1.8.1　添付文書（案）

次頁以降に添付文書（案）を示す。

AMGEN®

2021年●月作成（第●版）

抗悪性腫瘍剤/KRAS G12C阻害剤
ソトラシブ錠

日本標準商品分類番号
874291

ルマケラス®錠120mg

LUMAKRAS® Tablets 120mg

貯　　法：室温保存
有効期間：24箇月

承認番号	
販売開始	

処方箋医薬品注)
注）注意－医師等の処方箋により使用すること

1. 警告

本剤は、緊急時に十分対応できる医療施設において、がん化学療法に十分な知識・経験を持つ医師のもとで、本剤の使用が適切と判断される症例についてのみ投与すること。また、治療開始に先立ち、患者又はその家族に有効性及び危険性を十分説明し、同意を得てから投与すること。

2. 禁忌（次の患者には投与しないこと）

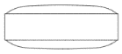
本剤の成分に対し過敏症の既往歴のある患者

3. 組成・性状

3.1 組成

販 売 名	ルマケラス錠120mg
有効成分	1錠中ソトラシブ120mg
添 加 剤	結晶セルロース、乳糖水和物、クロスカルメロースナトリウム、ステアリン酸マグネシウム、ポリビニルアルコール（部分けん化物）、酸化チタン、マクロゴール4000、タルク、黄色三二酸化鉄

3.2 製剤の性状

性 状		黄色のフィルムコーティング錠
外形	表面	
	裏面	
	側面	
大きさ	長径	16.00mm
	短径	7.11mm
	厚さ	5.58mm
識別コード		AMG

4. 効能又は効果

がん化学療法後に増悪したKRAS G12C変異陽性の切除不能な進行・再発の非小細胞肺癌

5. 効能又は効果に関連する注意

5.1 十分な経験を有する病理医又は検査施設における検査により、KRAS G12C変異陽性が確認された患者に投与すること。検査にあたっては、承認された体外診断用医薬品又は医療機器を用いること。なお、承認された体外診断用医薬品又は医療機器に関する情報については、以下のウェブサイトから入手可能である：
https://www.pmda.go.jp/review-services/drug-reviews/review-information/cd/0001.html

5.2 「17.臨床成績」の項の内容を熟知し、本剤の有効性及び安全性を十分に理解した上で、本剤以外の治療の実施についても慎重に検討し、適応患者の選択を行うこと。［17.1.1参照］

5.3 本剤の一次治療における有効性及び安全性は確立していない。

5.4 本剤の術後補助療法における有効性及び安全性は確立していない。

6. 用法及び用量

通常、成人にはソトラシブとして960mgを1日1回経口投与する。なお、患者の状態により適宜減量する。

7. 用法及び用量に関連する注意

7.1 他の抗悪性腫瘍剤との併用について、有効性及び安全性は確立していない。

7.2 本剤投与により副作用が発現した場合には、以下の基準を考慮して、休薬・減量・中止すること。240mg/日の投与量に対して忍容性が認められない場合は投与を中止すること。

本剤の減量レベル

減量レベル	投与量
通常投与量	960mg/日
1段階減量	480mg/日
2段階減量	240mg/日

副作用発現時の休薬、減量及び中止基準

副作用	程度	処置
肝機能障害［8.1、11.1.1参照］	症候性のGrade 2のAST増加若しくはALT増加又はGrade 3以上のAST増加若しくはALT増加	Grade 1以下又はベースラインに回復するまで休薬し、回復後は1段階減量して投与再開できる。
	正常値上限の3倍を超えるAST増加又はALT増加、かつ正常値上限の2倍を超える総ビリルビン増加	本剤の投与を中止する。
間質性肺疾患［8.2、11.1.2参照］	全Grade	本剤の投与を中止する。
上記以外の副作用	Grade 3又は4（ただし、悪心、嘔吐、下痢は適切な処置を行っても症状が継続する場合）	Grade 1以下又はベースラインに回復するまで休薬し、回復後は1段階減量して投与再開できる。

注）GradeはNCI-CTCAE version 5.0に準じる。

8. 重要な基本的注意

8.1 肝機能障害があらわれることがあるので、本剤の投与開始前及び投与中は定期的に肝機能検査を行い、患者の状態を十分に観察すること。［7.2、11.1.1参照］

8.2 間質性肺疾患があらわれることがあるので、本剤の投与にあたっては、初期症状（発熱、咳嗽、呼吸困難等）の確認及び胸部X線検査の実施等、観察を十分に行うこと。［7.2、11.1.2参照］

9. 特定の背景を有する患者に関する注意

9.3 肝機能障害患者

9.3.1 中等度以上の肝機能障害患者（ASTまたはALTが基準値上限の2.5倍以上、又は総ビリルビンが基準値上限の1.5倍以上）

本剤は主に肝臓で代謝されるため、血中濃度が上昇する可能性がある。なお、中等度以上の肝機能障害患者を対象とした臨床試験は実施していない。

9.5 妊婦

妊婦又は妊娠している可能性のある女性には、治療上の有益性が危険性を上回ると判断される場合にのみ投与すること。ウサギを用いた胚・胎児発生に関する試験において、臨床曝露量（AUC）の約2.2倍の曝露に相当する用量で、胎児の体重減少及び中手骨骨化数の減少が認められている。

9.6 授乳婦

治療上の有益性及び母乳栄養の有益性を考慮し、授乳の継続又は中止を検討すること。本剤の母乳中への移行は不明である。

9.7 小児等

小児等を対象とした臨床試験は実施していない。

10. 相互作用

本剤はCYP3Aの基質となり、CYP3Aの誘導作用及びP-gpの阻害作用を示す。また、本剤の溶解度はpHの上昇により低下する。

10.2 併用注意（併用に注意すること）

薬剤名等	臨床症状・措置方法	機序・危険因子
CYP3A誘導剤 リファンピシン、フェニトイン、カルバマゼピン等 [16.7.1参照]	本剤の有効性が減弱するおそれがあるため、併用を避けることが望ましい。	これらの薬剤がCYP3Aを誘導することにより、本剤の血中濃度が低下する可能性がある。
CYP3Aの基質となる薬剤 ミダゾラム、トリアゾラム、ロミタピド等 [16.7.2参照]	これらの薬剤の有効性が減弱するおそれがある。	本剤がCYP3Aを誘導することにより、これらの薬剤の血中濃度が低下する可能性がある。
治療域の狭いP-gpの基質となる薬剤 ジゴキシン、エベロリムス、シロリムス等 [16.7.3参照]	これらの薬剤の副作用が増強されるおそれがあるため、患者の状態を慎重に観察し、副作用の発現に十分注意すること。	本剤がP-gpを阻害することにより、これらの薬剤の血中濃度が上昇する可能性がある。
胃内pHを上昇させる薬剤 プロトンポンプ阻害剤 オメプラゾール、ラベプラゾール、ランソプラゾール等 H_2受容体拮抗剤 ファモチジン、ラニチジン、シメチジン等 [16.7.4、16.7.5参照]	本剤の有効性が減弱するおそれがあるため、これらの薬剤との併用を避けることが望ましい。	これらの薬剤による胃内pHの上昇により本剤の溶解性が低下し、本剤の血中濃度が低下する可能性がある。

11. 副作用

次の副作用があらわれることがあるので、観察を十分に行い、異常が認められた場合には投与を中止するなど適切な処置を行うこと。

11.1 重大な副作用

11.1.1 肝機能障害

ALT増加（16.3%）、AST増加（16.3%）等の肝機能障害があらわれることがある。［7.2、8.1参照］

11.1.2 間質性肺疾患

肺臓炎（1.1%）等があらわれることがある。［7.2、8.2参照］

11.2 その他の副作用

	5%以上	1%～5%未満	1%未満
感染症および寄生虫症			蜂巣炎、憩室炎、口腔カンジダ症、口腔真菌感染、膿疱性皮疹、上気道感染
良性、悪性および詳細不明の新生物（嚢胞およびポリープを含む）			血管筋脂肪腫
血液およびリンパ系障害		貧血、リンパ球減少、白血球減少、好中球減少、血小板減少	赤血球減少
免疫系障害			薬物過敏症
代謝および栄養障害		食欲減退、低カリウム血症、脱水、脂質異常症、高トリグリセリド血症、低マグネシウム血症、低リン酸血症	低血糖、低ナトリウム血症
精神障害			錯乱状態、不眠症
神経系障害		頭痛、味覚不全	浮動性めまい、知覚過敏、過眠症、神経系障害、末梢性ニューロパチー
眼障害			霧視、視力障害、眼球乾燥症
心臓障害			洞性徐脈
血管障害			高血圧、低血圧、末梢冷感
呼吸器、胸郭および縦隔障害		呼吸困難	咳嗽、鼻閉、湿性咳嗽
胃腸障害	下痢（27.9%）、悪心（16.3%）、嘔吐、腹痛	口内乾燥、腹部膨満、便秘、消化不良、胃食道逆流性疾患、口内炎	呼気臭、鼓腸、口腔粘膜水疱形成
肝胆道系障害			肝炎
皮膚および皮下組織障害		斑状丘疹状皮疹、皮膚乾燥、そう痒症、脱毛症、発疹	皮膚炎、ざ瘡様皮膚炎、多汗症、寝汗、光線過敏性反応、紫斑、乾皮症
筋骨格系および結合組織障害		筋肉痛、関節痛	関節炎、筋力低下、変形性関節症
腎および尿路障害			白血球尿、頻尿、蛋白尿
生殖系および乳房障害			女性化乳房
一般・全身障害および投与部位の状態	疲労（11.1%）	末梢性浮腫、無力症、倦怠感、発熱	びくびく感、限局性浮腫、粘膜の炎症、非心臓性胸痛、浮腫
臨床検査		体重減少、血中コレステロール増加、血中クレアチニン増加	AST減少、血中コルチコトロピン減少、血中クレアチンホスホキナーゼ増加、コルチゾール減少、心電図QT延長、胃内pH低下、リパーゼ増加

14. 適用上の注意

14.1 薬剤交付時の注意

PTP包装の薬剤はPTPシートから取り出して服用するよう指導すること。PTPシートの誤飲により、硬い鋭角部が食道粘膜へ刺入し、更には穿孔をおこして縦隔洞炎等の重篤な合併症を併発することがある。

14.2 薬剤投与時の注意

粉砕や分割して使用しないこと。

16. 薬物動態

16.1 血中濃度

16.1.1 単回及び反復投与

進行固形癌患者に、本剤180、360、720又は960mgを空腹時に1日1回反復経口投与[注)]したときのソトラシブの薬物動態パラメータ及び血漿中濃度推移を以下に示す。検討された用量範囲において、ソトラシブのC_{max}及びAUCは概ね類似した。反復投与した際、ソトラシブの蓄積は認められなかった（外国人データ）。[1)]

注）：本剤の承認用法・用量は960mgを1日1回経口投与である。

表1　進行固形癌患者に本剤180、360、720又は960mgを1日1回経口投与[注1)]したときの1日目及び8日目の薬物動態パラメータ［幾何平均値（CV%）］

用量 (mg)	投与 (n)	C_{max} (ng/mL)	T_{max}[注2)] (hr)	AUC_{0-24h} (ng·hr/mL)	$T_{1/2}$[注3)] (hr)
180	1日目 (6)	6,880 (51%)	1.0 (0.50 - 2.0)	43,600 (57%)	5.71[注4)] (0.815)
	8日目 (6)	6,440 (67%)	0.73 (0.50 - 1.2)	31,700 (89%)	5.13[注4)] (1.99)
360	1日目 (26)	6,190 (64%)	1.1 (0.57 - 6.2)	58,400[注5)] (63%)	6.45[注6)] (1.80)
	8日目 (24)	6,310 (43%)	1.0 (0.50 - 4.0)	38,900[注5)] (49%)	5.53[注7)] (1.84)
720	1日目 (11)	7,570 (59%)	1.2 (0.50 - 4.1)	84,000[注8)] (57%)	6.45[注9)] (1.95)
	8日目 (11)	5,450 (50%)	1.1 (0.53 - 4.0)	42,100 (49%)	4.75[注10)] (1.16)
960	1日目 (24)	8,400 (59%)	1.5 (0.25 - 4.8)	67,700[注5)] (77%)	5.49[注6)] (2.14)
	8日目 (24)	5,390 (65%)	1.1 (0.22 - 6.5)	32,400[注11)] (75%)	5.07[注12)] (1.08)

注1)：本剤の承認用法・用量は960mgを1日1回経口投与である、注2)：中央値（範囲）、注3)：平均値（標準偏差）、注4)：n = 5、注5)：n = 22、注6)：n = 17、注7)：n = 21、注8)：n = 9、注9)：n = 8、注10)：n = 7、注11)：n = 18、注12)：n = 15

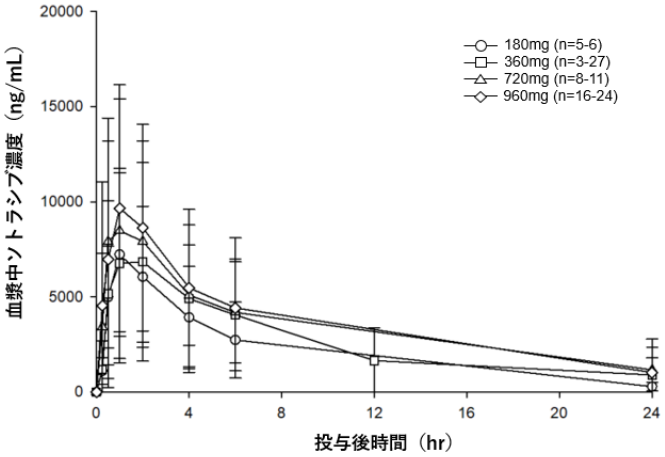


図1　進行固形癌患者に本剤180、360、720又は960mgを1日1回経口投与[注)]したときの1日目の血漿中濃度推移（平均値±標準偏差）

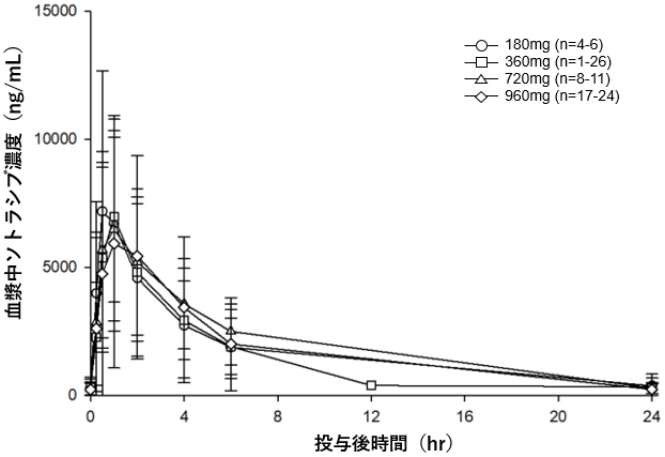


図2　進行固形癌患者に本剤180、360、720又は960mgを1日1回経口投与[注)]したときの8日目の血漿中濃度推移（平均値±標準偏差）

注)：本剤の承認用法・用量は960mgを1日1回経口投与である。

日本人固形癌患者に、本剤960mgを空腹時に1日1回反復経口投与したときのソトラシブの薬物動態パラメータを以下に示す。[2)]

表2　日本人患者に本剤960mgを1日1回経口投与したときの1日目及び8日目の薬物動態パラメータ［幾何平均値（CV%）］

投与 (n)	C_{max} (ng/mL)	T_{max}[注1)] (hr)	AUC_{0-24h}[注2)] (ng·hr/mL)	$T_{1/2}$[注2),3)] (hr)
1日目 (7)	5,190 (50%)	2.0 (0.53 - 6.1)	47,800 (38%)	4.59 (1.50)
8日目 (8)	4,150 (40%)	1.9 (0.90 - 5.9)	25,400 (23%)	3.95 (0.832)

注1)：中央値（範囲）、注2)：n = 5、注3)：平均値（標準偏差）

16.2 吸収

16.2.1 食事の影響

健康被験者（14例）に本剤360mgを単回経口投与[注)]したとき、空腹時投与に対する高脂肪食後投与におけるソトラシブのC_{max}及びAUC_{last}の最小二乗幾何平均値の比は、それぞれ1.03及び1.38であった（外国人データ）。[3)]

注)：本剤の承認用法・用量は960mgを1日1回経口投与である。

16.3 分布

非小細胞肺癌患者（21例）に本剤960mgを1日1回反復経口投与したときのソトラシブの定常状態における見かけの分布容積の幾何平均値は、211Lであった（外国人データ）。[1)]

ソトラシブのヒト血漿タンパク結合率は約89%であった（*in vitro*）。[4)]ソトラシブのヒト血液/血漿中濃度比は約0.7であった（*in vitro*）。[5)]

16.4 代謝

ソトラシブの代謝に関与する主な代謝酵素はCYP3Aである（*in vitro*）。[6)]

健康被験者（8例）に^{14}C-標識ソトラシブ720mgを単回経口投与[注)]したとき、投与192時間後までの血漿中には、主に未変化体、M10（システイン付加体）及びM24（ピペラジンアクリルアミドが脱離した酸化体）が認められ、血漿中総放射能のそれぞれ17.1%、26.8%及び7.81%を占めた（外国人データ）。[7)]

注)：本剤の承認用法・用量は960mgを1日1回経口投与である。

16.5 排泄

健康被験者（8例）に^{14}C-標識ソトラシブ720mgを単回経口投与[注)]したとき、投与312時間後までに、投与された全放射能の74.4%が糞中に、5.81%が尿中に排泄された。また、投与192時間後までに、投与された全放射能の53.0%が糞中に、1.39%が尿中に、それぞれ未変化体として排泄された（外国人データ）。[7)]

注)：本剤の承認用法・用量は960mgを1日1回経口投与である。

16.7 薬物相互作用

16.7.1 リファンピシン

健康被験者（14例）にリファンピシン（強いCYP3A誘導剤）600mgを1日1回15日間反復経口投与し、本剤960mgを単回経口投与したとき、本剤単独投与時に対するリファンピシン併用投与時のソトラシブのC_{max}及びAUC_{inf}の最小二乗幾何平均値の比は、それぞれ0.647及び0.487であった（外国人データ）。[8)]［10.2参照］

16.7.2 ミダゾラム

非小細胞肺癌患者（7例）に本剤960mgを1日1回15日間反復経口投与し、ミダゾラム（CYP3A基質）2mgを単回経口投与したとき、ミダゾラム単独投与時に対する本剤併用投与時のミダゾラムのC_{max}及びAUC_{6h}の最小二乗幾何平均値の比は、それぞれ0.52及び0.47であった（外国人データ）。[9)]［10.2参照］

16.7.3 ジゴキシン

健康被験者（14例）に本剤960mg及びジゴキシン（P-gp基質）0.5mgを単回経口投与したとき、ジゴキシン単独投与時に対する本剤併用投与時のジゴキシンのC_{max}及びAUC_{inf}の最小二乗幾何平均値の比は、それぞれ1.91及び1.21であった（外国人データ）。[10)]［10.2参照］

16.7.4 オメプラゾール

(1)　健康被験者（14例）にオメプラゾール（プロトンポンプ阻害

剤）40mgを1日1回6日間反復経口投与し、本剤960mgを空腹時に単回経口投与したとき、本剤単独投与時に対するオメプラゾール併用投与時のソトラシブのC_{max}及びAUC_{last}の最小二乗幾何平均値の比は、それぞれ0.431及び0.576であった（外国人データ）。[11] [10.2参照]

(2) 健康被験者（13例）にオメプラゾール（プロトンポンプ阻害剤）40mgを1日1回6日間反復経口投与し、本剤960mgを中脂肪食後に単回経口投与したとき、本剤単独投与時に対するオメプラゾール併用投与時のソトラシブのC_{max}及びAUC_{last}の最小二乗幾何平均値の比は、それぞれ0.349及び0.414であった（外国人データ）。[12] [10.2参照]

16.7.5 ファモチジン

健康被験者（14例）に本剤960mgを中脂肪食後に単回投与、並びにファモチジン（H_2受容体拮抗剤）40mgを本剤投与10時間前及び2時間後に経口投与したとき、本剤単独投与時に対するファモチジン併用投与時のソトラシブのC_{max}及びAUC_{last}の最小二乗幾何平均値の比は、それぞれ0.654及び0.619であった（外国人データ）。[12] [10.2参照]

16.7.6 その他

(1) 健康被験者（14例）にイトラコナゾール（強いCYP3A阻害剤）200mgを1日2回経口投与後に4日間1日1回反復経口投与し、本剤360mgを単回経口投与[注)]したとき、本剤単独投与時に対するイトラコナゾール併用投与時のソトラシブのC_{max}及びAUC_{inf}の最小二乗幾何平均値の比は、それぞれ1.04及び1.26であった（外国人データ）。[13]

注）：本剤の承認用法・用量は960mgを1日1回経口投与である。

(2) 健康被験者（13例）に本剤960mg及びメトホルミン（MATE1及びMATE2-K基質）850mgを単回経口投与したとき、メトホルミン単独投与時に対する本剤併用投与時のメトホルミンのC_{max}及びAUC_{inf}の最小二乗幾何平均値の比は、それぞれ0.996及び0.985であった（外国人データ）。[14]

(3) ソトラシブはBCRPを阻害した（*in vitro*）。[15]

17. 臨床成績

17.1 有効性及び安全性に関する試験

17.1.1 国際共同第Ⅰ/Ⅱ相試験（20170543試験、CodeBreaK 100試験）

がん化学療法後に増悪したKRAS G12C変異陽性の切除不能な進行・再発の固形癌患者を対象とした国際共同第Ⅰ/Ⅱ相試験の第Ⅱ相パートにおいて、非小細胞肺癌患者126例（日本人11例を含む）に本剤960mgを1日1回経口投与した。

主要評価項目であるRECIST ver.1.1に基づく独立中央画像判定機関による奏効率（データカットオフ日：2020年9月1日）は、有効性評価対象[注1)] 123例（日本人10例を含む）で37.4%（95%信頼区間：28.8, 46.6）であった。[16]

安全性評価対象[注2)] 190例（日本人13例を含む）中128例（67.4%）に副作用が認められ、主な副作用（発現率5%以上）は、下痢（27.9%）、悪心、ALT増加、AST増加（各16.3%）、疲労（11.1%）、血中アルカリホスファターゼ増加（7.9%）、嘔吐（7.4%）及び腹痛（5.3%）であった。［5.2参照］

注1) 中央判定によりベースライン時に測定可能病変を有さないと判定された3例（日本人1例を含む）が除外された。

注2) 第Ⅰ相及び第Ⅱ相パートにおいて本剤960mgを1回以上投与された非小細胞肺癌患者

18. 薬効薬理

18.1 作用機序

ソトラシブは、KRAS G12C変異を有するKRASに対する阻害作用を有する低分子化合物である。ソトラシブは、G12C変異を有するKRASに結合することで、KRASの活性化を阻害し、下流のシグナル伝達を阻害することにより、腫瘍増殖抑制作用を示すと考えられている。

18.2 抗腫瘍効果

ソトラシブは、KRAS G12C変異を有するヒト非小細胞肺癌由来NCI-H358細胞株を皮下移植したヌードマウスにおいて、腫瘍増殖抑制作用を示した。[17]

19. 有効成分に関する理化学的知見

一般的名称 ： ソトラシブ（Sotorasib）

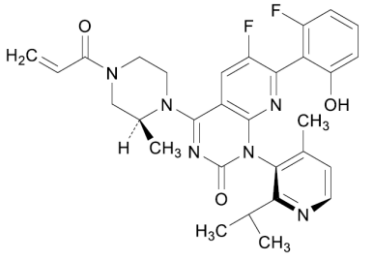
化学名 ： (1*M*)-6-Fluoro-7-(2-fluoro-6-hydroxyphenyl)-1-[4-methyl-2-(propan-2-yl)pyridin-3-yl]-4-[(2*S*)-2-methyl-4-(prop-2-enoyl)piperazin-1-yl]pyrido[2,3-*d*]pyrimidin-2(1*H*)-one

分子式 ： $C_{30}H_{30}F_2N_6O_3$

分子量 ： 560.59

性　状 ： 白色～薄い褐色の粉末である。水にほとんど溶けず、エタノールにやや溶けにくい。

化学構造式 ：



分配係数 ： Log D = 2.44(n-オクタノール/pH7.4 リン酸塩緩衝液)

22. 包装

56錠［8錠(PTP)×7］

23. 主要文献

1) 社内資料：20170543試験　患者における薬物動態（X年X月X日承認、CTD 2.7.2.2.1.1）
2) 社内資料：20170543試験　日本人患者における薬物動態（X年X月X日承認、CTD 2.7.2.5.1）
3) 社内資料：20190316試験　食事の影響を検討した試験（X年X月X日承認、CTD 2.7.6.1）
4) 社内資料：150530試験　ソトラシブのヒト血漿タンパク結合率（X年X月X日承認、CTD 2.6.4.4）
5) 社内資料：150532試験　ソトラシブのヒト血液／血漿中濃度比（X年X月X日承認、CTD 2.6.4.1）
6) 社内資料：150537試験　ソトラシブのヒトにおける代謝（X年X月X日承認、CTD 2.6.4.5.2）
7) 社内資料：20190321試験　マスバランス試験（X年X月X日承認、CTD 2.7.2.2.1.2）
8) 社内資料：20190319試験　薬物相互作用試験（X年X月X日承認、CTD 2.7.6.7）
9) 社内資料：20170543試験　薬物相互作用サブスタディ（X年X月X日承認、CTD 2.7.6.10）
10) 社内資料：20190315試験　薬物相互作用試験（X年X月X日承認、CTD 2.7.6.4）
11) 社内資料：20190320試験　薬物相互作用試験（X年X月X日承認、CTD 2.7.6.8）
12) 社内資料：20200199試験　薬物相互作用試験（X年X月X日承認、CTD 2.7.6.9）
13) 社内資料：20190318試験　薬物相互作用試験（X年X月X日承認、CTD 2.7.6.6）
14) 社内資料：20190317試験　薬物相互作用試験（X年X月X日承認、CTD 2.7.6.5）
15) 社内資料：150539試験　薬物トランスポーターに対するソトラシブの阻害作用試験（X年X月X日承認、CTD 2.6.4.7）
16) 社内資料：20170543試験　国際共同第Ⅰ/Ⅱ相試験（X年X月X日承認、CTD 2.7.6.11）
17) Canon J, et al.:Nature. 2019;575:217-223.

24. 文献請求先及び問い合わせ先

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0120-790-549

26. 製造販売業者等

26.1 製造販売

アムジェン株式会社
東京都港区赤坂九丁目7番1号

目次

略語一覧

略語又は用語	定義／説明
DLT	dose-limiting toxicity　用量制限毒性
ERK	extracellular signal-regulated kinase　細胞外シグナル調節キナーゼ
GDP	guanosine diphosphate　グアノシン二リン酸
KRAS	Kirsten rat sarcoma viral oncogene homolog
KRAS G12C	KRAS protein with a G12C amino acid substitution　12番目のアミノ酸グリシン（G）がシステイン（C）に置換されたKRASタンパク
MTD	maximum tolerated dose　最大耐量
NSCLC	non-small cell lung cancer　非小細胞肺癌
PK	pharmacokinetics　薬物動態
PR	partial response　部分奏効
QD	once daily　1日1回
RAF	RAF proto-oncogene serine/threonine-protein kinase　RAFプロトオンコジーンセリン／トレオニンプロテインキナーゼ
RP2D	recommended phase 2 dose　第II相部分における推奨用量

1. 効能又は効果、効能又は効果に関連する注意

効能又は効果（案）
がん化学療法後に増悪したKRAS G12C変異陽性の切除不能な進行・再発の非小細胞肺癌

＜効能又は効果に関連する注意（案）＞
5.1 十分な経験を有する病理医又は検査施設における検査により、KRAS G12C変異陽性が確認された患者に投与すること。検査にあたっては、承認された体外診断用医薬品又は医療機器を用いること。なお、承認された体外診断用医薬品又は医療機器に関する情報については、以下のウェブサイトから入手可能である：
https://www.pmda.go.jp/review-services/drug-reviews/review-information/cd/0001.html
5.2 「17.臨床成績」の項の内容を熟知し、本剤の有効性及び安全性を十分に理解した上で、本剤以外の治療の実施についても慎重に検討し、適応患者の選択を行うこと。
5.3 本剤の一次治療における有効性及び安全性は確立していない。
5.4 本剤の術後補助療法における有効性及び安全性は確立していない。

2. 効能又は効果の設定根拠

sotorasibは、KRAS G12C変異タンパクに特異的に結合し、不可逆的に阻害する低分子化合物である。sotorasibは、システインに変異した12番目のアミノ酸に隣接するKRAS G12CのP2ポケットと呼ばれる溝構造及びアミノ酸位置95のヒスチジンにおける溝構造に結合する。sotorasibは、チオール反応性部分を有し、システイン残基を共有結合により修飾することでKRAS G12Cをグアノシン二リン酸（GDP）が結合した不活性型の高次構造のまま保持する。これにより、Kirsten rat sarcoma viral oncogene homolog（KRAS）とRAFプロトオンコジーンセリン／トレオニンプロテインキナーゼ（RAF）等のエフェクターとの相互作用が阻害され、細胞外シグナル調節キナーゼ（ERK）のリン酸化を含め、下流のシグナル伝達が阻害される。sotorasibを用いた薬理試験でも、in vivoでこれらの作用が確認されており、KRAS G12C変異を有する腫瘍に対する選択的な細胞増殖阻害及び腫瘍退縮が認められている。sotorasibが結合する他の野生型又は変異型のタンパクや受容体は特定されておらず、KRAS G12C変異のない細胞ではsotorasibの影響は認められていない。In vitroでの選択性アッセイ及びシステインプロテオームプロファイリングの結果から、sotorasibはKRAS G12Cに対して高い選択性を有することが示唆された（モジュール2.4）。

KRAS G12C変異を有する固形癌患者を対象とした第I/II相試験である20170543試験の第II相部分の結果、既治療のKRAS G12C変異陽性非小細胞肺癌（NSCLC）患者に対するsotorasib単独療法による臨床的意義のある有効性及び良好な安全性プロファイルが認められ、sotorasibはKRAS G12C変異陽性NSCLC患者に対して良好なリスク・ベネフィットのプロファイルを有し、有用な治療選択肢となりうると考えられた（モジュール2.5）。

以上より、効能又は効果を「がん化学療法後に増悪したKRAS G12C変異陽性の切除不能な進行・再発の非小細胞肺癌」と設定した。

3. 効能又は効果に関連する注意の設定根拠

5.1 十分な経験を有する病理医又は検査施設における検査により、KRAS G12C変異陽性が確認された患者に投与すること。検査にあたっては、承認された体外診断用医薬品又は医療機器を用いること。なお、承認された体外診断用医薬品又は医療機器に関する情報については、以下のウェブサイトから入手可能である：
https://www.pmda.go.jp/review-services/drug-reviews/review-information/cd/0001.html

本剤の作用機序及び20170543試験の結果に基づき、本剤により期待される効果を得るためには、十分な経験を有する病理医又は検査施設における検査により、KRAS G12C変異陽性を確認する必要があると考え、設定した。なお、既承認の薬剤での記載に準じた。

5.2 「17.臨床成績」の項の内容を熟知し、本剤の有効性及び安全性を十分に理解した上で、本剤以外の治療の実施についても慎重に検討し、適応患者の選択を行うこと。

本剤の効能又は効果は、20170543試験の結果に基づき設定したことから、本剤の適応患者の選択に際し、臨床成績の項の内容を熟知し、本剤の有効性及び安全性を十分理解する必要があると考え、注意喚起することとした。また、本剤の延命効果に関する検証的な臨床試験成績は得られていないこと等を考慮し、本剤以外の治療の実施についても慎重に検討した上で、本剤投与の可否を判断する必要がある旨を注意喚起することが適切であると判断した。

5.3 本剤の一次治療における有効性及び安全性は確立していない。

本剤の一次治療における有効性及び安全性は、現時点では確立していないことから設定した。

5.4 本剤の術後補助療法における有効性及び安全性は確立していない。

本剤の術後補助療法における有効性及び安全性は、現時点では確立していないことから設定した。

4. 用法及び用量、用法及び用量に関連する注意

用法及び用量（案）
通常、成人にはソトラシブとして960mgを1日1回経口投与する。なお、患者の状態により適宜減量する。

＜用法及び用量に関連する注意（案）＞
7.1 他の抗悪性腫瘍剤との併用について、有効性及び安全性は確立していない。

7.2 本剤投与により副作用が発現した場合には、以下の基準を考慮して、休薬・減量・中止すること。240mg/日の投与量に対して忍容性が認められない場合は投与を中止すること。

本剤の減量レベル

減量レベル	投与量
通常投与量	960mg/日
1段階減量	480mg/日
2段階減量	240mg/日

副作用発現時の休薬、減量及び中止基準

副作用	程度	処置
肝機能障害	症候性のGrade 2のAST増加若しくはALT増加 又は Grade 3以上のAST増加若しくはALT増加	Grade 1以下又はベースラインに回復するまで休薬し、回復後は1段階減量して投与再開できる。
	正常値上限の3倍を超えるAST増加又はALT増加、かつ正常値上限の2倍を超える総ビリルビン増加	本剤の投与を中止する。
間質性肺疾患	全Grade	本剤の投与を中止する。
上記以外の副作用	Grade 3又は4（ただし、悪心、嘔吐、下痢は適切な処置を行っても症状が継続する場合）	Grade 1以下又はベースラインに回復するまで休薬し、回復後は1段階減量して投与再開できる。

注）GradeはNCI-CTCAE version 5.0に準じる。

5. 用法及び用量の設定根拠

用量漸増試験である20170543試験の第I相部分のパート1aの成績に基づいて、第II相部分における推奨用量（RP2D）を選択した。本パートではsotorasib 180、360、720及び960 mgの1日1回（QD）単独投与を検討した。その結果、いずれの用量にも用量制限毒性（DLT）は認められず、検討した最高用量である960 mgにおいても最大耐量（MTD）には到達しなかった。また、本パートでの予備的な有効性データの評価において、評価可能な進行NSCLC被験者17例中7例に部分奏効（PR）が認められ、960 mgの用量では評価可能な進行NSCLC被験者7例中4例にPRが認められた。これらの結果から、960 mg QD単独投与をRP2Dと決定した。

本試験の第II相部分では、KRAS G12C変異を有する進行NSCLC被験者において、RP2Dである960 mg QD単独投与により臨床的に意味のある客観的奏効率が認められた。また、忍容かつ良好な安全性が確認された。KRAS G12C変異を有する進行NSCLC被験者における960 mg QD単独投与では有害事象による中止割合は9.5%と低かった。さらに、用量変更が行われた割合は17.9%と低く、960 mgの用量選択の妥当性を支持している。

KRAS G12C変異を有する進行固形癌被験者にsotorasibを180 mgから960 mgまでQD経口投与したときの薬物動態（PK）データでは、sotorasibの曝露量は用量比を下回る増加を示した。反復投与による薬物の蓄積は認められなかった。また、960 mgを空腹時又は食後に投与したときのsotorasibの曝露量は、空腹時投与と食後投与で同様であった。母集団PK解析により、性別、人種、病勢、体重、年齢、軽度腎機能障害又は軽度肝機能障害の影響を検討した結果、sotorasibのPKに臨床的に意味のある差は認められず、これらの共変量に基づく用量調整は必要ないことが示唆された。

以上より、sotorasibの安全性及び有効性を含むエビデンスの包括的評価に基づき、KRAS G12C変異を有する進行NSCLC患者に対するsotorasibの推奨用法・用量は、960 mg QD単独投与とすることが妥当と判断された（モジュール2.7.3 4項）。

6. 用法及び用量に関連する注意の設定根拠

7.1 他の抗悪性腫瘍剤との併用について、有効性及び安全性は確立していない。

他の抗悪性腫瘍剤との併用療法における本剤の有効性及び安全性は、現時点では確立していないことから設定した。

7.2 本剤投与により副作用が発現した場合には、以下の基準を考慮して、休薬・減量・中止すること。240mg/日の投与量に対して忍容性が認められない場合は投与を中止すること。

20170543試験の結果、本剤の休薬・減量・中止を要した副作用のうち、多く認められたのは肝酵素増加や悪心、嘔吐、下痢であり（モジュール2.7.4 2.1.5項）、当該事象が認められた場合、本剤の休薬・減量・中止を検討する必要があると考え、20170543試験での設定に基づき、肝機能障害及びそれ以外の副作用が発現した場合について、休薬・減量・中止の基準を設定した。また、間質性肺疾患は死亡を含む重大な転帰に至る可能性のある事象であり、発現時には早期の対応を行うことが肝要であると考えられることから、いずれのGradeであっても発現が確認された場合は投与中止の処置が推奨されると考え、設定した。

1. 使用上の注意及びその設定根拠

使用上の注意（案）	設定根拠
1. 警告 本剤は、緊急時に十分対応できる医療施設において、がん化学療法に十分な知識・経験を持つ医師のもとで、本剤の使用が適切と判断される症例についてのみ投与すること。また、治療開始に先立ち、患者又はその家族に有効性及び危険性を十分説明し、同意を得てから投与すること。	副作用に適切に対応するため、本剤の投与はがん化学療法に関する十分な知識・経験を持つ医師のもとで、かつ副作用発現による緊急時に十分な措置ができる医療施設において、本剤の使用が適切と判断される症例についてのみ投与されることが安全対策上必要であることから設定した。また、本剤投与にあたり、患者又はその家族に有効性及び安全性を理解いただき、同意を得てから投与する必要があることから設定した。
2. 禁忌（次の患者には投与しないこと） 本剤の成分に対し過敏症の既往歴のある患者	過敏症に対する一般的な注意事項として設定した。また、本剤成分に過敏症の既往歴がある場合、本剤投与により過敏症が発現する可能性が高いことから設定した。
8. 重要な基本的注意 8.1肝機能障害があらわれることがあるので、本剤の投与開始前及び投与中は定期的に肝機能検査を行い、患者の状態を十分に観察すること。［7.2、11.1.1参照］	国際共同第I／II相試験（20170543試験）における安全性評価対象190例（本剤960 mgを1回以上投与された非小細胞肺癌患者）の結果及びCore Data Sheet（CDS）に基づき設定した。
8.2 間質性肺疾患があらわれることがあるので、本剤の投与にあたっては、初期症状（発熱、咳嗽、呼吸困難等）の確認及び胸部X線検査の実施等、観察を十分に行うこと。［7.2、11.1.2参照］	国際共同第I／II相試験（20170543試験）における安全性評価対象190例（本剤960 mgを1回以上投与された非小細胞肺癌患者）の結果に基づき設定した。
9. 特定の背景を有する患者に関する注意 9.3 肝機能障害患者 9.3.1 中等度以上の肝機能障害患者（AST若しくはALTが基準値上限の2.5倍以上、又は総ビリルビンが基準値上限の1.5倍以上） 本剤は主に肝臓で代謝されるため、血中濃度が上昇する可能性がある。なお、中等度以上の肝機能障害患者を対象とした臨床試験は実施していない。	本剤は主に肝臓で代謝されるため、血中濃度が上昇する可能性があること、中等度以上の肝機能障害患者を対象とした臨床試験は実施していないことから設定した。
9.5 妊婦 妊婦又は妊娠している可能性のある女性には、治療上の有益性が危険性を上回ると判断される場合にのみ投与すること。ウサギを用いた胚・胎児発生に関する試験において、臨床曝露量（AUC）の約2.2倍の曝露に相当する用量で、胎児の体重減少及び中手骨骨化数の減少が認められている。	妊婦又は妊娠している可能性のある女性における安全性は検討していないこと、非臨床試験の結果及びCDSに基づき設定した。
9.6 授乳婦 治療上の有益性及び母乳栄養の有益性を考慮し、授乳の継続又は中止を検討すること。本剤の母乳中への移行は不明である。	臨床試験及び非臨床試験等のデータがなく、ヒトで哺乳中の児における影響が不明であるため、設定した。
9.7 小児等 小児等を対象とした臨床試験は実施していない。	小児等を対象とした臨床試験は実施していないことから設定した。

<table>
<tr><th>使用上の注意（案）</th><th>設定根拠</th></tr>
<tr><td>10. 相互作用
本剤はCYP3Aの基質となり、CYP3Aの誘導作用及びP-gpの阻害作用を示す。また、本剤の溶解度はpHの上昇により低下する。
10.2 併用注意（併用に注意すること）
<table>
<tr><th>薬剤名等</th><th>臨床症状・措置方法</th><th>機序・危険因子</th></tr>
<tr><td>CYP3A誘導剤
リファンピシン、フェニトイン、カルバマゼピン等
[16.7.1参照]</td><td>本剤の有効性が減弱するおそれがあるため、併用を避けることが望ましい。</td><td>これらの薬剤がCYP3Aを誘導することにより、本剤の血中濃度が低下する可能性がある。</td></tr>
<tr><td>CYP3Aの基質となる薬剤
ミダゾラム、トリアゾラム、ロミタピド等
[16.7.2参照]</td><td>これらの薬剤の有効性が減弱するおそれがある。</td><td>本剤がCYP3Aを誘導することにより、これらの薬剤の血中濃度が低下する可能性がある。</td></tr>
<tr><td>治療域の狭いP-gpの基質となる薬剤
ジゴキシン、エベロリムス、シロリムス等
[16.7.3参照]</td><td>これらの薬剤の副作用が増強されるおそれがあるため、患者の状態を慎重に観察し、副作用の発現に十分注意すること。</td><td>本剤がP-gpを阻害することにより、これらの薬剤の血中濃度が上昇する可能性がある。</td></tr>
<tr><td>胃内pHを上昇させる薬剤
プロトンポンプ阻害剤
オメプラゾール、ラベプラゾール、ランソプラゾール等
H_2受容体拮抗剤
ファモチジン、ラニチジン、シメチジン等
[16.7.4、16.7.5参照]</td><td>本剤の有効性が減弱するおそれがあるため、これらの薬剤との併用を避けることが望ましい。</td><td>これらの薬剤による胃内pHの上昇により本剤の溶解性が低下し、本剤の血中濃度が低下する可能性がある。</td></tr>
</table></td><td>本剤は主に代謝酵素チトクロームP450 3A（CYP3A）で代謝され、またCYP3A誘導作用を有することが確認されている。また、本剤の併用によりP-gpの基質であるジゴキシンの血中濃度が上昇することが確認されている。さらに、オメプラゾールやファモチジン等による胃内pHの上昇により、本剤の血中濃度が低下することが確認されている。併用注意に関しては、臨床薬理試験等で相互作用が確認され、かつ有効性への影響が不明もしくは有効性を減弱させる可能性または副作用が増強される可能性のある薬剤について記載した。</td></tr>
<tr><td>11. 副作用
次の副作用があらわれることがあるので、観察を十分に行い、異常が認められた場合には投与を中止するなど適切な処置を行うこと。
11.1 重大な副作用
11.1.1 肝機能障害
ALT増加（16.3%）、AST増加（16.3%）等の肝機能障害があらわれることがある。［7.2、8.1参照］
11.1.2 間質性肺疾患
肺臓炎（1.1%）等があらわれることがある。［7.2、8.2参照］
11.2 その他の副作用
<table>
<tr><th></th><th>5%以上</th><th>1%～5%未満</th><th>1%未満</th></tr>
<tr><td>感染症および寄生虫症</td><td></td><td></td><td>蜂巣炎、憩室炎、口腔カンジダ症、口腔真菌感染、膿疱性皮疹、上気道感染</td></tr>
<tr><td>良性、悪性および詳細不明の新生物（嚢胞およびポリープを含む）</td><td></td><td></td><td>血管筋脂肪腫</td></tr>
<tr><td>血液およびリンパ系障害</td><td></td><td>貧血、リンパ球減少、白血球減少、</td><td>赤血球減少</td></tr>
</table></td><td>20170543試験の結果及び/又はCDSに基づき設定した。なお、本剤の臨床試験結果はMedDRAの基本語を用いて集計した。</td></tr>
</table>

<table>
<tr><th>使用上の注意（案）</th><th>設定根拠</th></tr>
<tr><td>
<table>
<tr><td></td><td></td><td>好中球減少、血小板減少</td><td></td></tr>
<tr><td>免疫系障害</td><td></td><td></td><td>薬物過敏症</td></tr>
<tr><td>代謝および栄養障害</td><td></td><td>食欲減退、低カリウム血症、脱水、脂質異常症、高トリグリセリド血症、低マグネシウム血症、低リン酸血症</td><td>低血糖、低ナトリウム血症</td></tr>
<tr><td>精神障害</td><td></td><td></td><td>錯乱状態、不眠症</td></tr>
<tr><td>神経系障害</td><td></td><td>頭痛、味覚不全</td><td>浮動性めまい、知覚過敏、過眠症、神経系障害、末梢性ニューロパチー</td></tr>
<tr><td>眼障害</td><td></td><td></td><td>霧視、視力障害、眼球乾燥症</td></tr>
</table>
</td><td></td></tr>
<tr><td>
<table>
<tr><th></th><th>5%以上</th><th>1%～5%未満</th><th>1%未満</th></tr>
<tr><td>心臓障害</td><td></td><td></td><td>洞性徐脈</td></tr>
<tr><td>血管障害</td><td></td><td></td><td>高血圧、低血圧、末梢冷感</td></tr>
<tr><td>呼吸器、胸郭および縦隔障害</td><td></td><td>呼吸困難</td><td>咳嗽、鼻閉、湿性咳嗽</td></tr>
<tr><td>胃腸障害</td><td>下痢（27.9%）、悪心（16.3%）、嘔吐、腹痛</td><td>口内乾燥、腹部膨満、便秘、消化不良、胃食道逆流性疾患、口内炎</td><td>呼気臭、鼓腸、口腔粘膜水疱形成</td></tr>
<tr><td>肝胆道系障害</td><td></td><td></td><td>肝炎</td></tr>
<tr><td>皮膚および皮下組織障害</td><td></td><td>斑状丘疹状皮疹、皮膚乾燥、そう痒症、脱毛症、発疹</td><td>皮膚炎、ざ瘡様皮膚炎、多汗症、寝汗、光線過敏性反応、紫斑、乾皮症</td></tr>
<tr><td>筋骨格系および結合組織障害</td><td></td><td>筋肉痛、関節痛</td><td>関節炎、筋力低下、変形性関節症</td></tr>
<tr><td>腎および尿路障害</td><td></td><td></td><td>白血球尿、頻尿、蛋白尿</td></tr>
<tr><td>生殖系および乳房障害</td><td></td><td></td><td>女性化乳房</td></tr>
<tr><td>一般・全身障害および投与部位の状態</td><td>疲労（11.1%）</td><td>末梢性浮腫、無力症、倦怠感、発熱</td><td>びくびく感、限局性浮腫、粘膜の炎症、非心臓性胸痛、浮腫</td></tr>
<tr><td>臨床検査</td><td></td><td>体重減少、血中コレステロール増加、血中クレアチニン増加、</td><td>AST減少、血中コルチコトロピン減少、血中クレアチンホスホキナーゼ増加、コルチゾール減少、心電図QT延長、胃内pH低下、リパーゼ増加</td></tr>
</table>
</td><td></td></tr>
<tr><td>14. 適用上の注意
14.1 薬剤交付時の注意
PTP包装の薬剤はPTPシートから取り出して服用するよう指導すること。PTPシートの誤飲により、硬い鋭角部が食道粘膜へ刺入し、更には穿孔をおこして縦隔洞炎等の重篤な合併症を併発することがある。</td><td>PTP包装の薬剤に対する一般的注意として設定した。</td></tr>
<tr><td>14.2 薬剤投与時の注意
粉砕や分割して使用しないこと。</td><td>本剤を粉砕や分割して使用したデータはないことから設定した。</td></tr>
</table>

1. JAN

医薬品一般的名称は、2021年4月13日付薬生薬審発0413第1号により、以下のとおり通知された。

JAN：

（日本名） ソトラシブ

（英　名） Sotorasib

化学名：

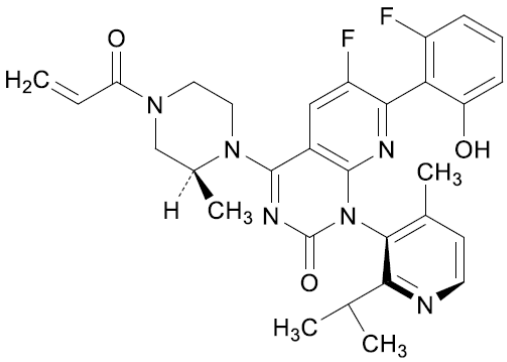
（日本名）

(1*M*)-6-フルオロ-7-(2-フルオロ-6-ヒドロキシフェニル)-1-[4-メチル-2-(プロパン-2-イル)ピリジン-3-イル]-4-[(2*S*)-2-メチル-4-(プロパ-2-エノイル)ピペラジン-1-イル]ピリド[2,3-*d*]ピリミジン-2(1*H*)-オン

（英　名）

(1*M*)-6-Fluoro-7-(2-fluoro-6-hydroxyphenyl)-1-[4-methyl-2-(propan-2-yl)pyridin-3-yl]-4-[(2*S*)-2-methyl-4-(prop-2-enoyl)piperazin-1-yl]pyrido[2,3-*d*]pyrimidin-2(1*H*)-one

化学構造式：



2. INN

r-INN：sotorasib

WHO Drug Information, Vol. 35, No.1, 2021, Recommended INN: List 85に掲載されている。

薬生薬審発 0413 第１号
令 和 ３ 年 ４ 月 13 日

各都道府県衛生主管部（局）長　殿

厚生労働省医薬・生活衛生局医薬品審査管理課長
（　　公　　印　　省　　略　　）

医薬品の一般的名称について

標記については、「医薬品の一般的名称の取扱いについて（平成 18 年３月 31 日薬食発第 0331001 号厚生労働省医薬食品局長通知）」等により取り扱っているところです。今般、我が国における医薬品の一般的名称（以下「JAN」という。）について、新たに別添のとおり定めたので、御了知の上、貴管下関係業者に周知方よろしく御配慮願います。

（参照）
「日本医薬品一般的名称データベース」https://jpdb.nihs.go.jp/jan/Default.aspx
（別添の情報のうち、JAN 以外の最新の情報は、当該データベースの情報で対応することとしています。）

別添

（別表２）INN に収載された品目の我が国における医薬品一般的名称
（平成 18 年 3 月 31 日薬食審査発第 0331001 号厚生労働省医薬食品局審査管理課長通知に示す別表２）

登録番号　302-4-B4
JAN（日本名）：スペソリマブ（遺伝子組換え）
JAN（英　名）：Spesolimab (Genetical Recombination)

アミノ酸配列及びジスルフィド結合

L鎖

QIVLTQSPGT LSLSPGERAT MTCTASSSVS SSYFHWYQQK PGQAPRLWIY

RTSRLASGVP DRFSGSGSGT DFTLTISRLE PEDAATYYCH QFHRSPLTFG

AGTKLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK

VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ

GLSSPVTKSF NRGEC

H鎖

QVQLVQSGAE VKKPGASVKV SCKASGYSFT SSWIHWVKQA PGQGLEWMGE

INPGNVRTNY NENFRNKVTM TVDTSISTAY MELSRLRSDD TAVYYCTVVF

YGEPYFPYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD

YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY

ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPEAAGGP SVFLFPPKPK

DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS

TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV

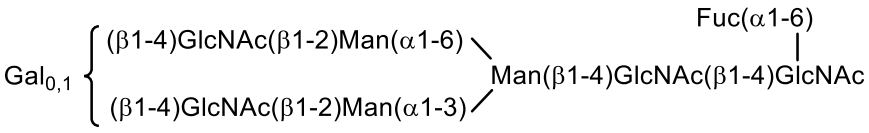
YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL

DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK

L 鎖 Q1，H 鎖 Q1：部分的ピログルタミン酸 ; H 鎖 N299：糖鎖結合 ; H 鎖 K449：部分的プロセシング

L 鎖 C215 – H 鎖 C222，H 鎖 C228 – H 鎖 C228，H 鎖 C231 – H 鎖 C231：ジスルフィド結合

主な糖鎖の推定構造



$C_{6480}H_{9988}N_{1736}O_{2012}S_{46}$（タンパク質部分，4 本鎖）

H 鎖 $C_{2201}H_{3392}N_{582}O_{674}S_{17}$

L 鎖 $C_{1039}H_{1606}N_{286}O_{332}S_{6}$

スペソリマブは遺伝子組換え抗ヒトインターロイキン-36 受容体モノクローナル抗体であり，その相補性決定部はマウス抗体に由来し，その他はヒト IgG1 に由来する．スペソリマブは，チャイニーズハムスター卵巣細胞により産生される．スペソリマブは，449 個のアミノ酸残基からなる H 鎖（γ1 鎖）2 本及び 215 個のアミノ酸残基からなる L 鎖（κ 鎖）2 本で構成される糖タンパク質（分子量：約 149,000）である．

Spesolimab is a recombinant anti-human interleukin-36 receptor monoclonal antibody, the complementarity-determining regions of which are derived from mouse antibody and other regions are derived from human IgG1. Spesolimab is produced in Chinese hamster ovary cells. Spesolimab is a glycoprotein (molecular weight: ca. 149,000) composed of 2 H-chains (γ1-chains) consisting of 449 amino acid residues each and 2 L-chains (κ-chains) consisting of 215 amino acid residues each.

登録番号　302-4-B6

JAN（日本名）：ガレトスマブ（遺伝子組換え）

JAN（英　名）：Garetosmab (Genetical Recombination)

アミノ酸配列及びジスルフィド結合

L鎖

EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY

GASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPWTFG

QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK

VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ

GLSSPVTKSF NRGEC

H鎖

QVQLQESGPG LVKPSETLSL TCTVSGGSFS SHFWSWIRQP PGKGLEWIGY

ILYTGGTSFN PSLKSRVSMS VGTSKNQFSL KLSSVTAADT AVYYCARARS

GITFTGIIVP GSFDIWGQGT MVTVSSASTK GPSVFPLAPC SRSTSESTAA

LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS

SLGTKTYTCN VDHKPSNTKV DKRVESKYGP PCPPCPAPEF LGGPSVFLFP

PKPKDTLMIS RTPEVTCVVV DVSQEDPEVQ FNWYVDGVEV HNAKTKPREE

QFNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKGLPSSIEK TISKAKGQPR

EPQVYTLPPS QEEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT

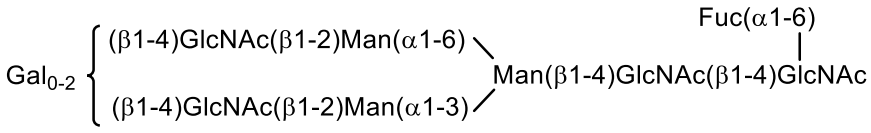
PPVLDSDGSF FLYSRLTVDK SRWQEGNVFS CSVMHEALHN HYTQKSLSLS

LGK

H 鎖 Q1：部分的ピログルタミン酸；H 鎖 N303：糖鎖結合；H 鎖 K453：部分的プロセシング

L 鎖 C215 – H 鎖 C140, H 鎖 C232 – H 鎖 C232, H 鎖 C235 – H 鎖 C235：ジスルフィド結合

主な糖鎖の推定構造



$C_{6472}H_{10004}N_{1712}O_{2024}S_{42}$（タンパク質部分，4 本鎖）

H 鎖　$C_{2205}H_{3409}N_{577}O_{677}S_{16}$

L 鎖　$C_{1031}H_{1597}N_{279}O_{335}S_{5}$

ガレトスマブはヒトアクチビン A，アクチビン AB 及びアクチビン AC に対する遺伝子組換えモノクローナル抗体であり，ヒト IgG4 に由来する．H 鎖の 234 番目のアミノ酸残基は Pro に置換されている．ガレトスマブはチャイニーズハムスター卵巣細胞により産生される．ガレトスマブは，453 個のアミノ酸残基からなる H 鎖（γ4 鎖）2 本及び 215 個のアミノ酸残基からなる L 鎖（κ 鎖）2 本で構成される糖タンパク質（分子量：約 148,000）である．

Garetosmab is a recombinant monoclonal antibody against human activin A, activin AB and activin AC derived from human IgG4. In the H-chain, amino acid residue at position 234 is substituted by Pro. Garetosmab is produced in Chinese hamster ovary cells. Garetosmab is a glycoprotein (molecular weight: ca. 148,000) composed of 2 H-chains (γ4-chains) consisting of 453 amino acid residues each and 2 L-chains (κ-chains) consisting of 215 amino acid residues each.

登録番号　302-4-B9

JAN（日本名）：ボソリチド（遺伝子組換え）

JAN（英　名）：Vosoritide (Genetical Recombination)

アミノ酸配列及びジスルフィド結合

PGQEHPNARK YKGANKKGLS KGCFGLKLDR IGSMSGLGC

$C_{176}H_{290}N_{56}O_{51}S_3$

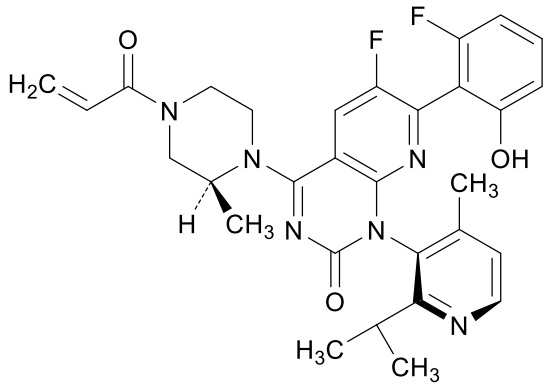
ボソリチドは，遺伝子組換えヒトC型ナトリウム利尿ペプチド（CNP）類縁体であり，ヒトCNP-53の17～53番目のアミノ酸残基に相当し，N末端に2個のアミノ酸残基（Pro-Gly）が付加している．ボソリチドは39個のアミノ酸残基からなるペプチドである．

Vosoritide is a recombinant human C-type natriuretic peptide (CNP) analog, which corresponds to amino acid residues at positions 17 – 53 of human CNP-53, and two amino acid residues (Pro-Gly) are attached to the N-terminus. Vosoritide is a peptide consisting of 39 amino acid residues.

登録番号　302-6-B1

JAN（日本名）：ソトラシブ

JAN（英　名）：Sotorasib



$C_{30}H_{30}F_2N_6O_3$

(1*M*)-6-フルオロ-7-(2-フルオロ-6-ヒドロキシフェニル)-1-[4-メチル-2-(プロパン-2-イル)ピリジン-3-イル]-4-[(2*S*)-2-メチル-4-(プロパ-2-エノイル)ピペラジン-1-イル]ピリド[2,3-*d*]ピリミジン-2(1*H*)-オン

(1*M*)-6-Fluoro-7-(2-fluoro-6-hydroxyphenyl)-1-[4-methyl-2-(propan-2-yl)pyridin-3-yl]-4-[(2*S*)-2-methyl-4-(prop-2-enoyl)piperazin-1-yl]pyrido[2,3-*d*]pyrimidin-2(1*H*)-one

※　JAN 以外の情報は、参考として掲載しました。

International Nonproprietary Names for Pharmaceutical Substances (INN)

RECOMMENDED International Nonproprietary Names: List 85

Notice is hereby given that, in accordance with paragraph 7 of the Procedure for the Selection of Recommended International Nonproprietary Names for Pharmaceutical Substances [*Off. Rec. Wld Health Org.*, 1955, **60**, 3 (Resolution EB15.R7); 1969, **173**, 10 (Resolution EB43.R9); Resolution EB115.R4 (EB115/2005/REC/1)], the following names are selected as Recommended International Nonproprietary Names. The inclusion of a name in the lists of Recommended International Nonproprietary Names does not imply any recommendation of the use of the substance in medicine or pharmacy.
Lists of Proposed (1–117) and Recommended (1–78) International Nonproprietary Names can be found in *Cumulative List No. 17, 2017* (available in CD-ROM only).

Dénominations communes internationales des Substances pharmaceutiques (DCI)

Dénominations communes internationales RECOMMANDÉES: Liste 85

Il est notifié que, conformément aux dispositions du paragraphe 7 de la Procédure à suivre en vue du choix de Dénominations communes internationales recommandées pour les Substances pharmaceutiques [*Actes off. Org. mond. Santé*, 1955, **60**, 3 (résolution EB15.R7); 1969, **173**, 10 (résolution EB43.R9); résolution EB115.R4 (EB115/2005/REC/1)] les dénominations ci-dessous sont choisies par l'Organisation mondiale de la Santé en tant que dénominations communes internationales recommandées. L'inclusion d'une dénomination dans les listes de DCI recommandées n'implique aucune recommandation en vue de l'utilisation de la substance correspondante en médecine ou en pharmacie.
On trouvera d'autres listes de Dénominations communes internationales proposées (1–117) et recommandées (1–78) dans la *Liste récapitulative No. 17, 2017* (disponible sur CD-ROM seulement).

Denominaciones Comunes Internacionales para las Sustancias Farmacéuticas (DCI)

Denominaciones Comunes Internacionales RECOMENDADAS: Lista 85

De conformidad con lo que dispone el párrafo 7 del Procedimiento de Selección de Denominaciones Comunes Internacionales Recomendadas para las Sustancias Farmacéuticas [*Act. Of. Mund. Salud*, 1955, **60**, 3 (Resolución EB15.R7); 1969, **173**, 10 (Resolución EB43.R9); Résolution EB115.R4 (EB115/2005/REC/1) EB115.R4 (EB115/2005/REC/1)], se comunica por el presente anuncio que las denominaciones que a continuación se expresan han sido seleccionadas como Denominaciones Comunes Internacionales Recomendadas. La inclusión de una denominación en las listas de las Denominaciones Comunes Recomendadas no supone recomendación alguna en favor del empleo de la sustancia respectiva en medicina o en farmacia.
Las listas de Denominaciones Comunes Internacionales Propuestas (1–117) y Recomendadas (1–78) se encuentran reunidas en *Cumulative List No. 17, 2017* (disponible sólo en CD-ROM).

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

Please find the names from proposed **INN List 124 – COVID-19 (special edition)** that have reached the status of recommended INN in annex.
Veuillez trouver les noms de la **Liste 124 des DCI proposées – COVID-19 (édition spéciale)** ayant atteint le statut de DCI recommandées en annexe.
Por favor, abajo se encuentran los nombres de la **Lista 124 de DCI propuestas – COVID-19 (edición especial)** que han alcanzado el estatus de DCI recomendadas.

acapatamabum #

acapatamab	immunoglobulin scFv-scFv-scFc, anti-[*Homo sapiens* FOLH1 (folate hydrolase, prostate specific membrane antigen, PSMA)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], monoclonal antibody single chain (scFv)2-scFc, bispecific; IG single chain scFv-scFv-scFc, anti FOLH1 and anti-CD3E (1-986) [scFv-VH-V-kappa anti-FOLH1 (1-243) [VH (*Homo sapiens* IGHV3-11*01 G49>C (44) (84.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -15-mer-tris(tetraglycyl-seryl) linker (122-136)-V-KAPPA (*Homo sapiens* IGKV1-16*01 (79.3%) -IGKJ2*01 Q120>C (236) (90.9%)) CDR-IMGT [6.3.9] (163-168.186-188.225-233) (137-243)] -6-mer seryl-tetraglycyl-seryl linker (244-249) -scFv-VH-V-lambda anti-CD3E (250-498) [VH (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (275-282.300-309.348-363) (250-374) -15-mer-tris(tetraglycyl-seryl) linker (375-389) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (415-423.441-443.480-488) (390-498)] -4-mer- tetraglycyl linker (499-502) -scFc (h-CH2-CH3)-(h-CH2-CH3) (503-986) [*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (hinge 6-15 (503-512), CH2 R83>C (574), N84.4>G (579), V85>C (584) (513-622), CH3 E12 (638), M14 (640) (623-727), CHS (728-729)) (503-729) -30-mer hexakis(tetraglycyl-seryl) linker (730-759) -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (hinge 6-15 (760-769), CH2 R83>C (831), N84.4>G (836), V85>C (841) (770-879), CH3 E12 (895), M14 (897) (880-984), CHS (985-986)) (760-986)]], non-glycosylated, produced in Chinese hamster ovary (CHO) cells
acapatamab	immunoglobuline scFv-scFv-scFc, anti-[*Homo sapiens* FOLH1 (folate hydrolase, antigène membranaire spécifique de la prostate, PSMA)], et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal à chaîne unique (scFv)2-scFc, bispécifique;

	IG à chaîne unique scFv-scFv-scFc, anti FOLH1 et anti-CD3E (1-986) [scFv-VH-V-kappa anti-FOLH1 (1-243) [VH (*Homo sapiens* IGHV3-11*01 G49>C (84.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -15-mer-tris(tétraglycyl-séryl) linker (122-136)-V-KAPPA (*Homo sapiens* IGKV1-16*01 (79.3%) -IGKJ2*01 Q120>C (236) (90.9%)) CDR-IMGT [6.3.9] (163-168.186-188.225-233) (137-243)] -6-mer-séryl-tétraglycyl-séryl linker (244-249) -scFv-VH-V-lambda anti-CD3E (250-498) [VH (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (275-282.300-309.348-363) (250-374) -15-mer-tris(tétraglycyl-séryl) linker (375-389) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (415-423.441-443.480-488) (390-498)] -4-mer-tétraglycyl linker (499-502) -scFc (h-CH2-CH3)-(h-CH2-CH3) (503-986) [*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (charnière 6-15 (503-512), CH2 R83>C (574), N84.4>G (579), V85>C (584) (513-622), CH3 E12 (638), M14 (640) (623-727), CHS (728-729)) (503-729) -30-mer-hexakis(tétraglycyl-séryl) linker (730-759) -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (charnière 6-15 (760-769), CH2 R83>C (831), N84.4>G (836), V85>C (841) (770-879), CH3 E12 (895), M14 (897) (880-984), CHS (985-986)) (760-986)]], non-glycosylé, produit dans des cellules ovariennes de hamster chinois (CHO)
acapatamab	inmunoglobulina scFv-scFv-scFc, anti-[*Homo sapiens* FOLH1 (folato hidrolasa, antígeno membranario específico de la prostata, PSMA)], y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal con cadena única (scFv)2-scFc, biespecífica; IG con cadena única scFv-scFv-scFc, anti FOLH1 y anti-CD3E (1-986) [scFv-VH-V-kappa anti-FOLH1 (1-243) [VH (*Homo sapiens* IGHV3-11*01 G49>C (84.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -15-mer-tris(tetraglicil-seril) linker (122-136)-V-KAPPA (*Homo sapiens* IGKV1-16*01 (79.3%) -IGKJ2*01 Q120>C (236) (90.9%)) CDR-IMGT [6.3.9] (163-168.186-188.225-233) (137-243)] -6-mer-seril-tetraglicil-seril linker (244-249) -scFv-VH-V-lambda anti-CD3E (250-498) [VH (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (275-282.300-309.348-363) (250-374) -15-mer-tris(tetraglicil-seril) linker (375-389) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (415-423.441-443.480-488) (390-498)] -4-mer- tetraglicil linker (499-502) -scFc (h-CH2-CH3)-(h-CH2-CH3) (503-986) [*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (bisagra 6-15 (503-512), CH2 R83>C (574), N84.4>G (579), V85>C (584) (513-622), CH3 E12 (638), M14 (640) (623-727), CHS (728-729)) (503-729) -30-mer-hexakis(tetraglicil-seril) linker (730-759) -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (bisagra 6-15 (760-769), CH2 R83>C (831), N84.4>G (836), V85>C (841) (770-879), CH3 E12 (895), M14 (897) (880-984), CHS (985-986)) (760-986)]], no glicosilado, producido en las células ováricas de hámster chino (CHO)

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG LVKPGESLRL SCAASGFTFS DYYMYWVRQA PGKCLEWVAI  50
ISDGGYYTYY SDIIKGRFTI SRDNAKNSLY LQMNSLKAED TAVYYCARGF 100
PLLRHGAMDY WGQGTLVTVS SGGGGSGGGG SGGGGSDIQM TQSPSSLSAS 150
VGDRVTITCK ASQNVDTNVA WYQQKPGQAP KSLIYSASYV YWDVPSRFSG 200
SASGTDFTLT ISSVQSEDFA TYYCQQYDQQ LITFGCGTKL EIKSGGGGSE 250
VQLVESGGGL VQPGGSLKLS CAASGFTFNK YAMNWVRQAP GKGLEWVARI 300
RSKYNNYATY YADSVKDRFT ISRDDSKNTA YLQMNNLKTE DTAVYYCVRH 350
GNFGNSYISY WAYWGQGTLV TVSSGGGGSG GGGSGGGGSQ TVVTQEPSLT 400
VSPGGTVTLT CGSSTGAVTS GNYPNWVQQK PGQAPRGLIG GTKFLAPGTP 450
ARFSGSLLGG KAALTLSGVQ PEDEAEYYCV LWYSNRWVFG GGTKLTVLGG 500
GGDKTHTCPP CPAPELLGGP SVFLFPPKPK DTLMISRTPE VTCVVVDVSH 550
EDPEVKFNWY VDGVEVHNAK TKPCEEQYGS TYRCVSVLTV LHQDWLNGKE 600
YKCKVSNKAL PAPIEKTISK AKGQPREPQV YTLPPSREEM TKNQVSLTCL 650
VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ 700
QGNVFSCSVM HEALHNHYTQ KSLSLSPGKG GGGSGGGGSG GGGSGGGGSG 750
GGGSGGGGSD KTHTCPPCPA PELLGGPSVF LFPPKPKDTL MISRTPEVTC 800
VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP CEEQYGSTYR CVSVLTVLHQ 850
DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL PPSREEMTKN 900
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSKLT 950
VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGK                986
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Post-translational modifications

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

Intra-V (C23 C104)	22-96	159-224	271-347	411-479
Intra-C (C23-C104)	543-603	649-707	800-860	906-964
Intra-CH2 (C83-C85)	574-584	831-841		
Inter-VH-VL (C49-C120)	44-236			
Inter-h11 (h 11 - h 11)	508-765			
Inter-h14 (h 14 - h 14)	511-768			

No N-glycosylation sites / pas de sites de N-glycosylation / ningún posición de N-glicosilación
CH2 N84.4>G:
579, 836
Aglycosylated

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
CHS K2:
986

adrenomedullinum pegolum #

adrenomedullin pegol

human adrenomedullin, C-terminal L-tyrosil amide, pegylated at O^4 of Y^1 with [(3*S*)-3-amino-4-{[(2R)-1-amino-3-{[(3*RS*)-2,5-dioxo-1-{3-oxo-3-[α-methyl(polyoxyethylene)-ω-amino]propyl}pyrrolidin-3-yl]sulfanyl}-1-oxopropan-2-yl]amino}-4-oxobutyl]carbamoyl; $O^{4.1}$-{[(3*S*)-3-amino-4-{[(2*R*)-1-amino-3-{[(3*RS*)-1-{3-[α-methylpoly(oxyethylene)-ω-amino]-3-oxopropyl}-2,5-dioxopyrrolidin-3-yl]sulfanyl}-1-oxopropan-2-yl]amino}-4-oxobutyl]carbamoyl}adrenomedullin (human)

adrénomedulline pégol

adrénomédulline humaine, L-tyrosil amide C-terminal, pégylée en O^4 de Y^1 avec [(3*S*)-3-amino-4-{[(2R)-1-amino-3-{[(3*RS*)-2,5-dioxo-1-{3-oxo-3-[α-méthyl(polyoxyéthylène)-ω-amino]propyl}pyrrolidin-3-yl]sulfanyl}-1-oxopropan-2-yl]amino}-4-oxobutyl]carbamoyle; $O^{4.1}$-({(3*S*)-3-amino-4-[(2*R*)-1-amino-3-{[(3*RS*)-1-{3-[α-méthylpoly(oxyéthylène)-ω-amino]-3-oxopropyl}-2,5-dioxopyrrolidin-3-yl]sulfanyl}-1-oxopropan-2-yl]-4-oxobutyl}carbamoyl)adrénomédulline (humaine)

adrenomedulina pegol

adrenomedulina humana, C-terminal L-tirosil amida, pegilada en O^4 de Y^1 con [(3S)-3-amino-4-{[(2R)-1-amino-3-{[(3*RS*)-2,5-dioxo-1-{3-oxo-3-[α-metil(polioxietileno)-ω-amino]propil}pirrolidin-3-il]sulfanil}-1-oxopropan-2-il]amino}-4-oxobutil]carbamoilo; $O^{4.1}$-({(3*S*)-3-amino-4-[(2*R*)-1-amino-3-{[(3*RS*)-1-{3-[α-metilpoli(oxietileno)-ω-amino]-3-oxopropil}-2,5-dioxopirrolidin-3-il]sulfanil}-1-oxopropan-2-il]-4-oxobutil}carbamoil)adrenomedulina (humana)

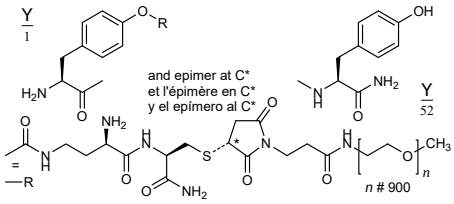
$C_{280}H_{430}N_{86}O_{83}S_4(C_2H_4O)_{\approx 900}$

Sequence / Séquence / Secuencia

YRQSMNNFQG LRSFGCRFGT CTVQKLAHQI YQFTDKDKDN VAPRSKISPQ 50
GY 52

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
36-86 43-89

Modified residues / Résidus modifiés / Restos modificados



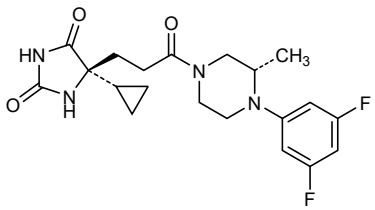
aldumastatum

aldumastat — (5*S*)-5-cyclopropyl-5-{3-[(3*S*)-4-(3,5-difluorophenyl)-3-methylpiperazin-1-yl]-3-oxopropyl}imidazolidine-2,4-dione

aldumastat — (5*S*)-5-cyclopropyl-5-{3-[(3*S*)-4-(3,5-difluorophényl)-3-méthylpipérazin-1-yl]-3-oxopropyl}imidazolidine-2,4-dione

aldumastat — (5*S*)-5-ciclopropil-5-{3-[(3*S*)-4-(3,5-difluorofenil)-3-metilpiperazin-1-il]-3-oxopropil}imidazolidina-2,4-diona

$C_{20}H_{24}F_2N_4O_3$



alnuctamabum #

alnuctamab — immunoglobulin G1-kappa/lambda with domain crossover, anti-[*Homo sapiens* TNFRSF17 (TNF receptor superfamily member 17, tumor necrosis factor receptor superfamily, member 17, B cell maturation antigen, BCMA, BCM, TNFRSF13A, CD269)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], monoclonal antibody, bispecific, trivalent; gamma1-lambda heavy chain anti-TNFRSF17 and anti-CD3E (VH-CH1-V-lambda-CH1-h-CH2-CH3) (1-671) [VH anti-TNFRSF17 (*Homo sapiens* IGHV3-23*01 (94.9%) -(IGHD) -IGHJ5*01 (93.3%)) CDR-IMGT [8.8.9] (26-33.51-58.97-105) (1-116) -*Homo sapiens* IGHG1*01, G1m17 (CH1 K26>E (146), K119>E (212), K120 (213) (117-214), hinge 1-6 (215-220)) (117-220) -10-mer bis(tetraglycyl-seryl) linker (221-230) -V-LAMBDA anti-CD3E (*Mus musculus* IGLV1*01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (80.0%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (256-264.282-284.321-329) (231-339)) -2-mer diseryl linker (340-341) -*Homo sapiens* IGHG1*01 G1m17,1, G1v14 CH2 A1.3, A1.2, G1v32 CH3 W22 (CH1 K120 (438) (342-439), hinge 1-15 (440-454), CH2 L1.3>A (458), L1.2>A (459), P114>G (553) (455-564), CH3 S10>C (578), D12 (580), L14 (582), T22>W (590) (565-669), CHS (670-671)) (342-671)],

(219-216')-disulfide with kappa light chain anti-TNFRSF17 (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (90.6%) -IGKJ1*01 (91.7%)) CDR-IMGT [7.3.10] (27-33.51-53.90-99) (1'-109') -*Homo sapiens* IGKC*01 (98.1%) E12>R (125), Q13>K (126), Km3 A45.1 (155), V101 (193) (110'-216')]; (444-232''')-disulfide with VH-C-kappa light chain anti-CD3E, (1'''-232''') [VH (*Homo sapiens* IGHV3-23*03 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) CDR-IMGT [8.10.16] (26-33.51-60.99-114) (1'''-125''') -*Homo sapiens* IGKC*01 (99.1%) T1.3>S (127), Km3 A45.1 (171), V101 (209) (126'''-232''')]; gamma1 heavy chain anti-TNFRSF17 (1''-446'') [VH (*Homo sapiens* IGHV3-23*01 (94.9%) -(IGHD) -IGHJ5*01 (93.3%)) CDR-IMGT [8.8.9] (26-33.51-58.97-105) (1''-116'') -*Homo sapiens* IGHG1*01 G1m17,1, G1v14 CH2 A1.3, A1.2, G1v33 CH3 S22, A24, V86 (CH1 K26>E (146), K119>E (212), K120 (213) (117''-214''), hinge 1-15 (215''-229''), CH2 L1.3>A (233), L1.2>A (234), P114>G (328) (230''-339''), CH3 Y5>C (348), D12 (355), L14 (357), T22>S (365), L24>A (367), Y86>V (406) (340''-444''), CHS (445''-446'')) (117''-446'')], (219''-216'''')-disulfide with kappa light chain anti-TNFRSF17 (1''''-216'''') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (90.6%) -IGKJ1*01 (91.7%)) CDR-IMGT [7.3.10] (27-33.51-53.90-99) (1''''-109'''') -*Homo sapiens* IGKC*01 (98.1%) E12>R (125), Q13>K (126), Km3 A45.1 (155), V101 (193) (110''''-216'''')]; dimer (450-225'':453-228'':578-348'')-trisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

alnuctamab

immunoglobuline G1-kappa/lambda avec domaines échangés, anti-[*Homo sapiens* TNFRSF17 (membre 17 de la superfamille des récepteurs du TNF, membre 17 de la superfamille des récepteurs du facteur de nécrose tumorale, antigène de maturation de cellule B, BCMA, BCM, TNFRSF13A, CD269)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal, bispécifique, trivalent; chaîne lourde gamma1 anti-TNFRSF17 et anti-CD3E (VH-CH1-V-lambda-CH1-h-CH2-CH3) (1-671) [VH anti-TNFRSF17 (*Homo sapiens* IGHV3-23*01 (94.9%) -(IGHD) -IGHJ4*01 (93.3%)) CDR-IMGT [8.8.9] (26-33.51-58.97-105) (1-116) -*Homo sapiens* IGHG1*01 G1m17 (CH1 K26>E (146), K119>E (212), K120 (213) (117-214), charnière 1-6 (215-220)) (117-220) -10-mer bis(tétraglycyl-séryl) linker (221-230) -V-LAMBDA anti-CD3E (*Mus musculus* IGLV1*01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* (IGLV7-46*01 (80.0%) -IGLJ3*02 (100%) CDR-IMGT [9.3.9] (256-264.282-284.321-329) (231-339)) -2-merdiséryl linker (340-341) -*Homo sapiens* IGHG1*01 G1m17,1,G1v14 CH2 A1.3, A1.2, G1v32 CH3 W22 (CH1 K120 (438) (342-439), charnière 1-15 (440-454), CH2 L1.3>A (458), L1.2>A (459), P114>G (553) (455-564), CH3 S10>C (578), D12 (580), L14 (582), T22>W (590) (565-669), CHS (670-671)) (342-671)], (219-216')-disulfure avec la chaîne légère kappa anti-TNFRSF17 (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (90.6%) -IGKJ1*01 (91.7%)) CDR-IMGT [7.3.10] (27-33.51-53.90-99) (1'-109') -*Homo sapiens* IGKC*01 (98.1%) E12>R (125), Q13>K (126), Km3 A45.1 (155), V101 (193) (110'-216')]; (444-232')-disulfure avec la chaîne légère VH-C-kappa anti-CD3E (1'''-232''') [VH (*Homo sapiens* IGHV3-23*03 (87.0%) -IGHJ6*01 (90.9%)) CDR-IMGT [8.10.16] (26-33.51-60.99-114) (1'''-125''') -*Homo sapiens* IGKC*01 (99.1%) T1.3>S (127), Km3 A45.1 (171), V101 (209) (126'''-232''')];

	chaîne lourde gamma1 anti-TNFRSF17 (1''-446'') [VH (*Homo sapiens* IGHV3-23*01 (94.9%) -(IGHD) -IGHJ4*01 (93.3%)) CDR-IMGT [8.8.9] (26-33.51-58.97-105) (1''-116'') -*Homo sapiens* IGHG1*01 G1m17,1, G1v14 CH2 A1.3, A1.2, G1v33 CH3 S22, A24, V86 (CH1 K26>E (146), K119>E (212), K120 (213) (117''-214''), charnière 1-15 (215''-229''), CH2 L1.3>A (233), L1.2>A (234), P114>G (328) (230''-339''), CH3 Y5>C (348), D12 (355), L14 (357), T22>S (365), L24>A (367), Y86>V (406) (340''-444''), CHS (445''-446'')) (117''-446'')], (219''-216'''')-disulfure avec la chaîne légère kappa anti-TNFRSF17 (1''''-216'''') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (90.6%) -IGKJ1*01 (91.7%)) CDR-IMGT [7.3.10] (27-33.51-53.90-99) (1''''-109'''') -*Homo sapiens* IGKC*01 (98.1%) E12>R (125), Q13>K (126), Km3 A45.1 (155), V101 (193) (110''''-216'''')]; dimère (450-225'':453-228'':578-348'')-trisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
alnuctamab	inmunoglobulina G1-kappa/lambda con dominios cruzados, anti-[*Homo sapiens* TNFRSF17 (miembro 17 de la superfamilia de los receptores del TNF, miembro 17 de la superfamilia de los receptores del factor de necrosis tumoral, antígeno de maduración de célula B, BCMA, BCM, TNFRSF13A, CD269)] y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal, biespecífico, trivalente; cadena pesada gamma1 anti-TNFRSF17 y anti-CD3E (VH-CH1-V-lambda-CH1-h-CH2-CH3) (1-671) [VH anti-TNFRSF17 (*Homo sapiens* IGHV3-23*01 (94.9%) -(IGHD) -IGHJ4*01 (93.3%)) CDR-IMGT [8.8.9] (26-33.51-58.97-105) (1-116) -*Homo sapiens* IGHG1*01 G1m17 (CH1 K26>E (146), K119>E (212), K120 (213) (117-214), bisagra 1-6 (215-220)) (117-220) -10-mer bis(tetraglicil-seril) linker (221-230) -V-LAMBDA anti-CD3E (*Mus musculus* IGLV1*01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* (IGLV7-46*01 (80.0%) -IGLJ3*02 (100%) CDR-IMGT [9.3.9] (256-264.282-284.321-329) (231-339)) -2-merdiseril linker (340-341) -*Homo sapiens* IGHG1*01 G1m17,1,G1v14 CH2 A1.3, A1.2, G1v32 CH3 W22 (CH1 K120 (438) (342-439), bisagra 1-15 (440-454), CH2 L1.3>A (458), L1.2>A (459), P114>G (553) (455-564), CH3 S10>C (578), D12 (580), L14 (582), T22>W (590) (565-669), CHS (670-671)) (342-671)], (219-216')-disulfuro con la cadena ligera kappa anti-TNFRSF17 (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (90.6%) -IGKJ1*01 (91.7%)) CDR-IMGT [7.3.10] (27-33.51-53.90-99) (1'-109') -*Homo sapiens* IGKC*01 (98.1%) E12>R (125), Q13>K (126), Km3 A45.1 (155), V101 (193) (110'-216')]; (444-232')-disulfuro con la cadena ligera VH-C-kappa anti-CD3E (1'''-232''') [VH (*Homo sapiens* IGHV3-23*03 (87.0%) -IGHJ6*01 (90.9%)) CDR-IMGT [8.10.16] (26-33.51-60.99-114) (1'''-125''') -*Homo sapiens* IGKC*01 (99.1%) T1.3>S (127), Km3 A45.1 (171), V101 (209) (126'''-232''')]; cadena pesada gamma1 anti-TNFRSF17 (1''-446'') [VH (*Homo sapiens* IGHV3-23*01 (94.9%) -(IGHD) -IGHJ4*01 (93.3%)) CDR-IMGT [8.8.9] (26-33.51-58.97-105) (1''-116'') -*Homo sapiens* IGHG1*01 G1m17,1, G1v14 CH2 A1.3, A1.2, G1v33 CH3 S22, A24, V86 (CH1 K26>E (146), K119>E (212), K120 (213) (117''-214''), bisagra 1-15 (215''-229''), CH2 L1.3>A (233), L1.2>A (234), P114>G (328) (230''-339''), CH3 Y5>C (348), D12 (355), L14 (357), T22>S (365), L24>A (367), Y86>V (406) (340''-444''), CHS (445''-446'')) (117''-446'')], (219''-216'''')-disulfuro con la cadena ligera kappa anti-TNFRSF17 (1''''-216'''') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (90.6%) -IGKJ1*01 (91.7%)) CDR-IMGT [7.3.10] (27-33.51-53.90-99) (1''''-109'''') -*Homo sapiens* IGKC*01 (98.1%) E12>R (125), Q13>K (126), Km3 A45.1 (155), V101 (193) (110''''-216'''')]; dímero (450-225'':453-228'':578-348'')-trisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada (1-671 anti-TNFRSF17 and anti-CD3)

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DNAMGWVRQA PGKGLEWVSA  50
ISGPGSSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVL 100
GWFDYWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVEDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DEKVEPKSCD GGGGSGGGGS QAVVTQEPSL TVSPGGTVTL 250
TCGSSTGAVT TSNYANWVQE KPGQAFRGLI GGTNKRAPGT PARFSGSLLG 300
GKAALTLSGA QPEDEAEYYC ALWYSNLWVF GGGTKLTVLS SASTKGPSVF 350
PLAPSSKSTS GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS 400
SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP SNTKVDKKVE PKSCDKTHTC 450
PPCPAPEAAG GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN 500
WYVDGVEVHN AKTKPREEQY NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK 550
ALGAPIEKTI SKAKGQPREP QVYTLPPCRD ELTKNQVSLW CLVKGFYPSD 600
IAVEWESNGQ PENNYKTTPP VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS 650
VMHEALHNHY TQKSLSLSPG K                                 671
```

Heavy chain / Chaîne lourde / Cadena pesada (1"-446" anti-TNFRSF17)

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DNAMGWVRQA PGKGLEWVSA  50
ISGPGSSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVL 100
GWFDYWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVEDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DEKVEPKSCD KTHTCPPCPA PEAAGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALGAP IEKTISKAKG QPREPQVCTL 350
PPSRDELTKN QVSLSCAVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLVSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGK     446
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Light chain / Chaîne légère / Cadena ligera (1'-216' and 1'"-216"" anti-TNFRSF17)

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS DEYLSWYQQK PGQAPRLLIH  50
SASTRATGIP DRFSGSGSGT DFTLAISRLE PEDFAVYYCQ QYGYPPDFTF 100
GQGTKVEIKR TVAAPSVFIF PPSDRKLKSG TASVVCLLNN FYPREAKVQW 150
KVDNALQSGN SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH 200
QGLSSPVTKS FNRGEC                                      216
```

Light chain / Chaîne légère / Cadena ligera (1'"-232"" anti-CD3E)

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS TYAMNWVRQA PGKGLEWVSR  50
IRSKYNNYAT YYADSVKGRF TISRDDSKNT LYLQMNSLRA EDTAVYYCVR 100
HGNFGNSYVS WFAYWGQGTL VTVSSASVAA PSVFIFPPSD EQLKSGTASV 150
VCLLNNFYPR EAKVQWKVDN ALQSGNSQES VTEQDSKDST YSLSSTLTLS 200
KADYEKHKVY ACEVTHQGLS SPVTKSFNRG EC                    232
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 143-199 252-320 368-424 485-545 591-649
22"-96" 143"-199" 260"-320" 366"-424"
Intra-L (C23-C104) 23'-89' 136'-196'
22'"-98"" 152'"-212'"
23'"-89"" 136'"-196'"
Inter-H-L (h 5-CL 126) 219-216' 444-232'" 219"-216""
Inter-H-H (h 11, h 14) 450-225" 453-228"
Inter-H-H engineered 578-348"

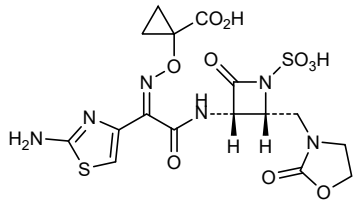
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
521, 296"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
671, 446"

ancremonamum

ancremonam	1-({(*Z*)-[1-(2-amino-1,3-thiazol-4-yl)-2-oxo-2-({(3*S*,4*R*)-2-oxo-4-[(2-oxo-1,3-oxazolidin-3-yl)methyl]-1-sulfoazetidin-3-yl}amino)ethylidene]amino}oxy) cyclopropane-1-carboxylic acid
ancrémonam	acide1-({(*Z*)-[1-(2-amino-1,3-thiazol-4-yl)-2-oxo-2-({(3*S*,4*R*)-2-oxo-4-[(2-oxo-1,3-oxazolidin-3-yl)méthyl]-1-sulfoazétidin-3-yl}amino)éthylidène]amino}oxy) cyclopropane-1-carboxylique
ancremonam	ácido1-({(*Z*)-[1-(2-amino-1,3-tiazol-4-il)-2-oxo-2-({(3*S*,4*R*)-2-oxo-4-[(2-oxo-1,3-oxazolidin-3-il)metil]-1-sulfoazetidin-3-il}amino)etilideno]amino}oxi) ciclopropano-1-carboxílico

$C_{16}H_{18}N_6O_{10}S_2$



apitegromabum #

apitegromab	immunoglobulin G4-lambda, anti-[*Homo sapiens* pro-MSTN (pro-growth differentiation factor 8, pro-GDF8, pro-myostatin, pro-GDF-8)], *Homo sapiens* monoclonal antibody; gamma4 heavy chain *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV3-30*03 (100%) -(IGHD) - IGHJ6*01 (94.4%)) CDR-IMGT [8.8.19] (26-33.51-58.97-115) (1-126)-*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (127-224), hinge 1-12 S10>P (234) (225-236), CH2 (237-346), CH3 (347-451), CHS K>del (452)) (127-452)], (140-214')-disulfide with lambda light chain *Homo sapiens* (1'-215') [V-LAMBDA (*Homo sapiens* IGLV1-44*01 (98%) -IGLJ2*01 (100%)) CDR-IMGT [8.3.10] (26-33.51-53.90-99) (1'-109') -*Homo sapiens* IGLC2*01 (100%) (110'-215')]; dimer (232-232":235-235")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
apitégromab	immunoglobuline G4-lambda, anti-[*Homo sapiens* pro-MSTN (pro-facteur de croissance et de différenciation 8, pro-GDF8, pro-myostatine, pro-GDF-8)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma4 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV3-30*03 (100%) -(IGHD) - IGHJ6*01 (94.4%)) CDR-IMGT [8.8.19] (26-33.51-58.97-115) (1-126)-*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (127-224), charnière 1-12 S10>P (234) (225-236), CH2 (237-346), CH3 (347-451), CHS K>del (452)) (127-452)], (140-214')-disulfure avec la chaîne légère lambda *Homo sapiens* (1'-215') [V-LAMBDA (*Homo sapiens* IGLV1-44*01 (98%) -IGLJ2*01 (100%)) CDR-IMGT [8.3.10] (26-33.51-53.90-99) (1'-109') -*Homo sapiens* IGLC2*01 (100%) (110'-215')]; dimère (232-232":235-235")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
apitegromab	inmunoglobulina G4-lambda, anti-[*Homo sapiens* pro-MSTN (pro-factor de crecimiento y de diferenciación 8, pro-GDF8, pro-miostatina, pro-GDF-8)], anticuerpo monoclonal *Homo sapiens*;

cadena pesada gamma4 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV3-30*03 (100%) -(IGHD) - IGHJ6*01 (94.4%)) CDR-IMGT [8.8.19] (26-33.51-58.97-115) (1-126)-*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (127-224), bisagra 1-12 S10>P (234) (225-236), CH2 (237-346), CH3 (347-451), CHS K>del (452)) (127-452)], (140-214')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-215') [V-LAMBDA (*Homo sapiens* IGLV1-44*01 (98%) -IGLJ2*01 (100%)) CDR-IMGT [8.3.10] (26-33.51-53.90-99) (1'-109') - *Homo sapiens* IGLC2*01 (100%) (110'-215')]; dímero (232-232":235-235")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVAV  50
ISYDGSNKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARDL 100
LVRFLEWSHY YGMDVWGQGT TVTVSSASTK GPSVFPLAPC SRSTSESTAA 150
LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS 200
SLGTKTYTCN VDHKPSNTKV DKRVESKYGP PCPPCPAPEF LGGPSVFLFP 250
PKPKDTLMIS RTPEVTCVVV DVSQEDPEVQ FNWYVDGVEV HNAKTKPREE 300
QFNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKGLPSSIEK TISKAKGQPR 350
EPQVYTLPPS QEEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSRLTVDK SRWQEGNVFS CSVMHEALHN HYTQKSLSLS 450
LG                                                      452
```

Light chain / Chaîne légère / Cadena ligera

```
QSVLTQPPSA SGTPGQRVTI SCSGSSSNIG SNTVHWYQQL PGTAPKLLIY  50
SDNQRPSGVP DRFSGSKSGT SASLAISGLQ SEDEADYYCA AWDDSLNGVF 100
GGGTKLTVLG QPKAAPSVTL FPPSSEELQA NKATLVCLIS DFYPGAVTVA 150
WKADSSPVKA GVETTTPSKQ SNNKYAASSY LSLTPEQWKS HRSYSCQVTH 200
EGSTVEKTVA PTECS                                        215
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 153-209 267-327 373-431
22"-96" 153"-209" 267"-327" 373"-431"
Intra-L (C23-C104) 22'-89' 137'-196'
22'"-89'" 137'"-196'"
Inter-H-L (h 10-CL 126) 140-214' 140"-214'"
Inter-H-H (h 8, h 11) 232-232" 235-235"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"
L VL Q1:
1', 1'"

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

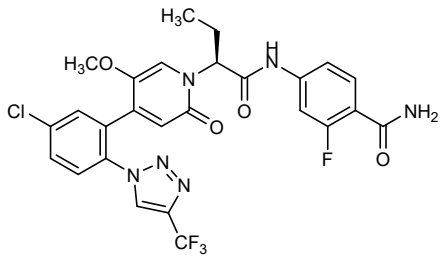
asundexianum

asundexian — (4*S*)-2^4-chloro-4-ethyl-7^3-fluoro-3^5-methoxy-3^2,5-dioxo-1^4-(trifluoromethyl)-3^2*H*-6-aza-3(4,1)-pyridina-1(1)-[1,2,3]triazola-2(1,2),7(1)-dibenzenaheptaphane-7^4-carboxamide

asundexian — (4*S*)-2^4-chloro-4-éthyl-7^3-fluoro-3^5-méthoxy-3^2,5-dioxo-1^4-(trifluorométhyl)-3^2*H*-6-aza-3(4,1)-pyridina-1(1)-[1,2,3]triazola-2(1,2),7(1)-dibenzénaheptaphane-7^4-carboxamide

asundexián — (4*S*)-2^4-cloro-4-etil-7^3-fluoro-3^5-metoxi-3^2,5-dioxo-1^4-(trifluorometil)-3^2*H*-6-aza-3(4,1)-piridina-1(1)-[1,2,3]triazola-2(1,2),7(1)-dibencenaheptafano-7^4-carboxamida

$C_{26}H_{21}ClF_4N_6O_4$



atidarsagenum autotemcelum #

atidarsagene autotemcel

Autologous CD34+ hematopoietic stem and progenitor cells transduced *ex vivo* with a replication-incompetent lentiviral vector encoding human arylsulfatase A (ARSA). Autologous CD34+ hematopoietic stem and progenitor cells (HSPC), obtained from bone marrow (BM) or mobilised peripheral blood (mPB), transduced *ex vivo* with a replication-incompetent pseudotyped HIV-1 based lentiviral vector encoding the human arylsulfatase A (ARSA) transgene under the control of a human phosphoglycerate kinase (PGK) promoter. The vector is pseudotyped with the vesicular stomatitis virus (VSV) envelope glycoprotein. The vector genome also contains a mutated Woodchuck hepatitis virus post-transcriptional regulatory element (WPRE), a fragment of the HIV-1 *gag,* the HIV-1 Rev response element (RRE), the HIV-1 central polypurine tract (cPPT) and a fragment of *nef*. The CD34+ cell population corresponds to an heterogenous population of stem and progenitor cells, some expressing the CD90 and/or CD133 markers.

atidarsagène autotemcel

Des cellules souches et progénitrices hématopoïétiques CD34+ autologues ont été transduites *ex vivo* avec un vecteur lentiviral incompétent à la réplication codant pour l'arylsulfatase A humaine (ARSA).
Des cellules souches et progénitrices hématopoïétiques CD34+ autologues (HSPC), obtenues à partir de moelle osseuse (BM) ou de sang périphérique mobilisé (mPB), ont été transduites *ex vivo* avec un vecteur lentiviral, à base de VIH-1 pseudotypé et incompétent à la réplication, codant pour le transgène de l'arylsulfatase A humaine (ARSA), sous le contrôle d'un promoteur de la phosphoglycérate kinase (PGK) humaine. Le vecteur est pseudotypé avec la glycoprotéine d'enveloppe du virus de la stomatite vésiculeuse (VSV). Le génome du vecteur contient également l'élément régulateur post-transcriptionnel Woodchuck (WPRE) du virus de l'hépatite, un fragment du *gag* du VIH-1, l'élément de réponse post-transcriptionnel (RRE) du VIH-1 et le tractus central de polypurine du VIH-1 (cPPT), ainsi qu'un fragment de *nef*. La population de cellules CD34+ correspond à une population hétérogène de cellules souches et progénitrices, certaines exprimant les marqueurs CD90 et/ou CD133.

atidarsagén autotemcel	Células troncales y progenitoras hematopoyéticas CD34+ autólogas transducidas *ex vivo* con un vector lentiviral incompetente en replicación que codifica para la arilsulfatasa A humana (ARSA). Las células troncales y progenitoras hematopoyéticas CD34+ autólogas, obtenidas de médula ósea o movilizadas de sangre periférica, se transducen *ex vivo* con un vector lentiviral basado en VIH-1 seudotipado y incompetente en replicación, que codifica el transgen de la arilsulfatasa A humana (ARSA) bajo el control de un promotor de la fosfoglicerato quinasa humana (PGK). El vector está seudotipado con la glicoproteína de la envuelta del virus de la estomatitis vesicular (VSV). El genoma del vector también contiene el elemento regulador post-transcipcional del virus de la hepatitis de la marmota (WPRE), un fragmento de *gag* del VIH-1, un elemento de respuesta post-transcripcional (RRE) del VIH-1 y un tramo central de poli-purinas (cPPT) de VIH-1, así como un fragmento de *nef*. La población de células CD34+corresponde en una población de celulas troncales y progenitoras, algunas expressando los marcadores CD90 y/o CD133.
avipendekinum pegolum #	
avipendekin pegol	human L-methionyl-interleukin 15, produced in *Escherichia coli*, pegylated at N^2 of Met^1 and N^6 of Lys residues with 4-[α-methylpoly(oxyethylene)-ω-oxy]butanoyl groups; L-methionyl-interleukin 15 (human, non-glycosylated), produced in *Escherichia coli*, substituted on an average of one site among N^2 of Met^1 and/or N^6 of lysyl residues with 4-[α-methylpoly(oxyethylene)-ω-oxy]butanoyl groups (~40 kDa each)
avipendékine pégol	L-méthionyl-interleukine 15 humaine, produite par *Escherichia coli*, pégylée en N^2 de Met^1 et N^6 des résidus Lys avec des groupes 4-[α-méthylpoly(oxyéthylène)-ω-oxy]butanoyle; L-méthionyl-interleukine 15 (humaine, non-glycosylée), produite dans *Escherichia coli*, substituée sur une moyenne d'un site parmi le N^2 du Met^1 et/ou N^6 des résidus lysyl par des groupes 4-[α-méthylpoly(oxyéthylène)-ω-oxy]butanoyle (~40 kDa chacun)
avipendekina pegol	L-metionil-interleukina 15 humana, producida en *Escherichia coli*, pegilada en N^2 de Met^1 y N^6 de residuos Lis con grupos 4-[α-metilpoli(oxietileno)-ω-oxi]butanoilo; L-metionil-interleukina 15 (humana, no glicosilada), producida en *Escherichia coli*, sustituida pro término medio de un sitio entre el N^2 del Met^1 y/o el N^6 de los residuos lisil por grupos 4-[α-metilpoli(oxietileno)-ω-oxi]butanoilo (~40 kDa cada uno)

$C_{563}H_{898}N_{144}O_{185}S_8[C_5H_8O_2(C_2H_4O)_n]_x$ n ≈ 900, x ≈ 1

Sequence / Séquence / Secuencia

```
MNWVNVISDL KKIEDLIQSM HIDATLYTES DVHPSCKVTA MKCFLLELQV   50
ISLESGDASI HDTVENLIIL ANNSLSSNGN VTESGCKECE ELEEKNIKEF  100
LQSFVHIVQM FINTS                                        115
```

Post-translational modifications

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

36-86, 43-89

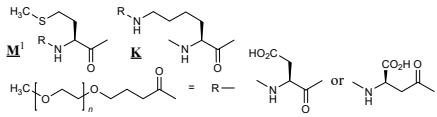
Partial deamidation / Désamidation partielle / Desamidación parcial

N78 (Asn>Asp, isoaspartyl)

Modified residues / Résidus modifiés / Restos modificados

avipendekin : pegol ~ 1:1

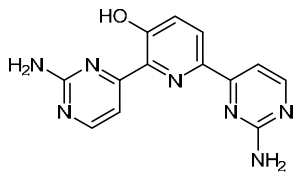
M[1] (Met 1: ~32-40 %), **K** (Lys 11, 37, 42, 87: ~33-42 %; Lys 12, 95, 98: ~18-35 %)



avotaciclibum

avotaciclib	2,6-bis(2-aminopyrimidin-4-yl)pyridin-3-ol
avotaciclib	2,6-bis(2-aminopyrimidin-4-yl)pyridin-3-ol
avotaciclib	2,6-bis(2-aminopirimidin-4-il)piridin-3-ol

$C_{13}H_{11}N_7O$



azercabtagenum zapreleucelum #

azercabtagene zapreleucel

Adult allogeneic CD4+ and CD8+ enriched T cells transduced with an anti-CD19 chimeric antigen receptor (CAR) that is site-specific integrated into the cellular genome.
Adult allogeneic CD4+ and CD8+ enriched T cells, gene edited through the electroporation of homing endonuclease mRNA, which is translated into endonuclease protein that introduces a double-stranded DNA break in exon 1 of the endogenous T cell receptor alpha constant (TRAC) locus. Cells are subsequently transduced with a recombinant non-replicating adeno-associated virus type 6 (rAAV6) vector, encoding an anti-CD19 CAR transgene consisting of a murine CD19-specific scFv (clone FMC63), a CD8 hinge/transmembrane domain, a novel 6 (N6) co-stimulatory domain and CD3 zeta signaling domain, under the control of the synthetic promoter JeT and the SV40 poly(A) signal. CAR transgene integration is achieved via homology directed recombination at the endonuclease target site (exon 1 of TRAC). Depletion of CD3+ cells is performed on the

	transduced cells to remove cells with functional endogenous T cell receptor (TCR). The substance is a mixture of non-effector (naive, stem cell memory, central memory) (CCR7+) and effector memory and effector (CCR7-) CD4+ and CD8+ T cells with generally ≥99% T cell receptor knockout, and ≥40% anti-CD19 CAR knock-in. Activation of the cells is accompanied *in vitro* by release of IFNγ, IL-2, IL-6, and TNFα in an antigen-dependent manner.
azercabtagène zapréleucel	Lymphocytes T adultes allogéniques de type CD4+ et CD8+ transduits avec un récepteur d'antigène chimérique (CAR) anti-CD19 qui est intégré de manière spécifique au site. Lymphocytes T allogéniques enrichies en cellules de type CD4+ et CD8+, dont les gènes ont été édités par l'électroporation du mRNA de l'endonucléase de ciblage, qui est traduite en une protéine endonucléase qui introduit une rupture d'ADN double brin dans l'exon 1 du locus du récepteur alpha endogène aux cellules T (TRAC). Les cellules sont transduites ensuite avec un vecteur du virus recombinant adéno-associé, non réplicatif de type 6 (rAAV6), qui code pour un trangène anti-CD19 CAR, qui consiste en un scFv spécifique à CD19 (clone FMC63), un domaine CD8 transmembranaire/charnière, en un nouveau domaine de co-stimulation 6 (N6) et en un domaine de signalisation CD3 zêta, sous le contrôle du promoteur synthétique JeT et d'un signal poly(A) SV40. L'intégration du transgène CAR est obtenue via la recombinaison homologue dirigée au site de ciblage de l'endonucléase (l'exon 1 du TRAC). La déplétion des cellules CD3+ est effectuée sur les cellules transduites pour éliminer les cellules avec des récepteurs T (TCR) endogènes. La substance est un mélange de lymphocytes T non-effecteurs (naïfs, cellules souches mémoire, mémoire centrale) (CCR7+) et lymphocytes T mémoire effecteurs et effecteurs (CCR7-) CD4+ et CD8+ avec en général ≥99% de récepteurs des lymphocytes T knock-out et ≥40% de CAR anti-CD19 knock-in. L'activation des cellules est accompagnée *in vitro* par le relâchement d'IFNγ, IL-2, IL-6, et TNFα d'une manière antigène-dépendante.
azercabtagén zapreleucel	Linfocitos T adultos, alogénicos, enriquecidos en CD4+ y CD8+, transducidos con un receptor de antígenos quimérico (CAR) anti-CD19 que se integra en el genoma celular de forma específica de sitio. Linfocitos T adultos, alogénicos, enriquecidos en CD4+ y CD8+, con genes editados mediante la electroporación del ARNm de una endonucleasa de homing, que se traduce a una proteína endonucleasa que introduce una rotura en el ADN de doble cadena en el exón 1 del locus de la región constante del receptor alfa de células T endógenas (TRAC). Las células son posteriormente transducidas con un vector recombinante, no replicativo, de virus adeno-asociado tipo 6 (rAAV6) que codifica para un transgén de CAR anti-CD19 que consiste en un scFv murino nti-CD19 (clon FMC63), un dominio bisagra/transmenbrana

CD8, un nuevo dominio de co-estimulación 6 (N6) y el dominio de señalización CD3 zeta, bajo el control del promotor sintético JeT y la señal poly(A) del SV40. La integración del transgén CAR se consigue mediante recombinación homóloga dirigida en el sitio diana de la endonucleasa (exón 1 de TRAC). Se realiza la depleción de células CD3+ en las células transducidas para eliminar las células con un receptor de células T (TCR) endógeno funcional. La sustancia es una mezcla de linfocitos T no efectores (ingenuos, células troncales memoria, memoria central) (CCR7+) y linfocitos T memoria efectores y efectores (CCR7-) CD4+ y CD8+ con en general ≥99% de receptores de linfocitos T (TCR) knock-out y ≥40% de CAR anti-CD19 knock-in. La activación de las células está acompañada *in vitro* por la liberación de IFNγ, IL-2, IL-6, y TNFα de una manera antígeno-dependiente.

bapotulimabum #

bapotulimab	immunoglobulin G2-kappa, anti-[*Homo sapiens* ILDR2 (immunoglobulin like domain containing receptor 2, C1orf32)], *Homo sapiens* monoclonal antibody; gamma2 heavy chain *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV1-69*10 (100%) -(IGHD) -IGHJ5*01 (81.2%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG2*01, G2m.. CH2 V45.1 (CH1 (121-218), hinge 1-12 (219-230), CH2 V45.1 (281) (231-339), CH3 (340-444), CHS K>del (445)) (121-445)], (134-219')-disulfide with kappa light chain *Homo sapiens* (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-28*01 (99%) -IGKJ4*01 (83.3%)) CDR-IMGT [11.3.9] (27-37.55-57.94-102) (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (222-222":223-223":226-226":229-229")-tetrakisdisulfide, produced in a Chinese hamster ovary (CHO)-derived cell line, glycoform alfa
bapotulimab	immunoglobuline G2-kappa, anti-[*Homo sapiens* ILDR2 (récepteur 2 contenant un domaine immunoglobuline-like, C1orf32)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma2 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV1-69*10 (100%) -(IGHD) -IGHJ5*01 (81.2%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG2*01, G2m.. CH2 V45.1 (CH1 (121-218), charnière 1-12 (219-230), CH2 V45.1 (281) (231-339), CH3 (340-444), CHS K>del (445)) (121-445)], (134-219')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-28*01 (99%) -IGKJ4*01 (83.3%)) CDR-IMGT [11.3.9] (27-37.55-57.94-102) (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (222-222":223-223":226-226":229-229")-tétrakisdisulfure, produite dans une lignée cellulaire dérivée des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

bapotulimab

inmunoglobulina G2-kappa, anti-[*Homo sapiens* ILDR2 (receptor 2 que contiene un dominio inmunoglobulina-like, C1orf32)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada gamma2 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV1-69*10 (100%) -(IGHD) -IGHJ5*01 (81.2%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG2*01, G2m.. CH2 V45.1 (CH1 (121-218), bisagra 1-12 (219-230), CH2 V45.1 (281) (231-339), CH3 (340-444), CHS K>del (445)) (121-445)], (134-219')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-28*01 (99%) -IGKJ4*01 (83.3%)) CDR-IMGT [11.3.9] (27-37.55-57.94-102) (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')];
dímero (222-222":223-223":226-226":229-229")-tetrakisdisulfuro, producido en una línea celular derivada de las células ováricas de hamster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG  50
IIPILGIANY AQKFQGRVTI TADKSTSTAY MELSSLRSED TAVYYCARGR 100
LPYGDFWDSW GQGTLVTVSS ASTKGPSVFP LAPCSRSTSE STAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSNFGTQT 200
YTCNVDHKPS NTKVDKTVER KCCVECPPCP APPVAGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTFR 300
VVSVLTVVHQ DWLNGKEYKC KVSNKGLPAP IEKTISKTKG QPREPQVYTL 350
PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPMLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPG      445
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL YSNGYNYLDW YLQKPGQSPQ  50
LLIYLGSNRA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP 100
LTFGGGTKLE IRRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

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

Intra-H (C23-C104)	22-96	147-203	260-320	366-424
	22"-96"	147"-203"	260"-320"	366"-424"
Intra-L (C23-C104)	23'-93'	139'-199'		
	23'"-93'"	139'"-199'"		
Inter-H-L (CH1 10-CL 126)*	134-219'	134"-219'"		
Inter-H-H (h 4, h 5, h 8, h 11)*	222-222"	223-223"	226-226"	229-229"

*A-isoform, predominant

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
296, 296"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

barecetamabum #
barecetamab

immunoglobulin G1-lambda, anti-[*Homo sapiens* ERBB3 (receptor tyrosine-protein kinase erbB-3, HER3)], *Homo sapiens* monoclonal antibody;
gamma1 heavy chain *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-23*01 (90.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -*Homo sapiens* IGHG1*01, nG1m1, G1m17 (CH1 K120 (218) (122-219), hinge 1-15 (220-234), CH2 (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-215')-disulfide with lambda light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-47*02 (92.9%) -IGLJ2*01 (100%)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC3*03 (100%) (111'-216')];
dimer (230-230":233-233")-bisdisulfide, produced in Chinese hamster ovary (CHO)-K1 cell line, glycoform alfa

barécétamab

immunoglobuline G1-lambda, anti-[*Homo sapiens* ERBB3 (récepteur à activité tyrosine kinase erbB-3, HER3)], *Homo sapiens* anticorps monoclonal;
chaîne lourde gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-23*01 (90.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -*Homo sapiens* IGHG1*01, nG1m1, G1m17 (CH1 K120 (218) (122-219), charnière 1-15 (220-234), CH2 (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (225-215')-disulfure avec la chaîne légère lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-47*02 (92.9%) -IGLJ2*01 (100%)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC3*03 (100%) (111'-216')]; dimère (230-230":233-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1, glycoforme alfa

barecetamab

inmunoglobulina G1-lambda, anti-[*Homo sapiens* ERBB3 (receptor de la actividad tirosina kinasa erbB-3, HER3)], *Homo sapiens* anticuerpo monoclonal;
cadena pesada gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-23*01 (90.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -*Homo sapiens* IGHG1*01, nG1m1, G1m17 (CH1 K120 (218) (122-219), bisagra 1-15 (220-234), CH2 (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (225-215')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-47*02 (92.9%) -IGLJ2*01 (100%)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC3*03 (100%) (111'-216')]; dímero (230-230":233-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYDMSWVRQA PGKGLEWVST  50
IDLDSGSIYY ADSVQGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDL 100
HMGPEGPFDY WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
QSVLTQPPSA SGTPGQRVTI SCSGSSSNIG SNSVSWYQQL PGTAPKLLIY  50
SDNHRPSGVP DRFSGSKSGT SASLAISGLR SEDEADYYCQ GWDTSLSGHV 100
FGGGTKLTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHKSYSCQVT 200
HEGSTVEKTV APTECS                                       216
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 148-204 265-325 371-429
22"-96" 148"-204" 265"-325" 371"-429"
Intra-L (C23-C104) 22'-89' 138'-197'
22'"-89'" 138'"-197'"
Inter-H-L (h 5-CL 126) 224-215' 224"-215'"
Inter-H-H (h 11, h 14) 230-230" 233-233"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
L VL Q1:
1', 1'"

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

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

batiraxceptum #

batiraxcept

human tyrosine-protein kinase receptor UFO (AXL oncogene) fragment (8-202, 1-195 in the current sequence), variant (G^{14}>S^{7}, A^{54}>V^{47}, D^{69}>G^{62}, V^{74}>A^{67}, G^{109}>R^{102}), fused via peptidyl linker (^{196}GGGGS^{200}) to a human immunoglobulin G1 Fc fragment (201-426, C-terminal Lys residue deleted), dimer, glycosylated, produced in Chinese hamster ovary (CHO) cells;
[G^{14}>S(7), A^{54}>V(47), D^{69}>G(62), V^{74}>A(67), G^{109}>R(102)] human AXL receptor tyrosine kinase (AXL oncogene, tyrosine-protein kinase receptor UFO) (8-202)-peptide (1-195), fused via a G_4S linker (196-200) to a human immunoglobulin G1 C-terminal K>del Fc fragment (201-426), dimer (206-206':209-209')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

batiraxcept

récepteur de la tyrosine kinase-protéine UFO (oncogène AXL), fragment (8-202, 1-195 dans la séquence présente), variant (G^{14}>S^{7}, A^{54}>V^{47}, D^{69}>G^{62}, V^{74}>A^{67}, G^{109}>R^{102}), fusionné via un peptide liant (^{196}GGGGS^{200}) à un fragment Fc de l'immunoglobuline humaine G1 (201-426, résidu Lys C-terminal supprimé), dimère, glycosylé, produit par des cellules ovariennes de hamsters chinois (CHO);
[G^{14}>S(7), A^{54}>V(47), D^{69}>G(62), V^{74}>A(67), G^{109}>R(102)] tyrosine kinase du récepteur AXL humaine (oncogène AXL, récepteur de la tyrosine kinase-protéine UFO) (8-202)-peptide (1-195), fusionné via un peptide liant G_4S (196-200) au fragment Fc C-terminal K>del de l'immunoglobuline G1 humaine (201-426), dimère (206-206':209-209')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

batiraxcept

receptor de la proteína tirosina kinasa humana UFO (oncogén AXL) fragmento (8-202, 1-195 en la secuencia actual), variante (G^{14}>S^{7}, A^{54}>V^{47}, D^{69}>G^{62}, V^{74}>A^{67}, G^{109}>R^{102}), fusionado a través de un conector peptidil (^{196}GGGGS^{200}) a una inmunoglobulina humana G1 Fc fragmento (201-426, residuo Lis C-terminal eliminado), dímero, glicosilado, producido en células ováricas de hámster Chino (CHO);
[G^{14}>S(7), A^{54}>V(47), D^{69}>G(62), V^{74}>A(67), G^{109}>R(102)] AXL receptor tirosina kinasa humana (oncogén AXL, receptor de la proteína tirosina-kinasa UFO) (8-202)-péptido (1-195), fusionado a través de un péptido G_4S (196-200) con un fragmento Fc C-terminal K>del de la inmunoglobulina G1 humana (201-426), dímero (206-206':209-209')-bisdisulfuro, producido en células ováricas de hámster Chino (CHO), glicosilada alfa

Sequence / Séquence / Secuencia

```
EESPFVSNPG NITGARGLTG TLRCQLQVQG EPPEVHWLRD GQILELVDST   50
QTQVPLGEDE QGDWIVASQL RITSLQLSDT GQYQCLVFLG HQTFVSQPGY  100
VRLEGLPYFL EEPEDRTVAA NTPFNLSCQA QGPPEPVDLL WLQDAVPLAT  150
APGHGPQRSL HVPGLNKTSS FSCEAHNAKG VTTSRTATIT VLPQQGGGGS  200
DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED  250
PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK  300
CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK  350
GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  400
NVFSCSVMHE ALHNHYTQKS LSLSPG                            426
```

Post-translational modifications

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

intra-AXL	24-85	128-173	intra-Fc	241-301	347-405
	24'-85'	128'-173'		241'-301'	347'-405'
inter-Fc	206-206'	209-209'			

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación
AXL: N11, N125, N166, N11', N125', N166';
Fc: N277, N277'

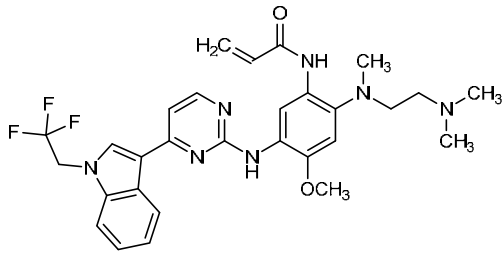
befotertinibum

befotertinib — *N*-[2-{[2-(dimethylamino)ethyl](methyl)amino}-4-methoxy-5-({4-[1-(2,2,2-trifluoroethyl)-1*H*-indol-3-yl]pyrimidin-2-yl}amino)phenyl]prop-2-enamide

béfotertinib — *N*-[2-{[2-(diméthylamino)éthyl](méthyl)amino}-4-méthoxy-5-({4-[1-(2,2,2-trifluoroéthyl)-1*H*-indol-3-yl]pyrimidin-2-yl}amino)phényl]prop-2-énamide

befotertinib — *N*-[2-{[2-(dimetilamino)etil](metil)amino}-4-metoxi-5-({4-[1-(2,2,2-trifluoroetil)-1*H*-indol-3-il]pirimidin-2-il}amino)fenil]prop-2-enamida

$C_{29}H_{32}F_3N_7O_2$



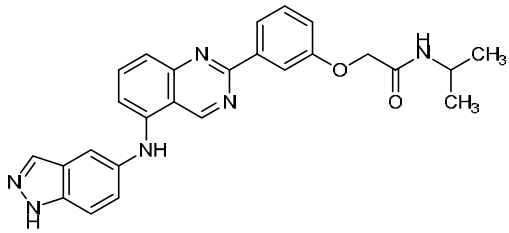
belumosudilum

belumosudil — 2-(3-{4-[(1*H*-indazol-5-yl)amino]quinazolin-2-yl}phenoxy)-*N*-(propan-2-yl)acetamide

bélumosudil — 2-(3-{4-[(1*H*-indazol-5-yl)amino]quinazolin-2-yl}phénoxy)-*N*-(propan-2-yl)acetamide

belumosudil — 2-(3-{4-[(1*H*-indazol-5-il)amino]quinazolin-2-il}fenoxi)-*N*-(propan-2-il)acetamida

$C_{26}H_{24}N_6O_2$



bentracimabum #

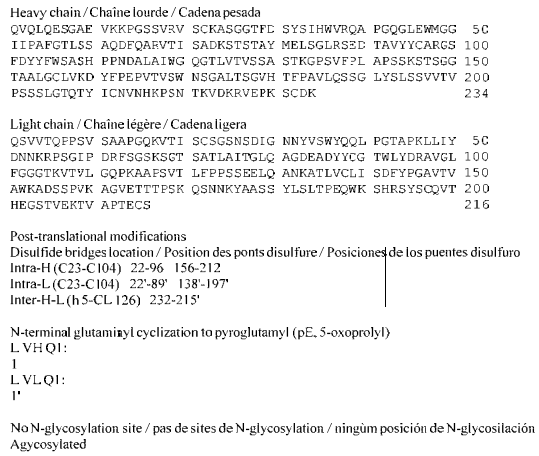
bentracimab — immunoglobulin Fab G1-lambda, anti-[*ticagrelor* and its active metabolite AR-C124910XX], *Homo sapiens* monoclonal antibody; VH-(CH1-hinge) gamma1 heavy chain *Homo sapiens* (1-234) [VH (*Homo sapiens* IGHV1-69*06 (85.7%) -(IGHD) -IGHJ1*01 (100%)) CDR-IMGT [8.7.14] (26-33.51-58.97-118) (1-129) -*Homo sapiens* IGHG1*03 (100%) G1m3 (CH1 R120 (226) (130-227), hinge 1-7 (228-234)) (130-234)], (232-215')-disulfide with lambda light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-51*01 (94.6%) -IGLJ2*01 (81.8%)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC2*01(100%) (111'-216')], non-glycosylated, produced in the bacteria *Escherichia coli* (*E. coli*)

bentracimab

immunoglobuline Fab G1-lambda, anti-[*ticagrelor* et son métabolite actif AR-C124910XX], anticorps monoclonal *Homo sapiens*;
VH-(CH1-charnière) chaîne lourde gamma1 *Homo sapiens* (1-234) [VH (*Homo sapiens* (1-234) [VH (*Homo sapiens* IGHV1-69*06 (85.7%) -(IGHD) -IGHJ1*01 (100%)) CDR-IMGT [8.7.14] (26-33.51-58.97-118) (1-129) -*Homo sapiens* IGHG1*03 (100%) G1m3 (CH1 R120 (226) (130-227), charnière 1-7 (228-234)) (130-234)], (232-215')-disulfure avec la chaîne légère lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-51*01 (94.6%) -IGLJ2*01 (81.8%)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC2*01(100%) (111'-216')], non-glycosylé, produit dans la bactérie *Escherichia coli* (*E. coli*)

bentracimab

inmunoglobulina Fab G1-lambda, anti-[*ticagrelor* y su metabolito activo AR-C124910XX], anticuerpo monoclonal *Homo sapiens*;
VH-(CH1-bisagra) cadena pesada gamma1 *Homo sapiens* (1-234) [VH (*Homo sapiens* (1-234) [VH (*Homo sapiens* IGHV1-69*06 (85.7%) -(IGHD) -IGHJ1*01 (100%)) CDR-IMGT [8.7.14] (26-33.51-58.97-118) (1-129) -*Homo sapiens* IGHG1*03 (100%) G1m3 (CH1 R120 (226) (130-227), bisagra 1-7 (228-234)) (130-234)], (232-215')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-51*01 (94.6%) -IGLJ2*01 (81.8%)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC2*01(100%) (111'-216')], no glicosilado, producido en la bacteria *Escherichia coli* (*E. coli*)



Heavy chain / Chaîne lourde / Cadena pesada
QVQLQESGAE VKKPGSSVRV SCKASGGTFD SYSIHWVRQA PGQGLEWMGG 50
IIPAFGTLSS AQDFQARVTI SADKSTSTAY MELSGLRSED TAVYYCARGS 100
FDYYFWSASH PPNDALAIWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG 150
TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV 200
PSSSLGTQTY ICNVNHKPSN TKVDKRVEPK SCDK 234

Light chain / Chaîne légère / Cadena ligera
QSVVTQPPSV SAAPGQKVTI SCSGSNSDIG NNYVSWYQQL PGTAPKLLIY 50
DNNKRPSGIP DRFSGSKSGT SATLAITGLQ AGDEADYYCG TWLYDRAVGL 100
FGGGTKVTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS 216

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 156-212
Intra-L (C23-C104) 22'-89' 138'-197'
Inter-H-L (h 5-CL 126) 232-215'

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
L VH Q1:
1
L VL Q1:
1'

No N-glycosylation site / pas de sites de N-glycosylation / ningùn posición de N-glycosilación
Agycosylated

bepirovirsenum

bepirovirsen

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

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

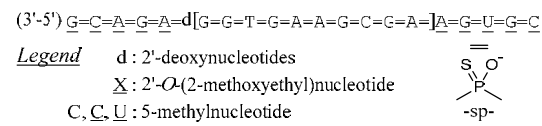
bépirovirsen

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

bepirovirsén

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

$C_{230}H_{309}N_{88}O_{115}P_{19}S_{19}$



beremagenum geperpavecum #

beremagene geperpavec

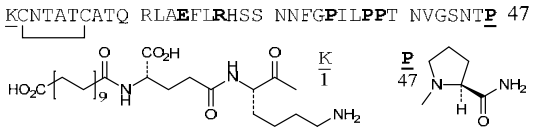
A replication-defective herpes simplex virus encoding human collagen type VII alpha 1 chain (COL7A1).

	A recombinant replication-defective, non-integrating herpes simplex virus-1 (HSV-1) (KOS strain) encoding two copies of human collagen type VII alpha 1 chain (COL7A1), inserted into the immediate early (IE) infected cell protein 4 (ICP4) gene regions after deletion of both copies of ICP4 genes, under the control of the human cytomegalovirus (hCMV) immediate early promoter and bovine growth hormone polyadenylation signal (bGHpA). The infected cell protein 22 (ICP22) gene is also deleted.
bérémagène géperpavec	Un virus herpès simplex à réplication défectueuse codant pour la chaîne du collagène humain de type VII alpha 1 (COL7A1). Un virus recombinant de l'herpès simplex-1 (HSV-1) (souche KOS), non intégrateur et à défaut de réplication, codant pour deux copies de la chaîne du collagène humain de type VII alpha 1 (COL7A1), insérées dans les régions du gène de la protéine d'infection cellulaire précoce 4 (ICP4) après délétion des deux copies des gènes ICP4, sous le contrôle du promoteur précoce immédiat du cytomégalovirus humain (hCMV) et du signal de polyadénylation de l'hormone de croissance bovine (bGHpA). Le gène de la protéine d'infection cellulaire précoce 22 (ICP22) est également supprimé.
beremagén geperpavec	Un virus herpes simplex deficiente para replicación que codifica para la cadena de colágeno humano de tipo VII alfa 1 (COL7A1). Un virus herpes simplex -1 (HSV-1) (cepa KOS) recombinante, no integrativo y deficiente en replicación, que codifica dos copias de la cadena de colágeno humano de tipo VII alfa 1 (COL7A1), insertadas en las regiones del gen de la proteína de infección celular inmediatamente temprana 4 (ICP4) tras la deleción de las dos copias de genes ICP4, bajo el control del promotor inmediatamente temprano del citomeglovirus humano (hCMV) y la señal de poliadenilación de la hormona de crecimiento bovina (bGHpA). El gen de la proteína de infección celular 22 (ICP22) está también delecionado.

cagrilintidum

cagrilintide	$N^{2.1}$-[*N*-(19-carboxynonadecanoyl)-L-γ-glutamyl]-[N^{14}>E, V^{17}>R, A^{25}>P, S^{28}>P, S^{29}>P, Y^{37}>P]-human amylin (islet amyloid polypeptide, IAPP, diabetes-associated peptide, DAP, insulinoma amyloid peptide, *INN: amlintide*), (35-40)-disulfide
cagrilintide	$N^{2.1}$-[*N*-(19-carboxynonadécanoyl)-L-γ-glutamyl]-[N^{14}>E, V^{17}>R, A^{25}>P, S^{28}>P, S^{29}>P, Y^{37}>P]-amyline humaine (polypeptide amyloïde des ilots, IAPP, peptide associé au diabète, DAP, polypeptide amyloïde de l'insulinome, *DCI: amlintide*), (35-40)-disulfure
cagrilintida	$N^{2.1}$-[*N*-(19-carboxinonadecanoil)-L-γ-glutamil]-[N^{14}>E, V^{17}>R, A^{25}>P, S^{28}>P, S^{29}>P, Y^{37}>P]-amilina humana (polipéptido amiloide de los islotes, IAPP, péptido asociado a la diabetes, DAP, polipéptido amiloide insulinoma, *DCI: amlintida*), (35-40)-disulfuro

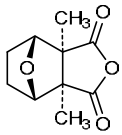
$C_{194}H_{312}N_{54}O_{59}S_2$



cantharidinum

cantharidin	(3a*R*,4*S*,7*R*,7a*S*)-3a,7a-dimethylhexahydro-4,7-epoxy-2-benzofuran-1,3-dione
cantharidine	(3a*R*,4*S*,7*R*,7a*S*)-3a,7a-diméthylhexahydro-4,7-époxy-2-benzofurane-1,3-dione
cantaridina	(3a*R*,4*S*,7*R*,7a*S*)-3a,7a-dimetilhexahidro-4,7-epoxi-2-benzofurano-1,3-diona

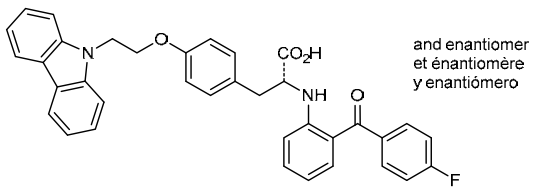
$C_{10}H_{12}O_4$



carfloglitazarum

carfloglitazar	*O*-[2-(9*H*-carbazol-9-yl)ethyl]-*N*-[2-(4-fluorobenzoyl)phenyl]-DL-tyrosine
carfloglitazar	*O*-[2-(9*H*-carbazol-9-yl)éthyl]-*N*-[2-(4-fluorobenzoyl)phényl]-DL-tyrosine
carfloglitazar	*O*-[2-(9*H*-carbazol-9-il)etil]-*N*-[2-(4-fluorobenzoil)fenil]-DL-tirosina

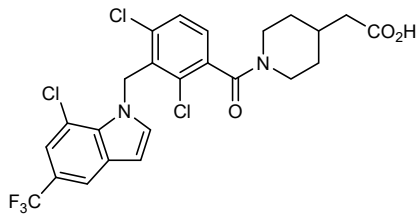
$C_{36}H_{29}FN_2O_4$



cedirogantum

cedirogant	[1-(2,4-dichloro-3-{[7-chloro-5-(trifluoromethyl)-1*H*-indol-1-yl]methyl}benzoyl)piperidin-4-yl]acetic acid
cédirogant	acide [1-(2,4-dichloro-3-{[7-chloro-5-(trifluorométhyl)-1*H*-indol-1-yl]méthyl}benzoyl)pipéridin-4-yl]acétique
cedirogant	ácido [1-(2,4-dicloro-3-{[7-cloro-5-(trifluorometil)-1*H*-indol-1-il]metil}benzoil)piperidin-4-il]acético

$C_{24}H_{20}Cl_3F_3N_2O_3$



cevaretigenum ritoparvovecum #

cevaretigene ritoparvovec

A non-replicating adeno-associated viral vector serotype 5 vector encoding human retinoid isomerohydrolase (RPE65).
A recombinant non-replicating adeno-associated viral vector serotype 5 (rAAV5), encoding codon-optimised human retinoid isomerohydrolase (retinal pigment epithelium-specific 65 kDa protein [RPE65]), under the control of the human RPE65 promoter and an SV40 poly(A) signal, flanked by AAV2 inverted terminal repeats (ITR).

cévarétigène ritoparvovec

Un vecteur adénoviral à réplication défectueuse de sérotype 5 et codant pour l'isomérohydrolase rétinoïde humaine (RPE65).
Un vecteur adénoviral recombinant à réplication défectueuse de sérotype 5 (rAAV5), codant pour une isomérohydrolase rétinoïde humaine, avec des codons optimisés (protéine de 65 kDa spécifique de l'épithélium pigmentaire rétinien [RPE65]), sous le contrôle du promoteur RPE65 humain et d'un signal SV40 poly(A), flanqué de répétitions terminales inversées (ITR) AAV2.

cevaretigén ritoparvovec

Un vector de virus adeno-asociado serotipo 5, no replicativo, que codifica para la isomerohidrolasa retinoide humana (RPE65).
Un vector de virus adeno-asociado recombinante serotipo 5, (rAAV5) no replicativo, que codifica para la isomerohidrolasa retinoide humana (proteína de 65 kDa específica del epitelio pigmentario retiniano [RPE65]) con los codones optimizados, bajo el control del promotor de RPE65 humano y una señal poly(A) de SV40, flanqueado por las repeticiones terminales invertidas (ITR) del AAV2.

cipaglucosidasum alfa #

cipaglucosidase alfa

human lysosomal α-glucosidase (acid alpha-glucosidase, acid maltase) fragment (57-952, 57-69 from the propeptide sequence), (1-896, 1-13 in the current sequence), produced in Chinese hamster ovary (CHO) cells, glycosylated;
human lysosomal α-glucosidase (acid alpha-glucosidase, GAA, acid maltase; EC 3.2.1.20) pre-pro-protein (57-952)-peptide (with 13 residues (57-69) of the propeptide (28-69)), produced in Chinese hamster ovary (CHO) cells, glycoform alfa

cipaglucosidase alfa

α-glucosidase lysosomale humaine (alpha-glucosidase acide, maltase acide) fragment (57-952, 57-69 de la séquence du propeptide), (1-896, 1-13 dans la séquence actuelle), produit dans des cellules ovariennes de hamster chinois (CHO), glycosylée; α-glucosidase lysosomale humaine (alpha-glucosidase acide, GAA, maltase acide; EC 3.2.1.20) pré-pro-protéine (57-952)-peptide (avec 13 résidus (57-69) du propeptide (28-69)), produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

cipaglucosidasa alfa

α-glucosidasa humana lisosomal (ácido alfa-glucosidasa, ácido maltasa) fragmento (57-952, 57-69 de la secuencia propétido), (1-896, 1-13 en la secuencia actual), producido en células ováricas de hámster Chino (CHO), glisosiladas;
α-glucosidasa lisosomal humana (alfa glucosidasa ácida, GAA, maltasa ácida; EC 3.2.1.20) pre-pro-proteína (57-952)-péptido, (con 13 residuos (57-69) del propéptido (28-69)), producido en las células ováricas de hámster Chino (CHO), glicosilada alfa

Sequence / Séquence / Secuencia

```
QQGASRPGPR DAQAHPGRPR AVPTQCDVPP NSRFDCAPDK AITQEQCEAR   50
GCCYIPAKQG LQGAQMGQPW CFFPPSYPSY KLENLSSSEM GYTATLTRTT  100
PTFFPKDILT LRLDVMMETE NRLHFTIKDP ANRRYEVPLE TPHVHSRAPS  150
PLYSVEFSEE PFGVIVRRQL DGRVLLNTTV APLFFADQFL QLSTSLPSQY  200
ITGLAEHLSP LMLSTSWTRI TLWNRDLAPT PGANLYGSHP FYLALEDGGS  250
AHGVFLLNSN AMDVVLQPSP ALSWRSTGGI LDVYIFLGPE PKSVVQQYLD  300
VVGYPFMPPY WGLGFHLCRW GYSSTAITRQ VVENMTRAHF PLDVQWNDLD  350
YMDSRRDFTF NKDGFRDFPA MVQELHQGGR RYMMIVDPAI SSSGPAGSYR  400
PYDEGLRRGV FITNETGQPL IGKVWPGSTA FPDFTNPTAL AWWEDMVAEF  450
HDQVPFDGMW IDMNEPSNFI RGSEDGCPNN ELENPPYVPG VVGGTLQAAT  500
ICASSHQFLS THYNLHNLYG LTEAIASHRA LVKARGTRPF VISRSTFAGH  550
GRYAGHWTGD VWSSWEQLAS SVPEILQFNL LGVPLVGADV CGFLGNTSEE  600
LCVRWTQLGA FYPFMRNHNS LLSLPQEPYS FSEPAQQAMR KALTLRYALL  650
PHLYTLFHQA HVAGETVARP LFLEFPKDSS TWTVDHQLLW GEALLITPVL  700
QAGKAEVTGY FPLGTWYDLQ TVPVEALGSL PPPPAAPREP AIHSEGQWVT  750
LPAPLDTINV HLRAGYIIPL QGPGLTTTES RQQPMALAVA LTKGGEARGE  800
LFWDDGESLE VLERGAYTQV IFLARNNTIV NELVRVTSEG AGLQLQKVTV  850
LGVATAPQQV LSNGVPVSNF TYSPDTKVLD ICVSLLMGEQ FLVSWC      896
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
26-53, 36-52, 47-71, 477-502, 591-602

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación
N84, N177, N334, N414, N596, N826, N869

cirtuvivintum

cirtuvivint

2-(4-methylpiperazin-1-yl)-*N*-[6-(1-methyl-1*H*-pyrazol-4-yl)isoquinolin-3-yl]pyridine-4-carboxamide

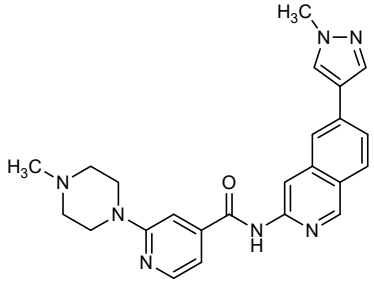
cirtuvivint

2-(4-méthylpipérazin-1-yl)-*N*-[6-(1-méthyl-1*H*-pyrazol-4-yl)isoquinoléin-3-yl]pyridine-4-carboxamide

cirtuvivint

2-(4-metilpiperazin-1-il)-*N*-[6-(1-metil-1*H*-pirazol-4-il)isoquinolein-3-il]piridina-4-carboxamida

$C_{24}H_{25}N_7O$



coprelotamabum #

coprelotamab	immunoglobulin G1-kappa, anti-[*Homo sapiens* ERBB2 (epidermal growth factor receptor 2, receptor tyrosine protein kinase erbB-2, EGFR2, HER2, HER-2, p185cerbB2, NEU, CD340)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-450) [VH humanized (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA humanized (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO)-DG44 cell line, glycoform alfa
coprélotamab	immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB2 (récepteur 2 du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-450) [VH humanisé (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA humanisé (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-DG44, glycoforme alfa
coprelotamab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor 2 del factor de crecimiento epidérmico, receptor tirosina-proteína kinasa erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-450) [VH humanizado (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA humanizado (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-DG44, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

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

Light chain / Chaîne légère / Cadena ligera

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

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

Intra-H (C23-C104)	22-96	147-203	264-324	370-428
	22"-96"	147"-203"	264"-324"	370"-428"
Intra-L (C23-C104)	23'-88'	134'-194'		
	23'"-88'"	134'"-194'"		
Inter-H-L (h 5-CL 126)	223-214'	223"-214'"		
Inter-H-H (h 11, h 14)	229-229"	232-232"		

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

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

cotoretigenum toliparvovecum

cotoretigene toliparvovec

A replication-defective adeno-associated viral vector encoding codon-optimised human retinitis pigmentosa GTPase regulator (RPGR).
A recombinant replication-defective adeno-associated viral vector serotype 8 (rAAV8) encoding codon-optimised human retinitis pigmentosa GTPase regulator (RPGR), under the control of human rhodopsin kinase (RK) promoter and bovine growth hormone poly(A) sequence, flanked by AAV2 inverted terminal repeats (ITR).

cotoretigène toliparvovec

Un vecteur adénoviral défectueux en terme de réplication et codant pour le régulateur de la GTPase de la rétinite pigmentaire humaine avec des codons optimisés (RPGR).
Un vecteur adénoviral recombinant de sérotype 8 (rAAV8) à réplication défectueuse codant pour un régulateur de la GTPase de la rétinite pigmentaire humaine (RPGR) avec des codons optimisés, sous contrôle du promoteur de la kinase de la rhodopsine humaine et de la séquence poly(A) de l'hormone de croissance bovine, flanqué de répétitions terminales inversées (ITR) de l'AAV2.

cotoretigén toliparvovec

Un vector de virus adeno-asociado, deficiente de replicación, que codifica para el regulador de la GTPasa implicado en la retinosis pigmentaria humana (RPGR) con los codones optimizados.
Un vector de virus adeno-asociado recombinante de serotipo 8 (rAAV8), deficiente de replicación, que codifica para el regulador de la GTPasa implicado en la retinosis pigmentaria humana (RPGR) con los codones optimizados, bajo el control del promotor de la rodopsin quinasa (RK) humana y la secuencia poly(A) de la hormona de crecimiento bovina, flanqueado por las repeticiones terminales invertidas (ITR) del AAV2.

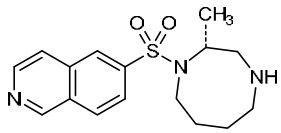
cotosudilum

cotosudil — 6-[(2*R*)-2-methyl-1,4-diazocane-1-sulfonyl]isoquinoline

cotosudil — 6-[(2*R*)-2-méthyl-1,4-diazocane-1-sulfonyl]isoquinoléine

cotosudil — 6-[(2*R*)-2-metil-1,4-diazocano-1-sulfonil]isoquinoleína

$C_{16}H_{21}N_3O_2S$



dafsolimabum #

dafsolimab — immunoglobulin G2B-kappa, anti-[CD3E (CD3 epsilon, Leu-4)], *Mus musculus* monoclonal antibody;
gamma2b heavy chain *Mus musculus* (1-456) [VH (*Mus musculus* IGHV1-4*01 (95.9%) -(IGHD) -IGHJ4*01 (94.1%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Mus musculus* IGHG2B*02 (100%) (CH1 (121-217), hinge 1-22 (218-239), CH2 (240-349), CH3 (350-454), CHS (455-456)) (121-456)], (135-213')-disulfide with kappa light chain *Mus musculus* (1'-213') [V-KAPPA (*Mus musculus* IGKV4-59*01 (100%) -IGKJ5*01 (100%)) CDR-IMGT [5.3.9] (27-31.49-51.88-96) (1'-106') -*Mus musculus* IGKC1*01 (100%) (107'-213')];
dimer (229-229":232-232":235-235":238-238")-tetrakisdisulfide, produced in SP2/0-derived mouse myeloma cells, glycoform alfa

dafsolimab — immunoglobuline G2B-kappa, anti-[CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal *Mus musculus*;
chaîne lourde gamma2b *Mus musculus* ((1-456) [VH (*Mus musculus* IGHV1-4*01 (95.9%) -(IGHD) -IGHJ4*01 (94.1%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Mus musculus* IGHG2B*02 (100%) (CH1 (121-217), charnière 1-22 (218-239), CH2 (240-349), CH3 (350-454), CHS (455-456)) (121-456)], (135-213')-disulfure avec la chaîne légère kappa *Mus musculus* (1'-213') [V-KAPPA (*Mus musculus* IGKV4-59*01 (100%) -IGKJ5*01 (100%)) CDR-IMGT [5.3.9] (27-31.49-51.88-96) (1'-106') -*Mus musculus* IGKC1*01 (100%) (107'-213')];
dimère (229-229":232-232":235-235":238-238")-tétrakisdisulfure, produit par une ligne cellulaire dérivée de myélome murin SP2/0, glycoforme alfa

dafsolimab — inmunoglobulina G2B-kappa, anti-[CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal *Mus musculus*;
cadena pesada gamma2b *Mus musculus* ((1-456) [VH (*Mus musculus* IGHV1-4*01 (95.9%) -(IGHD) -IGHJ4*01 (94.1%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Mus musculus* IGHG2B*02 (100%) (CH1 (121-217), bisagra 1-22 (218-239), CH2 (240-349), CH3 (350-454), CHS (455-456)) (121-456)], (135-213')-disulfuro con la cadena ligera kappa *Mus musculus* (1'-213') [V-KAPPA (*Mus musculus* IGKV4-59*01 (100%) -IGKJ5*01 (100%)) CDR-IMGT [5.3.9] (27-31.49-51.88-96) (1'-106') -*Mus musculus* IGKC1*01 (100%) (107'-213')];
dímero (229-229":232-232":235-235":238-238")-tetrakisdisulfuro, producido en una línea celular de mieloma murino SP2/0, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
QVQLQQSGAE LARPGASVKM SCKASGYTFT SYTMHWVKQR PGQGLEWIGY 50
INPSSGYTNY IQRFKDKATL TADKSSSTAY MQVSSLTSED SAVYYCARGS 100
RYDYYGMDYW GQGTSVTVSS AKTTPPSVYP LAPGCGDTTG SSVTLGCLVK 150
GYFPESVTVT WNSGSLSSSV HTFPALLQSG LYTMSSSVTV PSSTWPSQTV 200
TCSVAHPASS TTVDKKLEPS GPISTINPCP PCKECHKCPA PNLEGGPSVF 250
IFPPNIKDVL MISLTPKVTC VVVDVSEDDP DVQISWFVNN VEVHTAQTQT 300
HREDYNSTIR VVSTLPIQHQ DWMSGKEFKC KVNNKDLPSP IERTISKIKG 350
LVRAPQVYIL PPPAEQLSRK DVSLTCLVVG FNPGDISVEW TSNGHTEENY 400
KDTAPVLDSD GSYFIYSKLN MKTSKWEKTD SFSCNVRHEG LKNYYLKKTI 450
SRSPGK 456

Light chain / Chaîne légère / Cadena ligera
QIVLTQSPAI MSASPGEKVT MTCSASSSVS YMHWYQQKSG TSPKRWIYDT 50
SKLASGVPAR FSGSGSGTSY SLTISSMEAE DAATYYCQQW SSNPLTFGAG 100
TKLELKRADA APTVSIFPPS SEQLTSGGAS VVCFLNNFYP KDINVKWKID 150
GSERQNGVLN SWTDQDSKDS TYSMSSTLTL TKDEYERHNS YTCEATHKTS 200
TSPIVKSFNR NEC 213

Post-translational modifications
Disulfidebridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H(C23-C104) 22-96 147-202 270-330 376-434
22"-96" 147"-202" 270"-330' 376"-434"
Intra-L (C23-C104) 23'-87" 133'-193'
23"'-87"' 133"'-193"'
Inter-H-L (CH1 11-CL126) 135-213' 135"-213"'
Inter-H-H (h12, h15, h18, h21) 229-229" 232-232" 235-235" 238-238"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"
L VL Q1:
1', 1"'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
306, 306"

Fucosylated complex bi-antennary SP2/0-type glycans / glycanes de type SP2/0 bi-antennaires complexes fucosylés / glicanos de tipo SP2/0 biantenarios complejos fucosilados
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
456, 456"

dafsolimabum setaritoxum

dafsolimab setaritox — immunoglobulin G2B-kappa, anti-[CD3E (CD3 epsilon, Leu-4)], *Mus musculus* monoclonal antibody conjugated to aglycosylated ricin toxin A (RTA);
gamma2b heavy chain *Mus musculus* (1-456) [VH (*Mus musculus* IGHV1-4*01 (95.9%) -(IGHD) -IGHJ4*01 (94.1%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Mus musculus* IGHG2B*02 (100%) (CH1 (121-217), hinge 1-22 (218-239), CH2 (240-349), CH3 (350-454), CHS (455-456)) (121-456)], (135-213')-disulfide with kappa light chain *Mus musculus* (1'-213') [V-KAPPA (*Mus musculus* IGKV4-59*01 (100%) -IGKJ5*01 (100%)) CDR-IMGT [5.3.9] (27-31.49-51.88-96) (1'-106') -*Mus musculus* IGKC1*01 (100%) (107'-213')];
dimer (229-229":232-232":235-235":238-238")-tetrakisdisulfide, produced in SP2/0-derived mouse myeloma cells, glycoform alfa, substituted at N^6 of an average of 1.6 lysyl residues with 4-[(1*RS*)-1-{[L-methionyl-ricin toxin A-chain (Met-RTA, non-glycosylated, produced in *Escherichia coli*)-S^{260}-yl]sulfanyl}ethyl]benzoyl groups

dafsolimab sétaritox — immunoglobuline G2B-kappa, anti-[CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal *Mus musculus* conjugué à la toxine A de la ricine aglycosylée (RTA);
chaîne lourde gamma2b *Mus musculus* -(1-456) [VH (*Mus musculus* IGHV1-4*01 (95.9%) -(IGHD) -IGHJ4*01 (94.1%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Mus musculus* IGHG2B*02 (100%) (CH1 (121-217), charnière 1-22 (218-239), CH2 (240-349), CH3 (350-454), CHS (455-456)) (121-456)], (135-213')-disulfure avec la chaîne légère kappa *Mus musculus* (1'-213') [V-KAPPA (*Mus musculus* IGKV4-59*01 (100%) -IGKJ5*01 (100%)) CDR-IMGT [5.3.9] (27-31.49-51.88-96) (1'-106') -*Mus musculus* IGKC1*01 (100%) (107'-213')];
dimère (229-229":232-232":235-235":238-238")-tétrakisdisulfure, produit par une lignée cellulaire dérivée de myélome murin SP2/0, glycoforme alfa, substitué en N^6 sur un moyenne de 1.6 résidus lysyl par des groupes 4-[(1*RS*)-1-{[L-méthionyl-chaîne A de la toxine de ricine (Met-RTA, non-glycosylée, produite par *Escherichia coli*)-S^{260}-yl]sulfanyl}éthyl]benzoyle

dafsolimab setaritox

inmunoglobulina G2B-kappa, anti-[CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal *Mus musculus* conjugado con la toxina A de la ricina aglicosilada (RTA);
cadena pesada gamma2b *Mus musculus* -(1-456) [VH (*Mus musculus* IGHV1-4*01 (95.9%) -(IGHD) -IGHJ4*01 (94.1%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Mus musculus* IGHG2B*02 (100%) (CH1 (121-217), bisagra 1-22 (218-239), CH2 (240-349), CH3 (350-454), CHS (455-456)) (121-456)], (135-213')-disulfuro con la cadena ligera kappa *Mus musculus* (1'-213') [V-KAPPA (*Mus musculus* IGKV4-59*01 (100%) -IGKJ5*01 (100%)) CDR-IMGT [5.3.9] (27-31.49-51.88-96) (1'-106') -*Mus musculus* IGKC1*01 (100%) (107'-213')];
dímero (229-229":232-232":235-235":238-238")-tetrakisdisulfuro, producido en una línea celular de mieloma murino SP2/0, forma glicosilada alfa, sustituída en N^6 de un promedio de 1,6 residuos de lisilo con grupos de 4-[(1*RS*)-1-{[L-metionil-cadena A de toxina de ricina (Met-RTA, no glicosilada, producida por *Escherichia coli*)-S^{260}-il]sulfanil}etil]benzoilo

Heavy chain / Chaîne lourde / Cadena pesada
```
QVQLQQSGAE LARPGASVKM SCKASGYTFT SYTMHWVKQR PGQGLEWIGY  5C
INPSSGYTNY IQRFKDKATL TADKSSSTAY MQVSSLTSED SAVYYCARGS 100
RYDYYGMDYW GQGTSVTVSS AKTTPPSVYP LAPGCGDTTG SSVTLGCLVK 150
GYFPESVTVT WNSGSLSSSV HTFPALLQSG LYTMSSSVTV PSSTWPSQTV 200
TCSVAHPASS TTVDKKLEPS GPISTINPCP PCKECHKCPA PNLEGGPSVF 250
IFPPNIKDVL MISLTPKVTC VVVDVSEDDP DVQISWFVNN VEVHTAQTQT 300
HREDYNSTIR VVSTLPIQHQ DWMSGKEFKC KVNNKDLPSP IERTISKIKG 350
LVRAPQVYIL PPPAEQLSRK DVSLTCLVVG FNPGDISVEW TSNGHTEENY 400
KDTAPVLDSD GSYFIYSKLN MKTSKWEKTD SFSCNVRHEG LKNYYLKKTI 450
SRSPGK                                                  456
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Light chain / Chaîne légère / Cadena ligera
```
QIVLTQSPAI MSASPGEKVT MTCSASSSVS YMHWYQQKSG TSPKRWIYDT  5C
SKLASGVPAR FSGSGSGTSY SLTISSMEAE DAATYYCQQW SSNPLTFGAG 100
TKLELKRADA APTVSIFPPS SEQLTSGGAS VVCFLNNFYP KDINVKWKID 150
GSERQNGVLN SWTDQDSKDS TYSMSSTLTL TKDEYERHNS YTCEATHKTS 200
TSPIVKSFNR NEC                                         213
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Met-Ricin A chain / Met-chaîne A de la Ricine / Met-cadena A de la Ricina
```
MIFPKQYPII NFTTAGATVQ SYTNFIRAVR GRLTTGADVR HDIPVLPNRV  5C
GLPINQRFIL VELSNHAELS VTLALDVTNA YVVGYRAGNS AYFFHPDNQE 100
DAEAITHLFT DVQNRYTFAF GGNYDRLEQL AGNLRENIEL GNGPLEEAIS 150
ALYYYSTGGT QLPTLARSFI ICIQMISEAA RFQYIEGEMR TRIRYNRRSA 200
PDPSVITLEN SWGRLSTAIQ ESNQGAFASP IQLQRRNGSK FSVYDVSILI 250
PIIALMVYRC APPPSSQF                                    268
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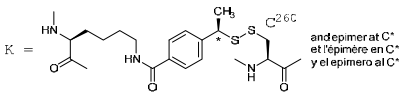
Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-202 270-330 376-434
22"-96" 147"-202" 270'-330' 376'-434"
Intra-L (C23-C104) 23'-87' 133'-193'
23"'-87"' 133"'-193"'
Inter-H-L (CH1 11-CL 126) 135-213' 135"-213"'
Inter-H-H (h 12, h 15, h 18, h 21) 229-229" 232-232" 235-235" 238-238"
Met-RTA: C172=Cys-SH,
C260=Cys-S-S-CH(CH3)-p-C6H4-CO-[N6-Lys(H,L)]

Conjugation sites / Sites de conjugaison / Posiciones de conjugación
major: K74 K141' K206'
K74" K141"' K206"'
minor: K326 K329 K349 K442 K447 K18' K52' K168'
K326" K329" K349" K442" K447" K18"' K52"' K168"'



N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
HVHQ1:
1, 1"
LVLQ1:
1', 1"'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
HCH2N84.4:
306, 306"
Fucosylated complex bi-antennary SP2/0-type glycans / glycanes de type SP2/0 bi-antennaires complexes fucosylés / glicanos de tipo SP2/0 biantenarios complejos fucosilados.

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
HCHSK2:
456, 456"

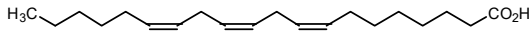
daleutonum

daleuton (8*Z*,11*Z*,14*Z*)-icosa-8,11,14-trienoic acid

daleuton acide (8*Z*,11*Z*,14*Z*)-icosa-8,11,14-triénoïque

daleutón ácido (8*Z*,11*Z*,14*Z*)-icosa-8,11,14-trienoico

$C_{20}H_{34}O_2$



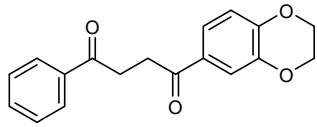
dalosirvatum

dalosirvat 1-(2,3-dihydro-1,4-benzodioxin-6-yl)-4-phenylbutane-1,4-dione

dalosirvat 1-(2,3-dihydro-1,4-benzodioxin-6-yl)-4-phénylbutane-1,4-dione

dalosirvat 1-(2,3-dihidro-1,4-benzodioxin-6-il)-4-fenilbutano-1,4-diona

$C_{18}H_{16}O_4$



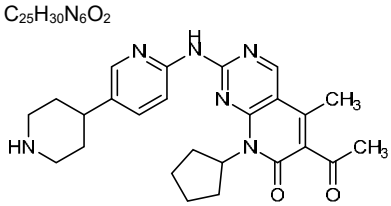
dalpiciclibum

dalpiciclib 6-acetyl-8-cyclopentyl-5-methyl-2-{[5-(piperidin-4-yl)pyridin-2-yl]amino}pyrido[2,3-*d*]pyrimidin-7(8*H*)-one

dalpiciclib 6-acétyl-8-cyclopentyl-5-méthyl-2-{[5-(pipéridin-4-yl)pyridin-2-yl]amino}pyrido[2,3-*d*]pyrimidin-7(8*H*)-one

dalpiciclib 6-acetil-8-ciclopentil-5-metil-2-{[5-(piperidin-4-il)piridin-2-il]amino}pirido[2,3-*d*]pirimidin-7(8*H*)-ona

$C_{25}H_{30}N_6O_2$

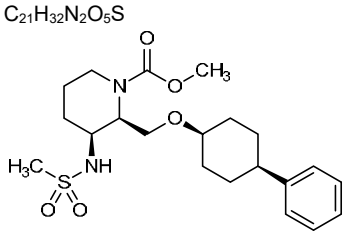


danavorextonum

danavorexton methyl (2*R*,3*S*)-3-(methanesulfonamido)-2-{[(*cis*-4-phenylcyclohexyl)oxy]methyl}piperidine-1-carboxylate

danavorexton (2*R*,3*S*)-3-(méthanesulfonamido)-2-{[(*cis*-4-phénylcyclohexyl)oxy]méthyl}pipéridine-1-carboxylate de méthyle

danavorextón (2*R*,3*S*)-2-{[(*cis*-4-fenilciclohexil)oxi]metil}-3-(metanosulfonamido)piperidina-1-carboxilato de metilo

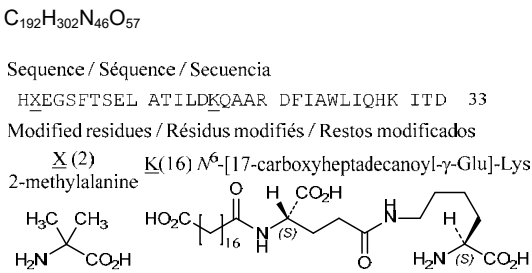


dapiglutidum

dapiglutide — human glucagon like peptide-2 (GLP-2) analogue; *N*$^{6.16}$-[*N*-(17-carboxyheptadecanoyl)-L-γ-glutamyl]-[A^{2}>Aib (2-methylalanine), D^{3}>E, S^{7}>T, D^{8}>S, M^{10}>L, N^{11}>A, N^{16}>K, L^{17}>Q, N^{24}>A, T^{29}>H]human glucagon-like peptide 2 (GLP-2)

dapiglutide — analogue du peptide 2 semblable au glucagon (GLP-2) humain; *N*$^{6.16}$-[*N*-(17-carboxyheptadécanoyl)-L-γ-glutamyl]-[A^{2}>Aib (2-méthylalanine), D^{3}>E, S^{7}>T, D^{8}>S, M^{10}>L, N^{11}>A, N^{16}>K, L^{17}>Q, N^{24}>A, T^{29}>H]peptide 2 semblable au glucagon humain (GLP-2)

dapiglutida — análogo del péptido 2 semejante al glucagón (GLP-2) humano; *N*$^{6.16}$-[*N*-(17-carboxiheptadecanoil)-L-γ-glutamil]-[A^{2}>Aib (2-metilalanina), D^{3}>E, S^{7}>T, D^{8}>S, M^{10}>L, N^{11}>A, N^{16}>K, L^{17}>Q, N^{24}>A, T^{29}>H]]péptido 2 semejante al glucagón humano (GLP-2)



daplusiranum

daplusiran — *all-P-ambo-O*-[(2*R*,3*S*)-2-(hydroxymethyl)oxolan-3-yl] hydrogen 5'-*O*-({[(2*R*,3*S*)-3-({[(*cis*-4-{(3*S*,8*S*)-17-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-3,8-bis[(2-{2-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]ethoxy}ethyl)carbamoyl]-6,11-dioxo-15-oxa-2,7,12-triazaheptadecan-1-oyl}cyclohexyl)oxy]hydroxyphosphorothioyl}oxy)oxolan-2-yl]methoxy}hydroxyphosphorothioyl)-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyl-*P*-thio-3'-uridylate duplex with *all-P-ambo*-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-deoxy-2'-fluoro-*P*-thioguanylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-*O*- methyladenylyl-

(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-deoxy-2'-fluoroguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methylcytidine

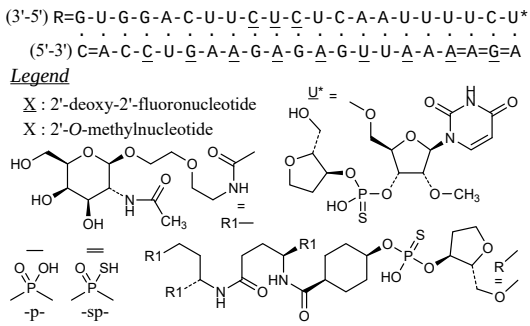
daplusiran

tout-P-ambo-5'-*O*-({[(2*R*,3*S*)-3-({[(*cis*-4-{(3*S*,8*S*)-17-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-3,8-bis[(2-{2-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]éthoxy}éthyl)carbamoyl]-6,11-dioxo-15-oxa-2,7,12-triazaheptadécan-1-oyl}cyclohexyl)oxy]hydroxyphosphorothioyl}oxy)oxolan-2-yl]méthoxy}hydroxyphosphorothioyl)-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-hydrogéno-2'-*O*-méthyl-*P*-thio-3'-uridylate de *O*-[(2*R*,3*S*)-2-(hydroxyméthyl)oxolan-3-yle]
duplex avec *tout-P-ambo*-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-désoxy-2'-fluoro-*P*-thioguanylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-désoxy-2'-fluoroguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthylcytidine

daplusirán

todo-P-ambo-5'-*O*-({[(2*R*,3*S*)-3-({[(*cis*-4-{(3*S*,8*S*)-17-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-3,8-bis[(2-{2-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]etoxi}etil)carbamoil]-6,11-dioxo-15-oxa-2,7,12-triazaheptadecan-1-oil}ciclohexil)oxi]hidroxifosforotioil}oxi)oxolan-2-il]metoxi}hidroxifosforotioil)-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-hidrógeno-2'-*O*-metil-*P*-tio-3'-uridilato de *O*-[(2*R*,3*S*)-2-(hidroximetil)oxolan-3-ilo]
duplex con *todo-P-ambo*-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-desoxi-2'-fluoro-*P*-tioguanilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-desoxi-2'-fluoroguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metilcitidina

$C_{492}H_{650}F_{12}N_{163}O_{310}P_{43}S_7$



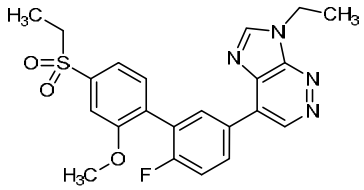
darigabatum

darigabat — 4-[4'-(ethanesulfonyl)-6-fluoro-2'-methoxy[1,1'-biphenyl]-3-yl]-7-ethyl-7*H*-imidazo[4,5-*c*]pyridazine

darigabat — 4-[4'-(éthanesulfonyl)-6-fluoro-2'-méthoxy[1,1'-biphényl]-3-yl]-7-éthyl-7*H*-imidazo[4,5-*c*]pyridazine

darigabat — 4-[4'-(etanosulfonil)-6-fluoro-2'-metoxi[1,1'-bifenil]-3-il]-7-etil-7*H*-imidazo[4,5-*c*]piridazina

$C_{22}H_{21}FN_4O_3S$



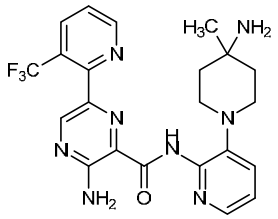
darovasertibum

darovasertib — 3-amino-*N*-[3-(4-amino-4-methylpiperidin-1-yl)pyridin-2-yl]-6-[3-(trifluoromethyl)pyridin-2-yl]pyrazine-2-carboxamide

darovasertib — 3-amino-*N*-[3-(4-amino-4-méthylpipéridin-1-yl)pyridin-2-yl]-6-[3-(trifluorométhyl)pyridin-2-yl]pyrazine-2-carboxamide

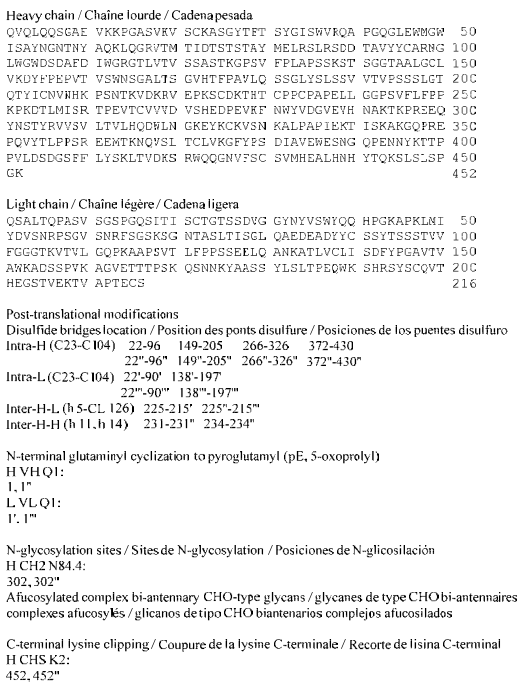
darovasertib — 3-amino-*N*-[3-(4-amino-4-metilpiperidin-1-il)piridin-2-il]-6-[3-(trifluorometil)piridin-2-il]pirazina-2-carboxamida

$C_{22}H_{23}F_3N_8O$



daxdilimabum #

daxdilimab	immunoglobulin G1-lambda, anti-[*Homo sapiens* LILRA4 (leukocyte immunoglobulin like receptor A4, ILT7, CD85g)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-18*01 (98.0%) -(IGHD) -IGHJ2*01 (92.9%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-215')-disulfide with lambda light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*01 (98.0%) -IGLJ2*01 (90.9%)) CDR-IMGT [9.3.10] (26-34.52-54.91-100) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimer (231-231'':234-234'')-bisdisulfide, produced in a Chinese hamster ovary (CHO)-derived cell line, glycoform alfa
daxdilimab	immunoglobuline G1-lambda, anti-[*Homo sapiens* LILRA4 (récepteur A4 immunoglobuline-like des leucocytes, ILT7, CD85g)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-18*01 (98.0%) -(IGHD) -IGHJ2*01 (92.9%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-215')-disulfure avec la chaîne légère lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*01 (98.0%) -IGLJ2*01 (90.9%)) CDR-IMGT [9.3.10] (26-34.52-54.91-100) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimère (231-231'':234-234'')-bisdisulfure, produite dans une lignée cellulaire dérivée des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
daxdilimab	inmunoglobulina G1-lambda, anti-[*Homo sapiens* LILRA4 (receptor A4 inmunoglobulina-like de los leucocitos, ILT7, CD85g)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-18*01 (98.0%) -(IGHD) -IGHJ2*01 (92.9%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-215')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*01 (98.0%) -IGLJ2*01 (90.9%)) CDR-IMGT [9.3.10] (26-34.52-54.91-100) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dímero (231-231'':234-234'')-bisdisulfuro, producido en una línea celular derivada de las células ováricas de hámster chino (CHO), forma glicosilada alfa



Heavy chain / Chaîne lourde / Cadena pesada
QVQLQQSGAE VKKPGASVKV SCKASGYTFT SYGISWVRQA PGQGLEWMGW 50
ISAYNGNTNY AQKLQGRVTM TIDTSTSTAY MELRSLRSDD TAVYYCARNG 100
LWGNDSDAFD IWGRGTLVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL GGPSVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE 350
PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP 450
GK 452

Light chain / Chaîne légère / Cadena ligera
QSALTQPASV SGSPGQSITI SCTGTSSDVG GYNYVSWYQQ HPGKAPKLMI 50
YDVSNRPSGV SNRFSGSKSG NTASLTISGL QAEDEADYYC SSYTSSSTVV 100
FGGGTKVTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS 216

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 149-205 266-326 372-430
22"-96" 149"-205" 266"-326" 372"-430"
Intra-L (C23-C104) 22'-90' 138'-197'
22'"-90'" 138'"-197'"
Inter-H-L (h 5-CL 126) 225-215' 225"-215'"
Inter-H-H (h 11-h 14) 231-231" 234-234"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"
L VL Q1:
1', 1'"

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CH3 K2:
452, 452"

dazodalibepum #

dazodalibep

engineered binding protein (1-85) anti-(human CD40 ligand) derived from the human tenascin third fibronectin type III domain (785-869), fused via the peptidyl linker ^{86}GGGGGGGGGGGGGGG^{100} to engineered binding protein (101-190) anti-(human CD40 ligand) derived from the human tenascin third fibronectin type III domain (780-869), fused via the peptidyl linker ^{191}GGGGGGGGGG^{200} to human albumin (201-785), variant (C^{34}>S^{234}), produced in *Escherichia coli*; [tenascin (785-869)-peptide (1-85) (containing a third fibronectin type III domain), engineered for binding to the CD40 ligand (CD40L)]-[G_{15} linker (86-100)]-[tenascin (780-869)-peptide (101-190) (containing a third fibronectin type III domain), engineered for binding to the CD40 ligand (CD40L)]-[G_{10} linker (91-100)]-[(C^{34}>S)-human serum albumin (HSA)] fusion protein, produced in *Escherichia coli*

dazodalibep

protéine de liaison mise au point (1-85) anti-(ligand de CD40 humain) dérivée du troisième domaine de la fibronectine de type III de la ténascine humaine, fusionnée via un peptide liant ^{86}GGGGGGGGGGGGGGG^{100} à la protéine de liaison mise au point (101-190) anti-(ligand de CD40 humain) dérivée du troisième domaine de la fibronectine de type III de la ténascine humaine, fusionnée via un peptide liant ^{191}GGGGGGGGGG^{200} à l'albumine humaine (201-785), variant (C^{34}>S^{234}), produite par *Escherichia coli*;
protéine de fusion de [ténascine (785-869)-peptide (1-85) (contenant un troisième domaine de fibronectine de type III), conçu pour se lier au ligand de CD40 (CD40L)]-[peptide G_{15} de liaison (86-100)]-[ténascine (780-869)-peptide (101-190) (contenant un troisième domaine de fibronectine de type III), conçu pour se lier au ligand de CD40 (CD40L)]-[peptide G_{10} de liaison (91-100)]-[(C^{34}>S)-albumine sérique humaine (ASH)], produite par *Escherichia coli*

dazodalibep

proteína de unión diseñada (1-85) anti-(ligando CD40 humano) derivada de un tercer dominio de fibronectina tipo III de tenascina humana (785-869), fusionada a través de un conector ^{86}GGGGGGGGGGGGGGG^{100} a la proteína de unión diseñada (101-190) anti-(ligando CD40 humano) derivado de un tercer dominio de fibronectina tipo III de tenascina humana (780-869), fusionado a través de un conector peptidil ^{191}GGGGGGGGGG^{200} a la albúmina humana (201-785), variante (C^{34}>S^{234}), producida en *Escherichia coli*;
proteína de fusión de [tenascina (785-869)-péptido (1-85) (que contiene un tercer dominio de fibronectina tipo III), diseñado para unirse al ligando de CD40 (CD40L)]-[péptido conector G_{15} (86-100)]-[tenascina (780-869)-péptido (101-190) (que contiene un tercer dominio de fibronectina tipo III), diseñado para unirse al ligando de CD40 (CD40L)]-[péptido conector G_{10} (91-100)]-[(C^{34}>S)-albúmina sérica humana (ASH)], producida por *Escherichia coli*

Sequence / Séquence / Secuencia

```
SQIEVKDVTD TTALITWSDD FGEYVWCELT YGIKDVPGDR TTIDLWYHHA   50
HYSIGNLKPD TEYEVSLICR SGDMSSNPAK ETFTTGGGGG GGGGGGGGGG  100
RLDAPSQIEV KDVTDTTALI TWSDDFGEYV WCELTYGIKD VPGDRTTIDL  150
WYHHAHYSIG NLKPDTEYEV SLICRSGDMS SNPAKETFTT GGGGGGGGGG  200
DAHKSEVAHR FKDLGEENFK ALVLIAFAQY LQQSPFEDHV KLVNEVTEFA  250
KTCVADESAE NCDKSLHTLF GDKLCTVATL RETYGEMADC CAKQEPERNE  300
CFLQHKDDNP NLPRLVRPEV DVMCTAFHDN EETFLKKYLY EIARRHPYFY  350
APELLFFAKR YKAAFTECCQ AADKAACLLP KLDELRDEGK ASSAKQRLKC  400
ASLQKFGERA FKAWAVARLS QRFPKAEFAE VSKLVTDLTK VHTECCHGDL  450
LECADDRADL AKYICENQDS ISSKLKECCE KPLLEKSHCI AEVENDEMPA  500
DLPSLAADFV ESKDVCKNYA EAKDVFLGMF LYEYARRHPD YSVVLLLRLA  550
KTYETTLEKC CAAADPHECY AKVFDEFKPL VEEPQNLIKQ NCELFEQLGE  600
YKFQNALLVR YTKKVPQVST PTLVEVSRNL GKVGSKCCKH PEAKRMPCAE  650
DYLSVVLNQL CVLHEKTPVS DRVTKCCTES LVNRRPCFSA LEVDETYVPK  700
EFNAETFTFH ADICTLSEKE RQIKKQTALV ELVKHKPKAT KEQLKAVMDD  750
FAAFVEKCCK ADDKETCFAE EGKKLVAASQ AALGL                   785
```

Mutations / Mutations / Mutaciones

$F^{18,123}$>S, $K^{19,124}$>D, $P^{20,125}$>D, $L^{21,126}$>F, $A^{22,127}$>G, $I^{24,129}$>Y, $D^{25,130}$>V, $G^{26,131}$>W, $I^{27,132}$>C, $T^{46,151}$>W, $E^{47,152}$>Y, $D^{48,153}$>H, $E^{49,154}$>H, $N^{50,155}$>A, $Q^{51,156}$>H, $S^{69,174}$>C, $R^{71,176}$>S, C^{234}>S

Post-translational modifications

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

27-69, 132-174, 253-262, 275-290, 291-301, 324-368, 369-377, 400-445, 446-453, 465-478, 479-489, 516-560, 561-569, 592-637, 638-648, 661-676, 677-687, 714-758, 759-767

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación

none / aucune / ninguna

depemokimabum #

depemokimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* IL5 (interleukin 5, IL-5)], humanized monoclonal antibody;
gamma1 heavy chain humanized (1-449) [VH humanized (*Homo sapiens* IGHV2-70*19 (75.8%) -(IGHD) -IGHJ4*01 (85.7%)) CDR-IMGT [8.7.13] (26-33.51-57.96-108) (1-119) -*Homo sapiens* IGHG1*03 G1m3, nG1m1, G1v21 CH2 Y15.1, T16, E18 (CH1 R120 (216) (120-217), hinge 1-15 (218-232), CH2 M15.1>Y (254), S16>T (256), T18>E (258) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-220')-disulfide with kappa light chain humanized (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (91.1%) -IGKJ2*02 (90.9%)) CDR-IMGT [12.3.9] (27-38.56-58.95-103) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (159), V101 (197) (114'-220')]; dimer (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO)-K1 cell line lacking the glutamine synthetase (GS) gene, glycoform alfa

dépémokimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* IL5 (interleukine 5, IL-5)], anticorps monoclonal humanisé;
chaîne lourde gamma1 humanisée (1-449) [VH humanisé (*Homo sapiens* IGHV2-70*19 (75.8%) -(IGHD) -IGHJ4*01 (85.7%)) CDR-IMGT [8.7.13] (26-33.51-57.96-108) (1-119) -*Homo sapiens* IGHG1*03 G1m3, nG1m1, G1v21 CH2 Y15.1, T16, E18 (CH1 R120 (216) (120-217), charnière 1-15 (218-232), CH2 M15.1>Y (254), S16>T (256), T18>E (258) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-220')-disulfure avec la chaîne légère kappa humanisée (1'-220') [V-KAPPA humanisé (*Homo sapiens* IGKV4-1*01 (91.1%) -IGKJ2*02 (90.9%)) CDR-IMGT [12.3.9] (27-38.56-58.95-103) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (159), V101 (197) (114'-220')];
dimère (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1 ne présentant pas le gène de la glutamine synthétase, glycoforme alfa

depemokimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL5 (interleukina 5, IL-5)], anticuerpo monoclonal humanizado;
cadena pesada gamma1 humanizada (1-449) [VH humanizado (*Homo sapiens* IGHV2-70*19 (75.8%) -(IGHD) -IGHJ4*01 (85.7%)) CDR-IMGT [8.7.13] (26-33.51-57.96-108) (1-119) -*Homo sapiens* IGHG1*03 G1m3, nG1m1, G1v21 CH2 Y15.1, T16, E18 (CH1 R120 (216) (120-217), bisagra 1-15 (218-232), CH2 M15.1>Y (254), S16>T (256), T18>E (258) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-220')-disulfuro con la cadena ligera kappa humanizada (1'-220') [V-KAPPA humanizado (*Homo sapiens* IGKV4-1*01 (91.1%) -IGKJ2*02 (90.9%)) CDR-IMGT [12.3.9] (27-38.56-58.95-103) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (159), V101 (197) (114'-220')];
dímero (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1 en ausencia del gen glutamina sintetasa (GS), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVTLRESGPA LVKPTQTLTL TCTVSGFSLT GSSVHWVRQP PGKGLEWLGV  50
IWASGGTDYN SALMSRLSIS KDTSRNQVVL TMTNMDPVDT ATYYCARDPP 100
SGLLRLDYWG RGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
DTLYITREPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPDS LAVSLGERAT INCKSSQSLL NSGNQKNYLA WYQQKPGQPP  50
KLLIYGASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQNVHSF 100
PFTFGGGTKL EIKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNNFYPREA 150
KVQWKVDNAL QSGNSQESVT EQDSKDSTYS LSSTLTLSKA DYEKHKVYAC 200
EVTHQGLSSP VTKSFNRGEC                                   220
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 146-202 263-323 369-427
22"-95" 146"-202" 263"-323" 369"-427"
Intra-L (C23-C104) 23'-94' 140'-200'
23'"-94'" 140'"-200'"
Inter-H-L (h 5-CL 126) 222-220' 222"-220'"
Inter-H-H (h 11, h 14) 228-228" 231-231"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
VH Q1:
1, 1"

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

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

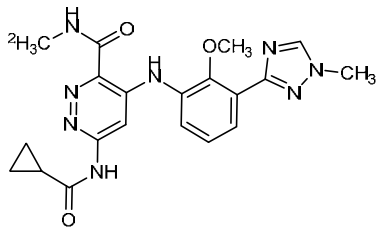
deucravacitinibum

deucravacitinib — 6-(cyclopropanecarboxamido)-4-[2-methoxy-3-(1-methyl-1*H*-1,2,4-triazol-3-yl)anilino]-*N*-($^2H_3$)methylpyridazine-3-carboxamide

deucravacitinib — 6-(ciclopropanocarboxamido)-4-[2-méthoxy-3-(1-méthyl-1*H*-1,2,4-triazol-3-yl)anilino]-*N*-($^2H_3$)méthylpyridazine-3-carboxamide

deucravacitinib — 6-(ciclopropanocarboxamido)-*N*-($^2H_3$)metil-4-[3-(1-metil-1*H*-1,2,4-triazol-3-il)-2-metoxianilino]piridazina-3-carboxamida

$C_{20}H_{19}{}^2H_3N_8O_3$



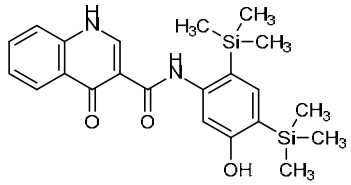
dirocaftorum

dirocaftor — *N*-[5-hydroxy-2,4-bis(trimethylsilyl)phenyl]-4-oxo-1,4-dihydroquinoline-3-carboxamide

dirocaftor — *N*-[5-hydroxy-2,4-bis(triméthylsilyl)phényl]-4-oxo-1,4-dihydroquinoléine-3-carboxamide

dirocaftor — *N*-[5-hidroxi-2,4-bis(trimetilsilil)fenil]-4-oxo-1,4-dihidroquinoleína-3-carboxamida

$C_{22}H_{28}N_2O_3Si_2$



divozilimabum #

divozilimab — immunoglobulin G1-kappa, anti-[*Homo sapiens* MS4A1 (membrane-spanning 4-domains subfamily A member 1, CD20)], monoclonal antibody;
gamma1 heavy chain (1-451) [VH (*Homo sapiens* IGHV1-46*01 (86.7%) -(IGHD) -IGHJ1*01 (86.7%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (218) (122-219), hinge 1-15 (220-234), CH2 (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-213')-disulfide with kappa light chain (1'-213') [V-KAPPA (*Mus musculus* IGKV4-72*01 (85.3%) -IGKJ1*01 (90.9%)/*Homo sapiens* IGKV3D-11*02 (73.3%) -IGKJ4*01 (100%)) CDR-IMGT [5.3.9] (27-31.49-51.88-96) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152), V101 (190) (107'-213')];
dimer (230-230'':233-233'')-bisdisulfide, produced in a Chinese hamster ovary (CHO)-S cell line, glycoform alfa

divozilimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* MS4A1 (membre 1 de la sous-famille A à 4 domaines transmembranaires, CD20)], anticorps monoclonal;
chaîne lourde gamma1 (1-451) [VH (*Homo sapiens* IGHV1-46*01 (86.7%) -(IGHD) -IGHJ1*01 (86.7%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (218) (122-219), charnière 1-15 (220-234), CH2 (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-213')-disulfure avec la chaîne légère kappa (1'-213') [V-KAPPA (*Mus musculus* IGKV4-72*01 (85.3%) -IGKJ1*01 (90.9%)/*Homo sapiens* IGKV3D-11*02 (73.3%) -IGKJ4*01 (100%)) CDR-IMGT [5.3.9] (27-31.49-51.88-96) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152), V101 (190) (107'-213')];
dimère (230-230":233-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-S, glycoforme alfa

divozilimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* MS4A1 (miembro 1 de la subfamilia A con 4 dominios transmembranarios, CD20)], anticuerpo monoclonal;
cadena pesada gamma1 (1-451) [VH (*Homo sapiens* IGHV1-46*01 (86.7%) -(IGHD) -IGHJ1*01 (86.7%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (218) (122-219), bisagra 1-15 (220-234), CH2 (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-213')-disulfuro con la cadena ligera kappa (1'-213') [V-KAPPA (*Mus musculus* IGKV4-72*01 (85.3%) -IGKJ1*01 (90.9%)/*Homo sapiens* IGKV3D-11*02 (73.3%) -IGKJ4*01 (100%)) CDR-IMGT [5.3.9] (27-31.49-51.88-96) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152), V101 (190) (107'-213')];
dímero (230-230":233-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQPGAE VVKPGASVKV SCKASGYTFT SYNMHWVRQA PGRGLEWMGA  50
IYPGNGDTSY NQKFKGRVTM TRDKSTSTVY MELSSLRSED TAVYYCARST 100
YYGGDWYFNV WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKRVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
QIVLSQSPAI LSASPGERVT LTCRASSSVS YIHWFQQKPG KAPKPLIYAT  50
SNLASGVPSR FSGSGSGTDF SLTISRVEPE DFAVYYCQQW TSNPPTFGGG 100
TKVEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC                                         213
```

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

```
Intra-H (C23-C104)   22-96    148-204    265-325    371-429
                     22"-96"  148"-204"  265"-325"  371"-429"
Intra-L (C23-C104)   23'-87'   133'-193'
                     23'"-87'" 133'"-193'"
Inter-H-L (h 5-CL 126)  224-213'  224"-213'"
Inter-H-H (h 11, h 14)  230-230"  233-233"
```

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
L VL Q1:
1', 1'"

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

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

ebronucimabum #

ebronucimab	immunoglobulin G1-lambda2, anti-[*Homo sapiens* PCSK9 (proprotein convertase subtilisin/kexin type 9, neural apoptosis-regulated convertase 1, NARC1, NARC-1, proprotein convertase 9, PC9)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV3-21*01 (91.8%) -(IGHD) - IGHJ3*01 (100%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123)-*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (220) (124-221), hinge 1-15 (222-236), CH2 (237-346), CH3 D12 (362), L14 (364) (347-451), CHS (452-453)) (124-453)], (226-216')-disulfide with lambda2 light chain *Homo sapiens* (1'-217') [V-LAMBDA (*Homo sapiens* IGLV2-11*01 (81.6%) -IGLJ1*01 (90.9%)) CDR-IMGT [9.3.11] (26-34.52-54.91-101) (1'-111') -*Homo sapiens* IGLC2*01 (100%) (112'-217')]; dimer (232-232":235-235")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
ébronucimab	immunoglobuline G1-lambda2, anti-[*Homo sapiens* PCSK9 (proprotéine convertase subtilisine/kexine type 9, convertase 1 régulée par l'apoptose neuronale, NARC1, NARC-1, proprotéine convertase 9, PC9)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV3-21*01 (91.8%) -(IGHD) - IGHJ3*01 (100%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (220) (124-221), charnière 1-15 (222-236), CH2 (237-346), CH3 D12 (362), L14 (364) (347-451), CHS (452-453)) (124-453)], (226-216')-disulfure avec la chaîne légère lambda2 *Homo sapiens* (1'-217') [V-LAMBDA (*Homo sapiens* IGLV2-11*01 (81.6%) -IGLJ1*01 (90.9%)) CDR-IMGT [9.3.11] (26-34.52-54.91-101) (1'-111') -*Homo sapiens* IGLC2*01 (100%) (112'-217')]; dimère (232-232":235-235")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
ebronucimab	inmunoglobulina G1-lambda2, anti-[*Homo sapiens* PCSK9 (proproteína convertasa subtilisina/kexina tipo 9, convertasa 1 regulada por la apoptosis neuronal, NARC1, NARC-1, proproteína convertasa 9, PC9)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV3-21*01 (91.8%) -(IGHD) - IGHJ3*01 (100%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (220) (124-221), bisagra 1-15 (222-236), CH2 (237-346), CH3 D12 (362), L14 (364) (347-451), CHS (452-453)) (124-453)], (226-216')-disulfuro con la cadena ligera lambda2 *Homo sapiens* (1'-217') [V-LAMBDA (*Homo sapiens* IGLV2-11*01 (81.6%) -IGLJ1*01 (90.9%)) CDR-IMGT [9.3.11] (26-34.52-54.91-101) (1'-111') -*Homo sapiens* IGLC2*01 (100%) (112'-217')]; dímero (232-232":235-235")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGRSLRL SCAASGFTFS SYSMNWVRQA PGKGLEWVSG  5C
ISSSSSYISY ADSVQGRFTI SRDNGKNSLY LQMNSLRAED TALYFCAREY 100
DFWSAYYDAF DVWGQGTMVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP 250
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR 350
EPQVYTLPPS RDELTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS 450
PGK                                                     453
```

Light chain / Chaîne légère / Cadena ligera

```
QSELTQPRSV SGSPGQSVTI SCTGTSRNIG GGNDVHWYQQ HPGKAPKLLI  5C
SGVIERSSGV PDRFSGSKSG NTASLTISGL QAEDEADYYC QSFDGSLSGS 100
VFGTGTDVTV LGQPKAAPSV TLFPPSSEEL QANKATLVCL ISDFYPGAVT 150
VAWKADSSPV KAGVETTTPS KQSNNKYAAS SYLSLTPEQW KSHRSYSCQV 200
THEGSTVEKT VAPTECS                                      217
```

Post-translational modifications

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

```
Intra-H (C23-C104)  22-96    150-206    267-327    373-431
                    22"-96"  150"-206"  267"-327"  373"-431"
Intra-L (C23-C104)  22'-90'    139'-198'
                    22'"-90'"  139'"-198'"
Inter-H-L (h5-CL 126)  226-216'  226"-216"
Inter-H-H (h11, h14)   232-232"  235-235"
```

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)

```
L VLQ1:
1', 1'"
```

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

```
H CH2 N84.4:
303, 303"
```

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

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

```
H CHSK2:
453, 453"
```

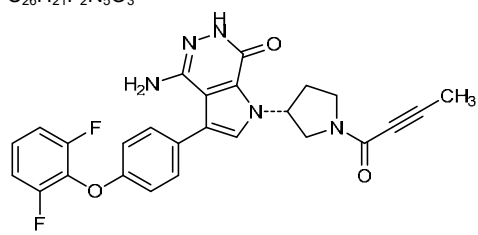
edralbrutinibum

edralbrutinib — 4-amino-1-[(3*R*)-1-(but-2-ynoyl)pyrrolidin-3-yl]-3-[4-(2,6-difluorophenoxy)phenyl]-1,6-dihydro-7*H*-pyrrolo[2,3-*d*]pyridazin-7-one

édralbrutinib — 4-amino-1-[(3*R*)-1-(but-2-ynoyl)pyrrolidin-3-yl]-3-[4-(2,6-difluorophénoxy)phényl]-1,6-dihydro-7*H*-pyrrolo[2,3-*d*]pyridazin-7-one

edralbrutinib — 4-amino-1-[(3*R*)-1-(but-2-inoil)pirrolidin-3-il]-3-[4-(2,6-difluorofenoxi)fenil]-1,6-dihidro-7*H*-pirrolo[2,3-*d*]piridazin-7-ona

$C_{26}H_{21}F_2N_5O_3$



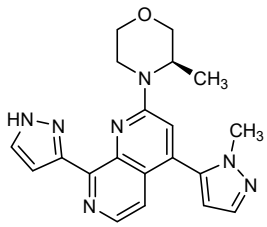
elimusertibum

elimusertib — 2-[(3*R*)-3-methylmorpholin-4-yl]-4-(1-methyl-1*H*-pyrazol-5-yl)-8-(1*H*-pyrazol-3-yl)-1,7-naphthyridine

élimusertib — 2-[(3*R*)-3-méthylmorpholin-4-yl]-4-(1-méthyl-1*H*-pyrazol-5-yl)-8-(1*H*-pyrazol-3-yl)-1,7-naphtyridine

elimusertib — 2-[(3*R*)-3-metilmorfolin-4-il]-4-(1-metil-1*H*-pirazol-5-il)-8-(1*H*-pirazol-3-il)-1,7-naftiridina

$C_{20}H_{21}N_7O$



eluvixtamabum #

eluvixtamab — immunoglobulin scFv-scFv, anti-[*Homo sapiens* CD33 (sialic acid binding Ig-like lectin 3, SIGLEC3, SIGLEC-3, gp67, p67)] and anti-[*Homo sapiens* CD3E (CD3 epsilon)], monoclonal antibody single chain, bispecific;
IG scFv-scFv single chain, anti-CD33 and anti-CD3E (1-511) [scFv-VH-V-kappa anti-CD33 (1-250) [VH (*Homo sapiens* IGHV1-18*01 (82.7%) -(IGHD) -IGHJ4*01 (93.3%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122)-15-mer tris(tetraglycyl-seryl) linker (123-137) -V-KAPPA (*Homo sapiens* IGKV4-1*01 (83.2%) -IGKJ5*01 (100%)) CDR-IMGT [12.3.9] (164-175.193-195.232-240) (138-250)] -6-mer seryl-tetraglycyl-seryl linker (251-256) -scFv-VH-V-lambda anti-CD3E (257-505) [VH (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD)-IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (282-289.307-316.355-370) (257-381) -15-mer tris(tetraglycyl-seryl) linker (382-396) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (422-430.448-450.487-495) (397-505)] -hexahistidine (506-511)], non-glycosylated, produced in Chinese hamster ovary (CHO) cells

éluvixtamab — immunoglobuline scFv-scFv, anti-[*Homo sapiens* CD33 (lectine 3 de type Ig-like liant l'acide sialique, SIGLEC3, SIGLEC-3, gp67, p67)] et anti-[*Homo sapiens* CD3E (CD3 epsilon)], anticorps monoclonal à chaîne unique, bispécifique;
IG scFv-scFv à chaîne unique, anti-CD33 et anti-CD3E (1-511) [scFv-VH-V-kappa anti-CD33 (1-250) [VH (*Homo sapiens* IGHV1-18*01 (82.7%) -(IGHD) -IGHJ4*01 (93.3%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122)-15-mer tris(tétraglycyl-séryl) linker (123-137) -V-KAPPA (*Homo sapiens* IGKV4-1*01 (83.2%) -IGKJ5*01 (100%)) CDR-IMGT [12.3.9] (164-175.193-195.232-240) (138-250)] -6-mer séryl-tétraglycyl-séryl linker (251-256) -scFv-VH-V-lambda anti-CD3E (257-505) [VH (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD)-IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (282-289.307-316.355-370) (257-381) -15-mer tris(tétraglycyl-séryl) linker (382-396) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%) CDR-IMGT [9.3.9] (422-430.448-450.487-495) (397-505)] -hexahistidine (506-511)], non-glycosylé, produit dans des cellules ovariennes de hamster chinois (CHO)

eluvixtamab — inmunoglobulina scFv-scFv, anti-[*Homo sapiens* CD33 (lectina 3 de tipo Ig-like aglutinando el ácido siálico, SIGLEC3, SIGLEC-3, gp67, p67)] y anti-[*Homo sapiens* CD3E (CD3 épsilon)], anticuerpo monoclonal con cadena única, biespecífico;

IG scFv-scFv con cadena única, anti-CD33 y anti-CD3E (1-511) [scFv-VH-V-kappa anti-CD33 (1-250) [VH (*Homo sapiens* IGHV1-18*01 (82.7%) -(IGHD) -IGHJ4*01 (93.3%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122)-15-mer tris(tetraglicil-seril) linker (123-137) -V-KAPPA (*Homo sapiens* IGKV4-1*01 (83.2%) -IGKJ5*01 (100%)) CDR-IMGT [12.3.9] (164-175.193-195.232-240) (138-250)] -6-mer seril-tetraglicil-seril linker (251-256) -scFv-VH-V-lambda anti-CD3E (257-505) [VH (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD)-IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (282-289.307-316.355-370) (257-381) -15-mer tris(tetraglicil-seril) linker (382-396) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%) CDR-IMGT [9.3.9] (422-430.448-450.487-495) (397-505)] -hexahistidina (506-511)], no glicosilado, producido en las células ováricas de hamster chino (CHO)

```
Heavy chain / Chaîne lourde / Cadena pesada
QVQLVQSGAE VKKPGESVKV SCKASGYTFT NYGMNWVXQA PGQGLEWMGW  50
INTYTGEPTY ADKFQGRVTM TTDTSTSTAY MEIRNLGGDD TAVYYCARWS 100
WSDGYYVYFD YWGQGTSVTV SSGGGGSGGG GSGGGGSDIV MTQSPDSLTV 150
SLGERTTINC KSSQSVLDSS TNKNSLAWYQ QKPGQPPKLL LSWASTRESG 200
IPDRFSGSGS GTDFTLTIDS PQPEDSATYY CQQSAHFPIT FGQGTRLEIK 250
SGGGGSEVQL VESGGGLVQP GGSLKLSCAA SGFTFNKYAM NWVRQAPGKG 300
LEWVARIRSK YNNYATYYAD SVKDRFTISR DDSKNTAYLQ MNNLKTEDTA 350
VYYCVRHGNF GNSYISYWAY WGQGTLVTVS SGGGGSGGGG SGGGGSQTVV 400
TQEPSLTVSP GGTVTLTCGS STGAVTSGNY PNWVQQKPGQ APRGLIGGTK 450
FLAPGTPARF SGSLLGGKAA LTLSGVQPED EAEYYCVLWY SNRWVFGGGT 500
KLTVLHHHHH H                                           511

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-V (C23 C104)  22-96  160-231  278-354  418-486

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
VH Q1: 1

No N-glycosylation sites / pas de sites de N-glycosylation / ningún posición de N-glycosilación
Aglycosylated
```

emerfetamabum #
emerfetamab

immunoglobulin scFv-scFv-scFc, anti-[*Homo sapiens* CD33 (sialic acid binding Ig-like lectin 3, SIGLEC3, SIGLEC-3, gp67, p67)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], monoclonal antibody single chain (scFv)2-scFc, bispecific;
IG scFv-scFv-scFc single chain, anti-CD33 and anti-CD3E (1-993) [scFv-VH-V-kappa anti-CD33 (1-250) [VH (*Homo sapiens* IGHV1-18*01 G49>C (44) (81.6%) -(IGHD) -IGHJ4*01 (93.3%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122) -15-mer tris(tetraglycyl-seryl) linker (123-137) -V-KAPPA (*Homo sapiens* IGKV4-1*01 (83.2%) -IGKJ5*01 Q120>C (243) (91.7%)) CDR-IMGT [12.3.9] (164-175.193-195.232-240) (138-250)] -6-mer seryl-tetraglycyl-seryl linker (251-256) -scFv-VH-V-lambda anti-CD3E (257-505) [VH (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (282-289.307-316.355-370) (257-381) -15-mer tris(tetraglycyl-seryl) linker (382-396) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (422-430.448-450.487-495) (397-505)] -4-mer tetraglycyl linker (506-509) -scFc (h-CH2-CH3)-(h-CH2-CH3) (510-993) [*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (hinge 6-15 (510-519), CH2 R83>C (581), N84.4>G (586), V85>C (591) (520-629), CH3 E12 (645), M14 (647) (630-734), CHS (735-736)) (510-736) -30-mer hexakis(tetraglycyl-seryl) linker (737-766) -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (hinge 6-15 (767-776), CH2 R83>C (838), N84.4>G (843), V85>C (848) (777-886), CH3 E12 (902), M14 (904) (887-991), CHS (992-993)) (767-993)]], non-glycosylated, produced in Chinese hamster ovary (CHO) cells

émerfétamab

immunoglobuline scFv-scFv-scFc, anti-[*Homo sapiens* CD33 (lectine 3 de type Ig-like liant l'acide sialique, SIGLEC3, SIGLEC-3, gp67, p67)], et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal à chaîne unique (scFv)2-scFc, bispécifique;
IG scFv-scFv-scFc chaîne unique, anti-CD33 et anti-CD3E (1-993) [scFv-VH-V-kappa anti-CD33 (1-250) [VH (*Homo sapiens* IGHV1-18*01 G49>C (44) (81.6%) -(IGHD) -IGHJ4*01 (93.3%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122) -15-mer-tris(tétraglycyl-séryl) linker (123-137) -V-KAPPA (*Homo sapiens* IGKV4-1*01 (83.2%) -IGKJ5*01 Q120>C (243) (91.7%)) CDR-IMGT [12.3.9] (164-175.193-195.232-240) (138-250)] -6-mer séryl-tétraglycyl-séryl linker (251-256) -scFv-VH-V-lambda anti-CD3E (257-505) [VH (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (282-289.307-316.355-370) (257-381) -15-mer tris(tétraglycyl-séryl) linker (382-396) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (422-430.448-450.487-495) (397-505)] -4-mer-tétraglycyl linker (506-509) -scFc (h-CH2-CH3)-(h-CH2-CH3) (510-993) [*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (charnière 6-15 (510-519), CH2 R83>C (581), N84.4>G (586), V85>C (591) (520-629), CH3 E12 (645), M14 (647) (630-734), CHS (735-736)) (510-736) -30-mer hexakis(tétraglycyl-séryl) linker (737-766) -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (charnière 6-15 (767-776), CH2 R83>C (838), N84.4>G (843), V85>C (848) (777-886), CH3 E12 (902), M14 (904) (887-991), CHS (992-993)) (767-993)]], non-glycosylé, produit dans des cellules ovariennes de hamster chinois (CHO)

emerfetamab

inmunoglobulina scFv-scFv-scFc, anti-[*Homo sapiens* CD33 (lectina 3 de tipo Ig-like aglutinando el ácido siálico, SIGLEC3, SIGLEC-3, gp67, p67)], y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal con cadena única (scFv)2-scFc, biespecífico;
IG scFv-scFv-scFc cadena única, anti-CD33 y anti-CD3E (1-993) [scFv-VH-V-kappa anti-CD33 (1-250) [VH (*Homo sapiens* IGHV1-18*01 G49>C (44) (81.6%) -(IGHD) -IGHJ4*01 (93.3%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122) -15-mer-tris(tetraglicil-seril) linker (123-137) -V-KAPPA (*Homo sapiens* IGKV4-1*01 (83.2%) -IGKJ5*01 Q120>C (243) (91.7%)) CDR-IMGT [12.3.9] (164-175.193-195.232-240) (138-250)] -6-mer seril-tetraglicil-seril linker (251-256) -scFv-VH-V-lambda anti-CD3E (257-505) [VH (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (282-289.307-316.355-370) (257-381) -15-mer tris(tetraglicil-seril) linker (382-396) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (422-430.448-450.487-495) (397-505)] -4-mer-tetraglicil linker (506-509) -scFc (h-CH2-CH3)-(h-CH2-CH3) (510-993) [*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (bisagra 6-15 (510-519), CH2 R83>C (581), N84.4>G (586), V85>C (591) (520-629), CH3 E12 (645), M14 (647) (630-734), CHS (735-736)) (510-736) -30-mer hexakis(tetraglicil-seril) linker (737-766) -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (bisagra 6-15 (767-776), CH2 R83>C (838), N84.4>G (843), V85>C (848) (777-886), CH3 E12 (902), M14 (904) (887-991), CHS (992-993)) (767-993)]], no glicosilado, producido en las células ováricas de hamster chino (CHO)

Heavy chain / Chaîne lourde / Cadena pesada

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QVQLVQSGAE VKKPGESVKV SCKASGYTFT NYGMNWVKQA PGQCLEWMGW  50
INTYTGEPTY ADKFQGRVTM TTDTSTSTAY MEIRNLGGDD TAVYYCARWS 100
WSDGYYVYFD YWGQGTSVTV SSGGGGSGGG GSGGGGSDIV MTQSPDSLTV 150
SLGERTTINC KSSQSVLDSS TNKNSLAWYQ QKPGQPPKLL LSWASTRESG 200
IPDRFSGSGS GTDFTLTIDS PQPEDSATYY CQQSAHFPIT FGCGTRLEIK 250
SGGGGSEVQL VESGGGLVQP GGSLKLSCAA SGFTFNKYAM NWVRQAPGKG 300
LEWVARIRSK YNNYATYYAD SVKDRFTISR DDSKNTAYLQ MNNLKTEDTA 350
VYYCVRHGNF GNSYISYWAY WGQGTLVTVS SGGGGSGGGG SGGGGSQTVV 400
TQEPSLTVSP GGTVTLTCGS STGAVTSGNY PNWVQQKPGQ APRGLIGGTK 450
FLAPGTPARF SGSLLGGKAA LTLSGVQPED EAEYYCVLWY SNRWVFGGGT 500
KLTVLGGGGD KTHTCPPCPA PELLGGPSVF LFPPKPKDTL MISRTPEVTC 550
VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP CEEQYGSTYR CVSVLTVLHQ 600
DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL PPSREEMTKN 650
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSKLT 700
VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGKGGGG SGGGGSGGGG 750
SGGGGSGGGG SGGGGSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS 800
RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPCEE QYGSTYRCVS 850
VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR EPQVYTLPPS 900
REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF 950
FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS PGK        993
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-V (C23-C104)	22-96	160-231	278-354	418-486	
Intra-C (C23-C104)	550-610	656-714	807-867	913-971	
Intra-CH2 (C83-C85)	581-591	838-848			
Inter-VH-VL (C49-C120)	44-243				
Inter-h11 (h11-h11)	515-772				
Inter-h14 (h14-h14)	518-775				

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
VH Q1:
1

No N-glycosylation sites / pas de sites de N-glycosylation / ningún posición de N-glicosilación
CH2 N84.4>G:
586, 843
Aglycosylated

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
CHS K2:
993

enibarcimabum

enibarcimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* ADM (adrenomedullin)], monoclonal antibody; gamma1 heavy chain (1-448) [VH (*Homo sapiens* IGHV1-69*01 (86.5%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (215) (119-216), hinge 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-219')-disulfide with kappa light chain (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (88.0%) -IGKJ2*01 (100%)/*Homo sapiens* IGKV2-30*01 (88.0%) -IGKJ2*01 (91.7%)) CDR-IMGT [11.3.9] (27-37.55-57.94-102) (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (227-227'':230-230'')-bisdisulfide, produced in Chinese hamster ovary (CHO)-DG44 cell line, glycoform alfa
énibarcimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* ADM (adrénomédulline)], anticorps monoclonal; chaîne lourde gamma1 (1-448) [VH (*Homo sapiens* IGHV1-69*01 (86.5%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (215) (119-216), charnière 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-219')-disulfure avec la chaîne légère kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (88.0%) -IGKJ2*01 (100%)/*Homo sapiens* IGKV2-30*01 (88.0%) -IGKJ2*01 (91.7%)) CDR-IMGT [11.3.9] (27-37.55-57.94-102) (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (227-227'':230-230'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-DG44, glycoforme alfa

enibarcimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* ADM (adrenomedulina)], anticuerpo monoclonal;
cadena pesada gamma1 (1-448) [VH (*Homo sapiens* IGHV1-69*01 (86.5%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (215) (119-216), bisagra 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-219')-disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (88.0%) -IGKJ2*01 (100%)/*Homo sapiens* IGKV2-30*01 (88.0%) -IGKJ2*01 (91.7%)) CDR-IMGT [11.3.9] (27-37.55-57.94-102) (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')];
dímero (227-227'':230-230'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-DG44, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

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QVQLVQSGAE VKKPGSSVKV SCKASGYTFS RYWIEWVRQA PGQGLEWIGE  50
ILPGSGSTNY NQKFQGRVTI TADTSTSTAY MELSSLRSED TAVYYCTEGY 100
EYDGFDYWGQ GTTVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
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Light chain / Chaîne légère / Cadena ligera

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DVVLTQSPLS LPVTLGQPAS ISCRSSQSIV YSNGNTYLEW YLQRPGQSPR  50
LLIYRVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCFQGSHIP 100
YTFGGGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 145-201 262-322 368-426
22''-96'' 145''-201'' 262''-322'' 368''-426''
Intra-L (C23-C104) 23'-93' 139'-199'
23'''-93''' 139'''-199'''
Inter-H-L (h 5-CL 126) 221-219' 221''-219'''
Inter-H-H (h 11, h 14) 227-227'' 230-230''

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1''

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

enomimeranum #

enomimeran

Messenger RNA encoding melanoma-associated antigen 3 (MAGE-A3).
Messenger RNA (mRNA), 5'-capped, encoding codon-optimised melanoma-associated antigen 3 (MAGE-A3, cancer/testis antigen 1.3) expressed as a fusion protein comprising a secretory signal peptide, MAGE-A3, P2P16 tetanus toxoid-derived helper epitopes and a major histocompatibility complex (MHC) class I transmembrane and cytoplasmic domain (MITD), connected by three glycine/serine-rich (GS) linker peptides, flanked by 5' and 3' untranslated regions and a 3' poly(A) tail.

énomiméran

ARN messager codant pour l'antigène 3 associé au mélanome (MAGE-A3).

	Un ARN messager (ARNm), protégé en 5', codant pour l'antigène 3 associé au mélanome (MAGE-A3, antigène 1.3 du cancer testiculaire) , avec des codons optimisés, exprimé sous la forme d'une protéine de fusion comprenant un peptide signal de sécrétion, MAGE-A3, les épitopes auxiliaires P2P16 dérivés de l'anatoxine tétanique et un domaine transmembranaire et cytoplasmique (MITD) du complexe majeur d'histocompatibilité (CMH) de classe I, reliés par trois peptides de liaison riches en glycine/sérine (GS), flanqués de régions non traduites en 5' et 3' et d'une queue poly(A) en 3'.
enomimerán	ARN mensajero que codifica para el antígeno asociado a melanoma 3 (MAGE-A3). ARN mensajero (ARNm), protegido en 5', que codifica para el antígeno asociado a melanoma 3 (MAGE-A3, antígeno de cáncer/testículo 1.3), con codones optimizados, expresado como una proteína de fusión que consta de un péptido señal de secreción, MAGE-A3, los epítopos auxiliares P2P16 derivados del toxoide tetánico y un dominio citoplásmico y transmembrana del complejo principal de histocompatibilidad (MHC) de clase I, conectados mediante tres péptidos de enlace ricos en glicina/serina (GS), flanqueado por las regiones 5' y 3' no traducidas y una cola poly(A) en 3'.

entacingenum turiparvovecum #

entacingene turiparvovec	A replication-defective adeno-associated viral vector encoding cone photoreceptor cyclic nucleotide-gated channel β3 (CNGB3). A recombinant non-replicating adeno-associated viral vector serotype 8 (rAAV8), encoding codon-optimised human cone photoreceptor cyclic nucleotide gated channel β3 (CNGB3), under the control of the human cone arrestin (hCAR) promoter and an SV40 poly(A) sequence, flanked by AAV2 inverted terminal repeats (ITR).
entacingène turiparvovec	Un vecteur adénoviral à réplication défectueuse codant pour le canal du photorécepteur conique β3 (CNGB3), dépendant des nucléotides cycliques. Un vecteur adénoviral recombinant non réplicatif de sérotype 8 (rAAV8), codant pour le canal du photorécepteur du cône humain β3 (CNGB3), dépendant des nucléotides cycliques, avec des codons optimisés, sous le contrôle du promoteur hCAR (arrestine du cône humain) et d'une séquence poly(A) SV40, flanquée de répétitions terminales inversées (ITR) AAV2.
entacingén turiparvovec	Un vector de virus adeno-asociado, deficiente de replicación, que codifica para el canal β3 regulado por nucleótidos cíclicos (CNGB3) del fotorreceptor de los conos. Un vector de virus adeno-asociado recombinante serotipo 8 (rAAV8), deficiente de replicación, que codifica para el canal β3 regulado por nucleótidos cíclicos (CNGB3) del fotorreceptor de los conos, con codones optimizados, bajo el control del promotor de la arrestina de cono humana (hCAR) y una secuencia poly(A) de SV40, flanqueado por las repeticiones invertidas terminales (ITR) del AAV2.

eplontersenum

eplontersen

all-P-ambo-5'-*O*-(28-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-16,16-bis{[3-({6-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]hexyl}amino)-3-oxopropoxy]methyl}-1-hydroxy-1,10,14,21-tetraoxo-2,18-dioxa-9,15,22-triaza-1λ^5-phosphaoctacosan-1-yl)-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyluridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyluridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)guanylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)adenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyluridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidine

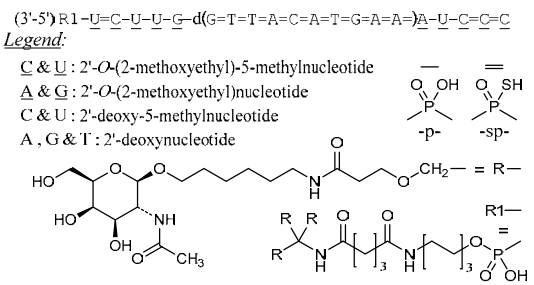
éplontersen

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

eplontersén

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

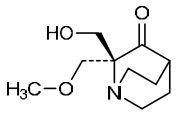
$C_{296}H_{437}N_{77}O_{156}P_{20}S_{13}$



eprenetapoptum

eprenetapopt	*rac*-(2*R*)-2-(hydroxymethyl)-2-(methoxymethyl)-1-azabicyclo[2.2.2]octan-3-one
éprénétapopt	*rac*-(2*R*)-2-(hydroxyméthyl)-2-(méthoxyméthyl)-1-azabicyclo[2.2.2]octan-3-one
eprenetapopt	*rac*-(2*R*)-2-(hidroximetil)-2-(metoximetil)-1-azabiciclo[2.2.2]octan-3-ona

$C_{10}H_{17}NO_3$



and enantiomer
et énantiomère
y enantiómero

etevritamabum #

etevritamab	immunoglobulin scFv-scFv, anti-[*Homo sapiens* EGFR (epidermal growth factor receptor, receptor tyrosine-protein kinase erbB-1, ERBB1, HER1, HER-1, ERBB) variant III (EGFRvIII)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], monoclonal antibody single chain, bispecific; IG scFv-scFv single chain (1-512) [scFv-VH-V-kappa anti-EGFRvIII(1-251) [VH (*Homo sapiens* IGHV3-33*01 G49>C (44) (93.9%) -IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.17] (26-33.51-58.97-113) (1-124) -15-mer tris(tetraglycyl-seryl) linker (125-139) -V-KAPPA (*Homo sapiens* IGKV2-24*01 (92.0%) -IGKJ1*01 Q120>C (244) (90.9%)) CDR-IMGT [11.3.9] (166-176.194-196.233-241) (140-251)] -6-mer seryl-tetraglycyl-seryl linker (252-257) -scFv-VH-V-lambda anti-CD3E (258-506) [VH (*Mus musculus* IGHV10-1*02 (91.9%)-(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87.0%)-(IGHD) -IGHJ5*01 (100%)) [8.10.16] (258-382) - 15-mer tris(tetraglycyl-seryl) linker (383-397) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%) CDR-IMGT [9.3.9] (423-431.449-451.488-496) (398-506)] -hexahistidine (507-512)], non-glycosylated, produced in Chinese hamster ovary (CHO) cells

étévritamab

immunoglobuline scFv-scFv, anti-[*Homo sapiens* EGFR (récepteur du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erb-1, ERBB1, HER1, HER-1, ERBB) variant III (EGFRvIII)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal à chaîne unique, bispécifique;
IG scFv-scFv chaîne unique (1-512) [scFv-VH-V-kappa anti-EGFRvIII(1-251) [VH (*Homo sapiens* IGHV3-33*01 G49>C (44) (93.9%) -IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.17] (26-33.51-58.97-113) (1-124) -15-mer tris(tétraglycyl-séryl) linker (125-139) – V-KAPPA (*Homo sapiens* IGKV2-24*01 (92.0%) -IGKJ1*01 Q120>C (244) (90.9%)) CDR-IMGT [11.3.9] (166-176.194-196.233-241) (140-251)] -6-mer séryl-tétraglycyl-séryl linker (252-257) -scFv-VH-V-lambda anti-CD3E (258-506) [VH (*Mus musculus* IGHV10-1*02 (91.9%)-(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87.0%)-(IGHD) -IGHJ5*01 (100%)) [8.10.16] (258-382) -15-mer tris(tétraglycyl-séryl) linker (383-397) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%) CDR-IMGT [9.3.9] (423-431.449-451.488-496) (398-506)] -hexahistidine (507-512)], non-glycosylé, produit dans des cellules ovariennes de hamsters chinois (CHO)

etevritamab

inmunoglobulina scFv-scFv, anti-[*Homo sapiens* EGFR (receptor del factor de crecimiento epidérmico, receptor tirosina-proteína kinasa erb-1, ERBB1, HER1, HER-1, ERBB) variante III (EGFRvIII)] y anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticuerpo monoclonal de cadena única, biespecífico;
IG scFv-scFv cadena única (1-512) [scFv-VH-V-kappa anti-EGFRvIII(1-251) [VH (*Homo sapiens* IGHV3-33*01 G49>C (44) (93.9%) -IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.17] (26-33.51-58.97-113) (1-124) -15-mer tris(tetraglicil-seril) linker (125-139) – V-KAPPA (*Homo sapiens* IGKV2-24*01 (92.0%) -IGKJ1*01 Q120>C (244) (90.9%)) CDR-IMGT [11.3.9] (166-176.194-196.233-241) (140-251)] -6-mer seril-tetraglicil-seril linker (252-257) -scFv-VH-V-lambda anti-CD3E (258-506) [VH (*Mus musculus* IGHV10-1*02 (91.9%)-(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87.0%)-(IGHD) -IGHJ5*01 (100%)) [8.10.16] (258-382) -15-mer tris(tetraglicil-seril) linker (383-397) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%) CDR-IMGT [9.3.9] (423-431.449-451.488-496) (398-506)] -hexahistidina (507-512)], no glicosilado, producido en las células ováricas de hámster chino (CHO)

Sequence / Séquence / Secuencia

```
QVQLVESGGG VVQSGRSLRL SCAASGFTFR NYGMHWVRQA PGKCLEWVAV  50
IWYDGSDKYY ADSVRGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARDG 100
YDILTGNPRD FDYWGQGTLV TVSSGGGGSG GGGSGGGGSD TVMTQTPLSS 150
HVTLGQPASI SCRSSQSLVH SDGNTYLSWL QQRPGQPPRL LIYRISRRFS 200
GVPDRFSGSG AGTDFTLEIS RVEAEDVGVY YCMQSTHVPR TFGCGTKVEI 250
KSGGGGSEVQ LVESGGGLVQ PGGSLKLSCA ASGFTFNKYA MNWVRQAPGK 300
GLEWVARIRS KYNNYATYYA DSVKDRFTIS RDDSKNTAYL QMNNLKTEDT 350
AVYYCVRHGN FGNSYISYWA YWGQGTLVTV SSGGGGSGGG GSGGGGSQTV 400
VTQEPSLTVS PGGTVTLTCG SSTGAVTSGN YPNWVQQKPG QAPRGLIGGT 450
KFLAPGTPAR FSGSLLGGKA ALTLSGVQPE DEAEYYCVLW YSNRWVFGGG 500
TKLTVLHHHH HH                                          512
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain (C23 C104):V 22-96 162-232 279-355 419-487
(C49-C120) V 44-244

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
VH Q1:
1

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

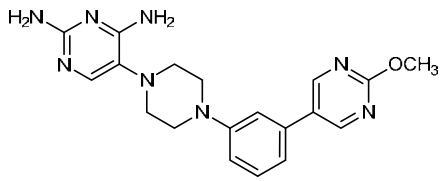
fanotaprimum

fanotaprim — 5-{4-[3-(2-methoxypyrimidin-5-yl)phenyl]piperazin-1-yl}pyrimidine-2,4-diamine

fanotaprim — 5-{4-[3-(2-méthoxypyrimidin-5-yl)phényl]pipérazin-1-yl}pyrimidine-2,4-diamine

fanotaprim — 5-{4-[3-(2-metoxipirimidin-5-il)fenil]piperazin-1-il}pirimidina-2,4-diamina

$C_{19}H_{22}N_8O$



favezelimabum #

favezelimab — immunoglobulin G4-kappa, anti-[*Homo sapiens* LAG3 (lymphocyte activating 3, lymphocyte-activation 3, CD223)], humanized monoclonal antibody;
gamma4 heavy chain humanized (1-446) [VH (*Homo sapiens* IGHV1-58*01 (85.6%) -(IGHD) -IGHJ1*01 (91.7%)) [8.8.12] (1-119) -*Homo sapiens* IGHG4*01 (CH1 (120-217), hinge 1-12 (218-229), CH2 (230-339), CH3 (340-444), CHS (445-446)) (120-446)], (133-218')-disulfide with kappa light chain humanized (1'-218') [V-KAPPA (*Homo sapiens* IGKV2D-29*01 (82.0%) -IGKJ4*01 (100%))[10.3.9] (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')];
dimer (225-225'':228-228'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

favézélimab — immunoglobuline G4-kappa, anti-[*Homo sapiens* LAG3 (activateur 3 des lymphocytes, lymphocyte-activation 3, CD223)], anticorps monoclonal humanisé;
chaîne lourde gamma4 humanisée (1-446) [VH (*Homo sapiens* IGHV1-58*01 (85.6%) -(IGHD) -IGHJ1*01 (91.7%)) [8.8.12] (1-119) -*Homo sapiens* IGHG4*01 (CH1 (120-217), charnière 1-12 (218-229), CH2 (230-339), CH3 (340-444), CHS (445-446)) (120-446)], (133-218')-disulfure avec la chaîne légère kappa humanisée (1'-218') [V-KAPPA (*Homo sapiens* IGKV2D-29*01 (82.0%) -IGKJ4*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')];
dimère (225-225'':228-228'')-bisdisulfure, produit dans des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa

favezelimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* LAG3 (activador 3 de los linfocitos, linfocito-activación 3, CD223)], anticuerpo monoclonal humanizado; cadena pesada gamma4 humanizada (1-446) [VH (*Homo sapiens* IGHV1-58*01 (85.6%) -(IGHD) - IGHJ1*01 (91.7%)) [8.8.12] (1-119) -*Homo sapiens* IGHG4*01 (CH1 (120-217), bisagra 1-12 (218-229), CH2 (230-339), CH3 (340-444), CHS (445-446)) (120-446)], (133-218')-disulfuro con la cadena ligera kappa humanizada (1'-218') [V-KAPPA (*Homo sapiens* IGKV2D-29*01 (82.0%) -IGKJ4*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (225-225":228-228")-bisdisulfuro, producido en las células ováricas de hamsters chinos (CHO), glicoforma alfa

Heavy chain / Chaîne lourde / Cadena pesada
```
QMQLVQSGPE VKKPGTSVKV SCKASGYTFT DYNVDWVRQA RGQRLEWIGD  50
INPNDGGTIY AQKFQERVTI TVDKSTSTAY MELSSLRSED TAVYYCARNY 100
RWFGAMDHWG QGTTVTVSSA STKGPSVFPL APCSRSTSES TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTKTY 200
TCNVDHKPSN TKVDKRVESK YGPPCPPCPA PEFLGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKGLPSS IEKTISKAKG QPREPQVYTL 350
PPSQEEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSRLT VDKSRWQEGN VFSCSVMHEA LHNHYTQKSL SLSLGK     446
```

Light chain / Chaîne légère / Cadena ligera
```
DIVMTQTPLS LSVTPGQPAS ISCKASQSLD YEGDSDMNWY LQKPGQPPQL  50
LIYGASNLES GVPDRFSGSG SGTDFTLKIS RVEAEDVGVY YCQQSTEDPR 100
TFGGGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC                                    218
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfu
Intra-H (C23-C104) 22-96 146-202 260-320 366-424
22"-96" 146"-202" 260"-320' 366"-424"
Intra-L (C23-C104) 23'-92' 138'-198'
23'"-92"' 138'"-198'"
Inter-H-L (CH1 10-CL 126) 133-218' 133"-218'"
Inter-H-H (h 11, h 14) 225-225" 228-228"

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

Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennai complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.
C-terminal lysine clipping:
H CHS K2:
446, 446"

firazorextonum

firazorexton

N-{(2*S*,3*S*)-1-(2-hydroxy-2-methylpropanoyl)-2-[(2,3',5'-trifluoro[1,1'-biphenyl]-3-yl)methyl]pyrrolidin-3-yl}methanesulfonamide

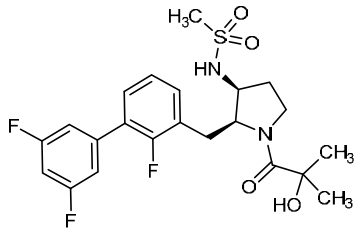
firazorexton

N-{(2*S*,3*S*)-1-(2-hydroxy-2-méthylpropanoyl)-2-[(2,3',5'-trifluoro[1,1'-biphényl]-3-yl)méthyl]pyrrolidin-3-yl}méthanesulfonamide

firazorextón

N-{(2*S*,3*S*)-1-(2-hidroxi-2-metilpropanoil)-2-[(2,3',5'-trifluoro[1,1'-bifenil]-3-il)metil]pirrolidin-3-il}metanosulfonamida

$C_{22}H_{25}F_3N_2O_4S$



flotufolastatum (^{18}F)

flotufolastat (^{18}F)

N^2-(*N*-{(4*S*)-4-carboxy-4-[4,7,10-tris(carboxymethyl)-1,4,7,10-tetraaza-cyclododecan-1-yl]butanoyl}-3-[4-(di-*tert*-butyl(^{18}F)fluorosilyl)benzamido]-D-alanyl)-*N*^{6}-[4-(*N*^{2}-{*N*-[(L-glutamic acid-*N*-yl)carbonyl]-L-γ-glutamyl}-D-ornithin-*N*^{5}-yl)-4-oxobutanoyl]-D-lysine

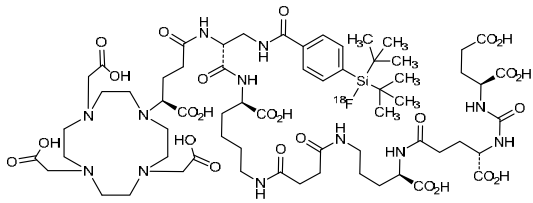
flotufolastat (^{18}F)

N^2-(*N*-{(4*S*)-4-carboxy-4-[4,7,10-tris(carboxyméthyl)-1,4,7,10-tétraaza-cyclododécan-1-yl]butanoyl}-3-[4-(di-*tert*-butyl(^{18}F)fluorosilyl)benzamido]-D-alanyl)-*N*^{6}-[4-(*N*^{2}-{*N*-[(acide L-glutamique-*N*-yl)carbonyl]-L-γ-glutamyl}-D-ornithin-*N*^{5}-yl)-4-oxobutanoyl]-D-lysine

flotufolastat (^{18}F)

N^2-(*N*-{(4*S*)-4-carboxi-4-[4,7,10-tris(carboximetil)-1,4,7,10-tetraazaciclo-dodecan-1-il]butanoil}-3-[4-(di-*terc*-butil(^{18}F)fluorosilil)benzamido]-D-alanil)-*N*^{6}-[4-(*N*^{2}-{*N*-[(ácido L-glutámico-*N*-il)carbonil]-L-γ-glutamil}-D-ornitin-*N*^{5}-il)-4-oxobutanoil]-D-lisina

$C_{63}H_{99}{}^{18}FN_{12}O_{25}Si$



flubentylosinum

flubentylosin

[(4*R*,5*S*,6*S*,7*R*,9*R*,11*E*,13*E*,15*R*,16*R*)-15-{[(6-deoxy-2,3-di-*O*-methyl-β-D-allopyranosyl)oxy]methyl}-6-{[3,6-dideoxy-4-*O*-{2,6-dideoxy-4-*O*-[(4-fluorophenyl)methyl]-3-*C*-methyl-α-L-*ribo*-hexopyranosyl}-3-(dimethylamino)-β-D-glucopyranosyl]oxy}-16-ethyl-4-hydroxy-5,9,13-trimethyl-2,10-dioxo-1-oxacyclohexadeca-11,13-dien-7-yl]acetaldehyde;
4^B-*O*-(4-fluorobenzyl)tylosin

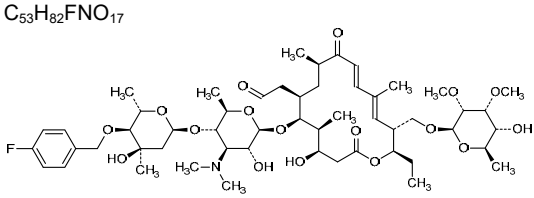
flubentylosine

[(4*R*,5*S*,6*S*,7*R*,9*R*,11*E*,13*E*,15*R*,16*R*)-15-{[(6-désoxy-2,3-di-*O*-méthyl-β-D-allopyranosyl)oxy]méthyl}-6-{[3,6-didésoxy-4-*O*-{2,6-didésoxy-4-*O*-[(4-fluorophényl)méthyl]-3-*C*-méthyl-α-L-*ribo*-hexopyranosyl}-3-(diméthylamino)-β-D-glucopyranosyl]oxy}-16-éthyl-4-hydroxy-5,9,13-triméthyl-2,10-dioxo-1-oxacyclohexadéca-11,13-dién-7-yl]acetaldehyde;
4^B-*O*-(4-fluorobenzyl)tylosine

flubentilosina

[(4*R*,5*S*,6*S*,7*R*,9*R*,11*E*,13*E*,15*R*,16*R*)-15-{[(6-desoxi-2,3-di-*O*-metil-β-D-alopiranosil)oxi]metil}-6-{[3,6-didesoxi-4-*O*-{2,6-didesoxi-4-*O*-[(4-fluorofenil)metil]-3-*C*-metil-α-L-*ribo*-hexopiranosil}-3-(dimetilamino)-β-D-glucopiranosil]oxi}-16-etil-4-hidroxi-5,9,13-trimetil-2,10-dioxo-1-oxaciclohexadeca-11,13-dien-7-il]acetaldehído; 4^B-*O*-(4-fluorobencil)tilosina

$C_{53}H_{82}FNO_{17}$



fordadistrogenum movaparvovecum #

fordadistrogene movaparvovec

A replication-defective adeno-associated viral vector encoding a codon-optimised mini-dystrophin (DMD).
A recombinant replication-defective adeno-associated viral vector serotype 9 (rAAV9), encoding a codon-optimised mini-dystrophin (DMD) gene comprising the N-terminus, hinge regions H1, H3 and H4, spectrin-like repeats R1, R2 and R22-24, and the C-terminal cysteine-rich region, under the control of a human muscle-specific synthetic enhancer/promoter and a synthetic poly(A) sequence, flanked by AAV2 inverted terminal repeats (ITR).

fordadistrogène movaparvovec

Un vecteur adénoviral à réplication défectueuse et codant pour une mini-dystrophine (DMD) avec des codons optimisés.
Un vecteur adénoviral recombinant de sérotype 9 (rAAV9) à réplication défectueuse, codant pour un gène de mini-dystrophine (DMD) avec des codons optimisés, comprenant l'extrémité N-terminale, les régions charnières H1, H3 et H4, les répétitions de type spectrine R1, R2 et R22-24, et la région C-terminale riche en cystéines, sous le contrôle d'un promoteur/amplificateur synthétique spécifique du muscle humain et d'une séquence synthétique poly(A), flanquée de répétitions terminales inversées (ITR) de l'AAV2.

fordadistrogén movaparvovec

Un vector de virus adeno-asociado, deficiente de replicación, que codifica para una mini-distrofina (DMD) con los codones optimizados.
Un vector de virus adeno-asociado recombinante de serotipo 9 (rAAV9), deficiente de replicación, que codifica para un gen de mini-distrofina (DMD) con los codones optimizados que contiene el extremo N-terminal, las regiones bisagra H1, H3 y H4, las repeticiones de tipo espectrina R1, R2 y R22-24, y la región C-terminal rica en cisteínas, bajo el control de un promotor/amplificador (enhancer) sintético específico de músculo humano y una secuencia poly(A) sintética, flanqueado por las repeticiones terminales invertidas (ITR) del AAV2.

gallium (^{68}Ga) gozetotidum

gallium (^{68}Ga) gozetotide

{*N*-[(*N*^{6}-{6-[3-(3-{[{2-[{[5-(2-carboxyethyl)-2-hydroxy-κ*O*-phenyl]methyl}(carboxy-κ*O*-methyl)amino-κ*N*]ethyl}(carboxy-κ*O*-methyl)amino-κ*N*]methyl}-4-hydroxy-κ*O*-phenyl)propanamido]hexanoyl}-L-lysin-*N*^{2}-yl)carbonyl]-L-glutamato(3−)}(^{68}Ga)gallium

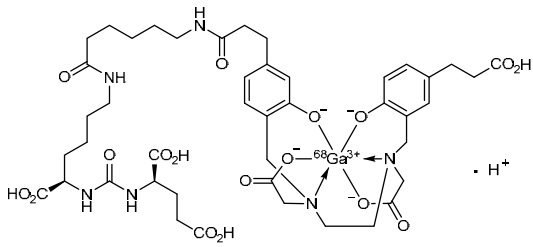
gallium (^{68}Ga) gozétotide

{*N*-[(*N*^{6}-{6-[3-(3-{[{2-[{[5-(2-carboxyéthyl)-2-hydroxy-κ*O*-phényl]méthyl}(carboxy-κ*O*-méthyl)amino-κ*N*]éthyl}(carboxy-κ*O*-méthyl)amino-κ*N*]méthyl}-4-hydroxy-κ*O*-phényl)propanamido]hexanoyl}-L-lysin-*N*^{2}-yl)carbonyl]-L-glutamato(3−)}(^{68}Ga)gallium

galio (^{68}Ga) gozetótida

{*N*-[(*N*^{6}-{6-[3-(3-{[{2-[{[5-(2-carboxietil)-2-hidroxi-κ*O*-fenil]metil}(carboxi-κ*O*-metil)amino-κ*N*]etil}(carboxi-κ*O*-metil)amino-κ*N*]metil}-4-hidroxi-κ*O*-fenil)propanamido]hexanoil}-L-lisin-*N*^{2}-il)carbonil]-L-glutamato(3−)}(^{68}Ga)galio

$C_{44}H_{59}{}^{68}GaN_6O_{17}$



garivulimabum #

garivulimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD274 (programmed death ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-446) [VH humanized (*Homo sapiens* IGHV3-NL1*01 (84.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.11] (26-33.51-57.96-106) (1-117) -*Homo sapiens* IGHG1*01 G1m17,1, G1v4 CH2 A114 (CH1 K120 (214) (118-215), hinge 1-15 (216-230) -CH2 V1.2>A (234), P114>A (329) (231-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (118-446)], (220-215')-disulfide with kappa light chain humanized (1'-215') [V-KAPPA humanized (*Homo sapiens* IGKV1-5*03 (84.0%) -IGKJ2*01 (91.7%)) CDR-IMGT [6.3.10] (27-32.50-52.89-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (226-226":229-229")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

garivulimab

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 humanisée (1-446) [VH humanisé (*Homo sapiens* IGHV3-NL1*01 (84.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.11] (26-33.51-57.96-106) (1-117) -*Homo sapiens* IGHG1*01 G1m17,1, G1v4 CH2 A114 (CH1 K120 (214) (118-215), charnière 1-15 (216-230) -CH2 V1.2>A (234), P114>A (329) (231-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (118-446)], (220-215')-disulfure avec la chaîne légère kappa humanisée (1'-215') [V-KAPPA humanisé (*Homo sapiens* IGKV1-5*03 (84.0%) -IGKJ2*01 (91.7%)) CDR-IMGT [6.3.10] (27-32.50-52.89-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (226-226":229-229")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

garivulimab

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 humanizada (1-446) [VH humanizado (*Homo sapiens* IGHV3-NL1*01 (84.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.11] (26-33.51-57.96-106) (1-117) -*Homo sapiens* IGHG1*01 G1m17,1, G1v4 CH2 A114 (CH1 K120 (214) (118-215), bisagra 1-15 (216-230) -CH2 V1.2>A (234), P114>A (329) (231-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (118-446)], (220-215')-disulfuro con la cadena ligera kappa humanizada (1'-215') [V-KAPPA humanizado (*Homo sapiens* IGKV1-5*03 (84.0%) -IGKJ2*01 (91.7%)) CDR-IMGT [6.3.10] (27-32.50-52.89-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (226-226":229-229")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAVSGFSLT SYGVHWVRQA PGKGLEWVAV  50
IWAGGSTNYA DSVKGRFTIS KDTSKNTVYL QMNSLRAEDT AVYYCAKPYG 100
TSAMDYWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APPAAGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALAAP IEKTISKAKG QPREPQVYTL 350
PPSRDELTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGK     446
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Light chain / Chaîne légère / Cadena ligera

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DIQMTQSPSS LSASVGDRVT ITCKASQDVG IVVAWYQQKP GKAPKLLIYW  50
ASIRHTGVPS RFSGSGSGTE FTLTISSLQP DDFATYYCQQ YSNYPLYTFG 100
QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 144-200 260-320 366-424
22"-95" 144"-200" 260"-320" 366"-424"
Intra-L (C23-C104) 23'-88' 135'-195'
23'"-88'" 135'"-195'"
Inter-H-L (h 5-CL 126) 220-215' 220"-215'"
Inter-H-H (h 11, h 14) 226-226" 229-229"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
296, 296"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

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

garveleucelum

garveleucel	Allogeneic T cell-enriched leukocyte preparation, devoid of alloreactive T cells. The cells are derived from peripheral blood mononuclear cells (PBMCs) collected by apheresis from a haploidentical stem cell donor. The cells are lymphocyte enriched, and during processing patient and donor cells are co-cultured *ex vivo* in an MLR (mixed lymphocyte reaction) to stimulate activation of host alloreactive T-cells and subsequent depletion of these cells using a proprietary rhodamine-based photodynamic treatment. In this process, monocytes are largely eliminated from the cell mixture. The cells are primarily T cells (average ~90%) consisting of both CD4+ T-helper cells and CD8+ T-cytotoxic cells (mean CD4:CD8 ratio of 2.1), and other leucocytes (average ~10%, with B-cells (~ 6-7%) and NK cells (~ 2-3%).
garvéleucel	Préparation de leucocytes enrichis en cellules T allogéniques, dépourvus de cellules T alloréactives. Les cellules sont dérivées de cellules mononucléaires du sang périphérique (PBMC) prélevées par aphérèse chez un donneur de cellules souches partiellement compatible pour les antigènes HLA. Les cellules sont enrichies en lymphocytes et, pendant le traitement, les cellules du patient et du donneur sont co-cultivées *ex vivo* selon une RML (réaction lymphocytaire mixte) pour stimuler l'activation des cellules T allo-réactives de l'hôte et l'épuisement ultérieur de ces cellules grâce à un traitement photodynamique exclusif à base de rhodamine. Dans ce processus, les monocytes sont largement éliminés du mélange de cellules. Les cellules sont principalement des cellules T (en moyenne ~90%) composées à la fois de cellules T auxiliaires CD4+ et de cellules T cytotoxiques CD8+ (rapport moyen CD4:CD8 de 2.1), et d'autres leucocytes (en moyenne ~10%, avec des cellules B (~6-7%) et des cellules NK (~ 2-3%).
garveleucel	Preparación de leucocitos enriquecidos en células T alogénicos, desprovistos de células T aloreactivas. Las células se obtienen a partir de células mononucleares de sangre periférica (PBMCs) recogidas por aféresis de un donante de células madre haploidéntico. Las células se enriquecen en linfocitos, y durante el procesamiento, las células del paciente y del donante se co-cultivan *ex vivo* en una MLR (reacción mixta de linfocitos) para estimular la activación de células T aloreactivas frente al huésped y la subsiguiente depleción de estas células usando un tratamiento fotodinámico basado en la rodamina. En este proceso, los monocitos en su mayoría se eliminan de la mezcla celular. Las células son principalmente células T (~90% como media) y consisten en células T colaboradoras CD4+ y células T citotóxicas CD8+ (ratio medio CD4:CD8 de 2.1), y otros leucocitos (media ~10%, con células B (~6-7%) y células NK (~2-3%).

gavocabtagenum autoleucelum #

gavocabtagene autoleucel	Autologous T cells transduced *ex vivo* with a self-inactivating lentiviral vector encoding an anti-mesothelin (MSLN) chimeric antigen receptor Autologous T cells transduced *ex vivo* with a non-replicating, self-inactivating (SIN) lentiviral vector, encoding an anti-mesothelin (MSLN) single-domain antibody (sdAb) based chimeric antigen receptor with a leader sequence derived from granulocyte-macrophage colony-stimulating factor receptor alpha (GMCSFR-alpha), fused to the CD3ε subunit of the T-cell receptor (TCR) via an A3(G4S)3LE flexible linker, which is incorporated into the endogenous TCR complex upon expression. The transgene is under control of elongation factor-1 alpha (EF-1α) promoter and woodchuck hepatitis virus post-transcriptional regulatory element. The vector genome also contains a packaging signal, a partial *gag* sequence, a Rev Response Element (RRE), a central polypurine tract (cPPT) and a 3' polypurine tract (3'PPT).
gavocabtagène autoleucel	Cellules T autologues transduites *ex vivo* avec un vecteur lentiviral non réplicatif codant pour un récepteur chimérique anti-mésothéline (MSLN). Cellules T autologues transduites *ex vivo* avec un vecteur lentiviral non réplicatif et auto-inactivable (SIN), codant pour un récepteur antigénique chimérique basé sur les anticorps anti-mésothéline (MSLN) à domaine unique (sdAb). Il comprend une séquence leader dérivée du récepteur alpha du facteur de stimulation des colonies de granulocytes-macrophages (GMCSFR-alpha), fusionné à la sous-unité CD3ε du récepteur des cellules T (TCR) via un polypeptide lieur flexible nommé A3(G4)3LE, qui est incorporé dans le complexe TCR endogène lors de l'expression. Le transgène est sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF-1α) ainsi que de l'élément régulateur post-transcriptionnel du virus de l'hépatite de la marmotte. Le génome du vecteur contient aussi un signal de conditionnement des gènes, une séquence *gag* partielle, un élément de réponse Rev (RRE), une région centrale avec tractus polypurin (cPPT) et un tractus polypurin 3' (3'PPT).
gavocabtagén autoleucel	Células T autólogas transducidas *ex vivo* con un vector lentiviral auto-inactivante que codifica para un receptor de antígenos quimérico anti-mesotelina (MSLN). Células T autólogas transducidas *ex vivo* con vector lentiviral auto-inactivante, no replicativo, que codifica para un receptor de antígenos quimérico basado en un anticuerpo de domino único (sdAb) anti-mesotelina (MSLN) con una secuencia líder derivada del receptor alfa del factor estimulador de colonias de granulocitos-macrófagos (GMCSFR-alfa), fusionado a la subunidad CD3ε del receptor de la célula T (TCR) mediante un conector (linker) flexible A3(G4S)3LE, que se incorpora en el complejo TCR endógeno al expresarse. El transgen está bajo el control del promotor del factor de elongación 1 alfa (EF-1α) y elemento regulador post-transcripcional del virus de la hepatitis de la marmota. El genoma del vector también contiene una señal empaquetadora, un secuencia *gag* parcial, un elemento de respuesta Rev (RRE), un segmento central de polipurinas (cPPT) y un segmento 3' de polipurinas (3'PPT).

geptanolimabum #

geptanolimab	immunoglobulin G4-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], monoclonal antibody; gamma4 heavy chain (1-440) [VH (*Homo sapiens*IGHV7-4-1*02 (85.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.7] (26-33.51-58.97-103) (1-114)-*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (115-212), hinge 1-12 S10>P (222) (213-224), CH2 (225-334), CH3 (335-439), CHS K>del (440) (115-440)], (28-217')-disulfide with kappa light chain (1'-217') [V-KAPPA (*Mus musculus* IGKV3-5*01 (89.9%) -IGKJ1*01 (90.9%)/*Homo sapiens* IGKV3D-11*02 (64.9%) -IGKJ2*01 (100%)) CDR-IMGT [10.3.8] (27-36.54-56.93-100) (1'-110') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (156), V101 (194) (111'-217')]; dimer (220-220":223-223")-bisdisulfide, produced in Chinese hamster ovary (CHO)-S cell line, glycoform alfa
geptanolimab	immunoglobuline G4-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal; chaîne lourde gamma4 (1-440) [VH (*Homo sapiens* IGHV7-4-1*02 (85.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.7] (26-33.51-58.97-103) (1-114) -*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (115-212), charnière 1-12 S10>P (222) (213-224), CH2 (225-334), CH3 (335-439), CHS K>del (440) (115-440)], (128-217')-disulfure avec la chaîne légère kappa (1'-217') [V-KAPPA (*Mus musculus* IGKV3-5*01 (89.9%) -IGKJ1*01 (90.9%)/*Homo sapiens* IGKV3D-11*02 (64.9%) -IGKJ2*01 (100%)) CDR-IMGT [10.3.8] (27-36.54-56.93-100) (1'-110') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (156), V101 (194) (111'-217')]; dimère (220-220":223-223")-bisdisulfure, produit dans des cellules ovariennes de hamsters chinois (CHO) lignée cellulaire CHO-S, glycoforme alfa
geptanolimab	inmunoglobulina G4-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal; cadena pesada gamma4 (1-440) [VH (*Homo sapiens* IGHV7-4-1*02 (85.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.7] (26-33.51-58.97-103) (1-114) -*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (115-212), bisagra 1-12 S10>P (222) (213-224), CH2 (225-334), CH3 (335-439), CHS K>del (440) (115-440)], (128-217')-disulfuro con la cadena ligera kappa (1'-217') [V-KAPPA (*Mus musculus* IGKV3-5*01 (89.9%) -IGKJ1*01 (90.9%)/*Homo sapiens* IGKV3D-11*02 (64.9%) -IGKJ2*01 (100%)) CDR-IMGT [10.3.8] (27-36.54-56.93-100) (1'-110') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (156), V101 (194) (111'-217')]; dímero (220-220":223-223")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
```
QIQLVQSGSE LKKPGASVKV SCKASGYTFT NFGMNWVRQA PGQGLKWMGW  50
ISGYTREPTY AADFKGRFVI SLDTSVSTAY LQISSLKAED TAVYYCARDV 100
FDYWGQGTLV TVSSASTKGP SVFPLAPCSR STSESTAALG CLVKDYFPEP 150
VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS SVVTVPSSSL GTKTYTCNVD 200
HKPSNTKVDK RVESKYGPPC PPCPAPEFLG GPSVFLFPPK PKDTLMISRT 250
PEVTCVVVDV SQEDPEVQFN WYVDGVEVHN AKTKPREEQF NSTYRVVSVL 300
TVLHQDWLNG KEYKCKVSNK GLPSSIEKTI SKAKGQPREP QVYTLPPSQE 350
EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL 400
YSRLTVDKSR WQEGNVFSCS VMHEALHNHY TQKSLSLSLG            440
```

Light chain / Chaîne légère / Cadena ligera
```
DIVLTQSPAS LAVSPGQRAT ITCRASESVD NYGYSFMNWF QQKPGQPPKL  50
LIYRASNLES GVPARFSGSG SRTDFTLTIN PVEADDTANY YCQQSNADPT 100
FGQGTKLEIK RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ 150
WKVDNALQSG NSQESVTEQD SKDSTYSLSS TLTLSKADYE KHKVYACEVT 200
HQGLSSPVTK SFNRGEC                                     217
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 141-197 255-315 361-419
22"-96" 141"-197" 255"-315" 361"-419"
Intra-L (C23-C104) 23'-92' 137'-197'
23'"-92'" 137'"-197'"
Inter-H-L (h 10-CL 126) 128-217' 128"-217'"
Inter-H-H (h 8, h 11) 220-220" 223-223"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
291, 291"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

gindameranum #

gindameran

Messenger RNA encoding cancer/testis antigen 1 (New York oesophageal squamous cell carcinoma antigen-1).
Messenger RNA (mRNA), 5'-capped, encoding codon-optimised New York esophageal squamous cell carcinoma antigen-1 (NY-ESO-1; cancer/testis antigen 1, CTAG1A) expressed as a fusion protein comprising a secretory signal peptide, NY-ESO-1, P2P16 tetanus toxoid-derived helper epitopes and a major histocompatibility complex (MHC) class I transmembrane and cytoplasmic domain (MITD), connected by three glycine/serine-rich (GS) linker peptides, flanked by 5' and 3' untranslated regions and a 3' poly(A) tail.

gindaméran

ARN messager codant pour l'antigène 1 du cancer testiculaire (antigène 1 du carcinome squameux de l'œsophage, dit de New York).
ARN messager (ARNm), protégé en 5', codant pour l'antigène 1 du carcinome squameux de l'œsophage, dit de New York (NY-ESO-1; antigène 1 du cancer testiculaire, CTAG1A), avec des codons optimisés, exprimé sous la forme d'une protéine de fusion comprenant un peptide signal de sécrétion, NY-ESO-1, les épitopes auxiliaires P2P16 dérivés de l'anatoxine tétanique et un domaine transmembranaire et cytoplasmique (MITD) du complexe majeur d'histocompatibilité (CMH) de classe I, reliés par trois peptides de liaison riches en glycine/sérine (GS), flanqués de régions non traduites en 5' et 3' et d'une queue poly(A) en 3'.

gindamerán	ARN mensajero que codifica para el antígeno 1 de cáncer/testículo (antígeno 1 de carcinoma escamoso del esófago Nueva York). ARN mensajero (ARNm), protegido en 5', que codifica para el antígeno 1 de carcinoma escamoso del esófago Nueva York (NY-ESO-1; antígeno cáncer/testículo 1, CTAG1A) con codones optimizados, que se expresa como una proteína de fusión que consta de un péptido señal de secreción, NY-ESO-1, los epítopos auxiliares P2P16 derivados del toxoide tetánico y un dominio citoplásmico y transmembrana del complejo principal de histocompatibilidad (MHC) de clase I (MITD), conectados mediante tres péptidos de enlace ricos en glicina/serina (GS), flanqueado por las regiones 5' y 3' no traducidas y una cola poly(A) en 3'.
grisnilimabum #	
grisnilimab	immunoglobulin G2A-lambda, anti-[CD7 (CD7 antigen (p41),GP40, LEU-9, TP41, Tp40)], *Mus musculus* monoclonal antibody; gamma2a heavy chain *Mus musculus* (1-453) [VH (*Mus musculus* IGHV9-3-1*01 (98%) -(IGHD) -IGHJ2*01 (93.3%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Mus musculus* IGHG2A*01 (100%) (CH1 (124-220), hinge 1-16 (221-236), CH2 (237-346), CH3 (347-451), CHS (452-453)) (124-453)], (138-214')-disulfide with lambda light chain *Mus musculus* (1'-215') [V-LAMBDA (*Mus musculus* IGLV1*01 (98%) -IGLJ1*01 (100%)) CDR-IMGT [9.3.9] (26-34.52-54.91-99) (1'-109') -*Mus musculus* IGLC1*01 (100%) (110'-215')]; dimer (230-230":233-233":235-235")-trisdisulfide, produced in SP2/0-derived mouse myeloma cells, glycoform alfa
grisnilimab	immunoglobuline G2A-lambda, anti-[CD7 (CD7 antigène (p41), GP40, LEU-9, TP41, Tp40)], anticorps monoclonal *Mus musculus*; chaîne lourde gamma2a *Mus musculus* (1-453) [VH (*Mus musculus* IGHV9-3-1*01 (98%) -(IGHD) -IGHJ2*01 (93.3%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Mus musculus* IGHG2A*01 (100%) (CH1 (124-220), charnière 1-16 (221-236), CH2 (237-346), CH3 (347-451), CHS (452-453)) (124-453)], (138-214')-disulfure avec la chaîne légère lambda *Mus musculus* (1'-215') [V-LAMBDA (*Mus musculus* IGLV1*01 (98%) -IGLJ1*01 (100%)) CDR-IMGT [9.3.9] (26-34.52-54.91-99) (1'-109') -*Mus musculus* IGLC1*01 (100%) (110'-215')]; dimère (230-230":233-233":235-235")-trisdisulfure, produit par une ligne cellulaire derivée de myélome murin SP2/0, glycoforme alfa
grisnilimab	inmunoglobulina G2A-lambda, anti-[CD7 (CD7 antígeno (p41), GP40, LEU-9, TP41, Tp40)], anticuerpo monoclonal *Mus musculus*;

cadena pesada gamma2a *Mus musculus* (1-453) [VH (*Mus musculus* IGHV9-3-1*01 (98%) -(IGHD) -IGHJ2*01 (93.3%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Mus musculus* IGHG2A*01 (100%) (CH1 (124-220), bisagra 1-16 (221-236), CH2 (237-346), CH3 (347-451), CHS (452-453)) (124-453)], (138-214')-disulfuro con la cadena ligera lambda *Mus musculus* (1'-215') [V-LAMBDA (*Mus musculus* IGLV1*01 (98%) -IGLJ1*01 (100%)) CDR-IMGT [9.3.9] (26-34.52-54.91-99) (1'-109') -*Mus musculus* IGLC1*01 (100%) (110'-215')];
dímero (230-230":233-233":235-235")-trisdisulfuro, producido en una línea celular de mieloma murino SP2/0, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
```
QIQLVQSGPE LKKPGETVKI SCKASGYTFT NYGMNWVKQA PGKGLMWLGW  50
INTYTGEPTY ADDFKGRFAF SLETSASTAY LQINNLKNED TATYFCARWA 100
YFYGSSPYFF DYWGQGTTLT VSSAKTTAPS VYPLAPVCGD TTGSSVTLGC 150
LVKGYFPEPV TLTWNSGSLS SGVHTFPAVL QSDLYTLSSS VTVTSSTWPS 200
QSITCNVAHP ASSTKVDKKI EPRGPTIKPC PPCKCPAPNL LGGPSVFIFP 250
PKIKDVLMIS LSPIVTCVVV DVSEDDPDVQ ISWFVNNVEV HTAQTQTHRE 300
DYNSTLRVVS ALPIQHQDWM SGKEFKCKVN NKDLPAPIER TISKPKGSVR 350
APQVYVLPPP EEEMTKKQVT LTCMVTDFMP EDIYVEWTNN GKTELNYKNT 400
EPVLDSDGSY FMYSKLRVEK KNWVERNSYS CSVVHEGLHN HHTTKSFSRT 450
PGK                                                     453
```

Light chain / Chaîne légère / Cadena ligera
```
QAVVTQESAL TTSPGETVTL TCRSSTGAVT TSNYANWVQE KPDHLFTGLI  50
GGTNNRAPGV PARFSGSLIG DKAALTITGA QTEDEAIYFC ALWCSNHLVF 100
GGGTKLTVLG QPKSSPSVTL FPPSSEELET NKATLVCTIT DFYPGVVTVD 150
WKVDGTPVTQ GMETTQPSKQ SNNKYMASSY LTLTARAWER HSSYSCQVTH 200
EGHTVEKSLS RADCS                                        215
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 150-205 267-327 373-431
22"-96" 150"-205" 267"-327" 373"-431"
Intra-L (C23-C104) 22'-90' 137'-196'
22'"-90'" 137'"-196'"
Inter-H-L (CH1 11-CL 126) 138-214' 138"-214'"
Inter-H-H (h 12, h 15, h 18) 230-230" 233-233" 235-235"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"
L VL Q1:
1', 1'"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
303, 303"
Fucosylated complex bi-antennary SP2/0-type glycans / glycanes de type SP2/0 bi-antennaires complexes fucosylés / glicanos de tipo SP2/0 biantenarios complejos fucosilados

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

grisnilimabum setaritoxum #
grisnilimab setaritox

immunoglobulin G2A-lambda, anti-[CD7 (CD7 antigen (p41),GP40, LEU-9, TP41, Tp40)], *Mus musculus* monoclonal antibody conjugated to ricin toxin A (RTA); gamma2a heavy chain *Mus musculus* (1-453) [VH (*Mus musculus* IGHV9-3-1*01 (98%) -(IGHD) -IGHJ2*01 (93.3%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Mus musculus* IGHG2A*01 (100%) (CH1 (124-220), hinge 1-16 (221-236), CH2 (237-346), CH3 (347-451), CHS (452-453)) (124-453)], (138-214')-disulfide

	with lambda light chain *Mus musculus* (1'-215') [V-LAMBDA (*Mus musculus* IGLV1*01 (98%) -IGLJ1*01 (100%)) CDR-IMGT [9.3.9] (26-34.52-54.91-99) (1'-109') -*Mus musculus* IGLC1*01 (100%) (110'-215')]; dimer (230-230":233-233":235-235")-trisdisulfide, produced in SP2/0-derived mouse myeloma cells, glycoform alfa, substituted at N^6 of an average of 1.6 lysyl residues with 4-[(1*RS*)-1-{[L-methionyl-ricin toxin A-chain (Met-RTA, non-glycosylated, produced in *Escherichia coli*)-S^{260}-yl]sulfanyl}ethyl]benzoyl groups
grisnilimab sétaritox	immunoglobuline G2A-lambda, anti-[CD7 (CD7 antigène (p41), GP40, LEU-9, TP41, Tp40)], anticorps monoclonal *Mus musculus* conjugué à la toxine A de la ricine (RTA); chaîne lourde gamma2a *Mus musculus* (1-453) [VH (*Mus musculus* IGHV9-3-1*01 (98%) -(IGHD) -IGHJ2*01 (93.3%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Mus musculus* IGHG2A*01 (100%) (CH1 (124-220), charnière 1-16 (221-236), CH2 (237-346), CH3 (347-451), CHS (452-453)) (124-453)], (138-214')-disulfure avec la chaîne légère lambda *Mus musculus* (1'-215') [V-LAMBDA (*Mus musculus* IGLV1*01 (98%) -IGLJ1*01 (100%)) CDR-IMGT [9.3.9] (26-34.52-54.91-99) (1'-109') -*Mus musculus* IGLC1*01 (100%) (110'-215')]; dimère (230-230":233-233":235-235")-trisdisulfure, produit par une lignée cellulaire dérivée de myélome murin SP2/0, glycoforme alfa, substitué en N^6 sur un moyenne de 1.6 résidus lysyl par des groupes 4-[(1*RS*)-1-{[L-méthionyl-chaîne A de la toxine de ricine (Met-RTA, non-glycosylée, produite par *Escherichia coli*)-S^{260}-yl]sulfanyl}éthyl]benzoyle
grisnilimab setaritox	inmunoglobulina G2A-lambda, anti-[CD7 (CD7 antígeno (p41), GP40, LEU-9, TP41, Tp40)], anticuerpo monoclonal *Mus musculus* conjugado con la toxina A de la ricina (RTA); cadena pesada gamma2a *Mus musculus* (1-453) [VH (*Mus musculus* IGHV9-3-1*01 (98%) -(IGHD) -IGHJ2*01 (93.3%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Mus musculus* IGHG2A*01 (100%) (CH1 (124-220), bisagra 1-16 (221-236), CH2 (237-346), CH3 (347-451), CHS (452-453)) (124-453)], (138-214')-disulfuro con la cadena ligera lambda *Mus musculus* (1'-215') [V-LAMBDA (*Mus musculus* IGLV1*01 (98%) -IGLJ1*01 (100%)) CDR-IMGT [9.3.9] (26-34.52-54.91-99) (1'-109') -*Mus musculus* IGLC1*01 (100%) (110'-215')]; dímero (230-230":233-233":235-235")-trisdisulfuro, producido en una línea celular de mieloma murino SP2/0, forma glicosilada alfa, sustituída en N^6 de un promedio de 1,6 residuos de lisilo con grupos de 4-[(1*RS*)-1-{[L-metionil-cadena A de toxina de ricina (Met-RTA, no glicosilada, producida por *Escherichia coli*)-S^{260}-il]sulfanil}etil]benzoilo

Heavy chain / Chaîne lourde / Cadena pesada

```
QIQLVQSGPE LKKPGETVKI SCKASGYTFT NYGMNWVKQA PGKGLMWLGW  50
INTYTGEPTY ADDFKGRFAF SLETSASTAY LQINNLKNED TATYFCARWA 100
YFYGSSPYFF DYWGQGTTLT VSSAKTTAPS VYPLAPVCGD TTGSSVTLGC 150
LVKGYFPEPV TLTWNSGSLS SGVHTFPAVL QSDLYTLSSS VTVTSSTWPS 200
QSITCNVAHP ASSTKVDKKI EPRGPTIKPC PPCKCPAPNL LGGPSVFIFP 250
PKIKDVLMIS LSPIVTCVVV DVSEDDPDVQ ISWFVNNVEV HTAQTQTHRE 300
DYNSTLRVVS ALPIQHQDWM SGKEFKCKVN NKDLPAPIER TISKPKGSVR 350
APQVYVLPPP EEEMTKKQVT LTCMVTDFMP EDIYVEWTNN GKTELNYKNT 400
EPVLDSDGSY FMYSKLRVEK KNWVERNSYS CSVVHEGLHN HHTTKSFSRT 450
PGK                                                     453
```

Light chain / Chaîne légère / Cadena ligera

```
QAVVTQESAL TTSPGETVTL TCRSSTGAVT TSNYANWVQE KPDHLFTGLI  50
GGTNNRAPGV PARFSGSLIG DKAALTITGA QTEDEAIYFC ALWCSNHLVF 100
GGGTKLTVLG QPKSSPSVTL FPPSSEELET NKATLVCTIT DFYPGVVTVD 150
WKVDGTPVTQ GMETTQPSKQ SNNKYMASSY LTLTARAWER HSSYSCQVTH 200
EGHTVEKSLS RADCS                                        215
```

Met-Ricin A chain / Met-chaîne A de la Ricine / Met-cadena A de la Ricina

```
MIFPKQYPII NFTTAGATVQ SYTNFIRAVR GRLTTGADVR HDIPVLPNRV 50
GLPINQRFIL VELSNHAELS VTLALDVTNA YVVGYRAGNS AYFFHPDNQE 100
DAEAITHLFT DVQNRYTFAF GGNYDRLEQL AGNLRENIEL GNGPLEEAIS 150
ALYYYSTGGT QLPTLARSFI ICIQMISEAA RFQYIEGEMR TRIRYNRRSA 200
PDPSVITLEN SWGRLSTAIQ ESNQGAFASP IQLQRRNGSK FSVYDVSILI 250
PIIALMVYRC APPPSSQF                                     268
```

Post-translational modifications

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

Intra-H (C23-C104) 22-96 150-205 267-327 373-431
22"-96" 150"-205" 267"-327" 373"-431"

Intra-L (C23-C104) 22'-90' 137'-196'
22'"-90'" 137'"-196'"

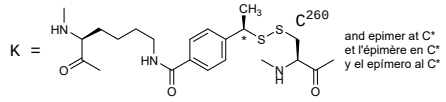
Inter-H-L (CH1 11-CL 126) 138-214' 138"-214'"

Inter-H-H (h 12, h 15, h 18) 230-230" 233-233" 235-235"
heterogeneous patterns involving 94' and 94'" e.g.:
96-94' 138-94' 150-94' 94'-137'
96"-94'" 138"-94'" 150"-94'" 94'"-137'"

Met-RTA: C172 = Cys-SH, C260 = Cys-S-S-CH(CH3)-p-C6H4-CO-[N6-Lys(H,L)]

Conjugation sites / Sites de conjugaison / Posiciones de coniugación

major: K87 K228 K72' K113'
K87" K228" K72'" K113'"
minor: K43 K215 K323 K332 K398 K421 K132'
K43" K215" K323" K332" K398" K421" K132'"



N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)

H VH Q1:
1, 1"
L VL Q1:
1', 1'"

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

H CH2 N84.4:
303, 303"
Fucosylated complex bi-antennary SP2/0-type glycans / glycanes de type SP2/0 bi-antennaires
complexes fucosylés / glicanos de tipo SP2/0 biantenarios complejos fucosilados.

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

H CHS K2:
453, 453"

hepcidinum

hepcidin — hepcidin (human) (hepatical bactericidal protein, hepcidin-25, liver-expressed antimicrobial peptide 1, LEAP-1, hepatic antimicrobial peptide, HAMP, ferroportin regulator protein): *S*^{7},*S*^{23}:*S*^{10},*S*^{13}:*S*^{11},*S*^{19}:*S*^{14},*S*^{22}-tetracyclo(L-α-aspartyl-L-threonyl-L-histidyl-L-phenylalanyl-L-prolyl-L-isoleucyl-L-cysteinyl-L-isoleucyl-L-phenylalanyl-L-cysteinyl-L-cysteinylglycyl-L-cysteinyl-L-cysteinyl-L-histidyl-L-arginyl-L-seryl-L-lysyl-L-cysteinylglycyl-L-methionyl-L-cysteinyl-L-cysteinyl-L-lysyl-L-threonine)

hepcidine — hepcidine (humaine) (protéine bactéricide hépatique, hepcidine-25, peptide antimicrobien exprimé par le foie 1, LEAP-1, peptide antimicrobien hépatique, HAMP, protéine régulatrice de la ferroportine):

S^7,S^{23}:S^{10},S^{13}:S^{11},S^{19}:S^{14},S^{22}-tétracyclo(L-α-aspartyl-L-thréonyl-L-histidyl-L-phénylalanyl-L-prolyl-L-isoleucyl-L-cystéinyl-L-isoleucyl-L-phénylalanyl-L-cystéinyl-L-cystéinylglycyl-L-cystéinyl-L-cystéinyl-L-histidyl-L-arginyl-L-séryl-L-lysyl-L-cystéinylglycyl-L-méthionyl-L-cystéinyl-L-cystéinyl-L-lysyl-L-thréonine)

hepcidina — hepcidina (humana) (proteína bactericida hepática, hepcidina-25, péptido antimicrobiano expresado en el hígado 1, LEAP-1, péptido antimicrobiano hepático, HAMP, proteína reguladora de ferroportina): S^7,S^{23}:S^{10},S^{13}:S^{11},S^{19}:S^{14},S^{22}-tetraciclo(L-α-aspartil-L-treonil-L-histidil-L-fenilalanil-L-prolil-L-isoleucil-L-cisteinil-L-isoleucil-L-fenilalanil-L-cisteinil-L-cisteinilglicil-L-cisteinil-L-cisteinil-L-histidil-L-arginil-L-seril-L-lisil-L-cisteinilglicil-L-metionil-L-cisteinil-L-cisteinil-L-lisil-L-treonina)

$C_{113}H_{170}N_{34}O_{31}S_9$

Sequence / Séquence / Secuencia
DTHFPICIFC CGCCHRSKCG MCCKT 25

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
7-23, 10-13, 11-19, 14-22

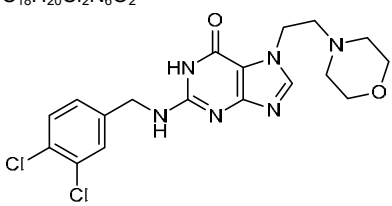
ibezapolstatum

ibezapolstat — 2-{[(3,4-dichlorophenyl)methyl]amino}-7-[2-(morpholin-4-yl)ethyl]-1,7-dihydro-6*H*-purin-6-one

ibézapolstat — 2-{[(3,4-dichlorophényl)méthyl]amino}-7-[2-(morpholin-4-yl)éthyl]-1,7-dihydro-6*H*-purin-6-one

ibezapolstat — 2-{[(3,4-diclorofenil)metil]amino}-7-[2-(morfolin-4-il)etil]-1,7-dihidro-6*H*-purin-6-ona

$C_{18}H_{20}Cl_2N_6O_2$



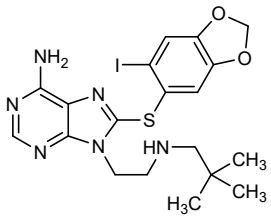
icapamespibum

icapamespib — 9-{2-[(2,2-dimethylpropyl)amino]ethyl}-8-[(6-iodo-2*H*-1,3-benzodioxol-5-yl)sulfanyl]-9*H*-purin-6-amine

icapamespib — 9-{2-[(2,2-diméthylpropyl)amino]éthyl}-8-[(6-iodo-2*H*-1,3-benzodioxol-5-yl)sulfanyl]-9*H*-purin-6-amine

icapamespib — 9-{2-[(2,2-dimetilpropil)amino]etil}-8-[(6-iodo-2*H*-1,3-benzodioxol-5-il)sulfanil]-9*H*-purin-6-amina

$C_{19}H_{23}IN_6O_2S$



idactamabum #

idactamab	immunoglobulin G1-kappa, anti-[*Homo sapiens* SLC1A5 (solute carrier family 1 member 5,neutral amino acid transporter, RDRC, M7V1,AAAT, ASCT2)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV4-34*01 (96.9%) -(IGHD) -IGHJ4*01 (100%)) [8.7.15] (1-121) -*Homo sapiens* IGHG1*03 G1m3, nG1m1 (CH1 R120 (218) (122-219), hinge 1-15 (220-234), CH2 3^4>ins^cysteinyl (244) (235-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452))(122-452)], (224-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (94.7%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (230-230'':233-233'')-bisdisulfide, produced in a Chinese hamster ovary (CHO) cell line derived from CHO-K1, glycoform alfa
idactamab	immunoglobuline G1-kappa, anti-[*Homo sapiens* SLC1A5 (famille du porteur soluté 1 membre 5, transporteur d'acide aminé neutre, RDRC, M7V1, AAAT, ASCT2)], anticorps monoclonal *Homo sapiens;* chaîne lourde gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV4-34*01 (96.9%) -(IGHD) -IGHJ4*01 (100%)) [8.7.15] (1-121) -*Homo sapiens* IGHG1*03 G1m3, nG1m1 (CH1 R120 (218) (122-219), charnière 1-15 (220-234), CH2 3^4>ins^cysteinyl (244) (235-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (122-452)], (224-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (94.7%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (230-230'':233-233'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) dérivant de la lignée cellulaire CHO-K1, glycoforme alfa
idactamab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* SLC1A5 (familia del portador de soluto 1 miembro 5, transportador de ácido amino neutral, RDRC, M7V1, AAAT, ASCT2)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV4-34*01 (96.9%) -(IGHD) -IGHJ4*01 (100%)) [8.7.15] (1-121) -*Homo sapiens* IGHG1*03 G1m3, nG1m1 (CH1 R120 (218) (122-219), bisagra 1-15 (220-234), CH2 3^4>ins^cisteinil (244) (235-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (122-452)], (224-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (94.7%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (230-230'':233-233'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular derivada de CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQQWGAG LLKPSETLSL TCAVYGGSFS GYYWSWIRQP PGKGLEWIGE  5C
IHHSGGANYN PSLKSRVTIS VDTSKNQFSL KLSSVTAADT AVYYCARGQG 100
KNWHYDYFDY WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKRVE PKSCDKTHTC PPCPAPELLG GPSCVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE 350
PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP 450
GK                                                      452
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPST LSASVGDRVT ITCRASQSIR SWLAWYQQKP GKAPKLLIYK  5C
ASILKIGVPS RFSGSGSGTE FTLTISSLQP DDFATYYCQQ YYSYSRTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                         214
```

Post-translational modifications

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

```
Intra-H (C23-C104)  22-95    148-204   266-326   372-430
                    22"-95"  148"-204"  266"-326"  372"-430"
Intra-L (C23-C104)  23'-88'  134'-194'
                    23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126)  224-214'  224"-214'"
Inter-H-H (h 11, h 14)  230-230"  233-233"
```

Cysteinyl inserted for conjugation capped by a cysteinyl
HCH2C3^4):
244, 244"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
HCH2N84.4:
302, 302"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

C-terminal lysine clipping:
HCHSK2:
452, 452"

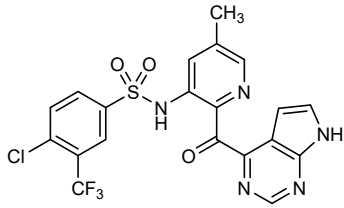
ilacirnonum

ilacirnon — 4-chloro-*N*-[5-methyl-2-(7*H*-pyrrolo[2,3-*d*]pyrimidine-4-carbonyl)pyridin-3-yl]-3-(trifluoromethyl)benzene-1-sulfonamide

ilacirnon — 4-chloro-*N*-[5-méthyl-2-(7*H*-pyrrolo[2,3-*d*]pyrimidine-4-carbonyl)pyridin-3-yl]-3-(trifluorométhyl)benzène-1-sulfonamide

ilacirnón — 4-cloro-*N*-[5-metil-2-(7*H*-pirrolo[2,3-*d*]pirimidina-4-carbonil)piridin-3-il]-3-(trifluorometil)benceno-1-sulfonamida

$C_{20}H_{13}ClF_3N_5O_3S$



insulinum icodecum

insulin icodec — human insulin A-chain (1-21) variant (Y>E^{14}), human insulin B-chain (1-29) variant (Y>H^{16}, F>H^{25}) conjugated at K^{29B} at its N^6 to (22*S*)-22,42-dicarboxy-10,19,24-trioxo-3,6,12,15-tetraoxa-9,18,23-triazadotetracontan-1-oyl; $N^{6.29B}$-[(22*S*)-22,42-dicarboxy-10,19,24-trioxo-3,6,12,15-tetraoxa-9,18,23-triazadotetracontan-1-oyl]-[Tyr14^A>Glu, Tyr16^B>His, Phe25^B>His]-des-Thr30^B-human insulin

insuline icodec

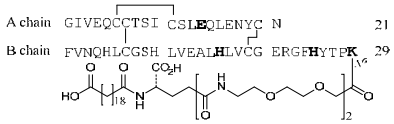
chaîne A de l'insuline humaine (1-21) variant (Y>E^{14}), chaîne B de l'insuline humaine (1-29) variant (Y>H^{16}, F>H^{25}), conjuguée en K^{29B} par son *N*^{6} à (22*S*)-22,42-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazadotétracontan-1-oyle; *N*$^{6.29B}$-[(22*S*)-22,42-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazadotétracontan-1-oyl]-[Tyr14^{A}>Glu, Tyr16^{B}>His, Phé25^{B}>His]-des-Thr30^{B}-insuline humaine

insulina icodec

insulina humana cadena-A (1-21) variante (Y>E^{14}), insulina humana cadena-B (1-29) variante (Y>H^{16}, F>H^{25}) conjugada con K^{29B} con su *N*^{6} al (22*S*)-22,42-dicarboxi-10,19,24-trioxo-3,6,12,15-tetraoxa-9,18,23-triazadotetracontan-1-oilo; *N*$^{6.29B}$-[(22*S*)-22,42-dicarboxi-10,19,24-trioxo-3,6,12,15-tetraoxa-9,18,23-triazadotetracontan-1-oil]-[Tir14^{A}>Glu, Tir16^{B}>His, Fen25^{B}>His]-des-Tre30^{B}-insulina humana

$C_{280}H_{435}N_{71}O_{87}S_6$

Sequences / Séquences / Secuencias



Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain 6^{A}-11^{A}
Inter-chain 7^{A}-7^{B}, 20^{A}-19^{B}

Modifications / Modifications / Modificaciones
Lys29^{B} conjugated at N^{ε}

inupadenantum

inupadenant

(+)-5-amino-3-{2-[4-(2,4-difluoro-5-{2-[(*S*)-methanesulfinyl]ethoxy}phenyl)piperazin-1-yl]ethyl}-8-(furan-2-yl)[1,3]thiazolo[5,4-*e*][1,2,4]triazolo[1,5-*c*]pyrimidin-2(3*H*)-one

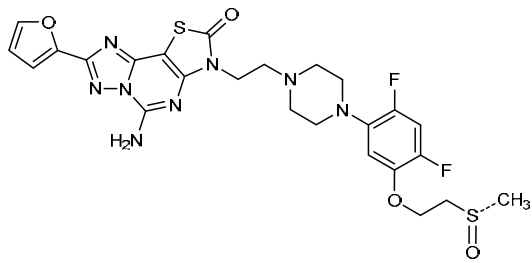
inupadénant

(+)-5-amino-3-{2-[4-(2,4-difluoro-5-{2-[(*S*)-méthanesulfinyl]éthoxy}phényl)pipérazin-1-yl]éthyl}-8-(furan-2-yl)[1,3]thiazolo[5,4-*e*][1,2,4]triazolo[1,5-*c*]pyrimidin-2(3*H*)-one

inupadenant

(+)-5-amino-3-{2-[4-(2,4-difluoro-5-{2-[(*S*)-metanosulfinil]etoxi}fenil)piperazin-1-il]etil}-8-(furan-2-il)[1,3]tiazolo[5,4-*e*][1,2,4]triazolo[1,5-*c*]pirimidin-2(3*H*)-ona

$C_{25}H_{26}F_2N_8O_4S_2$



invimestrocelum

invimestrocel	Allogeneic human multipotent adult progenitor cells (MAPC) derived from bone marrow and isolated by density gradient centrifugation. The cells are expanded *ex vivo* on fibronectin-coated surfaces under low-oxygen conditions and in the presence of growth media for the creation of a master cell bank (passage 4), a working cell bank (passage 6) and active substance (passage 9). The cells are adherent, secrete proangiogenic factors (including VEGF, IL-8 and CXCL5) and of mesenchymal progenitor lineage (*in vitro* differentiation to endothelial, hepatic and neuronal lineages). The cells express CD49c and CD90 (≥ 95% of the cells), and lack expression of CD45 and HLA II (< 5%). Additional markers include >90% CD13, CD44, CD73, CD105 and <5% CD34. The cells have also been shown to induce T cell suppression.
invimestrocel	Cellules humaines adultes progénitrices multipotentes qui sont allogéniques (MAPC), dérivées de la moelle osseuse et isolées par centrifugation à gradient de densité. Les cellules sont amplifiées *ex vivo* sur des surfaces recouvertes de fibronectine dans des conditions de faible teneur en oxygène et en présence de milieux de croissance pour la création d'une banque de cellules primaires (passage 4) et d'une banque de cellules de travail (passage 6) et d'une substance active produit fini (passage 9). Les cellules sont adhérentes, sécrètent des facteurs pro-angiogéniques (notamment le VEGF, l'IL-8 et la CXCL5) et sont de la lignée progénitrice mésenchymateuse (différenciation *in vitro* en lignées endothéliales, hépatiques et neuronales). Les cellules expriment CD49c et CD90 (≥ 95% des cellules), et sont négatives pour CD45 et HLA II (< 5%). Les marqueurs supplémentaires comprennent > 90 % de CD13, CD44, CD73, CD105 et < 5 % de CD34. Il a également été démontré que les cellules induisent la suppression des lymphocytes T.
invimestrocel	Células progenitoras adultas multipotentes humanas alogénicas (MAPC) derivadas de médula ósea y aisladas mediante centrifugación en gradiente de densidad. Las células se expanden *ex vivo* en superficies cubiertas de fibronectina en condiciones de oxígeno bajo y en presencia de medio de crecimiento para la creación de un banco de células maestro (pase 4) y un banco de células de trabajo (pase 6) y el principio activo (pase 9). Las células son adherentes, secretan factores proangiogénicos (incluyendo VEGF, IL-8 y CXCL5) y son de la línea progenitora mesenquimal (diferenciación *in vitro* a las líneas endotelial, hepática y neuronal). Las células expresan CD49c (≥ 95% de las células), y carecen de expresión de CD45 y HLA II (<5%). Otros marcadores adicionales incluyen >90% de CD13, CD44, CD73, CD105 y <5% de CD34. Se ha demostrado también que las células inducen supresión de linfocitos T.

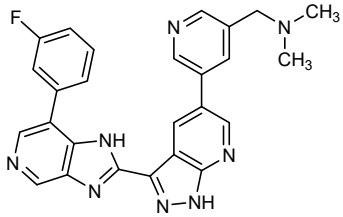
ipivivintum

ipivivint — 1-(5-{3-[7-(3-fluorophenyl)-1*H*-imidazo[4,5-*c*]pyridin-2-yl]-1*H*-pyrazolo[3,4-*b*]pyridin-5-yl}pyridin-3-yl)-*N*,*N*-dimethylmethanamine

ipivivint — 1-(5-{3-[7-(3-fluorophényl)-1*H*-imidazo[4,5-*c*]pyridin-2-yl]-1*H*-pyrazolo[3,4-*b*]pyridin-5-yl}pyridin-3-yl)-*N*,*N*-diméthylméthanamine

ipivivint — 1-(5-{3-[7-(3-fluorofenil)-1*H*-imidazo[4,5-*c*]piridin-2-il]-1*H*-pirazolo[3,4-*b*]piridin-5-il}piridin-3-il)-*N*,*N*-dimetilmetanamina

$C_{26}H_{21}FN_8$



izuralimabum #

izuralimab — immunoglobulin half-IG G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* ICOS (inductible T-cell costimulatory, activation-inducible lymphocyte immunomediatory molecule, AILIM, CD278)] and anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], monoclonal antibody, bispecific; gamma1 heavy chain anti-ICOS (1-454) [VH (*Homo sapiens* IGHV1-2*02 (99%) -(IGHD) -IGHJ3*02 (100%)) CDR-IMGT [8.8.18] (26-33.51-58.97-114) (1-125) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 N114>D (216) R120>K (222) (126-223), hinge 1-15 (224-238), CH2 E1.4,L1.3>P (241), L1.2>V (242), G1.1>A (243), S29>K (274), Q84.2>E (302) (239-347), CH3 E12 (363), M14 (365), L24>D (375), K26>S (377), N44>D (391), Q97>E (425), N100>D (428), M107>L (435), N114>S (441) (348-452), CHS (453-454)) (126-454)], (228-214')-disulfide with kappa light chain anti-ICOS (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (96.8%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')];
IG scFv-h-CH2-CH3 single chain, anti-PDCD1 (1''-480'') [scFv-V-kappa-VH anti-PDCD1 (1''-249'')[V-KAPPA (*Homo sapiens* IGKV3-15*01 (80.0%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1''-107'') -20-mer tetrakis(glycyl-lysyl-prolyl-glycyl-seryl) linker (108''-127'') -VH (*Mus musculus* IGHV6-6*02 (87.0%) -(IGHD) -IGHJ1*03 (86.7%)/*Homo sapiens* IGHV3-15*07 (81.8%) -(IGHD) -IGHJ2*01 (93.3%)) CDR-IMGT [8.10.13] (153-160.178-187.226-238) (128''-249'')] -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (250''-480'') [hinge 1-15 C5>S (254) (250-264) -CH2 E1.4,L1.3>P (267), L1.2>V (268), G1.1>A (269), S29>K (300) (265-373),CH3 E12 (389), E13>Q (390), M14 (391), S20>K (397), M107>L (461), N114>S (467) (374-478), CHS (479-480)]];
dimer (234-260'':237-263'')-bisdisulfide, produced in Chinese hamster ovary (CHO)-S cell line, glycoform alfa

izuralimab

immunoglobuline demi-IG G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* ICOS (costimulateur inductible du lymphocyte T, molécule immunomédiateur lymphocytaire inductible par activation, AILIM, CD278)] et anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal, bispécifique;
chaîne lourde gamma1 anti-ICOS (1-454) [VH (*Homo sapiens* IGHV1-2*02 (99%) -(IGHD) -IGHJ3*02 (100%)) CDR-IMGT [8.8.18] (26-33.51-58.97-114) (1-125) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 N114>D (216) R120>K (222) (126-223), charnière 1-15 (224-238), CH2 E1.4,L1.3>P (241), L1.2>V (242), G1.1>A (243), S29>K (274), Q84.2>E (302) (239-347), CH3 E12 (363), M14 (365), L24>D (375), K26>S (377), N44>D (391), Q97>E (425), N100>D (428), M107>L (435), N114>S (441) (348-452), CHS (453-454)) (126-454)], (228-214')-disulfure avec la chaîne légère kappa anti-ICOS (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (96.8%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')];
IG scFv-h-CH2-CH3 chaîne unique, anti-PDCD1 (1''-480'') [scFv V-kappa-VH anti-PDCD1 (1''-249'') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (80.0%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1''-107'') -20-mer tétrakis(glycyl-lysyl-prolyl-glycyl-séryl) linker (126''-145'') -VH (*Mus musculus* IGHV6-6*02 (87.0%) -(IGHD) -IGHJ1*03 (86.7%)/*Homo sapiens* IGHV3-15*07 (81.8%) -(IGHD) -IGHJ2*01 (93.3%)) CDR-IMGT [8.10.13] (153-160.178-187.226-238) (128''-249'')] -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (250''-480'') [charnière 1-15 C5>S (254) (250-264) -CH2 E1.4,L1.3>P (267), L1.2>V (268), G1.1>A (269), S29>K (300) (265-373), CH3 E12 (389), E13>Q (390), M14 (391), S20>K (397), M107>L (461), N114>S (467) (374-478), CHS (479-480)]];
dimère (234-260'':237-263'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-S, glycoforme alfa

izuralimab

inmunoglobulina demi-IG G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* ICOS (coestimulador inducible del linfocito T, molécula inmunomediadora linfocitaria inducible por activación, AILIM, CD278)] y anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal, biespecífico;
cadena pesada gamma1 anti-ICOS (1-454) [VH (*Homo sapiens* IGHV1-2*02 (99%) -(IGHD) -IGHJ3*02 (100%)) CDR-IMGT [8.8.18] (26-33.51-58.97-114) (1-125) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 N114>D (216) R120>K (222) (126-223), bisagra 1-15 (224-238), CH2 E1.4,L1.3>P (241), L1.2>V (242), G1.1>A (243), S29>K (274), Q84.2>E (302) (239-347), CH3 E12 (363), M14 (365), L24>D (375), K26>S (377), N44>D (391), Q97>E (425), N100>D (428), M107>L (435), N114>S (441) (348-452), CHS (453-454)) (126-454)], (228-214')-disulfuro con la cadena ligera kappa anti-ICOS (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (96.8%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')];
IG scFv-h-CH2-CH3 cadena única, anti-PDCD1 (1''-480'') [scFv V-kappa-VH anti-PDCD1 (1''-249'') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (80.0%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1''-107'') -20-mer tetrakis(glicil-lisil-prolil-glicil-seril) linker (126''-145'') -VH (*Mus musculus* IGHV6-6*02 (87.0%) -(IGHD) -IGHJ1*03 (86.7%)/*Homo sapiens* IGHV3-15*07 (81.8%) -(IGHD) -IGHJ2*01 (93.3%)) CDR-IMGT [8.10.13] (153-160.178-187.226-238) (128''-249'')] -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (250''-480'') [bisagra 1-15 C5>S (254) (250-264) -CH2 E1.4,L1.3>P (267), L1.2>V (268), G1.1>A (269), S29>K (300) (265-373), CH3 E12 (389), E13>Q (390), M14 (391), S20>K (397), M107>L (461), N114>S (467) (374-478), CHS (479-480)]];
dímero (234-260'':237-263'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-S, forma glicosilada alfa

1.Heavy chain / Chaîne lourde / Cadena pesada (anti-ICOS)

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT GYYMHWVRQA PGQGLEWMGW  50
INPHSGGTNY AQKFQGRVTM TRDTSISTAY MELSRLRSDD TAVYYCARTY 100
YYDSSGYYHD AFDIWGQGTM VTVSSASTKG PSVFPLAPSS KSTSGGTAAL 150
GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS 200
LGTQTYICNV NHKPSDTKVD KKVEPKSCDK THTCPPCPAP PVAGPSVFLF 250
PPKPKDTLMI SRTPEVTCVV VDVKHEDPEV KFNWYVDGVE VHNAKTKPRE 300
EEYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE KTISKAKGQP 350
REPQVYTLPP SREEMTKNQV SLTCDVSGFY PSDIAVEWES DGQPENNYKT 400
TPPVLDSDGS FFLYSKLTVD KSRWEQGDVF SCSVLHEALH SHYTQKSLSL 450
SPGK                                                    454
```

2. Light chain / Chaîne légère / Cadena ligera (anti-ICOS)

```
DIQMTQSPSS VSASVGDRVT ITCRASQGIS RLLAWYQQKP GKAPKLLIYV  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ ANSFPWTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

3. Chain / Chaîne / Cadena IG scFv-h-CH2-CH3 (anti-PDCD1)

```
EIVLTQSPAT LSASPGERVT LTCRASQSVG NDVAWYQQKP GQAPRLLINY  50
ASHRYTGVPD RFTGSGYGTE FTLTISSVQS EDFGVYYCQQ DFSSPRTFGG 100
GTKVEIKGKP GSGKPGSGKP GSGKPGSEVQ LVESGGGLVK PGGSLRLSCV 150
ASGFTFSNYW MNWVRQAPGK GLEWVAEIRL YSNNYATHYA ESVKGRFTIS 200
RDDSKSTLYL QMNNLKTEDT GVYYCTRYYG NYGGYFDVWG RGTLVTVSSE 250
PKSSDKTHTC PPCPAPPVAG PSVFLFPPKP KDTLMISRTP EVTCVVVDVK 300
HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK 350
EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSREQ MTKNQVKLTC 400
LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW 450
QQGNVFSCSV LHEALHSHYT QKSLSLSPGK                       480
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 152-208 268-328 374-432
Intra-L (C23-C104) 23'-88' 134'-194'
Intra-chain 3 23"-88" 149"-225" 294"-354" 400"-458"
Inter-H-L (h 5-CL 126) 228-214'
Inter-H-chain 3 (h 11, h 14) 234-260" 237-263"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
304, 330"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

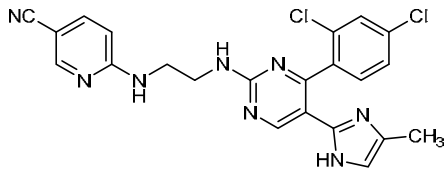
laduviglusibum

laduviglusib — 6-[(2-{[4-(2,4-dichlorophenyl)-5-(4-methyl-1*H*-imidazol-2-yl)pyrimidin-2-yl]amino}ethyl)amino]pyridine-3-carbonitrile

laduviglusib — 6-[(2-{[4-(2,4-dichlorophényl)-5-(4-méthyl-1*H*-imidazol-2-yl)pyrimidin-2-yl]amino}éthyl)amino]pyridine-3-carbonitrile

laduviglusib — 6-[(2-{[4-(2,4-diclorofenil)-5-(4-metil-1*H*-imidazol-2-il)pirimidin-2-il]amino}etil)amino]piridina-3-carbonitrilo

$C_{22}H_{18}Cl_2N_8$



lazucirnonum

lazucirnon — (4^2*R*)-1^4-chloro-*N*,*N*,1^3,7^6-tetramethyl-4^5,5-dioxo-6-aza-7(2)-pyridina-3(1,4)-piperidina-4(1,2)-pyrrolidina-1(1)-benzenaheptaphane-7^4-carboxamide

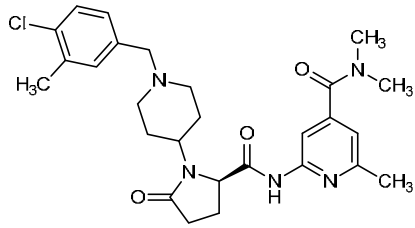
lazucirnon

(4^2*R*)-1^4-chloro-*N*,*N*,1^3,7^6-tétraméthyl-4^5,5-dioxo-6-aza-7(2)-pyridina-3(1,4)-pipéridina-4(1,2)-pyrrolidina-1(1)-benzénaheptaphane-7^4-carboxamide

lazucirnón

(4^2*R*)-1^4-cloro-*N*,*N*,1^3,7^6-tetrametil-4^5,5-dioxo-6-aza-7(2)-piridina-3(1,4)-piperidina-4(1,2)-pirrolidina-1(1)-bencenaheptafano-7^4-carboxamida

$C_{27}H_{34}ClN_5O_3$



lerodalcibepum #

lerodalcibep

engineered binding protein (1-96) anti-(human proprotein convertase subtilisin/kexin type 9), derived from human tenth fibronectin type III domain, fused via peptidyl linker (^{97}GSGSGS^{102}) to human serum albumin (103-687), variant (C^{34}>A^{136}), produced in Chinese hamster ovary (CHO) cells;
human fibronectin tenth type III domain variant anti-[human PCSK9 (pro-protein convertase subtilisin/kexin type 9, neural apoptosis-regulated convertase 1, NARC-1, proprotein convertase 9, PC9)] (1-96) fused via a $(GS)_3$ peptide linker (97-102) with [Cys^{34}>Ala (136)]-human serum albumin (HSA) (103-687), produced in Chinese hamster ovary (CHO) cells, non-glycosylated

lérodalcibep

protéine de liaison mise au point (1-96) anti-(proprotéine convertase subtilisine/kexine type 9), dérivée du dixième domaine de la fibronectine humaine de type III, fusionnée via un peptide de liaison (^{97}GSGSGS^{102}) à l'albumine sérique humaine (103-687), variant (C^{34}>A^{136}), produit dans des cellules ovariennes de hamster chinois (CHO);
peptide variant du dixième domaine de la fibronectine humaine de type III anti-[PCSK9 humain (proprotéine convertase subtilisine/kexine type 9, convertase 1 régulée par l'apoptose neuronale, NARC-1, proprotéine convertase 9, PC9)] (1-96) fusionné via un peptide $(GS)_3$ (97-102) à la [Cys^{34}>Ala (136)]-albumine sérique humaine (ASH) (103-687), produit dans des cellules ovariennes de hamsters chinois (CHO), non-glycosylé

lerodalcibep

proteína de unión diseñada (1-96) anti-(proproteína convertasa humana subtilisina/kexina tipo 9), derivada del décimo dominio de la fibronectina humana del tipo III, fusionada a través de un conector peptidil (^{97}GSGSGS^{102}) a la albúmina sérica humana (103-687), variante (C^{34}>A^{136}), producido en células ováricas de hámster Chino (CHO);

variante del décimo dominio de la fibronectina humana del tipo III anti-[PCSK9 humano (proproteína convertasa subtilisina/kexina tipo 9, convertasa 1 regulada por la apoptosa neuronal, NARC-1, proproteína convertasa 9, PC9)] fusionada mediante un péptido $(GS)_3$ (97-102) a la [Cis^{34}>Ala (136)]-albúmina sérica humana (ASH) (103-687), producido en células ováricas de hámster Chino (CHO), no glicosilado

Sequence / Séquence / Secuencia

```
VSDVPRDLEV VAATPTSLLI SWDAPAEGYG YYRITYGETG GNSPVQEFTV   50
PVSKGTATIS GLKPGVDYTI TVYAVEFDFP GAGYYHRPIS INYRTEGSGS  100
GSDAHKSEVA HRFKDLGEEN FKALVLIAFA QYLQQAPFED HVKLVNEVTE  150
FAKTCVADES AENCDKSLHT LFGDKLCTVA TLRETYGEMA DCCAKQEPER  200
NECFLQHKDD NPNLPRLVRP EVDVMCTAFH DNEETFLKKY LYEIARRHPY  250
FYAPELLFFA KRYKAAFTEC CQAADKAACL LPKLDELRDE GKASSAKQRL  300
KCASLQKFGE RAFKAWAVAR LSQRFPKAEF AEVSKLVTDL TKVHTECCHG  350
DLLECADDRA DLAKYICENQ DSISSKLKEC CEKPLLEKSH CIAEVENDEM  400
PADLPSLAAD FVESKDVCKN YAEAKDVFLG MFLYEYARRH PDYSVVLLLR  450
LAKTYETTLE KCCAAADPHE CYAKVFDEFK PLVEEPQNLI KQNCELFEQL  500
GEYKFQNALL VRYTKKVPQV STPTLVEVSR NLGKVGSKCC KHPEAKRMPC  550
AEDYLSVVLN QLCVLHEKTP VSDRVTKCCT ESLVNRRPCF SALEVDETYV  600
PKEFNAETFT FHADICTLSE KERQIKKQTA LVELVKHKPK ATKEQLKAVM  650
DDFAAFVEKC CKADDKETCF AEEGKKLVAA SQAALGL                687
```

Mutation / Mutation / Mutación

C^{136}>**A**

Post-translational modifications

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

155-164, 177-192, 193-203, 226-270, 271-279, 302-347, 348-355, 367-380, 381-391, 418-462, 463-471, 494-539, 540-550, 563-578, 579-589, 616-660, 661-669

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación

none / aucune / ninguna

letaplimabum #

letaplimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* CD47 (integrin associated protein, IAP, MER6, OA3)], *Homo sapiens* monoclonal antibody;
gamma4 heavy chain *Homo sapiens* (1-441) [VH (*Homo sapiens* IGHV4-59*01 (100%) -(IGHD) - IGHJ1*01 (100%)) CDR-IMGT [8.7.9] (26-33.51-57.96-104) (1-115)-*Homo sapiens* IGHG4*01, G4v4 CH2 A1.3, A1.2 (CH1 (116-213), hinge 1-12 S10>P (223) (214-225), CH2 F1.3>A (229), L1.2>A (230) (226-335), CH3 (336-440), CHS K>del (441) (116-441)], (129-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (96.8%) -IGKJ4*01 (91.7%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (221-221":224-224")-bisdisulfide, produced in Chinese hamster ovary (CHO)-S cell line, glycoform alfa

létaplimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* CD47 (protéine associée à l'intégrine, IAP, MER6, OA3)], anticorps monoclonal *Homo sapiens*;

	chaîne lourde gamma4 *Homo sapiens*(1-441) [VH (*Homo sapiens* IGHV4-59*01 (100%) -(IGHD) - IGHJ1*01 (100%)) CDR-IMGT [8.7.9] (26-33.51-57.96-104) (1-115) -*Homo sapiens* IGHG4*01, G4v4 CH2 A1.3, A1.2 (CH1 (116-213), charnière 1-12 S10>P (223) (214-225), CH2 F1.3>A (229), L1.2>A (230) (226-335), CH3 (336-440), CHS K>del (441) (116-441)], (129-214')-disulfure avec la chaîne légère kappa *Homo sapiens*(1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (96.8%) -IGKJ4*01 (91.7%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (221-221":224-224")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-S, glycoforme alfa
letaplimab	inmunoglobulina G4-kappa, anti-[*Homo sapiens* CD47 (proteína asociada a la integrina, IAP, MER6, OA3)], anticuerpo monoclonal *Homo sapiens;* cadena pesada gamma4 *Homo sapiens*(1-441) [VH (*Homo sapiens* IGHV4-59*01 (100%) -(IGHD) - IGHJ1*01 (100%)) CDR-IMGT [8.7.9] (26-33.51-57.96-104) (1-115) -*Homo sapiens* IGHG4*01, G4v4 CH2 A1.3, A1.2 (CH1 (116-213), bisagra 1-12 S10>P (223) (214-225), CH2 F1.3>A (229), L1.2>A (230) (226-335), CH3 (336-440), CHS K>del (441) (116-441)], (129-214')-disulfuro con la cadena ligera kappa *Homo sapiens*(1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (96.8%) -IGKJ4*01 (91.7%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (221-221":224-224")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYYWSWIRQP PGKGLEWIGY  50
IYYSGSTNYN PSLKSRVTIS VDTSKNQFSL KLSSVTAADT AVYYCARGKT 100
GSAAWGQGTL VTVSSASTKG PSVFPLAPCS RSTSESTAAL GCLVKDYFPE 150
PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS LGTKTYTCNV 200
DHKPSNTKVD KRVESKYGPP CPPCPAPEAA GGPSVFLFPP KPKDTLMISR 250
TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV 300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ 350
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF 400
LYSRLTVDKS RWQEGNVFSC SVMHEALHNH YTQKSLSLSL G          441
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS VSASVGDRVT ITCRASQGIS RWLAWYQQKP GKAPKLLIYA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TVSFPITFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 142-198 256-316 362-420
22"-95" 142"-198" 256"-316" 362"-420"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (CH1 10-CL 126) 129-214' 129"-214'"
Inter-H-H (h 8, h 11) 221-221" 224-224"

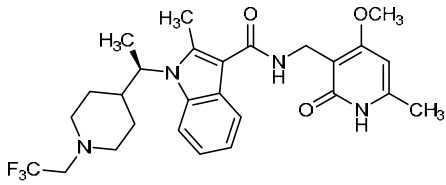
N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
L VH Q1:
1, 1"

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

lirametostatum

lirametostat	*N*-[(4-methoxy-6-methyl-2-oxo-1,2-dihydropyridin-3-yl)methyl]-2-methyl-1-{(1*R*)-1-[1-(2,2,2-trifluoroethyl)piperidin-4-yl]ethyl}-1*H*-indole-3-carboxamide
liramétostat	*N*-[(4-méthoxy-6-méthyl-2-oxo-1,2-dihydropyridin-3-yl)méthyl]-2-méthyl-1-{(1*R*)-1-[1-(2,2,2-trifluoroéthyl)pipéridin-4-yl]éthyl}-1*H*-indole-3-carboxamide
lirametostat	2-metil-*N*-[(6-metil-4-metoxi-2-oxo-1,2-dihidropiridin-3-il)metil]-1-{(1*R*)-1-[1-(2,2,2-trifluoroetil)piperidin-4-il]etil}-1*H*-indol-3-carboxamida

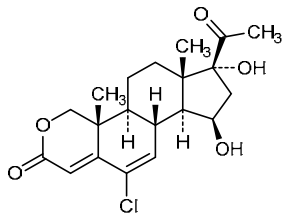
$C_{27}H_{33}F_3N_4O_3$



ludateronum

ludaterone	6-chloro-15β,17-dihydroxy-2-oxapregna-4,6-diene-3,20-dione
ludatérone	6-chloro-15β,17-dihydroxy-2-oxaprégna-4,6-diène-3,20-dione
ludaterona	6-cloro-15β,17-dihidroxi-2-oxapregna-4,6-dieno-3,20-diona

$C_{20}H_{25}ClO_5$



lutetium (^{177}Lu) vipivotidum tetraxetanum

lutetium (^{177}Lu) vipivotide tetraxetan	{*N*-[(N^6-{3-(naphthalen-2-yl)-*N*-[*trans*-4-({2-[4,7,10-tris(carboxy-κ$^3O^4$,O^7,O^{10}-methyl)-1,4,7,10-tetraazacyclododecan-1-yl-κ$^4N^1$,N^4,N^7,N^{10}]acetamido-κ*O*}methyl)cyclohexane-1-carbonyl]-L-alanyl}-L-lysin-N^2-yl)carbonyl]-L-glutamato(3−)}(^{177}Lu)lutetium

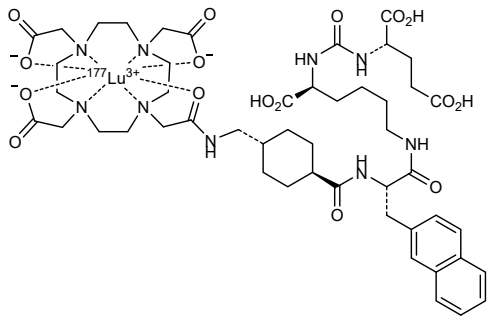
lutécium (^{177}Lu) vipivotide tétraxetan

{*N*-[(*N*^{6}-{3-(naphtalén-2-yl)-*N*-[*trans*-4-({2-[4,7,10-tris(carboxy-κ^3*O*^{4},*O*^{7},*O*^{10}-méthyl)-1,4,7,10-tétraazacyclododécan-1-yl-κ^4*N*^{1},*N*^{4},*N*^{7},*N*^{10}]acétamido-κ*O*}méthyl)cyclohexane-1-carbonyl]-L-alanyl}-L-lysin-*N*^{2}-yl)carbonyl]-L-glutamato(3−)}(^{177}Lu)lutecium

lutecio (^{177}Lu) vipivotida tetraxetán

{*N*-[(*N*^{6}-{3-(naftalen-2-il)-*N*-[*trans*-4-({2-[4,7,10-tris(carboxi-κ^3*O*^{4},*O*^{7},*O*^{10}-metil)-1,4,7,10-tetraazaciclododecan-1-il-κ^4*N*^{1},*N*^{4},*N*^{7},*N*^{10}]acetamido-κ*O*}metil)ciclohexano-1-carbonil]-L-alanil}-L-lisin-*N*^{2}-il)carbonil]-L-glutamato(3−)}(^{177}Lu)lutecio

$C_{49}H_{68}{}^{177}LuN_9O_{16}$



melrilimabum #

melrilimab

immunoglobulin G2-kappa, anti-[*Homo sapiens* IL1RL1 (interleukin 1 receptor like 1, DER4, FIT-1, growth stimulation expressed 2 gene, ST2, IL33R)], *Homo sapiens* monoclonal antibody;
gamma2 heavy chain *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV3-23*01 (91.8%) -(IGHD) -IGHJ4*01(92.9%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Homo sapiens* IGHG2*02v G2m23>G2m.., G2v3 CH2 A1.2, A1, S2, A30, L92, S115, S116 (CH1 T92 (195) (124-221), hinge 1-12 (222-233), CH2 V1.2>A (237), G1>A (239), P2>S (240), H30>A (270), M45.1>V (284), V92>L (311), A115>S (332), P116>S (333) (234-342), CH3 (343-447), CHS (448-449)) (124-449)], (137-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (95.6%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')];
dimer (225-225":226-226":229-229":232-232")-tetrakisdisulfide, produced in Chinese hamster ovary (CHO)-K1SV cell line lacking the Glutamine Synthetase (GS) gene, glycoform alfa

melrilimab

immunoglobuline G2-kappa, anti-[*Homo sapiens* IL1RL1 (récepteur like 1 de l'interleukine 1, DER4, FIT1, gène 2 exprimé lors de la stimulation de la croissance, ST2, IL33R)], anticorps monoclonal *Homo sapiens*;

chaîne lourde gamma2 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV3-23*01 (91.8%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Homo sapiens* IGHG2*02v G2m23>G2m.., G2v3 CH2 A1.2, A1, S2, A30, L92, S115, S116 (CH1 T92 (195) (124-221), charnière 1-12 (222-233), CH2 V1.2>A (237), G1>A (239), P2>S (240), H30>A (270), M45.1>V (284), V92>L (311), A115>S (332), P116>S (333) (234-342), CH3 (343-447), CHS (448-449)) (124-449)], (137-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (95.6%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (225-225":226-226":229-229":232-232")-tétrakisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1SV ne présentant pas le gène de la glutamine synthétase, glycoforme alfa

melrilimab

inmunoglobulina G2-kappa, anti-[*Homo sapiens* IL1RL1 (receptor like 1 de la interleukina 1, DER4, FIT1, gen 2 expresado durante la estimulación del crecimiento, ST2, IL33R)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma2 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV3-23*01 (91.8%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Homo sapiens* IGHG2*02v G2m23>G2m.., G2v3 CH2 A1.2, A1, S2, A30, L92, S115, S116 (CH1 T92 (195) (124-221), bisagra 1-12 (222-233), CH2 V1.2>A (237), G1>A (239), P2>S (240), H30>A (270), M45.1>V (284), V92>L (311), A115>S (332), P116>S (333) (234-342), CH3 (343-447), CHS (448-449)) (124-449)], (137-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (95.6%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (225-225":226-226":229-229":232-232")-tetrakisdisulfuro, producido en las células ováricas de hámsters chinos (CHO) línea celular CHO-K1SV en ausencia del gen Glutamina Sintetasa (GS)forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS IYDMIWVRQA PGKGLEWVSS  50
IRGEGGGTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARDP 100
WSTEGSFFVL DYWGQGTLVT VSSASTKGPS VFPLAPCSRS TSESTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVTSSNFG 200
TQTYTCNVDH KPSNTKVDKT VERKCCVECP PCPAPPAAAS SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSA EDPEVQFNWY VDGVEVHNAK TKPREEQFNS 300
TFRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK TKGQPREPQV 350
YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPML 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPAT LSLSPGERAT LSCRASQSVD DDLAWYQQKP GQAPRLLIYD  50
ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ YITAPLTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

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

```
Intra-H (C23-C104)   22-96     150-206  263-323  369-427
                    22"-96"  150"-206"  263"-323"  369"-427"
Intra-L (C23-C104)   23'-88'    134'-194'
                    23'"-88'"  134'"-194'"
Inter-H-L (CH1 10-CL 126)*    137-214'  137"-214'"
Inter-H-H (h 4, h 5, h 8, h 11)*  225-225"  226-226"  229-229"  232-232"
```

*In addition to the isoform A, isoform A/B characterized by an inter-H-H (h 4 - CH1 10) 225-137'" and an inter-H-L (h 4- CL 126) 225"-214'", instead of the inter-H-H (h 4 - h 4) 225-225" and of one of the two inter-H-L (CH1 10-CL 126) 137"-214'";
isoform B characterized by an inter-H-H (h 5 - CH1 10) 226-137 and an inter-H-L (h 5- CL 126) 226"-214', instead of the inter-H-H (h 5 - h 5) 226-226" and of the inter-H-L (CH1 10-CL 126) 137-214'.
* En plus de l'isoforme A, isoforme A/B caractérisée par un inter-H-H (h 4 - CH1 10) 225-137'" et un inter-H-L (h 4- CL 126) 225"-214'", au lieu de l'inter-H-H (h 4 - h 4) 225-225" et de l'un des deux inter-H-L (CH1 10-CL 126) 137"-214'";
isoforme B caractérisée par un inter-H-H (h 5 - CH1 10) 226-137 et un inter-H-L (h 5- CL 126) 226"-214', au lieu de l'inter-H-H (h 5 - h 5) 226-226" et de l'inter-H-L (CH1 10-CL 126) 137-214'.
* Además de la isoforma A, isoforma A/B caracterizado por un inter-H-H (h 4 - CH1 10) 225-137'" y un inter-H-L (h 4- CL 126) 225"-214'", enlugar del inter-H-H (h 4 - h 4) 225-225" y uno de los dos inter-H-L (CH1 10-CL 126) 137"-214'";
isoforma B caracterizado por un inter-H-H (h 5 - CH1 10) 226-137 y un inter-H-L (h 5- CL 126) 226"-214', en lugar del inter-H-H (h 5 - h 5) 226-226" y del inter-H-L (CH1 10-CL 126) 137-214'.

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

```
H CH2 N84.4:
299, 299'"
```

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

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

```
H CHS K2:
449, 449'"
```

milvexianum

milvexian

(5*R*,9*S*)-9-{4-[5-chloro-2-(4-chloro-1*H*-1,2,3-triazol-1-yl)phenyl]-6-oxopyrimidin-1(6*H*)-yl}-2^2-(difluoromethyl)-5-methyl-2^2*H*-3-aza-1(4,2)-pyridina-2(3,4)-pyrazolacyclononaphan-4-one

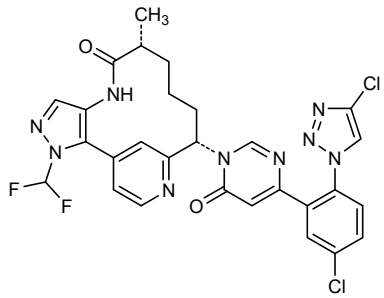
milvexian

(5*R*,9*S*)-9-{4-[5-chloro-2-(4-chloro-1*H*-1,2,3-triazol-1-yl)phényl]-6-oxopyrimidin-1(6*H*)-yl}-2^2-(difluorométhyl)-5-méthyl-2^2*H*-3-aza-1(4,2)-pyridina-2(3,4)-pyrazolacyclononaphan-4-one

milvexián

(5*R*,9*S*)-9-{4-[5-cloro-2-(4-cloro-1*H*-1,2,3-triazol-1-il)fenil]-6-oxopirimidin-1(6*H*)-il}-2^2-(difluorometil)-5-metil-2^2*H*-3-aza-1(4,2)-piridina-2(3,4)-pirazolaciclononafan-4-ona

$C_{28}H_{23}Cl_2F_2N_9O_2$



mipasetamabum #

mipasetamab

immunoglobulin G1-kappa, anti-[*Homo sapiens* AXL (AXL receptor tyrosine kinase, tyrosine-protein kinase receptor UFO)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-451) [VH humanized (*Homo sapiens* IGHV3-30*03 (92.9%) -(IGHD) -IGHJ4*01 (92.3%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122) -*Homo sapiens* IGHG1*03, G1m3>G1m17, nG1m1 (CH1 R>K 120 (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS K>del (451)) (123-451)], (225-215')-disulfide with kappa light chain humanized (1'-215') [V-KAPPA humanized (*Homo sapiens* IGKV3-11*01 (84.4%) -IGKJ4*01 (90.9%)) CDR-IMGT [7.3.9] (27-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')];
dimer (231-231":234-234")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

mipasétamab

immunoglobuline G1-kappa, anti-[*Homo sapiens* AXL (récepteur tyrosine kinase AXL, récepteur tyrosine-protéine kinase UFO)], anticorps monoclonal humanisé;

chaîne lourde gamma1 humanisée (1-451) [VH humanisé (*Homo sapiens* IGHV3-30*03 (92.9%) -(IGHD) -IGHJ4*01 (92.3%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122) -*Homo sapiens* IGHG1*03, G1m3>G1m17, nG1m1 (CH1 R>K 120 (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS K>del (451)) (123-451)], (225-215')-disulfure avec la chaîne légère kappa humanisée (1'-215') [V-KAPPA humanisé (*Homo sapiens* IGKV3-11*01 (84.4%) -IGKJ4*01 (90.9%)) CDR-IMGT [7.3.9] (27-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (231-231":234-234")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

mipasetamab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* AXL (receptor tirosina kinasa AXL, receptor tirosina-proteína kinasa UFO)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-451) [VH humanizado (*Homo sapiens* IGHV3-30*03 (92.9%) -(IGHD) -IGHJ4*01 (92.3%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122) -*Homo sapiens* IGHG1*03, G1m3>G1m17, nG1m1 (CH1 R>K 120 (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS K>del (451)) (123-451)], (225-215')-disulfuro con la cadena ligera kappa humanizada (1'-215') [V-KAPPA humanizado (*Homo sapiens* IGKV3-11*01 (84.4%) -IGKJ4*01 (90.9%)) CDR-IMGT [7.3.9] (27-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (231-231":234-234")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYGMSWVRQA PGKGLEWVAT  50
ISSGGSYTYY PDSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARHP 100
IYYTYDDTMD YWGQGTTVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELL GGPSVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE 350
PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP 450
G                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCSASSSVS SGNFHWYQQK PGLAPRLLIY  50
RTSNLASGIP ARFSGSGSGT DFTLTISSLE PEDFAVYYCQ QWSGYPWTFG 100
GGTKLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                        215
```

Post-translational modifications

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

Intra-H (C23-C104) 22-96 149-205 266-326 372-430
22"-96" 149"-205" 266"-326" 372"-430"
Intra-L (C23-C104) 23'-89' 135'-195'
23'"-89'" 135'"-195'"
Inter-H-L (h 5-CL 126) 225-215' 225"-215'"
Inter-H-H (h 11, h 14) 231-231" 234-234"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4 [glycoengineered GalNAcN3 (*N*-azidoacetyl-D-galactosamine)]:
302, 302"-bis[*N*-[*O*-2-(acetylamino)-6-azido-2,6-dideoxy- β-D-galactopyranosyl-(1->4)-*O*-[6-deoxy-α-L-galactopyranosyl-(1->6)]-2-(acetylamino)-2-deoxy- β-D-glucopyranosyl]-L-asparagine]

mipasetamabum uzoptirinum #

mipasetamab uzoptirine	immunoglobulin G1-kappa, anti-[*Homo sapiens* AXL (AXL receptor tyrosine kinase, tyrosine-protein kinase receptor UFO)], humanized monoclonal antibody conjugated to the pyrrolobenzodiazepine (PBD) dimer, SG3199; gamma1 heavy chain humanized (1-451) [VH humanized (*Homo sapiens* IGHV3-30*03 (92.9%) -(IGHD) -IGHJ4*01 (92.3%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122) -*Homo sapiens* IGHG1*03 nG1m1 (CH1 R120>K (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS K>del (451)) (123-451)], (225-215')-disulfide with kappa light chain humanized (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (84.4%) -IGKJ4*01 (90.9%)) CDR-IMGT [7.3.9] (27-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (231-231":234-234")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa; conjugated on the two glycoengineered N84.4, via a spacer and a cleavable valine-alanine linker, to the cytotoxic pyrrolobenzodiazepine (PBD) dimer, SG3199
mipasétamab uzoptirine	immunoglobuline G1-kappa, anti-[*Homo sapiens* AXL (récepteur tyrosine kinase AXL, récepteur tyrosine-protéine kinase UFO)], anticorps monoclonal humanisé conjugué au dimère de pyrrolobenzodiazépine (PDB), SG3199; chaîne lourde gamma1 humanisée (1-451) [VH (*Homo sapiens* IGHV3-30*03 (92.9%) -(IGHD) -IGHJ4*01 (92.3%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122) -*Homo sapiens* IGHG1*03 nG1m1 (CH1 R120>K (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS K>del (451)) (123-451)], (225-215')-disulfure avec la chaîne légère kappa humanisée (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (84.4%) -IGKJ4*01 (90.9%)) CDR-IMGT [7.3.9] (27-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (231-231":234-234")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa; conjugué sur les deux N84.4 glycomodifiés, via un espaceur et un linker clivable valine-alanine, au dimère pyrrolobenzodiazépine (PBD) cytotoxique, SG3199
mipasetamab uzoptirina	inmunoglobulina G1-kappa, anti-[*Homo sapiens* AXL (receptor tirosina kinasa AXL, receptor tirosina-proteína kinasa UFO)], anticuerpo monoclonal humanizado conjugado con el dímero de pirrolobenzodiazepina (PDB), SG3199; cadena pesada gamma1 humanizada (1-451) [VH (*Homo sapiens* IGHV3-30*03 (92.9%) -(IGHD) -IGHJ4*01 (92.3%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122) -*Homo sapiens* IGHG1*03 nG1m1 (CH1 R120>K (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS K>del (451)) (123-451)], (225-215')-disulfuro con la cadena ligera kappa humanizada (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (84.4%) -IGKJ4*01 (90.9%)) CDR-IMGT [7.3.9] (27-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')];

dímero (231-231":234-234")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa; conjugado sobre los dos N84.4 glicomodificados, mediante un espaciador y un conector escindible valina-alanina, al dímero pirrolobenzodiazepina (PBD) citotóxico, SG3199

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYGMSWVRQA PGKGLEWVAT  50
ISSGGSYTYY PDSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARHP 100
IYYTYDDTMD YWGQGTTVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELL GGPSVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE 350
PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP 450
G                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCSASSSVS SGNFHWYQQK PGLAPRLLIY  50
RTSNLASGIP ARFSGSGSGT DFTLTISSLE PEDFAVYYCQ QWSGYPWTFG 100
GGTKLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

Post-translational modifications

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

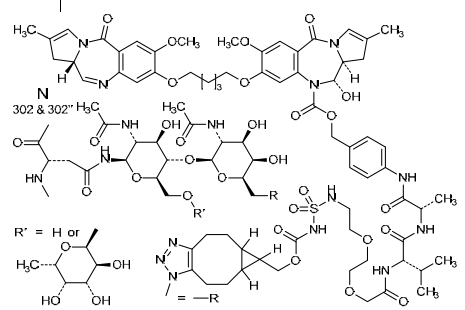
```
Intra-H (C23-C104)  22-96    149-205    266-326    372-430
                    22"-96"  149"-205"  266"-326"  372"-430"
Intra-L (C23-C104)  23'-89'    135'-195'
                    23'"-89'"  135'"-195'"
Inter-H-L (h 5-CL 126)  225-215'  225"-215'"
Inter-H-H (h 11, h 14)  231-231"  234-234"
```

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)

H VH Q1:
1, 1"

Chemically modified N-glycosylation sites / Sites de N-glycosylation chimiquement modifiés / Posiciones de N-glicosilación modificadas químicamente

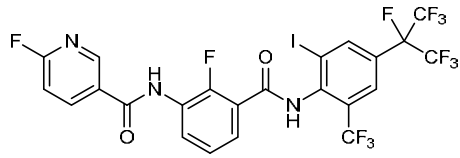
H CH2 N84.4:
302, 302"



modoflanerum

modoflaner	6-fluoro-*N*-(2-fluoro-3-{[4-(heptafluoropropan-2-yl)-2-iodo-6-(trifluoromethyl)phenyl]carbamoyl}phenyl)pyridine-3-carboxamide
modoflaner	6-fluoro-*N*-(2-fluoro-3-{[4-(heptafluoropropan-2-yl)-2-iodo-6-(trifluorométhyl)phényl]carbamoyl}phényl)pyridine-3-carboxamide
modoflaner	6-fluoro-*N*-(2-fluoro-3-{[4-(heptafluoropropan-2-il)-2-iodo-6-(trifluorometil)fenil]carbamoil}fenil)piridina-3-carboxamida

$C_{23}H_{10}F_{12}IN_3O_2$



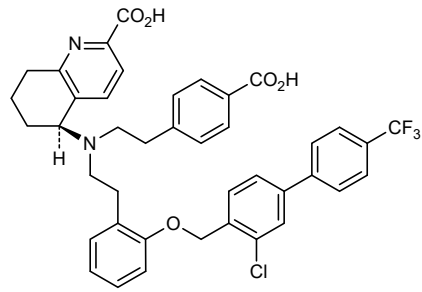
mosliciguatum

mosliciguat — (9^5*S*)-8-[2-(4-carboxyphenyl)ethyl]-2^3-chloro-1^4-(trifluoromethyl)-9^{5,6,7,8}-tetrahydro-4-oxa-8-aza-9(5)-quinolina-1(1),2(1,4),5(1,2)-tribenzenanonaphane-9^2-carboxylic acid

mosliciguat — acide (9^5*S*)-8-[2-(4-carboxyphényl)éthyl]-2^3-chloro-1^4-(trifluorométhyl)-9^{5,6,7,8}-tétrahydro-4-oxa-8-aza-9(5)-quinoléina-1(1),2(1,4),5(1,2)-tribenzénanonaphane-9^2-carboxylique

mosliciguat — ácido (9^5*S*)-8-[2-(4-carboxifenil)etil]-2^3-cloro-1^4-(trifluorometil)-9^{5,6,7,8}-tetrahidro-4-oxa-8-aza-9(5)-quinoleína-1(1),2(1,4),5(1,2)-tribencenanonafano-9^2-carboxílico

$C_{41}H_{36}ClF_3N_2O_5$



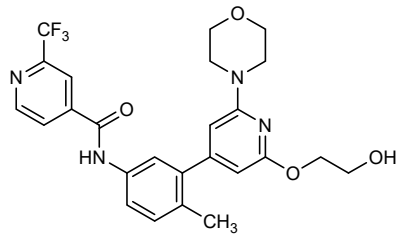
naporafenibum

naporafenib — *N*-{3-[2-(2-hydroxyethoxy)-6-(morpholin-4-yl)pyridin-4-yl]-4-methylphenyl}-2-(trifluoromethyl)pyridine-4-carboxamide

naporafénib — *N*-{3-[2-(2-hydroxyéthoxy)-6-(morpholin-4-yl)pyridin-4-yl]-4-méthylphényl}-2-(trifluorométhyl)pyridine-4-carboxamide

naporafenib — *N*-{3-[2-(2-hidroxietoxi)-6-(morfolin-4-il)piridin-4-il]-4-metilfenil}-2-(trifluorometil)piridina-4-carboxamida

$C_{25}H_{25}F_3N_4O_4$



nedosiranum

nedosiran

all-P-ambo-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluoroguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]pentanamido}ethoxy)ethoxy]methyl}guanylyl-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]pentanamido}ethoxy)ethoxy]methyl}adenylyl-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]pentanamido}ethoxy)ethoxy]methyl}adenylyl-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]pentanamido}ethoxy)ethoxy]methyl}adenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidine

duplex with *all-P-ambo*-2'-*O*-methyl-*P*-thioguanylyl-(5'→3')-2'-*O*-methyl-*P*-thioguanylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluorocytidylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thioguanylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thioadenylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thiocytidylyl-(5'→3')-methyl hydrogen 2'-*O*-methyl-5'-oxa-*O*-5'-carba-5'-uridylate

nédosiran

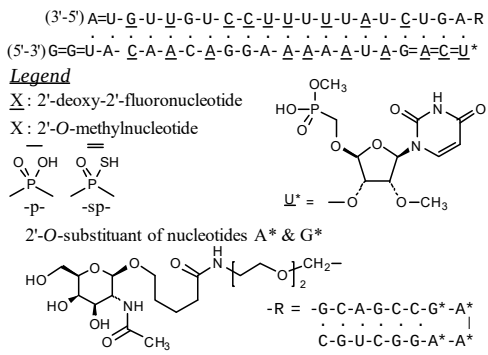
tout-P-ambo-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluoroguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-désoxy-2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

duplex avec acide *tout-P-ambo*-2'-*O*-méthyl-*P*-thioguanylyl-(5'→3')-2'-*O*-méthyl-*P*-thioguanylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyl-adénylyl-(5'→3')-2'-désoxy-2'-fluorocytidylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thioguanylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thioadénylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thiocytidylyl-(5'→3')-hydrogéno-2'-*O*-méthyl-5'-oxa-*O*-5'-carba-5'-uridylate de méthyle

nedosirán

todo-P-ambo-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluoroguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-des-oxi-2'-fluoroadenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluoro-citidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-pentanamido}etoxi)etoxi]metil}guanilil-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanamido}etoxi)etoxi]metil}adenilil-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanamido}etoxi)etoxi]metil}adenilil-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanamido}etoxi)etoxi]metil}adenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidina
dúplex con *todo-P-ambo*-2'-*O*-metil-*P*-tioguanilil-(5'→3')-2'-*O*-metil-*P*-tioguanilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluorocitidilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tioguanilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tioadenilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tiocitidilil-(5'→3')-hidrógeno-2'-*O*-metil-5'-oxa-*O*-5'-carba-5'-uridilato de metilo

$C_{662}H_{865}F_{19}N_{231}O_{413}P_{57}S_6$



nemvaleukinum alfa #

nemvaleukin alfa

human interleukin 2 fragment (1-59), variant (Cys^{125}>Ser^{51}), fused via peptidyl linker (^{60}GG^{61}) to human interleukin 2 fragment (62-132), fused via peptidyl linker (^{133}GSGGGS^{138}) to human interleukin 2 receptor α-chain fragment (139-303), produced in Chinese hamster ovary (CHO) cells, glycosylated; human interleukin 2 (IL-2) (75-133)-peptide [$Cys^{125(51)}$>Ser]-mutant (1-59), fused via a G_2 peptide linker (60-61) to human interleukin 2 (IL-2) (4-74)-peptide (62-132) and via a GSG_3S peptide linker (133-138) to human interleukin 2 receptor α-chain (IL2R subunit alpha, IL2Rα, IL2RA) (1-165)-peptide (139-303), produced in Chinese hamster ovary (CHO) cells, glycoform alfa

nemvaleukine alfa

fragment de l'interleukine 2 humaine (1-59), variant (Cys^{125}>Ser^{51}), fusionné via un peptide liant (^{60}GG^{61}) à un fragment de l'interleukine 2 humaine (62-132), fusionné via un peptide liant (^{133}GSGGGS^{138}) au fragment de la chaîne α du récepteur de l'interleukine 2 (139-303), produit dans des cellules ovariennes de hamsters chinois (CHO), glycosylé; peptide 75-133 d'interleukine 2 humaine (IL-2) mutante [$Cys^{125(51)}$>Ser] (1-59), fusionnée via un peptide G_2 (60-61) au peptide 4-74 d'inter-leukine humaine 2 (IL-2) (62-132) et via un peptide GSG_3S (133-138) au peptide 1-165 de la chaîne α du récepteur de l'interleukine 2 humaine (sous-unité alpha de IL2R, IL2Rα, IL2RA) (139-303), produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

nemvaleukina alfa

fragmento de interleukina 2 humana (1-59), variante (Cis^{125}>Ser^{51}), fusionado a través de un conector peptidil (^{60}GG^{61}) al fragmento de interleukina 2 humana (62-132), fusionado a través de un conector peptidil (^{133}GSGGGS^{138}) al fragmento humano de la cadena α del receptor de interleukina 2 (139-303), producido en células ováricas de hámster Chino (CHO), glicosilado;
péptido 75-133 de la interleukina 2 humana (IL-2) mutante [$Cis^{125(51)}$>Ser] (1-59), fusionado a través de un péptido G_2 (60-61) al péptido 4-74 de la interleukina 2 humana (IL-2) (62-132) y a través de un péptido GSG_3S (133-138) al péptido 1-165 de la cadena α del receptor de interleukina 2 humano (subunidad alfa de IL2R, IL2Rα, IL2RA) (139-303), producido en células ováricas de hámster Chino (CHO), glicosilada alfa

Sequence / Séquence / Secuencia

```
SKNFHLRPRD LISNINVIVL ELKGSETTFM CEYADETATI VEFLNRWITF   50
SQSIISTLTG GSSSTKKTQL QLEHLLLDLQ MILNGINNYK NPKLTRMLTF  100
KFYMPKKATE LKHLQCLEEE LKPLEEVLNL AQGSGGGSEL CDDDPPEIPH  150
ATFKAMAYKE GTMLNCECKR GFRRIKSGSL YMLCTGNSSH SSWDNQCQCT  200
SSATRNTTKQ VTPQPEEQKE RKTTEMQSPM QPVDQASLPG HCREPPPWEN  250
EATERIYHFV VGQMVYYQCV QGYRALHRGP AESVCKMTHG KTRWTQPQLI  300
CTG                                                     303
```

Mutation / Mutation / Mutación

C^{51}>S

Post-translational modifications

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

31-116, 141-285, 184-242, 269-301, 166-197 or 166-199, 168-199 or 168-197

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación

N187, N206, T212

obecabtagenum autoleucelum #

obecabtagene autoleucel

Autologous CD4+ and CD8+ T cells transduced *ex vivo* with a self-inactivating lentiviral vector encoding an anti-CD19 chimeric antigen receptor.
Autologous CD4+ and CD8+ T cells, enriched from peripheral blood mononuclear cells (PBMCs) obtained by apheresis transduced *ex vivo* with a non-replicating, self-inactivating (SIN) lentiviral vector, encoding a chimeric antigen receptor (CAR) consisting of an anti-CD19 specific scFv, a CD8α stalk, transmembrane domain and anchor, a 41BB endodomain and a CD3 zeta endodomain, under the control of a human PGK1 promoter and a modified Woodchuck post transcriptional response element. The vector genome also contains a 5' terminal CMV enhancer/promoter, a Ψ packaging signal, a Rev response element (RRE) and a central polypurine tract (cPPT).

obécabtagène autoleucel

Cellules T CD4+ et CD8+ autologues transduites *ex vivo* avec un vecteur lentiviral auto-inactivable codant pour un récepteur chimérique contre l'antigène CD19.
Cellules T CD4+ et CD8+ autologues, enrichies de cellules mononuclées de sang périphérique (PBMC) et obtenues par aphérèse, transduites *ex vivo* avec un vecteur lentiviral non réplicatif et auto-inactivable (SIN), codant pour un récepteur chimérique d'antigène (CAR) consistant en un scFv spécifique de CD19, un fragment extracellulaire, un domaine transmembranaire et la partie d'ancrage de CD8α, un endo-domaine de 41BB et un endo-domaine de CD3 zêta, sous le contrôle d'un promoteur PGK1 humain et d'un élément de réponse post-transcriptionnel Woodchuck modifié. Le génome du vecteur contient également un promoteur/amplificateur CMV placé en position terminale 5', un signal d'empaquetage Ψ, un élément de réponse Rev (RRE) et un segment central de polypurine (cPPT).

obecabtagén autoleucel

Células T CD4+ y CD8+ autólogas transducidas ex vivo con un vector lentiviral auto-inactivante que codifica para un receptor de antígenos quimérico anti-CD19.
Células T CD4+ y CD8+ autólogas, enriquecidas a partir de células mononucleares de sangre periférica (PBMCs) obtenidas por aféresis, transducidas *ex vivo* con un vector lentiviral no replicativo, auto-inactivante (SIN), que codifica para un receptor de antígenos quimérico (CAR) que consta de scFv específico anti-CD19, un tallo CD8α, un dominio transmembranal y de anclaje, un endodominio 41BB y un endodominio CD3 zeta, bajo el control de un promotor PGK1 humano y un elemento de respuesta post transcripcional de marmota modificado. El genoma del vector también contiene un potenciador (enhancer)/promotor de CMV en 5', una señal de empaquetamiento Ψ, un elemento de respuesta Rev (RRE) y un tramo central de polipurinas (cPPT).

obrindatamabum #

obrindatamab

immunoglobulin G1 scFv-h-CH2-CH3(_scFv)_h-CH2-CH3, anti-[*Homo sapiens* CD276 (B7H3, B7-H3, B7RP-2)] and anti-[*Homo sapiens* CD3E (CD3 epsilon)], monoclonal antibody, bispecific; IG scFv-h-CH2-CH3 single chain, anti-CD276 and anti-CD3E (1-504) [scFv-V-kappa-VH anti-CD276 and anti-CD3E (1-240) [V-KAPPA anti-CD276 (*Homo sapiens* IGKV1D-13*01 (85.1%) -IGHJ2*02 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1-107) -8-mer triglycyl-seryl-tetraglycyl linker (108-115) -VH anti-CD3E (*Mus musculus* IGHV10-1*02 (89.9%) -(IGHD) -GHJ3*01 (93.3%)/*Homo sapiens* IGHV3-72*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) CDR-IMGT [8.10.16] (141-148.166-175.214-229) (116-240)] -linker-E-coil (241-277) [6-mer diglycyl-cysteinyl-triglycyl linker (241-246) -28-mer tetrakis(glutamyl-valyl-dialanyl-leucyl-glutamyl-lysyl) E-coil motif (247-274) -3-mer triglycyl linker (275-277)] -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1, G1v14 CH2 A1.3, A1.2, G1v32 CH3 W22 (knob) (278-504) [hinge 6-15 (278-287), CH2 L1.3>A (291), L1.2>A (292) (288-397), CH3 E12 (413), M14 (415), T22>W (423) (398-502), CHS (503-504)]]; (243-243')-disulfide with the IG scFv single chain, anti-CD3E and anti-CD276 (1'-274') [scFv V-lambda-VH anti-CD3E and anti-CD276 (1'-240') [V-LAMBDA anti-CD3 (*Mus musculus* IGLV1*01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (77.9%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (26-34.52-54.91-99) (1'-109') -9-mer tetraglycyl-seryl-tetraglycyl linker (110'-118') -VH anti-CD276 (*Homo sapiens* IGHV3-48*02 (91.8%) -(IGHD) -IGHJ4*01 (85.7%)) CDR-IMGT [8.8.15] (144-151.169-176.215-229) (119'-240')] -6-mer diglycyl-cysteinyl-triglycyl linker (241'-246') -28-mer tetrakis(lysyl-valyl-dialanyl-leucyl-lysyl-glutamyl) K-coil motif (247'-274')];
(283-6'':286-9'')-bisdisulfide with the IG h-CH2-CH3 chain, IGHG1*03 nG1m1, G1v14 CH2 A1.3, A1.2, IGHG1v33 CH3 S22, A24, V86 (hole) (1''-227'') [hinge 6-15 (1''-10''), CH2 L1.3>A (14), L1.2>A (15) (11''-120''), CH3 E12 (136), M14 (138), T22>S (146), L24>A (148), Y86>V (187), H115>R (215) (121''-225''), CHS (226''-227'')], produced in Chinese hamster ovary (CHO) cells, glycoform alfa

obrindatamab

immunoglobuline G1 scFv-h-CH2-CH3(_scFv)_h-CH2-CH3, anti-[*Homo sapiens* CD276 (B7H3, B7-H3, B7RP-2)] et anti-[*Homo sapiens* CD3E (CD3 epsilon)], anticorps monoclonal, bispécifique; IG scFv-h-CH2-CH3 chaîne unique, anti-CD276 et anti-CD3E (1-504) [scFv-V-kappa-VH anti-CD276 et anti-CD3E (1-240) [V-KAPPA anti-CD276 (*Homo sapiens* IGKV1D-13*01 (85.1%) -IGHJ2*02 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1-107) -8-mer triglycyl-séryl-tétraglycyl linker (108-115) -VH anti-CD3E (*Mus musculus* IGHV10-1*02 (89.9%) -(IGHD) -GHJ3*01 (93.3%)/*Homo sapiens* IGHV3-72*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) CDR-IMGT [8.10.16] (141-148.166-175.214-229) (116-240)] -linker-E-coil (241-277) [-6-mer diglycyl-cystéinyl-triglycyl linker (241-246) -28-mer tétrakis(glutamyl-valyl-dialanyl-leucyl-glutamyl-lysyl) E-coil motif (247-274) -3-mer triglycyl linker (275-277)] -*Homo sapiens* IGHG1*03 h-CH2-CH3 nG1m1, G1v14 CH2 A1.3, A1.2, G1v32 CH3 W22 (knob) (278-504) [charnière 6-15 (278-287), CH2 L1.3>A (291), L1.2>A (292) (288-397), CH3 E12 (413), M14 (415), T22>W (423) (398-502), CHS (503-504)]; (243-243')-disulfure avec la chaîne unique IG scFv, anti-CD3E et

	anti-CD276 (1'-274') [scFv V-lambda-VH anti-CD3E et anti-CD276 (1'-240') [V-LAMBDA anti-CD3 (*Mus musculus* IGLV1*01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (77.9%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (26-34.52-54.91-99) (1'-109') -9-mer tétraglycyl-séryl-tétraglycyl linker (110'-118') -VH anti-CD276 (*Homo sapiens* IGHV3-48*02 (91.8%) -(IGHD) -IGHJ4*01 (85.7%)) CDR-IMGT [8.8.15] (144-151.169-176.215-229) (119'-240') -6-mer diglycyl-cystéinyl-triglycyl linker (241'-246') -28-mer tétrakis(lysyl-valyl-dialanyl-leucyl-lysyl-glutamyl) K-coil motif (247'-274')]; (283-6":286-9")-bisdisulfure avec la chaîne IG h-CH2-CH3, IGHG1*03 nG1m1, G1v14 CH2 A1.3, A1.2, IGHG1v33 CH3 S22, A24, V86 (hole) (1"-227") [charnière 6-15 (1"-10"), CH2 L1.3>A (14), L1.2>A (15) (11"-120"), CH3 E12 (136), M14 (138), T22>S (146), L24>A (148), Y86>V (187), H115>R (215) (121"-225"), CHS (226"-227")], produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
obrindatamab	inmunoglobulina G1 scFv-h-CH2-CH3(_scFv)_h-CH2-CH3, anti-[*Homo sapiens* CD276 (B7H3, B7-H3, B7RP-2)] y anti-[*Homo sapiens* CD3E (CD3 épsilon)], anticuerpo monoclonal, biespecífico; IG scFv-h-CH2-CH3 cadena única, anti-CD276 y anti-CD3E (1-504) [scFv-V-kappa-VH anti-CD276 y anti-CD3E (1-240) [V-KAPPA anti-CD276 (*Homo sapiens* IGKV1D-13*01 (85.1%) -IGHJ2*02 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1-107) -8-mer triglicil-seril-tetraglicil linker (108-115) -VH anti-CD3E (*Mus musculus* IGHV10-1*02 (89.9%) -(IGHD) -GHJ3*01 (93.3%)/*Homo sapiens* IGHV3-72*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) CDR-IMGT [8.10.16] (141-148.166-175.214-229) (116-240)] -linker-E-coil (241-277) [-6-mer diglicil-cisteinil-triglicil linker (241-246) -28-mer tetrakis(glutamil-valil-dialanil-leucil-glutamil-lisil) E-coli motif (247-274) -3-mer triglicil linker (275-277)] -*Homo sapiens* IGHG1*03 h-CH2-CH3 nG1m1, G1v14 CH2 A1.3, A1.2, G1v32 CH3 W22 (knob) (278-504) [bisagra 6-15 (278-287), CH2 L1.3>A (291), L1.2>A (292) (288-397), CH3 E12 (413), M14 (415), T22>W (423) (398-502), CHS (503-504)]; (243-243')-disulfuro con la cadena única IG scFv, anti-CD3E y anti-CD276 (1'-274') [scFv V-lambda-VH anti-CD3E y anti-CD276 (1'-240') [V-LAMBDA anti-CD3 (*Mus musculus* IGLV1*01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (77.9%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (26-34.52-54.91-99) (1'-109') -9-mer tetraglicil-seril-tetraglicil linker (110'-118') -VH anti-CD276 (*Homo sapiens* IGHV3-48*02 (91.8%) -(IGHD) -IGHJ4*01 (85.7%)) CDR-IMGT [8.8.15] (144-151.169-176.215-229) (119'-240') -6-mer diglicil-cisteinil-triglicil linker (241'-246') -28-mer tetrakis(lisil-valil-dialanil-leucil-lisil-glutamil) K-coli motif (247'-274')]; (283-6":286-9")-bisdisulfuro con la cadena IG h-CH2-CH3, IGHG1*03 nG1m1, G1v14 CH2 A1.3, A1.2, IGHG1v33 CH3 S22, A24, V86 (hole) (1"-227") [bisagra 6-15 (1"-10"), CH2 L1.3>A (14), L1.2>A (15) (11"-120"), CH3 E12 (136), M14 (138), T22>S (146), L24>A (148), Y86>V (187), H115>R (215) (121"-225"), CHS (226"-227")], producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

1. Chain / Chaîne / Cadena: IG scFv h-CH2-CH3 (V-kappa anti-CD276, VH anti-CD3E)

```
DIQLTQSPSF LSASVGDRVT ITCKASQNVD TNVAWYQQKP GKAPKALIYS  50
ASYRYSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YNNYPFTFGQ 100
GTKLEIKGGG SGGGGEVQLV ESGGGLVQPG GSLRLSCAAS GFTFSTYAMN 150
WVRQAPGKGL EWVGRIRSKY NNYATYYADS VKDRFTISRD DSKNSLYLQM 200
NSLKTEDTAV YYCVRHGNFG NSYVSWFAYW GQGTLVTVSS GGCGGGEVAA 250
LEKEVAALEK EVAALEKEVA ALEKGGGDKT HTCPPCPAPE AAGGPSVFLF 300
PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE 350
EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE KTISKAKGQP 400
REPQVYTLPP SREEMTKNQV SLWCLVKGFY PSDIAVEWES NGQPENNYKT 450
TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL 500
SPGK                                                    504
```

2. Chain / Chaîne / Cadena: IG scFv (V-lambda anti-CD3E, VH anti-CD276)

```
QAVVTQEPSL TVSPGGTVTL TCRSSTGAVT TSNYANWVQQ KPGQAPRGLI  50
GGTNKRAPWT PARFSGSLLG GKAALTITGA QAEDEADYYC ALWYSNLWVF 100
GGGTKLTVLG GGGSGGGGEV QLVESGGGLV QPGGSLRLSC AASGFTFSSF 150
GMHWVRQAPG KGLEWVAYIS SDSSAIYYAD TVKGRFTISR DNAKNSLYLQ 200
MNSLRDEDTA VYYCGRGREN IYYGSRLDYW GQGTTVTVSS GGCGGGKVAA 250
LKEKVAALKE KVAALKEKVA ALKE                              274
```

3. Chain / Chaîne / Cadena: IG h-CH2-CH3

```
DKTHTCPPCP APEAAGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED  50
PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK 100
CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLSCAVK 150
GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLVSKL TVDKSRWQQG 200
NVFSCSVMHE ALHNRYTQKS LSLSPGK                          227
```

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

Intra-chain 1 (C23-C104)	23-88	137-213	318-378	424-482	
Intra-chain 2 (C23-C104)	22'-90'	140'-214'			
Intra-chain 3 (C23-C104)	41"-101"	147"-205"			
Inter-chains 1 - 2	243-243'				
Inter-chains 1 - 3 (h 11 -h 11)	283-6"				
(h 14 -h 14)	286-9"				

N-terminal glutamine cyclization to pyroglutamate (pE, 5-oxoproline)
V-lambda Q1:
1'

Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
CH2 N84.4:
354, 77"

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
CHS K2:
504, 227"

ociperlimabum #

ociperlimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* TIGIT (T-cell immunoreceptor with Ig domain and ITIM, V-set Ig member 9, VSIG9, V-set and transmembrane member 3, VSTM3)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-449) [VH (*Homo sapiens* IGHV3-66*01 (88.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -*Homo sapiens* IGHG1*01 nG1m1**,** G1m17 (CH1 K120 (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (87.4%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')];
dimer (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

ociperlimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* TIGIT (immunorécepteur des lymphocytes T avec domaine Ig et ITIM, membre 9 de l'Ig V-set, VSIG9, membre 3 de l'Ig V-set et région transmembrane, VSTM3)], anticorps monoclonal humanisé;

chaîne lourde gamma1 humanisée (1-449) [VH (*Homo sapiens* IGHV3-66*01 (88.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -*Homo sapiens* IGHG1*01 nG1m1, G1m17 (CH1 K120 (216) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (87.4%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')];
dimère (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

ociperlimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* TIGIT (inmunoreceptor de los linfocitos T con dominio Ig y ITIM, miembro 9 de la Ig V-set, VSIG9, miembro 3 de la Ig V-set y región transmembrana, VSTM3)], anticuerpo monoclonal humanizado;
cadena pesada gamma1 humanizada (1-449) [VH (*Homo sapiens* IGHV3-66*01 (88.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -*Homo sapiens* IGHG1*01 nG1m1, G1m17 (CH1 K120 (216) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (87.4%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')];
dímero (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS DYYMYWVRQA PGKGLEWVAY  50
ITKGGGSTYY PDSVKGRFTI SRDNAKNTLY LQMNSLRAED TAVYYCARQT 100
NYDFTMDYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNNY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
EIVMTQSPAT LSVSPGERAT LSCKASQDVG TSVAWYQQKP GQAPRLLIYW  50
ASARHTGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ YSSYPLTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 146-202 263-323 369-427
22"-96" 146"-202" 263"-323" 369"-427"
Intra-L (C23-C104) 23'-88' 134'-194'
23"'-88"' 134"'-194"'
Inter-H-L (h 5-CL 126) 222-214' 222"-214"'
Inter-H-H (h 11, h 14) 228-228" 231-231"

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

C-terminal lysine clipping:
H CHS K2:
449,449"

omodenbamabum #

omodenbamab	immunoglobulin G3-kappa, anti-[*Staphylococcus aureus* SpA (Staphylococcal protein A)], *Homo sapiens* monoclonal antibody; gamma3 heavy chain *Homo sapiens* (1-502) [VH (*Homo sapiens* IGHV3-23*04 (90.8%) -(IGHD) -IGHJ5*01 (93.3%)) CDR-IMGT [8.8.18] (26-33.51-58.97-114) (1-125) -*Homo sapiens* IGHG3*01, G3m5* (G3m5,10,11,13,14,26,27) (CH1 (126-223), hinge 1-42 (224-285), CH2 (286-395), CH3 S44 (439), M84 (452), Q98 (474), I101 (477), R115 (490), F116 (491) (396-500), CHS (501-502)) (126-502)], (139-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (90.5%) -IGKJ5*01 (91.7%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (236-236'':239-239'':245-245'':251-251'':254-254'':260-260'':266-266'':269-269'':275-275'':281-281'':284-284'')-undecakisdisulfide, produced in Chinese hamster ovary (CHO)-K1SV cells, glycoform alfa
omodenbamab	immunoglobuline G3-kappa, anti-[*Staphylococcus aureus* SpA (protéine A de Staphylocoque)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma3 *Homo sapiens* (1-502) [VH (*Homo sapiens* IGHV3-23*04 (90.8%) -(IGHD) -IGHJ5*01 (93.3%)) CDR-IMGT [8.8.18] (26-33.51-58.97-114) (1-125) -*Homo sapiens* IGHG3*01, G3m5* (G3m5,10,11,13,14,26,27) (CH1 (126-223), charnière 1-42 (224-285), CH2 (286-395), CH3 S44 (439), M84 (452), Q98 (474), I101 (477), R115 (490), F116 (491) (396-500), CHS (501-502)) (126-502)], (139-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (90.5%) -IGKJ5*01 (91.7%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (236-236'':239-239'':245-245'':251-251'':254-254'':260-260'':266-266'':269-269'':275-275'':281-281'':284-284'')-undecakisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO)-K1SV, glycoforme alfa
omodenbamab	inmunoglobulina G3-kappa, anti-[*Staphylococcus aureus* SpA (proteína A de Estafilococo)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma3 *Homo sapiens* (1-502) [VH (*Homo sapiens* IGHV3-23*04 (90.8%) -(IGHD) -IGHJ5*01 (93.3%)) CDR-IMGT [8.8.18] (26-33.51-58.97-114) (1-125) -*Homo sapiens* IGHG3*01, G3m5* (G3m5,10,11,13,14,26,27) (CH1 (126-223), bisagra 1-42 (224-285), CH2 (286-395), CH3 S44 (439), M84 (452), Q98 (474), I101 (477), R115 (490), F116 (491) (396-500), CHS (501-502)) (126-502)], (139-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (90.5%) -IGKJ5*01 (91.7%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (236-236'':239-239'':245-245'':251-251'':254-254'':260-260'':266-266'':269-269'':275-275'':281-281'':284-284'')-undecakisdisulfuro, producido en las células ováricas de hámster chino (CHO)-K1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS TYGMSWVRQA PGKGLEWVSS  50
ITGSGRSTFY ADSVKGRFTI SRDNSTNTLS LQMNSLRAED TAVYYCARSP 100
ADIVTGYYPW WFDLWGQGTL VTVSSASTKG PSVFPLAPCS RSTSGGTAAL 150
GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS 200
LGTQTYTCNV NHKPSNTKVD KRVELKTPLG DTTHTCPRCP EPKSCDTPPP 250
CPRCPEPKSC DTPPPCPRCP EPKSCDTPPP CPRCPAPELL GGPSVFLFPP 300
KPKDTLMISR TPEVTCVVVD VSHEDPEVQF KWYVDGVEVH NAKTKPREEQ 350
YNSTFRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKTKGQPRE 400
PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESSG QPENNYNTTP 450
PMLDSDGSFF LYSKLTVDKS RWQQGNIFSC SVMHEALHNR FTQKSLSLSP 500
GK                                                      502
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASIGDRVT ITCRASQSIN TYLNWYQQKP GKAPRLLIAG  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ ANSFPLTFGQ 100
GTRLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 152-208 316-376 422-480
22"-96" 152"-208" 316"-376" 422"-480"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (CH1 10-CL 126) 139-214' 139"-214'"
Inter-H-H (h1 13, h1 16, 236-236" 239-239"
h2 5, h2 11, h2 14 245-245" 251-251" 254-254"
h3 5, h3 11, h3 14, 260-260" 266-266" 269-269"
h4 5, h4 11, h4 14) 275-275" 281-281" 284-284"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
352, 352"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
h2 S7 h3 S7 h4 S7
247, 247" 262, 262" 277, 277"
Sialylated glycans regularly present / glycanes sialylés régulièrement présents / glicanos sialilados regularmente presentes

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
502, 502"

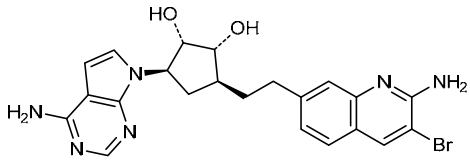
onametostatum

onametostat — (1*S*,2*R*,3*S*,5*R*)-3-[2-(2-amino-3-bromoquinolin-7-yl)ethyl]-5-(4-amino-7*H*-pyrrolo[2,3-*d*]pyrimidin-7-yl)cyclopentane-1,2-diol

onamétostat — (1*S*,2*R*,3*S*,5*R*)-3-[2-(2-amino-3-bromoquinoléin-7-yl)éthyl]-5-(4-amino-7*H*-pyrrolo[2,3-*d*]pyrimidin-7-yl)cyclopentane-1,2-diol

onametostat — (1*S*,2*R*,3*S*,5*R*)-3-[2-(2-amino-3-bromoquinolein-7-il)etil]-5-(4-amino-7*H*-pirrolo[2,3-*d*]pirimidin-7-il)ciclopentano-1,2-diol

$C_{22}H_{23}BrN_6O_2$



ontasameranum #

ontasameran — Messenger RNA encoding transmembrane phosphatase with tensin homology (TPTE).

	Messenger RNA (mRNA), 5'-capped, encoding codon-optimised transmembrane phosphatase with tensin homology (TPTE; cancer/testis antigen 44) expressed as a fusion protein comprising a secretory signal peptide, TPTE, P2P16 tetanus toxoid-derived helper epitopes and a major histocompatibility complex (MHC) class I transmembrane and cytoplasmic domain (MITD), connected by three glycine/serine-rich (GS) linker peptides, flanked by 5' and 3' untranslated regions and a 3' poly(A) tail.
ontasaméran	ARN messager codant pour la phosphatase transmembranaire homologue à la tensine (TPTE). Un ARN messager (ARNm), protégé en 5', codant pour la phosphatase transmembranaire homologue à la tensine (TPTE ; antigène 44 du cancer testiculaire), avec des codons optimisés, exprimé sous la forme d'une protéine de fusion comprenant un peptide signal de sécrétion, TPTE, les épitopes auxiliaires P2P16 dérivés de l'anatoxine tétanique et un domaine transmembranaire et cytoplasmique (MITD) du complexe majeur d'histocompatibilité (CMH) de classe I, reliés par trois peptides de liaison riches en glycine/sérine (GS), flanqués de régions non traduites en 5' et 3' et d'une queue poly(A) en 3'.
ontasamerán	ARN mensajero que codifica para la fosfatasa transmembranal con homología con la tensina (TPTE). ARN mensajero (ARNm), protegido en 5', que codifica para la fosfatasa transmembranal con homología con la tensina (TPTE; antígeno de cáncer/testículo 44), con codones optimizados, expresada como una proteína de fusión que consta de un péptido señal de secreción, TPTE, los epítopos auxiliares P2P16 derivados del toxoide tetánico y un dominio citoplásmico y transmembrana del complejo principal de histocompatibilidad (MHC) de clase I, conectados mediante tres péptidos de enlace ricos en glicina/serina (GS), flanqueado por las regiones 5' y 3' no traducidas y una cola poly(A) en 3'.
oplunofuspum #	
oplunofusp	*Actinomyces viscosus* L-methionyl sialidase (exo-α-sialidase) catalytic domain fragment (239-631, 2-394 in the current sequence), fused to human amphiregulin heparin binding domain fragment (25-45, 395-415 in the current sequence) anti-(binding to human heparin and cell surface glycosaminoglycans), produced in *Escherichia coli*; L-methionyl (1)-sialidase (exo-α-sialidase, EC:3.2.1.18) (*Actinomyces viscosus*) (239-631)-peptide (containing the sialidase domain) (2-394), fused to human amphiregulin (25-45)-peptide (binding to human heparin and glycosaminoglycans) (395-415), produced in *Escherichia coli*
oplunofusp	L-méthionyl, fragment du domaine catalytique (239-631, 2-394 dans la séquence actuelle) de la sialidase d'*Actinomyces viscosus* (exo-α-sialidase), fusionné à un fragment du domaine liant l'héparine de l'amphiréguline humaine (25-45, 395-415 dans la séquence actuelle) anti-(liant aux glycosaminoglycanes de surface cellulaire et à l'héparine, humains), produit dans *Escherichia coli;*

L-méthionyl (1)-peptide 239-631 de sialidase (exo-α-sialidase, EC:3.2.1.18) (*Actinomyces viscosus*) (contenant le domaine sialidase) (2-394), fusionné au peptide 25-45 de l'amphiréguline humaine (se liant aux glycosaminoglycanes et à l'héparine) (395-415), produit dans *Escherichia coli*

oplunofusp

L-metionil sialidasa(exo-α-sialidasa) *Actinomyces viscosus* fragmento con dominio catalítico (239-631, 2-394 en la secuencia actual), fusionado al fragmento del dominio de unión a la heparina de la anfiregulina humana (25-45, 395-415 en la secuencia actual) anti-(unión a la heparina humana y a los glicosaminoglicanos de superficie celular, humanos), producido in *Escherichia coli*;
L-metionil (1)-péptido 239-631 de sialidasa (exo-α-sialidasa, EC:3.2.1.18) (*Actinomyces viscosus*) (que contiene el dominio de sialidasa) (2-394), fusionado al péptido 25-45 de anfiregulina humana (se une a glicosaminoglicanos y heparina) (395-415), producido en *Escherichia coli*

Sequence / Séquence / Secuencia

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MSDHPQATPA PAPDASTELP ASMSQAQHLA ANTATDNYRI PAITTAPNGD   50
LLISYDERPK DNGNGGSDAP NPNHIVQRRS TDGGKTWSAP TYIHQGTETG  100
KKVGYSDPSY VVDHQTGTIF NFHVKSYDQG WGGSRGGTDP ENRGIIQAEV  150
STSTDNGWTW THRTITADIT KDKPWTARFA ASGQGIQIQH GPHAGRLVQQ  200
YTIRTAGGAV QAVSVYSDDH GKTWQAGTPI GTGMDENKVV ELSDGSLMLN  250
SRASDGSGFR KVAHSTDGGQ TWSEPVSDKN LPDSVDNAQI IRAFPNAAPD  300
DPRAKVLLLS HSPNPRPWSR DRGTISMSCD DGASWTTSKV FHEPFVGYTT  350
IAVQSDGSIG LLSEDAHNGA DYGGIWYRNF TMNWLGEQCG QKPAKRKKKG  400
GKNGKNRRNR KKKNP                                        415
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Post-translational modifications
Disulfide bridge location / Position du pont disulfure / Posición del puente disulfuro
329-389

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

pacanalotamabum #
pacanalotamab

immunoglobulin scFv-scFv, anti-[*Homo sapiens* TNFRSF17 (TNF receptor superfamily member 17, tumor necrosis factor receptor superfamily, member 17, B cell maturation antigen, BCMA, BCM, TNFRSF13A, CD269)] and anti-[*Homo sapiens* CD3E (CD3 epsilon)], monoclonal antibody single chain, bispecific;
IG scFv-scFv single chain, anti-TNFRSF17 and anti-CD3E (1-504) [scFv-VH-V-kappa anti-TNFRSF17 (1-243) [VH (*Homo sapiens* IGHV1-46*01 (85.7%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -15-mer tris(tetraglycyl-seryl) linker (122-136) -V-KAPPA (*Homo sapiens* IGKV1-33*01 (91.6%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (163-168.186-188.225-233) (137-243)] -6-mer seryl-tetraglycyl-seryl linker (244-249) -scFv-VH-V-lambda anti-CD3E (250-498) [VH (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (275-282.300-309.348-363) (250-374) -15-mer tris(tetraglycyl-seryl) linker (375-389) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%) CDR-IMGT [9.3.9 (415-423.441-443.480-488) (390-498)] -hexahistidine (499-504)], non-glycosylated, produced in Chinese hamster ovary (CHO) cells

pacanalotamab

immunoglobuline scFv-scFv, anti-[*Homo sapiens* TNFRSF17 (membre 17 de la superfamille des récepteurs du TNF, membre 17 de la superfamille des récepteurs du facteur de nécrose tumorale, antigène de maturation de cellule B, BCMA, BCM, TNFRSF13A, CD269)] et anti-[*Homo sapiens* CD3E (CD3 epsilon)], anticorps monoclonal à chaîne unique, bispécifique; IG scFv-scFv chaîne unique, anti-TNFRSF17 et anti-CD3E (1-504) [scFv-VH-V-kappa anti-TNFRSF17 (1-243) [VH (*Homo sapiens* IGHV1-46*01 (85.7%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121)-15-mer tris(tétraglycyl-séryl) linker (122-136) -V-KAPPA (*Homo sapiens* IGKV1-33*01 (91.6%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (163-168.186-188.225-233) (137-243)] -6-mer séryl-tétraglycyl-séryl linker (244-249) -scFv-V-lambda anti-CD3E (250-498) [VH (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD)-IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (275-282.300-309.348-363) (250-374) -15-mer tris(tétraglycyl-séryl) linker (375-389) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%) CDR-IMGT [9.3.9] (415-423.441-443.480-488) (390-498)] -hexahistidine (499-504)], non-glycosylé, produit dans des cellules ovariennes de hamster chinois (CHO)

pacanalotamab

inmunoglobulina scFv-scFv, anti-[*Homo sapiens* TNFRSF17 (miembro 17 de la superfamilia de los receptores del TNF, miembro 17 de la superfamilia de los receptores del factor de necrosis tumoral, antígeno de maduración de célula B, BCMA, BCM, TNFRSF13A, CD269)] y anti-[*Homo sapiens* CD3E (CD3 épsilon)], anticuerpo monoclonal con cadena única, biespecífico; IG scFv-scFv cadena única, anti-TNFRSF17 y anti-CD3E (1-504) [scFv-VH-V-kappa anti-TNFRSF17 (1-243) [VH (*Homo sapiens* IGHV1-46*01 (85.7%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121)-15-mer tris(tetraglicil-seril) linker (122-136) -V-KAPPA (*Homo sapiens* IGKV1-33*01 (91.6%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (163-168.186-188.225-233) (137-243)] -6-mer seril-tetraglicil-seril linker (244-249) -scFv-V-lambda anti-CD3E (250-498) [VH (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD)-IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (275-282.300-309.348-363) (250-374) -15-mer tris(tetraglicil-seril) linker (375-389) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%) CDR-IMGT [9.3.9] (415-423.441-443.480-488) (390-498)] -hexahistidina (499-504)], no glicosilado, producido en las células ováricas de hamster chino (CHO)

Heavy chain / Chaîne lourde / Cadena pesada

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QVQLVQSGAE VKKPGASVKV SCKASGYTFT NHIIHWVRQA PGQGLEWMGY  50
INPYPGYHAY NEKFQGRATM TSDTSTSTVY MELSSLRSED TAVYYCARDG 100
YYRDTDVLDY WGQGTLVTVS SGGGGSGGGG SGGGGSDIQM TQSPSSLSAS 150
VGDRVTITCQ ASQDISNYLN WYQQKPGKAP KLLIYYTSRL HTGVPSRFSG 200
SGSGTDFTFT ISSLEPEDIA TYYCQQGNTL PWTFGQGTKV EIKSGGGGSE 250
VQLVESGGGL VQPGGSLKLS CAASGFTFNK YAMNWVRQAP GKGLEWVARI 300
RSKYNNYATY YADSVKDRFT ISRDDSKNTA YLQMNNLKTE DTAVYYCVRH 350
GNFGNSYISY WAYWGQGTLV TVSSGGGGSG GGGSGGGGSQ TVVTQEPSLT 400
VSPGGTVTLT CGSSTGAVTS GNYPNWVQQK PGQAPRGLIG GTKFLAPGTP 450
ARFSGSLLGG KAALTLSGVQ PEDEAEYYCV LWYSNRWVFG GGTKLTVLHH 500
HHHH                                                    504
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-V (C23 C104) 22-96 159-224 271-347 411-479

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
VH Q1: 1

No N-glycosylation sites / pas de sites de N-glycosylation / ningún posición de N-glicosilación
Aglycosylated

pariglasgenum brecaparvovecum #

pariglasgene brecaparvovec	A non-replicating adeno-associated viral vector encoding codon-optimized human glucose-6-phosphatase (G6PC). A recombinant non-replicating adeno-associated viral vector serotype 8 (rAAV8), encoding codon-optimized human glucose-6-phosphatase (G6PC) under the control of the native human G6PC promoter/enhancer and an SV40 polyadenylation sequence, containing a chimeric intron in the 5' UTR between the promoter/enhancer and the transgene, flanked by AAV2 inverted terminal repeats (ITR).
pariglasgène brécaparvovec	Un vecteur adéno-viral non-réplicatif codant pour la glucose-6-phosphatase (G6PC) humaine avec des codons optimisés. Un vecteur recombinant adéno-viral non-réplicatif de sérotype 8 (rAAV8), codant pour la glucose-6-phosphatase (G6PC) humaine avec des codons optimisés, sous le contrôle du promoteur/activateur de la G6PC humaine native et d'une séquence de polyadénylation du SV40, contenant un intron chimérique dans l'UTR 5' entre le promoteur/activateur et le transgène, flanqué de répétitions terminales inversées (ITR) AAV2.
pariglasgén brecaparvovec	Un vector viral adeno-asociado, no replicativo, que codifica para la glucosa-6-fosfatasa (G6PC) humana, con codones optimizados. Un vector viral adeno-asociado recombinante de serotipo 8 (rAAV8) no replicativo, que codifica para la glucosa-6-fosfatasa (G6PC) humana, con codones optimizados, bajo el control del promotor/potenciador (enhancer) nativo de la G6PC humana y una secuencia de poliadenilación del SV40, conteniendo un intron quimérico en la región 5' UTR entre el promotor/potenciador y el transgén, flanqueado por repeticiones invertidas terminales (ITR) del AAV2.

pavurutamabum #

pavurutamab	immunoglobulin scFv-scFv-scFc, anti-[*Homo sapiens* TNFRSF17 (TNF receptor superfamily member 17, tumor necrosis factor receptor superfamily, member 17, B cell maturation antigen, BCMA, BCM, TNFRSF13A, CD269)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], monoclonal antibody single chain (scFv)2-scFc, bispecific; IG single chain scFv-scFv-scFc, anti-TNFRS17 and anti-CD3E (1-986) [scFv-VH-V-kappa anti-TNFRSF17 (1-243) [VH (*Homo sapiens* IGHV1-46*01 G49>C (44) (84.7%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -15-mer tris(tetraglycyl-seryl) linker (122-136)-V-KAPPA (*Homo sapiens* IGKV1-33*01 (91.6%) -IGKJ1*01 Q120>C (236) (91.7%)) CDR-IMGT [6.3.9] (163-168.186-188.225-233) (137-243)] -6 mer seryl-tetraglycyl-seryl linker (244-249) -scFv-VH-V-lambda anti-CD3E (250-498) [VH (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (275-282.300-309.348-363) (250-374) -15-mer tris(tetraglycyl-seryl) linker (375-389) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (415-423.441-443.480-488) (390-498)] -4-mer tetraglycyl linker

	(499-502) -scFc (h-CH2-CH3)-(h-CH2-CH3) (503-986) [*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (hinge 6-15 (503-512), CH2 R83>C (574), N84.4>G (579), V85>C (584) (513-622), CH3 E12 (638), M14 (640) (623-727), CHS (728-729)) (503-729) -30-mer hexakis(tetraglycyl-seryl) linker (730-759) -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (hinge 6-15 (760-769), CH2 R83>C (831), N84.4>G (836), V85>C (841) (770-879), CH3 E12 (895), M14 (897) (880-984), CHS (985-986)) (760-986)], non-glycosylated, produced in Chinese hamster ovary (CHO) cells
pavurutamab	immunoglobuline scFv-scFv-scFc, anti-[*Homo sapiens* TNFRSF17 (membre 17 de la superfamille des récepteurs du TNF, membre 17 de la superfamille des récepteurs du facteur de nécrose tumorale, antigène de maturation de cellule B, BCMA, BCM, TNFRSF13A, CD269)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal à chaîne unique (scFv)2-scFc, bispécifique; IG à chaîne unique scFv-scFv-scFc, anti-TNFRSF17 et anti-CD3E (1-986) [scFv-VH-V-kappa anti-TNFRSF17 (1-243) [VH (*Homo sapiens* IGHV1-46*01 G49>C (44) (84.7%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -15-mer tris(tétraglycyl-séryl) linker (122-136)-V-KAPPA (*Homo sapiens* IGKV1-33*01 (91.6%) -IGKJ1*01 Q120>C (236) (91.7%)) CDR-IMGT [6.3.9] (163-168.186-188.225-233) (137-243)] -6-mer séryl-tétraglycyl-séryl linker (244-249) -scFv-VH-V-lambda anti-CD3E (250-498) [VH (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (275-282.300-309.348-363) (250-374) -15-mer tris(tétraglycyl-séryl) linker (375-389) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (415-423.441-443.480-488) (390-498)] -4-mer tétraglycyl linker (499-502) -scFc (h-CH2-CH3)-(h-CH2-CH3) (503-986) [*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (503-729) (charnière 6-15 (503-512), CH2 R83>C (574), N84.4>G (579), V85>C (584) (513-622), CH3 E12 (638), M14 (640) (623-727), CHS (728-729)) -30-mer hexakis(tétraglycyl-séryl) linker (730-759) -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (charnière 6-15 (760-769), CH2 R83>C (831), N84.4>G (836), V85>C (841) (770-879), CH3 E12 (895), M14 (897) (880-984), CHS (985-986)) (760-986]], non-glycosylé, produit dans des cellules ovariennes de hamster chinois (CHO)
pavurutamab	inmunoglobulina scFv-scFv-scFc, anti-[*Homo sapiens* TNFRSF17 (miembro 17 de la superfamilia de los receptores del TNF, miembro 17 de la superfamilia de los receptores del factor de necrosis tumoral, antígeno de maduración de célula B, BCMA, BCM, TNFRSF13A, CD269)] y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal con cadena única (scFv)2-scFc, biespecífico;

IG con cadena única scFv-scFv-scFc, anti-TNFRSF17 y anti-CD3E (1-986) [scFv-VH-V-kappa anti-TNFRSF17 (1-243) [VH (*Homo sapiens* IGHV1-46*01 G49>C (44) (84.7%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -15-mer tris(tetraglicil-seril) linker (122-136)-V-KAPPA (*Homo sapiens* IGKV1-33*01 (91.6%) -IGKJ1*01 Q120>C (236) (91.7%)) CDR-IMGT [6.3.9] (163-168.186-188.225-233) (137-243)] -6-mer seril-tetraglicil-seril linker (244-249) -scFv-VH-V-lambda anti-CD3E (250-498) [VH (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (275-282.300-309.348-363) (250-374) -15-mer tris(tetraglicil-seril) linker (375-389) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (415-423.441-443.480-488) (390-498)] -4-mer tetraglicil linker (499-502) -scFc (h-CH2-CH3)-(h-CH2-CH3) (503-986) [*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (503-729) (bisagra 6-15 (503-512), CH2 R83>C (574), N84.4>G (579), V85>C (584) (513-622), CH3 E12 (638), M14 (640) (623-727), CHS (728-729)) -30-mer hexakis(tetraglicil-seril) linker (730-759) -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (bisagra 6-15 (760-769), CH2 R83>C (831), N84.4>G (836), V85>C (841) (770-879), CH3 E12 (895), M14 (897) (880-984), CHS (985-986)) (760-986]], no glicosilado, producido en las células ováricas de hamster chino (CHO)

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT NHIIHWVRQA PGQCLEWMGY   50
INPYPGYHAY NEKFQGRATM TSDTSTSTVY MELSSLRSED TAVYYCARDG  100
YYRDTDVLDY WGQGTLVTVS SGGGGSGGGG SGGGGSDIQM TQSPSSLSAS  150
VGDRVTITCQ ASQDISNYLN WYQQKPGKAP KLLIYYTSRL HTGVPSRFSG  200
SGSGTDFTFT ISSLEPEDIA TYYCQQGNTL PWTFGCGTKV EIKSGGGGSE  250
VQLVESGGGL VQPGGSLKLS CAASGFTFNK YAMNWVRQAP GKGLEWVARI  300
RSKYNNYATY YADSVKDRFT ISRDDSKNTA YLQMNNLKTE DTAVYYCVRH  350
GNFGNSYISY WAYWGQGTLV TVSSGGGGSG GGGSGGGGSQ TVVTQEPSLT  400
VSPGGTVTLT CGSSTGAVTS GNYPNWVQQK PGQAPRGLIG GTKFLAPGTP  450
ARFSGSLLGG KAALTLSGVQ PEDEAEYYCV LWYSNRWVFG GGTKLTVLGG  500
GGDKTHTCPP CPAPELLGGP SVFLFPPKPK DTLMISRTPE VTCVVVDVSH  550
EDPEVKFNWY VDGVEVHNAK TKPCEEQYGS TYRCVSVLTV LHQDWLNGKE  600
YKCKVSNKAL PAPIEKTISK AKGQPREPQV YTLPPSREEM TKNQVSLTCL  650
VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ  700
QGNVFSCSVM HEALHNHYTQ KSLSLSPGKG GGGSGGGGSG GGGSGGGGSG  750
GGGSGGGGSD KTHTCPPCPA PELLGGPSVF LFPPKPKDTL MISRTPEVTC  800
VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP CEEQYGSTYR CVSVLTVLHQ  850
DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL PPSREEMTKN  900
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSKLT  950
VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGK               986
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-V (C23 C104) 22-96 159-224 271-347 411-479
Intra-C (C23-C104) 543-603 649-707 800-860 906-964
Intra-CH2 (C83-C85) 574-584 831-841
Inter VH-VL (C49-C120) 44-236
Inter h11 (h 11-h 11) 508-765
Inter h14 (h 14-h 14) 511-768

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
VH Q1: 1

No N-glycosylation sites / pas de sites de N-glycosylation / ningún posición de N-glicosilación
H CH2 N84.4>G:
579, 836
Aglycosylated

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
CHS K2:
986

pegtibatinasum #

pegtibatinase

human cystathionine β-synthase fragment (2-413, M^1 cleaved) mutant (C^{15}>S), homodimer, produced in *Escherichia coli*, pegylated at N^6 of lysine residues with an average of five 5-[α-methylpoly(oxyethylene)-ω-oxy]-5-oxopentanoyl groups per protein monomer;
des-Met^1-[Cys^{15}>Ser] human cystathionine β-synthase (CBS, beta-thionase, serine sulfhydrase, EC:4.2.1.22) (2-413)-peptide, non-covalent dimer, produced in *Escherichia coli*, substituted with approximately five 5-[α-methylpoly(oxyethylene)-ω-oxy]-5-oxopentanoyl groups (20 kDa each) per protein monomer at N^6 of lysine residues

pegtibatinase

fragment de la cystathionine β-synthase humaine (2-413, M^1 supprimée) mutant (C^{15}>S), homodimère, produit dans *Escherichia coli*, pégylé en N^6 des résidus lysine avec une moyenne de cinq groupes 5-[α-méthylpoly(oxyéthylène)-ω-oxy]-5-oxopentanoyle par monomère de protéine;
peptide 2-413 de des-Met^1-[Cys^{15}>Sér] cystathionine β-synthase humaine (CBS, bêta-thionase, sérine sulfhydrase, EC: 4.2.1.22), dimère non covalent, produit dans *Escherichia coli*, substitué par environ cinq groupes 5-[α-méthylpoly(oxyéthylène)-ω-oxy]-5-oxopentanoyle (~20 kDa chacun) par monomère de protéine au N^6 des résidus de lysine

pegtibatinasa

fragmento de la cistationina β-sintasa humana (2-413, M^1 escindido) mutante (C^{15}>S), homodímero, producido en *Escherichia coli*, pegilada en N^6 residuos de lisina con una medida de cinco grupos 5-[α-metilpoli(oxietileno)-ω-oxi]-5-oxopentanoilo por monómero de proteína;
péptido 2-413 de des-Met^1-[Cis^{15}>Ser] cistationina β-sintasa humana (CBS, beta-tionasa, serina sulfhidrasa, EC: 4.2.1.22), dímero no covalente, producido en *Escherichia coli*, sustituido con aproximadamente cinco grupos 5-[α-metilpoli(oxietilen)-ω-oxi]-5-oxopentanoilo (~20 kDa cada uno) por proteína monomérica en N^6 de residuos de lisina

Sequence / Séquence / Secuencia

```
-PSETPQAEV GPTGSPHRSG PHSAKGSLEK GSPEDKEAKE PLNIRPDAPS   50
RCTWQLGRPA SESPHHHTAP AKSPKILPDI LKKIGDTPMV RINKIGKKFG  100
LKCELLAKCE FFNAGGSVKD RISLRMIEDA ERDGTLKPGG TIIEPTSGNT  150
GIGLALAAAV KGYRCIIVMP EKMSSEKVDV LRALGAEIVR TPTNARFDSP  200
ESHVGVAWRL KNEIPNSHIL DQYRNASNPL AHYDTTADEI LQQCDGKLDM  250
LVASVGTGGT ITGIARKLKE KCPGCRIIGV DPEGSILAEP EELNQTEQTT  300
YEVEGIGYDF IPTVLDRTVV DKWFKSNDEE AFTFARMLIA QEGLLCGGSA  350
GSTVAVAVKA AQELQEGQRC VVILPDSVRN YMTKFLSDRW MLQKGFLKEE  400
DLTEKKPWWW HLR                                          415
```

Mutation / Mutation / Mutación

C^{15}>S

Post-translational modifications

Removal of Met^1 / Suppression de Met^1 / Eliminación de Met^1

Disulfide bridges location / Position des ponts disulfure / Posición del puentes disulfuro

272-275, 272'-275' (and further variable potential bridges)

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación

none / aucune / ninguna

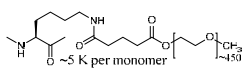
Cofactor binding sites / Sites de liaison des cofacteurs / Sitios de unión de cofactores

N^6-pyridoxylidene 5'-phosphate / 5'-phosphate de N^6-pyridoxylidène / 5'-fosfato de N^6-piridoxilideno K119, K119'

heme B (protoheme IX) / hème b (protohème IX) / hemo B (protohemo IX)

Cys52-S -Fe(II)- N^1-His65, Cys52'-S -Fe(II)- N^1-His65'

Chemical modification / Modification chimique / Modificación química



pegulicianinum

pegulicianine

N-[6-(1-{2-[3,6-bis(2,3-dihydro-1*H*-indol-1-yl)xanthylium-9-yl]benzene-1-sulfonyl}piperidine-4-carboxamido)hexanoyl]glycylglycyl-L-arginyl-N^6-(6-{2-[(1*E*,3*E*,5*Z*)-5-(1-ethyl-3,3-dimethyl-5-sulfonato-1,3-dihydro-2*H*-indol-2-ylidene)penta-1,3-dien-1-yl]-3,3-dimethyl-5-sulfonato-3*H*-indol-1-ium-1-yl}hexanoyl)-L-lysyl-[2-(2-aminoethoxy)ethoxy]acetyl-*S*-[(3*RS*)-1-{6-[α-methylpoly(oxyethylene)-ω-amino]-6-oxohexyl}-2,5-dioxopyrrolidin-3-yl]-L-cysteinamide

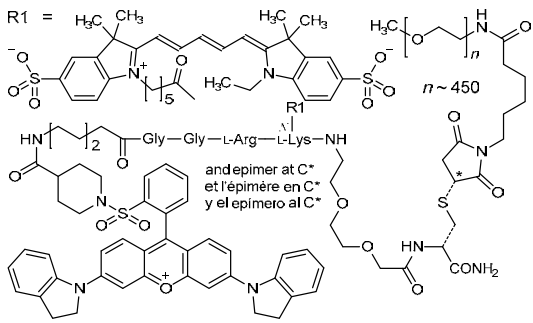
pégulicianine

N-[6-(1-{2-[3,6-bis(2,3-dihydro-1*H*-indol-1-yl)xanthylium-9-yl]benzène-1-sulfonyl}pipéridine-4-carboxamido)hexanoyl]glycylglycyl-L-arginyl-N^6-(6-{2-[(1*E*,3*E*,5*Z*)-5-(1-éthyl-3,3-diméthyl-5-sulfonato-1,3-dihydro-2*H*-indol-2-ylidene)penta-1,3-dién-1-yl]-3,3-diméthyl-5-sulfonato-3*H*-indol-1-ium-1-yl}hexanoyl)-L-lysyl-[2-(2-aminoéthoxy)éthoxy]acétyl-*S*-[(3*RS*)-1-{6-[α-méthylpoly(oxyethylène)-ω-amino]-6-oxohexyl}-2,5-dioxopyrrolidin-3-yl]-L-cystéinamide

pegulicianina

N-[6-(1-{2-[3,6-bis(2,3-dihidro-1*H*-indol-1-il)xantilio-9-il]benceno-1-sulfonil}piperidina-4-carboxamido)hexanoil]glicilglicil-L-arginil-N^6-(6-{2-[(1*E*,3*E*,5*Z*)-5-(1-etil-3,3-dimetil-5-sulfonato-1,3-dihidro-2*H*-indol-2-ilideno)penta-1,3-dien-1-il]-3,3-dimetil-5-sulfonato-3*H*-indol-1-io-1-il}hexanoil)-L-lisil-[2-(2-aminoetoxi)etoxi]acetil-*S*-[(3*RS*)-1-{6-[α-metilpoli(oxietileno)-ω-amino]-6-oxohexil}-2,5-dioxopirrolidin-3-il]-L-cisteinamida

$C_{116}H_{147}N_{19}O_{23}S_4(C_2H_4O)_n$



pelabresibum

pelabresib

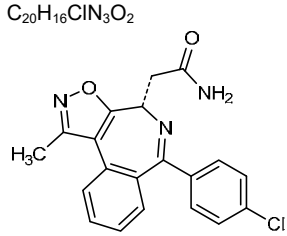
2-[(4*S*)-6-(4-chlorophenyl)-1-methyl-4*H*-[1,2]oxazolo[5,4-*d*][2]benzazepin-4-yl]acetamide

pélabrésib

2-[(4*S*)-6-(4-chlorophényl)-1-méthyl-4*H*-[1,2]oxazolo[5,4-*d*][2]benzazépin-4-yl]acetamide

pelabresib

2-[(4*S*)-6-(4-clorofenil)-1-metil-4*H*-[1,2]oxazolo[5,4-*d*][2]benzazepin-4-il]acetamida

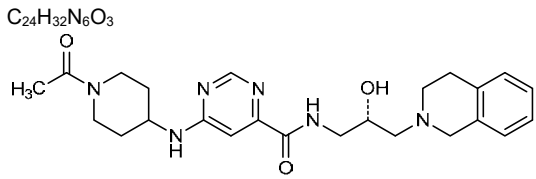


pemrametostatum

pemrametostat — 6-[(1-acetylpiperidin-4-yl)amino]-*N*-[(2*S*)-3-(3,4-dihydroisoquinolin-2(1*H*)-yl)-2-hydroxypropyl]pyrimidine-4-carboxamide

pemramétostat — 6-[(1-acétylpipéridin-4-yl)amino]-*N*-[(2*S*)-3-(3,4-dihydroisoquinoléin-2(1*H*)-yl)-2-hydroxypropyl]pyrimidine-4-carboxamide

pemrametostat — 6-[(1-acetilpiperidin-4-il)amino]-*N*-[(2*S*)-3-(3,4-dihidroisoquinolein-2(1*H*)-il)-2-hidroxipropil]pirimidina-4-carboxamida



penpulimabum #

penpulimab — immunoglobulin G1-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], monoclonal antibody;
gamma1 heavy chain (1-448) [VH (*Homo sapiens* IGHV3-23*04 (88.7%) -(IGHD) -IGHJ6*01 (90.9%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) - *Homo sapiens* IGHG1*01 G1m17,1, G1v14 CH2 A1.3, A1.2 (CH1 K120 (215) (119-216), hinge 1-15 (217-231), CH2 L1.3>A (235), L1.2>A (236), G1>A (238) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Mus musculus* IGKV14-111*01 (86.3%) -IGKJ5*01 (100%)/*Homo sapiens* IGKV1-16*01 (80%) -IGKJ2*01 (81.8%) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')];
dimer (227-227'':230-230'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

penpulimab — immunoglobuline G1-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal;

chaîne lourde gamma1 (1-448) [VH (*Homo sapiens* IGHV3-23*04 (88.7%) -(IGHD) -IGHJ6*01 (90.9%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo sapiens* IGHG1*01 G1m17,1, G1v14 CH2 A1.3, A1.2 (CH1 K120 (215) (119-216), charnière 1-15 (217-231), CH2 L1.3>A (235), L1.2>A (236), G1>A (238) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV14-111*01 (86.3%) -IGKJ5*01 (100%)/*Homo sapiens* IGKV1-16*01 (80%) -IGKJ2*01 (81.8%) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')];
dimère (227-227'':230-230'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

penpulimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal;
cadena pesada gamma1 (1-448) [VH (*Homo sapiens* IGHV3-23*04 (88.7%) -(IGHD) -IGHJ6*01 (90.9%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo sapiens* IGHG1*01 G1m17,1, G1v14 CH2 A1.3, A1.2 (CH1 K120 (215) (119-216), bisagra 1-15 (217-231), CH2 L1.3>A (235), L1.2>A (236), G1>A (238) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV14-111*01 (86.3%) -IGKJ5*01 (100%)/*Homo sapiens* IGKV1-16*01 (80%) -IGKJ2*01 (81.8%) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')];
dímero (227-227'':230-230'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFAFS SYDMSWVRQA PGKGLDWVAT 050
ISGGGRYTYY PDSVKGRFTI SRDNSKNNLY LQMNSLRAED TALYYCANRY 100
GEAWFAYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPEAAGAPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS MSASVGDRVT FTCRASQDIN TYLSWFQQKP GKSPKTLIYR 050
ANRLVSGVPS RFSGSGSGQD YTLTISSLQP EDMATYYCLQ YDEFPLTFGA 100
GTKLELKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications

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

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

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

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

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

H CHS K2:
448, 448"

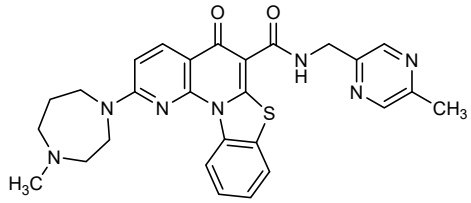
pidnarulexum

pidnarulex — 2-(4-methyl-1,4-diazepan-1-yl)-*N*-[(5-methylpyrazin-2-yl)methyl]-5-oxo-5*H*-[1,3]benzothiazolo[3,2-*a*][1,8]naphthyridine-6-carboxamide

pidnarulex — 2-(4-méthyl-1,4-diazépan-1-yl)-*N*-[(5-méthylpyrazin-2-yl)méthyl]-5-oxo-5*H*-[1,3]benzothiazolo[3,2-*a*][1,8]naphtyridine-6-carboxamide

pidnarulex — 2-(4-metil-1,4-diazepan-1-il)-*N*-[(5-metilpirazin-2-il)metil]-5-oxo-5*H*-[1,3]benzotiazolo[3,2-*a*][1,8]naftiridina-6-carboxamida

$C_{27}H_{27}N_7O_2S$



pimivalimabum #

pimivalimab — immunoglobulin G4-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], *Homo sapiens* monoclonal antibody; gamma4 heavy chain *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV1-46*01 (96.9%) -(IGHD) - IGHJ5*02 (100%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118)-*Homo sapiens* IGHG4*01 (CH1 (119-216), hinge 1-12 S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*01 (97.9%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (224-224":227-227")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

pimivalimab — immunoglobuline G4-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal *Homo sapiens*;
chaîne lourde gamma4 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV1-46*01 (96.9%) -(IGHD) - IGHJ5*02 (100%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), charnière 1-12 S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*01 (97.9%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (224-224":227-227")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

pimivalimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma4 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV1-46*01 (96.9%) -(IGHD) -IGHJ5*02 (100%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), bisagra 1-12 S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*01 (97.9%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (224-224":227-227")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFP SYYMHWVRQA PGQGLEWMGI  50
INPEGGSTAY AQKFQGRVTM TRDTSTSTVY MELSSLRSED TAVYYCARGG 100
TYYDYTYWGQ GTLVTVSSAS TKGPSVFPLA PCSRSTSEST AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTKTYT 200
CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFLGGPSVFL FPPKPKDTLM 250
ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV 300
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP 350
PSQEEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG 400
SFFLYSRLTV DKSRWQEGNV FSCSVMHEAL HNHYTQKSLS LSLGK       445
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPST LSASVGDRVT ITCRASQSIS SWLAWYQQKP GKAPKLLIYE  50
ASSLESGVPS RFSGSGSGTE FTLTISSLQP DDFATYYCQQ YNSFPPTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 145-201 259-319 365-423
22"-96" 145"-201" 259"-319" 365"-423"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194"
Inter-H-L (h 10-CL 126) 132-214' 132"-214'"
Inter-H-H (h 8, h 11) 224-224" 227-227"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
295, 295"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

C-terminal lysine clipping:
H CHS K2:
445, 445"

pirepematum

pirepemat

(3*S*)-3-(2,3-difluorophenyl)-3-methoxypyrrolidine

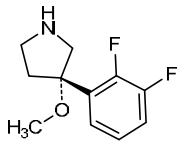
pirépémat

(3*S*)-3-(2,3-difluorophényl)-3-méthoxypyrrolidine

pirepemat

(3*S*)-3-(2,3-difluorofenil)-3-metoxipirrolidina

$C_{11}H_{13}F_2NO$



pomulmeranum #

pomulmeran	Messenger RNA encoding cystic fibrosis transmembrane conductance regulator (CFTR). Messenger RNA (mRNA), 5' capped, encoding codon-optimised human cystic fibrosis transmembrane conductance regulator (CFTR; channel conductance-controlling ATPase, cAMP-dependent chloride channel, ATP-binding cassette sub-family C member 7, ABCC7), flanked by 5' and 3' untranslated regions and a 3' poly(A) tail (200-1000 A).
pomulméran	ARN messager codant pour le régulateur de conductance transmembranaire de la mucoviscidose (CFTR). ARN messager (ARNm), protégé en 5', codant pour le régulateur de conductance transmembranaire de la mucoviscidose humaine avec des codons optimisés (CFTR ; canal ATPase contrôlant la conductance, canal chlorure dépendant de l'AMPc, sous-famille C membre 7, ABCC7), flanqué de régions 5' et 3' non traduites et d'une queue 3' poly(A) (200-1000 A).
pomulmerán	RNA mensajero que codifica para el regulador de la conductancia transmembrana de la fibrosis quística (CFTR). RNA mensajero (RNAm), protegido en 5', que codifica para el regulador de la conductancia transmembrana de la fibrosis quística (CFTR; canal ATPasa controlador de la conductancia, canal de cloro dependiente de AMPc, subfamilia C miembro 7 del casete de unión a ATP, ABCC7) con los codones optimizados, flanqueado por regiones 5' y 3' no traducidas y una cola poly(A) (200-1000 A) en 3'.

posoleucelum

posoleucel	Allogeneic human leukocyte antigen (HLA)-matched virus-specific T cells reactive to cytomegalovirus (CMV), EBV, BK virus, adenovirus and human herpesvirus-6 (HHV-6). The cells are derived from peripheral blood mononuclear cells (PBMCs) from donors seropositive for all five of these viruses. The cells are expanded and co-cultured with 15-mer peptides overlapping by 11 amino acids spanning antigenic proteins from polyomaviruses BK and JC (VP1 and large T), from adenovirus (hexon and penton), from cytomegalovirus (IE1 and pp65), from Epstein-Barr virus (LMP2, EBNA1, BZLF1), and from human herpesvirus-6 (U90, U11 and U14). The cells have specific anti-virus reactivity for each virus above a pre-specified potency threshold, and predominantly express CD3 (generally >95%) with a mixture of CD4+ (average 60%) and CD8+ (average 34%) subsets, including both central (CD45RA-/62L+/CCR7+) and effector (CD45RA-/62L-/CCR7-) memory markers.
posoleucel	Lymphocytes T allogéniques, compatibles pour les antigènes leucocytaires humains (HLA) et spécifiques pour le cytomégalovirus (CMV), l'EBV, le virus BK, l'adénovirus et le virus herpès humain 6 (HHV-6). Les cellules sont dérivées de cellules mononucléaires du sang périphérique (PBMC) provenant de donneurs séropositifs pour ces cinq virus. Les cellules sont amplifiées et cultivées avec des peptides de 15 résidus se chevauchant par 11 acides aminés couvrant les protéines antigéniques du polyomavirus BK et JC (VP1 et grand T), de l'adénovirus (hexon et penton), du cytomégalovirus (IE1 et pp65), du virus d'Epstein-Barr (LMP2, EBNA1, BZLF1), et du virus herpès humain 6 (U90, U11 et U14).

Les cellules ont une réactivité antivirus spécifique pour chacun des virus au-delà d'un seuil prédéfini, et expriment principalement CD3 (généralement >95%) avec un mélange de sous-populations de CD4+ (60% en moyenne) et de CD8+ (34% en moyenne), comprenant des marqueurs des mémoires centrale (CD45RA-/62L+/CCR7+) et effectrice (CD45RA-/62L-/CCR7-).

posoleucel

Células T alogénicas específicas de virus con compatibilidad para el antígeno leucocitario humano (HLA) reactivas frente a citomegalovirus (CMV), EBV, virus BK, adenovirus y herpesvirus humano 6 (HHV-6). Las células se obtienen a partir de células mononucleares de sangre periférica (PBMCs) de donantes seropositivos para estos cinco virus.
Las células tienen una reactividad antivirus específica para cada de estos virus por encima de un umbral de potencia preestablecido, y se expanden y co-cultivan con péptidos de 15 residuos que solapan en 11 amino ácidos cubriendo proteínas antigénicas de poliomavirus BK y JC (VP1 y T grande), de adenovirus (hexón y pentón), de citomegalovirus (IE1 y pp65), de virus de Epstein-Barr (LMP2, EBNA1, BZLF1), y de herpesvirus humano 6 (U90, U11 and U14).
Las células expresan predominantemente CD3 (generalmente >95%) con una mezcla de subtipos CD4+ (60% como media) y CD8+ (34% como media), incluyendo marcadores de memoria central (CD45RA-/62L+/CCR7+) y efectora (CD45RA-/62L-/CCR7-).

radgocitabinum

radgocitabine

4-amino-1-(2-cyano-2-deoxy-β-D-arabinofuranosyl)pyrimidin-2(1*H*)-one;
2'-cyano-2'-deoxy-D-*arabino*-cytidine

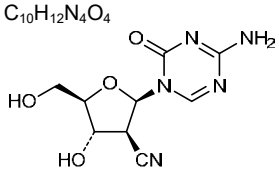
radgocitabine

4-amino-1-(2-cyano-2-désoxy-β-D-arabinofuranosyl)pyrimidin-2(1*H*)-one;
2'-cyano-2'-désoxy-D-*arabino*-cytidine

radgocitabina

4-amino-1-(2-ciano-2-desoxi-β-D-arabinofuranosil)pirimidin-2(1*H*)-ona;
2'-ciano-2'-desoxi-D-*arabino*-citidina

$C_{10}H_{12}N_4O_4$



rebonuputemcelum

rebonuputemcel

Allogenic human adult nucleus pulposus cells.
The cells are derived from the central region of intervertebral discs and isolated from the tissue using mechanical and enzymatic (collagenase) procedures. Isolated cells are expanded in culture involving

	adherent and non- adherent conditions until clusters of cells, 100-200 µm in diameter, are generated. Cells comprising the cell substance are dissociated out of these clusters and stored frozen. Cells (on average >95%) express the surface markers CD73, CD90, CD44 and HLA-ABC, and release proteoglycan, collagen and anti-inflammatory cytokines. Cells (on average <3%) lack expression of CD24 (classically associated with native nucleus pulposus cells), CD34, CD45, CD271, Stro-1 or HLA-DR/DP/DQ.
rébonuputemcel	Cellules allogènes du noyau pulpeux humain adulte. Les cellules sont dérivées de la région centrale des disques intervertébraux et isolées du tissu à l'aide de procédures mécaniques et enzymatiques (collagénase). Les cellules isolées sont multipliées en culture dans des conditions adhérentes et non adhérentes jusqu'à ce que des groupes de cellules, de 100 à 200 µm de diamètre, soient générés. Les cellules composant la substance cellulaire sont dissociées de ces amas et conservées congelées. Les cellules (en moyenne> 95%) expriment les marqueurs de surface CD73, CD90, CD44 et HLA-ABC, et libèrent du protéoglycane, du collagène et des cytokines anti-inflammatoires. Les cellules (en moyenne <3%) manquent d'expression de CD24 (classiquement associé aux cellules pulpeuses du noyau natif), CD34, CD45, CD271, Stro-1 ou HLA-DR/DP/DQ.
rebonuputemcel	Células alogénicas del núcleo pulposo adulto humano. Las células son derivadas de la región central de los discos intervertebrales y se aíslan del tejido usando procedimientos mecánicos y enzimáticos (colagenasa). Las células aisladas se expanden en cultivo en condiciones adherentes y no adherentes hasta que se generan grumos de células de 100-200 mm de diámetro. Las células que componen el principio activo se disocian de estos grumos y se almacenan congeladas. >95% de las células expresan los marcadores de superficie CD73, CD90, CD44 y HLA-ABC, y liberan proteoglicano, colágeno y citoquinas anti-inflamatorias. <3% de las células expresan CD24 (asociado clásicamente con células del núcleo pulposo nativo), CD34, CD45, CD271, Stro-1 o HLA-DR/DP/DQ.
recaticimabum # recaticimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* PCSK9 (proprotein convertase subtilisin/kexin type 9, neural apoptosis-regulated convertase 1, NARC1, NARC-1, proprotein convertase 9, PC9)], monoclonal antibody;

	gamma1 heavy chain (1-451) [VH (*Homo sapiens* IGHV1-2*02 (89.8%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -*Homo sapiens* IGHG1*01**,** G1m17,1, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (218) (122-219), hinge 1-15 (220-234), CH2 M15.1>Y (256), S16>T (258), T18>E (260) (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-219')-disulfide with kappa light chain (1'-219') [V-KAPPA (*Mus musculus* IGKV8-21*01 (85%) -IGKJ4*01 (91.7%)/*Homo sapiens* IGKV4-1*01 (76.8%) -IGKJ2*02 (100%)) CDR-IMGT [12.3.8] (27-38.56-58.95-102) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (158), V101 (196) (113-219')]; dimer (230-230":233-233")-bisdisulfide, produced in a Chinese hamster ovary (CHO) cell line (CHOK1SV GS-KO), glycoform alfa
récaticimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* PCSK9 (proprotéine convertase subtilisine/kexine type 9, convertase 1 régulée par l'apoptose neuronale, NARC1, NARC-1, proprotéine convertase 9, PC9)], anticorps monoclonal; chaîne lourde gamma1 (1-451) [VH (*Homo sapiens* IGHV1-2*02 (89.8%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -*Homo sapiens* IGHG1*01**,** G1m17,1, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (218) (122-219), charnière 1-15 (220-234), CH2 M15.1>Y (256), S16>T (258), T18>E (260) (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-219')-disulfure avec la chaîne légère kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV8-21*01 (85%) -IGKJ4*01 (91.7%)/*Homo sapiens* IGKV4-1*01 (76.8%) -IGKJ2*02 (100%)) CDR-IMGT [12.3.8] (27-38.56-58.95-102) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (158), V101 (196) (113-219')]; dimère (230-230":233-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHOK1SV GS-KO, glycoforme alfa
recaticimab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* PCSK9 (proproteína convertasa subtilisina/kexina tipo 9, convertasa 1 regulada por la apoptosis neuronal, NARC1, NARC-1, proproteína convertasa 9, PC9)], anticuerpo monoclonal; cadena pesada gamma1 (1-451) [VH (*Homo sapiens* IGHV1-2*02 (89.8%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -*Homo sapiens* IGHG1*01**,** G1m17,1, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (218) (122-219), bisagra 1-15 (220-234), CH2 M15.1>Y (256), S16>T (258), T18>E (260) (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-219')-disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV8-21*01 (85%) -IGKJ4*01 (91.7%)/*Homo sapiens* IGKV4-1*01 (76.8%) -IGKJ2*02 (100%)) CDR-IMGT [12.3.8] (27-38.56-58.95-102) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (158), V101 (196) (113-219')]; dímero (230-230":233-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHOK1SV GS-KO, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

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QVQLVQSGAE VKKPGASVKV SCKASGYTFT DYWMHWVRQA PGQGLEWMGY  50
INPSSGFTKY HQNFKDRVTM TRDTSISTAY MELSRLRSDD TAVYYCARQY 100
DYDEDWYFDV WGQGTTVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLYITRE PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                       451
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Light chain / Chaîne légère / Cadena ligera

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DIVMSQSPSS LSASVGDRVT ITCKSSQSLL NSRTRKNFLA WYQQKPGKSP  50
KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQPEDFA TYYCKQSFNL 100
FTFGQGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Post-translational modifications

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

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

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

Inter-H-L (h 5-CL 126) 224-219' 224"-219'"

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

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)

H VH Q1:
1, 1"

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

H CH2 N84.4:
301, 301"

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

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

H CHS K2:
451, 451"

relmacabtagenum autoleucelum #

relmacabtagene autoleucel

Autologous CD4+ and CD8+ enriched T cells transduced *ex vivo* with a self-inactivating lentivirus vector encoding an anti-CD19 chimeric antigen receptor.
Autologous CD4+ and CD8+ T cells, enriched from peripheral blood mononuclear cells (PBMCs) transduced with a non-replicative self-inactivating (SIN) lentiviral vector encoding a chimeric antigen receptor (CAR) consisting of the human CD19-specific scFv, an lgG4 hinge region, CD28 transmembrane domain, CD137 (4-1BB) co-stimulatory domain and CD3 zeta signalling domain, under the control of a hybrid Elongation Factor 1 alpha (EF1α) and Human T cell Leukemia Virus type 1 (HTLV-1) regulatory element promoter and woodchuck hepatitis virus post-transcriptional regulatory element (WPRE). The vector genome also encodes a truncated human epidermal growth factor receptor (EGFRt) that is co-expressed with the CAR and cleaved from it by the T2A self-cleaving peptide. The vector genome also contains a splice donor, a fragment of *gag*, a Rev response element (RRE), a mutated central polypurine tract (cPPT), and a splice acceptor.

relmacabtagène autoleucel

Cellules T autologues enrichies en CD4+ et CD8+ transduites *ex vivo* avec un vecteur lentiviral auto-inactivant codant pour un récepteur chimérique dirigé contre l'antigène CD19.

Cellules T CD4+ et CD8+ autologues, enrichies de cellules mononucléaires du sang périphérique (PBMC), transduites avec un vecteur lentiviral auto-inactivable et non réplicatif (SIN) codant pour un récepteur chimérique (CAR) constitué du scFv spécifique de l'antigène CD19 humain, d'une région charnière IgG4, d'un domaine transmembranaire CD28, du domaine co-stimulateur de CD137 (4-1BB) et du domaine de signalisation CD3 zeta, sous le contrôle d'un hybride du facteur d'allongement 1 alpha (EF1α) et du promoteur de l'élément régulateur du virus de la leucémie humaine à cellules T de type 1 (HTLV-1), ainsi que de l'élément régulateur post-transcriptionnel du virus de l'hépatite de la marmotte (WPRE). Le génome du vecteur code également pour un récepteur tronqué du facteur de croissance épidermique humain (EGFRt) qui est co-exprimé avec le CAR et en est relâché par le peptide T2A auto-coupant. Le génome du vecteur contient également un donneur d'épissage, un fragment de gag, un élément de réponse Rev (RRE), un segment central polypurine muté (cPPT) et un accepteur d'épissage.

relmacabtagén autoleucel

Células T autólogas enriquecidas en CD4+ y CD8+ transducidas *ex vivo* con un lentivirus auto-inactivante que codifica un receptor de antígenos quiméricos anti-CD19.
Las células T autólogas CD4+ y CD8+, enriquecidas a partir de células mononucleares de sangre periférica (PBMCs), transducidas con un vector lentiviral no replicativo y auto-inactivante (SIN) que codifica para un receptor de antígenos quimérico (CAR) consistente en un scFv específico de CD19 humano, una región bisagra IgG4, un dominio transmembrana CD28, un dominio co-estimulador CD137 (4-1BB) y un domino de señalización CD3 zeta, bajo el control de un promotor híbrido del factor de elongación 1 alfa (EF1α) y el elemento regulador del virus de la leucemia de células T de tipo 1 humano (HTLV-1), y elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE). El genoma del vector también codifica para un receptor del factor de crecimiento epidérmico humano truncado (EGFRt) que se coexpresa con el CAR y luego se escinde de él por el péptido de auto escisión T2A. El genoma del vector también contiene un sitio donante de procesamiento (splicing), un fragmento de *gag*, un elemento de respuesta Rev (RRE), un segmento central de polipurinas (cPPT) y un sitio aceptor de procesamiento (splicing).

resiniferatoxinum

resiniferatoxin

[(2*S*,3a*R*,3b*S*,6a*R*,9a*R*,9b*R*,10*R*,11a*R*)-2-benzyl-6a-hydroxy-8,10-dimethyl-7-oxo-11a-(prop-1-en-2-yl)-3a,3b,6,6a,9a,10,11,11a-octahydro-2*H*,7*H*-2,9b-epoxyazuleno[5,4-*e*][1,3]benzodioxol-5-yl]methyl (4-hydroxy-3-methoxyphenyl)acetate

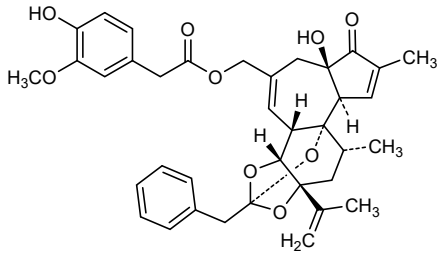
résinifératoxine

(4-hydroxy-3-méthoxyphényl)acétate de [(2*S*,3a*R*,3b*S*,6a*R*,9a*R*,9b*R*,10*R*,11a*R*)-2-benzyl-6a-hydroxy-8,10-diméthyl-7-oxo-11a-(prop-1-én-2-yl)-3a,3b,6,6a,9a,10,11,11a-octahydro-2*H*,7*H*-2,9b-époxyazuléno[5,4-*e*][1,3]benzodioxol-5-yl]méthyle

resiniferatoxina

(4-hidroxi-3-metoxifenil)acetato de [(2*S*,3a*R*,3b*S*,6a*R*,9a*R*,9b*R*,10*R*,11a*R*)-2-bencil-6a-hidroxi-8,10-dimetil-7-oxo-11a-(prop-1-en-2-il)-3a,3b,6,6a,9a,10,11,11a-octahidro-2*H*,7*H*-2,9b-epoxiazuleno[5,4-*e*][1,3]benzodioxol-5-il]metilo

$C_{37}H_{40}O_9$



revakinagenum taroretcelum #

revakinagene taroretcel

Allogeneic human adult retinal pigment epithelial (RPE) cell line stably transfected with a plasmid encoding human ciliary neurotrophic factor (CNTF).
An allogeneic human adult retinal pigment epithelial (RPE) cell line stably transfected with a plasmid encoding human ciliary neurotrophic factor (CNTF) fused in frame to the murine immunoglobulin mu-factor VDJ4C1 signal peptide, under the control of a mouse metallothionein promoter and a human growth hormone polyadenylation signal. The plasmid also contains three eukaryotic expression cassettes for the selectable markers neomycin resistance, mouse DHFR (dihydrofolate reductase) and HSV-TK (thymidine kinase), plus the bacterial components of the pUC18 backbone, including the ampicillin resistance gene (AmpR), origin of replication (ORI) and LacZ gene (alpha fragment of β-galactosidase).

révakinagène taroretcel

Lignée cellulaire épithéliale allogénique du pigment rétinien humain adulte (EPR) transfectée de façon stable avec un plasmide codant pour le facteur neurotrophique ciliaire humain (CNTF).
Une lignée cellulaire épithéliale allogénique du pigment rétinien humain adulte (RPE) transfectée de manière stable avec un plasmide codant pour le facteur neurotrophique ciliaire humain (CNTF) fusionné dans le cadre de lecture du peptide signal VDJ4C1 du facteur mu d'immunoglobuline murine, sous le contrôle d'un promoteur de la métallothionéine de souris et d'un signal de polyadénylation de l'hormone de croissance humaine. Le plasmide contient également des cassettes d'expression eucaryotes pour trois marqueurs de sélection, à savoir la résistance à la néomycine, la DHFR (réductase du dihydrofolate) et la HSV-TK (kinase de la thymidine) de souris, ainsi que les composants bactériens du plasmide pUC18, dont le gène de résistance à l'ampicilline (AmpR), l'origine de réplication (ORI) et le gène du LacZ (fragment alpha de la β-galactosidase).

revakinagén taroretcel

Línea celular epitelial alogénica de pigmento retiniano adulto (RPE) humano transfectada de forma estable con un plásmido que codifica para el factor neurotrófico ciliar (CNTF) humano.
Una línea celular epitelial alogénica de pigmento retiniano adulto (RPE) humano transfectada de forma estable con un plásmido que codifica para el factor neurotrófico ciliar (CNTF) humano fusionado en marco de lectura al péptido señal VDJ4AC1 del factor mu de la inmunoglobulina murina, bajo el control de un promotor de la metalotionina de ratón y una señal de poliadenilación de la hormona de crecimiento humana. El plásmido contiene también tres casetes de expresión eucariotas para los marcadores de selección de resistencia a neomicina, DHFR (dihidrofolato reductasa) de ratón y HSV-TK (timidin quinasa), más los componentes bacterianos del esqueleto de pUC18, incluyendo el gen de resistencia a ampicilina (AmpR), el origin de replicación (ORI) y el gen LacZ (fragmento alfa de la β-galactosidasa).

rezvilutamidum

rezvilutamide

4-(3-{4-[(2*S*)-2,3-dihydroxypropoxy]phenyl}-4,4-dimethyl-5-oxo-2-sulfanylideneimidazolidin-1-yl)-2-(trifluoromethyl)benzonitrile

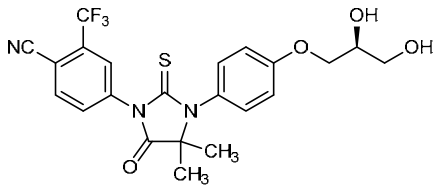
rezvilutamide

4-(3-{4-[(2*S*)-2,3-dihydroxypropoxy]phényl}-4,4-diméthyl-5-oxo-2-sulfanylidèneimidazolidin-1-yl)-2-(trifluorométhyl)benzonitrile

rezvilutamida

4-(3-{4-[(2*S*)-2,3-dihidroxipropoxi]fenil}-4,4-dimetil-5-oxo-2-sulfanilidenoimidazolidin-1-il)-2-(trifluorometil)benzonitrilo

$C_{22}H_{20}F_3N_3O_4S$



rineterkibum

rineterkib

4-{3-amino-6-[(1*S*,3*S*,4*S*)-3-fluoro-4-hydroxycyclohexyl]pyrazin-2-yl}-*N*-[(1*S*)-1-(3-bromo-5-fluorophenyl)-2-(methylamino)ethyl]-2-fluorobenzamide

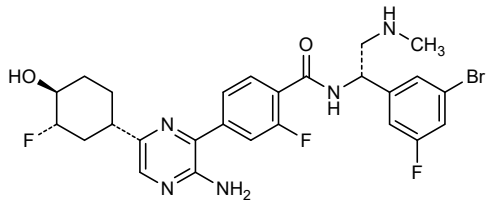
rinéterkib

4-{3-amino-6-[(1*S*,3*S*,4*S*)-3-fluoro-4-hydroxycyclohexyl]pyrazin-2-yl}-*N*-[(1*S*)-1-(3-bromo-5-fluorophényl)-2-(méthylamino)éthyl]-2-fluorobenzamide

rineterkib

4-{3-amino-6-[(1*S*,3*S*,4*S*)-3-fluoro-4-hidroxiciclohexil]pirazin-2-il}-*N*-[(1*S*)-1-(3-bromo-5-fluorofenil)-2-(metilamino)etil]-2-fluorobenzamida

$C_{26}H_{27}BrF_3N_5O_2$



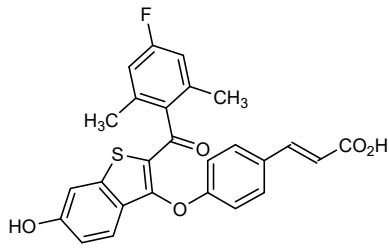
rintodestrantum

rintodestrant — (2*E*)-3-(4-{[2-(4-fluoro-2,6-dimethylbenzoyl)-6-hydroxy-1-benzothiophen-3-yl]oxy}phenyl)prop-2-enoic acid

rintodestrant — acide (2*E*)-3-(4-{[2-(4-fluoro-2,6-diméthylbenzoyl)-6-hydroxy-1-benzothiophén-3-yl]oxy}phényl)prop-2-énoïque

rintodestrant — ácido (2*E*)-3-(4-{[2-(4-fluoro-2,6-dimetilbenzoil)-6-hidroxi-1-benzotiofen-3-il]oxi}fenil)prop-2-enoico

$C_{26}H_{19}FO_5S$



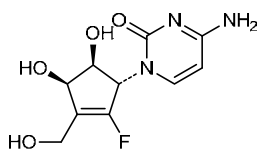
roducitabinum

roducitabine — 4-amino-1-[(1*S*,4*R*,5*S*)-2-fluoro-4,5-dihydroxy-3-(hydroxymethyl)cyclopent-2-en-1-yl]pyrimidin-2(1*H*)-one;
4'a-fluoro-4',4'a-didehydro-4'-*O*-carbacytidine

roducitabine — 4-amino-1-[(1*S*,4*R*,5*S*)-2-fluoro-4,5-dihydroxy-3-(hydroxyméthyl)cyclopent-2-én-1-yl]pyrimidin-2(1*H*)-one;
4'a-fluoro-4',4'a-didéhydro-4'-*O*-carbacytidine

roducitabina — 4-amino-1-[(1*S*,4*R*,5*S*)-2-fluoro-4,5-dihidroxi-3-(hidroximetil)ciclopent-2-en-1-il]pirimidin-2(1*H*)-ona;
4'a-fluoro-4',4'a-didehidro-4'-*O*-carbacitidina

$C_{10}H_{12}FN_3O_4$

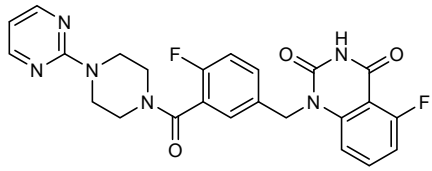


senaparibum
senaparib — 5-fluoro-1-({4-fluoro-3-[4-(pyrimidin-2-yl)piperazine-1-carbonyl]phenyl}methyl)quinazoline-2,4(1*H*,3*H*)-dione

sénaparib — 5-fluoro-1-({4-fluoro-3-[4-(pyrimidin-2-yl)pipérazine-1-carbonyl]phényl}méthyl)quinazoline-2,4(1*H*,3*H*)-dione

senaparib — 5-fluoro-1-({4-fluoro-3-[4-(pirimidin-2-il)piperazina-1-carbonil]fenil}metil)quinazolina-2,4(1*H*,3*H*)-diona

$C_{24}H_{20}F_2N_6O_3$

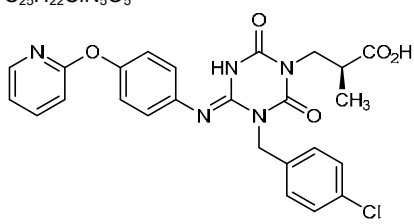


sivopixantum
sivopixant — (2*S*)-3-[(4*E*)-3-[(4-chlorophenyl)methyl]-2,6-dioxo-4-({4-[(pyridin-2-yl)oxy]phenyl}imino)-1,3,5-triazinan-1-yl]-2-methylpropanoic acid

sivopixant — acide (2*S*)-3-[(4*E*)-3-[(4-chlorophényl)méthyl]-2,6-dioxo-4-({4-[(pyridin-2-yl)oxy]phényl}imino)-1,3,5-triazinan-1-yl]-2-méthylpropanoïque

sivopixant — ácido (2*S*)-3-[(4*E*)-3-[(4-clorofenil)metil]-2,6-dioxo-4-({4-[(piridin-2-il)oxi]fenil}imino)-1,3,5-triazinan-1-il)-2-metilpropanoico

$C_{25}H_{22}ClN_5O_5$



sizavaleucelum
sizavaleucel — Allogeneic, HLA-matched CD3+ T-cells, derived from G-CSF mobilized peripheral blood stem cells (PBSC) collected by apheresis. Cells are transplant organ donor-derived, non-cultured and cryopreserved with CD34+ hematopoietic stem cells (HSC) *(firzotemcel (121)(83))* obtained from the same HLA-matched donor. Intended for delivery to a single HLA-matched recipient.

sizavaleucel	Des cellules T CD3+ allogéniques, exprimant des antigènes HLA compatibles, dérivées de cellules souches du sang périphérique (PBSC) mobilisées par le G-CSF et collectées par aphérèse. Les cellules sont dérivées de donneurs d'organes de transplantation, ne sont pas cultivées et sont cryoconservées avec des cellules souches hématopoïétiques (HSC) CD34+ *(firzotemcel (121)(83))* qui proviennent du même donneur compatible pour les antigènes HLA. Destinées à être données à un seul receveur compatible pour les antigènes HLA.
sizavaleucel	Células T CD3+ alogénicas, con HLA compatible, derivadas de células madre de sangre periférica (PBSC) movilizadas con G-CSF y recogidas por aféresis. Las células proceden de donantes de órganos para trasplante, no se cultivan y se criopreservan con células madre hematopoyéticas (HSC) CD34+ *(firzotemcel (121)(83))* obtenidas del mismo donante HLA compatible. Destinadas para administrarse a un sólo receptor HLA compatible.

sotigalimabum #

sotigalimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* CD40 (tumor necrosis factor receptor superfamily member 5, TNFRSF5)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV3-30*01 (79.8%) -(IGHD) -IGHJ1*01 (90.9%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 G1m17,1 (CH1 K120 (217) (121-218), hinge 1-15 (219-233), CH2 S29>E (270) (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-215')-disulfide with kappa light chain humanized (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (91%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.13] (27-32.50-52.89-101) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO)-derived cell line, glycoform alfa
sotigalimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* CD40 (membre 5 de la superfamille des récepteurs du TNF, TNFRSF5)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-450) [VH (*Homo sapiens* IGHV3-30*01 (79.8%) -(IGHD) -IGHJ1*01 (90.9%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 G1m17,1 (CH1 K120 (217) (121-218), charnière 1-15 (219-233), CH2 S29>E (270) (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-215')-disulfure avec la chaîne légère kappa humanisée (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (91%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.13] (27-32.50-52.89-101) (1'-108') (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (229-229":232-232")-bisdisulfure, produite dans une lignée cellulaire dérivée des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

sotigalimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD40 (miembro 5 de la superfamilia de los receptores del TNF, TNFRSF5)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-450) [VH (*Homo sapiens* IGHV3-30*01 (79.8%) -(IGHD) - IGHJ1*01 (90.9%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 G1m17,1 (CH1 K120 (217) (121-218), bisagra 1-15 (219-233), CH2 S29>E (270) (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-215')-disulfuro con la cadena ligera kappa humanizada (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (91%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.13] (27-32.50-52.89-101) (1'-108') (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')];
dímero (229-229":232-232")-bisdisulfuro, producido en una línea celular derivada de las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG VVQPGRSLRL SCAASGFSFS STYVCWVRQA PGKGLEWIAC  50
IYTGDGTNYS ASWAKGRFTI SKDSSKNTVY LQMNSLRAED TAVYFCARPD 100
ITYGFAINFW GPGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVE HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT IKCQASQSIS SRLAWYQQKP GKPPKLLIYR  50
ASTLASGVPS RFSGSGSGTD FTLTISSLQP EDVATYYCQC TGYGISWPIG 100
GGTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 35-50 147-203 264-324 370-428
22"-96" 35"-50" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 135'-195'
23'"-88'" 135'"-195'"
Inter-H-L (h 5-CL 126) 223-215' 223"-215'"
Inter-H-H (h 11, h 14) 229-229" 232-232"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H VH N65:
58, 58"
H CH2 N84.4:
300, 300"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

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

sotorasibum

sotorasib

(1*M*)-6-fluoro-7-(2-fluoro-6-hydroxyphenyl)-1-[4-methyl-2-(propan-2-yl)pyridin-3-yl]-4-[(2*S*)-2-methyl-4-(prop-2-enoyl)piperazin-1-yl]pyrido[2,3-*d*]pyrimidin-2(1*H*)-one

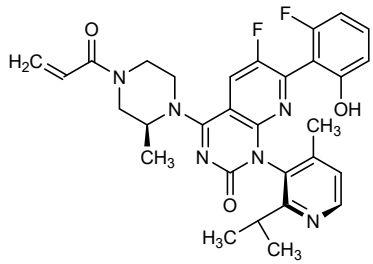
sotorasib

(1*M*)-6-fluoro-7-(2-fluoro-6-hydroxyphényl)-1-[4-méthyl-2-(propan-2-yl)pyridin-3-yl]-4-[(2*S*)-2-méthyl-4-(prop-2-énoyl)pipérazin-1-yl]pyrido[2,3-*d*]pyrimidin-2(1*H*)-one

sotorasib

(1*M*)-6-fluoro-7-(2-fluoro-6-hidroxifenil)-1-[4-metil-2-(propan-2-il)piridin-3-il]-4-[(2*S*)-2-metil-4-(prop-2-enoil)piperazin-1-il]pirido[2,3-*d*]pirimidin-2(1*H*)-ona

$C_{30}H_{30}F_2N_6O_3$



sulanemadlinum

sulanemadlin

C$^{2.11}$,*C*$^{2.4}$-[(4*E*)-undec-4-ene-1,11-diyl](*N*-acetyl-L-leucyl-L-threonyl-L-phenylalanyl-L-alanyl-L-α-glutamyl-L-tyrosyl-L-tryptophyl-L-alanyl-L-glutaminyl-L-leucyl-D-alanyl-L-alanyl-L-alanyl-L-alanyl-L-alanyl-L-alanyl-D-alaninamide)

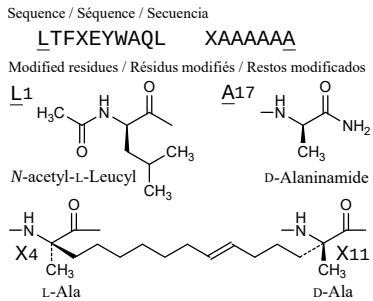
sulanémadline

C$^{2.11}$,*C*$^{2.4}$-[(4*E*)-undéc-4-ène-1,11-diyl](*N*-acétyl-L-leucyl-L-thréonyl-L-phénylalanyl-L-alanyl-L-α-glutamyl-L-tyrosyl-L-tryptophyl-L-alanyl-L-glutaminyl-L-leucyl-D-alanyl-L-alanyl-L-alanyl-L-alanyl-L-alanyl-L-alanyl-D-alaninamide)

sulanemadlina

C$^{2.11}$,*C*$^{2.4}$-[(4*E*)-undec-4-eno-1,11-diil](*N*-acetil-L-leucil-L-treonil-L-fenilalanil-L-alanil-L-α-glutamil-L-tirosil-L-triptofil-L-alanil-L-glutaminil-L-leucil-D-alanil-L-alanil-L-alanil-L-alanil-L-alanil-L-alanil-D-alaninamida)

$C_{95}H_{140}N_{20}O_{23}$



suntinorextonum

suntinorexton

N-[(2*S*,3*S*)-2-[(2,3'-difluoro[1,1'-biphenyl]-3-yl)methyl]-1-(2-hydroxy-2-methylpropanoyl)pyrrolidin-3-yl]ethanesulfonamide

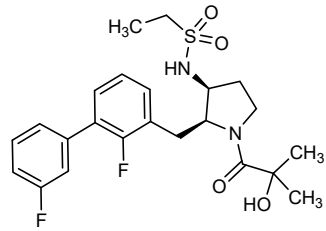
suntinorexton

N-[(2*S*,3*S*)-2-[(2,3'-difluoro[1,1'-biphényl]-3-yl)méthyl]-1-(2-hydroxy-2-méthylpropanoyl)pyrrolidin-3-yl]éthanesulfonamide

suntinorextón

N-[(2*S*,3*S*)-2-[(2,3'-difluoro[1,1'-bifenil]-3-il)metil]-1-(2-hidroxi-2-metilpropanoil)pirrolidin-3-il]etanosulfonamida

$C_{23}H_{28}F_2N_2O_4S$



suratadenoturevum #

suratadenoturev

A replication-competent adenovirus type 5 in which the E1A and E1B genes are under the control of a human telomerase reverse transcriptase (hTERT) and IRES, respectively.
A recombinant replication-competent adenovirus type 5 (Ad-5) in which the E1 gene, including its normal transcriptional regulatory element, has been deleted and replaced by an expression cassette containing an hTERT (human telomerase reverse transcriptase) promoter, the Ad E1A gene, an IRES (internal ribosome entry site) and the Ad E1B gene. E1A expression is controlled by the hTERT promoter; E1B translation is effected by the IRES.

suratadénoturev

Un adénovirus de type 5 réplicatif dans lequel les gènes E1A et E1B sont, respectivement, sous le contrôle de la transcriptase inverse de la télomérase humaine (hTERT) et d'IRES.
Un adénovirus recombinant réplicatif de type 5 (Ad-5) dans lequel le gène E1, y compris son élément normal de régulation de la transcription, a été supprimé et remplacé par une cassette d'expression contenant un promoteur hTERT (transcriptase inverse de la télomérase humaine), le gène Ad E1A, un IRES (site d'entrée interne du ribosome) et le gène Ad E1B. L'expression de E1A est contrôlée par le promoteur hTERT; la traduction de E1B est effectuée par l'IRES.

suratadenoturev

Un adenovirus tipo 5 competente de replicación en el que los genes E1A y E1B están bajo el control de la telomerasa transcriptasa inversa humana (hTERT) e IRES, respectivamente.
Un adenovirus tipo 5 (Ad-5) recombinante competente de replicación en el que el gen E1, incluyendo su elemento de regulación transcripcional normal, ha sido delecionado y reemplazado por un casete de expresión que contiene un promotor de hTERT (telomerasa transcriptasa inversa humana), el gen Ad E1A, un IRES (sitio interno de entrada al ribosoma) y el gen Ad E1B. La expresión de E1A esta controlada por el promotor hTERT; La traducción de E1B se efectúa por el IRES.

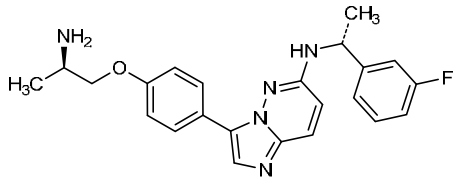
taletrectinibum

taletrectinib — 3-{4-[(2*R*)-2-aminopropoxy]phenyl}-*N*-[(1*R*)-1-(3-fluorophenyl)ethyl]imidazo[1,2-*b*]pyridazin-6-amine

talétrectinib — 3-{4-[(2*R*)-2-aminopropoxy]phényl}-*N*-[(1*R*)-1-(3-fluorophényl)éthyl]imidazo[1,2-*b*]pyridazin-6-amine

taletrectinib — 3-{4-[(2*R*)-2-aminopropoxi]fenil}-*N*-[(1*R*)-1-(3-fluorofenil)etil]imidazo[1,2-*b*]piridazin-6-amina

$C_{23}H_{24}FN_5O$



taniraleucelum

taniraleucel — Allogeneic natural killer (NK) cells derived from CD34+ umbilical cord blood (UCB) hematopoietic stem/progenitor cells.
The cells are expanded and differentiated in the presence of cytokines including thrombopoietin, SCF, Flt3 ligand, IL-7, IL-15 and IL-2 (average population doublings 15) to generate the NK cell population.
Cells (on average >95% of the cells) are CD56+/CD3- and have detectable levels of CD94, NKG2D and CD16.
The cells secrete IFN-γ, perforin and granzyme B, and have cytolytic activity against human tumour cell lines.

taniraleucel — Cellules tueuses naturelles (NK) allogéniques dérivées de cellules souches/progénitrices hématopoïétiques CD34+ du sang de cordon ombilical (UCB).
Les cellules sont amplifiées et différenciées en présence de cytokines, notamment la thrombopoïétine, le SCF, le ligand de Flt3, l'IL-7, l'IL-15 et l'IL-2 (la population double en moyenne 15 fois) pour générer la population de cellules NK.
Les cellules (en moyenne >95% des cellules) sont CD56+/CD3- et ont des niveaux détectables de CD94, NKG2D et CD16. Les cellules sécrètent l'IFN-γ, la perforine et la granzyme B, et ont une activité cytolytique contre les lignées de cellules tumorales humaines.

taniraleucel — Células natural killer (NK) alogénicas derivadas de células madre/progenitoras hematopoyéticas de sangre de cordón umbilical (UCB).
Las células se expanden y diferencian en presencia de citoquinas incluyendo trombopoyetina, SCF, ligando de Flt3, IL-7, IL-15 e IL-2 (la media de duplicaciones de la población es 15 veces) hasta generar la población de células NK. Las células (como media >95% de las células) son CD56+/CD3- y tienen niveles detectables de CD94, NKG2D y CD16. Las células secretan IFN-γ, perforina y granzima B, y tienen actividad citolítica frente a líneas celulares tumorales humanas.

tarlatamabum #

tarlatamab	immunoglobulin scFv-scFv-scFc, anti-[*Homo sapiens* DLL3 (delta-like ligand 3)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], monoclonal antibody single chain (scFv)2-scFc, bispecific; IG single chain scFv-scFv-scFc, anti-DLL3 and anti-CD3E (1-982) [scFv-VH-V-kappa anti-DLL3 (1-241) [VH (*Homo sapiens* IGHV4-59*01 G49>C (44) (96.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.12] (26-33.51-57.96-107) (1-118) -15-mer-tris(tetraglycyl-seryl) linker (119-133)-V-KAPPA (*Homo sapiens* IGKV3-20*01 (91.7%) -IGKJ2*01 Q120>C (234) (90.9%)) CDR-IMGT [7.3.9] (160-166.184-186.223-231) (134-241)] -6-mer-seryl-tetraglycyl-seryl linker (242-247) -scFv-VH-V-lambda anti-CD3E (248-496) [VH (*Mus musculus*IGHV10-1*02 (91.9%) -(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (273-280.298-307.346-361) (248-372)-15-mer-tris(tetraglycyl-seryl) linker (373-387) – V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (413-421.439-441.478-486) (388-496)] -4-mer-tetraglycyl linker (497-500) - scFc (h-CH2-CH3)-(h-CH2-CH3) (501-982) [*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (hinge 6-15 (501-510), CH2 R83>C (572), N84.4>G (577), V85>C (582) (511-620), CH3 E12 (636), M14 (638) (621-725), CHS>del) (501-725) -30-mer-hexakis(tetraglycyl-seryl) linker (726-755) -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (hinge 6-15 (756-765), CH2 R83>C (827), N84.4>G (832), V85>C (837) (766-875), CH3 E12 (891), M14 (893) (876-980), CHS (981-982)) (756-982)]], non-glycosylated, produced in Chinese hamster ovary (CHO) cells
tarlatamab	immunoglobuline scFv-scFv-scFc, anti-[*Homo sapiens* DLL3 (delta-like ligand 3)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal à chaîne unique (scFv)2-scFc, bispécifique; IG à chaîne unique scFv-scFv-scFc, anti-DLL3 et anti-CD3E (1-982) [scFv-VH-V-kappa anti-DLL3 (1-241) [VH (*Homo sapiens* IGHV4-59*01 G49>C (44) (96.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.12] (26-33.51-57.96-107) (1-118) -15-mer-tris(tétraglycyl-séryl) linker (119-133)-V-KAPPA (*Homo sapiens* IGKV3-20*01 (91.7%) -IGKJ2*01 Q120>C (234) (90.9%)) CDR-IMGT [7.3.9] (160-166.184-186.223-231) (134-241)] -6-mer-séryl-tétraglycyl-séryl linker (242-247) -scFv-VH-V-lambda anti-CD3E (248-496) [VH (*Mus musculus*IGHV10-1*02 (91.9%) -(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (273-280.298-307.346-361) (248-372) -15-mer-tris(tétraglycyl-séryl) linker (373-387) – V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (413-421.439-441.478-486) (388-496)] -4-mer-tétraglycyl linker (497-500) - scFc (h-CH2-CH3)-(h-CH2-CH3) (501-982) [*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (charnière 6-15 (501-510), CH2 R83>C (572), N84.4>G (577), V85>C (582) (511-620), CH3 E12 (636), M14 (638) (621-725), CHS>del) (501-725) -30-mer-hexakis(tétraglycyl-séryl) linker (726-755) -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (charnière 6-15 (756-765), CH2 R83>C (827), N84.4>G (832), V85>C (837) (766-875), CH3 E12 (891), M14 (893) (876-980), CHS (981-982)) (756-982)]], non-glycosylé, produit dans des cellules ovariennes de hamster chinois (CHO)

tarlatamab

inmunoglobulina scFv-scFv-scFc, anti-[*Homo sapiens* DLL3 (delta-like ligando 3)] y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal con cadena única (scFv)2-scFc, biespecífica;
IG con cadena única scFv-scFv-scFc, anti-DLL3 y anti-CD3E (1-982) [scFv-VH-V-kappa anti-DLL3 (1-241) [VH (*Homo sapiens* IGHV4-59*01 G49>C (44) (96.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.12] (26-33.51-57.96-107) (1-118) -15-mer-tris(tetraglicil-seril) linker (119-133)-V-KAPPA (*Homo sapiens* IGKV3-20*01 (91.7%) -IGKJ2*01 Q120>C (234) (90.9%)) CDR-IMGT [7.3.9] (160-166.184-186.223-231) (134-241)] -6-mer-seril-tetraglicil-seril linker (242-247) - scFv-VH-V-lambda anti-CD3E (248-496) [VH (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-73*01 (87%) -(IGHD) -IGHJ5*01 (100%)) CDR-IMGT [8.10.16] (273-280.298-307.346-361) (248-372) -15-mer-tris(tetraglicil-seril) linker (373-387) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.9] (413-421.439-441.478-486) (388-496)] -4-mer-tetraglicil linker (497-500) - scFc (h-CH2-CH3)-(h-CH2-CH3) (501-982) [*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (bisagra 6-15 (501-510), CH2 R83>C (572), N84.4>G (577), V85>C (582) (511-620), CH3 E12 (636), M14 (638) (621-725), CHS>del) (501-725) - 30-mer-hexakis(tetraglicil-seril) linker (726-755) -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (bisagra 6-15 (756-765), CH2 R83>C (827), N84.4>G (832), V85>C (837) (766-875), CH3 E12 (891), M14 (893) (876-980), CHS (981-982)) (756-982)]], no glicosilado, producido en las células ováricas de hámster chino (CHO)

Heavy chain / Chaîne lourde / Cadena pesada

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QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYYWSWIRQP PGKCLEWIGY  50
VYYSGTTNYN PSLKSRVTIS VDTSKNQFSL KLSSVTAADT AVYYCASIAV 100
TGFYFDYWGQ GTLVTVSSGG GGSGGGGSGG GGSEIVLTQS PGTLSLSPGE 150
RVTLSCRASQ RVNNNYLAWY QQRPGQAPRL LIYGASSRAT GIPDRFSGSG 200
SGTDFTLTIS RLEPEDFAVY YCQQYDRSPL TFGCGTKLEI KSGGGGSEVQ 250
LVESGGGLVQ PGGSLKLSCA ASGFTFNKYA MNWVRQAPGK GLEWVARIRS 300
KYNNYATYYA DSVKDRFTIS RDDSKNTAYL QMNNLKTEDT AVYYCVRHGN 350
FGNSYISYWA YWGQGTLVTV SSGGGGSGGG GSGGGGSQTV VTQEPSLTVS 400
PGGTVTLTCG SSTGAVTSGN YPNWVQQKPG QAPRGLIGGT KFLAPGTPAR 450
FSGSLLGGKA ALTLSGVQPE DEAEYYCVLW YSNRWVFGGG TKLTVLGGGG 500
DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED 550
PEVKFNWYVD GVEVHNAKTK PCEEQYGSTY RCVSVLTVLH QDWLNGKEYK 600
CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK 650
GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 700
NVFSCSVMHE ALHNHYTQKS LSLSPGGGGS GGGGSGGGGS GGGGSGGGGS 750
GGGGSDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD 800
VSHEDPEVKF NWYVDGVEVH NAKTKPCEEQ YGSTYRCVSV LTVLHQDWLN 850
GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR EEMTKNQVSL 900
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 950
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GK                    982
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Post-translational modifications

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

Intra-V (C23-C104)	22-95 156-222 269-345 409-477
Intra-C (C23-C104)	541-601 647-705 796-856 902-960
Intra-CH2 (C83-C85)	572-582 827-837
Inter-VH-VL (C49-C120)	44-234
Inter-h11 (h11-h11)	506-761
Inter-h14 (h14-h14)	509-764

No N-glycosylation sites / pas de sites de N-glycosylation / ningún posición de N-glicosilación
CH2 N84.4>G:
577, 832
Aglycosylated

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
CHS K2:
982

telpegfilgrastimum #

telpegfilgrastim — human granulocyte colony-stimulating factor (G-CSF, pluripoietin) short isoform, variant (A^1>M), produced in *Escherichia coli*, pegylated with one *N*-{[α-methylpoly(oxyethylene)-ω-oxy]acetyl}-*N*-[α-methylpoly(oxyethylene)-ω-yl]glycyl group at N^2 of M^1 (85-95%) or at N^6 of K^{17} (3-13%) or at N^6 of K^{24}, K^{35} and K^{41} (total not more than 5%);
[1-L-methionine]human granulocyte colony-stimulating factor (G-CSF, pluripoietin) short isoform, produced in *Escherichia coli,* substituted with one *N*-{[α-methylpoly(oxyeth-ylene)-ω-oxy]acetyl}-*N*-[α-methylpoly(oxyethylene)-ω-yl]glycyl group at N^2 of Met^1 (85-95%) or at N^6 of Lys^{17} (3-13 %) or one other lysine residue (total not more than 5%)

telpegfilgrastim — isoforme courte du facteur de stimulation des colonies de granulocytes humain (G-CSF, pluripoiétine), variant (A^1>M), produite dans *Escherichia coli,* pégylé avec un groupe *N*-{[α-méthylpoly(oxyéthylène)-ω-oxy]acétyl}-*N*-[α-méthylpoly(oxyéthylène)-ω-yl]glycyle en N^2 de M^1 (85-95%) ou en
N^6 de K^{17} (3-13%) ou en N^6 de K^{24}, K^{35} et K^{41} (pas plus de 5% au total);
[1-L-méthionine]isoforme courte du facteur de stimulation des colonies de granulocytes humain (G-CSF, pluripoiétine), produite dans *Escherichia coli,* substituée par un groupe *N*-{[α-méthylpoly(oxyéthylène-ω-oxy]acétyl}-*N*-[α-méthylpoly(oxyéthylène)-ω-yl]glycyle en N^2 du $Mét^1$ (85-95 %) ou en N^6 du Lys^{17} (3-13 %) ou d'un autre résidu de lysine (pas plus de 5 % au total)

telpegfilgrastim — factor humano de estimulación de colonias de granulocitos (G-CSF, pluripoyetina) isoforma corta, variante (A^1>M), producido en *Escherichia coli*, pegilado con un grupo *N*-{[α-metilpoli(oxietileno)-ω-oxi]acetil}-*N*-[α-metilpoli(oxietileno)-ω-il]glicilo en N^2 de M^1 (85-95%) o en N^6 de K^{17} (3-13%) o en N^6 de K^{24}, K^{35} y K^{41} (total no más del 5%);
[1-L-metionina]isoforma corta del factor humano de estimulación de colonias de granulocitos (G-CSF, pluripoyetina), producida en *Escherichia coli*, sustituido con un grupo *N*-{[α-metilpoli(oxietileno)-ω-oxi]acetil}-*N*-[α-metilpoli(oxietileno)-ω-il]glicilo en N^2 de la Met^1 (85-95 %) o en N^6 de la Lis^{17} (3-13 %) o un otro residuo de lisina (total no más del 5 %)

$C_{853}H_{1352}N_{224}O_{247}S_9[(C_2H_4O)_{2n}]$ (n ≈ 400-500)

Sequence / Séquence / Secuencia

```
MTPLGPASSL PQSFLLKCLE QVRKIQGDGA ALQEKLCATY KLCHPEELVL   50
LGHSLGIPWA PLSSCPSQAL QLAGCLSQLH SGLFLYQGLL QALEGISPEL  100
GPTLDTLQLD VADFATTIWQ QMEELGMAPA LQPTQGAMPA FASAFQRRAG  150
GVLVASHLQS FLEVSYRVLR HLAQP                             175
```

Mutation / Mutation / Mutación

A^1>M

Post-translational modifications

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

37-43, 65-75

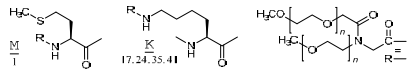
Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación

none / aucune / ninguna

Chemical modification sites / Sites de modification chimique / Posiciones de modificación química

major / principal / mayormente : M1, K17;

minor / secondaire / inferior : K24, K35, K41



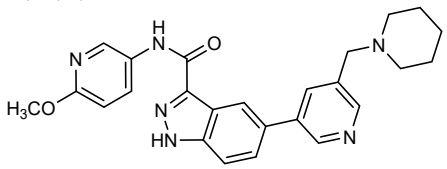
tenvumestrocelum

tenvumestrocel	Allogeneic human mesenchymal stromal cells derived from umbilical cord blood (hUCB-MSCs). The cells are isolated by density-gradient centrifugation and expanded by sub-culturing of the adherent cell population. Cells (on average > 95%) express mesenchymal stromal cell related antigens (CD105 and CD73). The cells are also positive for the CD29 antigen (integrin beta-1), the CD44 antigen (cell adhesion glycoprotein), the CD13 and CD90 antigens, and the HLA-ABC histocompatibility antigen. Cells do not express (on average < 1%) hematopoietic antigens (CD45, CD34 and CD14), histocompatibility antigen (HLA-DR), endothelial cell antigen (CD31), osteoclast antigen (CD51/61), and CD64.
tenvumestrocel	Cellules stromales mésenchymateuses humaines allogéniques dérivées du sang de cordon ombilical (hUCB-MSCs). Les cellules sont isolées par centrifugation à gradient de densité et amplifiées par sous-culture de la population des cellules adhérentes. Les cellules (en moyenne > 95%) expriment des antigènes liés aux cellules stromales mésenchymateuses (CD105 et CD73). Les cellules sont également positives pour l'antigène CD29 (intégrine beta-1), l'antigène CD44 (glycoprotéine d'adhésion cellulaire), les antigènes CD13 et CD90, et l'antigène d'histocompatibilité HLA-ABC. Les cellules n'expriment pas (en moyenne < 1%) les antigènes hématopoïétiques (CD45, CD34 et CD14), l'antigène d'histocompatibilité (HLA-DR), l'antigène des cellules endothéliales (CD31), l'antigène des ostéoclastes (CD51/61), ni l'antigène CD64.
tenvumestrocel	Células estromales mesenquimales humanas alogénicas derivadas de sangre de cordón umbilical (hUCB-MSCs). Las células se aíslan por centrifugación en un gradiente de densidad y se expanden mediante subcultivo de las poblaciones adherentes. Las células (de media >95%) expresan los antígenos relacionados con las células estromales mesenquimales (CD105 y CD73). Las células son también positivas para los antígenos CD29 (integrina beta-1), CD44 (receptor de matriz extracelular), CD13 y CD90, y para el antígeno de histocompatibilidad HLA-ABC. Las células no expresan (de media <1%) antígenos hematopoyéticos (CD45, CD34 y CD14), antígeno de histocomaptiblidad (HLA-DR), antígeno de células endoteliales (CD31), antígeno de osteoclastos (CD51/61), ni CD64.

teplinovivintum

teplinovivint	*N*-(6-methoxypyridin-3-yl)-5-{5-[(piperidin-1-yl)methyl]pyridin-3-yl}-1*H*-indazole-3-carboxamide
téplinovivint	*N*-(6-méthoxypyridin-3-yl)-5-{5-[(pipéridin-1-yl)méthyl]pyridin-3-yl}-1*H*-indazole-3-carboxamide
teplinovivint	*N*-(6-metoxipiridin-3-il)-5-{5-[(piperidin-1-il)metil]piridin-3-il}-1*H*-indazol-3-carboxamida

$C_{25}H_{26}N_6O_2$



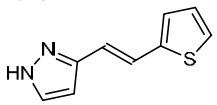
terevalefimum

terevalefim — 3-[(1*E*)-2-(thiophen-2-yl)ethen-1-yl]-1*H*-pyrazole

térévaléfim — 3-[(1*E*)-2-(thiophén-2-yl)éthén-1-yl]-1*H*-pyrazole

terevalefim — 3-[(1*E*)-2-(tiofen-2-il)eten-1-il]-1*H*-pirazol

$C_9H_8N_2S$



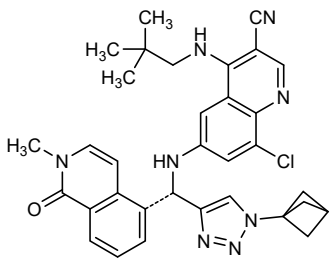
tilpisertibum

tilpisertib — 6-{[(*S*)-[1-(bicyclo[1.1.1]pentan-1-yl)-1*H*-1,2,3-triazol-4-yl](2-methyl-1-oxo-1,2-dihydroisoquinolin-5-yl)methyl]amino}-8-chloro-4-[(2,2-dimethylpropyl)amino]quinoline-3-carbonitrile

tilpisertib — 6-{[(*S*)-[1-(bicyclo[1.1.1]pentan-1-yl)-1*H*-1,2,3-triazol-4-yl](2-méthyl-1-oxo-1,2-dihydroisoquinoléin-5-yl)méthyl]amino}-8-chloro-4-[(2,2-diméthylpropyl)amino]quinoléine-3-carbonitrile

tilpisertib — 6-{[(*S*)-[1-(biciclo[1.1.1]pentan-1-il)-1*H*-1,2,3-triazol-4-il](2-metil-1-oxo-1,2-dihidroisoquinolein-5-il)metil]amino}-8-cloro-4-[(2,2-dimetilpropil)amino]quinoleína-3-carbonitrilo

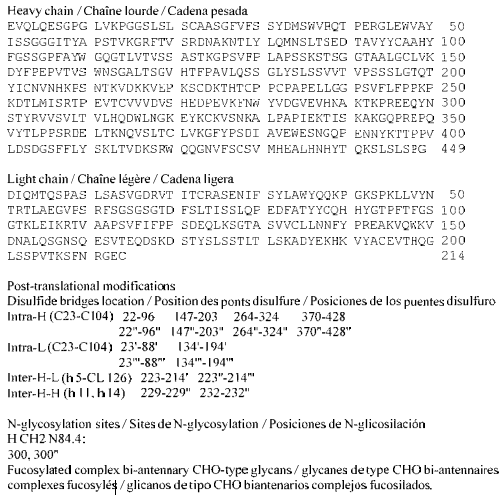
$C_{33}H_{33}ClN_8O$



tusamitamabum #

tusamitamab — immunoglobulin G1-kappa, anti-[*Homo sapiens* CEACAM5 (carcinoembryonic antigen-related cell adhesion molecule 5, CEA, CD66e)], monoclonal antibody;

	gamma1 heavy chain (1-449) [VH (*Mus musculus* IGHV5-12-1*01 (86.6%) -(IGHD) -IGHJ3*01 (92.9%)/*Homo sapiens* IGHV3-23*01 (77.3%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS K>del (449) (121-449)], (223-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Mus musculus* IGKV12-44*01 (87.4%) -IGKJ4*01 (100%)/*Homo sapiens* IGKV1-39*01 (82.1%) -IGKJ2*02 (90.9%)) CDR-IMGT [6.3.9](27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO)-derived cell line, glycoform alfa
tusamitamab	immunoglobuline G1-kappa, anti-[*Homo sapiens* CEACAM5 (molécule d'adhésion cellulaire 5 apparentée à l'antigène carcinoembryonaire, CEA, CD66e)], anticorps monoclonal; chaîne lourde gamma1 (1-449) [VH (*Mus musculus* IGHV5-12-1*01 (86.6%) -(IGHD) -IGHJ3*01 (92.9%)/*Homo sapiens* IGHV3-23*01 (77.3%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS K>del (449) (121-449)], (223-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV12-44*01 (87.4%) -IGKJ4*01 (100%)/*Homo sapiens* IGKV1-39*01 (82.1%) -IGKJ2*02 (90.9%)) CDR-IMGT [6.3.9](27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229'':232-232'')-bisdisulfure, produite dans une lignée cellulaire dérivée des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
tusamitamab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* CEACAM5 (molécula de adhesión celular 5 relacionada con el antígeno carcinoembrionario, CEA, CD66e)], anticuerpo monoclonal; cadena pesada gamma1 (1-449) [VH (*Mus musculus* IGHV5-12-1*01 (86.6%) -(IGHD) -IGHJ3*01 (92.9%)/*Homo sapiens* IGHV3-23*01 (77.3%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (217) (121-218), bisagra1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS K>del (449) (121-449)], (223-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV12-44*01 (87.4%) -IGKJ4*01 (100%)/*Homo sapiens* IGKV1-39*01 (82.1%) -IGKJ2*02 (90.9%)) CDR-IMGT [6.3.9](27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229'':232-232'')-bisdisulfuro, producido en una línea celular derivada de las células ováricas de hámster chino (CHO), forma glicosilada alfa



Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLQESGPG LVKPGGSLSL SCAASGFVFS SYDMSWVRQT PERGLEWVAY  50
ISSGGGITYA PSTVKGRFTV SRDNAKNTLY LQMNSLTSED TAVYYCAAHY 100
FGSSGPFAYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPG  449
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPAS LSASVGDRVT ITCRASENIF SYLAWYQQKP GKSPKLLVYN  50
TRTLAEGVPS RFSGSGSGTD FSLTISSLQP EDFATYYCQH HYGTPFTFGS 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                         214
```

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

```
Intra-H (C23-C104)  22-96    147-203   264-324    370-428
                    22"-96"  147"-203" 264"-324" 370"-428"
Intra-L (C23-C104)  23'-88'   134'-194'
                    23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126)  223-214'  223"-214'"
Inter-H-H (h 11, h 14)  229-229"  232-232"
```

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

tusamitamabum ravtansinum #

tusamitamab ravtansine

immunoglobulin G1-kappa, anti-[*Homo sapiens* CEACAM5 (carcinoembryonic antigen-related cell adhesion molecule 5, CEA, CD66e)], monoclonal antibody, conjugated to maytansinoid DM4; gamma1 heavy chain (1-449) [VH (*Mus musculus* IGHV5-12-1*01 (86.6%) -(IGHD) -IGHJ3*01 (92.9%)/*Homo sapiens* IGHV3-23*01 (77.3%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS K>del (449) (121-449)], (223-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Mus musculus* IGKV12-44*01 (87.4%) -IGKJ4*01 (100%)/*Homo sapiens* IGKV1-39*01 (82.1%) -IGKJ2*02 (90.9%)) CDR-IMGT [6.3.9](27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')];
dimer (229-229":232-232")-bisdisulfide, produced in a Chinese hamster ovary (CHO) cell line derived from CHO-K1SV, glycoform alfa; conjugated, on an average of 3 to 4 lysyl, to maytansinoid DM4 [*N2*'- deacetyl-*N2*'-(4-mercapto-4-methyl-1-oxopentyl)- maytansine] via the reducible SPDB linker [*N*-succinimidyl 4-(2-pyridyldithio)butanoate]
For the *ravtansine* part, please refer to the document "*INN for pharmaceutical substances: Names for radicals, groups and others*"*

tusamitamab ravtansine

immunoglobuline G1-kappa, anti-[*Homo sapiens* CEACAM5 (molécule d'adhésion cellulaire 5 apparentée à l'antigène carcinoembryonaire, CEA, CD66e)], anticorps monoclonal, conjugué au maytansinoïde DM4;
chaîne lourde gamma1 (1-449) [VH (*Mus musculus* IGHV5-12-1*01 (86.6%) -(IGHD) -IGHJ3*01 (92.9%)/*Homo sapiens* IGHV3-23*01 (77.3%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS K>del (449) (121-449)], (223-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV12-44*01 (87.4%) -IGKJ4*01 (100%)/*Homo sapiens* IGKV1-39*01 (82.1%) -IGKJ2*02 (90.9%)) CDR-IMGT [6.3.9](27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')];

tusamitamab ravtansina

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CEACAM5 (molécula de adhesión celular 5 con el antígeno carcinoembrionario, CEA, CD66e)], anticuerpo monoclonal, conjugado con maitansinoide DM4;
cadena pesada gamma1 (1-449) [VH (*Mus musculus* IGHV5-12-1*01 (86.6%) -(IGHD) -IGHJ3*01 (92.9%)/*Homo sapiens* IGHV3-23*01 (77.3%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS K>del (449) (121-449)], (223-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV12-44*01 (87.4%) -IGKJ4*01 (100%)/*Homo sapiens* IGKV1-39*01 (82.1%) -IGKJ2*02 (90.9%)) CDR-IMGT [6.3.9](27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')];
dímero (229-229'':232-232'')-bisdisulfuro, producido en las células ováricas de hámsters chinos (CHO) línea celular derivada de CHO-K1SV, forma glicosilada alfa; conjugado, en 3 a 4 residuos lisil por término medio, con maitansinoide DM4 [*N*2'-deacetil-*N*2'-(4-mercapto-4-metil-1-oxopentil)- maitansina]mediante un conector SPDB reducible [4-(2- piridilditio)butanoato de *N*-succinimidilo]
Para la fracción ravtansina, se ruega referirse al documento "*INN for pharmaceutical substances: Names for radicals, groups and others*"*

Heavy chain / Chaîne lourde / Cadena pesada
```
EVQLQESGPG LVKPGGSLSL SCAASGFVFS SYDMSWVRQT PERGLEWVAY  50
ISSGGGITYA PSTVKGRFTV SRDNAKNTLY LQMNSLTSED TAVYYCAARY 100
FGSSGPFAYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPG  449
```

Light chain / Chaîne légère / Cadena ligera
```
DIQMTQSPAS LSASVGDRVT ITCRASENIF SYLAWYQQKP GKSPKLLVYN  50
TRTLAEGVPS RFSGSGSGTD FSLTISSLQP EDFATYYCQH HYGTPFTFGS 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
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-h14) 229-229" 232-232"

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

For the ravtansine part, please refer to the document "INN for pharmaceutical substances: Names for radicals, groups and others"*
Pour la partie ravtansine, veuillez-vous référer au document "INN for pharmaceutical substances: Names for radicals, groups and others"*
Para la fracción ravtansina, se ruega referirse al documento "INN for pharmaceutical substances: Names for radicals, groups and others"*

upifitamabum rilsodotinum

upifitamab rilsodotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* SLC34A2 (solute carrier family 34 sodium phosphate member 2, sodium/phosphate cotransporter 2B, NaPi2b, NaPi3b, NAPI-3B)], monoclonal antibody, conjugated, via a thioether bond, to3 to 5 flexible polymers PHF-BA-EG2-MI-AF-HPA-Ala, each comprising maleimide (MI) bioconjugation linkers and
3 to 4 auristatin F- hydroxypropylamide-L-alanine (AF-HPA-Ala), with a drug ratio of 12:1 to 15:1;

	gamma1 heavy chain (1-449) [VH (*Homo sapiens* IGHV1-46*01 (81.6%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -glycinyl (120) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-215')-disulfide with kappa light chain (1'-215') [V-KAPPA (*Mus musculus* IGKV10-94*01 (84.2%) -IGKJ5*01 (91.7%)/*Homo sapiens* IGKV1-33*01 (83.2%) -IGKJ2*01 (90.9%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -arginyl (108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109''-215')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa; conjugated, via a thioether bond, from 3 to 5 flexible biodegradable polymers, poly(1-hydroxymethylethylene hydroxymethyl-formal) (PHF)-BA-EG2-MI-AF-HPA-Ala, each comprising maleimide (MI) conjugation linkers and 3 to 4 cytotoxic auristatin F- hydroxypropylamide-L-alanine (AF-HPA-Ala), with a drug ratio of 12:1 to 15:1
upifitamab rilsodotine	immunoglobuline G1-kappa, anti-[*Homo sapiens* SLC34A2 (membre 2 de la famille 34 sodium phosphate de transporteurs de solutés, cotransporteur 2B de sodium/phosphate, NaPi2b, NaPi3b, NAPI-3B)], anticorps monoclonal, conjugué, via une liaison thiéther, à 3 à 5 polymères flexibles PHF-BA-EG2-MI-AF-HPA-Ala, comprenant chacun des linkers de bioconjugaison maléimide (MI) et 3 à 4 auristatine F- hydroxypropylamide-alanine (AF-HPA-Ala), dans un rapport produit actif de 12:1 à 15:1; chaîne lourde gamma1 (1-449) [VH (*Homo sapiens* IGHV1-46*01 (81.6%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -glycinyl (120) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-215')-disulfure avec la chaîne légère kappa (1'-215') [V-KAPPA (*Mus musculus* IGKV10-94*01 (84.2%) -IGKJ5*01 (91.7%)/*Homo sapiens* IGKV1-33*01 (83.2%) -IGKJ2*01 (90.9%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -arginyl (108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (229-229'':232-232'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa; conjugué, via une liaison thiéther, de 3 à 5 polymères flexibles biodégradables poly(1-hydroxyméthyléthylène hydroxyméthyl-formal) (PHF)-BA-EG2-MI-AF-HPA-Ala, comprenant chacun des linkers de conjugaison maléimide (MI) et 3 à 4 auristatine F- hydroxypropylamide-L-alanine (AF-HPA-Ala) cytotoxiques, dans un rapport produit actif de 12:1 à 15:1
upifitamab rilsodotina	inmunoglobulina G1-kappa, anti-[*Homo sapiens* SLC34A2 (miembro 2 de la familia 34 sodio fosfato de transportadores de solutos, cotransportador 2B de sodio/fosfato, NaPi2b, NaPi3b, NAPI-3B)], anticuerpo monoclonal, conjugado, a través de un enlace tioéter, de 3 a 5 polímeros flexibles PHF-BA-EG2-MI-AF-HPA-Ala, que comprende cada uno de los enlaces de bioconjugación maleimida (MI) y 3 a 4 auristatina F- hidroxipropilamida-L-alanina (AF-HPA-Ala), en una relación de principio activo de 12:1 a 15:1;

cadena pesada gamma1 (1-449) [VH (*Homo sapiens* IGHV1-46*01 (81.6%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -glicinil (120) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-215')-disulfuro con la cadena ligera kappa (1'-215') [V-KAPPA (*Mus musculus* IGKV10-94*01 (84.2%) -IGKJ5*01 (91.7%)/*Homo sapiens* IGKV1-33*01 (83.2%) -IGKJ2*01 (90.9%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -arginil (108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')];
dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa; conjugado, a través de un enlace tioéter, a 3 a 5 polímeros flexibles biodegradables poli(1-hidroximetiletileno hidroximetil-formal) (PHF)-BA-EG2-MI-AF-HPA-Ala, que comprende cada unos de los enlaces de conjugación maleimida (MI) y
3 a 4 auristatina F- hidroxipropilamida-L-alanina (AF-HPA-Ala) citotóxicos, en una relación de principio activo de 12:1 a 15:1

Heavy chain / Chaîne lourde / Cadena pesada

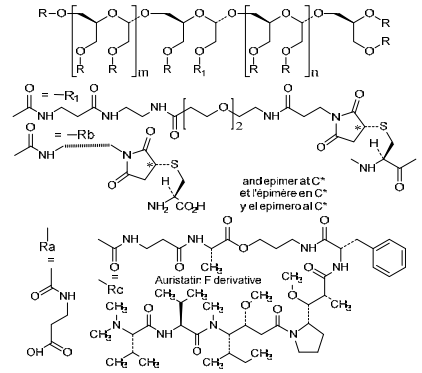
```
QVQLVQSGAE VVKPGASVKM SCKASGYTFT GYNIHWVKQA PGQGLEWIGA  5C
IYPGNGDTSY KQKFRGRATL TADTSTSTVY MELSSLRSED SAVYYCARGE 100
TARATFAYWG QGTLVTVSSG ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKRVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPG  449
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCSASQDIG NFLNWYQQKP GKTVKVLIYY  5C
TSSLYSGVPS RFSGSGSGTD YTLTISSLQP EDFATYYCQQ YSKLPLTFGQ 100
GTKLELKRRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGRS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 135'-195'
23'"-88'" 135'"-195'"
Inter-H-L (h 5-CL 126)* 223-215' 223"-215'"
Inter-H-H (h 11-h 14)* 229-229" 232-232"
*Two or three of the inter-chain disulfide bridges are not present, 3 to 5 cysteinyl being conjugated each via a thioether bond to one maleimide linker of one flexible polymer comprising 3 to 4 drug units.
*Deux ou trois des ponts disulfures inter-chaînes ne sont pas présents, 3 to 5 cystéinyl étant chacun conjugué via une liaison thioéther à un linker-maléimide d'un polymère flexible comprenant 3 à 4 unités de principe actif.
*Faltan dos o tres puentes disulfuro inter-catenarios. 3 a 5 cisteinil está conjugada a conectores de un polímero flexible que contiene 3 a 4 unidades de principio activo.

Modified residues / résidus modifiés / restos modificados:



m + n ~ 35-75 ; R = H , Ra , Rb or Rc ; ratio H : Ra : Rb : Rc ~ 70 : 20 : 2 : 8

N-terminal glutaminyl cyclization to pyroglutamyl (pE; 5-oxoprolyl)
L VHQ1:
1, 1"

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

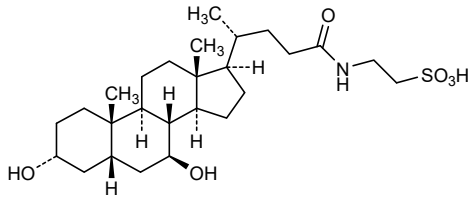
ursodoxicoltaurinum

ursodoxicoltaurine — 2-(3α,7β-dihydroxy-5β-cholan-24-amido)ethane-1-sulfonic acid

ursodoxicoltaurine — acide 2-(3α,7β-dihydroxy-5β-cholan-24-amido)éthane-1-sulfonique

ursodoxicoltaurina — ácido 2-(3α,7β-dihidroxi-5β-colan-24-amido)etano-1-sulfónico

$C_{26}H_{45}NO_6S$



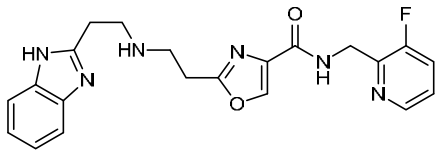
vamifeportum

vamifeport — 2-(2-{[2-(1*H*-benzimidazol-2-yl)ethyl]amino}ethyl)-*N*-[(3-fluoropyridin-2-yl)methyl]-1,3-oxazole-4-carboxamide

vamiféport — 2-(2-{[2-(1*H*-benzimidazol-2-yl)éthyl]amino}éthyl)-*N*-[(3-fluoropyridin-2-yl)méthyl]-1,3-oxazole-4-carboxamide

vamifeport — 2-(2-{[2-(1*H*-benzimidazol-2-il)etil]amino}etil)-*N*-[(3-fluoropiridin-2-il)metil]-1,3-oxazol-4-carboxamida

$C_{21}H_{21}FN_6O_2$



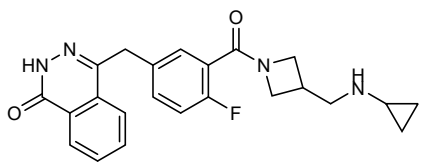
venadaparibum

venadaparib — 3^4-fluoro-7-aza-1(1)-phthalazina-5(1,3)-azetidina-3(1,3)-benzena-8(1)-cyclopropanaoctaphane-1^4(1^3H),4-dione

vénadaparib — 3^4-fluoro-7-aza-1(1)-phthalazina-5(1,3)-azétidina-3(1,3)-benzèna-8(1)-cyclopropanaoctaphane-1^4(1^3H),4-dione

venadaparib — 3^4-fluoro-7-aza-1(1)-ftalazina-5(1,3)-azetidina-3(1,3)-bencena-8(1)-ciclopropanaoctafano-1^4(1^3H),4-diona

$C_{23}H_{23}FN_4O_2$



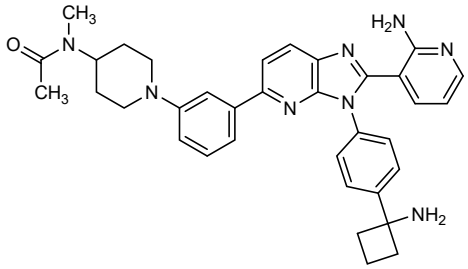
vevorisertibum

vevorisertib — *N*-[1-(3-{3-[4-(1-aminocyclobutyl)phenyl]-2-(2-aminopyridin-3-yl)-3*H*-imidazo[4,5-*b*]pyridin-5-yl}phenyl)piperidin-4-yl]-*N*-methylacetamide

vévorisertib — *N*-[1-(3-{3-[4-(1-aminocyclobutyl)phényl]-2-(2-aminopyridin-3-yl)-3*H*-imidazo[4,5-*b*]pyridin-5-yl}phényl)pipéridin-4-yl]-*N*-méthylacétamide

vevorisertib — *N*-[1-(3-{3-[4-(1-aminociclobutil)fenil]-2-(2-aminopiridin-3-il)-3*H*-imidazo[4,5-*b*]piridin-5-il}fenil)piperidin-4-il]-*N*-metilacetamida

$C_{35}H_{38}N_8O$



vibapapogenum autoleucelum #

vibapapogene autoleucel — Autologous peripheral blood mononuclear cells (PBMCs) expressing human papillomavirus types 16 and 18 antigens.
Autologous peripheral blood mononuclear cells (PBMCs), specifically B lymphocytes and monocytes that are T-cell depleted, transfected *ex vivo* with a non-replicating adenoviral vector that expresses a codon-optimised fusion of tumour-associated antigens (TAAs) E6 and E7 derived from human papillomavirus (HPV) types 16 and 18 (HPV-16/18 E6/E7). The antigen coding region is preceded by a tPA signal sequence and transcription is under the control of the cytomegalovirus (CMV)-tetracycline 10 promoter and the SV40 poly(A) termination sequence. The vector genome is flanked by inverted terminal repeats and contains an encapsidation signal and a K35 knob.

vibapapogène autoleucel — Cellules mononucléaires du sang périphérique autologues exprimant les antigènes de papillomavirus humains de type 16 et 18.
Cellules mononucléaires du sang périphérique autologues, spécifiquement les lymphocytes B et les monocytes qui sont déplétées en lymphocytes T, transfectées *ex vivo* avec une forme non réplicative du vecteur adénoviral exprimant un codon optimisé, fusion des antigènes associés à des tumeurs E6 et E7 dérivés du virus humain du papillome (HPV) types 16 et 18 (HPV-16/18 E6/E7). La région codant l'antigène est précédée d'une séquence signal tPA et la transcription est sous le contrôle du promoteur tétracycline 10 du cytomégalovirus et de la séquence de terminaison poly(A) SV40. Le génome du vecteur est flanqué de répétitions inverses et contient un signal d'encapsidation et un domaine globulaire distal (knob) K35.

vibapapogén autoleucel	Células monucleares de sangre periférica (PBMCs) autólogas que expresan antígenos del papilomavirus humano de tipo 16 y 18. Células monucleares de sangre periférica (PBMCs) autólogas, específicamente linfocitos B y monocitos que están deplecionadas de células T, transfectadas *ex vivo* con un vector adenoviral no replicative que expresa una fusion de los antígenos asociados a tumor (TAAs) E6 y E7 derivados del papillomavirus humano (HPV) de tipo 16 y 18 (HPV-16/18 E6/E7), con codones optimizados. La region codificadora de antigen está precedidad por una secuencia señal tPA y la transcripción está bajo el control del promotor de la tetraciclina 10 del cytomegalovirus (CMV) y la secuencia poly(A) de terminación del SV50. El genoma del vector está flanqueado por repeticiones invertidas terminales y contiene una señal de encapsidación y un dominio globular distal (knob) K35.
vibosameranum #	
vibosameran	Messenger RNA encoding tyrosinase. Messenger RNA (mRNA), 5'-capped, encoding codon-optimised tyrosinase (monophenol monooxygenase, tumour rejection antigen AB), expressed as a fusion protein comprising tyrosinase, P2P16 tetanus toxoid-derived helper epitopes and a major histocompatibility complex (MHC) class I transmembrane and cytoplasmic domain, connected by two glycine/serine-rich (GS) linker peptides, flanked by 5' and 3' untranslated regions and a 3' poly(A) tail.
vibosaméran	ARN messager codant pour la tyrosinase. ARN messager (ARNm), protégé en 5', codant pour la tyrosinase (monophénol monooxygénase, antigène de rejet de tumeur AB), avec des codons optimisés, exprimé sous la forme d'une protéine de fusion comprenant la tyrosinase, les épitopes auxiliaires P2P16 dérivés de l'anatoxine tétanique et un domaine transmembranaire et cytoplasmique du complexe majeur d'histocompatibilité (CMH) de classe I, reliés par deux peptides de liaison riches en glycine/sérine (GS), flanqués de régions non traduites en 5' et 3' et d'une queue poly(A) en 3'.
vibosamerán	ARN mensajero que codifica para tirosinasa. ARN mensajero (ARNm), protegido en 5' que codifica para tirosinasa (monofenol monooxigenasa, antígeno de rechazo tumoral AB), con codones optimizados, expresada como una proteína de fusión que consta de la tirosinasa, los epítopos auxiliares P2P16 derivados del toxoide tetánico y un dominio citoplásmico y transmembrana del complejo principal de histocompatibilidad (MHC) de clase I, conectados mediante dos péptidos de enlace ricos en glicina/serina (GS), flanqueado por las regiones 5' y 3' no traducidas y una cola poly(A) en 3'.

vidutolimodum

vidutolimod — immunostimulatory CG-rich palindromic oligodeoxyribonucleotide, flanked by 3'-dG_{10} and 5'-dG_{10} decanucleotides:
deca[2'-deoxyguanylyl-(3'→5')]-2'-deoxyguanylyl-(3'→5')-2'-deoxyadenylyl-(3'→5')-2'-deoxycytidylyl-(3'→5')-2'-deoxyguanylyl-(3'→5')-2'-deoxyadenylyl-(3'→5')-thymidylyl-(3'→5')-2'-deoxycytidylyl-(3'→5')-2'-deoxyguanylyl-(3'→5')-thymidylyl-(3'→5')-2'-deoxycytidylyl-(3'→5')-nona[2'-deoxyguanylyl-(3'→5')]-2'-deoxyguanosine

vidutolimod — oligodésoxyribonucléotide palindromique immunostimulateur riche en CG, flanqué de décanucléotides 3'-dG_{10} et 5'-dG_{10}:
déca[2'-désoxyguanylyl-(3'→5')]-2'-désoxyguanylyl-(3'→5')-2'-désoxyadénylyl-(3'→5')-2'-désoxycytidylyl-(3'→5')-2'-désoxyguanylyl-(3'→5')-2'-désoxyadénylyl-(3'→5')-thymidylyl-(3'→5')-2'-désoxycytidylyl-(3'→5')-2'-désoxyguanylyl-(3'→5')-thymidylyl-(3'→5')-2'-désoxycytidylyl-(3'→5')-nona[2'-désoxyguanylyl-(3'→5')]-2'-désoxyguanosine

vidutolimod — oligodesoxirribonucleótido palindrómico inmunoestimulador rico en CG, flanqueado por decanucleótidos 3'-dG_{10} y 5'-dG_{10}:
deca[2'-desoxiguanilil-(3'→5')]-2'-desoxiguanilil-(3'→5')-2'-desoxiadenilil-(3'→5')-2'-desoxicitidilil-(3'→5')-2'-desoxiguanilil-(3'→5')-2'-desoxiadenilil-(3'→5')-timidilil-(3'→5')-2'-desoxicitidilil-(3'→5')-2'-desoxiguanilil-(3'→5')-timidilil-(3'→5')-2'-desoxicitidilil-(3'→5')-nona[2'-desoxiguanilil-(3'→5')]-2'-desoxiguanosina

$C_{297}H_{363}N_{138}O_{178}P_{29}$

Sequence / Séquence / Secuencia

(3'→5') d(GGGGGGGGGG **GACGATCGTC** GGGGGGGGGG)

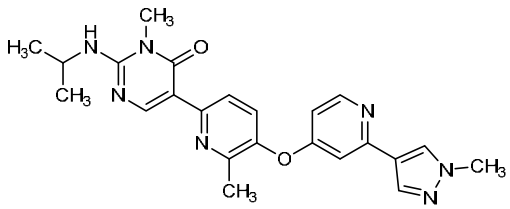
vimseltinibum

vimseltinib — 3-methyl-5-(6-methyl-5-{[2-(1-methyl-1*H*-pyrazol-4-yl)pyridin-4-yl]oxy}pyridin-2-yl)-2-[(propan-2-yl)amino]pyrimidin-4(3*H*)-one

vimseltinib — 3-méthyl-5-(6-méthyl-5-{[2-(1-méthyl-1*H*-pyrazol-4-yl)pyridin-4-yl]oxy}pyridin-2-yl)-2-[(propan-2-yl)amino]pyrimidin-4(3*H*)-one

vimseltinib — 3-metil-5-(6-metil-5-{[2-(1-metil-1*H*-pirazol-4-il)piridin-4-il]oxi}piridin-2-il)-2-[(propan-2-il)amino]pirimidin-4(3*H*)-ona

$C_{23}H_{25}N_7O_2$



vixarelimabum #

vixarelimab	immunoglobulin G4-G1-lambda2, anti-[*Homo sapiens* OSMR (oncostatin M receptor, OSMRB, OSMRbeta)], *Homo sapiens* monoclonal antibody; gamma4-gamma1 heavy chain *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-8*01 (95.9%) -(IGHD) -IGHJ6*01 (95.0%)) CDR-IMGT [8.8.19] (26-33.51-58.97-115) (1-126)-*Homo sapiens* IGHG4*01 CH1-h-CH2, G4v5 h P10, G4v36 CH2 Q84.4 (CH1 (127-224), hinge 1-12 S10>P (234) (225-236), CH2 N84.4>Q (303) (237-346)) -IGHG1*01 CH3-CHS, G1m1 (CH3 D12 (362), L14 (364) (347-451), CHS K>del (452)) (127-452)], (140-215')-disulfide with lambda2 light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-44*01 (90.8%) -IGLJ2*01 (100%)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimer (232-232":235-235")-bisdisulfide, non-glycosylated, produced in Chinese hamster ovary (CHO)-DG44i cell line
vixarélimab	immunoglobuline G4-G1-lambda2, anti-[*Homo sapiens* OSMR (récepteur de l'oncostatine M, OSMRB, OSMRbeta)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma4-gamma1 *Homo sapiens*(1-452) [VH (*Homo sapiens* IGHV1-8*01 (95.9%) -(IGHD) -IGHJ6*01 (95.0%)) CDR-IMGT [8.8.19] (26-33.51-58.97-115) (1-126)-*Homo sapiens* IGHG4*01 CH1-h-CH2, G4v5 h P10, G4v36 CH2 Q84.4 (CH1 (127-224), charnière 1-12 S10>P (234) (225-236), CH2 N84.4>Q (303) (237-346)) (127-346) -IGHG1*01 CH3-CHS, G1m1 (CH3 D12 (362), L14 (364) (347-451), CHS K>del (452)) (347-452)], (140-215')-disulfure avec la chaîne légère lambda2 *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-44*01 (90.8%) -IGLJ2*01 (100%)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimère (232-232":235-235")-bisdisulfure, non-glycosylé, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-DG44i
vixarelimab	inmunoglobulina G4-G1-lambda2, anti-[*Homo sapiens* OSMR (receptor de la oncostatina M, OSMRB, OSMRbeta)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma4-gamma1 *Homo sapiens*(1-452) [VH (*Homo sapiens* IGHV1-8*01 (95.9%) -(IGHD) -IGHJ6*01 (95.0%)) CDR-IMGT [8.8.19] (26-33.51-58.97-115) (1-126)-*Homo sapiens* IGHG4*01 CH1-h-CH2, G4v5 h P10, G4v36 CH2 Q84.4 (CH1 (127-224), bisagra 1-12 S10>P (234) (225-236), CH2 N84.4>Q (303) (237-346)) (127-346) -IGHG1*01 CH3-CHS, G1m1 (CH3 D12 (362), L14 (364) (347-451), CHS K>del (452)) (347-452)], (140-215')-disulfuro con la cadena ligera lambda2 *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-44*01 (90.8%) -IGLJ2*01 (100%)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dímero (232-232":235-235")-bisdisulfuro, no glicosilado, producido en las células ováricas de hámster chino (CHO) línea celular CHO-DG44i

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYEINWVRQA TGQGLEWMGW  50
MNPNSGYTGY AQKFQGRVTM TRDTSISTAY MEMSSLRSED TAVYYCARDI 100
VAANTDYYFY YGMDVWGQGT TVTVSSASTK GPSVFPLAPC SRSTSESTAA 150
LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS 200
SLGTKTYTCN VDHKPSNTKV DKRVESKYGP PCPPCPAPEF LGGPSVFLFP 250
PKPKDTLMIS RTPEVTCVVV DVSQEDPEVQ FNWYVDGVEV HNAKTKPREE 300
QFQSTYRVVS VLTVLHQDWL NGKEYKCKVS NKGLPSSIEK TISKAKGQPR 350
EPQVYTLPPS RDELTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS 450
PG                                                      452
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Light chain / Chaîne légère / Cadena ligera

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QSVLTQPPSA SGTPGQRVTI SCSGSNSNIG SNTVNWYHQL PGTAPKLLIY  50
NINKRPSGVP DRFSGSKSGS SASLAISGLQ SEDEADYYCS TWDDSLDGVV 100
FGGGTKLTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS                                      216
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 153-209 267-327 373-431
22"-96" 153"-209" 267"-327" 373"-431"
Intra-L (C23-C104) 22'-89' 138'-197'
22"'-89"' 138"'-197"'
Inter-H-L (CH1 10-CL 126) 140-215' 140"-215"'
Inter-H-H (h 8, h 11) 232-232" 235-235"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"
L VL Q1:
1', 1"'

No N-glycosylation sites / pas de sites de N-glycosylation / ningùn posición de N-glycosilación
H CH2 N84.4>Q (303)
Aglycosylated

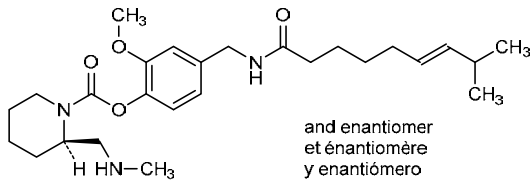
vocacapsaicinum

vocacapsaicin — *rac*-2-methoxy-4-{[(6*E*)-8-methylnon-6-enamido]methyl}phenyl (2*R*)-2-[(methylamino)methyl]piperidine-1-carboxylate

vocacapsaïcine — *rac*-(2*R*)-2-[(méthylamino)méthyl]pipéridine-1-carboxylate de 2-méthoxy-4-{[(6*E*)-8-méthylnon-6-énamido]méthyl}phényle

vocacapsaícina — *rac*-(2*R*)-2-[(metilamino)metil]piperidina-1-carboxilato de 4-{[(6*E*)-8-metilnon-6-enamido]metil}-2-metoxifenilo

$C_{26}H_{41}N_3O_4$



and enantiomer
et énantiomère
y enantiómero

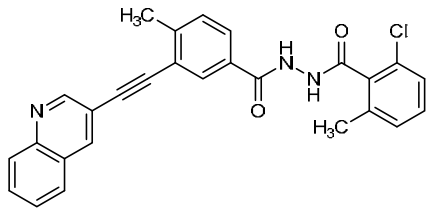
vodobatinibum

vodobatinib — 2-chloro-6-methyl-*N*′-{4-methyl-3-[(quinolin-3-yl)ethynyl]benzoyl}benzohydrazide

vodobatinib — 2-chloro-6-méthyl-*N*′-{4-méthyl-3-[(quinoléin-3-yl)éthynyl]benzoyl}benzohydrazide

vodobatinib — 2-cloro-6-metil-*N*′-{4-metil-3-[(quinolein-3-il)etinil]benzoil}benzohidrazida

$C_{27}H_{20}ClN_3O_2$



vudalimabum #

vudalimab	immunoglobulin half-IG G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* CTLA4 (cytotoxic T-lymphocyte-associated protein 4, CD152)] and anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], monoclonal antibody, bispecific; gamma1 heavy chain anti-CTLA4 (1-447) [VH (*Homo sapiens* IGHV3-48*03 (90.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107)(1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 N114>D (209) R120>K (215) (119-216), hinge 1-15 (217-231), CH2 E1.4,L1.3>P (234), L1.2>V (235), G1.1>A (236), S29>K (267), Q84.2>E (295) (232-340), CH3 E12 (356), M14 (358), L24>D (368), K26>S (370), N44>D (384), Q97>E (418), N100>D (421), M107>L (428), N114>S (434) (341-445), CHS (446-447)) (119-447)], (221-215')-disulfide with kappa light chain anti-CTLA4, *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (99.0%) -IGKJ1*01 (100%)) CDR-IMGT [7.3.9] (27-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; IG scFv-h-CH2-CH3 single chain, anti-PDCD1 (1"-480") [scFv V-kappa-VH anti-PDCD1 (1"-249") [V-KAPPA (*Homo sapiens*IGKV3-15*01 (80.0%)-IGHJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1"-107") -20-mer tetrakis(glycyl-lysyl-prolyl-glycyl-seryl) linker (108"-127") -VH (*Mus musculus* IGHV6-6*02 (87.0%) -(IGHD) -IGHJ1*03 (86.7%)/*Homo sapiens* IGHV3-15*07 (81.8%) -(IGHD) -IGHJ2*01 (93.3%)) CDR-IMGT [8.10.13] (153-160.178-187.226-238) (128"-249")] -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (250"-480") [hinge 1-15 C5>S (254) (250-264) -CH2 E1.4,L1.3>P (267), L1.2>V (268), G1.1>A (269), S29>K (300) (265-373),CH3 E12 (389), E13>Q (390), M14 (391), S20>K (397), M107>L (461), N114>S (467) (374-478), CHS (479-480)]]; dimer (227-260":230-263")-bisdisulfide, produced in Chinese hamster ovary (CHO)-S cell line, glycoform alfa
vudalimab	immunoglobuline demi-IG G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* CTLA4 (protéine 4 associée aux lymphocytes T cytotoxiques, CD152)] et anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal, bispécifique;

	chaîne lourde gamma1 anti-CTLA4, (1-447) [VH (*Homo sapiens* IGHV3-48*03 (90.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 N114>D (209) R120>K (215) (119-216), charnière 1-15 (217-231), CH2 E1.4,L1.3>P (234), L1.2>V (235), G1.1>A (236), S29>K (267), Q84.2>E (295) (232-340), CH3 E12 (356), M14 (358), L24>D (368), K26>S (370), N44>D (384), Q97>E (418), N100>D (421), M107>L (428), N114>S (434) (341-445), CHS (446-447)) (119-447)], (221-215')-disulfure avec la chaîne légère kappa anti-CTLA4,*Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (99.0%) -IGKJ1*01 (100%)) CDR-IMGT [7.3.9] (27-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; IG scFv-h-CH2-CH3 chaîne unique, anti-PDCD1 (1''-480'') [scFv V-kappa-VH anti-PDCD1 (1''-249'') [V-KAPPA (*Homo sapiens*IGKV3-15*01 (80.0%)-IGHJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1''-107'') -20-mer tétrakis(glycyl-lysyl-prolyl-glycyl-séryl) linker (108''-127'') -VH (*Mus musculus* IGHV6-6*02 (87.0%) -(IGHD) -IGHJ1*03 (86.7%)/*Homo sapiens* IGHV3-15*07 (81.8%) -(IGHD) -IGHJ2*01 (93.3%)) CDR-IMGT [8.10.13] (153-160.178-187.226-238) (128''-249'')] -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (250''-480'') [charnière 1-15 C5>S (254) (250-264) -CH2 E1.4,L1.3>P (267), L1.2>V (268), G1.1>A (269), S29>K (300) (265-373),CH3 E12 (389), E13>Q (390), M14 (391), S20>K (397), M107>L (461), N114>S (467) (374-478), CHS (479-480)]]; dimère (227-260'':230-263'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-S, glycoforme alfa
vudalimab	inmunoglobulina demi-IG G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* CTLA4 (proteína 4 asociada a los linfocitos T citotóxicos, CD152)] y anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal, biespecífico; cadena pesada gamma1 anti-CTLA4 (1-447) [VH (*Homo sapiens* IGHV3-48*03 (90.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 N114>D (209) R120>K (215) (119-216), bisagra 1-15 (217-231), CH2 E1.4,L1.3>P (234), L1.2>V (235), G1.1>A (236), S29>K (267), Q84.2>E (295) (232-340), CH3 E12 (356), M14 (358), L24>D (368), K26>S (370), N44>D (384), Q97>E (418), N100>D (421), M107>L (428), N114>S (434) (341-445), CHS (446-447)) (119-447)], (221-215')-disulfuro con la cadena ligera kappa anti-CTLA4,*Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (99.0%) -IGKJ1*01 (100%)) CDR-IMGT [7.3.9] (27-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; IG scFv-h-CH2-CH3 cadena única, anti-PDCD1 (1''-480'') [scFv V-kappa-VH anti-PDCD1 (1''-249'') [V-KAPPA (*Homo sapiens*IGKV3-15*01 (80.0%)-IGHJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1''-107'') -20-mer tetrakis(glicil-lisil-prolil-glicil-seril) linker (108''-127'') -VH (*Mus musculus* IGHV6-6*02 (87.0%) -(IGHD) -IGHJ1*03 (86.7%)/*Homo sapiens* IGHV3-15*07 (81.8%) -(IGHD) -IGHJ2*01 (93.3%)) CDR-IMGT [8.10.13] (153-160.178-187.226-238) (128''-249'')] -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (250''-480'') [bisagra 1-15 C5>S (254) (250-264) -CH2 E1.4,L1.3>P (267), L1.2>V (268), G1.1>A (269), S29>K (300) (265-373),CH3 E12 (389), E13>Q (390), M14 (391), S20>K (397), M107>L (461), N114>S (467) (374-478), CHS (479-480)]]; dímero (227-260'':230-263'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-S, forma glicosilada alfa

1.Heavy chain / Chaîne lourde / Cadena pesada (anti-CTLA4)

```
EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYTMHWVRQA PGKGLEWVSF  50
ISYDGNNKYY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARTG 100
WLGPFDYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSDT KVDKKVEPKS CDKTHTCPPC PAPPVAGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVKHED PEVKFNWYVD GVEVHNAKTK PREEEYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSREEMTK NQVSLTCDVS GFYPSDIAVE WESDGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWEQG DVFSCSVLHE ALHSHYTQKS LSLSPGK    447
```

2. Light chain / Chaîne légère / Cadena ligera (anti-CTLA4)

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

3. Chain / Chaîne / Cadena IG scFv-h-CH2-CH3 (anti-PDCD1)

```
EIVLTQSPAT LSASPGERVT LTCRASQSVG NDVAWYQQKP GQAPRLLINY  50
ASHRYTGVPD RFTGSGYGTE FTLTISSVQS EDFGVYYCQQ DFSSPRTFGG 100
GTKVEIKGKP GSGKPGSGKP GSGKPGSEVQ LVESGGGLVK PGGSLRLSCV 150
ASGFTFSNYW MNWVRQAPGK GLEWVAEIRL YSNNYATHYA ESVKGRFTIS 200
RDDSKSTLYL QMNNLKTEDT GVYYCTRYYG NYGGYFDVWG RGTLVTVSSE 250
PKSSDKTHTC PPCPAPPVAG PSVFLFPPKP KDTLMISRTP EVTCVVVDVK 300
HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK 350
EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSREQ MTKNQVKLTC 400
LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW 450
QQGNVFSCSV LHEALHSHYT QKSLSLSPGK                       480
```

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

Intra-H (C23-C104)	22-96	145-201	261-321	367-425	
Intra-L (C23-C104)	23'-89'	135'-195'			
Intra-chain 3	23"-88"	149"-225"	294"-354"	400"-458"	
Inter-H-L (h 5-CL 126)	221-215'				
Inter-H-chain 3 (h 11, h 14)	227-260"	230-263"			

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
297, 330"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
447, 480"

zalsenertantum tetraxetanum

zalsenertant tetraxetan

18^4,18^7,18^{10}-tris(carboxymethyl)-4^5-(2,6-dimethoxyphenyl)-7,11,15-trimethyl-3,6,16-trioxo-5^2-(propan-2-yl)-2,7,11,15-tetraaza-18(1)-(1,4,7,10-tetraazacyclododecana)-4(3,1)-pyrazola-1(2)-adamantana-5(1,4)-benzenaoctadecaphane-1^2-carboxylic acid

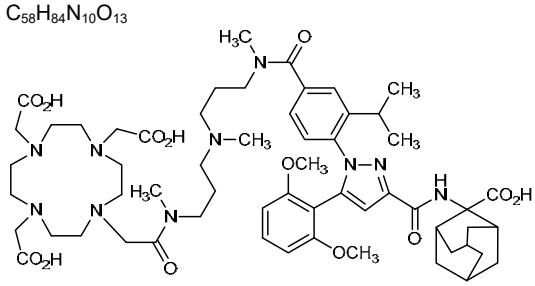
zalsénertant tétraxetan

acide 18^4,18^7,18^{10}-tris(carboxyméthyl)-4^5-(2,6-diméthoxyphényl)-7,11,15-triméthyl-3,6,16-trioxo-5^2-(propan-2-yl)-2,7,11,15-tétraaza-18(1)-(1,4,7,10-tétraazacyclododécana)-4(3,1)-pyrazola-1(2)-adamantana-5(1,4)-benzénaoctadécaphane-1^2-carboxylique

zalsenertant tetraxetán

ácido 18^4,18^7,18^{10}-tris(carboximetil)-4^5-(2,6-dimetoxifenil)-7,11,15-trimetil-3,6,16-trioxo-5^2-(propan-2-il)-2,7,11,15-tetraaza-18(1)-(1,4,7,10-tetraazaciclododecana)-4(3,1)-pirazola-1(2)-adamantana-5(1,4)-bencenaoctadecafano-1^2-carboxílico

$C_{58}H_{84}N_{10}O_{13}$



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immunoglobulin half-IG G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* ERBB2 (epidermal growth factor receptor 2, receptor tyrosine protein kinase erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], humanized monoclonal antibody, biparatopic (targeting two different non-overlapping epitopes on ERBB2, on extracellular domains 2 (ECD2) and 4 (ECD4), respectively), conjugated to auristatin E;
gamma1 heavy chain, anti-ERBB2 extracellular domain 2 (ECD2), humanized (1-449) [VH humanized (*Homo sapiens* IGHV3-66*01 (78.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT[8.8.12] (27-34.52-59.98-109) (1-120) -*Homo sapiens* IGHG1*01 G1m17,1 (CH1 K120 (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 T6>V (353), L7>Y (354), D12 (359), L14 (361), F85.1>A (408), Y86>V (410) (344-448), CHS K2>del (449)) (121-449)], (223- 215')-disulfide with kappa light chain, anti ERBB2 ECD2, humanized (1'-215') [V-KAPPA humanized (*Homo sapiens* IGKV1-16*01 (84.2%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (28-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')];
IG scFv-h-CH2-CH3 single chain, anti-ERBB2 extracellular domain 4 (ECD4), humanized (1"-481") [scFv V-kappa-VH anti-ERBB2 ECD4 (1'-248') [V-KAPPA humanized (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (28-33.51-53.90-98) (1'-108') -20-mer pentakis(diglycyl-seryl-glycyl) linker (109"-128") -VH humanized (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (154-161.179-186.225-237) (129"-248")] -dialanyl linker (249"-250") -*Homo sapiens* IGHG1*01 h-CH2-CH3, G1m1 (251"-481") [hinge 1-15, C5>S (255) (251-265), CH2 (266-375), CH3 T6>V (385), D12 (391), L14 (393), T22>L (401), K79>L (427), T81>W (429) (376-480), CHS K2>del (481)]];
dimer (229-261":232-264")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa, conjugated, on an average of 2 to 3 cysteinyl, to monomethylauristatin E (MMAE), via a cleavable maleimidocaproyl-valyl-citrullinyl-*p*-aminobenzylcarbonyl (mc-val-cit-PABC) type linker

zanidatamab zovodotine

immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB2 (récepteur 2 du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticorps monoclonal humanisé, biparatopique (ciblant deux épitopes différents non chevauchants sur ERBB2, respectivement sur les domaines extracellulaires 2 (ECD2) et 4 (ECD4)), conjugué à l'auristatine E;
chaîne lourde gamma1 anti-ERBB2 domaine extracellulaire 2 (ECD2), humanisée (1-449) [VH humanisé (*Homo sapiens* IGHV3-66*01 (78.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.12] (27-34.52-59.98-109) (1-120) -*Homo sapiens* IGHG1*01 G1m17,1 (CH1 K120 (217) (121-218), charnière 1-15 (219-233), CH2 (234- 343), CH3 T6>V (353), L7>Y (354), D12 (359), L14 (361), F85.1>A (408), Y86>V (410) (344-448), CHS K2>del (449)) (121-449)], (223-215')-disulfure avec la chaîne légère kappa, anti ERBB2 ECD2, humanisée (1'-215') [V-KAPPA humanisé (*Homo sapiens* IGKV1-16*01 (84.2%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (28-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')];

	IG scFv-h-CH2-CH3 chaîne unique, anti-ERBB2 domaine extracellulaire 4 (ECD4), humanisée (1"-481") [scFv V-kappa-VH anti-ERBB2 ECD4 (1'-248') [V-KAPPA humanisé (*Homo sapiens* IGKV1-39*01 (86.3%) - IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (28-33.51-53.90-98) (1'-108') -20-mer pentakis(diglycyl-seryl-glycyl) linker (109"- 128") -VH humanisé (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) - IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (154-161.179-186.225-237) (129"-248")] -dialanyl linker (249"-250") -*Homo sapiens* IGHG1*01 h-CH2-CH3, G1m1 (251"-481") [charnière 1-15 C5>S (255) (251- 265), CH2 (266-375), CH3 T6>V (385), D12 (391), L14 (393), T22>L (401), K79>L (427), T81>W (429) (376-480), CHS K2>del (481)]]; dimère (229-261":232- 264")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa; conjugué, sur 2 à 3 cystéinyl en moyenne, au monométhylauristatine E (MMAE), via un linker clivable de type maléimidécaproyl-valyl-citrullinyl-*p*-aminobenzylcarbonyl (mc-val-cit-PABC).
zanidatamab zovodotina	inmunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor 2 del factor de crecimiento epidérmico, receptor tirosina-proteína kinasa erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticuerpo monoclonal humanizado, biparatópico (dirigiendo dos epítopos diferentes no superpuestos sobre ERBB2, respectivamente sobre los dominios extracelulares 2 (ECD2) y 4 (ECD4)), conjugado con la auristatina E; cadena pesada gamma1 anti-ERBB2 dominio extracelular 2 (ECD2), humanizada (1-449) [VH humanizado (*Homo sapiens* IGHV3-66*01 (78.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.12] (27-34.52-59.98-109) (1-120) -*Homo sapiens* IGHG1*01 G1m17,1 (CH1 K120 (217) (121-218), bisagra 1-15 (219-233), CH2 (234- 343), CH3 T6>V (353), L7>Y (354), D12 (359), L14 (361), F85.1>A (408), Y86>V (410) (344-448), CHS K2>del (449)) (121-449)], (223-215')-disulfuro con la cadena ligera kappa, anti ERBB2 ECD2, humanizada (1'-215') [V-KAPPA humanizado (*Homo sapiens* IGKV1-16*01 (84.2%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (28-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')]; IG scFv-h-CH2-CH3 cadena única, anti-ERBB2 dominio extracelular 4 (ECD4), humanizada (1"-481") [scFv V-kappa-VH anti-ERBB2 ECD4 (1'-248') [V-KAPPA humanizado (*Homo sapiens* IGKV1-39*01 (86.3%) - IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (28-33.51-53.90-98) (1'-108') -20-mer pentakis(diglicil-seril-glicil) linker (109"- 128") -VH humanizado (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) - IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (154-161.179-186.225-237) (129"-248")] -dialanil linker (249"-250") -*Homo sapiens* IGHG1*01 h-CH2-CH3, G1m1 (251"-481") [bisagra 1-15 C5>S (255) (251- 265), CH2 (266-375), CH3 T6>V (385), D12 (391), L14 (393), T22>L (401), K79>L (427), T81>W (429) (376-480), CHS K2>del (481)]]; dímero (229-261":232- 264")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa; conjugado, sobre 2 a 3 restos cisteinil en término medio, con monometilauristatina E (MMAE), mediante un conector escindible de tipo maleimidecaproil-valil-citrulinil-*p*-aminobenzilcarbonil (mc-val-cit-PABC).

1.Heavy chain / Chaîne lourde / Cadena pesada (anti-ERBB2 ECD2)

```
GEVQLVESGG GLVQPGGSLR LSCAASGFTF ADYTMDWVRQ APGKGLEWVG  50
DVNPNSGGSI YNQRFKGRFT FSVDRSKNTL YLQMNSLRAE DTAVYYCARN 100
LGPSFYFDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYVYPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFALV SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPG  449
```

2. Light chain / Chaîne légère / Cadena ligera (anti-ERBB2 ECD2)

```
GDIQMTQSPS SLSASVGDRV TITCKASQDV SIGVAWYQQK PGKAPKLLIY  50
SASYRYTGVP SRFSGSGSGT DFTLTISSLQ PEDFATYYCQ QYYIYPATFG 100
QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

3. Chain / Chaîne / Cadena: IG scFv-h-CH2-CH3 (anti-ERBB2 ECD4)

```
GDIQMTQSPS SLSASVGDRV TITCRASQDV NTAVAWYQQK PGKAPKLLIY  50
SASFLYSGVP SRFSGSRSGT DFTLTISSLQ PEDFATYYCQ QHYTTPPTFG 100
QGTKVEIKGG SGGGSGGGSG GGSGGGGSGEV QLVESGGGLV QPGGSLRLSC 150
AASGFNIKDT YIHWVRQAPG KGLEWVARIY PTNGYTRYAD SVKGRFTISA 200
DTSKNTAYLQ MNSLRAEDTA VYYCSRWGGD GFYAMDYWGQ GTLVTVSSAA 250
EPKSSDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD 300
VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN 350
GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYVLPPSR DELTKNQVSL 400
LCLVKGFYPS DIAVEWESNG QPENNYLTWP PVLDSDGSFF LYSKLTVDKS 450
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP G                     481
```

Post-translational modifications

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

Intra-H (C23-C104) 23-97 147-203 264-324 370-428

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

Intra-chain 3 24"-89" 150"-224" 296"-356" 402"-460"

Inter-H-L (h 5-CL 126)* 223-215'

Inter-H-chain 3 (h 11, h 14)* 229-261" 232-264"

*At least two of the three inter-chain disulfide bridges are not present, an average of 2 to 3 cysteinyl being conjugated each via a thioether bond to a drug linker.

*Au moins deux des trois ponts disulfures inter-chaînes ne sont pas présents, 2 à 3 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif.

*Al menos dos de los tres puentes disulfuro inter-catenarios no estan presentes, una media de 2 a 3 cisteinil está conjugada a conectores de principio activo.

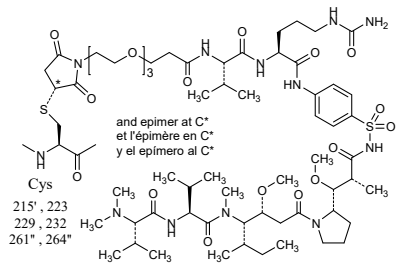
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación

H CH2 N84.4:

300, 332"

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

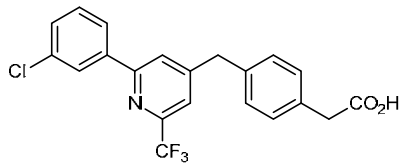
Modified residues / résidus modifiés / restos modificados:



zatolmilastum

zatolmilast	(4-{[2-(3-chlorophenyl)-6-(trifluoromethyl)pyridin-4-yl]methyl}phenyl)acetic acid
zatolmilast	acide (4-{[2-(3-chlorophényl)-6-(trifluorométhyl)pyridin-4-yl]méthyl}phényl)acétique
zatolmilast	ácido (4-{[2-(3-clorofenil)-6-(trifluorometil)piridin-4-il]metil}fenil)acético

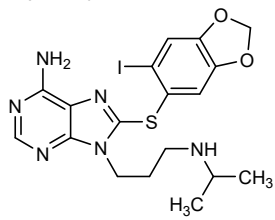
$C_{21}H_{15}ClF_3NO_2$



zelavespibum

zelavespib	8-[(6-iodo-2*H*-1,3-benzodioxol-5-yl)sulfanyl]-9-{3-[(propan-2-yl)amino]propyl}-9*H*-purin-6-amine
zélavespib	8-[(6-iodo-2*H*-1,3-benzodioxol-5-yl)sulfanyl]-9-{3-[(propan-2-yl)amino]propyl}-9*H*-purin-6-amine
zelavespib	8-[(6-iodo-2*H*-1,3-benzodioxol-5-il)sulfanil]-9-{3-[(propan-2-il)amino]propil}-9*H*-purin-6-amina

$C_{18}H_{21}IN_6O_2S$



zimberelimabum #

zimberelimab	immunoglobulin G4-lambda, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], *Homo sapiens* monoclonal antibody; gamma4 heavy chain *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV4-39*01 (87.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [10.7.15] (26-35.53-59.98-112) (1-123)-*Homo sapiens* IGHG4*01 (CH1 (124-221), hinge 1-12 S10>P (231) (222-233), CH2 (234-343), CH3 (344-448), CHS (449-450) (124-450)], (137-215')-disulfide with lambda light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*01 (94.9%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.10] (26-34.52-54.91-100) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO)-K1 cell line, glycoform alfa
zimbérélimab	immunoglobuline G4-lambda, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma4 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV4-39*01 (87.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [10.7.15] (26-35.53-59.98-112) (1-123)-*Homo sapiens* IGHG4*01 (CH1 (124-221), charnière 1-12 S10>P (231) (222-233), CH2 (234-343), CH3 (344-448), CHS (449-450) (124-450)], (137-215')-disulfure avec la chaîne légère

lambda *Homo sapiens*(1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*01 (94.9%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.10] (26-34.52-54.91-100) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dímero (229-229":232-232")-bisdisulfuro, producido en células ováricas de hámster chino (CHO) línea celular CHO-K1, glicosilada alfa

zimberelimab

inmunoglobulina G4-lambda, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada PD-1, PD1, CD279], anticuerpo monoclonal *Homo sapiens*;
cadena pesada gamma4 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV4-39*01 (87.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [10.7.15] (26-35.53-59.98-112) (1-123)-*Homo sapiens* IGHG4*01 (CH1 (124-221), bisagra 1-12 S10>P (231) (222-233), CH2 (234-343), CH3 (344-448), CHS (449-450) (124-450)], (137-215')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*01 (94.9%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.10] (26-34.52-54.91-100) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QLQLQESGPG LVKPSETLTL TCTVSADSIS STTYYWVWIR QPPGKGLEWI  50
GSISYSGSTY YNPSLKSRVT VSVDTSKNQF SLKLNSVAAT DTALYYCARH 100
LGYNGRYLPF DYWGQGTLVT VSSASTKGPS VFPLAPCSRS TSESTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TKTYTCNVDH KPSNTKVDKR VESKYGPPCP PCPAPEFLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKG LPSSIEKTIS KAKGQPREPQ 350
VYTLPPSQEE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SRLTVDKSRW QEGNVFSCSV MHEALHNHYT QKSLSLSLGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
QSALTQPASV SGSPGQSITI SCTGTSSDVG FYNYVSWYQQ HPGKAPELMI  50
YDVSNRPSGV SDRFSGSKSG NTASLTISGL QAEDEADYYC SSYTSISTWV 100
FGGGTKLTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS                                      216
```

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

Intra-H (C23-C104)	22-97	150-206	264-324	370-428
	22"-97"	150"-206"	264"-324"	370"-428"
Intra-L (C23-C104)	22'-90'	138'-197'		
	22'"-90'"	138'"-197'"		
Inter-H-L (CH1 10-CL 126)	137-215'	137"-215'"		
Inter-H-H (h 8, h 11)	229-229"	232-232"		

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
L VH Q1:
1, 1"
L VL Q1:
1', 1'"

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

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

Please find below the names from proposed **INN List 124 – COVID-19 (special edition)** that have reached the status of recommended INN.
Veuillez trouver ci-dessous les noms de la **Liste 124 des DCI proposées – COVID-19 (édition spéciale)** ayant atteint le statut de DCI recommandées.
Por favor, abajo se encuentran los nombres de la **Lista 124 de DCI propuestas – COVID-19 (edición especial)** que han alcanzado el estatus de DCI recomendadas.

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

abdavomeranum #

abdavomeran	messenger RNA (mRNA), 5'-capped, encoding the codon-optimised receptor binding domain (RBD) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2, GenBank: MN908947.3) spike (S) glycoprotein, expressed as a fusion protein 5' with an extended S glycoprotein signal peptide and connected 3' by a glycine/serine (GS)-rich linker peptide with a T4 fibritin trimerization domain, flanked by 5' and 3' untranslated regions and a 3' poly(A) tail; contains N1-methylpseudouridine instead of uridine (*all*-U>$m^1\Psi$).
abdavoméran	ARN messager (ARNm), protégé en 5', codant pour le domaine de liaison au récepteur (RBD) de la glycoprotéine spike (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère, GenBank: MN908947.3) avec des codons optimisés, exprimé comme une protéine de fusion 5'-avec un peptide signal de la glycoprotéine S allongé et lié en 3' par un peptide de liaison riche en glycine / sérine (GS) avec un domaine de trimérisation de la fibritine de T4, flanqué par des régions 5' et 3' non traduites et une queue poly(A); contient de la N1-méthylpseudouridine au lieu de l'uridine (*tout*-U>$m^1\Psi$).
abdavomerán	RNA mensajero (mRNA), protegido en 5', que codifica para el dominio de unión al receptor (RBD) de la glicoproteína de la espícula (S) de SRAS-CoV-2 (coronavirus 2 del síndrome respiratorio agudo severo, GenBank: MN908947.3) con codones optimizados, expresado como una proteína de fusión en 5' con un péptido señal de glicoproteína S extendido y conectado en 3' mediante un péptido enlazador (linker) rico en glicina/serina (GS) con un dominio fibritina de trimerización de T4, flanqueado por regiones 5' y 3' no traducidas y una cola poly(A); contiene N1-metilpseudouridina en lugar de uridina (*all*-U>$m^1\Psi$).

alunacedasum alfa #

alunacedase alfa	human angiotensin-converting enzyme 2 extracellular soluble domain (18-740, 1-723 in the current sequence), dimer, glycosylated, produced in Chinese hamster ovary (CHO) cells; human angiotensin-converting enzyme 2 (ACE2, angiotensin-converting enzyme homolog, ACEH, ACE-related carboxypeptidase, metalloprotease MPROT15, EC:3.4.17.23), soluble extracellular (18-740)-domain of the proprotein, non-covalent dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

alunacédase alfa

domaine extracellulaire soluble de l'enzyme de conversion de l'angiotensine de type 2 humaine (18-740, 1-723 dans la séquence actuelle), dimère, glycosylé, produit dans des cellules ovariennes de hamster chinois (CHO);enzyme de conversion de l'angiotensine de type 2 humaine (ECA2, enzyme de conversion homologue de l'angiotensine, HECA, carboxypeptidase liée à l'ECA, métalloprotéase MPROT15, EC: 3.4.17.23), domaine protéique extracellulaire soluble (18-740), dimère non covalent, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

alunacedasa alfa

enzima humana convertidora de la angiotensina 2 dominio extracelular soluble (18-740, 1-723 en la secuencia actual) dímero, glicosilado, producido en células ováricas de hámster Chino (CHO);
enzima humana convertidora de la angiotensina 2 (ECA2, homológo enzima covertidora de angiotensina, HECA, ECA-carboxipeptidasa relacionada, metaloproteasa MPROT15, EC:3.4.17.23), soluble extracelular (18-740)-dominio de la proproteína, dímero no covalente, producido en células ováricas de hámster Chino (CHO), glicoforma alfa

Sequence / Séquence / Secuencia

```
QSTIEEQAKT FLDKFNHEAE DLFYQSSLAS WNYNTNITEE NVQNMNNAGD   50
KWSAFLKEQS TLAQMYPLQE IQNLTVKLQL QALQQNGSSV LSEDKSKRLN  100
TILNTMSTIY STGKVCNPDN PQECLLLEPG LNEIMANSLD YNERLWAWES  150
WRSEVGKQLR PLYEEYVVLK NEMARANHYE DYGDYWRGDY EVNGVDGYDY  200
SRGQLIEDVE HTFEEIKPLY EHLHAYVRAK LMNAYPSYIS PIGCLPAHLL  250
GDMWGRFWTN LYSLTVPFGQ KPNIDVTDAM VDQAWDAQRI FKEAEKFFVS  300
VGLPNMTQGF WENSMLTDPG NVQKAVCHPT AWDLGKGDFR ILMCTKVTMD  350
DFLTAHHEMG HIQYDMAYAA QPFLLRNGAN EGFHEAVGEI MSLSAATPKH  400
LKSIGLLSPD FQEDNETEIN FLLKQALTIV GTLPFTYMLE KWRWMVFKGE  450
IPKDQWMKKW WEMKREIVGV VEPVPHDETY CDPASLFHVS NDYSFIRYYT  500
RTLYQFQFQE ALCQAAKHEG PLHKCDISNS TEAGQKLFNM LRLGKSEPWT  550
LALENVVGAK NMNVRPLLNY FEPLFTWLKD QNKNSFVGWS TDWSPYADQS  600
IKVRISLKSA LGDKAYEWND NEMYLFRSSV AYAMRQYFLK VKNQMILFGE  650
EDVRVANLKP RISFNFFVTA PKNVSDIIPR TEVEKAIRMS RSRINDAFRL  700
NDNSLEFLGI QPTLGPPNQP PVS                                723
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
116-124, 327-344, 513-525 116'-124', 327'-344', 513'-525'
Cys-SH: 244, 481, 244', 481'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
N36, N73, N86, N305, N415, N529, N36', N73', N86', N305', N415', N529' (97-100% each)
N673, N673' (4% each)

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
S704, S704' or T713, T713' or S723, S723'

Other modifications: Q1, Q1'>Glp (pyroGlu);
S723, S723': partially clipped (~4%)

atibuclimabum #

atibuclimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* CD14, membrane (mCD14) and soluble (sCD14)], chimeric monoclonal antibody; gamma4 heavy chain chimeric (1-442) [VH *Mus musculus* (Musmus IGHV3-2*02 (95.9%) -(IGHD) -Musmus IGHJ3*01 (92.9%) A128>S (115)) CDR-IMGT [9.7.8] (26-34.52-58.97-104) (1-115) -*Homo sapiens* IGHG4*01 (100%), CH1 (116-213),hinge 1-12 (214-225), CH2 (226-335), CH3 (336-440), CHS (441-442)) (116-442)], (129-218')-disulfide with kappa light chain chimeric (1'-218') [V-KAPPA *Mus musculus* (Musmus IGKV3-5*01 (97.0%) -IGKJ2*01 (100%)) CDR-IMGT [10.3.9] (27-36.54-56.93-101) (1'-111') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (221-221":224-224")-bisdisulfide, produced in a Chinese hamster ovary (CHO)-DG44 cell line, glycoform alfa

atibuclimab

immunoglobuline G4-kappa anti-[*Homo sapiens* CD14, membrane (mCD14) et soluble (sCD14)], anticorps monoclonal chimérique; chaîne lourde gamma4 chimérique (1-442) [VH *Mus musculus* (Musmus IGHV3-2*02 (95.9%) -(IGHD) -Musmus IGHJ3*01 (92.9%) A128>S (115)) CDR-IMGT [9.7.8] (26-34.52-58.97-104) (1-115) -*Homo sapiens* IGHG4*01 (100%), CH1 (116-213), charnière 1-12 (214-225), CH2 (226-335), CH3 (336-440), CHS (441-442)) (116-442)], (129-218')-disulfure avec la chaîne légère kappa chimérique (1'-218') [V-KAPPA *Mus musculus* (Musmus IGKV3-5*01 (97.0%) -IGKJ2*01 (100%)) CDR-IMGT [10.3.9] (27-36.54-56.93-101) (1'-111') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (221-221":224-224")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-DG44, glycoforme alfa

atibuclimab

inmunoglobulina G4-kappa anti-[*Homo sapiens* CD14, membrana (mCD14) y soluble (sCD14)], anticuerpo monoclonal quimérico; cadena pesada gamma4 quimérico (1-442) [VH *Mus musculus* (Musmus IGHV3-2*02 (95.9%) -(IGHD) -Musmus IGHJ3*01 (92.9%) A128>S (115)) CDR-IMGT [9.7.8] (26-34.52-58.97-104) (1-115) -*Homo sapiens* IGHG4*01 (100%), CH1 (116-213), bisagra 1-12 (214-225), CH2 (226-335), CH3 (336-440), CHS (441-442)) (116-442)], (129-218')-disulfuro con la cadena ligera kappa quimérica (1'-218') [V-KAPPA *Mus musculus* (Musmus IGKV3-5*01 (97.0%) -IGKJ2*01 (100%)) CDR-IMGT [10.3.9] (27-36.54-56.93-101) (1'-111') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (221-221":224-224")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-DG44, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
DVQLQQSGPG LVKPSQSLSL TCTVTGYSIT SDSAWNWIRQ FPGNRLEWMG   50
YISYSGSTSY NPSLKSRISI TRDTSKNQFF LQLNSVTTED TATYYCVRGL  100
RFAYWGQGTL VTVSSASTKG PSVFPLAPCS RSTSESTAAL GCLVKDYFPE  150
PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS LGTKTYTCNV  200
DHKPSNTKVD KRVESKYGPP CPSCPAPEFL GGPSVFLFPP KPKDTLMISR  250
TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ  350
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF  400
LYSRLTVDKS RWQEGNVFSC SVMHEALHNH YTQKSLSLSL GK          442
```

Light chain / Chaîne légère / Cadena ligera

```
DIVLTQSPAS LAVSLGQRAT ISCRASESVD SYVNSFLHWY QQKPGQPPKL   50
LIYRASNLQS GIPARFSGSG SRTDFTLTIN PVEADDVATY YCQQSNEDPY  100
TFGGGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV  150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV  200
THQGLSSPVT KSFNRGEC                                     218
```

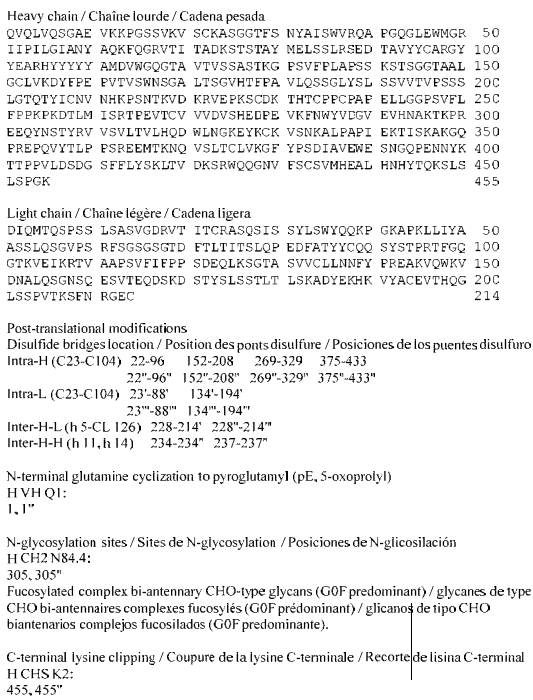
Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 142-198 256-316 362-420
22"-96" 142"-198" 256"-316" 362"-420"
Intra-L (C23-C104) 23'-92' 138'-198'
23'"-92'" 138'"-198'"
Inter-H-L (CH1 10-CL 126) 129-218' 129-218'"
Inter-H-H (h 8, h 11) 221-221" 224-224"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
292, 292"
Fucosylated complex bi-antennary CHO-type glycans (G0F predominant) / glycanes de type CHO bi-antennaires complexes fucosylés (G0F prédominant) / glicanos de tipo CHO biantenarios complejos fucosilados (G0F predominante).

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

bamlanivimabum #

bamlanivimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) protein], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-455) [VH (*Homo sapiens* IGHV1-69*04 (99.0%) -(IGHD) -IGHJ6*01 (90.9%) T123>A (120)) CDR-IMGT [8.8.18] (26-33.51-58.97-114) (1-125) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (222) (126-223), hinge 1-15 (224-238), CH2 (239-348), CH3 E12 (364), M14 (366) (349-453), CHS (454-455)) (126-454)], (228-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (97.9%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (234-234":237-237")-bisdisulfide, produced in a Chinese hamster ovary (CHO) cell line derived from CHO-K1SV, lacking the glutamine synthetase (GS) gene, glycoform alfa
bamlanivimab	immunoglobuline G1-kappa anti-[*Homo sapiens* protéine spike (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-455) [VH (*Homo sapiens* IGHV1-69*04 (99%) -(IGHD) -IGHJ6*01 (90.9%) T123>A (120)) CDR-IMGT [8.8.18] (26-33.51-58.97-114) (1-125) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (222) (126-223), charnière 1-15 (224-238), CH2 (239-348), CH3 E12 (364), M14 (366) (349-453), CHS (454-455)) (126-454)], (228-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (97.9%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (234-234":237-237")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) dérivant de la lignée cellulaire CHO-K1SV, ne présentant pas le gène de la glutamine synthétase, glycoforme alfa
bamlanivimab	inmunoglobulina G1-kappa anti-[*Homo sapiens* proteína espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SRAS-CoV-2)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-455) [VH (*Homo sapiens* IGHV1-69*04 (99%) -(IGHD) -IGHJ6*01 (90.9%) T123>A (120)) CDR-IMGT [8.8.18] (26-33.51-58.97-114) (1-125) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (222) (126-223), bisagra 1-15 (224-238), CH2 (239-348), CH3 E12 (364), M14 (366) (349-453), CHS (454-455)) (126-454)], (228-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (97.9%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (234-234":237-237")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular derivada de CHO-K1SV, en ausencia del gen glutamina sintetasa (GS), forma glicosilada alfa



Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS NYAISWVRQA PGQGLEWMGR  50
IIPILGIANY AQKFQGRVTI TADKSTSTAY MELSSLRSED TAVYYCARGY 100
YEARHYYYYY AMDVWGQGTA VTVSSASTKG PSVFPLAPSS KSTSGGTAAL 150
GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS 200
LGTQTYICNV NHKPSNTKVD KRVEPKSCDK THTCPPCPAP ELLGGPSVFL 250
FPPKPKDTLM ISRTPEVTCV VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR 300
EEQYNSTYRV VSVLTVLHQD WLNGKEYKCK VSNKALPAPI EKTISKAKGQ 350
PREPQVYTLP PSREEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK 400
TTPPVLDSDG SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS 450
LSPGK                                                   455
```

Light chain / Chaîne légère / Cadena ligera

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

Post-translational modifications

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

Intra-H (C23-C104) 22-96 152-208 269-329 375-433
22"-96" 152"-208" 269"-329" 375"-433"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 228-214' 228"-214"
Inter-H-H (h 11, h 14) 234-234" 237-237"

N-terminal glutamine cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
305, 305"
Fucosylated complex bi-antennary CHO-type glycans (G0F predominant) / glycanes de type CHO bi-antennaires complexes fucosylés (G0F prédominant) / glicanos de tipo CHO biantenarios complejos fucosilados (G0F predominante).

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

casirivimabum #

casirivimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) protein, receptor binding domain (RBD)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-11*01 (96.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (217) (121-218),hinge 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (96.8%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
casirivimab	immunoglobuline G1-kappa anti-[*Homo sapiens* protéine spike (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2), domaine de liaison au récepteur (RBD)], anticorps monoclonal *Homo sapiens*;

chaîne lourde gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-11*01 (96.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (96.8%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

casirivimab

inmunoglobulina G1-kappa anti-[*Homo sapiens* proteína espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SRAS-CoV-2), dominio de unión al receptor (RBD)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-11*01 (96.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (96.8%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG LVKPGGSLRL SCAASGFTFS DYYMSWIRQA PGKGLEWVSY  50
ITYSGSTIYY ADSVKGRFTI SRDNAKSSLY LQMNSLRAED TAVYYCARDR 100
GTTMVPFDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCQASQDIT NYLNWYQQKP GKAPKLLIYA  50
ASNLETGVPS RFSGSGSGTD FTFTISGLQP EDIATYYCQQ YDNLPLTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 223-214' 223"-214'"
Inter-H-H (h 11, h 14) 229-229" 232-232"

N-terminal glutamine cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

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

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

cilgavimabum #

cilgavimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) protein, receptor binding domain (RBD)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-461) [VH (*Homo sapiens* IGHV3-15*01 (96.0%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.10.22] (26-33.51-60.99-120) (1-131) -*Homo sapiens* IGHG1*03 G1m3, nG1m1, G1v21 CH2 Y15.1, T16, E18, G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (228) (132-229),hinge 1-15 (230-244), CH2 L1.3>F (248), L1.2>E (249), M15.1>Y (266), S16>T (268), T18>E (270), P116>S (345) (245-354), CH3 E12 (370), M14 (372) (355-459), CHS (460-461)) (132-461)], (234-219')-disulfide with kappa light chain *Homo sapiens* (1'-219') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (96.0%) -IGKJ4*01 (100%)) CDR-IMGT [12.3.8] (27-38.56-58.95-102) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (240-240":243-243")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
cilgavimab	immunoglobuline G1-kappa anti-[*Homo sapiens* protéine spike (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2), domaine de liaison au récepteur (RBD)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-461) [VH (*Homo sapiens* IGHV3-15*01 (96.0%) -(IGHD) - IGHJ4*01 (100%)) CDR-IMGT [8.10.22] (26-33.51-60.99-120) (1-131) -Homo sapiens IGHG1*03 G1m3, nG1m1, G1v21 CH2 Y15.1, T16, E18, G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (228) (132-229), charnière 1-15 (230-244), CH2 L1.3>F (248), L1.2>E (249), M15.1>Y (266), S16>T (268), T18>E (270), P116>S (345) (245-354), CH3 E12 (370), M14 (372) (355-459), CHS (460-461)) (132-461)], (234-219')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-219') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (96.0%) -IGKJ4*01 (100%)) CDR-IMGT [12.3.8] (27-38.56-58.95-102) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (240-240":243-243")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
cilgavimab	inmunoglobulina G1-kappa anti-[*Homo sapiens* proteína espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SRAS-CoV-2), dominio de unión al receptor (RBD)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-461) [VH (*Homo sapiens* IGHV3-15*01 (96.0%) -(IGHD) - IGHJ4*01 (100%)) CDR-IMGT [8.10.22] (26-33.51-60.99-120) (1-131) -*Homo sapiens* IGHG1*03 G1m3, nG1m1, G1v21 CH2 Y15.1, T16, E18, G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (228) (132-229), bisagra 1-15 (230-244), CH2 L1.3>F (248), L1.2>E (249), M15.1>Y (266), S16>T (268), T18>E (270), P116>S (345) (245-354), CH3 E12 (370), M14 (372) (355-459), CHS (460-461)) (132-461)], (234-219')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-219') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (96.0%) -IGKJ4*01 (100%)) CDR-IMGT [12.3.8] (27-38.56-58.95-102) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (240-240":243-243")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGFTFR DVWMSWVRQA PGKGLEWVGR  50
IKSKIDGGTT DYAAPVKGRF TISRDDSKNT LYLQMNSLKT EDTAVYYCTT 100
AGSYYYDTVG PGLPEGKFDY WGQGTLVTVS SASTKGPSVF PLAPSSKSTS 150
GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV 200
TVPSSSLGTQ TYICNVNHKP SNTKVDKRVE PKSCDKTHTC PPCPAPEFEG 250
GPSVFLFPPK PKDTLYITRE PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN 300
AKTKPREEQY NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPASIEKTI 350
SKAKGQPREP QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ 400
PENNYKTTPP VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY 450
TQKSLSLSPG K                                          461
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSSNNKNYLA WYQQKPGQPP  50
KLLMYWASTR ESGVPDRFSG SGSGAEFTLT ISSLQAEDVA IYYCQQYYST 100
LTFGGGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                  219
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-98 158-214 275-335 381-439
22"-98" 158"-214" 275"-335" 381"-439"
Intra-L (C23-C104) 23'-94' 139'-199'
23'"-94'" 139'"-199'"
Inter-H-L (h 5-CL 126) 234-219' 234"-219'"
Inter-H-H (h 11, h 14) 240-240" 243-243"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
311, 311"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
461, 461"

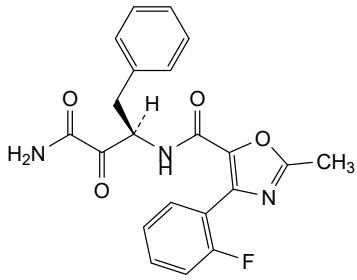
dazcapistatum

dazcapistat — *rac*-*N*-[(2*R*)-4-amino-3,4-dioxo-1-phenylbutan-2-yl]-4-(2-fluorophenyl)-2-methyl-1,3-oxazole-5-carboxamide

dazcapistat — *rac*-*N*-[(2*R*)-4-amino-3,4-dioxo-1-phénylbutan-2-yl]-4-(2-fluorophényl)-2-méthyl-1,3-oxazole-5-carboxamide

dazcapistat — *rac*-*N*-[(2*R*)-4-amino-3,4-dioxo-1-fenilbutan-2-il]-4-(2-fluorofenil)-2-metil-1,3-oxazol-5-carboxamida

$C_{21}H_{18}FN_3O_4$



and enantiomer
et énantiomère
y enantiómero

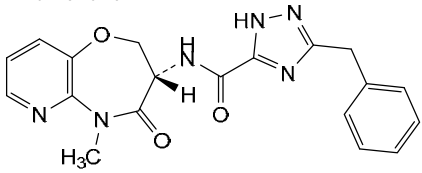
eclitasertibum

eclitasertib — 5-benzyl-*N*-[(3*S*)-5-methyl-4-oxo-2,3,4,5-tetrahydropyrido[3,2-*b*][1,4]oxazepin-3-yl]-1*H*-1,2,4-triazole-3-carboxamide

éclitasertib — 5-benzyl-*N*-[(3*S*)-5-méthyl-4-oxo-2,3,4,5-tétrahydropyrido[3,2-*b*][1,4]oxazépin-3-yl]-1*H*-1,2,4-triazole-3-carboxamide

eclitasertib — 5-bencil-*N*-[(3*S*)-5-metil-4-oxo-2,3,4,5-tetrahidropirido[3,2-*b*][1,4]oxazepin-3-il]-1*H*-1,2,4-triazol-3-carboxamida

$C_{19}H_{18}N_6O_3$



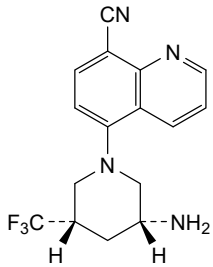
enpatoranum

enpatoran — 5-[(3*R*,5*S*)-3-amino-5-(trifluoromethyl)piperidin-1-yl]quinoline-8-carbonitrile

enpatoran — 5-[(3*R*,5*S*)-3-amino-5-(trifluorométhyl)pipéridin-1-yl]quinoléine-8-carbonitrile

enpatorán — 5-[(3*R*,5*S*)-3-amino-5-(trifluorometil)piperidin-1-il]quinoleína-8-carbonitrilo

$C_{16}H_{15}F_3N_4$



etesevimabum

etesevimab — immunoglobulin G1-kappa, anti-[*Homo sapiens* severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) protein, receptor binding domain (RBD)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV3-66*01 (96.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.13] (26-33.51-57.96-108) (1-119) -*Homo sapiens* IGHG1*03 G1m3, nG1m1, G1v14 A1.3, A1.2 (CH1 R120 (216) (120-217), hinge 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237), (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-216')-disulfide with kappa light chain *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (97.9%) -IGKJ2*01 (100%)) CDR-IMGT [6.3.11] (27-32.50-52.89-99) (1'-109') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (155), V101 (193) (110'-216')]; dimer (228-228":231-231")-bisdisulfide, produced in a Chinese hamster ovary (CHO) cell line derived from CHO-K1SV, lacking the glutamine synthetase (GS) gene, glycoform alfa

étésévimab

immunoglobuline G1-kappa anti-[*Homo sapiens* protéine spike (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2), domaine de liaison au récepteur (RBD)], anticorps monoclonal *Homo sapiens*;
chaîne lourde gamma1 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV3-66*01 (96.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.13] (26-33.51-57.96-108) (1-119) -*Homo sapiens* IGHG1*03 G1m3, nG1m1, G1v14 A1.3, A1.2 (CH1 R120 (216) (120-217), charnière 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237), (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-216')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (97.9%) -IGKJ2*01 (100%)) CDR-IMGT [6.3.11] (27-32.50-52.89-99) (1'-109') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (155), V101 (193) (110'-216')]; dimère (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) dérivant de la lignée cellulaire CHO-K1SV, ne présentant pas le gène de la glutamine synthétase, glycoforme alfa

etesevimab

inmunoglobulina G1-kappa anti-[*Homo sapiens* proteína espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SRAS-CoV-2), dominio de unión al receptor (RBD)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV3-66*01 (96.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.13] (26-33.51-57.96-108) (1-119) -*Homo sapiens* IGHG1*03 G1m3, nG1m1, G1v14 A1.3, A1.2 (CH1 R120 (216) (120-217), bisagra 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237), (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-216')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (97.9%) -IGKJ2*01 (100%)) CDR-IMGT [6.3.11] (27-32.50-52.89-99) (1'-109') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (155), V101 (193) (110'-216')]; dímero (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular derivada de CHO-K1SV, en ausencia del gen Glutamina Sintetasa (GS), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTVS SNYMSWVRQA PGKGLEWVSV  50
IYSGGSTFYA DSVKGRFTIS RDNSMNTLFL QMNSLRAEDT AVYYCARVLP 100
MYGDYLDYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPEAAGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPSS LSASVGDRVT ITCRASQSIS RYLNWYQQKP GKAPKLLIYA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYSTPPEYTF 100
GQGTKLEIKR TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW 150
KVDNALQSGN SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH 200
QGLSSPVTKS FNRGEC                                      216
```

Post-translational modifications

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

Intra-H (C23-C104) 22-95 146-202 263-323 369-427
22"-95" 146"-202" 263"-323" 369"-427"
Intra-L (C23-C104) 23'-88' 136'-196'
23'"-88'" 136'"-196'"
Inter-H-L (h 5-CL 126) 222-216' 222"-216'"
Inter-H-H (h 11, h 14) 228-228" 231-231"

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

H CH2 N84.4:
299, 299"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

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

H CHS K2:
449, 449"

ganulameranum #

ganulameran

messenger RNA (mRNA), 5'-capped, encoding the codon-optimised receptor binding domain (RBD) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2, GenBank: MN908947.3) spike (S) glycoprotein expressed as a fusion protein, 5' with an extended S glycoprotein signal peptide, and 3' with a T4 fibritin trimerization domain and the S glycoprotein transmembrane domain (TM) connected by two glycine/serine-rich (GS) linker peptides, flanked by 5' and 3' untranslated regions and a 3' poly(A) tail; contains N1-methylpseudouridine instead of uridine (*all*-U>m^{1}Ψ).

ganulaméran

ARN messager (ARNm), protégé en 5', codant pour le domaine de liaison au récepteur (RBD) de la glycoprotéine spike (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère, GenBank: MN908947.3) avec des codons optimisés, exprimés sous forme de protéine de fusion, 5' avec un peptide signal de la glycoprotéine S allongé et 3' avec un domaine de trimérisation de la fibritine de T4 et le domaine transmembranaire (TM) de la glycoprotéine S, liés au moyen de deux peptides de liaison (linker) riches en glycine / sérine (GS), flanqués de régions 5' et 3' non traduites et d'une queue poly(A); contient de la N1-méthylpseudouridine au lieu de l'uridine (*tout*-U>m^{1}Ψ).

ganulamerán

RNA mensajero (mRNA), protegido en 5', que codifica para el dominio de unión al receptor (RBD) de la glicoproteína de la espícula (S) de SRAS-CoV-2 (coronavirus 2 del síndrome respiratorio agudo severo, GenBank: MN908947.3) con codones optimizados, expresado como una proteína de fusión, en 5' con un péptido señal de glicoproteína S extendido y en 3' con un dominio fibritina de trimerización de T4 y el dominio transmembrana (TM) de la glicoproteína S, conectado mediante dos péptidos enlazadores (linker) ricos en glicina/serina (GS), flanqueado por regiones 5' y 3' no traducidas y una cola poly(A); contiene N1-metilpseudouridina en lugar de uridina (*all*-U>m^{1}Ψ).

goflikiceptum #

goflikicept

human interleukin-1 receptor accessory protein fragment (21-358, 1-338 in the current sequence) fused via peptidyl linker ^{339}GSGGG^{343} to a human immunoglobulin G1 Fc fragment (344-570, C-terminal Lys clipped) variant (S>C^{477}, T>W^{489}, K>A^{532}), covalent dimer with human interleukin-1 receptor type 1 fragment (21-333, 1-313 in the current sequence) fused via peptidyl linker ^{314}GSGG^{318} to a human immunoglobulin G1 Fc fragment (319-545, C-terminal Lys clipped) variant (Y>C^{447}, T>S^{464}, L>A^{466}, F>K^{503}, Y>V^{505}), glycosylated, produced in Chinese hamster ovary (CHO) cells;
fusion protein comprising the (1-338)-fragment of the human interleukin 1 receptor accessory protein (IL1RAP, IL-1RAcP, interleukin-1 receptor 3, IL1R3), a GSGGG linker (339-343), and the (S>C^{477}, T>W^{489}, K>A^{532}) variant of the C-terminal 227-peptide (Fc fragment) of human immunoglobulin G1 (344-570), (349-324':352-327':477-447')-trisdisulfide with a fusion protein comprising the (21-333)-fragment of the precursor of human interleukin 1 receptor type 1 (IL1R1, IL1Rα, IL1R type I, p80, CD121a) (1-313), a GSGGG linker (314-318), and the (Y>C^{447}, T>S^{464}, L>A^{466}, F>K^{503}, Y>V^{505}) variant of the C-terminal 227-peptide (Fc fragment) of human immunoglobulin G1 (319-545), produced in Chinese hamster ovary (CHO) cells, glycoform alfa

goflikicept	fragment de la protéine accessoire du récepteur de l'interleukine 1 humaine (21-358, 1-338 dans la séquence actuelle) fusionné via un peptide liant ^{339}GSGGG^{343} au fragment Fc de l'immunoglobuline humaine G1 (344-570, C-terminal attaché Lys) variant (S>C^{477}, T>W^{489}, K>A^{532}), dimère covalent avec fragment de récepteur de l'interleukine-1 humaine de type 1 (21-333, 1-313 dans la séquence actuelle) fusionné via un peptide liant ^{314}GSGG^{318} à un fragment Fc d'immunoglobuline humaine G1 (319-545, attaché au variant C-terminal Lys) (Y>C^{447}, T>S^{464}, L>A^{466}, F>K^{503}, Y>V^{505}), glycosylé, produit dans des cellules ovariennes de hamster chinois (CHO); une protéine de fusion comprenant le fragment (1-338) de la protéine accessoire du récepteur de l'interleukine 1 humaine (IL1RAP, IL-1RAcP, récepteur 3 de l'interleukine-1, IL1R3), un linker GSGGG (339-343), et le variant (S>C^{477}, T>W^{489}, K>A^{532}) du peptide C-terminal-227 (fragment Fc) de l'immunoglobuline humaine G1 (344-570), (349-324': 352-327': 477-447') -trisdisulfure avec une protéine de fusion comprenant le fragment- (21-333) du précurseur du récepteur de l'interleukine humaine de type 1 (IL1R1, IL1Rα, IL1R type I, p80, CD121a) (1-313), une liaison GSGGG (314-318) et le variant (Y>C^{447}, T>S^{464,} L>A^{466}, F>K^{503}, Y>V^{505}) du peptide C-terminal-227 (fragment Fc) de l'immunoglobuline humaine G1 (319-545), produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
goflikicept	receptor de la interleukina-1 humana fragmento de la proteína complemento (21-358, 1-338 en la secuencia actual) fusionado a través de un enlace peptidil ^{339}GSGGG^{343} a la inmunoglobulina humana G1 Fc fragmento (344-570, fijado al C-terminal Lis) variante (S>C^{477}, T>W^{489}, K>A^{532}), dímero covalente con receptor de interleukina-1 humana fragmento tipo 1 (21-333, 1-313 en la secuencia actual) fusionado a través del enlace peptidil ^{314}GSGG^{318} a una inmunoglobulina humana G1 Fc fragmento (319-545, fijado al C-terminal Lis) variante (Y>C^{447}, T>S^{464}, L>A^{466}, F>K^{503}, Y>V^{505}), glicosilado, producido en células ováricas de hámster Chino (CHO). una proteína de fusión que comprende el fragmento-(1-338) del receptor humano de la interleukina 1 proteína accesorio (IL1RAP, IL-1RAcP, interleukina-1 receptor 3, IL1R3), un enlace GSGGG (339-343), y la variante (S>C^{477}, T>W^{489}, K>A^{532}) del termina-C péptido-227 (Fc fragmento) de la inmunoglobulina humana G1 (344-570), (349-324':352-327':477-447')-trisdisulfuro con una proteína de fusión que comprende el fragmento-(21-333) del precursor del receptor tipo 1 de la interleukina humana (IL1R1, IL1Rα, IL1R tipo I, p80, CD121a) (1-313), un enlace GSGGG (314-318), y la (Y>C^{447}, T>S^{464}, L>A^{466}, F>K^{503}, Y>V^{505}) variante del terminal-C péptido-227 (Fc fragmento) de inmunoglobulina humana G1 (319-545), producido en células ováricas de hámster Chino (CHO), glicoforma alfa

Sequence / Séquence / Secuencia

IL1RAP-GSG$_3$-Fc

```
SERCDDWGLD TMRQIQVFED EPARIKCPLF EHFLKFNYST AHSAGLTLIW   50
YWTRQDRDLE EPINFRLPEN RISKEKDVLW FRPTLLNDTG NYTCMLRNTT  100
YCSKVAFPLE VVQKDSCFNS PMKLPVHKLY IEYGIQRITC PNVDGYFPSS  150
VKPTITWYMG CYKIQNFNNV IPEGMNLSFL IALISNNGNY TCVVTYPENG  200
RTFHLTRTLT VKVVGSPKNA VPPVIHSPND HVVYEKEPGE ELLIPCTVYF  250
SFLMDSRNEV WWTIDGKKPD DITIDVTINE SISHSRTEDE TRTQILSIKK  300
VTSEDLKRSY VCHARSAKGE VAKAAKVKQK VPAPRYTVGS GGGDKTHTCP  350
PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW  400
YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK EYKCKVSNKA  450
LPAPIEKTIS KAKGQPREPQ VYTLPPCRDE LTKNQVSLWC LVKGFYPSDI  500
AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SALTVDKSRW QQGNVFSCSV  550
MHEALHNHYT QKSLSLSPGK                                   570
```

IL1R1-GSG$_3$-Fc

```
DKCKEREEKI ILVSSANEID VRPCPLNPNE HKGTITWYKD DSKTPVSTEQ   50
ASRIHQHKEK LWFVPAKVED SGHYYCVVRN SSYCLRIKIS AKFVENEPNL  100
CYNAQAIFKQ KLPVAGDGGL VCPYMEFFKN ENNELPKLQW YKDCKPLLLD  150
NIHFSGVKDR LIVMNVAEKH RGNYTCHASY TYLGKQYPIT RVIEFITLEE  200
NKPTRPVIVS PANETMEVDL GSQIQLICNV TGQLSDIAYW KWNGSVIDED  250
DPVLGEDYYS VENPANKRRS TLITVLNISE IESRFYKHPF TCFAKNTHGI  300
DAAYIQLIYP VTNGSGGGDK THTCPPCPAP ELLGGPSVFL FPPKPKDTLM  350
ISRTPEVTCV VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV  400
VSVLTVLHQD WLNGKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVCTLP  450
PSRDELTKNQ VSLSCAVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG  500
SFKLVSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPGK       545
```

Mutations / Mutations / Mutaciones

S^{477}>**C**, T^{489}>**W**, K^{532}>**Δ**
Y^{447}>**C**, $T^{464'}$>**S**, $L^{466'}$>**A**, $F^{503'}$>**K**, $Y^{505'}$>**V**

Post-translational modifications

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

Inter-chain: 349-324' 352-327' 477-447'

Intra-chain IL1RAP-GSG3-Fc : 4-102 27-94 117-161 140-192 246-312 384-444 490-548

Intra-chain IL1R1-GSG3-Fc : 3'-84' 24'-76' 101'-144' 122'-176' 228'-292' 359'-419' 465'-523'

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación

N37, N87, N91, N98, N176, N189, N279, N420;
N80', N173', N213', N229', N243', N277', N313', N395'

Other modifications: K570, K545' clipped

imdevimabum #

imdevimab	immunoglobulin G1-lambda, anti-[*Homo sapiens* severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) protein, receptor binding domain (RBD)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-30*01 (96.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (217) (121-218),hinge 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-215')-disulfide with lambda light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*01 (93.9%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.10] (26-34.52-54.91-100) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
imdévimab	immunoglobuline G1-lambda anti-[*Homo sapiens* protéine spike (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2), domaine de liaison au récepteur (RBD)], anticorps monoclonal *Homo sapiens*;

chaîne lourde gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-30*01 (96.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-215')-disulfure avec la chaîne légère lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*01 (93.9%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.10] (26-34.52-54.91-100) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

imdevimab

inmunoglobulina G1-lambda anti-[*Homo sapiens* proteína espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SRAS-CoV-2), dominio de unión al receptor (RBD)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-30*01 (96.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-215')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*01 (93.9%) -IGLJ3*02 (100%)) CDR-IMGT [9.3.10] (26-34.52-54.91-100) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG VVQPGRSLRL SCAASGFTFS NYAMYWVRQA PGKGLEWVAV  50
ISYDGSNKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRTED TAVYYCASGS 100
DYGDYLLVYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
QSALTQPASV SGSPGQSITI SCTGTSSDVG GYNYVSWYQQ HPGKAPKLMI  50
YDVSKRPSGV SNRFSGSKSG NTASLTISGL QSEDEADYYC NSLTSISTWV 100
FGGGTKLTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS                                      216
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 22'-90' 138'-197'
22'"-90'" 138'"-197'"
Inter-H-L (h 5-CL 126) 223-215' 223"-215'"
Inter-H-H (h 11, h 14) 229-229" 232-232"

N-terminal glutamine cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"
L VL Q1:
1', 1'"

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

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

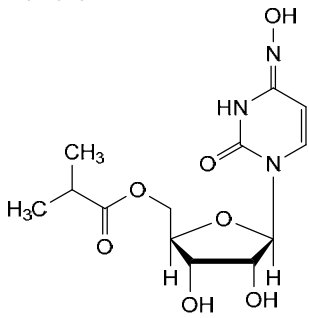
molnupiravirum

molnupiravir — N^4-hydroxycytidine 5'-(2-methylpropanoate)

molnupiravir — 5'-(2-méthylpropanoate) de N^4-hydroxycytidine

molnupiravir — 5'-(2-metilpropanoato) de N^4-hidroxicitidina

$C_{13}H_{19}N_3O_7$



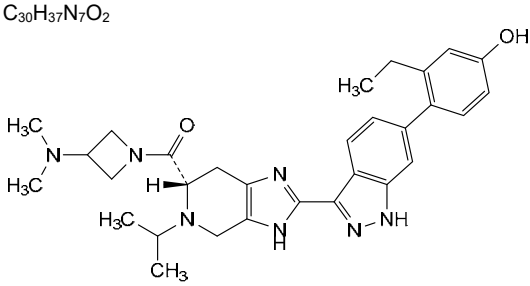
nezulcitinibum

nezulcitinib — [3-(dimethylamino)azetidin-1-yl]{(6*S*)-2-[6-(2-ethyl-4-hydroxyphenyl)-1*H*-indazol-3-yl]-5-(propan-2-yl)-4,5,6,7-tetrahydro-1*H*-imidazo[4,5-*c*]pyridin-6-yl}methanone

nézulcitinib — [3-(diméthylamino)azétidin-1-yl]{(6*S*)-2-[6-(2-éthyl-4-hydroxyphényl)-1*H*-indazol-3-yl]-5-(propan-2-yl)-4,5,6,7-tétrahydro-1*H*-imidazo[4,5-*c*]pyridin-6-yl}méthanone

nezulcitinib — [3-(dimetilamino)azetidin-1-il]{(6*S*)-2-[6-(2-etil-4-hidroxifenil)-1*H*-indazol-3-il]-5-(propan-2-il)-4,5,6,7-tetrahidro-1*H*-imidazo[4,5-*c*]piridin-6-il}metanona

$C_{30}H_{37}N_7O_2$



pemziviptadilum #

pemziviptadil — human L-methionyl vasoactive intestinal peptide (2-29) fused to 121 repeats of different elastin-derived pentapeptides (VPGVG, VPGGG, VPGAG, VPGWP) (30-634), produced in *Escherichia coli;*
fusion protein comprising L-methionyl (1)-vasoactive intestinal polypeptide (human VIP) (2-29) and an elastin-like artificial polymer (30-629) of 120 alternating pentapeptides of three types VPGVG, VPGGG, and VPGAG, and a C-terminal pentapeptide VPGWP (630-634), produced in *Escherichia coli*

pemziviptadil

L-méthionyl peptide vasoactif intestinal humain (2-29) fusionné à 121 répétitions de différents pentapeptides dérivés de l'élastine (VPGVG, VPGGG, VPGAG, VPGWP) (30-634), produits dans *Escherichia coli* ;
protéine de fusion comprenant le polypeptide intestinal vasoactif L-méthionyl (1) (VIP humain) (2-29) et un polymère artificiel de type élastine (30-629) de 120 pentapeptides alternés de trois types VPGVG, VPGGG et VPGAG, et un pentapeptide C-terminal VPGWP (630-634), produit dans *Escherichia coli*

pemziviptadil

péptido humano L-metionil vasoactivo intestinal (2-29) fusionado a 121 repeticiones de pentapéptidos derivados de elastina diferentes (VPGVG, VPGGG, VPGAG, VPGWP) (30-634), producido en *Escherichia coli;*
proteína de fusión que comprende polipéptido intestinal vasoactivo L-metionil (1) (humano VIP) (2-29) y un polímero artificial parecido a la elastina (30-629) de 120 pentapéptidos alternos de tres tipos VPGVG, VPGGG, y VPGAG, y un pentapéptido C-terminal VPGWP (630-634), producido en *Escherichia coli*

Sequence / Séquence / Secuencia

```
MHSDAVFTDN YTRLRKQMAV KKYLNSILNV PGVGVPGVGV PGGGVPGAGV   50
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  100
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  150
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  200
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  250
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  300
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  350
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  400
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  450
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  500
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  550
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  600
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGWP                   634
```

positions 30-634: 12 × pattern AABCAAABCB of 10 pentapeptides of three types A = **VPGVG**, B = **VPGGG,** and C = **VPGAG** plus a C-terminal pentapeptide **VPGWP**

pidacmeranum #

pidacmeran

self-replicating messenger RNA (mRNA), 5'-capped, encoding *Venezuelan equine encephalitis virus* (VEEV) RNA-dependent RNA polymerase (VEEV proteins nsP1, nsP2, nsP3 and nsP4) and a full-length codon-optimised pre-fusion stabilised conformation variant (K986P and V987P) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2, GenBank: MN908947.3) spike (S) glycoprotein, flanked by 5' and 3' untranslated regions and a 3' poly(A) tail; replication of the RNA is under control of a VEEV subgenomic promoter.

pidacméran

ARN messager (ARNm) auto-répliquant, protégé en 5', codant pour l'ARN polymérase ARN-dépendante du *virus de l'encéphalite équine vénézuélienne* (protéines VEEV nsP1, nsP2, nsP3 et nsP4) et une variante complète de pré-fusion de conformation stabilisée (K986P et V987P) de la glycoprotéine spike (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère, GenBank: MN908947.3) avec des codons optimisés, flanqués de régions 5 'et 3' non traduites une queue poly(A) 3'; la réplication de l'ARN est sous le contrôle du promoteur sous-génomique de VEEV.

pidacmerán	RNA mensajero auto replicativo (mRNA), protegido en 5', que codifica para la RNA polimerasa dependiente de RNA del *virus de la encefalitis equina venezolana* (proteínas VEEV nsP1, nsP2, nsP3 y nsP4) y una variante pre-fusión completa de conformación estabilizada (K986P and V987P) de la glicoproteína de la espícula (S) del SRAS-CoV-2 (coronavirus 2 del síndrome respiratorio agudo severo, GenBank: MN908947.3) con codones optimizados, flanqueada por regiones 5' y 3' no traducidas y una cola poly(A) en 3'; la replicación del ARN está bajo el control del promotor subgenómico de VEEV.
regdanvimabum # regdanvimab	immunoglobulin G1-lambda, anti-[*Homo sapiens* severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) protein, receptor binding domain (RBD)], humanized and *Homo sapiens* monoclonal antibody; gamma1 heavy chain humanized (1-458) [VH (*Homo sapiens* IGHV2-70*12 (92.9%) -(IGHD) - IGHJ6*01 (100%)) CDR-IMGT [10.7.20] (26-35.53-59.98-117) (1-128) -*Homo sapiens* IGHG1*08p (100%) G1m3,1 (CH1 R120 (225) (129-226), hinge 1-15 (227-241), CH2 (242-351), CH3 D12 (367), L14 (369) (352-456), CHS (457-458)) (129-458)], (231-215')-disulfide with lambda light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-51*01 (100%) - IGLJ2*01 (90.9%) K123>E (106)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC2*01 (98.1%) S45>G (156), T82>K (167) (111'-216')]; dimer (237-237":240-240")-bisdisulfide, produced in a Chinese hamster ovary (CHO) cell line derived from CHO-K1, glycoform alfa
regdanvimab	immunoglobuline G1-lambda anti-[*Homo sapiens* protéine spike (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2), domaine de liaison au récepteur (RBD)], anticorps monoclonal humanisé et *Homo sapiens*; chaîne lourde gamma1 humanisée (1-458) [VH (*Homo sapiens* IGHV2-70*12 (92.9%) -(IGHD) - IGHJ6*01 (100%)) CDR-IMGT [10.7.20] (26-35.53-59.98-117) (1-128) -*Homo sapiens* IGHG1*08p (100%) G1m3,1 (CH1 R120 (225) (129-226), charnière 1-15 (227-241), CH2 (242-351), CH3 D12 (367), L14 (369) (352-456), CHS (457-458)) (129-458)], (231-215')-disulfure avec la chaîne légère lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-51*01 (100%) -IGLJ2*01 (90.9%) K123>E (106)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC2*01 (98.1%) S45>G (156), T82>K (167) (111'-216')]; dimère (237-237":240-240")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) dérivant de la lignée cellulaire CHO-K1, glycoforme alfa

regdanvimab

inmunoglobulina G1-lambda anti-[*Homo sapiens* proteína espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SRAS-CoV-2), dominio de unión al receptor (RBD)], anticuerpo monoclonal humanizado y *Homo sapiens*; cadena pesada gamma1 humanizada (1-458) [VH (*Homo sapiens* IGHV2-70*12 (92.9%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [10.7.20] (26-35.53-59.98-117) (1-128) -*Homo sapiens* IGHG1*08p (100%) G1m3,1 (CH1 R120 (225) (129-226), bisagra 1-15 (227-241), CH2 (242-351), CH3 D12 (367), L14 (369) (352-456), CHS (457-458)) (129-458)], (231-215')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-51*01 (100%) -IGLJ2*01 (90.9%) K123>E (106)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC2*01 (98.1%) S45>G (156), T82>K (167) (111'-216')]; dímero (237-237":240-240")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular derivada de CHO-K1, forma glicosilada alfa

reluscovtogenum ralaplasmidum

reluscovtogene ralaplasmid

DNA plasmid expressing a consensus sequence* of the full-length SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) spike (S) glycoprotein, with an N-terminal IgE leader sequence, under control of the human CMV promoter (hCMV promoter) and a bovine growth hormone poly-adenylation signal (bGH poly(A)). The plasmid also contains a pUC origin of replication and a kanamycin antibiotic resistance gene.
*based upon sequences published on GISAID (Global Initiative on Sharing All Influenza Data) in early 2020.

réluscovtogène ralaplasmide	plasmide d'ADN exprimant une séquence consensus* complète de la glycoprotéine spike (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère), avec une séquence leader N-terminale d'IgE, sous contrôle du promoteur du CMV humain (promoteur hCMV) et d'un signal de polyadénylation de l'hormone de croissance bovine (bGH poly(A)). Le plasmide contient également une origine de réplication pUC et un gène de résistance à la kanamycine. *basé sur des séquences publiées dans GISAID (Global Initiative on Sharing All Influenza Data) début 2020.
reluscovtogén ralaplasmida	plásmido de DNA que expresa una secuencia consenso* completa de la glicoproteína de la espícula (S) de SARS-CoV-2 (coronavirus 2 del síndrome respiratorio agudo severo), con una secuencia líder N-terminal de la IgE, bajo el control del promotor de CMV humano (promotor hCMV) y una señal de poliadenilación de la hormona de crecimiento bovina (bGH poly(A)). El plásmido contiene también un origen de replicación pUC y un gen de resistencia al antibiótico kanamicina. *basada en secuencias publicadas en GISAID (Global Initiative on Sharing All Influenza Data) a principios de 2020.

sotrovimabum #

sotrovimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) protein, receptor binding domain (RBD)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-457) [VH (*Homo sapiens* IGHV1-18*01 (92.9%) -(IGHD) -IGHJ5*01 (92.9%)) CDR-IMGT [8.8.20] (26-33.51-58.97-116) (1-127) -*Homo sapiens* IGHG1*01 G1m17,1, G1v24 CH3 L107, S114(CH1 K120 (224) (128-225), hinge 1-15 (226-240), CH2 (241-350), CH3 D12 (366), L14 (368), M107>L (438), N114>S (444) (351-455), CHS (456-457)) (128-457)], (230-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (96.7%) -IGKJ4*01 (100%)) CDR-IMGT [7.3.8] (27-33.51-53.90-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (236-236":239-239")-bisdisulfide, produced in a Chinese hamster ovary (CHO)-K1 cell line, glycoform alfa
sotrovimab	immunoglobuline G1-kappa anti-[*Homo sapiens* protéine spike (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2), domaine de liaison au récepteur (RBD)], anticorps monoclonal *Homo sapiens*;

chaîne lourde gamma1 *Homo sapiens* (1-457) [VH (*Homo sapiens* IGHV1-18*01 (92.9%) -(IGHD) -IGHJ5*01 (92.9%)) CDR-IMGT [8.8.20] (26-33.51-58.97-116) (1-127) -*Homo sapiens* IGHG1*01 G1m17,1, G1v24 CH3 L107, S114 (CH1 K120 (224) (128-225), charnière 1-15 (226-240), CH2 (241-350), CH3 D12 (366), L14 (368), M107>L (438), N114>S (444) (351-455), CHS (456-457)) (128-457)], (230-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (96.7%) -IGKJ4*01 (100%)) CDR-IMGT [7.3.8] (27-33.51-53.90-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (236-236":239-239")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1, glycoforme alfa

sotrovimab

inmunoglobulina G1-kappa anti-[*Homo sapiens* proteína espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SRAS-CoV-2), dominio de unión al receptor (RBD)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada gamma1 *Homo sapiens* (1-457) [VH (*Homo sapiens* IGHV1-18*01 (92.9%) -(IGHD) -IGHJ5*01 (92.9%)) CDR-IMGT [8.8.20] (26-33.51-58.97-116) (1-127) -*Homo sapiens* IGHG1*01 G1m17,1, G1v24 CH3 L107, S114 (CH1 K120 (224) (128-225), bisagra 1-15 (226-240), CH2 (241-350), CH3 D12 (366), L14 (368), M107>L (438), N114>S (444) (351-455), CHS (456-457)) (128-457)], (230-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (96.7%) -IGKJ4*01 (100%)) CDR-IMGT [7.3.8] (27-33.51-53.90-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (236-236":239-239")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYPFT SYGISWVRQA PGQGLEWMGW  50
ISTYQGNTNY AQKFQGRVTM TTDTSTTTGY MELRRLRSDD TAVYYCARDY 100
TRGAWFGESL IGGFDNWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA 150
ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS 200
SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 250
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK 300
PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK 350
GQPREPQVYT LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN 400
YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVLHE ALHSHYTQKS 450
LSLSPGK                                               457
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQTVS STSLAWYQQK PGQAPRLLIY  50
GASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QHDTSLTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                       214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 154-210 271-331 377-435
22"-96" 154"-210" 271"-331" 377"-435"
Intra-L (C23-C104) 23'-89' 134'-194'
23'"-89'" 134'"-194'"
Inter-H-L (h 5-CL 126) 230-214' 230"-214'"
Inter-H-H (h 11, h 14) 236-236" 239-239"

N-terminal glutamine cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

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

Deamidation sites / Sites de désamidation / Posiciones de desamidación
H CH2 N98: 325, 325"
H CH3 N44: 394, 394"

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

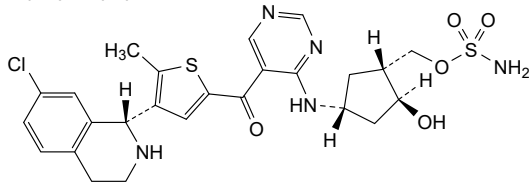
subasumstatum

subasumstat — {(1*R*,2*S*,4*R*)-4-[(5-{4-[(1*R*)-7-chloro-1,2,3,4-tetrahydroisoquinolin-1-yl]-5-methylthiophene-2-carbonyl}pyrimidin-4-yl)amino]-2-hydroxycyclopentyl}methyl sulfamate

subasumstat — sulfamate de {(1*R*,2*S*,4*R*)-4-[(5-{4-[(1*R*)-7-chloro-1,2,3,4-tétrahydroisoquinoléin-1-yl]-5-méthylthiophène-2-carbonyl}pyrimidin-4-yl)amino]-2-hydroxycyclopentyl}méthyle

subasumstat — sulfamato de {(1*R*,2*S*,4*R*)-4-[(5-{4-[(1*R*)-7-cloro-1,2,3,4-tetrahidroisoquinolein-1-il]-5-metiltiofeno-2-carbonil}pirimidin-4-il)amino]-2-hidroxiciclopentil}metilo

$C_{25}H_{28}ClN_5O_5S_2$



tixagevimabum #

tixagevimab — immunoglobulin G1-kappa, anti-[*Homo sapiens* severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) protein, receptor binding domain (RBD)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV1-58*01 (98.0%) -(IGHD) -IGHJ3*02 (93.8%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Homo sapiens* IGHG1*03 G1m3, nG1m1, G1v21 CH2 Y15.1, T16, E18, G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (220) (124-221), hinge 1-15 (222-236), CH2 L1.3>F (240), L1.2>E (241), M15.1>Y (258), S16>T (260), T18>E (262), P116>S (337) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-216')-disulfide with kappa light chain *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (98.9%) -IGKJ1*01 (100%)) CDR-IMGT [7.3.10] (27-33.51-53.90-99) (1'-109') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (155), V101 (193) (110'-216')]; dimer (232-232":235-235")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

tixagévimab — immunoglobuline G1-kappa anti-[*Homo sapiens* protéine spike (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2), domaine de liaison au récepteur (RBD)], anticorps monoclonal *Homo sapiens;*
chaîne lourde gamma1 *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV1-58*01 (98.0%) -(IGHD) -IGHJ3*02 (93.8%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Homo sapiens* IGHG1*03 G1m3, nG1m1, G1v21 CH2 Y15.1, T16, E18, G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (220) (124-221), charnière 1-15 (222-236), CH2 L1.3>F (240), L1.2>E (241), M15.1>Y (258), S16>T (260), T18>E (262), P116>S (337) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-216')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (98.9%) -IGKJ1*01 (100%)) CDR-IMGT [7.3.10] (27-33.51-53.90-99) (1'-109') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (155), V101 (193) (110'-216')]; dimère (232-232":235-235")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

tixagevimab

inmunoglobulina G1-kappa anti-[*Homo sapiens* proteína espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SRAS-CoV-2), dominio de unión al receptor (RBD)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada gamma1 *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV1-58*01 (98.0%) -(IGHD) -IGHJ3*02 (93.8%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Homo sapiens* IGHG1*03 G1m3, nG1m1, G1v21 CH2 Y15.1, T16, E18, G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (220) (124-221), bisagra 1-15 (222-236), CH2 L1.3>F (240), L1.2>E (241), M15.1>Y (258), S16>T (260), T18>E (262), P116>S (337) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-216')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (98.9%) -IGKJ1*01 (100%)) CDR-IMGT [7.3.10] (27-33.51-53.90-99) (1'-109') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (155), V101 (193) (110'-216')]; dímero (232-232":235-235")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QMQLVQSGPE VKKPGTSVKV SCKASGFTFM SSAVQWVRQA RGQRLEWIGW  50
IVIGSGNTNY AQKFQERVTI TRDMSTSTAY MELSSLRSED TAVYYCAAPY 100
CSSISCNDGF DIWGQGTMVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPEF EGGPSVFLFP 250
PKPKDTLYIT REPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPASIEK TISKAKGQPR 350
EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS 450
PGK                                                     453
```

Light chain / Chaîne légère / Cadena ligera

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

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 101-106 150-206 267-327 373-431
22"-96" 101"-106" 150"-206" 267"-327" 373"-431"
Intra- H (CDR3) 101-106
101"-106"
Intra-L (C23-C104) 23'-89' 136'-196'
23'"-89'" 136'"-196'"
Inter-H-L (h 5-CL 126) 226-216' 226"-216'"
Inter-H-H (h 11, h 14) 232-232" 235-235"

N-terminal glutamine cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

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

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

tozinameranum #

tozinameran

messenger RNA (mRNA), 5'-capped, encoding a full-length, codon-optimised pre-fusion stabilised conformation variant (K986P and V987P) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2, GenBank: MN908947.3) spike (S) glycoprotein, flanked by 5' and 3' untranslated regions and a 3' poly(A) tail; contains N1-methylpseudouridine instead of uridine (*all*-U>$m^1\Psi$).

tozinaméran	ARN messager (ARNm), protégé en 5', codant pour un variant de pré-fusion stabilisé en conformation (K986P et V987P) de la glycoprotéine spike (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère, GenBank: MN908947.3) complet, avec des codons optimisés, flanqués de régions 5' et 3' non traduites et d'une queue poly(A) 3'; contient de la N1-méthylpseudouridine au lieu de l'uridine (*tout*-U>m$^{1}\Psi$).
tozinamerán	RNA mensajero (mRNA), protegido en 5', que codifica para una variante pre-fusión de conformación estabilizada (K986P and V987P) de la glicoproteína de la espícula (S) del SRAS-CoV-2 (coronavirus 2 del síndrome respiratorio agudo severo, GenBank: MN908947.3) completa, con codones optimizados, flanqueada por regiones 5' y 3' no traducidas y una cola poly(A) en 3'; contiene N1-metilpseudouridina en lugar de uridina (*all*-U>m$^{1}\Psi$).

zansecimabum #

zansecimab	immunoglobulin G4-kappa, anti-[*Homo sapiens* ANGPT2 (angiopoietin 2)], humanized monoclonal antibody; gamma4 heavy chain humanized (1-447) [VH (*Homo sapiens* IGHV1-18*01 (86.7%) -(IGHD) -IGHJ4*01 (93.3%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -*Homo sapiens* IGHG4*01, G4v5 h P10,G4v4 CH2 A1.3, A1.2 (CH1 (122-219), hinge 1-12 S10>P (229) (220-231), CH2 F1.3>A (235), L1.2>A (236) (232-341), CH3 (342-446), CHS K>del (447)) (122-447)], (135-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (83.2%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (227-227":230-230")-bisdisulfide, produced in a Chinese hamster ovary (CHO) cell line derived from CHO-GSKO, glycoform alfa
zansécimab	immunoglobuline G4-kappa anti-[*Homo sapiens* ANGPT2 (angiopoietin 2)], anticorps monoclonal humanisé; chaîne lourde gamma4 humanisée (1-447) [VH (*Homo sapiens* IGHV1-18*01 (86.7%) -(IGHD) - IGHJ4*01 (93.3%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -*Homo sapiens* IGHG4*01 G4v5 h P10,G4v4 CH2 A1.3, A1.2 (CH1 (122-219), charnière 1-12 S10>P (229) (220-231), CH2 F1.3>A (235), L1.2>A (236) (232-341), CH3 (342-446), CHS K>del (447)) (122-447)], (135-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (83.2%) - IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (227-227":230-230")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) dérivant de la lignée cellulaire CHO-GSKO, glycoforme alfa
zansecimab	inmunoglobulina G4-kappa anti-[*Homo sapiens* ANGPT2 (angiopoyetina 2)], anticuerpo monoclonal humanizado;

cadena pesada gamma4 humanizada (1-447) [VH (*Homo sapiens* IGHV1-18*01 (86.7%) -(IGHD) - IGHJ4*01 (93.3%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -*Homo sapiens* IGHG4*01 G4v5 h P10,G4v4 CH2 A1.3, A1.2 (CH1 (122-219), bisagra 1-12 S10>P (229) (220-231), CH2 F1.3>A (235), L1.2>A (236) (232-341), CH3 (342-446), CHS K>del (447)) (122-447)], (135-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (83.2%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (227-227":230-230")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular derivada de CHO-GSKO, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYSFT DYNMVWVRQA PGQGLEWMGY  50
IDPYNGGTGY NQKFEGRVTM TTDTSTSTAY MELRSLRSDD TAVYYCARTR 100
DRYDVWYFDV WGQGTLVTVS SASTKGPSVF PLAPCSRSTS ESTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTK 200
TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEAAGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY 350
TLPPSQEEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSR LTVDKSRWQE GNVFSCSVMH EALHNHYTQK SLSLSLG    447
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS VSASVGDRVT ITCKASQDVY IAVAWYQQKP GKAPKLLIYW  50
ASTRDTGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCHQ YSSYPPTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

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

```
Intra-H (C23-C104)  22-96    148-204    262-322    368-426
                    22"-96"  148"-204"  262"-322"  368"-426"
Intra-L (C23-C104)  23'-88'    134'-194'
                    23'"-88'"  134'"-194'"
Inter-H-L (CH1 10-CL 126)  135-214'  135"-214'"
Inter-H-H (h 8, h 11)      227-227"  230-230"
```

N-terminal glutamine cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
298, 298"
Fucosylated complex bi-antennary CHO-type glycans (G0F predominant) / glycanes de type CHO bi-antennaires complexes fucosylés (G0F prédominant) / glicanos de tipo CHO biantenarios complejos fucosilados (G0F predominante).

zorecimeranum #

zorecimeran	messenger RNA (mRNA), 5'-capped, encoding a full-length codon-optimised pre-fusion stabilized conformation variant (K986P and V987P) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2; NC_045512.2) spike (S) glycoprotein, flanked by 5' and 3' untranslated regions; the 3' untranslated region comprises a part of the human alpha globin gene 3' UTR sequence element, a synthetic poly(A) tail and a poly(C)-rich sequence followed by a histone stem loop sequence as a 3' tail.
zoréciméran	ARN messager (ARNm), protégé en 5', codant pour un variant de pré-fusion stabilisé en conformation (K986P et V987P) de la glycoprotéine spike (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère), NC_045512.2) complet, avec des codons optimisés, flanqués de régions 5' et 3' non traduites. La région 3' non traduite comprend une partie de l'élément de séquence 3' UTR du gène de l'alpha globine humaine, une queue poly(A) synthétique et une séquence riche en poly(C) suivie d'une séquence d'histones stem-loop comme extrémité en 3'.

zorecimerán	RNA mensajero (mRNA), protegido en 5', que codifica para una variante pre-fusión de conformación estabilizada (K986P and V987P) de la glicoproteína de la espícula (S) del SRAS-Cov-2 (coronavirus 2 del síndrome respiratorio agudo severo, NC_045512.2) completa, con codones optimizados, flanqueada por regiones 5' y 3' no traducidas. La región 3' no traducida comprende una parte del elemento secuencia 3' UTR del gen de la alfa globina humana, una cola poly(A) sintética y una secuencia rica en poly(C) seguida de una secuencia de histona stem-loop cola 3'.

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 76
Dénominations communes internationales recommandées (DCI Rec.): Liste 76
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 76
(WHO Drug Information, Vol. 30, No. 3, 2016)

p.483 **blontuvetmabum #**

blontuvetmab *replace the description by the following one*
blontuvetmab *remplacer la description par la suivante*
blontuvetmab *sustitúyase la descripción por la siguiente*

immunoglobulin G2_V-kappa-C-lambda, anti-[***Canis lupus familiaris*** MS4A1 (membrane-spanning 4-domains subfamily A member 1, CD20)], caninized monoclonal antibody; gamma2 heavy chain chimeric (1-448) [*Mus musculus* VH (*Mus musculus* IGHV1-15*01 -(IGHD) -IGHJ1*03) [8.8.6] (1-113) -*Canis lupus familiaris* IGHG2*02 (CH1 T26>Q (131) (114-211), hinge (212-229), CH2 (230-339), CH3 (340-446), CHS (447-448)) (114-448)], (128-218')-disulfide with V-kappa-C-lambda light chain chimeric (1'-219') [*Mus musculus* V-KAPPA (*Mus musculus* IGKV8-30*01 -IGKJ5*01) [12.3.9] (1'-112') -*Canis lupus familiaris* IGL1CS1*01 V45.3>I (162) (114'-219')]; dimer (225-225'':228-228'')-bisdisulfide

immunoglobuline G2_V-kappa-C-lambda, anti-[***Canis lupus familiaris*** MS4A1 (membre 1 de la sous-famille A à 4 domaines transmembranaires, CD20)], anticorps monoclonal caninisé;
chaîne lourde gamma2 chimérique (1-448) [*Mus musculus* VH (*Mus musculus* IGHV1-15*01 -(IGHD) -IGHJ1*03) [8.8.6] (1-113) -*Canis lupus familiaris* IGHG2*02 (CH1 T26>Q (131) (114-211), charnière (212-229), CH2 (230-339), CH3 (340-446), CHS (447-448)) (114-448)], (128-218')-disulfure avec la chaîne légère V-kappa-C-lambda chimérique (1'-219') [*Mus musculus* V-KAPPA (*Mus musculus* IGKV8-30*01 -IGKJ5*01) [12.3.9] (1'-112') -*Canis lupus familiaris* IGL1CS1*01 V45.3>I (162) (114'-219')]; dimère (225-225'':228-228'')-bisdisulfure

inmunoglobulina G2_V-kappa-C-lambda, anti-[***Canis lupus familiaris*** MS4A1 (miembro 1 de la subfamilia A con 4 dominios transmembranarios, CD20)], anticuerpo monoclonal caninizado;
cadena pesada gamma2 quimérica (1-448) [*Mus musculus* VH (*Mus musculus* IGHV1-15*01 -(IGHD) -IGHJ1*03) [8.8.6] (1-113) -*Canis lupus familiaris* IGHG2*02 (CH1 T26>Q (131) (114-211), bisagra (212-229), CH2 (230-339), CH3 (340-446), CHS (447-448)) (114-448)], (128-218')-disulfuro con la cadena ligera V-kappa-C-lambda quimérica (1'-219') [*Mus musculus* V-KAPPA (*Mus musculus* IGKV8-30*01 -IGKJ5*01) [12.3.9] (1'-112') -*Canis lupus familiaris* IGL1CS1*01 V45.3>I (162) (114'-219')]; dímero (225-225'':228-228'')-bisdisulfuro

p.534 **tamtuvetmabum #**
-535 tamtuvetmab *replace the description by the following one*
tamtuvetmab *remplacer la description par la suivante*
tamtuvetmab *sustitúyase la descripción por la siguiente*

immunoglobulin G2_V-kappa-C-lambda, anti-[***Canis lupus familiaris*** CD52], caninized monoclonal antibody;
gamma2 heavy chain chimeric (1-456) [chimeric VH (*Rattus norvegicus* IGHV7S6*01 (97.00%) -(IGHD) -*Canis lupus familiaris* IGHJ-E2RCC8) [8.10.12] (1-121) -*Canis lupus familiaris* IGHG2*02 (CH1 (122-219), hinge (220-237), CH2 (238-347), CH3 (348-454), CHS (455-456))(122-456)], (136-212')-disulfide with V-kappa-C-lambda light chain chimeric (1'-213') [*Rattus norvegicus* V-KAPPA (*Rattus norvegicus* IGKV22S7 (93.70%) -IGKJ1*01) [6.3.9] (1'-107') -*Canis lupus familiaris* IGLC1S1*01 V45.3>I (156) (108'-213')]; dimer (233-233":236-236")-bisdisulfide

immunoglobuline G2_V-kappa-C-lambda, anti-[***Canis lupus familiaris*** CD52], anticorps monoclonal caninisé;
chaîne lourde gamma2 chimérique (1-456) [VH chimérique (*Rattus norvegicus* IGHV7S6*01 (97.00%) -(IGHD) -*Canis lupus familiaris* IGHJ-E2RCC8) [8.10.12] (1-121) -*Canis lupus familiaris* IGHG2*02 (CH1 (122-219), charnière (220-237), CH2 (238-347), CH3 (348-454), CHS (455-456)) (122-456)], (136-212')-disulfure avec la chaîne légère V-kappa-C-lambda chimérique (1'-213') [*Rattus norvegicus* V-KAPPA (*Rattus norvegicus* IGKV22S7 (93.70%) -IGKJ1*01) [6.3.9] (1'-107') -*Canis lupus familiaris* IGLC1S1*01 V45.3>I (156) (108'-213')]; dimère (233-233":236-236")-bisdisulfure

inmunoglobulina G2_V-kappa-C-lambda, anti-[***Canis lupus familiaris*** CD52], anticuerpo monoclonal caninizado;
cadena pesada gamma2 quimérica (1-456) [VH quimérico (*Rattus norvegicus* IGHV7S6*01 (97.00%) -(IGHD) -*Canis lupus familiaris* IGHJ-E2RCC8) [8.10.12] (1-121) -*Canis lupus familiaris* IGHG2*02 (CH1 (122-219), bisagra (220-237), CH2 (238-347), CH3 (348-454), CHS (455-456))(122-456)], (136-212')-disulfuro con la cadena ligera V-kappa-C-lambda quimérica (1'-213') [*Rattus norvegicus* V-KAPPA (*Rattus norvegicus* IGKV22S7 (93.70%) -IGKJ1*01) [6.3.9] (1'-107') -*Canis lupus familiaris* IGLC1S1*01 V45.3>I (156) (108'-213')]; dímero (233-233":236-236")-bisdisulfuro

Recommended International Nonproprietary Names (Rec. INN): List 77
Dénominations communes internationales recommandées (DCI Rec.): Liste 77
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 77
(WHO Drug Information, Vol. 31, No. 1, 2017)

p.118 **ranevetmabum #**
-119 ranevetmab *replace the description by the following one*
ranevetmab *remplacer la description par la suivante*
ranevetmab *sustitúyase la descripción por la siguiente*

immunoglobulin G1-kappa, anti-[***Canis lupus familiaris*** NGF (nerve growth factor, nerve growth factor beta polypeptide, NGFB, beta-NGF)], caninized monoclonal antibody;
gamma1 heavy chain (1-453) [caninized VH (*Rattus norvegicus* IGHV5S13*01 (71.40%) -(IGHD)-IGHJ4*01) [8.7.16] (1-122) -*Canis lupus familiaris* IGHG1*01 (CH1 (123-219), hinge (220-233), CH2 (234-343), CH3 (344-451), CHS (452-453)) (123-453)], (137-213')-disulfide with kappa light chain (1'-217') [caninized V-KAPPA (*Rattus norvegicus* IGKV12S34*01 (76.80%) -IGKJ2-3*01) [6.3.9] (1'-107') -*Canis lupus familiaris* IGKC*01 (108'-213') -4-mer (214'-217')]; dimer (224-224'':226-226'':232-232'')-trisdisulfide

immunoglobuline G2-kappa, anti-[***Canis lupus familiaris*** NGF (facteur de croissance du nerf, facteur de croissance du nerf polypeptide bêta, NGFB, bêta-NGF)], anticorps monoclonal caninisé;
chaîne lourde gamma2 (1-453) [VH caninisé (*Rattus norvegicus* IGHV5S13*01 (71.40%) -(IGHD)-IGHJ4*01) [8.7.16] (1-122) -*Canis lupus familiaris* IGHG1*01 (CH1 (123-219), charnière (220-233), CH2 (234-343), CH3 (344-451), CHS (452-453)) (123-453)], (137-213')-disulfure avec la chaîne légère kappa (1'-217') [V-KAPPA caninisé (*Rattus norvegicus* IGKV12S34*01 (76.80%) -IGKJ2-3*01) [6.3.9] (1'-107') -*Canis lupus familiaris* IGKC*01 (108'-213') -4-mer (214'-217')]; dimère (224-224'':226-226'':232-232'')-trisdisulfure

inmunoglobulina G2-kappa, anti-[***Canis lupus familiaris*** NGF (factor de crecimiento de los nervios, factor de crecimiento de nervios polipéptido beta, NGFB, beta-NGF)], anticuerpo monoclonal caninizado;
cadena pesada gamma2 (1-453) [VH caninizado (*Rattus norvegicus* IGHV5S13*01 (71.40%) -(IGHD)-IGHJ4*01) [8.7.16] (1-122) -*Canis lupus familiaris* IGHG1*01 (CH1 (123-219), bisagra (220-233), CH2 (234-343), CH3 (344-451), CHS (452-453)) (123-453)], (137-213')-disulfuro con la cadena ligera kappa (1'-217') [V-KAPPA caninizado (*Rattus norvegicus* IGKV12S34*01 (76.80%) -IGKJ2-3*01) [6.3.9] (1'-107') -*Canis lupus familiaris* IGKC*01 (108'-213') -4-mer (214'-217')]; dímero (224-224'':226-226'':232-232'')-trisdisulfuro

Recommended International Nonproprietary Names (Rec. INN): List 79
Dénominations communes internationales recommandées (DCI Rec.): Liste 79
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 79
(WHO Drug Information, Vol. 32, No. 1, 2018)

p.170	*suprimáse*	*insertese*
	t**o**glato de tigilanol	t**i**glato de tigilanol

Recommended International Nonproprietary Names (Rec. INN): List 81
Dénominations communes internationales recommandées (DCI Rec.): Liste 81
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 81
(WHO Drug Information, Vol. 31, No. 1, 2017)

olenasufligenum relduparvovecum #

olenasufligene relduparvovec	*A revised sequence has been uploaded to the INN MedNet, which includes three nucleotide insertions within the CAG promoter compared to the previous version, increasing the total length of the vector to 4075bp. The table of features was revised accordingly.*
olénasufligène relduparvovec	*Une séquence révisée a été téléchargée sur MedNet DCI, et comprend trois insertions de nucléotides dans le promoteur CAG par rapport à la version précédente, augmentant la longueur totale du vecteur à 4075 pb. Le tableau des caractéristiques a été révisé en conséquence.*
olenasufligén relduparvovec	*Se cargó una secuencia revisada en MedNet DCI e incluye tres inserciones de nucleótidos dentro del promotor CAG en comparación con la versión anterior, aumentando la longitud total del vector a 4075 pb. La tabla de características se revisó en consecuencia.*

Recommended International Nonproprietary Names (Rec. INN): List 83
Dénominations communes internationales recommandées (DCI Rec.): Liste 83
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 83
(WHO Drug Information, Vol. 34, No. 1, 2020)

p.41 -42

efbemalenograstimum alfa #

efbemalenograstim alfa	*replace the description and the structure by the following ones*
efbémalénograstim alfa	*remplacer la description et la structure par les suivantes*
efbemalenograstim alfa	*sustitúyase la descripción y la estructura por las siguientes*

human granulocyte colony-stimulating factor (G-CSF) fragment fused via a peptidyl linker to a human immunoglobulin G2 Fc fragment variant, dimer:
[human granulocyte colony-stimulating factor (G-CSF, pluripoietin) short **[V^{36}, S^{37}, E^{38}>del]** isoform (1-174)]-[GSG$_3$S(G$_4$S)$_2$ linker (175-190)]-[human immunoglobulin G2 Fc fragment (223 C-terminal residues) (*Homo sapiens* IGHG2*01 (natural S^{344}>A variant); hinge (191-197), CH2 (P^{297}>S) (198-306), CH3 (307-411), CHS (412-413) (191-413)] fusion protein, dimer (193-193':196-196')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

fragment du facteur de stimulation des colonies de granulocytes humain (G-CSF) lié par un peptide à un variant du fragment Fc de l'immunoglobuline humaine G2, dimère:
[facteur humain de stimulation des colonies de granulocytes (G-CSF, pluripoïétine) **[V^{36}, S^{37}, E^{38}>del]** isoforme courte (1-174)]-[GSG$_3$S(G$_4$S)$_2$ linker (175-190)]-[fragment Fc de l'immunoglobuline humaine G2 (résidus 223 C-terminaux) (*Homo sapiens* IGHG2*01 (variant natural S^{344}>A); charnière (191-197), CH2 (P^{297}>S) (198-306), CH3 (307-411), CHS (412-413) (191-413)] protéine de fusion, dimère (193-193':196-196')-bisdisulfure, produit par des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

fragmento del factor de estimulación de las colonias de granulocitos humano (G-CSF) que se une por un péptido a una variante del fragment Fc de la inmunoglobulina humana G2, dímero:
[factor humano de estimulación de las colonias de granulocitos (G-CSF, pluripoyetina) [**V^{36}, S^{37}, E^{38}**>del] isoforma corta (1-174)]-[$GSG_3S(G_4S)_2$ conector (175-190)]-[fragmento Fc de la inmunoglobulina humana G2 (residuo 223 C-terminal) (*Homo sapiens* IGHG2*01 (variante natural S^{344}>A); bisagra (191-197), CH2 (P^{297}>S) (198-306), CH3 (307-411), CHS (412-413) (191-413)] proteína de fusión, dímero (193-193':196-196')-bisdisulfuro, producido en las células ováricas de hamsters chinos (CHO), glicoforma alfa

Sequence / Séquence / Secuencia:

```
TPLGPASSLP QSFLLKCLEQ VRKIQGDGAA LQEKLCATYK LCHPEELVLL  50
GHSLGIPWAP LSSCPSQALQ LAGCLSQLHS GLFLYQGLLQ ALEGISPELG 100
PTLDTLQLDV ADFATTIWQQ MEELGMAPAL QPTQGAMPAF ASAFQRRAGG 150
VLVASHLQSF LEVSYRVLRH LAQPGSGGGS GGGGSGGGGS VECPPCPAPP 200
VAGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVQ FNWYVDGVEV 250
HNAKTKPREE QFNSTFRVVS VLTVVHQDWL NGKEYKCKVS NKGLPASIEK 300
TISKTKGQPR EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN 350
GQPENNYKTT PPMLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN 400
HYTQKSLSLS PGK                                         413
```

Disulfide bridge location / Position de la pont disulfure / Posición del puente disulfuro:
intra-G-CSF: 36-42, 64-74, 36'-42', 64'-74'
intra-IgG2 Fc: 227-287, 333-391, 227'-287', 333'-391'
inter-IgG2 Fc: 193-193', 196-196'

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación
N-linked glycans: Asn263, Asn263'
O-linked glycans: Thr133, Thr133'

p.298 -299 **narsoplimabum #**

narsoplimab	*replace the description by the following one*
narsoplimab	*remplacer la description par la suivante*
narsoplimab	*sustitúyase la descripción por la siguiente*

immunoglobulin G4-lambda, anti-[*Homo sapiens* MASP2 (mannan-binding lectin serine peptidase 2, mannan-binding lectin serine protease 2, mannan-binding lectin serine protease 1 pseudogene 1, MASP1P1)], *Homo sapiens* monoclonal antibody; gamma**4** heavy chain *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV2-26*01 (94.0%) -(IGHD) -IGHJ4*01 (100%)) [10.7.10] (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), hinge 1-12 S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-211')-disulfide with lambda light chain *Homo sapiens* (1'-212') [V-LAMBDA (*Homo sapiens* IGLV3-1*01 (93.5%) -IGLJ2*01 (100%)) [6.3.9] (1'-106') -*Homo sapiens* IGLC2*01 (100%) (107'-212')]; dimer (224-224":227-227")-bisdisulfide, produced in Chinese hamster ovary (CHO)-S cell line, glycoform alfa

immunoglobuline G4-lambda, anti-[*Homo sapiens* MASP2 (sérine peptidase 2 de la lectine liant le mannane, sérine protéase 2 de la lectine liant le mannane, pseudogène 1 de la protéase 1 de la lectine liant le mannane, MASP1P1)], anticorps monoclonal *Homo sapiens*;
chaîne lourde gamma**4** *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV2-26*01 (94.0%) -(IGHD) -IGHJ4*01 (100%)) [10.7.10] (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), charnière 1-12 S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-211')-disulfure avec la chaîne légère lambda *Homo sapiens* (1'-212') [V-LAMBDA (*Homo sapiens* IGLV3-1*01 (93.5%) -IGLJ2*01 (100%)) [6.3.9] (1'-106') -*Homo sapiens* IGLC2*01 (100%) (107'-212')]; dimère (224-224":227-227")-bisdisulfure, produit dans des cellules ovariennes de hamsters chinois (CHO) lignée cellulaire S, glycoforme alfa

inmunoglobulina G4-lambda, anti-[*Homo sapiens* MASP2 (serina peptidasa 2 de la lectina que se une al manano, serina proteasa 2 de la lectina unida al manano, pseudogen 1 de la proteasa 1 de la lectina unida al manano, MASP1P1)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma**4** *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV2-26*01 (94.0%) -(IGHD) -IGHJ4*01 (100%)) [10.7.10] (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), bisagra 1-12 S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-211')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-212') [V-LAMBDA (*Homo sapiens* IGLV3-1*01 (93.5%) -IGLJ2*01 (100%)) [6.3.9] (1'-106') -*Homo sapiens* IGLC2*01 (100%) (107'-212')]; dímero (224-224":227-227")-bisdisulfuro, producido en las células ováricas de hamsters chinos (CHO) línea celular S, glicoforma alfa

Proposed International Nonproprietary Names (Prop. INN): List 122
Dénominations communes internationales proposées (DCI Prop.): Liste 122
Denominaciones Comunes Internacionales Propuestas (DCI Prop.): Lista 122
(WHO Drug Information, Vol. 33, No. 2, 2019)

p.831 **eflepedocokinum alfa#**
-832 eflépédocokine alfa *remplacer la description par la suivante*
eflepedocokina alfa *sustitúyase la descripción por la siguiente*

interleukine 22 humaine (IL22, cytokine Zcyto18, facteur inductible dérivé des lymphocytes T lié à IL10, IL-TIF) (1-146), fusionnée via un peptide liant $GSG_3S(G_4S)_2$ (147-162) au fragment Fc C-terminal de l'immunoglobuline G2 humaine (163-385), P^{269}>S-mutant **S**^{316}>A-variant, dimère (165-165':168-168')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

interleukina 22 humana (IL22, citoquina Zcyto18, factor inducible derivado de los linfocitos T relacionado con IL10, IL-TIF) (1-146), fusionada a través de un péptido que se une a $GSG_3S(G_4S)_2$ (147-162) con el fragmento Fc C-terminal de la inmunoglobulina G2 humana (163-385), P^{269}>S-mutante **S**^{316}>A-variante, dímero (165-165':168-168')-bisdisulfuro, producido en las células ováricas de hamster chino (CHO), glicoforma alfa

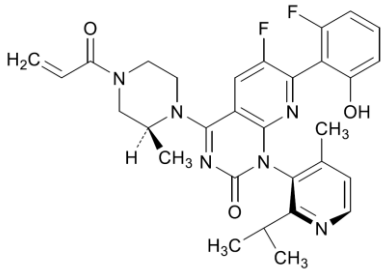
Procedure and Guiding Principles / Procédure et Directives / Procedimientos y principios generales

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.

毒薬・劇薬等の指定審査資料のまとめ

化学名・別名	(1*M*)-6-Fluoro-7-(2-fluoro-6-hydroxyphenyl)-1-[4-methyl-2-(propan-2-yl)pyridin-3-yl]-4-[(2*S*)-2-methyl-4-(prop-2-enoyl)piperazin-1-yl]pyrido[2,3-*d*]pyrimidin-2(1*H*)-one ［別名：Sotorasib・（ソトラシブ）］
構造式	
効能・効果	がん化学療法後に増悪したKRAS G12C変異陽性の切除不能な進行・再発の非小細胞肺癌
用法・用量	通常、成人にはソトラシブとして960mgを1日1回経口投与する。なお、患者の状態により適宜減量する。
劇薬等の指定	
市販名及び 有効成分・分量	［アムジェン株式会社］ 製剤：ルマケラス錠120mg（1錠中ソトラシブ120mg（力価）含有）
毒性	GLP条件下で実施したラットを用いた28日間反復投与毒性試において、sotorasibの30、100及び200 mg/kgを投与したときの忍容性は良好であり、使用した動物の10%に重篤な毒性が発現する投与量（STD10）は200 mg/kgを超えていた。ラットで認められたsotorasibに関連した主な変化は軽微から軽度であり、腎尿細管上皮の変性／壊死、脾臓重量の増加、白血球の増加、並びに網状赤血球数及び赤血球指数の変化を伴う循環赤血球（RBC）量の減少（ヘモグロビン、赤血球数及びヘマトクリット）と、病理組織学的検査における腎臓髄質外帯外側での腎尿細管上皮の変性／壊死であった。尿細管における変化は28日間の休薬期間終了後に部分的に回復したことから、回復あるいは修復が持続していることが確認された。しかしながら、少数の尿細管の周辺に間質性繊維増殖がみられた。ラットにおけるsotorasibの投与に関連した脾臓重量の増加は、28日間の休薬期間終了時には認められず、血液学的パラメータの変化はすべて対照群と同程度であった。ラットを用いた3カ月間反復投与及び2カ月間回復性試験では、sotorasibのより高い用量（60、180及び750 mg/kg）まで評価しており、ヒトの臨床曝露量を網羅する、より高い全身曝露が得られた。腎尿細管変性／壊死の発現頻度及び重症度（軽微から顕著）は、28日間反復投与毒性試験における腎臓の変化と比較して高かった。これは、試験期間が長いこと及びsotorasibの全身曝露量が高いことに起因したものと考えられた。休薬期間終了時、すべての用量において、sotorasibの投与に関連した腎臓の変化は部分的に回復した。ラットを用いた3カ月間反復投与毒性試験におけるSTD10は180 mg/kgであった。 GLP条件下で実施したイヌを用いた28日間反復投与毒性試験において、sotorasibの10、30及び300 mg/kgを投与したときの忍容性は良好であった。重篤な毒性が発現しない最大投与量（HNSTD）は300 mg/kgを超えていた。イヌにおけるsotorasibの投与に関連した主な変化は、網状赤血球数の減少を伴う軽微から軽度の赤血球系パラメータの減少であった。GLP条件下で実施したイヌを用いた3カ月間反復投与毒性試験では、sotorasibのより高い全身曝露を得るために、高い用量（200及び1000 mg/kg/dayを100及び500 mg/kgの用量で1日2回投与）を用いて評価した。しかしながら、sotorasibの1000 mg/kg/dayを投与しても、ラットを用いた3カ月間反復投与毒性試験と比較して高い曝露は得られなかった。sotorasibの投与に関連した所見

	として、胆嚢内の異物、軽微から軽度の血液学的検査及び血液生化学的検査パラメータの変化、肝臓、下垂体又は甲状腺の病理組織学的変化がみられたが、これらは重篤な毒性ではなく、肝細胞酵素誘導に対する適応性反応又は二次的反応と判断した。イヌにおいて腎毒性は認められなかった。本試験におけるHNSTDは1000 mg/kg/dayであった。
副作用	国際共同第I/II相試験である20170543試験の第 I 相及び第II相パートにおいて本剤960 mgを1回以上投与された非小細胞肺癌患者190例（日本人13例を含む）中128例（67.4%）に副作用が認められ、主な副作用（発現率5%以上）は、下痢（27.9%）、悪心、アラニンアミノトランスフェラーゼ増加、アスパラギン酸アミノトランスフェラーゼ増加（各16.3%）、疲労（11.1%）、血中アルカリホスファターゼ増加（7.9%）、嘔吐（7.4%）及び腹痛（5.3%）であった。
会社	アムジェン株式会社　製剤：製造販売

ソトラシブ

添付資料一覧

アムジェン株式会社

第3部　品質に関する文書

3.2　データ又は報告書

3.2.S　原薬

資料番号	資料表題	著者	実施期間	試験実施場所	評価・参考
3.2.S	原薬	Amgen	—	海外	評価

3.2.P　製剤

資料番号	資料表題	著者	実施期間	試験実施場所	評価・参考
3.2.P	製剤	Amgen	—	海外	評価

3.2.A　その他

資料番号	資料表題	著者	実施期間	試験実施場所	評価・参考
3.2.A	その他	Amgen	—	海外	評価

第3部　品質に関する文書
3.3 参考文献

資料番号	著者・表題・出典
3.3-1	[redacted]
3.3-2	[redacted]
3.3-3	[redacted]
3.3-4	[redacted]
3.3-5	[redacted]
3.3-6	[redacted]

第4部　非臨床試験報告書
4.2　試験報告書
4.2.1　薬理試験
4.2.1.1　効力を裏付ける試験

資料番号	資料表題	著者	実施期間（年／月／日）	試験実施場所	評価・参考
4.2.1.1-1	Study R20150198 - Biochemical Characterization of AMG 510 and Metabolites in KRAS$^{G12C/C118A}$ and KRAS^{C118A} Nucleotide Exchange Assays	Amgen	20[redacted]	海外	評価
4.2.1.1-2	Study R20150199 - Cellular Characterization of AMG 510	Amgen	20[redacted]	海外	評価
4.2.1.1-3	Study R20190078 - Effects of AMG 510 on KRAS Signaling in NCI-H358 and MIA PaCa-2 Cells In Vitro	Amgen	20[redacted]	海外	評価
4.2.1.1-4	Study 153894 - In Vitro Combination Effects of AMG 510 with MAPK Pathway, PI3K Pathway, and Other Targeted Inhibitors	Amgen	20[redacted]	海外	評価
4.2.1.1-5	Study R20150188 - AMG 510 Inhibits Phospho-ERK1/2 Signaling in *KRAS p.G12C* Pancreatic MIA PaCa-2 T2 Tumors in Female Athymic Nude Mice	Amgen	20[redacted]	海外	評価
4.2.1.1-6	Study R20190129 - AMG 510 Inhibits ERK1/2 Phosphorylation Signaling and Results in Covalent Occupancy of KRAS^{G12C} in *KRAS p.G12C* NSCLC NCI-H358 Tumors in Female Athymic Nude Mice	Amgen	20[redacted]	海外	評価
4.2.1.1-7	Study R20150192 - Effect of AMG 510 on Phospho-ERK1/2 Signaling at Early Timepoints (0.25 to 2 hours) in *KRAS p.G12C* Pancreatic MIA PaCa-2 T2 Tumors in Female Athymic Nude Mice	Amgen	20[redacted]	海外	評価
4.2.1.1-8	Study R20150189 - The Effect of Once-daily Dosing of AMG 510 on Tumor Growth in the *KRAS p.G12C* Pancreatic MIA PaCa-2 T2 Xenograft Model in Female Athymic Nude Mice	Amgen	20[redacted]	海外	評価
4.2.1.1-9	Study R20150190 - The Effect of Once-daily Dosing of AMG 510 on Tumor Growth in the *KRAS p.G12C* NSCLC H358 Xenograft Model in Female Athymic Nude Mice	Amgen	20[redacted]	海外	評価
4.2.1.1-10	Study R20150191 - The Effect of Once-daily Dosing of AMG 510 on Tumor Growth in the *KRAS p.G12V* Colorectal Carcinoma SW480-1AC Xenograft Model in Female Athymic Nude Mice	Amgen	20[redacted]	海外	評価
4.2.1.1-11	Study R20190130 - AMG 510 Inhibited ERK 1/2 Phosphorylation in a Time and Dose Dependent Manner in Human KRAS *p.G12C* CRC Patient-derived Xenograft Tumors in Female NOD/SCID IL2rg (NSG) Mices	Amgen	20[redacted]	海外	評価
4.2.1.1-12	Study R20190131 - Once Daily Dosing of AMG 510 Inhibited Tumor Growth in a Human *KRAS p.G12C* CRC Patient-derived Xenograft Model in Female NSG Mice	Amgen	20[redacted]	海外	評価
4.2.1.1-13	Study R20180033 - The Effect of AMG 510 in Combination with MEK Inhibitor 1009089 (PD-0325901) in the *KRAS p.G12C* NSCLC H358 Xenograft Model in Female Athymic Nude Mice	Amgen	20[redacted]	海外	評価
4.2.1.1-14	Study 153358 - Effect of AMG 510 in Combination with Afatinib on Tumor Growth in the *KRAS p.G12C* NSCLC NCI-H358 Xenograft Model in Female Athymic Nude Mice	Amgen	20[redacted]	海外	評価

4.2.1.1-15	Study 153397 - The Effect of AMG 510 in Combination with RMC-4550 (SHP2i), on Tumor Growth in the *KRAS p.G12C* NSCLC NCI-H358 Xenograft Model in Female Athymic Nude Mice	Amgen	20[redacted]	海外	評価
4.2.1.1-16	Study R20180032 - The Effect of AMG 510 in Combination with Carboplatin on Tumor Growth in the KRAS p.G12C NSCLC H358 Xenograft Model in Female Athymic Nude Mice	Amgen	20[redacted]	海外	評価
4.2.1.1-17	Study R20180002 - AMG 510 Inhibits ERK1/2 Phosphorylation in Murine Colorectal CT-26 *KRAS p.G12C* -H10 Tumors in Female Balb/c Mice	Amgen	20[redacted]	海外	評価
4.2.1.1-18	Study R20190110 - AMG 510 Inhibits ERK1/2 Phosphorylation in Murine Colorectal CT-26 *KRAS p.G12C* -H10 Tumors in Female Balb/c Mice	Amgen	20[redacted]	海外	評価
4.2.1.1-19	Study R20190128 - The Effect of Once-daily Dosing of AMG 510 on Tumor Growth in the Parental CT-26 *KRAS p.G12D* Colorectal Carcinoma Syngeneic Model in Female Balb/c Mice	Amgen	20[redacted]	海外	評価
4.2.1.1-20	Study R20180034 - The Effect of AMG 510 in Combination with anti-PD-1 antibody on Tumor Growth in the Murine Colorectal CT-26 *KRAS p.G12C* -H10 Syngeneic Model in Female Balb/c Mice	Amgen	20[redacted]	海外	評価
4.2.1.1-21	Study R20180035 - The Effect of AMG 510 on Tumor Infiltrating Lymphocytes in CT-26 *KRAS p.G12C* -H10 Colorectal Tumors in Female Balb/c Mice	Amgen	20[redacted]	海外	評価
4.2.1.1-22	Study R20190105 - The Effect of AMG 510 and/or Anti-PD-1 on CT-26 KRAS p.G12C-H10 Colorectal Tumors by Immunohistochemistry (IHC) in the Female BALB/c Mouse	Amgen	20[redacted]	海外	評価
4.2.1.1-23	Study R20180036 - The Effect of AMG 510 on Gene Expression and T-Cell Priming in CT-26 KRAS p.G12C-H10 Colorectal Tumors in Female Balb/c Mice	Amgen	20[redacted]	海外	評価

4.2.1.2 副次的薬理試験

資料番号	資料表題	著者	実施期間 （年／月／日）	試験実施場所	評価・参考
4.2.1.2-1	Study 125831 - mRNA Expression Assessment of KRAS	Amgen	20[redacted]	海外	評価
4.2.1.2-2	Study 124452 - *In Vitro* Pharmacology Study of 3365648 and 3365626 – Early Panel	Amgen	20[redacted]	海外	評価
4.2.1.2-3	Study 124453 - *In Vitro* Pharmacology Late Panel Study of 3365648 and 3365626	Amgen	20[redacted]	海外	評価
4.2.1.2-4	Study R20150219 - Cysteine Proteome Profiling of AMG 510 in NCI-H358	Amgen	20[redacted]	海外	評価
4.2.1.2-5	Study 124807 - *In Vitro* Pharmacology Study of 3368167 Early Panel	Amgen	20[redacted]	海外	評価
4.2.1.2-6	Study 124787 - KINOME*scan*™ Profiling Service Primary Screen Report	Amgen	20[redacted]	海外	評価
4.2.1.2-7	Study 124808 - *In Vitro* Pharmacology Study of 3368167 Late Panel	Amgen	20[redacted]	海外	評価

4.2.1.2-8	Study 153413 - *In Vitro* Pharmacology New Early Panel Study of 3375854 and 3413829	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.1.2-9	Study 153414 - *In Vitro* Pharmacology New Late Panel Study of 3375854 and 3413829	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.1.2-10	Study 153415 - KINOME*scan*™ Profiling Service Primary Screen Report	Amgen	20[redacted] - 20[redacted]	海外	評価

4.2.1.3 安全性薬理試験

資料番号	資料表題	著者	実施期間（年／月／日）	試験実施場所	評価・参考
4.2.1.3-1	Study 150431 - Effect of AMG 510 on Cloned hERG Potassium Channels Expressed in Human Embryonic Kidney Cells	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.1.3-2	Study 150458 - AMG 510: Single-Dose Oral Gavage Cardiovascular Safety Pharmacology Evaluation in Male Telemetry-Instrumented Conscious Dogs	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.1.3-3	Study 124803 - AMG3368167: Acute *In Vitro* Effect on hERG recorded From HEK Cells	Amgen	20[redacted] - 20[redacted]	海外	参考
4.2.1.3-4	Study 153419 - hERG ^{3}H-Dofetilide Filter Binding Assay –Study of 3375854#1 and 3413829#1	Amgen	20[redacted] - 20[redacted]	海外	参考

4.2.2 薬物動態試験

4.2.2.1 分析法及びバリデーション報告書

資料番号	資料表題	著者	実施期間（年／月／日）	試験実施場所	評価・参考
4.2.2.1-1	Study 150506 - Determination of AMG 510 in K_2EDTA Sprague Dawley Rat Plasma Using Plasma Using LC-MS/MS Following Protein Precipitation	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.2.1-2	Study 152694 - Validation of an LC-MS/MS Assay for AMG 510 in Rabbit Plasma with K_2EDTA	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.2.1-3	Study 150505 - Determination of AMG 510 in K_2EDTA Beagle Dog Plasma Using LC-MS/MS Following Protein Precipitation	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.2.1-4	Study 151603 - Validation of an LC-MS/MS Assay for AMG 510 in Rat Plasma with K_2EDTA (and Addendum 1)	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.2.1-5	Study 151604 - Validation of an LC-MS/MS Assay for AMG 510 in Dog Plasma with K_2EDTA (and Addendum 1)	Amgen	20[redacted] 20[redacted]	海外	評価

4.2.2.2 吸収

資料番号	資料表題	著者	実施期間（年／月／日）	試験実施場所	評価・参考
4.2.2.2-1	Study 150529 - Preclinical Pharmacokinetics of AMG 510	Amgen	20[redacted]	海外	評価

4.2.2.2-2	Study 125554 - Pharmacokinetics of AMG 510 Following Oral Solution, Suspension, or Tablet Dose Administration to Male Beagle Dogs	Amgen	20[redacted]	海外	評価

4.2.2.3 分布

資料番号	資料表題	著者	実施期間（年／月／日）	試験実施場所	評価・参考
4.2.2.3-1	Study 150563 - *In Vitro* Permeability Assessment of AMG 510 and Its Metabolite (AMG3368167) in MDCK Transwell Assay	Amgen	20[redacted]	海外	評価
4.2.2.3-2	Study 150530 - Mouse, Rat, Dog, Monkey, and Human In Vitro Plasma Protein Binding of AMG 510 and AMG3368167	Amgen	20[redacted]	海外	評価
4.2.2.3-3	Study 150532 - In Vitro Assessment of Blood-to-Plasma Partitioning of AMG 510 in Mouse, Rat, Dog, Monkey, and Human	Amgen	20[redacted]	海外	評価
4.2.2.3-4	Study 152495 - Pharmacokinetics, Distribution, Metabolism, and Excretion of ^{14}C-AMG510 Following Oral Administration to Rats	Amgen	20[redacted] - 20[redacted]	海外	評価

4.2.2.4 代謝

資料番号	資料表題	著者	実施期間（年／月／日）	試験実施場所	評価・参考
4.2.2.4-1	Study 150531 - Characterization of *In Vitro* Metabolites of AMG 510 Formed in Mouse, Rat, Dog, Monkey and Human Hepatic Microsomes and Hepatocytes	Amgen	20[redacted]	海外	評価

4.2.2.5 排泄

資料番号	資料表題	著者	実施期間（年／月／日）	試験実施場所	評価・参考
4.2.2.5-1	Study 124686 - Metabolism and Excretion of AMG 510 Following a Single Intravenous or Oral Dose to Male Sprague-Dawley Rats	Amgen	20[redacted]	海外	評価
4.2.2.5-2	Study 153304 - Pharmacokinetics, Absorption, Metabolism, and Excretion of ^{14}C-AMG 510 Following Oral Administration to Dogs	Amgen	20[redacted] - 20[redacted]	海外	評価

4.2.3 毒性試験

4.2.3.2 反復投与毒性試験

資料番号	資料表題	著者	実施期間（年／月／日）	試験実施場所	評価・参考
4.2.3.2-1	Study 124431 - AMG3365648: 7-Day Oral Toxicology Study in the Sprague Dawley Rat	Amgen	20[redacted] - 20[redacted]	海外	参考

4.2.3.2-2	Study 150428 - AMG 510: 28-Day Oral Toxicology Study in the Sprague Dawley Rat with a 28-Day Recovery Period	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.3.2-3	Study 150432 - AMG 510: A 3-Month Oral Toxicology Study in the Sprague Dawley Rat with a 2-Month Recovery Period	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.3.2-4	Study 124273 - AMG3365648: Exploratory 7-Day Oral Toxicology Study in the Female Beagle Dog	Amgen	20[redacted] - 20[redacted]	海外	参考
4.2.3.2-5	Study 151550 - AMG 510: Exploratory 7-Day Oral Toxicology Study in the Beagle Dog (and Amendment 1)	Amgen	20[redacted]	海外	参考
4.2.3.2-6	Study 150429 - AMG 510: 28-Day Oral Toxicology Study in the Beagle Dog	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.3.2-7	Study 150433 - AMG 510: A 3-Month BID Oral Toxicology Study in the Beagle Dog	Amgen	20[redacted] - 20[redacted]	海外	評価

4.2.3.3 遺伝毒性試験

4.2.3.3.1 In vitro試験

資料番号	資料表題	著者	実施期間（年／月／日）	試験実施場所	評価・参考
4.2.3.3.1-1	Study 124824 - Bacterial Reverse Mutation Assay in 24-well Plates (Micro Ames) with AMG3365648 #6	Amgen	20[redacted] - 20[redacted]	海外	参考
4.2.3.3.1-2	Study 124825 - *In Vitro* Micro HPBL Micronucleus Assay with AMG3365648 #6	Amgen	20[redacted] - 20[redacted]	海外	参考
4.2.3.3.1-3	Study 150436 - AMG 510: Bacterial Reverse Mutation Test in *Salmonella typhimurium* and *Escherichia coli*	Amgen	20[redacted] - 20[redacted]	海外	評価

4.2.3.3.2 In vivo試験

資料番号	資料表題	著者	実施期間（年／月／日）	試験実施場所	評価・参考
4.2.3.3.2-1	Study 150435 - AMG 510 - Combined In Vivo Mammalian Erythrocyte Micronucleus Test and Alkaline Comet Assay in Rat	Amgen	20[redacted] - 20[redacted]	海外	評価

4.2.3.5 生殖発生毒性試験

4.2.3.5.2 胚・胎児発生に関する試験

資料番号	資料表題	著者	実施期間（年／月／日）	試験実施場所	評価・参考
4.2.3.5.2-1	Study 150434 - AMG 510: Embryo-Fetal Development Toxicology Study in the Sprague Dawley Rat	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.3.5.2-2	Study 150808 - AMG 510: Maternal Tolerability Study in the Pregnant New Zealand White Rabbit	Amgen	20[redacted] - 20[redacted]	海外	参考
4.2.3.5.2-3	Study 150810 - AMG 510: Embryo-Fetal Development Study in the New Zealand White Rabbit	Amgen	20[redacted] - 20[redacted]	海外	評価

4.2.3.7　その他の毒性試験

4.2.3.7.3　メカニズム試験

資料番号	資料表題	著者	実施期間（年／月／日）	試験実施場所	評価・参考
4.2.3.7.3-1	Study 153127 - AMG 510: Exploratory 7-Day Oral Toxicology Study in the Male Sprague Dawley Rat	Amgen	20[redacted] - 20[redacted]	海外	参考
4.2.3.7.3-2	Study 153409 - AMG 510 and AMG3368167: Cytochrome P450 and UDP Glucuronosyltransferase Induction in Cultured Beagle Dog Hepatocytes	Amgen	20[redacted] - 20[redacted]	海外	参考

4.2.3.7.5　代謝物の毒性試験

資料番号	資料表題	著者	実施期間（年／月／日）	試験実施場所	評価・参考
4.2.3.7.5-1	Study 125020 - Bacterial Reverse Mutation Assay in 24-well Plates (Micro Ames) with AMG3368167#2	Amgen	20[redacted] - 20[redacted]	海外	参考
4.2.3.7.5-2	Study 125324 - *In Vitro* Micro HPBL Micronucleus Assay with AMG3368167#4	Amgen	20[redacted] - 20[redacted]	海外	参考
4.2.3.7.5-3	Study 153305 - In Silico Mutagenicity Predictions of AMG3413829 (M18)	Amgen	20[redacted] - 20[redacted]	海外	参考
4.2.3.7.5-4	Study 153306 - In Silico Mutagenicity Prediction of AMG3375854 (M10)	Amgen	20[redacted] - 20[redacted]	海外	参考

4.2.3.7.6　不純物の毒性試験

資料番号	資料表題	著者	実施期間（年／月／日）	試験実施場所	評価・参考
4.2.3.7.6-1	Study 152458 - Mixture of AMG 510 and Impurities: A 28-Day Oral Toxicology Study in the Sprague Dawley Rat	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.3.7.6-2	Study 153451 - Mixture of AMG 510 and Impurities: A 28-Day Oral Toxicology Study in the Sprague Dawley Rat	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.3.7.6-3	Study 125621 - Bacterial Reverse Mutation Assay in 24-well Plates (Micro Ames) with AMG3379613	Amgen	20[redacted] - 20[redacted]	海外	参考
4.2.3.7.6-4	Study 153049 - AMG3396902: GLP Bacterial Reverse Mutation Test in *Salmonella typhimurium* and *Escherichia coli*	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.3.7.6-5	Study 153050 - AMG3414168: GLP Bacterial Reverse Mutation Test in *Salmonella typhimurium* and *Escherichia coli*	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.3.7.6-6	Study 153051 - AMG3412607 GLP Bacterial Reverse Mutation Test in *Salmonella typhimurium* and *Escherichia coli*	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.3.7.6-7	Study 153052 - AMG3368167: GLP Bacterial Reverse Mutation Test in *Salmonella typhimurium* and *Escherichia coli*	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.3.7.6-8	Study 153053 - AMG3379613: GLP Bacterial Reverse Mutation Test in *Salmonella typhimurium* and *Escherichia coli*	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.3.7.6-9	Study 153054 - AMG3379620: GLP Bacterial Reverse Mutation Test in *Salmonella typhimurium* and *Escherichia coli*	Amgen	20[redacted] - 20[redacted]	海外	評価

4.2.3.7.6-10	Study 153494 - AMG3379613 Lot No. MH135223-001 and Lot No. MH144641-001: Bacterial Reverse Mutation Test in 24-well Plates (Micro Ames) in *Salmonella typhimurium* and *Escherichia coli*	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.3.7.6-11	Study 154030 - AMG3422551: Bacterial Reverse Mutation Test in 24-well Plates (Micro Ames) in *Salmonella Typhimurium* and *Escherichia Coli*	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.3.7.6-12	Study 154031 - AMG3422536: Bacterial Reverse Mutation Test in 24-well Plates (Micro Ames) in *Salmonella Typhimurium* and *Escherichia Coli*	Amgen	20[redacted] - 20[redacted]	海外	評価
4.2.3.7.6-13	Study 154032 - AMG3422547: Bacterial Reverse Mutation Test in 24-well Plates (Micro Ames) in *Salmonella Typhimurium* and *Escherichia Coli*	Amgen	20[redacted] - 20[redacted]	海外	評価

4.2.3.7.7　その他の試験

資料番号	資料表題	著者	実施期間 （年／月／日）	試験実施場所	評価・参考
4.2.3.7.7-1	Study 124666 - Screening Assay to Assess the Phototoxic Potential of AMG3365648	Amgen	20[redacted] - 20[redacted]	海外	参考

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第5部　臨床試験報告書

5.2　臨床試験一覧表

資料番号	資料表題	著者	試験実施期間（年／月／日）	試験実施場所（国内／海外）	評価・参考	申請電子データ提出の有無
5.2	Tabular Listing of All Clinical Studies	Amgen	－	－	－	－

5.3　試験報告書及び関連情報

5.3.1　生物薬剤学試験報告書

5.3.1.1　バイオアベイラビリティ（BA）試験報告書

資料番号	資料表題	著者	試験実施期間（年／月／日）	試験実施場所（国内／海外）	評価・参考	申請電子データ提出の有無
5.3.1.1-1	Study 20190316 - An Open-label, Randomized, 2-period, 2-treatment Crossover Study to Assess the Effect of Food on the Pharmacokinetics of AMG 510 in Healthy Subjects	Amgen	20[redacted]－20[redacted]	海外	参考	有

5.3.1.2　比較BA試験及び生物学的同等性（BE）試験報告書

資料番号	資料表題	著者	試験実施期間（年／月／日）	試験実施場所（国内／海外）	評価・参考	申請電子データ提出の有無
5.3.1.2-1	Study 20190500 - An Open-label, Randomized, 2-Period, 2-Treatment Crossover Study to Evaluate the Relative Bioavailability of AMG 510 Administered as Tablets and as a Water Dispersion in Healthy Subjects	Amgen	20[redacted]－20[redacted]	海外	参考	有

5.3.1.4　生物学的及び理化学的分析法検討報告書

資料番号	資料表題	著者	試験実施期間（年／月／日）	試験実施場所（国内／海外）	評価・参考	申請電子データ提出の有無
5.3.1.4-1	Study 150636 - Determination of AMG 510 in K_2EDTA Human Plasma Using LC-MS/MS Following Protein Precipitation	Amgen	20[redacted]－20[redacted]	海外	参考	無
5.3.1.4-2	Study 151842 Amendment 2 - Determination of AMG 510 in K_2EDTA Human Plasma Using LC-MS/MS Following Protein Precipitation (Revised Range)	Amgen	20[redacted]－20[redacted]	海外	参考	無
5.3.1.4-3	Study 153277 - Determination of AMG 510 in Human Urine Using LC-MS/MS Following Sample Dilution	Amgen	20[redacted]－20[redacted]	海外	参考	無
5.3.1.4-4.1	Study 150840 - Quantitation of AMG 510 in Human Plasma via HPLC with MS/MS Detection	Amgen	20[redacted]	海外	参考	無
5.3.1.4-4.2	Study 150840 Addendum 1 - Quantitation of AMG 510 in Human Plasma via HPLC with MS/MS Detection	Amgen	20[redacted]	海外	参考	無
5.3.1.4-4.3	Study 150840 Addendum 2 - Quantitation of AMG 510 in Human Plasma via HPLC with MS/MS Detection	Amgen	20[redacted]	海外	参考	無

5.3.1.4-4.4	Study 150840 Addendum 3 - Quantitation of AMG 510 in Human Plasma via HPLC with MS/MS Detection	Amgen	20[redacted]	海外	参考	無
5.3.1.4-4.5	Study 150840 Addendum 4 - Quantitation of AMG 510 in Human Plasma via HPLC with MS/MS Detection	Amgen	20[redacted]	海外	参考	無
5.3.1.4-5	Study 150840 Digoxin - Quantitation of Digoxin in Human Plasma via HPLC with MS/MS Detection	Amgen	20[redacted]	海外	参考	無
5.3.1.4-6	Study 150840 - Analytical Method Validation Report for Metformin in Human EDTA K_3 Plasma	Amgen	20[redacted]	海外	参考	無
5.3.1.4-7	Study 150840 - Validation of a High Performance Liquid Chromatograpidc Method Using Tandem Mass Spectrometry Detection for the Determination of Metformin (10 to 2500 ng/mL) in Human Urine	Amgen	20[redacted]	海外	参考	無
5.3.1.4-8	Study 150840 - Quantitation of Midazolam and 1-Hydroxymidazolam in Human Plasma via HPLC with MS/MS Detection	Amgen	20[redacted]	海外	参考	無
5.3.1.4-9	Study 150840 Itraconazole - Quantitation of Itraconazole and 2-Hydroxyitraconazole in Human Plasma via HPLC with MS/MS Detection	Amgen	20[redacted]	海外	参考	無
5.3.1.4-10.1	Study 153140 - Quantitation of AMG 510 in Human Urine via LC-MS/MS	Amgen	20[redacted]	海外	参考	無
5.3.1.4-10.2	Study 153140 Addendum 1 - Quantitation of AMG 510 in Human Urine via LC-MS/MS	Amgen	20[redacted]	海外	参考	無
5.3.1.4-11.1	Study 153141 - Quantitation of AMG 510 Metabolites M10 (AMG3375854), M18 (AMG3413829), and M24 (AMG3368167) in Human Plasma via LC-MS/MS	Amgen	20[redacted]	海外	参考	無
5.3.1.4-11.2	Study 153141 Addemdum 1 - Quantitation of AMG 510 Metabolites M10 (AMG3375854), M18 (AMG3413829), and M24 (AMG3368167) in Human Plasma via LC-MS/MS	Amgen	20[redacted]	海外	参考	無
5.3.1.4-11.3	Study 153141 Addendum 2 - Quantitation of AMG 510 Metabolites M10 (AMG3375854), M18 (AMG3413829), and M24 (AMG3368167) in Human Plasma via LC-MS/MS	Amgen	20[redacted]	海外	参考	無
5.3.1.4-12	bacsr-20190317 - Bioanalytical Report - Study 20190317 - A Phase I, Open-Label Study to Evaluate the Drug-Drug Interactions Between Metformin and AMG 510 in Healthy Subjects	Amgen	20[redacted]	海外	参考	無
5.3.1.4-13	bacsr-20190318 - Bioanalytical Report - Study 20190318 - Quantitation of Itraconazole in Human Plasma via HPLC with MS/MS Detection	Amgen	20[redacted]	海外	参考	無

5.3.2 ヒト生体試料を用いた薬物動態関連の試験報告書

5.3.2.1 血漿蛋白結合試験報告書

資料番号	資料表題	著者	試験実施期間（年／月／日）	試験実施場所（国内／海外）	評価・参考	申請電子データ提出の有無
5.3.2.1-1	Study 153486 - Human In Vitro Plasma Protein Binding of AMG3375854 and AMG3413829	Amgen	20[redacted]	海外	参考	無

5.3.2.2 肝代謝及び薬物相互作用試験報告書

資料番号	資料表題	著者	試験実施期間（年／月／日）	試験実施場所（国内／海外）	評価・参考	申請電子データ提出の有無
5.3.2.2-1	Study 150537 - Identification of the Major Enzymes Involved in the In Vitro Metabolism of AMG 510	Amgen	20[redacted]	海外	参考	無
5.3.2.2-2	Study 154076 - In Vitro Characterization of the Glutathione Conjugation of AMG 510	Amgen	20[redacted]	海外	参考	無
5.3.2.2-3	Study 150535 - Evaluation of the Inhibitory Potential of AMG 510 and AMG 3368167 Against Eight Principal Human Cytochrome P450 Isozymes Using Human Hepatic Microsomes	Amgen	20[redacted]	海外	参考	無
5.3.2.2-4	Study 153423 - Determination of the Inhibition of CYP1A2, CYP2B6, CYP2C8, CYP2C9, CYP2C19, CYP2D6, and CYP3A by AMG 3375854 and AMG 3413829 in Human Liver Microsomes	Amgen	20[redacted]	海外	参考	無
5.3.2.2-5	Study 150536 - Evaluation of AMG 510 and AMG3368167 as Inducers of CYP1A2, CYP2B6, CYP2C8, CYP2C9, CYP2C19, and CYP3A4 in Primary Human Hepatocytes	Amgen	20[redacted]	海外	参考	無
5.3.2.2-6	Study 153424 - An In Vitro Evaluation of the Effect of AMG3375854 and AMG3413829 on mRNA and Enzymatic Activity Levels of Cytochrome P450 Genes in Cultured Human Hepatocytes	Amgen	20[redacted]	海外	参考	無
5.3.2.2-7	Study 153303 - Peak Area Ratios for AMG 510 and Identified Human Metabolites in Matrix-normalized Rat, Dog, and Human Plasma Samples	Amgen	20[redacted]	海外	参考	無
5.3.2.2-8	Study 150539 - Assessment of AMG 510 and its Metabolite AMG3368167 as Inhibitors of Human BCRP, P-gp, MATE1, MATE2-K, OAT1, OAT3, OCT1, OCT2, OATP1B1, and OATP1B3 Mediated Transport	Amgen	20[redacted]－20[redacted]	海外	参考	無
5.3.2.2-9	Study 153425 - Assessment of AMG 3375854 and AMG 3413829 as inhibitors of human OAT1, OAT3, OCT1, OCT2, OATP1B1, OATP1B3, MATE1, MATE2-K, BCRP and P-gp mediated transport	Amgen	20[redacted]－20[redacted]	海外	参考	無

5.3.2.3 他のヒト生体試料を用いた試験報告書

資料番号	資料表題	著者	試験実施期間（年／月／日）	試験実施場所（国内／海外）	評価・参考	申請電子データ提出の有無
5.3.2.3-1	Study 150540 - Assessment of AMG 510 and its Metabolite AMG3368167 as a Substrate of Human BCRP and P-gp Mediated Transport	Amgen	20[redacted]－20[redacted]	海外	参考	無
5.3.2.3-2	Study 154075 - Nonspecific Binding of AMG 510 and Three of Its Metabolites to Human Liver Microsomes	Amgen	20[redacted]	海外	参考	無

5.3.3 臨床薬物動態（PK）試験報告書

5.3.3.1 健康被験者におけるPK及び初期忍容性試験報告書

資料番号	資料表題	著者	試験実施期間（年／月／日）	試験実施場所（国内／海外）	評価・参考	申請電子データ提出の有無
5.3.3.1-1.1	Study 20190321 - A Phase I, Open-label Study of the Absorption, Metabolism, and Excretion of [^{14}C]-AMG 510 Following a Single Oral Dose in Healthy Male Subjects	Amgen	20[redacted]－20[redacted]	海外	参考	無
5.3.3.1-1.2	Study 20190321 addendum - A Phase I, Open-label Study of the Absorption, Metabolism, and Excretion of [^{14}C]-AMG 510 Following a Single Oral Dose in Healthy Male Subjects	Amgen	20[redacted]－20[redacted]	海外	参考	無

5.3.3.4 外因性要因を検討したPK試験報告書

資料番号	資料表題	著者	試験実施期間（年／月／日）	試験実施場所（国内／海外）	評価・参考	申請電子データ提出の有無
5.3.3.4-1	Study 20190315 - An Open-label, Drug-drug Interaction Study to Evaluate the Effect of AMG 510 on the Pharmacokinetics of Digoxin, a P-glycoprotein Substrate, in Healthy Subjects	Amgen	20[redacted]－20[redacted]	海外	参考	有
5.3.3.4-2.1	Study 20190317 - A Phase I, Open-label Study to Evaluate the Drug-drug Interactions Between Metformin and AMG 510 in Healthy Subjects	Amgen	20[redacted]－20[redacted]	海外	参考	有
5.3.3.4-2.2	Study 20190317 errata - A Phase I, Open-label Study to Evaluate the Drug-drug Interactions Between Metformin and AMG 510 in Healthy Subjects	Amgen	20[redacted]－20[redacted]	海外	参考	無
5.3.3.4-3	Study 20190318 - An Open-label Study to Evaluate the Drug-drug Interaction Effect of Itraconazole, a CYP3A4 Inhibitor, on the Pharmacokinetics of AMG 510 in Healthy Subjects	Amgen	20[redacted]－20[redacted]	海外	参考	有
5.3.3.4-4	Study 20190319 - An Open-label Study to Evaluate the Drug-drug Interaction Effect of Rifampin, a CYP3A4 Inducer, on the Pharmacokinetics of AMG 510 in Healthy Subjects	Amgen	20[redacted]－20[redacted]	海外	評価	有
5.3.3.4-5	Study 20190320 - An Open-label Study to Evaluate the Drug-drug Interaction Effect of Omeprazole, a Proton-pump Inhibitor, on the Pharmacokinetics of AMG 510 in Healthy Subjects	Amgen	20[redacted]－20[redacted]	海外	評価	有
5.3.3.4-6.1	Study 20200199 - An Open-label Study to Evaluate the Impact of Acid-reducing Agents on the Pharmacokinetics of AMG 510 in Healthy Subjects under Fed Conditions	Amgen	20[redacted]－20[redacted]	海外	評価	有
5.3.3.4-6.2	Study 20200199 errata - An Open-label Study to Evaluate the Impact of Acid-reducing Agents on the Pharmacokinetics of AMG 510 in Healthy Subjects under Fed Conditions	Amgen	20[redacted]－20[redacted]	海外	評価	無
5.3.3.4-7	Study 153468 - Assessment of Clinical Drug-Drug Interaction of AMG 510 Using Physiologically Based Pharmacokinetic Modeling	Amgen	20[redacted]	－	参考	有

5.3.3.5 ポピュレーションPK試験報告書

資料番号	資料表題	著者	試験実施期間（年／月／日）	試験実施場所（国内／海外）	評価・参考	申請電子データ提出の有無
5.3.3.5-1	Study 152921 - Population Pharmacokinetic Evaluation of AMG 510 Monotherapy in Healthy and Advanced Solid Tumor Subjects With a Specific KRAS Mutation From Phase 1 and Phase 2 Studies	Amgen	20[redacted]	－	参考	有

5.3.4 臨床薬力学（PD）試験報告書

5.3.4.2 患者におけるPD試験及びPK/PD試験報告書

資料番号	資料表題	著者	試験実施期間（年／月／日）	試験実施場所（国内／海外）	評価・参考	申請電子データ提出の有無
5.3.4.2-1	Study 152922 - Exposure-Response of Sotorasib in Subjects With Advanced Solid Tumors With a Specific KRAS Mutation	Amgen	20[redacted]	－	参考	有

5.3.5 有効性及び安全性試験報告書

5.3.5.1 申請する適応症に関する比較対照試験報告書

資料番号	資料表題	著者	試験実施期間（年／月／日）	試験実施場所（国内／海外）	評価・参考	申請電子データ提出の有無
5.3.5.1-1	Ongoing Study Safety Report: Study 20190009 - A Phase 3 Multicenter, Randomized, Open Label, Active-controlled, Study of AMG 510 Versus Docetaxel for the Treatment of Previously Treated Locally Advanced and Unresectable or Metastatic NSCLC Subjects With Mutated *KRAS p.G12C*	Amgen	2020/6/4－実施中 Cutoff:2020/9/1	国内／海外	参考	無

5.3.5.2 非対照試験報告書

資料番号	資料表題	著者	試験実施期間（年／月／日）	試験実施場所（国内／海外）	評価・参考	申請電子データ提出の有無
5.3.5.2-1.1	Study 20170543 Phase-1 Portion interim analysis - A Phase 1/2, Open-label Study Evaluating the Safety, Tolerability, Pharmacokinetics, Pharmacodynamics, and Efficacy of AMG 510 Monotherapy in Subjects With Advanced Solid Tumors With *KRAS p.G12C* Mutation and AMG 510 Combination Therapy in Subjects With Advanced NSCLC With *KRAS p.G12C* Mutation (CodeBreak 100)	Amgen	2018/8/27－実施中 Cutoff：2020/7/6	国内／海外	評価	有
5.3.5.2-1.2	Study 20170543 errata - Phase-1 Portion interim analysis - A Phase 1/2, Open-label Study Evaluating the Safety, Tolerability, Pharmacokinetics, Pharmacodynamics, and Efficacy of AMG 510 Monotherapy in Subjects With Advanced Solid Tumors With *KRAS p.G12C* Mutation and AMG 510 Combination Therapy in Subjects With Advanced NSCLC With *KRAS p.G12C* Mutation (CodeBreak 100)	Amgen	2018/8/27－実施中 Cutoff：2020/7/6	国内／海外	評価	無
5.3.5.2-1.3	Study 20170543 errata2 - Phase-1 Portion interim analysis - A Phase 1/2, Open-label Study Evaluating the Safety, Tolerability, Pharmacokinetics, Pharmacodynamics, and Efficacy of AMG 510 Monotherapy in Subjects With Advanced Solid Tumors With *KRAS p.G12C* Mutation and AMG 510 Combination Therapy in Subjects With Advanced NSCLC With *KRAS p.G12C* Mutation (CodeBreak 100)	Amgen	2018/8/27－実施中 Cutoff：2020/7/6	国内／海外	評価	無
5.3.5.2-2.1	Study 20170543 Phase-2 Portion primary analysis- A Phase 1/2, Open-label Study Evaluating the Safety, Tolerability, Pharmacokinetics, Pharmacodynamics, and Efficacy of AMG 510 Monotherapy in Subjects With Advanced Solid Tumors With *KRAS p.G12C* Mutation and AMG 510 Combination Therapy in Subjects With Advanced NSCLC With *KRAS p.G12C* Mutation (CodeBreak 100)	Amgen	2019/8[redacted]－実施中 Cutoff:2020/9/1	国内／海外	評価	有

5.3.5.2-2.2	Study 20170543 errata - Phase-2 Portion primary analysis- A Phase 1/2, Open-label Study Evaluating the Safety, Tolerability, Pharmacokinetics, Pharmacodynamics, and Efficacy of AMG 510 Monotherapy in Subjects With Advanced Solid Tumors With *KRAS p.G12C* Mutation and AMG 510 Combination Therapy in Subjects With Advanced NSCLC With *KRAS p.G12C* Mutation (CodeBreak 100)	Amgen	2019/8[redacted]－実施中 Cutoff：2020/9/1	国内／海外	評価	無
5.3.5.2-3	Study 20170543 PRO Data - A Phase 1/2, Open-label Study Evaluating the Safety, Tolerability, Pharmacokinetics, Pharmacodynamics, and Efficacy of AMG 510 Monotherapy in Subjects With Advanced Solid Tumors With *KRAS p.G12C* Mutation and AMG 510 Combination Therapy in Subjects With Advanced NSCLC With *KRAS p.G12C* Mutation (CodeBreak 100)	Amgen	2019/8[redacted]－実施中 Cutoff：2020/9/1	国内／海外	評価	無
5.3.5.2-4	Study 20170543 Phase-2 Portion supplemental - A Phase 1/2, Open-label Study Evaluating the Safety, Tolerability, Pharmacokinetics, Pharmacodynamics, and Efficacy of AMG 510 Monotherapy in Subjects With Advanced Solid Tumors With *KRAS p.G12C* Mutation and AMG 510 Combination Therapy in Subjects With Advanced NSCLC With *KRAS p.G12C* Mutation (CodeBreak 100)	Amgen	2019/8[redacted]－実施中 Cutoff：2020/12/1	国内／海外	評価	無

5.3.5.3　複数の試験成績を併せて解析した報告書

資料番号	資料表題	著者	試験実施期間 （年／月／日）	試験実施場所 （国内／海外）	評価・参考	申請電子データ 提出の有無
5.3.5.3-1	Integrated Summary of Safety ISS TFLs Supplemental Statistical Analysis Plan	Amgen	－	－	－	無
5.3.5.3-2	Japan NDA analysis JNDA TFLs Supplemental Statistical Analysis Plan	Amgen	－	－	－	無

5.3.5.4　その他の臨床試験報告書

資料番号	資料表題	著者	試験実施期間 （年／月／日）	試験実施場所 （国内／海外）	評価・参考	申請電子データ 提出の有無
5.3.5.4-1	Observational Research Study 20180277 - A Retrospective Cohort Study of Patient Characteristics and Treatment Outcomes Among Patients With *KRAS p.G12C* Mutation-positive Advanced Non-small Cell Lung Cancer in the AACR Project GENIE Database	Amgen	20[redacted] （Date of report）	海外	参考	無
5.3.5.4-2	Observational Research Study 20190037 - Descriptive Analysis of Patients With *KRAS G12C* Mutant Solid Tumors in the Syapse Database	Amgen	20[redacted] （Date of report）	海外	参考	無
5.3.5.4-3	Observational Research Study 20200097 - A Retrospective Cohort Study of Patient Characteristics and Treatment Outcomes Among Patients With *KRAS p.G12C* Mutation-positive Advanced Non-small Cell Lung Cancer in the Flatiron Health-Foundation Medicine Clinico-Genomics Database	Amgen	20[redacted] （Date of report）	海外	参考	無
5.3.5.4-4	Observational Research Study 20200132 - A Retrospective Cohort Study of Patient Characteristics and Treatment Outcomes Among Patients With Advanced Non-small Cell Lung Cancer in the Flatiron Health-Foundation Medicine Clinico-Genomics Database	Amgen	20[redacted] （Date of report）	海外	参考	無

5.3.5.4-5	Observational Research Study 20190344 - *KRAS* ^{G12C} Mutation in Non-Small Cell Lung Cancer (NSCLC): Epidemiology and Clinical Outcomes: Systematic Literature Review	Amgen	20[redacted] (Date of report)	海外	参考	無
5.3.5.4-6	Observational Research Study 20200090 - Qualitative Interviews in Patients With *KRAS p.G12C* –Mutated Non–Small Cell Lung Cancer	Amgen	20[redacted] (Date of report)	海外	参考	無
5.3.5.4-7.1	Ongoing Study Safety Report: Study 20190135 - A Phase 1b Study Evaluating the Safety, Tolerability, Pharmacokinetics, and Efficacy of AMG 510 (pINN Sotorasib) in Combination With Trametinib in Subjects With Advanced Solid Tumors With *KRAS p.G12C* Mutation (CodeBreak 101 Subprotocol A)	Amgen	2019/12/[redacted] －実施中 Cutoff：2020/9/1	海外	参考	無
5.3.5.4-7.2	Ongoing Study Safety Report: Study 20190135 - A Phase 1b Study Evaluating the Safety, Tolerability, Pharmacokinetics, and Efficacy of AMG 510 (pINN Sotorasib) in Combination With RMC-4630 in Subjects With Advanced Solid Tumors With *KRAS p.G12C* Mutation (CodeBreaK 101 Subprotocol C)	Amgen	20[redacted] －実施中 Cutoff：2020/9/1	海外	参考	無
5.3.5.4-7.3	Ongoing Study Safety Report: Study 20190135 - A Phase 1b Study Evaluating the Safety, Tolerability, Pharmacokinetics, and Efficacy of AMG 510 in Combination With Afatinib in Subjects With Advanced Non-small Cell Lung Cancer (NSCLC) With *KRAS p.G12C* Mutation (CodeBreaK 101 Subprotocol D)	Amgen	20[redacted] －実施中 Cutoff：2020/9/1	海外	参考	無
5.3.5.4-7.4	Ongoing Study Safety Report: Study 20190135 - A Phase 1b Study Evaluating the Safety, Tolerability, Pharmacokinetics, and Efficacy of AMG 510 in Combination With Atezolizumab in Subjects With Advanced Non-small Cell Lung Cancer (NSCLC) With *KRAS p.G12C* Mutation (CodeBreaK 101 Subprotocol E)	Amgen	20[redacted] －実施中 Cutoff：2020/9/1	海外	参考	無
5.3.5.4-7.5	Ongoing Study Safety Report: Study 20190135 - A Phase 1b Study Evaluating the Safety, Tolerability, and Efficacy of AMG 510 in Combination With Panitumumab and in Combination with Panitumumab and FOLFIRI in Subjects With Advanced Solid Tumors With *KRAS p.G12C* Mutation (CodeBreaK 101 Subprotocol H)	Amgen	20[redacted] －実施中 Cutoff：2020/9/1	国内／海外	参考	無
5.3.5.4-8	Ongoing Study Safety Report: Study 20190147 - A Phase 1, Open-label Study Evaluating the Safety, Tolerability, Pharmacokinetics, and Efficacy of AMG 510 in Subjects of Chinese Descent With Advanced/Metastatic Solid Tumors With *KRAS p.G12C* Mutation (CodeBreaK105)	Amgen	2020/4/28－実施中 Cutoff：2020/9/1	海外	参考	無
5.3.5.4-9	Observational Research Study 20190325 - Patient Characteristics and Clinical Outcomes by the Presence of and Variants of *KRAS* Mutation in Japanese Advanced Non-small Cell Lung Cancer (NSCLC) Patients: LC-SCRUM-Japan	Amgen	20[redacted] (Date of report)	国内	参考	無

5.3.7 患者データー覧表及び症例記録

資料番号	資料表題	著者	試験実施期間（年／月／日）	試験実施場所（国内／海外）	評価・参考	申請電子データ提出の有無
5.3.7	患者データー覧表及び症例記録 JNDA Listings	Amgen	－	－	－	無

第5部　臨床試験報告書
5.4　参考文献

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