1 効能又は効果（案）、効能又は効果に関連する注意（案）、及びその設定根拠

1.1 効能又は効果（案）

既存治療で効果不十分な下記疾患

尋常性乾癬、膿疱性乾癬、乾癬性紅皮症

1.2 効能又は効果（案）の設定根拠

本剤の効能又は効果（案）は、局面型皮疹を有する乾癬患者を対象とした国際共同第 3 相比較試験である IM011-046 試験（046 試験）及び海外第 3 相比較試験である IM011-047 試験（047 試験）、並びに局面型皮疹を有する乾癬患者、膿疱性乾癬患者及び乾癬性紅皮症患者を対象とした国内第 3 相オープンラベル試験である IM011-066 試験（066 試験）から得られた結果に基づき設定した。なお、膿疱性乾癬は、汎発型と限局型（掌蹠膿疱症、アロポー稽留性肢端皮膚炎など）に大きく分類されるが、本申請資料において膿疱性乾癬は、汎発型膿疱性乾癬を指す。

第 3 相比較試験の 046 試験及び 047 試験のデザインは類似しており、同一の適格性基準を用いて中等症から重症の局面型皮疹を有する乾癬患者を選定した。いずれの試験もプラセボ及び実薬対照、ランダム化、二重盲検、ダブルダミー試験であり、投与 16 週まではプラセボ対照期間、投与 24 週まではアプレミラスト対照期間とし、試験全体の投与期間は 52 週間であった。また、2 つの主要評価項目である投与 16 週の sPGA（0/1）達成率及び PASI 75 達成率、並びに副次評価項目の多くが 2 試験で共通で、これらの評価項目は乾癬の臨床徴候及び症状を評価するために広く受け入れられている。2 つの第 3 相比較試験で、主要評価項目とした投与 16 週の sPGA（0/1）達成率及び PASI 75 達成率はいずれも、プラセボ群に比べデュークラバシチニブ群で統計学的に有意に高く、臨床的に意味のある改善が示された。また、デュークラバシチニブは、プラセボ及び既承認の経口治療薬で広く用いられているアプレミラストと比較し、皮膚病変に対する複数の評価項目について、統計学的に有意かつ臨床的に意味のある改善を示した。さらに、デュークラバシチニブの効果発現は速やかで、投与 24 週に最大効果が認められ、52 週間の投与期間にわたって効果が持続した（M2.7.3、3.2.1 項参照）。

国内第 3 相オープンラベル試験の 066 試験は、中等症から重症の局面型皮疹を有する乾癬患者、膿疱性乾癬患者又は乾癬性紅皮症患者を対象に、デュークラバシチニブの有効性及び安全性の評価を目的とした、52 週間、多施設共同、単一群、オープンラベル試験であった。主要評価項目とした投与 16 週の sPGA（0/1）達成率及び PASI 75 達成率について、デュークラバシチニブの投与により臨床的に意味のある改善が認められた。また、またその他の評価項目についても、デュークラバシチニブ投与による改善が認められ、これらの改善は投与 52 週まで維持された。膿疱性乾癬患者及び乾癬性紅皮症患者においても、被験者数に限りがあるものの、投与 16 週又は投与 52 週に PASI 75 及び sPGA（0/1）を達成した被験者が認められ、52 週間の投与期間にわたるデュークラバシチニブの改善効果

とその維持が確認された。膿疱性乾癬及び乾癬性紅皮症に対する疾患重症度の評価である GIS 及び JDA 総スコア（膿疱性乾癬のみ）についても、デュークラバシチニブの 52 週間の投与により皮膚及び全身症状、疾患重症度の全般的な改善とその維持が認められた（M2.7.3、3.2.2 項及び 3.3.3 項参照）。

以上より、本剤の効能又は効能（案）を以下のとおり設定し、製造販売承認申請を行った。

○ 局所療法で効果不十分な尋常性乾癬

○ 膿疱性乾癬、乾癬性紅皮症

しかしながら、製造販売承認申請後の審査過程において、医薬品医療機器総合機構の指示を受け、1.1 項のとおり本剤の効能又は効果（案）を設定した。

2 用法及び用量（案）及びその設定根拠

2.1 用法及び用量（案）

通常、成人にはデュークラバシチニブとして 1 回 6mg を 1 日 1 回経口投与する。

2.2 用法及び用量（案）の設定根拠

本剤の用法及び用量（案）は、局面型皮疹を有する乾癬患者を対象とした国際共同第 3 相比較試験である 046 試験及び海外第 3 相比較試験である 047 試験、並びに局面型皮疹を有する乾癬患者、膿疱性乾癬患者及び乾癬性紅皮症患者を対象とした国内第 3 相オープンラベル試験である 066 試験から得られた結果に基づき設定した。

第 3 相比較試験である 046 試験及び 047 試験で、デュークラバシチニブ 6 mg QD の有効性が示され（M2.7.3、3.2.1 項）、また忍容性及び安全性が確認されたことから（M2.7.4、2 項）、中等症から重症の局面型皮疹を有する乾癬患者に対するデュークラバシチニブの推奨用法・用量は 6 mg QD とした。日本を含む国際共同治験である第 2 相試験（011 試験）及び第 3 相比較試験（046 試験）において、日本人集団と全体集団の有効性主要評価項目の結果の一貫性が示され、日本人集団で特有の安全性上の懸念も認められていない（M2.7.3、3.3.2 項及び M2.7.4、5.1 項）。また、PPK 解析の結果から、日本人と外国人における 6 mg QD 投与時のデュークラバシチニブの予測曝露量に大きな違いはなかった（M2.7.2、3.5.1.4 項）。したがって、国際共同試験で構成される臨床データパッケージから得られた結果に基づくデュークラバシチニブの用量設定根拠は、日本人患者にも適用できると考える。

国内第 3 相試験の 066 試験でも同様に、デュークラバシチニブ 6 mg QD は、中等症から重症の局面型皮疹を有する乾癬患者での有効性が確認されたとともに、より重症かつ難治性である膿疱性乾癬

患者及び乾癬性紅皮症患者でも全身及び皮膚症状の改善効果が認められた（M2.7.3、3.2.2 項及び 3.3.3 項）。

これらの第 3 相試験の結果から、全身療法が適応となる中等症から重症の局面型皮疹を有する乾癬患者、膿疱性乾癬患者及び乾癬性紅皮症患者の治療にデュークラバシチニブ 6 mg QD の経口投与が有効であることが確認された。

以下に本承認申請における本剤の推奨用法及び用量の設定根拠を示す。

2.2.1 尋常性乾癬に対する臨床的有効性

プラセボ及び実薬（アプレミラスト）対照の第 3 相比較試験である 046 試験及び 047 試験では、主要評価項目及び主な副次評価項目（各検定グループ内の最終順位の副次評価項目を除く全て）について、デュークラバシチニブはプラセボ又はアプレミラストに比べ統計学的に有意な改善を示した。

いずれの試験でも、sPGA スコアが 3 以上（中等症又は重症）の局面型皮疹を有する乾癬患者において、主要評価項目である投与 16 週の sPGA（0/1）達成率（乾癬病変が無症状又はほぼ無症状）及び PASI 75 達成率は、プラセボと比べてデュークラバシチニブで統計学的に有意に高かった（いずれも $p < 0.0001$）。デュークラバシチニブ群及びプラセボ群の投与 16 週の sPGA（0/1）達成率は、046 試験ではそれぞれ 53.6%及び 7.2%、047 試験ではそれぞれ 49.5%及び 8.6%であり、投与 16 週の PASI 75 達成率は、046 試験でそれぞれ 58.4%及び 12.7%、047 試験で 53.0%及び 9.4%であった。アプレミラストとの比較でも同様に、両試験でのデュークラバシチニブ群の投与 16 週の sPGA（0/1）達成率及び PASI 75 達成率は統計学的に有意に高かった（いずれも $p \leq 0.0004$）。デュークラバシチニブ群及びアプレミラスト群の投与 16 週の sPGA（0/1）達成率は、046 試験でそれぞれ 53.6%及び 32.1%、047 試験でそれぞれ 49.5%及び 33.9%であり、投与 16 週の PASI 75 達成率は、046 試験でそれぞれ 58.4%及び 35.1%、047 試験で 53.0%及び 39.8%であった。全体として、sPGA（0/1）達成率及び PASI 75 達成率は、デュークラバシチニブの投与により投与 24 週まで経時的に増加した。

PASI 75 達成率及び sPGA（0/1）達成率の部分集団解析では、ベースラインの人口統計学的特性、疾患特性又は治療歴（生物学的製剤又は非生物学的製剤による全身療法を含む）にかかわらず、部分集団間で一貫してプラセボ群及びアプレミラスト群と比べてデュークラバシチニブ群で改善効果が認められた。

デュークラバシチニブはまた、疾患活動性に関する他の指標においても改善効果を示し、PASI 90 達成率、PASI 100 達成率及び sPGA（0）達成率により皮膚病変の改善及び消失を示し、乾癬の頭皮、爪及び掌蹠病変といった治療困難な部位でも改善をもたらした。また、これらの皮膚病変に対するベネフィットは、PSSD の改善及び DLQI、SF-36 PCS、EQ-5D-3L VAS などの他の患者報告アウトカム指標も改善させた。

2 つの第 3 相比較試験では、デュークラバシチニブを投与 52 週まで継続した被験者において、治療効果の維持が示された。両試験とも、投与 24 週に PASI 75 を達成し投与 24 週以降もデュークラバシ

チニブを継続投与した被験者のほとんど（80%～81%）が投与 52 週にも PASI 75 を達成した。国内第 3 相オープンラベル試験においても、デュークラバシチニブの 52 週間投与による治療効果の維持が確認された。この治療効果は、長期継続試験（075 試験）でデュークラバシチニブ 6 mg QD を更に 60 週間継続投与した被験者で維持されていた。

047 試験では、投与 24 週の PASI 75 を達成しデュークラバシチニブからプラセボに再ランダム化された被験者（投与中止群）のうち、投与 52 週までの間に PASI 75 反応が消失した被験者の割合は 78.7%であったが、残りの約 21%は投与 52 週まで PASI 75 を維持した。デュークラバシチニブの投与中止による PASI 75 反応が消失するまでの期間の中央値は約 12 週間であった。

第 3 相比較試験でプラセボ又はアプレミラストにランダム化され、投与 16 週又は投与 24 週にデュークラバシチニブに切り替えた被験者、又は 075 試験に移行しデュークラバシチニブに切り替えられた被験者は、最初にデュークラバシチニブにランダム化された被験者と同様に乾癬の改善が認められた。

デュークラバシチニブ 6 mg QD の安全性は、第 3 相比較試験の 046 試験及び 047 試験の統合解析である Controlled Safety Pool で評価し、デュークラバシチニブを 1 回以上投与された被験者 1364 例（うち 503 例は 52 週間以上投与された）が含まれた。Controlled Safety Pool の投与 16 週までの有害事象の発現割合は、デュークラバシチニブ群では 55.7%であり、プラセボ群（49.6%）と比べてやや高かったものの、既承認の経口治療薬であるアプレミラスト群（57.6%）と同程度であった。また、デュークラバシチニブの重篤な有害事象の発現割合は 1.8%と低く、プラセボ群（2.9%）及びアプレミラスト群（1.2%）と同程度であった。さらに、デュークラバシチニブの作用機序及び既承認の乾癬治療薬でのリスクに基づき、感染症、皮膚関連事象、悪性腫瘍、MACE、血栓塞栓症、自殺傾向等を評価した。これらの事象のデュークラバシチニブの発現割合は低く、皮膚関連事象及び感染症を除きプラセボ及びアプレミラストと同程度であった。また、デュークラバシチニブの長期投与により、これらの事象の発現割合が上昇する傾向は認められなかった。以上のことから、中等症から重症の尋常性乾癬患者でのデュークラバシチニブの許容可能な忍容性及び安全性が確認された。また、第 3 相試験 046 試験、047 試験及び 075 試験の統合解析である Phase 3 Safety Pool においても、最大 1519 例（うち 1068 例は 52 週間以上継続して投与された）でのデュークラバシチニブの長期安全性が確認され、Controlled Safety Pool の結果を裏付けるものであった（M2.7.4、2 項）。

2.2.2 薬物動態及び曝露-反応解析

デュークラバシチニブは迅速かつほぼ完全に吸収され、曝露量は用量依存的に増加し、時間依存的な PK の変化は認められなかった。また、デュークラバシチニブを錠剤として投与したときの PK は、3～36 mg の範囲で線形であり、申請用量の 6 mg QD はこの中に含まれる。日本人での PK パラメータについても、第 1 相試験（002 試験）で得られた日本人での曝露量は外国人と同様の用量比例性を示し（M2.7.2、2.2.1.4 項）、第 2 相試験（011 試験）及び 046 試験で得られたデュークラバシチニブの Ctrough の実測値に日本人集団と外国人集団又は全体集団とで差異は認められなかった（M2.7.2、

3.5.1.4 項）。さらに、011 試験及び第 3 相比較試験（046 試験及び 047 試験）を含むデュークラバシチニブの PPK 解析では、いずれの PK パラメータにおいても人種は有意な共変量ではないことが確認された。

011 試験及び第 3 相比較試験を用いた E-R 解析を実施し、乾癬患者におけるデュークラバシチニブの曝露量と有効性評価項目の sPGA（0/1）達成率及び PASI 75 達成率との関係を明らかにした。E-R 解析の結果、sPGA（0/1）達成率及び PASI 75 達成率は曝露量に依存して増加し、デュークラバシチニブの Cavgss は曝露量の指標として、sPGA モデル及び PASI モデルのいずれにおいても有効性の最良の予測因子であることが示された。デュークラバシチニブ 6 mg QD 投与による投与 16 週及び投与 24 週の PASI 75 達成率及び sPGA（0/1）達成率の予測値は、最大達成率に近い値を示した（M2.7.2、3.6.2.1 項）。

さらにモデル予測を用いて、デュークラバシチニブ 6 mg QD 投与時の PASI 75 達成率及び sPGA（0/1）達成率を共変量ごとに評価した。共変量として、PASI 75 達成率については体重、年齢、性別、ベースラインの PASI スコア及び生物学的製剤の使用の有無、sPGA（0/1）達成率については体重及び地域を評価した。デュークラバシチニブ 6 mg QD 投与時の PASI 75 達成率及び sPGA（0/1）達成率の予測値は、評価した共変量内のいずれの部分集団においても、最大達成率に近い値であった。したがって、デュークラバシチニブの 6 mg QD を上回る用量を投与し曝露量を増加しても、有効性の更なる増加は期待できないと考える（M2.7.2、3.6.2.1 項）。

安全性に関する E-R 解析の結果から、デュークラバシチニブの曝露量と安全性事象（重篤な感染症、帯状疱疹感染、MACE、Extended MACE、悪性腫瘍又はグレード 3 以上の CPK 上昇の発現）との間に明らかな E-R 関係は認められなかった。感染症および寄生虫症全体でなだらかな E-R 関係の傾向が認められたが、これは臨床的に意味のあるものではないと考えられた（M2.7.2、3.6.2.2 項）。

以上の臨床試験における安全性及び有効性データとともに薬物動態及び E-R 解析結果から、尋常性乾癬に対するデュークラバシチニブの推奨用法・用量は 6 mg QD であることが示唆される。なお、重度肝機能障害被験者のデュークラバシチニブの非結合形曝露量［AUC(INF)］は、肝機能正常被験者と比較して高い（131%）ことが示されており、重度肝機能障害患者へのデュークラバシチニブの投与は推奨されない。重度肝機能障害を除き、デュークラバシチニブの内因性要因及び外因性要因による用量調節は不要である（M2.7.2、3.7 項）。

2.2.3 膿疱性乾癬及び乾癬性紅皮症

国内第 3 相オープンラベル試験（066 試験）で膿疱性乾癬及び乾癬性紅皮症に対するデュークラバシチニブ 6 mg QD の有効性を評価し、いずれの疾患に対しても、デュークラバシチニブの 52 週間の投与により、GIS での評価による皮膚症状の改善が確認された。膿疱性乾癬に対する有効性として JDA 総スコアも評価し、52 週間の投与期間中に改善が認められた。また、膿疱性乾癬患者及び乾癬性紅

皮症患者での PASI 75 達成率及び sPGA（0/1）達成率においても、デュークラバシチニブによる改善効果が確認された。

膿疱性乾癬患者及び乾癬性紅皮症患者での安全性に関しても、尋常性乾癬患者と同様にデュークラバシチニブ 6 mg QD の安全性及び忍容性が確認され、これらの患者に特異的な安全性上の懸念は認められなかった。

検討した被験者数に限りがあるものの、膿疱性乾癬及び乾癬性紅皮症といった疾患活動性の高い病型においても、デュークラバシチニブ 6 mg QD の有効性及び安全性が確認された。

2.2.4 結論

第 3 相比較試験では、乾癬の皮膚病変の改善に関する客観的指標である複数の有効性評価項目及び患者報告アウトカムにおいて、プラセボ及び既承認の経口治療薬であるアプレミラストと比較して、デュークラバシチニブ 6 mg QD の優越性が示された。また、デュークラバシチニブ 6 mg QD は、第 2 相 011 試験データを用いた E-R 解析により最大効果に達すると予測され、その予測は第 3 相比較試験の結果で支持された。有効性及び安全性に関する E-R 解析の結果は、日本人及び外国人を含む第 3 相比較試験から得られたデュークラバシチニブ 6 mg QD の有効性及び安全性の結果を裏付けるものである。国内第 3 相オープンラベル試験でも、デュークラバシチニブ 6 mg QD による乾癬病変の改善効果が認められ、膿疱性乾癬患者及び乾癬性紅皮症患者での有効性及び安全性も確認された。

以上のデータから、中等症から重症の尋常性乾癬、膿疱性乾癬及び乾癬性紅皮症の治療薬として、デュークラバシチニブ 6 mg QD の用法・用量が推奨される。

1. 使用上の注意（案）及びその設定根拠

使用上の注意（案）	設定根拠
1. 警告 1.1 本剤は結核等の感染症を含む緊急時に十分に対応できる医療施設、あるいは当該医療施設との連携下において、本剤についての十分な知識と適応疾患の治療に十分な知識・経験をもつ医師のもとで、本剤による治療の有益性が危険性を上回ると判断される症例のみに使用すること。本剤は感染症のリスクを増大させる可能性があり、また結核の既往歴を有する患者では結核を活動化させる可能性がある。また、本剤との関連性は明らかではないが、悪性腫瘍の発現が報告されている。治療開始に先立ち、本剤が疾病を完治させる薬剤でないことも含め、本剤の有効性及び危険性を患者に十分説明し、患者が理解したことを確認した上で治療を開始すること。[2.1、2.2、8.1、8.2、8.6、9.1.1、9.1.2、11.1.1、15.1.2 参照] 1.2 重篤な感染症 ウイルス、細菌等による重篤な感染症が報告されているため、十分な観察を行うなど感染症の発症に注意し、本剤投与後に感染症の徴候又は症状があらわれた場合には、直ちに担当医に連絡するよう患者を指導すること。[2.1、8.1、9.1.1、11.1.1 参照] 1.3 本剤の治療を開始する前に、光線療法を含む既存の全身療法（生物製剤を除く）の適用を十分に勘案すること。[5. 参照]	1.1-1.2 既承認の乾癬治療薬の添付文書を参考に設定した。 1.3 本剤の効能又は効果を「既存治療で効果不十分な下記疾患　尋常性乾癬、膿疱性乾癬、乾癬性紅皮症」としたことから設定した。
2. 禁忌（次の患者には投与しないこと） 2.1 重篤な感染症の患者［症状を悪化させるおそれがある］[1.1、1.2、8.1、9.1.1、11.1.1 参照] 2.2 活動性結核の患者［症状を悪化させるおそれがある］[1.1、8.2、9.1.1、9.1.2 参照] 2.3 本剤の成分に対し過敏症の既往歴のある患者	2.1 重篤な感染症の患者では症状を悪化させるおそれがあることから設定した。 2.2 活動性結核の患者では症状を悪化させるおそれがあることから設定した。 2.3 一般的な注意事項として、本剤の成分に対する過敏症の既往歴のある患者を禁忌として設定した。
5. 効能又は効果に関連する注意 以下のいずれかを満たす尋常性乾癬、膿疱性乾癬又は乾癬性紅皮症の患者に投与すること。[1.3 参照] ・ 光線療法を含む既存の全身療法（生物製剤を除く）等で十分な効果が得られず、皮疹が体表面積の 10%以上に及ぶ患者 ・ 難治性の皮疹又は膿疱を有する患者	本剤の臨床試験における患者選択基準等を考慮して、既承認の乾癬治療薬の添付文書を参考に設定した。
7. 用法及び用量に関連する注意 7.1 本剤による治療反応は、通常投与開始から 24 週以内に得られる。24 週以内に治療反応が得られない場合は本剤の治療計画の継続を慎重に判断すること。	7.1 本剤の治療効果が得られる投与期間の目安として設定した。 7.2 適応疾患の生物製剤と併用した場合の安全性及び有効性に関する

使用上の注意（案）	設定根拠
7.2　本剤と適応疾患の生物製剤との併用について安全性及び有効性は確立していないので併用を避けること。	データは得られていないことから設定した。
8.　重要な基本的注意 8.1　本剤は、感染のリスクを増大させる可能性があるので、本剤の投与に際しては、十分な観察を行い、感染症の発症や増悪に注意すること。感染症の徴候又は症状があらわれた場合には、速やかに担当医に連絡するよう患者を指導すること。［1.1、1.2、2.1、9.1.1、11.1.1 参照］ 8.2　本剤投与に先立って結核に関する十分な問診及び胸部 X 線検査に加えてインターフェロンγ遊離試験又はツベルクリン反応検査を行い、適宜胸部 CT 検査等を行うことにより、結核感染の有無を確認すること。また、本剤投与中も、胸部 X 線検査等の適切な検査を定期的に行うなど結核の発現には十分に注意し、結核を疑う症状（持続する咳、体重減少、発熱等）が発現した場合には速やかに担当医に連絡するよう患者を指導すること。なお、結核の活動性が確認された場合は結核の治療を優先し、本剤を投与しないこと。［1.1、2.2、9.1.2 参照］ 8.3　帯状疱疹等のウイルスの再活性化が報告されていることから、ヘルペスウイルス等の再活性化の徴候や症状の発現が認められた場合には、患者に受診するよう説明し、本剤の投与を中断し速やかに適切な処置を行うこと。また、ヘルペスウイルス以外のウイルスの再活性化にも注意すること。 8.4　本剤投与による B 型肝炎ウイルスの再活性化のおそれがあるので、投与に先立って B 型肝炎ウイルス感染の有無を確認すること。［9.1.3 参照］ 8.5　本剤投与中は生ワクチン接種による感染症発現のリスクを否定できないため、生ワクチン接種を行わないこと。 8.6　臨床試験において皮膚及び皮膚以外の悪性腫瘍の発現が報告されている。本剤との因果関係は明確ではないが、悪性腫瘍の発現には注意すること。［1.1、15.1.2 参照］	8.1 本剤は感染のリスクを増大させる可能性があることから設定した。 8.2 本剤の臨床試験における患者選択基準等を踏まえ、本剤開始前に結核感染の有無を確認する必要があることから設定した。 8.3-8.4 既承認の乾癬治療薬の添付文書を参考に設定した。 8.5 本剤の作用機序及び臨床試験における患者選択基準等を考慮して、本剤投与に際してのワクチン接種に関する注意喚起を設定した。 8.6 本剤との因果関係は明確ではないが、臨床試験において悪性腫瘍の発現が報告されていることから設定した。
9.　特定の背景を有する患者に関する注意 9.1　合併症・既往歴等のある患者 9.1.1　感染症（重篤な感染症又は活動性結核を除く）の患者、感染症が疑われる患者又は再発性感染症の既往歴のある患者 感染症を悪化又は顕在化させるおそれがある。［1.1、1.2、2.1、2.2、8.1、11.1.1 参照］ 9.1.2　結核の既往歴を有する患者又は結核感染が疑われる患者［1.1、2.2、8.2 参照］ (1) 結核の既往歴を有する患者では、結核を活動化させるおそれがある。 (2) 結核の既往歴を有する場合又は結核感染が疑われる場合には、結核の診療経験がある医師に相談すること。下記のいずれかの患者には、原則として本剤の投与開始前に適切な抗結核薬を投与すること。	9.1.1 本剤は、感染のリスクを増大させる可能性を否定できないことから設定した。 9.1.2 結核の既往歴のある患者では、結核を活動化させるおそれがあるため、本剤投与開始前に適切な抗結核薬の投与を考慮する必要があることから設定した。 9.1.3 既承認の乾癬治療薬の添付文書を参考に設定した。

使用上の注意（案）	設定根拠
・　胸部画像検査で陳旧性結核に合致するか推定される陰影を有する患者 ・　結核の治療歴（肺外結核を含む）を有する患者 ・　インターフェロンγ遊離試験やツベルクリン反応検査等の検査により、既感染が強く疑われる患者 ・　結核患者との濃厚接触歴を有する患者 9.1.3　B 型肝炎ウイルスキャリアの患者又は既往感染者（HBs 抗原陰性、かつ HBc 抗体又は HBs 抗体陽性） 肝機能検査値や HBV DNA のモニタリングを行うなど、B 型肝炎ウイルスの再活性化の徴候や症状の発現に注意すること。［8.4 参照］	
9.3　肝機能障害患者 9.3.1　重度の肝機能障害（Child-Pugh 分類 C）のある患者 可能な限り投与を避けること。やむを得ず投与する場合には、患者の状態をより慎重に観察し、副作用の発現に十分注意すること。本剤非結合形の血中濃度が上昇し、副作用が強くあらわれるおそれがある。［16.6.2 参照］	重度の肝機能障害（Child-Pugh 分類 C）のある患者では、デュークラバシチニブの非結合形 AUC(INF)の 2 倍以上の増加が認められたことから設定した。
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。ラットで単回投与後にデュークラバシチニブ又はその代謝物は母動物の胎盤及び羊膜嚢に移行したが、胎児では検出されなかった。胚・胎児発生に関する試験において、AUC 比較で臨床曝露量の約 266 倍（ラット）及び約 20 倍（遊離血清中濃度、ウサギ）に相当する最高投与量まで、胚致死作用及び催奇形性は認められていない。 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。動物実験（ラット）において、デュークラバシチニブ又はその代謝物が乳汁中へ移行することが認められている（乳汁中濃度/血漿中濃度比：2.7～30.9）。動物実験（ラット）における妊娠及び哺育期間中の投与により、AUC 比較で臨床曝露量の約 110 倍に相当する投与量で、離乳前の期間に出生児の一過性の体重減少が認められている。	妊婦及び授乳婦に対する本剤の安全性は確立されていないため、本剤の CCDS 及び非臨床試験成績に基づき設定した。
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。
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 重篤な感染症（0.2%） ウイルス、細菌等による重篤な感染症があらわれることがある。本剤投与中に重篤な感染症を発現した場合は、感染症が消	本剤の CCDS を参考に設定した。副作用の発現頻度は、国際共同第 III相臨床試験（IM011-046 試験）、海外第III相臨床試験（IM011-047 試験）及び国内第III相臨床試験（IM011-066 試験）を統合した結果に基づき記載した。

<table>
<tr><th>使用上の注意（案）</th><th>設定根拠</th></tr>
<tr><td>失するまで本剤の投与を中止すること。［1.1、1.2、2.1、8.1、9.1.1 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>感染症及び寄生虫症</td><td>上気道感染</td><td>単純ヘルペス</td><td>帯状疱疹</td></tr>
<tr><td>胃腸障害</td><td></td><td>口腔潰瘍</td><td></td></tr>
<tr><td>皮膚及び皮下組織障害</td><td></td><td>ざ瘡様皮疹</td><td>毛包炎</td></tr>
<tr><td>臨床検査</td><td></td><td>血中 CK 増加</td><td></td></tr>
</table></td><td></td></tr>
<tr><td>13.　過量投与
13.1　処置
循環血液中のデュークラバシチニブは透析によりほとんど除去されない。［16.6.1 参照］</td><td>血液透析中の末期腎不全の被験者で、透析液中に回収されたデュークラバシチニブは投与量の 5.4%であったことから設定した。</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 シート包装に関する注意事項を設定した。</td></tr>
<tr><td>15.　その他の注意
15.1　臨床使用に基づく情報
15.1.1 免疫抑制剤又は光線療法と併用した場合の安全性及び有効性は確立していない。
15.1.2 国際共同第Ⅲ相臨床試験（IM011-046 試験）と海外第Ⅲ相臨床試験（IM011-047 試験）の統合解析において投与 0～52 週に本剤投与群（969 人・年）でリンパ腫 1 例を含む悪性腫瘍（非黒色腫皮膚癌を除く）が 0.2%（0.3/100 人・年）に報告された。この発現率は、一般的な乾癬患者やレジストリで報告されている悪性腫瘍（非黒色腫皮膚癌を除く）の発現率（0.4～2.3/100 人・年）と同程度であった。悪性腫瘍の発現における本剤との関連性は明らかではない。［1.1、8.6 参照］</td><td>15.1.1 免疫抑制剤又は光線療法と併用した場合の安全性及び有効性は確立していないため設定した。
15.1.2 悪性腫瘍の発現における本剤との関連性は明らかではないが、本剤の CCDS を参考に本剤の悪性腫瘍（非黒色腫皮膚癌を除く）の発現状況を記載した。</td></tr>
</table>

20XX 年 X 月作成（第 1 版）

***添付文書（案）は審査段階のものであり、最新の添付文書を参照すること。**

日本標準商品分類番号
8 7 3 9 9 9

貯法： 室温保存

有効期間： 36 箇月

承認番号	
販売開始	

劇薬、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

TYK2 阻害剤

デュークラバシチニブ錠

ソーティクツ錠 6mg

Sotyktu tablets

1. 警告

1.1 本剤は結核等の感染症を含む緊急時に十分に対応できる医療施設、あるいは当該医療施設との連携下において、本剤についての十分な知識と適応疾患の治療に十分な知識・経験をもつ医師のもとで、本剤による治療の有益性が危険性を上回ると判断される症例のみに使用すること。本剤は感染症のリスクを増大させる可能性があり、また結核の既往歴を有する患者では結核を活動化させる可能性がある。また、本剤との関連性は明らかではないが、悪性腫瘍の発現が報告されている。治療開始に先立ち、本剤が疾病を完治させる薬剤でないことも含め、本剤の有効性及び危険性を患者に十分説明し、患者が理解したことを確認した上で治療を開始すること。[2.1、2.2、8.1、8.2、8.6、9.1.1、9.1.2、11.1.1、15.1.2 参照]

1.2 重篤な感染症

ウイルス、細菌等による重篤な感染症が報告されているため、十分な観察を行うなど感染症の発症に注意し、本剤投与後に感染症の徴候又は症状があらわれた場合には、直ちに担当医に連絡するよう患者を指導すること。[2.1、8.1、9.1.1、11.1.1 参照]

1.3 本剤の治療を開始する前に、光線療法を含む既存の全身療法（生物製剤を除く）の適用を十分に勘案すること。[5. 参照]

2. 禁忌（次の患者には投与しないこと）

2.1 重篤な感染症の患者［症状を悪化させるおそれがある］[1.1、1.2、8.1、9.1.1、11.1.1 参照]

2.2 活動性結核の患者［症状を悪化させるおそれがある］[1.1、8.2、9.1.1、9.1.2 参照]

2.3 本剤の成分に対し過敏症の既往歴のある患者

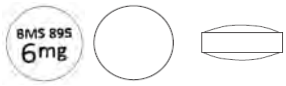
3. 組成・性状

3.1 組成

販売名	ソーティクツ錠 6mg
有効成分	1 錠中 デュークラバシチニブ 6mg
添加剤	ヒプロメロース酢酸エステルコハク酸エステル、無水乳糖、結晶セルロース、クロスカルメロースナトリウム、含水二酸化ケイ素、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、三二酸化鉄、黄色三二酸化鉄

3.2 製剤の性状

販売名	ソーティクツ錠 6mg
性状	薄い黄赤色の円形のフィルムコーティング錠
識別コード	BMS 895

外観	
直径	約 8.1 mm
厚さ	約 4.1 mm
重さ	約 206mg

4. 効能又は効果

既存治療で効果不十分な下記疾患
尋常性乾癬、膿疱性乾癬、乾癬性紅皮症

5. 効能又は効果に関連する注意

以下のいずれかを満たす尋常性乾癬、膿疱性乾癬又は乾癬性紅皮症の患者に投与すること。［1.3 参照］

- 光線療法を含む既存の全身療法（生物製剤を除く）等で十分な効果が得られず、皮疹が体表面積の 10%以上に及ぶ患者
- 難治性の皮疹又は膿疱を有する患者

6. 用法及び用量

通常、成人にはデュークラバシチニブとして 1 回 6mg を 1 日 1 回経口投与する。

7. 用法及び用量に関連する注意

7.1 本剤による治療反応は、通常投与開始から 24 週以内に得られる。24 週以内に治療反応が得られない場合は本剤の治療計画の継続を慎重に判断すること。

7.2 本剤と適応疾患の生物製剤との併用について安全性及び有効性は確立していないので併用を避けること。

8. 重要な基本的注意

8.1 本剤は、感染のリスクを増大させる可能性があるので、本剤の投与に際しては、十分な観察を行い、感染症の発症や増悪に注意すること。感染症の徴候又は症状があらわれた場合には、速やかに担当医に連絡するよう患者を指導すること。［1.1、1.2、2.1、9.1.1、11.1.1 参照］

8.2 本剤投与に先立って結核に関する十分な問診及び胸部 X 線検査に加えてインターフェロンγ 遊離試験又はツベルクリン反応検査を行い、適宜胸部 CT 検査等を行うことにより、結核感染の有無を確認すること。また、本剤投与中も、胸部 X 線検査等の適切な検査を定期的に行うなど結核の発現には十分に注意し、結核を疑う症状（持続する咳、体重減少、発熱等）が発現した場合には速やかに担当医に連絡するよう患者を指導すること。なお、結核の活動性が確認された場合は結核の治療を優先し、本剤を投与しないこと。［1.1、2.2、9.1.2 参照］

8.3 帯状疱疹等のウイルスの再活性化が報告されていることから、ヘルペスウイルス等の再活性化の徴候や症状の発現が認められた場合には、患者に受診するよう説明し、本剤の投与を中断し速やかに適切な処置を行うこと。

また、ヘルペスウイルス以外のウイルスの再活性化にも注意すること。

8.4　本剤投与によるB型肝炎ウイルスの再活性化のおそれがあるので、投与に先立ってB型肝炎ウイルス感染の有無を確認すること。［9.1.3参照］

8.5　本剤投与中は生ワクチン接種による感染症発現のリスクを否定できないため、生ワクチン接種を行わないこと。

8.6　臨床試験において皮膚及び皮膚以外の悪性腫瘍の発現が報告されている。本剤との因果関係は明確ではないが、悪性腫瘍の発現には注意すること。［1.1、15.1.2参照］

9.　特定の背景を有する患者に関する注意

9.1　合併症・既往歴等のある患者

9.1.1　感染症（重篤な感染症又は活動性結核を除く）の患者、感染症が疑われる患者又は再発性感染症の既往歴のある患者

感染症を悪化又は顕在化させるおそれがある。［1.1、1.2、2.1、2.2、8.1、11.1.1参照］

9.1.2　結核の既往歴を有する患者又は結核感染が疑われる患者［1.1、2.2、8.2参照］

(1) 結核の既往歴を有する患者では、結核を活動化させるおそれがある。

(2) 結核の既往歴を有する場合又は結核感染が疑われる場合には、結核の診療経験がある医師に相談すること。下記のいずれかの患者には、原則として本剤の投与開始前に適切な抗結核薬を投与すること。

- 胸部画像検査で陳旧性結核に合致するか推定される陰影を有する患者
- 結核の治療歴（肺外結核を含む）を有する患者
- インターフェロンγ遊離試験やツベルクリン反応検査等の検査により、既感染が強く疑われる患者
- 結核患者との濃厚接触歴を有する患者

9.1.3　B型肝炎ウイルスキャリアの患者又は既往感染者（HBs抗原陰性、かつHBc抗体又はHBs抗体陽性）

肝機能検査値やHBV DNAのモニタリングを行うなど、B型肝炎ウイルスの再活性化の徴候や症状の発現に注意すること。［8.4参照］

9.3　肝機能障害患者

9.3.1　重度の肝機能障害（Child-Pugh分類C）のある患者

可能な限り投与を避けること。やむを得ず投与する場合には、患者の状態をより慎重に観察し、副作用の発現に十分注意すること。本剤非結合形の血中濃度が上昇し、副作用が強くあらわれるおそれがある。［16.6.2参照］

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。ラットで単回投与後にデュークラバシチニブ又はその代謝物は母動物の胎盤及び羊膜嚢に移行したが、胎児では検出されなかった。胚・胎児発生に関する試験において、AUC比較で臨床曝露量の約266倍（ラット）及び約20倍（遊離血清中濃度、ウサギ）に相当する最高投与量まで、胚致死作用及び催奇形性は認められていない。

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。動物実験（ラット）において、デュークラバシチニブ又はその代謝物が乳汁中へ移行することが認められている（乳汁中濃度/血漿中濃度比：2.7～30.9）[1]。動物実験（ラット）における妊娠及び哺育期間中の投与により、AUC比較で臨床曝露量の約110倍に相当する投与量で、離乳前の期間に出生児の一過性の体重減少が認められている。

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。

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　重篤な感染症（0.2%）

ウイルス、細菌等による重篤な感染症があらわれることがある。本剤投与中に重篤な感染症を発現した場合は、感染症が消失するまで本剤の投与を中止すること。［1.1、1.2、2.1、8.1、9.1.1参照］

11.2　その他の副作用

	5%以上	1～5%未満	1%未満
感染症及び寄生虫症	上気道感染	単純ヘルペス	帯状疱疹
胃腸障害		口腔潰瘍	
皮膚及び皮下組織障害		ざ瘡様皮疹	毛包炎
臨床検査		血中CK増加	

13.　過量投与

13.1　処置

循環血液中のデュークラバシチニブは透析によりほとんど除去されない。［16.6.1参照］

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。

15.　その他の注意

15.1　臨床使用に基づく情報

15.1.1　免疫抑制剤又は光線療法と併用した場合の安全性及び有効性は確立していない。

15.1.2　国際共同第Ⅲ相臨床試験（IM011-046試験）と海外第Ⅲ相臨床試験（IM011-047試験）の統合解析において投与0～52週に本剤投与群（969人・年）でリンパ腫1例を含む悪性腫瘍（非黒色腫皮膚癌を除く）が0.2%（0.3/100人・年）に報告された。この発現率は、一般的な乾癬患者やレジストリで報告されている悪性腫瘍（非黒色腫皮膚癌を除く）の発現率（0.4～2.3/100人・年）と同程度であった[2),3)]。悪性腫瘍の発現における本剤との関連性は明らかではない。［1.1、8.6参照］

16.　薬物動態

16.1　血中濃度

16.1.1　単回投与

健康被験者（18例）に本剤6mgを空腹時単回投与したときの、デュークラバシチニブの薬物動態パラメータは下表のとおりであった[4)]（外国人データ）。

本剤を単回投与した時のデュークラバシチニブの薬物動態パラメータ

Cmax(ng/mL) N=18	Tmax(h) N=18	AUC(INF) (ng・h/mL) N=18	$t_{1/2}$ (h) N=18
36.5 (23)	3.00 (1.00, 4.05)	372 (30)	9.88 (1.42)

Tmax の値は中央値（範囲）、$t_{1/2}$の値は算術平均（標準偏差）を示す。Cmax 及び AUC(INF)の値は、幾何平均値［変動係数（CV%）］を示す。

16.1.2 反復投与

中等症から重症の乾癬を有する日本人患者（8 例）に本剤 6mg を 1 日 1 回反復投与したときの、定常状態におけるデュークラバシチニブの薬物動態パラメータは下表のとおりであった[5]。

本剤を反復投与した時の定常状態におけるデュークラバシチニブの薬物動態パラメータ

Cmax(ng/mL) N=8	Tmax(h) N=8	AUC(TAU) (ng･h/mL) N=7
59.0 (27)	1.79 (0.88, 2.37)	556 (34)

Tmax の値は中央値（範囲）を示す。Tmax 以外の値は、幾何平均値［変動係数（CV%）］を示す。

16.2 吸収

16.2.1 バイオアベイラビリティ

健康被験者（8 例）に本剤 12mg を単回経口投与[注)] したときのデュークラバシチニブの絶対的バイオアベイラビリティは 99%であった[6]（外国人データ）。

16.2.2 食事の影響

健康被験者（18 例）に本剤 6mg を高脂肪・高カロリー食摂取後に単回経口投与したとき、空腹時と比較して Cmax は 24%減少し、AUC(0-T)及び AUC(INF)は空腹時に投与した場合と同程度であった[4]（外国人データ）。

16.3 分布

健康成人被験者に静脈内投与後の定常状態における分布容積は 140L[6]であり、総体液量 42L[7]よりも大きいことから、血管外分布が示唆される。デュークラバシチニブのヒト血漿蛋白結合率は 81.6%であった[8]。デュークラバシチニブの血液/血漿中濃度比は 1.26 であった[9]。

16.4 代謝

デュークラバシチニブは、生体内でチトクローム P450（CYP）1A2、カルボキシエステラーゼ（CES）2、ウリジン 5'-二リン酸グルクロン酸転移酵素（UGT）1A9 並びに CYP2B6 及び CYP2D6 による代謝を受け、それぞれ BMT-153261（N-脱メチル化体）、加水分解物、グルクロン酸抱合体及び一酸化物が生成される[10),11)]。
健康成人被験者（6 例）に空腹時に ^{14}C-デュークラバシチニブ 24mg を単回経口投与[注)] したとき、投与 24 時間後までの血漿中放射能におけるデュークラバシチニブ及び活性代謝物である BMT-153261 の割合はそれぞれ 43%及び 11%であった[12]（外国人データ）。

16.5 排泄

健康成人被験者に ^{14}C-デュークラバシチニブを単回経口投与したとき、投与放射能の 13%がデュークラバシチニブとして、37%が代謝物として尿中に排泄されることが示された。また、投与放射能の 26%がデュークラバシチニブとして、22%が代謝物として糞中に排泄された[12]（外国人データ）。

16.6 特定の背景を有する患者

16.6.1 腎機能障害患者

軽度、中等度、重度の腎機能障害被験者及び血液透析中の末期腎不全（ESRD）の被験者並びに腎機能正常被験者に本剤 12mg を単回経口投与[注)] したとき、デュークラバシチニブ及び BMT-153261 並びに活性成分（デュークラバシチニブ及び BMT-153261 のモル濃度の合計として算出、以下同様）の薬物動態に及ぼす影響は下表のとおりであった。ESRD の被験者に本剤 12mg を単回経口投与[注)] したとき、透析液中に回収されたデュークラバシチニブは投与量の 5.4%であった[13]（外国人データ）。［13.1 参照］

腎機能障害の程度がデュークラバシチニブ及び BMT-153261 並びに活性成分の薬物動態に及ぼす影響

腎機能障害の程度	測定対象	幾何平均比（90%信頼区間） 腎機能障害被験者/腎機能正常被験者	
		Cmax	AUC(INF)
軽度腎機能障害被験者（eGFR：≥60 ～ <90 mL/min/1.73 m^2）	デュークラバシチニブ	0.86 (0.72, 1.03)	1.03 (0.76, 1.38)
	BMT-153261	0.89 (0.63, 1.26)	0.98 (0.70, 1.37)
	活性成分	0.86 (0.72, 1.02)	1.02 (0.77, 1.34)
中等度腎機能障害被験者（eGFR：≥30 ～ <60 mL/min/1.73 m^2）	デュークラバシチニブ	1.06 (0.89, 1.27)	1.39 (1.03, 1.88)
	BMT-153261	0.92 (0.65, 1.31)	1.24 (0.89, 1.74)
	活性成分	1.05 (0.88, 1.24)	1.36 (1.03, 1.79)
重度腎機能障害被験者（eGFR：<30 mL/min/1.73 m^2）	デュークラバシチニブ	1.00 (0.84, 1.19)	1.28 (0.95, 1.72)
	BMT-153261	1.28 (0.91, 1.82)	1.81 (1.29, 2.52)
	活性成分	1.00 (0.84, 1.19)	1.39 (1.05, 1.83)
ESRD	デュークラバシチニブ	1.00 (0.84, 1.18)	1.34 (0.99, 1.80)
	BMT-153261	1.09 (0.77, 1.54)	1.27 (0.91, 1.78)
	活性成分	0.99 (0.84, 1.18)	1.36 (1.03, 1.79)

16.6.2 肝機能障害患者

軽度、中等度、重度の肝機能障害被験者及び肝機能正常被験者に本剤 12mg を単回経口投与[注)] したとき、デュークラバシチニブ及び BMT-153261 並びに活性成分の薬物動態に及ぼす影響は下表のとおりであった[14]（外国人データ）。
［9.3.1 参照］

肝機能障害の程度がデュークラバシチニブ及び BMT-153261 並びに活性成分の薬物動態に及ぼす影響

肝機能障害の程度	測定対象	幾何平均比（90%信頼区間） 肝機能障害被験者/肝機能正常被験者	
		総 Cmax 非結合形 Cmax	総 AUC(INF) 非結合形 AUC(INF)
軽度肝機能障害被験者（Child-Pugh 分類 A、スコア 5 ～ 6）	デュークラバシチニブ	1.04 (0.80, 1.36) 1.07 (0.85, 1.33)	1.10 (0.85, 1.42) 1.13 (0.89, 1.43)
	BMT-153261	0.76 (0.44, 1.29) 0.77 (0.46, 1.29)	0.97 (0.68, 1.39) 1.01 (0.71, 1.43)
	活性成分	1.02 (0.79, 1.33) 1.05 (0.84, 1.30)	1.06 (0.83, 1.34) 1.08 (0.87, 1.34)
中等度肝機能障害被験者（Child-Pugh 分類 B、スコア 7 ～ 9）	デュークラバシチニブ	1.10 (0.85, 1.44) 1.26 (1.01, 1.57)	1.40 (1.09, 1.81) 1.60 (1.26, 2.03)
	BMT-153261	0.41 (0.24, 0.70) 0.47 (0.28, 0.78)	0.80 (0.56, 1.15) 0.88 (0.62, 1.24)
	活性成分	1.06 (0.81, 1.37) 1.20 (0.96, 1.49)	1.24 (0.98, 1.57) 1.40 (1.13, 1.73)
重度肝機能障害被験者（Child-Pugh 分類 C、スコア 10 ～ 14）	デュークラバシチニブ	1.01 (0.77, 1.31) 1.62 (1.30, 2.03)	1.43 (1.11, 1.85) 2.31 (1.82, 2.94)
	BMT-153261	0.21 (0.12, 0.38)	0.50 (0.25, 1.01)

		0.24 (0.14, 0.41)	0.58 (0.29, 1.14)
	活性成分	0.94 (0.73, 1.23) 1.51 (1.22, 1.88)	1.19 (0.94, 1.51) 1.87 (1.51, 2.32)

16.7 薬物相互作用

16.7.1 併用薬がデュークラバシチニブの薬物動態に及ぼす影響

In vitroにおいてデュークラバシチニブはCYP1A2、UGT1A9、CES2、P-gp、BCRP及びOCT1の基質である[15]。
薬物相互作用試験の結果は下表のとおりであった[16)～20)]（外国人データ）。

併用薬の存在下におけるデュークラバシチニブ及びBMT-153261並びに活性成分の薬物動態パラメータの変化

併用薬	併用薬投与量	本剤投与量[注]	測定対象	幾何平均比（90%信頼区間） 併用/非併用	
				Cmax	AUC
シクロスポリン（P-gp/BCRP阻害薬）	500mg 単回	6mg 1日1回	デュークラバシチニブ	1.16 (1.08, 1.24)	1.29 (1.24, 1.34)
			BMT-153261	1.15 (1.09, 1.20)	1.21 (1.16, 1.26)
			活性成分	1.15 (1.09, 1.22)	1.27 (1.23, 1.32)
リトナビル（CYP1A2誘導薬）	100mg 1日1回	12mg 単回	デュークラバシチニブ	1.08 (1.00, 1.16)	1.00 (0.96, 1.05)
			BMT-153261	1.49 (1.38, 1.61)	1.33 (1.26, 1.41)
			活性成分	1.11 (1.02, 1.20)	1.08 (1.04, 1.11)
フルボキサミン（CYP1A2阻害薬）	100mg 1日1回	12mg 単回	デュークラバシチニブ	1.15 (1.09, 1.22)	1.57 (1.47, 1.67)
			BMT-153261	0.07 (0.06, 0.09)	0.06 (0.05, 0.07)
			活性成分	1.06 (1.00, 1.12)	1.23 (1.18, 1.28)
ピリメタミン（国内未承認）（OCT1阻害薬）	50mg 単回	6mg 単回	デュークラバシチニブ	1.07 (0.98, 1.16)	1.05 (1.01, 1.09)
			BMT-153261	1.09 (1.00, 1.18)	1.12 (1.05, 1.20)
			活性成分	1.04 (0.96, 1.12)	1.06 (1.02, 1.10)
ジフルニサル（UGT1A9阻害薬）	500mg 1日2回	6mg 単回	デュークラバシチニブ	0.97 (0.88, 1.07)	1.19 (1.09, 1.30)
			BMT-153261	1.24 (1.12, 1.36)	1.50 (1.38, 1.63)
			活性成分	0.98 (0.90, 1.07)	1.29 (1.19, 1.39)

16.7.2 デュークラバシチニブが併用薬の薬物動態に及ぼす影響

In vitroにおいてデュークラバシチニブはBCRP及びOATP1B3を阻害する[21)]。
薬物相互作用試験の結果は下表のとおりであった[22～25)]（外国人データ）。

デュークラバシチニブ存在下における併用薬の薬物動態パラメータの変化

併用薬	併用薬投与量	本剤投与量[注]	幾何平均比（90%信頼区間） 併用/非併用	
			Cmax	AUC
ロスバスタチン（BCRP及びOATP基質）	10mg 単回	12mg 1日1回	1.14 (1.01, 1.29)	1.14 (1.04, 1.24)
ノルエチンドロン（経口避妊薬）	1.5mg 1日1回	12mg 1日2回	1.03 (0.94, 1.13)	1.10 (1.02, 1.19)
エチニルエストラジオール（経口避妊薬）	30μg 1日1回	12mg 1日2回	0.99 (0.89, 1.09)	1.04 (0.99, 1.10)
メトトレキサート	7.5mg 単回	12mg 1日1回	1.11 (1.00, 1.23)	1.04 (0.97, 1.11)
ミコフェノール酸モフェチル[a]	1000mg 単回	12mg 1日1回	1.08 (0.88, 1.33)	1.02 (0.96, 1.08)

a：ミコフェノール酸のパラメータを評価
注）本剤の承認された用法及び用量は「1回6mgを1日1回経口投与」である。

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Ⅲ相臨床試験（IM011-046試験）

局面型皮疹の病変が体表面積（BSA）の10%以上、PASI（Psoriasis Area and Severity Index）スコアが12以上、かつsPGA（医師による静的総合評価）スコアが3（中等度）以上の中等症から重症の局面型皮疹を有する乾癬患者666例（日本人66例含む）を対象とした52週間ランダム化プラセボ及びアプレミラスト対照並行群間比較試験を実施した[26)]。プラセボ、アプレミラスト（承認用法・用量に従い漸増後、30mg 1日2回）又は本剤（6mg 1日1回）を経口投与した。本剤投与群における投与16週後のPASIスコアがベースラインから75%以上改善した患者の割合（以下、PASI 75）及びsPGAが0又は1［sPGAが0（病変消失）又は1（病変軽快）］かつベースラインから2ポイント以上改善した割合（以下、sPGA 0/1）は、プラセボ投与群に比べて統計学的に有意に高かった。投与16週又は24週後のPASI 75、sPGA 0/1及びPASIスコアがベースラインから90%以上改善した患者の割合（以下、PASI 90）を表1に示す。

表1. 投与16週又は24週のPASI 75、sPGA 0/1及びPASI 90[a]

	16週			24週	
	本剤	プラセボ	アプレミラスト	本剤	アプレミラスト
PASI 75	58.4[b] (194/332)	12.7 (21/166)	35.1 (59/168)	69.3 (230/332)	38.1 (64/168)
sPGA 0/1	53.6[b] (178/332)	7.2 (12/166)	32.1 (54/168)	58.7 (195/332)	31.0 (52/168)
PASI 90	35.5 (118/332)	4.2 (7/166)	19.6 (33/168)	42.2 (140/332)	22.0 (37/168)

%（例数）
a：ノンレスポンダー補完法（NRI）
b:プラセボ群に対する$p < 0.0001$（地域、生物製剤使用歴の有無及び体重を層別因子としたCochran-Mantel-Haenszel検定）
52週時までの副作用発現頻度は、本剤投与群で22.0%（117/531例）であった。主な副作用は、下痢2.6%（14/531例）、上咽頭炎2.4%（13/531例）、上気道感染2.3%（12/531例）であった。

17.1.2 海外第Ⅲ相臨床試験（IM011-047試験）

中等症から重症の局面型皮疹を有する乾癬患者1020例（BSA10%以上、PASIスコアが12以上、かつsPGAスコアが3以上）を対象とした52週間ランダム化プラセボ及びアプレミラスト対照並行群間比較試験を実施した[27)]。プラセボ、アプレミラスト（承認用法・用量に従い漸増後、30mg 1日2回）又は本剤（6mg 1日1回）を経口投与した。本剤投与群における投与16週後のPASI 75及びsPGA 0/1は、プラ

セボ投与群に比べて統計学的に有意に高かった。投与16週又は24週のPASI 75、sPGA 0/1及びPASI 90を表2に示す。

表2. 投与16週又は24週のPASI 75、sPGA 0/1及びPASI 90[a]

	16週			24週	
	本剤	プラセボ	アプレミラスト	本剤	アプレミラスト
PASI 75	53.0[b] (271/511)	9.4 (24/255)	39.8 (101/254)	58.7 (296/504)	37.8 (96/254)
sPGA 0/1	49.5[b] (253/511)	8.6 (22/255)	33.9 (86/254)	49.8 (251/504)	29.5 (75/254)
PASI 90	27.0 (138/511)	2.7 (7/255)	18.1 (46/254)	32.5 (164/504)	19.7 (50/254)

% (例数)
a：NRI
b:プラセボ群に対するp < 0.0001（地域、生物製剤使用歴の有無及び体重を層別因子としたCochran-Mantel-Haenszel検定）

52週時までの副作用発現頻度は、本剤投与群で22.4%（187/833例）であった。主な副作用は、上咽頭炎2.4%（20/833例）、上気道感染2.2%（18/833例）であった。

17.1.3 国内第Ⅲ相臨床試験（IM011-066試験）

中等症から重症の局面型皮疹を有する乾癬患者（BSA10%以上、PASIスコアが12以上、かつsPGAスコアが3以上）63例、膿疱性乾癬（膿疱を伴う紅斑面積がBSAの10%以上）3例及び乾癬性紅皮症（炎症性紅斑面積がBSAの80%以上）8例を対象にした単一群、オープンラベル試験で、本剤6mgを1日1回52週まで投与した[28]。主要評価項目（NRI）である投与16週後のPASI 75及びsPGA 0/1は71.6%（53/74例）及び75.7%（56/74例）であった。また、投与16週のPASI 90は43.1%（31/72例）、投与52週後のPASI 75、PASI 90及びsPGA 0/1は82.6%（57/69例）、60.9%（42/69例）及び81.2%（56/69例）であった（observed cases）。また、16週後において膿疱性乾癬患者3例全例に日本皮膚科学会の膿疱性乾癬の重症度基準に基づいた総スコアの改善が、乾癬性紅皮症患者8例中6例及び膿疱性乾癬患者3例全例にGlobal Improvement Scoreの寛解又は改善が認められた。52週時までの副作用発現頻度は、25.7%（19/74例）であった。主な副作用は、口内炎5.4%（4［尋常性乾癬患者3例及び膿疱性乾癬患者1例］/74例）、上咽頭炎4.1%（3［尋常性乾癬患者3例］/74例）、ざ瘡2.7%（2［乾癬性紅皮症患者及び膿疱性乾癬患者各1例］/74例）であった。

18. 薬効薬理

18.1 作用機序

デュークラバシチニブは、チロシンキナーゼ2（TYK2）阻害薬である。TYK2の機能制御部位に結合し、この部位と触媒部位の間の相互作用を安定化することで、インターロイキン（IL）-23、IL-12、I型インターフェロン（IFN）などで誘導されるTYK2の活性化が阻害され、TYK2が介在する炎症や免疫応答が抑制される。

18.2 In vitroでのTYK2依存性シグナルに対する作用

デュークラバシチニブは、免疫系細胞においてIL-23、IL-12、I型IFNなどのサイトカインにより誘導されるTYK2依存性シグナル伝達経路を抑制する。デュークラバシチニブのTYK2依存性シグナル伝達経路に対する全血アッセイでの50%阻害濃度（IC50）は、他のヤヌスキナーゼ（JAK）ファミリーキナーゼJAK1、JAK2又はJAK3に依存するシグナル伝達経路に対するIC50に比べて約41分の1～208分の1以下であり、高い選択性が示されている[29]。

18.3 乾癬患者でのTYK2依存性シグナルに対する作用

乾癬患者を対象とした第Ⅱ相試験では、デュークラバシチニブにより乾癬皮膚における乾癬関連遺伝子の発現が用量依存的に減少し、特にIL-23経路及びI型IFN経路で調節される遺伝子の減少が認められた[30]。また、第Ⅲ相試験では、IL-17A、IL-19及びβデフェンシンの中央値は、ベースラインと比較してそれぞれ約48%～50%、72%及び81%～84%低下した[31),32)]。

18.4 マウス耳介炎症モデルに対する作用

デュークラバシチニブは、マウスでIL-23により誘発される耳介での表皮肥厚、表皮過形成及び炎症性細胞の浸潤並びに炎症性サイトカインの遺伝子発現を抑制する[33]。

19. 有効成分に関する理化学的知見

一般名：デュークラバシチニブ（Deucravacitinib）
化学名：6-(Cyclopropanecarboxamido)-4-[2-methoxy-3-(1-methyl-1*H*-1,2,4-triazol-3-yl)anilino]-*N*-($^2H_3$)methylpyridazine-3-carboxamide

分子式：$C_{20}H_{19}{}^2H_3N_8O_3$
分子量：425.46
構造式：

性状：白色～黄色の粉末で塊を含むことがある。

21. 承認条件

医薬品リスク管理計画を策定の上、適切に実施すること。

22. 包装

30錠［10錠（PTP）×3］

23. 主要文献

1）社内資料：乳汁移行（20XX年XX月XX日承認、CTD 2.6.4.4.5.5）
2）Kimball AB, et al. Br J Dermatol. 2015；173：1183-1190.
3）Reich K, et al. Arch Dermatol Res. 2015；307：875-883.
4）社内資料：市販予定錠剤に対する食事及びファモチジンの影響評価試験（20XX年XX月XX日承認、CTD 2.7.2.2.2.18）
5）社内資料：国内第Ⅲ相オープンラベル試験（20XX年XX月XX日承認、CTD 2.7.2.2.2.22）
6）社内資料：絶対的バイオアベイラビリティ評価試験（20XX年XX月XX日承認、CTD 2.7.1.2.3）
7）Davies B, et al. Pharmaceut Res. 1993；10：1093-1095.
8）社内資料：血清及び血漿蛋白結合（20XX年XX月XX日承認、CTD 2.6.4.4.3）
9）社内資料：全血中の分布（20XX年XX月XX日承認、CTD 2.6.4.4.2）

10）社内資料：デュークラバシチニブ代謝酵素の同定（20XX 年 XX 月 XX 日承認、CTD 2.6.4.5.1.3）
11）社内資料：ヒトでの代謝（20XX 年 XX 月 XX 日承認、CTD 2.6.4.5.2.4）
12）社内資料：放射性標識体投与時の薬物動態及び代謝試験（20XX 年 XX 月 XX 日承認、CTD 2.7.2.2.2.3）
13）社内資料：腎機能障害の影響評価試験（20XX 年 XX 月 XX 日承認、CTD 2.7.2.2.2.9）
14）社内資料：肝機能障害の影響評価試験（20XX 年 XX 月 XX 日承認、CTD 2.7.2.2.2.10）
15）社内資料：被相互作用薬としての in vitro 薬物相互作用評価（20XX 年 XX 月 XX 日承認、CTD 2.6.4.7.1）
16）社内資料：シクロスポリンとの薬物相互作用試験（20XX 年 XX 月 XX 日承認、CTD 2.7.2.2.2.7）
17）社内資料：リトナビルとの薬物相互作用試験（20XX 年 XX 月 XX 日承認、CTD 2.7.2.2.2.13）
18）社内資料：フルボキサミンとの薬物相互作用試験（20XX 年 XX 月 XX 日承認、CTD 2.7.2.2.2.14）
19）社内資料：Pyrimethamine との薬物相互作用試験（20XX 年 XX 月 XX 日承認、CTD 2.7.2.2.2.16）
20）社内資料：ジフルニサルとの薬物相互作用試験（20XX 年 XX 月 XX 日承認、CTD 2.7.2.2.2.17）
21）社内資料：相互作用薬としての in vitro 薬物相互作用評価（20XX 年 XX 月 XX 日承認、CTD 2.6.4.7.2）
22）社内資料：ロスバスタチンとの薬物相互作用試験（20XX 年 XX 月 XX 日承認、CTD 2.7.2.2.2.2）
23）社内資料：経口避妊薬との薬物相互作用試験（20XX 年 XX 月 XX 日承認、CTD 2.7.2.2.2.6）
24）社内資料：メトトレキサートとの薬物相互作用試験（20XX 年 XX 月 XX 日承認、CTD 2.7.2.2.2.4）
25）社内資料：ミコフェノール酸モフェチルとの薬物相互作用試験（20XX 年 XX 月 XX 日承認、CTD 2.7.2.2.2.12）
26）社内資料：IM011-046 試験（20XX 年 XX 月 XX 日承認、CTD 2.7.6.5.2）
27）社内資料：IM011-047 試験（20XX 年 XX 月 XX 日承認、CTD 2.7.6.5.3）
28）社内資料：IM011-066 試験（20XX 年 XX 月 XX 日承認、CTD 2.7.6.5.4）
29）社内資料：In vitro 薬効薬理試験（20XX 年 XX 月 XX 日承認、CTD 2.6.2.2.1.2.6）
30）社内資料：国際共同第Ⅱ相試験（20XX 年 XX 月 XX 日承認、CTD 2.7.2.2.2.19）
31）社内資料：国際共同第Ⅲ相比較試験（20XX 年 XX 月 XX 日承認、CTD 2.7.2.2.2.20）
32）社内資料：海外第Ⅲ相比較試験（20XX 年 XX 月 XX 日承認、CTD 2.7.2.2.2.21）
33）社内資料：In vivo 薬効薬理試験（20XX 年 XX 月 XX 日承認、CTD 2.6.2.2.2.3）

24. 文献請求先及び問い合わせ先

ブリストル・マイヤーズ スクイブ株式会社　メディカル情報グループ
（住所）東京都千代田区大手町 1-2-1
（TEL）0120-093-507

26. 製造販売業者等

26.1 製造販売元

ブリストル・マイヤーズ スクイブ株式会社
東京都千代田区大手町 1-2-1

1 国内の一般的名称（JAN）

令和 3 年 8 月 17 日付薬生薬審発 0817 第 1 号により通知された。

医薬品一般的名称

登録番号：302-5-B9

JAN（日本名）デュークラバシチニブ

JAN（英　名）Deucravacitinib

化学名

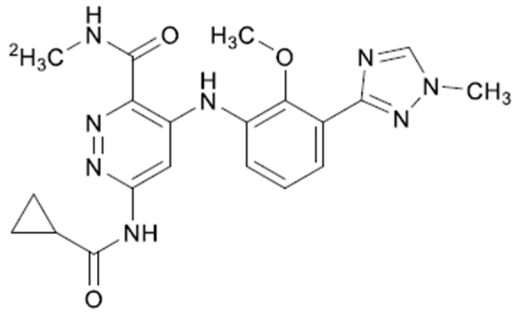
（日本名）

6-(シクロプロパンカルボキシアミド)-4-[2-メトキシ-3-(1-メチル-1*H*-1,2,4-トリアゾール-3-イル)アニリノ]-*N*-($^2H_3$)メチルピリダジン-3-カルボキシアミド

（英　名）

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

化学構造式



2 国際一般名（INN）

INN

deucravacitinib

INN 収載誌

International Nonproprietary Names for Pharmaceutical Substances（INN）, WHO Drug Information, Vol. 35, No.1 (2021) List 85 (p.131)

薬生薬審発 0817 第１号
令 和 ３ 年 ８ 月 17 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　302-5-B2

JAN（日本名）：ロペグインターフェロン　アルファ－2b（遺伝子組換え）

JAN（英　名）：Ropeginterferon Alfa-2b (Genetical Recombination)

アミノ酸配列及びジスルフィド結合

PCDLPQTHSL GSRRTLMLLA QMRRISLFSC LKDRHDFGFP QEEFGNQFQK

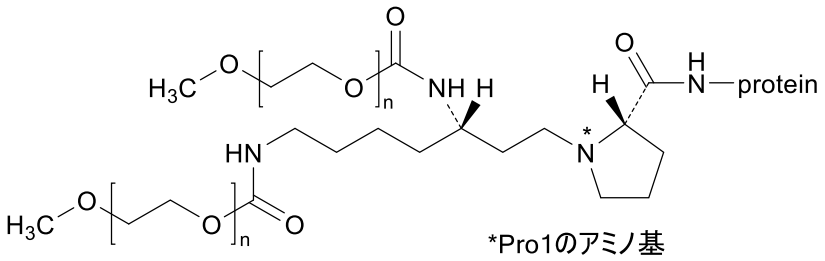
AETIPVLHEM IQQIFNLFST KDSSAAWDET LLDKFYTELY QQLNDLEACV

IQGVGVTETP LMKEDSILAV RKYFQRITLY LKEKKYSPCA WEVVRAEIMR

SFSLSTNLQE SLRSKE

P1：PEG 化部位

ポリエチレングリコールの結合様式



$C_{865}H_{1356}N_{230}O_{256}S_9$（タンパク質部分）

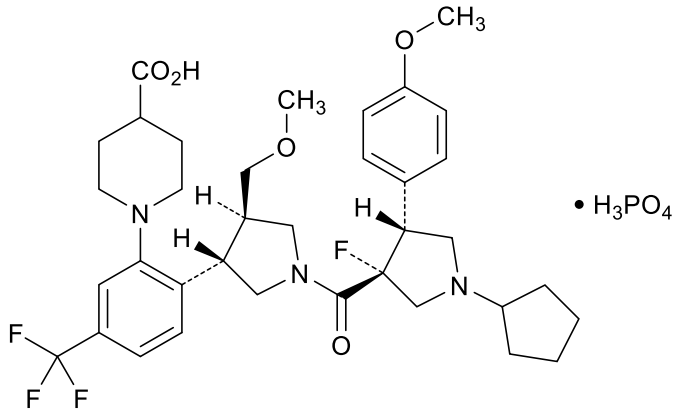
ロペグインターフェロン　アルファ－2b は，インターフェロン　アルファ－2b（遺伝子組換え）類縁体であり，N 末端に Pro が付加され，2 本のメトキシポリエチレングリコール鎖（分子量：約 43,000）がリンカーを介して結合している（PEG 結合部位：Pro1 残基）．ロペグインターフェロン　アルファ－2b は，166 個のアミノ酸残基からなる PEG 化タンパク質（分子量：約 61,000）である．

Ropeginterferon Alfa-2b is Interferon Alfa-2b (Genetical Recombination) analog in which Pro is attached to N-terminus, to which two methoxy polyethylene glycol polymers (molecular weight: ca. 43,000) are bound via a linker (pegylation site: Pro1 residue). Ropeginterferon Alfa-2b is a pegylated protein (molecular weight: ca. 61,000) consisting of 166 amino acid residues.

登録番号　302-5-B3

JAN（日本名）：デルシメラゴン　リン酸

JAN（英　名）：Dersimelagon Phosphoric Acid



$C_{36}H_{45}F_4N_3O_5 \cdot H_3PO_4$

1-{2-[(3*S*,4*R*)-1-[(3*R*,4*R*)-1-シクロペンチル-3-フルオロ-4-(4-メトキシフェニル)ピロリジン-3-カルボニル]-4-(メトキシメチル)ピロリジン-3-イル]-5-(トリフルオロメチル)フェニル}ピペリジン-4-カルボン酸　一リン酸

1-{2-[(3*S*,4*R*)-1-[(3*R*,4*R*)-1-Cyclopentyl-3-fluoro-4-(4-methoxyphenyl)pyrrolidine-3-carbonyl]-4-(methoxymethyl)pyrrolidin-3-yl]-5-(trifluoromethyl)phenyl}piperidine-4-carboxylic acid monophosphoric acid

登録番号　302-5-B4

JAN（日本名）：ロザノリキシズマブ（遺伝子組換え）

JAN（英　名）：Rozanolixizumab (Genetical Recombination)

アミノ酸配列及びジスルフィド結合

L鎖

DIQMTQSPSS LSASVGDRVT ITCKSSQSLV GASGKTYLYW LFQKPGKAPK

RLIYLVSTLD SGIPSRFSGS GSGTEFTLTI SSLQPEDFAT YYCLQGTHFP

HTFGQGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK

VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE

VTHQGLSSPV TKSFNRGEC

H鎖

EVPLVESGGG LVQPGGSLRL SCAVSGFTFS NYGMVWVRQA PGKGLEWVAY

IDSDGDNTYY RDSVKGRFTI SRDNAKSSLY LQMNSLRAED TAVYYCTTGI

VRPFLYWGQG TLVTVSSAST KGPSVFPLAP CSRSTSESTA ALGCLVKDYF

PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTKTYTC

NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF PPKPKDTLMI

SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV

SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP

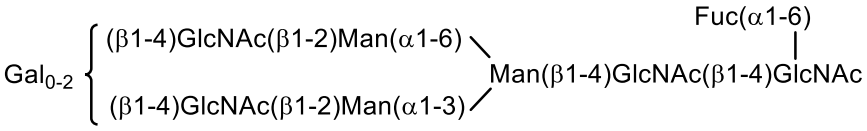
SQEEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS

FFLYSRLTVD KSRWQEGNVF SCSVMHEALH NHYTQKSLSL SLGK

H鎖N294：糖鎖結合；H鎖K444：部分的プロセシング

L鎖C219 – H鎖C131, H鎖C223 – H鎖C223, H鎖C226 – H鎖C226 : ジスルフィド結合

主な糖鎖の推定構造



$C_{6462}H_{9984}N_{1704}O_{2016}S_{44}$（タンパク質部分，4本鎖）

H鎖　$C_{2174}H_{3350}N_{572}O_{670}S_{16}$

L鎖　$C_{1057}H_{1646}N_{280}O_{338}S_{6}$

ロザノリキシズマブは，遺伝子組換えヒト化及びキメラ抗ヒト新生児型Fc受容体（FcRn）モノクローナル抗体であり，H鎖はラット抗FcRn抗体の相補性決定部，ヒトフレームワーク部及びヒトIgG4の定常部からなり，L鎖はラット抗FcRn抗体の可変部及びヒトIgGの定常部からなる．H鎖の225番目のアミノ酸残基はProに置換されている．ロザノリキシズマブは，チャイニーズハムスター卵巣細胞により産生される．ロザノリキシズマブは，444 個のアミノ酸残基からなるH鎖（γ4鎖）2本及び219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．

Rozanolixizumab is a recombinant humanized and chimeric anti-human neonatal Fc receptor (FcRn) monoclonal antibody in which the H-chains are composed of complementarity-determining regions derived from rat anti-FcRn monoclonal antibody, human framework regions and a human IgG4 constant regions and the L-chains are composed of variable regions derived from rat anti-FcRn antibody and human IgG constant regions. The amino acid residue at position 225 in the H-chain is substituted by Pro. Rozanolixizumab is produced in Chinese hamster ovary cells. Rozanolixizumab is a glycoprotein (molecular weight: ca. 148,000) composed of 2 H-chains (γ4-chains) consisting of 444 amino acid residues each and 2 L-chains (κ-chains) consisting of 219 amino acid residues each.

登録番号　302-5-B5

JAN（日本名）：フェラジリマブ（遺伝子組換え）

JAN（英　名）：Feladilimab (Genetical Recombination)

アミノ酸配列及びジスルフィド結合

L鎖

```
EIVLTQSPAT LSLSPGERAT LSCSASSSVS YMHWYQQKPG QAPRLLIYDT

SKLASGIPAR FSGSGSGTDY TLTISSLEPE DFAVYYCFQG SGYPYTFGQG

TKLEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD

NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL

SSPVTKSFNR GEC
```

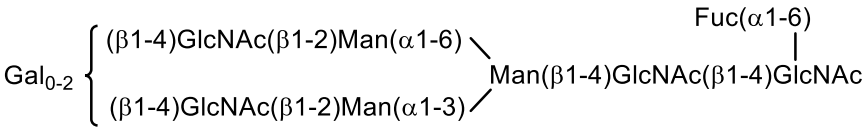
H鎖

```
QVQLVQSGAE VKKPGSSVKV SCKASGYTFT DYAMHWVRQA PGQGLEWMGL

ISIYSDHTNY NQKFQGRVTI TADKSTSTAY MELSSLRSED TAVYYCGRNN

YGNYGWYFDV WGQGTTVTVS SASTKGPSVF PLAPCSRSTS ESTAALGCLV

KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTK

TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEFEGGPS VFLFPPKPKD

TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST

YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY

TLPPSQEEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD

SDGSFFLYSR LTVDKSRWQE GNVFSCSVMH EALHNHYTQK SLSLSLGK
```

H 鎖 Q1：部分的ピログルタミン酸；H 鎖 N298：糖鎖結合；H 鎖 K448：部分的プロセシング

L 鎖 C213－H 鎖 C135，H 鎖 C227－H 鎖 C227，H 鎖 C230－H 鎖 C230：ジスルフィド結合

主な糖鎖の推定構造



$C_{6450}H_{9888}N_{1696}O_{2036}S_{46}$（タンパク質部分，4本鎖）

H鎖　$C_{2199}H_{3368}N_{580}O_{685}S_{17}$

L鎖　$C_{1026}H_{1580}N_{268}O_{333}S_{6}$

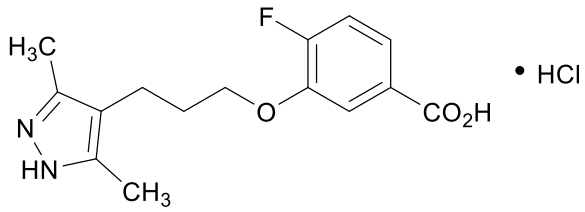
フェラジリマブは，遺伝子組換え抗ヒト誘導性 T 細胞共刺激因子（ICOS）モノクローナル抗体であり，その相補性決定部はマウス抗体に由来し，その他はヒト IgG4 に由来する．H 鎖の 229 及び 236 番目のアミノ酸残基はそれぞれ Pro 及び Glu に置換されている．フェラジリマブは，チャイニーズハムスター卵巣細胞により産生される．フェラジリマブは，448 個のアミノ酸残基からなる H 鎖（γ4 鎖）2 本及び 213 個のアミノ酸残基からなる L 鎖（κ 鎖）2 本で構成される糖タンパク質（分子量：約 148,000）である．

Feladilimab is a recombinant anti-human inducible T-cell costimulator (ICOS) monoclonal antibody, the complementarity-determining regions of which are derived from mouse antibody and other regions are derived from human IgG4. In the H-chain, the amino acid residues at positions 229 and 236 are substituted by Pro and Glu, respectively. Feladilimab is produced in Chinese hamster ovary cells. Feladilimab is a glycoprotein (molecular weight: ca. 148,000) composed of 2 H-chains (γ4-chains) consisting of 448 amino acid residues each and 2 L-chains (κ-chains) consisting of 213 amino acid residues each.

登録番号　302-5-B6

JAN（日本名）：アコラミジス塩酸塩

JAN（英　名）：Acoramidis Hydrochloride



$C_{15}H_{17}FN_2O_3$・HCl

3-[3-(3,5-ジメチル-1*H*-ピラゾール-4-イル)プロポキシ]-4-フルオロ安息香酸　一塩酸塩

3-[3-(3,5-Dimethyl-1*H*-pyrazol-4-yl)propoxy]-4-fluorobenzoic acid monohydrochloride

登録番号　302-5-B7

JAN（日本名）：レカネマブ（遺伝子組換え）

JAN（英　名）：Lecanemab (Genetical Recombination)

アミノ酸配列及びジスルフィド結合

L鎖

DVVMTQSPLS LPVTPGAPAS ISCRSSQSIV HSNGNTYLEW YLQKPGQSPK

LLIYKVSNRF SGVPDRFSGS GSGTDFTLRI SRVEAEDVGI YYCFQGSHVP

PTFGPGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK

VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE

VTHQGLSSPV TKSFNRGEC

H鎖

EVQLVESGGG LVQPGGSLRL SCSASGFTFS SFGMHWVRQA PGKGLEWVAY

ISSGSSTIYY GDTVKGRFTI SRDNAKNSLF LQMSSLRAED TAVYYCAREG

GYYYGRSYYT MDYWGQGTTV TVSSASTKGP SVFPLAPSSK STSGGTAALG

CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS SVVTVPSSSL

GTQTYICNVN HKPSNTKVDK RVEPKSCDKT HTCPPCPAPE LLGGPSVFLF

PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE

EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE KTISKAKGQP

REPQVYTLPP SREEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT

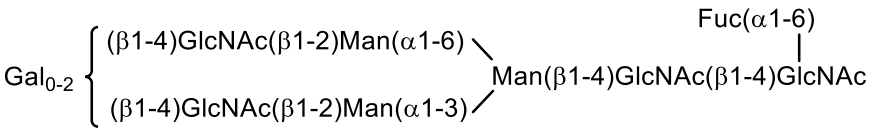
TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL

SPGK

H 鎖 N304：糖鎖結合；H 鎖 K454：部分的プロセシング

L 鎖 C219－H 鎖 C227，H 鎖 C233－H 鎖 C233，H 鎖 C236－H 鎖 C236：ジスルフィド結合

主な糖鎖の推定構造



$C_{6544}H_{10088}N_{1744}O_{2032}S_{46}$（タンパク質部分，4本鎖）

H 鎖　$C_{2216}H_{3407}N_{587}O_{681}S_{17}$

L鎖　$C_{1056}H_{1641}N_{285}O_{335}S_{6}$

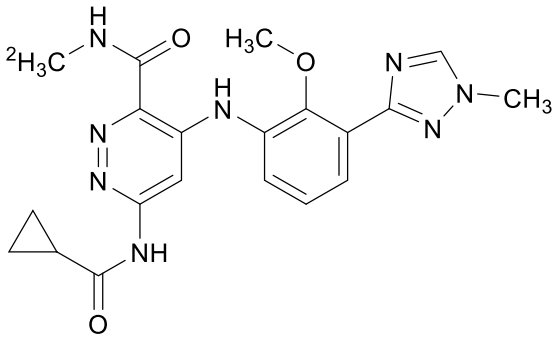
レカネマブは，遺伝子組換え抗ヒトアミロイドベータペプチドモノクローナル抗体であり，その相補性決定部はマウス抗体に由来し，その他はヒトIgG1に由来する．レカネマブは，チャイニーズハムスター卵巣細胞により産生される．レカネマブは，454個のアミノ酸残基からなるH鎖（γ1鎖）2本及び219個のアミノ酸残基からなるL鎖（κ鎖）2本で構成される糖タンパク質（分子量：約150,000）である．

Lecanemab is a recombinant anti-human amyloid beta peptide monoclonal antibody, the complementarity-determining regions of which are derived from mouse antibody and other regions are derived from human IgG1. Lecanemab is produced in Chinese hamster ovary cells. Lecanemab is a glycoprotein (molecular weight: ca. 150,000) composed of 2 H-chains (γ1-chains) consisting of 454 amino acid residues each and 2 L-chains (κ-chains) consisting of 219 amino acid residues each.

登録番号　302-5-B9

JAN（日本名）：デュークラバシチニブ

JAN（英　名）：Deucravacitinib



$C_{20}H_{19}{}^{2}H_{3}N_{8}O_{3}$

6-(シクロプロパンカルボキシアミド)-4-[2-メトキシ-3-(1-メチル-1*H*-1,2,4-トリアゾール-3-イル)アニリノ]-*N*-($^{2}H_{3}$)メチルピリダジン-3-カルボキシアミド

6-(Cyclopropanecarboxamido)-4-[2-methoxy-3-(1-methyl-1*H*-1,2,4-triazol-3-yl)anilino]-*N*-($^{2}H_{3}$)methylpyridazine-3-carboxamide

登録番号　302-6-B3

JAN（日本名）：サバトリマブ（遺伝子組換え）

JAN（英　名）：Sabatolimab (Genetical Recombination)

アミノ酸配列及びジスルフィド結合

L 鎖

```
AIQLTQSPSS  LSASVGDRVT  ITCRASESVE  YYGTSLMQWY  QQKPGKAPKL
LIYAASNVES  GVPSRFSGSG  SGTDFTLTIS  SLQPEDFATY  FCQQSRKDPS
TFGGGTKVEI  KRTVAAPSVF  IFPPSDEQLK  SGTASVVCLL  NNFYPREAKV
QWKVDNALQS  GNSQESVTEQ  DSKDSTYSLS  STLTLSKADY  EKHKVYACEV
THQGLSSPVT  KSFNRGEC
```

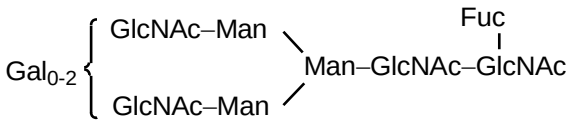
H 鎖

```
QVQLVQSGAE  VKKPGSSVKV  SCKASGYTFT  SYNMHWVRQA  PGQGLEWMGD
IYPGNGDTSY  NQKFKGRVTI  TADKSTSTVY  MELSSLRSED  TAVYYCARVG
GAFPMDYWGQ  GTTVTVSSAS  TKGPSVFPLA  PCSRSTSEST  AALGCLVKDY
FPEPVTVSWN  SGALTSGVHT  FPAVLQSSGL  YSLSSVVTVP  SSSLGTKTYT
CNVDHKPSNT  KVDKRVESKY  GPPCPPCPAP  EFLGGPSVFL  FPPKPKDTLM
ISRTPEVTCV  VVDVSQEDPE  VQFNWYVDGV  EVHNAKTKPR  EEQFNSTYRV
VSVLTVLHQD  WLNGKEYKCK  VSNKGLPSSI  EKTISKAKGQ  PREPQVYTLP
PSQEEMTKNQ  VSLTCLVKGF  YPSDIAVEWE  SNGQPENNYK  TTPPVLDSDG
SFFLYSRLTV  DKSRWQEGNV  FSCSVMHEAL  HNHYTQKSLS  LSLG
```

H 鎖 Q1：部分的ピログルタミン酸；H 鎖 N295：糖鎖結合

L 鎖 C218 – H 鎖 C132，H 鎖 C224 – H 鎖 C224，H 鎖 C227 – H 鎖 C227：ジスルフィド結合

主な糖鎖の推定構造



$C_{6398}H_{9886}N_{1698}O_{2032}S_{48}$（タンパク質部分，4 本鎖）

H 鎖　$C_{2162}H_{3330}N_{570}O_{674}S_{18}$

L 鎖　$C_{1037}H_{1617}N_{279}O_{342}S_{6}$

サバトリマブは，遺伝子組換え抗ヒト T 細胞免疫グロブリンムチンファミリーメンバー3（TIM-3）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 IgG4 に由来する．H 鎖の 226 番目のアミノ酸残基は Pro に置換されており，C 末端の Lys は除去されている．サバトリマブは，チャイニーズハムスター卵巣細胞により産生される．サバトリマブは，444 個のアミノ酸残基からなる H 鎖（γ4 鎖）2 本及び 218 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．

Sabatolimab is a recombinant anti-human T-cell immunoglobulin mucin family member 3 (TIM-3) monoclonal antibody, the complementarity-determining regions of which are derived from mouse antibody and other regions are derived from human IgG4. In the H-chain, the amino acid residue at position 226 is substituted by Pro, and Lys at the C-terminus is deleted. Sabatolimab is produced in Chinese hamster ovary cells. Sabatolimab is a glycoprotein (molecular weight: ca. 149,000) composed of 2 H-chains (γ4-chains) consisting of 444 amino acid residues each and 2 L-chains (κ-chains) consisting of 218 amino acid residues each.

※　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
```

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 [(3*S*)-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)

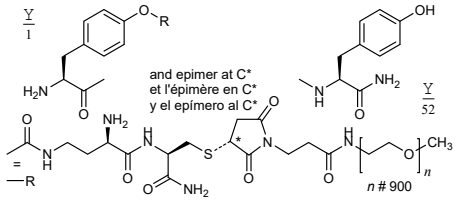
$C_{280}H_{430}N_{86}O_{83}S_4(C_2H_4O)_{\approx 900}$

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



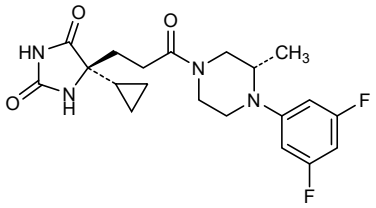
aldumastatum

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
```

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"

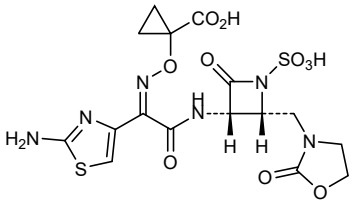
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
521, 296"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

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.

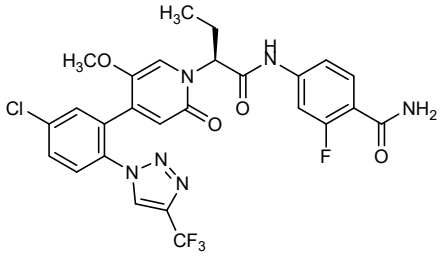
asundexianum

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)

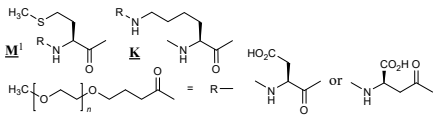
$C_{563}H_{898}N_{144}O_{185}S_8[C_5H_8O_2(C_2H_4O)_n]_x$ n ≈ 900, x ≈ 1

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)

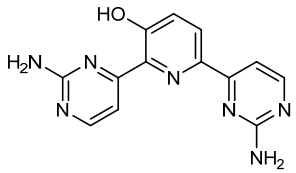
Modified residues / Résidus modifiés / Restos modificados
avipendekin : pegol ~ 1:1
M[1] (Met 1: ~32-40 %), **K** (Lys 11, 37, 42, 87: ~33-42 %; Lys 12, 95, 98: ~18-35 %)



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'

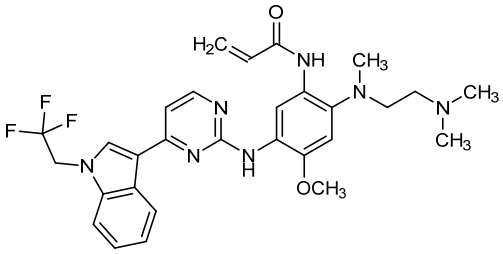
befotertinibum

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

$C_{29}H_{32}F_3N_7O_2$



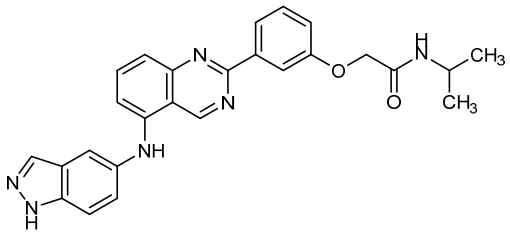
belumosudilum

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 / ningùm 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

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

(3'-5') G=C=A=G=A=d[G=G=T=G=A=A=G=C=G=A=]A=G=U=G=C

Legend d : 2'-deoxynucleotides
X : 2'-*O*-(2-methoxyethyl)nucleotide
C, C, U : 5-methylnucleotide

-sp-

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

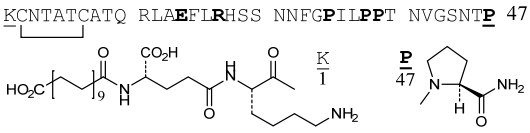
cagrilintide

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

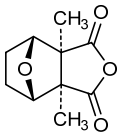
$C_{194}H_{312}N_{54}O_{59}S_2$



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

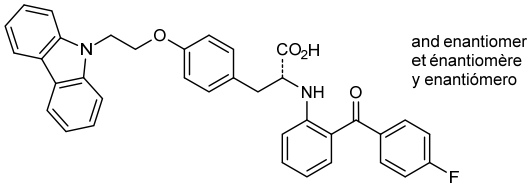
$C_{10}H_{12}O_4$



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

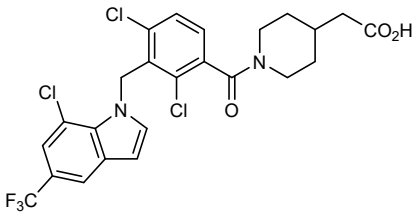
$C_{36}H_{29}FN_2O_4$



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 IGKVVWPGSTA 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

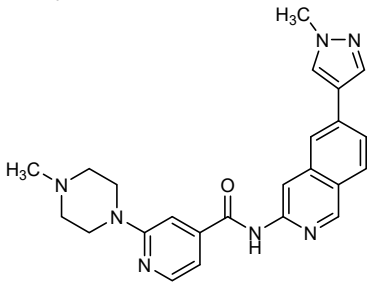
cirtuvivint

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"

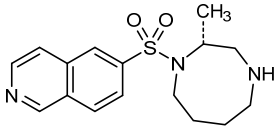
cotoretigenum toliparvovecum

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
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"

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  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

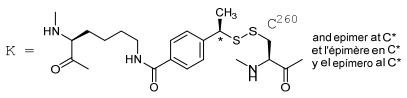
```
QIVLTQSPAI MSASPGEKVT MTCSASSSVS YMHWYQQKSG TSPKRWIYDT  50
SKLASGVPAR FSGSGSGTSY SLTISSMEAE DAATYYCQQW SSNPLTFGAG 100
TKLELKRADA APTVSIFPPS SEQLTSGGAS VVCFLNNFYP KDINVKWKID 150
GSERQNGVLN SWTDQDSKDS TYSMSSTLTL TKDEYERHNS YTCEATHKTS 200
TSPIVKSFNR NEC                                         213
```

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) 22-96 147-202 270-330 376-434
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 coniugación
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)
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"

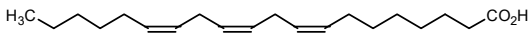
daleutonum

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

$C_{20}H_{34}O_2$



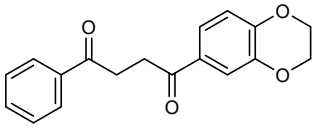
dalosirvatum

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

$C_{18}H_{16}O_4$



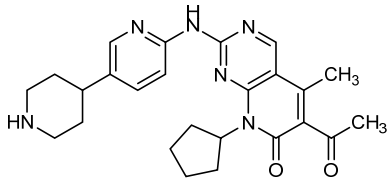
dalpiciclibum

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

$C_{25}H_{30}N_6O_2$



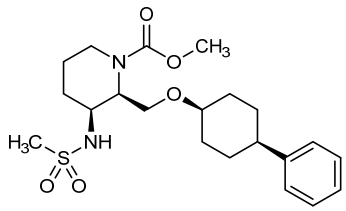
danavorextonum

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

$C_{21}H_{32}N_2O_5S$



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)

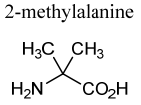
$C_{192}H_{302}N_{46}O_{57}$

Sequence / Séquence / Secuencia

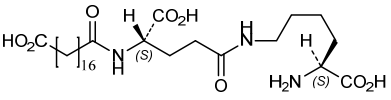
HXEGSFTSEL ATILDKQAAR DFIAWLIQHK ITD 33

Modified residues / Résidus modifiés / Restos modificados

X (2) 2-methylalanine



K(16) N^6-[17-carboxyheptadecanoyl-γ-Glu]-Lys



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

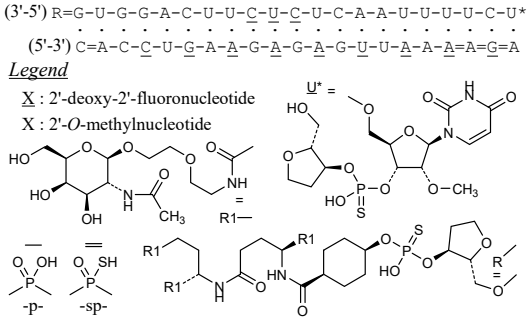
daplusiran

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*-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*-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

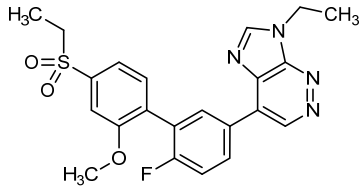
$C_{492}H_{650}F_{12}N_{163}O_{310}P_{43}S_7$



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

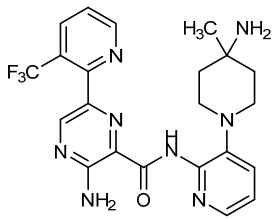
$C_{22}H_{21}FN_4O_3S$



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
LWGWDSDAFD 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 CHS 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"

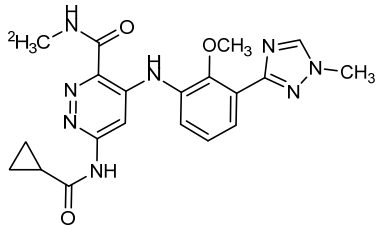
deucravacitinibum

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

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

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

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



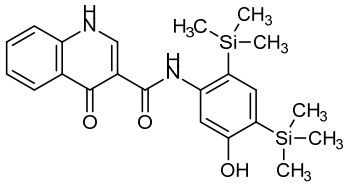
dirocaftorum

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  50
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  50
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 (h 5-CL 126) 226-216' 226"-216"
Inter-H-H (h 11, h 14) 232-232" 235-235"

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:
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"

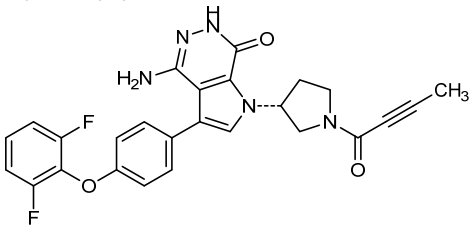
edralbrutinibum

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

$C_{26}H_{21}F_2N_5O_3$



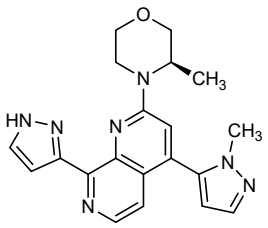
elimusertibum

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 NYGMNWVKQA 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 / ningùn 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

```
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
```

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 (h 11 - h 11)	515-772				
Inter-h14 (h 14 - h 14)	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

```
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
```

Light chain / Chaîne légère / Cadena ligera

```
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
```

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

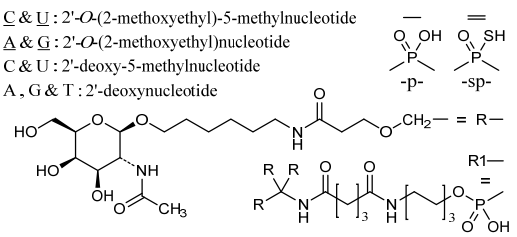
eplontersen	*all-P-ambo*-5'-*O*-(28-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-16,16-bis{[3-({6-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]hexyl}amino)-3-oxopropoxy]methyl}-1-hydroxy-1,10,14,21-tetraoxo-2,18-dioxa-9,15,22-triaza-1λ^5-phosphaoctacosan-1-yl)-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidyly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

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

(3'-5') R1-U=C-U-U-G-d(G=T=T=A=C=A=T=G=A=A=)A-U-C=C=C

Legend:

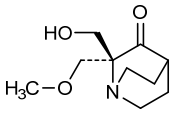
C & U : 2'-*O*-(2-methoxyethyl)-5-methylnucleotide
A & G : 2'-*O*-(2-methoxyethyl)nucleotide
C & U : 2'-deoxy-5-methylnucleotide
A , G & T : 2'-deoxynucleotide



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

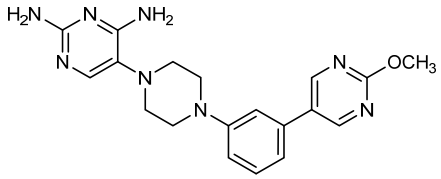
N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
VH Q1:
1

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

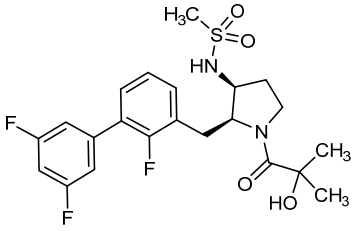
firazorexton

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

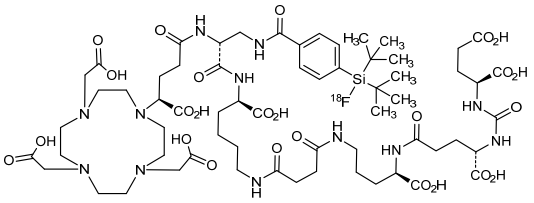
flotufolastat (^{18}F)

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

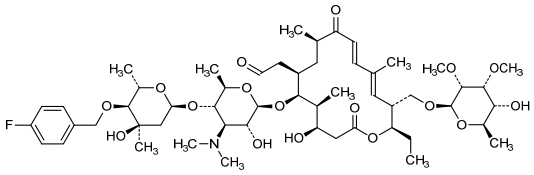
flubentylosine

[(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

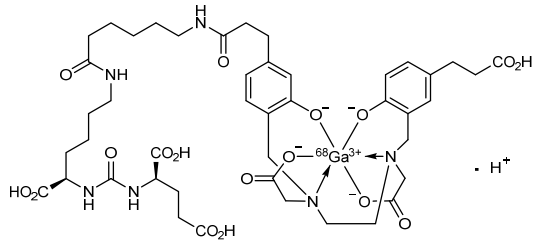
gallium (^{68}Ga) gozétotide

{*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
```

Light chain / Chaîne légère / Cadena ligera

```
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'"

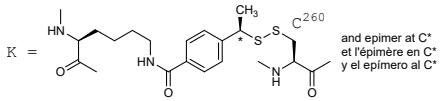
Inter-H-H (h 12, h 15, h 18) 230-230" 233-233" 235-235"
heterogeneous patterns involving 94' and 94'" e.g.:
96-94' 138-94' 150-94' 94'-137'
96"-94'" 138"-94'" 150"-94'" 94'"-137'"

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

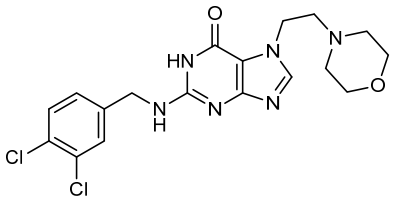
ibézapolstat

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

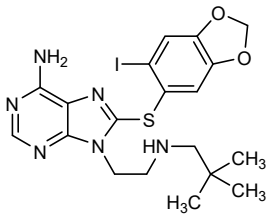
icapamespib

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  50
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  50
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
H CH2 C3^4):
244, 244"

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

C-terminal lysine clipping:
H CHS K2:
452, 452"

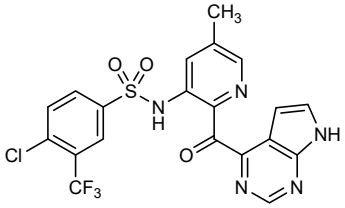
ilacirnonum

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^{ε} 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

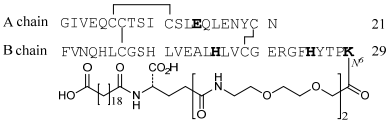
chaîne A de l'insuline humaine (1-21) variant (Y>E^{14}), chaîne B de l'insuline humaine (1-29) variant (Y>H^{16}, F>H^{25}), conjuguée en K^{29B} par son N^6 à (22*S*)-22,42-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazadotétracontan-1-oyle; $N^{6.29B}$-[(22*S*)-22,42-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazadotétracontan-1-oyl]-[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

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

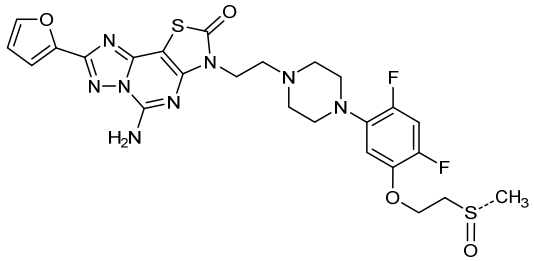
inupadénant

(+)-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.

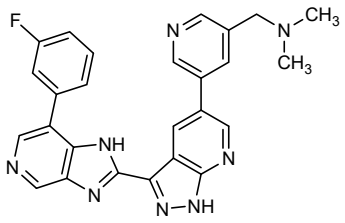
ipivivintum

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.

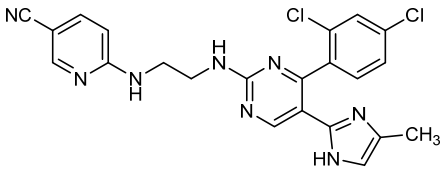
laduviglusibum

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 — (4^2R)-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

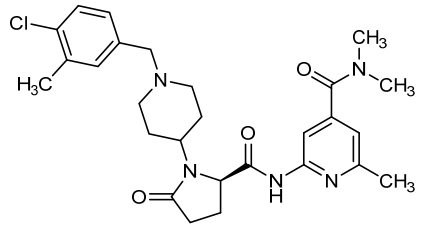
lazucirnon

(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"

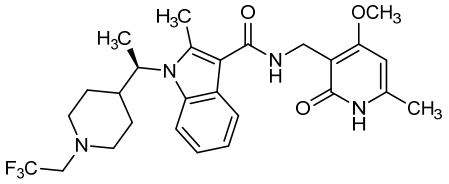
N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
L VH Q1:
1, 1"

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

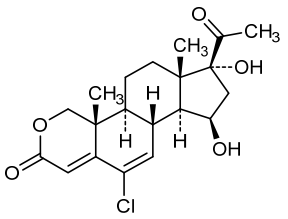
$C_{27}H_{33}F_3N_4O_3$



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^3*O*^{4},*O*^{7},*O*^{10}-methyl)-1,4,7,10-tetraazacyclododecan-1-yl-κ^4*N*^{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

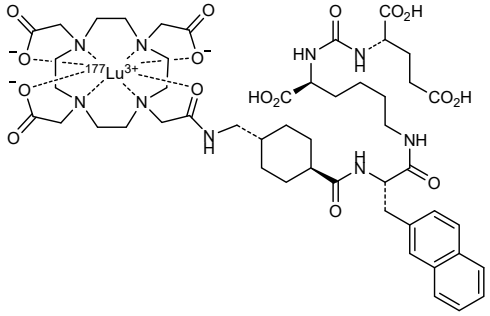
lutécium (^{177}Lu) vipivotide tétraxetan

{*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"

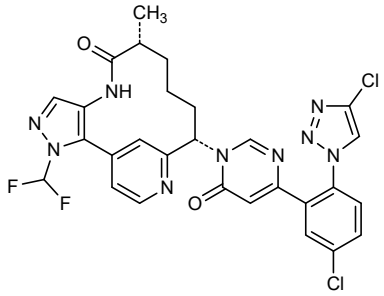
milvexianum

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'"

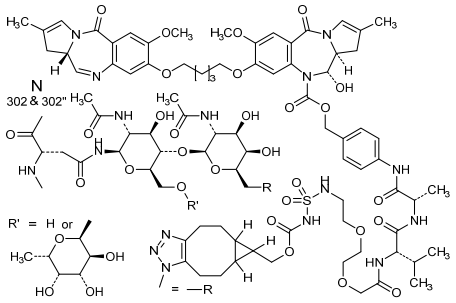
Inter-H-H (h 11, h 14) 231-231" 234-234"

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

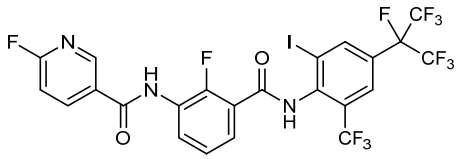
H CH2 N84.4:
302, 302"



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

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



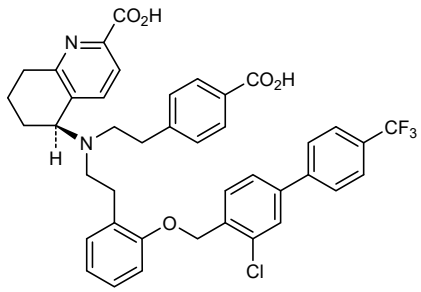
mosliciguatum

mosliciguat — (9^5S)-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 (9^5S)-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 (9^5S)-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

$C_{41}H_{36}ClF_3N_2O_5$



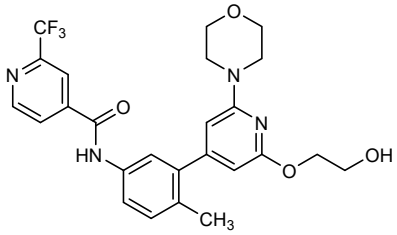
naporafenibum

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'-*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

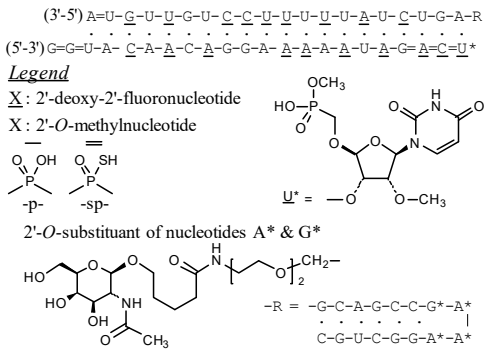
tout-P-ambo-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluoroguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-désoxy-2'-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 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

```
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"

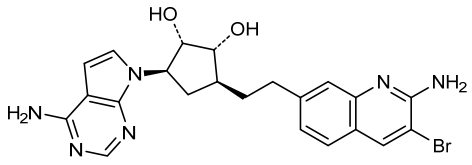
onametostatum

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

```
MGDHPQATPA 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
```

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

```
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
```

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
```

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-$Mét^1$-[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 PLWIRPDAPS   50
RCTWQLGRPA SESPHHHTAP AKSPKILPDI LKKIGDTPMV RINKIGKKFG  100
LKCELLAKCE FFNAGGSVKD RISLRMIEDA ERDGTLKPGD TIIEPTSGNT  150
GIGLALAAAV RGYRCIIVMP 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

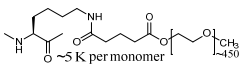
Post-translational modifications
Removal of Met^1 / Suppression de Met^1 / Eliminación de Met^1

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

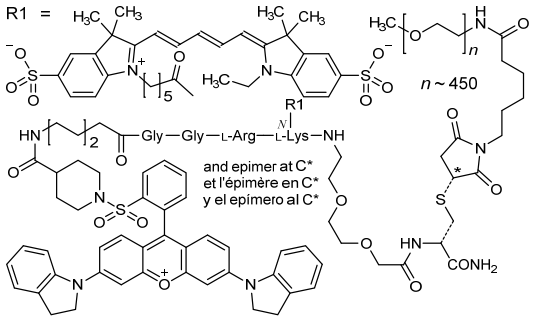
pégulicianine

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

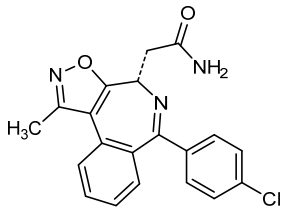
pélabrésib

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

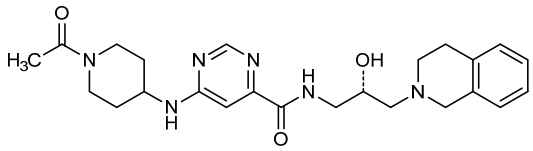
$C_{20}H_{16}ClN_3O_2$



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

$C_{24}H_{32}N_6O_3$



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"

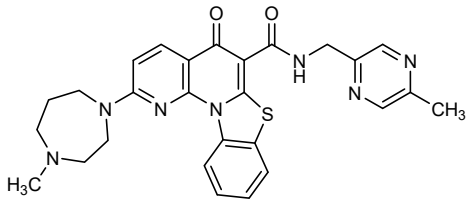
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
298, 298"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

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

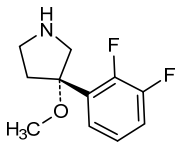
pirépémat

(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

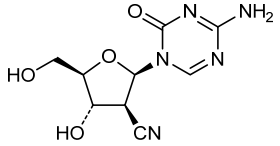
radgocitabine

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

```
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
```

Light chain / Chaîne légère / Cadena ligera

```
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

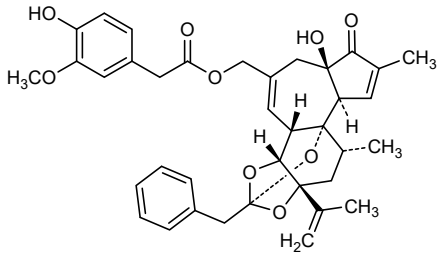
résinifératoxine

(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

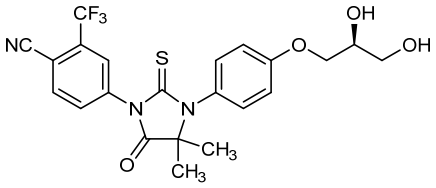
rezvilutamide

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

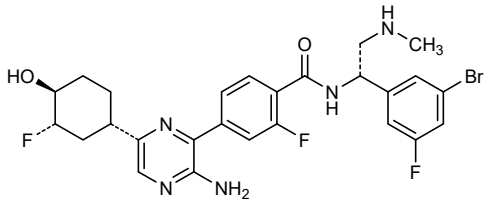
rinéterkib

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

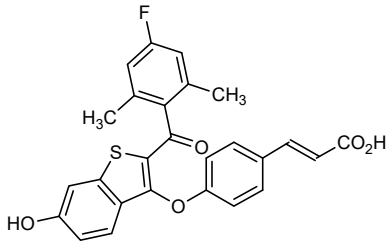
$C_{26}H_{27}BrF_3N_5O_2$



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

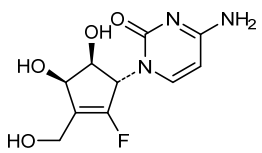
$C_{26}H_{19}FO_5S$



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

$C_{10}H_{12}FN_3O_4$



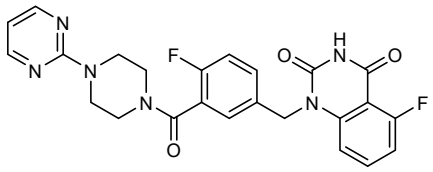
senaparibum

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

$C_{24}H_{20}F_2N_6O_3$



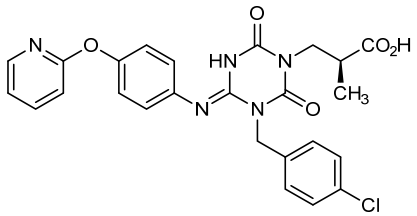
sivopixantum

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

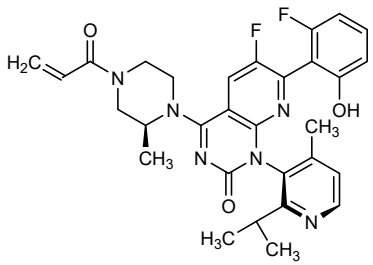
sotorasib

(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)

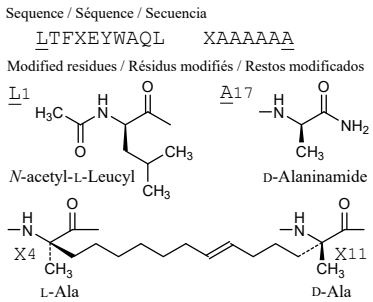
sulanémadline

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

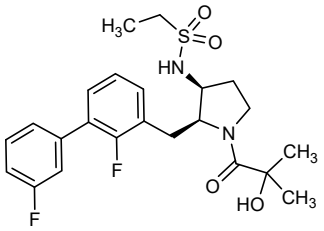
suntinorexton

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.

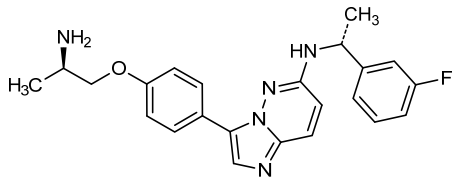
taletrectinibum

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

```
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
```

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 (h 11 - h 11)	506-761				
Inter-h14 (h 14 - h 14)	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

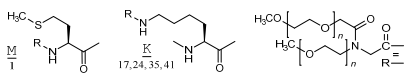
Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación

none / aucune / ninguna

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

major / principal / mayormente : **M**1, **K**17;

minor / secondaire / inferior : **K**24, **K**35, **K**41



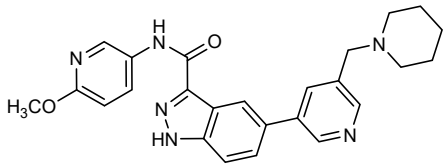
tenvumestrocelum

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

$C_{25}H_{26}N_6O_2$



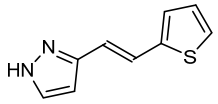
terevalefimum

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

$C_9H_8N_2S$



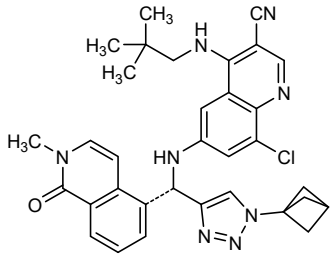
tilpisertibum

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 [*N*2'- deacetyl-*N*2'-(4-mercapto-4-methyl-1-oxopentyl)- maytansine] via the reducible SPDB linker [*N*-succinimidyl 4-(2-pyridyldithio)butanoate]
For the *ravtansine* part, please refer to the document "*INN for pharmaceutical substances: Names for radicals, groups and others*"*

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 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, 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

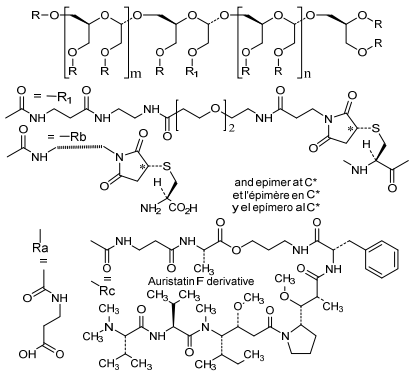
```
QVQLVQSGAE VVKPGASVKM SCKASGYTFT GYNIHWVKQA PGQGLEWIGA  50
IYPGNGDTSY KQKFRGRATL TADTSTSTVY MELSSLRSED SAVYYCARGE 100
TARATFAYWG QGTLVTVSSG ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKRVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP 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  50
TSSLYSGVPS RFSGSGSGTD YTLTISSLQP EDFATYYCQQ YSKLPLTFGQ 100
GTKLELKRRT 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) 22-96 147-203 264-324 370-428
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 polimero 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 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.

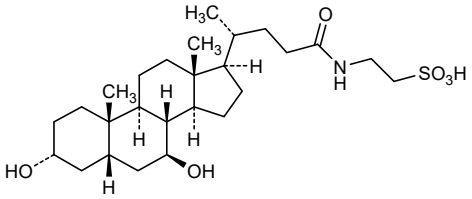
ursodoxicoltaurinum

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

$C_{26}H_{45}NO_6S$



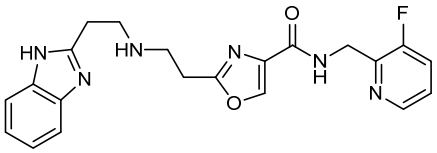
vamifeportum

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

$C_{21}H_{21}FN_6O_2$



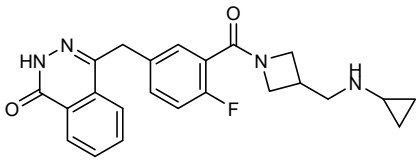
venadaparibum

venadaparib — 3^4-fluoro-7-aza-1(1)-phthalazina-5(1,3)-azetidina-3(1,3)-benzena-8(1)-cyclopropanaoctaphane-1^4(1^3*H*),4-dione

vénadaparib — 3^4-fluoro-7-aza-1(1)-phthalazina-5(1,3)-azétidina-3(1,3)-benzèna-8(1)-cyclopropanaoctaphane-1^4(1^3*H*),4-dione

venadaparib — 3^4-fluoro-7-aza-1(1)-ftalazina-5(1,3)-azetidina-3(1,3)-bencena-8(1)-ciclopropanaoctafano-1^4(1^3*H*),4-diona

$C_{23}H_{23}FN_4O_2$



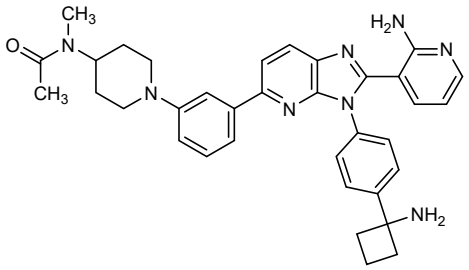
vevorisertibum

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)

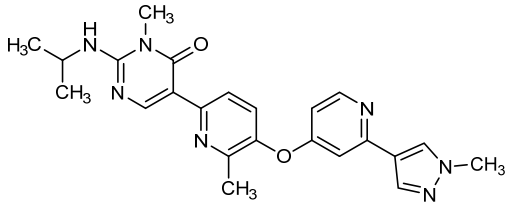
vimseltinibum

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
```

Light chain / Chaîne légère / Cadena ligera

```
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

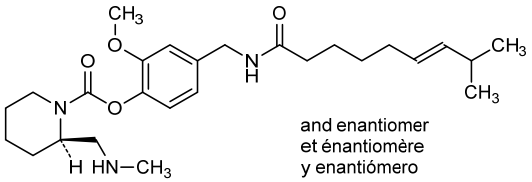
vocacapsaicinum

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

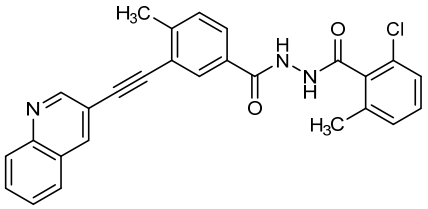
vodobatinibum

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
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-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"

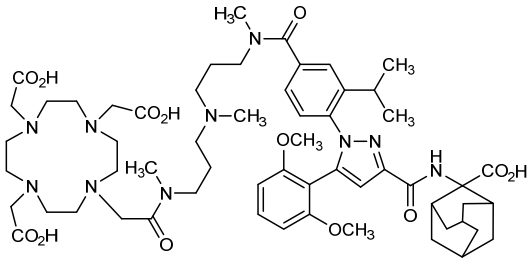
zalsenertantum tetraxetanum

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

$C_{58}H_{84}N_{10}O_{13}$



zanidatamabum zovodotinum #

zanidatamab zovodotin

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
```

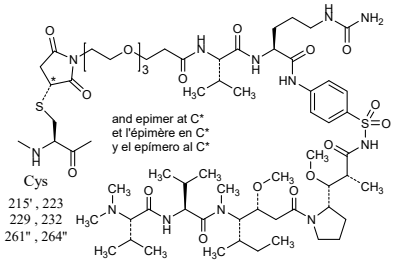
3. Chain / Chaîne / Cadena: IG scFv-h-CH2-CH3 (anti-ERBB2 ECD4)

```
GDIQMTQSPS SLSASVGDRV TITCRASQDV NTAVAWYQQK PGKAPKLLIY  50
SASFLYSGVP SRFSGSRSGT DFTLTISSLQ PEDFATYYCQ QHYTTPPTFG 100
QGTKVEIKGG SGGGSGGGSG GGSGGGSGEV 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.

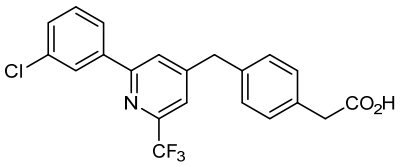
Modified residues / résidus modifiés / restos modificados:



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

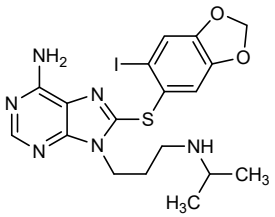
$C_{21}H_{15}ClF_3NO_2$



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')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1, glycoforme 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"

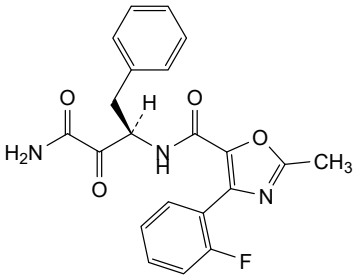
dazcapistatum

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

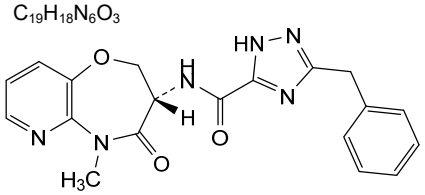
eclitasertibum

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

$C_{19}H_{18}N_6O_3$



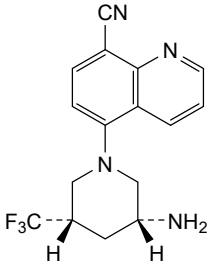
enpatoranum

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>$m^1\Psi$).

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>$m^1\Psi$).

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>$m^1\Psi$).

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}>A
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"

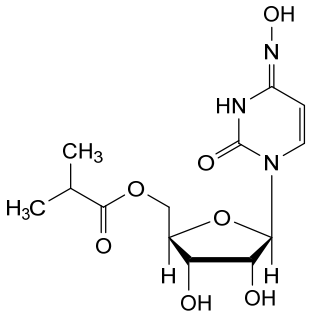
molnupiravirum

molnupiravir — N^4-hydroxycytidine 5'-(2-methylpropanoate)

molnupiravir — 5'-(2-méthylpropanoate) de N^4-hydroxycytidine

molnupiravir — 5'-(2-metilpropanoato) de N^4-hidroxicitidina

$C_{13}H_{19}N_3O_7$



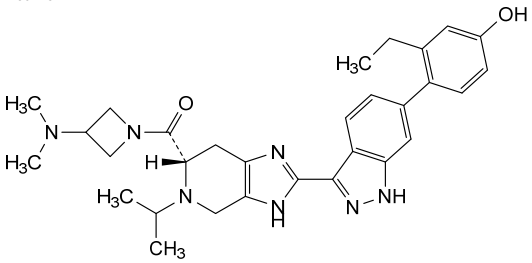
nezulcitinibum

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 KKYLNSILN**V 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

Heavy chain / Chaîne lourde / Cadena pesada

```
QITLKESGPT LVKPTQTLTL TCSFSGFSLS TSGVGVGWIR QPPGKALEWL  50
ALIDWDDNKY HTTSLKTRLT ISKDTSKNQV VLTMTNMDPV DTATYYCARI 100
PGFLRYRNRY YYYGMDVWGQ GTTVTVSSAS TKGPSVFPLA PSSKSTSGGT 150
AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP 200
SSSLGTQTYI CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPELLGGPS 250
VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT 300
KPREEQYNST YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA 350
KGQPREPQVY TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN 400
NYKTTPPVLD SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK 450
SLSLSPGK                                               458
```

Light chain / Chaîne légère / Cadena ligera

```
ELVLTQPPSV SAAPGQKVTI SCSGSSSNIG NNYVSWYQQL PGTAPKLLIY  50
DNNKRPSGIP DRFSGSKSGT SATLGITGLQ TGDEADYYCG TWDSSLSAGV 100
FGGGTELTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADGSPVK AGVETTKPSK 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) 22-97 155-211 272-332 378-436
22"-97" 155"-211" 272"-332" 378"-436"
Intra-L (C23-C104) 22'-89' 138'-197'
22'"-89'" 138'"-197'"
Inter-H-L (h 5-CL 126) 231-215' 231"-215'"
Inter-H-H (h 11, h 14) 237-237" 240-240"

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:
308, 308"
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:
458, 458"

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"

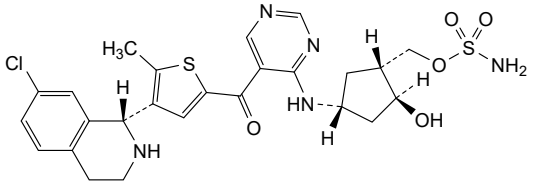
subasumstatum

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
tamtuvetmab
tamtuvetmab

replace the description by the following one
remplacer la description par la suivante
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*
	to**g**lato de tigilanol	ti**g**lato 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

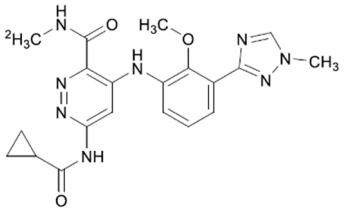
Procedure and Guiding Principles / Procédure et Directives / Procedimientos y principios generales

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.

1　毒薬・劇薬等の指定審査資料のまとめ

<table>
<tr><td>化学名・別名</td><td>6-(Cyclopropanecarboxamido)-4-[2-methoxy-3-(1-methyl-1H-1,2,4-triazol-3-yl)anilino]-N-($^{2}H_3$)methylpyridazine-3-carboxamide</td></tr>
<tr><td>構造式</td><td>  </td></tr>
<tr><td>効能・効果</td><td>既存治療で効果不十分な下記疾患
尋常性乾癬、膿疱性乾癬、乾癬性紅皮症</td></tr>
<tr><td>用法・用量</td><td>通常、成人にはデュークラバシチニブとして 1 回 6mg を 1 日 1 回経口投与する。</td></tr>
<tr><td>劇薬等の指定</td><td></td></tr>
<tr><td>市販名及び
有効成分・分量</td><td>原薬：デュークラバシチニブ
製剤：ソーティクツ錠 6mg（1 錠中デュークラバシチニブとして 6mg 含有）</td></tr>
<tr><td>毒　性</td><td>単回投与毒性
<table>
<tr><th>概略の致死量 (mg/kg)</th><th>経口</th></tr>
<tr><td>マウス　雌雄
ラット　雌雄
サル　雌雄</td><td>＞200 mg/kg
＞400 mg/kg
＞30 mg/kg</td></tr>
</table>
反復投与毒性
<table>
<tr><th>動物種</th><th>投与期間、投与経路</th><th>投与量 (mg/kg/day)</th><th>無毒性量 (mg/kg/day)</th><th>主な所見</th></tr>
<tr><td>ラット</td><td>1 ヵ月間（qd）、経口</td><td>5, 15, 75</td><td>5</td><td>5 mg/kg/day 以上：リンパ球数、白血球数及び脾臓重量の減少
15 mg/kg/day 以上：脾臓の小型化及び白脾髄のリンパ球減少、血小板数の減少（雌）
75 mg/kg/day：胸腺の小型化、重量及びリンパ球の減少</td></tr>
<tr><td>ラット</td><td>3 ヵ月間（qd）、経口</td><td>2, 5, 15</td><td>15</td><td>2 mg/kg/day 以上：リンパ球数及び白血球数の減少
5 mg/kg/day 以上：脾臓の小型化及び重量の減少（雌）
15 mg/kg/day：脾臓の白脾髄小型化及びリンパ球減少（雌）</td></tr>
</table></td></tr>
</table>

	ラット	6 ヵ月間（qd）、経口	5, 15, 50	5	5 mg/kg/day 以上：リンパ球数、白血球数及び脾臓重量の減少、KLH 感作に対する TDAR の低下 15 mg/kg/day 以上：体重及び摂餌量減少（雌）、脾臓の小型化、血小板数及び赤血球系パラメータ、網状赤血球数、骨髄細胞数の減少、下顎及び腸間膜リンパ節のリンパ球数減少 50 mg/kg/day：体重減少（雄）
	サル	1 ヵ月間（qd）、経口	0.5, 1.5, 5	5	1.5 mg/kg/day 以上 : 赤血球系パラメータの減少 5 mg/kg/day 以上：血小板数の減少、好酸球数の増加（雄）
	サル	3 ヵ月間（qd）、経口	0.75, 1.5, 5	5	0.75 mg/kg/day 以上：皮膚変化、好酸球数の増加 5 mg/kg/day : 赤血球系パラメータ及び血小板数の減少
	サル	9 ヵ月間（qd）、経口	1, 3, 10/5[a]	<1	1 mg/kg/day 以上：皮膚変化、液状便、赤血球系パラメータの減少、好酸球数の増加、KLH 感作に対する TDAR の低下 3 mg/kg/day 以上：活動性低下、円背位、歯肉の蒼白化、体温上昇 10/5 mg/kg/day：尿潜血（雄）、血小板数の減少
	[a] 10 mg/kg/day の用量で Day 1～49 に投与した後、1 週間の休薬期間を設け、その後 Day 57 から投与期間終了まで 5 mg/kg の用量で投与した。 qd：1 日 1 回投与 KLH：キーホールリンペットヘモシアニン、TDAR：T 細胞依存性抗体反応				
副作用	治験薬との関連のある有害事象が安全性解析対象集団 1,438 例中 323 例［22.5%］に認められた。多く認められた治験薬との関連のある有害事象は、「上咽頭炎」［2.5%（36/1438 例）］、「上気道感染」［2.1%（30/1438 例）］、「下痢」［2.0%（29/1438 例）］、「頭痛」［1.6%（23/1438 例）］、「ざ瘡」［1.0%（14/1438 例）］であった。また、多く認められた治験薬との関連のある有害事象のうちの臨床検査異常は、「血中クレアチンホスホキナーゼ増加」［1.0%（14/1438 例）］、「血中免疫グロブリン E 増加」［0.2%（3/1438 例）］、「C-反応性蛋白増加」［0.2%（3/1438 例）］、「好酸球数増加」［0.2%（3/1438 例）］、「糸球体濾過率減少」［0.2%（3/1438 例）］であった。				
会社	ブリストル・マイヤーズ スクイブ株式会社　　製剤：輸入				

第3部　品質に関する文書

3.2.S　原薬

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/ 参考
3.2.S	Drug Substance	-	20[redacted]年[redacted]月～[redacted]	海外	社内報	評価

3.2.P　製剤

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/ 参考
3.2.P	Drug Product	-	20[redacted]年[redacted]月～[redacted]	海外	社内報	評価

3.2.A　その他

(該当なし)

3.2.R　各極の要求資料

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/ 参考
3.2.R	Regional Information	-	-	-	-	-

3.3　参考文献

(該当なし)

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

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/ 参考
4.2.1.1-1	Characterization of Tyk2 inhibitor, BMS-986165, in biochemical and human immune cell assays	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Amendment01	-	-	-	-	-
4.2.1.1-2	Biochemical and cellular potency and selectivity of BMT-153261 and BMT-158170, metabolites of BMS-986165	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Amendment01	-	-	-	-	-
	Amendment02	-	-	-	-	-
4.2.1.1-3	Potencies of BMS-986165 and inhibitors of JAK1, JAK2, and JAK3 in an IL-7-induced human whole blood assay	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.1.1-4	In vitro analysis of BMS-986165 in assays using whole blood from rats and cynomolgus monkeys	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Amendment01	-	-	-	-	-
4.2.1.1-5	A head-to-head comparison in human whole blood potency between BMS-153261 (metabolite) and BMS-986165 (parent)	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.1.1-6	Human whole blood potency of BMT-334616, a metabolite of BMS-986165	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.1.1-7	Whole blood potency of BMT-153261 and BMT-158170, metabolites of BMS-986165	[redacted]	20[redacted]年[redacted]月～[redacted]年[redacted]月	海外	社内報	評価
4.2.1.1-8	Potencies of BMS-986165 and inhibitors of JAK1, JAK2, and JAK3 in human whole blood assays	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.1.1-9	In vivo pre-clinical pharmacology with the Tyk2 inhibitor, BMS‑986165	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

	Amendment01	-	-	-	-	-
	Amendment02	-	-	-	-	-

4.2.1.2 副次的薬理試験

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/ 参考
4.2.1.2-1	BMS-986165 (BMT-143848): In vitro receptor, ion channel, transporter binding and enzyme interaction assessment	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.1.2-2	BMT-158170: In vitro receptor, ion channel, transporter binding and enzyme interaction assessment	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.1.2-3	BMT-153261: In vitro receptor, ion channel, transporter binding and enzyme interaction assessment	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.1.2-4	In vitro analysis of BMT-153261 and BMT-158170, metabolites of BMS-986165 in whole blood from rats and cynomolgus monkeys stimulated with IL-2 or TPO	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.1.2-5	In vitro analysis of BMS-986165 in whole blood from rats and cynomolgus monkeys stimulated with IL-2 or TPO	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

4.2.1.3 安全性薬理試験

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/ 参考
4.2.1.3-1	BMS-986165 (BMT-143848): Effects on cardiac ion channels	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.1.3-2	BMT-143848 (BMS-986165): Exploratory in vitro cardiomyocyte, isolated-perfused heart and aortic smooth muscle studies	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.1.3-3	BMS-986165 (BMT-143848): Single-dose oral investigative cardiovascular study in telemetrized male rats	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

4.2.1.3-4	BMT-143848: Electrophysiological effects in anesthetized rabbits	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.1.3-5	BMS-986165/BMT-143848: Single-dose oral exploratory cardiovascular telemetry study in dogs	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Amendment01	-	-	-	-	-
4.2.1.3-6	BMS-986165 (BMT-143848): Single-dose exploratory cardiovascular telemetry study in monkeys	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Amendment01	-	-	-	-	-
4.2.1.3-7	BMS-986165: Single-dose oral cardiovascular telemetry study in monkeys	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Amendment01	-	-	-	-	-
	Amendment02	-	-	-	-	-

4.2.1.4 薬力学的薬物相互作用試験
(該当なし)

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

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考
4.2.2.1-1	Quantitative determination of BMS-986165 in mouse EDTA plasma by LC-MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Addendum No.1 to the report entitled "Quantitative determination of BMS-986165 in mouse EDTA plasma by LC-MS/MS"	[redacted]	20[redacted]年[redacted]月	海外	社内報	評価
	Addendum No.2 to the report entitled "Quantitative determination of BMS-986165 in mouse EDTA plasma by LC-MS/MS"	[redacted]	20[redacted]年[redacted]月	海外	社内報	評価
	Addendum No.3 to the report entitled "Quantitative determination of BMS-986165 in mouse EDTA plasma by LC-MS/MS"	[redacted]	20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.1-2	Quantitative determination of BMS-986165 in rat EDTA plasma by LC-MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

	Amendment No. 1 to the report entitled “Quantitative determination of BMS-986165 in rat EDTA plasma by LC-MS/MS”	[redacted]	-	海外	社内報	評価
	Amendment No. 2 to the report entitled “Quantitative determination of BMS-986165 in rat EDTA plasma by LC-MS/MS”	[redacted]	-	海外	社内報	評価
	Addendum No. 1 to the report entitled “Quantitative determination of BMS-986165 in rat EDTA plasma by LC-MS/MS”	[redacted]	20[redacted]年[redacted]月	海外	社内報	評価
	Addendum No. 2 to the report entitled “Quantitative determination of BMS-986165 in rat EDTA plasma by LC-MS/MS”	[redacted]	20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.1-3	Quantitative determination of BMS-986165 in rabbit EDTA plasma by LC-MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Addendum No. 1 to the report entitled “Quantitative determination of BMS-986165 in rabbit EDTA plasma by LC-MS/MS”	[redacted]	20[redacted]年[redacted]月	海外	社内報	評価
	Addendum No. 2 to the report entitled “Quantitative determination of BMS-986165 in rabbit EDTA plasma by LC-MS/MS”	[redacted]	20[redacted]年[redacted]月	海外	社内報	評価
	Addendum No. 3 to the report entitled “Quantitative determination of BMS-986165 in rabbit EDTA plasma by LC-MS/MS”	[redacted]	20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.1-4	Quantitative determination of BMS-986165 in dog EDTA plasma by LC-MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.1-5	Method validation for the quantitation of BMS-986165 in mouse plasma by turbo ion spray LC/MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.1-6	Method validation for the quantitation of BMT-153261 and BMT-158170 in mouse plasma by turbo ion spray LC/MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Addendum 1 to the method validation for the quantitation of BMT-153261 and BMT-158170 in mouse plasma by turbo ion spray LC/MS/MS	[redacted]	20[redacted]年[redacted]月	海外	社内報	評価

4.2.2.1.-7	Method validation for the quantitation of BMS-986165 in rat plasma by turbo ion spray LC/MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Addendum 1 to the method validation for the quantitation of BMS-986165 in rat plasma by turbo ion spray LC/MS/MS	[redacted]	20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.1-8	Method validation for the quantitation of BMT-153261 and BMT-158170 in rat plasma by turbo ion spray LC/MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Addendum 1 to method validation for the quantitation of BMT-153261 and BMT-158170 in rat plasma by turbo ion spray LC/MS/MS	[redacted]	20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.1-9	Method validation for the quantitation of BMS-986165 in rabbit plasma by turbo ion spray LC/MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Addendum 1 to the method validation for the quantitation of BMS-986165 in rabbit plasma by turbo ion spray LC/MS/MS	[redacted]	20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.1-10	Method validation for the quantitation of BMT-153261 and BMT-158170 in rabbit plasma by turbo ion spray LC/MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Addendum 1 to method validation for the quantitation of BMT-153261 and BMT-158170 in rabbit plasma by turbo ion spray LC/MS/MS	[redacted]	20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.1-11	Quantitative determination of BMS-986165 in monkey EDTA plasma by LC-MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Addendum No. 1 to the report entitled “Quantitative determination of BMS-986165 in monkey EDTA plasma by LC-MS/MS”	[redacted]	20[redacted]年[redacted]月	海外	社内報	評価
	Amendment No. 1 to the report entitled “Quantitative Determination of BMS-986165 in monkey EDTA plasma by LC-MS/MS”	[redacted]	-	海外	社内報	評価

4.2.2.1-12	Quantitative determination of BMS-986165 metabolites BMT-153261 and BMT-158170 in mouse EDTA plasma by LC-MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.1-13	Quantitative determination of BMS-986165 metabolites BMT-153261 and BMT-158170 in rat EDTA plasma by LC-MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Amendment No. 1 to the report entitled “Quantitative determination of BMS-986165 metabolites BMT-153261 and BMT-158170 in rat EDTA plasma by LC-MS/MS”	[redacted]	-	海外	社内報	評価
4.2.2.1-14	Quantitative determination of BMS-986165 metabolites BMT-153261 and BMT-158170 in monkey EDTA plasma by LC-MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.1-15	Quantitative determination of BMS-986165 metabolite BMT-334616 in mouse EDTA plasma by LC-MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.1-16	Quantitative determination of BMS-986165 metabolite BMT-334616 in rat EDTA plasma by LC-MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.1-17	Quantitative determination of BMS-986165 metabolite BMT-334616 in monkey EDTA plasma by LC-MS/MS	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

4.2.2.2 吸収

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考
4.2.2.2-1	In vitro characterization of absorption, distribution, metabolism, and elimination properties of BMS-986165	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.2-2	Substrate potential of BMS-986165 towards human P-glycoprotein	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.2-3	In vitro determination of transport kinetics for BMS-986165 using human BCRP and MDR1 efflux transporter expressing cells	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

4.2.2.2-4	Nonclinical evaluation of the pharmacokinetics and metabolism of BMS-986165	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Nonclinical evaluation of the pharmacokinetics and metabolism of BMS-986165 (Report amendment No.01)	[redacted]	-	海外	社内報	評価

4.2.2.3 分布

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考
4.2.2.3-1	Assessment of red blood cell partitioning and the blood-to-plasma ratio for BMS-986165 and its metabolite, BMT-153261	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Assessment of red blood cell partitioning and the blood-to-plasma ratio for BMS-986165 and its metabolite, BMT-153261 (Report amendment No.01)	[redacted]	-	海外	社内報	評価
4.2.2.3-2	Evaluation of in vitro human plasma protein binding of BMS-986165 and metabolite BMT-153261 by equilibrium dialysis	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.3-3	Binding of BMS-986165 and its metabolite, BMT-153261, to the human plasma proteins, serum albumin, and α1 acid glycoprotein	[redacted]	20[redacted]年[redacted]月~20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.3-4	In vitro assessment of substrate potential of BMS-986165 and its metabolite BMT-153261 towards human organic cation transporter 1	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	In vitro assessment of substrate potential of BMS-986165 and its metabolite BMT-153261 towards human organic cation transporter 1 (Report amendment No. 01)	[redacted]	-	海外	社内報	評価
4.2.2.3-5	In vitro assessment of the inhibitory effect of cyclosporine A on the transporter-mediated hepatic uptake of BMS-986165 into human hepatocytes in suspension	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

4.2.2.3-6	In vitro assessment of substrate potential of BMS-986165 and its metabolite BMT-153261 towards human organic anion transporter (OAT)1, OAT2, OAT3, organic cation transporter (OCT)2, multidrug and toxin extrusion protein (MATE) 1, and MATE2-K	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.3-7	Assessment of the uptake clearance of BMT-153261 (an active metabolite of BMS-986165) into human hepatocytes in suspension	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.3-8	Assessment of the uptake clearance of BMT-158170, a metabolite of BMS-986165, into human hepatocytes in suspension	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.3-9	Tissue distribution of radioactivity following a single oral dose of [^{14}C]BMS-986165 (20 mg/kg) dose in male Long-Evans rats using quantitative whole body autoradiography (QWBA)	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.3-10	Placental transfer, lacteal excretion, and tissue distribution of radioactivity in pregnant female rats and tissue distribution of radioactivity in male and non-pregnant female rats following oral administration of [^{14}C]BMS-986165	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

4.2.2.4 代謝

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考
4.2.2.4-1	Assessment of metabolic clearance of BMS-986165 in human hepatocytes via the relay method	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Assessment of metabolic clearance of BMS-986165 in human hepatocytes via the relay method (Report amendment No. 1)	[redacted]	-	海外	社内報	評価

4.2.2.4-2	Metabolism of BMS-986165 (deuterated [redacted]) and *不純物B in human liver microsomes	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.4-3	Investigation of cytochrome P450 enzymes responsible for the formation of BMT-153261 (N-desmethyl metabolite) from BMS-986165 in human liver microsomes	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.4-4	Investigation of glucuronidation kinetics of BMS-986165 in human liver microsomes	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.4-5	Biotransformation of [^{14}C]BMS-986165 after a single oral dose administration to CBYB6F1 hybrid mice	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.4-6	Biotransformation of [^{14}C]BMS-986165 after oral administration to bile duct-cannulated and intact rats	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.4-7	Biotransformation of [^{14}C]BMS-986165 after oral administration to bile duct-cannulated monkeys	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.4-8	Biotransformation of [^{14}C]BMS-986165 in humans following a single oral dose administration	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

4.2.2.5 排泄

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考
4.2.2.5-1	Plasma pharmacokinetics and excretion balance of [^{14}C]BMS-986165-derived radioactivity following a single oral dose of [^{14}C]BMS-986165 to male CByB6F1 hybrid mice	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

＊新薬承認情報提供時に置き換え

4.2.2.5-2	Determination of pharmacokinetics and elimination of total radioactivity in bile, urine, and feces after oral administration of [^{14}C]BMS-986165 to bile duct- cannulated monkeys	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.5-3	Radioanalysis in support of clinical protocol No. IM011016	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

4.2.2.6 薬物動態学的薬物相互作用（非臨床）

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/ 参考
4.2.2.6-1	In vitro characterization of absorption, distribution, metabolism, and elimination properties of BMT-158170, a metabolite of BMS-986165	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.6-2	In vitro characterization of absorption, distribution, metabolism, and elimination properties of BMT-153261, a metabolite of BMS-986165	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.6-3	Inhibition potential of BMS-986165 and its metabolite, BMT-153261, towards uridine 5'-diphospho-glucuronosyltransferases (UGTs) in human recombinant UGTs and human liver microsomes	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.6-4	Inhibition of human recombinant carboxylesterase (CES) 2 by BMS-986165	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.6-5	In vitro evaluation of BMS-986165 potential to induce transcription of the human cytochrome P450 genes CYP3A4, 2B6, and 1A2 in human primary hepatocytes	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.6-6	In vitro characterization of BMS-986165 for CYP induction potential using sandwich-cultured transporter certified hepatocytes	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

4.2.2.6-7	In vitro evaluation of the effects of BMS-986165 on the activity of human transporters: OCT1, OCT2, and MATE1	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.6-8	Inhibition potential of BMS-986165 and its metabolites, BMT-153261 and BMT-158170, towards human multidrug and toxin extrusion protein (MATE) 2-K	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.2.6-9	In vitro characterization of BMS-986165 distribution properties: Human liver microsomal protein binding	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

4.2.2.7 その他の薬物動態試験
(該当なし)

4.2.3 毒性試験
4.2.3.1 単回投与毒性試験

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考
4.2.3.1-1	BMS-986165: Single-dose oral exploratory toxicokinetic and tolerability study in rats	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.1-2	BMT-143848: Single dose oral exploratory toxicokinetic and tolerability study in dogs	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.1-3	BMT-143848: Single-dose oral exploratory toxicokinetic and tolerability study in monkeys	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考

4.2.3.2 反復投与毒性試験

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考
4.2.3.2-1	BMT-143848 (BMS-986165): Three-day oral exploratory toxicokinetic and tolerability study in male mice	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.2-2	BMS-986165: 5-day oral exploratory toxicity study in CByB6F1 mice	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考

4.2.3.2-3	BMS-986165: Five-day oral toxicokinetic and tolerability study in CByB6F1 mice	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
	Amendment 01	-	-	-	-	-
4.2.3.2-4	BMT-143848: Four-day oral exploratory toxicity study in male rats	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.2-5	BMS-986165: Five-day oral exploratory toxicokinetic study in sprague dawley rats	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.2-6	BMS-986165: Five-day oral toxicokinetic and tolerability study in rats	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.2-7	BMT-143848: Two-week oral exploratory toxicity study in rats	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
	Metabolomics report	-	-	-	-	-
4.2.3.2-8	BMS-986165: One-month oral toxicity study in rats with a 2-week recovery	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.3.2-9	BMS-986165: Three-month oral toxicity study in rats with a one-month post-dose recovery	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.3.2-10	BMS-986165: Six-month oral toxicity study in rats with a two-month post-dose recovery	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.3.2-11	BMS-986165: Five-day oral exploratory toxicokinetic and tolerability study in monkeys	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.2-12	BMS-986165: Five-day oral exploratory toxicokinetic study in monkeys	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.2-13	BMS-986165: One-month oral toxicity study in monkeys with a two-week recovery	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Amendment 01	-	-	-	-	-
4.2.3.2-14	BMS-986165: Three-month oral toxicity study in monkeys with a one-month post-dose recovery	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.3.2-15	BMS-986165: Nine-month oral toxicity study in monkeys with a two-month post-dose recovery	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Amendment 01	-	-	-	-	-
	Amendment 02	-	-	-	-	-

	Amendment 03	-	-	-	-	-

4.2.3.3 遺伝毒性試験

4.2.3.3.1 In vitro試験

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考
4.2.3.3.1-1	BMT-143848: Exploratory Ames bacterial reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.3.1-2	BMS-986165: Ames reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.3.3.1-3	BMT-158170: Exploratory Ames bacterial reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.3.1-4	BMT-158170: Ames reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.3.3.1-5	BMT-153261: Exploratory Ames bacterial reverse-mutation study in Salmonella typhimurium	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.3.1-6	BMT-153261: Ames reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.3.3.1-7	BMT-143848: Exploratory in vitro micronucleus study in chinese hamster ovary cells	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.3.1-8	BMS-986165: Cytogenetics study in chinese hamster ovary cells	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.3.3.1-9	BMT-158170: Exploratory in vitro micronucleus study in chinese hamster ovary cells	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.3.1-10	BMT-158170: In vitro micronucleus study in chinese hamster ovary cells	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

4.2.3.3.1-11	BMT-153261: Exploratory in vitro micronucleus study in chinese hamster ovary cells	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.3.1-12	BMT-153261: In vitro micronucleus study in chinese hamster ovary cells	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

4.2.3.3.2 In vivo試験
(該当なし)

4.2.3.4 がん原性試験
4.2.3.4.1 長期がん原性試験

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考
4.2.3.4.1-1	BMS-986165: Five-day and 28-day oral toxicity study in CByB6F1 mice	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.3.4.1-2	BMS-986165: Six-month oral carcinogenicity study in CByB6F1/Tg rasH2 hemizygous mice	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.3.4.1-3	BMS-986165: Two-year oral gavage carcinogenicity study in rats	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

4.2.3.4.2 短期又は中期がん原性試験
(該当なし)

4.2.3.4.3 その他の試験
(該当なし)

4.2.3.5 生殖発生毒性試験
4.2.3.5.1 受胎能及び着床までの初期胚発生に関する試験

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考
4.2.3.5.1-1	BMS-986165: Oral study of fertility and early embryonic development in female rats	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Amendment 01	-	-	-	-	-

4.2.3.5.2 胚・胎児発生に関する試験

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/ 参考
4.2.3.5.2-1	BMS-986165: Ten-day oral expanded range-finding study in pregnant rats	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.5.2-2	BMS-986165: Oral study of embryo-fetal development in rats	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.3.5.2-3	BMS-986165: A 10-day oral toxicokinetic study in pregnant rats	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.3.5.2-4	BMS-986165: Thirteen-day oral exploratory expanded range-finding study in pregnant rabbits	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.5.2-5	BMS-986165: Oral study of embryo-fetal development in rabbits	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
4.2.3.5.2-6	BMS-986165: A 13-day oral toxicokinetic study in pregnant rabbits	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

4.2.3.5.3 出生前及び出生後の発生並びに母体の機能に関する試験

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/ 参考
4.2.3.5.3-1	BMS-986165: Oral study of pre- and postnatal development in rats	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

4.2.3.5.4 新生児を用いた試験
(該当なし)

4.2.3.6 局所刺激性試験
(該当なし)

4.2.3.7 その他の毒性試験
4.2.3.7.1 抗原性試験
(該当なし)

4.2.3.7.2 免疫毒性試験
(該当なし)

4.2.3.7.3 毒性発現の機序に関する試験
(該当なし)

4.2.3.7.4 依存性試験
(該当なし)

4.2.3.7.5 代謝物の毒性試験
(該当なし)

4.2.3.7.6 不純物の毒性試験

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考
4.2.3.7.6-1	BMS-986165: One-month oral impurity qualifying toxicity study in rats	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価
	Amendment 01	-	-	-	-	-
	Amendment 02	-	-	-	-	-
	Amendment 03	-	-	-	-	-
4.2.3.7.6-2	*有機化合物1 : Ames reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.7.6-3	*不純物D : Ames reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.7.6-4	*不純物E ([redacted]): Ames reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.7.6-5	*不純物F : Ames reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.7.6-6	*不純物G [redacted]): Ames reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考

＊新薬承認情報提供時に置き換え

	Amendment 01	-	-	-	-	-
4.2.3.7.6-7	*不純物H ([redacted]): Ames reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
	Amendment 01	-	-	-	-	-
4.2.3.7.6-8	*不純物I : Reverse mutation assay 'Ames test' using Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.7.6-9	*有機化合物2: Ames reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.7.6-10	*不純物J ([redacted]): Ames reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.7.6-11	*有機化合物3 [[redacted]]: Ames reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.7.6-12	*有機化合物3 : 30-Day oral investigative Pig-A mutant erythrocyte evaluation in male Sprague Dawley rats with peripheral blood micronucleus and liver comet analysis	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.7.6-13	*不純物K ([redacted]): Exploratory Ames bacterial reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.7.6-14	*有機化合物4 ([redacted]): Reverse mutation assay "Ames test" using Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考

＊新薬承認情報提供時に置き換え

4.2.3.7.6-15	*有機化合物5: Ames reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.7.6-16	*有機化合物6: Ames reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.7.6-17	*不純物L : Ames reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考
4.2.3.7.6-18	*不純物M [redacted]: Ames reverse-mutation study in Salmonella typhimurium and Escherichia coli	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	参考

4.2.3.7.7 その他の試験

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考
4.2.3.7.7-1	BMS-986165: Neutral red uptake phototoxicity assay in Balb/c 3T3 mouse fibroblasts	[redacted]	20[redacted]年[redacted]月～20[redacted]年[redacted]月	海外	社内報	評価

4.3 参考文献

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考
-	A critical function for transforming growth factor-beta, interleukin 23 and proinflammatory cytokines in driving and modulating human $T_{(H)}$-17 responses.	Volpe E, Servant N, Zollinger R, et al.	-	-	Nat Immunol 2008;9:650-7.	-
-	A natural mutation in the Tyk2 pseudokinase domain underlies altered susceptibility of B10.Q/J mice to infection and autoimmunity.	Shaw MH, Boyartchuk V, Wong S, et al.	-	-	Proc Nat Acad Sci 2003; 100:11594-9.	-
-	A review of background findings in cynomolgus monkeys (Macaca fascicularis) from three different geographical origins.	Drevon-Gaillot E, Perron-Lepage MF, Clément C, et al.	-	-	Exp Toxicol Pathol 2006;58:77-88.	-

＊新薬承認情報提供時に置き換え

-	Activated STING in a vascular and pulmonary syndrome.	Liu Y, Jesus AA, Marrero B, et al.	-	-	N Engl J Med 2014;371:507-18.	-
-	Anifrolumab, an anti-interferon-alpha receptor monoclonal antibody, in moderate-to-severe systemic lupus erythematosus.	Furie R, Khamashta M, Merrill JT.	-	-	Arthritis Rheumatol 2017;69:376-86.	-
-	Assessment of male rodent fertility in general toxicology 6-month studies.	Mitchard T, Jarvis P, and Stewart J.	-	-	Birth Defects Res B Dev Reprod Toxicol 2012;95:410-20.	-
-	Association of increased interferon-inducible gene expression with disease activity and lupus nephritis in patients with systemic lupus erythematosus.	Feng X, Wu H, Grossman JM, et al.	-	-	Arthritis Rheum 2006;54:2951-62.	-
-	Autoimmune pathways in mice and humans are blocked by pharmacological stabilization of the TYK2 pseudokinase domain.	Burke JR, Cheng L, Gillooly KM, et al.	-	-	Sci Transl Med 2019;11:eaaw1736.	-
-	Best practices for evaluation of bone marrow in nonclinical toxicity studies.	Reagan WJ, Irizarry-Rovira A, Poitout-Belissent F, et al.	-	-	Toxicol Pathol 2011;39:435-48.	-
-	Biology and significance of the JAK/STAT signalling pathways.	Kiu H, Nicholson SE.	-	-	Growth Factors 2012;30:88-106.	-
-	Comparison of human duodenum and Caco-2 gene expression profiles for 12,000 gene sequence tags and correlation with permeability of 26 drugs.	Sun D, Lennernas H, Welage LS, et al.	-	-	Pharm Res 2002;19:1400-16.	-
-	Compromised humoral and delayed-type hypersensitivity responses in IL-23-deficient mice.	Ghilardi N, Kljavin N, Chen Q, et al.	-	-	J Immunol 2004;172:2827-33.	-
-	Crosstalk between platelets and microbial pathogens.	Li C, Li J, and Ni H.	-	-	Front Immunol 2020;11:1962.	-
-	Cytokines IL-17 and IL-22 in the host response to infection.	Valeri M and Raffatellu M.	-	-	Pathog Dis 2016;74:ftw111.	-

-	Decrease in intracellular concentration causes the shift in Km value of efflux pump substrates.	Korjamo T, Kemilainen H, Heikkinen AT, et al.	-	-	Drug Metab Dispos 2007;35:1574-9.	-
-	Differential selectivity of efflux transporter inhibitors in Caco-2 and MDCK-MDR1 monolayers: a strategy to assess the interaction of a new chemical entity with P-gp, BCRP, and MRP2.	Mease K, Sane R, Podila L, et al.	-	-	J Pharm Sci 2012;101:1888-97.	-
-	Discovery of competitive and noncompetitive ligands of the organic cation transporter 1 (OCT1; SLC22A1).	Chen EC, Khuri N, Liang X, et al.	-	-	J Med Chem 2017;60:2685-96.	-
-	Drug-induced acneiform eruption.	Du-Thanh A, Kluger N, Bensalleh H, et al.	-	-	Am J Clin Dermatol 2011;12:233-45.	-
-	Early occurrence of spontaneous tumors in CD-1 mice and Sprague-Dawley rats.	Son WC, Gopinath C.	-	-	Toxicol Pathol 2004;32:371-4.	-
-	Effects of a MATE protein inhibitor, pyrimethamine, on the renal elimination of metformin at oral microdose and at therapeutic dose in healthy subjects.	Kusuhara H, Ito S, Kumagai Y, et al.	-	-	Clin Pharmacol Ther 2011;89:837-44.	-
-	Efficacy and safety of ustekinumab in psoriatic arthritis patients with peripheral arthritis and physician-reported spondylitis: post-hoc analyses from two phase III, multicentre, double-blind, placebo-controlled studies (PSUMMIT-1/PSUMMIT-2).	Kavanaugh A, Puig L, Gottlieb AB et al.	-	-	Ann Rheum Dis 2016;75:1984-8.	-
-	Efficacy and safety results from a phase III, randomized controlled trial comparing the safety and efficacy of briakinumab with etanercept and placebo in patients with moderate to severe chronic plaque psoriasis.	Strober BE, Crowley JJ, Yamauchi PS, et al.	-	-	Br J Dermatol 2011;165:661-8.	-
-	Enhanced and persistent inhibition of organic cation transporter 1 activity by preincubation of cyclosporine A.	Panfen E, Chen W, et al.	-	-	Drug Metab Dispos 2019;47:1352-60.	-

-	Exposure-response relationships for the efficacy and safety of risankizumab in Japanese subjects with psoriasis.	Suleiman AA, Khatri A, Oberoi RK, et al.	-	-	Clin Pharmacokinet 2020;59:575-89.	-
-	Guidance for industry. In vitro drug interaction studies-cytochrome P450 enzyme- and transporter-mediated drug interactions.	Department of Health and Human Services, Food and Drug Administration, Center for Drug Evaluation and Research.	-	-	Published 2020.	-
-	Guideline on the investigation of drug interactions.	European Medicines Agency, Committee for Medicinal Products for Human Use.	-	-	Adopted 2012.	-
-	Hemostasis. In: Latimer KS editor.	Bordeaux MK, Spangler EA, and Welles EG.	-	-	Duncan and Prasse's Veterinary Laboratory Medicine: Clinical Pathology. 5th ed. Wiley-Blackwell; 2011:107-44.	-
-	Highly selective inhibition of Tyrosine Kinase 2 (TYK2) for the treatment of autoimmune diseases: Discovery of the allosteric inhibitor BMS-986165.	Wrobleski ST, Moslin R, Lin S, et al.	-	-	J Med Chem 2019;62:8973-95.	-
-	Human TYK2 deficiency: mycobacterial and viral infections without hyper-IgE syndrome.	Kreins AY, Ciancanelli MJ, Okada S, et al.	-	-	J Exp Med 2015;212:1641-62.	-
-	Human tyk2 kinase deficiency: another primary immunodeficiency syndrome.	Watford WT, O'Shea JJ.	-	-	Immunity 2006;25:695-7.	-
-	Human tyrosine kinase 2 deficiency reveals its requisite roles in multiple cytokine signals involved in innate and acquired immunity.	Minegishi Y, Saito M, Morio T, et al.	-	-	Immunity 2006;25:745-55.	-

-	IFN-alpha/beta enhances BCR-dependent B cell responses.	Braun D, Caramalho I, Demengeot J.	-	-	Int Immunol 2002;14:411-9.	-
-	IL-23-responsive innate lymphoid cells are increased in inflammatory bowel disease.	Geremia A, Arancibia-Carcamo CV, Fleming MP, et al.	-	-	J Exp Med 2011;208:1127–33.	-
-	In vitro p-glycoprotein inhibition assays for assessment of clinical drug interaction potential of new drug candidates: a recommendation for probe substrates.	Rautio J, Humphreys JE, Webster LO, et al.	-	-	Drug Metab Dispos 2006;34:786-92.	-
-	Incidences and range of spontaneous findings in control cynomolgus monkeys (Macaca fascicularis) used in toxicity studies.	Chamanza R, Marxfeld HA, Blanco AI, et al.	-	-	Toxicol Pathol 2010;38:642-57.	-
-	Induction of dendritic cell differentiation by IFN-alpha in systemic lupus erythematosus.	Blanco P, Palucka AK, Gill M, et al.	-	-	Science 2001;294:1540-3.	-
-	Interferon and biologic signatures in dermatomyositis skin: specificity and heterogeneity across diseases.	Wong D, Kea B, Pesich R, et al.	-	-	PLoS One 2012;7:e29161.	-
-	Interferon-alpha-dependent activation of Tyk2 requires phosphorylation of positive regulatory tyrosines by another kinase.	Gauzzi MC, Velazquez L, McKendry R, et al.	-	-	J Biol Chem 1996;271:20494-500.	-
-	Interferon-inducible gene expression signature in peripheral blood cells of patients with severe lupus.	Baechler EC, Batliwalla FM, Karypis G, et al.	-	-	Proc Natl Acad Sci U S A 2003;100:2610-5.	-
-	Interferons and scleroderma—a new clue to understanding the pathogenesis of scleroderma?	Coelho LFL, de Oliveira JG, Kroon EG.	-	-	Immunol Lett 2008;118:110-5.	-
-	Membrane transporters in drug development.	International Transporter Consortium	-	-	Nat Rev Drug Discov. 2010; 9:215-36.	-
-	Model analysis of the concentration dependent permeability of P-gp substrates.	Tachibana T, Kitamura S, Kato M, et al.	-	-	Pharm Res 2010;27:442-6.	-

-	Modular transcriptional repertoire analyses of adults with systemic lupus erythematosus reveal distinct type I and type II interferon signatures.	Chiche L, Jourde-Chiche N, Whalen E, et al.	-	-	Arthritis Rheumatol 2014;66:1583-95.	-
-	Modulation of human BCRP (ABCG2) activity by anti-HIV drugs.	Weiss J, Rose J, Storch CH, et al.	-	-	J Antimicrob Chemother. 2007;59:238-45.	-
-	Natural occurrence of neoplastic lesions in young Sprague-Dawley rats.	Ikezaki S, Takagi M, Tamura K.	-	-	J Toxicol Pathol 2011;24:37-40.	-
-	Olumiant (baricitinib) Pharmacology Review(s).	Department of Health and Human Services, Public Health Service, Food and Drug Administration, Center for Drug Evaluation and Research.	-	-	NDA 207924; 2018.	-
-	Overexpression of interleukin-12 and T helper 1 predominance in lupus nephritis.	Tucci M, Lombardi L, Richards HB, et al.	-	-	Clin Exp Immunol 2008;154:247-54.	-
-	Partial impairment of cytokine responses in TYK2-deficient mice.	Karaghiosoff M, Neubauer H, Lassnig C, et al.	-	-	Immunity 2000;13:549-60.	-
-	Physiological parameters in laboratory animals and humans.	Davies, B, Morris T.	-	-	Pharm Res 1993;10:1093-5.	-
-	Plasmacytoid dendritic cells induce plasma cell differentiation through type I interferon and interleukin 6.	Jego G, Palucka AK, Blanck JP, et al.	-	-	Immunity 2003;19:225-34.	-
-	Plasmacytoid predendritic cells initiate psoriasis through interferon-alpha production.	Nestle FO, Conrad C, Tun-Kyi A, et al.	-	-	J Exp Med 2005;202:135-43.	-
-	Platelet consumption and sequestration in severe acute respiratory failure.	Schneider RC, Zapol WM, and Carvalho AC.	-	-	Amer Rev Respir Dis 1980;122:445-51.	-

-	Pooling of platelets in the spleen: role in the pathogenesis of “hypersplenic” thrombocytopenia.	Aster RH.	-	-	J Clin Invest 1966;45:645-57.	-
-	Quantitative contribution of six major transporters to the hepatic uptake of drugs: "SLC-phenotyping" using primary human hepatocytes.	Bi Y, Costales C, Mathialagan S, et al.	-	-	J Pharmacol Exp Ther 2019;370:72-83.	-
-	Reliable rate measurements for active and passive hepatic uptake using plated human hepatocytes.	Bi Y, Scialis RJ, Lazzaro S, et al.	-	-	AAPS J 2017;19:787-96.	-
-	Role of P-selectin in platelet sequestration in pulmonary capillaries during endotoxemia.	Kiefmann R, Heckel K, Schenkat S, et al.	-	-	J Vasc Res 2006;43:473-81.	-
-	Sifalimumab, an anti-interferon-alpha monoclonal antibody, in moderate to severe systemic lupus erythematosus: a randomised, double-blind, placebo-controlled study.	Khamashta M, Merrill JT, Werth VP, et al.	-	-	Ann Rheum Dis 2016;75:1909-16.	-
-	Signaling by IL-12 and IL-23 and the immunoregulatory roles of STAT4.	Watford WT, Hissong BD, Bream JH, et al.	-	-	Immunol Rev 2004;202:139-56.	-
-	Spontaneous findings in the heart of Mauritian-origin cynomolgus macaques (Macaca fascicularis).	Vidal JD, Drobatz LS, Holliday DF, et al.	-	-	Toxicol Pathol 2010;38:297-302.	-
-	Spontaneous lesions of the cardiovascular system in purpose-bred laboratory nonhuman primates.	Chamanza R, Parry NMA, Rogerson P, et al.	-	-	Toxicol Pathol 2006;34:357-63.	-
-	Spontaneous malignant T-cell lymphoma in a young adult Crl:CD (SD) rat.	Matsushima K, Yamakawa S, Edamoto H, et al.	-	-	J Toxicol Pathol 2010;23:49-52.	-
-	Targeting the Janus kinase family in autoimmune skin diseases.	Howell MD, Kuo FI, Smith PA,	-	-	Front Immunol 2019;10:2342.	-
-	The influence of nonspecific microsomal binding on apparent intrinsic clearance, and its prediction from physicochemical properties.	Austin RP, Barton P, Cockroft SL, et al.	-	-	Drug Metab Dispos 2002;30:1497-503.	-

-	The JAK-STAT signaling pathway: input and output integration.	Murray PJ.	-	-	J Immunol 2007;178:2623-9.	-
-	The molecular regulation of Janus kinase (JAK) activation.	Babon JJ, Lucet IS, Murphy JM, et al.	-	-	Biochem J 2014;462:1-13.	-
-	The thrombopoietin receptor: structural basis of traffic and activation by ligand, mutations, agonists, and mutated calreticulin.	Varghese LN, Defour JP, Pecquet C, et al.	-	-	Front Endocrinol (Lausanne) 2017;8:59.	-
-	Thrombopoietin signal transduction requires functional JAK2, not TYK2.	Drachman JG, Millett KM, Kaushansky K.	-	-	J Biol Chem 1999;274:13480-4.	-
-	Tofacitinib suppresses antibody responses to protein therapeutics in murine hosts.	Onda M, Ghoreschi K, Steward-Tharp S, et al.	-	-	J Immunol 2014;193:48-55.	-
-	TYK2 plays a restricted role in IFN alpha signaling, although it is required for IL-12-mediated T cell function.	Shimoda K, Kato K, Aoki K, et al.	-	-	Immunity 2000;13:561-71.	-
-	Type I IFN drives a distinctive dendritic cell maturation phenotype that allows continued class II MHC synthesis and antigen processing.	Simmons DP, Wearsch PA, Canaday DH, et al.	-	-	J Immunol 2012;188:3116-26.	-
-	Type I interferon signaling in hematopoietic cells is required for survival in mouse polymicrobial sepsis by regulating CXCL10.	Kelly-Scumpia KM, Scumpia PO, Delano MJ, et al.	-	-	J Exp Med 2010;207:319-26.	-
-	Type I interferons keep activated T cells alive.	Marrack P, Kappler J, Mitchell T.	-	-	J Exp Med 1999;189:521-30.	-
-	Tyrosine kinase 2-mediated signal transduction in T lymphocytes is blocked by pharmacological stabilization of its pseudokinase domain.	Tokarski JS, Zupa-Fernandez A, Tredup JA, et al.	-	-	J Biol Chem 2015;290:11061-74.	-

-	Upadacitinib Non-clinical Review(s).	Department of Health and Human Services, Public Health Service, Food and Drug Administration, Center for Drug Evaluation and Research.	-	-	NDA 211675; 2018.	-
-	Ustekinumab induction and maintenance therapy in refractory Crohn's disease.	Sandborn WJ, Gasink C, Gao LL, et al.	-	-	N Engl J Med 2012;367:1519-28.	-
-	Xeljanz (tofacitinib) Pharmacology Review(s).	Department of Health and Human Services, Public Health Service, Food and Drug Administration, Center for Drug Evaluation and Research.	-	-	NDA 203214; 2011.	-

第5部　臨床試験報告書

5.2　全臨床試験一覧表

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
5.2	全臨床試験一覧表	-	-	-	-	-	-

5.3　臨床試験報告書
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

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
5.3.1.1-1	A Phase 1, Randomized, Open-Label, Single-Dose, Crossover Study to Evaluate the Bioavailability of BMS-986165 Tablet Formulation Relative to BMS-986165 Capsule Formulation and the Effect of a High-Fat/High-Calorie Meal and Increased Gastric pH on the Bioavailability of BMS-986165 Tablet Formulation in Healthy Subjects	-	2017年9月～2018年1月	海外	-	参考	無
	Erratum	-	-	-	-	-	-
5.3.1.1-2	Study to Evaluate the Absolute Bioavailability of BMS-986165 Tablet in Healthy Male Participants	-	2018年12月～2019年2月	海外	-	参考	無
	Addendum 01	-	-	-	-	-	-
5.3.1.1-3	An Open-label 3×3 Cross-over Study to Compare Effects of Famotidine Pretreatment and of Food on the Relative Bioavailability of Single Doses of BMS-986165 in Healthy Volunteers	-	2019年12月～2020年2月	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
(該当なし)

5.3.1.3 In Vitro-In Vivoの関連を検討した試験報告書
(該当なし)

5.3.1.4 生物学的及び理化学的分析法検討報告書

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
5.3.1.4-1	Quantitative determination of BMS-986165 in human EDTA plasma by LC-MS/MS	-	2015年11月	海外	-	-	無
	Addendum 01	-	2015年12月	海外	-	-	無
	Addendum 02	-	2016年4月	海外	-	-	無
	Addendum 03	-	2017年1月	海外	-	-	無
	Addendum 04	-	2021年2月	海外	-	-	無
5.3.1.4-2	Method Validation for the Quantitation of BMS-986165 in Human Plasma by Turbo Ion Spray LC/MS/MS	-	2016年12月	海外	-	-	無
	Revised Method Validation Report	-	2018年2月	海外	-	-	無
	Addendum 01	-	2018年2月	海外	-	-	無
5.3.1.4-3	Method Validation for the Quantitation of BMS-986165 in Human Plasma (Low Range) by Turbo Ion Spray LC/MS/MS	-	2017年8月	海外	-	-	無
	Addendum 01	-	2018年2月	海外	-	-	無
5.3.1.4-4	Method Validation for the Quantitation of BMS-986165 and BMT-153261 in Human Plasma by Turbo Ion Spray LC/MS/MS	-	2018年10月	海外	-	-	無
	Addendum 01	-	2019年7月	海外	-	-	無
	Addendum 02	-	2021年3月	海外	-	-	無
5.3.1.4-5	Validation of an LC-MS/MS method for the determination of BMS-986165 and BMT-153261 in human plasma (K_2EDTA)	-	2020年4月	海外	-	-	無
	Amendment 01	-	2020年4月	海外	-	-	無
5.3.1.4-6	Method Validation for the Quantitation of BMT-158170 in Human Plasma by Turbo Ion Spray LC/MS/MS	-	2018年10月	海外	-	-	無

	Addendum 01	-	2020年2月	海外	-	-	無
	Addendum 02	-	2021年3月	海外	-	-	無
5.3.1.4-7	Validation of an LC-MS/MS method for the determination of BMT-158170 in Human Plasma	-	2019年7月	海外	-	-	無
	Amendment 01	-	2019年7月	海外	-	-	無
	Amendment 02	-	2019年7月	海外	-	-	無
	Amendment 03	-	2019年7月	海外	-	-	無
5.3.1.4-8	Method Validation for the Quantitation of BMT-334616 in Human Plasma by Turbo Ion Spray LC/MS/MS	-	2020年3月	海外	-	-	無
	Addendum 01	-	2020年9月	海外	-	-	無
5.3.1.4-9	Quantitative determination of BMS-986165 in 0.2% CHAPS Human Urine by LC-MS/MS	-	2015年11月	海外	-	-	無
	Addendum 01	-	2016年1月	海外	-	-	無
	Addendum 02	-	2016年3月	海外	-	-	無
	Addendum 03	-	2016年4月	海外	-	-	無
	Addendum 04	-	2021年2月	海外	-	-	無
5.3.1.4-10	Method Validation for the Quantitation of BMS-986165 in Treated Human Urine by Turbo Ion Spray LC/MS/MS	-	2017年6月	海外	-	-	無
	Addendum 01	-	2018年9月	海外	-	-	無
5.3.1.4-11	Method Validation for the Quantitation of BMT-153261 and BMT-158170 in Treated Human Urine by Turbo Ion Spray LC/MS/MS	-	2019年4月	海外	-	-	無
	Addendum 01	-	2020年12月	海外	-	-	無
5.3.1.4-12	Method Validation for the Quantitation of BMT-334616 in Treated Human Urine by Turbo Ion Spray LC/MS/MS	-	2020年3月	海外	-	-	無
	Addendum 01	-	2020年9月	海外	-	-	無
5.3.1.4-13	Method Validation for the Quantitation of BMS-986165 and BMT-409408-02 in Human Plasma by Turbo Ion Spray LC/MS/MS	-	2019年6月	海外	-	-	無

5.3.1.4-14	Method Validation for the Quantitation of BMS-986165, BMT-153261, and BMT-158170 in Treated Human Dialysis Buffer by Turbo Ion Spray LC/MS/MS	-	2020年5月	海外	-	-	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

(該当なし)

5.3.2.2 肝代謝及び薬物相互作用試験報告書

(該当なし)

5.3.2.3 他のヒト生体試料を用いた試験報告書

(該当なし)

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

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
5.3.3.1-1	Randomized, Double-Blind, Placebo-Controlled, Single and Multiple Ascending Dose Study to Evaluate the Safety, Tolerability, Pharmacokinetics, and Pharmacodynamics of BMS-986165 in Healthy Subjects and to Evaluate the Safety, Tolerability, Pharmacokinetics, Pharmacodynamics, and Clinical Efficacy of BMS-986165 in Subjects with Moderate to Severe Psoriasis	-	2015年10月～2016年11月	海外	-	評価	有
	Addendum 01	-	-	-	-	-	-
	Addendum 02	-	-	-	-	-	-
	Exploratory Bioanalytical Study Report	-	-	-	-	-	-

5.3.3.1-2	Pharmacokinetics and Metabolism of [^{14}C]BMS-986165 in Healthy Male Participants	-	2017年1月～2017年2月	海外	-	参考	無

5.3.3.2 患者におけるPK及び初期忍容性試験報告書
(該当なし)

5.3.3.3 内因性要因を検討したPK試験報告書

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
5.3.3.3-1	An Open-Label, Single-Dose Study to Evaluate the Pharmacokinetics and Safety of BMS-986165 in Participants with Normal Renal Function and Participants with Mild, Moderate, and Severe Renal Impairment and in Participants with End-Stage Renal Disease (ESRD) on Hemodialysis	-	2019年4月～2020年2月	海外	-	参考	有
	Addendum 01	-	-	-	-	-	-
	Erratum	-	-	-	-	-	-
5.3.3.3-2	An Open-Label, Single-Dose Study to Evaluate the Pharmacokinetics and Safety of BMS-986165 in Participants with Normal Hepatic Function and Participants with Mild, Moderate and Severe Hepatic Impairment	-	2019年3月～2019年11月	海外	-	参考	有

5.3.3.4 外因性要因を検討したPK試験報告書

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
5.3.3.4-1	Effect of BMS-986165 on the Pharmacokinetics of Rosuvastatin	-	2017年2月～2017年4月	海外	-	参考	有
	Revised Bioanalytical Report – 170178APEJ_BPN_R1 – Long Term Stability Update	-	-	-	-	-	-

	Erratum	-	-	-	-	-	-
5.3.3.4-2	An Open-Label, Single-Sequence Study to Investigate the Effects of BMS-986165 on the Single-Dose Pharmacokinetics of Methotrexate in Healthy Male Subjects	-	2018年2月～2018年3月	海外	-	参考	無
	Addendum 01	-	-	-	-	-	-
	Erratum	-	-	-	-	-	-
5.3.3.4-3	The Effect of BMS-986165 on the Pharmacokinetics of a Combined Oral Contracepitive (Ethinyl Estradiol/Norethindrone) in Healthy Female Subjects	-	2017年8月～2017年12月	海外	-	参考	無
	Erratum	-	-	-	-	-	-
5.3.3.4-4	An Open-Label, Single-Sequence Study to Investigate the Effects of Cyclosporine on the Pharmacokinetics of BMS-986165 at Steady State in Healthy Male Participants	-	2018年3月～2018年5月	海外	-	参考	有
	Erratum	-	-	-	-	-	-
	Addendum 01	-	-	-	-	-	-
5.3.3.4-5	An Open-label, Single-sequence Study to Investigate the Effects of BMS-986165 at Steady-State on the Single Dose Pharmacokinetics of Mycophenolate Mofetil (MMF) in Healthy Male Subjects	-	2018年8月～2018年10月	海外	-	参考	有
5.3.3.4-6	An Open-label, Single-sequence Study to Investigate the Effects of Cytochrome P450 1A2 Induction by Ritonavir on the Pharmacokinetics of BMS-986165 in Healthy Participants	-	2019年8月～2019年10月	海外	-	参考	有
	Revised Bioanalytical Report – 191634ARM_BPN_R1 – Long Term Stability Update	-	-	-	-	-	-

5.3.3.4-7	An Open-label, Single-sequence Study to Investigate the Effects of Cytochrome P450 1A2 Inhibition on the Pharmacokinetics of BMS-986165 in Healthy Participants	-	2019年5月～2019年5月	海外	-	参考	有
5.3.3.4-8	An Open-Label, Single-Sequence Study to Investigate the Effects of Gastric Acid Suppression by Rabeprazole on the Pharmacokinetics of BMS-986165 in Healthy Participants	-	2019年5月～2019年7月	海外	-	参考	無
5.3.3.4-9	An Open-label, Single-sequence, Crossover Study to Investigate the Effects of OCT1 Inhibition Utilizing Pyrimethamine on Pharmacokinetics of BMS-986165 in Healthy Male Volunteers	-	2019年9月～2019年10月	海外	-	参考	無
5.3.3.4-10	An Open-label, Single-sequence, Crossover Study to Investigate the Effects of UGT1A9 Inhibitor Diflunisal, at Steady-State, on Pharmacokinetics of a Single Dose of BMS-986165 in Healthy Male and Female Volunteers	-	2019年10月～2019年11月	海外	-	参考	有

5.3.3.5 ポピュレーションPK試験報告書

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
5.3.3.5-1	Population PK analysis of BMS-986165 in healthy subjects and psoriasis patients, and exposure-response analysis of BMS-986165 in psoriasis patients	-	2018年1月	海外	-	参考	無
5.3.3.5-2	Population Pharmacokinetic Analysis of Deucravacitinib in Subjects with Moderate-to-Severe Psoriasis	-	2021年6月	海外	-	評価	有
5.3.3.5-3	Exposure-Response Analyses of Deucravacitinib in Subjects with Moderate to Severe Psoriasis	-	2021年7月	海外	-	評価	有

5.3.3.5-4	Population Pharmacokinetics of Deucravacitinib in Japanese Subjects with Moderate-to-Severe Psoriasis Addendum	-	2021年11月	海外	-	評価	有
5.3.3.5-5	Exposure-Response Addendum of Deucravacitinib in Japanese Subjects with Moderate to Severe Psoriasis	-	2021年11月	海外	-	評価	有

5.3.4 臨床薬力学（PD）試験報告書

5.3.4.1 健康被験者におけるPD試験及びPK/PD試験報告書

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
5.3.4.1-1	A Randomized, Double-Blind, Positive-Controlled, Placebo-Controlled, 4-Period Crossover Study to Investigate the Electrocardiographic Effects of BMS-986165 in Healthy Subjects	-	2018年6月～2018年9月	海外	-	評価	有
	Erratum	-	-	-	-	-	-

5.3.4.2 患者におけるPD試験及びPK/PD試験報告書

(該当なし)

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

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
5.3.5.1-1	IM011-011 Final CSR: A Multi-Center, Randomized, Double-Blind, Placebo-Controlled, Parallel Group Phase 2 Study to Evaluate the Clinical Efficacy and Safety of BMS-986165 in Subjects with Moderate to Severe Psoriasis	-	2016年11月～2018年11月	国内/海外	-	評価	有
	Addendum to Clinical Study Report for Study IM011011	-	-	-	-	-	-

5.3.5.1-2	IM011046 Primary CSR: A Multi-Center, Randomized, Double-Blind, Placebo- and Active Comparator-Controlled Phase 3 Study to Evaluate the Efficacy and Safety of BMS-986165 in Subjects with Moderate-to Severe Plaque Psoriasis	-	2018年8月～2021年8月	国内/海外	-	評価	有
5.3.5.1-3	IM011-047 Primary CSR: A Multi-center, Randomized, Double-Blind, Placebo- and Active Comparator-Controlled Phase 3 Study with Randomized Withdrawal and Retreatment to Evaluate The Efficacy and Safety of BMS-986165 in Subjects with Moderate-to-Severe Plaque Psoriasis	-	2018年7月～2021年8月	海外	-	評価	有

5.3.5.2 非対照試験報告書

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
5.3.5.2-1	IM011-066 Primary CSR: An Open-Label, Single-arm, Multi-Center, Phase 3 Study to Evaluate the Efficacy and Safety of BMS-986165 in Japanese Subjects with Moderate-to-Severe Psoriasis	-	2019年4月～2021年10月	国内	-	評価	有
5.3.5.2-2	IM011075 Interim CSR: An Open-Label, Multi-Center Extension Study to Characterize the Long-Term Safety and Efficacy of BMS-986165 in Subjects with Moderate-to-Severe Plaque Psoriasis	-	2019年8月～20[redacted]年[redacted]月	国内/海外	-	参考	無

5.3.5.3 複数の試験成績を併せて解析した報告書

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
5.3.5.3-1	Selective TYK2 Inhibition With Deucravacitinib Compared to JAK Inhibitors	-	2021年3月	-	-	-	-

5.3.5.3-2	Deucravacitinib is the Founding Member of a Novel Class, Selective Allosteric TYK2 Inhibitor, Distinct from the ATP-Competitive JAK Inhibitor Class	-	2021年7月	-	-	-	-
5.3.5.3-3	Integrated PK	-	2021年10月	-	-	-	有
5.3.5.3-4	Integrated Summary of Efficacy	-	2021年8月	-	-	-	有
5.3.5.3-5	Integrated Summary of Safety	-	2021年8月	-	-	-	有
5.3.5.3-6	J-Safety Pool: Summary of Clinical Safety Japan PsO	-	2021年10月	-	-	-	有

5.3.5.4 その他の試験報告書
(該当なし)

5.3.6 市販後の使用経験に関する報告書
(該当なし)

5.3.7 患者データ一覧表及び症例記録
5.3.7.1 主要な臨床試験の症例一覧表

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
5.3.7.1	主要な臨床試験の症例一覧表	-	-	-	-	-	-

5.3.7.2 有害事象発現症例一覧表

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
5.3.7.2	有害事象発現症例一覧表	-	-	-	-	-	-

5.3.7.3 重篤な有害事象発現症例一覧表

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
5.3.7.3	重篤な有害事象発現症例一覧表	-	-	-	-	-	-

5.3.7.4 臨床検査値異常変動発現症例一覧表

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
5.3.7.4	臨床検査値異常変動発現症例一覧表	-	-	-	-	-	-

5.3.7.5 臨床検査値の変動図

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
5.3.7.5	臨床検査値の変動図	-	-	-	-	-	-

5.4 参考文献

添付資料番号	タイトル	著者	試験実施期間	実施場所 国内/海外	掲載誌	評価/参考	申請電子データ有無
-	Adherence, satisfaction and preferences for treatment in patients with psoriasis in the European Union: a systematic review of the literature.	Belinchón I, Rivera R, Blanch C, et al.	-	-	Patient Prefer Adherence. 2016 Nov 17;10:2357-67	-	-
-	Age at disease onset: a key factor for understanding psoriatic disease.	Queiro R, Tejón P, Alonso S et al.	-	-	Rheumatology (Oxford) 2014;53(7):1178-85.	-	-
-	Attributable risk estimate of severe psoriasis on major cardiovascular events.	Mehta NN, Yu Y, Pinnelas R, et al.	-	-	Am J Med 2011;124:775.e1-e6.	-	-
-	Definition of treatment goals for moderate to severe psoriasis: a European consensus.	Mrowietz U, Kragballe K, Reich K, et al.	-	-	Arch Dermatol Res. 2011 Jan;303(1):1-10.	-	-
-	Dermatologist and patient preferences in choosing treatments for moderate to severe psoriasis.	Alcusky M, Lee S, Lau G, et al.	-	-	Dermatol Ther (Heidelb). 2017;7:463-83.	-	-

-	Enhanced platelet aggregation with TRAP-6 and collagen in platelet aggregometry in patients with venous thromboembolism.	Weber M, Gerdsen F, Gutensohn K, et al.	-	-	Thromb Res. 2002 Sep 15;107(6):325-8.	-	-
-	Environment, inflammation, and cancer.	Sansone P, Bromberg J.	-	-	Curr Opin Genet Dev. 2011 Feb;21(1):80-5.	-	-
-	Epidemiological survey from 2009 to 2012 of psoriatic patients in Japanese Society for Psoriasis Research.	Ito T, Takahashi H, Kawada A, et al.	-	-	J Dermatol 2018; 45: 293-301	-	-
-	Epidemiology of psoriasis and palmoplantar pustulosis: a nationwide study using the Japanese national claims database.	Kubota K, Kamijima Y, Sato T, et al.	-	-	BMJ Open 2015;5	-	-
-	Establishing the role of tyrosine kinase 2 in cancer.	Ubel C, Mousset S, Trufa D, et al.	-	-	OncoImmunology 2013;2:e22840	-	-
-	Global epidemiology of psoriasis: a systematic review of incidence and prevalence.	Parisi R, Symmons DP, Griffiths CE, et al.	-	-	J Invest Dermatol 2013;133(2):377-85.	-	-
-	Global Report on psoriasis.	World Health Organization.	-	-	WHO 2016.	-	-
-	Guidelines of care for the management of psoriasis and psoriatic arthritis: section 4. Guidelines of care for the management and treatment of psoriasis with traditional systemic agents.	Menter A, Korman NJ, Elmets CA et al.	-	-	J Am Acad Dermatol. 2009;61(3):451-85	-	-
-	Herpes zoster, hepatitis C, and tuberculosis risk with apremilast compared to biologics, DMARDs and corticosteroids to treat psoriasis and psoriatic arthritis.	Hagberg KW, Persson R, Vasilakis-Scaramozza C, et al.	-	-	Clin Epidemiol 2020;12:153-61.	-	-
-	Incidence rates of comorbidities among patients with psoriasis in the United States.	Feldman SR, Hur P, Zhao Y et al.	-	-	Dermatol Online J 2018;24:13030/qt2m18n6vj	-	-
-	Inhibition of interleukin-12 and/or interleukin-23 for the treatment of psoriasis: What is the evidence for an effect on malignancy?	Ergen EN, Yusuf N.	-	-	Exp Dermatol. 2018 Jul;27(7):737-47.	-	-

-	JAK inhibition as a therapeutic strategy for immune and inflammatory diseases.	Schwartz DM, Kanno Y, Villarino A, et al.	-	-	Nat Rev Drug Discov. 2017;16(12):843-62.	-	-
-	Janus kinases to jakinibs: from basic insights to clinical practice.	Gadina M, Le MT, Schwartz DM	-	-	Rheumatology (Oxford) 2019;58:i4-i16	-	-
-	Mechanisms of Disease: Psoriasis.	Nestle FO, Kaplan DH, Barker J.	-	-	N Engl J Med 2009;361:496-509.	-	-
-	Overview of venous thromboembolism.	Phillippe HM.	-	-	Am J Manag Care. 2017;23(20 Suppl):S376-S382.	-	-
-	Pathophysiology, Clinical Presentation, and Treatment of Psoriasis, A Review.	Armstrong AW, Read C.	-	-	JAMA 2020;323:1945-60.	-	-
-	Patient-reported reasons for the discontinuation of commonly used treatments for moderate to severe psoriasis.	Yeung H, Wan J, Van Voorhees AS, et al.	-	-	J Am Acad Dermatol 2013;68:64-72.	-	-
-	Patients with severe psoriasis are at increased risk of cardiovascular mortality: cohort study using the General Practice Research Database.	Mehta NN, Afzar RS, Shin DB et al.	-	-	Eur Heart J 2010;31:1000-6.	-	-
-	Protection from Psoriasis-Related Thrombosis after Inhibition of IL-23 or IL-17A.	Li Y, Golden JB, Camhi MI, et al.	-	-	J Invest Dermatol. 2018 Feb;138(2):310-5.	-	-
-	Psoriasis and Cardiovascular Comorbidities: Focusing on Severe Vascular Events, Cardiovascular Risk Factors and Implications for Treatment.	Hu S CH and Lan CCE.	-	-	Int J Mol Sci 2017;18:2211.	-	-
-	Psoriasis and risk of malignant lymphoma: a population-based cohort study.	Kamstrup MR, Skov L, Zachariae C, T et al.	-	-	Br J Dermatol. 2018;178(6):1435-6.	-	-
-	Psoriasis and Suicidality: A Review of the Literature.	Liang SE, Cohen JM, and Ho RS.	-	-	Dermatologic Ther. 2018;32(1):e12771.	-	-

-	Psoriasis carries an increased risk of venous thromboembolism: A danish nationwide cohort study.	Ahlehoff O, Gislason GH, Lindhardsen J, et al.	-	-	PLoS One 2011;6:e18125.	-	-
-	Psoriasis Pathogenesis and Treatment.	Rendon A, Schäkel K.	-	-	Int J Mol Sci 2019;20:1475.	-	-
-	Psoriasis: epidemiology, clinical features, and quality of life.	Langley RG, Krueger GG, Griffiths CE.	-	-	Ann Rheum Dis 2005;64:18-23.	-	-
-	Risk of malignancy with systemic psoriasis treatment in the Psoriasis Longitudinal Assessment Registry.	Fiorentino D, Ho V, Lebwohl MG, et al.	-	-	J Am Acad Dermatol 2017;77:845-54.e5.	-	-
-	S3 Guideline for the treatment of psoriasis vulgaris , update – Short version part 1 – Systemic treatment.	Nast A, Amelunxen L, Augustin M, et al.	-	-	J Dtsch Dermatol Ges 2018;16:645-69.	-	-
-	The Risk of Cancer in Patients With Psoriasis: A Population-Based Cohort Study in the Health Improvement Network.	Chiesa Fuxench ZC, Shin DB, Ogdie Beatty A, Gelfand JM.	-	-	JAMA Dermatol 2016;152(3):282-90.	-	-
-	The risk of depression, anxiety, and suicidality in patients with psoriasis: a population-based cohort study.	Kurd SK, Troxel AB, Crits-Christoph P et al.	-	-	Arch Dermatol 2010;146(8):891-5.	-	-
-	The risk of lymphoma in patients with psoriasis.	Gelfand JM, Shin DB, Neimann AL et al.	-	-	J Invest Dermatol. 2006;126 (10):2194-201	-	-
-	Treatment of erythrodermic psoriasis with biologics: A systematic review.	Carrasquillo O, Pabon-Cartagena G, Falto-Aizpurua L, et al.	-	-	J Am Acad Dermatol. 2020;83(1):151-8.	-	-
-	日本皮膚科学会乾癬生物学的製剤検討委員会　乾癬における生物学的製剤の使用ガイダンス（2019年版）	大槻マミ太郎, 佐伯秀久, 照井正 et al.	-	-	日皮会誌　2019;129(9):1845-64	-	-