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WHO Drug Information

WHO Drug Information provides an overview of topics relating to medicines development, regulation, quality and safety. The journal also publishes and reports on guidance documents and includes lists of International Nonproprietary Names for Pharmaceutical Substances (INN), ATC/DDD classification and monographs for The International Pharmacopoeia. It presents and describes WHO policies and activities while reflecting on technical and pharmaceutical topics of international and regional interest.

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Abbreviations and websites

CHMP	Committee for Medicinal Products for Human Use (EMA)
EMA	European Medicines Agency (www.ema.europa.eu)
EU	European Union
FDA	U.S. Food and Drug Administration (www.fda.gov)
Health Canada	Federal department responsible for health product regulation in Canada (www.hc-sc.gc.ca)
HPRA	Health Products Regulatory Authority, Ireland(www.hpra.ie)
HSA	Health Sciences Authority, Singapore (www.hsa.gov.sg)
ICDRA	International Conference of Drug Regulatory Authorities
ICH	International Council for Harmonisation of Technical Requirements for Pharmaceuticals for Human Use (www.ich.org)
IGDRP	International Generic Drug Regulators Programme (https://www.igdrp.com)
MHLW	Ministry of Health, Labour and Welfare, Japan
MHRA	Medicines and Healthcare Products Regulatory Agency, United Kingdom (www.mhra.gov.uk)
Medsafe	New Zealand Medicines and Medical Devices Safety Authority (www.medsafe.govt.nz)
Ph. Int	*The International Pharmacopoeia* (http://apps.who.int/phint/)
PMDA	Pharmaceuticals and Medical Devices Agency, Japan (www.pmda.go.jp/english/index.htm)
Swissmedic	Swiss Agency for Therapeutic Products(www.swissmedic.ch)
TGA	Therapeutic Goods Administration, Australia(www.tga.gov.au)
WHO	World Health Organization (www.who.int)
WHO MHP	WHO Access to Medicines and Health Products Division (www.who.int/medicines/en/)
WHO RPQ	WHO Regulation and Prequalification Department
WHO PQT	WHO Prequalification Unit (https://www.who.int/topics/prequalification/en/)
WHO HPS	WHO Health Product Policy and Standards Department

Note: The online version of this issue is available at www.who.int/medicines/publications/druginformation)

55th Expert Committee on Specifications for Pharmaceutical Preparations (ECSPP) meeting

1. Summary and recommendations

The World Health Organization (WHO) Expert Committee on Specifications for Pharmaceutical Preparations (ECSPP) advises the Director-General of WHO in the area of medicines quality assurance. It oversees the maintenance of *The International Pharmacopoeia* and provides guidance for use by relevant WHO units and regulatory authorities in WHO Member States to ensure that medicines meet unified standards of quality, safety and efficacy. The ECSPP's guidance texts are developed through a broad consensus-building process, including iterative public consultation. Representatives from international organizations, State actors, non-State actors, pharmacopoeias and relevant WHO departments are invited to the ECSPP's annual meetings, to provide updates and input to the Expert Committee's discussions.

At its Fifty-fifth meeting, held virtually from 12 to 19 October 2020, the ECSPP received updates on cross-cutting issues from other WHO bodies, including the Prequalification team, the Regulatory Systems Strengthening unit and the International Nonproprietary Names team. Updates were also provided by partner organizations, including the International Meeting of World Pharmacopoeias (IMWPs), the International Atomic Energy Agency (IAEA) and the United Nations Population Fund (UNFPA), on collaborative projects. The ECSPP was further updated on the latest efforts to ensure manufacturers and inspectors tackle antimicrobial resistance.

The European Directorate for the Quality of Medicines & HealthCare (EDQM) updated the ECSPP on its activities as the custodial centre in charge of international chemical reference substances (ICRS) for use with monographs of *The International Pharmacopoeia*. Results from the latest phase of the External Quality Assurance Assessment Scheme (EQAAS), which is organized by WHO with the assistance of EDQM, were also shared with the ECSPP.

The ECSPP reviewed new and revised specifications and general texts for quality control testing of medicines for inclusion in *The International Pharmacopoeia*. The Expert Committee adopted 17 pharmacopoeial texts (4 general chapters, 11 new and revised monographs, including 10 subject to a final review by a subgroup (*), and 2 corrections); and confirmed the release of 2 new ICRS established by the custodial centre for use in connection with *The International Pharmacopoeia*.

The ECSPP reviewed proposals for new and updated quality assurance and regulatory guidance, adopting 10 new guidance texts. In line with last year's recommendations, the ECSPP updated the WHO Biowaiver List as an annex to its report. Moreover, it agreed to annex *a consolidated list of all current guidelines and guidance texts adopted by the ECSPP* to date to the report (Annex 1).

Following an update from the Regulatory Systems Strengthening unit and further discussion therein, the Expert Committee adopted a definition for WHO-listed authorities (WLAs).

The sections that follow summarize the specific decisions and recommendations made by the ECSPP during its Fifty-fifth meeting in 2020.

1.1. Guidelines and decisions adopted and recommended for use

The following guidelines and decisions were adopted and recommended for use:

- *Points to consider when including Health Based Exposure Limits (HBELs) in cleaning validation* (Annex 2)
- *Good manufacturing practices: water for pharmaceutical use* (Annex 3)
- *WHO Guideline on data integrity* (Annex 4)
- *UNFPA/WHO Recommendations for condom storage and shipping* (Annex 5)
- *UNFPA/WHO Guidance on testing of male latex condoms* (Annex 6)
- *UNFPA/WHO Guidance on conducting post-market surveillance of condoms* (Annex 7)
- *WHO Biowaiver List* (Annex 8)
- *WHO Certification Scheme on the quality of pharmaceutical products moving in international commerce* (Annex 9)
- *Good reliance practices in the regulation of medical products: high level principles and considerations* (Annex 10)
- *Good regulatory practices for regulation of medical products* (Annex 11)

1.2. Texts adopted for inclusion in *The International Pharmacopoeia*

The ECSPP adopted a series of texts, chapters and monograph, as listed below.

1.2.1. General chapters

- Dissolution test for solid oral dosage forms (revision)
- General identification tests (revision)

1.2.2. Monographs

General monographs for dosage forms

- Powders for inhalation (new)
- Liquid preparations for oral use (revision)

COVID-19 therapeutics

- dexamethasone sodium phosphate (correction)
- dexamethasone phosphate injection (correction)
- remdesivir (new)*
- remdesivir intravenous infusion (new)*

Antiviral medicines, including antiretrovirals

- dolutegravir sodium (new) *
- dolutegravir tablets (new) *
- zanamivir (new) *
- zanamivir powder for inhalation, pre-metered (new) *

Medicines for tropical diseases

- albendazole chewable tablets (revision) *
- ivermectin tablets (revision)

Excipients

- sodium starch glycolate (new) *
- sodium laurilsulfate (new) *
- hydroxypropylcellulose, low-substituted (new) *

1.2.3. Omissions

The ECSPP agreed to omit the following texts from *The International Pharmacopoeia*:

- test for histamine-like substances (vasodepressor substances), including the whole of Chapter 3.6 and all reference to vasodepressor substances in the monographs on bleomycin sulfate, spectinomycin hydrochloride and streptomycin sulfate.

1.2.4. International chemical reference substances

The ECSPP confirmed the release of the following ICRS that have been newly characterized by the custodial centre, EDQM:

- estradiol valerate ICRS, batch 1; and
- moxifloxacin hydrochloride ICRS, batch 1.

1.3. Recommendations

The ECSPP made a series of recommendations related to quality assurance, as listed below. Progress on the suggested actions will be reported to the ECSPP at its Fifty-sixth meeting in October 2021.

The Expert Committee recommended that the WHO Secretariat, in collaboration with experts as appropriate, should take the actions listed next.

1.3.1. *The International Pharmacopoeia*

- Continue the development of monographs, general methods and texts and general supplementary information, including IAEA/WHO specifications for radiopharmaceuticals, in accordance with the 2020–2021 workplan and as decided at the meeting.
- Develop a concept for future work on excipient monographs in *The International Pharmacopoeia*, considering the need for such monographs from a public health perspective, addressing known quality deficiencies, and exploring ways to harmonize specifications with other pharmacopoeias.

1.3.2. Quality control – national laboratories

- Continue the EQAAS in support of national and regional Pharmaceutical Quality Control Laboratories (PQCLs), including continuing the post-assessment assistance programme.

1.3.3. Good manufacturing practices and related areas

- Continue collaborating with the European Union (EU), European Medicines Agency (EMA) and Pharmaceutical Inspection Co-operation Scheme (PIC/S) to harmonize guidance on sterile products and, if feasible, present such guidance for possible adoption at its next meeting in 2021.
- Continue the development of a new good manufacturing practices (GMP) text for radiopharmaceuticals for investigational use.
- Open the existing WHO guideline on cleaning validation to review and update it in accordance with the latest good practices, including the newly adopted *Points to consider when including Health Based Exposure Limits (HBELs) in cleaning validation.*
- Publish results of the survey of pharmaceutical manufacturers engaging in synthesis and/or production of antimicrobials on their waste and wastewater management practices in a regulatory journal.
- Assist national inspectorates and manufacturers towards implementing recommendations made in the *Points to Consider for manufacturers and inspectors: environmental aspects of manufacturing practices for the prevention of antimicrobial resistance.*

- Update the *WHO GMP for investigational pharmaceutical products for clinical trials in humans.*
- Explore the need for updated *WHO guidelines on transfer of technology in pharmaceutical manufacturing.*
- Explore the need for a new guideline to address good practices during the research and development of medicinal products

1.3.4. Distribution and supply chain

- Encourage WHO colleagues involved in procurement to support implementation of *Points to consider for setting the remaining shelf life of medical products upon delivery.*
- Circulate for public consultation the proposed amendment to consider emergency health kits for use in humanitarian emergency response as an additional example to the *Points to consider for setting the remaining shelf life of medical products upon delivery* guideline.

1.3.5. Regulatory mechanisms

- Start the next phase of the WHO Biowaiver Project (Cycle IV) to continue the Biopharmaceutics Classification System (BCS)-based classification of ten further active pharmaceutical ingredients (APIs): dexamethasone, doxycycline, ethambutol, isoniazid, hydroxycholoroquine, lamivudine, levonorgestrel, nifurtimox and proguanil.
- Undertake a pilot expansion study in Cycle IV of the WHO Biowaiver Project to consider API stability under pH conditions representative of stomach and small intestine.
- Promote the results of the WHO Biowaiver Project through publication, advocacy, engagement and partnership.
- Explore the feasibility of presenting the WHO Prequalification of Medicines team's product-specific guidance texts on how to design bioequivalence studies to the ECSPP with a view to making them more generally available to regulators.
- Continue efforts to update the *WHO List of International Comparator Products.*
- Evaluate a possible revision of *WHO Multisource (generic) pharmaceutical products: guidelines on registration requirements to establish interchangeability* (Annex 6, WHO Technical Report Series, No. 1003, 2017).
- Ensure a speedy implementation by WHO of the revised *WHO Certification Scheme on the quality of pharmaceutical products moving in international commerce.*
- Work with interested parties to facilitate the WHO Certification Scheme's implementation through electronic systems, including e-CPPs (certificates of a pharmaceutical product).

- Develop a situation analysis and proposed way forward for replacing references to stringent regulatory authorities (SRAs) with WLAs in relevant WHO documents and guidance.

1.3.6. Other

- Continue to serve as the Secretariat for IMWPs; and strive to publish articles about the IMWP, especially the pharmacopoeial global alert on COVID-19, in open-access peer-reviewed journals.
- Continue updating the Quality Assurance of Medicines Terminology Database on an annual basis.
  Promote the use of existing guidelines and guidance in the context of the COVID-19 pandemic.

***

WHO Certification Scheme on the Quality of Pharmaceutical Products moving in International Commerce

Update for improving reliance and adaptation to the new pharmaceutical environment

Summary

The *World Health Organization (WHO) Certification Scheme on the Quality of Pharmaceutical Products moving in International Commerce* (hereinafter referred to as the "Scheme") has demonstrated its value as a tool for quality assurance during the importation and exportation of medicines for WHO Member States. Since its approval in 1969, it became more and more widely used by national regulatory authorities and its main document, *The Certificate of a Pharmaceutical Product*, has proved to be an essential instrument in providing information about relevant provisions already approved in marketing authorization, including the good manufacturing practices of manufacturers and for the prevention and detection of the export, import and smuggling of falsified or substandard pharmaceutical preparations. This voluntary agreement has evolved constantly in order to respond to the regulatory and pharmaceutical environment demands.

This article summarizes the steps of the updating process of the Scheme since its creation, and particularly the modifications adopted during the last 14 years, until the endorsement of the revised Scheme by the Fifty-fifth WHO Expert Committee on Specifications for Pharmaceutical Preparations (ECSPP) in 2020. The milestones of the evolution of the Scheme are listed and described herein and show the active follow-up by the ECSPP and the World Health Assembly on the matters arising during its implementation. In addition, the main 25 changes made to the Scheme are explained. These have been discussed and approved in the last period of revision based on the comments and suggestions received during the public consultations and the inputs of expert working group meetings, the pharmaceutical industry, and the national and regional regulatory authorities.

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The amendments made to the Scheme address the problems identified and the opportunities for improvement. Participating experts and regulators consider that the Scheme will serve and respond to the current and anticipated challenges. The surveillance and timely analysis of its proper use will be essential in order to obtain the expected benefits of reliance and access to medicines, according to the Scheme's objectives.

Introduction

The *World Health Organization (WHO) Certification Scheme on the Quality of Pharmaceutical Products moving in International Commerce* (hereinafter referred to as the "Scheme") was adopted in 1969 by the Twenty-second World Health Assembly, with resolution WHA22.50 *(1)* which recommended to WHO Member States, to adopt and apply the requirements for *Good practices in the manufacture and quality control of drugs* (GMP). These internationally-recognized and respected standards provided the basis for the Scheme and were identified as a prerequisite for participation. Both the GMP and the Scheme were adopted by the same resolution.

The Scheme is a voluntary agreement intended to provide assurance to participating countries about the quality of pharmaceutical products moving in international commerce. It is considered as an important tool towards assuring the desired level of quality control on medical products in international commerce. At the beginning, its focus was on the manufacturer. Basically, the first edition certified that the product had been authorized for marketing by the competent authority and the manufacturers were inspected for GMP compliance. It also comprised the certification for batches.

A series of modifications have occurred in order to respond to the changing regulatory environment. Since its approval, the Scheme has attracted both controversy and support and there have been many discussions about its value. With this article, the evolution process of the Scheme is characterized with emphasis on the steps involved during the past 14 years, from 2006 until the last update developed in 2020, and the principal changes based on proposed solutions to the compiled key issues endorsed by the Fifty-fifth WHO Expert Committee on Specifications of Pharmaceutical Product (ECSPP), which report is published in WHO Technical Report Series No. 1033.

Chronology of amendments and updating of the Scheme

The Scheme was amended in 1975, by resolution WHA28.65 *(2)*. At that time, the Twenty-eight World Health Assembly adopted the revised texts of both the GMP and the Scheme. It was recommended to Member States to apply the revised requirements for GMP and to participate in the revised Scheme. After this time, the updating of these quality assurance tools run separately. The main changes in the Scheme were addressed to the basis of the certification, the exchange of information and details about the participation. A model of the *Certificate of Pharmaceutical Product(s)* (CPP), with explanatory notes, was included.

In 1988, the second amendment of the Scheme was approved by the Forty-first World Health Assembly, held from 2-13 May 1988. By resolution WHA41.18 *(3)*, the Assembly adopted the revised text of the expanded Scheme, invited those Member States which were not yet participating in the Scheme to join and all Member States to implement the recommendations, and all provisions of the expanded WHO Scheme, as far as possible.

Very significant changes were included in this second amendment. The scope of the Scheme was extended to veterinary use, with the modification of the concept of a pharmaceutical product as *¨any medicine intended for human use, or a veterinary product administered to food-producing animals, presented in its finished dosage form, or as a starting material for use in such a dosage form, when it is subject to control by legislation in the exporting and in the importing Member States*¨. Provisions were also made to include the complete product information as approved in the country of origin, together with its date of approval.

In 1989, WHO consulted both national regulatory authorities (NRAs) and international pharmaceutical industry associations on the implementation of the Scheme. The prime objective was to consider how the existing certification procedure might be effectively modified to mitigate the risks of fraudulent use of the Scheme and prevent illicit trade in falsified and substandard pharmaceutical products. The revision attempted to provide a procedure applicable to all circumstances of trade which ensured more rigorous control through a more effective exchange of information.

In 1990, the provisional guidelines and certificates were refined following field trials in a number of Member States and discussions during the sixth and seventh biennial International Conference of Drug Regulatory Authorities (ICDRA). They were endorsed by the WHO ECSPP during its Thirty-second meeting from 10-15 December 1990**,** without prejudice to any changes that might be considered necessary in the course of further consultation *(4)*.

The Expert Committee provisionally endorsed the guidelines for implementing the expanded Certification Scheme and three different forms of attestation were proposed:

- a product certificate issued by the competent authority in the exporting country, which should be requested by the importing authority primarily when it intends to issue or vary a product license (CPP);
- a statement of licensing status, also issued by the competent authority in the exporting country, which may be requested by an importing agent who simply needs confirmation as to whether or not specified products are licensed in the country of origin; information that is important when screening any bid made in response to an international tender; and
- a batch certificate, which is usually issued by the manufacturer as a warranty that a specific consignment of a product conforms to documented specification.

The Expert Committee considered that the objectives of the Scheme would be advanced if the three forms, once adopted in their definitive form, were used without further adjustment by all participating countries.

A process of consultation of the guidelines was opened until June of 1991 *(5)*, and in 1992 the Forty-fifth World Health Assembly, which met from 4-14 May, endorsed the *Guidelines for implementation of the WHO Certification Scheme* by resolution WHA45.29. These guidelines were intended to be evaluated and revised as necessary, and Members States were urged to implement them and to issue certificates within five years in a form to be agreed upon in light of the experience gained in preliminary field testing *(5)*. Provisions for certification of active ingredients were also included within the scope of the Scheme but they would be the subject of separated guidelines *(6)*.

The Thirty-third meeting of the WHO ECSPP, held from 30 November to 4 December 1992, discussed the work carried out on proposals for the Certification of active pharmaceutical ingredients (APIs), and the significant difference between active ingredients and pharmaceutical products was noted because many Member States did not assess nor register the former *per se.* In this sense, the Expert Committee agreed that, in finalizing the draft proposals in consultation with Member States, it should be stressed that certification of an active ingredient would be an additional safeguard and not a substitute for analysis of the material by those responsible for the manufacture of the dosage forms *(7)*.

The Thirty-fourth WHO ECSPP meeting was convened from 28 November to 2 December 1994. It adopted the revised guidelines for implementing the expanded Certification Scheme and emphasized that the extent to which the Scheme would meet its objectives would depend on the integrity with which it was operated by WHO Member States. In that year, 138 Member States, both importing and exporting pharmaceutical products, were signatories to the Scheme. The Expert Committee considered ways in which WHO, in discussion with medicines regulatory authorities, might take further steps to strengthen and promote the Scheme. It recognized the need for more advice and training on the implementation of the Scheme by importing Member States *(8)*.

During the meeting, WHO's active role in implementing the Scheme was acknowledged. As a basis for discussion, the Expert Committee suggested that all those using the Scheme should be encouraged to notify WHO of any problems and serious abuses of the Scheme which should be investigated and duly sanctioned.

Discussions that took place at the Eight ICDRA, held in Bahrain in 1996, showed that the use of the Scheme was steadily increasing and that some regulatory authorities, including the European Medicines Evaluation Agency (EMEA), were already using the WHO-type Certificates in the approved format.

As a further step relating to the Scheme for finished pharmaceutical products, the WHO Executive Board, in its Ninety-ninth session held in January 1997, endorsed through its resolution EB99.R1 the revised guidelines approved by the Thirty-fourth meeting of the WHO ECSPP and transmitted them to the Fiftieth World Health Assembly for adoption. The date of 1 January 1998 was recommended to start issuing/requesting WHO-type product certificates.

With regard to the active ingredients, a status report was provided on the development of the specific guidelines. In light of some initiatives at national and regional levels to extend regulatory control to starting materials (active ingredients and excipients), the Expert Committee recommended that such developments be closely followed since they would be of direct relevance to the further development of the WHO certification guidelines *(9)*.

The Fiftieth World Health Assembly met from 5-12 May 1997 and endorsed the revised guidelines on the implementation of the WHO Certification Scheme by resolution WHA50.3 as the result of field trials in a number of WHO Member States and discussions during the sixth and seventh biennial ICDRAs. The World Health Assembly urged the Member States to implement the guidelines, to request WHO-type certificates in the form contained in the guidelines, and to issue the certificates in the form proposed as from 1 January 1998. The resolution also urged the Member States to inform the Director-General of the WHO of their intent to apply the Scheme

and of any significant reservations they intended to express relating to their participation as provided for in article 2.1 of the guidelines *(10)*.

Because of the concern relating to the control of starting materials, a meeting was held in 1998 during which proposals were made for a model certificate of analysis and for expansion of the WHO Certification Scheme to include pharmaceutical starting materials, as well as a provision for brokers and traders of such materials. The information was presented at the Thirty-sixth meeting of the WHO ECSPP which met from 31 May to 4 June 1999 *(11)*.

During its Thirty-seventh meeting held from 22-26 October 2001, the WHO ECSPP was briefed on the recommendations made at the Tenth ICDRA in 1999 with regard to issuing certificates of the Scheme and a paper advocating the preparation of electronic certificates on the websites of regulatory authorities. The opinion of some members of the Expert Committee was that this should be difficult for both exporting and importing countries. The Expert Committee noted the update and agreed that a small working group be established to discuss and introduce any further improvements that would increase the credibility of the Scheme.

In relation to the *WHO Scheme for the Certification of Pharmaceutical Starting Materials Moving in International Commerce: guidelines on implementation (SMACS)*, the Expert Committee considered the draft document in which two model certificates were proposed: one for issue by national authorities and the other for completion by manufacturers of starting materials. It was noted that there was still a call for further comments to be sent to WHO by the end of 2001. WHO should seek ways of discussing the proposed model certificates with national drug regulatory authorities in international fora in order to obtain feedback on the operational aspects of their implementation in regulatory practice *(12)*.

During the Thirty-eight meeting of the WHO ECSPP held from 10-14 March 2003, on the topic of the new WHO pharmaceutical SMACS, a discussion took place on the implementation of minimum requirements by relevant authorities. It was suggested that this new scheme be reviewed after a pilot phase. Additionally, training materials should be developed on this subject. The Expert Committee supported the proposal and adopted the document for submission to the World Health Assembly and implementation by Member States.

Regarding the Certification Scheme for finished products, the Expert Committee was briefed on its implementation in which about 140 members were participating. The issue of differences in the implementation of GMP requirements was also raised. The Expert Committee suggested that every effort should be made in order to ensure the credibility of the Scheme which was based on self-assessment by the participating country, agreed that a small working group be formed to discuss its current status, and recommended further measures to improve its effectiveness for presentation at the next WHO ECSPP meeting *(13)*.

The Thirty-ninth meeting of the WHO ECSPP, held from 25-29 October 2004, reviewed the implementation of the Scheme, its linkage to harmonization, and comments from some Member States about its unreliability, particularly because some Member States were issuing certificates when they lacked legal requirements to enforce all aspects of WHO GMP (e.g. validation), and because certificates were being issued by countries that were not members of the Scheme. The Expert Committee urged Member States to ensure that the Scheme was being properly used.

The Expert Committee recommended that the WHO Secretariat prepare a proposal on a possible amendment to the Scheme, including the need for NRAs to be assessed before they could join, for consideration by the Expert Committee at its next meeting. The Expert Committee was informed by the European Federation of Pharmaceutical Industries Associations (EFPIA) of a significant increase in duplication of GMP inspections by different inspectorates that was being experienced by manufacturers worldwide and of the cost burden involved.

During the meeting, the Expert Committee was informed about SMACS, which still might be discussed by WHO´s Governing Bodies. It was also informed about the interest of the EMEA in the WHO document, particularly with regard to making use of the different certificates contained in the document for the forthcoming European system for controlling manufacturers of starting materials *(14)*.

The Fortieth meeting of the WHO ECSPP, held from 24-28 October 2005, noted the value of the Scheme in relation to some WHO guidelines, such as the *Model of quality assurance system for procurement agencies* (recommendations focusing on prequalification of products and manufacturers, purchasing, storage and distribution of pharmaceutical products), and also in relation with the existing certificates and their use in Prequalification. The *Good distribution practices for pharmaceutical products* also included the application of the Scheme in several parts. As a result, the integration of the Scheme was reinforced by different quality assurance tools *(15)*.

In the Forty-first meeting of the WHO ECSPP, held from 16-20 October 2006, the Expert Committee recommended to provide further details with a view to reviewing the Scheme and to discuss it during its next meeting *(16)*.

From 15-19 October 2007, the Forty-second meeting of the WHO ECSPP *(17)* identified a number of perceived problems with the operation of the Scheme and with proposals of its improvement. The Expert Committee further reviewed the possible solutions and endorsed, in principle, the main strategies as follows:

- Revise the Certification Scheme to make it responsive to the needs of countries that rely on it.
- Revise criteria for membership to the Scheme.
- Prepare a list of Member States implementing the Scheme.
- Create awareness and understanding of the Scheme.
- Delisting and negative publication (e.g. if a country issues a certificate without being part of the Scheme).
- Strengthen national regulatory systems.

The Expert Committee recommended that further discussion of the measures and steps to be taken should take place in a future consultation, taking due consideration of the comments received during the consultation phase of the discussion paper. The consultation was based on the changing environment, including the rapid globalization of the pharmaceutical manufacturing sector, coupled with changes in the make-up of both the regulators and the groups involved in procurement.

During its Forty-third meeting, from 13-17 October 2008, the WHO ECSPP *(18)* analyzed the report of the consultation on the WHO Certification Scheme developed from 22-24 July 2008. Participants at the consultation discussed the recommendations made on the working document QAS/07.240 (*Proposal for improvement of the WHO Certification Scheme*) and the comments received thereof. They acknowledged the value of the Scheme but also recognized that it had some limitations, which were identified. The consultation group was of the opinion that implementation of these recommendations would strengthen the Scheme and improve compliance with its goals towards quality medicines circulating in international commerce.

Feedback from the International Federation of Pharmaceutical Manufacturers and Associations (IFPMA) and from EFPIA was reported to the ECSPP, which noted that the pharmaceutical industry regarded the WHO Certification as a very important tool.

The Expert Committee endorsed the following recommendations:

1. The WHO Certification Scheme should be revised.
2. The proposal for revision of the Scheme and modification of the guidelines should be discussed by the relevant Governing Bodies - the WHO Executive Board and the World Health Assembly - and in consultation with WHO´s Legal Counsel.
3. In the interim, a questions and answers (Q&A) paper should be prepared on the function of the Scheme.

The recommendations from the consultation were also reported to the Thirteenth ICDRA, held in Bern, Switzerland in September 2008, for information and possible comments. The value of the Scheme was the subject of a presentation with the title *¨WHO Certification Scheme for finished pharmaceutical products, where are we today?¨*. Recommendations of the conference were to review reports of recent meetings held at WHO and to give feedback to WHO for further discussion *(19)*.

The Forty-fourth WHO ECSPP met from 12-16 October 2009 and reviewed the Q&A paper prepared in the interim on the function of the Scheme, based on the Expert Committee's recommendations. The first working document was based on the feedback, and draft Q&A received from IFPMA/EFPIA. A working document was subsequently circulated for comments.

By reviewing all the comments received and the materials already available, a new set of Q&A was prepared and made available. An additional question and answer was provided for further discussion at the Expert Committee, raised by the specialist who had reviewed all the comments received and drafted a revised version. This question referred to the possibility of a CPP to be used to provide evidence of an administrative review and approval, for example, as certification of acceptability of a company name change (QAS/10.374) *(20)*.

The Expert Committee noted the updated report from the WHO Secretariat; reviewed the document and considered the additional question; approved the revised set of Q&A on the functioning of the Scheme on the revised document on the WHO website; and agreed to include it in *WHO Drug Information*, with the possibility of receiving comments and reviewing any question(s) that might raise major concerns. It also recommended to continue the steps to be taken regarding the Scheme in consultation with WHO Member States and WHO Legal Counsel and proposed that the progress be reported to the Expert Committee at its next meeting *(21)*.

During the Forty-fifth WHO ECSPP, held from 18-22 October 2010, the Expert Committee was updated on the WHO Certification Scheme. It was informed that a Circular Letter had been sent to Member States on 15 January 2010 asking them to comment on the report of the Expert Committee and to provide updated contact addresses of the respective competent authorities of Member States participating in the WHO Certification Scheme. The response received thus far had been extremely limited and the comments received on the suggestions and recommendations made in previous Expert Committee meetings lacked uniformity. Countries made a number of requests to be covered by the Certification Scheme, including the attachment of summary product characteristics (SPC), access to the WHO assessment report, the creation of a list of low-risk products, a separate certificate for low-risk products, and the inclusion of a date of validity of the issued certificate, amongst others.

The Expert Committee was also informed that Poland had joined the WHO SMACS as the first competent authority adhering to that scheme.

The Expert Committee noted the updated report from the WHO Secretariat about the Q&A paper prepared on the function of the Scheme and recommended further encouragement to Member States to respond to the Circular Letter, for example, during the forthcoming ICDRA meeting to continue the steps to be taken regarding the WHO Certification Scheme in consultation with WHO Member States and WHO Legal Counsel *(22)*.

At the Forty-sixth WHO ECSPP, held from 10-14 October 2011, a summary was provided on the history and the last events related to the Scheme, since 2008 when the Expert Committee asked for the Scheme to be reviewed in light of the changing situation. As part of the actions, two question and answer documents on the Scheme were prepared by the WHO Secretariat and were approved by the Expert Committee for publication on the WHO Medicines website.

Only 12 out of 194 Member States responded to the Circular Letter, examples of which were presented to the Expert Committee. The conclusion was drawn that, in spite of some limitations, Member States acknowledged the value of the WHO Certification Scheme.

The Expert Committee noted the report, stressed the importance of the WHO Certification Scheme for starting materials (APIs and excipients) and requested a follow-up to ensure that the appropriate regulatory staff received the communication. It also recommended to:

- Continue efforts towards a possible review of the WHO Certification Scheme.
- Develop a special WHO website for the WHO Certification Scheme for APIs *(23)*.

At the Forty-eight WHO ECSPP, held from 14-18 October 2013, the Expert Committee analyzed and took note of a report updating the evolution of the Scheme. The primary document of the Scheme is the model CPP. It was proposed to send a Circular Letter to Member States regarding their use of the CPP, together with a questionnaire requesting basic information such as the contact addresses of the respective competent authorities. The Expert Committee endorsed the new initiative to gather further information on the Scheme *(24)*.

During the Forty-ninth WHO ECSPP, held from 13-17 October 2014, the Expert Committee listened to updates about the Scheme which included 146 Member States and the European Medicines Agency (EMA). Recent changes in the pharmaceutical industry and in the evolution of business models had made the application of the Scheme more and more challenging. Yet, in spite of its limitations, some Member States appreciated its value. It was felt that, if used appropriately, the Scheme could be a powerful instrument to assist NRAs in sharing information and avoiding duplication.

The Expert Committee agreed to the proposal to send a Circular Letter from WHO to the Organization's Member States regarding their use of and requirements for the CPP, to renew the request for information on their use of the WHO Certification Scheme *(25)*.

At the Fiftieth WHO ECSPP, held from 12-16 October 2015, the Expert Committee examined updates about the Scheme *(26)*. At its previous meeting in 2014, it had recommended that the Q&A should be updated. In consequence, the CPP Network Team of the IFPMA proposed a revised document which was circulated for comments in August 2015. The comments were reviewed by a small working group in September 2015 and the proposed revision of Q&A was presented and examined during this meeting. The Expert Committee heard from the WHO Regulatory Systems Strengthening Team and from a number of organizations represented at the meeting session about their experience with the use of the Scheme. The Expert Committee adopted the proposed revised guidance *¨WHO Certification Scheme on the quality of pharmaceutical products moving in international commerce: questions and answers (Q&A) ¨*. Prior to its adoption, the text was posted for public comment on the WHO website as working document QAS/15.623, June 2016 *(27)*.

During the Fifty-second WHO ECSPP, held from 16-20 October 2017, the Expert Committee reviewed the need for updating the WHO Certification Scheme and considered that it was still deemed to be valuable in principle, but issues of misuse had been noted in global pharmaceutical markets. In view of the feedback received from the users of the Scheme, the Expert Committee noted the update and recommended that the WHO Secretariat prepare a proposal for revision of the Scheme for public consultation *(28)*.

The last phase in the updating process of the Scheme, 2018-2019

From February to March 2018, a working document was prepared by the WHO Secretariat with a suggestion for an updated version of the Scheme based on all the feedback received and documented during the past years. This version was widely circulated for comments (from April to May 2018) and posted on the WHO website. The consolidated comments and feedback received during the informal consultation on Regulatory Tools for Medicines were discussed from 19-20 May 2018. A revised working document was again circulated for public consultation from June-August 2018. Comments received were consolidated and presented, together with the suggested Scheme, to the Eighteenth ICDRA held in Dublin, Ireland, in September 2018. The ICDRA recommended that the Scheme be updated by WHO and made a number of suggestions, particularly in view of the increasing use of electronic documentation.

This outcome was presented during the Fifty-third WHO ECSPP, held from 22-26 October 2018. The Expert Committee recommended to continue the updating process for the Scheme, with a subgroup and active involvement of Member States. It was proposed that a group of regulators be convened to review the recommendations and comments received, with a view to revise the document. It was the Expert Committee's view that this document was of a technical nature and suggested that the WHO Secretariat explore the possibilities for the formal process of adoption of the revised text *(29)*.

From November 2018 to October 2019, all the comments received were reviewed and working documents prepared to serve the consultation with regulators from exporting and importing countries, pending available resources.

The Fifty-fourth WHO ECSPP met from 14-18 October 2019 and was updated about the revision process of the Scheme, as recommended by the Expert Committee, and about the work of the WHO Secretariat which was preparing a list of regulatory authorities interested in collaborating with WHO in consolidating and addressing these comments. The Expert Committee noted the update and endorsed the next steps, as proposed, to continue with preparatory work to revise the WHO Certification Scheme *(30)*.

From November 2018 to October 2019, the background documents for the consultation with regulators from exporting and importing countries were prepared, pending available resources. Moreover, the WHO Secretariat identified and compiled a list of regulatory authorities that were interested in collaborating with WHO in consolidating and addressing these comments.

The second round of consultation in 2019 raised more than 180 comments, from 18 entities including, amongst others, 9 NRAs, 1 regional authority, 3 pharmaceutical associations, 1 pharmaceutical manufacturer and 4 other parties. By the end of 2019, and the first semester of 2020, a comprehensive overview of the suggested amendments was prepared, and a proposal developed on how to address this feedback for each of the comments received. Furthermore, a section-by-section overview on the changes proposed was drafted identifying those suggested to be taken on board and those that needed more ample discussion.

In 2020, the WHO Secretariat consolidated the list of regulatory authorities that were interested in collaborating with WHO in addressing these comments. From January to August 2020, a review of the comments was undertaken in a series of virtual meetings in lieu of the planned consultation (March 2020) with an international working group, comprised of regulators from 14 national and regional regulatory authorities from importing and exporting countries, including China, Cuba, EMA, Ethiopia, Ghana, Indonesia, India, Japan, Kenya, South Africa, Tanzania, Thailand, United States of America and Zimbabwe (Brazil was unable to attend) and

brought these stakeholders together in a virtual meeting held from 26-28 August 2020. The comments received during the second public consultation were reviewed in detail during the virtual meeting and, in addition, the practical experiences and challenges observed by the participating regulatory authorities were shared and resulted in numerous changes in the text.

Following the meeting, the Scheme was further refined as a follow-up on the decisions taken and a new version prepared following the suggestions and experience of the participating regulatory authorities, pharmaceutical industry and specialized teams of WHO. It was also accommodating to the current reality and pharmaceutical context, as well as the needs of timely access to medicines.

This proposal for the WHO Certification Scheme was further revised and modified as per additional feedback from the circulation of comments to the participating authorities as a follow-up to the virtual meeting (working documents QAS18.768/Rev.1 and Rev.2) *(31,32)*. This resulting proposal, and all related details regarding the comments received and changes made to the Scheme, were presented to the Fifty-fifth WHO ECSPP held from 12-16 October 2020 and discussed in its virtual meeting. The proposed document was endorsed by the Expert Committee with additional major changes triggered by the discussion.

Following the meeting, the updated draft of the Scheme was refined as a follow-up on the decisions taken during the virtual meeting.

Milestones. In Table 1, the milestones are chronologically summarized.

Table 1. Milestones of the evolution of the WHO Scheme

Date	Forum	Results
1969	22th World Health Assembly	The World Health Assembly adopted the *World Health Organization (WHO) Certification Scheme on the Quality of Pharmaceutical Products moving in International Commerce* (the "Scheme"), by resolution WHA22.50.
1975	28th World Health Assembly	The World Health Assembly adopted the revised texts of the Scheme and of the good manufacturing practices (GMP) by resolution WHA28.65.
2-13 May 1988	41st World Health Assembly	The World Health Assembly adopted the second amendment of the revised text of the expanded Scheme by resolution WHA41.18.
10-15 Dec 1990	32nd meeting of the WHO Expert Committee on Specifications for Pharmaceutical Preparations (ECSPP)	The Expert Committee endorsed the provisional guidelines, refined following field trials and discussions during the sixth and seventh biennial International Conference of Drug Regulatory Authorities (ICDRA).

28 Nov-02 Dec 1994	34th meeting of the WHO ECSPP	The Expert Committee adopted the revised guidelines for implementing the expanded Certification Scheme and emphasized that the Scheme would meet its objectives according the integrity with which it was operated by WHO Member States.
5-12 May 1997	50th World Health Assembly	The World Health Assembly endorsed the revised guidelines on the implementation of the WHO Certification Scheme by resolution WHA50.3, as the result of field trials in a number of WHO Member States and discussions during the sixth and seventh biennial ICDRAs. The World Health Assembly urged Member States to implement the guidelines, and to request WHO-type certificates and to issue the certificates, as from 1 January 1998.
24-28 Oct 2005	40th meeting of the WHO ECSPP	The Expert Committee reinforced the integration of the Scheme to different tools of quality assurance. It noted its value in relation to the WHO guidelines for procurement agencies and Prequalification.
15-19Oct 2007	42nd meeting of the WHO ECSPP	The Expert Committee identified perceived problems with the operation of the Scheme and proposals for its improvement. It reviewed the possible solutions and endorsed the main strategies.
13-17 Oct 2008	43rd meeting of the WHO ECSPP	The Expert Committee analyzed the report of the consultation on the WHO Certification Scheme, developed from 22-24 July 2008, and endorsed a set of recommendations.
12-16 Oct 2020	55th meeting of the WHO ECSPP	The Expert Committee endorsed the proposal for the revision of the WHO Certification Scheme, based on the outcome of the feedback received during the public consultations, the virtual meetings with the regulators and the additional changes made during the meeting (WHO Technical Report Series, No. 1033, Annex 9).

Main changes of the revision.

As more than twenty years have passed since the last update, the new version contains important modifications. Several changes in wording were made in order to orient the use of the revised Scheme to avoid deviations and mistakes in its implementation. These had previously been identified as key issues during consultations, meetings and previous published Q&A documents. Table 2, below, lists the main amendments.

Table 2. Main amendments of the WHO Scheme

No.	Section of the Scheme	Modification
1	3. Provisions and objectives	It newly includes the actual status of commercialization of the certified product on the market of the certifying authority, when authorized (3.3).
2	4. Membership	Inclusion of regional organizations as participants of the Scheme; for example, the European Union *(4.1).*
3 4 5		Several aspects were included/detailed as requirements for certifying authorities (4.2); • to possess an effective system for vigilance and market surveillance and control, and not only for marketing authorization, as it historically was;

No.	Section of the Scheme	Modification
		• it was specified that GMP compliance should refer to the current publication of the WHO guidelines; • the factors supporting the capacity of the certifying authority for issuing certificates efficiently and to identify and to inform potentially serious quality defect or other hazard in a timely manner.
6		The declarations of the members to the Scheme were modified, they now need to declare their commitment of implementing the WHO guideline related to the Scheme, the WHO Model Certificate (WHO template), and to notify any change of the information submitted related to the certifying and/or requesting members (4.3). The wording for declaration of accomplishment of requirements by Member States intending to participate in the Scheme as certificate-issuing countries was changed, so they should affirm that the competent authority meets the requirements in the notification to the Director-General of the WHO (4.3).
7		A model notification to the Director-General of the WHO for joining the Scheme has been added as a new annex to the document. It is not a part of the Scheme (Appendix 4).
8		Information about the aspects that certifying and requesting members should notify to WHO were modernized by the inclusion of email and website addresses, for easier location (4.3).
9	5. Requesting a certificate	The number of certificates to be requested within the scope of the Scheme were reduced to two (5.1): • a certificate of a pharmaceutical product (CPP) and; • a batch certificate of a pharmaceutical product. The Statement of License Status could be requested/issued but it remains now out of the scope of the Scheme, as it was reported without application in practice (5 Note).
10	Certificate of a pharmaceutical product (CPP)	The situation for using the CPP for a marketing authorization was modified including the information of the marketing status of a product in the country of the certifying authority (3.3 and 5.5).
11		In order to remark the objectives and importance of the CPP for the Scheme, a new point was incorporated: ¨*The CPP is intended to facilitate the trade of pharmaceutical products. Its use should have an impact for regulatory authorities and regional bodies in terms of quality and time on the assessment of dossiers for the marketing authorization. The Scheme facilitates reliance among the participating authorities and its use will enable a timely access to medicines*¨ (5.6).
12		The Summary of Product Characteristics (SPC) was added to the information to be submitted for the applicant when requesting a CPP to the certifying authority (Appendix 1, 2.A.5).
13		A new point was inserted to fix the limits of the information within the scope of the Scheme to be provided by the certifying authority: ¨*Additional information is not within the scope of the Scheme. The certifying authority is under no obligations to supply additional information*¨ (5.13).

No.	Section of the Scheme	Modification
14	A note was adjoined with the examples and descriptions of the Statement of Marketing Authorization Status and the Certificate of Batch/Lot Release for Vaccines, both issued in connection with the Scheme but that are not considered to be part of it. The note explains what they are, when they are used and their role in the international commerce.	As mentioned before, the Statement of Marketing Authorization Status was removed and is out of the scope of the Scheme. As certifying authorities/competent laboratories normally issue Certificates of Batch/Lot Release for Vaccines, which is not included under the scope of the Scheme, for the moment it was considered convenient to mention it, as a recognition of its value. In consequence, were included the references of the *Guidelines for independent lot release of vaccines by regulatory authorities (33)* for the Model Certificate proposed by the WHO National Control Laboratory Network for Biologicals *(34)* and also the references to the GMP mentioned in this certificate, the *WHO good manufacturing practices: main principles for pharmaceutical products (24)* and *WHO Good manufacturing practices for biological products (35)* (5 Note).
15	6. Issuing a certificate	The excess of time used for the legalization of certificates and its valueless were criticized. A sentence was included to remark the correct approach: ¨.... *requesting authorities are discouraged to introduce legalization procedures or any form of authentication procedures such as notarization, embassy legalization and apostillation that may cause the undue delay of certificates*¨ (6.6).
16		In order to stimulate efficiency for issuing certificates and to promote best practices, a standard time frame for the issuance of certificates was recommended (ideally within 30 working days); at the same time, for identical copies, the ideal timeframe suggested was within 20 working days (6.7 and 6.8).
17	7. Notifying and investigating a quality defect	Precision was included about the nature of the complaint and the origin of the defect: • the complaint is considered to be of a serious nature *in terms of risk* by the latter authority; and • the defect, if it appeared after the delivery of the product into the importing country, is not attributable *to local climatic or storage conditions* (both 7.1).
18		WHO are to be notified in the case of substandard or falsified pharmaceutical products: the WHO Global Surveillance and Monitoring System for Substandard and Falsified Medical Products *(36)*. The ways of publication were also brought up-to-date, including the websites of the certifying authority and the WHO Medical Product Alert *(37)* (7.3).
19	Appendix 1. Model certificate of a pharmaceutical product	The introduction of the Model was extended explaining what it establishes and why it is related only to a single and not to several products: ¨*It establishes the status of the pharmaceutical product and of the applicant for the certificate by the national certifying authority in the country or within the jurisdiction of the regional certifying authority. It is for a single product only since the manufacturing arrangements and approved information for different dosage forms and different strengths can vary*¨.

No.	Section of the Scheme	Modification
20		Most of the Explanatory notes were integrated into the template in order to make the document easier to fill.
21	1. Basic information	Information about the brand name of the pharmaceutical product was added for both the country of the certifying authority and the foreign country. In the latter case, it is clarified that it was declared by the requester, if different *(1.1)*.
22	2. Information on marketing authorization	In a consistent way, with the inclusion of the SPC in the CPP explained before, the modified model CPP format, now includes a point for declaration of this information as an attachment (2.A.5).
23	3. Information on manufacturing and inspections	The subtitle formerly referred to information about manufacturing, and now it refers to manufacturing and inspection which reflects more exactly its contents (3).
24		In order to promote the identification of the different sites of manufacturing of various steps of the manufacturing process of the pharmaceutical product, a table to fill with a list of names and addresses of the manufacturing site(s) and activities was included, at least for information on manufacturers responsible for: (a) the manufacturing of dosage forms, (b) certificates of the finished pharmaceutical product batch (batch release), and (c) the packaging and/or labelling of the dosage form. In addition, CPPs should allow other manufacturing site information (e.g. quality control of finished pharmaceutical products) to be included (3).
25	More contact information of the certifying authority was included, such as website, email address, stamp and date; electronic whenever possible. This information allows for the easier location of the certifying authority for verification and confirmation in case of doubts with the CPP.	

The amended WHO Scheme has answered the problems and opportunities identified for improvement and it is now ready for the next challenges, therefore the surveillance and a timely analysis of its proper use and results will be essential in order to obtain the expected benefits of reliance and access to medicines, according to its objectives.

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ETHANOL 96% (*V/V*)

(*ETHANOLUM 96% (V/V)*)

DRAFT FOR COMMENTS

Please send any comments you may have on this draft working document to **Dr Herbert Schmidt**, Technical Officer, Norms and Standards for Pharmaceuticals, Technical Standards and Specifications (*schmidth@who.int*), with a copy to **Ms Claire Vogel** (*vogelc@who.int*) by **31 March 2021**.

Our working documents are sent out electronically and they will also be placed on the WHO Medicines website https://www.who.int/teams/health-product-and-policy-standards/standards-and-specifications/pharmaceuticals/current-projects for comments under the "Working documents in public consultation" link.

If you wish to receive our draft guidelines, please send your e-mail address to ***jonessi@who.int*** and your name will be added to our electronic mailing list.

*[**Note from the Secretariat.** It is proposed to include the monograph on Ethanol 96% (V/V) in The International Pharmacopoeia.*

The monograph is based on the corresponding, internationally-harmonized text developed by the Pharmacopoeial Discussion Group (PDG). Editorial modifications have been made in order to be in line with the style used in The International Pharmacopoeia.*]*

ETHANOL 96% (V/V)

(*ETHANOLUM 96% (V/V)*)

This monograph is based on the corresponding, internationally-harmonized text developed by the Pharmacopoeial Discussion Group (PDG). Editorial modifications have been made in order to be in line with the style used in The International Pharmacopoeia.

Graphic formula

Molecular formula. C2H6O

Relative molecular mass. 46.07

Chemical name. Ethyl alcohol; ethanol; CAS Reg. No. 64-17-5.

Other name. Alcohol 96% (V/V).

Description. A colourless, clear and mobile liquid.

Miscibility. Miscible with water R.

Category. Solvent; antiseptic.

Storage. Ethanol 96% (V/V) should be kept in a well-closed container and stored, whenever possible, at a temperature between 8 and 15 °C.

Additional information. Ethanol 96% (V/V) contains approximately 4% (V/V) of water. It is flammable, burning with a blue smokeless flame, and hygroscopic. Boiling point, about 79 °C.

Requirements

Definition. Ethanol 96% (V/V) contains not less than 95.1% (V/V) and not more than 96.9% (V/V) of C2H6O, corresponding to not less than 92.6% (m/m) and not more than 95.2% (m/m) of C2H6O, at 20 °C.

Identity tests

A. Determine the relative density d_{20}^{20} of the test substance as described under 1.3 Determination of mass density, relative density and weight per millilitre. The relative density d_{20}^{20} is 0.805 to 0.812.

B. Carry out the test as described under 1.7 Spectrophotometry in the infrared region. The infrared absorption spectrum of the test substance is concordant with the reference spectrum of ethanol 96% (V/V)[A reference spectrum of ethanol 96% (V/V) will be recorded.]

Clarity and colour of solution. The test substance is clear when tested as described under 1.18 Clarity and degree of opalescence of liquids [Note from the Secretariat. Chapter 1.18 is currently under elaboration] and colourless when compared with water R as described under 1.11.2 Degree of coloration of liquids, Method II. Dilute 1.0 mL to 20 mL with water R. After standing for 5 minutes, the dilution remains clear when compared with water R.[The "General Notices: Clarity of solution" shall be replaced by the new chapter 1.18 Clarity and degree of opalescence of liquids.]

Non-volatile residue. Place 100 mL of the test substance in a porcelain dish and heat on a water-bath until volatilized, dry the residue at 105 °C for 1 hour, and weigh; not more than 2.5 mg (25 ppm m/V).

Acidity or alkalinity. Add 20 mL of carbon-dioxide-free water R and 0.1 mL of phenolphthalein solution TS to 20 mL of the test substance; the solution is colourless. Add 0.1 mL of carbonate-free sodium hydroxide (0.01 mol/L) VS; the solution is pink (30 ppm, expressed as acetic acid).

Absorbance. Record the absorption spectrum (1.6) of the test substance in a cuvette or cell with an optical pathlength of 50 mm against water R between 235 nm and 340 nm. The absorbance at 240 nm is not more than 0.40, not more than 0.30 between 250 nm and 260 nm, and not more than 0.10 between 270 nm and 340 nm. The spectrum shows a steadily descending curve with no observable peaks or shoulders.

Volatile impurities. Carry out the test as described under 1.14.5 Gas chromatography.

Use a fused-silica column (30 m × 0.32 mm) coated with a stationary phase of cyanopropyl(3)phenyl(3)methyl(94)polysiloxane R (1.8 µm).

As a detector, use a flame ionization detector.

Use helium R as the carrier gas with a linear velocity of 35 cm/s. Use a split ratio of 1:20.

Maintain the temperature of the column at 40 °C for 12 minutes. Increase the temperature at a rate of 10 °C per minute to 240 °C, and then maintain it at this temperature for 10 minutes. Maintain the temperatures of the injection port and that of the detector at 200 °C and 280 °C, respectively.

Prepare the following six solutions: For solution (1), use the test substance. For solution (2), add 150 µL of 4-methylpentan-2-ol R to 500.0 mL of the test substance. For solution (3), dilute 100 µL of anhydrous methanol R to 50.0 mL with the test substance. Dilute 5.0 mL of the solution to 50.0 mL with the test substance. For solution (4), dilute 50 µL of anhydrous methanol R and 50 µL of acetaldehyde R to 50.0 mL with the test substance. Dilute 100 µL of the solution to 10.0 mL with the test substance. For solution (5), dilute 150 µL of acetal R to 50.0 mL with the test substance. Dilute 100 µL of the solution to 10.0 mL with the test substance. For solution (6), dilute 100 µL of benzene R to 100.0 mL with the test substance. Dilute 100 µL of the solution to 50.0 mL with the test substance.

Inject alternately 1 µL each of solutions (1), (2), (3), (4), (5) and (6) and record the chromatograms.

The test is not valid unless the resolution between the peaks corresponding to acetaldehyde (the first peak) and methanol (the second peak) in the chromatogram obtained with solution (4) is at least 1.5.

Methanol (impurity F)

In the chromatogram obtained with solution (1), the area of any peak corresponding to methanol is not greater than 0.5 times the area of the peak due to methanol in the chromatogram obtained with solution (3) (200 ppm *(V/V)*).

Acetaldehyde (impurity B) and acetal (impurity A)

Calculate the sum of the contents of acetaldehyde and acetal in parts per million *(V/V)* using the following expression:

$$\frac{10 \times A_E}{A_T - A_E} + \frac{30 \times C_E}{C_T - C_E} \times \frac{44.05}{118.2}$$

where

A_E = area of any peak corresponding to acetaldehyde in the chromatogram obtained with solution (1);

A_T = area of the peak due to acetaldehyde in the chromatogram obtained with solution (4);

C_E = area of any peak corresponding to acetal in the chromatogram obtained with solution (1);

C_T = area of the peak due to acetal in the chromatogram obtained with reference solution (5);

44.05 = molecular mass of acetaldehyde;

118.2 = molecular mass of acetal.

The sum of the contents is not greater than 10 ppm *(V/V)*, expressed as acetaldehyde.

Benzene (impurity D)

Calculate the content of benzene in parts per million *(V/V)* using the following expression:

$$\frac{2B_E}{B_T - B_E}$$

where

B_E = area of any peak corresponding to benzene in the chromatogram obtained with solution (1);

B_T = area of the peak due to benzene in the chromatogram obtained with solution (6).

The content of benzene is not greater than 2 ppm *(V/V)*.

If necessary, the identity of benzene can be confirmed using another suitable chromatographic system (stationary phase with a different polarity).

Other volatile impurities

In the chromatogram obtained with solution (2), the sum of the areas of the peaks for any other impurities is not greater than the area of the peak due to 4-methylpentan-2-ol (300 ppm). Disregard any peak with an area less than 0.03 times than the area of the peak due to 4-methylpentan-2-ol (9 ppm).

Assay. Calculate the mass density at 20 °C (ρ20) of the test substance using the value for the relative density d_{20}^{20} obtained in identity test A[AK: The formula for mass density in the PhInt is inconsistent with that of the PhEur]. Determine the % (*V/V*) of C_2H_6O using the alcoholimetric table given in 1.3.2. *[**Note from the Secretariat.** Chapter 1.3.2 is currently under revision. The revised version will include the mentioned alcoholimetric table]*

Impurities

***[Note from the Secretariat.** The chemical structures will be added at a later stage.]*

A. 1,1-Diethoxyethane (acetal)
B. Acetaldehyde
C. Propan-2-one (acetone)
D. Benzene
E. Cyclohexane
F. Methanol
G. Butan-2-one (methyl ethyl ketone)
H. 4-Methylpentan-2-one (methyl isobutyl ketone)
I. Propan-1-ol (propanol)
J. Propan-2-ol (isopropyl alcohol)
K. Butan-1-ol (butanol)
L. Butan-2-ol
M. 2-Methylpropan-1-ol (isobutanol)
N. Furan-2-carbaldehyde (furfural)
O. 2-Methylpropan-2-ol (1,1-dimethylethyl alcohol)
P. 2-Methylbutan-2-ol
Q. Pentan-2-ol
R. Pentan-1-ol (pentanol)
S. Hexan-1-ol (hexanol)
T. Heptan-2-ol
U. Hexan-2-ol
V. Hexan-3-ol

New reagents for Anhydrous Ethanol and Ethanol 96% (*V/V*) monographs

Phenolphthalein solution TS

Procedure. Dissolve 0.1 g of phenolphthalein R in 80 mL of ethanol (~750 g/L) TS and dilute to 100 mL with water R.

Test for sensitivity. Add 0.1 mL of the phenolphthalein solution to 100 mL of carbon dioxide-free water R; the solution is colourless. Not more than 0.2 mL of sodium hydroxide (0.02 mol/L) VS is required to change the colour to pink.

Colour change. pH 8.2 (colourless) to pH 10.0 (red).

Cyanopropyl(3)phenyl(3)methyl(94)polysiloxane R

Polysiloxane substituted with 3% cyanopropyl groups, 3% of phenyl groups and 94% of methyl groups.

4-Methylpentan-2-ol R

4-Methyl-2-pentanol; C6H14O

Description. Clear, colourless, volatile liquid.

Refractive index. n_D^{20} = about 1.411

Relative density. d_4^{20} = about 0.802

Boiling point. About 132 °C.

Methanol, anhydrous R

Procedure. Treat 1000 mL of methanol R with 5 g of magnesium R. If necessary initiate the reaction by adding 0.1 mL of mercuric chloride (54 g/L) TS. When the evolution of gas has ceased, distil the liquid and collect the distillate in a dry container protected from moisture.

Water (2.8). Not more than 0.3 g/L.

Magnesium R

Mg

Description. Silver-white ribbon, turnings or wire, or a grey powder.

Mercuric chloride (54 g/L) TS

A solution of mercuric chloride R containing 54 g of $HgCl_2$ per litre.

Acetal R

Acetaldehyde diethyl acetal; 1,1-Diethoxyethane; $C_6H_{14}O_2$

Description. Clear, colourless, volatile liquid.

Miscibility. Miscible with water and with ethanol (~750 g/L) TS.

Refractive index. n_D^{20} = about 1.382

Relative density. d_{20}^{20} = about 0.824

Boiling point. About 103°C

Amendment to existing reagent entry

The existing entry for Benzene will be replaced with the following:

Benzene

C_6H_6 (SRIP, 1963, p.48)

Where benzene is used to prepare a reference solution, for safety reasons, the pure reagent may be replaced by a commercially available reference material containing a certified amount of benzene.

***

ETHANOL, ANHYDROUS

(ETHANOLUM, ANHYDRICUM)

DRAFT FOR COMMENTS

Please send any comments you may have on this draft working document to **Dr Herbert Schmidt**, Technical Officer, Norms and Standards for Pharmaceuticals, Technical Standards and Specifications (*schmidth@who.int*), with a copy to **Ms Claire Vogel** (*vogelc@who.int*) by 31 March 2021.

Our working documents are sent out electronically and they will also be placed on the WHO Medicines website (https://www.who.int/teams/health-product-and-policy-standards/standards-and-specifications/pharmaceuticals/current-projects) for comments under the "Working documents in public consultation" link.

If you wish to receive our draft guidelines, please send your e-mail address to ***jonessi@who.int*** and your name will be added to our electronic mailing list.

*[**Note from the Secretariat.** It is proposed to revise the monograph on Ethanol in* The International Pharmacopoeia.

The revision is based on the corresponding, internationally-harmonized text developed by the Pharmacopoeial Discussion Group (PDG). Editorial modifications have been made in order to be in line with the style used in The International Pharmacopoeia.

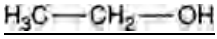
Changes to the current chapter are indicated in the text by insert or ~~delete~~.]

ETHANOL, ANHYDROUS

(ETHANOLUM, ANHYDRICUM)

This monograph is based on the corresponding, internationally-harmonized text developed by the Pharmacopoeial Discussion Group (PDG). Editorial modifications have been made in order to be in line with the style used in The International Pharmacopoeia.

Graphic formula.



Molecular formula. C_2H_6O

Relative molecular mass. 46.07

Chemical name. Ethyl alcohol; ethanol; CAS Reg. No. 64-17-5.

Other name. Absolute alcohol; dehydrated alcohol; anhydrous ethanol.

Description. A colourless, clear and mobile liquid.

Miscibility. Miscible with water.

Category. Solvent; antiseptic.

Storage. Anhydrous ethanol should be kept in a well-closed container and stored, whenever possible, at a temperature between 8 and 15 °C.

Additional information. Anhydrous ethanol is flammable, burning with a blue smokeless flame, and hygroscopic. Boiling point, about 79 °C.

Requirements

Definition. Anhydrous ethanol contains not less than 99.5% (*V/V*) of C_2H_6O, corresponding to not less than 99.2% (*m/m*) of C_2H_6O, at 20 °C.

Identity tests

A. Determine the relative density d_{20}^{20} of the test substance as described under *1.3 Determination of mass density, relative density and weight per millilitre*. The relative density d_{20}^{20} is 0.790 to 0.793.

B. Carry out the test as described under *1.7 Spectrophotometry in the infrared region*. The infrared absorption spectrum of the test substance is concordant with the reference spectrum of anhydrous ethanol.

Clarity and colour of solution. The test substance is clear when tested, as described under *1.18 Clarity and degree of opalescence of liquids, [**Note from the Secretariat**. Chapter 1.18 is currently under elaboration]* and colourless when compared with water R, as described under *1.11.2 Degree of coloration of liquids*, Method II. Dilute 1.0 mL to 20 mL with water R. After standing for 5 minutes, the dilution remains clear when compared with water R.

Non-volatile residue. Place 100 mL of the test substance in a porcelain dish and heat on a water-bath until volatilized, dry the residue at 105 °C for 1 hour, and weigh; not more than 2.5 mg (25 ppm *m/V*).

Acidity or alkalinity. Add 20 mL of carbon-dioxide-free water R and 0.1 mL of phenolphthalein solution TS to 20 mL of test substance; the solution is colourless. Add 0.1 mL of carbonate-free sodium hydroxide (0.01 mol/L) VS; the solution is pink (30 ppm, expressed as acetic acid).

Absorbance. Record the absorption spectrum (*1.6*) of the test substance in a cuvette or cell with an optical pathlength of 50 mm cell against water R between 235 nm and 340 nm. The absorbance at 240 nm is not more than 0.40, not more than 0.30 between 250 nm and 260 nm and not more than 0.10 between 270 nm and 340 nm. The spectrum shows a steadily descending curve with no observable peaks or shoulders.

Volatile impurities. Carry out the test, as described under *1.14.5 Gas chromatography*.

Use a fused-silica column (30 m × 0.32 mm) coated with a stationary phase of cyanopropyl(3)phenyl(3)methyl(94)polysiloxane R (1.8 µm).

As a detector, use a flame ionization detector.

Use helium R as the carrier gas with a linear velocity of 35 cm/s. Use a split ratio of 1:20.

Maintain the temperature of the column at 40 °C for 12 minutes. Increase the temperature at a rate of 10 °C per minute to 240 °C and then maintain it at this temperature for 10 minutes. Maintain the temperatures of the injection port and that of the detector at 200 °C and 280 °C, respectively.

Prepare the following six solutions: For solution (1), use the test substance. For solution (2), add 150 µL of 4-methylpentan-2-ol R to 500.0 mL of the test substance. For solution (3), dilute 100 µL of anhydrous methanol R to 50.0 mL with the test substance. Dilute 5.0 mL of the solution to 50.0 mL with the test substance. For solution (4), dilute 50 µL of anhydrous methanol R and 50 µL of acetaldehyde R to 50.0 mL with the test substance.

Dilute 100 µL of the solution to 10.0 mL with the test substance. For solution (5), dilute 150 µL of acetal R to 50.0 mL with the test substance. Dilute 100 µL of the solution to 10.0 mL with the test substance. For solution (6), dilute 100 µL of benzene R to 100.0 mL with the test substance. Dilute 100 µL of the solution to 50.0 mL with the test substance.

Inject alternately 1 µL each of solutions (1), (2), (3), (4), (5) and (6) and record the chromatograms.

The test is not valid unless the resolution between the peaks corresponding to acetaldehyde (the first peak) and methanol (the second peak) in the chromatogram obtained with solution (4) is at least 1.5.

Methanol (impurity F)

In the chromatogram obtained with solution (1), the area of any peak corresponding to methanol is not greater than 0.5 times the area of the peak due to methanol in the chromatogram obtained with solution (3) (200 ppm (*V/V*)).

Acetaldehyde (impurity B) and acetal (impurity A)

Calculate the sum of the contents of acetaldehyde and acetal in parts per million (*V/V*) using the following expression:

$$\frac{10 \times A_E}{A_T - A_E} + \frac{30 \times C_E}{C_T - C_E} \times \frac{44.05}{118.2}$$

where

A_E	=	area of any peak corresponding to acetaldehyde in the chromatogram obtained with solution (1);
A_T	=	area of the peak due to acetaldehyde in the chromatogram obtained with solution (4);
C_E	=	area of any peak corresponding to acetal in the chromatogram obtained with solution (1);
C_T	=	area of the peak due to acetal in the chromatogram obtained with reference solution (5);
44.05	=	molecular mass of acetaldehyde;
118.2	=	molecular mass of acetal.

The sum of the contents is not greater than 10 ppm (*V/V*), expressed as acetaldehyde.

Benzene (impurity D)

Calculate the content of benzene in parts per million (*V/V*) using the following expression: $\frac{2B_E}{B_T - B_E}$

where

B_E	=	area of any peak corresponding to benzene in the chromatogram obtained with solution (1);
B_T	=	area of the peak due to benzene in the chromatogram obtained with solution (6).

The content of benzene is not greater than 2 ppm (*V/V*).

If necessary, the identity of benzene can be confirmed using another suitable chromatographic system (stationary phase with a different polarity).

Other volatile impurities

In the chromatogram obtained with solution (2), the sum of the areas of the peaks for any other impurities is not greater than the area of the peak due to 4-methylpentan-2-ol (300 ppm). Disregard any peak with an area less than 0.03 times than the area of the peak due to 4-methylpentan-2-ol (9 ppm).

Assay. Calculate the mass density at 20 °C (ρ_{20}) of the test substance using the value for the relative density d_{20}^{20} obtained in identity test A. Determine the % (*V/V*) of C_2H_6O using the alcoholimetric table given in 1.3.2. *[**Note from the Secretariat**. Chapter 1.3.2 is currently under revision. The revised version will include the mentioned alcoholimetric table]*

Impurities

[Note from the Secretariat. *The chemical structures will be added at a later stage.]*

A. 1,1-diethoxyethane (acetal)
B. acetaldehyde
C. propan-2-one (acetone)
D. benzene
E. cyclohexane
F. methanol
G. butan-2-one (methyl ethyl ketone)
H. 4-methylpentan-2-one (methyl isobutyl ketone)
I. propan-1-ol (propanol)
J. propan-2-ol (isopropyl alcohol)
K. butan-1-ol (butanol)
L. butan-2-ol
M. 2-methylpropan-1-ol (isobutanol)
N. furan-2-carbaldehyde (furfural)
O. 2-methylpropan-2-ol (1,1-dimethylethyl alcohol)
P. 2-methylbutan-2-ol
Q. pentan-2-ol
R. pentan-1-ol (pentanol)
S. hexan-1-ol (hexanol)
T. heptan-2-ol
U. hexan-2-ol
V. hexan-3-ol

New reagents for the monographs on Anhydrous ethanol and Ethanol 96% (*V/V*)

Phenolphthalein solution TS

Procedure. Dissolve 0.1 g of phenolphthalein R in 80 mL of ethanol (~750 g/L) TS and dilute to 100 mL with water R.
Test for sensitivity. Add 0.1 mL of the phenolphthalein solution to 100 mL of carbon dioxide-free water R; the solution is colourless. Not more than 0.2 mL of sodium hydroxide (0.02 mol/L) VS is required to change the colour to pink.

Colour change. pH 8.2 (colourless) to pH 10.0 (red).

Cyanopropyl(3)phenyl(3)methyl(94)polysiloxane R

Polysiloxane substituted with 3% cyanopropyl groups, 3% of phenyl groups and 94% of methyl groups.

4-Methylpentan-2-ol R

4-Methyl-2-pentanol; $C_6H_{14}O$.

Description. Clear, colourless, volatile liquid.

Refractive index. n_D^{20} = about 1.411.

Relative density. d_4^{20} = about 0.802.

Boiling point. About 132 °C.

Methanol, anhydrous R

Procedure. Treat 1,000 mL of methanol R with 5 g of magnesium R. If necessary, initiate the reaction by adding 0.1 mL of mercuric chloride (54 g/L) TS. When the evolution of gas has ceased, distil the liquid and collect the distillate in a dry container protected from moisture.

Water (2.8). Not more than 0.3 g/L.

Magnesium R

Mg.

Description. Silver-white ribbon, turnings or wire, or a grey powder.

Mercuric chloride (54 g/L) TS

A solution of mercuric chloride R containing 54 g of $HgCl_2$ per litre.

Acetal R

Acetaldehyde diethyl acetal; 1,1-Diethoxyethane; $C_6H_{14}O_2$.

Description. Clear, colourless, volatile liquid.

Miscibility. Miscible with water and with ethanol (~750 g/L) TS.

Refractive index. n_D^{20} = about 1.382.

Relative density. d_{20}^{20} = about 0.824.

Boiling point. About 103 °C.

Amendment to existing reagent entry

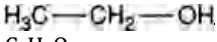
Replace the existing entry for Benzene with the following:

Benzene

C_6H_6 (SRIP, 1963, p.48).

Where benzene is used to prepare a reference solution, for safety reasons, the pure reagent may be replaced by a commercially available reference material containing a certified amount of benzene.

~~Ethanol (Ethanolum)~~



~~C_2H_6O~~

~~Relative molecular mass. 46.07~~

~~Chemical name. Ethyl alcohol; ethanol; CAS Reg. No. 64-17-5.~~

~~Other name. Absolute alcohol, dehydrated alcohol.~~

~~Description. A colourless, clear and mobile liquid; odour, characteristic.~~

~~Miscibility. Miscible with water and ether R.~~

~~Category. Solvent; antiseptic.~~

~~Storage. Ethanol should be kept in a well-closed container, and stored whenever possible at a temperature between 8 and 15 °C.~~

~~Additional information. Ethanol is flammable, burning with a blue smokeless flame. Hygroscopic. Boiling point, about 79 °C.~~

~~Requirements~~

~~Ethanol contains not less than 98.8% *v/v* and not more than the equivalent of 100.0% *v/v* of C_2H_6O, corresponding to not less than 98.1% *m/m* and not more than the equivalent of 100.0% *m/m* of C_2H_6O.~~

~~Identity tests~~

~~A. Place 0.25 mL in a small beaker, add 1 mL of potassium permanganate (10 g/l) TS and 0.5 mL of sulfuric acid (0.5 mol/l) VS, and cover the beaker immediately with a filter-paper moistened with a recently prepared solution of 0.1 g of sodium nitroprusside R and 0.5 g of piperazine hydrate R in 5 mL of water; a dark blue colour is produced on the filter-paper, that fades after a few minutes.~~
~~B. To a few drops add 1 mL of sulfuric acid (~1760 g/l) TS and a few drops of potassium dichromate (100 g/l) TS; a green colour is produced and an odour of acetaldehyde is perceptible.~~

~~Relative density. d_{20}^{20} = 0.7904 – 0.7935~~
~~Non-volatile residue. Place 100 mL in a porcelain dish and heat on a water-bath until volatilized, dry the residue at 105 °C for 1 hour, and weigh; not more than 5 mg.~~

~~Water-insoluble substances. Dilute a volume of Ethanol with an equal volume of water; the mixture is clear and, after cooling to 10 °C, it remains clear for 30 minutes.~~

~~Acidity. Add 20 mL of carbon-dioxide-free water R and 3 drops of phenolphthalein/ethanol TS to 20 mL of Ethanol; the colour remains unchanged. Titrate with carbonate-free sodium hydroxide (0.02 mol/l) VS; not more than 0.5 mL is required to obtain the midpoint of the indicator (pink).~~

~~Aldehydes and other foreign organic substances. Thoroughly clean a glass-stoppered cylinder with hydrochloric acid (~250 g/l) TS, rinse with water and the Ethanol to be examined. Place 20 mL of Ethanol in the cylinder. Cool the contents to about 15 °C and, by means of a carefully cleaned pipette, add 0.1 mL of potassium permanganate (0.02 mol/l) VS, noting the time of the addition. Mix at once by inverting the stoppered cylinder, and allow to stand at 15 °C for exactly 5 minutes; the pink colour does not entirely disappear.~~

~~Fusel oil and allied impurities. Allow 25 mL to evaporate spontaneously from a porcelain dish, carefully protected from dust, until the surface of the dish is barely moist; no foreign odour is perceptible, and on the addition of a few drops of sulfuric acid (~1760 g/l) TS, no red or brown colour develops.~~

~~Methanol. To 1 drop add 1 drop of water, 1 drop of phosphoric acid (~105 g/l) TS, and 2 drops of potassium permanganate (25 g/l) TS. Mix, allow to stand for 1 minute, and add, drop by drop, sodium metabisulfite (50 g/l) TS until the permanganate colour is discharged. If a brown colour remains, add 1 drop of phosphoric acid (~105 g/l) TS. To the colourless solution add 5 mL of freshly prepared disodium chromotropate TS, and heat on a water-bath at 60 °C for 10 minutes; no violet colour appears.~~

~~Benzene. Record an absorption spectrum of the Ethanol in a 1-cm layer against water between 220 nm and 350 nm. The absorbance at about 220 nm is not more than 0.30, at about 230 nm not more than 0.18, at about 240 nm not more than 0.08, and at about 270 to 350 nm not more than 0.02. A curve drawn through these points is smooth.~~

***

GELATIN

(GELATINA)

DRAFT FOR COMMENTS

Please send any comments you may have on this draft working document to **Dr Herbert Schmidt**, Technical Officer, Norms and Standards for Pharmaceuticals, Technical Standards and Specifications (*schmidth@who.int*), with a copy to Ms Claire Vogel (*vogelc@who.int*) by **31 March 2021**.

Our working documents are sent out electronically and they will also be placed on the WHO Medicines website (https://www.who.int/teams/health-product-and-policy-standards/standards-and-specifications/pharmaceuticals/current-projects) for comments under the "*Working documents in public consultation*" link.

If you wish to receive our draft guidelines, please send your e-mail address to ***jonessi@who.int*** and your name will be added to our electronic mailing list.

*[**Note from the Secretariat**. It is proposed to revise the monograph on Gelatin in* The International Pharmacopoeia*.*

The monograph is based on the corresponding, internationally-harmonized text developed by the Pharmacopoeial Discussion Group (PDG). Editorial modifications have been made in order to be in line with the style used in The International Pharmacopoeia*.*

Changes to the current chapter are indicated in the text by insert or ~~delete.~~]

GELATIN (GELATINA)

This monograph is based on the corresponding, internationally-harmonized text developed by the Pharmacopoeial Discussion Group (PDG). Editorial modifications have been made in order to be in line with the style used in The International Pharmacopoeia .

Chemical name. Gelatin; CAS Reg. No. 9000-70-8.

Description

Gelling grades: faintly yellow or light yellowish-brown solid, usually occurring as translucent sheets, shreds, granules or powder.

Non-gelling grades: faintly yellow or white granules or powder.

Solubility
Gelling grades: practically insoluble in common organic solvents; swell in cold water and give on heating a colloidal solution which on cooling forms a more or less firm gel.

Non-gelling grades: soluble in cold or warm water, practically insoluble in common organic solvents.

Category. Encapsulating agent; tablet binder; coating agent; suspending agent; viscosity-increasing agent.

Storage. Gelatin should be kept in a well-closed container.

Labelling. For gelling grades, the designation on the container should state the nominal gel strength of the gelatin.

Additional information. These specifications do not necessarily apply to gelatin for parenteral use or other particular application. Attention should be paid to the microbiological quality since gelatin is of natural origin.

Requirements

Definition. Gelatin is a purified protein obtained from collagen of animals by partial alkaline and/or acid hydrolysis and/or enzymatic hydrolysis, or by thermal hydrolysis. The hydrolysis leads to either gelling or non-gelling product grades. This monograph covers both gelling grades and non-gelling grades.

Solution S. Dissolve 1.00 g of the test substance in carbon-dioxide-free water R, heat to about 55 °C, and dilute to 100 mL with the same solvent. Keep the solution at this temperature to carry out the tests in which the use of solution S is indicated.

Identity tests

For gelling grades, carry out tests A and B. For non-gelling grades, carry out tests A, B and C.

A. To 2 mL of solution S add 0.05 mL of copper(II) sulfate (80 g/L) TS, mix, and add 0.5 mL of sodium hydroxide (~85 g/L) TS; a violet colour is produced.

B. Transfer 0.5 g of the test substance to a test-tube, add 10 mL of water, and allow to stand for 10 minutes. Heat at 60 °C for 15 minutes and keep the tube in a vertical position at 2-8 °C for 6 hours. Invert the tube; for gelling grades, the contents do not flow out immediately; for non-gelling grades, the contents flow out immediately.

C. To 0.5 g of the test substance in a 250 mL bottle, add 10 mL of water R and 5 mL of sulfuric acid (~1760 g/L) R. Place the bottle, partly but not completely closed (for example, using a watch glass), in an oven at 105 °C for 4 hours. Allow to cool and add 200 mL of water R. Adjust to pH 6.0-8.0 using sodium hydroxide (~200 g/L) TS. Place 2 mL of the solution in a test-tube and add 2 mL of a solution prepared immediately before use containing 14 g/L of tosylchloramide sodium R in phosphate buffer solution pH 6.8 R. Mix and allow to stand for 20 minutes. Add 2 mL of 4-dimethylaminobenzaldehyde TS8. Mix and place in a water-bath at 60 °C for 15 minutes; a red to violet colour develops.

pH value. pH of solution S, measured at 55 °C; 3.8-7.6.

Conductivity. Use a 10.0 g/L solution of the test substance at 30 ± 1.0 °C. Proceed with the test as described under *1.18 Conductivity [**Note from the Secretariat**. The chapter on conductivity is currently under elaboration].*without the use of a temperature compensation device; the conductivity is not more than 1 $mS \cdot cm^{-1}$.

Heavy metals. Use 1.0 g of the test substance for the preparation of the test solution as described under *2.2.3 Limit test for heavy metals*, Procedure 3; determine the heavy metals content according to Method A; not more than 10 µg/g.

Loss on drying. Dry 5 g of the test substance at 105 °C for 16 hours; it loses not more than 150 mg/g.

Sulfur dioxide. Proceed with the test described under *2.11 Determination of Sulphur Dioxide [**Note from the Secretariat**. This chapter is currently under elaboration.]*; the sulfur dioxide concentration is not more than 50 µg/g.

Peroxides. Carry out the test described below using peroxide test strips R that contain peroxidase and that comply with the suitability test described below. The peroxidase present in the test strips transfers oxygen from peroxides to an organic redox indicator which is converted to a blue oxidation product. The intensity of the colour obtained is proportional to the quantity of peroxide and can be compared with a colour scale provided with the test strips, to determine the peroxide concentration.

Suitability test. Dip a test strip for 1 second into hydrogen peroxide standard (2 µg H_2O_2/mL) TS, such that the reaction zone is properly wetted. Remove the test strip, shake off excess liquid and, after 15 seconds, compare the reaction zone with the colour scale provided. The test strips are suitable if the colour matches that of the 2 ppm concentration.

Test. Weigh 20.0 ± 0.1 g of the test substance in a beaker and add 80.0 ± 0.2 mL of water R. Stir to moisten all the gelatin and allow the sample to stand at room temperature for 1-3 hours. Cover the beaker with a watch-glass. If dissolution is not complete, place the beaker for 20 ± 5 minutes in a water-bath at 65 ± 2 °C to dissolve the sample. Stir the contents of the beaker with a glass rod to achieve a homogeneous solution. Dip a test strip for 1 second into the test solution, such that the reaction zone is properly wetted. Remove the test strip, shake off excess liquid and, after 15 seconds, compare the reaction zone with the colour scale provided. Multiply the concentration read from the colour scale by a factor of 5 to calculate the concentration in µg/g of peroxide in the test substance; the peroxide concentration is not more than 10 µg/g.

Gel strength (Bloom value). For gelling grades, carry out the following test:
The gel strength is expressed as the mass in grams necessary to produce the force which, applied to a plunger 12.7 mm in diameter, makes a depression 4 mm deep in a gel having a concentration of 6.67 per cent (*m/m*) and matured at 10 °C.

The apparatus consists of a texture analyser or gelometer with a cylindrical piston 12.7 ± 0.1 mm in diameter with a plane pressure surface with a sharp bottom edge; and a bottle 59 ± 1 mm in internal diameter and 85 mm high.

Adjust the apparatus according to the manufacturer's manual. Settings are: distance 4 mm, test speed 0.5 mm/s.

Prepare a gel as follows: Place 7.5 g of the test substance in the bottle. Add 105 mL of water R, close the bottle and allow to stand for 1-4 hours. Heat in a water-bath at 65 ± 2 °C for 15 minutes. While heating, stir gently with a glass rod. Ensure that the solution is uniform and that any condensed water on the inner walls of the bottle is incorporated. Allow to cool at room temperature for 15 minutes and transfer the bottle to a thermostatically controlled bath at 10.0 ± 0.1 °C, fitted with a device to ensure that the platform on which the bottle stands is perfectly horizontal. Close the bottle with a rubber stopper and allow to stand for 17 ± 1 hours.

Remove the bottle from the bath and quickly wipe the water from the exterior of the bottle. Centre the bottle on the platform of the apparatus so that the plunger contacts the sample as near to its midpoint as possible and start the measurement.

The gel strength is not less than 80 per cent and not more than 120 per cent of the nominal value stated on the labelling.

Iron. Determine by atomic absorption spectrophotometry as described under *1.8 Atomic spectrometry: emission and absorption*, Method 2 ***[Note from the Secretariat.*** *Chapter 1.8 Atomic spectrometry: emission and adsorption is currently under revision.]*, at a wavelength of 248.3 nm. Prepare the test solution as follows: To 5.00 g of the test substance to be examined, in a conical flask, add 10 mL of hydrochloric acid (~420 g/L) TS. Close the flask and place in a water-bath at 75-80 °C for 2 hours (if necessary for proper solubilisation, the gelatin may be allowed to swell after addition of the acid and before heating, the heating time may be prolonged, and a higher temperature may be used). Allow to cool and adjust the contents of the flask to 100.0 g with water R. Use iron standard (8 µg Fe/mL) TS to prepare the reference solutions, diluting with water R; the iron content is not more than 30 µg per g.

Chromium. Determine by atomic absorption spectrophotometry as described under *1.8 Atomic spectrometry: emission and absorption*, Method 2, at a wavelength of 357.9 nm. Prepare the test solution as described in the test for Iron. Use chromium standard (100 µg Cr/mL) TS to prepare the reference solutions, diluting with water R; the chromium content is not more than 10 µg per g.

Zinc. Determine by atomic absorption spectrophotometry as described under *1.8 Atomic spectrometry: emission and absorption*, Method 2, at a wavelength of 213.9 nm. Prepare the test solution as described in the test for Iron. Use zinc standard (10 µg Zn/mL) TS to prepare the reference solutions, diluting with water R; the zinc content is not more than 30 µg per g.

Microbial contamination. Determine as described under *3.3. Microbiological examination of non-sterile products.* The acceptance criteria are: TAMC 103 CFU/g (3.3.1), TYMC 102 CFU/g (3.3.1), Absence of *Escherichia coli* (3.3.2) and Absence of *Salmonella* (3.3.2).

REAGENTS to be amended

Tosylchloramide sodium R
Amend the entry to include the synonym '*chloramine T*'.

Hydrogen peroxide (~30 g/L) TS
Change the content statement from '*about 30 g of H_2O_2 per litre*' to '*.....not less than 25 g and nt more than 35 g of H_2O_2 per litre."*

REAGENTS to be added

Phosphate buffer solution pH 6.8 R
Procedure. Mix 77.3 mL of a 71.5 g/L solution of disodium hydrogen phosphate R with 22.7 mL of a 21 g/L solution of citric acid R.

4-Dimethylaminobenzaldehyde TS8
Procedure. Dissolve 1.0 g of 4-dimethylaminobenzaldehyde R in 3.5 mL of perchloric acid (~600 g/L) TS and slowly add 6.5 mL of 2-propanol R.
Note: 4-Dimethylaminobenzaldehyde TS8 should be prepared immediately before use.

Perchloric acid (~600 g/L) TS
Perchloric acid (~1170 g/L) TS, diluted with water to contain 600 g/L of $HClO_4$.

Peroxide test strips R
Use commercial test strips with a suitable scale in the range from 0 ppm to 25 ppm peroxide.

Hydrogen peroxide standard (2 µg H_2O_2/mL) TS
Procedure. Dilute 10.0 mL of hydrogen peroxide (~30 g/L) TS to 300.0 mL with water R. Dilute 2.0 mL of this solution to 1000.0 mL with water R.

Note: Hydrogen peroxide standard (2 µg H_2O_2/mL) TS should be prepared immediately before use.

Iron standard (8 µg Fe/mL) TS
Procedure. Dissolve 80 mg of reduced iron R in 50 mL of hydrochloric acid (~220 g/L) TS and dilute to 1000.0 mL with water R. Immediately before use, dilute this solution to 10 times its volume using water R. Each mL of the resultant solution contains 8 µg of iron.

Hydrochloric acid (~220 g/L) TS
A solution of hydrochloric acid (~420 g/L) TS in water containing approximately 220 g of HCl per litre (about 6 mol/L).

Chromium standard (100 µg Cr/mL) TS
Procedure. Dissolve potassium dichromate R equivalent to 0.283 mg of $K_2Cr_2O_7$ in water R and dilute to 1000.0 mL with the same solvent. Each mL of this solution contains 100 µg of chromium.

Zinc standard (10 µg Zn/mL) TS
Procedure. Dissolve 0.440 g of zinc sulfate R and 1 mL of acetic acid (~300 g/L) TS in water R and dilute to 100.0 mL with the same solvent. Immediately before use, dilute this solution to 100 times its volume using water R. Each mL of the resultant solution contains 10 µg of zinc.

~~Gelatin (Gelatina)~~

~~**Chemical name**. Gelatin; CAS Reg. No. 9000-70-8.~~

~~**Description.** Faintly yellow to amber-coloured sheets, flakes, granules, or powder; practically odourless; in solution it has a slight, characteristic, bouillon-like odour.~~

~~**Solubility.** Practically insoluble in most organic solvents. In cold water it swells and softens, absorbing 5-10 times its own mass of water. After swelling, soluble in hot water, in acetic acid (~300 g/l) TS, and in a hot mixture of glycerol R and water.~~

~~**Category.** Encapsulating agent; tablet binder; coating agent; suspending agent; viscosity-increasing agent.~~

~~**Storage.** Gelatin should be kept in a well-closed container.~~

~~**Additional information.** These specifications do not necessarily apply to gelatin for parenteral use or other particular application. Attention should be paid to the microbiological quality since gelatin is of natural origin.~~

~~The type of gelatin may be distinguished by the following test:~~
~~Dissolve 1 g in 100 mL of hot water. Place aliquots of 5 mL into six separate test-tubes and add 5 mL of a buffer to each tube, using buffers of pH 4.0, 5.0, 6.0, 7.0, 8.0, and 9.0 (citrate buffer, pH 4.0, TS, phosphate buffer, pH 4.0, TS, or phthalate buffer, pH 4.0, TS; acetate buffer, pH 5.0, TS; phosphate/citrate buffer, pH 6.0, TS or acetate buffer, pH 6.0, TS; phosphate buffer, pH 7.0, TS; phosphate buffer, pH 8.0, TS or buffer borate, pH 8.0, TS; buffer borate, pH 9.0, TS). Cool the test-tubes and allow them to stand at 4 °C for 24 hours; the type of gelatin is recognized by the resulting opalescence – a maximum opalescence appearing at pH 5.0 indicates gelatin type B, while a maximum opalescence between pH 7.0 and pH 9.0 indicates gelatin type A.~~

Requirements

Definition. Gelatin is a purified protein obtained either by the partial acid hydrolysis (type A) or by the partial alkali hydrolysis (type B) of animal collagen. It can exist as a mixture of both types.

Identity tests

A. Dissolve 1 g in carbon-dioxide-free water R, heat to about 55 °C, and dilute to 100 mL with the same solvent. Keep the solution at this temperature throughout the following test (retain the solution for test C): to 2 mL add 0.05 mL of copper(II) sulfate (160 g/l) TS, mix, and add 0.5 mL of sodium hydroxide (~80 g/l) TS; a violet colour is produced.
B. Transfer 0.5 g to a test-tube, add 10 mL of water, and allow to stand for 10 minutes. Heat at 60 °C for 15 minutes and keep the tube in a vertical position at 0 °C for 6 hours. Invert the tube; the content does not immediately flow out.

C. Acidify 2 mL of the solution prepared for test A and add 0.5 mL of potassium dichromate (100 g/l) TS; a yellow precipitate is formed.

Heavy metals. Use 1.0 g for the preparation of the test solution as described under, Procedure 3; determine the heavy metals content according to Method A; not more than 10 µg/g.

Arsenic. Use a solution of 1.0 g in a mixture of 2.5 mL of sulfuric acid (~1760 g/l) TS, 2.5 mL of nitric acid (~1000 g/l) TS, and a slight excess of bromine TS1, allow to stand for 30 minutes, and boil under a reflux condenser for 1 hour. Proceed with the test as described under; the arsenic content is not more than 1 µg/g.

Odour and water-insoluble substances. Dissolve 1 g in 40 mL of hot water; no disagreeable odour is perceptible. Observe the solution through a layer of 2 cm; only a slight opalescence appears.

Sulfated ash. Use 2.0 g; not more than 30 mg/g.

Loss on drying. Weigh 10 g and dry to constant mass at 105 °C; it loses not more than 150 mg/g.

~~**Sulfur dioxide**. Dissolve 20 g in 150 mL of hot water using a round-bottom flask with a long neck. Add 5 mL of phosphoric acid (~1440 g/l) TS and 1 g of sodium hydrogen carbonate R, and without delay connect the flask to a condenser. (*Note*. Excessive foaming can be reduced by adding a few drops of an antifoaming agent.) Distil 50 mL, allowing the distillate to be collected under a 50 mL surface of iodine (0.05 mol/l) VS. Acidify the distillate with a few drops of hydrochloric acid (~70 g/l) TS, add 2 mL of barium chloride (50 g/l) TS, and heat on a water-bath until the liquid is nearly colourless. If any, filter the precipitated barium sulfate, wash, ignite, and weigh. Repeat the procedure without the Gelatin being examined and make any necessary corrections. The content of barium sulfate is not more than 109.3 mg, which corresponds to not more than 1.5 mg/g of sulfur dioxide.~~

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GUIDANCE ON SETTING REMAINING SHELF LIFE FOR THE SUPPLY AND PROCUREMENT OF EMERGENCY HEALTH KITS

DRAFT FOR COMMENTS

Please send your comments to **Ms Sophie Laroche**, Quality Officer, Global Supply Policies (*laroches@who.int*), with a copy to **Ms Claire Vogel** (*vogelc@who.int*) before **15 April 2021**.

Our working documents are sent out electronically and they will also be placed on the WHO Medicines website (https://www.who.int/teams/health-product-and-policy-standards/standards-and-specifications/pharmaceuticals/current-projects) for comments under the "*Working documents in public consultation*" link.

If you wish to receive all our draft guidelines, please send your email address to *jonessi@who.int* and your name will be added to our electronic mailing list.

GUIDANCE ON SETTING REMAINING SHELF LIFE FOR THE SUPPLY AND PROCUREMENT OF EMERGENCY HEALTH KITS

Background

During the Fifth-fourth World Health Organization (WHO) Expert Committee on Specifications for Pharmaceutical Preparations (ECSPP), the Expert Committee members adopted the *Points to consider for setting the remaining shelf life of medical products upon delivery* guideline (WHO Technical Report Series, No. 1025, Annex 8, 2020).

This document aims to facilitate the national authorization of imports; support efficient processing; ensure sufficient stocks; address barriers to access and supply; prevent dumping and stock-outs; and prevent donations of near and out-of-date medical products.

The ECSPP acknowledged the value of this document in guiding procurement agencies, regulators and other stakeholders; harmonizing policies in this area; and addressing the problem of short remaining shelf life of donated medicines during emergencies.

During the public consultation of the *Points to consider for setting the remaining shelf life of medical products upon deliver guidance text,* some UN agencies and humanitarian organizations involved in procurement had made the comment to include health kits for use in emergencies in this new guidance, the reason being that a streamlined international approach would serve all agencies and reduce waste. In the finalization of the new guidance, it was agreed not to include this yet and, rather, to first focus on individual medical products.

A group of colleagues from agencies and humanitarian organizations procuring health kits (including, for example, the International Committee of the Red Cross, Médecins Sans Frontières, Save the Children, United Nations Children's Fund, United Nations Population Fund and WHO) have submitted a draft proposal to the WHO Secretariat for an *Amendment to consider Emergency Health Kits for use in humanitarian emergency response as an additional example* for consideration.

This proposal below is intended to serve as an ***additional example*** to the ***Points to consider on remaining shelf life of medical products upon delivery*** (i.e. as an amendment ***to consider Emergency Health Kits for use in an humanitarian emergency response***).

Proposal for an addition to the *Points to consider on remaining shelf life of medical products upon delivery* for Emergency Health Kits

Emergency Health Kits are designed to facilitate the provision of priority health services to affected populations in humanitarian emergencies without access to medical facilities or where medical facilities are disrupted during a crisis. Depending on the type of Emergency Health Kit, they contain a mix of essential medicines, health supplies and equipment designed to be used for a limited period of time and for a specific number of people.

Many different international and national organizations will be providing these Emergency Health Kits in an acute or post-acute humanitarian response; some examples of these organizations include (but are not limited to):

- International Committee of the Red Cross (ICRC)
- Médecins Sans Frontières (MSF)
- Save the Children
- United Nations Children's Fund (UNICEF)
- United Nations Population Fund (UNFPA)
- World Health Organization (WHO)

Examples of these kits include (but are not limited to) the Interagency Emergency Health Kits, the Interagency Emergency Reproductive Health Kits, the MSF Emergency Health Kits, Cholera Kits, the ICRC Surgical Team Kits, and so on. "Kits" manufactured and validated as such are not considered in the amendment (such as in vitro diagnostic kits, laboratory reagent kits or PCR kits) and are not intended to be covered by this annex.

1. Definitions

Expiry date of an Emergency Health Kit. Each Emergency Health Kit should have a manufacturing date defined as an "assembly date" and an expiry date defined as the "first item to be expired in the kit", allocated by the supplier or the manufacturer assembling the kit.

The shelf life of an Emergency Health Kit is defined by the "first item to be expired in the kit." In other words, the item in the kit with the shortest expiry date will define the expiry date of the entire kit. This implies that all the other items composing the Emergency Health Kit have a longer shelf life.

The expiry date of the "first item to be expired in the kit" should follow the principles described in the document. Products, such as pharmaceutical products, should have an expiry date allocated by the manufacturer. The expiry date should be established based on the stability testing results obtained on the relevant packaging (primary and secondary packaging, where appropriate) and the required stability conditions. These are presented in the number of years, based on the calculation from the date of manufacture.

Remaining shelf life of an Emergency Health Kit. The remaining shelf life is calculated based on the expiry date, storage conditions and risks. The remaining shelf life of an Emergency Health Kit should consider the expiry date of the entire kit (*see definition of expiry date of an Emergency Health Kit above*) as the end date of possible use of the kit.

Criteria which influence the recommended remaining shelf life are the purpose of the emergency kit (immediate response or prepositioning) and the phase of the emergency-acute or post-acute (protracted or recovery). Please note that Emergency Health Kit prepositioning requires careful attention to be paid to stock rotation in order to ensure the expiry dates do not arrive before use.

Examples of remaining shelf life (RSL) at the different point of delivery for the shelf life, up to the total shelf-life (TSL), are laid out below.

2. Recommended remaining shelf life (RSL) of Emergency Health Kits

Acute Emergency Response[1]

Expiry date as defined above	RSL at time of dispatch from supplier's premises	RSL at time of delivery at port of entry of country	RSL at time of delivery at end-user level
48 months <TSL ≤ 60 months	24 months	12 months	6 months
36 months <TSL ≤ 48 months	20 months	12 months	6 months
24 months < TSL ≤ 36 months	18 months	12 months	6 months
14 months <TSL ≤ 24 months	12 months	7 months	3 months
Less than 14 months	Special arrangements and conditions apply*		

[1] An Acute Emergency refers to a period of time where there are sudden, often unpredicted, humanitarian needs due to a natural or man-made crisis, where the complexities of the crisis-setting lead to added complexities in the delivery of humanitarian response, or where the scale of humanitarian needs exceeds the capacity of local/national actors; this may or may not refer to an official or unofficial scale-up of a coordinated interagency response.

Prepositioning in Preparedness OR Post-Acute Emergency Response[2]

Expiry date as defined above	RSL at time of dispatch from supplier's premises	RSL at time of delivery at port of entry of country	RSL at time of delivery at end-user level
48 months <TSL ≤ 60 months	40 months	30 months	12 months
36 months <TSL ≤ 48 months	30 months	24 months	12 months
24 months < TSL ≤ 36 months	20 months	15 months	6 months
14 months <TSL ≤ 24 months	14 months	12 months	3 months
Less than 14 months	Special arrangements and conditions apply*		

*There are some items that will never have more than 12 months of total shelf life: for example, anti-blood group reagents.

Please keep in mind that when an Emergency Health Kit has expired, many of the items in the kit will still be viable for use. The expired item/s should be disposed of and replaced. In case these cannot be replaced, the remaining items can be used as bulk individual items and integrated into the health system, provided these individual components of the kits have been manufactured for dedicated use as a "single product".

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[2] A Post-Acute Emergency refers to a period of time where there are significant humanitarian needs due to a natural or man-made crisis, where complexities of the crisis-setting have remained stable for a significant period of time (protracted) or where the crisis has begun to subsite with an implied gradual return to stability (recovery).

INQUIRY REGARDING WHO PRODUCT-SPECIFIC GUIDANCE ON THE DESIGN OF BIOEQUIVALENCE STUDIES

DRAFT FOR COMMENTS

Please send your comments to **Dr Steve Estevão Cordeiro**, Technical Officer, Norms and Standards for Pharmaceuticals, Technical Standards and Specifications (*estevaos@who.int*), with a copy to **Ms Claire Vogel** (*vogelc@who.int*) before **26 March 2021**.

Our working documents are sent out electronically and they will also be placed on the WHO Medicines website (https://www.who.int/teams/health-product-and-policy-standards/standards-and-specifications/pharmaceuticals/current-projects) for comments under the "*Working documents in public consultation*" link.

If you wish to receive all our draft guidelines, please send your email address to ***jonessi@who.int*** and your name will be added to our electronic mailing list.

INQUIRY REGARDING WHO PRODUCT-SPECIFIC GUIDANCE ON THE DESIGN OF BIOEQUIVALENCE STUDIES

Background

During the Fifty-fifth World Health Organization (WHO) Expert Committee on Specifications for Pharmaceutical Preparations (ECSPP), Expert Committee members were updated on the annual consultation on Regulatory Guidance for Multisource Products between the WHO Norms and Standards for Pharmaceuticals Team and the Prequalification of Medicines Team – Assessment Group (PQTm) which took place as a virtual meeting in June 2020 due to the Coronavirus disease 2019 (COVID-19) pandemic. Further to this meeting, the group of experts suggested whether PQTm's product-specific guidance texts on how to design bioequivalence studies could be presented to the ECSPP with a view to making them more widely available to regulators.

At present, the guidance developed by PQTm is uniquely meant for products contained in an Expression of Interest for Product Evaluation (EoI) with the sole purpose of helping manufacturers with their product development to meet the WHO Prequalification Programme standards. This guidance should not be understood as being enforceable as deviations can be considered acceptable if justified by sound scientific evidence and without prejudice of the compliance with existing requirements. Furthermore, these product-specific texts should always be read and followed in line with the general WHO guideline on *Multisource (generic) pharmaceutical products: guidelines on registration requirements to establish interchangeability*[3] adopted at the Fifty-first meeting of the WHO ECSPP.

The Expert Committee asked the WHO Secretariat to explore the feasibility of the above-mentioned proposal, specifically to collect feedback and assess whether making such guidance widely available (in particular to regulators worldwide) would be welcomed and advantageous.

[3] World Health Organization (2017) *Multisource (generic) pharmaceutical products: guidelines on registration requirements to establish interchangeability.* Fifty-first report of the WHO Expert Committee on specifications for pharmaceutical preparations, Geneva (WHO Technical Report Series, No. 1003, 2017, Annex 6)

In view of the fact that these guidance texts are currently developed by the WHO Prequalification Programme, it was proposed to use the existing approach (namely the scope, such as products contained in an EoI and document structure-content) as a basis for product-specific guidance documents on the design of bioequivalence studies to be recommended for implementation to WHO Member States and other parties.

In light of the above, feedback is being sought on:

- **whether it would be advantageous to recommend these guidance texts to other audiences, namely national regulatory authorities, in addition to the relevant manufacturers;**

- **whether any modification to the structure-content of the existing document(s) is needed to meet the needs of other stakeholders and, if so, suggestions to be welcomed; and**

- **whether these guidance texts should preferably be developed for a specific group of medicines[4].**

Note: This is an inquiry document to find out how best to move forward and will not be published as an annex to the ECSPP report.

The outcome of this inquiry document will be reported to the Fifty-Sixth ECSPP in October 2021.

[4] World Health Organization (2019) *Guidance on bioequivalence studies for reproductive health medicines.* WHO Prequalification Team.

An example of product-specific guidance on the design of bioequivalence studies developed by PQTm can be found as Annex 1 to this document for ease of reference. Further examples can be found here:

1. World Health Organization Medicines Prequalification Guidance on Bioequivalence: guidance documents on study design. Available at: https://extranet.who.int/pqweb/medicines/who-medicines-prequalification-guidance (accessed on 25 January 2021).

2. World Health Organization (2018): *Notes on the design of bioequivalence study: sofosbuvir/velpatasvir*. WHO Prequalification Team. Available at: https://extranet.who.int/pqweb/sites/default/files/documents/BE_sofos-velpa_Jan2018.pdf (accessed on 25 January 2021).

3. World Health Organization (2019): *Guidance on bioequivalence studies for reproductive health medicines*. WHO Prequalification Team. Available at: https://extranet.who.int/pqweb/sites/default/files/documents/31%20BE_guidance_RH_medicines_Oct2019_new%20templ.pdf (accessed on 25 January 2021).

4. World Health Organization (2020): *Notes on the design of bioequivalence study: dexamethasone*. WHO Prequalification Team. Available at: https://extranet.who.int/pqweb/sites/default/files/documents/BE_Dexamethasone_July2020.pdf (accessed on 25 January 2021).

5. World Health Organization (2021): *Notes on the design of bioequivalence study: raltegravir*. WHO Prequalification Team. Available at: https://extranet.who.int/pqweb/sites/default/files/documents/BE_raltegravir_January2021.pdf (accessed on 25 January 2021).

Annex 1

Notes on the design of bioequivalence study: dexamethasone

A WHO product-specific guidance on the design of bioequivalence studies may follow the structure-content, as suggested below, or may be appropriately modified based on the feedback received.

1. Pharmacokinetics of dexamethasone

1.1. The pharmacokinetics of dexamethasone after intravenous administration are linear. A second peak after intravenous administration can be explained by enterohepatic recirculation. The disposition of dexamethasone is biexponential. After oral administration, the bioavailability is 76%. The maximum concentration is reached after 0.75 - 1.5 h (0.5 – 2.0 h) and the elimination half-life is 3.6 - 4.0 h. Dexamethasone should be taken with or after food to minimise irritation to the gastrointestinal tract.

2. Guidance for the design of bioequivalence studies

Taking into account the pharmacokinetic properties of dexamethasone, the following guidance with regard to the study design should be taken into account:

2.1. **Study design:** A cross-over design is recommended.

2.2. **Dose:** As the EoI includes dexamethasone 1.5 mg, 2 mg, and 6 mg tablets, the highest strength of the series to be developed should be administered. The bioequivalence study for the additional lower strengths may be waived if the conditions for an "additional strength biowaiver" are met with regard to manufacturing method, qualitative and quantitative composition and similarity of the dissolution profiles. In the case of oral solutions, the EoI includes 2 mg/5 ml and 10 mg/5 ml (expressed as dexamethasone base). In this case, the bioequivalence study should be conducted with the 6 mg dose (i.e. 15 ml of 2 mg/5 ml or 3 m of 10 mg/5 ml oral solutions).

2.3. **Fasting/fed:** Although dexamethasone is administered during or after meals to avoid gastrointestinal adverse effects, a single dose in healthy volunteers is considered to be tolerable. Therefore, the bioequivalence study should be conducted in the fasting state, since it is considered the most discriminative study condition.

2.4. **Subjects:** Healthy adult subjects should be recruited. It is not necessary to include patients in the bioequivalence study.

2.5. **Sample size:** Dexamethasone C_{max} exhibits moderate intra-subject variability (18 – 21%), whereas AUC_{0-t}, exhibits low variability (9 - 13%) in the fasting state when administering a dose of 4 or 8 mg, based on information available in the literature[1-3]. However, a study with intra-subject CV of 33% for C_{max} and 22% for AUC when administering a dose of 2 mg has been reported in the literature[4]. These data will facilitate the calculation of a sufficient sample size for the bioequivalence study.

2.6. **Washout:** 7 days.

2.7. **Blood sampling:** Predose, 0.25, 0.50, 0.75, 1.00, 1.25, 1.50, 1.75, 2.00, 2.25, 2.50, 2.75, 3.00, 4.00, 5.00, 8.00, 12.00, 16.00 and 24.00 h after drug administration.

2.8. **Analytical method:** Information currently available indicates that it is possible to measure dexamethasone in human plasma using LC-MS/MS analytical methodology. The bioanalytical method should be sufficiently sensitive to detect concentrations that are 5% of the C_{max} in most profiles of each formulation (test or comparator).

2.9. **Parent or metabolite data for assessment of bioequivalence:** The parent drug is considered to best reflect the biopharmaceutical quality of the proposed product. The data for the parent compound should be used to assess bioequivalence.

2.10. **Statistical considerations:** The data for dexamethasone should meet the following bioequivalence standards in a single-dose cross-over design study:

- The 90% confidence interval of the relative mean AUC_{0-t} of the test to reference product should be within 80–125%;

- The 90% confidence interval of the relative mean C_{max} of the test to reference product should be within 80–125%.

2.11. **Waiver of the in vivo demonstration of bioequivalence:** The Invitation to Manufacturers of therapeutics against COVID-19 to submit an EoI for product evaluation includes dexamethasone solution for injection, containing dexamethasone base 3.3 mg/ml or 6.6 mg/ml, as the sodium phosphate (equivalent to dexamethasone phosphate 4 mg/ml or 8 mg/ml, respectively). Multisource pharmaceutical products are considered to be equivalent without the need for further documentation when the pharmaceutical product is to be administered parenterally (e.g. intravenously, subcutaneously, or intramuscularly) as an aqueous solution containing the same API in the same molar concentration as the comparator product and the same or similar excipients in comparable concentrations to those in the comparator product. Certain excipients (e.g. buffer, preservative, and antioxidant) may be different provided it can be shown that the change(s) in these excipients would not affect the safety and/or efficacy of the pharmaceutical product.

The Invitation to Manufacturers of therapeutics against COVID-19 to submit an EoI for product evaluation includes dexamethasone oral solution, containing dexamethasone base 2 mg/5 ml or 10 mg/5 ml, as the base or sodium phosphate. Multisource pharmaceutical products are considered to be equivalent without the need for further documentation when pharmaceutically equivalent products are solutions for oral use (e.g. syrups, elixirs, and tinctures), contain the API in the same molar concentration as the comparator product, contain similar excipients in usual concentrations (if the API is BCS Class I) and the same excipients (i.e. cosolvents, surfactants, viscosity agents or critical excipients like sorbitol) in similar concentrations (for APIs from other BCS classes), although buffers, flavours, colourants, antioxidants or preservatives may be changed. One of the presently authorised dexamethasone oral solutions in the UK, which may have been employed in the RECOVERY trial, is Martapan 2 mg/5 ml oral solution. According to the SmPC of Martapan[5], the amount of the critical excipients and cosolvent per 5 ml of oral solution are: 0.6 g of liquid sorbitol, 1.4 g of liquid maltitol and 0.5 g of Propylene glycol. This quantitative composition may serve as basis to obtain a waiver for the in vivo demonstration of bioequivalence oral solution irrespective of the BCS classification of dexamethasone, taking into account that the other excipients are preservatives (5 mg/5 ml of Benzoic acid), flavours (Garden mint flavour (contains propylene glycol E1520)) and buffer agents (citric acid monohydrate, sodium citrate and citric acid 10% solution for pH adjustment), that might be changed without any expected impact on bioavailability. The quantitative composition of functional and critical excipients of the other dexamethasone oral solution marketed in UK does not seem to be publicly available. Therefore, a waiver based on that product is not feasible.

The Invitation to Manufacturers of therapeutics against COVID-19 to submit an EoI for product evaluation includes dexamethasone tablets, containing 1.5, 2, and 6 mg. Although at the maximum single therapeutic dose for other indications (e.g. 300 mg/day) dexamethasone (base) is classified as a low solubility drug, a BCS-based biowaiver approach might be accepted exceptionally if the indications for the applied product are limited to COVID-19, where the maximum single therapeutic dose is 6 mg. Therefore, if the Applicant demonstrates that the polymorph, if any, used in the applied product is the same as the morphic form used in the comparator product and the active pharmaceutical ingredient is highly soluble, according to the BCS criterion, based on a 6 mg dose, and stable, a BCS-based biowaiver would be acceptable, taking into account that the submitted information on permeability/absorption would impact the requirements on excipient composition and dissolution profile comparison since these requirements differ for BCS class I and III drugs. For a BCS-based biowaiver the same strengths of test and reference should be compared (i.e. 2 mg test tablet vs. 2 mg comparator tablet). In this exceptional case, for those strengths that are not available in the comparator product (i.e. 1.5 and 6 mg tablets), the dissolution profile comparison should be conducted not only with one tablet per vessel (e.g. 1 x 1.5 mg test tablet vs. 1 x 2 mg comparator tablet and 1 x 6 mg test tablet vs. 1 x 4 mg or 8 mg tablet), but also with the lowest common dose per vessel (e.g. 1 x 1.5 mg tablet vs. 3 x 0.5 mg comparator tablet and 1 x 6 mg test tablet vs. 3 x 2 mg comparator tablet).

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GOOD MANUFACTURING PRACTICES FOR MEDICAL GASES

DRAFT FOR COMMENTS

Please send your comments to **Dr Sabine Kopp**, Team Lead, Norms and Standards for Pharmaceuticals, Technical Standards and Specifications (*kopps@who.int*), with a copy to **Ms Claire Vogel** (*vogelc@who.int*) before **30 March 2021**.

Our working documents are sent out electronically and they will also be placed on the WHO Medicines website (https://www.who.int/teams/health-product-and-policy-standards/standards-and-specifications/pharmaceuticals/current-projects) for comments under the "*Working documents in public consultation*" link.

If you wish to receive all our draft guidelines, please send your email address to *jonessi@who.int* and your name will be added to our electronic mailing list.

GOOD MANUFACTURING PRACTICES FOR MEDICAL GASES

Introduction

1.1. Arising from an increased demand for medical gases, in particular the use of oxygen in the treatment of patients with Coronavirus disease 2019 (COVID-19), the World Health Organization (WHO) Health Products Policy and Standards Department (formerly Essential Medicines and Health Products) and other departments involved in the supply of oxygen and the inspection of production sites of medical gases, raised the urgency for the preparation of the *WHO good manufacturing practices for medical gases* guidance text.

1.2. There is an urgent need to scale-up the production of medical gases, in particular oxygen, meeting the required quality specifications.

1.3. Although there are other published guidelines, such as those in the European Union (EU) and the Pharmaceutical Inspection Co-operation Scheme (PIC/S), the COVID-19 pandemic resulted in a rapid and increased need for the use of medical oxygen in many WHO Member States.

1.4. Whilst the urgent supply of medical gases is necessary, we must be certain that appropriate standards in all countries are followed for the production, control, storage and distribution of oxygen and other medical gases to guarantee that gases for medical use are of assured quality when they reach the patients.

1.5. The recommendations in this guideline are harmonized with the principles from other similar and published guidelines.

1.6. WHO good manufacturing practices (GMP) guidelines are reviewed, updated regularly, and available in the WHO Technical Report Series. Manufacturers and distributors of medical gases should comply with the relevant parts of WHO GMP guidelines, as well as the content of this document. For ease of reference, a list of some applicable guidelines, such as those reflecting the main principles in GMP *(1)*, Water for pharmaceutical use *(2)*, Data integrity *(3)*, Good quality control laboratory practices *(4)*, Good storage and distribution practices *(5)* and others, are referenced below.

2. Scope

2.1. This guideline focuses on the production, control, storage and distribution of medical gases.

2.2. This document does not cover the manufacturing of medical gases in hospitals or at home for personal use. However, the principles contained in this document may be applied in those instances to ensure that oxygen generated at hospitals or at home are suitable for their intended use and meet the appropriate quality standards.

3. Glossary

The definitions of terms relating to the manufacture of medical gases, as described in this guideline, are described below.

Active substance gas. Any gas intended to be an active substance for a medical product.

Air separation. A separation of atmospheric air into its constituent gases using fractional distillation at cryogenic temperatures.

Compressed gas. Gas which, when packaged under pressure, is entirely gaseous at all temperatures above –500 ° C.

Container. A container is a cryogenic vessel (tank, tanker or other type of mobile cryogenic vessel), a cylinder, a cylinder bundle or any other package that is in direct contact with the gas.

Cryogenic gas. Gas which liquefies at 1.013 bar at temperatures below –150 ° C .

Cylinder. A container, usually cylindrical suited for compressed, liquefied or dissolved gas, fitted with a device to regulate the spontaneous outflow of gas at atmospheric pressure and room temperature.

Cylinder bundle. An assembly of cylinders which are fastened together, interconnected by a manifold, transported and used as a unit.

Evacuate. To remove the residual gas from a container/system to a pressure less than 1.013 bar using a vacuum system.

Gas. Any substance that is completely gaseous at 1.013 bar and +200 ° C or has a vapour pressure exceeding 3 bar at +500 ° C.

Home cryogenic vessel. A mobile cryogenic vessel designed to hold liquid oxygen and dispense gaseous oxygen at patient's home.

Hydrostatic pressure test. A test performed, as required by national or international regulations, in order to ensure that pressure containers are able to withstand pressures up to the container's design pressure.

Liquefied gas. Gas which, when packaged for transport, is partially liquid (or solid) at a temperature above –50 ° C.

Manifold. Equipment or an apparatus designed to enable one or more gas containers to be emptied and filled at the same time.

Maximum theoretical residual impurity. A gaseous impurity coming from a possible backflow that remains after the cylinders pre-treatment before filling. The calculation of the maximum theoretical residual impurity is only relevant for compressed gases and supposes that these gases act as perfect gases.

Medical gas. Any gas or mixture of gases classified as a medical product.

Minimum pressure retention valve. A cylinder valve, which maintains a positive pressure above atmospheric pressure in a gas cylinder after use, in order to prevent any internal contamination of the cylinder.

Mobile cryogenic vessel. A mobile thermally insulated container designed to maintain the contents in a liquid state.

Non-return valve. A valve which permits flow in one direction only.

Purge. To remove the residual gas from a container/system by first pressurising and then venting the gas used for purging to 1.013 bar.

Tank. A static thermally insulated container designed for the storage of liquefied or cryogenic gas. They are also called "fixed cryogenic vessels".

Tanker. A thermally insulated container fixed on a vehicle for the transport of liquefied or cryogenic gas.

Valve. A device for opening and closing containers.

Vent. To remove the residual gas from a container/system down to 1.013 bar by opening the container/system to the atmosphere.

4. Quality management

4.1. Companies that are involved in the manufacture, control, storage and distribution of medical gases should document and implement a comprehensively designed and clearly defined quality management system. This is the responsibility of senior management.

4.2. Senior management should also assume responsibility for the quality of the medical gases manufactured, controlled, stored and distributed.

4.3. All parts of the quality system should be adequately resourced and maintained.

4.4. The quality system should incorporate the principles of good practices (GxP) which should be applied to the life cycle stages of medical gases.

4.5. The quality system should ensure that:

- medical gases are manufactured, controlled, stored and distributed in accordance with the recommendations in this document and other associated guidelines such as good quality control laboratory practices and good storage and distribution practices, where appropriate;
- managerial responsibilities are clearly specified in job descriptions;
- operations and other activities are clearly described in a written form such as standard operating procedures (SOPs) and work instructions;
- arrangements are made for the manufacture, supply and use of the correct containers and labels;
- all necessary controls are in place;
- there is a system for quality risk management;
- calibrations and validations are carried out where necessary;
- the finished product is correctly processed and checked according to the defined procedures and specifications;
- deviations and changes are investigated and recorded with an appropriate level of root cause analysis done;
- appropriate corrective actions and preventive actions (CAPAs) are identified and taken where required;
- there is a system for handling complaints, returns, and recalls from the market;
- there is a system for self-inspection; and
- satisfactory arrangements exist to ensure that medical gases are filled, stored, distributed and subsequently handled so that their quality is maintained.

4.6. The system for quality risk management should cover a systematic process for the assessment, control, communication and review of risks in the production, filling, control, storage and distribution of medical gases and, ultimately, protect the patient from receiving the wrong or contaminated product.

5. Personnel

5.1. Personnel involved in the manufacture, control, storage and distribution of medical gases should have the appropriate qualifications and experience.

5.2. Personnel should receive the appropriate training in relevant guidelines covering GxP and company procedures.

5.3. Personnel should be aware of the risks and potential hazards to products and patients.

5.4. Personnel of outsourced service providers should be appropriately trained, especially where activities could influence the quality of medical gases and containers, such as the maintenance and cleaning of cylinders or valves.

6. Documentation

6.1. Specifications, SOPs and related documents, as appropriate for the manufacture, control, storage and distribution of medical gases, should be available.

6.2. Documents should be designed, prepared, reviewed and distributed with care.

6.3. Documents should be authorized (approved, signed and dated) by the appropriate responsible persons. No document should be changed without prior authorization and approval.

6.4. Documents should have unambiguous contents and be laid out in an orderly fashion. The title, nature and purpose should be clearly stated.

6.5. Documents should be periodically reviewed and kept up-to-date.

6.6. Superseded documents should not be used. These should be retained for a specified period of time.

6.7. Where documents require the entry of data, these entries should be clear, legible and indelible, in compliance with good documentation practices and data integrity requirements.

6.8. Records should be made or completed when any action is taken and in such a way that all significant activities are traceable. Records should be retained for a specified period of time.

6.9. Labels should be clear, unambiguous and in the company's agreed format.

6.10. Labels on the cylinders of medical gases should comply with legislation and contain at least the following information:
   a) the name of the medical gas;
   b) the batch number assigned by the manufacturer;
   c) the expiry or use before date;
   d) any special storage conditions or handling precautions that may be necessary;
   e) directions for use;
   f) warnings and precautions if required; and
   g) the name and address of the manufacturer.

6.11. Authorized specifications and testing procedures should be available.

6.12. Records should be maintained for each batch of gas manufactured.

Standard operating procedures and records

6.13. SOPs and associated records should be available for at least, but not limited to:
   a) equipment;
   b) analytical apparatus and instruments;
   c) maintenance, calibration;
   d) cleaning and sanitization;
   e) personnel matters such as training, clothing and hygiene;
   f) qualification and validation;
   g) self-inspection
   h) complaints;
   i) recalls; and
   j) returns.

6.14. The SOPs for sampling should specify the person(s) authorized to take samples and the sampling instructions.

6.15. The SOPs describing the details of the batch (lot) numbering system should ensure that each batch of medical gas is identified with a specific batch number.

6.16. Records of analysis should be maintained.

6.17. Written release and rejection procedures should be available, in particular for the release of the finished product for sale.

6.18. Records should be maintained of the distribution of each batch of medical gas.

6.19. Records should be kept for major and critical equipment, as appropriate, of any qualifications, calibrations, maintenance, cleaning or repair operations, including the dates and the identities of the people who carried out these operations.

7. Complaints

7.1. There should be a written procedure describing the handling of complaints.

7.2. Any complaint concerning a defect of a medical gas should be recorded in detail and thoroughly investigated.

7.3. Where necessary, the appropriate follow-up action should be taken after the investigation and evaluation of a complaint. Where necessary, a recall of the batch or batches should be considered.

7.4. All decisions made and measures taken as a result of a complaint should be recorded and referenced to the corresponding batch records.

7.5. The competent authorities should be informed if a manufacturer is considering action following the identification of serious quality problems with a medical gas that may be impacting patients.

8. Recalls

8.1. There should be a written, authorized procedure describing the managing of a recall of medical gases.

8.2. The recall of a medical gas should be documented. Records should be kept.

9. Returns

9.1. There should be a written, authorized procedure describing the managing of returns of medical gases.

9.2. Once distributed, medical gases may only be returned under agreed conditions as defined by the manufacturer.

9.3. Returned medical gases should be stored in a controlled manner, in a dedicated area. Returned goods should be clearly identified and kept until a decision is made as to what should be done with the returned goods.

9.4. Inventory records of returned medical gases should be kept.

10. Self-inspection

10.1. Self-inspections should be carried out according to a written, authorized procedure. The objective should be to detect any shortcomings in the implementation of GMP and to recommend the necessary corrective actions.

10.2. Self-inspections should be performed routinely and may be, in addition, performed on special occasions.

10.3. Self-inspections should be done by a team of personnel who is able to evaluate compliance with GxP.

10.4. Self-inspections should cover for example:
- a) personnel;
- b) premises;
- c) maintenance;
- d) equipment;
- e) production;
- f) quality control;
- g) documentation;
- h) sanitation and hygiene;
- i) validation and qualification;
- j) calibration;
- k) recall procedures;
- l) complaints management; and
- m) results of previous self-inspections and any corrective steps taken.

10.5. A report should be made at the completion of a self-inspection.

10.6. All recommendations for corrective action should be implemented and an effective follow-up programme should be implemented. The effectiveness of corrective actions taken should be verified.

10.7. Self-inspections may be supplemented by quality audits and conducted by outside or independent specialists.

11. Premises

11.1. The premises, where medical gases are manufactured, should be located, designed, constructed and maintained to suit the operations to be carried out.

11.2. The layout and design of the premises should aim to minimize the risk of errors, mix-ups, contamination and cross-contamination. In addition, it should allow for effective cleaning and maintenance without any adverse effect on the quality of the products.

11.3. The premises should provide sufficient space for manufacturing, quality control testing and storage operations.

11.4. There should be:

a) separate marked areas for different gases; and
b) clear identification and segregation of cylinders/mobile cryogenic vessels at various stages of processing (e.g. “filled cylinders/mobile cryogenic vessels”, “waiting checking”, "awaiting filling", "quarantine", "certified", “rejected“, “prepared deliveries”, “empty cylinders/home cryogenic vessels”).

Note: The method used to achieve these various levels of segregation will depend on the nature, extent and complexity of the overall operation. Marked-out floor areas, partitions, barriers, signs, labels or other appropriate means could be used.

11.5. Empty cylinders/home cryogenic vessels (after sorting or maintenance), as well as filled cylinders/mobile cryogenic vessels, should be stored under cover and be protected from adverse weather conditions.

11.6. Filled cylinders/mobile cryogenic vessels should be stored in a manner that ensures that they will be delivered in a clean state, compatible with the environment in which they will be used. Specific storage conditions should be provided as required (e.g. for gas mixtures where phase separation occurs upon freezing).

12. Equipment and utilities

12.1. Equipment and utilities should be selected, located, constructed and maintained to suit the operations to be carried out.

12.2. The layout, design, installation and use of equipment and utilities should aim to minimize the risk of errors and permit effective cleaning and maintenance in order to avoid cross-contamination, build-up of dust or dirt and, in general, any adverse effect on the quality of products.

12.3. Equipment should be designed to ensure that the correct gas is filled into the correct container. There should normally be no cross connections between pipelines carrying different gases. If cross connections are needed (e.g. filling equipment of mixtures), qualification and controls should ensure that there is no risk of cross-contamination between the different gases. In addition, the manifolds should be equipped with specific connections. These connections may be subject to international or national standards. The use of connections meeting different standards at the same filling site should be carefully controlled, as well as the use of adaptors needed in some situations to bypass the specific fill connection systems.

12.4. Tanks and tankers should be dedicated to a single and defined quality of gas. However, medical gases may be stored or transported in the same tanks, other containers used for intermediate storage, or tankers, as the same nonmedical gas, provided that the quality of the latter is at least equal to the quality of the medical gas and that GMP standards are maintained. In such cases, quality risk management should be performed and documented.

12.5. A common system supplying gas to medical and non-medical gas manifolds is only acceptable if there is a validated method to prevent backflow from the non-medical gas line to the medical gas line.

12.6. Filling manifolds should be dedicated to a single medical gas or to a given mixture of medical gases. In exceptional cases, filling gases used for other medical purposes on manifolds dedicated to medical gases may be acceptable if justified and performed under control. In these cases, the quality of the non-medical gas should be at least equal to the required quality of the medical gas and GMP standards should be maintained. Filling should then be carried out by campaigns.

12.7. Repairs, maintenance, cleaning and purging operations of equipment should not adversely affect the quality of the medical gases. Procedures should describe the measures to be taken after repair and maintenance operations involving breaches of the system's integrity. It should be demonstrated that the equipment is free from any contamination that may adversely affect the quality of the finished product before releasing it for use. Records should be maintained.

12.8. A procedure should describe the measures to be taken when a tanker is back into medical gas service (after transporting non-medical gas, or after a maintenance operation). This should include analytical testing.

13. Qualification and validation

13.1. The scope and extent of qualification and validation should be determined based on risk management principles.

13.2. Risk assessment should be done and cover, for example, the premises, equipment, processing, filling, storage and transport of medical gases.

13.3. Authorized procedures, protocols and records should be maintained.

14. Production

14.1. The manufacturing of medical gases should generally be carried out in closed equipment.

Note: Active substance gases can be prepared by chemical synthesis or be obtained from natural sources followed by purification steps, if necessary (e.g. in an air separation plant).

14.2. Controls should be identified and implemented to minimise the risks of contamination and cross-contamination, for example, because of the reuse of containers.

14.3. Manufacturing data and information should be included in the records for each batch of cylinders/mobile cryogenic vessels produced.

14.4. Records should be maintained for each batch of gas manufactured. These records should, as appropriate, include relevant information such as the following:

a) name of the product;
b) batch number;
c) identification of the person(s) carrying out each significant step;
d) equipment used (e.g. filling manifold);
e) quantity of cylinders/mobile cryogenic vessels before filling, including individual identification references and water capacity(ies);
f) pre-filling operations performed;
g) key parameters that are needed to ensure correct fill at standard conditions;
h) results of appropriate checks to ensure the containers have been filled;
i) specification of the finished product and the results of quality control tests (including reference to the calibration status of the test equipment);
j) quantity of rejected cylinders/mobile cryogenic vessels, with individual identification references and reasons for rejections;
k) details of any problems or unusual events, and signed authorisation for any deviation from instructions; and
l) specification of the finished product and results of quality control tests (including reference to the calibration status of the test equipment) by the responsible person, date and signature.

14.5. Each filled cylinder should be traceable to significant aspects of the production and filling operations.

14.6. Cylinders and mobile cryogenic vessels should be checked, prepared, filled and stored in a separate area from non-medical gases.

14.7. There should be no exchange of cylinders/mobile cryogenic vessels used for medical and non-medical gases these areas, unless all comply with the specifications of medical gases and the manufacturing operations are performed according to GMP standards.

14.8. The production through a continuous process such as air separation should be continuously monitored for quality. The results of this monitoring should be kept in a manner permitting trend evaluation.

14.9. The transfers and deliveries of active substance gases in bulk should comply with the same requirements as those for the medical gases.

14.10. The filling of active substance gases into cylinders or into mobile cryogenic vessels should comply with the same requirements as those for the medical gases.

14.11. Requirements applying to cylinders should also apply to cylinders bundles (except storage and transportation under cover).

14.12. Records should be maintained for each batch of gas transferred to tankers. These records should, as appropriate, include relevant information such as the following:

a) name of the product;
b) batch number;
c) identification reference for the tank (tanker) in which the batch is certified;
d) date and time of the filling operation;
e) identification of the person(s) carrying out the filling of the tank (tanker);
f) identification of the person(s) carrying out each significant step (e.g. line clearance, receipt, preparation before filling, filling, etc.);
g) reference to the supplying tanker (tank), reference to the source gas as applicable;
h) relevant details concerning the filling operation;
i) equipment used (e.g. filling manifold);
j) pre-filling operations performed;
k) key parameters that are needed to ensure correct fill at standard conditions;
l) a sample of the batch label;
m) specification of the finished product and results of quality control tests (including reference to the calibration status of the test equipment);
n) details of any problems or unusual events, and signed authorisation for any deviation from filling instructions; and
o) certification statement by the authorized responsible person, date and signature.

Transfers and deliveries of cryogenic and liquefied gas

14.13. The transfers of cryogenic or liquefied gases from primary storage, including controls before transfers, should be in accordance with validated procedures designed to avoid any contamination. Transfer lines should be equipped with non-return valves or other suitable alternatives. Flexible connections and coupling hoses and connectors should be flushed with the relevant gas before use.

14.14. The transfer hoses used to fill tanks and tankers should be equipped with product-specific connections. The use of adaptors allowing the connection of tanks and tankers not dedicated to the same gases should be adequately controlled.

14.15. Deliveries of gas may be added to tanks containing the same quality of gas provided that a sample is tested to ensure that the quality of the delivered gas is acceptable. This sample may be taken from the gas to be delivered or from the receiving tank after delivery.

Filling and labelling of cylinders and mobile cryogenic vessels

14.16. Before filling cylinders and mobile cryogenic vessels, a batch (batches) of gas(es) should be determined, controlled according to specifications, and approved for filling.

14.17. In the case of continuous processes, adequate in-process controls should be performed to ensure that the gas complies with specifications.

14.18. Cylinders, mobile cryogenic vessels and valves should conform to appropriate technical specifications and any relevant requirements by the applicable regulatory authorities. They should be dedicated to a single medical gas or to a given mixture of medical gases.

14.19. Cylinders should be colour-coded according to relevant standards. They should preferably be fitted with minimum pressure retention valves with non-return mechanism in order to get adequate protection against contamination.

14.20. Cylinders, mobile cryogenic vessels and valves should be checked before first use in production and should be properly maintained.

14.21. Checks and maintenance operations should not affect the quality and the safety of the medical gas. The water used for the hydrostatic pressure testing carried out on cylinders should be at least of drinking quality.

14.22. As part of the checks and maintenance operations, cylinders should be subject to an internal visual inspection before fitting the valve, to make sure they are not contaminated with water or other contaminants.

14.23. Internal visual inspection should be done:
- a) when they are new and initially put into medical gas service;
- b) following any hydrostatic statutory pressure test or equivalent test where the valve is removed; and
- b) whenever the valve is replaced.

Note: After fitting, the valve should be kept closed to prevent any contamination from entering the cylinder.

14.24. The maintenance and repair operations of cylinders, mobile cryogenic vessels and valves are the responsibility of the manufacturer of the medical product. If subcontracted, they should only be carried out by approved subcontractors, and contracts including technical agreements should be established. Subcontractors should be audited to ensure that appropriate standards are maintained.

14.25. There should be a system in place to ensure traceability of cylinders, mobile cryogenic vessels and valves.

14.26. Checks to be performed before filling should be done in accordance with an authorized procedure. The following checks should be observed:
- a) in the case of cylinders fitted with a minimum pressure retention valve, for a positive residual pressure in each cylinder;
- b) in the case of cylinders that are not fitted with a minimum pressure retention valve, to make sure it is not contaminated with water or other contaminants;
- c) ensuring that all previous batch labels have been removed;
- d) the removal and replacement of damaged product labels;
- e) a visual external inspection of each cylinder, mobile cryogenic vessel and valve for dents, arc burns, debris, other damage and contamination with oil or grease; cleaning should be done if necessary;
- f) on each cylinder or mobile cryogenic vessel outlet connection to determine that it is the proper type for the particular gas involved;
- g) for the date of the next test to be performed on the valve (in the case of valves that need to be periodically tested);
- h) on cylinders or mobile cryogenic vessels to ensure that any tests required by national or international regulations (e.g. hydrostatic pressure test or equivalent for cylinders) have been conducted and still is valid; and
- i) that each container is colour-coded as specified in the legislation (e.g. colour-coding of the relevant national/international standards).

14.27. A batch should be defined for filling operations.

14.28. Cylinders and mobile cryogenic vessels which have been returned for refilling should be prepared with care in order to minimise risks for contamination. These procedures, which should include evacuation and/or purging operations, should be validated.

Note: For compressed gases, a maximum theoretical impurity should be defined for a filling pressure at specified temperature.

14.29. There should be appropriate checks to ensure that each cylinder/mobile cryogenic vessel has been properly filled.

14.30. Each filled cylinder should be tested for leaks using an appropriate method, prior to fitting the tamper evident seal or device. The test method should not introduce any contaminant into the valve outlet and, if applicable, should be performed after any quality sample is taken.

14.31. After filling, cylinder valves should be fitted with covers to protect the outlets from contamination. Cylinders and mobile cryogenic vessels should be fitted with tamper-evident seals or devices.

14.32. Each cylinder or mobile cryogenic vessel should be labelled. The batch number and the expiry date may be on a separate label.

14.33. In the case of medical gases produced by mixing two or more different gases (in-line before filling or directly into the cylinders), the mixing process should be validated to ensure that the gases are properly mixed in every cylinder and that the mixture is homogeneous.

15. Quality control

15.1. Each batch of medical gas (cylinders, mobile cryogenic vessels, hospital tanks) should be tested in accordance with the requirements of the authorized specification and or pharmacopoeia.

Sampling

15.2. There should be an authorized sampling procedure with a sampling plan for testing medical gases.

15.3. In the case of a single medical gas:

a) filled via a multi-cylinder manifold, the gas from at least one cylinder from each manifold filling cycle should be tested for identity and assay each time the cylinders are changed on the manifold; and

b) filled into cylinders one at a time, the gas from at least one cylinder of each uninterrupted filling cycle should be tested for identity and assay.

Note: An example of an uninterrupted filling cycle is one shift's production using the same personnel, equipment, and batch of gas to be filled.

15.4. In the case of a medical gas produced by mixing two or more gases in a cylinder from the same manifold, the gas from every cylinder should be tested for assay and identity.

15.5. In the case of a medical gas produced by mixing two or more gases in a cylinder from the same manifold, the gas from every cylinder should be tested for assay and identity of each component gas.

15.6. For excipients, if any, testing on identity could be performed on one cylinder per manifold filling cycle (or per uninterrupted filling cycle in case of cylinders filled one at a time). Fewer cylinders may be tested in case of validated automated filling system.

15.7. Premixed gases should follow the same principles as single gases when continuous in-line testing of the mixture to be filled is performed. Premixed gases should follow the same principle as medical gases produced by mixing gases in the cylinders when there is no continuous inline testing of the mixture to be filled.

15.8. The testing for water content should be performed unless otherwise justified.

15.9. Other sampling and testing procedures that provide at least equivalent level of quality assurance may be justified.

15.10. Final testing on mobile cryogenic vessels should include a test for assay and identity on each vessel, unless otherwise authorized by the medicines regulatory authority. Testing by batches should only be carried out if it has been demonstrated that the critical attributes of the gas remaining in each vessel before refilling have been maintained.

15.11. Cryogenic vessels retained by customers (hospital tanks or home cryogenic vessels) which are refilled in place from dedicated tankers do not need to be sampled after filling, provided that a certificate of analysis on the contents of the tanker accompanies the delivery. However, it should be demonstrated that the specification of the gas in the vessels is maintained over the successive re-fillings.

15.12. Records of analysis should include at least the following:

a) name of the medical gas;
b) batch number;
c) references to the relevant specifications and testing procedures;
d) test results and reference to any specifications (limits);
e) date(s) and reference number(s) of testing;
f) initials of the persons who performed the testing;
g) date and initials of the persons who verified the testing and the calculations, where appropriate; and
h) a clear statement of release or rejection (or other status decision) and the dated signature of the designated responsible person.

15.13. Reference and retention samples are not required, unless otherwise specified.

15.14. On-going stability studies are not required in case initial stability studies have been replaced by bibliographic data.

16. Product life cycle and continuous improvement

16.1. Manufacturers of medical gases should consider adopting a life cycle approach and continuous improvement. These principles should be applied in the relevant areas of the facility, equipment, instrument, utility, product and processes.

16.2. Means should be identified for continuous improvement to enable optimizing production and control, while meeting current demands for supply and satisfying quality requirements of medical gases.

17. Storage and distribution

17.1. Precautions should be taken to prevent unauthorized persons from entering storage areas.

17.2. Storage areas should be under cover, an enclosed area, with sufficient capacity to allow the orderly storage of the different medical gases.

17.3. Storage areas should be appropriately designed, constructed, and maintained. They should be kept clean and dry and there should be sufficient space and ventilation.

17.4. In general, medical gases should be protected from extreme temperatures during storage. Where special storage conditions are required, these should be provided, controlled, monitored and recorded.

17.5. Empty cylinders should be stored separately.

17.6. A written cleaning programme should be available indicating the frequency of cleaning and the methods to be used to clean the storage areas.

17.7. There should be a written programme for pest control.

17.8. Broken or damaged cylinders that can no longer be used should be withdrawn from usable stock and stored separately.

17.9. Periodic stock reconciliation should be performed at defined intervals by comparing the actual and recorded stocks. Discrepancies should be identified and investigated. The appropriate corrective action should be taken.

Distribution and transport

17.10. Filled gas cylinders and home cryogenic vessels should be handled in a manner to ensure that they are delivered to customers in a clean state compatible with the environment in which they will be used.

17.11. Medical gases should be transported in accordance with the conditions stated on the labels. There should be no risk to their quality during transport and distribution.

17.12. Product, batch and container identity should be maintained at all times. All labels should remain legible.

17.13. Distribution records should be sufficiently detailed to allow for a recall when required.

17.14. Appropriately equipped vehicles should be suitable for the transport of medical gases, with sufficient space.

17.15. The design and use of vehicles should aim to minimize the risk of errors and permit effective cleaning and maintenance to avoid contamination, build-up of dust or dirt and/or any adverse effect on the medical gases and containers.

17.16. In case of tankers, dedicated vehicles and equipment should be used. Where non-dedicated vehicles and equipment are used, procedures should be in place to ensure that the quality of the medical gases will not be compromised.

17.17. Defective vehicles and equipment should not be used. These should either be labelled as such or removed from service.

17.18. There should be procedures in place for the operation and maintenance of all vehicles and equipment.

17.19. There should be written procedures, programmes and records for cleaning of tankers and vehicles. Agents used should not have any adverse effect on product quality or be a source of contamination.

17.20. Where required, appropriate environmental conditions should be provided, checked, monitored and recorded.

17.21. There should be documented, detailed procedures for the dispatch of medical gases. Records for the dispatch should include relevant information to allow traceability. Such records should facilitate the recall of a batch of a medical gas when necessary.

17.22. Tankers and cylinders should be secured to prevent unauthorized access.

17.23. Procedures for transport should ensure that:
- a) the identity of the medical gas is not lost;
- b) there is no risk of contamination of the medical gas;
- c) precautions are taken against damage and theft; and
- d) environmental conditions are maintained if required.

17.24. The appropriate signs and warnings, where required, should be visible on tankers and vehicles.

References

Note: Some parts of the text may have been adapted from other WHO GMP guidelines, as well as those published by the European Union and Pharmaceutical Inspection Co-operation Scheme. The intention is to establish a document which reflects current requirements and is harmonized with these texts. For further details on some of the topics, further reading of original guidelines is recommended.

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2. WHO good manufacturing practices: water for pharmaceutical use. In. WHO Expert Committee on Specifications for Pharmaceutical Preparations: forty-sixth report. Geneva: World Health Organization; 2020: Annex 3 (WHO Technical Report Series, No.1025; http://www.who.int/medicines/areas/quality_safety/quality_assurance/expert_committee/trs_970/en/, accessed 29 January 2021).

3. WHO guideline on good integrity. In. WHO Expert Committee on Specifications for Pharmaceutical Preparations: fifty-fifth report. Geneva: World Health Organization; 2021: Annex 4 (WHO Technical Report Series, No. XXXX (*in preparation*).

4. WHO good practices for pharmaceutical quality control laboratories. In. WHO Expert Committee on Specifications for Pharmaceutical Preparations: forty-fourth report. Geneva: World Health Organization; 2010: Annex 1 (WHO Technical Report Series, No. 957; http://www.who.int/medicines/publications/, accessed 29 January 2021).

5. WHO good storage and distribution practices for medical products. In. WHO Expert Committee on Specifications for Pharmaceutical Preparations: fifty-fourth report. Geneva: World Health Organization; 2020: Annex 7 (WHO Technical Report Series, No. 1025; https://www.who.int/publications/m/item/trs-1025-annex-7-gdp-medical-products, accessed 29 January 2021).

6. WHO guidelines for sampling of pharmaceutical products and related materials. In. WHO Expert Committee on Specifications for Pharmaceutical Preparations: thirty-ninth report. Geneva: World Health Organization; 2005: Annex 4 (WHO Technical Report Series, No. 929; http://whqlibdoc.who.int/trs/WHO_TRS_929_eng.pdf?ua=1, accessed 29 January 2021).

7. WHO guidelines on heating, ventilation and air-conditioning systems for non-sterile pharmaceutical products. In. WHO Expert Committee on Specifications for Pharmaceutical Preparations: fifty-second report. Geneva: World Health Organization; 2018: Annex 8 (WHO Technical Report Series, No. 1010; http://www.who.int/medicines/areas/quality_safety/quality_assurance/expert_committee/trs_1010/en/, accessed 29 January 2021).

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9. WHO good practices for pharmaceutical microbiology laboratories. In. WHO Expert Committee on Specifications for Pharmaceutical Preparations: forty-fifth report. Geneva, World Health Organization; 2011: Annex 2 (WHO Technical Report Series, No. 961; http://whqlibdoc.who.int/trs/WHO_TRS_961_eng.pdf?ua=1, accessed 29 January 2021).

10. WHO guidelines on quality risk management. In. WHO Expert Committee on Specifications for Pharmaceutical Preparations: forty-seventh report. Geneva, World Health Organization; 2013: Annex 2 (WHO Technical Report Series, No. 981; https://www.who.int/medicines/areas/quality_safety/quality_assurance/expert_committee/trs_981/en/; accessed 29 January 2021).

11. WHO technical supplements to model guidance for storage and transport of time – and temperature – sensitive pharmaceutical products. In. WHO Expert Committee on Specifications for Pharmaceutical Preparations: forty-ninth report. Geneva, World Health Organization; 2015: Annex 5 (WHO Technical Report Series, No. 992; http://www.who.int/medicines/areas/quality_safety/quality_assurance/expert_committee/WHO_TRS_992_web.pdf, accessed 29 January 2021).

12. Inspection of medicinal gases; www.picscheme.org.

13. EudraLex - Volume 4 - Good Manufacturing Practices (GMP) guidelines; https://ec.europa.eu/health/documents/eudralex/vol-4_en. https://ec.europa.eu/health/sites/health/files/files/eudralex/vol-4/2009_07_annex6.pdf#:~:text=Manufacture%20of%20medicinal%20gases%20is%20generally%20carried%20out,particular%20because%20of%20the%20reuse%20of%20containers.%204

14. *The International Pharmacopoeia*, 10th edition, 2021 (*in preparation*).

Abbreviations

°C	Celsius
CAPA	corrective action and preventive action
EU	European Union
GMP	good manufacturing practices
GxP	good practices
PIC/S	Pharmaceutical Inspection Co-operation Scheme
SOP(s)	standard operating procedure(s)

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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

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

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

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

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

CH2 N84.4>G:
579, 836
Aglycosylated

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

CHS K2:
986

adrenomedullinum pegolum #

adrenomedullin pegol

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

adrénomedulline pégol

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

adrenomedulina pegol

adrenomedulina humana, C-terminal L-tirosil amida, pegilada en O^4 de Y^1 con [(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)

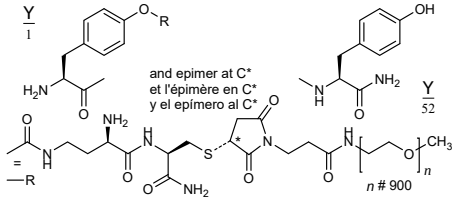
$C_{280}H_{430}N_{86}O_{83}S_4(C_2H_4O)_{\approx 900}$

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



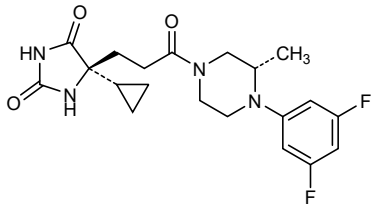
aldumastatum

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
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Light chain / Chaîne légère / Cadena ligera (1'-216' and 1'"-216'"" anti-TNFRSF17)

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

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

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

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

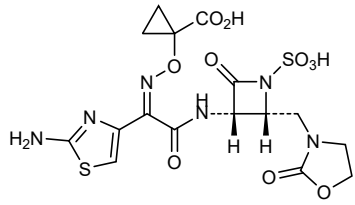
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
521, 296"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

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

ancremonamum

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

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



apitegromabum #

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

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

Heavy chain / Chaîne lourde / Cadena pesada

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

Light chain / Chaîne légère / Cadena ligera

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

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

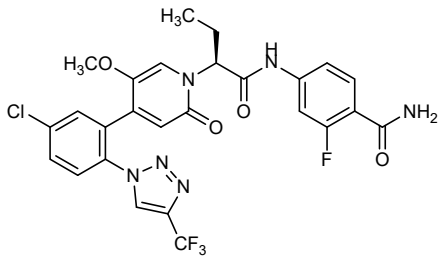
N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"
L VL Q1:
1', 1'"

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

asundexianum

asundexian	(4*S*)-2^4-chloro-4-ethyl-7^3-fluoro-3^5-methoxy-3^2,5-dioxo-1^4-(trifluoromethyl)-3^2*H*-6-aza-3(4,1)-pyridina-1(1)-[1,2,3]triazola-2(1,2),7(1)-dibenzenaheptaphane-7^4-carboxamide
asundexian	(4*S*)-2^4-chloro-4-éthyl-7^3-fluoro-3^5-méthoxy-3^2,5-dioxo-1^4-(trifluorométhyl)-3^2*H*-6-aza-3(4,1)-pyridina-1(1)-[1,2,3]triazola-2(1,2),7(1)-dibenzénaheptaphane-7^4-carboxamide
asundexián	(4*S*)-2^4-cloro-4-etil-7^3-fluoro-3^5-metoxi-3^2,5-dioxo-1^4-(trifluorometil)-3^2*H*-6-aza-3(4,1)-piridina-1(1)-[1,2,3]triazola-2(1,2),7(1)-dibencenaheptafano-7^4-carboxamida

$C_{26}H_{21}ClF_4N_6O_4$



atidarsagenum autotemcelum #

atidarsagene autotemcel

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

atidarsagène autotemcel

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

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

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

Sequence / Séquence / Secuencia

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

Post-translational modifications

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

36-86, 43-89

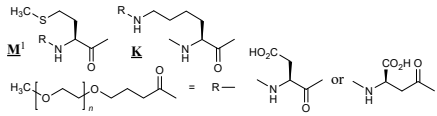
Partial deamidation / Désamidation partielle / Desamidación parcial

N78 (Asn>Asp, isoaspartyl)

Modified residues / Résidus modifiés / Restos modificados

avipendekin : pegol ~ 1:1

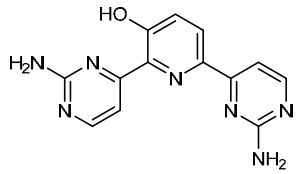
M[1] (Met 1: ~32-40 %), **K** (Lys 11, 37, 42, 87: ~33-42 %; Lys 12, 95, 98: ~18-35 %)



avotaciclibum

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

$C_{13}H_{11}N_7O$



azercabtagenum zapreleucelum

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

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

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

bapotulimabum #

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

bapotulimab

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

Heavy chain / Chaîne lourde / Cadena pesada

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

Light chain / Chaîne légère / Cadena ligera

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

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

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

*A-isoform, predominant

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

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

barecetamabum #

barecetamab

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

barécétamab

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

barecetamab

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

Heavy chain / Chaîne lourde / Cadena pesada

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

Light chain / Chaîne légère / Cadena ligera

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

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

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

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
301, 301"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires 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'

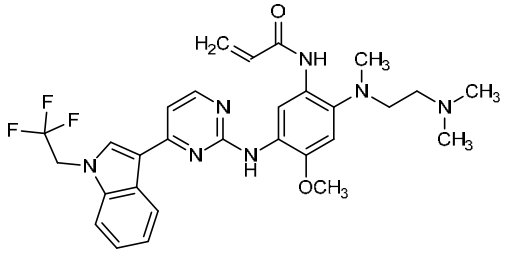
befotertinibum

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

$C_{29}H_{32}F_3N_7O_2$



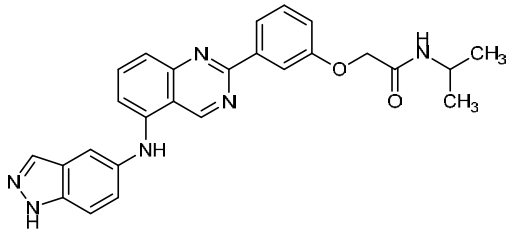
belumosudilum

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 #

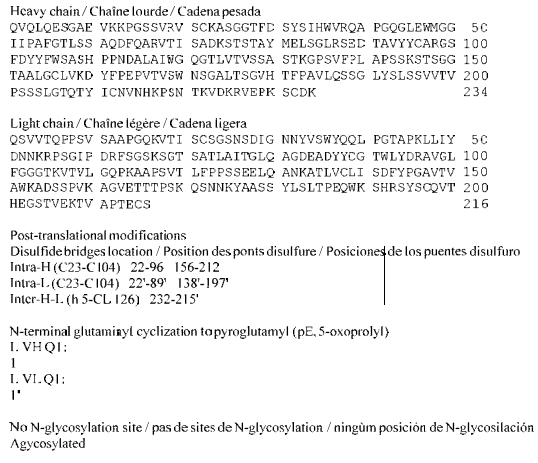
bentracimab — immunoglobulin Fab G1-lambda, anti-[*ticagrelor* and its active metabolite AR-C124910XX], *Homo sapiens* monoclonal antibody; VH-(CH1-hinge) gamma1 heavy chain *Homo sapiens* (1-234) [VH (*Homo sapiens* IGHV1-69*06 (85.7%) -(IGHD) -IGHJ1*01 (100%)) CDR-IMGT [8.7.14] (26-33.51-58.97-118) (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)
1, VH Q1:
1
1, VL Q1:
1'

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

bepirovirsenum
bepirovirsen

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

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

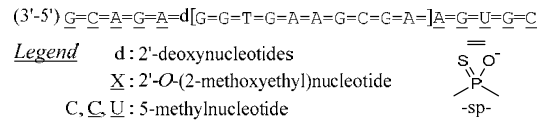
bépirovirsen

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

bepirovirsén

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

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



beremagenum geperpavecum #

beremagene geperpavec

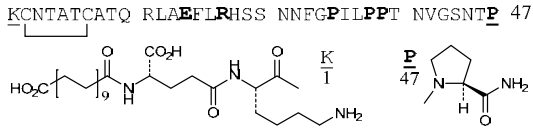
A replication-defective herpes simplex virus encoding human collagen type VII alpha 1 chain (COL7A1).

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

cagrilintidum

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

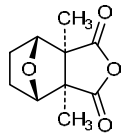
$C_{194}H_{312}N_{54}O_{59}S_2$



cantharidinum

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

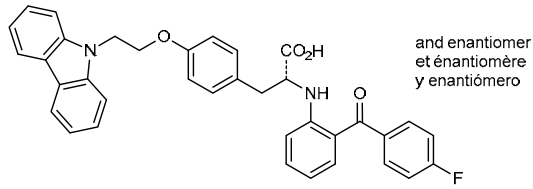
$C_{10}H_{12}O_4$



carfloglitazarum

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

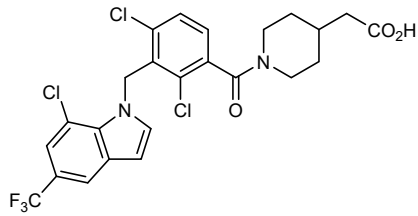
$C_{36}H_{29}FN_2O_4$



cedirogantum

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

$C_{24}H_{20}Cl_3F_3N_2O_3$



cevaretigenum ritoparvovecum #

cevaretigene ritoparvovec

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

cévarétigène ritoparvovec

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

cevaretigén ritoparvovec

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

cipaglucosidasum alfa #

cipaglucosidase alfa

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

cipaglucosidase alfa

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

cipaglucosidasa alfa

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

Sequence / Séquence / Secuencia

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

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

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

cirtuvivintum

cirtuvivint

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

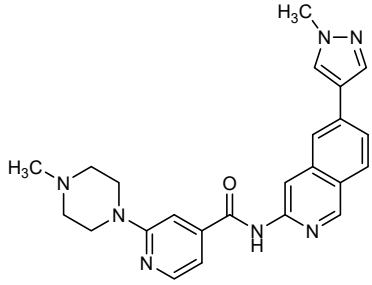
cirtuvivint

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

cirtuvivint

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

$C_{24}H_{25}N_7O$



coprelotamabum #

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

Heavy chain / Chaîne lourde / Cadena pesada

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

Light chain / Chaîne légère / Cadena ligera

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

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

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

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

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

cotoretigenum toliparvovecum

cotoretigene toliparvovec

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

cotoretigène toliparvovec

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

cotoretigén toliparvovec

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

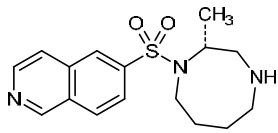
cotosudilum

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

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

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

$C_{16}H_{21}N_3O_2S$



dafsolimabum

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

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

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

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

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

Post-translational modifications
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 (h12, h15, h18, h21) 229-229" 232-232" 235-235" 238-238"

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

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

Fucosylated complex bi-antennary SP2/0-type glycans / glycanes de type SP2/0 bi-antennaires complexes fucosylés / glicanos de tipo SP2/0 biantenarios complejos fucosilados
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CH3 K2:
456, 456"

dafsolimabum setaritoxum

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

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

dafsolimab setaritox

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

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQQSGAE LARPGASVKM SCKASGYTFT SYTMHWVKQR PGQGLEWIGY  5C
INPSSGYTNY IQRFKDKATL TADKSSSTAY MQVSSLTSED SAVYYCARGS 10C
RYDYYGMDYW GQGTSVTVSS AKTTPPSVYP LAPGCGDTTG SSVTLGCLVK 15C
GYFPESVTVT WNSGSLSSSV HTFPALLQSG LYTMSSSVTV PSSTWPSQTV 20C
TCSVAHPASS TTVDKKLEPS GPISTINPCP PCKECHKCPA PNLEGGPSVF 25C
IFPPNIKDVL MISLTPKVTC VVVDVSEDDP DVQISWFVNN VEVHTAQTQT 30C
HREDYNSTIR VVSTLPIQHQ DWMSGKEFKC KVNNKDLPSP IERTISKIKG 35C
LVRAPQVYIL PPPAEQLSRK DVSLTCLVVG FNPGDISVEW TSNGHTEENY 40C
KDTAPVLDSD GSYFIYSKLN MKTSKWEKTD SFSCNVRHEG LKNYYLKKTI 45C
SRSPGK                                                  456
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Light chain / Chaîne légère / Cadena ligera

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QIVLTQSPAI MSASPGEKVT MTCSASSSVS YMHWYQQKSG TSPKRWIYDT  5C
SKLASGVPAR FSGSGSGTSY SLTISSMEAE DAATYYCQQW SSNPLTFGAG 10C
TKLELKRADA APTVSIFPPS SEQLTSGGAS VVCFLNNFYP KDINVKWKID 15C
GSERQNGVLN SWTDQDSKDS TYSMSSTLTL TKDEYERHNS YTCEATHKTS 20C
TSPIVKSFNR NEC                                          213
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Met-Ricin A chain / Met-chaîne A de la Ricine / Met-cadena A de la Ricina

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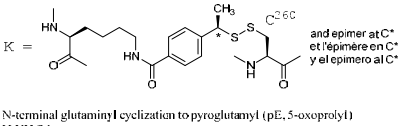
MIFPKQYPII NFTTAGATVQ SYTNFIRAVR GRLTTGADVR HDIPVLPNRV 5C
GLPINQRFIL VELSNHAELS VTLALDVTNA YVVGYRAGNS AYFFHPDNQE 10C
DAEAITHLFT DVQNRYTFAF GGNYDRLEQL AGNLRENIEL GNGPLEEAIS 15C
ALYYYSTGGT QLPTLARSFI ICIQMISEAA RFQYIEGEMR TRIRYNRRSA 20C
PDPSVITLEN SWGRLSTAIQ ESNQGAFASP IQLQRRNGSK FSVYDVSILI 25C
PIIALMVYRC 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 conjugación
major: K74 K141' K206'
K74" K141"' K206"'
minor: K326 K329 K349 K442 K447 K18' K52' K168'
K326" K329" K349" K442" K447" K18"' K52"' K168"'



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

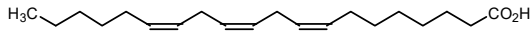
daleutonum

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

$C_{20}H_{34}O_2$



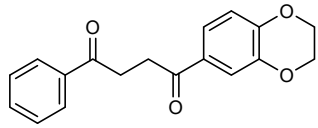
dalosirvatum

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

$C_{18}H_{16}O_4$



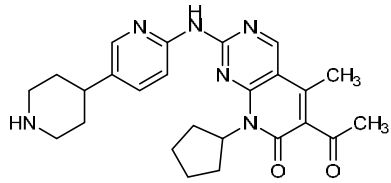
dalpiciclibum

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

$C_{25}H_{30}N_6O_2$



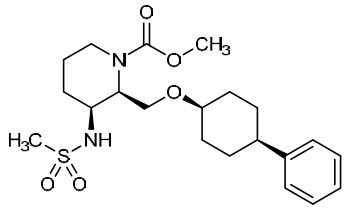
danavorextonum

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)

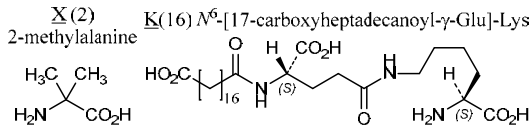
dapiglutida — análogo del péptido 2 semejante al glucagón (GLP-2) humano; *N*$^{6.16}$-[*N*-(17-carboxiheptadecanoil)-L-γ-glutamil]-[A^2>Aib (2-metilalanina), D^3>E, S^7>T, D^8>S, M^{10}>L, N^{11}>A, N^{16}>K, L^{17}>Q, N^{24}>A, T^{29}>H]]péptido 2 semejante al glucagón humano (GLP-2)

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

Sequence / Séquence / Secuencia

HXEGSFTSEL ATILDKQAAR DFIAWLIQHK ITD 33

Modified residues / Résidus modifiés / Restos modificados



daplusiranum

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

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

daplusiran

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

daplusirán

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

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

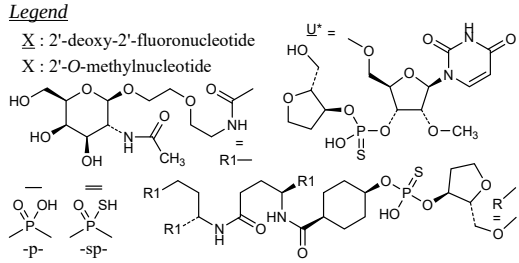
(3'-5') R=G-U-G-G-A-C-U-U-C-U-C-U-C-A-A-U-U-U-C-U*

(5'-3') C=A-C-C-U-G-A-A-G-A-G-A-G-U-U-A-A-A=A=G=A

Legend

X : 2'-deoxy-2'-fluoronucleotide

X : 2'-*O*-methylnucleotide



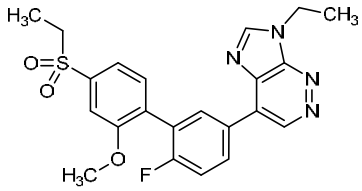
darigabatum

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

$C_{22}H_{21}FN_4O_3S$



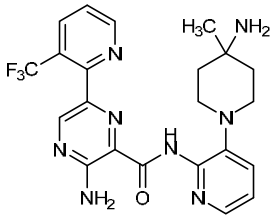
darovasertibum

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 TTDTSTSTAY 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 (h5-C1, 126) 225-215' 225"-215'"
Inter-H-H (h11, h14) 231-231" 234-234"

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

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

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

dazodalibepum #

dazodalibep

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

dazodalibep

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

dazodalibep

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

Sequence / Séquence / Secuencia

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

Mutations / Mutations / Mutaciones

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

Post-translational modifications

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

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

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación

none / aucune / ninguna

depemokimabum #

depemokimab

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

dépémokimab

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

depemokimab

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

Heavy chain / Chaîne lourde / Cadena pesada

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

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

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

Intra-H (C23-C104)	22-95	146-202	263-323	369-427
	22"-95"	146"-202"	263"-323"	369"-427"
Intra-L (C23-C104)	23'-94'	140'-200'		
	23'"-94'"	140'"-200'"		
Inter-H-L (h 5-CL 126)	222-220'	222"-220'"		
Inter-H-H (h 11, h 14)	228-228"	231-231"		

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

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

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

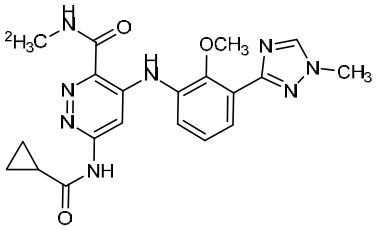
deucravacitinibum

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

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

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

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



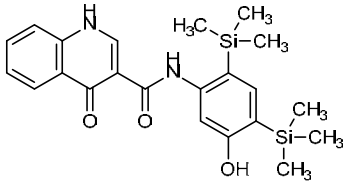
dirocaftorum

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

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

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

$C_{22}H_{28}N_2O_3Si_2$



divozilimabum #

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

divozilimab

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

divozilimab

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

Heavy chain / Chaîne lourde / Cadena pesada

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

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

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 148-204 265-325 371-429
22"-96" 148"-204" 265"-325" 371"-429"
Intra-L (C23-C104) 23'-87' 133'-193'
23'"-87'" 133'"-193'"
Inter-H-L (h 5-CL 126) 224-213' 224"-213'"
Inter-H-H (h 11, h 14) 230-230" 233-233"

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

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

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

ebronucimabum #

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

Heavy chain / Chaîne lourde / Cadena pesada

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

Light chain / Chaîne légère / Cadena ligera

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

Post-translational modifications

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

```
Intra-H (C23-C104)  22-96    150-206    267-327    373-431
                    22"-96"  150"-206"  267"-327"  373"-431"
Intra-L (C23-C104)  22'-90'    139'-198'
                    22'"-90'"  139'"-198'"
Inter-H-L (h 5-CL 126)  226-216'  226"-216'"
Inter-H-H (h11, h14)    232-232"  235-235"
```

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

L 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.

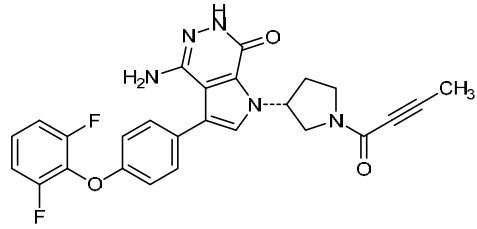
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal

H CH3 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

$C_{26}H_{21}F_2N_5O_3$



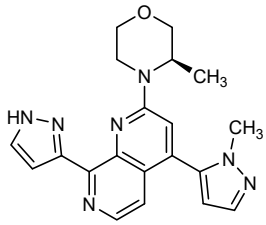
elimusertibum

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

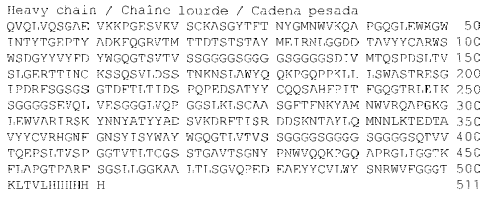
éluvixtamab

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)



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Heavy chain / Chaîne lourde / Cadena pesada
QVQLVQSGAE VKKPGESVKV SCKASGYTFT NYGMNWVKQA PGQGLEWMGW  50
INTYTGEPTY ADKFQGRVTM TTDTSTSTAY MELRNLGGDD TAVYYCARWS 100
WSDGYYVYFD YWGQGTSVTV SSGGGGSGGG GSGGGGSDIV MTQSPDSLTV 150
SLGERTTINC KSSQSVLDSS TNKNSLAWYQ QKPGQPPKLL LSWASTRESG 200
TPDRFSGSGS 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
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-V (C23 C104) 22-96 160-231 278-354 418-486

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

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

emerfetamabum #
emerfetamab

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

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

Heavy chain / Chaîne lourde / Cadena pesada

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QVQLVQSGAE VKKPGESVKV SCKASGYTFT NYGMNWVKQA PGQGLEWMGW  50
INTYTGEPTY ADKFQGRVTM TTDTSTSTAY MELRNLGGDD TAVYYCARRS 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
KLTVLGGGGG KTHTCPPCPA PELLGGPSVF LFPPKPKDTL MISRTPEVTC 550
VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP CREQYGSTYR 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 HNAKTKPCRE QYGSTYRCVS 850
VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR EPQVYTLPPS 900
REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF 950
FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS PGK        993
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

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

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

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DVVLTQSPLS LPVTLGQPAS ISCRSSQSIV YSNGNTYLEW YLQRPGQSPR  50
LLIYRVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCFQGSHIP 100
YTFGGGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 145-201 262-322 368-426
22"-96" 145"-201" 262"-322" 368"-426"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (h 5-CL 126) 221-219' 221"-219'"
Inter-H-H (h 11, h 14) 227-227" 230-230"

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

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

enomimeranum #

enomimeran

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

énomiméran

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

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

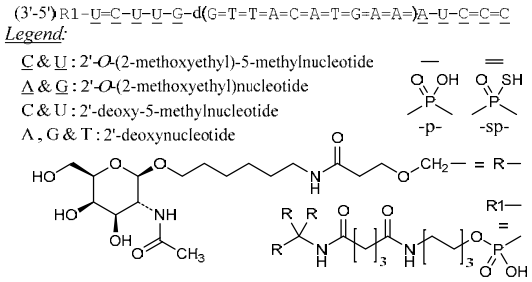
entacingenum turiparvovecum #

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

eplontersenum

eplontersen	*all-P-ambo*-5'-*O*-(28-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-16,16-bis{[3-({6-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]hexyl}amino)-3-oxopropoxy]methyl}-1-hydroxy-1,10,14,21-tetraoxo-2,18-dioxa-9,15,22-triaza-1λ^5-phosphaoctacosan-1-yl)-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyluridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyluridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)guanylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)adenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyluridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidine
éplontersen	*tout-P-ambo*-5'-*O*-(28-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-16,16-bis{[3-({6-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]hexyl}-amino)-3-oxopropoxy]méthyl}-1-hydroxy-1,10,14,21-tétraoxo-2,18-dioxa-9,15,22-triaza-1λ^5-phosphaoctacosan-1-yl)-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyluridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyluridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)guanylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)adénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyluridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidine
eplontersén	*todo-P-ambo*-5'-*O*-(28-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-16,16-bis{[3-({6-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]hexil}amino)-3-oxopropoxi]metil}-1-hidroxi-1,10,14,21-tetraoxo-2,18-dioxa-9,15,22-triaza-1λ^5-fosfaoctacosan-1-il)-2'-*O*-(2-metoxietil)-5-metil-*P*-tiouridilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metilcitidilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metiluridilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metiluridilil-(3'→5')-2'-*O*-(2-metoxietil)guanilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-*O*-(2-metoxietil)adenilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metiluridilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metilcitidina

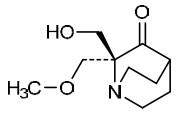
$C_{296}H_{437}N_{77}O_{156}P_{20}S_{13}$



eprenetapoptum

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

$C_{10}H_{17}NO_3$



and enantiomer
et énantiomère
y enantiómero

etevritamabum #

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

étévritamab

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

etevritamab

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

Sequence / Séquence / Secuencia

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

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

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

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

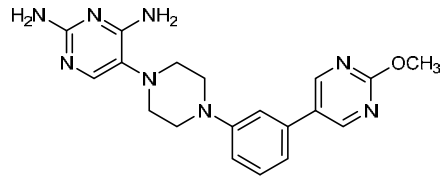
fanotaprimum

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

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

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

$C_{19}H_{22}N_8O$



favezelimabum #

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

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

favezelimab

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

Heavy chain / Chaîne lourde / Cadena pesada

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

Light chain / Chaîne légère / Cadena ligera

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

Post-translational modifications

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

Intra-H (C23-C104) 22-96 146-202 260-320 366-424
22"-96" 146"-202" 260"-320' 366"-424"
Intra-L (C23-C104) 23'-92' 138'-198'
23'"-92'" 138'"-198'"
Inter-H-L (CH1 10-CL 126) 133-218' 133"-218'"
Inter-H-H (h 11, h 14) 225-225" 228-228"

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

H CH2 N84.4:
296, 296"

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

C-terminal lysine clipping:
H CHS K2:
446, 446"

firazorextonum

firazorexton

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

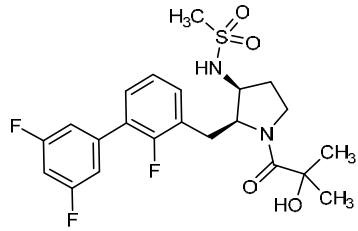
firazorexton

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

firazorextón

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

$C_{22}H_{25}F_3N_2O_4S$



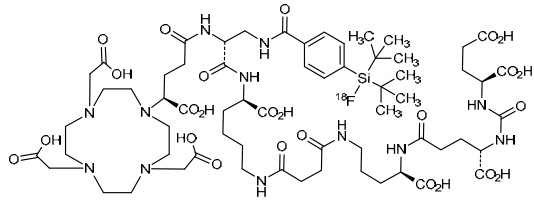
flotufolastatum (^{18}F)

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

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

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

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



flubentylosinum

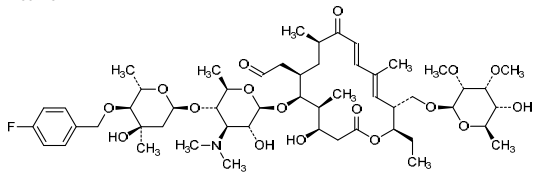
flubentylosin — [(4*R*,5*S*,6*S*,7*R*,9*R*,11*E*,13*E*,15*R*,16*R*)-15-{[(6-deoxy-2,3-di-*O*-methyl-β-D-allopyranosyl)oxy]methyl}-6-{[3,6-dideoxy-4-*O*-{2,6-dideoxy-4-*O*-[(4-fluorophenyl)methyl]-3-*C*-methyl-α-L-*ribo*-hexopyranosyl}-3-(dimethylamino)-β-D-glucopyranosyl]oxy}-16-ethyl-4-hydroxy-5,9,13-trimethyl-2,10-dioxo-1-oxacyclohexadeca-11,13-dien-7-yl]aceta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

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

flubentilosina

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

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



fordadistrogenum movaparvovecum #

fordadistrogene movaparvovec

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

fordadistrogène movaparvovec

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

fordadistrogén movaparvovec

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

gallium (^{68}Ga) gozetotidum

gallium (^{68}Ga) gozetotide

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

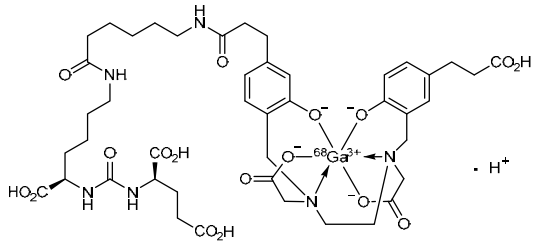
gallium (^{68}Ga) gozétotide

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

galio (^{68}Ga) gozetótida

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

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



garivulimabum #

garivulimab

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

garivulimab

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

chaîne lourde gamma1 humanisée (1-446) [VH humanisé (*Homo sapiens* IGHV3-NL1*01 (84.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.11] (26-33.51-57.96-106) (1-117) -*Homo sapiens* IGHG1*01 G1m17,1, G1v4 CH2 A114 (CH1 K120 (214) (118-215), charnière 1-15 (216-230) -CH2 V1.2>A (234), P114>A (329) (231-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (118-446)], (220-215')-disulfure avec la chaîne légère kappa humanisée (1'-215') [V-KAPPA humanisé (*Homo sapiens* IGKV1-5*03 (84.0%) -IGKJ2*01 (91.7%)) CDR-IMGT [6.3.10] (27-32.50-52.89-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (226-226":229-229")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

garivulimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD274 (ligando 1 de muerte programada, PDL1, PD-L1, homólogo 1 de B7, B7H1)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-446) [VH humanizado (*Homo sapiens* IGHV3-NL1*01 (84.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.11] (26-33.51-57.96-106) (1-117) -*Homo sapiens* IGHG1*01 G1m17,1, G1v4 CH2 A114 (CH1 K120 (214) (118-215), bisagra 1-15 (216-230) -CH2 V1.2>A (234), P114>A (329) (231-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (118-446)], (220-215')-disulfuro con la cadena ligera kappa humanizada (1'-215') [V-KAPPA humanizado (*Homo sapiens* IGKV1-5*03 (84.0%) -IGKJ2*01 (91.7%)) CDR-IMGT [6.3.10] (27-32.50-52.89-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (226-226":229-229")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

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

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

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

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

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

garveleucelum

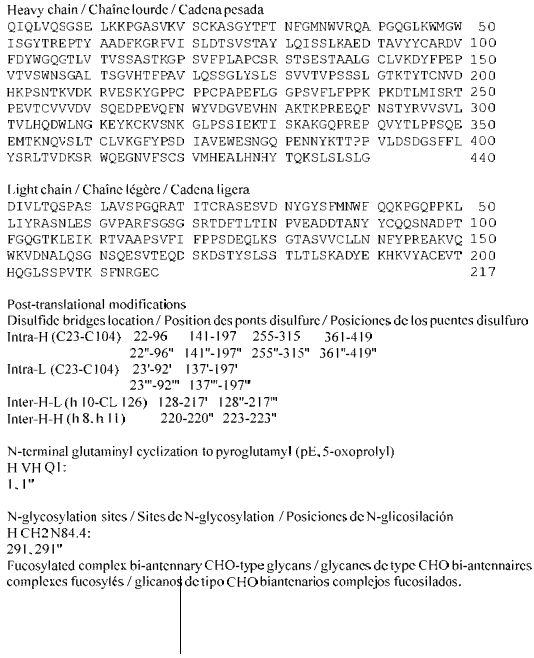
garveleucel	Allogeneic T cell-enriched leukocyte preparation, devoid of alloreactive T cells. The cells are derived from peripheral blood mononuclear cells (PBMCs) collected by apheresis from a haploidentical stem cell donor. The cells are lymphocyte enriched, and during processing patient and donor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

gavocabtagenum autoleucelum #

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

geptanolimabum #

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



gindameranum #

gindameran

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

gindaméran

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

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

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

Heavy chain / Chaîne lourde / Cadena pesada

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

Light chain / Chaîne légère / Cadena ligera

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

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

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

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

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

grisnilimabum setaritoxum #
grisnilimab setaritox

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

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

Heavy chain / Chaîne lourde / Cadena pesada

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

Light chain / Chaîne légère / Cadena ligera

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

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

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

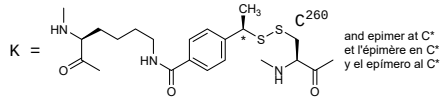
Post-translational modifications

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

Intra-H (C23-C104) 22-96 150-205 267-327 373-431
22"-96" 150"-205" 267"-327" 373"-431"
Intra-L (C23-C104) 22'-90' 137'-196'
22'"-90'" 137'"-196'"
Inter-H-L (CH1 11-CL 126) 138-214' 138"-214'"
Inter-H-H (h 12, h 15, h 18) 230-230" 233-233" 235-235"
heterogeneous patterns involving 94' and 94'" e.g.:
96-94' 138-94' 150-94' 94'-137'
96"-94'" 138"-94'" 150"-94'" 94'"-137'"
Met-RTA: C172 = Cys-SH, C260 = Cys-S-S-CH(CH3)-p-C6H4-CO-[N6-Lys(H,L)]

Conjugation sites / Sites de conjugaison / Posiciones de coniugación

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



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

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

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

hepcidinum

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

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

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

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

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

Sequence / Séquence / Secuencia
DTHFPICIFC CGCCHRSKCG MCCKT 25

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

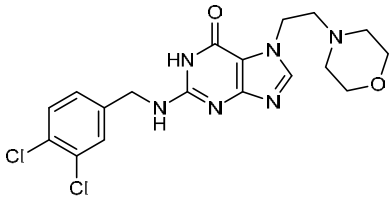
ibezapolstatum

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

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

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

$C_{18}H_{20}Cl_2N_6O_2$



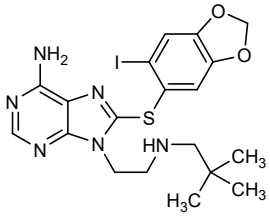
icapamespibum

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

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

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

$C_{19}H_{23}IN_6O_2S$



idactamabum #

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

Heavy chain / Chaîne lourde / Cadena pesada

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

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

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 148-204 266-326 372-430
22"-95" 148"-204" 266"-326" 372"-430"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 224-214' 224"-214'"
Inter-H-H (h 11, h 14) 230-230" 233-233"

Cysteinyl inserted for conjugation capped by a cysteinyl
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 CHSK2:
452, 452"

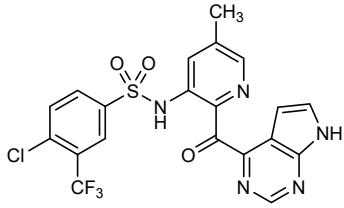
ilacirnonum

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

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

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

$C_{20}H_{13}ClF_3N_5O_3S$



insulinum icodecum

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

insuline icodec

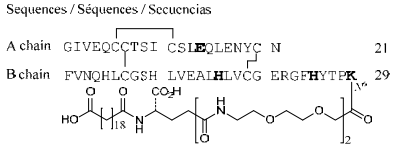
chaîne A de l'insuline humaine (1-21) variant (Y>E^{14}), chaîne B de l'insuline humaine (1-29) variant (Y>H^{16}, F>H^{25}), conjuguée en K^{29B} par son *N*^{6} à (22*S*)-22,42-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazadotétracontan-1-oyle; *N*$^{6.29B}$-[(22*S*)-22,42-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazadotétracontan-1-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

insulina icodec

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

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

Sequences / Séquences / Secuencias



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

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

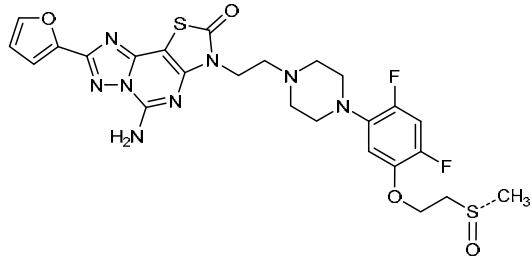
inupadénant

(+)-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.

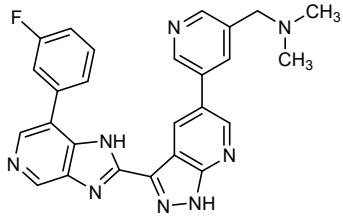
ipivivintum

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

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

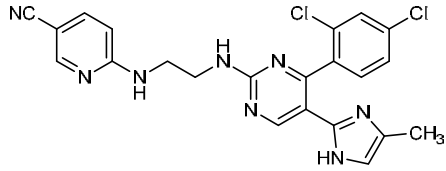
laduviglusibum

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

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

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

$C_{22}H_{18}Cl_2N_8$



lazucirnonum

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

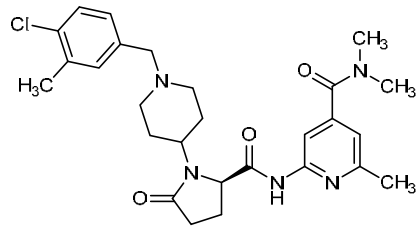
lazucirnon

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

lazucirnón

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

$C_{27}H_{34}ClN_5O_3$



lerodalcibepum #

lerodalcibep

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

lérodalcibep

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

lerodalcibep

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

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

Sequence / Séquence / Secuencia

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

Mutation / Mutation / Mutación

C^{136}>**Δ**

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

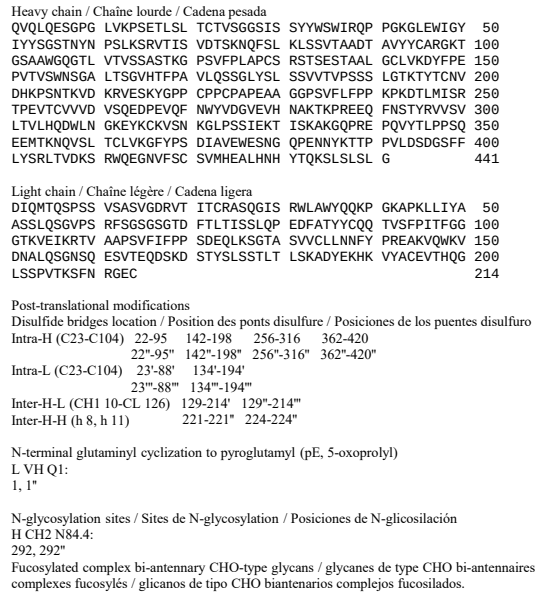
létaplimab

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"		

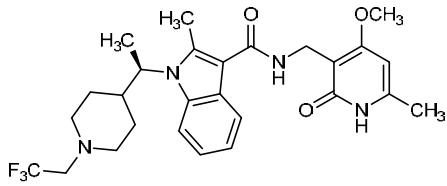
N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
L VH Q1:
1, 1"

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

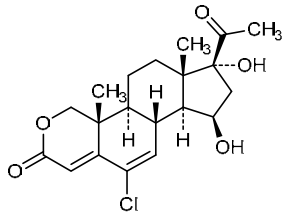
$C_{27}H_{33}F_3N_4O_3$



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

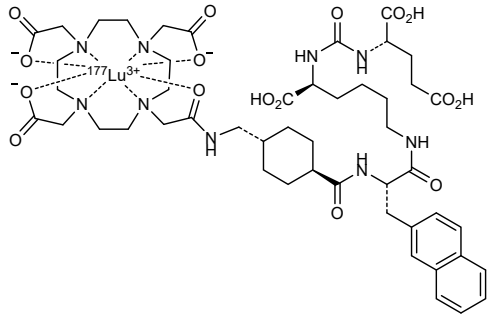
lutécium (^{177}Lu) vipivotide tétraxetan

{*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

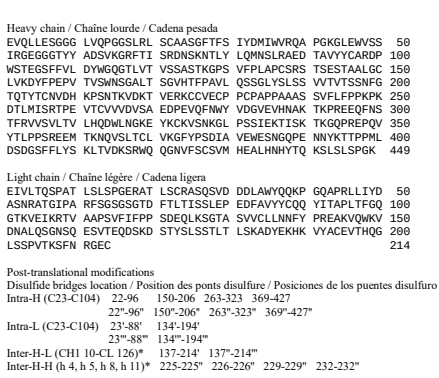
immunoglobulin G2-kappa, anti-[*Homo sapiens* IL1RL1 (interleukin 1 receptor like 1, DER4, FIT-1, growth stimulation expressed 2 gene, ST2, IL33R)], *Homo sapiens* monoclonal antibody;
gamma2 heavy chain *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV3-23*01 (91.8%) -(IGHD) -IGHJ4*01(92.9%)) CDR-IMGT [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

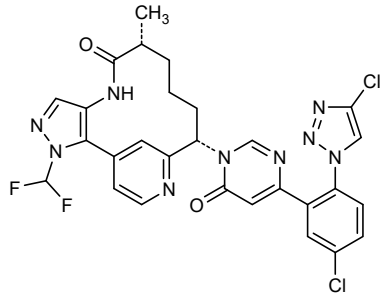
milvexian

(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
IYYTYDDTND YWGQGTTVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELL GGPSVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE 350
PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP 450
G                                                       451
```

Light chain / Chaîne légère / Cadena ligera

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

Post-translational modifications

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

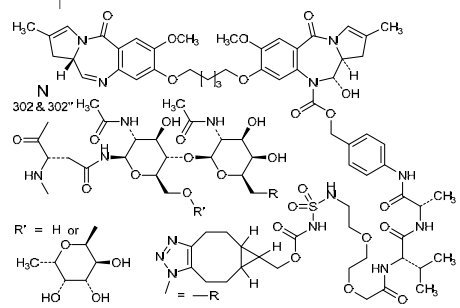
```
Intra-H (C23-C104)  22-96    149-205   266-326   372-430
                    22"-96"  149"-205" 266"-326" 372"-430"
Intra-L (C23-C104)  23'-89'   135'-195'
                    23"'-89"' 135"'-195"'
Inter-H-L (h 5-CL 126)  225-215'  225"-215"'
Inter-H-H (h 11, h 14)  231-231"  234-234"
```

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

```
H VH Q1:
1, 1"
```

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

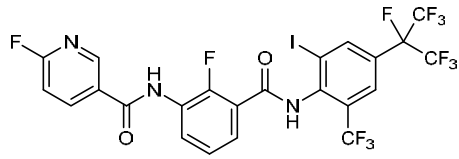
```
H CH2 N84.4:
302, 302"
```



modoflanerum

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

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



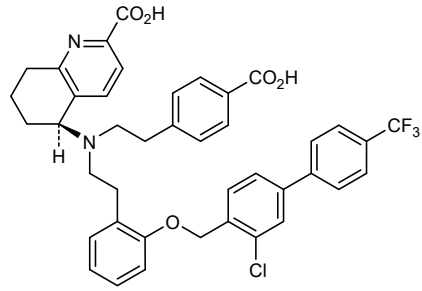
mosliciguatum

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

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

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

$C_{41}H_{36}ClF_3N_2O_5$



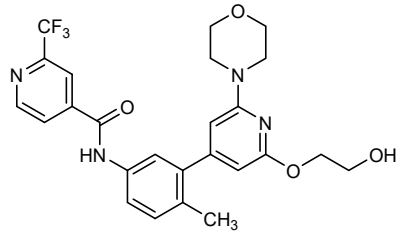
naporafenibum

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

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

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

$C_{25}H_{25}F_3N_4O_4$



nedosiranum

nedosiran

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

nédosiran

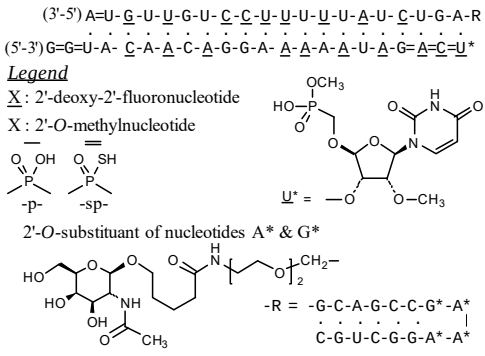
tout-P-ambo-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluoroguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-désoxy-2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

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

nedosirán

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

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



nemvaleukinum alfa #

nemvaleukin alfa

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

nemvaleukine alfa

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

nemvaleukina alfa

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

Sequence / Séquence / Secuencia

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

Mutation / Mutation / Mutación

C^{51}>S

Post-translational modifications

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

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

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación

N187, N206, T212

obecabtagenum autoleucelum #

obecabtagene autoleucel

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

obécabtagène autoleucel

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

obecabtagén autoleucel

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

obrindatamabum #

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

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

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

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

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

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

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

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

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain 1 (C23-C104) 23-88 137-213 318-378 424-482
Intra-chain 2 (C23-C104) 22'-90' 140'-214'
Intra-chain 3 (C23-C104) 41"-101" 147"-205"
Inter-chains 1 - 2 243-243'
Inter-chains 1 - 3 (h 11 -h 11) 283-6"
(h 14 -h 14) 286-9"

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

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

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

ociperlimabum #

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

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

ociperlimab

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

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS DYYMYWVRQA PGKGLEWVAY  50
ITKGGGSTYY PDSVKGRFTI SRDNAKNTLY LQMNSLRAED TAVYYCARQT 100
NYDFTMDYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH 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 CHSK2:
449, 449"

omodenbamabum #

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

Heavy chain / Chaîne lourde / Cadena pesada

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

Light chain / Chaîne légère / Cadena ligera

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

Post-translational modifications

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

Intra-H (C23-C104) 22-96 152-208 316-376 422-480
22"-96" 152"-208" 316"-376" 422"-480"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (CH1 10-CL 126) 139-214' 139"-214'"
Inter-H-H (h1 13, h1 16, 236-236" 239-239"
h2 5, h2 11, h2 14 245-245" 251-251" 254-254"
h3 5, h3 11, h3 14, 260-260" 266-266" 269-269"
h4 5, h4 11, h4 14) 275-275" 281-281" 284-284"

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

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

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

h2 S7 h3 S7 h4 S7
247, 247" 262, 262" 277, 277"
Sialylated glycans regularly present / glycanes sialylés régulièrement présents / glicanos sialilados regularmente presentes

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

H CHS K2:
502, 502"

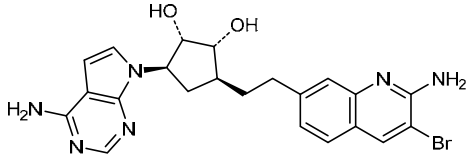
onametostatum

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

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

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

$C_{22}H_{23}BrN_6O_2$



ontasameranum

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

	Messenger RNA (mRNA), 5'-capped, encoding codon-optimised transmembrane phosphatase with tensin homology (TPTE; cancer/testis antigen 44) expressed as a fusion protein comprising a secretory signal peptide, TPTE, P2P16 tetanus toxoid-derived helper epitopes and a major histocompatibility complex (MHC) class I transmembrane and cytoplasmic domain (MITD), connected by three glycine/serine-rich (GS) linker peptides, flanked by 5' and 3' untranslated regions and a 3' poly(A) tail.
ontasaméran	ARN messager codant pour la phosphatase transmembranaire homologue à la tensine (TPTE). Un ARN messager (ARNm), protégé en 5', codant pour la phosphatase transmembranaire homologue à la tensine (TPTE ; antigène 44 du cancer testiculaire), avec des codons optimisés, exprimé sous la forme d'une protéine de fusion comprenant un peptide signal de sécrétion, TPTE, les épitopes auxiliaires P2P16 dérivés de l'anatoxine tétanique et un domaine transmembranaire et cytoplasmique (MITD) du complexe majeur d'histocompatibilité (CMH) de classe I, reliés par trois peptides de liaison riches en glycine/sérine (GS), flanqués de régions non traduites en 5' et 3' et d'une queue poly(A) en 3'.
ontasamerán	ARN mensajero que codifica para la fosfatasa transmembranal con homología con la tensina (TPTE). ARN mensajero (ARNm), protegido en 5', que codifica para la fosfatasa transmembranal con homología con la tensina (TPTE; antígeno de cáncer/testículo 44), con codones optimizados, expresada como una proteína de fusión que consta de un péptido señal de secreción, TPTE, los epítopos auxiliares P2P16 derivados del toxoide tetánico y un dominio citoplásmico y transmembrana del complejo principal de histocompatibilidad (MHC) de clase I, conectados mediante tres péptidos de enlace ricos en glicina/serina (GS), flanqueado por las regiones 5' y 3' no traducidas y una cola poly(A) en 3'.

oplunofuspum #

oplunofusp	*Actinomyces viscosus* L-methionyl sialidase (exo-α-sialidase) catalytic domain fragment (239-631, 2-394 in the current sequence), fused to human amphiregulin heparin binding domain fragment (25-45, 395-415 in the current sequence) anti-(binding to human heparin and cell surface glycosaminoglycans), produced in *Escherichia coli*; L-methionyl (1)-sialidase (exo-α-sialidase, EC:3.2.1.18) (*Actinomyces viscosus*) (239-631)-peptide (containing the sialidase domain) (2-394), fused to human amphiregulin (25-45)-peptide (binding to human heparin and glycosaminoglycans) (395-415), produced in *Escherichia coli*
oplunofusp	L-méthionyl, fragment du domaine catalytique (239-631, 2-394 dans la séquence actuelle) de la sialidase d'*Actinomyces viscosus* (exo-α-sialidase), fusionné à un fragment du domaine liant l'héparine de l'amphiréguline humaine (25-45, 395-415 dans la séquence actuelle) anti-(liant aux glycosaminoglycanes de surface cellulaire et à l'héparine, humains), produit dans *Escherichia coli;*

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

oplunofusp

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

Sequence / Séquence / Secuencia

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MSDHPQATPA PAPDASTELP ASMSQAQHLA ANTATDNYRI PAITTAPNGD   50
LLISYDERPK DNGNGGSDAF NPNHIVQRRS TDGGKTWSAF 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
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-V (C23 C104) 22-96 159-224 271-347 411-479

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

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

pariglasgenum brecaparvovecum #

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

pavurutamabum #

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

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

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

Heavy chain / Chaîne lourde / Cadena pesada

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

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

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

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

pegtibatinasum #

pegtibatinase

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

pegtibatinase

fragment de la cystathionine β-synthase humaine (2-413, M^1 supprimée) mutant (C^{15}>S), homodimère, produit dans *Escherichia coli*, pégylé en N^6 des résidus lysine avec une moyenne de cinq groupes 5-[α-méthylpoly(oxyéthylène)-ω-oxy]-5-oxopentanoyle par monomère de protéine;
peptide 2-413 de des-$Mét^1$-[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 GPTCSPHRSC PHSAKCSLEK CSPEDKEAKE PLWIRPDAPS   50
RCTWQLGRPA SESPHHHTAP AKSPKILPDI LKKICDTPMV RINKICKKFG  100
LKCELLAKCE FFNACGSVKD RISLRMIEDA ERDCTLKPGE TIIEPTSGNT  150
GIGLALAAAV RGYRCIIVMP EKMSSEKVDV LRALGAEIVR TPTNARFDSP  200
ESHVGVAWRL KNEIPNSHIL DQYRNASNPL AHYDTTADEI LQQCDGKLDM  250
LVASVGTGGT ITGIARKLKE KCPGCRIIGV DPEGSILAEP EELNQTEQTT  300
YEVEGIGYDF TPTVLDRTVV DKWFKSNDEE AFTFARMLTA QEGLLCGGSA  350
GSTVAVAVKA AQELQEGQRC VVILPDSVRN YMTKFLSDRW MLQKGFLKEE  400
DLTFKKPWWW HLR                                          415
```

Mutation / Mutation / Mutación
C^{15}>S

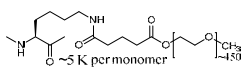
Post-translational modifications
Removal of Met^1 / Suppression de Met^1 / Eliminación de Met^1

Disulfide bridges location / Position des ponts disulfure / Posición del puentes disulfuro
272-275, 272'-275' (and further variable potential bridges)

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

Cofactor binding sites / Sites de liaison des cofacteurs / Sitios de unión de cofactores
N^6-pyridoxylidene 5'-phosphate / 5'-phosphate de N^6-pyridoxylidène / 5'-fosfato de N^6-piridoxilideno K119, K119'
heme B (protoheme IX) / hème b (protohème IX) / hemo B (protohemo IX)
Cys52-S -Fe(II)- N^1-His65, Cys52'-S -Fe(II)- N^1-His65'

Chemical modification / Modification chimique / Modificación química



pegulicianinum

pegulicianine

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

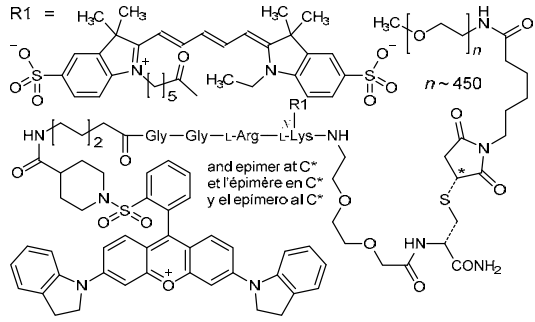
pégulicianine

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

pegulicianina

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

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



pelabresibum

pelabresib

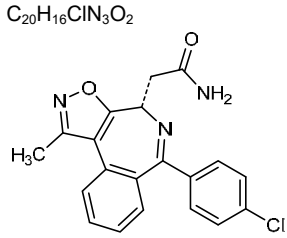
2-[(4*S*)-6-(4-chlorophenyl)-1-methyl-4*H*-[1,2]oxazolo[5,4-*d*][2]benzazepin-4-yl]acetamide

pélabrésib

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

pelabresib

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

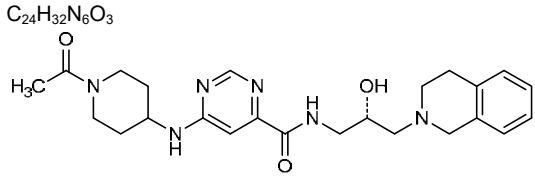


pemrametostatum

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

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

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



penpulimabum #

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

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

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

penpulimab

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

Heavy chain / Chaîne lourde / Cadena pesada

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

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

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 145-201 262-322 368-426
22"-96" 145"-201" 262"-322" 368"-426"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 221-214' 221"-214'"
Inter-H-H (h 11, h 14) 227-227" 230-230"

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

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

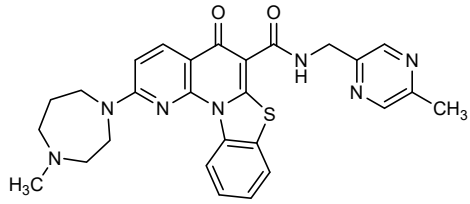
pidnarulexum

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

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

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

$C_{27}H_{27}N_7O_2S$



pimivalimabum #

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

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

pimivalimab

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

Heavy chain / Chaîne lourde / Cadena pesada

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

Light chain / Chaîne légère / Cadena ligera

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

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

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

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

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

pirepematum

pirepemat

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

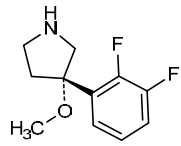
pirépémat

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

pirepemat

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

$C_{11}H_{13}F_2NO$



pomulmeranum #

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

posoleucelum

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

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

posoleucel

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

radgocitabinum

radgocitabine

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

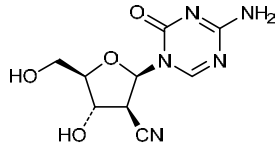
radgocitabine

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

radgocitabina

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

$C_{10}H_{12}N_4O_4$



rebonuputemcelum

rebonuputemcel

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

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

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

Heavy chain / Chaîne lourde / Cadena pesada

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

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

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

Intra-H (C23-C104) 22-96 148-204 265-325 371-429
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 IgG4 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.

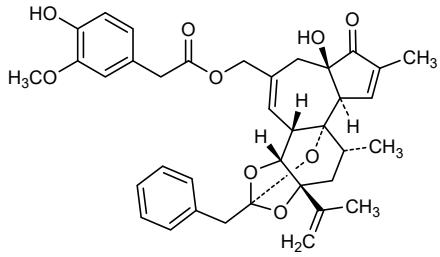
relmacabtagène autoleucel

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 #

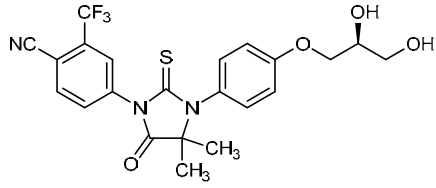
revakinagene taroretcel	Allogeneic human adult retinal pigment epithelial (RPE) cell line stably transfected with a plasmid encoding human ciliary neurotrophic factor (CNTF). An allogeneic human adult retinal pigment epithelial (RPE) cell line stably transfected with a plasmid encoding human ciliary 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

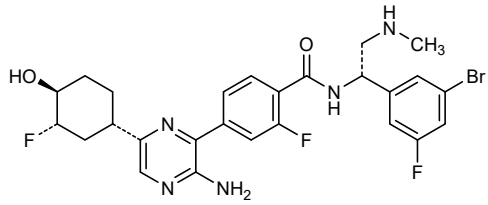
$C_{22}H_{20}F_3N_3O_4S$



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

$C_{26}H_{27}BrF_3N_5O_2$



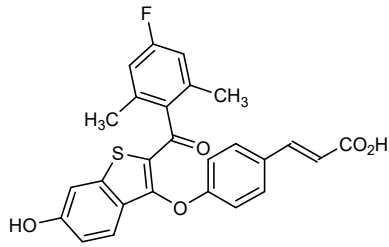
rintodestrantum

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

$C_{26}H_{19}FO_5S$



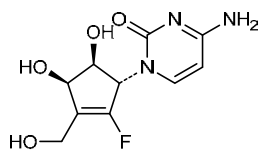
roducitabinum

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

$C_{10}H_{12}FN_3O_4$



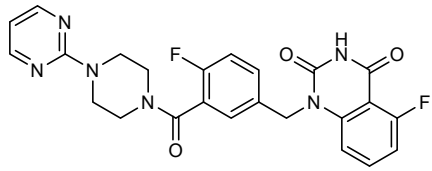
senaparibum

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

$C_{24}H_{20}F_2N_6O_3$



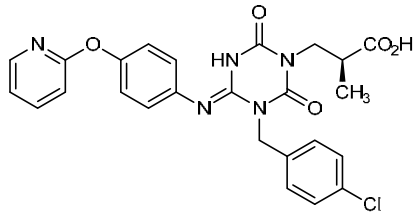
sivopixantum

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

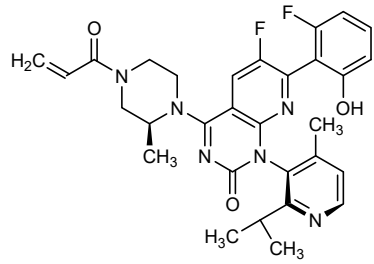
sotorasib

(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)

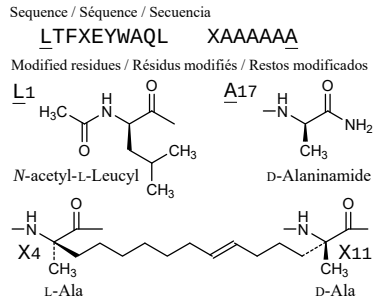
sulanémadline

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

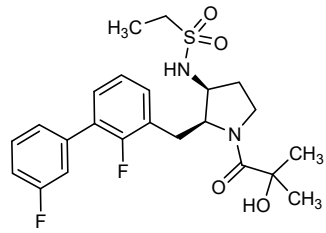
suntinorexton

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.

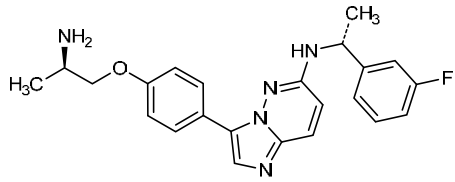
taletrectinibum

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
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Post-translational modifications

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

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

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

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

telpegfilgrastimum #

telpegfilgrastim

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

telpegfilgrastim

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

telpegfilgrastim

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

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

Sequence / Séquence / Secuencia

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

Mutation / Mutation / Mutación

A^{1}>**M**

Post-translational modifications

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

37-43, 65-75

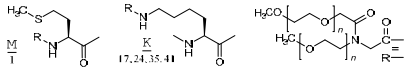
Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación

none / aucune / ninguna

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

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

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



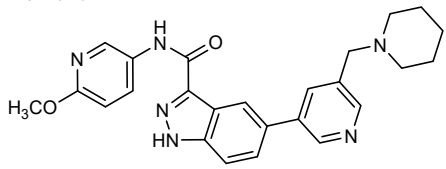
tenvumestrocelum

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

$C_{25}H_{26}N_6O_2$



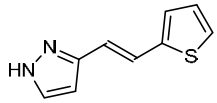
terevalefimum

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

$C_9H_8N_2S$



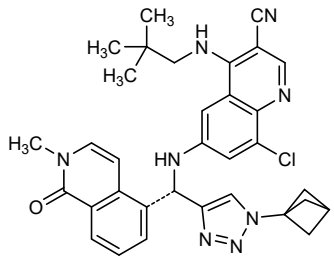
tilpisertibum

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

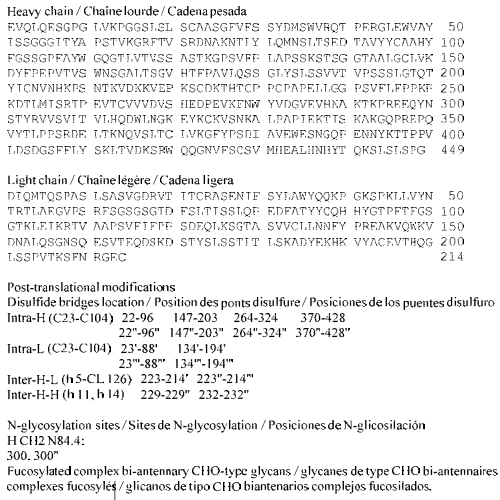
$C_{33}H_{33}ClN_8O$



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
TSSGGGTYYA 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 HYGTPPTFGS 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQKKV 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 PERRGLEWVAY  50
TSSGGGTTYA PSTVKGRFTV SRDNAKNTLY LQMNSLTSED TAVYYCAARY 100
FGSSGPFAYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPG  449
```

Light chain / Chaîne légère / Cadena ligera

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

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 134'-194'
23"'-88"' 134"'-194"'
Inter-H-L (h 5-CL 126) 223-214' 223"-214"'
Inter-H-H (h 11, h14) 229-229" 232-232"

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

For the ravtansine part, please refer to the document "INN for pharmaceutical substances: Names for radicals, groups and others"*
Pour la partie ravtansine, veuillez-vous référer au document "INN for pharmaceutical substances: Names for radicals, groups and others"*
Para la fracción ravtansina, se ruega referirse al documento "INN for pharmaceutical substances: Names for radicals, groups and others"*

upifitamabum rilsodotinum

upifitamab rilsodotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* SLC34A2 (solute carrier family 34 sodium phosphate member 2, sodium/phosphate cotransporter 2B, NaPi2b, NaPi3b, NAPI-3B)], monoclonal antibody, conjugated, via a thioether bond, to3 to 5 flexible polymers PHF-BA-EG2-MI-AF-HPA-Ala, each comprising maleimide (MI) bioconjugation linkers and
3 to 4 auristatin F- hydroxypropylamide-L-alanine (AF-HPA-Ala), with a drug ratio of 12:1 to 15:1;

	gamma1 heavy chain (1-449) [VH (*Homo sapiens* IGHV1-46*01 (81.6%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -glycinyl (120) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-215')-disulfide with kappa light chain (1'-215') [V-KAPPA (*Mus musculus* IGKV10-94*01 (84.2%) -IGKJ5*01 (91.7%)/*Homo sapiens* IGKV1-33*01 (83.2%) -IGKJ2*01 (90.9%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -arginyl (108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109''-215')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa; conjugated, via a thioether bond, from 3 to 5 flexible biodegradable polymers, poly(1-hydroxymethylethylene hydroxymethyl-formal) (PHF)-BA-EG2-MI-AF-HPA-Ala, each comprising maleimide (MI) conjugation linkers and 3 to 4 cytotoxic auristatin F- hydroxypropylamide-L-alanine (AF-HPA-Ala), with a drug ratio of 12:1 to 15:1
upifitamab rilsodotine	immunoglobuline G1-kappa, anti-[*Homo sapiens* SLC34A2 (membre 2 de la famille 34 sodium phosphate de transporteurs de solutés, cotransporteur 2B de sodium/phosphate, NaPi2b, NaPi3b, NAPI-3B)], anticorps monoclonal, conjugué, via une liaison thiéther, à 3 à 5 polymères flexibles PHF-BA-EG2-MI-AF-HPA-Ala, comprenant chacun des linkers de bioconjugaison maléimide (MI) et 3 à 4 auristatine F- hydroxypropylamide-alanine (AF-HPA-Ala), dans un rapport produit actif de 12:1 à 15:1; chaîne lourde gamma1 (1-449) [VH (*Homo sapiens* IGHV1-46*01 (81.6%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -glycinyl (120) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-215')-disulfure avec la chaîne légère kappa (1'-215') [V-KAPPA (*Mus musculus* IGKV10-94*01 (84.2%) -IGKJ5*01 (91.7%)/*Homo sapiens* IGKV1-33*01 (83.2%) -IGKJ2*01 (90.9%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -arginyl (108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (229-229'':232-232'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa; conjugué, via une liaison thiéther, de 3 à 5 polymères flexibles biodégradables poly(1-hydroxyméthyléthylène hydroxyméthyl-formal) (PHF)-BA-EG2-MI-AF-HPA-Ala, comprenant chacun des linkers de conjugaison maléimide (MI) et 3 à 4 auristatine F- hydroxypropylamide-L-alanine (AF-HPA-Ala) cytotoxiques, dans un rapport produit actif de 12:1 à 15:1
upifitamab rilsodotina	inmunoglobulina G1-kappa, anti-[*Homo sapiens* SLC34A2 (miembro 2 de la familia 34 sodio fosfato de transportadores de solutos, cotransportador 2B de sodio/fosfato, NaPi2b, NaPi3b, NAPI-3B)], anticuerpo monoclonal, conjugado, a través de un enlace tioéter, de 3 a 5 polímeros flexibles PHF-BA-EG2-MI-AF-HPA-Ala, que comprende cada uno de los enlaces de bioconjugación maleimida (MI) y 3 a 4 auristatina F- hidroxipropilamida-L-alanina (AF-HPA-Ala), en una relación de principio activo de 12:1 a 15:1;

cadena pesada gamma1 (1-449) [VH (*Homo sapiens* IGHV1-46*01 (81.6%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -glicinil (120) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-215')-disulfuro con la cadena ligera kappa (1'-215') [V-KAPPA (*Mus musculus* IGKV10-94*01 (84.2%) -IGKJ5*01 (91.7%)/*Homo sapiens* IGKV1-33*01 (83.2%) -IGKJ2*01 (90.9%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -arginil (108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')];
dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa; conjugado, a través de un enlace tioéter, a 3 a 5 polímeros flexibles biodegradables poli(1-hidroximetiletileno hidroximetil-formal) (PHF)-BA-EG2-MI-AF-HPA-Ala, que comprende cada unos de los enlaces de conjugación maleimida (MI) y
3 a 4 auristatina F- hidroxipropilamida-L-alanina (AF-HPA-Ala) citotóxicos, en una relación de principio activo de 12:1 a 15:1

Heavy chain / Chaîne lourde / Cadena pesada

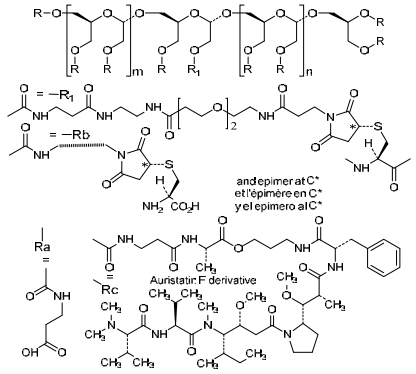
```
QVQLVQSGAE VVKPGASVKM SCKASGYTFT GYNIHWVKQA PGQGLEWIGA  50
IYPGNGDTSY KQKFRGRATL TADTSTSTVY MELSSLRSED SAVYYCARGE 100
TARATFAYWG QGTLVTVSSG ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKRVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP 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-C1, 126)* 223-215' 223"-215"'
Inter-H-H (h 11, h 14)* 229-229" 232-232"
*Two or three of the inter-chain disulfide bridges are not present, 3 to 5 cysteinyl being conjugated each via a thioether bond to one maleimide linker of one flexible polymer comprising 3 to 4 drug units.
*Deux ou trois des ponts disulfures inter-chaînes ne sont pas présents, 3 to 5 cystéinyl étant chacun conjugué via une liaison thioéther à un linker-maléimide d'un polymère flexible comprenant 3 à 4 unités de principe actif.
*Faltan dos o tres puentes disulfuro inter-catenarios, 3 a 5 cisteinil está conjugada a conectores de un polímero flexible que contiene 3 a 4 unidades de principio activo.

Modified residues / résidus modifiés / restos modificados:



m + n ~ 35-75 ; R = H , Ra , Rb or Rc ; ratio H : Ra : Rb : Rc ~ 70 : 20 : 2 : 8

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

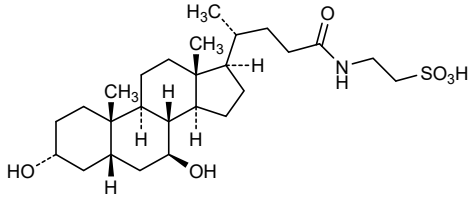
ursodoxicoltaurinum

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

$C_{26}H_{45}NO_6S$



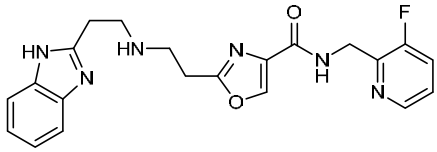
vamifeportum

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

$C_{21}H_{21}FN_6O_2$



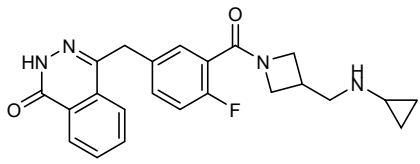
venadaparibum

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

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

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

$C_{23}H_{23}FN_4O_2$



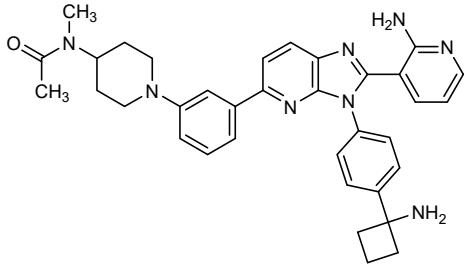
vevorisertibum

vevorisertib — *N*-[1-(3-{3-[4-(1-aminocyclobutyl)phenyl]-2-(2-aminopyridin-3-yl)-3*H*-imidazo[4,5-*b*]pyridin-5-yl}phenyl)piperidin-4-yl]-*N*-methylacetamide

vévorisertib — *N*-[1-(3-{3-[4-(1-aminocyclobutyl)phényl]-2-(2-aminopyridin-3-yl)-3*H*-imidazo[4,5-*b*]pyridin-5-yl}phényl)pipéridin-4-yl]-*N*-méthylacétamide

vevorisertib — *N*-[1-(3-{3-[4-(1-aminociclobutil)fenil]-2-(2-aminopiridin-3-il)-3*H*-imidazo[4,5-*b*]piridin-5-il}fenil)piperidin-4-il]-*N*-metilacetamida

$C_{35}H_{38}N_8O$



vibapapogenum autoleucelum #

vibapapogene autoleucel — Autologous peripheral blood mononuclear cells (PBMCs) expressing human papillomavirus types 16 and 18 antigens. Autologous peripheral blood mononuclear cells (PBMCs), specifically B lymphocytes and monocytes that are T-cell depleted, transfected *ex vivo* with a non-replicating adenoviral vector that expresses a codon-optimised fusion of tumour-associated antigens (TAAs) E6 and E7 derived from human papillomavirus (HPV) types 16 and 18 (HPV-16/18 E6/E7). The antigen coding region is preceded by a tPA signal sequence and transcription is under the control of the cytomegalovirus (CMV)-tetracycline 10 promoter and the SV40 poly(A) termination sequence. The vector genome is flanked by inverted terminal repeats and contains an encapsidation signal and a K35 knob.

vibapapogène autoleucel — Cellules mononucléaires du sang périphérique autologues exprimant les antigènes de papillomavirus humains de type 16 et 18.
Cellules mononucléaires du sang périphérique autologues, spécifiquement les lymphocytes B et les monocytes qui sont déplétées en lymphocytes T, transfectées *ex vivo* avec une forme non réplicative du vecteur adénoviral exprimant un codon optimisé, fusion des antigènes associés à des tumeurs E6 et E7 dérivés du virus humain du papillome (HPV) types 16 et 18 (HPV-16/18 E6/E7). La région codant l'antigène est précédée d'une séquence signal tPA et la transcription est sous le contrôle du promoteur tétracycline 10 du cytomégalovirus et de la séquence de terminaison poly(A) SV40. Le génome du vecteur est flanqué de répétitions inverses et contient un signal d'encapsidation et un domaine globulaire distal (knob) K35.

vibapapogén autoleucel	Células monucleares de sangre periférica (PBMCs) autólogas que expresan antígenos del papilomavirus humano de tipo 16 y 18. Células monucleares de sangre periférica (PBMCs) autólogas, específicamente linfocitos B y monocitos que están deplecionadas de células T, transfectadas *ex vivo* con un vector adenoviral no replicative que expresa una fusion de los antígenos asociados a tumor (TAAs) E6 y E7 derivados del papillomavirus humano (HPV) de tipo 16 y 18 (HPV-16/18 E6/E7), con codones optimizados. La region codificadora de antigen está precedidad por una secuencia señal tPA y la transcripción está bajo el control del promotor de la tetraciclina 10 del cytomegalovirus (CMV) y la secuencia poly(A) de terminación del SV50. El genoma del vector está flanqueado por repeticiones invertidas terminales y contiene una señal de encapsidación y un dominio globular distal (knob) K35.

vibosameranum #

vibosameran	Messenger RNA encoding tyrosinase. Messenger RNA (mRNA), 5'-capped, encoding codon-optimised tyrosinase (monophenol monooxygenase, tumour rejection antigen AB), expressed as a fusion protein comprising tyrosinase, P2P16 tetanus toxoid-derived helper epitopes and a major histocompatibility complex (MHC) class I transmembrane and cytoplasmic domain, connected by two glycine/serine-rich (GS) linker peptides, flanked by 5' and 3' untranslated regions and a 3' poly(A) tail.
vibosaméran	ARN messager codant pour la tyrosinase. ARN messager (ARNm), protégé en 5', codant pour la tyrosinase (monophénol monooxygénase, antigène de rejet de tumeur AB), avec des codons optimisés, exprimé sous la forme d'une protéine de fusion comprenant la tyrosinase, les épitopes auxiliaires P2P16 dérivés de l'anatoxine tétanique et un domaine transmembranaire et cytoplasmique du complexe majeur d'histocompatibilité (CMH) de classe I, reliés par deux peptides de liaison riches en glycine/sérine (GS), flanqués de régions non traduites en 5' et 3' et d'une queue poly(A) en 3'.
vibosamerán	ARN mensajero que codifica para tirosinasa. ARN mensajero (ARNm), protegido en 5' que codifica para tirosinasa (monofenol monooxigenasa, antígeno de rechazo tumoral AB), con codones optimizados, expresada como una proteína de fusión que consta de la tirosinasa, los epítopos auxiliares P2P16 derivados del toxoide tetánico y un dominio citoplásmico y transmembrana del complejo principal de histocompatibilidad (MHC) de clase I, conectados mediante dos péptidos de enlace ricos en glicina/serina (GS), flanqueado por las regiones 5' y 3' no traducidas y una cola poly(A) en 3'.

vidutolimodum

vidutolimod — immunostimulatory CG-rich palindromic oligodeoxyribonucleotide, flanked by 3'-dG$_{10}$ and 5'-dG$_{10}$ decanucleotides:
deca[2'-deoxyguanylyl-(3'→5')]-2'-deoxyguanylyl-(3'→5')-2'-deoxyadenylyl-(3'→5')-2'-deoxycytidylyl-(3'→5')-2'-deoxyguanylyl-(3'→5')-2'-deoxyadenylyl-(3'→5')-thymidylyl-(3'→5')-2'-deoxycytidylyl-(3'→5')-2'-deoxyguanylyl-(3'→5')-thymidylyl-(3'→5')-2'-deoxycytidylyl-(3'→5')-nona[2'-deoxyguanylyl-(3'→5')]-2'-deoxyguanosine

vidutolimod — oligodésoxyribonucléotide palindromique immunostimulateur riche en CG, flanqué de décanucléotides 3'-dG$_{10}$ et 5'-dG$_{10}$:
déca[2'-désoxyguanylyl-(3'→5')]-2'-désoxyguanylyl-(3'→5')-2'-désoxyadénylyl-(3'→5')-2'-désoxycytidylyl-(3'→5')-2'-désoxyguanylyl-(3'→5')-2'-désoxyadénylyl-(3'→5')-thymidylyl-(3'→5')-2'-désoxycytidylyl-(3'→5')-2'-désoxyguanylyl-(3'→5')-thymidylyl-(3'→5')-2'-désoxycytidylyl-(3'→5')-nona[2'-désoxyguanylyl-(3'→5')]-2'-désoxyguanosine

vidutolimod — oligodesoxirribonucleótido palindrómico inmunoestimulador rico en CG, flanqueado por decanucleótidos 3'-dG$_{10}$ y 5'-dG$_{10}$:
deca[2'-desoxiguanilil-(3'→5')]-2'-desoxiguanilil-(3'→5')-2'-desoxiadenilil-(3'→5')-2'-desoxicitidilil-(3'→5')-2'-desoxiguanilil-(3'→5')-2'-desoxiadenilil-(3'→5')-timidilil-(3'→5')-2'-desoxicitidilil-(3'→5')-2'-desoxiguanilil-(3'→5')-timidilil-(3'→5')-2'-desoxicitidilil-(3'→5')-nona[2'-desoxiguanilil-(3'→5')]-2'-desoxiguanosina

$C_{297}H_{363}N_{138}O_{178}P_{29}$

Sequence / Séquence / Secuencia

(3'→5') d(GGGGGGGGGG **GACGATCGTC** GGGGGGGGGG)

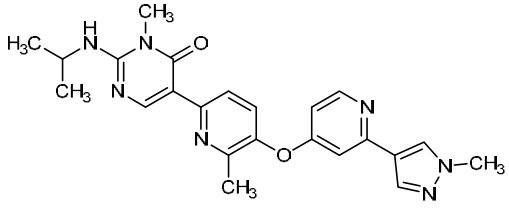
vimseltinibum

vimseltinib — 3-methyl-5-(6-methyl-5-{[2-(1-methyl-1*H*-pyrazol-4-yl)pyridin-4-yl]oxy}pyridin-2-yl)-2-[(propan-2-yl)amino]pyrimidin-4(3*H*)-one

vimseltinib — 3-méthyl-5-(6-méthyl-5-{[2-(1-méthyl-1*H*-pyrazol-4-yl)pyridin-4-yl]oxy}pyridin-2-yl)-2-[(propan-2-yl)amino]pyrimidin-4(3*H*)-one

vimseltinib — 3-metil-5-(6-metil-5-{[2-(1-metil-1*H*-pirazol-4-il)piridin-4-il]oxi}piridin-2-il)-2-[(propan-2-il)amino]pirimidin-4(3*H*)-ona

$C_{23}H_{25}N_7O_2$



vixarelimabum #

vixarelimab	immunoglobulin G4-G1-lambda2, anti-[*Homo sapiens* OSMR (oncostatin M receptor, OSMRB, OSMRbeta)], *Homo sapiens* monoclonal antibody; gamma4-gamma1 heavy chain *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-8*01 (95.9%) -(IGHD) -IGHJ6*01 (95.0%)) CDR-IMGT [8.8.19] (26-33.51-58.97-115) (1-126)-*Homo sapiens* IGHG4*01 CH1-h-CH2, G4v5 h P10, G4v36 CH2 Q84.4 (CH1 (127-224), hinge 1-12 S10>P (234) (225-236), CH2 N84.4>Q (303) (237-346)) -IGHG1*01 CH3-CHS, G1m1 (CH3 D12 (362), L14 (364) (347-451), CHS K>del (452)) (127-452)], (140-215')-disulfide with lambda2 light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-44*01 (90.8%) -IGLJ2*01 (100%)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimer (232-232":235-235")-bisdisulfide, non-glycosylated, produced in Chinese hamster ovary (CHO)-DG44i cell line
vixarélimab	immunoglobuline G4-G1-lambda2, anti-[*Homo sapiens* OSMR (récepteur de l'oncostatine M, OSMRB, OSMRbeta)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma4-gamma1 *Homo sapiens*(1-452) [VH (*Homo sapiens* IGHV1-8*01 (95.9%) -(IGHD) -IGHJ6*01 (95.0%)) CDR-IMGT [8.8.19] (26-33.51-58.97-115) (1-126)-*Homo sapiens* IGHG4*01 CH1-h-CH2, G4v5 h P10, G4v36 CH2 Q84.4 (CH1 (127-224), charnière 1-12 S10>P (234) (225-236), CH2 N84.4>Q (303) (237-346)) (127-346) -IGHG1*01 CH3-CHS, G1m1 (CH3 D12 (362), L14 (364) (347-451), CHS K>del (452)) (347-452)], (140-215')-disulfure avec la chaîne légère lambda2 *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-44*01 (90.8%) -IGLJ2*01 (100%)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimère (232-232":235-235")-bisdisulfure, non-glycosylé, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-DG44i
vixarelimab	inmunoglobulina G4-G1-lambda2, anti-[*Homo sapiens* OSMR (receptor de la oncostatina M, OSMRB, OSMRbeta)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma4-gamma1 *Homo sapiens*(1-452) [VH (*Homo sapiens* IGHV1-8*01 (95.9%) -(IGHD) -IGHJ6*01 (95.0%)) CDR-IMGT [8.8.19] (26-33.51-58.97-115) (1-126)-*Homo sapiens* IGHG4*01 CH1-h-CH2, G4v5 h P10, G4v36 CH2 Q84.4 (CH1 (127-224), bisagra 1-12 S10>P (234) (225-236), CH2 N84.4>Q (303) (237-346)) (127-346) -IGHG1*01 CH3-CHS, G1m1 (CH3 D12 (362), L14 (364) (347-451), CHS K>del (452)) (347-452)], (140-215')-disulfuro con la cadena ligera lambda2 *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-44*01 (90.8%) -IGLJ2*01 (100%)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dímero (232-232":235-235")-bisdisulfuro, no glicosilado, producido en las células ováricas de hámster chino (CHO) línea celular CHO-DG44i

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYEINWVRQA TGQGLEWMGW  50
MNPNSGYTGY AQKFQGRVTM TRDTSISTAY MEMSSLRSED TAVYYCARDI 100
VAANTDYYFY YGMDVWGQGT TVTVSSASTK GPSVFPLAPC SRSTSESTAA 150
LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS 200
SLGTKTYTCN VDHKPSNTKV DKRVESKYGP PCPPCPAPEF LGGPSVFLFP 250
PKPKDTLMIS RTPEVTCVVV DVSQEDPEVQ FNWYVDGVEV HNAKTKPREE 300
QFQSTYRVVS VLTVLHQDWL NGKEYKCKVS NKGLPSSIEK TISKAKGQPR 350
EPQVYTLPPS RDELTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS 450
PG                                                      452
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Light chain / Chaîne légère / Cadena ligera

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QSVLTQPPSA SGTPGQRVTI SCSGSNSNIG SNTVNWYHQL PGTAPKLLIY  50
NINKRPSGVP DRFSGSKSGS SASLAISGLQ SEDEADYYCS TWDDSLDGVV 100
FGGGTKLTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS                                      216
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 153-209 267-327 373-431
22"-96" 153"-209" 267"-327" 373"-431"
Intra-L (C23-C104) 22'-89' 138'-197'
22'"-89'" 138'"-197'"
Inter-H-L (CH1 10-CL 126) 140-215' 140"-215'"
Inter-H-H (h 8, h 11) 232-232" 235-235"

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

No N-glycosylation sites / pas de sites de N-glycosylation / ningùn posición de N-glycosilación
H CH2 N84.4>Q (303)
Aglycosylated

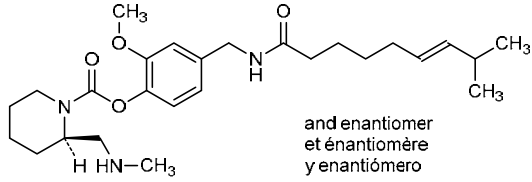
vocacapsaicinum

vocacapsaicin — *rac*-2-methoxy-4-{[(6*E*)-8-methylnon-6-enamido]methyl}phenyl (2*R*)-2-[(methylamino)methyl]piperidine-1-carboxylate

vocacapsaïcine — *rac*-(2*R*)-2-[(méthylamino)méthyl]pipéridine-1-carboxylate de 2-méthoxy-4-{[(6*E*)-8-méthylnon-6-énamido]méthyl}phényle

vocacapsaícina — *rac*-(2*R*)-2-[(metilamino)metil]piperidina-1-carboxilato de 4-{[(6*E*)-8-metilnon-6-enamido]metil}-2-metoxifenilo

$C_{26}H_{41}N_3O_4$



and enantiomer
et énantiomère
y enantiómero

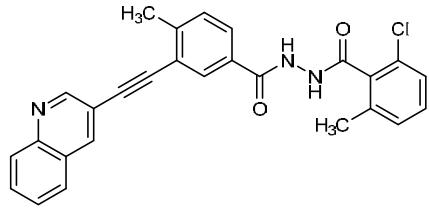
vodobatinibum

vodobatinib — 2-chloro-6-methyl-*N*′-{4-methyl-3-[(quinolin-3-yl)ethynyl]benzoyl}benzohydrazide

vodobatinib — 2-chloro-6-méthyl-*N*′-{4-méthyl-3-[(quinoléin-3-yl)éthynyl]benzoyl}benzohydrazide

vodobatinib — 2-cloro-6-metil-*N*′-{4-metil-3-[(quinolein-3-il)etinil]benzoil}benzohidrazida

$C_{27}H_{20}ClN_3O_2$



vudalimabum #

vudalimab — immunoglobulin half-IG G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* CTLA4 (cytotoxic T-lymphocyte-associated protein 4, CD152)] and anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], monoclonal antibody, bispecific;
gamma1 heavy chain anti-CTLA4 (1-447) [VH (*Homo sapiens* IGHV3-48*03 (90.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107)(1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 N114>D (209) R120>K (215) (119-216), hinge 1-15 (217-231), CH2 E1.4,L1.3>P (234), L1.2>V (235), G1.1>A (236), S29>K (267), Q84.2>E (295) (232-340), CH3 E12 (356), M14 (358), L24>D (368), K26>S (370), N44>D (384), Q97>E (418), N100>D (421), M107>L (428), N114>S (434) (341-445), CHS (446-447)) (119-447)], (221-215')-disulfide with kappa light chain anti-CTLA4, *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (99.0%) -IGKJ1*01 (100%)) CDR-IMGT [7.3.9] (27-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')];
IG scFv-h-CH2-CH3 single chain, anti-PDCD1 (1"-480") [scFv V-kappa-VH anti-PDCD1 (1"-249") [V-KAPPA (*Homo sapiens*IGKV3-15*01 (80.0%)-IGHJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1"-107") -20-mer tetrakis(glycyl-lysyl-prolyl-glycyl-seryl) linker (108"-127") -VH (*Mus musculus* IGHV6-6*02 (87.0%) -(IGHD) -IGHJ1*03 (86.7%)/*Homo sapiens* IGHV3-15*07 (81.8%) -(IGHD) -IGHJ2*01 (93.3%)) CDR-IMGT [8.10.13] (153-160.178-187.226-238) (128"-249")] -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (250"-480") [hinge 1-15 C5>S (254) (250-264) -CH2 E1.4,L1.3>P (267), L1.2>V (268), G1.1>A (269), S29>K (300) (265-373),CH3 E12 (389), E13>Q (390), M14 (391), S20>K (397), M107>L (461), N114>S (467) (374-478), CHS (479-480)]];
dimer (227-260":230-263")-bisdisulfide, produced in Chinese hamster ovary (CHO)-S cell line, glycoform alfa

vudalimab — immunoglobuline demi-IG G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* CTLA4 (protéine 4 associée aux lymphocytes T cytotoxiques, CD152)] et anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal, bispécifique;

chaîne lourde gamma1 anti-CTLA4, (1-447) [VH (*Homo sapiens* IGHV3-48*03 (90.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 N114>D (209) R120>K (215) (119-216), charnière 1-15 (217-231), CH2 E1.4,L1.3>P (234), L1.2>V (235), G1.1>A (236), S29>K (267), Q84.2>E (295) (232-340), CH3 E12 (356), M14 (358), L24>D (368), K26>S (370), N44>D (384), Q97>E (418), N100>D (421), M107>L (428), N114>S (434) (341-445), CHS (446-447)) (119-447)], (221-215')-disulfure avec la chaîne légère kappa anti-CTLA4,*Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (99.0%) -IGKJ1*01 (100%)) CDR-IMGT [7.3.9] (27-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')];
IG scFv-h-CH2-CH3 chaîne unique, anti-PDCD1 (1''-480'') [scFv V-kappa-VH anti-PDCD1 (1''-249'') [V-KAPPA (*Homo sapiens*IGKV3-15*01 (80.0%)-IGHJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1''-107'') -20-mer tétrakis(glycyl-lysyl-prolyl-glycyl-séryl) linker (108''-127'') -VH (*Mus musculus* IGHV6-6*02 (87.0%) -(IGHD) -IGHJ1*03 (86.7%)/*Homo sapiens* IGHV3-15*07 (81.8%) -(IGHD) -IGHJ2*01 (93.3%)) CDR-IMGT [8.10.13] (153-160.178-187.226-238) (128''-249'')] -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (250''-480'') [charnière 1-15 C5>S (254) (250-264) -CH2 E1.4,L1.3>P (267), L1.2>V (268), G1.1>A (269), S29>K (300) (265-373),CH3 E12 (389), E13>Q (390), M14 (391), S20>K (397), M107>L (461), N114>S (467) (374-478), CHS (479-480)]];
dimère (227-260'':230-263'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-S, glycoforme alfa

vudalimab

inmunoglobulina demi-IG G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* CTLA4 (proteína 4 asociada a los linfocitos T citotóxicos, CD152)] y anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal, biespecífico; cadena pesada gamma1 anti-CTLA4 (1-447) [VH (*Homo sapiens* IGHV3-48*03 (90.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 N114>D (209) R120>K (215) (119-216), bisagra 1-15 (217-231), CH2 E1.4,L1.3>P (234), L1.2>V (235), G1.1>A (236), S29>K (267), Q84.2>E (295) (232-340), CH3 E12 (356), M14 (358), L24>D (368), K26>S (370), N44>D (384), Q97>E (418), N100>D (421), M107>L (428), N114>S (434) (341-445), CHS (446-447)) (119-447)], (221-215')-disulfuro con la cadena ligera kappa anti-CTLA4,*Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (99.0%) -IGKJ1*01 (100%)) CDR-IMGT [7.3.9] (27-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')];
IG scFv-h-CH2-CH3 cadena única, anti-PDCD1 (1''-480'') [scFv V-kappa-VH anti-PDCD1 (1''-249'') [V-KAPPA (*Homo sapiens*IGKV3-15*01 (80.0%)-IGHJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1''-107'') -20-mer tetrakis(glicil-lisil-prolil-glicil-seril) linker (108''-127'') -VH (*Mus musculus* IGHV6-6*02 (87.0%) -(IGHD) -IGHJ1*03 (86.7%)/*Homo sapiens* IGHV3-15*07 (81.8%) -(IGHD) -IGHJ2*01 (93.3%)) CDR-IMGT [8.10.13] (153-160.178-187.226-238) (128''-249'')] -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 (250''-480'') [bisagra 1-15 C5>S (254) (250-264) -CH2 E1.4,L1.3>P (267), L1.2>V (268), G1.1>A (269), S29>K (300) (265-373),CH3 E12 (389), E13>Q (390), M14 (391), S20>K (397), M107>L (461), N114>S (467) (374-478), CHS (479-480)]];
dímero (227-260'':230-263'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-S, forma glicosilada alfa

1.Heavy chain / Chaîne lourde / Cadena pesada (anti-CTLA4)

```
EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYTMHWVRQA PGKGLEWVSF  50
ISYDGNNKYY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARTG 100
WLGPFDYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSDT KVDKKVEPKS CDKTHTCPPC PAPPVAGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVKHED PEVKFNWYVD GVEVHNAKTK PREEEYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSREEMTK NQVSLTCDVS GFYPSDIAVE WESDGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWEQG DVFSCSVLHE ALHSHYTQKS LSLSPGK    447
```

2. Light chain / Chaîne légère / Cadena ligera (anti-CTLA4)

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY  50
GAFSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPWTFG 100
QGTKVEIKGT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

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

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

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

Intra-H (C23-C104)	22-96 145-201 261-321 367-425
Intra-L (C23-C104)	23'-89' 135'-195'
Intra-chain 3	23"-88" 149"-225" 294"-354" 400"-458"
Inter-H-L (h 5-CL 126)	221-215'
Inter-H-chain 3 (h 11, h 14)	227-260" 230-263"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
297, 330"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
447, 480"

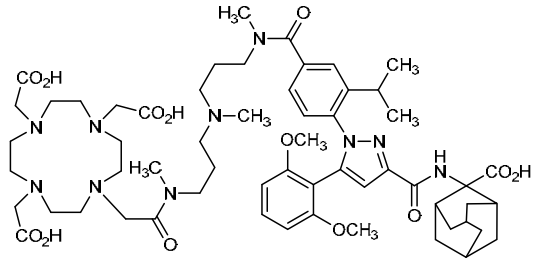
zalsenertantum tetraxetanum

zalsenertant tetraxetan — 18^4,18^7,18^{10}-tris(carboxymethyl)-4^5-(2,6-dimethoxyphenyl)-7,11,15-trimethyl-3,6,16-trioxo-5^2-(propan-2-yl)-2,7,11,15-tetraaza-18(1)-(1,4,7,10-tetraazacyclododecana)-4(3,1)-pyrazola-1(2)-adamantana-5(1,4)-benzenaoctadecaphane-1^2-carboxylic acid

zalsénertant tétraxetan — acide 18^4,18^7,18^{10}-tris(carboxyméthyl)-4^5-(2,6-diméthoxyphényl)-7,11,15-triméthyl-3,6,16-trioxo-5^2-(propan-2-yl)-2,7,11,15-tétraaza-18(1)-(1,4,7,10-tétraazacyclododécana)-4(3,1)-pyrazola-1(2)-adamantana-5(1,4)-benzénaoctadécaphane-1^2-carboxylique

zalsenertant tetraxetán — ácido 18^4,18^7,18^{10}-tris(carboximetil)-4^5-(2,6-dimetoxifenil)-7,11,15-trimetil-3,6,16-trioxo-5^2-(propan-2-il)-2,7,11,15-tetraaza-18(1)-(1,4,7,10-tetraazaciclododecana)-4(3,1)-pirazola-1(2)-adamantana-5(1,4)-bencenaoctadecafano-1^2-carboxílico

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



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.

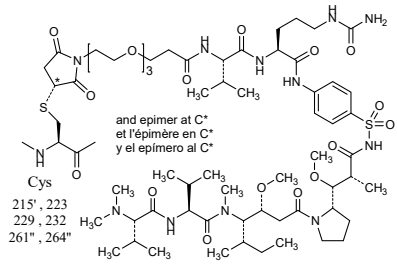
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación

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.

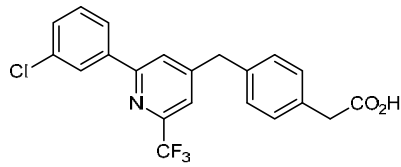
Modified residues / résidus modifiés / restos modificados:



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

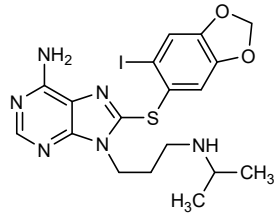
$C_{21}H_{15}ClF_3NO_2$



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*

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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"

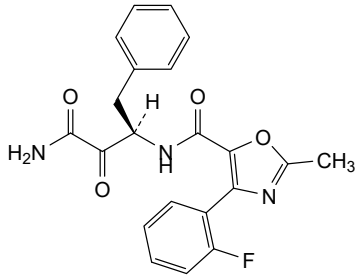
dazcapistatum

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

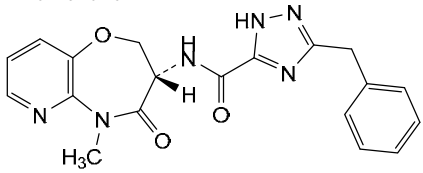
eclitasertibum

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

$C_{19}H_{18}N_6O_3$



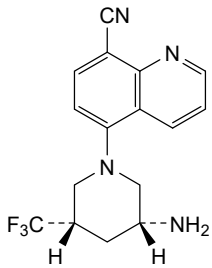
enpatoranum

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"

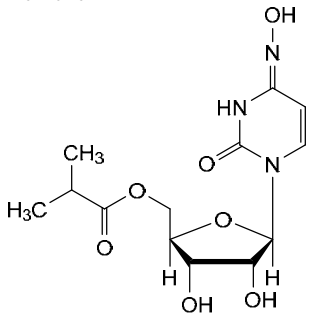
molnupiravirum

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

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

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

$C_{13}H_{19}N_3O_7$



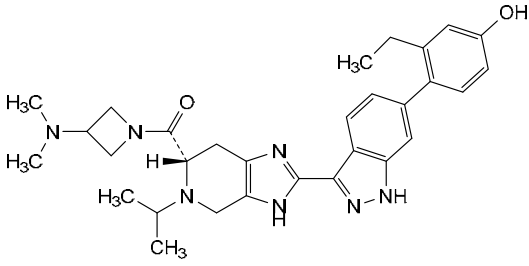
nezulcitinibum

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 KKYLNSILNV PGVGVPGVGV PGGGVPGAGV   50
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  100
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  150
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  200
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  250
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  300
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  350
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  400
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  450
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  500
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  550
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGVGVPGVGV PGGGVPGAGV  600
PGVGVPGVGV PGVGVPGGGV PGAGVPGGGV PGWP                   634
```

positions 30-634: 12 × pattern AABCAAABCB of 10 pentapeptides of three types A = **VPGVG**, B = **VPGGG,** and C = **VPGAG** plus a C-terminal pentapeptide **VPGWP**

pidacmeranum #

pidacmeran

self-replicating messenger RNA (mRNA), 5'-capped, encoding *Venezuelan equine encephalitis virus* (VEEV) RNA-dependent RNA polymerase (VEEV proteins nsP1, nsP2, nsP3 and nsP4) and a full-length codon-optimised pre-fusion stabilised conformation variant (K986P and V987P) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2, GenBank: MN908947.3) spike (S) glycoprotein, flanked by 5' and 3' untranslated regions and a 3' poly(A) tail; replication of the RNA is under control of a VEEV subgenomic promoter.

pidacméran

ARN messager (ARNm) auto-répliquant, protégé en 5', codant pour l'ARN polymérase ARN-dépendante du *virus de l'encéphalite équine vénézuélienne* (protéines VEEV nsP1, nsP2, nsP3 et nsP4) et une variante complète de pré-fusion de conformation stabilisée (K986P et V987P) de la glycoprotéine spike (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère, GenBank: MN908947.3) avec des codons optimisés, flanqués de régions 5 'et 3' non traduites une queue poly(A) 3'; la réplication de l'ARN est sous le contrôle du promoteur sous-génomique de VEEV.

pidacmerán	RNA mensajero auto replicativo (mRNA), protegido en 5', que codifica para la RNA polimerasa dependiente de RNA del *virus de la encefalitis equina venezolana* (proteínas VEEV nsP1, nsP2, nsP3 y nsP4) y una variante pre-fusión completa de conformación estabilizada (K986P and V987P) de la glicoproteína de la espícula (S) del SRAS-CoV-2 (coronavirus 2 del síndrome respiratorio agudo severo, GenBank: MN908947.3) con codones optimizados, flanqueada por regiones 5' y 3' no traducidas y una cola poly(A) en 3'; la replicación del ARN está bajo el control del promotor subgenómico de VEEV.
regdanvimabum # regdanvimab	immunoglobulin G1-lambda, anti-[*Homo sapiens* severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) protein, receptor binding domain (RBD)], humanized and *Homo sapiens* monoclonal antibody; gamma1 heavy chain humanized (1-458) [VH (*Homo sapiens* IGHV2-70*12 (92.9%) -(IGHD) - IGHJ6*01 (100%)) CDR-IMGT [10.7.20] (26-35.53-59.98-117) (1-128) -*Homo sapiens* IGHG1*08p (100%) G1m3,1 (CH1 R120 (225) (129-226), hinge 1-15 (227-241), CH2 (242-351), CH3 D12 (367), L14 (369) (352-456), CHS (457-458)) (129-458)], (231-215')-disulfide with lambda light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-51*01 (100%) - IGLJ2*01 (90.9%) K123>E (106)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC2*01 (98.1%) S45>G (156), T82>K (167) (111'-216')]; dimer (237-237":240-240")-bisdisulfide, produced in a Chinese hamster ovary (CHO) cell line derived from CHO-K1, glycoform alfa
regdanvimab	immunoglobuline G1-lambda anti-[*Homo sapiens* protéine spike (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2), domaine de liaison au récepteur (RBD)], anticorps monoclonal humanisé et *Homo sapiens*; chaîne lourde gamma1 humanisée (1-458) [VH (*Homo sapiens* IGHV2-70*12 (92.9%) -(IGHD) - IGHJ6*01 (100%)) CDR-IMGT [10.7.20] (26-35.53-59.98-117) (1-128) -*Homo sapiens* IGHG1*08p (100%) G1m3,1 (CH1 R120 (225) (129-226), charnière 1-15 (227-241), CH2 (242-351), CH3 D12 (367), L14 (369) (352-456), CHS (457-458)) (129-458)], (231-215')-disulfure avec la chaîne légère lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-51*01 (100%) -IGLJ2*01 (90.9%) K123>E (106)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC2*01 (98.1%) S45>G (156), T82>K (167) (111'-216')]; dimère (237-237":240-240")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) dérivant de la lignée cellulaire CHO-K1, glycoforme alfa

regdanvimab

inmunoglobulina G1-lambda anti-[*Homo sapiens* proteína espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SRAS-CoV-2), dominio de unión al receptor (RBD)], anticuerpo monoclonal humanizado y *Homo sapiens*; cadena pesada gamma1 humanizada (1-458) [VH (*Homo sapiens* IGHV2-70*12 (92.9%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [10.7.20] (26-35.53-59.98-117) (1-128) -*Homo sapiens* IGHG1*08p (100%) G1m3,1 (CH1 R120 (225) (129-226), bisagra 1-15 (227-241), CH2 (242-351), CH3 D12 (367), L14 (369) (352-456), CHS (457-458)) (129-458)], (231-215')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-51*01 (100%) -IGLJ2*01 (90.9%) K123>E (106)) CDR-IMGT [8.3.11] (26-33.51-53.90-100) (1'-110') -*Homo sapiens* IGLC2*01 (98.1%) S45>G (156), T82>K (167) (111'-216')]; dímero (237-237":240-240")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular derivada de CHO-K1, forma glicosilada alfa

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"

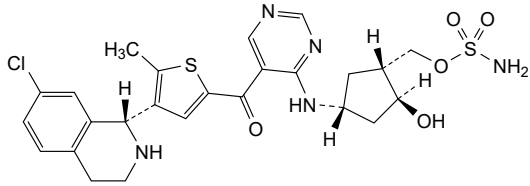
subasumstatum

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
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Light chain / Chaîne légère / Cadena ligera

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DIQMTQSPSS VSASVGDRVT ITCKASQDVY IAVAWYQQKP GKAPKLLIYW  50
ASTRDTGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCHQ YSSYPPTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 148-204 262-322 368-426
22"-96" 148"-204" 262"-322" 368"-426"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88"' 134'"-194'"
Inter-H-L (CH1 10-CL 126) 135-214' 135"-214'"
Inter-H-H (h 8, h 11) 227-227" 230-230"

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

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
298, 298"
Fucosylated complex bi-antennary CHO-type glycans (G0F predominant) / glycanes de type CHO bi-antennaires complexes fucosylés (G0F prédominant) / glicanos de tipo CHO biantenarios complejos fucosilados (G0F predominante).

zorecimeranum #

zorecimeran

messenger RNA (mRNA), 5'-capped, encoding a full-length codon-optimised pre-fusion stabilized conformation variant (K986P and V987P) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2; NC_045512.2) spike (S) glycoprotein, flanked by 5' and 3' untranslated regions; the 3' untranslated region comprises a part of the human alpha globin gene 3' UTR sequence element, a synthetic poly(A) tail and a poly(C)-rich sequence followed by a histone stem loop sequence as a 3' tail.

zoréciméran

ARN messager (ARNm), protégé en 5', codant pour un variant de pré-fusion stabilisé en conformation (K986P et V987P) de la glycoprotéine spike (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère), NC_045512.2) complet, avec des codons optimisés, flanqués de régions 5' et 3' non traduites. La région 3' non traduite comprend une partie de l'élément de séquence 3' UTR du gène de l'alpha globine humaine, une queue poly(A) synthétique et une séquence riche en poly(C) suivie d'une séquence d'histones stem-loop comme extrémité en 3'.

zorecimerán	RNA mensajero (mRNA), protegido en 5', que codifica para una variante pre-fusión de conformación estabilizada (K986P and V987P) de la glicoproteína de la espícula (S) del SRAS-Cov-2 (coronavirus 2 del síndrome respiratorio agudo severo, NC_045512.2) completa, con codones optimizados, flanqueada por regiones 5' y 3' no traducidas. La región 3' no traducida comprende una parte del elemento secuencia 3' UTR del gen de la alfa globina humana, una cola poly(A) sintética y una secuencia rica en poly(C) seguida de una secuencia de histona stem-loop cola 3'.

Electronic structure available on Mednet: http://mednet.who.int/
Structure électronique disponible sur Mednet: http://mednet.who.int/
Estructura electrónica disponible en Mednet: http://mednet.who.int/
* http://www.who.int/medicines/services/inn/publication/en/

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

Recommended International Nonproprietary Names (Rec. INN): List 76
Dénominations communes internationales recommandées (DCI Rec.): Liste 76
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 76
(WHO Drug Information, Vol. 30, No. 3, 2016)

p.483 **blontuvetmabum #**

blontuvetmab	*replace the description by the following one*
blontuvetmab	*remplacer la description par la suivante*
blontuvetmab	*sustitúyase la descripción por la siguiente*

immunoglobulin G2_V-kappa-C-lambda, anti-[***Canis lupus familiaris*** MS4A1 (membrane-spanning 4-domains subfamily A member 1, CD20)], caninized monoclonal antibody; gamma2 heavy chain chimeric (1-448) [*Mus musculus* VH (*Mus musculus* IGHV1-15*01 -(IGHD) -IGHJ1*03) [8.8.6] (1-113) -*Canis lupus familiaris* IGHG2*02 (CH1 T26>Q (131) (114-211), hinge (212-229), CH2 (230-339), CH3 (340-446), CHS (447-448)) (114-448)], (128-218')-disulfide with V-kappa-C-lambda light chain chimeric (1'-219') [*Mus musculus* V-KAPPA (*Mus musculus* IGKV8-30*01 -IGKJ5*01) [12.3.9] (1'-112') -*Canis lupus familiaris* IGL1CS1*01 V45.3>I (162) (114'-219')]; dimer (225-225":228-228")-bisdisulfide

immunoglobuline G2_V-kappa-C-lambda, anti-[***Canis lupus familiaris*** MS4A1 (membre 1 de la sous-famille A à 4 domaines transmembranaires, CD20)], anticorps monoclonal caninisé; chaîne lourde gamma2 chimérique (1-448) [*Mus musculus* VH (*Mus musculus* IGHV1-15*01 -(IGHD) -IGHJ1*03) [8.8.6] (1-113) -*Canis lupus familiaris* IGHG2*02 (CH1 T26>Q (131) (114-211), charnière (212-229), CH2 (230-339), CH3 (340-446), CHS (447-448)) (114-448)], (128-218')-disulfure avec la chaîne légère V-kappa-C-lambda chimérique (1'-219') [*Mus musculus* V-KAPPA (*Mus musculus* IGKV8-30*01 -IGKJ5*01) [12.3.9] (1'-112') -*Canis lupus familiaris* IGL1CS1*01 V45.3>I (162) (114'-219')]; dimère (225-225":228-228")-bisdisulfure

inmunoglobulina G2_V-kappa-C-lambda, anti-[***Canis lupus familiaris*** MS4A1 (miembro 1 de la subfamilia A con 4 dominios transmembranarios, CD20)], anticuerpo monoclonal caninizado; cadena pesada gamma2 quimérica (1-448) [*Mus musculus* VH (*Mus musculus* IGHV1-15*01 -(IGHD) -IGHJ1*03) [8.8.6] (1-113) -*Canis lupus familiaris* IGHG2*02 (CH1 T26>Q (131) (114-211), bisagra (212-229), CH2 (230-339), CH3 (340-446), CHS (447-448)) (114-448)], (128-218')-disulfuro con la cadena ligera V-kappa-C-lambda quimérica (1'-219') [*Mus musculus* V-KAPPA (*Mus musculus* IGKV8-30*01 -IGKJ5*01) [12.3.9] (1'-112') -*Canis lupus familiaris* IGL1CS1*01 V45.3>I (162) (114'-219')]; dímero (225-225":228-228")-bisdisulfuro

p.534 **tamtuvetmabum #**
-535 tamtuvetmab *replace the description by the following one*
tamtuvetmab *remplacer la description par la suivante*
tamtuvetmab *sustitúyase la descripción por la siguiente*

immunoglobulin G2_V-kappa-C-lambda, anti-[***Canis lupus familiaris*** CD52], caninized monoclonal antibody;
gamma2 heavy chain chimeric (1-456) [chimeric VH (*Rattus norvegicus* IGHV7S6*01 (97.00%) -(IGHD) -*Canis lupus familiaris* IGHJ-E2RCC8) [8.10.12] (1-121) -*Canis lupus familiaris* IGHG2*02 (CH1 (122-219), hinge (220-237), CH2 (238-347), CH3 (348-454), CHS (455-456))(122-456)], (136-212')-disulfide with V-kappa-C-lambda light chain chimeric (1'-213') [*Rattus norvegicus* V-KAPPA (*Rattus norvegicus* IGKV22S7 (93.70%) -IGKJ1*01) [6.3.9] (1'-107') -*Canis lupus familiaris* IGLC1S1*01 V45.3>I (156) (108'-213')]; dimer (233-233'':236-236'')-bisdisulfide

immunoglobuline G2_V-kappa-C-lambda, anti-[***Canis lupus familiaris*** CD52], anticorps monoclonal caninisé;
chaîne lourde gamma2 chimérique (1-456) [VH chimérique (*Rattus norvegicus* IGHV7S6*01 (97.00%) -(IGHD) -*Canis lupus familiaris* IGHJ-E2RCC8) [8.10.12] (1-121) -*Canis lupus familiaris* IGHG2*02 (CH1 (122-219), charnière (220-237), CH2 (238-347), CH3 (348-454), CHS (455-456)) (122-456)], (136-212')-disulfure avec la chaîne légère V-kappa-C-lambda chimérique (1'-213') [*Rattus norvegicus* V-KAPPA (*Rattus norvegicus* IGKV22S7 (93.70%) -IGKJ1*01) [6.3.9] (1'-107') -*Canis lupus familiaris* IGLC1S1*01 V45.3>I (156) (108'-213')]; dimère (233-233'':236-236'')-bisdisulfure

inmunoglobulina G2_V-kappa-C-lambda, anti-[***Canis lupus familiaris*** CD52], anticuerpo monoclonal caninizado;
cadena pesada gamma2 quimérica (1-456) [VH quimérico (*Rattus norvegicus* IGHV7S6*01 (97.00%) -(IGHD) -*Canis lupus familiaris* IGHJ-E2RCC8) [8.10.12] (1-121) -*Canis lupus familiaris* IGHG2*02 (CH1 (122-219), bisagra (220-237), CH2 (238-347), CH3 (348-454), CHS (455-456))(122-456)], (136-212')-disulfuro con la cadena ligera V-kappa-C-lambda quimérica (1'-213') [*Rattus norvegicus* V-KAPPA (*Rattus norvegicus* IGKV22S7 (93.70%) -IGKJ1*01) [6.3.9] (1'-107') -*Canis lupus familiaris* IGLC1S1*01 V45.3>I (156) (108'-213')]; dímero (233-233'':236-236'')-bisdisulfuro

Recommended International Nonproprietary Names (Rec. INN): List 77
Dénominations communes internationales recommandées (DCI Rec.): Liste 77
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 77
(WHO Drug Information, Vol. 31, No. 1, 2017)

p.118 **ranevetmabum #**
-119 ranevetmab *replace the description by the following one*
ranevetmab *remplacer la description par la suivante*
ranevetmab *sustitúyase la descripción por la siguiente*

immunoglobulin G1-kappa, anti-[***Canis lupus familiaris*** NGF (nerve growth factor, nerve growth factor beta polypeptide, NGFB, beta-NGF)], caninized monoclonal antibody;
gamma1 heavy chain (1-453) [caninized VH (*Rattus norvegicus* IGHV5S13*01 (71.40%) -(IGHD)-IGHJ4*01) [8.7.16] (1-122) -*Canis lupus familiaris* IGHG1*01 (CH1 (123-219), hinge (220-233), CH2 (234-343), CH3 (344-451), CHS (452-453)) (123-453)], (137-213')-disulfide with kappa light chain (1'-217') [caninized V-KAPPA (*Rattus norvegicus* IGKV12S34*01 (76.80%) -IGKJ2-3*01) [6.3.9] (1'-107') -*Canis lupus familiaris* IGKC*01 (108'-213') -4-mer (214'-217')]; dimer (224-224'':226-226'':232-232'')-trisdisulfide

immunoglobuline G2-kappa, anti-[***Canis lupus familiaris*** NGF (facteur de croissance du nerf, facteur de croissance du nerf polypeptide bêta, NGFB, bêta-NGF)], anticorps monoclonal caninisé;
chaîne lourde gamma2 (1-453) [VH caninisé (*Rattus norvegicus* IGHV5S13*01 (71.40%) -(IGHD)-IGHJ4*01) [8.7.16] (1-122) -*Canis lupus familiaris* IGHG1*01 (CH1 (123-219), charnière (220-233), CH2 (234-343), CH3 (344-451), CHS (452-453)) (123-453)], (137-213')-disulfure avec la chaîne légère kappa (1'-217') [V-KAPPA caninisé (*Rattus norvegicus* IGKV12S34*01 (76.80%) -IGKJ2-3*01) [6.3.9] (1'-107') -*Canis lupus familiaris* IGKC*01 (108'-213') -4-mer (214'-217')]; dimère (224-224'':226-226'':232-232'')-trisdisulfure

inmunoglobulina G2-kappa, anti-[***Canis lupus familiaris*** NGF (factor de crecimiento de los nervios, factor de crecimiento de nervios polipéptido beta, NGFB, beta-NGF)], anticuerpo monoclonal caninizado;
cadena pesada gamma2 (1-453) [VH caninizado (*Rattus norvegicus* IGHV5S13*01 (71.40%) -(IGHD)-IGHJ4*01) [8.7.16] (1-122) -*Canis lupus familiaris* IGHG1*01 (CH1 (123-219), bisagra (220-233), CH2 (234-343), CH3 (344-451), CHS (452-453)) (123-453)], (137-213')-disulfuro con la cadena ligera kappa (1'-217') [V-KAPPA caninizado (*Rattus norvegicus* IGKV12S34*01 (76.80%) -IGKJ2-3*01) [6.3.9] (1'-107') -*Canis lupus familiaris* IGKC*01 (108'-213') -4-mer (214'-217')]; dímero (224-224'':226-226'':232-232'')-trisdisulfuro

Recommended International Nonproprietary Names (Rec. INN): List 79
Dénominations communes internationales recommandées (DCI Rec.): Liste 79
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 79
(WHO Drug Information, Vol. 32, No. 1, 2018)

p.170	*suprimáse*	*insertese*
	t**o**glato de tigilanol	t**i**glato de tigilanol

Recommended International Nonproprietary Names (Rec. INN): List 81
Dénominations communes internationales recommandées (DCI Rec.): Liste 81
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 81
(WHO Drug Information, Vol. 31, No. 1, 2017)

olenasufligenum relduparvovecum #

olenasufligene relduparvovec	*A revised sequence has been uploaded to the INN MedNet, which includes three nucleotide insertions within the CAG promoter compared to the previous version, increasing the total length of the vector to 4075bp. The table of features was revised accordingly.*
olénasufligène relduparvovec	*Une séquence révisée a été téléchargée sur MedNet DCI, et comprend trois insertions de nucléotides dans le promoteur CAG par rapport à la version précédente, augmentant la longueur totale du vecteur à 4075 pb. Le tableau des caractéristiques a été révisé en conséquence.*
olenasufligén relduparvovec	*Se cargó una secuencia revisada en MedNet DCI e incluye tres inserciones de nucleótidos dentro del promotor CAG en comparación con la versión anterior, aumentando la longitud total del vector a 4075 pb. La tabla de características se revisó en consecuencia.*

Recommended International Nonproprietary Names (Rec. INN): List 83
Dénominations communes internationales recommandées (DCI Rec.): Liste 83
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 83
(WHO Drug Information, Vol. 34, No. 1, 2020)

p.41 -42 **efbemalenograstimum alfa #**

efbemalenograstim alfa	*replace the description and the structure by the following ones*
efbémalénograstim alfa	*remplacer la description et la structure par les suivantes*
efbemalenograstim alfa	*sustitúyase la descripción y la estructura por las siguientes*

human granulocyte colony-stimulating factor (G-CSF) fragment fused via a peptidyl linker to a human immunoglobulin G2 Fc fragment variant, dimer:
[human granulocyte colony-stimulating factor (G-CSF, pluripoietin) short **[V^{36}, S^{37}, E^{38}**>del] isoform (1-174)]-[GSG$_3$S(G$_4$S)$_2$ linker (175-190)]-[human immunoglobulin G2 Fc fragment (223 C-terminal residues) (*Homo sapiens* IGHG2*01 (natural S^{344}>A variant); hinge (191-197), CH2 (P^{297}>S) (198-306), CH3 (307-411), CHS (412-413) (191-413)] fusion protein, dimer (193-193':196-196')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

fragment du facteur de stimulation des colonies de granulocytes humain (G-CSF) lié par un peptide à un variant du fragment Fc de l'immunoglobuline humaine G2, dimère:
[facteur humain de stimulation des colonies de granulocytes (G-CSF, pluripoïétine) **[V^{36}, S^{37}, E^{38}**>del] isoforme courte (1-174)]-[GSG$_3$S(G$_4$S)$_2$ linker (175-190)]-[fragment Fc de l'immunoglobuline humaine G2 (résidus 223 C-terminaux) (*Homo sapiens* IGHG2*01 (variant natural S^{344}>A); charnière (191-197), CH2 (P^{297}>S) (198-306), CH3 (307-411), CHS (412-413) (191-413)] protéine de fusion, dimère (193-193':196-196')-bisdisulfure, produit par des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

fragmento del factor de estimulación de las colonias de granulocitos humano (G-CSF) que se une por un péptido a una variante del fragment Fc de la inmunoglobulina humana G2, dímero:
[factor humano de estimulación de las colonias de granulocitos (G-CSF, pluripoyetina) [**V^{36}, S^{37}, E^{38}**>del] isoforma corta (1-174)]-[$GSG_3S(G_4S)_2$ conector (175-190)]-[fragmento Fc de la inmunoglobulina humana G2 (residuo 223 C-terminal) (*Homo sapiens* IGHG2*01 (variante natural S^{344}>A); bisagra (191-197), CH2 (P^{297}>S) (198-306), CH3 (307-411), CHS (412-413) (191-413)] proteína de fusión, dímero (193-193':196-196')-bisdisulfuro, producido en las células ováricas de hamsters chinos (CHO), glicoforma alfa

Sequence / Séquence / Secuencia:

```
TPLGPASSLP QSFLLKCLEQ VRKIQGDGAA LQEKLCATYK LCHPEELVLL  50
GHSLGIPWAP LSSCPSQALQ LAGCLSQLHS GLFLYQGLLQ ALEGISPELG 100
PTLDTLQLDV ADFATTIWQQ MEELGMAPAL QPTQGAMPAF ASAFQRRAGG 150
VLVASHLQSF LEVSYRVLRH LAQPGSGGGS GGGGSGGGGS VECPPCPAPP 200
VAGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVQ FNWYVDGVEV 250
HNAKTKPREE QFNSTFRVVS VLTVVHQDWL NGKEYKCKVS NKGLPASIEK 300
TISKTKGQPR EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN 350
GQPENNYKTT PPMLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN 400
HYTQKSLSLS PGK                                         413
```

Disulfide bridge location / Position de la pont disulfure / Posición del puente disulfuro:
intra-G-CSF: 36-42, 64-74, 36'-42', 64'-74'
intra-IgG2 Fc: 227-287, 333-391, 227'-287', 333'-391'
inter-IgG2 Fc: 193-193', 196-196'

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación
N-linked glycans: Asn263, Asn263'
O-linked glycans: Thr133, Thr133'

p.298 -299 **narsoplimabum #**

narsoplimab	*replace the description by the following one*
narsoplimab	*remplacer la description par la suivante*
narsoplimab	*sustitúyase la descripción por la siguiente*

immunoglobulin G4-lambda, anti-[*Homo sapiens* MASP2 (mannan-binding lectin serine peptidase 2, mannan-binding lectin serine protease 2, mannan-binding lectin serine protease 1 pseudogene 1, MASP1P1)], *Homo sapiens* monoclonal antibody; gamma**4** heavy chain *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV2-26*01 (94.0%) -(IGHD) -IGHJ4*01 (100%)) [10.7.10] (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), hinge 1-12 S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-211')-disulfide with lambda light chain *Homo sapiens* (1'-212') [V-LAMBDA (*Homo sapiens* IGLV3-1*01 (93.5%) -IGLJ2*01 (100%)) [6.3.9] (1'-106') -*Homo sapiens* IGLC2*01 (100%) (107'-212')];
dimer (224-224":227-227")-bisdisulfide, produced in Chinese hamster ovary (CHO)-S cell line, glycoform alfa

immunoglobuline G4-lambda, anti-[*Homo sapiens* MASP2 (sérine peptidase 2 de la lectine liant le mannane, sérine protéase 2 de la lectine liant le mannane, pseudogène 1 de la protéase 1 de la lectine liant le mannane, MASP1P1)], anticorps monoclonal *Homo sapiens*;
chaîne lourde gamma**4** *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV2-26*01 (94.0%) -(IGHD) -IGHJ4*01 (100%)) [10.7.10] (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), charnière 1-12 S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-211')-disulfure avec la chaîne légère lambda *Homo sapiens* (1'-212') [V-LAMBDA (*Homo sapiens* IGLV3-1*01 (93.5%) -IGLJ2*01 (100%)) [6.3.9] (1'-106') -*Homo sapiens* IGLC2*01 (100%) (107'-212')];
dimère (224-224":227-227")-bisdisulfure, produit dans des cellules ovariennes de hamsters chinois (CHO) lignée cellulaire S, glycoforme alfa

inmunoglobulina G4-lambda, anti-[*Homo sapiens* MASP2 (serina peptidasa 2 de la lectina que se une al manano, serina proteasa 2 de la lectina unida al manano, pseudogen 1 de la proteasa 1 de la lectina unida al manano, MASP1P1)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma**4** *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV2-26*01 (94.0%) -(IGHD) -IGHJ4*01 (100%)) [10.7.10] (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), bisagra 1-12 S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-211')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-212') [V-LAMBDA (*Homo sapiens* IGLV3-1*01 (93.5%) -IGLJ2*01 (100%)) [6.3.9] (1'-106') -*Homo sapiens* IGLC2*01 (100%) (107'-212')]; dímero (224-224":227-227")-bisdisulfuro, producido en las células ováricas de hamsters chinos (CHO) línea celular S, glicoforma alfa

Proposed International Nonproprietary Names (Prop. INN): List 122
Dénominations communes internationales proposées (DCI Prop.): Liste 122
Denominaciones Comunes Internacionales Propuestas (DCI Prop.): Lista 122
(WHO Drug Information, Vol. 33, No. 2, 2019)

p.831 **eflepedocokinum alfa#**
-832 eflépédocokine alfa *remplacer la description par la suivante*
eflepedocokina alfa *sustitúyase la descripción por la siguiente*

interleukine 22 humaine (IL22, cytokine Zcyto18, facteur inductible dérivé des lymphocytes T lié à IL10, IL-TIF) (1-146), fusionnée via un peptide liant $GSG_3S(G_4S)_2$ (147-162) au fragment Fc C-terminal de l'immunoglobuline G2 humaine (163-385), P^{269}>S-mutant **S**^{316}>A-variant, dimère (165-165':168-168')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

interleukina 22 humana (IL22, citoquina Zcyto18, factor inducible derivado de los linfocitos T relacionado con IL10, IL-TIF) (1-146), fusionada a través de un péptido que se une a $GSG_3S(G_4S)_2$ (147-162) con el fragmento Fc C-terminal de la inmunoglobulina G2 humana (163-385), P^{269}>S-mutante **S**^{316}>A-variante, dímero (165-165':168-168')-bisdisulfuro, producido en las células ováricas de hamster chino (CHO), glicoforma alfa

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

The text of the *Procedures for the Selection of Recommended International Nonproprietary Names for Pharmaceutical Substances* and *General Principles for Guidance in Devising International Nonproprietary Names for Pharmaceutical Substances* will be reproduced in proposed INN lists only.

Les textes de la *Procédure à suivre en vue du choix de dénominations communes internationales recommandées pour les substances pharmaceutiques* et des *Directives générales pour la formation de dénominations communes internationales applicables aux substances pharmaceutiques* seront publiés seulement dans les listes des DCI proposées.

El texto de los *Procedimientos de selección de denominaciones comunes internacionales recomendadas para las sustancias farmacéuticas* y de los *Principios generales de orientación para formar denominaciones comunes internacionales para sustancias farmacéuticas* aparece solamente en las listas de DCI propuestas.

Selected WHO publications of related interest

WHO Expert Committee on Biological Standardization. Sixty-seventh Report. WHO Technical Report Series, No. 1004, 2017

WHO Expert Committee on Drug Dependence. Thirty-ninth Report. WHO Technical Report Series, No. 1009, 2018

The Selection and Use of Essential Medicines. Report of the WHO Expert Committee, 2017 (including the 20th WHO Model List of Essential Medicines and the 6th WHO Model List of Essential Medicines for Children). WHO Technical Report Series, No. 1006, 2017

Quality assurance of pharmaceuticals 2018. WHO guidelines, good practices, related regulatory guidance and GXP training materials. (CD-ROM, USB and online)

WHO Expert Committee on Specifications for Pharmaceutical Preparations. Fifty-third Report. WHO Technical Report Series, No. 1019, 2019

International Nonproprietary Names (INN) for Pharmaceutical Substances. CD-ROM. 2017

The International Pharmacopoeia. Eighth edition 2018. CD-ROM. (CD-ROM, USB and online)

WHO Expert Committee on Biological Standardization. Guidelines on management of blood and blood components as essential medicines. 2016. Adopted by the Committee at its Sixty-seventh Meeting; published as Annex 3 to the WHO Technical Report Series, No. 1004, 2017

Council for International Organizations of Medical Sciences (CIOMS)

International Ethical Guidelines for Health-related Research Involving Humans. 2016 (e-training module about this guideline is available at https://cioms.ch/online-training/)

Drug-induced liver injury (DILI): Current status and future directions for drug development and the post-market setting. 2020

CIOMS Guide to Active Vaccine Safety Surveillance. 2017

CIOMS Guide to Vaccine Safety Communication. 2018

Evidence Synthesis and Meta-Analysis for Drug Safety. 2016

Development and Rational Use of Standardised MedDRA Queries (SMQs): Retrieving Adverse Drug Reactions with MedDRA. Second Edition. 2016

CIOMS e-publications are also available free at: https://cioms.ch/publications/

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