

# WHO Drug Information

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**Proposed INN: List 128**

International Nonproprietary Names for Pharmaceutical Substances



**World Health  
Organization**

## 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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# WHO Drug Information

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### Abbreviations and websites

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

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## Evaluation of the Saccharide Content of the WHO 2nd International Standard for *Haemophilus Influenzae* Polysaccharide Polyribosyl Ribitol Phosphate (PRP) by HPAEC- PAD Analysis Following Acid Hydrolysis

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### Abstract

With this report, we present the results of a collaborative study evaluating the content in mg per ampoule of the “WHO 2<sup>nd</sup> International Standard (IS) for *Haemophilus influenzae* polysaccharide Polyribosyl Ribitol Phosphate (PRP), NIBSC code: 12/306” (WHO 2<sup>nd</sup> IS for PRP), by applying High Performance Anion Exchange Chromatography with Pulsed Amperometric Detection (HPAEC-PAD) following acid hydrolysis of the PRP.

Seventeen laboratories from eleven countries participated in the collaborative study. The outcome of this study revealed a PRP content of the WHO 2<sup>nd</sup> IS for PRP of  $4.338 \pm 0.203$  mg/ampoule. Results of a previous collaborative study that included eleven participating laboratories, yielded a content of  $4.904 \pm 0.185$  mg/ampoule when applying the ribose assays (i.e., by orcinol method). Based on the outcome of this study, using HPAEC-PAD and acid hydrolysis of PRP, it is concluded that the determination of the PRP content is method dependent and therefore assigned values for the WHO 2<sup>nd</sup> IS for PRP should be tailored according to the applied method.

**Keywords:** *Haemophilus influenzae* type b, Hib Polysaccharide International Standard, High Performance Anion Exchange Chromatography (HPAEC), Pulsed amperometric detection (PAD), acid hydrolysis.

## 1. Introduction

This study was organised and coordinated by the Technical Assistance & Laboratory Services (TAL) - Vaccines Group (subsequently renamed the Laboratory Networks and Services - LNS) within the Regulatory System Strengthening (RSS) Team, the Regulation of Medicines and Other Health Technologies (RHT) Unit, the Essential Medicines and Health Products (EMP) Department in the Health Systems and Innovation (HIS) Cluster of the World Health Organization (WHO), and was done in collaboration with the Unit of Biological and Biotechnological Products, Bacterial Vaccine Section of the Istituto Superiore di Sanità (ISS), Rome, Italy.

The aim of this study was to ascertain whether the PRP content of the WHO 2<sup>nd</sup> IS for PRP (NIBSC code: 12/306), when assessed by HPAEC-PAD following acid hydrolysis, was in line with the assigned value using the orcinol method [1].

## 2. Materials and Methods

### 2.1 Participants

A total number of 17 laboratories participated in the study; out of these, nine are National Control Laboratories and eight are quality control laboratories from vaccine manufacturers. Appendix A provides a list of participants and related institutions in alphabetical order by country. Herein, an arbitrarily allocated code number [1-17], which is not related to the order of listing, refers to the participating laboratories.

### 2.2 Study material

The study material, the WHO 2<sup>nd</sup> IS for PRP (NIBSC code: 12/306), was kindly donated by the National Institute for Biological Standards and Control (NIBSC), Potters Bar, Hertfordshire, EN6 3QG, WHO International Laboratory for Biological Standards, UK Official Medicines Control Laboratory.

Participants received one ampoule of the WHO 2<sup>nd</sup> IS for PRP. According to the instructions for use [2], each ampoule contains the freeze-dried powder of 2 ml of PRP in 0.56 mg/ml NaCl. When estimated by weighing after freeze-drying, each ampoule contains about 6.0 mg of dry material and has a moisture content of about 1.45%. The ampoule should be stored at or below -20°C.

### 2.3 Study design and reporting of results

Participants were requested to quantify the PRP content per ampoule in three independent runs (i.e., 3 separate testing days), according to the analytical protocol of a previously performed collaborative study [3]. The protocol method quantifies the *Haemophilus influenzae* type b (Hib) saccharide content by determining, using HPAEC-PAD, the ribitol obtained after acidic hydrolyses. Thus, the calculation was based on the calibration curve of the monosaccharide, D-ribitol (adonitol).

As ribitol accounts for 41.3% of the PRP dry weight, a conversion factor of 2.42 was indicated to convert ribitol to a PRP content on a per gram basis [1, 4].

Laboratories were asked to report the total content of PRP per ampoule in mg/ampoule and rounded to three decimals.

Participants were asked to record results from three independent test runs into a standardized electronic data reporting sheet that had been provided in advance by the coordinators of the study. The reported results were used for further calculations and statistical analyses performed at ISS. Test results were submitted between February 2019 and December 2019.

### 2.4 Sample preparation

According to the instructions for use [2], the ampoule had to be reconstituted with 1 ml sterile distilled water and stored at -20°C in small aliquots until use. Further dilutions to yield a test solution in the correct concentration range for the assay were provided in the study protocol. Thus, a working solution containing 19.732 PRP ng/mL (based on ribose content) had to be prepared and then diluted 1:20 in MilliQ water. To 1 mL of this solution, 50 µL 6N HCl was added and then incubated for 2 hours at 100 °C to hydrolyse the PRP. Afterwards the sample was cooled for 10 min at 5 ± 3 °C and 400 µL of 1 M NaOH was added.

The monosaccharide, D-ribitol, was used for a five-point calibration curve ranging from 0.075 mcg/mL to 1.05 mcg/mL and treated as the PRP solution (i.e. hydrolysis and addition of NaOH).

## 2.5 Assay by HPAEC-PAD

Prior to the analysis by HPAEC-PAD, all samples were filtered. Ribitol was separated on a CarboPac MA1 analytical column (4 × 250, Dionex,) connected with a CarboPac MA1 guard column (Dionex). The analytical protocol defined the chromatographic conditions to be applied and these are shown in the Table 1.

**Table 1.** *Chromatographic conditions.*

<b>Parameters</b>	<b>Setting</b>
Column temperature	30°C
Detection	Pulsed amperometric detection (PAD)
Wave Form	Carbohydrate standard quadruple potential
Gold electrode	Not disposable
Reference electrode	AgCl
Elution conditions / eluent	Isocratic / 580 mM NaOH
Autosampler temperature	4°C
Injection volume	100 µL
Flow rate	0.4 mL/min
Run time	40 min
Software for data acquisition and processing	Chromeleon version 6 or 7



## 2.6 Statistical analysis

All data were analysed by ISS using the software IBM SPSS 26.0 and MS Excel 16.0.

Precision of the method was calculated as intra-laboratory precision, inter-laboratory precision and reproducibility (see Table 2 for details) [5].

**Table 2.** Precision analysis.

VAR Component	VAR Estimate	% of tot	SD	RSD (%)
<b>Inter-Laboratories (between)</b>	0.096	64	0.31	
<b>Intra-Laboratory (within)</b>	0.055	36	0.235	<b>5.5</b>
<b>Reproducibility</b>	0.152	100	0.39	<b>9.1</b>

*VAR*: Variance, in (mg/ampoule)<sup>2</sup>; *SD*: Standard Deviation, in mg/ampoule; *RSD*: Relative Standard Deviation, in %

$S_{Run}$ : Intra-Laboratory SD; it represents the “Variability among Runs + Repeatability of the Method”

$S_{Run}$  is obtained by the pooled SD within the 3 Runs results, per each of the N=17 Labs

$S_{Lab}$ : Inter-Laboratories SD; it represents the variability among the participating Laboratories. It

is obtained by  $\sqrt{S_b^2 - \frac{S_{Run}^2}{N_{run}}}$

With  $S_b$ : Standard Deviation between laboratories, and  $N_{run}$  = number of Runs (i.e., 3)

$S_{Repr}$  is the Standard Deviation of Reproducibility; it is obtained by  $= \sqrt{S_{Run}^2 + S_{Lab}^2}$

To establish the content of the PRP per ampoule, an analysis of the raw data was carried out by a pre-assessment of potential outliers; for this purpose, both Dixon and Grubb's tests were performed. The hypothesis of normality was assessed by means of the Shapiro-Wilk Test. This is considered the most powerful normality test when there is a small sample size, as in this case of 17 laboratories. If the p-value of the Shapiro-Wilk test is less than the classical threshold of 0.05, the results indicate a significant deviation from the assumption of normality, whereas Shapiro-Wilk p-values greater than 0.05 indicate no significant deviation from normality. However, for the purposes of this report, a more conservative approach was used. Specifically, a distribution was considered normal if normality was consistent with visual inspection of

exploratory graphs of the data and if the Shapiro-Wilk p-value was greater than 0.5. This conservative approach was adopted because the classical estimator of central tendency is very sensitive even to small deviations from normality. The content of the PRP in mg/ampoule was estimated after the above cited exploratory analysis of the data in order to choose a robust estimator instead of the classical calculation (i.e., which is based on the mean value). The uncertainty of measurement [6] associated with the estimated PRP content value per ampoule was determined by considering the uncertainty sources that derived from the preparation of the IS stock solution (i.e., purity, weighing and moisture content of the standard), the uniformity of content of ampoules (i.e., homogeneity of filling weight), and the reproducibility of the test method (i.e., experimental part).

The uncertainties associated with homogeneity of filling weight of the WHO 2<sup>nd</sup> IS for PRP has been derived from the data reported by Mawas and colleagues [7], as NIBSC is the custodian. The uncertainty associated with the purity of the ribitol standard is estimated by the declared contents on the Certificate of Analysis and under the assumption of a rectangular distribution from 99% to 100%.

The uncertainty associated with the moisture content of the ribitol standard was estimated under the assumption of a rectangular distribution from 0.0% to 0.4% (values provided by the participants).

The uncertainty of measurement due to weighing of ribitol standard was determined from calibration data for the balance used at ISS.

The uncertainty associated with the reproducibility of the test method is estimated by the standard error, i.e.,  $S_{\text{Repr}}/\sqrt{N}$ , with  $S_{\text{Repr}}$  obtained by a one way Random ANOVA (see Table 3) and N equal to the number of the participating laboratories (i.e., 17).

**Table 3.** Robust estimators vs mean value.

	Robust Estimators							Mean Value
	Shapiro Wilk p-value	Huber's M-Estimator <sup>a</sup>	Tukey's Biweight <sup>b</sup>	Hampel's M-Estimator <sup>c</sup>	Andrews Wave <sup>d</sup>	Alg_A <sup>e</sup>	Median	
<b>WHO 2nd IS</b>	<i>0.088</i>	<b>4.338</b>	4.368	4.339	4.371	4.330	4.310	4.290

All results (except the p-value) are in mg/ampoule. In bold the adopted value for content

a. The weighting constant is 1.339.

b. The weighting constant is 4.685.

c. The weighting constants are 1.700, 3.400, and 8.500

d. The weighting constant is 1.340\* $\pi$ .

e. The weighting constant is 1.483.

### 3. Results

All 17 laboratories reported their assay results for the WHO 2<sup>nd</sup> IS for PRP. All 17 laboratories that are included in the data analyses reported below carried out three assays (i.e., test runs) in accordance with the study protocol. With the exception of one laboratory, all other laboratories used the same standard material, namely D-ribitol (adonitol) supplied by Sigma-Aldrich for the calibration curve. This material had a purity greater than 99% (99.5% on average). Only laboratory 13 used the ribitol supplied by Acros Organic. Moisture content of the in-house ribitol standard ranged from 0.1% to 2.4%. When calculating the ribitol concentration, the moisture content was taken into account in case of the highest value.

Table 4 shows a complete listing of values reported by the laboratories. The table presents the results per individual run, the rounded geometric mean (GM) of the three runs, the geometric coefficient of variation (GCV, %) of the three runs, and the overall GM and GCV (%).

**Table 4.** Results from participating laboratories. Individual results received from the participating laboratories reported in milligram of PRP per ampoule.

Laboratory	Run 1	Run 2	Run 3	GM	GCV (%)
1	4.728	3.981	3.986	<b>4.22</b>	<b>9.92</b>
2	4.235	4.114	3.993	<b>4.11</b>	<b>2.94</b>
3	4.459	4.394	4.367	<b>4.41</b>	<b>1.07</b>
4	4.124	4.258	4.205	<b>4.20</b>	<b>1.61</b>
5	4.296	4.316	4.257	<b>4.29</b>	<b>0.70</b>
6	3.893	3.681	3.237	<b>3.59</b>	<b>9.48</b>
7	4.431	4.848	4.543	<b>4.60</b>	<b>4.65</b>
8	4.088	4.132	4.213	<b>4.14</b>	<b>1.53</b>
9	4.446	4.486	4.495	<b>4.48</b>	<b>0.58</b>
10	4.312	4.322	4.298	<b>4.31</b>	<b>0.28</b>
11	4.085	4.127	4.062	<b>4.09</b>	<b>0.80</b>
12	3.476	3.625	3.525	<b>3.54</b>	<b>2.14</b>
13	4.595	4.238	4.426	<b>4.42</b>	<b>4.05</b>
14	4.544	4.628	4.670	<b>4.61</b>	<b>1.39</b>
15	4.622	4.570	4.505	<b>4.57</b>	<b>1.29</b>
16	5.467	4.041	4.911	<b>4.77</b>	<b>15.41</b>
17	4.524	4.668	4.569	<b>4.59</b>	<b>1.60</b>
			<b>GM</b>	<b>4.28</b>	
	<b>Overall</b>		<b>GCV</b>		
			<b>(%)</b>	<b>8.21</b>	

GM: Geometric Mean; GCV: Geometric Coefficient of Variation (defined by  $\sqrt{(e^{\omega} - 1) * 100}$ , with  $\omega$  = Sample Variance of the ln-transformed results). GCVs for each Lab are single measures of Intra-Lab Precision. These measures should be used assuming a Log-Normal distribution.

The reported amount of PRP per ampoule ranged from 3.54 to 4.77 mg, with a geometric mean value of 4.28 and a GCV (%) equal to 8.21.

Figure 1 plots the GMs and the individual test results for each of the 17 laboratories, while in Figure 2, the frequency of all 51 determinations of PRP per ampoule is reported in a histogram plot format.

Figure 1. Descriptive plot of the three values of the PRP content in mg per ampoule obtained by the laboratories.

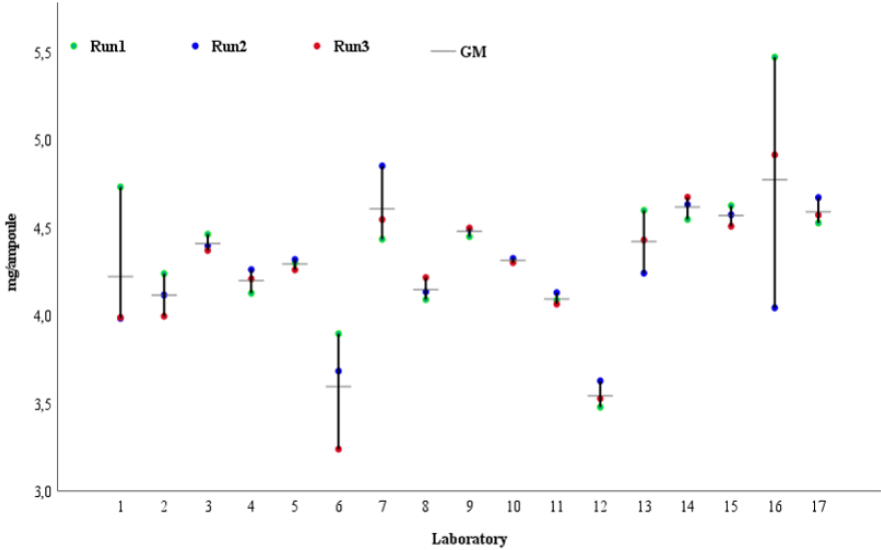


Figure 2. Individual results for the three determinations of the PRP content in mg per ampoule obtained by the laboratories. Numbers in the boxes represent the laboratory codes.

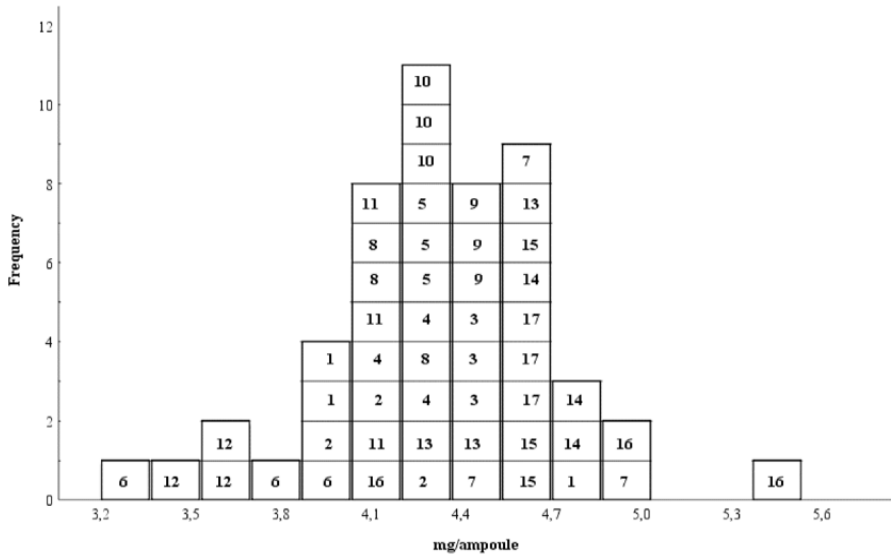
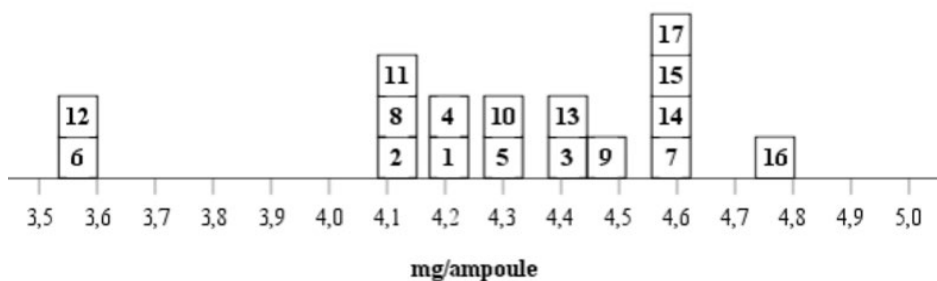


Figure 3 reports, in dot plot format, the distribution of the GMs of the 17 laboratories.

**Figure 3.** Geometric means of the PRP content in mg per ampoule of the laboratories. Numbers in the boxes represent the laboratory codes.



With respect to the precision of the analytical method (Table 2), the decomposition of the total variability (i.e., reproducibility) into the two sources (i.e., intra-laboratory and the inter-laboratory) was in line with what is expected in an inter-laboratory study since the inter-laboratory component, (which should likely be the major contributor but not the only relevant one) accounted for the 64% of the total variability, leaving the intra-laboratory component the remaining 36%.

With respect to detection of outliers, both Dixon and Grubb's tests were not significant whether performed on the 17 GM values (p-values 0.837 and 0.275, respectively) or on the 51 raw data values (p-values 0.056 and 0.071, respectively). Therefore, despite some anomalous values, all the results were included in the final dataset.

Based on the criteria in 2.6 (i.e., the Shapiro-Wilk p-value was  $<0.5$ ), it was not possible to safely assume a normal distribution, and therefore the classical calculation of mean value and standard deviation was not used. Instead, a robust calculation based on Huber *et al.* [8] was preferred. A list of results from robust estimators compared to the mean value is provided in Table 3.

The standard uncertainty of measurement associated with the estimated content per ampoule of the WHO 2<sup>nd</sup> IS for PRP was calculated in relative terms, since the sources of variation to be pooled to obtain the combined uncertainty have different units.

Although the contributions from homogeneity of ampoule filling weight, purity, moisture content and weighing of the ribitol standard are definitely less than one fifth of the major contribution (i.e., standard error), and they would not change significantly the estimated measurement uncertainty [9, 10], they are all included in the combination of uncertainty sources (Table 5).

**Table 5.** Relative standard uncertainties.

Uncertainty sources (%)				
Experimental: Standard Error	Purity of ribitol standard	Moisture content of ribitol standard	Weighing (balance)	Homogeneity of filling weight
$\frac{u(Repr)}{Repr}$	$\frac{u(p)}{p}$	$\frac{u(m)}{m}$	$\frac{u(w)}{w}$	$\frac{u(h)}{h}$
2.18	0.29	0.12	0.10	0.12

Thus, the combined relative standard uncertainty is derived as:

$$\frac{u_x}{x} = \sqrt{\left(\frac{u(Repr)}{Repr}\right)^2 + \left(\frac{u(w)}{w}\right)^2 + \left(\frac{u(p)}{p}\right)^2 + \left(\frac{u(m)}{m}\right)^2 + \left(\frac{u(h)}{h}\right)^2} = 2.21\% = 0.096$$

mg/ampoule

Based on all the statistical analyses, the content of the WHO 2<sup>nd</sup> IS for PRP per ampoule was obtained by the Huber's robust estimators and corresponds to 4.338 with an expanded uncertainty of measurement equal to  $\pm 0.203$  mg/ampoule (relative U = 4.7%; k= 2.12, which corresponds to an approximate 95% level of confidence).

#### 4. Discussion and conclusions

The quantification of the Hib conjugate saccharide in both forms (i.e., total and free saccharide) is a critical and mandatory release test for Hib containing vaccines. The determination of the total and free PRP content needs to be performed by both the manufacturers and the national control laboratories in charge of the regulatory oversight of the vaccine. When combination vaccines containing whole cell pertussis, for example, pentavalent vaccine (DTwP-HepB-Hib), are tested for the content of total and free Hib saccharide, an acidic hydrolysis step is necessary due to the interference by the whole cell pertussis component [3, 11].

The availability and appropriate use of reference preparations in independent testing is of critical importance for the interpretation of the results and allows for better comparison of biological measurements worldwide and the normalization of test results between different laboratories.

In 2013, an international collaborative study for the establishment of the WHO 2<sup>nd</sup> IS for PRP was carried out [1]. Based on the ribose assays performed by 11 participating laboratories, a PRP content of  $4.904 \pm 0.185$  mg/ampoule (i.e., expanded uncertainty calculated using a coverage factor of 2.23 which corresponds to an approximate 95% level of confidence) was assigned to the WHO 2<sup>nd</sup> IS for PRP [7].

In the 2013 collaborative study [7], a similar value for the content per ampoule of WHO 2<sup>nd</sup> IS for PRP (i.e., 4.940 mg/ampoule) was obtained by nine laboratories performing HPAEC-PAD after the alkaline depolymerization method and using the 1<sup>st</sup> WHO IS as a standard. A correlation between the orcinol method (ribose) and HPAEC-PAD - alkaline depolymerization method was also verified by van der Put and colleagues [12] who stated that for the down-stream processing samples, *“it was found that the correlation between the results obtained by HPAEC-PAD specific quantification of the PRP monomeric repeat unit released by alkaline hydrolysis, and those from the orcinol method was high ( $R^2 = 0.8762$ ).”*

The present collaborative study was specifically designed to evaluate the PRP content per ampoule by HPAEC-PAD based on the measurement of ribitol obtained after acid hydrolysis [3]. In recent years, various laboratories have obtained a lower value for the PRP content of the WHO 2<sup>nd</sup> IS for PRP when applying this test protocol, a method which employs a calibration curve based on D-ribitol. The outcome of the current collaborative study confirmed that the measured content of PRP per ampoule is lower when determined by HCl acid hydrolysis followed by HPAEC-PAD than when measured by the orcinol method.



Bardotti and colleagues [11] also found on average that a method using trifluoroacetic acid hydrolysis followed by HPAEC-PAD, led to a slightly lower value of PRP than was obtained using the orcinol (ribose) assay. The reason for this was not given. A similar result was observed when the WHO 1<sup>st</sup> IS was tested by HPAEC-PAD after trifluoroacetic acid hydrolysis [4].

The results of the current collaborative study demonstrate that a value of  $4.338 \pm 0.203$  mg/ampoule was obtained for the WHO 2<sup>nd</sup> IS for PRP when quantifying the content according to the acid hydrolysis protocol reported in Roskopf and colleagues [3].

Given that the acid hydrolysis method is needed when testing vaccines with a whole cell pertussis component, discussions should be initiated to evaluate whether method-dependent adjustments are required for the international standard to ensure accurate PRP quantitation when different methods are employed.

**Authors Contributions:**

Conceptualization, Christina von Hunolstein, Andrea Gaggioli and Ute Roszkopf; Formal analysis, Christina von Hunolstein and Andrea Gaggioli; Funding acquisition, Ute Roszkopf; Methodology, Andrea Gaggioli; Project administration, Ute Roszkopf; Supervision, Ute Roszkopf; Writing – original draft, Christina von Hunolstein, Andrea Gaggioli and Ute Roszkopf; Writing – review & editing, Christina von Hunolstein.

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**Conflict of Interest:** The authors declare no conflict of interest.

**Disclaimer:** The authors alone are responsible for the views expressed in this article and they do not necessarily represent the views, decisions or policies of the institutions with which they are affiliated.

The funder had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

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- Bruce Meade for editorial review of the report.

**Appendix A****List of participants, in alphabetical order by country.**

<b>Country</b>	<b>Name</b>	<b>Institution</b>
Bangladesh	Dr Mohammad Mainul AHASAN	Incepta Vaccine Ltd.
China	Dr Qiang YE Dr Maoguang LI Ms Dan ZHAO	National Institute for Food and Drug Control (NIFDC) Division of Respiratory Bacterial Vaccines
Germany	Dr Wolf Hagen HOLTKAMP	Paul-Ehrlich Institut (PEI) Section 3/1 Product testing of immunological medicinal products
India	Dr Dipankar DAS	Bharat Biotech International Ltd.
India	Dr Srinivas KOSARAJU	Biological E. Limited
India	Mr Jaipal MEENA Mr Ade Ajay KUMAR	National Institute of Biologicals (NIB)
India	Dr Sunil GAIROLA	Serum Institute of India PVT LTD
India	Dr Radhakrishnam Raju MANTENA	Sanofi Healthcare India Private Limited (formerly: Shantha Biotechnics Limited (A Sanofi Company))
Indonesia	Dra Togi Junice HUTADJULU Ms Elisabeth ARISSETININGSIH	National Quality Control Laboratory of Drug and Food (NQCLDF) National Agency of Drug and Food Control
Indonesia	Dr Dori UGIYADI Ms Lin SUSANTI	PT Bio Farma (Persero)
Italy	Dr Cristina PEZZELLA Dr Luisa RALLI	Istituto Superiore di Sanità (ISS)

Mexico	Ms Imelda Rocío GUZMÁN CERVANTES Ms Laura MUNGUÍA Dr Guillermo VEGA RODRIGUEZ	Commission for Analytical Control and Expansion of Coverage (CCAYAC) Federal Commission for Protection against Health Risks (COFEPRIS)
Republic of Korea	Ms Helen KIM Dr ByoungKook HYUN	LG Chem Ltd.
Republic of Korea	Dr Chulhyun LEE Dr Hyun LEE	National Institute of Food and Drug Safety Evaluation (NIFDS) Vaccines Division
South Africa	Dr Ruan ELLS	National Control Laboratory for Biological Products (NCLBP)
Thailand	Dr Supaporn PHUMIAMORN Mrs Wereyarmarst JAROENKUNATHUM	Institute of Biological Products (IBP), Department of Medical Sciences, Ministry of Public Health
United Kingdom	Dr Fang GAO Dr Barbara BOLGIANO Mrs Karena BURKIN	National Institute for Biological Standards and Control (NIBSC) Bacterial Division

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**LAMIVUDINE AND TENOFOVIR DISOPROXIL FUMARATE TABLETS**  
***(LAMIVUDINI ET TENOFOVIRI DISOPROXILI FUMARATI COMPRESSI)***

**Draft proposal for inclusion in**  
***The International Pharmacopoeia***

This draft working document was sent out electronically and 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. Period for comments on this draft working document is now closed with all comments received by **21 October 2022**.

All comments were sent to **Dr Herbert Schmidt**, Technical Officer, Norms and Standards for Pharmaceuticals, Technical Standards and Specifications (email: [schmidth@who.int](mailto:schmidth@who.int)), with a copy to Ms Sinéad Jones (email: [jonessi@who.int](mailto:jonessi@who.int))

Should you wish to receive our draft guidelines, please send your e-mail address to [jonessi@who.int](mailto:jonessi@who.int) and your name will be added to our electronic mailing list.

## LAMIVUDINE AND TENOFOVIR DISOPROXIL FUMARATE TABLETS

### *(LAMIVUDINI ET TENOFOVIRI DISOPROXILI FUMARATI COMPRESSI)*

**Category.** Antiretroviral (Nucleoside/Nucleotide reverse transcriptase inhibitor).

**Storage.** Lamivudine and tenofovir disoproxil tablets should be kept in a tightly closed container.

**Additional information.** Strength in the 20th Invitation to Manufacturers and Suppliers of Medicinal Products for HIV Infections and Related Diseases to Submit an Expression of Interest (EOI) for Product Evaluation to the WHO Prequalification Unit – Medicines Team: 300 mg Lamivudine and 300 mg Tenofovir disoproxil fumarate.

#### Requirements

Comply with the monograph for *Tablets*.

**Definition.** Lamivudine and tenofovir disoproxil fumarate tablets contain Lamivudine and Tenofovir disoproxil fumarate. They contain not less than 90.0% and not more than 110.0% of the amount of lamivudine ( $C_8H_{11}N_3O_3S$ ) and tenofovir disoproxil fumarate ( $C_{19}H_{30}N_5O_{10}P \cdot C_4H_4O_4$ ) stated on the label.

**Manufacture.** The manufacturing process and the product packaging are designed and controlled so as to minimize the moisture content of the tablets. They ensure that, if tested, the tablets would comply with a water content limit of not more than 50 mg/g when determined as described under *2.8 Determination of water by the Karl Fischer method*, Method A, using 0.5 g of the powdered tablets.

#### Identity tests

- Either test A or test B may be performed.
- A. Carry out the test as described under *1.14.1 Chromatography*, High-performance liquid chromatography, using the conditions and solutions given under “Assay”. The retention time of the principal peak in the chromatogram obtained with solution (1) corresponds to the retention time of the corresponding peak due to lamivudine and tenofovir disoproxil in the chromatograms obtained with solution (2) and (3).



- B. Carry out the test as described under *1.14.1 Chromatography*. Thin-layer chromatography, using silica gel R6 as the coating substance and a freshly prepared mixture of ethyl acetate R, water R, anhydrous formic acid R and glacial acetic acid R (71:14:7:7 v/v/v/v) as the mobile phase. Apply separately to the plate 5 µL of each of the following 3 solutions in a mixture of methanol R and formic acid (~1080 g/L) TS (9:1 v/v). For solution (A), disperse a quantity of the powdered tablets, nominally containing 12 mg of tenofovir disoproxil fumarate, in 2 mL, sonicate for 5 minutes and filter. For solution (B), use a solution containing 6 mg of lamivudine RS per mL. For solution (C), use a solution containing 6 mg of tenofovir disoproxil fumarate RS. After removing the plate from the chromatographic chamber, allow it to dry in air or in a current of air. Allow the plate to cool and examine the chromatogram under ultraviolet light (254 nm and 365 nm). The two principal spots in the chromatogram obtained with solution (A) corresponds in position, appearance and intensity with the corresponding spots due to lamivudine and tenofovir disoproxil obtained with solution (B) and (C).

**Dissolution.** Carry out the test described under *5.5 Dissolution test for oral dosage forms*, using as the dissolution medium 900 mL of hydrochloric acid (~4 g/L) TS and rotating the paddle at 50 revolutions per minute. At 30 minutes, withdraw a sample of 10 mL of the medium through an in-line filter. Allow the filtered sample to cool to room temperature. Dilute 5.0 mL of the solution to 25.0 mL with the diluent, described under “Assay”.

Carry out the test as described under *1.14.1 Chromatography*. High-performance liquid chromatography, using the chromatographic conditions and solutions as described under “Assay”.

For each of the tablets tested, calculate the total amount each of lamivudine and tenofovir disoproxil fumarate in the medium from the results obtained, using the declared content of lamivudine ( $C_8H_{11}N_3O_3S$ ) in lamivudine RS and the declared content of tenofovir disoproxil fumarate ( $C_{19}H_{30}N_5O_{10}P \cdot C_4H_4O_4$ ) in tenofovir disoproxil fumarate RS.

Evaluate the results as described under *5.5 Dissolution test for oral dosage forms*. Acceptance criteria. The amount of lamivudine ( $C_8H_{11}N_3O_3S$ ) and tenofovir disoproxil fumarate ( $C_{19}H_{30}N_5O_{10}P \cdot C_4H_4O_4$ ) released after 45 minutes is not less than 80% (Q) of the corresponding amounts declared on the label.

**Tests for related substances.** Carry out the test as described under *1.14.1 Chromatography*. High-performance liquid chromatography, using a stainless steel column (25 cm x 4.6 mm) packed with end-capped particles of silica gel, the surface of which has been modified with chemically-bonded octadecylsilyl groups (5 µm).<sup>1</sup>

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<sup>1</sup> An Inertsil ODS-3v column was found suitable.

Use the following conditions for gradient elution:

- mobile phase A: acetate buffer pH 4.2; and
- mobile phase B: acetonitrile R.

Prepare the acetate buffer pH 4.2 by dissolving 9.64 g of ammonium acetate R in 900 mL of water R, adjust the pH to 4.2 with glacial acetic acid R and dilute to 1000 mL with water R.

Time (minutes)	Mobile phase A (% v/v)	Mobile phase B (% v/v)	Comments
0–2	100	0	Isocratic
2–17	100 to 95	0 to 5	Linear gradient
17–47	95 to 60	5 to 40	Linear gradient
47–62	60 to 25	40 to 75	Linear gradient
62–63	25 to 100	75 to 0	Return to initial composition
63–75	100	0	Re-equilibration

Operate with a flow rate of 1.0 mL per minute. As a detector, use an ultraviolet spectrophotometer set at a wavelength of 260 nm. Maintain the column temperature at 25 °C and the autosampler temperature at 6 °C.

Prepare the following solutions using water R as diluent.

For solution (1), transfer a quantity of the powdered tablets, nominally containing 225 mg of Tenofovir disoproxil fumarate, to a 250 mL volumetric flask. Add about 175 mL of diluent and sonicate at room temperature for about 30 minutes with intermittent shaking. Allow to cool to room temperature, dilute to volume and filter.

For solution (2), dilute 1.0 mL of solution (1) to 100.0 mL.

For solution (3), dilute 10.0 mL of solution (2) to 100.0 mL.

For solution (4), use a solution containing 0.5 mg of tenofovir disoproxil for system suitability (containing tenofovir disoproxil and the impurity H) per mL.

For solution (5), dissolve 10 mg of tenofovir disoproxil fumarate RS in 10 mL. Heat the solution carefully in a boiling water-bath for 20 minutes. Cool to room temperature and dilute 1 mL of the solution to 10 mL.

For solution (6), use a solution containing 0.2 mg of fumaric acid R per mL.

For solution (7), dissolve 25 mg of cytosine R and 25 mg of uracil R and dilute to 50.0 mL. Dilute 1.0 mL of this solution to 100.0 mL.

For solution (8), dissolve a suitable amount of each of the excipients stated on the label in 10 mL of a suitable solvent and dilute to 100.0 mL with the diluent.

Inject 10  $\mu$ L each of solutions (1), (2), (3), (4), (5), (6), (7) and (8).

Use the chromatogram obtained with solution (4) and the chromatogram supplied with tenofovir disoproxil for system suitability RS to identify the peak due to the tenofovir disoproxil impurity H in the chromatogram obtained with solution (1), if present.

Use the chromatogram obtained with solution (5) to identify the peak due to the tenofovir disoproxil impurity A in the chromatogram obtained with solution (1), if present.

Use the chromatogram obtained with solution (6) to identify the peak due to fumaric acid in the chromatogram obtained with solution (1). The peak due to fumaric acid is eluted at about 2.5 minutes and may appear as a single or split peaks.

Use the chromatogram obtained with solution (7) to identify the peaks due to lamivudine impurities E (cytosine) and F (uracil) in the chromatogram obtained with solution (1), if present.

Use the chromatogram obtained with solution (8) to identify the peaks due to excipients. The impurities, if present, are eluted at the following relative retentions with reference to tenofovir disoproxil (retention time about 48 minutes):

Impurity	Relative retention	Impurity Classification
Lamivudine impurity E	0.09	Synthesis/Degradation
Lamivudine impurity F	0.11	Synthesis/Degradation
Lamivudine impurity A	0.17	Synthesis
Lamivudine impurity G	0.20	Synthesis/Degradation
Lamivudine impurity H	0.21	Synthesis/Degradation
Lamivudine impurity B	0.38	Synthesis
Lamivudine	0.39	-
Lamivudine impurity J	0.45	Degradant
Lamivudine impurity C	0.54	Synthesis
Tenofovir disoproxil impurity R	0.30	
Tenofovir disoproxil impurity N	0.33	Synthesis/Degradation
Tenofovir disoproxil impurity A	0.63	Synthesis/Degradation
Tenofovir disoproxil impurity F	0.73	Degradation
Tenofovir disoproxil impurity E	0.76	Synthesis/Degradation
Tenofovir disoproxil impurity B	0.80 and 0.81	Synthesis
Tenofovir disoproxil impurity L	0.87	Synthesis
Tenofovir disoproxil impurity C	0.88	Synthesis
Tenofovir disoproxil impurity D	0.90	Synthesis
Tenofovir disoproxil impurity M	0.94	Synthesis
Tenofovir disoproxil impurity P	0.96	Synthesis
Tenofovir disoproxil impurity O	0.97	Synthesis
Tenofovir disoproxil impurity I	0.98	Synthesis/Degradation
Tenofovir disoproxil impurity H	1.01	Synthesis
Tenofovir disoproxil impurity Q	1.10	Synthesis/Degradation
Tenofovir disoproxil impurity J	1.19	Synthesis/Degradation

*Note: Tenofovir disoproxil impurities B and C may appear as single or split peaks. If they appear as split peaks, use the sum of the two peaks in the calculation of the concentration. (“Synthesis” stands for synthesis-related impurity; “Degradation” for degradation product.)*

The test is not valid unless:

- in the chromatogram obtained with solution (3), the signal-to-noise ratio of the peak due to tenofovir disoproxil is at least 20; and
- in the chromatogram obtained with solution (4), the resolution between the peaks due to tenofovir disoproxil and tenofovir disoproxil impurity H is at least 1.2.

*[Note from the Secretariat. It is intended to use the peak-to-valley ratio in the verification of the system suitability once the International Chemical Reference Substance on tenofovir disoproxil for system suitability has been established.]*

In the chromatogram obtained with solution (1):

- the area of any peak corresponding to tenofovir impurity A, when multiplied by a correction factor of 0.7, is not greater than five times the area of the peak due to tenofovir disoproxil in the chromatogram obtained with solution (2) (5.0%).
- the area of any peak corresponding to either tenofovir impurity F, tenofovir impurity I or tenofovir impurity J, is not greater than 0.75 times the area of the peak due to tenofovir disoproxil in the chromatogram obtained with solution (2) (0.75%);
- the area of any peak corresponding to impurity D is not greater than 3 times the area of the peak due to tenofovir disoproxil in the chromatogram obtained with solution (3) (0.3%);
- the area of any peak corresponding to tenofovir impurity N, when multiplied by a correction factor of 0.5, is not greater than two times the area of the peak due to tenofovir disoproxil in the chromatogram obtained with solution (3) (0.2%);
- the area of any peak corresponding to tenofovir impurity E or impurity Q is not greater than two times the area of the peak due to tenofovir disoproxil in the chromatogram obtained with solution (3) (0.2%);
- the area of any peak corresponding to lamivudine impurity E, when multiplied by a correction factor of 0.6, is not greater than two times the area of the peak due to lamivudine in the chromatogram obtained with solution (3) (0.2%);
- the area of any peak corresponding to lamivudine impurity F or J, when multiplied by a correction factor of 2.2, is not greater than two times the area of the peak due to lamivudine in the chromatogram obtained with solution (3) (0.2%); and
- the area of any peak corresponding to either lamivudine impurity G or H, is not greater than two times the area of the peak due to lamivudine in the chromatogram obtained with solution (3) (0.2%).
- Determine the sum of the areas of any peaks corresponding to lamivudine impurities G and H and the corrected areas of any peaks corresponding to lamivudine impurities E, F and J. Calculate the percentage content of lamivudine related impurities using the area of the peak due to lamivudine in the chromatogram obtained with solution (2) as a reference. Disregard any peak with an area or a corrected area of less than 0.5 times the area of the peak due to lamivudine in the chromatogram obtained with solution (3) (0.05%).

- Determine the sum of the areas of any peaks corresponding to tenofovir impurities F, E, I, D, Q and J and the corrected areas of any peaks corresponding to tenofovir impurities N and A. Calculate the percentage content of tenofovir disoproxil related impurities using the area of the peak due to tenofovir disoproxil in the chromatogram obtained with solution (2) as a reference. Disregard any peak with an area or a corrected area of less than 0.5 times the area of the peak due to tenofovir disoproxil in the chromatogram obtained with solution (3) (0.05%) and any peak due to fumaric acid.
- The sum of the lamivudine and tenofovir disoproxil related impurities is not greater than 5.0%.

**Assay.** Perform the test in subdued light and without any prolonged interruptions, preferably using low-actinic glassware. Carry out the test as described under *1.14.1 Chromatography*. High-performance liquid chromatography, using a stainless steel column (15 cm x 4.6 mm) packed with end-capped particles of silica gel, the surface of which has been modified with chemically-bonded octylsilyl groups (3.5 µm).<sup>2</sup>

Use the following conditions for gradient elution:

- mobile phase A: 0.1% (v/v) of trifluoroacetic acid R in water R;
- mobile phase B: Acetonitrile R.

Time (minutes)	Mobile phase A (% v/v)	Mobile phase (% v/v)	Comments
0 – 2.0	97	3	Isocratic
2.0 – 12.0	97 to 50	3 to 50	Linear gradient
12.0 – 15.0	50	50	Isocratic
15.0 – 16.0	50 to 97	50 to 3	Return to initial composition
16.0 – 20.0	97	3	Re-equilibration

Operate at a flow rate of 1.5 mL per minute. As a detector, use an ultraviolet spectrophotometer set at a wavelength of 260 nm. Maintain the column temperature at 30 °C.

Use as a diluent a mixture of 95 volumes of 0.1% (v/v) of trifluoroacetic acid R in water R and 5 volumes of acetonitrile R.

Prepare the following solution. For solution (1), weigh and powder 20 tablets. Transfer a quantity of the powdered tablets, nominally containing 300.0 mg of lamivudine, to a 100 mL volumetric flask. Add about 30 mL of the diluent and sonicate for about 10 minutes with intermittent shaking until the larger pieces have disintegrated. Add 50 mL acetonitrile and sonicate for about 30 minutes. Allow to cool to room temperature, dilute to volume with the

<sup>2</sup> An Eclipse XDB C8 column was found suitable.

diluent and filter. Dilute 5.0 mL of this solution to 100.0 mL with the diluent. For solution (2), dissolve 30.0 mg of lamivudine RS in diluent and dilute to 100.0 mL with the same solvent.

Dilute 5.0 mL of this solution to 10.0 mL with diluent. For solution (3), dissolve 30.0 mg of tenofovir disoproxil fumarate RS in diluent and dilute to 100.0 mL with the same solvent. Dilute 5.0 mL of this solution to 10.0 mL with diluent.

Inject 20 µL each of solutions (1), (2) and (3).

Measure the areas of the peaks corresponding to lamivudine and tenofovir disoproxil obtained in the chromatograms of solutions (1), (2) and (3) and calculate the percentage content of lamivudine ( $C_8H_{11}N_3O_3S$ ) and tenofovir disoproxil fumarate ( $C_{19}H_{30}N_5O_{10}P \cdot C_4H_4O_4$ ) in the tablets using the declared content of lamivudine ( $C_8H_{11}N_3O_3S$ ) in lamivudine RS and the declared content of tenofovir disoproxil fumarate ( $C_{19}H_{30}N_5O_{10}P \cdot C_4H_4O_4$ ) in tenofovir disoproxil fumarate RS.

**Impurities.** The impurities limited by the requirements of this monograph include those listed in the monographs on Lamivudine and Tenofovir disoproxil fumarate, excluding lamivudine impurity D and tenofovir disoproxil impurity G.

#### Reference substances invoked

##### Lamivudine RS

Established International Chemical Reference Substance.

**Tenofovir disoproxil for system suitability RS** (containing tenofovir disoproxil and the impurity H)

International Chemical Reference Substance to be established.

##### Tenofovir disoproxil fumarate RS

Established International Chemical Reference Substance.

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**TENOFOVIR DISOPROXIL FUMARATE TABLETS**  
***(TENOFVIRI DISOPROXILI FUMARATI COMPRESSI)***

**Draft proposal for inclusion in**  
***The International Pharmacopoeia***

This draft working document was sent out electronically and 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. Period for comments on this draft working document is now closed with all comments received by **21 October 2022**.

All comments were sent to **Dr Herbert Schmidt**, Technical Officer, Norms and Standards for Pharmaceuticals, Technical Standards and Specifications (email: [schmidth@who.int](mailto:schmidth@who.int)), with a copy to Ms Sinéad Jones (email: [jonessi@who.int](mailto:jonessi@who.int))

Should you wish to receive our draft guidelines, please send your e-mail address to [jonessi@who.int](mailto:jonessi@who.int) and your name will be added to our electronic mailing list.



# TENOFOVIR DISOPROXIL FUMARATE TABLETS

## *(TENOFVIRI DISOPROXILI FUMARATI COMPRESSI)*

**Category.** Antiretroviral (Nucleoside/Nucleotide reverse transcriptase inhibitor).

**Storage.** Tenofovir disoproxil tablets should be kept in a tightly closed container.

**Additional information.** Strength in the current WHO Model List of Essential Medicines: 300 mg Tenofovir disoproxil fumarate. 300 mg of tenofovir disoproxil fumarate is equivalent to approximately 245 mg of tenofovir disoproxil.

### Requirements

Comply with the monograph for *Tablets*.

**Definition.** Tenofovir disoproxil tablets contain Tenofovir disoproxil fumarate. They contain not less than 90.0% and not more than 110.0% of the amount of tenofovir disoproxil fumarate ( $C_{19}H_{30}N_5O_{10}P \cdot C_4H_4O_4$ ) stated on the label.

**Manufacture.** The manufacturing process and the product packaging are designed and controlled so as to minimize the moisture content of the tablets. They ensure that, if tested, the tablets would comply with a water content limit of not more than 50 mg/g when determined as described under *2.8 Determination of water by the Karl Fischer method*, Method A, using 0.5 g of the powdered tablets.

### Identity tests

- Either test A or test B may be performed.
- A. Carry out the test as described under *1.14.1 Chromatography*, High-performance liquid chromatography, using the conditions and solutions given under “Assay”. The retention time of the principal peak in the chromatogram obtained with solution (1) corresponds to the retention time of the corresponding peak due to tenofovir disoproxil in the chromatograms obtained with solution (2).

- B. Carry out the test as described under *1.14.1 Chromatography*, Thin-layer chromatography, using silica gel R6 as the coating substance and a freshly prepared mixture of ethyl acetate R, water R, anhydrous formic acid R and glacial acetic acid R (71:14:7:7 v/v/v/v) as the mobile phase. Apply separately to the plate 5 µL of each of the following 2 solutions in a mixture of methanol R and formic acid (~1080 g/L) TS (9:1 v/v). For solution (A), disperse a quantity of the powdered tablets, nominally containing 12 mg of tenofovir disoproxil fumarate, in 2 mL, sonicate for 5 minutes and filter. For solution (B), use a solution containing 6 mg of tenofovir disoproxil fumarate RS. After removing the plate from the chromatographic chamber, allow it to dry in air or in a current of air. Allow the plate to cool and examine the chromatogram under ultraviolet light (254 nm and 365 nm). The principal spot in the chromatogram obtained with solution (A) corresponds in position, appearance and intensity with the corresponding spots due to tenofovir disoproxil obtained with solution (B).

**Dissolution.** Carry out the test described under *5.5 Dissolution test for oral dosage forms*, using as the dissolution medium 900 mL of hydrochloric acid (0.1 mol/L) VS and rotating the paddle at 50 revolutions per minute. At 30 minutes, withdraw a sample of 10 mL of the medium through an in-line filter. Allow the filtered sample to cool to room temperature. Measure the absorbance (1.6) of a 1 cm layer of the resulting solution, suitably diluted if necessary, at the maximum of about 260 nm. For each of the tablets tested, calculate the total amount of tenofovir disoproxil fumarate ( $C_{19}H_{30}N_5O_{10}P \cdot C_4H_4O_4$ ) in the medium using the absorptivity value of 22.3 ( $A_{1\text{ cm}}^{1\%} = 223$ ) for tenofovir disoproxil fumarate.

Evaluate the results as described under *5.5 Dissolution test for oral dosage forms*, Acceptance criteria. The amount of tenofovir disoproxil fumarate ( $C_{19}H_{30}N_5O_{10}P \cdot C_4H_4O_4$ ) released is not less than 80% (Q) of the amount declared on the label.

**Tests for related substances.** Perform the test in subdued light and without any prolonged interruptions, preferably using low-actinic glassware. Carry out the test as described under *1.14.1 Chromatography*: High-performance liquid chromatography, using a stainless steel column (25 cm x 4.6 mm) packed with end-capped particles of silica gel, the surface of which has been modified with chemically-bonded octadecylsilyl groups (5 µm).<sup>3</sup>

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<sup>3</sup> An Inertsil ODS-3v column was found suitable.

Use the following conditions for gradient

- mobile phase A: acetate buffer pH 4.2; and  
elution: mobile phase B: acetonitrile R.

Prepare the acetate buffer pH 4.2 by dissolving 9.64 g of ammonium acetate R in 900 mL of water R, adjust the pH to 4.2 with glacial acetic acid R and dilute to 1000 mL with water R.

Time (minutes)	Mobile phase A (% v/v)	Mobile phase B (% v/v)	Comments
0–2	100	0	Isocratic
2–17	100 to 95	0 to 5	Linear gradient
17–47	95 to 60	5 to 40	Linear gradient
47–62	60 to 25	40 to 75	Linear gradient
62–63	25 to 100	75 to 0	Return to initial composition
63–75	100	0	Re-equilibration

Operate with a flow rate of 1.0 mL per minute. As a detector, use an ultraviolet spectrophotometer set at a wavelength of 260 nm. Maintain the column temperature at 25 °C and the autosampler temperature at 6 °C.

Prepare the following solutions using water R as diluent.

For solution (1), transfer a quantity of the powdered tablets, nominally containing 225 mg of Tenofovir disoproxil fumarate, to a 250 mL volumetric flask. Add about 175 mL of diluent and sonicate at room temperature for about 30 minutes with intermittent shaking. Allow to cool to room temperature, dilute to volume and filter.

For solution (2), dilute 1.0 mL of solution (1) to 100.0 mL.

For solution (3), dilute 10.0 mL of solution (2) to 100.0 mL.

For solution (4), use a solution containing 0.5 mg of tenofovir disoproxil for system suitability (containing tenofovir disoproxil and the impurity H) per mL.

For solution (5), dissolve 10 mg of tenofovir disoproxil fumarate RS in 10 mL. Heat the solution carefully in a boiling water-bath for 20 minutes. Cool to room temperature and dilute 1 mL of the solution to 10 mL.

For solution (6), use a solution containing 0.2 mg of fumaric acid R per mL.

For solution (7), dissolve a suitable amount of each of the excipients stated on the label in 10 mL of a suitable solvent and dilute to 100.0 mL with the diluent.

Inject 10 µL each of solutions (1), (2), (3), (4), (5), (6) and (7).

Use the chromatogram obtained with solution (4) and the chromatogram supplied with tenofovir disoproxil for system suitability RS to identify the peak due to the tenofovir disoproxil impurity H in the chromatogram obtained with solution (1), if present.

Use the chromatogram obtained with solution (5) to identify the peak due to the tenofovir disoproxil impurity A in the chromatogram obtained with solution (1), if present.

Use the chromatogram obtained with solution (6) to identify the peak due to fumaric acid in the chromatogram obtained with solution (1). The peak due to fumaric acid is eluted at about 2.5 minutes and may appear as a single or split peaks.

Use the chromatogram obtained with solution (7) to identify the peaks due to excipients. The impurities, if present, are eluted at the following relative retentions with reference to tenofovir disoproxil (retention time about 48 minutes):

<b>Impurity</b>	<b>Relative retention</b>	<b>Impurity Classification</b>
Tenofovir disoproxil impurity R	0.30	
Tenofovir disoproxil impurity N	0.33	Synthesis/Degradation
Tenofovir disoproxil impurity A	0.63	Synthesis/Degradation
Tenofovir disoproxil impurity F	0.73	Degradation
Tenofovir disoproxil impurity E	0.76	Synthesis/Degradation
Tenofovir disoproxil impurity B	0.80 and 0.81	Synthesis
Tenofovir disoproxil impurity L	0.87	Synthesis
Tenofovir disoproxil impurity C	0.88	Synthesis
Tenofovir disoproxil impurity D	0.90	Synthesis
Tenofovir disoproxil impurity M	0.94	Synthesis
Tenofovir disoproxil impurity P	0.96	Synthesis
Tenofovir disoproxil impurity O	0.97	Synthesis
Tenofovir disoproxil impurity I	0.98	Synthesis/Degradation
Tenofovir disoproxil impurity H	1.01	Synthesis
Tenofovir disoproxil impurity Q	1.10	Synthesis/Degradation
Tenofovir disoproxil impurity J	1.19	Synthesis/Degradation

*Note: Tenofovir disoproxil impurities B and C may appear as single or split peaks. If they appear as split peaks, use the sum of the two peaks in the calculation of the concentration. ("Synthesis" stands for synthesis-related impurity; "Degradation" for degradation product.)*

The test is not valid unless:

- in the chromatogram obtained with solution (3), the signal-to-noise ratio of the peak due to tenofovir disoproxil is at least 20; and
- in the chromatogram obtained with solution (4), the resolution between the peaks due to tenofovir disoproxil and tenofovir disoproxil impurity H is at least 1.2.

*[Note from the Secretariat. It is intended to use the peak-to-valley ratio in the verification of the system suitability once the International Chemical Reference Substance on tenofovir disoproxil for system suitability has been established.]*

In the chromatogram obtained with solution (1):

- the area of any peak corresponding to tenofovir impurity A, when multiplied by a correction factor of 0.7, is not greater than five times the area of the peak due to tenofovir disoproxil in the chromatogram obtained with solution (2) (5.0%);
- the area of any peak corresponding to either tenofovir impurity F, tenofovir impurity I or tenofovir impurity J, is not greater than 0.75 times the area of the peak due to tenofovir disoproxil in the chromatogram obtained with solution (2) (0.75%);
- the area of any peak corresponding to impurity D is not greater than 3 times the area of the peak due to tenofovir disoproxil in the chromatogram obtained with solution (3) (0.3%);
- the area of any peak corresponding to tenofovir impurity N, when multiplied by a correction factor of 0.5, is not greater than two times the area of the peak due to tenofovir disoproxil in the chromatogram obtained with solution (3) (0.2%); and
- the area of any peak corresponding to tenofovir impurity E or impurity Q is not greater than two times the area of the peak due to tenofovir disoproxil in the chromatogram obtained with solution (3) (0.2%).
- The sum of the areas of all impurity peaks, including the corrected areas of any peaks corresponding to tenofovir impurities N and A is not greater than 5 times the area of the peak due to tenofovir disoproxil in the chromatogram obtained with solution (2) (5.0%). Disregard any peak with an area or a corrected area of less than 0.5 times the area of the peak due to tenofovir disoproxil in the chromatogram obtained with solution (3) (0.05%) and any peak due to fumaric acid.

**Assay.** Perform the test in subdued light and without any prolonged interruptions, preferably using low-actinic glassware. Carry out the test as described under *1.14.1 Chromatography*. High-performance liquid chromatography, using a stainless steel column (25 cm x 4.6 mm) packed with end-capped particles of silica gel, the surface of which has been modified with chemically-bonded octylsilyl groups (5 µm).<sup>4</sup>

As the mobile phase use a mixture of a sodium dihydrogen phosphate buffer pH 2.3 and acetonitrile for chromatography R (60:40 v/v).

<sup>4</sup> An Inertsil ODS-3v column was found suitable.

Prepare the sodium dihydrogen phosphate buffer pH 2.3 by dissolving 6.9 g of sodium dihydrogen phosphate R in 900 ml of water R, adding 1.0 mL of triethylamine R, adjusting the pH to 2.3 with phosphoric acid (~105 g/l) TS, and diluting to 1000 ml with water R.

Operate at a flow rate of 1.0 mL per minute. As a detector, use an ultraviolet spectrophotometer set at a wavelength of 260 nm. Maintain the column temperature at 30 °C.

Use as a diluent a mixture of 95 volumes of 0.1% (v/v) of trifluoroacetic acid R in water R and 5 volumes of acetonitrile R.

Prepare the following solution. For solution (1), weigh and powder 20 tablets. Transfer a quantity of the powdered tablets, nominally containing 300.0 mg of tenofovir disoproxil fumarate, to a 100 mL volumetric flask. Add about 30 mL of diluent and sonicate for about 10 minutes with intermittent shaking until the larger pieces have disintegrated. Add 50 mL acetonitrile and sonicate for about 30 minutes. Allow to cool to room temperature, dilute to volume with diluent and filter. Dilute 5.0 mL of this solution to 100.0 mL with diluent. For solution (2), dissolve 30.0 mg of tenofovir disoproxil fumarate RS in diluent and dilute to 100.0 mL with the same solvent. Dilute 5.0 mL of this solution to 10.0 mL with diluent.

Inject 20 µL each of solutions (1) and (2).

Measure the areas of the peaks corresponding to tenofovir disoproxil obtained in the chromatograms of solutions (1) and (2) and calculate the percentage content of tenofovir disoproxil fumarate ( $C_{19}H_{30}N_5O_{10}P \cdot C_4H_4O_4$ ) in the tablets using the declared content of tenofovir disoproxil fumarate ( $C_{19}H_{30}N_5O_{10}P \cdot C_4H_4O_4$ ) in tenofovir disoproxil fumarate RS.

**Impurities.** The impurities limited by the requirements of this monograph include those listed in the monographs on Tenofovir disoproxil fumarate, excluding tenofovir disoproxil impurity G.

#### Reference substances invoked

**Tenofovir disoproxil for system suitability RS** (containing tenofovir disoproxil and the impurity H)

International Chemical Reference Substance to be established.

#### Tenofovir disoproxil fumarate RS

Established International Chemical Reference Substance.

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## ATC/DDD Classification (Temporary)

The following ATC codes and DDDs were agreed at the meeting of the WHO International Working Group for Drug Statistics Methodology in October 2022.

Comments or objections to the decisions from the meeting should be forwarded to the WHO Collaborating Centre for Drug Statistics Methodology before 1 February 2023. If no objections are received before this date, the new ATC codes and DDDs will be considered final and included in the January 2024 version of the ATC/DDD Index.

### New ATC 5th level codes:

New ATC code	ATC level name/INN
A02BC51	omeprazole, combinations
A02BD17	vonoprazan and amoxicillin
A02BX16	irsogladine
A05AA05	ursodoxicoltaurine
A07FA03	escherichia coli
A10AE07	insulin icodec
A10BD28	metformin and teneligliptin
A10BD29	sitagliptin and dapagliflozin
A16AB26	eladocagene exuparovec
A16AB27	pabinafusp alfa
A16AX23	leriglitazone
B01AF51	rivaroxaban and acetylsalicylic acid
B02BD15	valoctocogene roxaparovec
B02BX10	concizumab
B06AX05	exagamglogene autotemcel
C01CA28	centhaquine
C01CX10	omecamtiv mecarbil
C05AX06	phenylephrine
C05XX01	bepmerminogene perplasmid
C09BX06	perindopril, bisoprolol, amlodipine and indapamide
C10BX20	rosuvastatin and telmisartan
D05AX06	roflumilast
D05AX07	tapinarof
G04BD15	vibegron
G04BX17	sodium salicylate and methenamine
J01DC52	cefuroxime and beta-lactamase inhibitor
J01DE51	cefepime and beta-lactamase inhibitor
J07BN05	covid-19, virus-like particles

New ATC code	ATC level name/INN
J07BX05	respiratory syncytial virus vaccines
L01BC58	decitabine, combinations
L01EJ04	momelotinib
L01EK04	fruquintinib
L01EL04	orelabrutinib
L01EL05	pirtobrutinib
L01FF11	sugemalimab
L01FF12	serplulimab
L01FX24	teclistamab
L01FX25	mosunetuzumab
L01XK52	niraparib and abiraterone
L01XL08	lisocabtagene maraleucel
L01XL09	tabelecleucel
L02BA04	elacestrant
L02BX53	abiraterone and prednisolone
L03AB17	sampeginterferon beta-1a
L03AX22	leniolisib
L04AC24	mirikizumab
L04AC25	levilimab
L04AF08	ritlecitinib
L04AG15	divozilimab
L04AJ06	zilucoplan
M01AE57	naproxen and diphenhydramine
M04AC51	colchicine and probenecid
M09AX14	givinostat
N02AD51	pentazocine and naloxone
N02AJ22	hydrocodone and paracetamol
N02AJ23	hydrocodone and ibuprofen
N02BA67	magnesium salicylate, combinations excl. psycholeptics
N02CC51	sumatriptan and naproxen
N05CJ03	daridorexant
N06DX04	lecanemab
N07XX19	sodium phenylbutyrate and ursodoxicoltaurine
N07XX21	eplontersen
P02BA03	arpraziquantel
S01AA32	bacitracin
S01AX24	polihexanide
S01BA16	difluprednate
S01CA12	loteprednol and antiinfectives
S01XA31	pegcetacoplan
V03AB54	pralidoxime and atropine



**New ATC 4<sup>th</sup> and 3<sup>rd</sup> levels:**

<b>ATC code</b>	<b>New ATC level name</b>
C05X	OTHER VASOPROTECTIVES
C05XX	Other vasoprotectives
L04AE	Sphingosine 1-phosphate (S1P) receptor modulators
L04AF	Janus-associated kinase (JAK) inhibitors
L04AG	Monoclonal antibodies
L04AH	Mammalian target of rapamycin (mTOR) kinase inhibitors
L04AJ	Complement inhibitors
L04AK	Dihydroorotate dehydrogenase (DHODH) inhibitors
N05CJ	Orexin receptor antagonists

**ATC level alterations:**

<b>Previous ATC code</b>	<b>ATC level name</b>	<b>New ATC code</b>
L04AA02	muromonab-CD3	L04AG01
L04AA10	sirolimus	L04AH01
L04AA13	leflunomide	L04AK01
L04AA18	everolimus	L04AH02
L04AA21	efalizumab	L04AG02
L04AA23	natalizumab	L04AG03
L04AA25	eculizumab	L04AJ01
L04AA26	belimumab	L04AG04
L04AA27	fingolimod	L04AE01
L04AA29	tofacitinib	L04AF01
L04AA31	teriflunomide	L04AK02
L04AA33	vedolizumab	L04AG05
L04AA34	alemtuzumab	L04AG06
L04AA35	beigelomab	L04AG07
L04AA36	ocrelizumab	L04AG08
L04AA37	baricitinib	L04AF02
L04AA38	ozanimod	L04AE02
L04AA39	emapalumab	L04AG09
L04AA42	siponimod	L04AE03
L04AA43	ravulizumab	L04AJ02
L04AA44	upadacitinib	L04AF03
L04AA45	filgotinib	L04AF04

Previous ATC code	ATC level name	New ATC code
L04AA46	itacitinib	L04AF05
L04AA47	inebilizumab	L04AG10
L04AA49	peficitinib	L04AF06
L04AA50	ponesimod	L04AE04
L04AA51	anifrolumab	L04AG11
L04AA52	ofatumumab	L04AG12
L04AA53	teprotumumab	L04AG13
L04AA54	pegcetacoplan	L04AJ03
L04AA55	sutimlimab	L04AJ04
L04AA56	deucravacitinib	L04AF07
L04AA57	ublituximab	L04AG14
L04AA59	avacopan	L04AJ05
N05CM19	suvorexant	N05CJ01
N05CM21	lemborexant	N05CJ02

### ATC level name alterations:

ATC code	Previous ATC level name	New ATC level name
J07BX01	smallpox vaccines	smallpox and monkeypox vaccines

### New DDDs:

ATC code	ATC level name	New DDD	Unit	Adm. route
A10BH08	teneligliptin	20	mg	O
C03DA05	finerenone	20	mg	O
H02CA02	osilodrostat	10	mg	O
J01AA13	eravacycline	0.14	g	P
J01DC52	cefuroxime and beta-lactamase inhibitor	0.5	g	O
J01DI04	cefiderocol	6	g	P
J05AH04	laninamivir	0.16	g	Inhal.solution
J05AX28	bulevirtide	2	mg	P
L01EX21	tepotinib	0.45	g	O
L04AA51	anifrolumab	10.7	mg	P
L04AC19	satralizumab	4.3	mg	P
N02CC08	lasmiditan	0.1	g	O

## ATC/DDD Classification (Final)

The following ATC codes and DDDs were agreed at the meeting of the WHO International Working Group for Drug Statistics Methodology in March 2022.

These are considered as final and will be included in the **January 2023 version of the ATC/DDD Index**.

### New ATC 5th level codes:

New ATC code	Substance name
A03FA10	acotiamide
A10BX16	tirzepatide
A10BX17	carfloglitazar
A10BX18	dorzagliatin
A16AB24	pegzilarginase
A16AB25	olipudase alfa
C02KX54	macitentan and tadalafil
C09BB13	benazepril and amlodipine
C09DX08	telmisartan, amlodipine and hydrochlorothiazide
G01AF21	tinidazole
G02CX06	fezolinetant
A03FA10	acotiamide
A10BX16	tirzepatide
A10BX17	carfloglitazar
A10BX18	dorzagliatin
A16AB24	pegzilarginase
A16AB25	olipudase alfa
C02KX54	macitentan and tadalafil
C09BB13	benazepril and amlodipine
C09DX08	telmisartan, amlodipine and hydrochlorothiazide
G01AF21	tinidazole

New ATC code	Substance name
G02CX06	fezolinetant
G04CB51	finasteride and tadalafil
H01AC09	lonapegsomatropin
H01CC53	elagolix, estradiol and norethisterone
H02CA04	levoketoconazole
J01RA16	cefixime and azithromycin
J02AX08	rezafungin acetate
J04BA50	dapsone and rifampicin
J04BA51	dapsone, rifampicin and clofazimine
J05AB18	molnupiravir
J05AE30	nirmatrelvir and ritonavir
J07BN04	covid-19, protein subunit
J07XA01	malaria vaccines
L01EB11	aumolertinib
L01EG04	sirolimus
L01EX25	umbralisib
L01FX22	loncastuximab tesirine
L01FX23	tisotumab vedotin
L01XL05	ciltacabtagene autoleucel
L01XL06	brexucabtagene autoleucel
L01XL07	idecabtagene vicleucel
L01XX77	adagrasib
L03AA18	efbemalenograstim alfa
L04AA59	avacopan*
L04AC23	olokizumab
N06AX29	brexanolone

New ATC code	Substance name
R02AD05	ambroxol
R06AA61	dimenhydrinate, combinations
S01KX02	trypan blue
S01XA28	varenicline
S01XA29	sepfarsen
V04CX10	pafolacianine
V09AX07	flortaucipir ( <sup>18</sup> F)

\* New ATC 5th level to be included in new ATC 4th level L04AJ *Complement inhibitors* in the Index 2024

### New ATC 4<sup>th</sup> and 3<sup>rd</sup> levels:

ATC code	New ATC level name
J07XA	Parasitic vaccines
L01XL	Antineoplastic cell and gene therapy
N02BF	Gabapentinoids

### ATC level alterations:

Previous ATC code	ATC level name	New ATC code
L01XX37	sitimogene ceradenovec	L01XL01
L01XX51	talimogene laherparepvec	L01XL02
L01XX70	axicabtagene ciloleucel	L01XL03
L01XX71	tisagenlecleucel	L01XL04
N02BG11	mirogabalin	N02BF03
N03AX12	gabapentin	N02BF01
N03AX16	pregabalin	N02BF02

## New DDDs:

ATC code	ATC level name	New DDD	Unit	Adm. route
C10AX15	bempedoic acid	0.18	g	O
D11AH07	tralokinumab	16.1	mg	P
D11AH08	abrocitinib	0.15	g	O
G01AF21	tinidazole	0.2	g	V
J05AB18	molnupiravir	1.6	g	O
J05AE30	nirmatrelvir and ritonavir	0.6	g	O
J06BD05	sotrovimab	0.5	g	P
L04AA45	filgotinib <sup>1</sup>	0.2	g	O
L04AA50	ponesimod <sup>2</sup>	20	mg	O
L04AA59	avacopan <sup>3</sup>	60	mg	O
L04AC21	bimekizumab	5.7	mg	P
L04AX09	diroximel fumarate	0.924	g	O
M05BX05	burosumab	2.5	mg	P
N02CD06	rimegepant	37.5	mg	O
N03AX26	fenfluramine	8	mg	O
N07BC01	buprenorphine	1.6	mg	implant

<sup>1</sup> New ATC 5th level L04AF04 to be included in the new ATC 4th level L04AF *Janus-associated kinase (JAK) inhibitors* in the Index 2024

<sup>2</sup> New ATC 5th level L04AE04 to be included in the new ATC 4th level L04AE *Sphingosine 1-phosphate (S1P) receptor modulators* in the Index 2024

<sup>3</sup> New ATC 5th level L04AJ05 to be included in the new ATC 4th level L04AJ *Complement inhibitors* in the Index 2024

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# International Nonproprietary Names for Pharmaceutical Substances (INN)

Notice is hereby given that, in accordance with article 3 of the Procedure for the Selection of Recommended International Nonproprietary Names for Pharmaceutical Substances, the names given in the list on the following pages are under consideration by the World Health Organization as Proposed International Nonproprietary Names. The inclusion of a name in the lists of Proposed 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). The statements indicating action and use are based largely on information supplied by the manufacturer. **This information is merely meant to provide an indication of the potential use of new substances at the time they are accorded Proposed International Nonproprietary Names.** WHO is not in a position either to uphold these statements or to comment on the efficacy of the action claimed. Because of their provisional nature, these descriptors will neither be revised **nor included in the Cumulative Lists of INNs.**

## Dénominations communes internationales des Substances pharmaceutiques (DCI)

Il est notifié que, conformément aux dispositions de l'article 3 de la Procédure à suivre en vue du choix de Dénominations communes internationales recommandées pour les Substances pharmaceutiques les dénominations ci-dessous sont mises à l'étude par l'Organisation mondiale de la Santé en tant que dénominations communes internationales proposées. L'inclusion d'une dénomination dans les listes de DCI proposées 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). Les mentions indiquant les propriétés et les indications des substances sont fondées sur les renseignements communiqués par le fabricant. **Elles ne visent qu'à donner une idée de l'utilisation potentielle des nouvelles substances au moment où elles sont l'objet de propositions de DCI.** L'OMS n'est pas en mesure de confirmer ces déclarations ni de faire de commentaires sur l'efficacité du mode d'action ainsi décrit. En raison de leur caractère provisoire, ces informations **ne figureront pas dans les listes récapitulatives de DCI.**

## Denominaciones Comunes Internacionales para las Sustancias Farmacéuticas (DCI)

De conformidad con lo que dispone el párrafo 3 del "Procedimiento de Selección de Denominaciones Comunes Internacionales Recomendadas para las Sustancias Farmacéuticas", se comunica por el presente anuncio que las denominaciones detalladas en las páginas siguientes están sometidas a estudio por la Organización Mundial de La Salud como Denominaciones Comunes Internacionales Propuestas. La inclusión de una denominación en las listas de las DCI

Propuestas 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). Las indicaciones sobre acción y uso que aparecen se basan principalmente en la información facilitada por los fabricantes. **Esta información tiene por objeto dar una idea únicamente de las posibilidades de aplicación de las nuevas sustancias a las que se asigna una DCI Propuesta.** La OMS no está facultada para respaldar esas indicaciones ni para formular comentarios sobre la eficacia de la acción que se atribuye al producto. Debido a su carácter provisional, esos datos descriptivos **no deben incluirse en las listas recapitulativas de DCI.**

## Proposed International Nonproprietary Names: List 128

Comments on, or formal objections to, the proposed names may be forwarded by any person to the INN Programme of the World Health Organization within four months of the date of their publication in *WHO Drug Information*, i.e., for **List 128 of Proposed INN not later than 19 May 2023. Publication date:** 20.01.2023

## Dénominations communes internationales proposées: Liste 128

Des observations ou des objections formelles à l'égard des dénominations proposées peuvent être adressées par toute personne au Programme des Dénominations communes internationales de l'Organisation mondiale de la Santé dans un délai de quatre mois à compter de la date de leur publication dans *WHO Drug Information*, c'est à dire pour la **Liste 128 de DCI Proposées le 19 mai 2023 au plus tard. Date de publication :** 20.01.2023

## Denominaciones Comunes Internacionales Propuestas: Lista 128

Cualquier persona puede dirigir observaciones u objeciones respecto de las denominaciones propuestas, al Programa de Comunes Internacionales de la Organización Mundial de la Salud, en un plazo de cuatro meses, contados desde la fecha de su publicación en *WHO Drug Information*, es decir, para **la Lista 128 de DCI Propuestas el 19 de Mayo de 2023 a más tardar.**

**Fecha de publicación:** 20.01.2023

<i>Proposed INN</i> (Latin, English, French, Spanish)	<i>Chemical name or description: Action and use: Molecular formula</i> <i>Chemical Abstracts Service (CAS) registry number:</i> <i>Graphic formula</i>
<i>DCI Proposée</i>	<i>Nom chimique ou description: Propriétés et indications: Formule brute</i> <i>Numéro dans le registre du CAS: Formule développée</i>
<i>DCI Propuesta</i>	<i>Nombre químico o descripción: Acción y uso: Fórmula molecular</i> <i>Número de registro del CAS: Fórmula desarrollada</i>

**acimtamigum #**  
acimtamig

immunoglobulin chain VH-V-kappa-VH'-V-lambda homodimer, anti-[*Homo sapiens* FCGR3A (Fc gamma receptor IIIa, CD16a)] and anti-[*Homo sapiens* TNFRSF8 (TNF receptor superfamily member 8, CD30)], monoclonal antibody *Homo sapiens* and *Mus musculus* VH-V-kappa-VH'-V-lambda chain non covalent head to tail homodimer, bispecific, tetravalent;



- IG chain VH-V-kappa-VH'-V-lambda *Homo sapiens* and *Mus musculus* (1-483) [anti-FCGR3A VH (*Homo sapiens*IGHV1-46\*01 (98.0%) -(IGHD) -IGHJ5\*01 (92.3%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -9-mer tris(bisglycyl-seryl) linker (121-129) -anti-TNFRSF8 V-KAPPA (*Mus musculus*IGKV6-15\*01 (93.7%) -(IGHD) -IGKJ1\*02 (90.0%) K127>N (236), CDR-IMGT [6.3.9] (156-161.179-181.218-226)) (130-236) -9-mer tris(bisglycyl-seryl) linker (237-245) -anti-TNFRSF8 VH' (*Mus musculus*IGHV1-4\*01 (87.8%) -(IGHD) -IGHJ3\*01 (86.7%) L123>T (363), A128>S (368), CDR-IMGT [8.8.16] (271-278.296-303.342-357)) (246-368) -9-mer tris(bisglycyl-seryl) linker (369-377) -anti-FCGR3A V-LAMBDA (*Homo sapiens*IGLV3-9\*01 (83.7%) -(IGHD) -IGLJ2\*01 (91.7%), CDR-IMGT [6.3.9] (403-408.426-428.465-473)) (378-483)]; homodimer head to tail non covalent, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa  
*antineoplastica*
- acimtamig immunoglobuline chaîne VH-V-kappa-VH'-V-lambda homodimère, anti-[*Homo sapiens* FCGR3A (Fc gamma récepteur IIIa, CD16a)] et anti-[*Homo sapiens* TNFRSF8 (membre 8 de la superfamille des récepteurs du TNF, CD30)], anticorps monoclonal chaîne *Homo sapiens* et *Mus musculus* VH-V-kappa-VH'-V-lambda homodimère tête-bêche non covalent, bispécifique, tétravalent;  
IG chaîne VH-V-kappa-VH'-V-lambda *Homo sapiens* and *Mus musculus* (1-483) [anti-FCGR3A VH (*Homo sapiens*IGHV1-46\*01 (98.0%) -(IGHD) -IGHJ5\*01 (92.3%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -9-mer tris(bisglycyl-séryl) linker (121-129) -anti-TNFRSF8 V-KAPPA (*Mus musculus*IGKV6-15\*01 (93.7%) -(IGHD) -IGKJ1\*02 (90.0%) K127>N (236), CDR-IMGT [6.3.9] (156-161.179-181.218-226)) (130-236) -9-mer tris(bisglycyl-séryl) linker (237-245) -anti-TNFRSF8 VH' (*Mus musculus*IGHV1-4\*01 (87.8%) -(IGHD) -IGHJ3\*01 (86.7%) L123>T (363), A128>S (368), CDR-IMGT [8.8.16] (271-278.296-303.342-357)) (246-368) -9-mer tris(bisglycyl-séryl) linker (369-377) -anti-FCGR3A V-LAMBDA (*Homo sapiens*IGLV3-9\*01 (83.7%) -(IGHD) -IGLJ2\*01 (91.7%), CDR-IMGT [6.3.9] (403-408.426-428.465-473)) (378-483)]; homodimère tête-bêche non covalent, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa  
*antineoplasique*
- acimtamig inmunoglobulina VH-V-kappa-VH'-V-lambda homodímero, anti-[*Homo sapiens* FCGR3A (Fc gamma receptor IIIa, CD16a)] y anti-[*Homo sapiens* TNFRSF8 (miembro 8 de la superfamilia de los receptores del TNF, CD30)], anticuerpo monoclonal *Homo sapiens* y *Mus musculus* VH-V-kappa-VH'-V-lambda homodímero de cabeza a cola no covalente, biespecífico, tetraivalente;  
IG cadena VH-V-kappa-VH'-V-lambda *Homo sapiens* and *Mus musculus* (1-483) [anti-FCGR3A VH (*Homo sapiens*IGHV1-46\*01 (98.0%) -(IGHD) -IGHJ5\*01 (92.3%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -9-mer tris(bisglicil-seril) enlace (121-129) -anti-TNFRSF8 V-KAPPA (*Mus musculus*IGKV6-15\*01 (93.7%) -(IGHD) -IGKJ1\*02 (90.0%) K127>N (236), CDR-IMGT [6.3.9] (156-161.179-181.218-226)) (130-236) -9-mer tris(bisglicil-seril) enlace (237-245) -anti-TNFRSF8 VH' (*Mus musculus*IGHV1-4\*01 (87.8%) -(IGHD) -IGHJ3\*01 (86.7%) L123>T (363), A128>S (368), CDR-IMGT [8.8.16] (271-278.296-303.342-357)) (246-368) -9-mer tris(bisglicil-seril) enlace (369-377) -anti-FCGR3A V-LAMBDA (*Homo sapiens*IGLV3-9\*01 (83.7%) -(IGHD) -IGLJ2\*01 (91.7%), CDR-IMGT [6.3.9] (403-408.426-428.465-473)) (378-483)]; homodímero de dabeza a cola no covalente, producido en las células ováricas de hamster chino (CHO), línea celular CHO-DG44, forma glicosilada alfa  
*antineoplásico*

2738880-26-5

Heavy chain / Chaîne lourde / Cadena pesada  
 QVQLVQSGAE VKKPGESLKV SKKASGYTFE SYMHWRQRA PGQGLEWMI 50  
 INPSGGSTSY AQRFLQGRVTM TRDTSTSTVY MELSLRSED TAVYYCARGS 100  
 AYYDFADYD GQGLTLVTVSS GSGGGSGSD IVMTQSPKFM STSVGDRVTV 150  
 TCKASQNVGT NVAWFQKQKPG QSPKVLIIYA SYRYSQVPRD FTGSGSCTDF 200  
 TLTISNVQSE DLAEYFCQQY HTYPLTFGGG TKLEINGGSG GSGGSQVQLQ 250  
 QSGAELARPG ASVKMSCKAS GYTFPTYTIH WVRQRPGHDL EWIGYINPSS 300  
 GYSDYNQNFK GKTTTLTADKS SMTAYMQLNS LTESDSAVYY CARRADYGNV 350  
 EYTWFAIYWGQ GTTIVTVSSG GSGGGSGSYV LTQFSSVSYA PGQTATISCG 400  
 GHNIGSKNVH WYQRFQKQSP VLVIIYQDNKR PSGIPEPFSG SNSGNTATLT 450  
 ISGTQAMDEA DYICQVWDNY SVLFGGGTKL TVL 483

**Post-translational modifications**

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

Intra chain (C23-C104) 22-96 152-217 267-341 399-464  
 22'-96' 152'-217' 267'-341' 399'-464'

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

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxopropililo)  
 VH Q1: 1, 1'

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación:  
 VH Y112.2

350, 350' (12-20% Glycosylated / 12-20% Glycosylé / 12-20% Glicosilado)  
 (Hex1HexNAc1NeuAc1 (<13%), Hex1HexNAc1 (<5%), Hex1HexNAc1NeuAc2 (<3%), HexNAc1 (<0.1%)

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación:  
 V-LAMBDA N109:469, 469' (Not glycosylated / Non glycosylé / No glicosilado)

**adrixetinibum**  
 adrixetinib

*N*-{5-[(6,7-dimethoxyquinolin-4-yl)oxy]pyridin-2-yl}-1-propyl-4-(2,2,2-trifluoroethoxy)-1*H*-pyrazole-3-carboxamide  
*tyrosine kinase inhibitor, antineoplastic*

adrixétinib

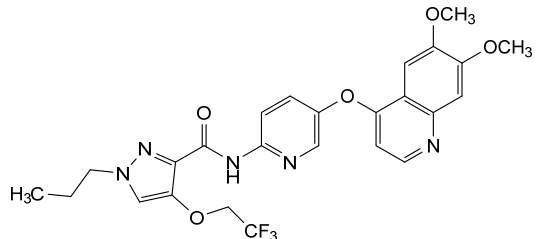
*N*-{5-[(6,7-diméthoxyquinoléin-4-yl)oxy]pyridin-2-yl}-1-propyl-4-(2,2,2-trifluoroéthoxy)-1*H*-pyrazole-3-carboxamide  
*inhibiteur de tyrosine kinase, antinéoplasique*

adrixetinib

*N*-{5-[(6,7-dimetoxiquinolein-4-il)oxi]piridin-2-il}-1-propil-4-(2,2,2-trifluoroetoxi)-1*H*-pirazolo-3-carboxamida  
*inhibidor de tirosina kinasa, antineoplásico*

C<sub>25</sub>H<sub>24</sub>F<sub>3</sub>N<sub>5</sub>O<sub>5</sub>

2394874-66-7



**alemtuzumabum beta #**  
 alemtuzumab beta

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD52 (CD52 antigen, CAMPATH-1 antigen, CDW52)], humanized monoclonal antibody;

	<p>gamma1 heavy chain humanized (1-451) [VH (<i>Homo sapiens</i>IGHV4-30-4*01 (73.5%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.10.12] (26-33.51-60.99-110)) (1-121) -<i>Homo sapiens</i>IGHG1*01 (100%), G1m17,1, CH1 K120, CH3 D12, L14 (CH1 K120 (218) (122-219), hinge 1-15 (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (<i>Homo sapiens</i>IGKV1-33*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -<i>Homo sapiens</i>IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimer (230-230":233-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa <i>immunomodulator, antineoplastic</i></p>
alemtuzumab bêta	<p>immunoglobuline G1-kappa, anti-[<i>Homo sapiens</i> CD52 (antigène CD52, antigène CAMPATH-1, CDW52)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-451) [VH (<i>Homo sapiens</i>IGHV4-30-4*01 (73.5%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.10.12] (26-33.51-60.99-110)) (1-121) -<i>Homo sapiens</i>IGHG1*01 (100%), G1m17,1, CH1 K120, CH3 D12, L14 (CH1 K120 (218) (122-219), charnière 1-15 (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (<i>Homo sapiens</i>IGKV1-33*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -<i>Homo sapiens</i>IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimère (230-230":233-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa <i>immunomodulateur, antinéoplasique</i></p>
alemtuzumab beta	<p>immunoglobulina G1-kappa, anti-[<i>Homo sapiens</i> CD52 (antígeno CD52, antígeno CAMPATH-1, CDW52)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-451) [VH (<i>Homo sapiens</i>IGHV4-30-4*01 (73.5%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.10.12] (26-33.51-60.99-110)) (1-121) -<i>Homo sapiens</i>IGHG1*01 (100%), G1m17,1, CH1 K120, CH3 D12, L14 (CH1 K120 (218) (122-219), bisagra 1-15 (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (<i>Homo sapiens</i>IGKV1-33*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -<i>Homo sapiens</i>IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dímero (230-230":233-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa <i>immunomodulador, antineoplásico</i></p>

2750001-58-0

Heavy chain / Chaîne lourde / Cadena pesada  
 QVQLQESGPG LVRPSQTLSL TCTVSGFTFT DFYMNWVRP PGRGLEWIGF 50  
 IRDKAKGYTT EYNPSVKRVR TMLVDTSKNQ FSLRLSSVTA ADTAVYYCAR 100  
 EGHTAAPFDY WQGQSLVTYS SASTKGRSVF PLAPSSKSTS GGTAALGCLV 150  
 KDYFPEPVTV SWNSGALTSG VHTFFAVLQS SGLYLSLSSVY TVPSSSLGTQ 200  
 TYICNVNHPK SNTKVDKKEE PKSCDKTHTC PPCAPELLG GPSVFLFPFK 250  
 PKDTLMSRPT FEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300  
 NSTYRVVSVL TVLHQDWLNG KEYCKKVSNK ALPAFIEKTI SKAKGQPREP 350  
 QVYTLPPSRD ELTKNQVSLT CLVKGFPYSD IAVWEESNGQ PENNYKTTFP 400  
 VLDSDGGSFFL YSKLTVDKSR WQQGNVFCSS VMHEALHNYH TQKSLSLSPG 450  
 K 451

Light chain / Chaîne légère / Cadena ligera  
 DIQMTQSPSS LSASVGRDRT ITCKASQDID KYLNWYQQKP GKAPKLLIYN 50  
 TNNLQTGVPS RFGSGSGTD FTFTISSLQP EDIATYYCLQ HISRPRTFGQ 100  
 GTKVEIKRTV AAPSVEIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150  
 DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200  
 LSSPEVTKSFN RGEC 214

**Post-translational modifications**  
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro  
 Intra-H (C23-C104) 22"-98" 148"-204" 265"-325" 371"-429"  
 22"-98" 148"-204" 265"-325" 371"-429"  
 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"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutamínilo N-terminal  
 Q<sup>26</sup> pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxoprotyle) / piroglutamilo (pE, 5-oxoprolilo)  
 HVH 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 biantenarijos complejos fucosilados

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

**alintegimodum**  
 alintegimod

[ethane-1,2-diylbis(oxyethane-2,1-diyl)]  
 bis{bis[(thiophen-2-yl)methyl]carbamate}  
*immunomodulator*

alintégimod

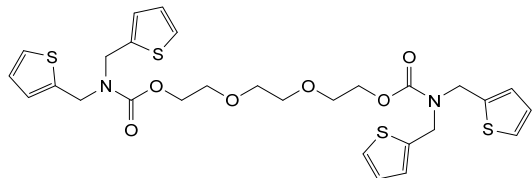
bis{bis[(thiophén-2-yl)méthyl]carbamate} d'[éthane-1,2-  
 diylbis(oxyéthane-2,1-diyle)]  
*immunomodulateur*

alintegimod

bis{bis[(tiofen-2-il)metil]carbamato} de [etano-1,2-  
 diilbis(oxietano-2,1-diilo)]  
*immunomodulador*

C<sub>28</sub>H<sub>32</sub>N<sub>2</sub>O<sub>6</sub>S<sub>4</sub>

1378535-08-0



**anitocabtagem autoleucelum #**  
 anitocabtagene autoleucel

autologous T lymphocytes obtained from peripheral blood mononuclear cells by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector encoding a chimeric antigen receptor (CAR)

comprising a three-helix bundle D domain polypeptide (DDpp) targeting human B-cell maturation antigen (BCMA). The expressed transgene comprises a chymotrypsinogen B leader sequence, the anti-BCMA binding domain, a CD8 $\alpha$  hinge and transmembrane domain, and a 4-1BB (CD137) and CD3 $\zeta$  signalling domain, under control of the elongation factor 1 alpha (EF1 $\alpha$ ) promoter. The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a  $\psi$  packaging signal, a central polypurine tract (cPPT) sequence and a Woodchuck hepatitis virus posttranscriptional regulatory element (WPRE). The vector is pseudotyped with vesicular stomatitis virus (VSV) G glycoprotein. The leukapheresis material is enriched for CD4+ and CD8+ T lymphocytes by positive immunoselection. The cells are then activated by CD3 and CD28 agonists and transduced with the lentiviral vector. The cells are further culture expanded in growth media containing interleukin 2 (IL-2) and human AB serum. The cell suspension consists of T lymphocytes (>83%), with greater than 10% of the T lymphocytes expressing the CAR-BCMA transgene. The transduced T lymphocytes demonstrate cytotoxicity against BCMA-expressing cells and secrete interferon gamma (IFN- $\gamma$ ) and IL-2

*cell-based gene therapy (antineoplastic)*

anitocabtagène autoleucel

lymphocytes T autologues obtenus à partir de cellules mononucléaires de sang périphérique par leucaphérèse, transduits avec un vecteur lentiviral auto-inactivant et non répliquant codant un récepteur antigénique chimérique (CAR) comprenant un polypeptide à domaine D regroupant trois hélices (DDpp) ciblant l'antigène de maturation des cellules B humaines (BCMA). Le transgène exprimé comprend une séquence de tête de chymotrypsinogène B, le domaine de liaison anti-BCMA, un domaine charnière et transmembranaire CD8 $\alpha$ , et un domaine de signalisation 4-1BB (CD137) et CD3 $\zeta$ , sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF1 $\alpha$ ). La construction est flanquée de répétitions longues terminales (LTR) en 5' et 3' et contient également un signal d'encapsulation  $\psi$ , une séquence de tractus polypurine central (cPPT) et un élément régulateur post-transcriptionnel (WPRE) du virus de l'hépatite de Woodchuck. Le vecteur est pseudotypé avec la glycoprotéine G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est enrichi en lymphocytes T CD4+ et CD8+ par immunosélection positive. Les cellules sont ensuite activées par des agonistes CD3 et CD28 et transduites avec le vecteur lentiviral. Les cellules sont ensuite mises en culture dans un milieu de croissance contenant de l'interleukine 2 (IL-2) et du sérum AB humain. La suspension cellulaire est composée de lymphocytes T (>83%), avec plus de 10% des lymphocytes T exprimant le transgène CAR-BCMA. Les lymphocytes T transduits font preuve de cytotoxicité contre les cellules exprimant le BCMA et sécrètent de l'interféron gamma (IFN- $\gamma$ ) et IL-2

*thérapie génique à base de cellules (antineoplasique)*

aniticabtagén autoleucel

linfocitos T autólogos obtenidos de células mononucleares de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica para un receptor de antígenos quimérico (CAR) que contiene el dominio D de un polipéptido con un paquete de tres hélices (DDpp) dirigido al antígeno de maduración de células B (BCMA) humano. El transgén expresado contiene una secuencia líder de quimotripsinógeno B, el dominio de unión anti-BCMA, un dominio bisagra y transmembrana de CD8 $\alpha$ , y un dominio de señalización 4-1BB (CD137) y CD3 $\zeta$ , bajo el control del promotor del factor de elongación 1 alfa (EF1 $\alpha$ ). El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento  $\psi$ , una secuencia de tracto de polipurina central (cPPT) y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE). El vector está seudotipado con la glicoproteína G del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se enriquece para linfocitos T CD4+ y CD8+ mediante inmunoselección positiva. Las células se activan después mediante agonistas de CD3 y CD28 y se transducen con el vector lentiviral. Las células se expanden más en cultivo con medio de crecimiento que contiene interleuquina 2 (IL-2) y suero AB humano. La suspensión celular consiste en linfocitos T (>83%) con más del 10% de los linfocitos T que expresan el transgén del CAR-BCMA. Los linfocitos T transducidos demuestran citotoxicidad frente a células que expresan BCMA y secretan interferon gamma (IFN- $\gamma$ ) e IL-2 *terapia génica basada en células (antineoplásico)*

**anpocoginum #**  
anpocogin

*Ancylostoma canium* nematode anticoagulant protein c2, variant (C-terminal P<sup>85</sup> added), produced in *Pichia pastoris*  
*anticoagulant*

anpocogine

protéine anticoagulante c2 du nématode *Ancylostoma canium*, variante (ajout de P<sup>85</sup> en C-terminal), produite chez *Pichia pastoris*  
*anticoagulant*

anpocogina

*Ancylostoma canium* proteína c2 anticoagulante de nematodo, variante (C-terminal P<sup>85</sup> añadida), producida por *Pichia pastoris*  
*anticoagulante*

2725767-44-0

Sequence / Séquence / Secuencia  
KATMQCGENE KYDSCGSKEC DKKCKYDGV EEDDEEFPNP CLVRVCHQDC 50  
VCEEGFYRNK DDKCVSAEDC ELDNMDFIYP GTRN**P** 85

Mutation / Mutation / Mutación  
**P85** >added

**Post-translational modifications**  
Disulfide bridge locations / Position des ponts disulfure / Posiciones de los puentes disulfuro  
6-50, 15-46, 20-41, 24-70, 52-64

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

**avibactam tomilopilum**

avibactam tomilopil

ethyl 3-[[[[(1*R*,2*S*,5*R*)-2-carbamoyl-7-oxo-1,6-diazabicyclo[3.2.1]octan-6-yl]oxy]sulfonyl]oxy]-2,2-dimethylpropanoate  
*beta-lactamase inhibitor*

avibactam tomilopil

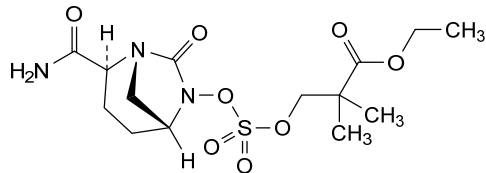
3-[[[[(1*R*,2*S*,5*R*)-2-carbamoyl-7-oxo-1,6-diazabicyclo[3.2.1]octan-6-yl]oxy]sulfonyl]oxy]-2,2-diméthylpropanoate d'éthyle  
*inhibiteur de bêta-lactamase*

avibactam tomilopil

3-[[[[(1*R*,2*S*,5*R*)-2-carbamoiil-7-oxo-1,6-diazabicio[3.2.1]octan-6-il]oxi]sulfonyl]oxi]-2,2-dimetilpropanoato de etilo  
*inhibidor de beta lactamasa*

C<sub>14</sub>H<sub>23</sub>N<sub>3</sub>O<sub>8</sub>S

2245880-46-8

**basiliximabum sarotalocanum #**

basiliximab sarotalocan

immunoglobulin G1-kappa, anti-[*Homo sapiens* IL2RA (interleukin 2 receptor subunit alpha; IL-2RA, TAC, p55, CD25)], chimeric monoclonal antibody conjugated to IRDye 700DX (IR700) near-infrared photosensitizing dye;

gamma1 heavy chain chimeric (1-447) [VH (*Mus musculus* IGHV1-5\*01 (92.9%) -(IGHD) -IGHJ2\*01 (93.3%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1\*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (214) (118-215), hinge 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-211')-disulfide with kappa light chain chimeric (1'-211') [V-KAPPA (*Mus musculus* IGKV4-70\*01 (98.9%) -IGKJ1\*01 (100%), CDR-IMGT [11.3.10] (27-31.49-51.88-94)) (1'-104') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (150), V101 (188) (105'-211')]; dimer (226-226":229-229")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa; conjugated on an average of 2 or 3 lysyl to photosensitizing dye IRDye 700DX  
*antineoplastic*

basiliximab sarotalocan

immunoglobuline G1-kappa, anti-[*Homo sapiens* IL2RA (sous-unité alpha du récepteur de l'interleukine 2; IL-2RA, TAC, p55, CD25)]; anticorps monoclonal chimérique; conjugué au photosensibilisateur proche de l'infrarouge IRDye 700DX (IR700); chaîne lourde gamma1 chimérique (1-447) [VH (*Mus musculus* IGHV1-5\*01 (92.9%) -(IGHD) - IGHJ2\*01 (93.3%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1\*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (214) (118-215), charnière 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-211')-disulfure avec la chaîne légère kappa chimérique (1'-211') [V-KAPPA (*Mus musculus* IGKV2-24\*01 (90.0%) -IGKJ2\*01 (100%), CDR-IMGT [11.3.10] (27-37.55-57.94-103)) (1'-113') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (150), V101 (188) (105'-211')]; dimère (226-226":229-229")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa; conjugué sur 2 ou 3 lysyl en moyenne au photosensibilisateur IRDye 700DX  
*antineoplasique*

basiliximab sarotalocán

immunoglobulina G1-kappa, anti-[*Homo sapiens* IL2RA (subunidad alfa del receptor de la interleukina 2; IL-2RA, TAC, p55, CD25)]; anticuerpo monoclonal quimérico; conjugado con fotosensibilizante de infrarrojo cercano IRDye 700DX (IR700); cadena pesada gamma1 quimérica (1-447) [VH (*Mus musculus* IGHV1-5\*01 (92.9%) -(IGHD) - IGHJ2\*01 (93.3%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1\*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (214) (118-215), bisagra 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-211')-disulfuro con la cadena ligera kappa quimérica (1'-211') [V-KAPPA (*Mus musculus* IGKV2-24\*01 (90.0%) -IGKJ2\*01 (100%), CDR-IMGT [11.3.10] (27-37.55-57.94-103)) (1'-113') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (150), V101 (188) (105'-211')]; dímero (226-226":229-229")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa; conjugada en 2 o 3 restos lisil por término medio con fotosensibilizante IRDye 700DX  
*antineoplásico*



## Heavy chain / Chaîne lourde / Cadena pesada

EVQLQQSGTV LARFGASVKM SCKASGYSFT RYWMHWIKQR PGQGLEWIGA 50  
 IYFNGSDTSY NQKFEKGAKL TAVTSASTAY MELSSLTHED SAVYICSRDY 100  
 GYFDWFQGG TLLTVSSAST KGPSVFLPAP SSKSTSGGTA ALGCLVKDYF 150  
 PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200  
 NVNHKPSNTK VDKRVEPKSC DKHTCPFCF APELLGGPSV FLFPPKPKDT 250  
 LMISRTPEVT CVVVVDSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300  
 RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTSKAK GQPREPQVYT 350  
 LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTFPVLDS 400  
 DGSFFLYSKL TVDKSRWQQG NVFSCSVMEH ALHNHYTQKS LSLSPGK 447

## Light chain / Chaîne légère / Cadena ligera

QIVLTQSPAI MSASPGKVT MTCASASSIS YMOWYQQKPG TSPKRWIYDT 50  
 SKLASGVPAR FSGSGSGTYS LTITSSMEA EDAATYCHQR SSYTFGGGTK 100  
 LEIKRTVAAP SVFIFFPSDE QLKSGTASVV CLLNFFYPRE AKVQWKVDNA 150  
 LQSGNSQESV TEQDSKDSY SLSTLTLSK ADYERKHKVYA CEVTHQGLSS 200  
 PVTKSNRGE C 211

## Post-translational modifications

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

Intra-H (C23-C104) 22-96 144-200 261-321 367-425  
 22<sup>o</sup>-96<sup>o</sup> 144<sup>o</sup>-200<sup>o</sup> 261<sup>o</sup>-321<sup>o</sup> 367<sup>o</sup>-425<sup>o</sup>

Intra-L (C23-C104) 23<sup>o</sup>-87<sup>o</sup> 131<sup>o</sup>-191<sup>o</sup>  
 23<sup>o</sup>-87<sup>o</sup> 131<sup>o</sup>-191<sup>o</sup>

Inter-H-L (h 5-CL 126) 220-211<sup>o</sup> 220<sup>o</sup>-211<sup>o</sup>

Inter-H-H (h 11, h 14) 226-226<sup>o</sup> 229-229<sup>o</sup>

N-terminal glutaminylation / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxopropililo)

L VL Q1: 1, 1<sup>o</sup>

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

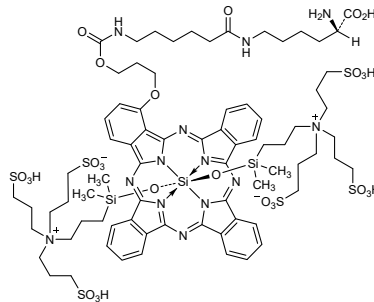
H CH2 N84.4: 297, 297<sup>o</sup>

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

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

H CHS K2: 447, 447<sup>o</sup>

Potential modified residues / résidus modifiés potentiels / restos modificados potenciales



**benmelstobartum #**  
 benmelstobart

immunoglobulin G1-kappa, anti-*Homo sapiens* CD274 (programmed cell death 1 ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1, B7-H1, PDCD1LG1)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-446) [VH (*Homo sapiens* IGHV2-5\*01 (78.6%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.7.10] (26-33.51-57.96-105))] (1-116) -*Homo sapiens* IGHG1\*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v66 CH2 A27 (CH1 K120 (213) (117-214), hinge 1-15 (215-229), CH2 D27>A (264) (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33\*01 (82.1%) -IGKJ2\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimer (225-225''-228-228'')-bisdisulfide

*immunostimulant, antineoplastic*

benmelstobart immunoglobuline G1-kappa, anti-[*Homo sapiens* CD274 (ligand 1 de mort cellulaire programmée 1, PDL1, PD-L1, B7 homologue 1, B7H1, B7-H1, PDCD1LG1)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-446) [VH (*Homo sapiens* IGHV2-5\*01 (78.6%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.7.10] (26-33.51-57.96-105)) (1-116) -*Homo sapiens* IGHG1\*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v66 CH2 A27 (CH1 K120 (213) (117-214), charnière 1-15 (215-229), CH2 D27>A (264) (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33\*01 (82.1%) -IGKJ2\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimère (225-225''-228-228'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO)-S, glycoforme alfa *immunostimulant, antinéoplasique*

benmelstobart inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD274 (ligando 1 de muerte celular programada 1, PDL1, PD-L1, B7 homólogo 1, B7H1, B7-H1, PDCD1LG1)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-446) [VH (*Homo sapiens* IGHV2-5\*01 (78.6%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.7.10] (26-33.51-57.96-105)) (1-116) -*Homo sapiens* IGHG1\*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v66 CH2 A27 (CH1 K120 (213) (117-214), bisagra 1-15 (215-229), CH2 D27>A (264) (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33\*01 (82.1%) -IGKJ2\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dímero (225-225''-228-228'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO)-S, forma glicosilada alfa *inmunoestimulante, antineoplásico*

2303884-58-2

## Heavy chain / Chaîne lourde / Cadena pesada

QITLKESGPT LVKPTQTLLT TCTVSGFSLT TYGVHWIRQP PGKALEWLGV 50  
IWRGVTTDYN AAFMSRLTIT KDNSKNQWVL TMNNMDPVDI ATYYCARLGF 100  
YAMDYWGQGT LVTYSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150  
EPVTVSNWNG ALTSVGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200  
VNHKPSNTRV DKKVEPKSCD KTHTCPPCPA PELLGGPSVF LFPKPKDTL 250  
MISRTPEVTC VVVAVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300  
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTIKAKG QPREPQVYTL 350  
PFSRDELTKN QVSLTCLVYG FYPSDIAVEW ESNQGPENNY KTFPPVLDS 400  
GSFFLYSKLT VDKSRWQQGN VFSCSVMEHA LHNHYTQKSL SLSPGK 446

## Light chain / Chaîne légère / Cadena ligera

DIQMTQSPFS LSAAGVDRVT ITCKASQSVS NDVAWYQQKP GKAPKLLIYY 50  
AANRYTGVDP RFGSGGYGTD FTFITISLQP EDIATYFCQQ DYTSPTYTFGQ 100  
GTKLEIKRTP AAPSVEFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150  
DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200  
LSSPVTKSN RGE 214

## Post-translational modifications

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

Intra-H (C23-C104) 22-95 143-199 260-320 366-424  
22"-95" 143"-199" 260"-320" 366"-424"  
Intra-L (C23-C104) 23'-88' 134'-194'  
23'''-88''' 134'''-194'''

Inter-H-L (h 5-CL 126) 219-214' 219"-214''

Inter-H-H (h 11, h 14) 225-225'' 228-228''

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

glutamínilo N-terminal

Q &gt; pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo

(pE, 5-oxoprolilo)

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 biantennarios complejos fucosilados

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

H CHS K2: 446, 446"

**berahyaluronidasum alfa #**  
berahyaluronidase alfa

human hyaluronidase isozyme-5 (HYAL5, sperm adhesion molecule 1, SPAM1, hyaluronidase PH-20, EC:3.2.1.35) fragment (3-433, 1-431 in the current sequence) engineered variant with the structural domain replaced by the corresponding region of human hyaluronidase isozyme-1 (HYAL1) (<sup>306</sup>TLSIMRSMKSCLLDDNYMET<sup>322</sup>><sup>304</sup>SWENTRTKESCQAIKEYMDTT<sup>324</sup>), produced in Chinese hamster ovary (CHO) cells, cell line DG44, glycoform alfa  
*hyaluronidase analogue*

bérahyaluronidase alfa

variant modifié d'un fragment (3-433, 1-431 dans la séquence actuelle) de l'isozyme-5 de la hyaluronidase humaine (HYAL5, molécule d'adhésion des spermatozoïdes 1, SPAM1, hyaluronidase PH-20, EC:3.2.1.35) dont le domaine structural a été remplacé par la région correspondante de l'isozyme-1 de la hyaluronidase humaine (HYAL1) (<sup>306</sup>TLSIMRSMKSCLLDDNYMET<sup>322</sup>><sup>304</sup>SWENTRTKESCQAIKEYMDTT<sup>324</sup>), produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire DG44, glycoforme alfa  
*analogue de la hyaluronidase*

berahialuronidasa alfa

hialuronidasa humana isoenzima-5 (HYAL5, molécula de adhesión de esperma 1, SPAM1, hialuronidasa PH-20, EC:3.2.1.35) fragmento (3-433, 1-431 en la secuencia actual) variante diseñada con el dominio estructural reemplazado por la región correspondiente a la hialuronidasa humana isoenzima-1 (HYAL1) (<sup>306</sup>TLSIMRSMKSCLLDDNYMET<sup>322</sup>><sup>304</sup>SWENTRTKESCQAIKEYMDTT<sup>324</sup>), producida en células ováricas de hámster Chino (CHO), línea celular DG44, forma glicosilada alfa  
*análogo de la hialuronidasa*

2636716-20-4

Sequence / Séquence / Secuencia

FRAP FVIENV PFLWAWNAPS EFCLGKFDEP LDMSLFVFIG SPRINATGGG	50
VTIFYVDRLG YYPYIDSITG VTVNGGIPQK ISLQDHLDKA KKDITFYMPV	100
DNLGMAVIDW EWRRTWARN WPKPDVYKWR SIELVQQQNV QLSLTEATEK	150
AKQEFERAGK DFLVETIKLG KLLRPNHLWG YLFPDCYNH HYKKPGYNGS	200
CFNVEIKRND DLSWLWNEST ALYPSIYLNT QQSPVAATLY VRNRVREAIR	250
VSKIPDAKSP LÉVFAYTRIV FTDQVLKFLS QDELVYTFGE TVALGASGIV	300
IWGSWENTRT KESCQAIKEY MDTTLNPIYII NVTLAARKMS QVLCQEQGVC	350
IRKNWNSDY LHLNPDNFAI QLEKRGKFTV RGRFTLEDELF QFSEKFCYSC	400
YSTLSCKEKA DVKDTDAVDV CIADGVVIDA F	431

**Post-translational modifications**

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro  
23-314, 187-201, 339-350, 344-398, 400-406, 421-427

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación

N45, N129, N198, N217, N331, N356 (3 to 6 glycans per N-glycosylation site)

Deamidation sites / Sites de désamidation / Posiciones de desamidación

N74, Q84, N120, N139, N189, Q391 (for residues Q341/Q345/Q347 and N354/N364/N367 the specific deamidation site could not be determined due to close proximity among these residues)

**besvatresgenum autoleucelum #**

besvatresgene autoleucel

autologous T lymphocytes obtained from peripheral blood lymphocytes by leukapheresis transduced with a self-inactivating, non-replicating lentiviral vector encoding an affinity-enhanced cancer testis antigen (NY-ESO-1<sup>c259</sup>) specific T-cell receptor (TCR) and co-expressing the CD8 $\alpha$  chain of the CD8 co-receptor. The TCR is based on *letetresgene autoleucel* and specifically recognises a peptide (SLLMWITQC), which is shared by the cancer antigens NY-ESO-1 (CTAG1B) and LAGE-1a (CTAG2) presented on human leukocyte antigen HLA-A\*02. The expressed transgene comprises CD8 $\alpha$  joined by the foot-and-mouth disease virus ribosome skipping sequence (F2A) to the TCR $\alpha$  chain, joined by the porcine teschovirus-1 ribosome skipping sequence (P2A) to the TCR  $\beta$  chain and is under control of the elongation factor 1 alpha (EF1 $\alpha$ ) promoter. The construct is flanked by long terminal repeats (LTR) that have a deletion in the U3 part of the LTR, and also contains a  $\psi$  packaging signal, Rev response element (RRE), central polypurine tract (cPPT) and a central termination sequence (CTS). The vector is pseudotyped with vesicular stomatitis virus (VSV) G glycoprotein. The leukapheresis material is enriched for CD4/CD8 T lymphocytes by positive immunoselection, activated by CD3 and CD28 agonists and transduced with the lentiviral vector. The cells are then expanded initially in media supplemented with AB serum and interleukin 2 (IL-2), and then in media supplemented with only IL-2. The T lymphocytes ( $\geq 95\%$ ) are positive for the transgene ( $\geq 10\%$  CAR positive), and are cytotoxic to T2 cells loaded with the target peptide *cell-based gene therapy (antineoplastic)*

besvatresgène autoleucel

lymphocytes T autologues obtenus à partir de lymphocytes de sang périphérique par leucaphérèse, transduits avec un vecteur lentiviral auto-inactivant et non répliquant codant un récepteur de cellules T (TCR) spécifique d'un antigène du cancer du testicule à affinité renforcée (NY-ESO-1<sup>c259</sup>) et co-exprimant la chaîne CD8 $\alpha$  du corécepteur CD8. Le TCR est basé sur le *lététresgène autoleucel* et reconnaît spécifiquement un peptide (SLLMWITQC), qui est partagé par les antigènes de cancer NY-ESO-1 (CTAG1B) et LAGE-1a (CTAG2) présentés sur l'antigène de leucocyte humain HLA-A\*02. Le transgène exprimé comprend le CD8 $\alpha$  lié par la séquence de saut (skipping) du ribosome du virus de la fièvre aphteuse (F2A) à la chaîne TCR $\alpha$ , lié par la séquence de saut (skipping) du ribosome du teschovirus-1 porcin (P2A) à la chaîne TCR  $\beta$  et est sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF1 $\alpha$ ). La construction est flanquée de longues répétitions terminales (LTR) qui présentent une délétion dans la partie U3 de la LTR, et contient également un signal d'encapsulation  $\psi$ , un élément de réponse Rev (RRE), un tractus polypurine central (cPPT) et une séquence de terminaison centrale (CTS). Le vecteur est pseudotypé avec la glycoprotéine G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est enrichi en lymphocytes T CD4/CD8 par immunosélection positive, activé par des agonistes CD3 et CD28 et transduit avec le vecteur lentiviral. Les cellules sont ensuite développées dans un premier temps dans un milieu complété par du sérum AB et de l'interleukine 2 (IL-2), puis dans un milieu complété uniquement par de l'IL-2. Les lymphocytes T ( $\geq 95\%$ ) sont positifs pour le transgène ( $\geq 10\%$  CAR positif), et sont cytotoxiques pour les cellules T2 chargées avec le peptide cible *thérapie génique à base de cellules (antineoplasique)*

## besvatresgén autoleucel

linfocitos T autólogos obtenidos de linfocitos de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica para un receptor de linfocitos T (TCR) con afinidad aumentada, específico del antígeno de cáncer de testículo (NY-ESO-1<sup>c259</sup>) y que coexpresa la cadena CD8α del correceptor CD8. El TCR está basado en *letetresgén autoleucel* y reconoce específicamente un péptido (SLLMWITQC), compartido por los antígenos de cáncer NY-ESO-1 (CTAG1B) y LAGE-1a (CTAG2), presentado en el antígeno común leucocitario HLA-A\*02. El transgén expresado contiene CD8α unido, mediante la secuencia de salto ribosómico del virus de la fiebre aftosa (F2A), a la cadena TCRA, unida, mediante la secuencia de salto ribosómico del teschovirus 1 porcino (P2A), a la cadena TCRb y está bajo el control del promotor del factor de elongación 1 alfa (EF1α). El constructo está flanqueado por repeticiones terminales largas (LTR) que tienen una deleción en la parte U3 del LTR, y también contiene una señal de empaquetamiento ψ, un elemento de respuesta Rev (RRE), una secuencia de tracto de polipurina central (cPPT) y una secuencia de terminación central (CTS). El vector está pseudotipado con la glicoproteína G del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se enriquece para linfocitos T CD4/CD8 mediante inmunoselección positiva, se activa mediante agonistas de CD3 y CD28 y se transduce con el vector lentiviral. Las células son después expandidas inicialmente en medio suplementado con suero AB e interleuquina 2 (IL-2), y después en medio suplementado sólo con IL-2. Los linfocitos T (≥95%) son positivos para el transgén (≥10% positivos para el CAR) y son citotóxicos frente a células T2 cargadas con el péptido diana

*terapia génica basada en células (antineoplásico)*

## bevacizumabum gamma #

## bevacizumab gamma

immunoglobulin G1-kappa, anti-[*Homo sapiens* VEGFA (vascular endothelial growth factor A, VEGF-A, VEGF)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-453) [VH (*Homo sapiens*IGHV3-30\*02 (76.8%) -(IGHD) -IGHJ4\*01 (93.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112))] (1-123) -*Homo sapiens*IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (220) (124-221), hinge 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-16\*01 (88.4%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97))] (1'-107') -*Homo sapiens*IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214'); dimer (232-232":235-235")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa *angiogenesis inhibitor*

bévacizumab gamma immunoglobuline G1-kappa, anti-[*Homo sapiens* VEGF (facteur de croissance A de l'endothélium vasculaire, VEGF-A, VEGF)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-453) [VH (*Homo sapiens* IGHV3-30\*02 (76.8%) -(IGHD) - IGHJ4\*01 (93.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (220) (124-221), charnière 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16\*01 (88.4%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01(100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimère (232-232":235-235")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa *inhibiteur de l'angiogénèse*

bevacizumab gamma inmunoglobulina G1-kappa, anti-[*Homo sapiens* VEGF (factor de crecimiento A del endotelio vascular, VEGF-A, VEGF)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-453) [VH (*Homo sapiens* IGHV3-30\*02 (76.8%) -(IGHD) - IGHJ4\*01 (93.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (220) (124-221), bisagra 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfuro con la cadena ligera humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16\*01 (88.4%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01(100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dímero (232-232":235-235")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa *inhibidor de la angiogénesis*

216974-75-3

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG	LVQPGGSLRL	SCAASGYTFT	NYGMNWRVRA	PGKGLEWVWG	50
INTYTGPEPT	AADFKRRRFT	SLDTSKSTAY	LQMNLSRAED	TAVYYCAKYP	100
HYGGSSHWYF	DVWGQGLTIV	VSSASTKGPS	VFFLAPFSKSS	TSGGTAALGG	150
LVKDYFFPEPV	TWVSNMGALT	SGVHTFFPAVL	QSSGLYSLSS	VVTVPFSSSLG	200
TQTYICNVNHW	KFSNTKVDKK	VEPKSCDKTH	TCFPCPAPEL	LGGPSVFLFF	250
PKPKDTLMIS	RTPEVTCVVV	DVSHEDPEVK	FNWYVDGVEV	HNARTRKPRE	300
QYNSTYRVVS	VLTVLHQDWL	NGKEYKCKVS	NKALPAPIEK	TISKARGQPR	350
EPQVYTLPPS	REEMTKNQVS	LTCLVKGFPY	SDIAVEWESN	GQPENNYKTR	400
PFVLDSDSGF	FLYSKLTVDK	SRWQQGNVFS	CSVMHEALHN	HYTKQKSLSL	450
PGK					453

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPFS	LSASVGDRTV	ITCSASQDIS	NYLNWYQQPK	GKAPKVLIIYF	50
TSLSLHSGVPS	RFGSGSGSDT	FTLTISLSLP	EDFATYYCQQ	YSTVPWFTEG	100
GTKVEIKRTV	AAPSVFIFFP	SDEQLKSGTA	SVVCLLNIFY	PREAKVQHWV	150
DNALQSGNSQ	ESVTEQDSKD	STYLSLSLTL	LSKADYKHKH	VYACEVTHQG	200
LSSPVTKSFN	RGEC				214

**Post-translational modifications**

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

Intra-H (C23-C104) 22"-96" 150"-206" 267"-327" 373"-431"  
 22"-96" 150"-206" 267"-327" 373"-431"

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

Inter-H-L (h 5-CL 126) 226-214' 226"-214"

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

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

H CH2 N84.4: 303, 303"

Fucosylated (sum of G0F, G1F, G2F &gt;14%) and afucosylated (sum of G0, G1, G2 &gt;5%)

complex bi-antennary CHO-type glycans without sialylation / glycanes fucosylés (somme

de G0F, G1F, G2F &gt;14%) et afucosylés (somme de G0, G1, G2 &gt;5%) de type CHO bi-antennaires

complexes sans sialylation / glicanos fucosilados (suma de G0F, G1F, G2F &gt;14%) y afucosilados

(suma de G0, G1, G2 &gt;5%) de tipo CHO biantennarios complejos sin sialilación

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

H CHS K2: 453, 453"

**bevonescinum**

bevonescin

*N*<sup>2</sup>-(3',6'-dihydroxy-3-oxo-3*H*-spiro[[2]benzofuran-1,9'-xanthene]-5-carbonyl)-L-glutamyl-L-valyl-L-prolyl-L-tryptophyl-L-α-glutamyl-L-α-glutamyl-L-prolyl-L-tyrosyl-L-tyrosyl-L-valyl-L-valyl-L-lysyl-L-lysyl-L-seryl-L-serylglycylglycinamide  
*diagnostic imaging agent*

bévonescéine

*N*<sup>2</sup>-(3',6'-dihydroxy-3-oxo-3*H*-spiro[[2]benzofuran-1,9'-xanthène]-5-carbonyl)-L-glutamyl-L-valyl-L-prolyl-L-tryptophyl-L-α-glutamyl-L-α-glutamyl-L-prolyl-L-tyrosyl-L-tyrosyl-L-valyl-L-valyl-L-lysyl-L-lysyl-L-séryl-L-sérylglycylglycinamide  
*agent diagnostique*

bevonescéina

*N*<sup>2</sup>-(3',6'-dihidroxi-3-oxo-3*H*-spiro[[2]benzofuran-1,9'-xanteno]-5-carbonil)-L-glutamínil-L-valil-L-prolil-L-triptofil-L-α-glutamil-L-α-glutamil-L-prolil-L-tirosil-L-tirosil-L-valil-L-valil-L-lisil-L-lisil-L-seril-L-serilglicilglicinamida  
*agente de diagnóstico*

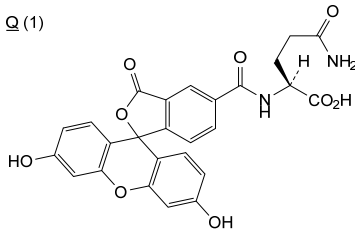
C<sub>112</sub>H<sub>144</sub>N<sub>22</sub>O<sub>32</sub>

2276787-79-0

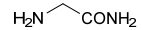
QVPWEEPYV VKKSSGG 17

Modified residues / Résidus modifiés / Restos modificados

Q (1)



G (17)



**bidoleucelum**

bidoleucel

allogeneic invariant natural killer T cells (iNKT), isolated from peripheral blood leukapheresis of HLA-A2 positive donors. The iNKT cells are enriched using antibody-specific positive selection, and expanded through a two-step stimulation procedure, initially by co-culture with irradiated peripheral blood mononuclear cells (PBMCs) derived from the same donor and alpha-galactosylceramide (αGalCer), and then by co-culture with αGalCer-pulsed irradiated PBMCs, each in media containing human AB serum and interleukin 2 (IL-2). The final cell substance is >99% iNKTs (CD3 and invariant T cell receptor α chain positive) and are in an activated state (CD25 and CD69 positive). The cells can induce dose-dependent target cell killing of glycolipid-presenting tumour cell lines  
*cell therapy (immunomodulator)*

bidoleucel

cellules T tueuses naturelles invariantes allogéniques (iNKT), isolées à partir de la leucaphérèse de sang périphérique de donneurs HLA-A2 positifs. Les cellules

iNKT sont enrichies à l'aide d'une sélection positive spécifique à un anticorps, et amplifiées par une procédure de stimulation en deux étapes, d'abord par co-culture avec des cellules mononucléaires irradiées du sang périphérique (PBMC) provenant du même donneur et de l'alpha-galactosylcéramide ( $\alpha$ GalCer), puis par co-culture avec des PBMC irradiées pulsées par  $\alpha$ GalCer, chacune dans un milieu contenant du sérum AB humain et de l'interleukine 2 (IL-2). La substance cellulaire finale est composée à >99% de iNKTs (CD3 et chaîne  $\alpha$  invariante du récepteur des cellules T) et sont dans un état activé (CD25 et CD69 positifs). Les cellules peuvent induire une destruction dose-dépendante des cellules cibles des lignées de cellules tumorales présentant des glycolipides  
*thérapie cellulaire (immunomodulateur)*

bidoleucel

células T natural killer invariantes (iNKT) alogénicas, aisladas de leucoaféresis de sangre periférica de donantes HLA-A2 positivos. Las células iNKT se enriquecen usando selección positiva específica de anticuerpo y se expanden a través de un procedimiento de estimulación en dos pasos, inicialmente por cocultivo con células mononucleares de sangre periférica (PBMCs) irradiadas derivadas del mismo donante y galactosilceramide alfa ( $\alpha$ GalCer), y después mediante cocultivo con PBMCs irradiadas pulsadas con  $\alpha$ GalCer, ambos en medio que contiene suero AB e interleuquina 2 (IL-2). La substancia celular final es >99% iNKTs (CD3 y cadena invariante  $\alpha$  del receptor de linfocitos T) y están en un estado activado (positivas para CD25 y CD69). Las células pueden inducir, de forma dependiente de dosis, la muerte de líneas celulares tumorales que presentan glicolípidos  
*terapia celular (inmunomodulador)*

**boditrectinibum**

boditrectinib

(2E)-3-{5-[(2R)-2-(2,5-difluorophenyl)pyrrolidin-1-yl]pyrazolo[1,5-a]pyrimidin-3-yl}-1-(piperazin-1-yl)prop-2-en-1-one  
*tyrosine kinase inhibitor, antineoplastic*

boditrectinib

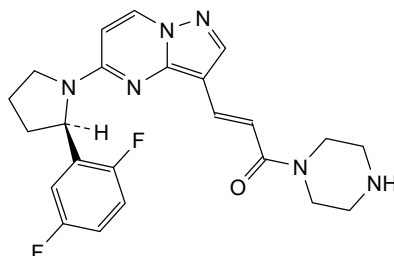
(2E)-3-{5-[(2R)-2-(2,5-difluorophényl)pyrrolidin-1-yl]pyrazolo[1,5-a]pyrimidin-3-yl}-1-(pipérazin-1-yl)prop-2-én-1-one  
*inhibiteur de tyrosine kinase, antinéoplasique*

boditrectinib

(2E)-3-{5-[(2R)-2-(2,5-difluorofenil)pirrolidin-1-il]pirazolo[1,5-a]pirimidin-3-il}-1-(piperazin-1-il)prop-2-en-1-ona  
*inhibidor de tirosina kinasa, antineoplásico*

C<sub>23</sub>H<sub>24</sub>F<sub>2</sub>N<sub>6</sub>O

1940165-80-9





**brenetafuspum #**

brenetafus

humanized immunoglobulin anti-(human T-cell surface glycoprotein CD3 epsilon chain) single chain variable fragment (scFv) (1-253) containing the light chain variable (VL) region (1-107), the linker <sup>108</sup>GGGGSGGGSGGGSGGGSGGGSGGG<sup>131</sup> and the heavy chain variable (VH) region (132-253) fused via the peptide linker <sup>254</sup>GGGG<sup>258</sup> to a human T-cell receptor beta chain anti-(human HLA-A2 antigen complex with preferentially expressed antigen in melanoma (PRAME) protein) fragment (259-502 in the current sequence) engineered variant (S<sup>429</sup>>C, C<sup>447</sup>>A, N<sup>461</sup>>D), disulfide bridged to a human T cell receptor alpha chain anti-(human HLA-A2 antigen complex with preferentially expressed antigen in melanoma (PRAME) protein) fragment (1-201), engineered variant (T<sup>163</sup>>C), non-glycosylated, produced in *Escherichia coli*;

humanized monoclonal scFv antibody fusion with human T-cell receptor; CDR source: *Mus musculus*; antigen: human T-cell surface glycoprotein CD3 epsilon chain, T-cell surface antigen T3/Leu-4 epsilon chain, CD3e (CD3E); type: Fv-kappa scFv; light chain class: kappa; LV germline: *Homo sapiens* IGKV1-NL1\*01; LJ germline: *Homo sapiens* IGKJ1\*01; VL: 1-107; CDR Kabat L1: RASQDIRNYLN (24-34); CDR Kabat L2: YTSRLES (50-56); CDR Kabat L3: QQGNTLPWT (89-97); linker: 108-131; HV germline: *Homo sapiens* IGHV3-23\*04; HJ germline: *Homo sapiens* IGHJ4\*01; VH: 132-253; CDR Kabat H1: GYTMM (162-166); CDR Kabat H2: LINPYKGVSTYNQKFKD (181-197); CDR Kabat H3: SGYYGDSWDYFDV (230-242); linker: 254-258; fusion protein: 259-372; T-cell receptor beta chain (CB) variable domain [TRBV19\*01-TRBJ2-7\*01]; fusion protein: 373-502 (S429C C447A N461D); T-cell receptor beta chain constant domain [TRBC2\*01]; mutation: S429C (disulfide with CA); mutation: C447A (removed disulfide); mutation: N461D (natural variant); fusion protein: 1-115; T-cell receptor alpha chain (CA) variable domain [TRAV26.1\*01-TRAJ15\*02]; fusion protein: 116-201 (T163C); T-cell receptor alpha chain constant domain [TRAC\*01]; mutation: T163C (disulfide with CB) *immunostimulant, antineoplastic*

brénétafus

fragment variable à chaîne unique (scFv) de l'immunoglobuline humanisée anti-(chaîne epsilon de la glycoprotéine de surface des lymphocytes T humains CD3) (1-253, ) contenant la région variable (VL) de la chaîne légère (1-107), la liaison <sup>108</sup>GGGGSGGGSGGGSGGGSGGGSGGG<sup>131</sup> et la région variable (VH) de la chaîne lourde (132-253) fusionnées via la liaison peptidique <sup>254</sup>GGGG<sup>258</sup> à un fragment (259-502 dans la séquence actuelle) de la chaîne bêta du récepteur des lymphocytes T humains anti-(complexe antigénique HLA-A2 humain avec l'antigène préférentiellement exprimé dans le mélanome (PRAME), variant modifié (S<sup>429</sup>>C, C<sup>447</sup>>A, N<sup>461</sup>>D), disulfure ponté à un fragment (1-201) de la chaîne alpha du récepteur des lymphocytes T humains anti-(complexe antigénique HLA-A2 humain avec l'antigène préférentiellement exprimé dans le mélanome (PRAME)), variant modifié (T<sup>163</sup>>C), non glycosylé, produite chez *Escherichia coli*;

fusion d'un anticorps monoclonal scFv humanisé avec le récepteur des lymphocytes T humains; source CDR: *Mus musculus*; antigène: chaîne epsilon de la glycoprotéine de surface des lymphocytes T humains CD3, antigène T3 de surface des cellules T /Leu-4 chaîne epsilon, CD3e (CD3E); type: Fv-kappa scFv; classe de la chaîne légère: kappa; LV lignée germinale: *Homo sapiens* IGKV1-NL1\*01; LJ lignée germinale: *Homo sapiens* IGKJ1\*01; VL: 1-107; CDR Kabat L1: RASQDIRNYLN (24-34); CDR Kabat L2: YTSRLES (50-56); CDR Kabat L3: QQGNTLPWT (89-97); liaison: 108-131; HV lignée germinale: *Homo sapiens* IGHV3-23\*04; HJ lignée germinale: *Homo*

*sapiens* IGHJ4\*01; VH: 132-253; CDR Kabat H1: GYTMN (162-166); CDR Kabat H2: LINPYKGVSTYNQKFKD (181-197); CDR Kabat H3: SGYYGDSWYFDV (230-242); liaison: 254-258; protéine de fusion: 259-372; domaine variable de la chaîne bêta (CB) du récepteur des lymphocytes T [TRBV19\*01-TRBJ2-7\*01]; protéine de fusion: 373-502 (S429C C447A N461D); domaine constant de la chaîne bêta du récepteur des lymphocytes T [TRBC2\*01]; mutation: S429C (disulfure avec CA); mutation: C447A (disulfure supprimé); mutation: N461D (variant naturel); protéine de fusion: 1-115; domaine variable de la chaîne alpha (CA) du récepteur des lymphocytes T [TRAV26.1\*01-TRAJ15\*02]; protéine de fusion: 116-201 (T163C); domaine constant de la chaîne alpha du récepteur des lymphocytes T [TRAC\*01]; mutation: T163C (disulfure avec CB)  
*immunostimulant, antinéoplasique*

brenetafusp

inmunoglobulina humanizada anti-(cadena épsilon CD3 de glicoproteína de superficie de linfocitos T humanos) fragmento variable de cadena única (scFv) (1-253,) conteniendo la cadena ligera variable (VL) región (1-107) el enlace <sup>108</sup>GGGGSGGGSGGGSGGGSGGGSGGG<sup>131</sup> y la cadena pesada variable (VH) región (132-253) fusionado a través del enlace peptídico <sup>254</sup>GGGG<sup>258</sup> a una cadena beta del receptor de linfocitos T humanos anti-(complejo antígeno humano HLA-A2 con antígeno expresado preferentemente en melanoma (PRAME)) fragmento (259-502 en la secuencia actual) variante diseñada (S<sup>429</sup>>C, C<sup>447</sup>>A, N<sup>461</sup>>D), unido por puente disulfuro a una cadena alfa del receptor de linfocitos T humanos anti-(complejo antígeno humano HLA-A2 con antígeno expresado preferentemente en melanoma (PRAME)) fragmento (1-201), variante diseñada (T<sup>163</sup>>C), no glicosilada, producida en *Escherichia coli*;  
anticuerpo monoclonal scFv de fusión con receptor de linfocitos T humanos; fuente CDR: *Mus musculus*; antígeno: cadena épsilon CD3 de glicoproteína de superficie de linfocitos T humanos, cadena épsilon de antígeno de superficie de células T T3/Leu-4, CD3e (CD3E); tipo: Fv-kappa scFv; clase cadena ligera: kappa; línea germinal LV: *Homo sapiens* IGKV1-NL1\*01; línea germinal LJ: *Homo sapiens* IGKJ1\*01; VL: 1-107; CDR Kabat L1: RASQDIRNYLN (24-34); CDR Kabat L2: YTSRLES (50-56); CDR Kabat L3: QQGNTLPWT (89-97); enlace: 108-131; línea germinal HV: *Homo sapiens* IGHV3-23\*04; línea germinal HJ: *Homo sapiens* IGHJ4\*01; VH: 132-253; CDR Kabat H1: GYTMN (162-166); CDR Kabat H2: LINPYKGVSTYNQKFKD (181-197); CDR Kabat H3: SGYYGDSWYFDV (230-242); enlace: 254-258; proteína de fusión: 259-372; dominio variable de la cadena beta (CB) del receptor de linfocitos T [TRBV19\*01-TRBJ2-7\*01]; proteína de fusión: 373-502 (S429C C447A N461D); dominio constante de la cadena beta del receptor de linfocitos T [TRBC2\*01]; mutación: S429C (disulfuro con CA); mutación: C447A (disulfuro eliminado); mutación: N461D (variante natural); proteína de fusión: 1-115; dominio variable de la cadena alfa (CA) del receptor de linfocitos T [TRAV26.1\*01-TRAJ15\*02]; proteína de fusión: 116-201 (T163C); dominio constante de la cadena alfa del receptor de linfocitos T [TRAC\*01]; mutación: T163C (disulfuro con CB)  
*inmunostimulante, antineoplásico*

2736407-54-6

Sequence / Séquence / Secuencia  
 ScFv-T cell receptor beta chain  
**AIQMTQSPSS** **LSASVGDVRT** **ITCRASQDIR** **NYLNWYQQKP** **GKAPKLLIYY** 50  
**TSRLESGVPS** **RFSGSGSGTD** **YTLTISSLQP** **EDFATYYCQQ** **GNTLPWTFGQ** 100  
**GTVEIKGGG** **GGGGGGGGG** **GGGGGGGGG** **SEVQLVESGG** **GLVQPGGSLR** 150  
**LSCAASGYF** **TCYTMNWVRQ** **APGKGLEWVA** **LINPKGVST** **YNQKFKDRFT** 200  
**ISVDKSKNTA** **YLQMNSLRAE** **DTAVYYCARS** **GYGDSDDWYF** **DVWGQGTLLVT** 250  
**VSSGGGSDG** **GITQSPKYL** **RKEGQNVTL** **CEQNLNHDAM** **YWYRQDPGQG** 300  
 LRLIYYQIM GDEQKGDIAE GYSVSRKKE SFPLTVTSAQ KNPTAFYLCA 350  
 SSWWTGASP IRFGPGTRLT VTEDLKNVFP PEVAVFEPSE AEISHTQKAT 400  
 LVCLATGFYP **DHVELSWWN** **GKEVHSGVCT** **DPQLKEQPA** **LNSRYALSS** 450  
 RLRVSATFWQ DPRNHFRQV QFYGLSENDE WTQDRAKPVT QIVSAEAWGR 500  
 AD 502

T-cell receptor alpha chain  
 GDAKTTQPNM MESNEEPEVH LPCNHSTISG TDYIHWRQL PSQGPEYVIH 50  
 GLTSNVNRM ASLAIADRK SSTLILHRAT LRDAVYVCI LILGHSRLGN 100  
 YIATFGKGTK LSVIFNIQNP DPAVYQLRDS KSSDKSVCLF TDFDSQTNVS 150  
 QSKDSVYIT **DKC**VLDLRSM DFKSNSAVAW SNKSDFACAN AFNNSIIPED 200  
 T 201

Peptide linkers / Peptides liants / Péptidos de unión  
**GGGGGGGGGGGGGGGGGGGGGG** 108-131, **GGGG** 254-258

Mutation / Mutation / Mutación  
 T-Cell Receptor beta chain: S429>**C**, C447>**A**, N461>**D**  
 T-Cell Receptor alpha chain: T163>**C**

**Post-translational modifications**  
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro  
 Intra-scFv: 23-88, 153-227  
 Intra-TCR beta chain: 281-349, 403-468  
 Intra-TCR alpha chain: 23-89, 138-188  
 Inter-TCR alpha chain - TCR beta chain: 163-429

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

**brigimadlinum**

brigimadlin

(3*S*,3'*S*,3*a*'*S*,10*a*'*S*)-6-chloro-3'-(3-chloro-2-fluorophenyl)-1'-(cyclopropylmethyl)-6'-methyl-2-oxo-1,2,3',3*a*',10',10*a*'-hexahydro-1'*H*-spiro[indole-3,2'-pyrrolo[2',3':4,5]pyrrolo[1,2-*b*]indazole]-7'-carboxylic acid

*E3 ubiquitin-protein ligase Mdm2 inhibitor, antineoplastic*

brigimadline

acide (3*S*,3'*S*,3*a*'*S*,10*a*'*S*)-6-chloro-3'-(3-chloro-2-fluorophényl)-1'-(cyclopropylméthyl)-6'-méthyl-2-oxo-1,2,3',3*a*',10',10*a*'-hexahydro-1'*H*-spiro[indole-3,2'-pyrrolo[2',3':4,5]pyrrolo[1,2-*b*]indazole]-7'-carboxylique

*inhibiteur de l'ubiquitine-protéine ligase E3 Mdm2, antinéoplasique*

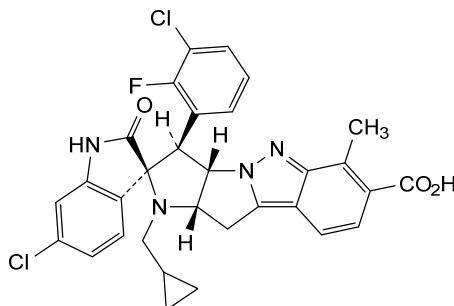
brigimadlina

ácido (3*S*,3'*S*,3*a*'*S*,10*a*'*S*)-6-cloro-3'-(3-cloro-2-fluorofenil)-1'-(ciclopropilmetil)-6'-metil-2-oxo-1,2,3',3*a*',10',10*a*'-hexahidro-1'*H*-spiro[indol-3,2'-pirrolo[2',3':4,5]pirrolo[1,2-*b*]indazol]-7'-carboxílico

*inhibidor de ubiquitina-proteína ligasa E3 Mdm2, antineoplásico*

C<sub>31</sub>H<sub>25</sub>Cl<sub>2</sub>FN<sub>4</sub>O<sub>3</sub>

2095116-40-6



**cemavafuspum #**

**cemavafusp** enterobacteria phage H19B L-methionyl-Shiga-like toxin 1 subunit A1 (SLT-1 subunit A1, SLT-1a1, verotoxin 1 subunit A1, verocytotoxin 1 subunit A1, EC:3.2.2.22) (2-252), variant (S<sup>45</sup>>I<sup>46</sup>, V<sup>54</sup>>I<sup>55</sup>, R<sup>55</sup>>L<sup>56</sup>, I<sup>57</sup>>F<sup>58</sup>, P<sup>59</sup>>F<sup>60</sup>, E<sup>60</sup>>T<sup>61</sup>, E<sup>61</sup>>L<sup>62</sup>, G<sup>110</sup>>A<sup>111</sup>, R<sup>188</sup>>A<sup>189</sup>, C<sup>242</sup>>S<sup>243</sup>, R<sup>248</sup>>A<sup>249</sup>, R<sup>251</sup>>A<sup>252</sup>) fused via the peptide linker <sup>253</sup>EFPKPSTPPGSSGGAP<sup>268</sup> to an anti-(human programmed cell death 1 ligand 1 (PD-L1, CD274)) murine immunoglobulin single chain variable fragment (scFv) (269-501) containing the heavy chain variable region (VH) region (269-390), a <sup>391</sup>GGGS<sup>395</sup> peptide linker and the light chain variable region (VL) region (396-501) fused via peptide linker <sup>502</sup>HHA<sup>505</sup> to an HLA-A\*02 immunodominant MHC class I restricted epitope derived from human cytomegalovirus (CMV) pp65 (UL83) protein (506-514), disulfide bridged dimer, produced in *Escherichia coli*;  
human scFv dimer monoclonal antibody fusion with human SLTA and MHC-I antigen; antigen: human programmed cell death 1 ligand 1, PD-L1, programmed death ligand 1, PDCD1 ligand 1, B7 homolog 1, B7-H1 (CD274); fusion protein (Shiga-like toxin 1, *Escherichia coli* subunit A1): 1-251 (ins1M T46I V55I R56L I58F P60F E61T E62L G111A R189A C243S R249A, R252A); linker: 252-268; type: Fv-heavy scFv; VH: 269-390; HV germline: *Homo sapiens* IGHV1-2\*02; HJ germline: *Homo sapiens* IGHJ4\*01; CDR Kabat H1: EYTMH (299-303); CDR Kabat H2: GINPNNGGTWYNQKFKG (318-334); CDR Kabat H3: PYYGSRDYFDY (367-379); linker: 391-395; Type: Fv-kappa scFv; light chain class: kappa; LV germline: *Homo sapiens* IGKV1-39\*01; LJ germline: *Homo sapiens* IGKJ2\*01; VL: 396-501; CDR Kabat L1: SASSSVSYMY (419-428); CDR Kabat L2: LTSNLAS (444-450); CDR Kabat L3: QQWSSNPPT (483-491); Linker: 502-505; fusion protein: 506-514 (major histocompatibility complex I HLA-A\*02-restricted epitope, derived from human cytomegalovirus viral tegument protein UL83/pp65) *immunomodulator, antineoplastic*

**cémavafusp**

sous-unité A1 de la toxine 1 du phage H19B d'entérobactéries de type L-méthionyl-Shiga (SLT-1 sous-unité A1, SLT-1a1, vérotoxine 1 sous-unité A1, vérocytotoxine 1 sous-unité A1, EC:3.2.2.22) (2-252), variant (S S<sup>45</sup>>I<sup>46</sup>, V<sup>54</sup>>I<sup>55</sup>, R<sup>55</sup>>L<sup>56</sup>, I<sup>57</sup>>F<sup>58</sup>, P<sup>59</sup>>F<sup>60</sup>, E<sup>60</sup>>T<sup>61</sup>, E<sup>61</sup>>L<sup>62</sup>, G<sup>110</sup>>A<sup>111</sup>, R<sup>188</sup>>A<sup>189</sup>, C<sup>242</sup>>S<sup>243</sup>, R<sup>248</sup>>A<sup>249</sup>, R<sup>251</sup>>A<sup>252</sup>) fusionnée via la liaison peptidique <sup>253</sup>EFPKPSTPPGSSGGAP<sup>268</sup> à un anti-(ligand 1 humain de mort cellulaire programmée 1 (PD-L1, CD274)) d'immunoglobuline murine au fragment variable à chaîne unique (scFv) (269-501) contenant la région (269-390) de la région variable de la chaîne lourde (VH), la liaison peptidique <sup>391</sup>GGGS<sup>395</sup> et la région (396-501) de la région variable de la chaîne légère (VL) fusionnée via la liaison peptidique <sup>502</sup>HHA<sup>505</sup> à un épitope restreint du CMH de classe I immunodominant HLA-A\*02 dérivé de la protéine (506-514) pp65 (UL83) du cytomégalovirus humain (CMV), homodimère à pont disulfure, produit chez *Escherichia coli*;  
fusion d'un anticorps monoclonal humain scFv dimère avec l'antigène humain SLTA et MHC-I; antigène: ligand 1 humain de mort cellulaire programmée 1, PD-L1, ligand de mort programmée 1, PDCD1 ligand 1, homologue 1 de B7, B7-H1 (CD274); protéine de fusion (toxine 1 de type Shiga, sous-unité A1 d'*Escherichia coli*): 1-251 (ins1M T46I V55I R56L I58F P60F E61T E62L G111A R189A C243S R249A, R252A); liaison: 252-268; type: Fv-lourde scFv; VH: 269-390; HV lignée germinale: *Homo sapiens* IGHV1-2\*02; HJ lignée germinale: *Homo sapiens* IGHJ4\*01; CDR Kabat H1: EYTMH (299-303); CDR Kabat H2: GINPNNGGTWYNQKFKG (318-334); CDR Kabat H3: PYYGSRDYFDY (367-379); liaison: 391-395; Type: Fv-kappa scFv; classe de la chaîne légère: kappa; LV lignée germinale: *Homo sapiens* IGKV1-39\*01; LJ lignée germinale: *Homo sapiens* IGKJ2\*01; VL: 396-501; CDR Kabat L1: SASSSVSYMY (419-428); CDR Kabat L2: LTSNLAS (444-450); CDR Kabat L3: QQWSSNPPT (483-491); liaison: 502-505; protéine de fusion: 506-514 (épitope restreint au complexe majeur d'histocompatibilité I HLA-A\*02, dérivé de la protéine tégumentale virale UL83/pp65 du cytomégalovirus humain) *immunomodulateur, antinéoplasique*

cemavafusp

enterobacteria fago H19B L-metionil-Shiga-like toxina 1 subunidad A1 (SLT-1 subunidad A1, SLT-1a1, verotoxina 1 subunidad A1, verocitotoxina 1 subunidad A1, EC:3.2.2.22) (2-252), variante (S<sup>45</sup>>I<sup>46</sup>, V<sup>54</sup>>I<sup>55</sup>, R<sup>55</sup>>L<sup>56</sup>, I<sup>57</sup>>F<sup>58</sup>, P<sup>59</sup>>F<sup>60</sup>, E<sup>60</sup>>T<sup>61</sup>, E<sup>61</sup>>L<sup>62</sup>, G<sup>110</sup>>A<sup>111</sup>, R<sup>188</sup>>A<sup>189</sup>, C<sup>242</sup>>S<sup>243</sup>, R<sup>248</sup>>A<sup>249</sup>, R<sup>251</sup>>A<sup>252</sup>) fusionada a través del enlace peptídico <sup>253</sup>EFPKPSTPPGSSGGAP<sup>268</sup> a un anti-(ligando 1 de muerte celular programada humana 1 (PD-L1, CD274)) fragmento variable de cadena única de inmunoglobulina murina (scFv) (269-501) que contiene la región variable de cadena pesada (VH) región (269-390), un enlace peptídico <sup>391</sup>GGGGS<sup>395</sup> y la región variable de cadena ligera (VL) región (396-501) fusionado a través de un enlace peptídico <sup>502</sup>HHA<sup>505</sup> a un epítipo HLA-A\*02 restringido inmunodominante MHC de clase I derivado del citomegalovirus humano (CMV) pp65 (UL83) proteína (506-514), homodímero con puente disulfuro, producido en *Escherichia coli*; anticuerpo monoclonal humano con dímero scFv de fusión con SLTA humano y antígeno MHC-I; antígeno: ligando 1 de muerte celular programada humana, PD-L1, ligando 1 de muerte programada, ligando 1 PDCD1, B7 homólogo 1, B7-H1 (CD274); proteína de fusión (toxina 1 de tipo Shiga, subunidad A1 de *Escherichia coli*): 1-251 (ins1M T46I V55I R56L I58F P60F E61T E62L G111A R189A C243S R249A, R252A); enlace: 252-268; type: Fv-pesado scFv; VH: 269-390; línea germinal HV: *Homo sapiens* IGHV1-2\*02; línea germinal HJ: *Homo sapiens* IGHJ4\*01; CDR Kabat H1: EYTMH (299-303); CDR Kabat H2: GINPNNGGTWYNQKFKG (318-334); CDR Kabat H3: PYYYGSREDFDY (367-379); enlace: 391-395; tipo: Fv-kappa scFv; cadena ligera: chain class: kappa; LV línea germinal: *Homo sapiens* IGKV1-39\*01; LJ línea germinal: *Homo sapiens* IGKJ2\*01; VL: 396-501; CDR Kabat L1: SASSSVSYMY (419-428); CDR Kabat L2: LTSNLAS (444-450); CDR Kabat L3: QQWSSNPPT (483-491); enlace: 502-505; proteína de fusión: 506-514 (epítipo restringido del complejo de histocompatibilidad mayor I HLA-A\*02, derivado de la proteína del tegumento viral de citomegalovirus humano UL83/pp65) *inmunomodulador, antineoplásico*

2711705-98-3

Sequence / Séquence / Secuencia

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MKEFTLDFST AKTYVDSLNV IRSAIGTFLQ TISSGGTSLL MIDSGIGDNL 50
FAVDILGFDL TLGRFNLRRL IVERNLYVT GFVNRNTRNVF YRFADFSHVT 100
FPGTTAVTLS ADSSYTTLQR VAGISRTRMQ INRHSLTTSY LDLMSSHSGTS 150
LTQSVARAML RFBVTVAEAL RFRQIQRGFR TTLDDLSGAS YVMTAEDVDL 200
TLNWGRLLSS LPDYHQGDSV RVGRISFGSI NALLGSVALI LNSHHHSAV 250
AAEFKPKSTP PGSSGGAPFV QLQSGPELV KPGASVKISC KTSGYTFTEY 300
TMHNVQRHG KSLIEWIGGIN PNNGGTWYNQ KFKGKATLTV DKSSSTAYME 350
LRLSLSDSA VYFCARPYYY GSREDFDYW GQGTTLVVSS GGGGSDIQMT 400
QSPSSLSASV GDRVTITCSA SSSVSYMYWY QOKPRSSPKP WYILTSNLAS 450
GVPARFSGSG SGTYSYLTIS SMEAEDAATY YCQQWSSNPP TFGGGTKLEL 500
KHAANLVPM VATV 514
    
```

Mutation / Mutation / Mutación

N-L-methionyl added (M<sup>1</sup>), S<sup>45</sup>>I<sup>46</sup>, V<sup>54</sup>>I<sup>55</sup>, R<sup>55</sup>>L<sup>56</sup>, I<sup>57</sup>>F<sup>58</sup>, P<sup>59</sup>>F<sup>60</sup>, E<sup>60</sup>>T<sup>61</sup>, E<sup>61</sup>>L<sup>62</sup>, G<sup>110</sup>>A<sup>111</sup>, R<sup>188</sup>>A<sup>189</sup>, C<sup>242</sup>>S<sup>243</sup>, R<sup>248</sup>>A<sup>249</sup>, R<sup>251</sup>>A<sup>252</sup>

Peptide linkers / Peptides liants / Péptidos de unión

EFKPKPSTPPGSSGGAP 253-268; GGGGS 391-395, HHA 502-505

Post-translational modifications

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

Intra VH: 290-364, 290'-364'

Intra VL: 418-482, 418'-482'

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

none

**cemsidomidum**

cemsidomide

(3*S*)-3-(6-([4-(morpholin-4-ylmethyl)phenyl]methyl)-2-oxobenz[*cd*]indol-1(2*H*)-yl)piperidine-2,6-dione  
*antineoplastic*

cemsidomide

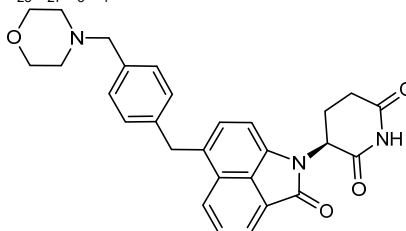
(3*S*)-3-(6-([4-(morpholin-4-ylméthyl)phényl]méthyl)-2-oxobenz[*cd*]indol-1(2*H*)-yl)pipéridine-2,6-dione  
*antineoplasique*

cemsidomida

(3*S*)-3-(6-([4-(morfolin-4-ilmetil)fenil]metil)-2-oxobenz[*cd*]indol-1(2*H*)-yl)piperidina-2,6-diona  
*antineoplásico*

C<sub>28</sub>H<sub>27</sub>N<sub>3</sub>O<sub>4</sub>

2504235-67-8

**crisugabalinum**

crisugabalin

[(1*S*,2*S*,3*R*,6*S*,8*S*)-2-(aminométhyl)tricyclo[4.2.1.0<sup>3,8</sup>]nonan-2-yl]acetic acid  
*diagnostic imaging agent*

crisugabaline

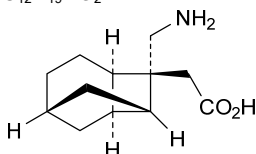
acide [(1*S*,2*S*,3*R*,6*S*,8*S*)-2-(aminométhyl)tricyclo[4.2.1.0<sup>3,8</sup>]nonan-2-yl]acétique  
*agent diagnostique*

crisugabalina

ácido [(1*S*,2*S*,3*R*,6*S*,8*S*)-2-(aminométíl)tríciclo[4.2.1.0<sup>3,8</sup>]nonan-2-il]acético  
*agente de diagnóstico*

C<sub>12</sub>H<sub>19</sub>NO<sub>2</sub>

2209104-84-5

**daniluromerum**

daniluromer

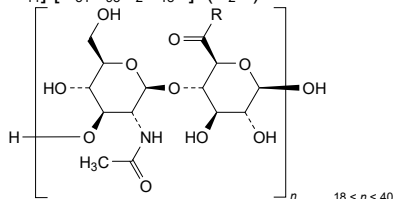
hyaluronic acid, degraded, partially amidated with (2*R*)-3-[[2-aminoethoxy](hydroxy)phosphoryl]oxy]propane-1,2-diyl di(hexadecanoate)  
*anti-inflammatory*

daniluromère

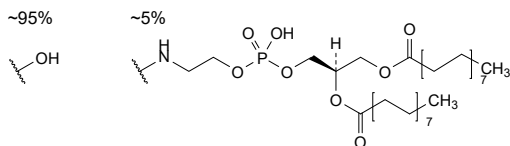
acide hyaluronique, dégradé, partiellement amidifié par le di(hexadécanoate) de (2*R*)-3-[[2-aminoéthoxy](hydroxy)phosphoryl]oxy]propane-1,2-diyle  
*anti-inflammatoire*

danilurómero

ácido hialurónico, degradado, parcialmente amidificado por (2*R*)-3-[[2-aminoetoxi](hidroxi)fosforil]oxi]propano-1,2-diilo di(hexadecanoato)  
*antiinflamatorio*

[C<sub>14</sub>H<sub>21</sub>NO<sub>11</sub>]<sub>n</sub>[C<sub>51</sub>H<sub>93</sub>N<sub>2</sub>O<sub>16</sub>P]<sub>m</sub>(H<sub>2</sub>O) 2644728-09-4

R :

**darizmetinibum**

darizmetinib

*N*-{2,6-difluoro-3-[5-(pyridin-4-yl)-1*H*-pirazolo[3,4-*b*]piridina-3-carbonil]fenil]propano-1-sulfonamida  
*mitogen-activated protein kinase (MAP kinase) kinase inhibitor*

darizmetínib

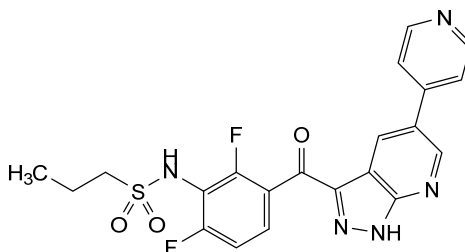
*N*-{2,6-difluoro-3-[5-(piridin-4-yl)-1*H*-pirazolo[3,4-*b*]piridina-3-carbonil]fenil]propano-1-sulfonamida  
*inhibiteur de la kinase de la protéine kinase activée par des mitogènes (MAP kinase)*

darizmetinib

*N*-{2,6-difluoro-3-[5-(piridin-4-il)-1*H*-pirazolo[3,4-*b*]piridina-3-carbonil]fenil]propano-1-sulfonamida  
*inhibidor de la kinasa de la proteina kinasa activada por mitógeno (MAP kinasa)*

C<sub>21</sub>H<sub>17</sub>F<sub>2</sub>N<sub>5</sub>O<sub>3</sub>S

2369583-33-3

**davutamigum #**

davutamig

immunoglobulin G4-kappa, anti-MET (met proto-oncogene, hepatocyte growth factor (HGF) receptor, HGFR, scatter factor (SF) receptor, HGF/SF receptor, receptor tyrosine-protein kinase c-met, papillary renal cell carcinoma 2, RCCP2)], *Homo sapiens* monoclonal antibody, biparatopic (targeting two different non-overlapping epitopes on MET);

gamma4 heavy chain anti-MET *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-9\*01 (94.9%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (122-219), hinge 1-12 S10>P (229) (220-231), CH2 L92 (310) (232-341), CH3 (342-446), CHS (447-448)) (122-448)], (135-215')-disulfide with kappa light chain anti-MET *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (100%) -IGKJ5\*01 (100%), CDR-IMGT [6.3.10] (27-32.50-52.89-98)) (1'-108') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215'))]; gamma4 heavy chain anti-MET *Homo sapiens* (1"-444") [VH (*Homo sapiens* IGHV3-53\*04 (90.6%) -(IGHD) -IGHJ3\*02 (93.8%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1"-117") -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10, G4v8 R115, F116, P125 (CH1 (118"-215"), hinge 1-12 S10>P (225) (216"-227")), CH2 L92 (306) (228"-337")), CH3 H115>R (432), Y116>F (433), L125>P (442) (338"-442")), CHS (443"-444")) (118"-444"), (131"-215'")-disulfide with kappa light chain anti-MET *Homo sapiens* (1'"-215'") [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (100%) -IGKJ5\*01 (100%), CDR-IMGT [6.3.10] (27-32.50-52.89-98)) (1'"-108'") -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (154), V101 (192) (109'"-215'")); dimer (227-223'':230-226'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa  
*antineoplastique*

davutamig

immunoglobuline G4-kappa, anti-MET (proto-oncogène met, récepteur du facteur de croissance hépatocytaire, HGFR, récepteur du facteur de dispersion (SF), récepteur de l'HGF/SF, récepteur protéine-tyrosine kinase c-met, carcinome papillaire à cellules rénales 2, RCCP2)], anticorps monoclonal *Homo sapiens*, biparatopique (ciblant deux épitopes différents non chevauchants sur MET); chaîne lourde gamma4 anti-MET *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-9\*01 (94.9%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (122-219), charnière 1-12 S10>P (229) (220-231), CH2 L92 (310) (232-341), CH3 (342-446), CHS (447-448)) (122-448)], (135-215')-disulfure avec la chaîne légère kappa anti-MET *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (100%) -IGKJ5\*01 (100%), CDR-IMGT [6.3.10] (27-32.50-52.89-98)) (1'-108') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215'))]; chaîne lourde gamma4 anti-MET *Homo sapiens* (1"-444") [VH (*Homo sapiens* IGHV3-53\*04 (90.6%) -(IGHD) -IGHJ3\*02 (93.8%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1"-117") -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10, G4v8 R115, F116, P125 (CH1 (118"-215"), charnière 1-12 S10>P (225) (216"-227")), CH2 L92 (306) (228"-337")), CH3 H115>R (432), Y116>F (433), L125>P (442) (338"-442")), CHS (443"-444")) (118"-444"), (131"-215'")-disulfure avec la chaîne légère kappa anti-MET *Homo sapiens* (1'"-215'") [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (100%) -IGKJ5\*01 (100%), CDR-IMGT [6.3.10] (27-32.50-52.89-98)) (1'"-108'") -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (154), V101 (192) (109'"-215'")); dimère (227-223'':230-226'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa  
*antineoplastique*



davutamig

immunoglobulina G4-kappa, anti-MET (proto-oncogen met, receptor del factor de crecimiento hepatocitario, HGFR, receptor del factor de dispersión (SF), receptor del HGF/SF, receptor proteína-tirosina kinasa c-met, carcinoma papilar con células renales 2, RCCP2)], anticuerpo monoclonal *Homo sapiens*, biparatópico (apuntando dos epítomos diferentes no superpuestos sobre MET);  
 cadena pesada gamma4 anti-MET *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-9\*01 (94.9%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (122-219), bisagra 1-12 S10>P (229) (220-231), CH2 L92 (310) (232-341), CH3 (342-446), CHS (447-448)) (122-448)], (135-215')-disulfuro con la cadena ligera kappa anti-MET *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (100%) -IGKJ5\*01 (100%), CDR-IMGT [6.3.10] (27-32.50-52.89-98)) (1'-108') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215'')];  
 cadena pesada gamma4 anti-MET *Homo sapiens* (1''-444'') [VH (*Homo sapiens* IGHV3-53\*04 (90.6%) -(IGHD) -IGHJ3\*02 (93.8%), CDR-IMGT [8.7.11](26-33.51-57.96-106)) (1''-117'') -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10, G4v8 R115, F116, P125 (CH1 (118'-215''), bisagra 1-12 S10>P (225) (216''-227''), CH2 L92 (306) (228''-337''), CH3 H115>R (432), Y116>F (433), L125>P (442) (338''-442''), CHS (443''-444'')) (118''-444''), (131''-215''')-disulfuro con la cadena ligera kappa anti-MET *Homo sapiens* (1'''-215''') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (100%) -IGKJ5\*01 (100%), CDR-IMGT [6.3.10] (27-32.50-52.89-98)) (1'''-108''') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (154), V101 (192) (109'''-215'''); dímero (227-223'':230-226'')-bisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa **antineoplásico**

2648058-48-2

Heavy chain / Chaîne lourde / Cadena pesada: anti-MET (H)

```
EVQLVESGGG LVQPGLTSLRL SCAASGFTFD DYAMHWVRQA PGKGLEWVSG 50
ITWNSYNIDY ADSVKGRFTI SRDNARNSLY LQMNSLRAED TALYYCAKDD 100
DYSNYYVFDY WGGQGLTVTVS SASTKGPSVF FLAPCSRSTS ESTAAALGLV 150
KDYFPEPVTV SWNSGALTSV VHTFPAVLQS SGLYSLSSVV TVPSSSLGK 200
TYTCNVDHKP SNTKVDKRVK SKYGGPCPPC PAPEFLGGPS VFLFPKPKD 250
TLMISRTPEV TCVVVDVQSE DPEVQFNWYV DGVEVHNAKT KPREEQFNST 300
YRVVSVLTVL HQDWLNGREY KCKVSNKGLP SSIERTKSKA KGQPREPQVY 350
TLPSPQEMT KNOVSLTCLV KGFYPSDIAV EWESNGQFEN NYKTPPVL 400
SDGSFFLYSR LTVDKSRWQE GNVFSCVMH EALHNYTQK SLSLSLKG 448
```

Heavy chain / Chaîne lourde / Cadena pesada: anti-MET (H')

```
EVQLVESGGG LVQPGGLSLRL SCAASGFIVT TNYMTWLRQA PGKGLEWVSL 50
IYSSGHGTYA DSVKGRFTIS RHNSKNTLYL QMDSLRAEDT AVYICASAF 100
ADVFDIWGGQ TMTVSSAST KGPSVFPLAP CSRSTSESTA ALGCLVKDYF 150
PEPVTWNSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGKTYTC 200
NVDHKPSTNK VDKRVESKYG PCPCPPAPE FLGGPSVLEF PPKPKDTLMI 250
SRTPEVTCVW VDSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV 300
SVLTVLHQDW LNKKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLFP 350
SQEEMTKNQV SLTCLVKGFI PSDIAVENES NGQPENNYKT TPVLDSDSGS 400
FFLYSRLTVD KSRWQEGNVF SCSVMHEALH NRPTQKSLSL SPGK 444
```

Light chain / Chaîne légère / Cadena ligera: anti-MET (L, L')

```
DIQMTQSPSS LSASVGRDVT ITCRAQSIS SYLNWYQQKPK GKAPKLLIYA 50
ASSLQSGVPS RFGSGSGTD FTLTISSLQP EDFATYTCQQ SYSTPPITFG 100
QGTRLLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNFF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYLSSTL TLSKADYERH KVAACEVTHQ 200
GLSSPVTKSF NRGEC 215
```

Post-translational modifications

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

Intra-H (C23-C104)	22-96	148-204	262-322	368-426
	22"-95"	144"-200"	258"-318"	364"-422"
Intra-L (C23-C104)	23'-88'	135'-195'		
	23'''-88'''	135'''-195'''		
Inter-H-L (CH1 10-CL 126)	135-215'	131"-215''		
Inter-H-H (h 8, h 11)	227-223"	230-226'''		

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

H CH2 N84.4: 298, 294"

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

C-terminal lysine clipping / Coupeure de la lysine C-terminale / Recorte de lisina C-terminal  
 H CHS K2: 448, 444"

**dazostinagum**

dazostinag

cyclo[(*P*<sup>3</sup>*R*)-2'-deoxy-2'-fluoro-*P*-thioadenylyl-(3'→5')-(*P*<sup>2</sup>*R*)-7-fluoro-*P*-thio-7-deazainosinyl-(2'→5')]  
stimulator of interferon genes (*STING*) protein agonist,  
antineoplastic

dazostinag

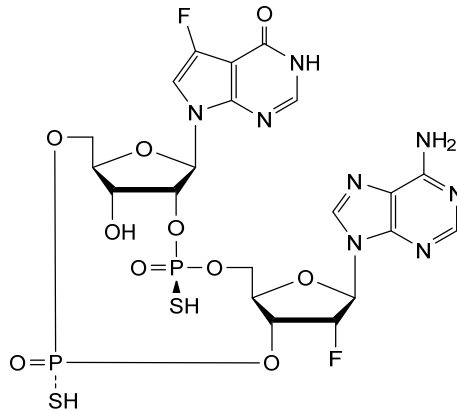
cyclo[(*P*<sup>3</sup>*R*)-2'-désoxy-2'-fluoro-*P*-thioadénylyl-(3'→5')-(*P*<sup>2</sup>*R*)-7-fluoro-*P*-thio-7-désazainosinyl-(2'→5')]  
agoniste de la protéine stimulant les gènes de  
l'interféron, antinéoplasique

dazostinag

ciclo[(*P*<sup>3</sup>*R*)-2'-desoxi-2'-fluoro-*P*-tioadenilil-(3'→5')-(*P*<sup>2</sup>*R*)-7-fluoro-*P*-tio-7-desazainosinil-(2'→5')]  
agonista de la proteína estimulador del gen de  
interferón, antineoplásico

C<sub>21</sub>H<sub>22</sub>F<sub>2</sub>N<sub>8</sub>O<sub>10</sub>P<sub>2</sub>S<sub>2</sub>

2553413-86-6

**dazukibartum #**

dazukibart

immunoglobulin G1-kappa, anti-[*Homo sapiens* IFNB1 (interferon beta)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV1-69\*11 (84.7%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v14-1 CH2 A1.3, A1.2, A1 (CH1 K120 (216) (120-217), hinge 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237), G1>A (239) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16\*01 (87.8%) -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 (228-228'':231-231'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from CHO-K1 cell line, lacking the glutamine synthetase (GS-KO) gene, glycoform alfa  
*immunomodulator*

dazukibart

immunoglobuline G1-kappa, anti-[*Homo sapiens* IFNB1 (interféron bêta)], anticorps monoclonal humanisé;

chaîne lourde gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV1-69\*11 (84.7%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v14-1 CH2 A1.3, A1.2, A1 (CH1 K120 (216) (120-217), charnière 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237), G1>A (239) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16\*01 (87.8%) -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 (230-230':233-233')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa *immunomodulateur*

dazukibart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* IFNB1 (interferón beta)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV1-69\*11 (84.7%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v14-1 CH2 A1.3, A1.2, A1 (CH1 K120 (216) (120-217), bisagra 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237), G1>A (239) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16\*01 (87.8%) -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 (230-230':233-233')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa *immunomodulador*

2639474-65-8

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VKKPGSSVKV SCKASGYTFS RYWMHWVRQA PGQGLEWMGH 50  
IDPDSYTY Y NQKFRGRVTI TADESTSTAY MELSSLRSED TAVYCARWD 100  
YGNLLFEYWG QGTLVTVSSA STKGPSVFP L APSSKSTSGG TAALGCLVKD 150  
YFPEPVTWSW NSGALTSVGH TTPAVLQSSG LYSLSVVTV PSSLGTQTY 200  
ICNVNHKFSN TKVDKVEPK SCDKTHCTCP CAPEAAGAP SVFLFPKPK 250  
DTLMSIRTP E VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300  
TYRVVSVLTV LHQDNLNGKE YKCKVSNKAL PAPIERTISK AKGQPREPQV 350  
YTLPPSREEM TKNQVSLTCL VKGIFYPSDIA VEWESNGQPE NNYKTTFPVL 400  
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPG 448

## Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGDRTV ITCRTSQDIG NYLNWYQQKPK GKAFKLLIYS 50  
TSRLHSGVPS RFGSGSGSDT FTLTISSLQP EDFATYYCOQ GIILPITFGG 100  
GTRKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQMKV 150  
DNALQSGNSQ ESVTEQDSK STYLSSTLT LSKADYEKHK VYACEVTHQG 200  
LSSPVTKSFN RGECC 214

## Post-translational modifications

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

Intra-H (C23-C104) 22-96 146-202 263-323 369-427  
22"-96" 146"-202" 263"-323" 369"-427"

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

Inter-H-L (h 5-CL 126) 222-214" 222"-214"  
Inter-H-H (h 11, h 14) 228-228" 231-231"

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

Q > pyroglutamy (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoproliolo)  
H 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 biantenaricos complejos fucosilados.

**debamestrocelum**

debamestrocel

autologous bone marrow-derived mesenchymal stromal cells (MSC) differentiated to secrete high levels of neurotrophic factors (NTF). The MSCs are isolated from the bone marrow aspirate and cultured in xeno-free growth medium containing 10% platelet lysate. To induce MSC differentiation, the cells are cultured in serum-free media supplemented with dibutyl cyclic AMP (dbcAMP), human basic fibroblast growth factor (bFGF), human platelet derived growth factor (PDGF-AA), and human heregulin- $\beta$ 1. The cells express mesenchymal progenitor cell marker cluster of differentiation 73 (CD73), CD90, and CD105 (>90%) and secrete high levels of NTF (glial cell line-derived neurotrophic factor (GDNF), brain derived neurotrophic factor (BDNF), vascular endothelial growth factor (VEGF) and hepatocyte growth factor (HGF)), having VEGF ( $\geq 7000$  pg/ $10^6$  cells) as the most representative cell therapy (*neurodegenerative diseases*)

débamestrocel

cellules stromales mésenchymateuses (MSC) autologues dérivées de la moelle osseuse, différenciées pour sécréter des niveaux élevés de facteurs neurotrophiques (NTF). Les MSC sont isolées à partir d'une aspiration de moelle osseuse et cultivées dans un milieu de croissance non-xéno contenant 10% de lysat de plaquettes. Pour induire la différenciation des MSC, les cellules sont cultivées dans un milieu sans sérum complété par de l'AMP cyclique dibutyle (dbcAMP), du facteur de croissance basique des fibroblastes humain (bFGF), du facteur de croissance dérivé des plaquettes humaines (PDGF-AA) et de l'héréguline  $\beta$ 1 humaine. Les cellules expriment les marqueurs des classes de différenciation 73 (CD73) de cellules progénitrices mésenchymateuses, CD90 et CD105 (>90%) et sécrètent des niveaux élevés de NTF (facteur neurotrophique dérivé de la lignée de cellules gliales (GDNF), facteur neurotrophique dérivé du cerveau (BDNF), facteur de croissance endothéliale vasculaire (VEGF) et facteur de croissance des hépatocytes (HGF)), le VEGF ( $\geq 7000$  pg/ $10^6$  cellules) étant le plus représentatif  
*thérapie cellulaire (maladies neurodégénératives)*

debamestrocel

células mesenquimales estromales (MSC) autólogas, derivadas de médula ósea, diferenciadas para secretar niveles altos de factores neurotróficos (NFT). Las MSCs se aíslan del aspirado de médula ósea y se cultivan en medio de crecimiento sin componentes xenogénicos que contiene 10% de lisado plaquetario. Para inducir la diferenciación de las MSC, las células se cultivan en medio sin suero suplementado con dibutilil AMP cíclico (dbcAMP), factor de crecimiento de fibroblastos básico (bFGF) humano, factor de crecimiento derivado de plaquetas humano (PDGF-AA) y heregulina  $\beta$ 1 humana. Las células expresan marcadores de células mesenquimales progenitoras grupo de diferenciación 73 (CD73), CD90 y CD105 (>90%) y secretan niveles altos de NTF (factor neurotrófico derivado de la línea de células gliales (GDNF), factor neurotrófico derivado de cerebro (BDNF), factor de crecimiento del endotelio vascular (VEGF) y factor de crecimiento de hepatocitos (HGF)), teniendo al VEGF ( $\geq 7000$  pg/ $10^6$  células) como el más representativo  
*terapia celular (enfermedades neurodegenerativas)*

**detalimogenum voraplasmidum #**

detalimogene voraplasmid

DNA plasmid encoding codon-optimized human interleukin-12 (IL-12) subunits p40 ( $\beta$ ) and p35 ( $\alpha$ ) joined by a ten amino acid linker sequence (VPGVG)<sub>2</sub>, under control of a cytomegalovirus (CMV) enhancer-promoter and a bovine growth hormone (bGH) polyadenylation signal, plus two retinoic acid-inducible gene I (RIG-I) agonists (non-protein coding double-stranded RNA eRNA11a and adenovirus VA RNAI) under control of RNA Pol-III promoters. The plasmid also contains an origin of replication, a human T-cell leukemia virus type 1 (HTLV-1) R region, and a  $\beta$ -globin intron  
*gene therapy (antineoplastic)*

détalimogène voraplasme

plasmide d'ADN codant les sous-unités p40 ( $\beta$ ) et p35 ( $\alpha$ ) de l'interleukine-12 (IL-12) humaine aux codons optimisés et réunies par une séquence de liaison de dix acides aminés (VPGVG)<sub>2</sub>, sous le contrôle d'un amplificateur-promoteur du cytomégalovirus (CMV) et d'un signal de polyadénylation de l'hormone de croissance bovine (bGH), plus deux agonistes du gène I inducible par l'acide rétinolique (RIG-I) (ARN eRNA11a double brin non codant des protéines et le RNAI de l'adénovirus VA) sous le contrôle de promoteurs RNA Pol-III. Le plasmide contient également une origine de réplication, une région R du virus de la leucémie humaine à lymphocytes T de type 1 (HTLV-1) et un intron de la  $\beta$ -globine.  
*thérapie génique (antinéoplasique)*

detalimogén voraplásmido

plásmido de ADN que codifica, con codones optimizados, para las subunidades p40 ( $\beta$ ) y p35 ( $\alpha$ ) de la interleuquina-12 (IL-12) humana unida a una secuencia de unión de diez amino ácidos (VPGVG)<sub>2</sub>, bajo el control de un potenciador-promotor de citomegalovirus (CMV) y una señal de poliadenilación de la hormona de crecimiento bovina (bGH), más dos agonistas del gen inducible por ácido retinoico I (RIG-I) (ARN no codificante de doble cadena eRNA11a y VA RNAI de adenovirus) bajo el control de promotores de ARN pol-III. El plásmido también contiene un origen de la replicación, una región R del virus de la leucemia de linfocitos T humano tipo 1 (HTLV-1) y un intrón de la  $\beta$ -globina  
*terapia génica (antineoplásico)*

2660044-23-3

**deupirfenidonum**

deupirfenidone

5-(<sup>2</sup>H<sub>3</sub>)methyl-1-phenylpyridin-2(1H)-one  
*anti-inflammatory, antifibrotic*

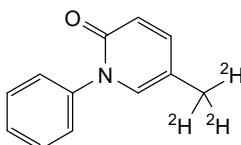
deupirfénidone

5-(<sup>2</sup>H<sub>3</sub>)méthyl-1-phénylpyridin-2(1H)-one  
*anti-inflammatoire, antifibrotique*

deupirfenidona

5-(<sup>2</sup>H<sub>3</sub>)metil-1-fenilpiridin-2(1H)-ona  
*antiinflamatorio, antifibrótico*C<sub>12</sub>H<sub>8</sub><sup>2</sup>H<sub>3</sub>NO

1093951-85-9

**dibutepinephrinum**

dibutepinephrine

4-[(1R)-1-hydroxy-2-(methylamino)ethyl]-1,2-phenylene bis(2-methylpropanoate)  
*sympathomimetic*

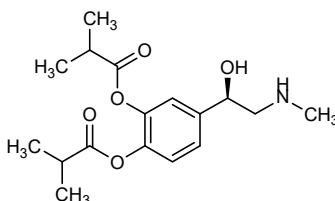
dibutépinéphrine

bis(2-metilpropanoato) de 4-[(1R)-1-hidroxi-2-(methylamino)etil]-1,2-fenileno  
*sympathomimétique*

dibutepinefrina

bis(2-metilpropanoato) de 4-[(1R)-1-hidroxi-2-(metilamino)etil]-1,2-fenileno  
*simpaticomimético*C<sub>17</sub>H<sub>25</sub>NO<sub>5</sub>

2735735-23-4

**durcabtagenum autoleucelum #**

durcabtogene autoleucel

autologous T lymphocytes obtained from peripheral blood mononuclear cells by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector encoding a chimeric antigen receptor (CAR) targeting human B cell maturation antigen (BCMA). The expressed transgene comprises a CD8 $\alpha$  leader sequence, an anti-BCMA single chain variable fragment (scFv), a CD8 $\alpha$  hinge and transmembrane domain, and a 4-1BB (CD137) and CD3 $\zeta$  signalling domain, under control of the human elongation factor 1 $\alpha$  (EF-1 $\alpha$ ) promoter. The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a  $\psi$  packaging signal, a truncated *gag*, a Rev response element (RRE), a central polypurine tract (cPPT) sequence and a synthetic ID tag sequence. The leukapheresis material is enriched for CD4<sup>+</sup> and CD8<sup>+</sup> T lymphocytes by positive immunoselection, activated by CD3 and CD28 agonists and transduced with the lentiviral vector in serum-free media containing interleukin 2 (IL-2). Without further cell propagation *in*

*vitro*, the T lymphocytes are washed, formulated for infusion, and cryopreserved. The T lymphocytes phenotype very closely resembles that of the initial leukapheresis material. The cell suspension consists of T lymphocytes ( $\geq 80\%$ ;  $\leq 1\%$  B cells), with a minimum of 4.0% of the T lymphocytes expressing the CAR-BCMA transgene. The T lymphocytes secrete interferon gamma (IFN- $\gamma$ ) and IL-2 following co-culture with BCMA-expressing cells  
*cell-based gene therapy (antineoplastic)*

durcabtagène autoleucel

lymphocytes T autologues obtenus à partir de cellules mononucléaires de sang périphérique par leucaphérèse, transduits avec un vecteur lentiviral auto-inactivant et non répliquant codant un récepteur antigénique chimérique (CAR) ciblant l'antigène de maturation des cellules B humaines (BCMA). Le transgène exprimé comprend une séquence de tête CD8 $\alpha$ , un fragment variable à chaîne unique (scFv) anti-BCMA, un domaine charnière et transmembranaire CD8 $\alpha$ , et un domaine de signalisation 4-1BB (CD137) et CD3 $\zeta$ , sous le contrôle du promoteur du facteur d'élongation 1 $\alpha$  (EF-1 $\alpha$ ) humain. La construction est flanquée de répétitions longues terminales (LTR) en 5' et 3' et contient également un signal d'encapsulation  $\psi$ , un *gag* tronqué, un élément de réponse Rev (RRE), une séquence de tractus polypurine central (cPPT) et une séquence synthétique avec étiquette d'identification. Le matériel de leucaphérèse est enrichi en lymphocytes T CD4+ et CD8+ par immunosélection positive, activé par des agonistes CD3 et CD28 et transduit avec le vecteur lentiviral dans un milieu sans sérum contenant de l'interleukine 2 (IL-2). Sans propagation cellulaire supplémentaire *in vitro*, les lymphocytes T sont lavées, formulées pour la perfusion et cryoconservées. Le phénotype des lymphocytes T ressemble beaucoup à celui du matériel de leucaphérèse initial. La suspension cellulaire est constituée de lymphocytes T ( $\geq 80\%$ ;  $\leq 1\%$  de lymphocytes B), avec un minimum de 4.0 % des lymphocytes T exprimant le transgène CAR-BCMA. Les lymphocytes T sécrètent de l'interféron gamma (IFN-  $\gamma$ ) et IL-2 suite à la coculture avec des cellules exprimant BCMA  
*thérapie génique à base de cellules (antinéoplasique)*

durcabtagén autoleucel

linfocitos T autólogos obtenidos de células mononucleares de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica para un receptor de antígenos quimérico (CAR) dirigido al antígeno de maduración de células B (BCMA). El transgén expresado contiene una secuencia líder de CD8 $\alpha$ , un fragmento variable de cadena sencilla (scFv) anti-BCMA, un dominio bisagra y transmembrana de CD8 $\alpha$ , y un dominio de señalización 4-1BB (CD137) y CD3 $\zeta$ , bajo el control del promotor del factor de elongación 1 alfa (EF1 $\alpha$ ). El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento  $\psi$ , un *gag* truncado, un elemento de respuesta Rev (RRE), una secuencia de tracto de polipurina central (cPPT) y una secuencia etiqueta ID sintética. El material de leucoaféresis se enriquece para linfocitos T CD4+ y CD8+ mediante inmunoselección positiva, se activa mediante agonistas de CD3 y CD28 y se transduce con el vector lentiviral en medio sin suero que contiene interleuquina 2 (IL-2). Sin más

propagación *in vitro*, los linfocitos T se lavan, se formulan para infusión y se criopreservan. El fenotipo de los linfocitos T se parece mucho al del material de leucoaféresis inicial. La suspensión celular consiste en linfocitos T ( $\geq 80\%$ ;  $\leq 1\%$  de linfocitos B), con un mínimo del 4.0% de linfocitos T que expresan el transgén CAR-BCMA. Los linfocitos T secretan interferón gamma (IFN- $\gamma$ ) e IL-2 tras el cocultivo con células que expresan BCMA  
*terapia génica basada en células (antineoplásico)*

**duvakitugum #**

duvakitug

immunoglobulin G1-lambda, anti-[*Homo sapiens* TNFSF15 (tumor necrosis factor (TNF) superfamily member 15, vascular endothelial cell growth inhibitor, VEGI, TNF superfamily ligand TL1A)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV1-8\*01 (92.9%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-215')-disulfide with lambda light chain *Homo sapiens*(1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-40\*01 (85.7%) -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 (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV, glycoform alfa  
*anti-inflammatory*

duvakitug

immunoglobuline G1-lambda, anti-[*Homo sapiens* TNFSF15 (membre 15 de la superfamille du facteur de nécrose tumorale (TNF), inhibiteur de la croissance des cellules endothéliales vasculaires, VEGI, ligand TL1A de la superfamille du TNF), anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV1-8\*01 (92.9%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1CH1 K120, CH3 D12, L14 (CH1 K120 (216) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-215')-disulfure avec la chaîne légère lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-40\*01 (85.7%) -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 (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO- K1SV, glycoforme alfa  
*anti-inflammatoire*

duvakitug

inmunoglobulina G1-lambda, anti-[*Homo sapiens* TNFSF15 (miembro 15 de la superfamilia del factor de necrosis tumoral (TNF), inhibidor del crecimiento de las células endoteliales vasculares, VEGI, ligando TL1A de la superfamilia del TNF), anticuerpo monoclonal *Homo sapiens*;



cadena pesada gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV1-8\*01 (92.9%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14(CH1 K120 (216) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-215')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-40\*01 (85.7%) -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 (228-228''-231-231'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO- K1SV, forma glicosilada alfa **antiinflamatorio**

2750005-84-4

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYDINWVRQA PGQGLEWMGW 50  
LNPNSGYTGY AQRKQGRVTM TADRSTSTAY MELSSLRSED TAVYVCAREV 100  
PETAFAFEYWG QGTLVTVSSA STKGPSVFPPL APSSKSTSGG TAALGCLVKD 150  
YFPEPFTVSW NSGALTSGVH TTPAVLQSSG LYSLSSTVTV PSSSLGTQTY 200  
ICNVNHKPSN TKVDKKVEPK SCDKTHCTPP CPAPPELLGGF SVFLFPPKPK 250  
DTLMISRTPE VTCVVDVSH EDEPEVKFNWY VDGVEVHNAK TKPREQYNS 300  
TYRVVSVLTV LHQDNLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350  
YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEVESNGQPE NNYKTTTPVVL 400  
DSDGSFFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPG 448

## Light chain / Chaîne légère / Cadena ligera

QSVLTQPPSV SGAPGQRVTI SCTSSSSDGI AGLGVHMYQQ LPGTAPKLLI 50  
EGYVYRPSGV PDRFSGSKSG TSASLITLGL LPEDEGDYIC QSWDGLSAL 100  
FGGOTKLTVL GQPKAAPSVT LFPSSSEELQ ANKATLVCLI SDFYPGAVTV 150  
AWKADSSPVK AGVETTTPSK QSNMKYAAAS YLSLTPEQWK SHRSYSCQVT 200  
HEGSTVEKTV APTTECS 216

## 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) 22''-90'' 138''-197''  
22'''-90''' 138'''-197'''

Inter-H-L (h 5-CL 126) 222-215'' 222''-215''

Inter-H-H (h 11, h 14) 228-228'' 231-231''

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

Q &gt; pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxopropilo)

H VH Q1: 1, 1''

L VL Q1: 1', 1'''

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

H CH2 N84.4: 299, 299''

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

**ederimotidum**  
ederimotide

[R126>Y]-human Wilms tumor protein (WT33)-(126-134)-peptide;  
L-tyrosyl-L-methionyl-L-phenylalanyl-L-prolyl-L-asparaginyl-L-alanyl-L-prolyl-L-tyrosyl-L-leucine  
*immunological agent for active immunization*  
*(antineoplastic)*

édérimotide

[R126>Y]-protéine humaine de la tumeur de Wilms (WT33)-(126-134)-peptide;  
L-tyrosyl-L-méthionyl-L-phénylalanyl-L-prolyl-L-asparaginyl-L-alanyl-L-prolyl-L-tyrosyl-L-leucine  
*agent immunologique d'immunisation active*  
*(antineoplasique)*

ederimotida

[R126>Y]-proteína humana del tumor de Wilms (WT33)-(126-134)-péptido;  
L-tirosil-L-metionil-L-fenilalanil-L-prolil-L-asparaginil-L-alanil-L-prolil-L-tirosil-L-leucina  
*agente inmunológico para inmunización activa (antineoplásico)*

C<sub>55</sub>H<sub>74</sub>N<sub>10</sub>O<sub>13</sub>S

852243-39-1

H – Tyr – Met – Phe – Pro – Asn – Ala – Pro – Tyr – Leu – OH

**efbalropendekinum alfa #**  
efbalropendekinum alfa

human interleukin-15 (IL-15) fragment (1-114) variant (D<sup>30</sup>>N, E<sup>64</sup>>Q, N<sup>65</sup>>D) fused via peptide linker <sup>115</sup>GGGGS<sup>119</sup> to a human immunoglobulin G1 C-terminal Fc fragment (120-350) variant, [*Homo sapiens* IGHG1\*03; hinge: 120-134 (C124S); CH2: 135-243 (E137P, L138V, L139A, G139-140del, S170K, Q198E whereby E137P, L138V, L139A, G139-140del matches IGHG2\*02); CH3: 244-348 (L271D, K273S, N287D, Q321E, N324D, M331L, N337S); CHS: 349-350], disulfide bridge with human interleukin-15 receptor subunit alpha fragment (1-65) fused via the <sup>66</sup>GGGGS<sup>70</sup> peptide linker to a human immunoglobulin G1 Fc fragment (71-301) variant [*Homo sapiens* IGHG1\*03; Hinge: 71-85 (C75S); CH2: 86-194 (E88P, L89V, L90A, G90-91del, S121K); CH3: 195-299 (E211Q, S218K, M282L, N288S); CHS: 300-301], disulfide bridged heterodimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa  
*interleukin-15 analogue, immunomodulator*

efbalropendékine alfa

variant (D<sup>30</sup>>N, E<sup>64</sup>>Q, N<sup>65</sup>>D) du fragment (1-114) de l'interleukine-15 (IL-15) humaine fusionné via la liaison peptidique <sup>115</sup>GGGGS<sup>119</sup> à un variant du fragment Fc C-terminal de l'immunoglobuline G1 humaine (120-350), [*Homo sapiens* IGHG1\*03; charnière: 120-134 (C124S); CH2: 135-243 (E137P, L138V, L139A, G139-140del, S170K, Q198E par lequel E137P, L138V, L139A, G139-140del correspond à IGHG2\*02); CH3: 244-348 (L271D, K273S, N287D, Q321E, N324D, M331L, N337S); CHS: 349-350], pont disulfure avec le fragment alpha de la sous-unité du récepteur de l'interleukine-15 humaine (1-65) fusionné via la liaison peptidique <sup>66</sup>GGGGS<sup>70</sup> à un variant du fragment Fc de l'immunoglobuline G1 humaine (71-301) [*Homo sapiens* IGHG1\*03; charnière: 71-85 (C75S); CH2 : 86-194 (E88P, L89V, L90A, G90-91del, S121K); CH3: 195-299 (E211Q, S218K, M282L, N288S); CHS: 300-301], hétérodimère à pont disulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa  
*analogue de l'interleukine 15, immunomodulateur*

efbalropendekina alfa

interleukina-15 humana (IL-15) fragmento (1-114) variante (D<sup>30</sup>>N, E<sup>64</sup>>Q, N<sup>65</sup>>D) fusionado a través del enlace peptídico <sup>115</sup>GGGGS<sup>119</sup> al fragmento Fc de una inmunoglobulina humana terminal G1 C (120-350) variante, [*Homo sapiens* IGHG1\*03; bisagra: 120-134

(C124S); CH2: 135-243 (E137P, L138V, L139A, G139-140del, S170K, Q198E por lo cual E137P, L138V, L139A, G139-140del se corresponde con IGHG2\*02); CH3: 244-348 (L271D, K273S, N287D, Q321E, N324D, M331L, N337S); CHS: 349-350], puente disulfuro con el fragment de la subunidad alfa del receptor de la interleukina-15 humana (1-65) fusionado a través del enlace peptídico <sup>66</sup>GGGS<sup>70</sup> al fragment Fc de la inmunoglobulina humana G1 (71-301) variante [*Homo sapiens* IGHG1\*03; bisagra: 71-85 (C75S); CH2: 86-194 (E88P, L89V, L90A, G90-91del, S121K); CH3: 195-299 (E211Q, S218K, M282L, N288S); CHS: 300-301], heterodímero con puente disulfuro, prodido en células ováricas de hámster Chino (CHO), forma glicosilada alfa *análogo de la interleukina 15, inmunomodulador*

2736449-62-8

Sequence / Séquence / Secuencia

IL15-Fc:  
**NWVNVISDLK KIEDLIQSMH IDATLYTESN VHPSCVKVTAM KCFLELQVI** 50  
**SLESGDASH DTVDLILILA NNSLSSNGNV TEGCKECEE LEEKNIKEFL** 100  
**QSFVHIVQMF INTSGGGGSE** PKSDKTHTC PFCFAPFVA G PSVFLFPFKP 150  
 KDTLMISRTF EVTCVVVDV **K** HEDPEVKFN YVDGVEVHNA KTKPREE **E**YN 200  
 STYRVVSVLT VLVHQQDLNGLG EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 250  
 VYTLPPSREE MTKNQVSLT **D**VSGFYPSDI AVEWESD **Q**GP ENNYKTT **P**VP 300  
 LDSGDSFFLY SKLTVDKSR **E**QGDV **F**SCSV **L**HEALH **S**HYT QKSLSLSPGK 350

IL15R-Fc:  
**ITCPPPMSVE HADIWVKYS LYSRERYICN SGFKRKA GTS SLTECVLNKA** 50  
**TNVAHWTPPS LKCI RGGGGS** EPKSDKTHTC CPPCPAP **FVA** GPSVFLFPFK 100  
 PKDTLMISRT PEVTCVVVDV **K**HEDPEVKFN WYVDGVEVHN AKTKPREBQY 150  
 NSTYRVVSVL TVLVHQQDLNGLG KEYKCKVSNK ALPAPIEKTIS SKARGQPREP 200  
 QVYTLPPSRE **Q**MTKNQV **K**LT CLVKGFYPSD IAVEWESNGQ PENNYKTT **P** 250  
 VLDSGDSFFL YSKLTVDKSR WQQGNV **F**SCSV **V**LHEALH **S**HYT QKSLSLSPG 300  
 K 350

Peptide linkers / Peptides liants / Péptidos de unión

IL15-IgG1Fc: **GGGG** 115-119  
 IL15R-IgG1Fc: **GGGG** 66-70

Mutation / Mutation / Mutación

IL-15: D<sup>30</sup>>N, E<sup>64</sup>>Q, N<sup>65</sup>>D  
 IL15-Fc: C<sup>124</sup>>S, E<sup>137</sup>>P, L<sup>138</sup>>Y, L<sup>139</sup>>A, G<sup>139-140</sup>>del, S<sup>170</sup>>K, Q<sup>198</sup>>E, L<sup>271</sup>>D, K<sup>273</sup>>S, N<sup>287</sup>>D, Q<sup>321</sup>>E, N<sup>324</sup>>D, M<sup>331</sup>>L, N<sup>337</sup>>S  
 IL15R-Fc: C<sup>75</sup>>S, E<sup>88</sup>>P, L<sup>89</sup>>Y, L<sup>90</sup>>A, G<sup>90-91</sup>>del, S<sup>121</sup>>K, E<sup>211</sup>>Q, S<sup>218</sup>>K, M<sup>282</sup>>L, N<sup>288</sup>>S

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro  
 Intra-chain IL15-IgG1 Fc: 35-85, 42 - 88, 164 - 224, 270 - 328  
 Intra-chain IR15R-IgG1Fc: 3'-45', 29'-63', 115'-175', 221'-279'  
 Inter-chain: IL15Fc-IL15RFc: 130-81', 133-84'

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

IL15-IgG1Fc: N71, N79, N112, N200  
 IL15R-IgG1Fc: N151'

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

IL15R-IgG1Fc: T2'

**efzimfotasum alfa #**  
 efzimfotase alfa

human alkaline phosphatase, tissue-nonspecific isozyme (AP-TNAP, TNS-ALP, EC:3.1.3.1) soluble fragment (1-491), variant (E<sup>108</sup>>M, N<sup>213</sup>>Q, N<sup>286</sup>>Q) fused to a human immunoglobulin G4 heavy chain

constant region fragment (492-714) [*Homo sapiens* IGHG4\*01; hinge: 492-498 (ERKCC 491-492del, P492V, P493E, S496P (matches IGHG2\*02)); CH2: 499-607 (E501P, F502V, L503A, G503-504del (matches IGHG2\*02)); CH3: 608-712; CHS: 713-714], fused to a deca-aspartate peptide (<sup>715</sup>DDDDDDDDDD<sup>724</sup>), disulfide bridged dimer, produced in Chinese hamster ovary (CHO) cells, cell line K1SV, glycoform alfa  
*enzyme replacement therapy (hypophosphatasia)*

efzimfotase alfa

fragment soluble (1-491) de l'isozyme humaine de la phosphatase alcaline non spécifique des tissus (AP-TNAP, TNS-ALP, EC:3.1.3.1), variant (E<sup>108</sup>>M, N<sup>213</sup>>Q, N<sup>286</sup>>Q) fusionné à un fragment de la région constante de la chaîne lourde de l'immunoglobuline G4 humaine (492-714) [*Homo sapiens* IGHG4\*01; charnière: 492-498 (ERKCC 491-492del, P492V, P493E, S496P (correspond à IGHG2\*02)); CH2: 499-607 (E501P, F502V, L503A, G503-504del (correspond à IGHG2\*02)); CH3: 608-712; CHS: 713-714], fusionné à un peptide déca-aspartate (<sup>715</sup>DDDDDDDDDD<sup>724</sup>), dimère à pont disulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire K1SV, glycoforme alfa  
*traitement enzymatique substitutif (hypophosphatasie)*

efzimfotasa alfa

fosfatasa humana alcalina isoenzima tisular no específica (AP-TNAP, TNS-ALP, EC:3.1.3.1) fragmento soluble (1-491), variante (E<sup>108</sup>>M, N<sup>213</sup>>Q, N<sup>286</sup>>Q) fusionada a una cadena pesada de la inmunoglobulina humana G4 fragmento de la región constante (492-714) [*Homo sapiens* IGHG4\*01; bisagra: 492-498 (ERKCC 491-492del, P492V, P493E, S496P (corresponde IGHG2\*02)); CH2: 499-607 (E501P, F502V, L503A, G503-504del (corresponde IGHG2\*02)); CH3: 608-712; CHS: 713-714], fusionada a un péptido deca-aspartato (<sup>715</sup>DDDDDDDDDD<sup>724</sup>), dímero con puente disulfuro, producida en células ováricas de hámster Chino (CHO), línea celular K1SV, forma glicosilada alfa  
*tratamiento enzimático de sustitución (hipofosfatasa)*

2746354-58-3

Sequence / Séquence / Secuencia	
LVPEKEKDPK YWRDQAQETL KYALELQKLN TNVAKNVIMF LGDGMGVSTV	50
TAARILKGLL HNNPGEETRL EMDKFFPFVAL SKTYNTNAQV PDSAGTATAY	100
LCGVKAMGGT VGVSAATERS RCNTFQGNEV TSLRWAKDA GRSVGIWTTT	150
RVNHATFSA AYAHSADRDWY SDNEMPPPEAL SQGCKDIAYQ LMHNIRIDIV	200
IMGGGRKYMY PKQKTDVEYE SDEKARGTRL DGLDLVDTWK SFKPRYKHS	250
FIMNRTELLT LDPHNVYLL GLEFEPGMQY ELNRNQTDP SLSEMYVVAI	300
QILRNPKGF PLLVEGGRID HGHHEGKAKQ ALHEAVEMDR AIGQAGSLTS	350
SEDTLTVVTA DSHSVETFGG YTPRGNSIFG LAPMLSOTDK KPFTAILYGN	400
GPYKVVGGG RENVMVDYA HNNYQAQSAV PLRHETHGGE DVAVFSKGM	450
AHLHGVHEQ NYVPHVMAYA ACIGANLGHG APASSAGSLA AVECFPCPAP	500
PVAGSVEFLP PPKPKDITMI SRTPEVTCVV VDVSDPEVE QFNWYVDGVE	550
VHNAKTKFRE EQFNSTYRVV SVLTVLHQDW LNKKEYKCKV SNKGLPSSIE	600
KTISKAKGQP REPQVITLPP SQEEMTKNQV SLTCLVKGFY PSDIAVEWES	650
NQQFPENNYKT TPFVLDSDGS FFLYSRLTVD KSRWQEGNVF SCVSMHEALH	700
NHYYQKSLSL SLGKDDDDDD DDDD	724

Mutation / Mutación / Mutación  
 E108>M, N213>Q, N286>Q

**Post-translational modifications**  
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro  
 Intra-chain: 122'-184, 472'-480, 528'-588, 634'-692  
 122'-184', 472'-480', 528'-588', 634'-692'  
 Inter-chain: 494'-494', 497'-497'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación  
 N123, N254, N413, N564, N123', N254', N413', N564'

Potential O-glycosylation sites / Sites de O-glycosylation potentielle / Posiciones de O-glicosilación potencial  
 S484, S485, S488, or S506 (one site only)

**elenestininibum**

elenestininib

2-{4-[4-(4-{5-[(1S)-1-amino-1-(4-fluorophenyl)ethyl]pyrimidin-2-yl}piperazin-1-yl)pyrrolo[2,1-f][1,2,4]triazin-6-yl]-1H-pyrazol-1-yl}ethan-1-ol  
*tyrosine kinase inhibitor, antineoplastic*

élénestinib

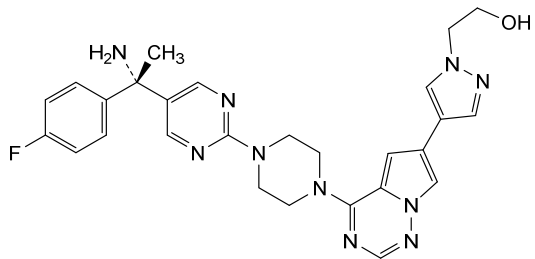
2-{4-[4-(4-{5-[(1S)-1-amino-1-(4-fluorophényl)éthyl]pyrimidin-2-yl}pipérazin-1-yl)pyrrolo[2,1-f][1,2,4]triazin-6-yl]-1H-pyrazol-1-yl}éthan-1-ol  
*inhibiteur de tyrosine kinase, antinéoplasique*

elenestininib

2-{4-[4-(4-{5-[(1S)-1-amino-1-(4-fluorofenil)etil]pirimidin-2-il}pipérazin-1-il)pirrolo[2,1-f][1,2,4]triazin-6-il]-1H-pirazol-1-il}etan-1-ol  
*inhibidor de tirosina kinasa, antineoplásico*

C<sub>27</sub>H<sub>29</sub>FN<sub>10</sub>O

2505078-08-8

**elriterceptum #**

elritercept

human activin receptor type 2-A (activin receptor type IIA, ACTR-IIA) extracellular domain (ECD) fragment (1-109) engineered variant (F<sup>15</sup>>Y, <sup>21</sup>KD<sup>22</sup>>LE, P<sup>31</sup>>R, Y<sup>33</sup>>E, D<sup>35</sup>>E, R<sup>40</sup>>L, F<sup>43</sup>>Y, K<sup>47</sup>>R, Q<sup>58</sup>>K, I<sup>65</sup>>F, <sup>76</sup>KKDS<sup>79</sup>>TEEN, E<sup>81</sup>>Q) fused via the peptide linker <sup>110</sup>GGG<sup>112</sup> to a human immunoglobulin G1 heavy chain fragment C-terminal Fc fragment (113-338), [*Homo sapiens* IGHG1\*01; hinge: 113-122 (EPKSC 112-113del); CH2: 123-232; CH3: 233-337; CHS: 338-338 (K339del)]; disulfide bridged dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa *hematopoietic*

elritercept

variant modifié du fragment (1-109) du domaine extracellulaire (ECD) du récepteur de l'activine humaine de type 2-A (récepteur de l'activine de type IIA, ACTR-IIA) (F<sup>15</sup>>Y, <sup>21</sup>KD<sup>22</sup>>LE, P<sup>31</sup>>R, Y<sup>33</sup>>E, D<sup>35</sup>>E, R<sup>40</sup>>L, F<sup>43</sup>>Y, K<sup>47</sup>>R, Q<sup>58</sup>>K, I<sup>65</sup>>F, <sup>76</sup>KKDS<sup>79</sup>>TEEN, E<sup>81</sup>>Q) fusionné via la liaison peptidique <sup>110</sup>GGG<sup>112</sup> à un fragment Fc en C-terminal de la chaîne lourde de l'immunoglobuline G1 humaine (113-338), [*Homo sapiens* IGHG1\*01; charnière: 113-122 (EPKSC 112-113del); CH2: 123-232 ; CH3: 233-337; CHS: 338-338 (K339del)]; dimère à pont disulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa *hématopoiétique*

elritercept

receptor humano de la activina de tipo 2-A (receptor de la activina tipo IIA, ACTR-IIA) dominio extracelular (ECD) fragmento (1-109) variante diseñada (F<sup>15</sup>>Y, <sup>21</sup>KD<sup>22</sup>>LE, P<sup>31</sup>>R, Y<sup>33</sup>>E, D<sup>35</sup>>E, R<sup>40</sup>>L, F<sup>43</sup>>Y, K<sup>47</sup>>R, Q<sup>58</sup>>K, I<sup>65</sup>>F, <sup>76</sup>KKDS<sup>79</sup>>TEEN, E<sup>81</sup>>Q) fusionada a través de un enlace peptídico <sup>110</sup>GGG<sup>112</sup> a la cadena pesada de la inmunoglobulina humana G1 fragmento C-terminal Fc fragmento (113-338), [*Homo sapiens* IGHG1\*01; bisagra: 113-122 (EPKSC 112-113del); CH2: 123-232; CH3: 233-337; CHS: 338-338 (K339del)]; dímero con puente disulfuro, producido en células ováricas de hámster Chino (CHO), forma glicosilada alfa *hematopoyético*

2727114-26-1

## Sequence / Séquence / Secuencia

```
GAILGRSETQ ECLFYNANWE LERTNQTGVE RCECCKDKRL HCYATWRNIS 50
GSIEIVRKGC WLDDFNCYDR TDCVETEENP QVYFCCCEGN MCNEKFSYFP 100
EMEVITQPTSG GGDKTHTCPP CFAPELLGGP SVFLFPPKPK DTLMISRTP 150
VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS TYRVVSVLTV 200
LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV YTLPPSRDEL 250
TRNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTTPVL DSDGSFFFLYS 300
KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPG 338
```

## Peptide linker / Peptides liant / Péptido de unión

*GGG* 110-112

## Mutation / Mutation / Mutación

F<sup>15</sup>>Y, <sup>21</sup>KD<sup>22</sup>>LE, P<sup>31</sup>>R, Y<sup>33</sup>>E, D<sup>35</sup>>E, R<sup>40</sup>>L, F<sup>43</sup>>Y, K<sup>47</sup>>R, Q<sup>58</sup>>K, I<sup>65</sup>>E, <sup>76</sup>KKDS<sup>79</sup>>TEEN, E<sup>81</sup>>Q

## Post-translational modifications

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

Intra-chain 12 - 42, 32 - 60, 67 - 86, 73 - 85, 87 - 92, 153 - 213, 259 - 317  
12'-42', 32'-60', 67'-86', 73'-85', 87'-92', 153'-213', 259'-317'

Inter-chain 118-118', 121-121'

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

N25, N48, N189, N25', N48', N189'

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

S97, S97'

## emzeltrectinibum

emzeltrectinib

2-amino-5-[(2*R*,4*S*)-2-(2,5-difluorophenyl)-4-fluoropyrrolidin-1-yl]-pyrazolo[1,5-*a*]pyrimidine-3-carboxamide  
*tyrosine kinase inhibitor, antineoplastic*

emzeltrectinib

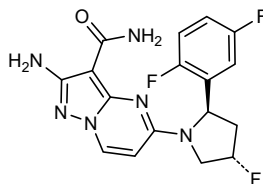
2-amino-5-[(2*R*,4*S*)-2-(2,5-difluorophényl)-4-fluoropyrrolidin-1-yl]-pyrazolo[1,5-*a*]pyrimidine-3-carboxamide  
*inhibiteur de tyrosine kinase, antinéoplasique*

emzeltrectinib

2-amino-5-[(2*R*,4*S*)-2-(2,5-difluorofenil)-4-fluoropirrolidin-1-il]-pirazolo[1,5-*a*]pirimidina-3-carboxamida  
*inhibidor de tirosina kinasa, antineoplásico*

C<sub>17</sub>H<sub>15</sub>F<sub>3</sub>N<sub>6</sub>O

2223678-97-3



**enlicitidi chloridum**

enlicitide chloride

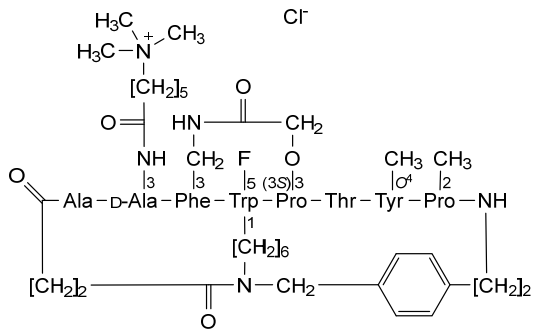
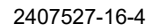
1,4:3,5:4,8-trianhydro[L-alanyl-3-[6-(trimethylazaniumyl)hexanamido]-D-alanyl-3-(aminomethyl)-L-phenylalanyl-1-{6-[[[4-(2-aminoethyl)phenyl]methyl]}(3-carboxypropanoyl)amino]hexyl]-5-fluoro-L-tryptophyl-(3S)-3-(carboxymethoxy)-L-prolyl-L-threonyl-O-methyl-L-tyrosyl-2-methyl-L-proline] chloride  
*proprotein convertase subtilisin/ kexin type 9 (PCSK9) inhibitor*

chlorure d'enlicitide

chlorure de 1,4:3,5:4,8-trianhydro[L-alanyl-3-[6-(triméthylazaniumyl)hexanamido]-D-alanyl-3-(aminométhyl)-L-phénylalanyl-1-{6-[[[4-(2-aminoéthyl)phényl]méthyl]}(3-carboxypropanoyl)amino]hexyl]-5-fluoro-L-tryptophyl-(3S)-3-(carboxyméthoxy)-L-prolyl-L-thréonyl-O-méthyl-L-tyrosyl-2-méthyl-L-proline]  
*inhibiteur de la proprotéine convertase subtilisine/ kexine de type 9 (PCSK9)*

cloruro de enlicitida

cloruro de 1,4:3,5:4,8-trianhidro[L-alanil-3-[6-(trimetilazaniumil)hexanamido]-D-alanil-3-(aminometil)-L-fenilalanil-1-{6-[[[4-(2-aminoetil)fenil]metil]}(3-carboxipropanoil)amino]hexil]-5-fluoro-L-triptofil-(3S)-3-(carboximetoxi)-L-prolil-L-treonil-O-metil-L-tirosil-2-metil-L-prolina]  
*inhibidor de la proprotéina convertasa subtilisina/ kexina tipo 9 (PCSK9)*



**enlonstobartum #**

enlonstobart

immunoglobulin G4-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD1, PD-1, CD279)], *Homo sapiens* monoclonal antibody; gamma4 heavy chain *Homo sapiens* (1-440) [VH (*Homo sapiens* IGHV3-33\*01 (92.8%) -(IGHD) - IGHJ4\*01 (100%), CDR-IMGT [8.8.6] (26-33.51-58.97-102)) (1-113) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (114-211), hinge 1-12 S10>P (221) (212-223), CH2 L92 (302) (224-333),

	<p>CH3 (334-438), CHS (439-440)) (114-440)], (127-214')-disulfide with kappa light chain <i>Homo sapiens</i> (1'-214') [V-KAPPA (<i>Homo sapiens</i> IGKV3-11*01 (97.9%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -<i>Homo sapiens</i> IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (219-219":222-222")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa <i>immunostimulant, antineoplastic</i></p>
enlonstobart	<p>immunoglobuline G4-kappa, anti-[<i>Homo sapiens</i> PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal <i>Homo sapiens</i>; chaîne lourde gamma4 <i>Homo sapiens</i> (1-440) [VH (<i>Homo sapiens</i> IGHV3-33*01 (92.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.6] (26-33.51-58.97-102)) (1-113) -<i>Homo sapiens</i> IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (114-211), charnière 1-12 S10&gt;P (221) (212-223), CH2 L92 (302) (224-333), CH3 (334-438), CHS (439-440)) (114-440)], (127-214')-disulfure avec la chaîne légère kappa <i>Homo sapiens</i> (1'-214') [V-KAPPA (<i>Homo sapiens</i> IGKV3-11*01 (97.9%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -<i>Homo sapiens</i> IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (219-219":222-222")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa <i>immunostimulant, antinéoplasique</i></p>
enlonstobart	<p>inmunoglobulina G4-kappa, anti-[<i>Homo sapiens</i> PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal <i>Homo sapiens</i>; cadena pesada gamma4 <i>Homo sapiens</i> (1-440) [VH (<i>Homo sapiens</i> IGHV3-33*01 (92.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.6] (26-33.51-58.97-102)) (1-113) -<i>Homo sapiens</i> IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (114-211), bisagra 1-12 S10&gt;P (221) (212-223), CH2 L92 (302) (224-333), CH3 (334-438), CHS (439-440)) (114-440)], (127-214')-disulfuro con la cadena ligera kappa <i>Homo sapiens</i> (1'-214') [V-KAPPA (<i>Homo sapiens</i> IGKV3-11*01 (97.9%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -<i>Homo sapiens</i> IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (219-219":222-222")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa <i>inmunostimulante, antineoplásico</i></p>



C<sub>63720</sub>H<sub>9878</sub>N<sub>1712</sub>O<sub>1989</sub>S<sub>42</sub>

2651230-53-2

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLVESGGG VVQPGKSLRL TCKASGLTFS SSGMHVWRQA PGKGLEWVAV 50  
 IWYDGSKRYY ADSVKGRFTI SRDNSKNTLF LQMNSLRAED TAVYYCATNN 100  
 DYWGQGTLLVT VSSASTKGPS VFPLAPCSRS TSESTAALGC LVKDYFPEPV 150  
 TVSWNSGALT SGVHTFFPAVL QSSGLYSLSS VVTVFSSSLG TKTYTCNVDH 200  
 KFSNTKVDKR VESKYGPPCF PCPAPEFLGG PSVFLFPPPK KDTLMSRTP 250  
 EVTCVVVDVS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN STYRVVSVLT 300  
 VLHQDWLNGK EYKCKVSNKG LPSSIEKTIS KAKGQPREPQ VYTLPPSQEE 350  
 MTKNQVSLTC LVRGIFYPSDI AVEWESNGQP ENNYKTTTPV LDSDGSFFLY 400  
 SRLTVDKSRW QEGNVFSCSV MHEALHNHYT QKSLSLSLGLK 440

## Light chain / Chaîne légère / Cadena ligera

EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYT 50  
 ASNRATGIPA RFGSGSGSDT FTLTISLLEP EDFAVYYCQQ YSNWPRTFGQ 100  
 GTKVEIKRTV AAPSVEIFPP SDEQLKSGTA SUVCLLNIFY PREAKVQMKV 150  
 DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200  
 LSSPVTKSFN RGEC 214

## Post-translational modifications

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

Intra-H (C23-C104) 22-96 140-196 254-314 360-418  
 22<sup>o</sup>-96<sup>o</sup> 140<sup>o</sup>-196<sup>o</sup> 254<sup>o</sup>-314<sup>o</sup> 360<sup>o</sup>-418<sup>o</sup>  
 Intra-L (C23-C104) 23<sup>o</sup>-88<sup>o</sup> 134<sup>o</sup>-194<sup>o</sup>  
 23<sup>o</sup>-88<sup>o</sup> 134<sup>o</sup>-194<sup>o</sup>  
 Inter-H-L (CH1 10-CL 126) 127-214<sup>o</sup> 127<sup>o</sup>-214<sup>o</sup>  
 Inter-H-H (h 8, h 11) 219-219<sup>o</sup> 222-222<sup>o</sup>

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

Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)  
 H VH Q1: 1, 1<sup>o</sup>

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

H CH2 N84.4: 290, 290<sup>o</sup>

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: 440, 440<sup>o</sup>

ersodetugum #  
ersodetug

immunoglobulin G2-kappa, anti-[*Homo sapiens* INSR (insulin receptor)], *Homo sapiens* monoclonal antibody, allosteric;  
 gamma2 heavy chain *Homo sapiens* (1-444) [VH (*Homo sapiens* IGHV3-20\*01 (98.0%) -(IGHD) - IGHJ6\*01 (93.8%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG2\*02 (100%), G2m23 CH2 M45.1 (CH1 (119-216), hinge 1-12 (217-228), CH2 M45.1 (279) (229-337), CH3 (338-442), CHS (443-444)) (119-444)], (132-219)-disulfide with kappa light chain humanized (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-30\*01 (93.0%) -IGKJ2\*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC\*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (220-220<sup>o</sup>:221-221<sup>o</sup>:224-224<sup>o</sup>:227-227<sup>o</sup>)-tetrakisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa  
*insulin receptor allosteric inhibitor, antihypoglycaemic*

## ersodétug

immunoglobuline G2-kappa, anti-[*Homo sapiens* INSR (récepteur de l'insuline)], anticorps monoclonal *Homo sapiens*, allostérique;

chaîne lourde gamma2 *Homo sapiens* (1-444) [VH (*Homo sapiens* IGHV3-20\*01 (98.0%) -(IGHD) -IGHJ6\*01 (93.8%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG2\*02 (100%), G2m23 CH2 M45.1 (CH1 (119-216), charnière 1-12 (217-228), CH2 M45.1 (279) (229-337), CH3 (338-442), CHS (443-444)) (119-444)], (132-219')-disulfure avec la chaîne légère kappa humanisée (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-30\*01 (93.0%) -IGKJ2\*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC\*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (220-220":221-221":224-224":227-227")- tétrakisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa  
*inhibiteur allostérique du récepteur de l'insuline, antihypoglycémiant*

ersodetug

inmunoglobulina G2-kappa, anti-[*Homo sapiens* INSR (receptor de la insulina)], anticuerpo monoclonal *Homo sapiens*, alostérico;  
cadena pesada gamma2 *Homo sapiens* (1-444) [VH (*Homo sapiens* IGHV3-20\*01 (98.0%) -(IGHD) -IGHJ6\*01 (93.8%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG2\*02 (100%), G2m23 CH2 M45.1 (CH1 (119-216), bisagra 1-12 (217-228), CH2 M45.1 (279) (229-337), CH3 (338-442), CHS (443-444)) (119-444)], (132-219')-disulfuro con la cadena ligera kappa humanizada (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-30\*01 (93.0%) -IGKJ2\*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC\*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (220-220":221-221":224-224":227-227")-tetrakisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa  
*inhibidor alostérico del receptor de la insulina, antihipoglucemiante*

2410976-61-1

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVETGGG VVQPGRSLRL SCAASGFTFS SYAMHWVRQA PGKLEWVAV 50  
ISYDGSNKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARHE 100  
WFGMDVWVGQ GTTIVTVSSAS TKGPSVFLPA PCRSSTSEST AALGCLVKDY 150  
FPEPVTVSWN SGALTSVHT FPAVLQSSGL YSLSSVTVT SSNFGTQTYT 200  
CNVDHKPSNT KVDKTVVERK CVECPCPPAP PVAGPSVLEF PPKPKDTLMI 250  
SRTPEVTCVV VDVSHEDPEV QFNWYVDGME VHNAKTKERE EQPNSTFRVV 300  
SVLTVVHQDW LNGKEYKCKV SNKGLPAPIE KTISKTKGQP REPQVYLLP 350  
SREEMTNQV SLTCLVKGFY PSDIAYEWES NGQPENNYKT TTPMLDSDGS 400  
FPLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKLSL SPGK 444

Light chain / Chaîne légère / Cadena ligera

DVVMTQSPFLS LSVTLGQPAS ISCRSSLSLV YGDENTYLNW FQQRPGQSPR 50  
RLLYKVSRRD SGVPRDFSGS GSGTDFTLKI SRVEADDVGV YYCMQGTWHP 100  
YTFGQGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVL LNIFYREAK 150  
VQWKVDNALQ SGNSQESVTE QDSKSTYSLS STLTLSKAD YERHKVYACE 200  
VTHQGLSSPV TRSFNRGEC 219

Post-translational modifications

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

Intra-H (C23-C104) 22"-96" 145"-201" 258"-318" 364"-422"  
22"-96" 145"-201" 258"-318" 364"-422"  
Intra-L (C23-C104) 23"-93" 139"-199"  
23"-93" 139"-199"  
Inter-H-L (CH1 10-CL 126) 132"-219" 132"-219"  
Inter-H-H (h 4, h 5, h 8, h11) 220"-220" 221"-221" 224"-224" 227"-227"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación  
H CH2 N84.4:294, 294"

C-terminal lysine clipping / Coupeure de la lysine C-terminale / Recorte de lisina C-terminal  
H CHS K2: 444, 444"

**erzotabartum #**

erzotabart

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD38 (ADP-ribosyl cyclase 1, cyclic ADP-ribose hydrolase 1, cADPr hydrolase 1, cADPR1)], *Homo sapiens* monoclonal antibody;  
 gamma1 heavy chain *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV1-69\*04 (93.8%) -(IGHD) -IGHJ3\*02 (93.8%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121)-*Homo sapiens* IGHG1\*03, G1m3, nG1m1 CH1 R120 CH3 E12, M14, IGHG1v34 CH3 G109 (CH1 R120 (218) (122-219), hinge 1-15 (220-234), CH2 (235-344), CH3 E12 (360), M14 (362), E109>G (434) (345-449), CHS K2>del (450)) (122-450)], (224-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-16\*01 (98.9%) -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 (230-230":233-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa  
*antineoplastic*

erzotabart

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD38 (ADP-ribosyl cyclase 1, ADP cyclique-ribose hydrolase 1, cADPr hydrolase 1, cADPR1)], anticorps monoclonal *Homo sapiens*;  
 chaîne lourde gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV1-69\*04 (93.8%) -(IGHD) - IGHJ3\*02 (93.8%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1\*03, G1m3, nG1m1 CH1 R120 CH3 E12, M14, IGHG1v34 CH3 G109 (CH1 R120 (218) (122-219), charnière 1-15 (220-234), CH2 (235-344), CH3 E12 (360), M14 (362), E109>G (434) (345-449), CHS K2>del (450)) (122-450)], (224-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-16\*01 (98.9%) -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 (230-230":233-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa  
*antineoplasique*

erzotabart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD38 (ADP-ribosil ciclaza 1, ADP cíclico-ribosa hidrolasa 1, cADPr hidrolasa 1, cADPR1)], anticuerpo monoclonal *Homo sapiens*;  
 cadena pesada gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV1-69\*04 (93.8%) -(IGHD) - IGHJ3\*02 (93.8%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1\*03, G1m3, nG1m1 CH1 R120 CH3 E12, M14, IGHG1v34 CH3 G109 (CH1 R120 (218) (122-219), bisagra 1-15 (220-234), CH2 (235-344), CH3 E12 (360), M14 (362), E109>G (434) (345-449), CHS K2>del (450)) (122-450)], (224-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-16\*01 (98.9%) -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 (230-230":233-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa  
*antineoplásico*

2430792-01-9

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VKKPGSSVKV SCKAFGGTFS SYAISWVRQA PGQGLEWMGR 50  
 IIRFLGIANY AQKFQGRVTL IADKSTNTAY MELSSLRSED TAVYYCAGEP 100  
 GERDPAVDI WGGGTMVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150  
 KDYFPEFVTV SWNSGALTSV VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200  
 TYICNVNHKP SNTKVDKRVK PKSCDKTHTC PCCPAPELLG GPSVFLFPPK 250  
 PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEEQ 300  
 NSTYRVVSVL TVLHQDWLNG KEYEKVSNK ALPAIEKTI SKAKGPREF 350  
 QVYTLPPSRE EMTRKQVSLT CLVKGFPYSD IAVEWESNGQ PENNYKTPFP 400  
 VLDSGGSFFL YSKLTVDKSR WQQGNVFSCS VMHGALHNYH TQKSLSLSPG 450

## Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGDVRT ITCRASGGIR SWLAWYQQKPK EKAPKSLIYA 50  
 ASSLQSGVPS RFGSGSGTD FTLTISSLQP EDFATYICQQ YNSYPLTFGG 100  
 GTKVEIKRTV AAPSVPFIAPP SDEQLKSGTA SVVCLLNIFY PREAKVQWVK 150  
 DNALQSGNSQ ESVTEQDSKD STYISLSSLT LSKADYERHK VYACEVTHQG 200  
 LSSPVTKSFN RGEK 214

## Post-translational modifications

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

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

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°

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

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxopropililo)  
 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 biantennarios complejos fucosilados

**esonadogenum imvoparvecum #**  
 esonadogene imvoparvec

recombinant, non-replicating adeno-associated virus serotype 2 (AAV2) vector encoding codon-optimised human NADH dehydrogenase subunit 4 (also known as NADH-ubiquinone oxidoreductase chain 4; MTND4, NADH4, ND4) preceded by a Kozak sequence and a mitochondrial targeting sequence from human heme A: farnesyltransferase cytochrome C oxidase assembly factor (also known as protoheme IX farnesyltransferase, mitochondrial; gene COX10), under control of a human cytomegalovirus enhancer/promoter plus a Macacine herpesvirus-3 chimeric intron, followed with a COX10 gene 3'-untranslated region (UTR), and terminated by a simian virus 40 (SV40) polyadenylation signal, and flanked by AAV2 inverted terminal repeats (ITRs)  
*gene therapy (Leber's hereditary optic neuropathy)*

ésonadogène imvoparvec

vecteur recombinant et non répliquant du virus adéno-associé de sérotype 2 (AAV2) codant la sous-unité 4 de la NADH déshydrogénase humaine aux codons optimisés (également connue sous le nom de chaîne 4 de la NADH-ubiquinone oxydoréductase; MTND4, NADH4, ND4) précédée d'une séquence Kozak et d'un hème A humain: facteur d'assemblage de la farnesyltransférase cytochrome C oxydase (également connu sous le nom de farnesyltransférase protohème IX, mitochondriale; gène COX10) ciblant les mitochondries, sous le contrôle d'un amplificateur/promoteur du cytomégalovirus humain plus d'un intron chimérique de l'herpèsvirus-3 Macacine, suivi d'une région 3' non traduite (UTR)

	du gène COX10, et terminé par un signal de polyadénylation du virus simien 40 (SV40), et flanqué de répétitions terminales inversées (ITR) de l'AAV2. <i>thérapie génique (neuropathie optique héréditaire de Leber)</i>
esonadogén imvoparovec	vector de virus adenoasociado recombinante del serotipo 2 (AAV2), no replicativo, que codifica, con codones optimizados, para la subunidad 4 de la NADH deshidrogenasa humana (también conocida como cadena 4 de la NADH-ubiquinona oxidorreductasa; MTND4, NADH4, ND4) precedida por una secuencia Kozak y un hemo A humano: factor de ensamblaje de citocromo C oxidasa de farnesiltransferasa (también conocido como protohemo IX farnesiltransferasa, mitocondrial; gen COX10), bajo el control de un potenciador/promotor del citomegalovirus humano más un intrón quimérico del herpesvirus-3 Macacine, seguido de una región no traducida (UTR) en 3' del gen COX10, y terminado con una señal de poliadenilación del virus simio 40 (SV40) y flanqueado por repeticiones terminales invertidas (ITRs) del AAV2 <i>terapia génica (neuropatía óptica hereditaria de Leber)</i>
	2678565-23-4
<b>etimumotidum</b> etimumotide	L-phenylalanyl-L-methionyl-L-threonyl-L-tyrosyl-L-tryptophyl-L-histidyl-L-leucyl-L-leucyl-L-asparaginy-L-alanyl-L-phenylalanyl-L-threonyl-L-valyl-L-threonyl-L-valyl-L-prolyl-L-lysyl-L-α-aspartyl-L-leucine <i>immunological agent for active immunization (antineoplastic)</i>
étimumotide	L-phénylalanyl-L-méthionyl-L-thréonyl-L-tyrosyl-L-tryptophyl-L-histidyl-L-leucyl-L-leucyl-L-asparaginy-L-alanyl-L-phénylalanyl-L-thréonyl-L-valyl-L-thréonyl-L-valyl-L-prolyl-L-lysyl-L-α-aspartyl-L-leucine <i>agent immunologique d'immunisation active (antineoplasique)</i>
etimumotida	L-fenilalanil-L-metionil-L-treonil-L-tirosil-L-triptofil-L-histidil-L-leucil-L-leucil-L-asparaginil-L-alanil-L-fenilalanil-L-treonil-L-valil-L-treonil-L-valil-L-prolil-L-lisil-L-α-aspartil-L-leucina <i>agente inmunológico para inmunización activa (antineoplásico)</i>
	C <sub>111</sub> H <sub>162</sub> N <sub>24</sub> O <sub>27</sub> S
	1431550-68-3
	FMTYWHLINA FTVTVPKDL 21
<b>eurestobartum #</b> eurestobart	immunoglobulin G1-kappa, anti-[ <i>Homo sapiens</i> ENTPD1 (ectonucleoside triphosphate diphosphohydrolase 1, CD39)], humanized monoclonal antibody;

- gamma1 heavy chain humanized (1-453) [VH (*Homo sapiens*IGHV1-3\*01 (80.4%) -(IGHD) -IGHJ3\*01 (92.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens*IGHG1\*03v, G1m3>G1m17, nG1m1, CH1 K120, CH3 E12, M14, G1v14 CH2 A1.3, A1.2 (CH1 R120>K (220) (124-221), hinge 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-213')-disulfide with kappa light chain humanized (1'-213') [V-KAPPA (*Homo sapiens*IGKV3-11\*01 (82.1%) -IGKJ2\*02 (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 (232-232":235-235")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1 lacking the glutamine synthetase (GS-KO) gene, glycoform alfa  
*immunostimulant, antineoplastic*
- eurestobart immunoglobuline G1-kappa, anti-[*Homo sapiens*ENTPD1 (ectonucleoside triphosphate diphosphohydrolase 1, CD39)], anticorps monoclonal humanisé;  
chaîne lourde gamma1 humanisée (1-453) [VH (*Homo sapiens*IGHV1-3\*01 (80.4%) -(IGHD) -IGHJ3\*01 (92.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens*IGHG1\*03v, G1m3>G1m17, nG1m1, CH1 K120, CH3 E12, M14, G1v14 CH2 A1.3, A1.2 (CH1 R120>K (220) (124-221), charnière 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-213')-disulfure avec la chaîne légère kappa humanisée (1'-213') [V-KAPPA (*Homo sapiens*IGKV3-11\*01 (82.1%) -IGKJ2\*02 (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 (232-232":235-235")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1 ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa  
*immunostimulant, antinéoplasique*
- eurestobart inmunoglobulina G1-kappa, anti-[*Homo sapiens*ENTPD1 (ectonucleósido trifosfato difosfohidrolasa 1, CD39)], anticuerpo monoclonal humanizado;  
cadena pesada gamma1 humanizada (1-453) [VH (*Homo sapiens*IGHV1-3\*01 (80.4%) -(IGHD) -IGHJ3\*01 (92.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens*IGHG1\*03v, G1m3>G1m17, nG1m1, CH1 K120, CH3 E12, M14, G1v14 CH2 A1.3, A1.2 (CH1 R120>K (220) (124-221), bisagra 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-213')-disulfuro con la cadena ligera kappa humanizada (1'-213') [V-KAPPA (*Homo sapiens*IGKV3-11\*01 (82.1%) -IGKJ2\*02 (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 (232-232":235-235")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1 en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa  
*inmunoestimulante, antineoplásico*

2682847-53-4

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VKKPGASVKV SCKASGYNLK DTFLLHWVRQA PGQGLEWMGR 50  
 IDPAQGNIKY DPKFQGRVTI TADTSANTAY MELISLRSED TAVYYCANSF 100  
 YYYGSGYRIF DWWGQTTVT VSSASTKGPS VFPLAPSSKS TSGTAAALGC 150  
 LVKDYFFPEPV TVSWNSGALT SGVHTFFAVL QSSGLYSLSS VVTVPSSSLG 200  
 TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCFPCFAPEA AGGPSVFLFP 250  
 PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300  
 QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR 350  
 EFQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400  
 PFLVDSGDSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HTYQKSLSL 450  
 PGK 453

## Light chain / Chaîne légère / Cadena ligera

QIVLTQSPAT LSLSPGERAT LSCSAFSSVN YMHWYQQKPG QAPRLLIYTT 50  
 SNLASGIPTR FSGSGSGTSY TLTISLSLEPE DPAVYYCQQR STYPTFTGQG 100  
 TKLEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150  
 NALQSGNSQE SVTEQDSKDS TYSLSLTLTL 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) 22-96 150-206 267-327 373-431  
 22"-96" 150"-206" 267"-327" 373"-431"

Intra-L (C23-C104) 23'-87' 133'-193'  
 23"-87'" 133"-193'"

Inter-H-L (h 5-CL 126) 226-213' 226"-213"

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

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

Q &gt; pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoproliolo)

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 biantennarios complejos fucosilados

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

H CHS K2: 453, 453"

falbikitugum  
falbikitug

immunoglobulin G1-kappa, anti-[*Homo sapiens* LIF (LIF interleukin 6 family cytokine, leukemia inhibitory factor)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV3-15\*07 (86.9%) -(IGHD) -IGHJ1\*01 (90.9%), CDR-IMGT [8.10.9] (26-33.51-60.99-107))(1-118) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (215) (119-216), hinge 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-220')-disulfide with kappa light chain humanized (1'-220') [V-KAPPA (*Homo sapiens* IGKV2-24\*01 (90.0%) -IGKJ2\*01 (100%), CDR-IMGT [11.3.10] (27-37.55-57.94-103)) (1'-113') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (159), V101 (197) (114'-220')]; dimer (227-227"':230-230")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa  
*antineoplastic*

## falbikitug

immunoglobuline G1-kappa, anti-[*Homo sapiens* LIF (cytokine LIF de la famille 6 des interleukines, facteur inhibiteur de la leucémie)]; anticorps monoclonal humanisé;

chaîne lourde gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV3-15\*07 (86.9%) -(IGHD) -IGHJ1\*01 (90.9%), CDR-IMGT [8.10.9] (26-33.51-60.99-107)) (1-118) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (215) (119-216), charnière 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-220')-disulfure avec la chaîne légère kappa humanisée (1'-220') [V-KAPPA (*Homo sapiens* IGKV2-24\*01 (90.0%) -IGKJ2\*01 (100%), CDR-IMGT [11.3.10] (27-37.55-57.94-103)) (1'-113') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (159), V101 (197) (114'-220')]; dimère (227-227":230-230")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa  
*antineoplasique*

falbikitug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* LIF (citoquina LIF de la familia 6 de las interleukinas, factor inhibidor de la leucemia)]; anticuerpo monoclonal humanizado;

cadena pesada gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV3-15\*07 (86.9%) -(IGHD) -IGHJ1\*01 (90.9%), CDR-IMGT [8.10.9] (26-33.51-60.99-107)) (1-118) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (215) (119-216), bisagra 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-220')-disulfuro con la cadena ligera kappa humanizada (1'-220') [V-KAPPA (*Homo sapiens* IGKV2-24\*01 (90.0%) -IGKJ2\*01 (100%), CDR-IMGT [11.3.10] (27-37.55-57.94-103)) (1'-113') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (159), V101 (197) (114'-220')]; dímero (227-227":230-230")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa  
*antineoplásico*

2740565-02-8

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLQESGGG	LVPKGGSLRL	SCAASGFTFS	HAMMHVVRQA	PGKGLEWVGG	50
IKAKSDDYAT	YVAESVKGGRF	TISRDSKNT	LVLQMSLKT	EDTAVVYCTC	100
WEWDLDFWGG	GTMTVSSAS	TKGPSVFPLA	PSKRSTSGGT	AALGCLVKDY	150
FPEFVTVSWN	SGALTSVGHV	FPFVQLQSSGL	YSLSSVVTVP	SSSLGTQTYI	200
CNVNHPKSN	KVDKQVEPKS	CDRTHTCPPC	PAPELLGGPS	VFLFPPKPKD	250
TLMSRSTPEV	TCVVVDVSH	DPEVKFNWYV	DGVEVHNAKT	KPREEQYNST	300
YRVVSVLTVL	HQDWWLNGKEY	KCKVSNKALP	APIEKTIISKA	KGQPREPQVY	350
TLFPPSRDEL	TKNQVSLTCLV	KGFYPSDIAV	EWESNGQPEN	NYKTTTTPVLD	400
SDGSFFFLYS	LTVDKSRWQQ	GNVFSCSVHM	EALHNNHYTK	SLSLSPGK	448

## Light chain / Chaîne légère / Cadena ligera

DIVMTQTFLS	SPVTLGQPAS	ISCRSSQSL	DSHGHTYLNW	LQQRPGQPPR	50
LLIYSVSNLE	SGVPDRFSGS	GAGTDFTLKI	SRVEAEDVGV	YYCMQATHAP	100
PYTFGGQTKL	EIKRTVAAPS	VFIFPPSDEQ	LKSGTASVVC	LLNNFYPREA	150
KVQWKVDNAL	QSGNSQESV	EQDSKSTYS	LSLSTLTSKA	DYEKHKVYAC	200
EVTHQGLSSP	VTKSFNRGEC				220

## Post-translational modifications

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

Intra-H (C23-C104)	22-98	145-201	262-322	368-426
	22"-98"	145"-201"	262"-322"	368"-426"

Intra-L (C23-C104)	23-93'	140-200'
	23"-93"	140"-200"

Inter-H-L (h 5-CL 126) 221-220' 221"-220"

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

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

Q &gt; pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxoprolilo)

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 biantennarios complejos fucosilados

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

H CHS K2: 448, 448"



**fazamorexantum**

fazamorexant

(4<sup>1</sup>S,4<sup>2</sup>R,4<sup>5</sup>S)-7<sup>5</sup>-fluoro-2<sup>4</sup>-methyl-6-oxa-4<sup>8</sup>-aza-1(2)-pyrimidina-7(2)-pyridina-4(8,2)-bicyclo[3.2.1]octana-2(1,2)-benzenaheptaphan-3-one  
*orexin receptor antagonist*

fazamorexant

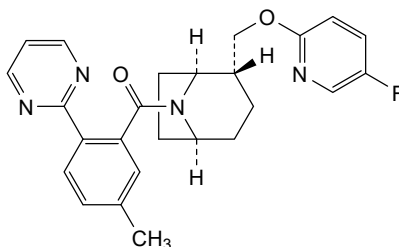
(4<sup>1</sup>S,4<sup>2</sup>R,4<sup>5</sup>S)-7<sup>5</sup>-fluoro-2<sup>4</sup>-méthyl-6-oxa-4<sup>8</sup>-aza-1(2)-pyrimidina-7(2)-pyridina-4(8,2)-bicyclo[3.2.1]octana-2(1,2)-benzénaheptaphan-3-one  
*antagoniste du récepteur de l'orexine*

fazamorexant

(4<sup>1</sup>S,4<sup>2</sup>R,4<sup>5</sup>S)-7<sup>5</sup>-fluoro-2<sup>4</sup>-metil-6-oxa-4<sup>8</sup>-aza-1(2)-pirimidina-7(2)-piridina-4(8,2)-bicyclo[3.2.1]octana-2(1,2)-benzenaheptafan-3-ona  
*antagonista del receptor de la orexina*

C<sub>25</sub>H<sub>25</sub>FN<sub>4</sub>O<sub>2</sub>

1808918-69-5

**faznolutamidum**

faznolutamide

4-[4,4-dimethyl-3-(6-methylpyridin-3-yl)-5-oxo-2-sulfanylideneimidazolidin-1-yl]-3-fluoro-2-methoxybenzonnitrile  
*antiandrogen*

faznolutamide

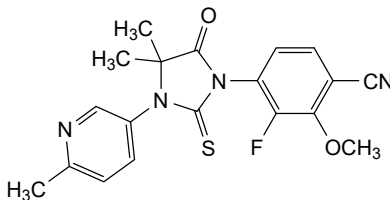
4-[4,4-diméthyl-3-(6-méthylpyridin-3-yl)-5-oxo-2-sulfanylidèneimidazolidin-1-yl]-3-fluoro-2-méthoxybenzonnitrile  
*antiandrogène*

faznolutamida

4-[4,4-dimetil-3-(6-metilpiridin-3-il)-5-oxo-2-sulfanilidenimidazolidin-1-il]-3-fluoro-2-metoxibenzonitrilo  
*antiandrógeno*

C<sub>19</sub>H<sub>17</sub>FN<sub>4</sub>O<sub>2</sub>S

1272719-08-0



**ficonalkibum**

ficonalkib

*N*<sup>2</sup>-{4-[4-(diméthylamino)piperidin-1-yl]-2-méthoxyphényl}-*N*<sup>4</sup>-[2-(propane-2-sulfonyl)phényl]-6,7-dihydro-5*H*-pyrrolo[2,3-*d*]pyrimidine-2,4-diamine  
*anaplastic lymphoma kinase (ALK) tyrosine kinase receptor inhibitor, antineoplastic*

ficonalkib

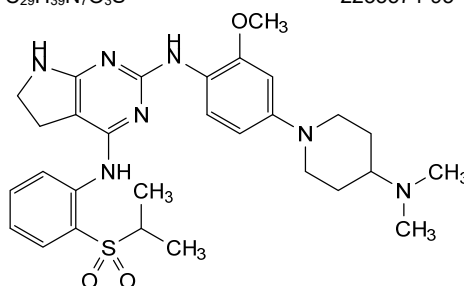
*N*<sup>2</sup>-{4-[4-(diméthylamino)pipéridin-1-yl]-2-méthoxyphényl}-*N*<sup>4</sup>-[2-(propane-2-sulfonyl)phényl]-6,7-dihydro-5*H*-pyrrolo[2,3-*d*]pyrimidine-2,4-diamine  
*inhibiteur du récepteur de la tyrosine kinase du lymphome anaplasique (ALK), antinéoplasique*

ficonalkib

*N*<sup>2</sup>-{4-[4-(dimetilamino)piperidin-1-il]-2-metoxifenil}-*N*<sup>4</sup>-[2-(propano-2-sulfonyl)fenil]-6,7-dihidro-5*H*-pirrolo[2,3-*d*]pirimidina-2,4-diamina  
*inhibidor del receptor de la tirosina kinasa del linfoma anaplásico (ALK), antineoplásico*

C<sub>29</sub>H<sub>39</sub>N<sub>7</sub>O<sub>3</sub>S

2233574-95-1

**firastotugum #**

firastotug

immunoglobulin G1-kappa, anti-[*Homo sapiens* CTLA4 (cytotoxic T-lymphocyte associated protein 4, CTLA-4, CD152)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-446) [VH (*Homo sapiens* IGHV3-7\*01 (77.8%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [9.7.9] (26-34.52-58.97-105)) (1-116) -*Homo sapiens* IGHG1\*01 (100%), G1m17, 1 CH1 K120, D12, L14 (CH1 K120 (213) (117-214), hinge 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-215')-disulfide with kappa light chain humanized (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-13\*02 (85.3%) -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')]; dimer (225-225":228-228")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa  
*immunostimulant, antineoplastic*

firastotug

immunoglobuline G1-kappa, anti-[*Homo sapiens* CTLA4 (protéine 4 associée aux lymphocytes T cytotoxiques, CTLA-4, CD152)], anticorps monoclonal humanisé;

chaîne lourde gamma1 humanisée (1-446) [VH (*Homo sapiens* IGHV3-7\*01 (77.8%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [9.7.9] (26-34.52-58.97-105)) (1-116) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, D12, L14 (CH1 K120 (213) (117-214), charnière 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-215')-disulfure avec la chaîne légère humanisée (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-13\*02 (85.3%) -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')]; dimère (225-225":228-228")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa  
*immunostimulant, antinéoplasique*

firastotug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CTLA4 (proteína 4 asociada a los linfocitos T citotóxicos, CTLA-4, CD152)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-446) [VH (*Homo sapiens* IGHV3-7\*01 (77.8%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [9.7.9] (26-34.52-58.97-105)) (1-116) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, D12, L14 (CH1 K120 (213) (117-214), bisagra 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-215')-disulfuro con la cadena ligera kappa humanizada (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-13\*02 (85.3%) -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')]; dímero (225-225":228-228")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa  
*inmunostimulante, antineoplásico*

2750031-14-0

Heavy chain / Chaîne lourde / Cadena pesada

```

EVQLVESGGG LVQPGGSLRL SCARSGYSIS SGYHWSMIRG APGKGLEWLA 50
RIDWDDDKYY STSLKSRSLTI SRDMSKNTLY LQLNLSLRAED TAVVYCARSY 100
VYFDYWGQGT LVTVSSASTK GPSVFFLAPS SKSTSGGTAA LGCLVKDYFP 150
EPTVTSWNSG ALTSGVHTFP AVLQSSGLYS LSSVTVFSS SLGTQTYICN 200
VNHKFSNTRV DKKVEPKSCD KTHTCPPCPA PELLGGPSVF LFPKPKDPL 250
MISRTPPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGREYKC KVSNAKALPAP IEKTISKAKG QPREPVYTL 350
PPSRDELTHN QVSLTCLVKG FYPSDIAVEW ESNQGPENNY KTTTPVLDS 400
GSFFLYSKLT VDKSRWQQGN VFSCVMHEA LHNHYTQKSL SLSPGK 446
    
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Light chain / Chaîne légère / Cadena ligera

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DIQLTQSPSS LSASVGRDVT ITCRASQSVR GRFLAWYQQK PGKAPKLLIY 50
DASNRAATGIP SRFSGSGSGT DFTLTISLQ PEDFATYYCQ QSSSWPPTFG 100
QGTRKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNMF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSEFVTKSF NRGEC 215
    
```

Post-translational modifications

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

Intra-H (C23-C104) 22"-96" 143"-199" 260"-320" 366"-424"  
 22"-96" 143"-199" 260"-320" 366"-424"  
 Intra-L (C23-C104) 23"-89" 135"-195"  
 23"-89" 135"-195"  
 Inter-H-L (h 5-CL 126) 219-215' 219'-215"  
 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-antennaires complexes fucosylés / glicanos de tipo CHO biantennarios complejos fucosilados

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

**flizasertibum**

flizasertib

cyclopropyl[(5S,7S)-7-fluoro-5-phenyl-6,7-dihydro-5H-pyrrolo[1,2-b][1,2,4]triazol-2-yl]methanone  
*serine/ threonine kinase inhibitor*

flizasertib

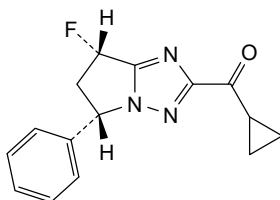
cyclopropyl[(5S,7S)-7-fluoro-5-phényl-6,7-dihydro-5H-pyrrolo[1,2-b][1,2,4]triazol-2-yl]méthanone  
*inhibiteur de sérine/ thréonine kinase*

flizasertib

ciclopropil[(5S,7S)-7-fluoro-5-fenil-6,7-dihidro-5H-pirrol[1,2-b][1,2,4]triazol-2-il]metanona  
*inhibidor de serina/ treonina kinasa*

C<sub>15</sub>H<sub>14</sub>FN<sub>3</sub>O

2268739-68-8

**flurimedrimerum (<sup>18</sup>F)**flurimedrimer (<sup>18</sup>F)

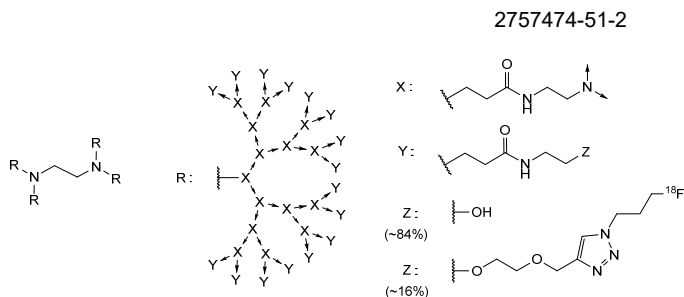
2-({1-[3-(<sup>18</sup>F)fluoropropyl]-1H-1,2,3-triazol-4-yl)methoxy}ethyl ether with about 16 % of hydroxyl end groups of a regular 4-dendron poly(amidoamine)-type dendrimer;  
 $\alpha, \alpha', \alpha'', \alpha'''$ -(ethane-1,2-diyl dinitrilo)tetrakis( $\omega$ -hexacontakis{3-[(2-hydroxyethyl)amino]-3-oxopropyl}-*dendro*<sup>G4</sup>-(3-oxopropane-1,3-diyl)azanediylethylenitrilo})  
*diagnostic imaging agent*

flurimédrimère (<sup>18</sup>F)

éther 2-({1-[3-(<sup>18</sup>F)fluoropropyl]-1H-1,2,3-triazol-4-yl)méthoxy}éthyl) avec approximativement 16 % de groupes terminaux hydroxyles d'un dendrimère régulier de type 4-dendron poly(amidoamine);  
 $\alpha, \alpha', \alpha'', \alpha'''$ -(éthane-1,2-diyl dinitrilo)tétrakis( $\omega$ -hexacontakis{3-[(2-hydroxyéthyl)amino]-3-oxopropyl}-*dendro*<sup>G4</sup>-(3-oxopropane-1,3-diyl)azanediyléthylénitrilo})  
*agent diagnostique*

flurimedrímero (<sup>18</sup>F)

éter 2-({1-[3-(<sup>18</sup>F)fluoropropil]-1H-1,2,3-triazol-4-il}metoxi)etilico con aproximadamente 16% de los grupos terminados hidroxiles de uno dendrímero regular de tipo 4-dendron poly(amidoamina);  
 $\alpha, \alpha', \alpha'', \alpha'''$ -(etano-1,2-diildinitrilo)tetrakis( $\omega$ -hexacontakis{3-[(2-hidroxietyl)amino]-3-oxopropil}-*dendro*<sup>G4</sup>-(3-oxopropano-1,3-diil)azanodiiletilenonitrilo})  
*agente de diagnóstico*

**foslevcromakalimum**

foslevcromakalim

(3*S*,4*R*)-6-cyano-2,2-diméthyl-4-(2-oxopyrrolidin-1-yl)-3,4-dihydro-2*H*-1-benzopyran-3-yl dihydrogen phosphate  
*potassium channel opener*

foslevcromakalim

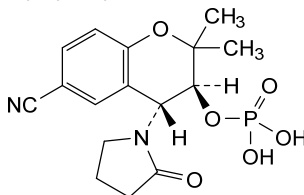
dihydrogénophosphate de (3*S*,4*R*)-6-cyano-2,2-diméthyl-4-(2-oxopyrrolidin-1-yl)-3,4-dihydro-2*H*-1-benzopyran-3-yle  
*ouvreur des canaux potassiques*

foslevcromakalim

dihidrogenofosfato de (3*S*,4*R*)-6-ciano-2,2-dimetil-4-(2-oxopirrolidin-1-il)-3,4-dihidro-2*H*-1-benzopiran-3-ilo  
*activador de los canales de potasio*

C<sub>16</sub>H<sub>19</sub>N<sub>2</sub>O<sub>6</sub>P

1802655-72-6

**fulzerasibum**

fulzerasib

(4*aR*,8*M*)-11-chloro-10-(2-fluoro-6-hydroxyphenyl)-6-méthyl-8-[2-(propan-2-yl)-4-méthylpyridin-3-yl]-3-prop-2-énoyl-2,3,4,4*a*,6,8-hexahydro-1*H*-pyrazino[1',2':4,5]pyrazino[2,3-*c*][1,8]naphthyridine-5,7-dione  
*Kirsten rat sarcoma viral oncogene homolog (KRAS) inhibitor, antineoplastic*

fulzérasib

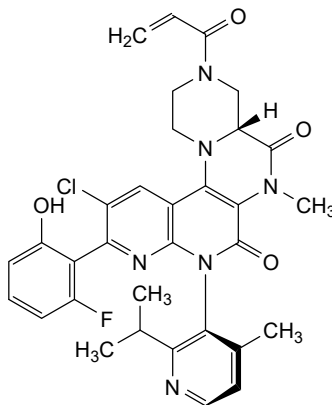
(4*aR*,8*M*)-11-chloro-10-(2-fluoro-6-hydroxyphényl)-6-méthyl-8-[2-(propan-2-yl)-4-méthylpyridin-3-yl]-3-prop-2-énoyl-2,3,4,4*a*,6,8-hexahydro-1*H*-pyrazino[1',2':4,5]pyrazino[2,3-*c*][1,8]naphthyridine-5,7-dione  
*inhibiteur de l'homologue de l'oncogène du virus du sarcome du rat de Kirsten (KRAS), antinéoplasique*

fulzerasib

(4a*R*,8*M*)-11-cloro-10-(2-fluoro-6-hidroxifenil)-6-metil-8-[2-(propan-2-il)-4-metilpiridin-3-il]-3-prop-2-enoil-2,3,4,4a,6,8-hexahidro-1*H*-pirazino[1',2':4,5]pirazino[2,3-c][1,8]naftiridina-5,7-diona  
*inhibidor homólogo del oncogén del virus del sarcoma de rata de Kirsten (KRAS), antineoplásico*

C<sub>32</sub>H<sub>30</sub>ClFN<sub>6</sub>O<sub>4</sub>

2641747-54-6

**gallium (<sup>68</sup>Ga) rofapitidum tetraxetanum**

gallium (<sup>68</sup>Ga) rofapitide tetraxetanum [2,2',2''-{10-[2-(oxo-κO)-2-[[2-(((1<sup>2</sup>S,3<sup>2</sup>S,5*R*,13*R*,16*S*,19*S*,22*S*)-19-(3-amino-3-oxopropyl)-16-benzyl-13-carboxy-5-hexanamido-22-[(1*R*)-1-hydroxyethyl]-2,4,15,18,21,24-hexaoxo-7,11-dithia-14,17,20,23-tetraaza-1(1,2),3(2,1)-dipyrrolidina-9(1,3)-benzenacyclotetracosaphan-9<sup>5-</sup>yl)methyl)sulfanyl]ethyl]amino]ethyl]-1,4,7,10-tetraazacyclododecane-1,4,7-triyl-κ<sup>4</sup>*N*<sup>1</sup>,*N*<sup>4</sup>,*N*<sup>7</sup>,*N*<sup>10</sup>}tri(acetato-κO)](<sup>68</sup>Ga)gallium  
*diagnostic imaging agent*

**gallium (<sup>68</sup>Ga) rofapitide tétraxétan**

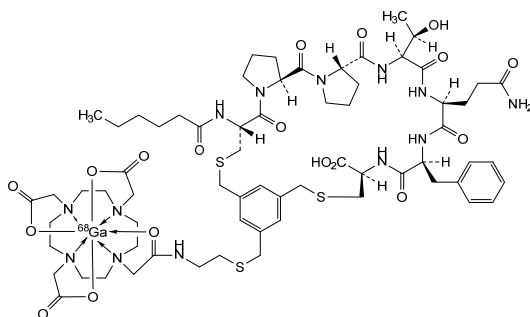
[2,2',2''-{10-[2-(oxo-κO)-2-[[2-(((1<sup>2</sup>S,3<sup>2</sup>S,5*R*,13*R*,16*S*,19*S*,22*S*)-19-(3-amino-3-oxopropyl)-16-benzyl-13-carboxy-5-hexanamido-22-[(1*R*)-1-hydroxyéthyl]-2,4,15,18,21,24-hexaoxo-7,11-dithia-14,17,20,23-tétraza-1(1,2),3(2,1)-dipyrrolidina-9(1,3)-benzénacyclotétracosaphan-9<sup>5-</sup>yl)méthyl)sulfanyl]éthyl]amino]éthyl]-1,4,7,10-tétrazacyclododécane-1,4,7-triyl-κ<sup>4</sup>*N*<sup>1</sup>,*N*<sup>4</sup>,*N*<sup>7</sup>,*N*<sup>10</sup>}tri(acétato-κO)](<sup>68</sup>Ga)gallium  
*agent diagnostique*

**galio (<sup>68</sup>Ga) rofapitida tetraxetán**

[2,2',2''-{10-[2-(oxo-κO)-2-[[2-(((1<sup>2</sup>S,3<sup>2</sup>S,5*R*,13*R*,16*S*,19*S*,22*S*)-19-(3-amino-3-oxopropil)-16-bencil-13-carboxi-5-hexanamido-22-[(1*R*)-1-hidroxietil]-2,4,15,18,21,24-hexaoxo-7,11-ditia-14,17,20,23-tetraaza-1(1,2),3(2,1)-dipirrolidina-9(1,3)-bencenaciotetracosafan-9<sup>5-</sup>il]metil)sulfanil]etil]amino]etil]-1,4,7,10-tetraazacyclododecano-1,4,7-triyl-κ<sup>4</sup>*N*<sup>1</sup>,*N*<sup>4</sup>,*N*<sup>7</sup>,*N*<sup>10</sup>}tri(acetato-κO)](<sup>68</sup>Ga)galio  
*agente de diagnóstico*

$C_{67}H_{96}^{68}GaN_{13}O_{18}S_3$ 

2584414-86-6



**ganfaborolum**  
ganfaborole

(3*S*)-3-(aminomethyl)-4-chloro-7-(2-hydroxyethoxy)-  
2,1-benzoxaborol-1(3*H*)-ol  
*antibacterial*

ganfaborole

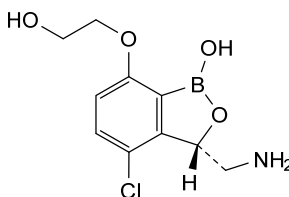
(3*S*)-3-(aminométhyl)-4-chloro-7-(2-hydroxyéthoxy)-  
2,1-benzoxaborol-1(3*H*)-ol  
*antibactérien*

ganfaborol

(3*S*)-3-(aminometil)-4-cloro-7-(2-hidroxiético)-2,1-  
benzoxaborol-1(3*H*)-ol  
*antibacteriano*

 $C_{10}H_{13}BCINO_4$ 

2131798-12-2



**gemlapodectum**  
gemlapodect

1-methyl-4-[(morpholin-4-yl)carbonyl]-*N*-(2-  
phenyl[1,2,4]triazolo[1,5-*a*]pyridin-7-yl)-1*H*-pyrazole-5-  
carboxamide  
*phosphodiesterase 10A (PDE10A) inhibitor*

gemlapodect

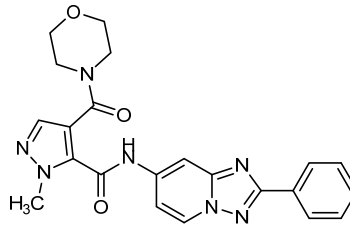
1-méthyl-4-[(morpholin-4-yl)carbonyl]-*N*-(2-  
phényl[1,2,4]triazolo[1,5-*a*]pyridin-7-yl)-1*H*-pyrazole-5-  
carboxamide  
*inhibiteur de la phosphodiésterase 10A (PDE10A)*

gemlapodect

1-metil-4-[(morfolin-4-il)carbonil]-*N*-(2-  
fenil[1,2,4]triazolo[1,5-*a*]piridin-7-il)-1*H*-pirazolo-5-  
carboxamida  
*inhibidor de la fosfodiesterasa 10A (PDE10A)*

C<sub>22</sub>H<sub>21</sub>N<sub>7</sub>O<sub>3</sub>

1380329-87-2



**gotistobartum #**  
gotistobart

immunoglobulin G1-kappa, anti-[*Homo sapiens* CTLA4 (cytotoxic T-lymphocyte-associated protein 4, CTLA-4, CD152)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-454) [VH (*Homo sapiens* IGHV4-59\*01 (86.6%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [8.7.19] (26-33.51-57.96-114)) (1-125) -*Homo sapiens* IGHG1\*01, G1m17,1 CH1 K120 CH3 D12, L14, G1v6CH2 A85.4, A118, A119, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (222) (126-223), hinge 1-15 (224-238), CH2 M15.1>Y (260), S16>T (262), T18>E (264), S85.4>A (306), E118>A (341), K119>A (342) (239-348), CH3 D12 (364), L14 (366) (349-453), CHS K2>del (454)) (126-454)], (228-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1\*01 (84.2%) -IGKJ2\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimer (234-234":237-237")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa  
*immunostimulant, antineoplastique*

gotistobart

immunoglobuline G1-kappa, anti-[ *Homo sapiens* CTLA4 (protéine 4 associée aux lymphocytes T cytotoxiques, CTLA-4, CD152)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-454) [VH (*Homo sapiens* IGHV4-59\*01 (86.6%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [8.7.19] (26-33.51-57.96-114)) (1-125) -*Homo sapiens* IGHG1\*01, G1m17,1 CH1 K120 CH3 D12, L14, G1v6 CH2 A85.4, A118, A119, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (222) (126-223), hinge 1-15 (224-238), CH2 M15.1>Y (260), S16>T (262), T18>E (264), S85.4>A (306), E118>A (341), K119>A (342) (239-348), CH3 D12 (364), L14 (366) (349-453), CHS K2>del (454)) (126-454)], (228-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1\*01 (84.2%) -IGKJ2\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimère (234-234":237-237")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa  
*immunostimulant, antinéoplasique*



gotistobart

immunoglobulina G1-kappa, anti-[ *Homo sapiens* CTLA4 (proteína 4 asociada a los linfocitos T citotóxicos, CTLA-4, CD152)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-454) [VH (*Homo sapiens* IGHV4-59\*01 (86.6%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [8.7.19] (26-33.51-57.96-114))] (1-125) -*Homo sapiens* IGHG1\*01, G1m17,1 CH1 K120 CH3 D12, L14, G1v6 CH2 A85.4, A118, A119, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (222) (126-223), bisagra 1-15 (224-238), CH2 M15.1>Y (260), S16>T (262), T18>E (264), S85.4>A (306), E118>A (341), K119>A (342) (239-348), CH3 D12 (364), L14 (366) (349-453), CHS K2>del (454)) (126-454)], (228-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1\*01 (84.2%)-IGKJ2\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97))] (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dímero (234-234":237-237")-bisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

*inmunostimulante, antineoplásico*

2226344-78-9

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLQESGPG LVKPSSETLSL TCTVSGFSLT SYGLSWIRQP PGKLEWIGY	50
INVDGNTNFH SPLKSRVTIS VDTSKNQFSL KLSVTAADT AVYCAKTEG	100
HYGSDNYGYY ALDYWGQGLT VTVSSASTKG PSVFPLAPSS KSTSGGTAAL	150
GCLVKDYFPE PVTYSWNSGA LTVSGVHTFPA VLQSSGLYSL SSVVTVPSSS	200
LCTQYICNV NHPKSNKVD KKVEPKSCDK THTCPPCPAP ELLGQPSVFL	250
FPKPKDTLLI ITREPEVTCV VVDVSHEDPE VKFNWYVDGV EVMNAKTKPR	300
EEQYQATYRV VSVLTVLHQD WLVGKEYKCK VSNKALPAPI AATISKAKGQ	350
PREPQVYTLF PSRDELTRKQ VSLTCLVKG FPSDIAVEWE SNGQFENNYK	400
TTPFVLDSDG SFFLYSKLTV DKSRWQQGNV FSCVMHEAL HNHYTQKSL	450
LSPG	454

## Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGRVIT ITCRASENIY SNLAWYQQK GRAPKLLLYA	50
ATNLDQGVPS RFGSGSGSDT YTLTISLQF EDFATYFCQH LWGTPYTFGQ	100
GTKLEIKRTV AAPSVEIFPP SDEQLKSGTA SVVCLLNFFY PREAKVQWVK	150
DNALQSGNSQ ESVTEQDSKD STYLSSTLT LSKADYEKHK VYACEVTHGQ	200
LSSPVTKSFN RGEK	214

## Post-translational modifications

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

Intra-H (C23-C104)	22-95	152-208	269-329	375-433
	22"-95"	152"-208"	269"-329"	375"-433"
Intra-L (C23-C104)	23-88	134-194		
	23"-88"	134"-194"		
Inter-H-L (h 5-CL 126)	228-214'	228"-214"		
Inter-H-H (h 11, h 14)	234-234"	237-237"		

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

Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolylo)  
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 / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantennarios complejos fucosilados

**gulgafafuspum alfa #**  
gulgafafusp alfa

humanized immunoglobulin G2-kappa, anti-(human glucagon-like peptide 1 receptor, GLP1R) (heavy chain 1-451, variant S<sup>382</sup>>A) fused at the N-terminus of each light chain (53-266) via the peptide linker <sup>30</sup>GSGSATGGSGSGASSGSGSATGS<sup>52</sup> to a glucagon-like peptide-1 (GLP-1) fragment (7-35, 1-29 in the current sequence), variant (A<sup>2</sup>>G), disulfide bridged dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa;

humanized monoclonal antibody fusion with human Glucagon-like peptide 1 (GLP1); type: IgG2-kappa; antigen: human glucagon-like peptide 1 receptor, GLP-1 receptor, GLP-1-R, GLP-1R (GLP1R); CDR source: *Mus musculus* (humanized by Kabat CDR grafting); heavy chain class: gamma2; heavy chain length: 451; HV germline: *Homo sapiens* IGHV3-33\*01; HJ germline: *Homo sapiens* IGHJ6\*01; HC germline: *Homo sapiens* IGHG2\*01; VH: 1-125; CH1: 126-223; hinge: 224-235; CH2: 236-344; CH3: 345-449 (S382A, non-functional mutation); CHS: 450-451; CDR Kabat H1: SYGMH (31-35); CDR Kabat H2: VIWYDGSNKYYADSVKG (50-66); CDR Kabat H3: GGGSGSYRYYYYGLDV (99-114); fusion protein: 1-29 (human 7-35 glucagon-like peptide-1); linker: 30-52; light chain class: kappa; light chain length: 266; LV germline: *Homo sapiens* IGKV1-12\*01; LJ germline: *Homo sapiens* IGKJ1\*01; LC germline: *Homo sapiens* IGKC\*01; VL: 53-159; CL: 160-266; CDR Kabat L1: RASQININLLA (76-86); CDR Kabat L2: TASSLQS (102-108); CDR Kabat L3: QQAHRFPPT (141-149)  
*glucagon-like peptide 1 (GLP-1) receptor agonist*

gulgafafusp alfa

immunoglobuline humanisée G2-kappa, anti-(récepteur humain du peptide 1 de type glucagon, GLP1R) (chaîne lourde 1-451, variant S<sup>382</sup>>A) fusionnée à l'extrémité N-terminale de chaque chaîne légère (53-266) via la liaison peptidique  
<sup>30</sup>GGSGATGGSGSGASSGSGSATGS<sup>52</sup> à un fragment du peptide-1 de type glucagon (GLP-1) (7-35, 1-29 dans la séquence actuelle), variant (A<sup>2</sup>>G), dimère à pont disulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa;  
 fusion d'un anticorps monoclonal humanisé avec le peptide 1 de type glucagon (GLP1) humain; type: IgG2-kappa; antigène: récepteur humain du peptide 1 de type glucagon récepteur GLP-1, GLP-1-R, GLP-1R (GLP1R); source CDR: *Mus musculus* (humanisé par greffe de CDR Kabat); classe de chaîne lourde: gamma2; longueur de la chaîne lourde: 451; HV lignée germinale: *Homo sapiens* IGHV3-33\*01; HJ lignée germinale: *Homo sapiens* IGHJ6\*01; HC lignée germinale: *Homo sapiens* IGHG2\*01; VH: 1-125; CH1: 126-223; charnière: 224-235; CH2: 236-344; CH3: 345-449 (S382A, mutation non fonctionnelle); CHS: 450-451; CDR Kabat H1: SYGMH (31-35); CDR Kabat H2: VIWYDGSNKYYADSVKG (50-66); CDR Kabat H3: GGGSGSYRYYYYGLDV (99-114); protéine de fusion: 1-29 (peptide-1 de type glucagon humain 7-35); liaison: 30-52; classe de chaîne légère: kappa; longueur de chaîne légère: 266; LV lignée germinale: *Homo sapiens* IGKV1-12\*01; LJ lignée germinale: *Homo sapiens* IGKJ1\*01; LC lignée germinale: *Homo sapiens* IGKC\*01; VL: 53-159; CL: 160-266; CDR Kabat L1: RASQININLLA (76-86); CDR Kabat L2: TASSLQS (102-108); CDR Kabat L3: QQAHRFPPT (141-149)  
*agoniste du récepteur au peptide-1 similaire au glucagon (GLP-1)*

gulgafafusp alfa

inmunoglobulina humana G2-kappa, anti-(receptor del péptido 1 similar al glucagón humano, GLP1R) (cadena pesada 1-451, variante S<sup>382</sup>>A) fusionada al N-terminal de cada cadena ligera (53-266) a través del enlace peptídico  
<sup>30</sup>GGSGATGGSGSGASSGSGSATGS<sup>52</sup> al receptor del péptido 1 similar al glucagón humano (GLP-1) fragmento (7-35, 1-29 en la secuencia actual), variante (A<sup>2</sup>>G), dímero con puente disulfuro, producido en células ováricas de hámster Chino (CHO), forma glicosilada alfa;

anticuerpo monoclonal humanizado de fusión con receptor del péptido 1 similar al glucagón (GLP1); tipo: IgG2-kappa; antígeno: receptor del péptido 1 similar al glucagón, receptor GLP-1, GLP-1-R, GLP-1R (GLP1R); fuente CDR: *Mus musculus* (humanizado por injerto de CDR de Kabat); clase cadena pesada: gamma2; longitud cadena pesada: 451; línea germinal HV: *Homo sapiens* IGHV3-33\*01; línea germinal HJ: *Homo sapiens* IGHJ6\*01; línea germinal HC: *Homo sapiens* IGHG2\*01; VH: 1-125; CH1: 126-223; bisagra: 224-235; CH2: 236-344; CH3: 345-449 (S382A, mutación no funcional); CHS: 450-451; CDR Kabat H1: SYGMH (31-35); CDR Kabat H2: VIWYDGSNKYYADSVKG (50-66); CDR Kabat H3: GGGSGSYRYYYGLDV (99-114); proteína de fusión: 1-29 (péptido 1 similar al glucagón humano 7-35); enlace: 30-52; clase de cadena ligera: kappa; longitud de cadena ligera: 266; línea germinal LV: *Homo sapiens* IGKV1-12\*01; línea germinal LJ: *Homo sapiens* IGKJ1\*01; línea germinal LC: *Homo sapiens* IGKC\*01; VL: 53-159; CL: 160-266; CDR Kabat L1: RASQININLLA (76-86); CDR Kabat L2: TASSLQS (102-108); CDR Kabat L3: QQAHRFPPT (141-149)  
*agonista del receptor del péptido similar al glucagón (GLP-1)*

2642374-02-3

## Sequence / Séquence / Secuencia

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLVESGGG	VYQPGKSLRL	SCAASGFTLS	SYGMHWVRQA	PGKLEWVAV	50
IWYDGSNKYY	ADSVKGRFTI	SRDNSKNTLY	LQMNSLRAED	TAVYICARGG	100
GSGSYRYYYY	GLDVWGQGTI	VTVSSASTKG	PSVFPLAPCS	RSTSESTAAL	150
GCLVKDYFPE	FVTVSWNSGA	LTSGVHTFFA	VLQSSGLYSL	SSVTVVPSN	200
FGTQTYTCNV	DHKPSNTKVD	KTVERKCCVE	CPPCAPPVA	GPSVFLFPPK	250
PKDTLMISRT	PEVTCVVVDV	SHEDPEVQFN	WYVDGVEVHN	AKTKPREEQF	300
NSTFRVSVLV	TVVHQDWLNG	KEYKCKVSNK	GLPAPIERTI	SKTKGQPREP	350
QVYTLPPSRE	EMTKNQVSLT	CLVKGFPYSD	IAVEWESNGQ	PENNYKTPPT	400
MLDSDGSFFL	YSKLTVDKSR	WQQGNVFCSS	VMHEALHNHY	TQKSLSLSPG	450
K					451

## Light chains / Chaînes légères / Cadenas ligeras: GLP-1- IgG2 kappa

<b>HCEGTFTSDV</b>	<b>SSYLEGQAAK</b>	<b>EFIAWLKVG</b>	<u>SGSATGGSGS</u>	<u>GASSGGSAT</u>	50
GSIAIQMTQSP	SSVSASIGDR	VTITCRASQN	INLLAWYQQ	KPGKAPKLLI	100
YTASSLQSEV	PSRFSGSGSG	TDFTLTISSL	QPEDFAIYCC	QQAHRFPPTF	150
GQGTKVEIRR	TVAAPSVFIF	PPSDEQLKSG	TASVCLLNN	FYPREAKVQW	200
KVDNALQSGN	SQESVTEQDS	KDSTYLSLST	LTLISKADYEK	HKVYACEVTH	250
QGLSSPVTKS	FNRGEC				266

## Mutation / Mutation / Mutación

S382, S382<sup>→</sup>A, A2<sup>→</sup>, A2<sup>→</sup>G

## Peptide linker / Peptides liant / Péptido de unión

GSATGGSGSGASSGSGSATGS 30-52

## Post-translational modifications

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

Intra-H 22-96, 152-208, 265-325, 371-429

22<sup>°</sup>-96<sup>°</sup>, 152<sup>°</sup>-208<sup>°</sup>, 265<sup>°</sup>-325<sup>°</sup>, 371<sup>°</sup>-429<sup>°</sup>Intra-L 75<sup>°</sup>-140<sup>°</sup>, 186<sup>°</sup>-246<sup>°</sup>75<sup>°</sup>-140<sup>°</sup>, 186<sup>°</sup>-246<sup>°</sup>Inter-H-L 139-266<sup>°</sup>, 139<sup>°</sup>-266<sup>°</sup>Inter-H-H 227-227<sup>°</sup>, 228-228<sup>°</sup>, 231-231<sup>°</sup>, 234-234<sup>°</sup>

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

N301, N301<sup>°</sup>

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

glutaminilo N-terminal

H VH Q1> pyroglutamyl (pE, 5-oxopropyl): 1, 1<sup>°</sup>

**gumelutamidum**  
gumelutamide

2-chloro-4-(4-([5-(2-hydroxypropan-2-yl)pyridin-2-yl]amino)-5,8-dihydropyrido[3,4-d]pyrimidin-7(6H)-yl)benzonitrile  
*antiandrogen, antineoplastic*

gumélutamide

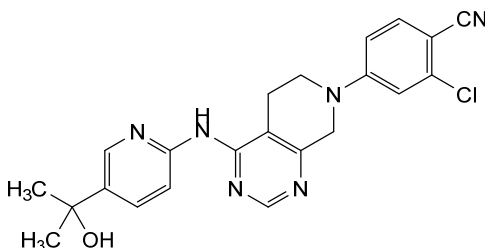
2-chloro-4-(4-[[5-(2-hydroxypropan-2-yl)pyridin-2-yl]amino]-5,8-dihydropyrido[3,4-*d*]pyrimidin-7(6*H*)-yl]benzonnitrile  
*antiandrogène, antinéoplasique*

gumelutamida

2-cloro-4-(4-[[5-(2-hidroxiopropan-2-il)piridin-2-il]amino]-5,8-dihidropirido[3,4-*d*]pirimidin-7(6*H*)-il]benzonnitrilo  
*antiandrògeno, antineoplàsico*

C<sub>22</sub>H<sub>21</sub>ClN<sub>6</sub>O

1831085-48-3

**hypericinum**

hypericin

*rac*-(3*aM*,10*aM*)-1,3,4,6,8,13-hexahydroxy-10,11-dimethylphenanthro[1,10,9,8-*opqra*]perylene-7,14-dione  
*photosensitizer*

hypéricine

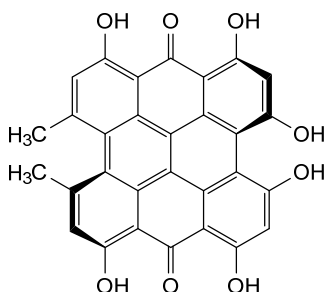
*rac*-(3*aM*,10*aM*)-1,3,4,6,8,13-hexahydroxy-10,11-diméthylphénanthro[1,10,9,8-*opqra*]pérylène-7,14-dione  
*photosensibilisant*

hipericina

*rac*-(3*aM*,10*aM*)-1,3,4,6,8,13-hexahidroxi-10,11-dimetilfenantro[1,10,9,8-*opqra*]perileno-7,14-diona  
*fotosensibilizante*

C<sub>30</sub>H<sub>16</sub>O<sub>8</sub>

1372719-41-9



and enantiomer  
et énantiomère  
y enantiómero

**ifebentinibum**

ifebentinib

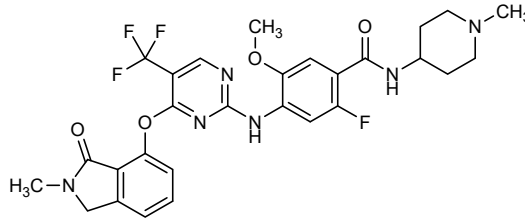
2-fluoro-5-methoxy-4-({4-[(2-methyl-3-oxo-2,3-dihydro-1*H*-isoindol-4-yl)oxy]-5-(trifluoromethyl)pyrimidin-2-yl}amino)-*N*-(1-methylpiperidin-4-yl)benzamide  
*tyrosine kinase inhibitor, antineoplastic*

ifébertinib 2-fluoro-5-méthoxy-4-({4-[(2-méthyl-3-oxo-2,3-dihydro-1*H*-isoinдол-4-yl)oxy]-5-(trifluorométhyl)pyrimidin-2-yl}amino)-*N*-(1-méthylpiperidin-4-yl)benzamíde  
*inhibiteur de tyrosine kinase, antinéoplasique*

ifebertinib 2-fluoro-5-metoxi-4-({4-[(2-metil-3-oxo-2,3-dihidro-1*H*-isoinдол-4-il)oxi]-5-(trifluorometil)pirimidin-2-il}amino)-*N*-(1-metilpiperidin-4-il)benzamida  
*inhibidor de tirosina kinasa, antineoplásico*

C<sub>28</sub>H<sub>28</sub>F<sub>4</sub>N<sub>6</sub>O<sub>4</sub>

1227948-82-4



**iluzanebartum #**  
iluzanebart

immunoglobulin G1-kappa, anti-[*Homo sapiens* TREM2 (triggering receptor expressed on myeloid cells 2)], *Homo sapiens* monoclonal antibody, agonist;

gamma1 heavy chain *Homo sapiens* (1-451) [VH (*Homo sapiens*IGHV5-51\*01 (96.9%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens*IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120>K (218) (122-219), hinge 1-15 (220-234), CH2 R83>C (296), N84.4>G (301), V85>C (306) (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV3-15\*01 (94.7%) -IGKJ1\*01 (90.9%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC\*01 (100%) (108'-214')]; dimer (230-230":233-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa  
*neuroprotectant*

iluzanebart

immunoglobuline G1-kappa, anti-[*Homo sapiens* TREM2 (récepteur déclenchant exprimé sur les cellules myéloïdes 2)], anticorps monoclonal *Homo sapiens*, agoniste;  
chaîne lourde gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens*IGHV5-51\*01 (96.9%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens*IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120>K (218) (122-219), charnière 1-15 (220-234), CH2 R83>C (296), N84.4>G (301), V85>C (306) (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV3-15\*01 (94.7%) -IGKJ1\*01 (90.9%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC\*01 (100%) (108'-214')]; dimère (230-230":233-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa  
*neuroprotecteur*

iluzanebart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* TREM2 (receptor desencadenante expresado sobre las células mieloides 2)], anticuerpo monoclonal *Homo sapiens*, agonista;  
 cadena pesada gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV5-51\*01 (96.9%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120>K (218) (122-219), bisagra 1-15 (220-234), CH2 R83>C (296), N84.4>G (301), V85>C (306)(235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15\*01 (94.7%) -IGKJ1\*01 (90.9%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%) (108'-214')]; dímero (230-230":233-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa *neuroprotector*

2733621-19-5

## Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKPGESLKI SCKGSGYSFT SYWIGWVRQM PCKGLEMMGI 50
IYFGDADARY SPSFQCVTTI SADKSI STAY LQWSSLKASD TAMYFCARRR 100
QGIFGCDALDF WQQGTLTVTS SASTKGPSVF FLAPSSKSTS GCTAALGCLV 150
KDYFFPEPVTV SWNSGALTSQ VHTFFAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKEV FKEDCKTHTC FPCPAPELLG GFSVFLFFPK 250
PKDTLMSRST PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPCEEQY 300
GSTYRCVSVL TVLHQDWLNG KEYCKVSNK ALPAPIEKTI SKARGQPREP 350
QVYTLPPSRE EMTKNQVSLT CLVKGFPYSD IAVEWESNGQ PENNYKTPFP 400
VLDSGGSFFL YSKLTVDKSR WQQGNVFPSCS VMHEALHNNHY TQKSLSLSPG 450
K 451
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## Light chain / Chaîne légère / Cadena ligera

```
EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWFQKQP GQAPRLLIYQ 50
ASTRATGIPA RFGSGSGSTE FTLTISLQF EDFAVYYCLQ DNNFPPTFGQ 100
GTRKVDIKRTV AAPSVEIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEK 214
```

## Post-translational modifications

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

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

22"-96" 148"-204" 265"-325" 371"-429"

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"

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

H CH2 N84.4&gt;G (G1v30): 301, 301"

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

L- $\alpha$ -aspartyl-L-threonyl-L-leucyl-L-leucyl-L-lysyl-L-alanyl-L-leucyl-L-leucyl-L- $\alpha$ -glutamyl-L-isoleucyl-L-alanyl-L-seryl-L-cysteinyl-L-leucyl-L- $\alpha$ -glutamyl-L-lysyl-L-alanyl-L-leucyl-L-glutamyl-L-valyl-L-phenylalanine  
*immunological agent for active immunization*  
*(antineoplastic)*

imsamotide	<p>L-<math>\alpha</math>-aspartyl-L-thréonyl-L-leucyl-L-leucyl-L-lysyl-L-alanyl-L-leucyl-L-leucyl-L-<math>\alpha</math>-glutamyl-L-isoleucyl-L-alanyl-L-séryl-L-cystéinyl-L-leucyl-L-<math>\alpha</math>-glutamyl-L-lysyl-L-alanyl-L-leucyl-L-glutaminy-L-valyl-L-phénylalanine</p> <p><i>agent immunologique d'immunisation active (antinéoplasique)</i></p>
imsamotida	<p>L-<math>\alpha</math>-aspartil-L-treonil-L-leucil-L-leucil-L-lisil-L-alanil-L-leucil-L-leucil-L-<math>\alpha</math>-glutamil-L-isoleucil-L-alanil-L-seril-L-cisteinil-L-leucil-L-<math>\alpha</math>-glutamil-L-lisil-L-alanil-L-leucil-L-glutaminil-L-valil-L-fenilalanina</p> <p><i>agente inmunológico para inmunización activa (antineoplásico)</i></p> <p><math>C_{106}H_{180}N_{24}O_{31}S</math> <span style="float: right;">2130836-27-8</span></p> <p>DTLLKALLEI ASCLEKALQV F 21</p>
<b>inaticabtagenum autoleucelum #</b> inaticabtagene autoleucel	<p>autologous T lymphocytes obtained from peripheral blood mononuclear cells by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector, encoding a chimeric antigen receptor targeting CD19. The expressed transgene comprises a CD8<math>\alpha</math> leader sequence, an anti-CD19 single chain variable fragment (scFv) derived from clone HI19a, a CD8<math>\alpha</math> hinge and transmembrane region, and a 4-1BB and CD3<math>\zeta</math> signalling domain and is under control of the elongation factor 1 alpha (EF1<math>\alpha</math>) promoter. The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a <math>\psi</math> packaging signal, parts of the <i>gag</i> and <i>env</i> genes, a Rev response element (RRE), a central polypurine tract (cPPT) sequence, a Kozak sequence, and a Woodchuck hepatitis virus posttranscriptional regulatory element (WPRE). The vector is pseudotyped with vesicular stomatitis virus (VSV) G glycoprotein. The leukapheresis material is enriched for CD4/CD8 T lymphocytes by positive immunoselection, activated by CD3 and CD28 magnetic beads and transduced with the vector. The cells are then expanded in media supplemented with serum replacement and interleukin 2 (IL-2). The T lymphocytes (<math>\geq 90\%</math>) are positive for the transgene (<math>\geq 15\%</math> CAR positive), secrete interferon gamma, and demonstrate cytotoxicity against CD19 expressing cells</p> <p><i>cell-based gene therapy (antineoplastic)</i></p>
inaticabtagène autoleucel	<p>lymphocytes T autologues obtenus à partir de cellules mononucléaires de sang périphérique par leucaphérese, transduits avec un vecteur lentiviral auto-inactivant et non répliquant, codant un récepteur antigénique chimérique ciblant CD19. Le transgène exprimé comprend une séquence leader CD8<math>\alpha</math>, un fragment variable à chaîne unique (scFv) anti-CD19 dérivé du clone HI19a, une charnière CD8<math>\alpha</math> et une région transmembranaire, ainsi qu'un domaine de signalisation 4-1BB et CD3<math>\zeta</math> et est sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF1<math>\alpha</math>). La construction est flanquée de répétitions longues terminales (LTR) en 5' et 3' et contient</p>

également un signal d'encapsidation  $\psi$ , des parties des gènes *gag* et *env*, un élément de réponse Rev (RRE), une séquence du tractus polypurine central (cPPT), une séquence Kozak et un élément de régulation post-transcriptionnel du virus de l'hépatite de Woodchuck (WPRE). Le vecteur est pseudotypé avec la glycoprotéine G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est enrichi en lymphocytes T CD4/CD8 par immunosélection positive, activé par des billes magnétiques CD3 et CD28 et transduit avec le vecteur. Les cellules sont ensuite développées dans un milieu complété par du sérum de remplacement et de l'interleukine 2 (IL-2). Les lymphocytes T ( $\geq 90\%$ ) sont positifs pour le transgène ( $\geq 15\%$  CAR positif), sécrètent de l'interféron gamma et démontrent une cytotoxicité contre les cellules exprimant le CD19

*thérapie génique à base de cellules (antineoplasique)*

inaticabtagén autoleucel

linfocitos T autólogos obtenidos de células mononucleares de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica para un receptor de antígenos quimérico dirigido a CD19. El transgén expresado contiene una secuencia líder de CD8 $\alpha$ , un fragmento variable de cadena sencilla (scFv) anti-CD19 derivado del clon HI19a, una región bisagra y transmembrana de CD8 $\alpha$ , y un dominio de señalización 4-1BB y CD3 $\zeta$ , y está bajo el control del promotor del factor de elongación 1 alfa (EF1 $\alpha$ ). El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento  $\psi$ , partes de los genes *gag* y *env*, un elemento de respuesta Rev (RRE), una secuencia de tracto de polipurina central (cPPT), una secuencia Kozak y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE). El vector está seudotipado con la glicoproteína G del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se enriquece para linfocitos T CD4/CD8 mediante inmunoselección positiva, se activa mediante bolas magnéticas de CD3 y CD28 y se transduce con el vector. Las células son después expandidas en medio suplementado con sustituto de suero e interleuquina 2 (IL-2). Los linfocitos T ( $\geq 90\%$ ) son positivos para el transgén ( $\geq 15\%$  CAR positivas), secretan interferón gamma y demuestran citotoxicidad contra células que expresan CD19

*terapia génica basada en células (antineoplásico)*

**inpegsomatropinum #**  
inpegsomatropin

recombinant human somatotropin (growth hormone, GH), conjugated to a multi-arm polyethylene glycol carrier molecule;  
somatotropin (human), produced by *Pichia pastoris*, non-glycosylated, N-terminal or N<sup>6</sup>-Lys mono-substituted with one (2-[ $\omega$ -methoxypoly(oxyethylene)- $\alpha$ -yl]-N-{2-[ $\omega$ -methoxypoly(oxyethylene)- $\alpha$ -yl]ethyl}acetamido)acetyl group (~40 kDa)

*growth hormone analogue*



- inpegsomatropine somatotropine humaine recombinante (hormone de croissance, GH), conjuguée à une molécule transporteur multi-bras de polyéthylène glycol;  
somatotropine (humaine), produite par *Pichia pastoris*, non glycosylée, mono-substituée à l'extrémité N-terminale ou en N<sup>6</sup>.Lys par un groupe (2-[ω-méthoxypoly(oxyéthylène)-α-yl]-N-[2-[ω-méthoxypoly(oxyéthylène)-α-yl]éthyl]acétamido)acétyle (~40 kDa)  
*analogue de l'hormone de croissance*
- inpegsomatropina somatotropina humana recombinante (hormona de crecimiento, GH), conjugada con una molécula transportadora multi-brazo de polietileno glicol;  
somatotropina (humana), producida por *Pichia pastoris*, no glicosilada, mono-sustituida con el extremo N-terminal o con N<sup>6</sup>.Lys por un grupo (2-[ω-metoxipoli(oxietileno)-α-il]-N-[2-[ω-metoxipoli(oxietileno)-α-il]etil]acetamido)acetil (~40 kDa)  
*análogo de la hormona de crecimiento*

2656386-75-1

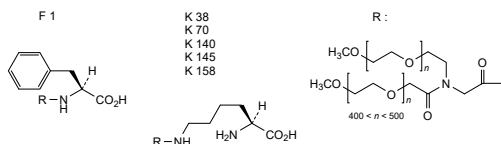
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EPTIPLSRRLF DNAMLRARHL HQLAFDTYQE FEEAYIPKEQ KYSFLQNPQT 50
SLCFSESIPT PSNREETQQK SNLELLRISL LLIQSWLEPV QFLRSVFANS 100
LVYGASDSNV YDLLKDLEEG IQTLMGRLED GSPRTGQIFK QTYSKFDTNS 150
HNDDALLKNY GLLYCFRKM DKVETFLRIV QCRSVEGSCG F 191

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

Potential modified residues / Résidus modifiés potentiels / restos modificados potenciales



**izumerogantum**  
izumerogant

4-{4-[3-(2-chloro-6-fluorophenyl)-4-(pyrimidin-2-yl)-1,2-oxazol-5-yl]-5-(trifluoromethyl)-1H-pyrazol-1-yl]-2-methylbutan-2-ol  
*retinoid-related orphan receptor-gamma (RORγ) inverse agonist*

izumérogant

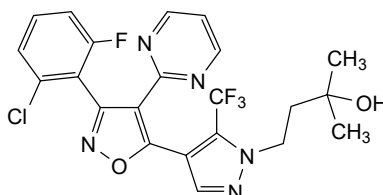
4-{4-[3-(2-chloro-6-fluorophényl)-4-(pyrimidin-2-yl)-1,2-oxazol-5-yl]-5-(trifluorométhy)-1H-pyrazol-1-yl]-2-méthylbutan-2-ol  
*agoniste inverse des récepteurs gamma orphelins liés aux rétinoïdes (RORγ)*

izumerogant

4-{4-[3-(2-cloro-6-fluorofenil)-4-(pirimidin-2-il)-1,2-oxazol-5-il]-5-(trifluorometil)-1H-pirazol-1-il]-2-metilbutan-2-ol  
*agonista inverso de los receptores gamma huérfanos relacionados con los retinoides (RORγ)*

C<sub>22</sub>H<sub>18</sub>ClF<sub>4</sub>N<sub>5</sub>O<sub>2</sub>

2299252-72-3



**labafenogenum marselecobacum #**

labafenogene marselecobac recombinant live *Escherichia coli* strain Nissle 1917 (EcN) bacteria, genetically engineered as follows:

- Insertion across the genome of four copies of a modified phenylalanine ammonia lyase (mPAL) gene from *Phototribidus laumondii* subsp. *laumondii* with mutations S92G, H133M, I167K, L432I, V470A under control of the  $\text{Lacl}$  repressor/ $\text{P}_{\text{tac}}$  inducible promoter.
- Insertion of one extra copy of the endogenous high affinity phenylalanine specific permease (PheP), under control of the  $\text{Lacl}$  repressor/ $\text{P}_{\text{tac}}$  inducible promoter.
- Insertion of the gene L-amino acid deaminase (LAAD), derived from *Proteus mirabilis*, under control of the endogenous AraC transcriptional regulator/ $\text{P}_{\text{BAD}}$  inducible promoter.
- Deletion of the *dapA* gene, which renders bacteria cells auxotrophic unless supplemented with diaminopimelate (DAP) exogenously.
- Deletion of its endogenous prophage  $\Phi$ .

*genetically modified bacteria (phenylalanine hydroxylase deficiency)*

labafénogène marsélécobac bactérie recombinante vivante *Escherichia coli* souche Nissle 1917 (EcN), génétiquement modifiée comme suit:

- Insertion dans le génome de quatre copies d'un gène de phénylalanine ammoniac lyase (mPAL) modifié de *Phototribidus laumondii* subsp. *laumondii* avec les mutations S92G, H133M, I167K, L432I, V470A sous le contrôle du répresseur  $\text{Lacl}$ /promoteur inductible  $\text{P}_{\text{tac}}$ .
- Insertion d'une copie supplémentaire de la perméase spécifique de la phénylalanine endogène à haute affinité (PheP), sous le contrôle du répresseur  $\text{Lacl}$ /promoteur inductible  $\text{P}_{\text{tac}}$ .
- Insertion du gène L-aminoacide désaminase (LAAD), dérivé de *Proteus mirabilis*, sous le contrôle du régulateur de transcription endogène AraC/promoteur inductible  $\text{P}_{\text{BAD}}$ .
- La délétion du gène *dapA*, qui rend les cellules bactériennes auxotrophes à moins d'être complémentées par du diaminopimélate (DAP) de manière exogène.
- Suppression de son prophage endogène  $\Phi$ .

*bactérie génétiquement modifiée (déficit en phénylalanine hydroxylase)*

labafenogén marselecobac bacteria recombinante viva *Escherichia coli* cepa Nissle 1917 (EcN), modificada genéticamente como sigue:

- Inserción a lo largo del genoma de cuatro copias de un gen modificado de fenilalanina amonio liasa (mPAL) de *Phototribidus laumondii* subsp. *laumondii* con mutaciones S92G, H133M, I167K, L432I, V470A bajo el control del represor  $\text{Lacl}$ /promotor inducible  $\text{P}_{\text{tac}}$ .
- Inserción de una copia extra de la permeasa de alta afinidad endógena específica de fenilalanina (PheP), bajo el control del represor  $\text{Lacl}$ /promotor inducible  $\text{P}_{\text{tac}}$ .
- Inserción el gen de la L-amino ácido deaminasa (LAAD), derivado de *Proteus mirabilis*, bajo el control del regulador transcripcional endógeno AraC/promotor inducible  $\text{P}_{\text{BAD}}$ .
- Delección del gen *dapA*, que produce células de bacteria auxotróficas salvo que se las suplemente exógenamente con diaminopimelato (DAP).

e) Delección de su profago endógeno Φ.

*bacteria genéticamente modificada (deficiencia de fenilalanina hidroxilasa)*

**lafuvitugum #**

lafuvitug

immunoglobulin G1-kappa, anti-[HIV-1 (human immunodeficiency virus type 1) gp120 envelope glycoprotein, CD4-binding site)], *Homo sapiens* monoclonal antibody;  
 gamma1 heavy chain *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV1-2\*02 (62.7%) -(IGHD) -IGHJ3\*01 (85.7%), CDR-IMGT [8.8.12] (26-33.51-58.101-112), FR3 insertion D84.1, F84.2, D85.2, T85.1 (77-80)) (1-123) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (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)], (226-206')-disulfide with kappa light chain *Homo sapiens* (1'-206') [V-KAPPA (*Homo sapiens* IGKV1-33\*01 (72.8%) -IGKJ5\*01 (41,6%) del(F118, G119, Q120) 92^93, E125>D (97), I126>L (98), CDR-IMGT [2.3.8] (27-28.46-48.85-92)) (1'-99') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (145), V101 (183) (100'-206')]; dimer (232-232":235-235")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHOK1SV, glycoform alfa  
*antiviral*

lafuvitug

immunoglobuline G1-kappa, anti-[site de liaison au CD4 de la protéine d'enveloppe gp120 du virus de l'immunodéficience humaine de type 1 (HIV-1)], anticorps monoclonal *Homo sapiens*;  
 chaîne lourde gamma1 *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV1-2\*02 (62.7%) -(IGHD) -IGHJ3\*01 (85.7%), CDR-IMGT [8.8.12] (26-33.51-58.101-112), FR3 insertion D84.1, F84.2, D85.2, T85.1 (77-80)) (1-123) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (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)], (226-206')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-206') [V-KAPPA (*Homo sapiens* IGKV1-33\*01 (72.8%) -IGKJ5\*01 (41,6%) del(F118, G119, Q120) 92^93, E125>D (97), I126>L (98), CDR-IMGT [2.3.8] (27-28.46-48.85-92)) (1'-99') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (145), V101 (183) (100'-206')]; dimère (232-232":235-235")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHOK1SV, glycoforme alfa  
*antiviral*

lafuvitug

inmunoglobulina G1-kappa, anti-[lugar de unión al CD4 de la proteína de recubrimiento gp120 del virus de la inmunodeficiencia humana de tipo 1 (HIV-1)], anticuerpo monoclonal *Homo sapiens*;  
 cadena pesada gamma1 *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV1-2\*02 (62.7%) -(IGHD) -IGHJ3\*01 (85.7%), CDR-IMGT [8.8.12] (26-33.51-58.101-112), FR3 inserción D84.1, F84.2, D85.2, T85.1 (77-80)) (1-123) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14(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)], (226-206')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-206') [V-KAPPA (*Homo sapiens* IGKV1-33\*01 (72.8%) -IGKJ5\*01 (41,6%) del(F118, G119, Q120) 92^93, E125>D (97), I126>L (98), CDR-IMGT [2.3.8] (27-28.46-48.85-92)) (1'-99') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (145), V101 (183) (100'-206')]; dímero (232-232":235-235")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHOK1SV, forma glicosilada alfa  
*antiviral*

2743342-91-6

## Heavy chain / Chaîne lourde / Cadena pesada

VQQLQSGAA VTKPGASRVV SCEASGYNIR DYFIHWWRQA PGQGLQWVGW 50  
 INPKTGQFNN PRQFQGRVSL TRHASWDFDT FSFYMDLKAL RSDDTAVYFC 100  
 ARQRSDYWFV DVWGSQTQVT VSSASTKGPS VFFLAPS SSKS TSGGTAALGC 150  
 LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSL VVTVPSSSLG 200  
 TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL LGGSPVFLFP 250  
 PKPKDFLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300  
 QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKARQQPR 350  
 EPQVYTLPPS RDELTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400  
 PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSMVHEALHN HYTKQSLSL 450  
 PGK 453

## Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGDIVT ITCQANGYLW WYQQRGKAP KLLIYDGSKL 50  
 ERGVPSRFSG RRWGQENYLT INNLQPEDIA TYFCQVVEFV VPGTRLDLKR 100  
 TVAAPSVEFIF PPSDEQLKSG TASVVCLLNN FYPREARQVW KVDNALQSGN 150  
 SQESVTEQDS KDSTYLSLST LTLISKADYEK HKVYACEVTH QGLSSPVTKS 200  
 FNRGEC 206

## Post-translational modifications

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

Intra-H (C23-C104) 22°-100° 150°-206° 267°-327° 373°-431°  
 22°-100° 150°-206° 267°-327° 373°-431°

Intra-L (C23-C104) 23°-84° 126°-186°

23°-84° 126°-186°

Inter-H-L (h 5-CL 126) 226°-206° 226°-206°

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

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

Q &gt; pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolyle)

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  
 V-KAPPA N88: 68°, 68"

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

H CHS K2: 453, 453"

**lartesertibum**

lartesertib

8-(1,3-dimethyl-1*H*-pyrazol-4-yl)-1-(3-fluoro-5-methoxy-*pyridin*-4-yl)-7-methoxy-3-methyl-1,3-dihydro-2*H*-imidazo[4,5-*c*]quinolin-2-one  
*serine/ threonine kinase inhibitor, antineoplastic*

lartésertib

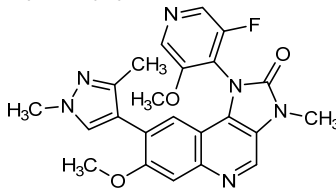
8-(1,3-diméthyl-1*H*-pyrazol-4-yl)-1-(3-fluoro-5-méthoxy-*pyridin*-4-yl)-7-méthoxy-3-méthyl-1,3-dihydro-2*H*-imidazo[4,5-*c*]quinoléin-2-one  
*inhibiteur de sérine/ thréonine kinase, antinéoplasique*

lartesertib

8-(1,3-dimetil-1*H*-pirazol-4-il)-1-(3-fluoro-5-metoxipiridin-4-il)-7-metoxi-3-metil-1,3-dihidro-2*H*-imidazo[4,5-*c*]quinolein-2-ona  
*inhibidor de serina/ treonina kinasa, antineoplásico*

C<sub>23</sub>H<sub>21</sub>FN<sub>6</sub>O<sub>3</sub>

2495096-26-7



**lenumlostatum**

lenumlostat

(3-[[4-(aminométhyl)-6-(trifluorométhyl)pyridin-2-yl]oxy]phényl)[(3*R*,4*R*)-3-fluoro-4-hydroxypyrrolidin-1-yl]méthanone  
*lysyl oxidase homolog 2 (LOXL2) inhibitor, antifibrotic*

lénumlostat

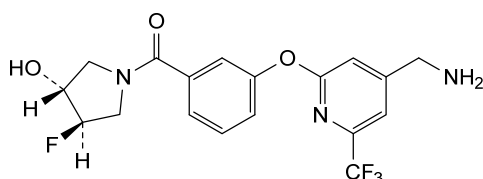
(3-[[4-(aminométhy)-6-(trifluorométhy)pyridin-2-yl]oxy]phényl)[(3*R*,4*R*)-3-fluoro-4-hydroxypyrrolidin-1-yl]méthanone  
*inhibiteur de l'homologue 2 de la lysyl-oxydase (LOXL2), antifibrotique*

lenumlostat

(3-[[4-(aminometil)-6-(trifluorometil)piridin-2-il]oxi]fenil)[(3*R*,4*R*)-3-fluoro-4-hidroxi-pirrolidin-1-il]metanona  
*inhibidor homólogo 2 de la lisil oxidasa (LOXL2), antifibrótico*

C<sub>18</sub>H<sub>17</sub>F<sub>4</sub>N<sub>3</sub>O<sub>3</sub>

2098884-52-5

**lirafugratinibum**

lirafugratinib

*N*-[4-(4-amino-5-{3-fluoro-4-[(4-méthylpyrimidin-2-yl)oxy]phényl}-7-méthyl-7*H*-pyrrolo[2,3-*d*]pyrimidin-6-yl)phényl]-2-méthylprop-2-énamide  
*tyrosine kinase inhibitor, antineoplastic*

lirafugratinib

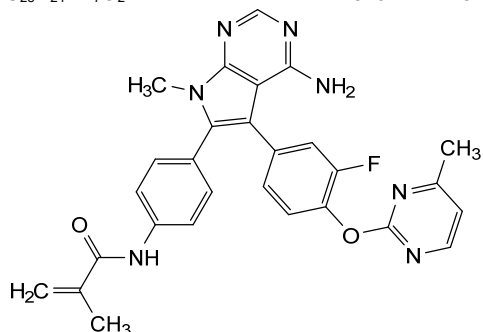
*N*-[4-(4-amino-5-{3-fluoro-4-[(4-méthylpyrimidin-2-yl)oxy]phényl}-7-méthyl-7*H*-pyrrolo[2,3-*d*]pyrimidin-6-yl)phényl]-2-méthylprop-2-énamide  
*inhibiteur de tyrosine kinase, antinéoplasique*

lirafugratinib

*N*-[4-(4-amino-5-{3-fluoro-4-[(4-metilpirimidin-2-il)oxi]fenil}-7-metil-7*H*-pirrolo[2,3-*d*]pirimidin-6-il)fenil]-2-metilprop-2-enamida  
*inhibidor de tirosina kinasa, antineoplásico*

C<sub>28</sub>H<sub>24</sub>FN<sub>7</sub>O<sub>2</sub>

2549174-42-5



**lixudebartum #**

lixudebart

immunoglobulin G1-kappa, anti-[*Homo sapiens* CLDN1 (claudin-1) conformational epitope of the first extracellular loop (EL1)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV3-21\*01 (94.9%) -(IGHD) -IGHJ1\*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1\*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, CH2 IGHG1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (216) (120-217), hinge 1-15 (218-232), CH2 L1.3>F (236) , L1.2>E (237), P116>S (333) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15\*01 (84.2%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa  
*claudin 1 protein inhibitor*

lixudébart

immunoglobuline G1-kappa, anti-[*Homo sapiens* CLDN1 (claudine 1) épitope conformationnel de la première boucle extracellulaire (EL1)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV3-21\*01 (94.9%) -(IGHD) -IGHJ1\*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1\*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, CH2 IGHG1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (216) (120-217), charnière 1-15 (218-232), CH2 L1.3>F (236), L1.2>E (237), P116>S (333) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16\*01 (87.8%) -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 (230-230":233-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa  
*inhibiteur de la protéine claudine 1*

lixudebart

immunoglobulina G1-kappa, anti-[*Homo sapiens* CLDN1 (claudina 1) epítipo conformacional del primer bucle extracelular (EL1)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV3-21\*01 (94.9%) -(IGHD) -IGHJ1\*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1\*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, CH2 IGHG1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (216) (120-217), bisagra 1-15 (218-232), CH2 L1.3>F (236), L1.2>E (237), P116>S (333) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16\*01 (87.8%) -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 (230-230":233-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa  
*inhibidor de la proteína claudin 1*

C<sub>6442</sub>H<sub>9928</sub>N<sub>1726</sub>O<sub>1997</sub>S<sub>44</sub>

2749515-10-2

## Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG LVKPGGSLRL SCAASGFSEF SYGMNWRQA PGKLEWVSS 50  
 ISFGSYFYF ADSVKRFTI SRDANKNSLY LQMSLRAED TAVYCARLP 100  
 GFNPPDFHWG QGTLVTVSSA STKGPSVFPFL APSKSTSGG TAALGCLVKD 150  
 YFPEPVTVSW NSGALTSGVH TFFPAVLQSSG LYSLSVVTV PSSSLGTQTY 200  
 ICNWNHKFSN TKVDKRVFK SCDKTHTCPP CPAPEFEGGP SVFLFPKPK 250  
 DTLMISRTEF VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREQYNS 300  
 TYRVSVLTV LHQDNLNGKE YKCKVSNKAL PASIEKTIK ARGQPREPQV 350  
 YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPEVL 400  
 DSDGSFFLYS KLTVDKSRWQ QGNVFSQVM HEALHNHYTQ KSLSLSPG 448

## Light chain / Chaîne légère / Cadena ligera

DIQMTQSPAT LSVSPGERAT LSCKASQNVG GNVDWYQWKP GQAPRLLIYG 50  
 ASNRYTGIPA RFRGSGSGTE FTLTISLQOS EDFAVYYCLO YKNNPWTFGQ 100  
 GTKVEIKRTV AAPSIVFIFPP SDEQLKSGTA SVVCLLNIFY BREAKVQWKV 150  
 DNALQSGNSQ ESVTEQDSKD STYLSSTLT 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 biantennarios complejos fucosilados.

**lutetium (<sup>177</sup>Lu) edotreotidum**  
 lutetium (<sup>177</sup>Lu) edotreotide

[N<sup>2,1</sup>-({4,7,10-tris[(carboxylato-κO)methyl]-1,4,7,10-tetraazacyclododecan-1-yl-κ<sup>4</sup>N<sup>1</sup>,N<sup>4</sup>,N<sup>7</sup>,N<sup>10</sup>)}acetyl-κO)-S<sup>3,2</sup>,S<sup>3,7</sup>-cyclo(D-phenylalanyl-L-cysteinyl-L-tyrosyl-D-tryptophyl-L-lysyl-L-threonyl-L-cysteinyl-L-threoninol)](<sup>177</sup>Lu)lutetium  
*antineoplastic*

lutécium (<sup>177</sup>Lu) édotréotide

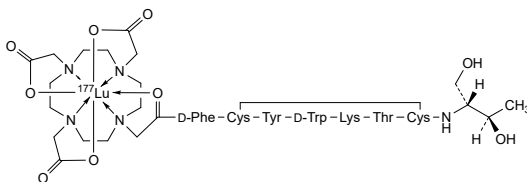
[N<sup>2,1</sup>-({4,7,10-tris[(carboxylato-κO)méthyl]-1,4,7,10-tétrazacyclododécane-1-yl-κ<sup>4</sup>N<sup>1</sup>,N<sup>4</sup>,N<sup>7</sup>,N<sup>10</sup>)}acétyl-κO)-S<sup>3,2</sup>,S<sup>3,7</sup>-cyclo(D-phénylalanyl-L-cystéinyl-L-tyrosyl-D-tryptophyl-L-lysyl-L-thréonyl-L-cystéinyl-L-thréoninol)](<sup>177</sup>Lu)lutécium  
*antineoplasique*

lutecio (<sup>177</sup>Lu) edotreotida

[N<sup>2,1</sup>-({4,7,10-tris[(carboxilato-κO)metil]-1,4,7,10-tetraazaciclododecan-1-il-κ<sup>4</sup>N<sup>1</sup>,N<sup>4</sup>,N<sup>7</sup>,N<sup>10</sup>)}acetyl-κO)-S<sup>3,2</sup>,S<sup>3,7</sup>-ciclo(D-fenilalanil-L-cisteinil-L-tirosil-D-triptofil-L-lisil-L-treonil-L-cisteinil-L-treoninol)](<sup>177</sup>Lu)lutecio  
*antineoplásico*

C<sub>65</sub>H<sub>89</sub><sup>177</sup>LuN<sub>14</sub>O<sub>18</sub>S<sub>2</sub>

321835-55-6



**lutetium (<sup>177</sup>Lu) rofapitidum tetraxetanum**lutetium (<sup>177</sup>Lu) rofapitide tetraxetan

[2,2',2''-{10-[2-(oxo-κO)-2-[[2-(((1<sup>2</sup>S,3<sup>2</sup>S,5R,13R,16S,19S,22S)-19-(3-amino-3-oxopropyl)-16-benzyl-13-carboxy-5-hexanamido-22-[(1R)-1-hydroxyethyl]-2,4,15,18,21,24-hexaoxo-7,11-dithia-14,17,20,23-tetraaza-1(1,2),3(2,1)-dipyrrolidina-9(1,3)-benzenacyclotetracosaphan-9<sup>5</sup>-yl)methyl}sulfanyl)ethyl]amino}ethyl]-1,4,7,10-tetraazacyclododecane-1,4,7-triyl-κ<sup>4</sup>N<sup>1</sup>,N<sup>4</sup>,N<sup>7</sup>,N<sup>10</sup>}]tri(acetato-κO)](<sup>177</sup>Lu)lutetium  
*antineoplastique*

lutécium (<sup>177</sup>Lu) rofapitide tétraxétan

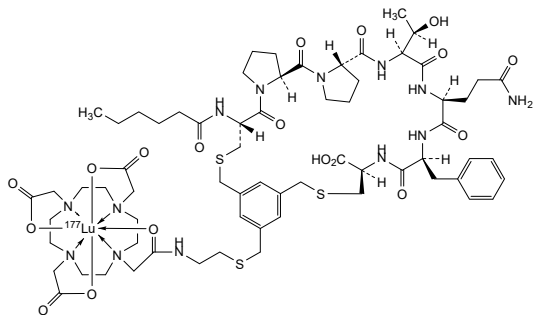
[2,2',2''-{10-[2-(oxo-κO)-2-[[2-(((1<sup>2</sup>S,3<sup>2</sup>S,5R,13R,16S,19S,22S)-19-(3-amino-3-oxopropyl)-16-benzyl-13-carboxy-5-hexanamido-22-[(1R)-1-hydroxyéthyl]-2,4,15,18,21,24-hexaoxo-7,11-dithia-14,17,20,23-tétraaza-1(1,2),3(2,1)-dipyrrolidina-9(1,3)-benzénacyclotétracosaphan-9<sup>5</sup>-yl)méthyl}sulfanyl)éthyl]amino}éthyl]-1,4,7,10-tétraazacyclododécane-1,4,7-triyl-κ<sup>4</sup>N<sup>1</sup>,N<sup>4</sup>,N<sup>7</sup>,N<sup>10</sup>}]tri(acétato-κO)](<sup>177</sup>Lu)lutécium  
*antineoplasique*

lutecio (<sup>177</sup>Lu) rofapitida tetraxetán

[2,2',2''-{10-[2-(oxo-κO)-2-[[2-(((1<sup>2</sup>S,3<sup>2</sup>S,5R,13R,16S,19S,22S)-19-(3-amino-3-oxopropil)-16-bencil-13-carboxi-5-hexanamido-22-[(1R)-1-hidroxietyl]-2,4,15,18,21,24-hexaoxo-7,11-ditia-14,17,20,23-tetraaza-1(1,2),3(2,1)-dipirrolidina-9(1,3)-bencenaciotetracosafan-9<sup>5</sup>-il]metil}sulfanil)etil]amino}etil]-1,4,7,10-tetraazaciclododecano-1,4,7-triyl-κ<sup>4</sup>N<sup>1</sup>,N<sup>4</sup>,N<sup>7</sup>,N<sup>10</sup>}]tri(acetato-κO)](<sup>177</sup>Lu)lutecio  
*antineoplásico*

C<sub>67</sub>H<sub>96</sub><sup>177</sup>LuN<sub>13</sub>O<sub>18</sub>S<sub>3</sub>

2583700-68-7

**maridebartum #**

maridebart

immunoglobulin G1-kappa, anti-[*Homo sapiens* GIPR (gastric inhibitory polypeptide receptor)], *Homo sapiens* monoclonal antibody;



	<p>gamma1 heavy chain <i>Homo sapiens</i> (1-450) [VH (<i>Homo sapiens</i> IGHV3-33*01 (92.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -<i>Homo sapiens</i> IGHG1*03v, G1m3&gt;G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v64 CH2 C36, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120&gt;K (217) (121-218), hinge 1-15 (219-233), CH2 E36&gt;C (275), R83&gt;C (295), N84.4&gt;G (300), V85&gt;C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain <i>Homo sapiens</i> (1'-214') [V-KAPPA (<i>Homo sapiens</i> IGKV3-15*01 (97.9%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.51-53.89-97)) (1'-107') -<i>Homo sapiens</i> 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 <i>gastric inhibitory polypeptide (GIP) receptor antagonist</i></p>
maridébart	<p>immunoglobuline G1-kappa, anti-[<i>Homo sapiens</i> GIPR (récepteur du polypeptide inhibiteur gastrique)], anticorps monoclonal <i>Homo sapiens</i>; chaîne lourde gamma1 <i>Homo sapiens</i> (1-450) [VH (<i>Homo sapiens</i> IGHV3-33*01 (92.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -<i>Homo sapiens</i> IGHG1*03v, G1m3&gt;G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v64 CH2 C36, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120&gt;K (217) (121-218), charnière 1-15 (219-233), CH2 E36&gt;C (275), R83&gt;C (295), N84.4&gt;G (300), V85&gt;C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa <i>Homo sapiens</i> (1'-214') [V-KAPPA (<i>Homo sapiens</i> IGKV3-15*01 (97.9%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.51-53.89-97)) (1'-107') -<i>Homo sapiens</i> 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 <i>antagoniste du récepteur du polypeptide insulinothéropé dépendant du glucose (GIP)</i></p>
maridebart	<p>immunoglobulina G1-kappa, anti-[<i>Homo sapiens</i> GIPR (receptor del polipéptido inhibidor gástrico)], anticuerpo monoclonal <i>Homo sapiens</i>; cadena pesada gamma1 <i>Homo sapiens</i> (1-450) [VH (<i>Homo sapiens</i> IGHV3-33*01 (92.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -<i>Homo sapiens</i> IGHG1*03v, G1m3&gt;G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v64 CH2 C36, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120&gt;K (217) (121-218), bisagra 1-15 (219-233), CH2 E36&gt;C (275), R83&gt;C (295), N84.4&gt;G (300), V85&gt;C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa <i>Homo sapiens</i> (1'-214') [V-KAPPA (<i>Homo sapiens</i> IGKV3-15*01 (97.9%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.51-53.89-97)) (1'-107') -<i>Homo sapiens</i> 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 <i>antagonista del receptor del polipéptido insulinothéropé dependiente de la glucosa (GIP)</i></p>



maridébart cafraglutide

immunoglobuline G1-kappa, anti-[*Homo sapiens* GIPR (récepteur du polypeptide inhibiteur gastrique)], anticorps monoclonal *Homo sapiens*; conjugué avec deux peptides identiques analogues du peptide-1 similaire au glucagon (GLP-1); chaîne lourde gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-33\*01 (92.9%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v64 CH2 C36, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 E36>C (275), R83>C (295), N84.4>G (300), V85>C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15\*01 (97.9%) -IGKJ4\*01 (100%), CDR-IMGT [6.3.9] (27-32.51-53.89-97)) (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; 275,275''-bis(thioéther) conjugué à un analogue du glucagon-like peptide 1 (GLP-1)(GCG (glucagon) 98-126, GLP-1 7-35 A8>méthylalanine (2), V16>Y (10), G22>E (16)), via un linker fusionné de 18-mer (diglycyl- tris(tétraglycyl-séryl)- lysinamide)  
*antagoniste du récepteur du polypeptide insulinothrepe dépendant du glucose (GIP), agoniste du récepteur du peptide-1 similaire au glucagon (GLP-1)*

maridebart cafraglutida

inmunoglobulina G1-kappa, anti-[*Homo sapiens* GIPR (receptor del polipéptido inhibidor gástrico)], anticuerpo monoclonal *Homo sapiens*; conjugado con dos péptidos idénticos análogos del péptido tipo glucagón 1 (GLP-1); cadena pesada gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-33\*01 (92.9%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v64 CH2 C36, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 E36>C (275), R83>C (295), N84.4>G (300), V85>C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15\*01 (97.9%) -IGKJ4\*01 (100%), CDR-IMGT [6.3.9] (27-32.51-53.89-97)) (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; 275,275''-bis(tioéter) conjugado con un análogo del péptido de tipo glucagón 1 (GLP-1)(GCG (glucagón) 98-126, GLP-1 7-35 A8>metilalanina (2), V16>Y (10), G22>E (16)), a través de un enlace fusionado de 18-mer (diglicil- tris(tetraglicil-seril)-lisinamida)  
*antagonista del receptor del polipéptido insulinothrópico dependiente de la glucosa (GIP), agonista del receptor del péptido similar al glucagón (GLP-1)*

2760218-55-9

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVDSGGG VVQFGRSLRL SCAASGFTFS NYGMHWVRQA PGEGLNVAA 50  
 IWFDAADKYI ADAVKGRFTI SRDMSKNTLY LQMNLSRAED TAVYYCARDQ 100  
 AIFGVVPDYW GQGTLVTVSS ASTKGPSVFP LAFSSKSTSG GTAALGCLVK 150  
 DYFPEPVTVS WNSGALTSGV HTPFVAVLQSS GLYSLSSVVT VFSSSLGTQT 200  
 YICNVVHKPS NTKVDRKVEP KSCDKHTHCP FCPAPELLGG PSVFLFPPKP 250  
 KDTLMISRTPEVTCVVVDVSP HEDPCVRFNW YVDGVEVHNA KTKPCCEQYG 300  
 STYRCVSLT VLNQDNLNGK EYKCKVSNKA LPAPIERTIS KAKGQPREPQ 350  
 VYTLPPSREE MTRKQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTTTPV 400  
 LDSGDSFFLY SKLTVDKSRW QCGNVFSCSV MHEALHNYT QKSLSLSPGK 450

Light chain / Chaîne légère / Cadena ligera

EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQK QGAPRLLIY 50  
 AATRATGIPA RVSGSGSGTE FTLTISLQSS EDFAVYYCQQ YNNWPLTEGG 100  
 GTKVEIKRTV AAPSVEIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150  
 DNALQSGNSQ ESVTEQDSKD STYLSSTLT LSKADYEKHK VYACEVTHQG 200  
 LSSPVTKSFN RGEC 214

Conjugated peptide / Peptide conjugué / Péptido conjugado

HXEGFTSDY SSYLEEQAAK EFLAWLVKGG GGGGGSGGG SGGGGSK 47  
 X=methylalanine

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-CH2 C83-C85 (G1v54) 295-305 295"-305"  
 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 glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxopropililo)  
 H VH Q1: 1, 1"

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

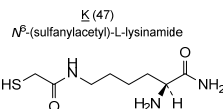
H CH2 N84.4->G (G1v30): 300, 300"

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

H CHS K2: 450, 450"

Modified residues / Résidus modifiés / Restos modificados

A(2)  
 2-methyl-Ala, Aib  
 aminoisobutyric acid



marlumotidum  
 marlumotide

[R126>Y]-human Wilms tumor protein (WT33)-(122-140)-peptide;

L-serylglycyl-L-glutaminyL-L-alanyl-L-tyrosyl-L-methionyl-L-phenylalanyl-L-prolyl-L-asparaginyL-L-alanyl-L-prolyl-L-tyrosyl-L-leucyl-L-prolyl-L-seryl-L-cysteinyl-L-leucyl-L-α-glutamyl-L-serine  
*immunological agent for active immunization (antineoplastic)*

marlumotide

[R126>Y]-protéine humaine de la tumeur de Wilms (WT33)-(122-140)-peptide;

L-sérylglycyl-L-glutaminyL-L-alanyl-L-tyrosyl-L-méthionyl-L-phénylalanyl-L-prolyl-L-asparaginyL-L-alanyl-L-prolyl-L-tyrosyl-L-leucyl-L-prolyl-L-séryl-L-cystéinyl-L-leucyl-L-α-glutamyl-L-sérine  
*agent immunologique d'immunisation active (antinéoplasique)*

marlumotida

[R126>Y]-proteína humana del tumor de Wilms (WT33)-(122-140)-péptido;  
L-serilglicil-L-glutaminil-L-alanil-L-tirosil-L-metionil-L-fenilalanil-L-prolil-L-asparaginil-L-alanil-L-prolil-L-tirosil-L-leucil-L-prolil-L-seril-L-cisteinil-L-leucil-L- $\alpha$ -glutamil-L-serina  
*agente inmunológico para inmunización activa (antineoplásico)*

C<sub>93</sub>H<sub>135</sub>N<sub>21</sub>O<sub>29</sub>S<sub>2</sub>

952720-86-4

SGQAYMFPNA PYLPSCLES 19

**merigolixum**

merigolix

4-[[[(1*R*)-2-(1-[[2-fluoro-6-(trifluorometil)fenil]metil]-2,4-dioxo-1'-[[5-(trifluorometil)furan-2-yl]metil]-1,2,4,7-tetrahydro-3*H*-spiro[furo[3,4-*d*]pirimidina-5,4'-piperidin]-3-yl)-1-fenyletil]amino]butanoico acid  
*gonadotrophin releasing hormone (GnRH) antagonist*

mérigolix

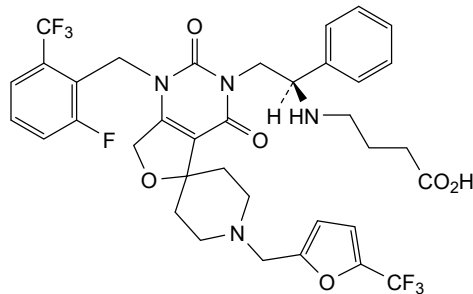
acide 4-[[[(1*R*)-2-(1-[[2-fluoro-6-(trifluorométyl)phényl]métyl]-2,4-dioxo-1'-[[5-(trifluorométyl)furan-2-yl]métyl]-1,2,4,7-tétrahydro-3*H*-spiro[furo[3,4-*d*]pyrimidine-5,4'-pipéridin]-3-yl)-1-phénylétyl]amino]butanoïque  
*antagoniste du facteur libérant les gonadotrophines (GnRH)*

merigolix

ácido 4-[[[(1*R*)-2-(1-[[2-fluoro-6-(trifluorometil)fenil]metil]-2,4-dioxo-1'-[[5-(trifluorometil)furan-2-il]metil]-1,2,4,7-tetrahidro-3*H*-spiro[furo[3,4-*d*]pirimidina-5,4'-piperidin]-3-il)-1-feniletil]amino]butanoico  
*antagonista del factor liberador de gonadotrofinas (GnRH)*

C<sub>36</sub>H<sub>35</sub>F<sub>7</sub>N<sub>4</sub>O<sub>6</sub>

1454272-94-6

**mifanertinibum**

mifanertinib

(2*E*)-*N*-[4-(3-chloro-4-fluoroanilino)-7-(difluorometoxi)quinazolin-6-yl]-4-(dimetilamino)but-2-enamida  
*tyrosine kinase inhibitor, antineoplastic*

mifanertinib

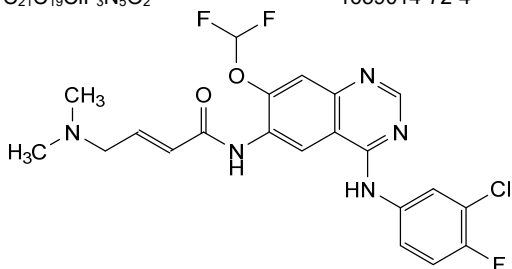
(2*E*)-*N*-[4-(3-chloro-4-fluoroanilino)-7-(difluorométhoxy)quinazolin-6-yl]-4-(diméthylamino)but-2-énamide  
*inhibiteur de tyrosine kinase, antinéoplasique*

mifanertinib

(2*E*)-*N*-[4-(3-cloro-4-fluoroanilino)-7-(difluorometoxi)quinazolin-6-il]-4-(dimetilamino)but-2-enamida  
*inhibidor de tirosina kinasa, antineoplásico*

C<sub>21</sub>H<sub>19</sub>ClF<sub>3</sub>N<sub>5</sub>O<sub>2</sub>

1639014-72-4



**migoprotafibum**  
migoprotafib

(3*R*)-1'-[3-(3,4-dihydro-1,5-naphthyridin-1(2*H*)-yl)-1*H*-pyrazolo[3,4-*b*]pyrazin-6-yl]-spiro[benzofuran-2(3*H*),4'-piperidin]-3-amine  
*protein tyrosine phosphatase (HPTP) inhibitor, antineoplastic*

migoprotafib

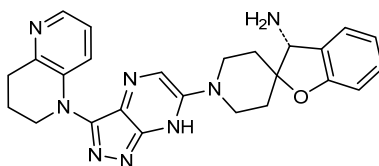
(3*R*)-1'-[3-(3,4-dihydro-1,5-naphthyridin-1(2*H*)-yl)-1*H*-pyrazolo[3,4-*b*]pyrazin-6-yl]-spiro[benzofuran-2(3*H*),4'-pipéridin]-3-amine  
*inhibiteur de la protéine tyrosine phosphatase (HPTP), antinéoplasique*

migoprotafib

(3*R*)-1'-[3-(3,4-dihydro-1,5-naftiridin-1(2*H*)-il)-1*H*-pirazolo[3,4-*b*]pirazin-6-il]-spiro[benzofuran-2(3*H*),4'-piperidin]-3-amina  
*inhibidor de la proteína tirosina fosfatasa (HPTP), antineoplásico*

C<sub>25</sub>H<sub>26</sub>N<sub>8</sub>O

2377352-49-1



**milrebrutinibum**  
milrebrutinib

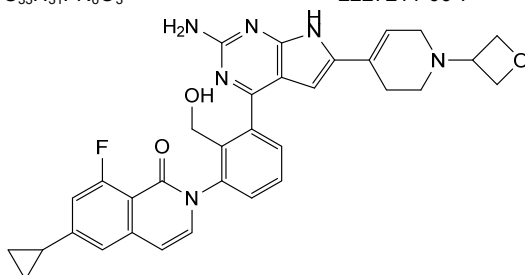
2-[3-{2-amino-6-[1-(oxetan-3-yl)-1,2,3,6-tetrahydropyridin-4-yl]-7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl]-2-(hydroxymethyl)phenyl]-6-cyclopropyl-8-fluoroisoquinolin-1(2*H*)-one  
*Bruton's tyrosine kinase inhibitor, antineoplastic*

milrébrutinib  
 2-[3-{2-amino-6-[1-(oxétan-3-yl)-1,2,3,6-tétrahydropyridin-4-yl]-7H-pyrrolo[2,3-d]pyrimidin-4-yl}-2-(hydroxyméthyl)phényl]-6-cyclopropyl-8-fluoroisoquinoléin-1(2H)-one  
*inhibiteur de la tyrosine kinase de Bruton, antinéoplasique*

milrebrutinib  
 2-[3-{2-amino-6-[1-(oxetan-3-yl)-1,2,3,6-tetrahydropyridin-4-yl]-7H-pyrrolo[2,3-d]pyrimidin-4-yl}-2-(hidroximetil)fenil]-6-ciclopropil-8-fluoroisoquinolein-1(2H)-ona  
*inhibidor de la tirosina kinasa de Bruton, antineoplásico*

 $C_{33}H_{31}FN_6O_3$ 

2227211-00-7

**monzosertibum**

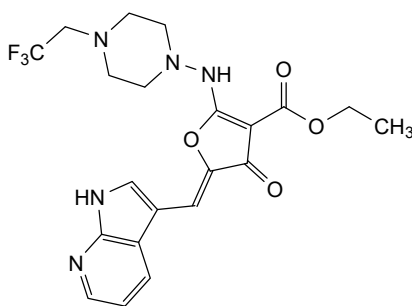
monzosertib  
 ethyl 5-[( $\Xi$ )-(1H-pyrrolo[2,3-b]pyridin-3-yl)methylene]-4-oxo-2-[[4-(2,2,2-trifluoroethyl)piperazin-1-yl]amino]-4,5-dihydrofuran-3-carboxylate  
*serine/ threonine kinase inhibitor, antineoplastic*

monzosertib  
 5-[( $\Xi$ )-(1H-pyrrolo[2,3-b]pyridin-3-yl)méthylène]-4-oxo-2-[[4-(2,2,2-trifluoroéthyl)pipérazin-1-yl]amino]-4,5-dihydrofurane-3-carboxylate d'éthyle  
*inhibiteur de sérine/ thréonine kinase, antinéoplasique*

monzosertib  
 5-[( $\Xi$ )-(1H-pirrolo[2,3-b]piridin-3-il)metileno]-4-oxo-2-[[4-(2,2,2-trifluoroetil)piperazin-1-il]amino]-4,5-dihidrofurano-3-carboxilato de etilo  
*inhibidor de serina/ treonina kinasa, antineoplásico*

 $C_{21}H_{22}F_3N_5O_4$ 

1402057-88-8



**murcidencelum**

murcidencel

autologous dendritic cells (DCs) derived from peripheral blood mononuclear cells (PBMCs) obtained from glioblastoma patients. A sample of the same patients' glioblastoma is also collected, and a tumour lysate prepared. The purified adherent monocytes isolated from PBMCs are initially grown in media containing granulocyte-macrophage colony-stimulating factor (GM-CSF) and interleukin 4 (IL-4) to induce differentiation into dendritic cells, followed by loading of the dendritic cells with the tumour lysate in culture media supplemented with GM-CSF and IL-4. The final cell suspension contains  $\geq 60\%$  dendritic cells (MHC Class II+, CD86+; CD14-), with  $\leq 40\%$  of the cells in the suspension being other autologous cells, such as T lymphocytes, B lymphocytes, and natural killer cells. The dendritic cells induce T cell proliferation in a co-stimulation assay  
*cell therapy (antineoplastic)*

murcidencel

cellules dendritiques (DC) autologues dérivées de cellules mononucléaires de sang périphérique (PBMC) obtenues de patients atteints de glioblastome. Un échantillon du glioblastome de ces mêmes patients est également prélevé et un lysat tumoral est préparé. Les monocytes adhérents purifiés isolés des PBMC sont d'abord cultivés dans un milieu contenant le facteur de stimulation des colonies de granulocytes-macrophages (GM-CSF) et l'interleukine 4 (IL-4) pour induire la différenciation en cellules dendritiques, puis les cellules dendritiques sont chargées avec le lysat tumoral dans un milieu de culture complété en GM-CSF et IL-4. La suspension cellulaire finale contient  $\geq 60\%$  de cellules dendritiques (MHC Classe II+, CD86+; CD14-), et  $\leq 40\%$  des cellules de la suspension sont d'autres cellules autologues, telles que des lymphocytes T, des lymphocytes B et des cellules tueuses naturelles. Les cellules dendritiques induisent la prolifération des lymphocytes T dans un test de costimulation  
*thérapie cellulaire (antineoplasique)*

murcidencel

células dendríticas (DCs) autólogas derivadas de células mononucleares de sangre periférica (PBMCs) obtenidas de pacientes con glioblastoma. Se recoge también una muestra de glioblastoma del mismo paciente y se prepara un lisado tumoral. Los monocitos adherentes purificados, aislados de las PBMCs, se crecen inicialmente en medio que contiene factor estimulador de colonias de monocitos-macrófagos (GM-CSF) e interleuquina 4 (IL-4) para inducir la diferenciación en células dendríticas, seguido de la carga de las células dendríticas con el lisado tumoral en medio de cultivo suplementado con GM-CSF e IL-4. La suspensión celular final contiene  $\geq 60\%$  de células dendríticas (MHC Clase II+, CD96+, CD14-), con  $\leq 40\%$  de otras células autólogas como linfocitos T, linfocitos B y células NK. Las células dendríticas inducen la proliferación de linfocitos T en un ensayo de coestimulación  
*terapia celular (antineoplásico)*



**muvalaplinum**

muvalaplin

(1<sup>3</sup>S,2R,10R,11<sup>3</sup>S)-6-[(3-[(2S)-2-carboxy-2-[(3R)-pyrrolidin-3-yl]éthyl]phényl)méthyl]-6-aza-1,11(3)-dipyrrolidina-4,8(1,3)-dibenzénaundécaphane-2,10-dicarboxylique acid

*lipoprotein (a) formation inhibitor, antiatherosclerotic*

muvalapline

acide (1<sup>3</sup>S,2R,10R,11<sup>3</sup>S)-6-[(3-[(2S)-2-carboxy-2-[(3R)-pyrrolidin-3-yl]éthyl]phényl)méthyl]-6-aza-1,11(3)-dipyrrolidina-4,8(1,3)-dibenzénaundécaphane-2,10-dicarboxylique

*inhibiteur de la formation de lipoprotéine (a), antiathérosclérotique*

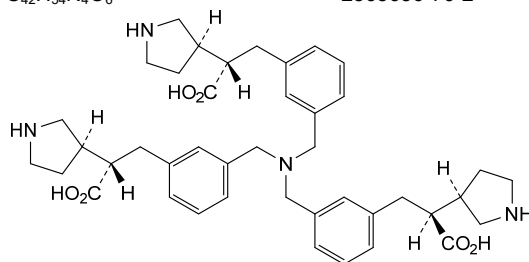
muvalaplina

ácido (1<sup>3</sup>S,2R,10R,11<sup>3</sup>S)-6-[(3-[(2S)-2-carboxi-2-[(3R)-pirrolidina-3-il]etil]fenil)metil]-6-aza-1,11(3)-dipirrolidina-4,8(1,3)-dibencenaundecafano-2,10-dicarboxílico

*inhibidor de la formación de la lipoproteína (a), antiarteroesclerótico*

C<sub>42</sub>H<sub>54</sub>N<sub>4</sub>O<sub>6</sub>

2565656-70-2

**muzastotugum #**

muzastotug

immunoglobulin G1-kappa, anti-[*Homo sapiens* CTLA4 (cytotoxic T-lymphocyte associated protein 4, CTLA-4, CD152)], humanized monoclonal antibody with cleavable prodomain;

gamma1 heavy chain humanized (1-446) [VH (*Homo sapiens*IGHV3-7\*01 (77.8%) -(IGHD)-IGHJ4\*01 (100%), CDR-IMGT [9.7.9] (26-34.52-58.97-105)) (1-116) -*Homo sapiens*IGHG1\*01 (100%), G1m17,1 CH1 K120, D12, L14 (CH1 K120 (213) (117-214), hinge 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-256')-disulfide with kappa light chain humanized (1'-256') [cleavable prodomain (1'-41') fused to V-KAPPA (*Homo sapiens*IGKV1-13\*02 (85.3%) -IGKJ1\*01 (100%), CDR-IMGT [7.3.9] (68-74.92-94.131-139)) (42'-149') -*Homo sapiens*IGKC\*01 (100%), Km3 A45.1 (195), V101 (233) (150'-256')]; dimer (225-225':228-228'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

*immunostimulant, antineoplastic*

muzastotug

immunoglobuline G1-kappa, anti-[*Homo sapiens* CTLA4 (protéine 4 associée aux lymphocytes T cytotoxiques, CTLA-4, CD152)], anticorps monoclonal humanisé avec prodomaine clivable;

chaîne lourde gamma1 humanisée (1-446) [VH (*Homo sapiens* IGHV3-7\*01 (77.8%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [9.7.9] (26-34.52-58.97-105)) (1-116) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 (CH1 K120 (213) (117-214), charnière 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-256')-disulfure avec la chaîne légère kappa humanisée (1'-256') [prodromaine clivable (1'-41') fusionné à V-KAPPA (*Homo sapiens* IGKV1-13\*02 (85.3%) - IGKJ1\*01 (100%), CDR-IMGT [7.3.9] (68-74.92-94.131-139)) (42'-149') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (195), V101 (233) (150'-256')]; dimère (225-225":228-228")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa  
*immunostimulant, antinéoplasique*

muzastotug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CTLA4 (proteína 4 asociada con los linfocitos T citotóxicos, CTLA-4, CD152)], anticuerpo monoclonal humanizado con prodominio escindible; cadena pesada gamma1 humanizada (1-446) [VH (*Homo sapiens* IGHV3-7\*01 (77.8%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [9.7.9] (26-34.52-58.97-105)) (1-116) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 (CH1 K120 (213) (117-214), bisagra 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-256')-disulfuro con la cadena ligera kappa humanizada (1'-256') [prodrominio escindible (1'-41') fusionado con V-KAPPA (*Homo sapiens* IGKV1-13\*02 (85.3%) - IGKJ1\*01 (100%), CDR-IMGT [7.3.9] (68-74.92-94.131-139)) (42'-149') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (195), V101 (233) (150'-256')]; dímero (225-225":228-228")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa  
*inmunoestimulante, antineoplásico*

2750031-18-4

## Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGYSTIS SGYHWSWIRQ APGKGLEWLA 50
RIDWDDKYY STSLKSRLLT SRDNSKNTLY LQLNSLRAED TAVYVCARSY 100
VYFDYWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSNMSG ALTSGVHTFP AVLQSSGLYS LSSVTVFPSS SLGFTQYICN 200
VNHKPSNTRV DKKVPEKSCD KTHTCFPCFA PELLGGPSVF LFFPKFKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL 350
PPSRDELTKN QVSLTCLVKG FYPSDIAVEW ESNQGPENNY KTTFPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGK 446
```

## Light chain / Chaîne légère / Cadena ligera

```
EVGSPNPSS DCVPPYYACA YSGRSAGGGG TPLGLAGSGG SDIQLTQSPS 50
SLSASVGDV TITCRASQSV RGRFLAWYQQ KPGKAPKLLI YDASNRTGI 100
PSRFSGSGSG TDFTLTISSL QPEDFATYYC QQSSSWPPTF GQGTQKVEIKR 150
TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN 200
SQESVTEQDS KDSTYLSLST LTLSKADYEK HKVYACEVTH QGLSSPVTKS 250
FNRGEC 256
```

## Post-translational modifications

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

Intra-H (C23-C104) 22-96 143-199 260-320 366-424  
22"-96" 143"-199" 260"-320" 366"-424"  
Intra-L (C23-C104) 64'-130' 176"-236'  
64"-130" 176"-236"  
Inter-H-L (h 5-CL 126) 219-256' 219"-256"  
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-antennaires complexes fucosylés / glicanos de tipo CHO biantennarios complejos fucosilados

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

H CHS K2: 446, 446"

**narmafotinibum**

narmafotinib

2-{2-[2-{{2-methoxy-4-(1-methylpiperidin-4-yl)phenyl}amino}-5-(trifluoromethyl)pyrimidin-4-yl]ethyl}benzeneacetamide  
*tyrosine kinase inhibitor, antifibrotic, antineoplastic*

narmafotinib

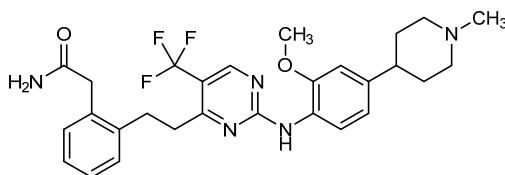
2-{2-[2-{{2-méthoxy-4-(1-méthylpipéridin-4-yl)phényl}amino}-5-(trifluorométhyl)pyrimidin-4-yl]éthyl}benzèneacétamide  
*inhibiteur de tyrosine kinase, antinéoplasique*

narmafotinib

2-{2-[2-{{2-metoxi-4-(1-metilpiperidin-4-il)fenil}amino}-5-(trifluorometil)pirimidin-4-il]etil}bencenoacetamida  
*inhibidor de tirosina kinasa, antineoplásico*

C<sub>28</sub>H<sub>32</sub>F<sub>3</sub>N<sub>5</sub>O<sub>2</sub>

1393653-34-3

**navacaprantum**

navacaprant

1-[6-ethyl-8-fluoro-4-methyl-3-(3-methyl-1,2,4-oxadiazol-5-yl)quinolin-2-yl]-N-(oxan-4-yl)piperidin-4-amine  
*kappa-opioid receptor antagonist*

navacaprant

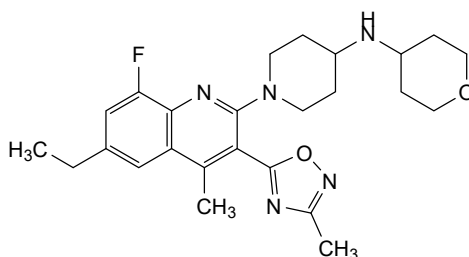
1-[6-éthyl-8-fluoro-4-méthyl-3-(3-méthyl-1,2,4-oxadiazol-5-yl)quinoléin-2-yl]-N-(oxan-4-yl)pipéridin-4-amine  
*agoniste du récepteur opioïde kappa*

navacaprant

1-[6-etil-8-fluoro-4-metil-3-(3-metil-1,2,4-oxadiazol-5-il)quinolein-2-il]-N-(oxan-4-il)piperidin-4-amina  
*agonista del receptor opioide kappa*

C<sub>25</sub>H<sub>32</sub>FN<sub>5</sub>O<sub>2</sub>

2244614-14-8

**nebratamigum #**

nebratamig

immunoglobulin scFv-G1-scFv-scFv<sub>L</sub>-kappa, anti-[*Homo sapiens* TNFRSF9 (TNF receptor superfamily member 9, 4-1BB, ILA, CD137)], anti-[*Homo sapiens* CD274 (programmed cell death 1 ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1, B7-H1, PDCD1LG1)], anti-[*Homo sapiens* ROR1 (receptor tyrosine kinase like orphan receptor 1)] and anti-[*Homo sapiens* CD3D (CD3 delta) and CD3E (CD3 epsilon, Leu-4) dimer], humanized monoclonal antibody, tetraspecific, octavalent;

scFv-G1-scFv-scFv fused heavy chain humanized (1-1227) [scFv kappa-heavy anti-TNFRSF9 humanized (1-246) [V-KAPPA (*Homo sapiens* IGKV1-12\*01 (83.1%) -IGKJ4\*01 (100%), CDR-IMGT [6.3.13] (27-32.50-52.89-111)) (1-111)-20-mer tetrakis(tetraglycyl-seryl) linker (112-131) -VH (*Homo sapiens* IGHV3-64\*04 (82.1%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.7.10] (156-163.181-187.226-235)) (132-246)]-10-mer bis(tetraglycyl-seryl) linker (247-256)-gamma-1 heavy chain anti-CD274 humanized (257-700) [VH (*Homo sapiens* IGHV3-23\*03 (77.7%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.7.10] (281-288.306-312.351-360)) (257-371) -*Homo sapiens* IGHG1\*01v, G1m17,1>G1m3,1, CH1 R120, CH3 D12, L14, G1v14-1 CH2 A1.3, A1.2, A1, G1v20 CH2 A105 (CH1 K120>R (468) (372-469), hinge 1-15 (470-484), CH2 L1.3>A (488), L1.2>A (489), G1>A (491), K105>A (576) (485-594), CH3 D12 (610), L14 (612) (595-699), CHS K2>del (700)) (372-700)] -10-mer bis(tetraglycyl-seryl) linker (701-710) -scFv heavy-kappa anti-ROR1 humanized (711-965) [VH (*Homo sapiens* IGHV3-23\*03 (81.6%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.8.15] (736-743.761-768.807-821)) (711-832) -20-mer tetrakis(tetraglycyl-seryl) linker (833-852) -V-KAPPA (*Homo sapiens* IGKV1-27\*01 (88.9%) -(IGHD) -IGKJ4\*01 (83.3%), CDR-IMGT [8.3.13] (879-886.904-906.943-955)) (853-965)] -10-mer bis(tetraglycyl-seryl) linker (966-975) -scFv heavy-kappa anti-CD3D-CD3E dimer humanized (976-1227) [VH (*Homo sapiens* IGHV3-66\*01 (86.6%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.7.14] (1001-1008.1026-1032.1071-1084)) (976-1095) -20-mer tetrakis(tetraglycyl-seryl) linker (1096-1115) -V-KAPPA (*Homo sapiens* IGKV1-5\*01 (90.1%) -IGKJ4\*01 (90.9%), CDR-IMGT [6.3.14] (1142-1047.1165-1167.1204-1217)) (1116-1227)]; (474-217)-disulfide with kappa light chain anti-CD274 humanized (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-12\*01 (89.7%) -IGKJ4\*01 (100%), CDR-IMGT [6.3.12] (27-32.50-52.89-100)) (1'-110') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (156), V101 (194) (111'-217')]; dimer (480-480":483-483")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa *antineoplastic*

## nébratamig

immunoglobuline scFv-G1-scFv-scFv\_L-kappa, anti-[*Homo sapiens* TNFRSF9 (membre 9 de la superfamille des récepteurs du TNF, 4-1BB, ILA, CD137)], anti-[*Homo sapiens* CD274 (ligand 1 de mort programmée 1, PDL1, PD-L1, B7 homologue 1, B7H1, B7-H1, PDCD1LG1)], anti-[*Homo sapiens* ROR1 (récepteur orphelin 1 récepteur tyrosine kinase like)] et anti-[*Homo sapiens* CD3D (CD3 delta) et CD3E (CD3 epsilon, Leu-4) dimère], anticorps monoclonal humanisé, tétraspécifique, octavalent; chaîne lourde fusionnée scFv-G1-scFv-scFv humanisée (1-1227) [scFv kappa-lourde anti-TNFRSF9 humanisé (1-246) [V-KAPPA (*Homo sapiens* IGKV1-12\*01 (83.1%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [6.3.13] (27-32.50-52.89-111)) (1-111) -20-mer tetrakis(tetraglycyl-séryl) linker (112-131) -VH (*Homo sapiens* IGHV3-64\*04 (82.1%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.7.10] (156-163.181-187.226-235)) (132-246)] -10-mer bis(tétraglycyl-séryl) linker (247-256)-chaîne lourde gamma-1 anti-CD274 humanisée (257-700) [VH (*Homo sapiens* IGHV3-23\*03 (77.7%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.7.10] (281-288.306-312.351-360)) (257-371) -*Homo sapiens* IGHG1\*01v, G1m17,1>G1m3,1, CH1 R120, CH3 D12, L14, G1v14-1 CH2 A1.3, A1.2, A1, G1v20 CH2 A105 (CH1 K120>R (468) (372-469), charnière 1-15 (470-484), CH2 L1.3>A (488), L1.2>A (489), G1>A (491), K105>A (576) (485-594), CH3 D12 (610), L14 (612) (595-699), CHS K2>del (700)) (372-700)] -10-mer bis(tétraglycyl-séryl) linker (701-710) -scFv lourde-kappa anti-ROR1 humanisé (711-965) [VH (*Homo sapiens* IGHV3-23\*03 (81.6%) -(IGHD) -

- IGHJ1\*01 (100%), CDR-IMGT [8.8.15] (736-743.761-768.807-821)) (711-832) -20-mer tétrakis(tétraglycyl-séryl) linker (833-852) -V-KAPPA (*Homo sapiens* IGKV1-27\*01 (88.9%) -(IGHD) -IGKJ4\*01 (83.3%), CDR-IMGT [8.3.13] (879-886.904-906.943-955)) (853-965)] -10-mer bis(tétraglycyl-séryl) linker (966-975) -scFv lourde-kappa anti-CD3D-CD3E humanisé (976-1227) [VH (*Homo sapiens* IGHV3-66\*01 (86.6%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.7.14] (1001-1008.1026-1032.1071-1084)) (976-1095) -20-mer tétrakis(tétraglycyl-séryl) linker (1096-1115) -[V-KAPPA (*Homo sapiens* IGKV1-5\*01 (90.1%) -(IGHD) -IGKJ4\*01 (90.9%), CDR-IMGT [6.3.14] (1142-1047.1165-1167.1204-1217)) (1116-1227)]]; (474-217')-disulfure avec la chaîne légère kappa anti-CD274 humanisée (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-12\*01 (89.7%) -IGKJ4\*01 (100%), CDR-IMGT [6.3.12] (27-32.50-52.89-100)) (1'-110') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (156), V101 (194) (111'-217')]]; dimère (480-480":483-483")-bisdisulfide, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa  
*antinéoplasique*
- nebratamig immunoglobulina scFv-G1-scFv-scFv\_L-kappa, anti-[*Homo sapiens* anti-TNFRSF9 (miembro 9 de la superfamilia de los receptores del TNF, 4-1BB, ILA, CD137)], anti-[*Homo sapiens* CD274 (ligando 1 de muerte programada 1, PDL1, PD-L1, B7 homólogo 1, B7H1, B7-H1, PDCD1LG1)], anti-[*Homo sapiens* ROR1 (receptor huérfano 1 receptor tipo tirosina kinasa)] y anti-[*Homo sapiens* anti-CD3D (CD3 delta) y anti-CD3E (CD3 épsilon, Leu-4) dímero], anticuerpo monoclonal humanizado, tetraespecífico, octavalente; cadena pesada fusionada scFv-G1-scFv-scFv humanizada (1-1227) [scFv kappa-pesada anti-TNFRSF9 humanizada (1-246) [V-KAPPA (*Homo sapiens* IGKV1-12\*01 (83.1%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [6.3.13] (27-32.50-52.89-111)) (1-111) -20-mer tetrakis(tetraglicil-seril) enlace (112-131) -VH (*Homo sapiens* IGHV3-64\*04 (82.1%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.7.10] (156-163.181-187.226-235)) (132-246)] -10-mer bis(tetraglicil-seril) enlace (247-256)-cadena pesada gamma-1 anti-CD274 humanizada (257-700) [VH (*Homo sapiens* IGHV3-23\*03 (77.7%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.7.10] (281-288.306-312.351-360)) (257-371) -*Homo sapiens* IGHG1\*01v, G1m17, 1>G1m3,1, CH1 R120, CH3 D12, L14, G1v14-1 CH2 A1.3, A1.2, A1, G1v20 CH2 A105(CH1 K120>R (468) (372-469), bisagra 1-15 (470-484), CH2 L1.3>A (488), L1.2>A (489), G1>A (491), K105>A (576) (485-594), CH3 D12 (610), L14 (612) (595-699), CHS K2>del (700)) (372-700)] -10-mer bis(tetraglicil-seril) enlace (701-710) -scFv pesada-kappa anti-ROR1 humanizada (711-965) [VH (*Homo sapiens* IGHV3-23\*03 (81.6%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.8.15] (736-743.761-768.807-821)) (711-832) -20-mer tetrakis(tetraglicil-seril) enlace (833-852) -V-KAPPA (*Homo sapiens* IGKV1-27\*01 (88.9%) -(IGHD) -IGKJ4\*01 (83.3%), CDR-IMGT [8.3.13] (879-886.904-906.943-955)) (853-965)] -10-mer bis(tetraglicil-seril) enlace (966-975) -scFv pesada-kappa anti-CD3D-CD3E humanizada (976-1227) [VH (*Homo sapiens* IGHV3-66\*01 (86.6%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.7.14] (1001-1008.1026-1032.1071-1084)) (976-1095) -20-mer tetrakis(tetraglicil-seril) enlace (1096-1115) -[V-KAPPA (*Homo sapiens* IGKV1-5\*01 (90.1%) -(IGHD) -IGKJ4\*01 (90.9%), CDR-IMGT [6.3.14] (1142-1047.1165-1167.1204-1217)) (1116-1227)]]; (474-217')-disulfuro com la cadena ligera kappa anti-CD274 humanizada (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-12\*01 (89.7%) -IGKJ4\*01 (100%), CDR-IMGT [6.3.12] (27-32.50-52.89-100)) (1'-110') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (156), V101 (194) (111'-217')]]; dímeero (480-480":483-483")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa  
*antineoplásico*

Heavy chain / Chaîne lourde / Cadena pesada: [scFv (anti-TNFRSF9)-G1 (anti-CD274)-scFv (anti-ROR1)-scFv (anti-CD3D-CD3E)]

DVVMTQSPSS VSASVGDVRT ITCQASQNR TYLSWYQQPK GKAPKLLIYA 50  
 AANLASGVPS RFGSGSGGTD FTLTISDLEP GDAATYYCQS TYLGTDYVGG 100  
 AFGGGTKVEI KGGGGSGGGG SGGGGSGGGG SRSLVESGGG LVQPGGSLRL 150  
 SCTASGFTIS SYHMQVVRQA PGKLEYIGT ISSGNNVYYA SSARGRFTIS 200  
 RFPSSKNTVDL QMNSLRAEDT AVYYCARDSDG YSDPMWGGQT LVTVSSGGGG 250  
 SGGGGSQSV ESGGGLVQPG GSLRLSCTAS GIDLNTYDMI WVRQAPGKGL 300  
 EWVGIIITYSG SRYANWAKG RFTISKDNKT NTVYLQMNLS RAEDTAVYYC 350  
 ARDYMSSGSHL WGGQTLVTVS SASTKGPVSF PLAPSSKSTS GGTAALGCLV 400  
 KDYFPEPVTV SWNSGALTSV VHTFFAVLQS SGLYSLSSVV TFPSSSLGTQ 450  
 TYICNVNHKP SNTKVKDRVE PKSCDKTHTC PPCAPEAAG APSVFLFPPK 500  
 PKDTLMSIRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 550  
 NSTYRVVSVL TVLHQDMLNG KEYKCAVSNK ALPAPIEKTI SKAKQPREP 600  
 QVYTLPPSRD ELTKNQVSLT CLVKGFPYSD IAVEWESNGQ PENNYKTPP 650  
 VLDSGGSFFL YSKLTVDKSR WQQGNVFPSC VMHEALHNHY TQKSLSLSPG 700  
 GGGGSGGGGS EVQLLESQGG LVQPGGSLRL SCAASGFTIS RYHMTWVRQA 750  
 PGKGLEWIGH IYVNDTDDY ASSAKGRFTI SRDNSKNTLY LQMNSLRAED 800  
 TATYFCARLD VGGGGAYIGD IWGQGTLLTV SGGGGSGGG GSGGGSGGG 850  
 GSDIQMTQSP SLSASVGDRT VTTTCQSSQS VYNNNDLAWY QPKPKVFKL 900  
 LIYYASTLAS GVPSPRFSGG SGTDFTLTIS SLQPEDVATY YCAGGYDIDG 950  
 LDTFAFGGGT KVEIKGGGGG GGGGSEVQLV ESGGGLVQPG GSLRLSCTAS 1000  
 GFTISTNAMS WVRQAPGKGL EWIGVITGRD ITYYASWAKG RFTISRDNK 1050  
 NTLYLQMNLS RAEDTAVYYC ARDGGSAIT SNNIWWGQGT LVTVSSGGGG 1100  
 GGGGSGGGGS GGGGSDVVMT QSPSTLSASV GDRVTINCQA SESISSWLAW 1150  
 YQKPKGKAPK LLIYEASKLA SGVPSRFSGS GSGTEFTLTI SSLQPDFDFA 1200  
 YYCQGYFYFI SRTYVNSFVG GTKVEIK 1227

Light chain / Chaîne légère / Cadena ligera

AYDMTQSPSS VSASVGDVRT IKCQASEDIY SFLAWYQQPK GKAPKLLIHS 50  
 ASSLASGVPS RFGSGSGGTD FTLTISSLPQ EDFATYYCQQ GYGKNNVDNA 100  
 FGGGTKVEIK RTVAAPSVEI FPPSDEQLKS GTASVVCLLN NFPYPREAKVQ 150  
 WKVDNALQSG NSQESVTEQD SKDSTYSLSS TLTLKADYEH KHKVYACEVT 200  
 HQGLSSPVTK SFRNGEC 217

Post-translational modifications

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

Intra-H (C23-C104) 23-88 152-225 277-350 398-454 515-575  
 23"-88" 152"-225" 277"-350" 398"-454" 515"-575"  
 621-679 732-806 875-942 997-1070 1138-1203  
 621"-679" 732"-806" 875"-942" 997"-1070" 1138"-1203"

Intra-L (C23-C104) 23"-88" 137"-197"  
 23"-88" 137"-197"  
 Inter-H-L (h 5-CL 126) 474-217" 474"-217"  
 Inter-H-H (h 11, h 14) 480-480" 483-483"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación  
 H CH2 N84.4: 551, 551"

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

nelistotugum #  
 nelistotug

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD96 (T cell activation increased late expression, TACTILE, T-cell surface protein tactile)], *Homo sapiens* monoclonal antibody;  
 gamma1 heavy chain *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-69\*01 (95.9%) -(IGHD) - IGHJ1\*01 (90.9%) L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-213')-disulfide with kappa light chain *Homo sapiens* (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (95.7%) -IGKJ4\*01 (91.7%), CDR-IMGT [6.3.8] (27-32.50-52.89-96)) (1'-106') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (152), V101 (190) (107'-213')]; dimer (231-231":234-234")-bisdisulfide, produced in Chinese Hamster Ovary (CHO) Cell line, glycoform alfa immunostimulant, antineoplastic

- nélistotug** immunoglobuline G1-kappa, anti-[*Homo sapiens* CD96 (protéine de l'activation des cellules T exprimée tardivement, TACTILE, protéine tactile de la surface des cellules T)]; chaîne lourde gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-69\*01 (95.9%) -(IGHD) -IGHJ1\*01 (90.9%) L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-213')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (95.7%) -IGKJ4\*01 (91.7%), CDR-IMGT [6.3.8] (27-32.50-52.89-96)) (1'-106') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (152), V101 (190) (107'-213')]; dimère (231-231":234-234")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa *immunostimulant, antinéoplasique*
- nelistotug** inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD96 (proteína de la activación de las células T expresadas en etapas tardías, TACTILE, proteína tactile de la superficie de las células T)]; cadena pesada gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-69\*01 (95.9%) -(IGHD) -IGHJ1\*01 (90.9%) L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-213')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (95.7%) -IGKJ4\*01 (91.7%), CDR-IMGT [6.3.8] (27-32.50-52.89-96)) (1'-106') -*Homo sapiens* IGKC\*01(100%), Km3, A45.1 (152), V101 (190) (107'-213')]; dímero (231-231":234-234")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa *inmunoestimulante, antineoplásico*

2645437-82-5

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VKKPGSGSVKV SCKASGGTFV EYAIISWRQA PGQGLEWMMG 50  
 IIPAFGTAQY AQRFGQRTVI TADESTSTAY MELSSLRSED TAVYYCARGA 100  
 GYYGDKDFMD WVGQGTFTVTY SSASTKGPSV FFLAPSSKST SGGTAAALGCL 150  
 VKDYFPEFPT VSWNSGALTS GVHTFPAPVLQ SSGLYSLSSV VTPVSSSLGT 200  
 QTYICNVNHK PSNTRKDKVK EPKSCDKTHT CPPCPAPELL GGPSVFLFPP 250  
 KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NRYVDGVEVH NARTKPREEQ 300  
 YNSTYRVVSV LTVLHQDWLNL GKVEYKCKVSN KALPAPIEKT ISKAKGQPRE 350  
 PQYITLPPSR DELTKNQVSL TCVLKGFPYS DIAVEWESNG QPENNYKTFP 400  
 FVLDSGDSFF LYSKLTVDKRS RQQQGNVFSC SVMHEALHNH YTKQSLSLSP 450  
 GK 452

## Light chain / Chaîne légère / Cadena ligera

DIQLTQSPSS LSASVGDRTV ITCRASQIS SYLNWYQKPK GKAPKLLIYA 50  
 ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ VLHITIFGGG 100  
 TKVEIKRTVA APSVFIFFPS DEQLKSGTAS VVCLLNPFY REAKVQWKVD 150  
 NALQSGNSQE SVTEQDSKDS TYLSLSTLTL SKADYEKHKV YACEVTHQGL 200  
 SSPVTKSFNR GEC 213

## Post-translational modifications

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

Intra-H (C23-C104) 22-96 149-205 266-326 372-430  
 22"-96" 149"-205" 266"-326" 372"-430"

Intra-L (C23-C104) 23'-88" 133'-193"  
 23"-88" 133"-193"

Inter-H-L (h 5-CL 126) 225-213" 225"-213"

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

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

Q>pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxoprolilo)  
 H VHQI: 1, 1"

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

H CH2 N84.4: 302, 302"

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

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

H CHS K2: 452, 452"

**neracorvirum**

neracorvir *N*-{[2-(2*S*)-1,4-dioxan-2-yl]ethyl}-2-méthyl-5,5,11-trioxo-10,11-dihydro-5λ<sup>6</sup>*H*-pyrrolo[1,2-*b*][1,2,5]benzothiadiazepine-8-carboxamide *antiviral*

néracorvir

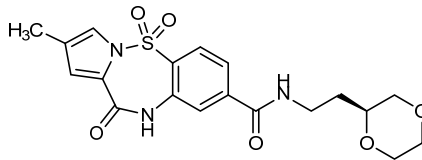
*N*-{[2-(2*S*)-1,4-dioxan-2-yl]éthyl}-2-méthyl-5,5,11-trioxo-10,11-dihydro-5λ<sup>6</sup>*H*-pyrrolo[1,2-*b*][1,2,5]benzothiadiazépine-8-carboxamide *antiviral*

neracorvir

*N*-{[2-(2*S*)-1,4-dioxan-2-il]etil}-2-metil-5,5,11-trioxo-10,11-dihydro-5λ<sup>6</sup>*H*-pirrolo[1,2-*b*][1,2,5]benzotiadiazepina-8-carboxamida *antiviral*

C<sub>19</sub>H<sub>21</sub>N<sub>3</sub>O<sub>6</sub>S

2243162-66-3

**nezutatugum #**

nezutatug

immunoglobulin G1-kappa, anti-[*Homo sapiens* ERBB3 (receptor tyrosine-protein kinase erbB-3, HER3)], humanized monoclonal antibody;  
gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV4-31\*01 (89.9%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [9.7.13] (26-34.52-58.97-109)) (1-120) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, D12, L14 (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 (*Homo sapiens* IGKV1-12\*01 (85.3%) -IGKJ2\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa *antineoplastic*

nézutatug

immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB3 (récepteur à activité tyrosine kinase erbB-3, HER3)], anticorps monoclonal humanisé;  
chaîne lourde gamma1 humanisée (1-450) [VH (*Homo sapiens* IGHV4-31\*01 (89.9%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [9.7.13] (26-34.52-58.97-109)) (1-120) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, D12, L14 (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')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12\*01 (85.3%) -IGKJ2\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa *antinéoplasique*



nezutatug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB3 (receptor con actividad tirosina kinasa erbB-3, HER3)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-450) [VH (*Homo sapiens* IGHV4-31\*01 (89.9%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [9.7.13] (26-34.52-58.97-109)) (1-120) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, D12, L14 (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 (*Homo sapiens* IGKV1-12\*01 (85.3%) -IGKJ2\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214'')]; dímero (229-229"-232-232'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa  
*antineoplásico*

2673271-78-6

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLQESGPG LVKPSQTLSL TCTVSGYSIT SGYSWHWIRQ HPGKGLEWIG 50  
SIRYSGGTDY NPSLKSLSVTI SADTSKNQFS LKLSSTVAAD TAVYICARMT 100  
TAPWYPFDDYV GQGTTVTVSS ASTKGPSVFP LAFSSKSTSG GTAALGLVK 150  
DYFPEPVTVS WNSGALTSGV HTPFAVLQSS GLYSLSSVVT VPSSSLGTQT 200  
YICNVNHPKS NTKVDKVEEP KSCDKTHTCP PCPAPELLGG PSVFLFPPK 250  
KDTLMISSRTP EPTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300  
STYRVVSVLT VLNQDNLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350  
VYTLPPSRDE LTRKQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTTPV 400  
LDSGGSFFLY SKLTVDKSRW QQGNVFSVCSV MHEALHNHYT QKSLSLSPGK 450

## Light chain / Chaîne légère / Cadena ligera

DIQMTQSPFS VSASVGDRTV ITCKASQIVG SNVAWYQQKPK GKAPLEPLIYS 50  
ASYLYSGVPS RFSGSGSGTD FTLTISLSLQF EDFATYYCQQ YSSHPLTFGQ 100  
GTKLEIKRIV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150  
DNLQSGNSQV ESVTQDQSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200  
LSSFPVTKSFN RGEK 214

## Post-translational modifications

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

Intra-H (C23-C104) 22-96 147-203 264-324 370-428  
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 glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q &gt; pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo

(pE, 5-oxoprolilo)

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 biantenaríos complejos fucosilados

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

H CHS K2: 450, 450"

nimucitinibum

nimucitinib

(9<sup>3</sup>S)-1<sup>3</sup>,5<sup>1</sup>-difluoro-8-oxo-3,5,7-triaza-4(4,2)-pyridina-9(3)-piperidina-1(1),6(1,3)-dibenzonanaphane-4<sup>5</sup>-carboxamide

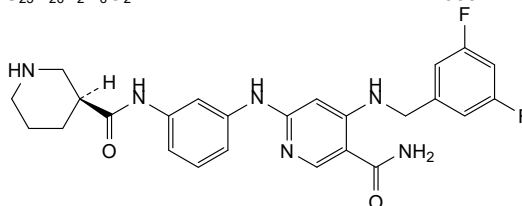
*Janus kinase inhibitor*

nimucitinib (9<sup>3</sup>S)-1<sup>3</sup>,1<sup>5</sup>-difluoro-8-oxo-3,5,7-triaza-4(4,2)-pyridina-9(3)-piperidina-1(1),6(1,3)-dibenzénanonaphane-4<sup>5</sup>-carboxamide  
*inhibiteur de la kinase de Janus*

nimucitinib (9<sup>3</sup>S)-1<sup>3</sup>,1<sup>5</sup>-difluoro-8-oxo-3,5,7-triaza-4(4,2)-piridina-9(3)-piperidina-1(1),6(1,3)-dibencenanonafano-4<sup>5</sup>-carboxamida  
*inhibidor de la kinasa de Janus*

C<sub>25</sub>H<sub>26</sub>F<sub>2</sub>N<sub>6</sub>O<sub>2</sub>

2740557-24-6

**nizubaglustatum**

nizubaglustat

(2S,3R,4R,5S)-1-{5-[(2-fluoro-[1,1'-biphenyl]-4-yl)methoxy]pentyl}-2-(hydroxymethyl)piperidine-3,4,5-triol  
*ceramide glucosyltransferase inhibitor*

nizubaglustat

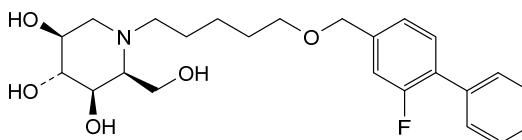
(2S,3R,4R,5S)-1-{5-[(2-fluoro-[1,1'-biphenyl]-4-yl)méthoxy]pentyl}-2-(hydroxyméthyl)pipéridine-3,4,5-triol  
*inhibiteur de la céramide glucosyltransférase*

nizubaglustat

(2S,3R,4R,5S)-1-{5-[(2-fluoro-[1,1'-biphenil]-4-il)metoxi]pentil}-2-(hidroximetil)piperidina-3,4,5-triol  
*inhibidor de la ceramida glucosiltransferasa*

C<sub>24</sub>H<sub>32</sub>FNO<sub>5</sub>

1633666-49-5

**nolavetbartum #**

nolavetbart

immunoglobulin G2-kappa, anti-[*Canis lupus familiaris* IL31RA (interleukin 31 receptor A)], caninized monoclonal antibody; gamma2 heavy chain caninized (1-453) [VH (*Canis lupus familiaris* IGHV4-1\*01 (77.8%) -(IGHD) -IGHJ4\*01 (86.7%), CDR-IMGT [8.8.12] (26-33.51-58.97-108))] (1-119) -*Canis lupus familiaris* IGHG2\*02, G2v2 CH2 A1.3, A1.2, G114 (CH1 (120-216), hinge 1-19 (217-235), CH2 M1.3>A (239), L1.2>A (240), P114>G (334) (236-345), CH3 (346-452), CHS K2>del (453)) (120-453)], (134-213')-disulfide with kappa light chain caninized (1'-213') [V-KAPPA (*Canis lupus familiaris* IGKV4-15\*01 (76.0%) -IGKJ3\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Canis lupus familiaris* IGKC\*01 (100%) (108'-213')]; dimer (231-231":234-234")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa  
*immunomodulator (veterinary use)*

nolavetbart

immunoglobuline G2-kappa, anti-[*Canis lupus familiaris* IL31RA (récepteur A de l'interleukine 31)], anticorps monoclonal caninisé;  
 chaîne lourde gamma2 caninisée (1-453) [VH (*Canis lupus familiaris* IGHV4-1\*01 (77.8%) -(IGHD) -IGHJ4\*01 (86.7%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Canis lupus familiaris* IGHG2\*02, G2v2 CH2 A1.3, A1.2, G114 (CH1 (120-216), charnière 1-19 (217-235), CH2 M1.3>A (239), L1.2>A (240), P114>G (334) (236-345), CH3 (346-452), CHS K2>del (453)) (120-453)], (134-213')-disulfure avec la chaîne légère kappa caninisée (1'-213') [V-KAPPA (*Canis lupus familiaris* IGKV4-15\*01 (76.0%) -IGKJ3\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Canis lupus familiaris* IGKC\*01 (100%) (108'-213')]; dimère (231-231":234-234")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa  
*immunomodulateur (usage vétérinaire)*

nolavetbart

immunoglobulina G2-kappa, anti-[*Canis lupus familiaris* IL31RA (receptor A de la interleukina 31)], anticuerpo monoclonal caninizado;  
 cadena pesada gamma2 caninizada (1-453) [VH (*Canis lupus familiaris* IGHV4-1\*01 (77.8%) -(IGHD) -IGHJ4\*01 (86.7%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Canis lupus familiaris* IGHG2\*02, G2v2 CH2 A1.3, A1.2, G114 (CH1 (120-216), bisagra 1-19 (217-235), CH2 M1.3>A (239), L1.2>A (240), P114>G (334) (236-345), CH3 (346-452), CHS K2>del (453)) (120-453)], (134-213')-disulfuro con la cadena ligera kappa caninizada (1'-213') [V-KAPPA (*Canis lupus familiaris* IGKV4-15\*01 (76.0%) -IGKJ3\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Canis lupus familiaris* IGKC\*01 (100%) (108'-213')]; dímero (231-231":234-234")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, forma glicosilada alfa  
*inmunomodulador (uso veterinario)*

2750248-93-0

Heavy chain / Chaîne lourde / Cadena pesada

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EVTLQESGPG LVKPSQTLSL TCVASGFSIK SSFIHWLRQR PGRGLEWIGR 50
IDPAFGATEY NPAFQGRFSI TADTAKNQAS LQLSSMTTED SAVYCYRHY 100
YAASHFDAMG QGTFLVTVSSA STTAPSVFPL APSCGSTSGS TVALACLVSG 150
YFPEFVTVSW NSGSLTSGVH TFFSVLQSSG LYLSLSSMTV PSSRWPSETF 200
TCNVAHPASK TKVDKPVKRR ENGRVPRPPD CPKCPAPEAA GGPSVFIFFP 250
KPKDILLIAR TPEVTCVVVD LDPEDPEVQI SWFVDGKQMQ TARTQPREEQ 300
FNGTYRVVSV LPIGHQDWLK GKQFTCKVNN KALGSPPIERT ISKARGQAHQ 350
PSVYVLPFSR EELSKNTVSL TCLIKDFFPP DIDVEWQNSG QQEPESKYRT 400
TPPQLDEDGS YFLYSKLSVD KSRWQRGDTF ICAVMHEALH NHYTQESLSH 450
SPG 453
    
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Light chain / Chaîne légère / Cadena ligera

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RIVMTQSPGS LAGSVGESVS INCKSSQSVT NDLTWYQKQP GEAPKVLITY 50
ASQRYTGVA RFGSGYGTD FLTIINLQA EDVGDYFCQQ DYASPTFGQ 100
GTKLEIKRND AQPAVYLFQP SPDQLHTGSA SVVCLLNSFY PKDINVKWV 150
DGVIQDTGIQ ESVTEQDKDS TYLSLSTLTM SSTEYLSHEL YSCEITHKSL 200
PSTLIKSFQR SEC 213
    
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Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro  
 Intra-H (C23-C104) 22-96 146-202 266-326 372-432  
 22"-96" 146'-202" 266"-326" 372"-432"  
 Intra-L (C23-C104) 23'-88" 134'-193"  
 23"-88" 134"-193"  
 Inter-H-L (CHI 11-CL 126) 134-213' 134"-213"  
 Inter-H-H (h 15, h 18) 231-231" 234-234"

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

H CH2 N84.4: 302, 302"  
 Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantennarios complejos fucosilados

**oberotatum #**

oberotatum

immunoglobulin G1-kappa, anti-[*Homo sapiens* LY75 (human lymphocyte antigen 75, C-type lectin domain family 13 member B, CLEC13B, DEC-205, CD205)], *Homo sapiens* monoclonal antibody;

gamma1 heavy chain *Homo sapiens* (1-448) [VH (*Homo sapiens*IGHV3-15\*01 (98.0%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.10.10] (26-33.51-60.99-108)) (1-119) -*Homo sapiens*IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-39\*01 (88.4%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimer (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1SV, glycoform alfa  
*antineoplastica*

obérotatum

immunoglobuline G1-kappa, anti-[*Homo sapiens* LY75 (antigène 75 des lymphocytes humains, membre B de la famille 13 des lectines à domaine de type C, CLEC13B, DEC-205, CD205)], anticorps monoclonal *Homo sapiens*;

chaîne lourde gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens*IGHV3-15\*01 (98.0%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.10.10] (26-33.51-60.99-108)) (1-119) -*Homo sapiens*IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (216) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-39\*01 (88.4%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimère (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1SV, glycoforme alfa  
*antineoplasique*

oberotatum

immunoglobulina G1-kappa, anti-[*Homo sapiens* LY75 (antígeno 75 de los linfocitos humanos, miembro B de la familia 13 de las lectinas con dominio de tipo C, CLEC13B, DEC-205, CD205)], anticuerpo monoclonal *Homo sapiens*;

cadena pesada gamma1 *Homo sapiens* (1-448) [VH humanizado (*Homo sapiens*IGHV3-15\*01 (98.0%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.10.10] (26-33.51-60.99-108)) (1-119) -*Homo sapiens*IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (216) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-39\*01 (88.4%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dímero (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1SV, forma glicosilada alfa  
*antineoplásico*

2641919-35-7

## Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG LVKPGGSLRL SCAASGFTYS NAWMSWRQA PGKLEWVGR 50  
 IKSKTGGT DYAAPVQGRF TISRDDSKNT LYLQMNLSKT EDTAVYYCTI 100  
 FGVVSDYWG QGTLVTSSA STKGPSVFEL APSSKSTSGG TAALGCLVKD 150  
 YFPEPTVSW NSGALTSVH TFPVAVLQSSG LYSLSVTVV PSSLGQTQY 200  
 ICNVNHKPSN TKVDKVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250  
 DTLMISRTPV VTCVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300  
 YTRVSVLTV LHQDNLNGKE YKCKVSNKAL PAPEKTIKSK AKGQPREPQV 350  
 YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTTPVL 400  
 DSDGSFFLYS KLTVDKSRWQ QGNVFSQVVM HEALHNYTQ KSLSLSPG 448

## Light chain / Chaîne légère / Cadena ligera

DVQMTQSPSS LSASVGRDVT ITCRASQGIS DYLSWYQQRP GKAPNLLIYA 50  
 ASNLTKTGPS RFGSGSGSDT FTLTISTLQP EDFATYCYQQ SYRSPWTFQG 100  
 GTKVEIKRTP AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQKWK 150  
 DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEHKK VYACEVTHQG 200  
 LSSPVTKSPN RGEC 214

## Post-translational modifications

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

Intra-H (C23-C104) 22-98 146-202 263-323 369-427  
 22"-98" 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 biantennarios complejos fucosilados.

**oberotatugum ravtansinum #**

oberotatug ravtansine

immunoglobulin G1-kappa, anti-[*Homo sapiens* LY75 (human lymphocyte antigen 75, C-type lectin domain family 13 member B, CLEC13B, DEC-205, CD205)], *Homo sapiens* monoclonal antibody; conjugated to maytansinoid DM4; gamma1 heavy chain *Homo sapiens* (1-448) [VH (*Homo sapiens*IGHV3-15\*01 (98.0%) -(IGHD)-IGHJ4\*01 (100%), CDR-IMGT [8.10.10] (26-33.51-60.99-108)) (1-119) -*Homo sapiens*IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-39\*01 (88.4%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimer (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1SV, glycoform alfa; conjugated, on an average of 3 to 4 lysyl, to maytansinoid DM4 [*N*<sup>2</sup>- deacetyl-*N*<sup>2</sup>-(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"**antineoplastic**

obérotatug ravtansine

immunoglobuline G1-kappa, anti-[*Homo sapiens* LY75 (antigène 75 des lymphocytes humains, membre B de la famille 13 des lectines à domaine de type C, CLEC13B, DEC-205, CD205)], anticorps monoclonal *Homo sapiens*; conjugué au maytansinoïde DM4; chaîne lourde gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens*IGHV3-15\*01 (98.0%) -(IGHD)-IGHJ4\*01 (100%), CDR-IMGT [8.10.10] (26-33.51-60.99-108)) (1-119) -*Homo sapiens*IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (216) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfure avec la chaîne légère

kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (88.4%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimère (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1SV, glycoforme alfa; conjugué, sur 3 ou 4 lysyl en moyenne, au maitansinoïde DM4 [N<sup>2</sup>-déacétyl-N<sup>2</sup>-(4-mercapto-4-méthyl-1-oxopentyl)-maitansine] via le linker SPDB réductible [4-(2-pyridylthio)butanoate de *N*-succinimidyle]  
 Pour la partie *ravtansine*, veuillez-vous référer au document "INN for pharmaceutical substances: Names for radicals, groups and others"  
**antinéoplasique**

oberotatug ravtansina

inmunoglobulina G1-kappa, anti-[*Homo sapiens* LY75 (antígeno 75 de los linfocitos humanos, miembro B de la familia 13 de las lectinas con dominio tipo C, CLEC13B, DEC-205, CD205)], anticuerpo monoclonal *Homo sapiens*; conjugado con maitansinoide DM4; cadena pesada gamma1 *Homo sapiens* (1-448) [VH humanizado (*Homo sapiens* IGHV3-15\*01 (98.0%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.10.10] (26-33.51-60.99-108)) (1-119) -*Homo sapiens* IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (216) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (88.4%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dímero (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1SV, forma glicosilada alf; conjugado, en 3 o 4 restos lisil por término medio, con maitansinoide DM4 [N<sup>2</sup>-deacetil-N<sup>2</sup>-(4-mercapto-4-metil-1-oxopentil)-maitansina] a través del enlace SPDB reducible [4-(2-piridiliditio)butanoato de *N*-succinimidilo]  
 Para la fracción *ravtansine*, se pueda referirse al documento "INN for pharmaceutical substances: Names for radicals, groups and others"  
**antineoplásico**

2641919-35-7

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG	LVKPFGSLRL	SCAASGFTYS	NAWMSVVRQA	PGKGLEWVGR	50
IRSKTDGGTT	DYAAPVQGRF	TISRDDSKNT	LYLQMSLKT	EDTAVYYCTI	100
FGVVSFDYWG	QGTLVTVSSA	STKGFVFFL	APSSKSTSGG	TAALGCLVKD	150
YFPEPVTVSW	NSGALTSGVH	TFFAVLQSSG	LYLSLSVTVV	PSSSLGTQTY	200
ICNVNHPKSN	TKVDKKEVEK	SCRKTHTCFP	CPAPELLGGP	SVFLFPKPK	250
DTLMSRTPTE	VTCVVVDVSH	EDPEVKFNWY	VDGVVHNAR	TKPREEQYNS	300
TYRIVSVLTV	LHQDNLNGKE	YKCKVSNKAL	PAPIEKTISK	AKGQPREPQV	350
YTLPPSREEM	TKNQVSLTCL	VKGFPYSDIA	VEWESNGQPE	NNYKTTPPVL	400
DSGDSFFLYS	KLTVDKSRWQ	QGNVFCSCVM	HEALHNHYTQ	KSLSLSPG	448

Light chain / Chaîne légère / Cadena ligera

DVQMTQSPSS	LSASVGDRTV	ITCRASQGIS	DYLSWYQGRP	GKAPNLLIYA	50
ASNLKTVGPS	RFSGSGGSDT	FLTITISLQP	EDFATYYCQQ	SYRSPWTFGQ	100
GTKVEIKRTV	AAPSVFIFPP	SDEQLKSGTA	SVVCLNNFY	PREAKVQWKV	150
DNALQSGNSQ	ESVTEQDSKD	STYLSLSTLT	LSKADYERKH	VYACEVTHGQ	200
LSSPVTKSFN	RGEC				214

Post-translational modifications

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

Intra-H (C23-C104) 22-98 146-202 263-323 369-427

22"-98" 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.

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"\*

**obertamigum #**

## obertamig

immunoglobulin half IG G1-lambda2/scFv-h-CH2-CH3, anti-[*Homo sapiens* CD3E (CD3 epsilon)] and anti-[*Homo sapiens* HLA-G (class I major histocompatibility (MH1) antigen G, human leucocyte antigen G) C-like domain], *Homo sapiens* monoclonal antibody, bispecific, bivalent; gamma1 heavy chain anti-CD3E *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV6-1\*01 (88.1%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [10.9.10] (26-35.53-61.100-109)) (1-120) -*Homo sapiens* IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v14-67 CH2 A1.3, A1.2, S27, G1v69 V6, Y7, A85.1, V86 (CH1 R120>K (217) (121-218), hinge 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), D27>S (268) (234-343), CH3 E12 (359), M14 (361), T6>V (353), L7>Y (354), F85.1>A (408), Y86>V (410) (344-448), CHS (449-450)) (121-450)], (223-216')-disulfide with lambda light chain anti-CD3E *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-23\*02 (84.4%) -IGKJ2\*01 (90.9%), CDR-IMGT [9.3.10] (26-34.52-54.91-100)) (1'-110') -*Homo sapiens* IGLC2\*01 (100%) (111'-216')];

IG scFv-h-CH2-CH3 chain single chain, anti-HLA-G *Homo sapiens* (1"-452") [scFv V-kappa-VH anti-HLA-G (1"-258") [V-KAPPA (*Homo sapiens* IGKV4-1\*01 (96.0%) -IGKJ1\*01 (100%), CDR-IMGT [12.3.9] (27-38.56-58.95-103)) (1"-113") -20-mer linker (114"-133") -VH (*Homo sapiens* IGHV6-1\*01 (99.0%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [10.9.15] (159-168.186-194.233-247)) (134"-258")] -*Homo sapiens* IGHG1\*03 h-CH2-CH3, nG1m1 CH3 E12, M14, G1v37 h S5, G1v14-67 CH2 A1.3, A1.2, S27, G1v68 CH3 V6, L22, L79; W81 (259"-490") [hinge 1-15 C5>S (263) (259"-273"), CH2 L1.3>A (277), L1.2>A (278), D27>S (308) (274"-383"), CH3 T6>V (393), E12 (399), M14 (401), T22>L (409), K79>L (435), T81>W (437) (384"-488"), CHS (489"-490")]; dimer (229-269"-232-272")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa  
*antineoplastic*

## obertamig

immunoglobuline demi-IG G1-lambda2/scFv-h-CH2-CH3, anti-[*Homo sapiens* CD3E (CD3 epsilon)] et anti-[*Homo sapiens* HLA-G (antigène G d'histocompatibilité majeure de classe I (MH1), antigène G leucocytaire humain) domaine C-like], anticorps monoclonal *Homo sapiens*, bispécifique, bivalent;  
chaîne lourde H-gamma1 anti-CD3E *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV6-1\*01 (88.1%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [10.9.10] (26-35.53-61.100-109)) (1-120) -*Homo sapiens* IGHG1\*03v, G1m3>G1m17, nG1m1bCH1 K120, CH3 E12, M14, G1v14-67 CH2 A1.3, A1.2, S27, G1v69 V6, Y7, A85.1, V86 (CH1 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), D27>S (268) (234-343), CH3 E12 (359), M14 (361), T6>V (353), L7>Y (354), F85.1>A (408), Y86>V (410) (344-448), CHS (449-450)) (121-450)], (223-216')-disulfure avec la chaîne légère lambda anti-CD3E *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-23\*02 (84.4%) -IGKJ2\*01 (90.9%), CDR-IMGT [9.3.10] (26-34.52-54.91-100)) (1'-110') -*Homo sapiens* IGLC2\*01 (100%) (111'-216')];

	<p>IG scFv-h-CH2-CH3 chaîne unique, anti-HLA-G <i>Homo sapiens</i> (1"-452") [scFv V-kappa-VH anti-HLA-G (1"-258") [V-KAPPA (<i>Homo sapiens</i> IGKV4-1*01 (96.0%) - IGKJ1*01 (100%), CDR-IMGT [12.3.9] (27-38.56-58.95-103)) (1"-113")-20-mer linker (114"-133") -VH (<i>Homo sapiens</i> IGHV6-1*01 (99.0%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [10.9.15] (159-168.186-194.233-247)) (134"-258") -<i>Homo sapiens</i> IGHG1 h-CH2-CH3, nG1m1 CH3 E12, M14, G1v37 h S5, G1v14-67 CH2 A1.3, A1.2, S27, G1v68 CH3 V6, L22, L79; W81 (259"-490") [charnière 1-15 C5&gt;S (263) (259"-273"), CH2 L1.3&gt;A (277), L1.2&gt;A (278), D27&gt;S (308) (274"-383"), CH3 T6&gt;V (393), E12 (399), M14 (401), T22&gt;L (409), K79&gt;L (435), T81&gt;W (437) (384"-488"), CHS (489"-490")]]; dimère (229-269":232-272")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa <i>antineoplasique</i></p>
obertamig	<p>inmunoglobulina demi-IG G1-lambda2/scFv-h-CH2-CH3, anti-[<i>Homo sapiens</i> CD3E (CD3 epsilon)] y anti-[<i>Homo sapiens</i> HLA-G (antígeno G de histocompatibilidad de clase I (MH1), antígeno G leucocitario humano de tipo C), anticuerpo monoclonal <i>Homo sapiens</i>, biespecífico, bivalente;</p> <p>cadena pesada H-gamma1 anti-CD3E <i>Homo sapiens</i> (1-450) [VH (<i>Homo sapiens</i> IGHV6-1*01 (88.1%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.9.10] (26-35.53-61.100-109)) (1-120) -<i>Homo sapiens</i> IGHG1*03v, G1m3&gt;G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v14-67 CH2 A1.3, A1.2, S27, G1v69 V6, Y7, A85.1, V86 (CH1 R120&gt;K (217) (121-218), bisagra 1-15 (219-233), CH2 L1.3&gt;A (237), L1.2&gt;A (238), D27&gt;S (268) (234-343), CH3 E12 (359), M14 (361), T6&gt;V (353), L7&gt;Y (354), F85.1&gt;A (408), Y86&gt;V (410) (344-448), CHS (449-450)) (121-450)], (223-216')-disulfuro con la cadena ligera lambda anti-CD3 E <i>Homo sapiens</i> (1'-216') [V-LAMBDA (<i>Homo sapiens</i> IGLV2-23*02 (84.4%) -IGKJ2*01 (90.9%), CDR-IMGT [9.3.10] (26-34.52-54.91-100)) (1'-110') -<i>Homo sapiens</i> IGLC2*01 (100%) (111'-216')]]; IG scFv-h-CH2-CH3 cadena única, anti-HLA-G <i>Homo sapiens</i> (1"-452") [scFv V-kappa-VH anti-HLA-G (1"-258") [V-KAPPA (<i>Homo sapiens</i> IGKV4-1*01 (96.0%) - IGKJ1*01 (100%), CDR-IMGT [12.3.9] (27-38.56-58.95-103)) (1"-113")-20-mer enlace (114"-133") -VH (<i>Homo sapiens</i> IGHV6-1*01 (99.0%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [10.9.15] (159-168.186-194.233-247)) (134"-258") -<i>Homo sapiens</i> IGHG1 h-CH2-CH3, nG1m1 CH3 E12, M14, G1v37 h S5, G1v14-67 CH2 A1.3, A1.2, S27, G1v68 CH3 V6, L22, L79; W81 (259"-490") [bisagra 1-15 C5&gt;S (263) (259"-273"), CH2 L1.3&gt;A (277), L1.2&gt;A (278), D27&gt;S (308) (274"-383"), CH3 T6&gt;V (393), E12 (399), M14 (401), T22&gt;L (409), K79&gt;L (435), T81&gt;W (437) (384"-488"), CHS (489"-490")]]; dímero (229-269":232-272")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa <i>antineoplásico</i></p>



2750126-32-8

**Heavy chain / Chaîne lourde / Cadena pesada: anti-CD3E (H)**

QVQLQQSGPR LVRPSQTLSL TCAISGDSVFN NNAAWSWIR QSPSRGLEWL 50  
 GRITYRSKWL YDYAVSVKSR ITVNPDTSRN QFTLQLNSVT PEDTALYCA 100  
 RGYSSSFDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGLVK 150  
 DYFPEFVTVS WNSGALTSVG HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200  
 YICNVNHKPS NTKVDKVEEP KSCDKTHTCP PCPAPEAAGG PSVFLFPPK 250  
 KDTLMISRTP EVTCVVVSVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300  
 STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350  
 VYVYVPSREE MTRKQVSLTC LVRKGFYPSDI AVEWESNGQP ENNYKTTFPV 400  
 LDSDGSFALV SKLTVDKSRW QQGNVFSCSV MHEALHNYT QKSLSLSPGK 450

**Light chain / Chaîne légère / Cadena ligera: anti-CD3E (L)**

QSALTQPASV SGSPGQSITI SCTGTSSNIG TYKFEVSWYQQ HPDKAPKVL 50  
 YEVSKRPSGV SSRFSGSKSG NTASLTISGL QAEDQADYHC VSYAGSGTLL 100  
 FGGGKTLTVL GQPKAAPSVT LFPPSSEELQ ANKATLWCLI SDFYPGAQVT 150  
 ANKADSSPVK AGVETTTFSK QSMNKYAASS YLSLTPQWQK SHRSYSCQVT 200  
 HEGSTVETRV APTTECS 216

**Heavy chain / Chaîne lourde / Cadena pesada: anti-HLA-G (H')**

DIVMTQSPDS LAVSLGERAT INCKSSQSVL HSNNNKNYLT WFQKPKGQPP 50  
 KLLIYWASTR ESGVPRDFRSG SSGGTFDTLL ISSLQAEDVA VYCHQYYST 100  
 PPTFGQGTVK EIRKGSSEKSG SSGSGSEKST GGSQVQLQSS GPGLVKPVSQT 150  
 LSLTCAISGD SVSSNSAAMN WIRQSPSRGL EWLGRTYRYS KWNNDYAVSV 200  
 KSRITINPDT SKNQLSLQLN SVTPEDTAVY YCAGDRRYGI VGLPFAYWGG 250  
 GTLVTVSSEP KSSDKTHTCP PCPAPEAAGG PSVFLFPPK KDTLMISRTP 300  
 EVTCVVVSVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT 350  
 VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYVLPSPREE 400  
 MTRKQVSLLC LVRKGFYPSDI AVEWESNGQP ENNYLTWPPV LDSDGSFFLY 450  
 SKLTVDKSRW QQGNVFSCSV MHEALHNYT QKSLSLSPGK 490

**Post-translational modifications**

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro  
 Intra-H (C23-C104) 22-99 147-203 264-324 370-428  
 23"-94" 155"-232" 304"-364" 410"-468"  
 Intra-L (C23-C104) 22'-90' 138'-197'  
 Inter-H-L (CH1 10-CL 126) 223-215'  
 Inter-H-H (h 8, h 11) 229-269" 232-272"

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

Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)  
 H VH Q1: I  
 L VL Q1: I'

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

H CH2 N84.4: 300, 340"

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal  
 H CHS K2: 450, 490"

**oditrasertibum**

oditrasertib

4-(3,3-difluoro-2,2-dimethylpropanoyl)-2,3,4,5-tetrahydropyrido[3,4-f][1,4]oxazepine-9-carbonitrile  
*serine/ threonine kinase inhibitor*

oditrasertib

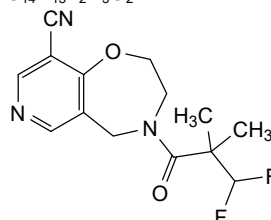
4-(3,3-difluoro-2,2-diméthylpropanoïl)-2,3,4,5-tétrahydropyrido[3,4-f][1,4]oxazépine-9-carbonitrile  
*inhibiteur de sérine/ thréonine kinase*

oditrasertib

4-(3,3-difluoro-2,2-dimetilpropanoïl)-2,3,4,5-tetrahidropirido[3,4-f][1,4]oxazepina-9-carbonitrilo  
*inhibidor de serina/ treonina kinasa*

C<sub>14</sub>H<sub>15</sub>F<sub>2</sub>N<sub>3</sub>O<sub>2</sub>

2252271-93-3



**oloctinebartum #**

oloctinebart

immunoglobulin G4-kappa, anti-[*Homo sapiens* LGALS3 (galectin 3)], humanized monoclonal antibody;  
 gamma4 heavy chain humanized (1-442) [VH (*Homo sapiens* IGHV1-3\*01 (88.7%) -(IGHD) -IGHJ6\*01 (93.3%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (117-214), hinge 1-12 S10>P (224) (215-226), CH2 L92 (305) (227-336), CH3 (337-441), CHS K2>del (442)) (117-442)], (130-219')-disulfide with kappa light chain humanized (1'-219') [V-KAPPA (*Homo sapiens* IGKV2D-29\*02 (89.0%) -IGKJ2\*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (222-222":225-225")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa  
*reduction of amyloid beta oligomers formation*

oloctinebart

immunoglobuline G4-kappa, anti-[*Homo sapiens* LGALS3 (galectine 3)], anticorps monoclonal humanisé;  
 chaîne lourde gamma4 humanisée (1-442) [VH (*Homo sapiens* IGHV1-3\*01 (88.7%) -(IGHD) -IGHJ6\*01 (93.3%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (117-214), charnière 1-12 S10>P (224) (215-226), CH2 L92 (305) (227-336), CH3 (337-441), CHS K2>del (442)) (117-442)], (130-219')-disulfure avec la chaîne légère kappa humanisée (1'-219') [V-KAPPA (*Homo sapiens* IGKV2D-29\*02 (89.0%) -IGKJ2\*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (222-222":225-225")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa  
*réduction de la formation d'amyloïde bêta*

oloctinebart

immunoglobulina G4-kappa, anti-[*Homo sapiens* LGALS3 (galectina 3)], anticuerpo monoclonal humanizado;  
 cadena pesada gamma4 humanizada (1-442) [VH (*Homo sapiens* IGHV1-3\*01 (88.7%) -(IGHD) -IGHJ6\*01 (93.3%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (117-214), bisagra 1-12 S10>P (224) (215-226), CH2 L92 (305) (227-336), CH3 (337-441), CHS K2>del (442)) (117-442)], (130-219')-disulfuro com la cadena ligera kappa humanizada (1'-219') [V-KAPPA (*Homo sapiens* IGKV2D-29\*02 (89.0%) -IGKJ2\*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (222-222":225-225")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa  
*reducción de la formación de amiloide beta*

2669063-84-5

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VKKPGASVKV SCKASGYSTF NYMHWVRQA PGQRLWMMGW 50  
 IYPGSGNTNY NEKFGQGRVTI TADTSASTAY MELSSLRSED TAVVYCSTAP 100  
 GGFDFWGGQT TTVTSSASTK GPSVFPLAPC SRSTSESTAA LGCLVKDYFP 150  
 EPVTVSWNSG ALTSGVHTFF AVLQSSGLYS LSSVTVFSS SLGKTYTCN 200  
 VDHKPSNTKV DKRVESKYGF PCPPCPAPEF LGGPSVFELF PKPKDTLMIS 250  
 RTPEVTCVVV DVSQEDPEVQ FNWYVDGVEV HNAKTKFREE QFNSTYRVVS 300  
 VLTVLHQDWL NGKEYKCKVS NKGLPSSIEK TISKAKGQPR EPQVYTLPPS 350  
 QEEMTKNQVS LTLCLVKGFPY SDIAVEWESN GQPENNYKTT PPVLDSDGSF 400  
 FLYSRLTVDK SRWQEGNVFS CSMVHEALHN HYTKKSLSLG LG 442

## Light chain / Chaîne légère / Cadena ligera

DIVMTQTPLS LSVTPGQPAS ISCKSSKSLD HSDGITLYLV YLQKPGQSPQ 50  
 LLIYRMSNLA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCAQMLEFP 100  
 LTFGQGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVEL LNNFYPREAK 150  
 VQWFKVDNALQ SGNSQESVTE QDSKDSSTYSL SSTLTLSKAD YEKHKVYACE 200  
 VTRQGLSSPV TKSFNRGEC 219

## Post-translational modifications

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

Intra-H (C23-C104) 22-96 143-199 257-317 363-421  
 22<sup>o</sup>-96<sup>o</sup> 143<sup>o</sup>-199<sup>o</sup> 257<sup>o</sup>-317<sup>o</sup> 363<sup>o</sup>-421<sup>o</sup>  
 Intra-L (C23-C104) 23<sup>o</sup>-93<sup>o</sup> 139<sup>o</sup>-199<sup>o</sup>  
 23<sup>o</sup>-93<sup>o</sup> 139<sup>o</sup>-199<sup>o</sup>  
 Inter-H-L (CH1 10-CL 126) 130-219<sup>o</sup> 130<sup>o</sup>-219<sup>o</sup>  
 Inter-H-H (h 8, h 11) 222-222<sup>o</sup> 225-225<sup>o</sup>

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

Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)  
 H VH Q1: 1, 1<sup>o</sup>

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

H CH2 N84.4: 293, 293<sup>o</sup>  
 Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantennarios complejos fucosilados.

**onvitrelinum ucalontidum**

onvitrelin ucalontide

L-lysyl-L-phenylalanyl-L-alanyl-L-lysyl-L-phenylalanyl-L-  
 alanyl-L-lysyl-L-lysyl-L-phenylalanyl-L-alanyl-L-lysyl-L-  
 phenylalanyl-L-alanyl-L-lysyl-L-lysyl-L-phenylalanyl-L-  
 alanyl-L-lysyl-L-glutaminyL-L-histidyl-L-tryptophyl-L-  
 seryl-L-tyrosylglycyl-L-leucyl-L-arginyl-L-prolylglycine  
*luteinizing hormone releasing hormone (LHRH)  
 analogue, antineoplastic*

onvitréline ucalontide

L-lysyl-L-phénylalanyl-L-alanyl-L-lysyl-L-phénylalanyl-L-  
 alanyl-L-lysyl-L-lysyl-L-phénylalanyl-L-alanyl-L-lysyl-L-  
 phénylalanyl-L-alanyl-L-lysyl-L-lysyl-L-phénylalanyl-L-  
 alanyl-L-lysyl-L-glutaminyL-L-histidyl-L-tryptophyl-L-  
 séryl-L-tyrosylglycyl-L-leucyl-L-arginyl-L-prolylglycine  
*analogue de l'hormone de libération de l'hormone  
 lutéinisante (LHRH), antineoplasique*

onvitreline ucalontida

L-lisil-L-fenilalanil-L-alanil-L-lisil-L-fenilalanil-L-alanil-L-  
 lisil-L-lisil-L-fenilalanil-L-alanil-L-lisil-L-fenilalanil-L-alanil-  
 L-lisil-L-lisil-L-fenilalanil-L-alanil-L-lisil-L-glutaminyL-L-  
 histidil-L-triptofil-L-seril-L-tirosilglicil-L-leucil-L-arginil-L-  
 proliliglicina  
*análogo de la hormona liberadora de hormona  
 luteinizante (LHRH), antineoplásico*

C<sub>163</sub>H<sub>243</sub>N<sub>43</sub>O<sub>32</sub>

1174415-90-7

KFAKFAKKFA KFAKKFAKQH WSYGLRPG 28

**opnurasibum**

opnurasib

1-{6-[(4*M*)-4-(5-chloro-6-methyl-1*H*-indazol-4-yl)-5-methyl-3-(1-methyl-1*H*-indazol-5-yl)-1*H*-pyrazol-1-yl]-2-azaspiro[3.3]heptan-2-yl}prop-2-en-1-one  
*Kirsten rat sarcoma viral oncogene homolog (KRAS) inhibitor, antineoplastic*

opnurasib

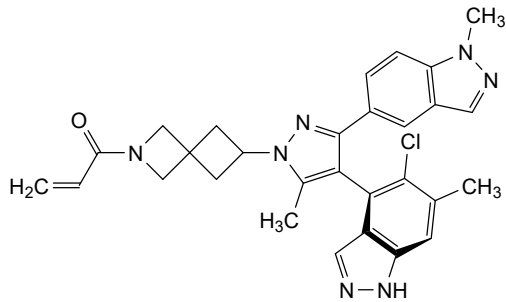
1-{6-[(4*M*)-4-(5-chloro-6-méthyl-1*H*-indazol-4-yl)-5-méthyl-3-(1-méthyl-1*H*-indazol-5-yl)-1*H*-pyrazol-1-yl]-2-azaspiro[3.3]heptan-2-yl}prop-2-èn-1-one  
*inhibiteur de l'homologue de l'oncogène du virus du sarcome du rat de Kirsten (KRAS), antinéoplasique*

opnurasib

1-{6-[(4*M*)-4-(5-cloro-6-metil-1*H*-indazol-4-il)-5-metil-3-(1-metil-1*H*-indazol-5-il)-1*H*-pirazol-1-il]-2-azaspiro[3.3]heptan-2-il}prop-2-en-1-ona  
*inhibidor homólogo del oncogén del virus del sarcoma de rata de Kirsten (KRAS), antineoplásico*

C<sub>29</sub>H<sub>28</sub>ClN<sub>7</sub>O

2653994-08-0

**orforglipronum**

orforglipron

(3<sup>4</sup>S,6<sup>1</sup>S,6<sup>2</sup>S)-5<sup>5</sup>-[(4*S*)-2,2-diméthyloxan-4-yl]-1<sup>4</sup>-fluoro-3<sup>2</sup>-(4-fluoro-3,5-diméthylphényl)-1<sup>1</sup>,3<sup>4</sup>,6<sup>2</sup>-triméthyl-3<sup>2</sup>,3<sup>4</sup>,3<sup>6</sup>,3<sup>7</sup>-tétrahydro-1<sup>1</sup>*H*,2<sup>2</sup>*H*-3(3,5)-pyrazolo[4,3-*c*]pyridina-1(5)-indazola-5(2,1)-indola-7(3)-[1,2,4]oxadiazola-2(1,3)-imidazola-6(1,1)-cyclopropanaheptaphane-2<sup>2</sup>,4,7<sup>5</sup>(7<sup>2</sup>*H*)-trione  
*glucagon-like peptide 1 (GLP-1) receptor agonist*

orforglipron

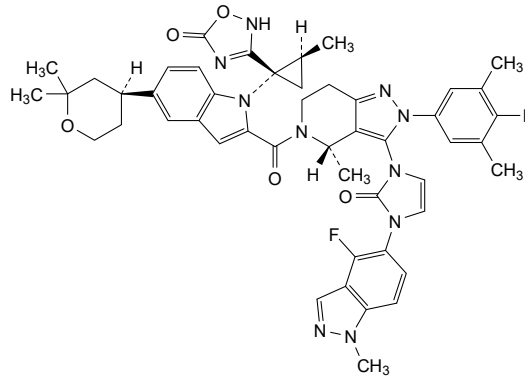
(3<sup>4</sup>S,6<sup>1</sup>S,6<sup>2</sup>S)-5<sup>5</sup>-[(4*S*)-2,2-diméthyloxan-4-yl]-1<sup>4</sup>-fluoro-3<sup>2</sup>-(4-fluoro-3,5-diméthylphényl)-1<sup>1</sup>,3<sup>4</sup>,6<sup>2</sup>-triméthyl-3<sup>2</sup>,3<sup>4</sup>,3<sup>6</sup>,3<sup>7</sup>-tétrahydro-1<sup>1</sup>*H*,2<sup>2</sup>*H*-3(3,5)-pyrazolo[4,3-*c*]pyridina-1(5)-indazola-5(2,1)-indola-7(3)-[1,2,4]oxadiazola-2(1,3)-imidazola-6(1,1)-cyclopropanaheptaphane-2<sup>2</sup>,4,7<sup>5</sup>(7<sup>2</sup>*H*)-trione  
*agoniste du récepteur au peptide-1 similaire au glucagon (GLP-1)*

orforgliprón

(3<sup>4</sup>S,6<sup>1</sup>S,6<sup>2</sup>S)-5<sup>5</sup>-[(4*S*)-2,2-dimetiloxan-4-il]-1<sup>4</sup>-fluoro-3<sup>2</sup>-(4-fluoro-3,5-dimetilfenil)-1<sup>1</sup>,3<sup>4</sup>,6<sup>2</sup>-trimetil-3<sup>2</sup>,3<sup>4</sup>,3<sup>6</sup>,3<sup>7</sup>-tetrahidro-1<sup>1</sup>*H*,2<sup>2</sup>*H*-3(3,5)-pirazolo[4,3-*c*]piridina-1(5)-indazola-5(2,1)-indola-7(3)-[1,2,4]oxadiazola-2(1,3)-imidazola-6(1,1)-ciclopropanaheptafano-2<sup>2</sup>,4,7<sup>5</sup>(7<sup>2</sup>*H*)-triona  
*agonista del receptor del péptido similar al glucagón (GLP-1)*

C<sub>48</sub>H<sub>48</sub>F<sub>2</sub>N<sub>10</sub>O<sub>5</sub>

2212020-52-3

**osivelotorum**

osivelotor

2-hydroxy-6-[[[(3S)-4-[[2-(2-hydroxyethyl)pyridin-3-yl]carbonyl]morpholin-3-yl]methoxy]benzaldehyde  
*haemoglobin S allosteric modulator*

osivelótor

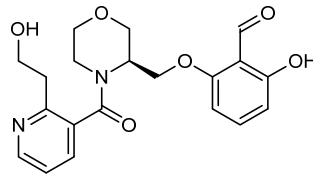
2-hydroxy-6-[[[(3S)-4-[[2-(2-hydroxyéthyl)pyridin-3-yl]carbonyl]morpholin-3-yl]méthoxy]benzaldéhyde  
*modulateur allostérique de l'hémoglobine S*

osivelotor

2-hidroxi-6-[[[(3S)-4-[[2-(2-hidroxietil)piridin-3-il]carbonil]morfolin-3-il]metoksi]benzaldehido  
*modulador alostérico de la hemoglobina S*

C<sub>20</sub>H<sub>22</sub>N<sub>2</sub>O<sub>6</sub>

2417955-18-9

**ozekibartum #**

ozekibart

only-heavy-chain immunoglobulin G1, anti-[*Homo sapiens* TNFRSF10B (TNF receptor superfamily member 10B, death receptor 5, DR5, TNF-related apoptosis-inducing ligand TRAIL receptor 2, TRAILR2, TRAIL-R2, TR-2, CD262)], humanized monoclonal antibody, monospecific, tetravalent, agonist; gamma1 heavy chain humanized (1-480) [VH humanized (*Homo sapiens*IGHV3-23\*01 (82.5%) -(IGHD)-IGHJ4\*01 (91.7%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -6-mer bis(bisglycylseryl linker (124-129) -[VH humanized (*Homo sapiens*IGHV3-23\*01 (82.5%) -(IGHD)-IGHJ4\*01 (91.7%), CDR-IMGT [8.8.16] (155-162.180-187.226-241)) (80-252) -4-mer tetraglycyl linker (253-256) -*Homo sapiens*IGHG1\*01, h-CH2-CH3, G1m1 CH3 D12, L14, G1v65 CH2 del(E1.4, L1.3, L1.2) (hinge 6-15 (257-266), CH2 (E1.4, L1.3, L1.2)>del 268^269 (267-373), CH3 D12 (389), L14 (391) (374-478), CHS (479-480)) (257-480)]; dimer (262-262":265-265")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa  
*antineoplastic*

ozékibart

immunoglobuline G1 à chaînes lourdes seulement, anti-[*Homo sapiens* TNFRSF10B (membre 10B de la superfamille des récepteurs du TNF, récepteur de mort 5, DR5, récepteur 2 du ligand TRAIL apparenté au TNF induisant l'apoptose, TRAIL-R2, TR2, CD262)], anticorps monoclonal humanisé, monospécifique, tétravalent, agoniste;

chaîne lourde gamma1 humanisée (1-480) [VH humanisé (*Homo sapiens* IGHV3-23\*01 (82.5%) -(IGHD) -IGHJ4\*01 (91.7%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -6-mer bis(bisglycyl-séryl linker (124-129) -[VH humanisé (*Homo sapiens* IGHV3-23\*01 (82.5%) -(IGHD) -IGHJ4\*01 (91.7%), CDR-IMGT [8.8.16] (155-162.180-187.226-241)) (80-252) -4-mer tétraglycyl linker (253-256) -*Homo sapiens* IGHG1\*01, h-CH2-CH3, G1m1 CH3 D12, L14, G1v65 CH2 del(E1.4, L1.3, L1.2) (charnière 6-15 (257-266), CH2 (E1.4, L1.3, L1.2)>del 268<sup>A</sup>269 (267-373), CH3 D12 (389), L14 (391) (374-478), CHS (479-480)) (257-480)]; dimère (262-262":265-265")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa *antinéoplasique*

ozekibart

inmunoglobulina G1 de cadena pesada única, anti-[*Homo sapiens* TNFRSF10B (miembro 10B de la superfamilia de los receptores del TNF, receptor de muerte 5, DR5, receptor 2 del ligando TRAIL relacionado con TNF que induce la apoptosis, TRAIL-R2, TR2, CD262)], anticuerpo monoclonal humanizado, monospécífico, tetravalente, agonista;

cadena pesada gamma1 humanizada (1-480) [VH humanizado (*Homo sapiens* IGHV3-23\*01 (82.5%) -(IGHD) -IGHJ4\*01 (91.7%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -6-mer bis(bisglicil-séryl linker (124-129) -[VH humanizado (*Homo sapiens* IGHV3-23\*01 (82.5%) -(IGHD) -IGHJ4\*01 (91.7%), CDR-IMGT [8.8.16] (155-162.180-187.226-241)) (80-252) -4-mer tetraglicil enlace (253-256) -*Homo sapiens* IGHG1\*01, h-CH2-CH3, G1m1 CH3 D12, L14, G1v65 CH2 del(E1.4, L1.3, L1.2) (bisagra 6-15 (257-266), CH2 (E1.4, L1.3, L1.2)>del 268<sup>A</sup>269 (267-373), CH3 D12 (389), L14 (391) (374-478), CHS (479-480)) (257-480)]; dímero (262-262":265-265")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa *antineoplásico*

2539847-03-3

## Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG EVQPGGSLRL SCAASGLTFF NYGMGWRQA PKKEREFVSA 50
IYWSGGTVVY AESVKGRFTI SRDNARKNTLY LQMSLSRAED TAVYYCAVTI 100
RGAATQTWKY DYWGQGLTIV VKPGGSGGSE VQLLESGGGE VQPGGSLRLS 150
CAASGLTFPN YGMGWRQAP GKEREFSVAI YWSGGTVVYA ESKVGRFTIS 200
RDNAKNTLYL QMSLSRAEDT AVYYCAVTIR GAATQTWKYD YWGQGLTIVT 250
KPGGGGDKTH TCPPCPAFGG PSVFLFPKPK KDTLMISRTPEVTCVVVDVS 300
HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLNQDNLNGK 350
EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE LTRKQVSLTC 400
LVKGFYPSDI AVEWESNGQP ENNYKTTPEV LDSGSPFLY SKLTVDKSRW 450
QQGNVFCSSV MHEALHNHYT QKSLSLSPGK 480
```

## Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro  
 Intra-H(C23-C104) 22-96 151-225 294-354 400-458  
 22"-96" 151"-225" 294"-354" 400"-458"  
 Inter-H-H (h 11, h 14) 262-262" 265-265"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación  
 HCH2 N84.4: 330, 330"

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal  
 HCHS K2: 480, 480"

**palazestrantum**

palazestrant

(1*R*,3*R*)-2-(2-fluoro-2-méthylpropyl)-3-méthyl-1-{4-[(1-propylazétidin-3-yl)oxy]phényl}-2,3,4,9-tétrahydro-1*H*-pyrido[3,4-*b*]indole  
*antiœstrogène, antinéoplasique*

palazestrant

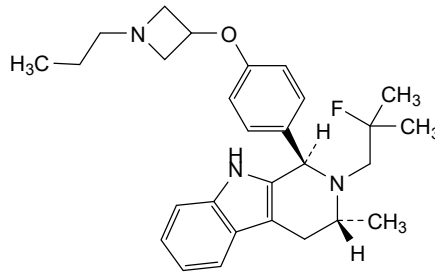
(1*R*,3*R*)-2-(2-fluoro-2-méthylpropyl)-3-méthyl-1-{4-[(1-propylazétidin-3-yl)oxy]phényl}-2,3,4,9-tétrahydro-1*H*-pyrido[3,4-*b*]indole  
*anti-œstrogène, antinéoplasique*

palazestrant

(1*R*,3*R*)-2-(2-fluoro-2-méthylpropyl)-3-méthyl-1-{4-[(1-propylazétidin-3-yl)oxy]phényl}-2,3,4,9-tétrahydro-1*H*-pyrido[3,4-*b*]indol  
*antiœstrógeno, antineoplásico*

C<sub>28</sub>H<sub>36</sub>FN<sub>3</sub>O

2092925-89-6

**patecibartum #**

patecibart

immunoglobulin G4-kappa, anti-[*Homo sapiens* EDNRA (endothelin receptor type A, ETA, ET-A, ETA-R, ET-AR)], humanized monoclonal antibody;  
gamma4 heavy chain humanized (1-446) [VH (*Homo sapiens* IGHV2-5\*09 (88.9%) -(IGHD) -IGHJ4\*01 (93.3%), CDR-IMGT [10.7.12] (26-35.53-59.98-109)) (1-120) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10, G4v4 CH2 A1.3, A1.2 (CH1 (121-218), hinge 1-12 S10>P (228) (219-230), CH2 F1.3>A (234), L1.2>A (235), L92 (309) (231-340), CH3 (341-445), CHS K2>del (446)) (121-446)], (134-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV6-21\*02 (90.5%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (226-226":229-229")-bisdisulfide, produced in Chinese Hamster Ovary (CHO) Cell line, glycoform alfa  
*endothelin receptor antagonist*

patécibart

immunoglobuline G4-kappa, anti-[*Homo sapiens* EDNRA (récepteur de type A de l'endothéline, ETA, ET-A, ETA-R, ET-AR)], anticorps monoclonal humanisé;  
chaîne lourde gamma4 humanisée (1-446) [VH (*Homo sapiens* IGHV2-5\*09 (88.9%) -(IGHD) -IGHJ4\*01 (93.3%), CDR-IMGT [10.7.12] (26-35.53-59.98-109)) (1-120) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10, G4v4 CH2 A1.3, A1.2 (CH1 (121-218), charnière 1-12 S10>P (228) (219-230), CH2 F1.3>A (234), L1.2>A (235), L92 (309) (231-340), CH3 (341-445), CHS K2>del (446)) (121-446)], (134-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV6-21\*02 (90.5%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (226-226":229-229")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa  
*antagoniste du récepteur de l'endothéline*

patecibart

inmunoglobulina G4-kappa, anti-[*Homo sapiens* EDNRA (receptor de tipo A de la endotelina, ETA, ET-A, ETA-R, ET-AR)], anticuerpo monoclonal humanizado;  
 cadena pesada gamma4 humanizada (1-446) [VH (*Homo sapiens* IGHV2-5\*09 (88.9%) -(IGHD) -IGHJ4\*01 (93.3%), CDR-IMGT [10.7-12] (26-35.53-59.98-109)) (1-120) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10, G4v4 CH2 A1.3, A1.2 (CH1 (121-218), bisagra 1-12 S10>P (228) (219-230), CH2 F1.3>A (234), L1.2>A (235), L92 (309) (231-340), CH3 (341-445), CHS K2>del (446)) (121-446)], (134-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV6-21\*02 (90.5%) -IGKJ1\*01 (100%), CDR-IMGT [6.3-9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (226-226":229-229")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa  
**antagonista del receptor de la endotelina**

2642374-04-5

Heavy chain / Chaîne lourde / Cadena pesada

QVTLKESGPT LVKPTQTLTL TCTFSGFSLT TSGLGVAWIR QPPGKALEWL	50
AHIWSDGDTR YYPALKNRLT ITKDTSRKNQV VLTMTNMDV DTATYYCAHM	100
KDDSLYFDNR GQGTLVTVSS ASTKGPSVFP LAPCSRSTSE STAALGLVK	150
DYFPEPVTVS WNSGALTSV HTPFAVLQSS GLYSLSSVVT VPSSSLGTKT	200
YTCNVDPKPS NTKVDKRVES KYGPPCPFP APEAAGGPSV FLFFPKPKDT	250
LMISRTPEVT CVVVDVSDQED PEVQENWYVD GVEVHNAKTK PREEQFNSTY	300
RVVSVLTVLH QDNLNGKEYK CKVSNKGLPS SIEKTSKAK GQPREPQVYT	350
LPPSQEEMTK NQVSLTCLVK GFYPSDIAVE WESNGQFENN YKTTPEVLDS	400
DGSFFLYSRL TVDKSRWQEG NVFSCVMHE ALHNHYTQKS LLSLSLG	446

Light chain / Chaîne légère / Cadena ligera

EIVLTQSPDF QSVTPKEKVT ITCRASQNIQ TSIHWYQKPK DQYPKLLIKY	50
ASKSISGVPS RFGSGSGSTD FTLTINSLEA EDAATYYCQH SYSPFWTFGQ	100
GTRVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWKV	150
DNALQSGNSQ ESVTEQDSK D STYLSLSTLT LSKADYKHKK VYACEVTHQG	200
LSSPVTKSN RGEK	214

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

Intra-H (C23-C104)	22-97	147-203	261-321	367-425
	22"-97"	147"-203"	261"-321"	367"-425"
Intra-L (C23-C104)	23'-88'	134'-194'		
	23"-88"	134"-194"		
Inter-H-L (CH1 10-CL 126)	134-214'	134"-214"		
Inter-H-H (h 8, h 11)	226-226"	229-229"		

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal  
 Q > pyroglutamy (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolylo)  
 H VH Q1: 1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación  
 H CH2 N84.4: 297, 297"  
 Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

**pegfosimerum manganesum**

pegfosimer manganese

polymer nanoparticles synthesized from tetramethyl *P,P'*-[1,7-bis(triethoxysilyl)heptane-4,4-diyl]bisphosphonate (~52 molecules per particle on average) by  
 (i) hydrolysis of the triethoxysilyl groups and ~75% of the dimethyl phosphonate groups and condensation of the resulting bis-silanetriol to a polymeric network with Si-O-Si linkages,  
 (ii) coating of the core particles by hydrolysis of  $\alpha$ -{[3,5-bis[3-(triethoxysilyl)propoxy]phenyl)methyl]- $\omega$ -methoxypoly(oxyethylene) (~18 molecules per particle on average) and condensation of the resulting silanetriol groups with surficial silanol groups, and  
 (iii) addition of a manganese(2+) salt to form hydrated polymeric ammonium manganese(2+) sodium ( $\approx$  29:13:65) phosphonate complexes  
**diagnostic imaging agent**



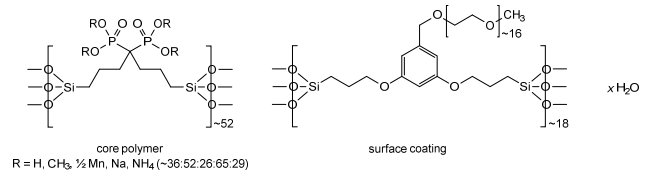
pegfosimère manganèse

nanoparticules polymériques synthétisées à partir de  $P,P'$ -[1,7-bis(triéthoxysilyl)heptane-4,4-diyl]bisphosphonate de tétraméthyle (~52 molécules par particule en moyenne) par (i) hydrolyse des groupes triéthoxysilyle et ~75 % des groupes phosphonate de diméthyle et condensation des groupes silanetriol résultants en un réseau polymérique avec des liaisons Si-O-Si, (ii) enrobage de ce noyau de particule par hydrolyse de  $\alpha$ -({3,5-bis[3-(triéthoxysilyl)propoxy]phényl)méthyl)- $\omega$ -méthoxypoly(oxyéthylène) (~18 molécules par particule en moyenne) et condensation des groupes silanetriol résultants avec des groupes silanol superficiels, et (iii) addition d'un sel de manganèse(2+) pour former des complexes de polymères hydratés sous forme de phosphonate d'ammonium et de manganèse(2+) et de sodium ( $\approx$  29:13:65) *agent diagnostique*

pegfosímero manganeso

nanopartículas poliméricas sintetizadas a partir de  $P,P'$ -[1,7-bis(trietoxisilil)heptano-4,4-diil]bisfosfonato de tetrametilo (~52 moléculas por partícula por término medio) por (i) hidrólisis de los grupos trietoxisilil y ~75 % de los grupos fosfonato de dimetilo y condensación de los grupos silanetriol resultantes en una red polimérica con las uniones Si-O-Si, (ii) revestimiento de este núcleo de partícula por hidrólisis de  $\alpha$ -({3,5-bis[3-(trietoxisilil)propoxil]fenil)metil)- $\omega$ -metoxipoli(oxietileno) (~18 moléculas por partícula por término medio) y condensación de los grupos silanetriol resultantes con los grupos silanol superficiales, y (iii) adición de una sal de manganeso(2+) para formar los complejos de polímeros hidratados bajo la forma de fosfonato de amonio y de manganeso(2+) y de sodio ( $\approx$  29:13:65) *agente de diagnóstico*

2641234-28-6



pegtarazimodum  
pegtarazimod

3-{2-[ $\omega$ -(L-isoleucyl-L-alanyl-L-leucyl-L-isoleucyl-L-leucyl-L- $\alpha$ -glutamyl-L-prolyl-L-isoleucyl-L-cysteinyl-L-cysteinyl-L-glutamyl-L- $\alpha$ -glutamyl-L-arginyl-L-alanyl-L-alanyl-amino)poly(oxyethylene)- $\alpha$ -yl]éthyl}propanoic acid  
*immunomodulator*

pegtarazimod

acide 3-{2-[ $\omega$ -(L-isoleucyl-L-alanyl-L-leucyl-L-isoleucyl-L-leucyl-L- $\alpha$ -glutamyl-L-prolyl-L-isoleucyl-L-cystéinyl-L-cystéinyl-L-glutamyl-L- $\alpha$ -glutamyl-L-arginyl-L-alanyl-L-alanyl-amino)poly(oxyéthylène)- $\alpha$ -yl]éthyl}propanoïque  
*immunomodulateur*

pegтаразимод

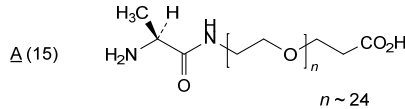
ácido 3-{2-[w-(L-isoleucil-L-alanil-L-leucil-L-isoleucil-L-leucil-L- $\alpha$ -glutamil-L-prolil-L-isoleucil-L-cisteinil-L-cisteinil-L-glutaminil-L- $\alpha$ -glutamil-L-arginil-L-alanil-L-alanilamino)poli(oxietileno)- $\alpha$ -il]etil} propanoico  
*immunomodulador*

C<sub>76</sub>H<sub>132</sub>N<sub>20</sub>O<sub>23</sub>S<sub>2</sub>(C<sub>2</sub>H<sub>4</sub>O)<sub>n</sub>

2056232-82-5

IALILEPICC QERAA 15

Modified residues / Résidus modifiés / Restos modificados



picankibartum #

picankibart

immunoglobulin G1-kappa, anti-[*Homo sapiens* IL23A (interleukin 23 subunit alpha; IL-23A, IL-23 subunit p19, IL23p19)], humanized monoclonal antibody;

gamma1 heavy chain humanized (1-444) [VH (*Homo sapiens* IGHV1-2\*02 (93.9%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.8] (27-32.51-58.97-104)) (1-115) -*Homo sapiens* IGHG1\*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (212) (116-213), hinge 1-15 (214-228), CH2M15.1>Y (250), S16>T (252), T18>E (254) (229-338), CH3 D12 (354), L14 (356) (339-443), CHS K2>del (444)) (116-444)], (218-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (88.4%) -IGKJ2\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimer (224-224":227-227")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, glycoform alfa  
*immunomodulador*

picankibart

immunoglobuline G1-kappa, anti-[*Homo sapiens* IL23A (interleukine 23 sous-unité alpha, IL-23A, IL-23 sous-unité p19, IL23p19)], anticorps monoclonal humanisé;  
chaîne lourde gamma1 humanisée (1-444) [VH (*Homo sapiens* IGHV1-2\*02 (93.9%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.8] (26-33.51-58.97-104)) (1-115) -*Homo sapiens* IGHG1\*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (212) (116-213), charnière 1-15 (214-228), CH2 M15.1>Y (250), S16>T (252), T18>E (254) (229-338), CH3 D12 (354), L14 (356) (339-443), CHS K2>del (444)) (116-444)], (218-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (88.4%) -IGKJ2\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimère (224-224":227-227")-bisdisulfure; produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa  
*immunomodulateur*

picankibart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL23A (interleukina 23 subunidad alfa, IL-23A, IL-23 subunidad p19, IL23p19)], anticuerpo monoclonal humanizado;

cadena pesada gamma1 humanizada (1-444) [VH (*Homo sapiens* IGHV1-2\*02 (93.9%) -(IGHD) - IGHJ4\*01 (100%), CDR-IMGT [8.8.8] (26-33.51-58.97-104)) (1-115) -*Homo sapiens* IGHG1\*01, G1m17,1 CH1 K120, CH3 D12, L14,G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (212) (116-213), bisagra 1-15 (214-228), CH2 M15.1>Y (250), S16>T (252), T18>E (254) (229-338), CH3 D12 (354), L14 (356) (339-443), CHS K2>del (444)) (116-444)], (218-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (88.4%) -IGKJ2\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dímero (224-224":227-227")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GS-KO), glicosilada alfa  
*inmunomodulador*

2622900-74-5

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYLHWVVRQA PGQGLEWMGY 50  
INPYNQETNY AAKFQGRVMT TRDTSISTAY MELSLRSDDD TAVVYICARNW 100  
DLPYWGQGLT VTSSASTKG PSVFPFLAPSS KSTSGGTAAL GCLVKDYFPE 150  
PVTWSNWSGA LTSGVHTFFA VLQSSGLYSL SSVVTVPSSS LGTQTYICNV 200  
NHKPSNTKVD KKVPEKSCDK THTCPPCPAP ELLGGPSVFL FPPKPKDTLY 250  
ITREPEVTCV VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV 300  
VSVLTVLHQD WLNKKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVYITLP 350  
PSRDELTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG 400  
SFFLYSKLTV DKSRWQQGNV FSCSVHREAL HNHVTQKSL S LSPG 444

## Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGDRTV ITCRASQSSIS DYLHWYQQKPK GKAPKLLIKY 50  
ASQMSMGVPS RFGSGSGSD FTLTISLQPF EDFATYYCQQ GHSFPTTFGQ 100  
GTKLEIKRTV AAFSVFIFFP SDEQLKSGTA SVVCLLNIFY PREAKVQWKV 150  
DNALQSGNSQ ESVEQDQSKD STYLSLSTLT LSKADYERKK VYACEVTHQG 200  
LSSPVTKSFN RGECC 214

## Post-translational modifications

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

Intra-H (C23-C104) 22-96 142-198 259-319 365-423  
22"-96" 142"-198" 259"-319" 365"-423"

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

Inter-H-L (h 5-CL 126) 218-214' 218"-214"

Inter-H-H (h 11, h 14) 224-224" 227-227"

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

Q &gt; pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxoprolilo)

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 biantenaricos complejos fucosilados

**plixorafenibum**  
plixorafenib

(8<sup>3</sup>R)-5<sup>2</sup>,5<sup>6</sup>,8<sup>3</sup>-trifluoro-3'*H*-7λ<sup>6</sup>-thia-6-aza-3(5,3)-pyrrolo[2,3-*b*]pyridina-2(2,5)-pyrimidina-8(1)-pyrrolidina-5(1,3)-benzena-1(1)-cyclopropanoactaphane-4,7,7-trione  
*antineoplastica*

plixorafénib

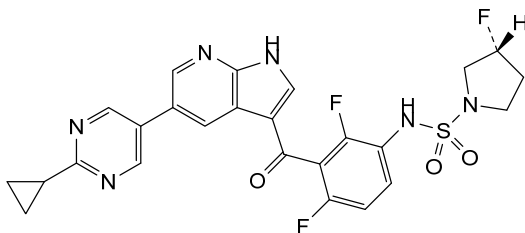
(8<sup>3</sup>R)-5<sup>2</sup>,5<sup>6</sup>,8<sup>3</sup>-trifluoro-3'*H*-7λ<sup>6</sup>-thia-6-aza-3(5,3)-pyrrolo[2,3-*b*]pyridina-2(2,5)-pyrimidina-8(1)-pyrrolidina-5(1,3)-benzéna-1(1)-cyclopropanoactaphane-4,7,7-trione  
*antineoplasique*

ploxorafenib

(8<sup>3R</sup>)-5<sup>2</sup>,5<sup>6</sup>,8<sup>3</sup>-trifluoro-3<sup>1H</sup>-7<sup>λ<sup>6</sup></sup>-tia-6-aza-3(5,3)-  
pirrolo[2,3-*b*]piridina-2(2,5)-pirimidina-8(1)-pirrolidina-  
5(1,3)-bencena-1(1)-ciclopropanaocetafano-4,7,7-triona  
*antineoplásico*

C<sub>25</sub>H<sub>21</sub>F<sub>3</sub>N<sub>6</sub>O<sub>3</sub>S

1393466-87-9



**pocenbrodibum**  
pocenbrodib

(1*R*,3*R*)-3-((7*S*)-2-[(*R*)-(5-fluoro-2-  
methoxyphenyl)(hydroxy)methyl]-6-(methoxycarbonyl)-  
7-méthyl-6,7,8,9-tétrahydro-3*H*-imidazo[4,5-*f*]quinolin-  
3-yl)cyclohexane-1-carboxylic acid  
*inhibitor of the histone acetyltransferase p300 and  
CREB-binding protein, antineoplastic*

pocenbrodib

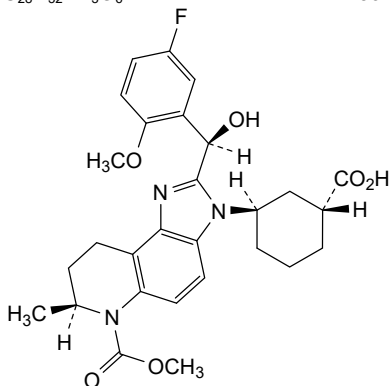
acide (1*R*,3*R*)-3-((7*S*)-2-[(*R*)-(5-fluoro-2-  
méthoxyphényl)(hydroxy)méthyl]-6-(méthoxycarbonyl)-  
7-méthyl-6,7,8,9-tétrahydro-3*H*-imidazo[4,5-*f*]quinolin-  
3-yl)cyclohexane-1-carboxylique  
*inhibiteur de l'histone acétyltransférase p300 et de la  
protéine de liaison de l'élément de réponse à l'AMP  
cyclique, antinéoplasique*

pocenbrodib

ácido (1*R*,3*R*)-3-((7*S*)-2-[(*R*)-(5-fluoro-2-  
metoxifenil)(hidroxi)metil]-6-(metoxicarbonil)-7-metil-  
6,7,8,9-tetrahydro-3*H*-imidazo[4,5-*f*]quinolin-3-  
il)ciclohexano-1-carboxílico  
*inhibidor de la acetiltransferasa de histonas p300 y de  
la proteína de unión a CREB, antineoplásico*

C<sub>28</sub>H<sub>32</sub>FN<sub>3</sub>O<sub>6</sub>

2304372-79-8



**pralurbactamum**

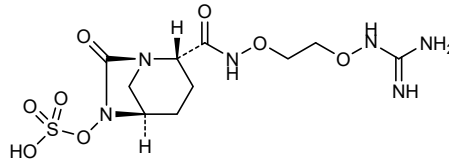
pralurbactam (1*R*,2*S*,5*R*)-2-[[2-(guanidinoxy)ethoxy]carbamoyle]-7-oxo-1,6-diazabicyclo[3.2.1]octan-6-yl hydrogen sulfate  
*beta-lactamase inhibitor*

pralurbactam hydrogénosulfate de (1*R*,2*S*,5*R*)-2-({2-[(carbamidoylamino)oxy]éthoxy}carbamoyle)-7-oxo-1,6-diazabicyclo[3.2.1]octan-6-yle  
*inhibiteur de bêta-lactamase*

pralurbactam hidrogenosulfato de (1*R*,2*S*,5*R*)-2-({2-[(carbamidoylamino)oxy]etoxi}carbamoyle)-7-oxo-1,6-diazabicyclo[3.2.1]octan-6-ilo  
*inhibidor de beta lactamasa*

C<sub>10</sub>H<sub>18</sub>N<sub>6</sub>O<sub>9</sub>S

2163782-59-8

**prizloncabtagemum autoleucelum #**

prizloncabtage autoleucel autologous T lymphocytes obtained from peripheral blood lymphocytes by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector, encoding a bispecific chimeric antigen receptor targeting CD19 and CD20. The expressed transgene comprises a CD8 $\alpha$  leader sequence, anti-CD19 and anti-CD20 single chain fragment variable (scFv) (derived from FMC-63 and *ofatumumab*, respectively), an IgG4 hinge and a CD28 transmembrane region, a 4-1BB and a CD3 $\zeta$  signalling domain, and is under control of the elongation factor 1 alpha (EF1 $\alpha$ ) short promoter. The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a  $\psi$  packaging signal, a Rev response element (RRE), a central polyurine tract (cPPT) sequence and a mutated Woodchuck hepatitis virus posttranscriptional regulatory element (WPRE). The vector is pseudotyped with vesicular stomatitis virus (VSV) G envelope protein. The leukapheresis material is enriched for CD4/CD8 T lymphocytes by positive immunoselection, activated by CD3 and CD28 agonists and transduced with the lentiviral vector. The cells are then expanded in media with serum replacement and interleukin 2 (IL-2). The T lymphocytes ( $\geq 95\%$ ) are positive for the transgene ( $\geq 10\%$  CAR positive), and secrete interferon gamma in response to CD19 and CD20 expressing tumour cell lines  
*cell-based gene therapy (antineoplastic)*

prizloncabtage autoleucel lymphocytes T autologues obtenus à partir de lymphocytes de sang périphérique par leucaphérèse, transduits avec un vecteur lentiviral auto-inactivant et non répliquant, codant un récepteur antigénique chimérique bispécifique ciblant CD19 et CD20. Le transgène exprimé comprend une séquence de tête CD8 $\alpha$ , un fragment variable à chaîne unique (scFv) anti-CD19 et anti-CD20 (dérivé de FMC-63 et *d'ofatumumab*, respectivement), une charnière IgG4 et une

région transmembranaire CD28, un domaine de signalisation 4-1BB et CD3 $\zeta$ , et est sous le contrôle du promoteur court du facteur d'élongation 1 alpha (EF1 $\alpha$ ). La construction est flanquée de répétitions longues terminales (LTR) en 5' et 3' et contient également un signal d'encapsidation  $\psi$ , un élément de réponse Rev (RRE), une séquence du tractus polypurine central (cPPT) et un élément régulateur post-transcriptionnel (WPRES) muté du virus de l'hépatite de Woodchuck. Le vecteur est pseudotypé avec la protéine d'enveloppe G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est enrichi en lymphocytes T CD4/CD8 par immunosélection positive, activé par des agonistes CD3 et CD28 et transduit avec le vecteur lentiviral. Les cellules sont ensuite développées dans un milieu avec remplacement du sérum et interleukine 2 (IL-2). Les lymphocytes T ( $\geq 95\%$ ) sont positifs pour le transgène ( $\geq 10\%$  CAR positif), et sécrètent de l'interféron gamma en réponse à des lignées de cellules tumorales exprimant CD19 et CD20  
*thérapie génique à base de cellules (antinéoplasique)*

prizloncabtagn autoleucel

linfocitos T autólogos obtenidos de linfocitos de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica para un receptor de antígenos quimérico biespecífico dirigido a CD19 y CD20. El transgén expresado contiene una secuencia líder de CD8 $\alpha$ , un fragmento variable de cadena sencilla (scFv) anti-CD19 y otro anti-CD20 (derivados de FMC-63 y *ofatumumab*, respectivamente), una bisagra IgG4 y una región transmembrana de CD28, un dominio de señalización 4-1BB y CD3 $\zeta$ , y está bajo el control del promotor corto del factor de elongación 1 alfa (EF1 $\alpha$ ). El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento  $\psi$ , un elemento de respuesta Rev (RRE), una secuencia de tracto de polipurina central (cPPT) y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRES) mutado. El vector está seudotipado con la proteína G de la envuelta del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se enriquece para linfocitos T CD4/CD8 mediante inmunoselección positiva, se activa mediante agonistas de CD3 y CD28 y se transduce con el vector lentiviral. Las células son después expandidas en medio con sustituto de suero e interleuquina 2 (IL-2). Los linfocitos T ( $\geq 95\%$ ) son positivos para el transgén ( $\geq 10\%$  positivos para el CAR) y secretan interferón gamma en respuesta a líneas de células tumorales que expresan CD19 y CD20  
*terapia génica basada en células (antineoplásico)*

**pumecitinibum**  
pumecitinib

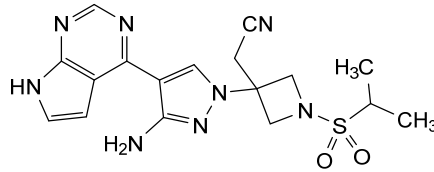
{3-[3-amino-4-(7H-pyrrolo[2,3-d]pyrimidin-4-yl)-1H-pyrazol-1-yl]-1-(propane-2-sulfonyl)azetidín-3-yl}acetónitrilo  
*Janus kinase inhibitor, anti-inflammatory*

pumécitinib {3-[3-amino-4-(7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)-1*H*-pyrazol-1-yl]-1-(propane-2-sulfonyl)azétidin-3-yl}acétonitrile  
*inhibiteur de la kinase de Janus, anti-inflammatoire*

pumecitinib {3-[3-amino-4-(7*H*-pirrolo[2,3-*d*]pirimidin-4-il)-1*H*-pirazol-1-il]-1-(propano-2-sulfonyl)azetidid-3-il}acetonitrilo  
*inhibidor de la kinasa de Janus, antiinflamatorio*

C<sub>17</sub>H<sub>20</sub>N<sub>8</sub>O<sub>2</sub>S

2401057-12-1



**puxitatugum #**  
puxitatug

immunoglobulin G1-kappa, anti-[*Homo sapiens* VTCN1 (V-set domain containing T cell activation inhibitor 1, B7 family member H4, B7H4, B7-H4)], *Homo sapiens* monoclonal antibody;

gamma1 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-34\*01 (95.9%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG1\*03 (100%), G1m3, nG1m1 CH1 R120, E12, M14 (CH1 R120 (214) (118-215), hinge 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17\*01 (96.8%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimer (226-226":229-229")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa  
*antineoplastique*

puxitatug

immunoglobuline G1-kappa, anti-[*Homo sapiens* VTCN1 (inhibiteur 1 de l'activation des cellules T contenant un domaine V-set, membre H4 de la famille B7, B7-H4, B7H4)], anticorps monoclonal *Homo sapiens*;  
chaîne lourde gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-34\*01 (95.9%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG1\*03 (100%), G1m3, nG1m1 CH1 R120, E12, M14 (CH1 R120 (214) (118-215), charnière 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17\*01 (96.8%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimère (226-226":229-229")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa  
*antineoplastique*

puxitatug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* VTCN1 (inhibidor 1 de la activación de las células T que contiene un dominio V-set, miembro H4 de la familia B7, B7-H4, B7H4)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-34\*01 (95.9%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG1\*03 (100%), G1m3, nG1m1 CH1 R120, E12, M14 (CH1 R120 (214) (118-215), bisagra 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17\*01 (96.8%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dímero (226-226":229-229")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa *antineoplásico*

2760250-47-1

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLQWAG LLKPSETLSL ACTVYGGFS GYYWNIRQP PGKLEWIGE 50  
 INHSGSTSYN PSLKSRVTIS VDTSKNQFSL KLSSTVTAADT AVYICARVLV 100  
 NWNVDSWGGQ TLTVTSSAST KGPSVFLAP SSKSTSGGTA ALGCLVKDYF 150  
 PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSVVTVPSS SGLTQTYIC 200  
 NVNHKPSNTK VDKRVEPKSC DKHTCPCCP APPELLGGPSV FLFPPKPKDT 250  
 LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK FREQYINSTY 300  
 RRVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTIKAK GQPREPQVYT 350  
 LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPEPVLD 400  
 DGSFPLYSKL TVDKSRWQQG NVFSCSVMEH ALHNHYTQKS LSLSPGK 447

## Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGRVIT ITCRASQDIR NDVGYWYQKPK GKAPKRLIYA 50  
 ASRLQSGVPS RFGSGSGSTE FTLTISLQPF EDFATYICLQ HNSYFRTFGQ 100  
 GTKVEIKRTV AAPSVEIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWVKV 150  
 DNALQSGNSQ ESVTEQDSKD STYLSSTLT LSKADYERKHK VYACEVTHQG 200  
 LSSPVTKSFN RGEK 214

## Post-translational modifications

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

Intra-H (C23-C104) 22-95 144-200 261-321 367-425  
 22"-95" 144"-200" 261"-321" 367"-425"

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

Inter-H-L (h 5-CL 126) 220-214' 220"-214"

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

N-terminal glutaminylation / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q &gt; pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyl (pE, 5-oxoprolyl) / piroglutamilo

(pE, 5-oxoprolyl)

H VH Q1: 1, 1"

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

H VH CDR2 N57: 52, 52"

Deamidation, no glycosylation / déamidation, pas de glycosylation / desamidación, sin glicosilación

H CH2 N84.4: 297, 297"

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

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

H CHS K2: 447, 447"

**puxitatugum samrotecanum #**

puxitatug samrotecan

immunoglobulin G1-kappa, anti-[*Homo sapiens* VTCN1 (V-set domain containing T cell activation inhibitor 1, B7 family member H4, B7H4, B7-H4)], *Homo sapiens* monoclonal antibody; conjugated to a topoisomerase I inhibitor;



- gamma1 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-34\*01 (95.9%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG1\*03 (100%), G1m3, nG1m1 CH1 R120, E12, M14 (CH1 R120 (214) (118-215), hinge 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17\*01 (96.8%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimer (226-226":229-229")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa; 220, 214', 220", 214"', 226, 226", 229, 229" -octakis (thioether) conjugated with *N*-[31-(3-mercapto-2,5-dioxo-3-pyrrolidinyl)-1,29-dioxo-4,7,10,13,16,19,22,25-octaosa-28-azahentriacont-1-yl]-*L*-valyl-*N*-[(9*S*)-9-ethyl-2,3,9,10,13,15-hexahydro-9-hydroxy-10,13-dioxo-1*H*,12*H*-benzo[de]pyrano[3',4':6,7]indolizino[1,2-*b*]quinolin-4-yl]-*L*-alaninamide  
*antineoplastique*
- puxitatug samrotécán immunoglobuline G1-kappa, anti-[*Homo sapiens* VTCN1 (inhibiteur 1 de l'activation des cellules T contenant un domaine V-set, membre H4 de la famille B7, B7-H4, B7H4)], anticorps monoclonal *Homo sapiens*; conjugué à un inhibiteur de la topoisomérase I; chaîne lourde gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-34\*01 (95.9%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG1\*03 (100%), G1m3, nG1m1 CH1 R120, E12, M14 (CH1 R120 (214) (118-215), charnière 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17\*01 (96.8%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimère (226-226":229-229")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa; 220, 214', 220", 214"', 226, 226", 229, 229" -octakis (thioéther) conjugué with *N*-[31-(3-mercapto-2,5-dioxo-3-pyrrolidinyl)-1,29-dioxo-4,7,10,13,16,19,22,25-octaosa-28-azahentriacont-1-yl]-*L*-valyl-*N*-[(9*S*)-9-ethyl-2,3,9,10,13,15-hexahydro-9-hydroxy-10,13-dioxo-1*H*,12*H*-benzo[de]pyrano[3',4':6,7]indolizino[1,2-*b*]quinolin-4-yl]-*L*-alaninamide  
*antineoplasique*
- puxitatug samrotecán inmunoglobulina G1-kappa, anti-[*Homo sapiens* VTCN1 (inhibidor 1 de la activación de las células T que contiene un dominio V-set, miembro H4 de la familia B7, B7-H4, B7H4)], anticuerpo monoclonal *Homo sapiens*; conjugado con un inhibidor de la topoisomerasa I; cadena pesada gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-34\*01 (95.9%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG1\*03 (100%), G1m3, nG1m1 CH1 R120, E12, M14 (CH1 R120 (214) (118-215), bisagra 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfuro con la cadena ligera kappa *Homo sapiens*

(1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17\*01 (96.8%) - IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dímero (226-226'':229-229'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa; 220, 214', 220'', 214''', 226, 226'', 229, 229''-octakis (tioéter) conjugado con *N*-[31-(3-mercapto-2,5-dioxo-3-pirrolidinil)-1,29-dioxo-4,7,10,13,16,19,22,25-octaoxa-28-azahentricont-1-il]-L-valil-*N*-[(9*S*)-9-etil-2,3,9,10,13,15-hexahidro-9-hidroxi-10,13-dioxo-1*H*,12*H*-benzo[de]pirano[3',4':6,7]indolizino[1,2-*b*]quinolin-4-il]-L-alaninamida  
**antineoplásico**

## 2760250-80-2

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLQQWAG LLKPESETLSL ACTVYGGSF S GYYWNWIRQP PGKGLEWIGE 50  
 INHSGSTSYN PSLKSRVTIS VDTSKNQPSL KLSSVTAADT AVYYCARVLY 100  
 NWNVDSWGQG TLTVTSSAST KGPSVFPLAP SSKSTSGGTA ALGLVLRDYF 150  
 FEPVTVSWSN GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200  
 NVNHKPSNTK VDKRVEPKSC DKHTCPCPC APELLGGPSV FLFPPKPKDT 250  
 LMISRTPEVT CVVVDVSHED FEVKFNWYVD GVEVHNARTK PREEQYNSTY 300  
 RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTIKAK GQPREPQVYV 350  
 LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPPEN YKTTPEPVLD 400  
 DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK 447

## Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGDRTV ITCRASQDIR NDVGWYQKPK GKAPKRLIYA 50  
 ASRLQSGVPS RFSGSGSGTE FTLTISLQPE EDFATYCYCLQ HNSYPRTFGQ 100  
 GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY BREAKVQMKV 150  
 DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYERHK VYACEVTHQG 200  
 LSSPVTKSFN RGEK 214

## Post-translational modifications

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

Intra-H (C23-C104) 22-95 144-200 261-321 367-425  
 22''-95'' 144''-200'' 261''-321'' 367''-425''

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

Inter-H-L (h 5-CL 126)\* 220-214' 220''-214''

Inter-H-H (h 11, h 14)\* 226-226'' 229-229''

\*The inter-chain disulfide bridges are not present, the 8 cysteinyl being conjugated each via a thioether bond to a drug linker.

\*Les ponts disulfures inter-chaînes ne sont pas présents, les 8 cystéinyl étant chacun conjugué via une liaison thioéther à un linker-principe actif.

\*Los puentes disulfuro entre cadenas no están presentes, cada uno de los 8 cisteinil está conjugada a través de un enlace tioéter a un linker-principio activo.

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

Q > pyroglutamyl (pE, 5-oxoprolil) / pyroglutamy (pE, 5-oxoprolile) / piroglutamilo (pE, 5-oxoprolilo)  
 H VH Q1: 1, 1''

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

H VH N57: 52, 52''

Deamidation, no glycosylation / déamidation, pas de glycosylation / desamidación, sin glicosilación

H CH2 N84.4: 297, 297''

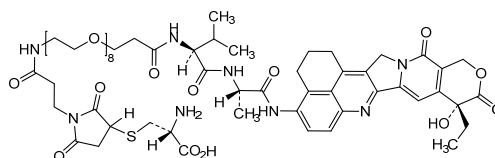
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenaríos complejos fucosilados

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

H CHS K2: 447, 447''

Modified residues / Résidus modifiés / Restos modificados

C(214'',214''',220,220',226,226'',229,229'')



**quazomotidum**

quazomotide

human Wilms tumor protein (WT33)-(427-445)-peptide;  
 L-arginyl-L-seryl-L- $\alpha$ -aspartyl-L- $\alpha$ -glutamyl-L-leucyl-L-valyl-  
 L-arginyl-L-histidyl-L-histidyl-L-asparaginyl-L-methionyl-L-  
 histidyl-L-glutamyl-L-arginyl-L-asparaginyl-L-methionyl-L-  
 threonyl-L-lysyl-L-leucine  
*immunological agent for active immunization*  
*(antineoplastic)*

quazomotide

protéine humaine de la tumeur de Wilms (WT33)-(427-  
 445)-peptide;  
 L-arginyl-L-séryl-L- $\alpha$ -aspartyl-L- $\alpha$ -glutamyl-L-leucyl-L-valyl-  
 L-arginyl-L-histidyl-L-histidyl-L-asparaginyl-L-méthionyl-L-  
 histidyl-L-glutamyl-L-arginyl-L-asparaginyl-L-méthionyl-L-  
 thréonyl-L-lysyl-L-leucine  
*agent immunologique d'immunisation active*  
*(antinéoplasique)*

quazomotida

proteína humana del tumor de Wilms (WT33)-(427-445)-  
 péptido;  
 L-arginil-L-seril-L- $\alpha$ -aspartil-L- $\alpha$ -glutamil-L-leucil-L-valil-L-  
 arginil-L-histidil-L-histidil-L-asparaginil-L-metionil-L-histidil-  
 L-glutaminil-L-arginil-L-asparaginil-L-metionil-L-treonil-L-  
 lisil-L-leucina  
*agente inmunológico para inmunización activa*  
*(antineoplásico)*

C<sub>98</sub>H<sub>164</sub>N<sub>38</sub>O<sub>29</sub>S<sub>2</sub>

935395-33-8

RSEDELVRHHN MHQRNMTKL 19

**rademikibartum #**

rademikibart

immunoglobulin G4-kappa, anti-[*Homo sapiens* IL4R  
 (interleukin 4 receptor, IL4RA, IL-4RA, interleukin 13  
 receptor, CD124)], *Homo sapiens* monoclonal antibody;  
 gamma4 heavy chain *Homo sapiens* (1-441) [VH (*Homo*  
*sapiens* IGHV3-23\*04 (88.8%) -(IGHD) -IGHJ4\*01  
 (100%), CDR-IMGT [8.7.9] (26-33.51-57.96-104)) (1-115)  
 -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h  
 P10 (CH1 (116-213), hinge 1-12 S10>P (223) (214-225),  
 CH2 L92 (304) (226-335), CH3 (336-440), CHS K2>del  
 (441)) (116-441)], (129-216')-disulfide with kappa light  
 chain *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens*  
 IGKV3-20\*01 (97.9%) -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 (221-221":224-224")-bisdisulfide, produced in  
 Chinese hamster ovary (CHO) cells, glycoform alfa  
*anti-inflammatory*

rademikibart

immunoglobuline G4-kappa, anti-[*Homo sapiens* IL4R  
 (récepteur de l'interleukine 4, IL4RA, IL-4RA, récepteur de  
 l'interleukine 13, CD124)], anticorps monoclonal *Homo*  
*sapiens*;

chaîne lourde gamma4 *Homo sapiens* (1-441) [VH (*Homo sapiens* IGHV3-23\*04 (88.8%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.7.9] (26-33.51-57.96-104)) (1-115) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (116-213), hinge 1-12 S10>P (223) (214-225), CH2 L92 (304) (226-335), CH3 (336-440), CHS K2>del (441)) (116-441)], (129-216')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20\*01 (97.9%) -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 (221-221":224-224")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa *anti-inflammatoire*

rademikibart

immunoglobulina G4-kappa, anti-[*Homo sapiens* IL4R (receptor de la interleukina 4, IL4RA, IL-4RA, receptor de la interleukina, CD124)], anticuerpo monoclonal *Homo sapiens*;

cadena pesada gamma4 *Homo sapiens* (1-441) [VH (*Homo sapiens* IGHV3-23\*04 (88.8%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.7.9] (26-33.51-57.96-104)) (1-115) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (116-213), 1-12 bisagra S10>P (223) (214-225), CH2 L92 (304) (226-335), CH3 (336-440), CHS K2>del (441)) (116-441)], (129-216')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20\*01 (97.9%) -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 (221-221":224-224")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa *antiinflamatorio*

2648260-80-2

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS RNAMFWVRQA PGKLEWVSG 50
IGTGGATSYA DSVKGRFTIS RDNAKNSLYL QMNSLRAEDT AVYYCARGRY 100
YFDYWGQQTLL VTVSSASTKG PSVFPLAPCS RSTSESTAAAL GCLVKDYFPE 150
FVTVSWNSGA LTSGVHTFFA VLQSSGLYSL SSVTVFSSS LGTKYITCNV 200
DHKFSNTRVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP KFKDTLMISR 250
TPEVTCVVVD VSQEDPEVQF NMYVDGVEVH NAKTKPREEQ FNSTYRVVSV 300
LTVLHQDWLW GKEYRCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ 350
EEMTRKQVSL TCLVRGFYPS DIAVEWESNG QPENNYKTTT PVLDSGGSFF 400
LYSRLTVDKS RWQEGNVFSC SVMHEALHNN YTQKSLSLSL G 441
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Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSSLAWYQQK PGQAPRLLIY 50
GASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYDHSAGWTF 100
QGQTKVEIKR TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW 150
KVDNALQSGN SQESVTEQDS KDSTYLSLST 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'-95 142-198 256-316 362-420  
22''-95'' 142''-198'' 256''-316'' 362''-420''

Intra-L (C23-C104) 23'-89'' 136'-196''  
23''-89'' 136''-196''

Inter-H-L (CH1 10-CL 126) 129-216' 129''-216''

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

**relutriginum**

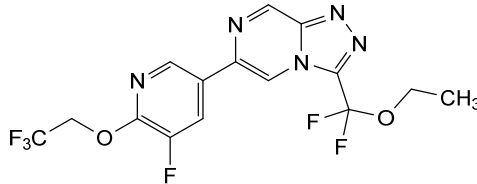
relutrigine 3-(ethoxydifluoromethyl)-6-[5-fluoro-6-(2,2,2-trifluoroethoxy)pyridin-3-yl][1,2,4]triazolo[4,3-a]pyrazine  
*sodium channel blocker*

rélutrigine 3-(éthoxydifluorométhyl)-6-[5-fluoro-6-(2,2,2-trifluoroéthoxy)pyridin-3-yl][1,2,4]triazolo[4,3-a]pyrazine  
*bloqueur des canaux sodiques*

relutrigina 3-(etoxidifluorometil)-6-[5-fluoro-6-(2,2,2-trifluoroetoxi)piridin-3-il][1,2,4]triazolo[4,3-a]pirazina  
*bloqueante de los canales del sodio*

C<sub>15</sub>H<sub>11</sub>F<sub>6</sub>N<sub>5</sub>O<sub>2</sub>

2392951-29-8

**remternetugum #**

remternetug

immunoglobulin G1-kappa, anti-[*Homo sapiens* APP (amyloid beta A4 precursor protein) Abeta42 N3pGlu peptide (N-terminal truncated and pyroglutamate-modified amyloid beta 3-42 peptide), *Homo sapiens* monoclonal antibody;  
gamma1 heavy chain *Homo sapiens* (1-451) [VH (*Homo sapiens*IGHV3-23\*01 (98.0%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens*IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS K2>del (451)) (123-451)], (225-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-5\*03 (93.4%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.51-53.89-97)) (1'-107') -*Homo sapiens*IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimer (231-231'':234-234'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-GSKO, glycoform alfa  
*clearance of amyloid beta*

remternetug

immunoglobuline G1-kappa, anti-[*Homo sapiens* APP (protéine précurseur A4 amyloïde bêta) Abêta42 N3pGlu peptide (peptide amyloïde bêta 3-42 tronqué, avec un pyroglutamate N-terminal)]; chaîne lourde gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens*IGHV3-23\*01 (98.0%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens*IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS K2>del (451)) (123-451)], (225-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-5\*03 (93.4%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.51-53.89-97)) (1'-107') -*Homo sapiens*IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimère (231-231'':234-234'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-GSKO, glycoforme alfa  
*élimination d'amyloïde bêta*

remternetug

immunoglobulina G1-kappa, anti-[*Homo sapiens* APP (proteína precursor A4 amiloide beta) Abeta42 N3pGlu péptido (péptido amiloide beta 3-42 truncado, con un piroglutamato N-terminal)]; cadena pesada gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-23\*01 (98.0%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS K2>del (451)) (123-451)], (225-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5\*03 (93.4%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.51-53.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dímero (231-231":234-234")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-GSKO, forma glicosilada alfa  
*eliminación del amiloide beta*

2571940-41-3

## Heavy chain / Chaîne lourde / Cadena pesada

```

EQQLLESGGG LVQPGGSLRL SCAASGFTFS SYPMSWVRQA PGKGLEWVSA 50
ISGSGGSTYY ADSVKGRTI SRDNSKNTLY LQMNSLRAED TAVYYCAREG 100
GSGSYNGFD YWGGTLVTV SSASTKGPSV FPLAPSSKST SGGTAAALGCL 150
VKDYFPEPVT VSMNSGALTS GVHTFFAVLQ SSGLYSLSSV VTFVSSSLGT 200
QTYICNVNHK PSNTKVDKVK EPKSCDKTHT CPPCPAPELL GGSYVFLFP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDMLN GREYKCKVSN KALPARIKKT ISKAKGQPRE 350
PQVYTLPPSR DELTKNQVSL TCVLKGFYPS DIAVEWESNG OPENNYKTT 400
PVLDSDSGFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNR YTKQSLSLSP 450
G 451

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## Light chain / Chaîne légère / Cadena ligera

```

DIQMTQSPST LSASVGRVIT ITCRASQSLG NWLAWYQQKPK GKAPKLLIYQ 50
ASTLESQVPS RFGSGSGSTE FTLTISSLQP DDFATYYCQH YKGSFRTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNFFY PREAKVQMKV 150
DNALQSGNSQ ESVTEQDSKD STYLSLSSTL LSKADYEKHK YVACEVTHQG 200
LSSPVTKSFN RGEK 214

```

## Post-translational modifications

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

Intra-H (C23-C104) 22-96 149-205 266-326 372-430  
22"-96" 149"-205" 266"-326" 372"-430"

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

Inter-H-L (h 5-CL 126) 225-214' 225"-214"''

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

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

H CH2 N84.4:

302, 302"

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

renvistobartum #

renvistobart

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)], *Homo sapiens* monoclonal antibody;  
gamma1 heavy chain *Homo sapiens* (1-459) [VH (*Homo sapiens* IGHV4-61\*01 (98.0%) -(IGHD) -IGHJ3\*01 (92.3%), CDR-IMGT [10.7.22] (26-35.53-59.98-119)) (1-130) -*Homo sapiens* IGHG1\*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v43 CH2 A1.3, E1.2, A1, G1v60 S115, S116 (CH1 R120 (227) (131-228), hinge 1-15 (229-243), CH2 L1.3>A (247), L1.2>E (248), G1>A (250), A115>S (343), P116>S (344) (244-353), CH3 E12 (369), M14 (371) (354-458), CHS K2>del (459)) (131-459)], (233-216')-disulfide with kappa light chain *Homo*

- sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-11\*01 (100%) -IGKJ3\*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 (239-239":242-242")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1 lacking the glutamine synthetase (GS-KO) gene, glycoform alfa *immunostimulant, antineoplastic*
- renvistobart immunoglobuline G1-kappa, anti-[*Homo sapiens* TIGIT (immunorécepteur des cellules T avec domaines Ig et ITIM, membre 9 de l'Ig V-set, VSIG9, membre 3 de l'Ig V-set et région transmembranaire, VSTM3)], anticorps monoclonal *Homo sapiens*;  
chaîne lourde gamma1 *Homo sapiens* (1-459) [VH (*Homo sapiens* IGHV4-61\*01 (98.0%) -(IGHD) -IGHJ3\*01 (92.3%), CDR-IMGT [10.7.22] (26-35.53-59.98-119)) (1-130) -*Homo sapiens* IGHG1\*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v43 CH2 A1.3, E1.2, A1, G1v60 S115, S116 (CH1 R120 (227) (131-228), charnière 1-15 (229-243), CH2 L1.3>A (247), L1.2>E (248), G1>A (250), A115>S (343), P116>S (344) (244-353), CH3 E12 (369), M14 (371) (354-458), CHS K2>del (459)) (131-459)], (233-216')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-11\*01 (100%) -IGKJ3\*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 (239-239":242-242")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1 ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa *immunostimulant, antinéoplasique*
- renvistobart inmunoglobulina G1-kappa, anti-[*Homo sapiens* TIGIT (immunoreceptor de las células T con dominios Ig e ITIM, miembro 9 de la Ig V-set, VSIG9, miembro 3 de la Ig V-set y región transmembranaria, VSTM3)], anticuerpo monoclonal *Homo sapiens*;  
cadena pesada gamma1 *Homo sapiens* (1-459) [VH (*Homo sapiens* IGHV4-61\*01 (98.0%) -(IGHD) -IGHJ3\*01 (92.3%), CDR-IMGT [10.7.22] (26-35.53-59.98-119)) (1-130) -*Homo sapiens* IGHG1\*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v43 CH2 A1.3, E1.2, A1, G1v60 S115, S116 (CH1 R120 (227) (131-228), bisagra 1-15 (229-243), CH2 L1.3>A (247), L1.2>E (248), G1>A (250), A115>S (343), P116>S (344) (244-353), CH3 E12 (369), M14 (371) (354-458), CHS K2>del (459)) (131-459)], (233-216')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-11\*01 (100%) -IGKJ3\*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 (239-239":242-242")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa *inmunoestimulante, antineoplásico*

## Heavy chain / Chaîne lourde / Cadena pesada

QVHLQESGPG LVKPSSETLSL TCTVSGGSVS SGIYYWSWIR QPPGKGLEWI 50  
 GYIYSGSTN YNPSLKSRTV ISVDTSKNQF SLKLSVSTAA DTAVVYCARD 100  
 YVYSGNYNV DYYFFGVDVM GQGTTVTVSS ASTKGPSVFP LAPSSKSTSG 150  
 GTAALGLCLVK DYFPEPVTVS WNSGALTSQV HTFPAVLQSS GLYSLSSVVT 200  
 VPSSSLGTQT YICNVNHKPS NTKVDKRVPEP KSCDKTHTCP PCPAPEAEGA 250  
 PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA 300  
 KTKPREEQYN STYRVVSVLT VLNQDNLNGK EYKCKVSNKA LPSSIEKTIS 350  
 KAKGQPREPQ VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP 400  
 ENNYKTTFPV LDDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNYHT 450  
 QKLSLSLSPG 459

## Light chain / Chaîne légère / Cadena ligera

EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQPK GQAPRLLIYD 50  
 ASNRATGIPA RFGSGSGSDT FTLTISLSEF EDFAVVYCOQ RSNWPLPTFF 100  
 GPGTKVDIKR TVAAPSVEFIF PPSDEQLKSG TASVUCLLNN FYPREKRVQW 150  
 KVDNALQSGN SQESVTEQDS KDSYISLSST LTLKADYEK HKVYACEVTH 200  
 QGLSSPVTKS FNRGEC 216

## Post-translational modifications

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

Intra-H (C23-C104) 22-97 157-213 274-334 380-438  
 22\*-97" 157\*-213" 274\*-334" 380\*-438"

Intra-L (C23-C104) 23\*-88" 136\*-196"

23"-88" 136"-196"

Inter-H-L (h 5-CL 126) 233-216" 233"-216"

Inter-H-H (h 11, h 14) 239-239" 242-242"

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

Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamy (pE, 5-oxoprolyle) / piroglutamilo

(pE, 5-oxoprolyle)

H VH Q1: 1, 1"

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

H CH2 N84.4: 310, 310"

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

**resencatinibum**

resencatinib

6-[[{(2R)-2-hydroxy-2-methylbut-3-yn-1-yl]oxy]-4-(6-{6-  
 [(6-methoxypyridin-3-yl)methyl]-3,6-  
 diazabicyclo[3.1.1]heptan-3-yl}pyridin-3-  
 yl)pyrazolo[1,5-a]pyridine-3-carbonitrile  
*tyrosine kinase inhibitor, antineoplastic*

résencatinib

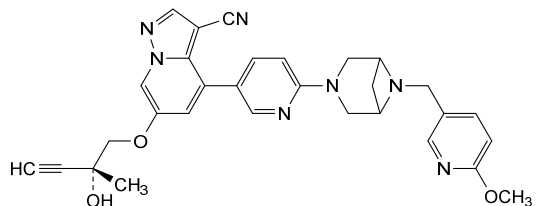
6-[[{(2R)-2-hydroxy-2-méthylbut-3-yn-1-yl]oxy]-4-(6-{6-  
 [(6-méthoxypyridin-3-yl)méthyl]-3,6-  
 diazabicyclo[3.1.1]heptan-3-yl}pyridin-3-  
 yl)pyrazolo[1,5-a]pyridine-3-carbonitrile  
*inhibiteur de tyrosine kinase, antinéoplasique*

resencatinib

6-[[{(2R)-2-hidroxi-2-metilbut-3-in-1-il]oxi]-4-(6-{6-  
 metoxipiridin-3-il}metil]-3,6-diazabicyclo[3.1.1]heptan-3-  
 il)piridin-3-il)pirazolo[1,5-a]piridina-3-carbonitrilo  
*inhibidor de tirosina kinasa, antineoplásico*

C<sub>30</sub>H<sub>29</sub>N<sub>7</sub>O<sub>3</sub>

2546117-79-5





**retatrutidum**

retatrutide

L-tyrosyl-2-methylalanyl-L-glutaminyglycyl-L-threonyl-L-phenylalanyl-L-threonyl-L-seryl-L- $\alpha$ -aspartyl-L-tyrosyl-L-seryl-L-isooleucyl-2-methyl-L-leucyl-L-leucyl-L- $\alpha$ -aspartyl-L-lysyl- $N^6$ -{2-[2-(2-{[N-(19-carboxynonadecanoyl)-L- $\gamma$ -glutamyl]amino}ethoxy)ethoxy]acetyl}-L-lysyl-L-alanyl-L-glutaminy-2-methylalanyl-L-alanyl-L-phenylalanyl-L-isooleucyl-L- $\alpha$ -glutamyl-L-tyrosyl-L-leucyl-L-leucyl-L- $\alpha$ -glutamylglycylglycyl-L-prolyl-L-seryl-L-serylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-serinamide  
*glucagon, gastric inhibitory polypeptide (GIP) and glucagon-like peptide 1 (GLP-1) receptors agonist*

rétatrutide

L-tyrosyl-2-méthylalanyl-L-glutaminyglycyl-L-thréonyl-L-phénylalanyl-L-thréonyl-L-séryl-L- $\alpha$ -aspartyl-L-tyrosyl-L-séryl-L-isooleucyl-2-méthyl-L-leucyl-L-leucyl-L- $\alpha$ -aspartyl-L-lysyl- $N^6$ -{2-[2-(2-{[N-(19-carboxynonadécanoyl)-L- $\gamma$ -glutamyl]amino}éthoxy)éthoxy]acétyl}-L-lysyl-L-alanyl-L-glutaminy-2-méthylalanyl-L-alanyl-L-phénylalanyl-L-isooleucyl-L- $\alpha$ -glutamyl-L-tyrosyl-L-leucyl-L-leucyl-L- $\alpha$ -glutamylglycylglycyl-L-prolyl-L-séryl-L-sérylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-sérinamide  
*agoniste des récepteurs du glucagon, du peptide insulinotrope dépendant du glucose (GIP) et du peptide-1 d'action type glucagon (GLP-1)*

retatrutida

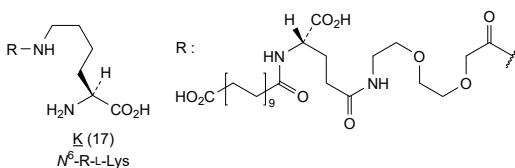
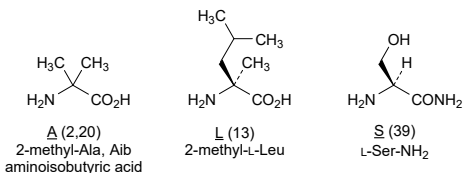
L-tirosil-2-metilalanil-L-glutaminilglicil-L-treonil-L-fenilalanil-L-treonil-L-seril-L- $\alpha$ -aspartil-L-tirosil-L-seril-L-isooleucil-2-metil-L-leucil-L-leucil-L- $\alpha$ -aspartil-L-lisil- $N^6$ -{2-[2-(2-{[N-(19-carboxinonadecanoil)-L- $\gamma$ -glutamyl]amino}etoxi)etoxi]acetil}-L-lisil-L-alanil-L-glutaminil-2-metilalanil-L-alanil-L-fenilalanil-L-isooleucil-L- $\alpha$ -glutamil-L-tyrosil-L-leucil-L-leucil-L- $\alpha$ -glutamilglicilglicil-L-proilil-L-seril-L-serilglicil-L-alanil-L-proilil-L-proilil-L-proilil-L-serinamida  
*agonista de los receptores del glucagón, del péptido insulinotrópico dependiente de la glucosa y del péptido similar al glucagón (GLP-1)*

C<sub>221</sub>H<sub>342</sub>N<sub>46</sub>O<sub>68</sub>

2381089-83-2

YAQGTFTSDY SILLDKKAQA AFIEYLLEGG PSSGAPPPS 39

Modified residues / Résidus modifiés / Restos modificados



**rildinadstrocelum**

rildinadstrocel

allogeneic mesenchymal stromal cells (MSC) prepared from subcutaneous adipose tissue of healthy donors, collected by liposuction. The adipose tissue is digested and the released cells placed in culture media containing bovine serum albumin (BSA), fetal bovine serum (FBS), hydrocortisone, recombinant human epidermal growth factor (rh-EGF), recombinant human fibroblast growth factor (rh-FGF), recombinant human transferrin and insulin, heparin and L-alanyl-L-glutamine. The cells are frozen to generate a master cell bank (MCB) at an early passage, and then resuscitated and culture-expanded. The cells express mesenchymal stromal cell marker cluster of differentiation 73 (CD73), CD90, and CD105 (> 80%) and do not express human leukocyte antigen-DR isotype (HLA DR), CD34, CD11b, CD19, and CD45 (<5%). Resting cells are expressing CD274 (PDL1, >2%). The activated cells secrete vascular endothelial growth factor (VEGF) and upregulate expression of indoleamine 2,3-dioxygenase 1 (IDO1) mRNA when activated *in vitro*.  
*cell therapy (anti-inflammatory)*

rildinadstrocel

cellules stromales mésenchymateuses (MSC) allogènes préparées à partir du tissu adipeux sous-cutané de donneurs sains, prélevé par liposuction. Le tissu adipeux est digéré et les cellules libérées sont placées dans des milieux de culture contenant de l'albumine de sérum bovin (BSA), du sérum bovin fœtal (FBS), de l'hydrocortisone, du facteur de croissance épidermique humain recombinant (rh-EGF), du facteur de croissance des fibroblastes humain recombinant (rh-FGF), de la transferrine humaine recombinante et de l'insuline, de l'héparine et de la L-alanyl-L-glutamine. Les cellules sont congelées pour générer une banque cellulaire primaire (MCB) lors d'un passage précoce, puis ressuscitées et amplifiées en culture. Les cellules expriment les marqueurs de la classe de différenciation 73 (CD73) des cellules stromales mésenchymateuses, CD90 et CD105 (>80%) et n'expriment pas l'antigène leucocytaire humain - isotype DR (HLA DR), CD34, CD11b, CD19 et CD45 (<5%). Les cellules au repos expriment CD274 (PDL1, >2%). Les cellules activées sécrètent le facteur de croissance endothélial vasculaire (VEGF) et régulent à la hausse l'expression de l'ARNm de l'indoleamine 2,3-dioxygénase 1 (IDO1) lorsqu'elles sont activées *in vitro*.  
*thérapie cellulaire (anti-inflammatoire)*

rildinadstrocel

células estromales mesenquimales (MSC) alogénicas preparadas a partir de tejido adiposo subcutáneo de donantes sanos, obtenido por liposucción. El tejido adiposo se digiere y las células liberadas se ponen en medio de cultivo que contiene albúmina sérica bovina (BSA), suero bovino fetal (FBS), hidrocortisona, factor de crecimiento epidérmico humano recombinante (rh-EGF), factor de crecimiento de fibroblastos humano recombinante (rh-FGF), transferrina e insulina humanas recombinantes, heparina y L-alanil-L-glutamina. Las células se congelan para generar un banco de células maestro (MCB) en un pase temprano y después se resucitan y se expanden en cultivo. Las células expresan los marcadores de células estromales mesenquimales, grupo de diferenciación 73 (CD73), CD90 y CD105 (>80%) y no expresan el antígeno común leucocitario - isotipo DR (HLA DR), CD34, CD11b, CD19 y CD45 (<5%). Las células en reposo expresan CD274 (PDL1, >2%). Las células activadas secretan factor de crecimiento del endotelio vascular (VEGF) y aumentan la expresión de ARNm de indoleamina 2,3-dioxygenasa 1 (IDO1) cuando se activan *in vitro*.  
*terapia celular (antiinflamatorio)*

**riliprubartum #**

riliprubart

immunoglobulin G4-kappa, anti-[*Homo sapiens* C1S (complement C1s)], chimeric monoclonal antibody;  
 gamma4 heavy chain chimeric (1-446) [VH Musmus/Homsap (*Mus musculus* IGHV14-3\*02 (82.7%) -(IGHD) -IGHJ2\*01 (92.9%)/*Homo sapiens* IGHV1-46\*02 (75.5%) -(IGHD) -IGHJ4\*01 (92.9%) L123>T (114)), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10, G4v3 CH2 E1.2, G4v24 CH3 L107, S114 (CH1 (120-217), hinge 1-12 S10>P (227) (218-229), CH2 L1.2>E (234), L92 (308) (230-339), CH3 M107>L (427), N114>S (433) (340-444), CHS (445-446)) (120-446)], (133-218')-disulfide with kappa light chain chimeric (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-4\*01 (88.9%) -IGKJ1\*01 (91.7%)/*Homo sapiens* IGKV4-1\*01 (74.3%) -IGKJ4\*01 (100%)), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218)]; dimer (225-225'::228-228')-bisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa  
*immunosuppressant*

riliprubart

immunoglobuline G4-kappa, anti-[*Homo sapiens* C1S (complément C1s)], anticorps monoclonal chimérique;  
 chaîne lourde gamma4 chimérique (1-446) [VH Musmus/Homsap (*Mus musculus* IGHV14-3\*02 (82.7%) -(IGHD) -IGHJ2\*01 (92.9%)/*Homo sapiens* IGHV1-46\*02 (75.5%) -(IGHD) -IGHJ4\*01 (92.9%) L123>T (114)), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10, G4v3 CH2 E1.2, G4v24 CH3 L107, S114 (CH1 (120-217), charnière 1-12 S10>P (227) (218-229), CH2 L1.2>E (234), L92 (308) (230-339), CH3 M107>L (427), N114>S (433) (340-444), CHS (445-446)) (120-446)], (133-218')-disulfure avec la chaîne légère kappa chimérique (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-4\*01 (88.9%) -IGKJ1\*01 (91.7%)/*Homo sapiens* IGKV4-1\*01 (74.3%) -IGKJ4\*01 (100%)), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218)]; dimère (225-225'::228-228')-bisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa  
*immunosuppresseur*

riliprubart

immunoglobulina G4-kappa, anti-[*Homo sapiens* C1S (complemento C1s)], anticuerpo monoclonal quimérico;  
 cadena pesada gamma4 quimérica (1-446) [VH Musmus/Homsap (*Mus musculus* IGHV14-3\*02 (82.7%) -(IGHD) -IGHJ2\*01 (92.9%)/*Homo sapiens* IGHV1-46\*02 (75.5%) -(IGHD) -IGHJ4\*01 (92.9%) L123>T (114)), CDR-IMGT [8.7.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10, G4v3 CH2 E1.2, G4v24 CH3 L107, S114 (CH1 (120-217), bisagra 1-12 S10>P (227) (218-229), CH2 L1.2>E (234), L92 (308) (230-339), CH3 M107>L (427), N114>S (433) (340-444), CHS (445-446)) (120-446)], (133-218')-disulfuro con la cadena ligera kappa quimérica (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-4\*01 (88.9%) -IGKJ1\*01 (91.7%)/*Homo sapiens* IGKV4-1\*01 (74.3%) -IGKJ4\*01 (100%)), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218)]; dímero (225-225'::228-228')-bisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa  
*immunosupresor*

**Heavy chain / Chaîne lourde / Cadena pesada**  
 QVQLVQSGAE VKKPGASVKL SCTASGFNIK DDYIHVWKQA PGQGLEWIGR 50  
 IDPADGHTKY APKFQVKVTI TADTSTSTAY LELSSLRSED TAVYYCARYG 100  
 YGREVFDYWG QGTTVTVSSA STKGPSVFPPL APCSRSTSES TAALGCLVKD 150  
 YFPEPVTVSW NSGALTSGVH TFPVAVLQSSG LYSLSVSVTV PSSSLGKTKY 200  
 TCNVDPKPSN TKVDKRVESK YGPPCPPCA PEFEGGSPVF LFPKPKDYL 250  
 MISRTPEVTC VVVDVSDQED EVQFNWYVDG VEVHNAKTKP REEQFNSTYR 300  
 VVSVLTVLHQ DWLNGKEYKC KVSNGKLPSS IEKTIKAKG QPREPQVYTL 350  
 PPSQEEMTKN QVSLTCLVKG FYPDSIAVEW ESNQGFENNY KTTFPVLDS 400  
 GSFFLYSRLT VDKSRWQEGN VFSCSVLHEA LHSHTYQKSL SLSLKG 446

**Light chain / Chaîne légère / Cadena ligera**  
 DIVLTQSPDS LAVSLGERAT ISCKASQSGVD YDGDSYMNWY QKPKGQPPKI 50  
 LYDASNLES GIPARFSGSG SGTDFLTITIS SLEPEDFAIY XCQQSNEDPW 100  
 TFGGGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150  
 QMKVDNALQS 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) 22-96 146-202 260-320 366-424  
 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 8, h 11) 225-225" 228-228"

**N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutamilo N-terminal**  
 Q > pyroglutamyl (pE, 5-oxoprollyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)  
 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 biantenarijos complejos fucosilados.

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

**rinvecalinasum alfa #**  
 rinvecalinase alfa

human kallikrein-1 (tissue kallikrein, KLK1, EC:3.4.21.35) mature form, engineered variant (E<sup>121</sup>>Q, A<sup>164</sup>>V) produced in Chinese hamster ovary (CHO) cells, glycoform alfa *kallikrein-1 analogue*

rinvécalinase alfa

forme mature de la kallikréine-1 humaine (kallikréine tissulaire, KLK1, EC:3.4.21.35), variant modifié (E<sup>121</sup>>Q, A<sup>164</sup>>V) produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa *analogue de la kallikréine-1*

rinvecalinasa alfa

calicreína-1 humana (calicreína tisular, KLK1, EC:3.4.21.35) forma madura, variante diseñada (E<sup>121</sup>>Q, A<sup>164</sup>>V) producida en células ováricas de hámster Chino (CHO), forma glicosilada alfa *análogo de la calicreína-1*

2419877-37-3

**Sequence / Séquence / Secuencia**  
 IVGGWECEQH SQPWQAALYH FSTFQCGGIL VHRQWLTAA HCISDNYQLW 50  
 LGRHNLFDDE NTAQFVHVSE SFPHPGFNMS LLENHTRQAD EDYSHDLMLL 100  
 RLTEPADTIT DAVKVVLEPT QEPEVGSSTC ASGWGSIIEP NFSFPDDLQC 150  
 VDLKILFNDE CKKVAHQKVT DFMLCVGHLE GGDTCVGDSD GGFLMCDGVL 200  
 QGVTSWGYVP CGTPNKPSVA VRVLSVYKWI EDTIAENS 238

**Mutation / Mutation / Mutación**  
 E121>Q, A164>V

**Post-translational modifications**  
**Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro**  
 7-150, 7-186, 7-211, 26-42, 129-196, 150-186, 150-211, 161-175, 175-186, 186-211

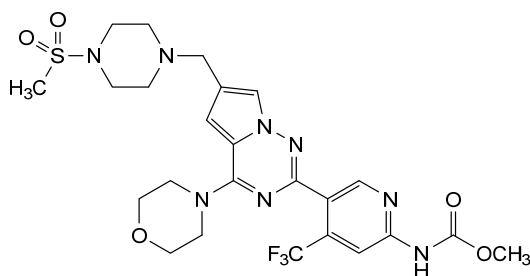
**Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación**  
 N78, N84, N141 (partially glycosylated)

**risovalisibum**

- risovalisib methyl {5-[6-{{4-(methanesulfonyl)piperazin-1-yl}methyl}-4-(morpholin-4-yl)pyrrolo[2,1-f][1,2,4]triazin-2-yl]-4-(trifluoromethyl)pyridine-2-yl}carbamate  
*phosphatidylinositol 3-kinase (PI3K) inhibitor, antineoplastic*
- risovalisib {5-[6-{{4-(méthanesulfonyl)pipérazin-1-yl}méthyle}-4-(morpholin-4-yl)pyrrolo[2,1-f][1,2,4]triazin-2-yl]-4-(trifluorométhyle)pyridine-2-yl}carbamate de méthyle  
*inhibiteur de phosphatidylinositol 3-kinase (PI3K), antinéoplasique*
- risovalisib {5-[6-{{4-(metanosulfonyl)piperazin-1-il}metil}-4-(morfolin-4-il)pirrolo[2,1-f][1,2,4]triazin-2-il]-4-(trifluorometil)piridina-2-il}carbamato de metilo  
*inhibidor de fosfatidilinositol 3-kinasa (PI3K), antineoplásico*

C<sub>24</sub>H<sub>29</sub>F<sub>3</sub>N<sub>8</sub>O<sub>5</sub>S

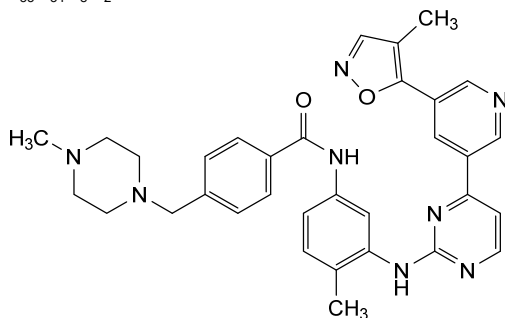
1494684-28-4

**risvodetinibum**

- risvodetinib *N*-[4-methyl-3-{{4-[5-(4-methyl-1,2-oxazol-5-yl)pyridin-3-yl]pyrimidin-2-yl}amino}phenyl]-4-[(4-methylpiperazin-1-yl)methyl]benzamide  
*tyrosine kinase inhibitor*
- risvodétinib *N*-[4-méthyl-3-{{4-[5-(4-méthyl-1,2-oxazol-5-yl)pyridin-3-yl]pyrimidin-2-yl}amino}phényl]-4-[(4-méthylpipérazin-1-yl)méthyle]benzamide  
*inhibiteur de tyrosine kinase*
- risvodetinib *N*-[4-metil-3-{{4-[5-(4-metil-1,2-oxazol-5-il)piridin-3-il]pirimidin-2-il}amino}fenil]-4-[(4-metilpiperazin-1-il)metil]benzamida  
*inhibidor de tirosina kinasa*

C<sub>33</sub>H<sub>34</sub>N<sub>8</sub>O<sub>2</sub>

2031185-00-7



**ritivixibat**

ritivixibat

3-[[3,3-dibutyl-7-(methylsulfanyl)-1,1-dioxo-5-phenyl-2,3,4,5-tetrahydro-1,2,5-benzothiadiazepin-8-yl]oxy]-propanoic acid

*ileal bile acid transporter inhibitor*

ritivixibat

acide 3-[[3,3-dibutyl-7-(méthylsulfanyl)-1,1-dioxo-5-phényl-2,3,4,5-tétrahydro-1,2,5-benzothiadiazépin-8-yl]oxy]-propanoïque

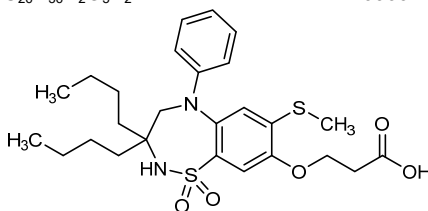
*inhibiteur du transporteur iléal d'acides biliaires*

ritivixibat

ácido 3-[[3,3-dibutil-7-(metilsulfanil)-1,1-dioxo-5-fenil-2,3,4,5-tetrahidro-1,2,5-benzotiadiazepin-8-il]oxi]-propanoico

*inhibidor del transportador ilíaco de ácidos biliares*C<sub>26</sub>H<sub>36</sub>N<sub>2</sub>O<sub>5</sub>S<sub>2</sub>

2460667-52-9

**rizedisbenum**

rizedisben

2-(9<sup>4</sup>-amino-6<sup>3</sup>-methoxy-2,2-dioxo-2-thia-1(1)-piperazina-3(1,4),6(1,4),9(1,4)-tribenzenanonaphane-4,7-dien-9<sup>4</sup>-yl)ethanol*diagnostic imaging agent*

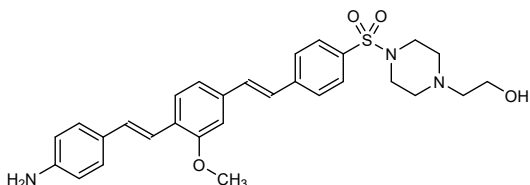
rizédisbène

2-(9<sup>4</sup>-amino-6<sup>3</sup>-méthoxy-2,2-dioxo-2-thia-1(1)-pipérazina-3(1,4),6(1,4),9(1,4)-tribenzenanonaphane-4,7-dién-9<sup>4</sup>-yl)éthanol*agent diagnostique*

rizedisbén

2-(9<sup>4</sup>-amino-6<sup>3</sup>-metoxi-2,2-dioxo-2-tia-1(1)-piperazina-3(1,4),6(1,4),9(1,4)-tribencenanonafano-4,7-dien-9<sup>4</sup>-il)etanol*agente de diagnóstico*C<sub>29</sub>H<sub>33</sub>N<sub>3</sub>O<sub>4</sub>S

1311570-07-6

**rolistobartum #**

rolistobart

immunoglobulin G4-kappa, anti-[*Homo sapiens* LILRB4 (leukocyte immunoglobulin like receptor B4, ILT3, LIR-5, CD85k)], humanized monoclonal antibody;

- gamma4 heavy chain humanized (1-449) [VH (*Homo sapiens* IGHV3-7\*01 (86.7%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (123-220), hinge 1-12 S10>P (230) (221-232), CH2 L92 (311) (233-342), CH3 (343-447), CHS (448-449)) (123-449)], (136-218')-disulfide with kappa light chain humanized (1'-218') [V-KAPPA (*Homo sapiens* IGKV1-9\*03 (81.6%) -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 (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa  
*immunostimulant, antineoplastic*
- rolistobart  
immunoglobuline G4-kappa, anti-[*Homo sapiens* LILRB4 (récepteur similaire à l'immunoglobuline leucocytaire B4, ILT3, LIR-5, CD85k)], anticorps monoclonal humanisé;  
chaîne lourde gamma4 humanisée (1-449) [VH (*Homo sapiens* IGHV3-7\*01 (86.7%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (123-220), charnière 1-12 S10>P (230) (221-232), CH2 L92 (311) (233-342), CH3 (343-447), CHS (448-449)) (123-449)], (136-218')-disulfure avec la chaîne légère kappa humanisée (1'-218') [V-KAPPA (*Homo sapiens* IGKV1-9\*03 (81.6%) -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 (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa  
*immunostimulant, antinéoplasique*
- rolistobart  
immunoglobulina G4-kappa, anti-[*Homo sapiens* LILRB4 (receptor B4 inmunoglobulina tipo de los leucocitos, ILT3, LIR-5, CD85k)], anticuerpo monoclonal humanizado;  
cadena pesada gamma4 humanizada (1-449) [VH (*Homo sapiens* IGHV3-7\*01 (86.7%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (123-220), bisagra 1-12 S10>P (230) (221-232), CH2 L92 (311) (233-342), CH3 (343-447), CHS (448-449)) (123-449)], (136-218')-disulfuro com la cadena ligera kappa humanizada (1'-218') [V-KAPPA (*Homo sapiens* IGKV1-9\*03 (81.6%) -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 (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa  
*inmunostimulante, antineoplásico*

2723442-10-0

## Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG LVQPFGSLRL SCAASGFTFS NYGMSWVRQA PGKGLEWVAT 50  
 ISGGGDYTNV PDSVRRFTI SRDNAKNSLY LQMNSLRAED TAVYICGRRL 100  
 WFRSLYAMD YWGQGLTVTV SSASTKGPSV FPLAPCSRST SESTAALGCL 150  
 VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTFPSSSLGT 200  
 KTYTCNVDPHK PSNTKVDKRV ESKYGPCCPP CPAPEFLGGP SVFLFPPKPK 250  
 DTLMISRTPE VTCVVVDVDSQ EDEPVQFNWY VDGVEVHNAK TKPREEQFNS 300  
 TYRVVSVLTV LHQDNLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV 350  
 YTLPPSQEEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTTPVL 400  
 DSDGSFFLYS RLTVDKSRWQ EGNVFSQCSVM HEALHNHYTQ KSLSLSLGK 449

## Light chain / Chaîne légère / Cadena ligera

DIQLTQSPSS LSASVGDRTV ITCRASEKVD SFGQSFMHVY QOKPGKAPKL 50  
 LIYLTSNLDG GVPSPRFSGSG SGTDFTLTIS SLQPEDFATY YCQQNEDPY 100  
 TFGQGTKEII KRTVAAPSVF IFPPSDEQLK SGTASVCLL NNFVYPREAKV 150  
 QWKVDNALQS GNSQESVTEQ DSKDSTYSLT STLTLKADY EKHKVYACEV 200  
 THQGLSSPVT KSFNRGEC

## Post-translational modifications

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

Intra-H (C23-C104) 22-96 149-205 263-323 369-427  
 22"-96" 149"-205" 263"-323" 369"-427"  
 Intra-L (C23-C104) 23"-92" 138"-198"  
 23"-92" 138"-198"

Inter-H-L (CH1 10-CL 126) 136-218 136"-218"

Inter-H-H (h 8, h 11) 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 biantennarios complejos fucosilados.

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

rolusafine

2-(4-ethylphenoxy)-4'-methoxy-3,3'-bipyridine  
*antifungal*

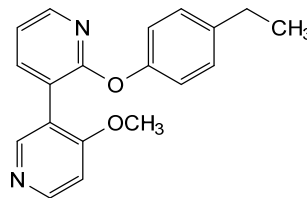
rolusafine

2-(4-éthylphénoxy)-4'-méthoxy-3,3'-bipyridine  
*antifongique*

rolusafina

2-(4-etilfenoxi)-4'-metoxi-3,3'-bipiridina  
*antifúngico*C<sub>19</sub>H<sub>18</sub>N<sub>2</sub>O<sub>2</sub>

2089153-78-4

**rovaliditininibum**

rovaliditininib

(3*R*)-3-[3-amino-4-(7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)-1*H*-pyrazol-1-yl]-3-cyclopentylpropanenitrile  
*Janus kinase inhibitor, anti-inflammatory*

rovaliditininib

(3*R*)-3-[3-amino-4-(7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)-1*H*-pyrazol-1-yl]-3-cyclopentylpropanenitrile  
*inhibiteur de la kinase de Janus, anti-inflammatoire*

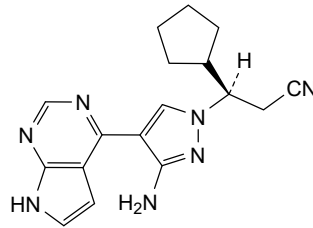
rovaliditininib

(3*R*)-3-[3-amino-4-(7*H*-pirrolo[2,3-*d*]pirimidin-4-il)-1*H*-pirazol-1-il]-3-ciclopentilpropanenitrilo  
*inhibidor de la kinasa de Janus, antiinflamatorio*



C<sub>17</sub>H<sub>19</sub>N<sub>7</sub>

1948242-59-8



**sabestomigum #**  
sabestomig

immunoglobulin G1-kappa/lambda, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD1, PD-1, CD279) and HAVCR2 (hepatitis A virus cellular receptor 2, T cell immunoglobulin and mucin domains family member 3, TIM3, TIM-3, TIMD3, CD366)], humanized and *Homo sapiens* monoclonal antibody, bispecific, bivalent; gamma1 heavy chain anti-PDCD1 humanized (1-452) [VH humanized (*Homo sapiens* IGHV3-48\*01 (92.9%) -(IGHD) - IGHJ4\*01 (93.3%) L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1\*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120 (219) (123-220), hinge 1-15 (221-235), CH2 L1.3>F (239), L1.2>E (240), P116>S (336) (236-345), CH3 E12 (361), M14 (363), Y5>C (354), T22>S (371), L24>A (373), Y86>V (412) (346-450), CHS (451-452)) (123-452)], (225-219')-disulfide with kappa light chain anti-PDCD1 humanized (1'-219') [V-KAPPA humanized (*Homo sapiens* IGKV3D-7\*01 (81.1%) -IGKJ2\*02 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; gamma1 heavy chain anti-HAVCR2 *Homo sapiens* (1"-452") [VH (*Homo sapiens* IGHV3-23\*01 (99.0%) -(IGHD) - IGHJ4\*01 (93.3%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1"-122") -*Homo sapiens* IGHG1\*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v32 CH3 W22 (knob), G1v58 CH1 C5, h V5 (CH1 F5>C (131), R120 (219) (123"-220"), hinge 1-15 C5>V (225)(221"-235"), CH2 L1.3>F (239), L1.2>E (240), P116>S (336) (236"-345"), CH3 S10>C (359), E12 (361), M14 (363), T22>W (371) (346"-450"), CHS (451"-452")) (123"-452"), (131"-123")-disulfide with lambda light chain anti-HAVCR2 *Homo sapiens* (1'''-214''') [V-LAMBDA (*Homo sapiens* IGLV3-21\*01 (94.8%) -IGKJ2\*02 (90.9%), CDR-IMGT [6.3.11] (26-31.49-51.88-98)) (1'''-108''') -*Homo sapiens* IGLC2\*01 (98.1%) LC2v58 C10, V126 (S10>C (123), C126>V (213)) (109'''-214''')]; dimer (231-231":234-234":354-359)-trisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CATS, glycoform alfa *immunostimulant, antineoplastic*

sabestomig

immunoglobuline G1-kappa/lambda, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD1, PD-1, CD279) et anti-[*Homo sapiens* HAVCR2 (récepteur cellulaire 2 du virus de l'hépatite A, membre 3 de la famille à domaines immunoglobuline et mucine des cellules T, TIM3, TIM-3, TIMD3, CD366)], anticorps monoclonal humanisé et *Homo sapiens*, bispécifique, bivalent;

chaîne lourde gamma1 anti-PDCD1 humanisée (1-452) [VH humanisé (*Homo sapiens* IGHV3-48\*01 (92.9%) -(IGHD) -IGHJ4\*01 (93.3%) L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1\*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120 (219) (123-220), charnière 1-15 (221-235), CH2 L1.3>F (239), L1.2>E (240), P116>S (336) (236-345), CH3 Y5>C (354), E12 (361), M14 (363), T22>S (371), L24>A (373), Y86>V (412) (346-450), CHS (451-452)) (123-452)], (225-219')-disulfure avec la chaîne légère kappa anti-PDCD1 humanisée (1'-219') [V-KAPPA humanisé (*Homo sapiens* IGKV3D-7\*01 (81.1%) -IGKJ2\*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; chaîne lourde gamma1 anti- HAVCR2 *Homo sapiens* (1"-452") [VH (*Homo sapiens* IGHV3-23\*01 (99.0%) -(IGHD) -IGHJ4\*01 (93.3%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1"-122") -*Homo sapiens* IGHG1\*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v32 CH3 W22 (knob), G1v58 CH1 C5, h V5 (CH1 F5>C (131), R120 (219) (123"-220")), charnière 1-15 C5>V (225) (221"-235"), CH2 L1.3>F (239), L1.2>E (240), P116>S (336) (236"-345"), CH3 S10>C (359), E12 (361), M14 (363), T22>W (371) (346"-450"), CHS (451"-452")) (123"-452)], (131"-123")-disulfure avec la chaîne légère lambda anti-HAVCR2 *Homo sapiens* (1""-214"" [V-LAMBDA (*Homo sapiens* IGLV3-21\*01 (94.8%) -IGKJ2\*01 (90.9%), CDR-IMGT [6.3.11] (26-31.49-51.88-98)) (1""-108"" -*Homo sapiens* IGLC2\*01 (98.1%) LC2v58 C10, V126 (S10>C (123), C126>V (213)) (109""-214"")); dimère (231-231"":234-234"":354-359""))-trisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CATS, glycoforme alfa  
*immunostimulant, antinéoplasique*

sabestomig immunoglobulina G1-kappa/lambda, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD1, PD-1, CD279) y anti-[*Homo sapiens* HAVCR2 (receptor celular 2 del virus de la hepatitis A, miembro 3 de la familia con dominios inmunoglobulina y mucina de las células T, TIM3, TIM-3, TIMD3, CD366)], anticuerpo monoclonal humanizado y *Homo sapiens*, biespecífico, bivalente;  
cadena pesada gamma1 anti-PDCD1 humanizada (1-452) [VH humanizado (*Homo sapiens* IGHV3-48\*01 (92.9%) -(IGHD) -IGHJ4\*01 (93.3%) L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1\*03, G1m3, nG1 m1CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120 (219) (123-220), bisagra 1-15 (221-235), CH2 L1.3>F (239), L1.2>E (240), P116>S (336) (236-345), CH3 Y5>C (354), E12 (361), M14 (363), T22>S (371), L24>A (373), Y86>V (412) (346-450), CHS (451-452)) (123-452)], (225-219')-disulfuro con la cadena ligera kappa anti-PDCD1 humanizada (1'-219') [V-KAPPA humanizado (*Homo sapiens* IGKV3D-7\*01 (81.1%) -IGKJ2\*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; cadena pesada gamma1 anti-HAVCR2 *Homo sapiens* (1"-452") [VH (*Homo sapiens* IGHV3-23\*01 (99.0%) -(IGHD) -IGHJ4\*01 (93.3%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1"-122") -*Homo sapiens* IGHG1\*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v32 CH3 W22 (knob), G1v58 CH1 C5, h V5 (CH1 F5>C (131), R120 (219) (123"-220")), bisagra 1-15 C5>V (225) (221"-235"), CH2 L1.3>F (239), L1.2>E (240), P116>S (336) (236"-345"), CH3 S10>C (359), E12 (361), M14 (363), T22>W (371) (346"-450"), CHS (451"-452")) (123"-452)], (131"-123")-disulfuro con la cadena ligera lambda anti-HAVCR2 *Homo sapiens* (1""-214"" [V-LAMBDA (*Homo sapiens* IGLV3-21\*01 (94.8%) -IGKJ2\*01 (90.9%), CDR-IMGT [6.3.11] (26-31.49-51.88-98)) (1""-108"" -*Homo sapiens* IGLC2\*01 (98.1%) LC2v58 C10, V126 (S10>C (123), C126>V (213)) (109""-214"")); dímero (231-231"":234-234"":354-359""))-trisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CATS, forma glicosilada alfa  
*inmunostimulante, antineoplásico*

Heavy chain / Chaîne lourde / Cadena pesada: anti-PDCD1 (H)

EVQLVESGGG	LVQPFGSLRL	SCAASGFTFS	DYGMHWVRQA	PGKGLEWVAY	50
ISSGSGYTYIS	ADSVKGRFTI	SRDNAKNSLY	LQMNSLRAED	TAVYVCARRA	100
PNSFYEYFDF	YWGQGTIVTV	SSASTKGPSV	FPLAPSSKST	SGGTAALGCL	150
VKDYFPEFVIT	VSNWNGALTS	GVHTFFPAVLQ	SSGLYSLSSV	VTVPSSSLGT	200
QTYICNVNHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPEFE	GGPSVFLFPP	250
KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPASIEKT	ISKAKGQPRE	350
PQVCTLPFSR	EMTKNQVSL	SCAVKGFYPS	DIAVEWESNG	QPENNYKTPP	400
PVLDSDGSFF	LVSKLTVDKS	RWQQGNVFC	SVMHEALHNN	YTQKLSLSLP	450
GK					452

Light chain / Chaîne légère / Cadena ligera: anti-PDCD1 kappa (L')

QIVLTQSFAT	LSPSPGERAT	LSCSASSKHT	NLYWSRHMVW	YQQKPGQAPR	50
LLIYLTSNRA	TGIPARFSGS	GSQDTFLTI	SSLEPEDFAV	YYCQQNSNP	100
FTFQQGTKLE	IKRTVAAPSV	FIFPPSDEQL	KSGTASVVCCL	LNIFYPREAK	150
VQMKVDNALQ	SGNSQESVTE	QDSKDYSTYS	SSTLTLSKAD	YEKHKVYACE	200
VTHQGLSSPV	TKSFRNGEC				219

Heavy chain / Chaîne lourde / Cadena pesada: anti-HAVCR2 (H')

EVQLLESGGG	LVQPFGSLRL	SCAASGFTFS	SYAMSWVRQA	PGKGLEWVSA	50
ISGSGGTYIY	ADSVKGRFTI	SRDNSKNTLY	LQMNSLRAED	TAVYVCARGS	100
YGYTYGNVFE	YWGQGTIVTV	SSASTKGPSV	CPLAPSSKST	SGGTAALGCL	150
VKDYFPEFVIT	VSNWNGALTS	GVHTFFPAVLQ	SSGLYSLSSV	VTVPSSSLGT	200
QTYICNVNHK	PSNTKVDKRV	EPKSVDRKHT	CPPCPAPEFE	GGPSVFLFPP	250
KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPASIEKT	ISKAKGQPRE	350
PQVYVTLPCR	EMTKNQVSL	WCLVKGFYPS	DIAVEWESNG	QPENNYKTPP	400
PVLDSDGSFF	LYSKLTVDKS	RWQQGNVFC	SVMHEALHNN	YTQKLSLSLP	450
GK					452

Light chain / Chaîne légère / Cadena ligera: anti-HAVCR2 lambda (L'')

SYVLTQPFPSV	SVAPGKTARI	TCGGDNIGGK	SVHWYQQKFG	QAPVLYIYYD	50
SDRPSGIFER	FGSGNSGNTA	TLTISRVEAG	DEADYQCQVL	DRRSDFHFLG	100
GGTKLTVLGG	FKAAPSPTLF	PPCSEELQAN	KATLVCLISD	FYPGAVTVAW	150
KADSSPVKAG	VETTPSKQK	NNKYAASSYL	SLTPEQWKSH	RSYSCQVTHE	200
GSTVEKTVAP	TEVS				214

**Post-translational modifications**

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

Intra-H (C23-C104) 22<sup>o</sup>-96 149-205 266-326 372-430  
 22<sup>o</sup>-96<sup>\*</sup> 149<sup>o</sup>-205<sup>\*</sup> 266<sup>o</sup>-326<sup>o</sup> 372<sup>o</sup>-430<sup>o</sup>

Intra-L (C23-C104) 23<sup>o</sup>-93<sup>o</sup> 139<sup>o</sup>-199<sup>o</sup>  
 22<sup>o</sup>-87<sup>o</sup>m 136<sup>o</sup>-195<sup>o</sup>m

Inter-H-L (CH1 10-CL 126) 225-219<sup>o</sup> (CH1 5-CL 10)\* 131<sup>o</sup>-123<sup>o</sup>Inter-H-H (h 8, h 11) 231-231<sup>o</sup> 234-234<sup>o</sup> (CH3 5-CH3 10)\* 354-359<sup>o</sup>

\*Engineered alternative Inter-H-L (instead of 225<sup>o</sup>-213<sup>o</sup>) and additional Inter-H-H, owing to 4 amino acid changes to cysteinyl.

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

Q &gt; pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyl (pE, 5-oxoprolyl) / piroglutamilo (pE, 5-oxoprolyl)

L VL Q1: 1, 1'

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

H CH2 N84.4: 302, 302<sup>o</sup>

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

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

H CHS K2: 452, 452<sup>o</sup>**sabirnetugum #  
sabirnetug**

immunoglobulin G2-kappa, anti-[*Homo sapiens* APP (amyloid beta A4 precursor protein) Abeta42 and Abeta40 soluble non-fibrillar oligomers], humanized monoclonal antibody;  
 gamma2 heavy chain humanized (1-443) [VH (*Homo sapiens* IGHV3-48\*01 (92.9%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG2\*01, G2m.. CH2 V45.1 (CH1 (118-215), hinge 1-12 (216-227), CH2 V45.1 (278) (228-336), CH3 (337-441), CHS (442-443)) (118-443)], (131-219)-disulfide with kappa light chain humanized (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-28\*01 (89.5%) -IGKJ2\*03 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (219-219<sup>o</sup>:220-220<sup>o</sup>:223-223<sup>o</sup>:226-226<sup>o</sup>)-tetrakisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa  
*clearance of amyloid beta*

sabirnetug

immunoglobuline G2-kappa, anti-[*Homo sapiens* APP (protéine précurseur A4 amyloïde bêta) oligomères solubles non fibrillaires d'Abeta42 et Abeta40], anticorps monoclonal humanisé;  
chaîne lourde gamma2 humanisée (1-443) [VH (*Homo sapiens* IGHV3-48\*01 (92.9%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG2\*01, G2m.. CH2 V45.1 (CH1 (118-215), charnière 1-12 (216-227), CH2 V45.1 (278) (228-336), CH3 (337-441), CHS (442-443)) (118-443)], (131-219')-disulfure avec la chaîne légère kappa humanisée (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-28\*01 (89.5%) -IGKJ2\*03 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (219-219":220-220":223-223":226-226")- tétrakisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa  
*élimination d'amyloïde bêta*

sabirnetug

inmunoglobulina G2-kappa, anti-[*Homo sapiens* APP (proteína precursor 4 amiloide beta) oligómeros solubles no fibrilares de Abeta42 t Abeta40], anticuerpo monoclonal humanizado;  
cadena pesada gamma2 humanizada (1-443) [VH (*Homo sapiens* IGHV3-48\*01 (92.9%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG2\*01, G2m.. CH2 V45.1 (CH1 (118-215), bisagra1-12 (216-227), CH2 V45.1 (278) (228-336), CH3 (337-441), CHS (442-443)) (118-443)], (131-219')-disulfuro con la cadena ligera kappa humanizada (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-28\*01 (89.5%) -IGKJ2\*03 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (219-219":220-220":223-223":226-226")- tetrakisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa  
*eliminación del amiloide beta*

2747959-38-0

Heavy chain / Chaîne lourde / Cadena pesada

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EQQLVESGGG LVPGGSLRL SCAASGFTFS SFGMHWVRQA PGKGLEWVAY 50
ISRGSSIIYY ADTVKGRFTI SRDNARNSLY LQMNSLRAED TAVYYCARGI 100
TTALDYWGQG LTVTVSSAST KGPSVFPFLAP CSRSTSESTA ALGLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPV SNFGTQTYTC 200
NVDHKFSNTK VDKTVERKCC VECPPCPAPP VAGPSVFLFP PKPKDTLMIS 250
RTPVEVTCVVV DVSHEDEPEVQ FNWYVDGVEV HNAKTKPREE QFNSTFRVVS 300
VLTVVHQDWL NGKEYEKCKVS NKGLEPAIEK TISKTKGQPR EPQVYTLPPS 350
REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPMLDSGGSF 400
FLYSKLTVDK SRWQQGNVFS CSMHEALHN HYTKQSLSLG PGK 443
    
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Light chain / Chaîne légère / Cadena ligera

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DVTMTQSPLS LPVTPGEPAS ISCRSSQIV HSGNNTYLEW YLQKPGQSPQ 50
LLIYKASNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCFQGSRLG 100
PSFGGQTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVL LNNFYFREAK 150
VQWVKVDNALQ SGNSQESVTE QDSKDYSL SSTITLSKAD YEKHKVYACE 200
VTHQGLSSEV TKSFNREGC 219
    
```

Post-translational modifications

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

Intra-H (C23-C104) 22-96 144-200 257-317 363-421  
 22"-96" 144"-200" 257"-317" 363"-421"  
 Intra-L (C23-C104) 23'-93' 139'-199'  
 23"-93" 139"-199"  
 Inter-H-L (CH1 10-CL 126) 131-219' 131"-219"  
 Inter-H-H (h 4, h 5, h 8, h11) 219-219" 220-220" 223-223" 226-226"

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal  
 H CHS K2: 443, 443"

**saruparibum**

saruparib

5-{4-[(7-ethyl-5,6-dihydro-6-oxo-1,5-naphthyridin-3-yl)methyl]piperazin-1-yl}-*N*-methylpyridine-2-carboxamide  
*poly (ADP-ribose) polymerase (PARP) inhibitor, antineoplastic*

saruparib

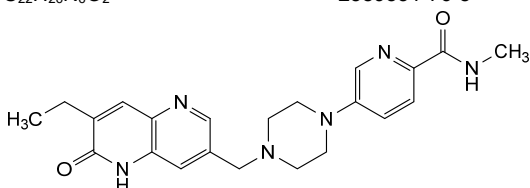
5-{4-[(7-éthyl-5,6-dihydro-6-oxo-1,5-naphtyridin-3-yl)méthyl]pipérazin-1-yl}-*N*-méthylpyridine-2-carboxamide  
*inhibiteur de poly-ADP-ribose polymérase (PARP), antinéoplasique*

saruparib

5-{4-[(7-etil-5,6-dihidro-6-oxo-1,5-naftiridin-3-il)metil]piperazin-1-il}-*N*-metilpiridina-2-carboxamida  
*inhibidor de poli-ADP-ribosa polimerasa (PARP), antineoplásico*

C<sub>22</sub>H<sub>26</sub>N<sub>6</sub>O<sub>2</sub>

2589531-76-8

**sevasemtenum**

sevasemten

2-[(5-fluoropyridin-3-yl)methyl]-6-[2-(2,2,2-trifluoroethoxy)pyrimidin-5-yl]pyridazin-3(2*H*)-one  
*skeletal muscle myosin allosteric inhibitor*

sévasemten

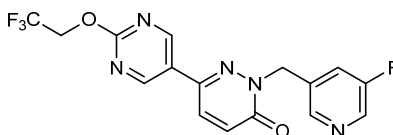
2-[(5-fluoropyridin-3-yl)méthyl]-6-[2-(2,2,2-trifluoroéthoxy)pyrimidin-5-yl]pyridazin-3(2*H*)-one  
*inhibiteur allostérique de la myosine du muscle squelettique*

sevasemtén

2-[(5-fluoropiridin-3-il)metil]-6-[2-(2,2,2-trifluoroetoxi)pirimidin-5-il]piridazin-3(2*H*)-ona  
*inhibidor alostérico de la miosina del músculo esquelético*

C<sub>16</sub>H<sub>11</sub>F<sub>4</sub>N<sub>5</sub>O<sub>2</sub>

2417395-15-2

**sofnobrutinibum**

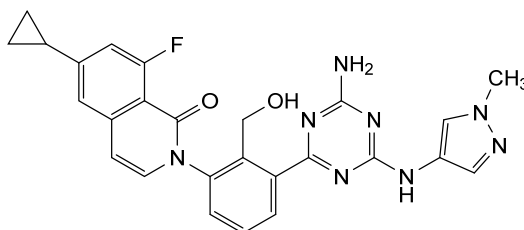
sofnobrutinib

2-[3-{4-amino-6-[(1-methyl-1*H*-pyrazol-4-yl)amino]-1,3,5-triazin-2-yl}-2-(hydroxymethyl)phenyl]-6-cyclopropyl-8-fluoroisoquinolin-1(2*H*)-one  
*Bruton's tyrosine kinase inhibitor, antineoplastic*

- sofno Brutinib 2-[3-[4-amino-6-[(1-méthyl-1*H*-pyrazol-4-yl)amino]-1,3,5-triazin-2-yl]-2-(hydroxyméthyl)phényl]-6-cyclopropyl-8-fluoroisoquinoléin-1(2*H*)-one  
*inhibiteur de la tyrosine kinase de Bruton, antinéoplasique*
- sofno Brutinib 2-[3-[4-amino-6-[(1-metil-1*H*-pirazol-4-il)amino]-1,3,5-triazin-2-il]-2-(hidroximetil)fenil]-6-ciclopropil-8-fluoroisoquinolin-1(2*H*)-ona  
*inhibidor de la tirosina kinasa de Bruton, antineoplásico*

C<sub>26</sub>H<sub>23</sub>N<sub>8</sub>O<sub>2</sub>

1646608-10-7

**sonpiretigenous isteparvovecum #**

- sonpiretigenous isteparvovec recombinant, non-replicating adeno-associated virus serotype 2 (AAV2) vector, encoding a codon-optimized *Chlamydomonas*-derived ambient light-activatable multi-characteristic opsin (MCO) fusion protein with a *Discosoma* red fluorescent bioluminescence reporter (mCherry), under control of the cytomegalovirus (CMV) promoter and human metabotropic glutamate receptor mGluR6 enhancer, terminated with a human growth hormone (hGH) polyadenylation signal, flanked by AAV2 inverted terminal repeats (ITRs)  
*gene therapy (retinal dystrophy)*

- sonpiretigenous isteparvovec vecteur recombinant et non répliquant du virus adéno-associé de sérotype 2 (AAV2), codant une protéine de fusion d'opsine multicaractéristique (MCO) activable par la lumière ambiante dérivée de *Chlamydomonas* aux codons optimisés avec un rapporteur de bioluminescence fluorescent rouge *Discosoma* (mCherry), sous le contrôle du promoteur du cytomégalo virus (CMV) et de l'amplificateur mGluR6 du récepteur métabotrope de glutamate humain, terminé par un signal de polyadénylation de l'hormone de croissance humaine (hGH), flanqué de répétitions terminales inversées (ITR) de l'AAV2  
*thérapie génique (dystrophie rétinienne)*

- sonpiretigenous isteparvovec vector de virus adenoasociado del serotipo 2 (AAV2) recombinante, no replicativo, que codifica, con codones optimizados, una proteína de fusión de la opsina multicaracterística (MCO) activable por luz ambiental derivada de *Chlamydomona* con el reportero de bioluminiscencia fluorescente rojo (mCherry) de *Discosoma*, bajo el control del promotor de citomegalovirus (CMV) y el potenciador del receptor metabotrópico de glutamato humano mGluR6, terminado con una señal de poliadenilación de la hormona de crecimiento humana (hGH), flanqueado por las repeticiones terminales invertidas (ITRs) del AAV2  
*terapia génica (distrofia retiniana)*

2658561-40-9

**sonrotoclaxum**

sonrotoclax

*N*-[4-({[(1*r*,4*r*)-4-hydroxy-4-methylcyclohexyl]methyl}amino)-3-nitrobenzene-1-sulfonyl]-4-(2-{{(2*S*)-2-[2-(propan-2-yl)phenyl]pyrrolidin-1-yl}-7-azaspiro[3.5]nonan-7-yl)-2-[(1*H*-pyrrolo[2,3-*b*]pyridin-5-yl)oxy]benzamide  
*antineoplastique*

sonrotoclax

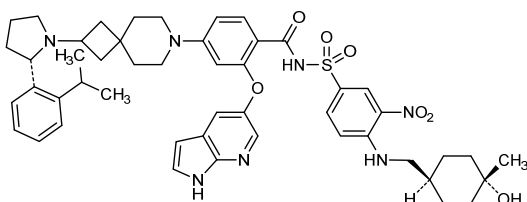
*N*-[4-({[(1*r*,4*r*)-4-hydroxy-4-méthylcyclohexyl]méthyl}amino)-3-nitrobenzène-1-sulfonyl]-4-(2-{{(2*S*)-2-[2-(propan-2-yl)phényl]pyrrolidin-1-yl}-7-azaspiro[3.5]nonan-7-yl)-2-[(1*H*-pyrrolo[2,3-*b*]pyridin-5-yl)oxy]benzamide  
*antinéoplasique*

sonrotoclax

*N*-[4-({[(1*r*,4*r*)-4-hidroxi-4-metilciclohexil]metil}amino)-3-nitrobenzeno-1-sulfonyl]-2-[(1*H*-pirrolo[2,3-*b*]piridin-5-il)oxi]-4-(2-{{(2*S*)-2-[2-(propan-2-il)fenil]pirrolidin-1-il}-7-azaspiro[3.5]nonan-7-il)benzamida  
*antineoplásico*

C<sub>49</sub>H<sub>59</sub>N<sub>7</sub>O<sub>7</sub>S

2383086-06-2

**sotiburafuspum alfa #**

sotiburafusp alfa

humanized vascular endothelial growth factor receptor 1 (VEGFR-1, Fms-like tyrosine kinase 1, FLT-1) extracellular domain fragment (129-228, 1-100 in the current sequence) fused via the peptide linker <sup>101</sup>GGSGGGSGGSGGSGGS<sup>115</sup> to the N-terminus of the heavy chain (116-564) of a humanized immunoglobulin G1-kappa anti-(human programmed cell death 1 ligand 1 (PD-L1, CD274) heavy chain variant L<sup>352</sup>>A, L<sup>353</sup>>A; disulfide bridged dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa; humanized monoclonal antibody fusion with human VEGF receptor type 1; antigen: human programmed cell death 1 ligand 1, PD-L1, programmed death ligand 1, PDCD1 ligand 1, B7 homolog 1, B7-H1 (CD274); CDR Source: *Mus musculus*; chain length: 564; fusion protein: 1-100 (domain 2 of the mature human extracellular domain of vascular endothelial growth factor receptor type-1 (VEGFR-1, VEGFR1) VEGF type 1 receptor); linker: 101-115; type: IgG1-kappa; heavy chain class: gamma1; HV germline: *Homo sapiens* IGHV1-3\*01; HJ germline: *Homo sapiens* IGHJ4\*01; HC germline: *Homo sapiens* IGHG1\*03; VH: 116-235; CH1: 236-333; hinge: 334-348; CH2: 349-458 (L352A L353A, reduce FcGammaR and C1q binding); CH3: 459-563; CHS: 564-564 (K565del); CDR Kabat H1: GYTIH (146-150); CDR Kabat H2: WFYPGSGTLKYSEKFGQ (165-181); CDR Kabat H3: HGTGTLAMADY (214-224); light chain class: kappa; light chain length: 219; LV germline: *Homo sapiens* IGKV2-29\*02; LJ germline: *Homo sapiens* IGKJ2\*01; LC germline: *Homo sapiens* IGKC\*01; VL: 1-112; CL: 113-219; CDR Kabat L1: KSSQSLANSYGNTYLS (24-39); CDR Kabat L2: GISNRFS (55-61); CDR Kabat L3: LQGTHQPPT (94-102)  
*angiogenesis inhibitor, antineoplastique*

sotiburafusp alfa

fragment du domaine extracellulaire du récepteur 1 du facteur de croissance endothélial vasculaire humanisé (VEGFR-1, tyrosine kinase 1 de type Fms, FLT-1) (129-228, 1-100 dans la séquence actuelle) fusionné via la liaison peptidique<sup>101</sup>GGSGGGSGSGSGGS<sup>115</sup> à l'extrémité N-terminale de la chaîne lourde (116-564) du variant de la chaîne lourde L<sup>352></sup>A, L<sup>353></sup>A d'une immunoglobuline G1-kappa anti-(ligand 1 humain de mort cellulaire programmée 1(PD-L1, CD274) humanisée; dimère à pont disulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa; fusion d'un anticorps monoclonal humanisé avec le récepteur humain du VEGF de type 1; antigène: ligand humain 1 de mort cellulaire programmée 1, PD-L1, ligand 1 de mort programmée, ligand 1 de PDCD1, homologue 1 de B7, B7-H1 (CD274); source CDR: *Mus musculus*; longueur de la chaîne: 564; protéine de fusion: 1-100 (domaine 2 du domaine extracellulaire humain mature du récepteur du facteur de croissance endothélial vasculaire de type 1 (VEGFR-1, VEGFR1) VEGF type 1); liaison: 101-115; type: IgG1-kappa; classe de la chaîne lourde: gamma1; HV lignée germinale: *Homo sapiens* IGHV1-3\*01; HJ lignée germinale: *Homo sapiens* IGHJ4\*01; HC lignée germinale: *Homo sapiens* IGHG1\*03; VH: 116-235; CH1: 236-333; charnière: 334-348; CH2: 349-458 (L352A L353A, réduit la liaison de FcGammaR et C1q); CH3: 459-563; CHS: 564-564 (K565del); CDR Kabat H1: GYTIH (146-150); CDR Kabat H2: WFYPGSGTLKYSEKFQG (165-181); CDR Kabat H3: HGTGTLMAMDY (214-224); classe de la chaîne légère: kappa; longueur de la chaîne légère: 219; LV lignée germinale: *Homo sapiens* IGKV2-29\*02; LJ lignée germinale: *Homo sapiens* IGKJ2\*01; LC lignée germinale: *Homo sapiens* IGKC\*01; VL: 1-112; CL: 113-219; CDR Kabat L1: KSSQSLANSYGNTYLS (24-39); CDR Kabat L2: GISNRFS (55-61); CDR Kabat L3: LQGTHQPPT (94-102)  
*inhibiteur de l'angiogenèse, antinéoplasique*

sotiburafusp alfa

receptor 1 del factor de crecimiento endotelial vascular humanizado (VEGFR-1, tirosina kinasa de tipo Fms, FLT-1) fragmento de dominio extracelular (129-228, 1-100 en la secuencia actual) fusionado a través del enlace peptídico<sup>101</sup>GGSGGGSGSGSGGS<sup>115</sup> al N-terminal de la cadena pesada (116-564) de la inmunoglobulina humanizada G1-kappa anti-(ligando 1 de muerte celular 1 programada humana 1 (PD-L1, CD274) variante de cadena pesada L<sup>352></sup>A, L<sup>353></sup>A; dímero con puente disulfuro, producido en células ováricas de hámster Chino (CHO), forma glicosilada alfa; anticuerpo monoclonal humanizado de fusión con receptor VEGF de tipo 1; antígeno: ligando 1 de muerte celular programada humana 1, PD-L1, ligando 1 de muerte programada, PDCD1 ligando 1, B7 homólogo 1, B7-H1 (CD274); fuente CDR: *Mus musculus*; longitud cadena: 564; proteína de fusión: 1-100 (dominio 2 del dominio extracelular maduro humano del receptor tipo 1 del factor de crecimiento endotelial vascular (VEGFR-1, VEGFR1) receptor VEGF tipo 1); enlace: 101-115; tipo: IgG1-kappa; clase cadena pesada: gamma1; línea germinal HV: *Homo sapiens* IGHV1-3\*01; línea germinal HJ: *Homo sapiens* IGHJ4\*01; línea germinal HC: *Homo sapiens* IGHG1\*03; VH: 116-235; CH1: 236-333; bisagra: 334-348; CH2: 349-458 (L352A L353A, unión reducida FcGammaR y C1q); CH3: 459-563; CHS: 564-564 (K565del); CDR Kabat H1: GYTIH (146-150); CDR Kabat H2: WFYPGSGTLKYSEKFQG (165-181); CDR Kabat H3: HGTGTLMAMDY (214-224); clase cadena ligera: kappa; longitud cadena ligera: 219; línea germinal LV: *Homo sapiens* IGKV2-29\*02; línea germinal LJ: *Homo sapiens* IGKJ2\*01; línea germinal LC: *Homo sapiens* IGKC\*01; VL: 1-112; CL: 113-219; CDR Kabat L1: KSSQSLANSYGNTYLS (24-39); CDR Kabat L2: GISNRFS (55-61); CDR Kabat L3: LQGTHQPPT (94-102)  
*inhibidor de la angiogénesis, antineoplásico*



Sequence / Séquence / Secuencia

Heavy chain / Chaîne lourde / Cadena pesada: VEGFR1-IgG1

<b>SDTGRPFVEM</b>	<b>YSEIPEIIHM</b>	<b>TEGRELVIPC</b>	<b>RVTSNPITVT</b>	<b>LKKFFLDTLI</b>	50
<b>PDGKRIIWDS</b>	<b>RKGFIIISNAT</b>	<b>YKIGLLTCE</b>	<b>ATVNGHLKYT</b>	<b>NYLTHRQNTN</b>	100
<u>GGSGGGGGG</u>	<u>GGGG</u> QVQLV	QSGAEVKKPG	ASVKVSCKAS	GYAFTGYTIH	150
WVRQAPGQRL	EMMGWFYFPGS	GTLKYSEKFG	GRVTITRDKS	LSTAYMELSS	200
LRSEDTAVVY	CARHGTGTLM	AMDYWGQSTL	VTVSSASTRG	PSVFLAPLSS	250
KSTSGGTAAL	GCLVKDYFPE	PVTVSWNSGA	LTSGVHTFPA	VLQSSGLYSL	300
KSVTVVPSSS	LGDTQYICNV	NHKPSNKTVD	KRVEPKSCDK	THCPPCPAP	350
<b>EA</b> GGPSVFL	FPKPKDTLM	ISRTPQVTCV	VVDVSHEDPE	VKFNWYVDGV	400
EVHNAKTKPR	EEQYNSTYRV	VSVLTVLHQD	WLNKKEYCKK	VSNKALPAPI	450
EKTISKAKGQ	PREPQVYTLP	PSREEMTKNQ	VSLTCLVKGF	YPSDIAVEWE	500
SGKQPPENYK	TTPVLDSDG	SFFLYSKITV	DKSRWQQGNV	FSCVMHEAL	550
HNHYTQKSL	LSPG				564

Light chains / Chaînes légères / Cadenas ligeras

DVVMQTPLS	LSVTPGQPAS	ISCKSSQSLA	NSYNGNTYLSW	YLHKPGQSPQ	50
LLIYGISNRF	SGVDFRFSGS	GSQTDFTLKI	SRVEAEDVGV	YYCLQGTQHP	100
PTFGQGTLE	IKRTVAAPSIV	FIFPPSDEQL	KSGTASVVCL	LNNFYPREAK	150
VQWKVDNALQ	SGNSQESVTE	QDSKDSYISL	SSTLTLSKAD	YEKKHVVYACE	200
VTHQGLSSPV	TKSFNRGEC				219

Peptide linker / Peptides liant / Péptido de unión

GGSGGGGGGGGGG 101-115

Mutation / Mutation / Mutación

L352, L352>A, L353, L353>A

Post-translational modifications

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

Intra-VEGFR1	30-79, 30 <sup>o</sup> -79 <sup>o</sup>
Intra-H	137 - 211, 262 - 318, 379 - 439, 485 - 543 137 <sup>o</sup> -211 <sup>o</sup> , 262 <sup>o</sup> -318 <sup>o</sup> , 379 <sup>o</sup> -439 <sup>o</sup> , 485 <sup>o</sup> -543 <sup>o</sup>
Intra-L	23 <sup>o</sup> - 93 <sup>o</sup> , 139 <sup>o</sup> - 199 <sup>o</sup> , 23 <sup>o</sup> - 93 <sup>o</sup> , 139 <sup>o</sup> - 199 <sup>o</sup>
Inter-H-L	338-219, 338 <sup>o</sup> -219 <sup>o</sup>
Inter-H-H	344-344 <sup>o</sup> , 347-347 <sup>o</sup>

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

VEGFR1-IgG1 heavy chain: N36, N68, N415, N36<sup>o</sup>, N68<sup>o</sup>, N415<sup>o</sup>

Oxidation sites / Sites de oxidation / Posiciones de oxidación

VEGFR1-HC: M10, M163, M196, M220, M370, M546,  
M10<sup>o</sup>, M163<sup>o</sup>, M196<sup>o</sup>, M220<sup>o</sup>, M370<sup>o</sup>, M546<sup>o</sup>  
LC: M4<sup>o</sup>, M4<sup>o</sup>

Deamidation sites / Sites de désamidation / Posiciones de desamidación

VEGFR1-HC (succinimide formation): N84, N433, N502, N507, N508,  
N84<sup>o</sup>, N433<sup>o</sup>, N502<sup>o</sup>, N507<sup>o</sup>, N508<sup>o</sup>  
LC: N31<sup>o</sup>, N35<sup>o</sup>, N58<sup>o</sup>, N31<sup>o</sup>, N35<sup>o</sup>, N58<sup>o</sup>

**sovipostobartum #**  
sovipostobart

immunoglobulin G1-kappa, anti-[*Homo sapiens* CTLA4 (cytotoxic T-lymphocyte associated protein 4, CTLA-4, CD152)], *Homo sapiens* monoclonal antibody with cleavable prodomain; gamma1 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-30\*01 (94.9%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1\*01v, G1m17, 1>G1m3, 1 CH1 R120, CH3 D12, L14 (CH1 R120 (215) (119-216), hinge 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS K2>del (447)) (119-447)], (221-259')-disulfide with kappa light chain *Homo sapiens* (1'-259') [cleavable prodomain (1'-44') fused to V-KAPPA (*Homo sapiens* IGKV3-20\*01 (97.9%) -IGKJ1\*01 (100%), CDR-IMGT [7.3.9] (71-77.95-97.134-142)) (45'-152') - *Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (198), V101 (236) (153'-259')]; dimer (227-227":230-230")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa *immunostimulant, antineoplastic*

sovipostobart

immunoglobuline G1-kappa, anti-[*Homo sapiens* CTLA4 (protéine 4 associée aux lymphocytes T cytotoxiques, CTLA-4, CD152)], anticorps monoclonal *Homo sapiens* avec prodomaine clivable;

chaîne lourde gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-30\*01 (94.9%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1\*01v, G1m17,1>G1m3,1 CH1 R120, CH3 D12, L14 (CH1 R120 (215) (119-216), charnière 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS K2>del (447)) (119-447)], (221-259')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-259') [prodomaine clivable (1'-44') fusionné to V-KAPPA (*Homo sapiens* IGKV3-20\*01 (97.9%) -IGKJ1\*01 (100%), CDR-IMGT [7.3.9] (71-77.95-97.134-142)) (45'-152') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (198), V101 (236) (153'-259')]; dimère (227-227":230-230")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa  
*immunostimulant, antinéoplasique*

sovipostobart

immunoglobulina G1-kappa, anti-[*Homo sapiens* CTLA4 (proteína 4 asociada a los linfocitos T citotóxicos, CTLA-4, CD152)], anticuerpo monoclonal *Homo sapiens* con prodominio escindible; cadena pesada gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-30\*01 (94.9%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1\*01v, G1m17,1>G1m3,1 CH1 R120, CH3 D12, L14 (CH1 R120 (215) (119-216), bisagra 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS K2>del (447)) (119-447)], (221-259')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-259') [prodominio escindible (1'-44') fusionado a V-KAPPA (*Homo sapiens* IGKV3-20\*01 (97.9%) -IGKJ1\*01 (100%), CDR-IMGT [7.3.9] (71-77.95-97.134-142)) (45'-152') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (198), V101 (236) (153'-259')]; dímero (227-227":230-230")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa  
*immunoestimulante, antineoplásico*

2649371-19-5

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLVESGEGG VVQPGRSRLRL SCAASGFTFS SYTMHWVRQA PGRGLEWVTF	50
ISYDGNKNYY ADSVKGKRFIT SRDNRKNTLY LQMNSLRAED TAIYYCARTG	100
WLGPFDFYWGQ GTLVTVSSAS TKGSPVFLPA PSSKSTSGGT AALGCLVKDY	150
FPEPVTVSWN SGALTSVGHV FPAVLQSSGL YSLSSVTVTP SSSLGTQTYI	200
CNVNHHKPSNT KVDKRVEPKS CDKTHCTPPC PAPELLGGPS VFLPPFKPKD	250
TLMSIRTPEV TCVVVDVSH EDPVKFNWYV DGEVHNAKT KPREEQYNST	300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY	350
TLPPSRDELDT KNQVSLTCLV KGFVPSDIAV EWESNGQPEN NYKTTFPVLD	400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNYTQK SLSLSPG	447

## Light chain / Chaîne légère / Cadena ligera

QGQSGS CRTQ LYGNLCPYG GGSSGGSISS GLLSGRSDNP GGGSEIVLTQ	50
SPGTLSSLSPG ERATLSCRAS QVSGSSYLAW YQQKPGQAPR LLIYGAFSRA	100
TGIPDRFSGS GSGTDFTLTI SRLEPEDFAV YCQQYGSSP WTFGQGTKVE	150
IKRTVAAPSV FIFPFSDQL KSGTASVVLCL LNNFYPREAK VQWKVDNALQ	200
SGNSQESVTE QDSKDSYSL SSTLTLSKAD YEKHKVYACE VTHQGLSSPV	250
TKSFNRGEC	259

## 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)	67'-133'	179'-239'		
	67"-133"	179"-239"		
Inter-H-L (h 5-CL 126)	221-259'	221"-259"		
Inter-H-H (h 11, h 14)	227-227"	230-230"		

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

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxopropilo)  
H VH Q1: I, I'

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

H CH2 N84.4: 298, 298"

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

**stapokibartum #**

stapokibart

immunoglobulin G4-kappa, anti-[*Homo sapiens* IL4R (interleukin 4 receptor, IL4RA, IL-4RA, interleukin 13 receptor, CD124)], humanized monoclonal antibody; gamma4 heavy chain humanized(1-446) [VH (*Homo sapiens* IGHV3-23\*03 (92.9%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (120-217), hinge 1-12 S10>P (227) (218-229), CH2 L92 (308) (230-339), CH3 (340-444), CHS (445-446)) (120-446)], (133-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33\*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 (225-225'':228-228'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1 lacking the glutamine synthetase (GS-KO) gene, glycoform alfa  
*anti-inflammatory*

stapokibart

immunoglobuline G4-kappa, anti-[*Homo sapiens* IL-4R (récepteur de l'interleukine 4, IL4RA, IL-4RA, récepteur de l'interleukine 13, CD124)], anticorps monoclonal humanisé; chaîne lourde gamma4 humanisée (1-446) [VH (*Homo sapiens* IGHV3-23\*03 (92.9%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (120-217), charnière 1-12 S10>P (227) (218-229), CH2 L92 (308) (230-339), CH3 (340-444), CHS (445-446)) (120-446)], (133-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33\*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 (225-225'':228-228'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1 ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa  
*anti-inflammatoire*

estapokibart

immunoglobulina G4-kappa, anti-[*Homo sapiens* IL-4R (receptor de la interleukina 4, IL4RA, IL-4RA, receptor de la interleukina 13, CD124)], anticuerpo monoclonal humanizado; cadena pesada gamma4 humanizada (1-446) [VH (*Homo sapiens* IGHV3-23\*03 (92.9%) -(IGHD) -IGHJ4\*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (120-217), bisagra 1-12 S10>P (227) (218-229), CH2 L92 (308) (230-339), CH3 (340-444), CHS (445-446)) (120-446)], (133-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33\*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 (225-225'':228-228'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa  
*antiinflamatorio*

## Heavy chain / Chaîne lourde / Cadena pesada

EVQLLESGGG LVQPGGSLRL SCAASGFTFS RYAMSWVRQA PGKLEWVST 50  
 ISSGGSYTNY ADSVRGRFTI SRDNVKNLTY LQMNSLRAED TAVYCARAT 100  
 ARATEFAYWG QGTLVTVSSA STKGPSVFP L APCSRSSTSES TAALGCLVKD 150  
 YFPEPVTVSW NSGALTSGVH TFFPAVLQSSG LYSLSVVTV PSSLGKTKTY 200  
 TCNVDRHKPSN TKVDRKVESK YGPPCPVCPA PEFLLGGPVSF LFPPKPKDTL 250  
 MISRTPEVTC VVVVDSQEDF EVQFNWYVDP VEVHNAKTKP REEQFNSTYR 300  
 VVSVLTVLHQ DWLNGKEYK KVSNNKLPSS IEKTIKAKG QPREPQVYTL 350  
 PPSQEQEMTKN QVSLTCLVKG FYPSDIAVEW ESNQGPENNY KTTPEPVLDS 400  
 GSFFLYSRLT VDKSRWQEGN VFSCVMHEA LHNHYTQKSL SLSLGG 446

## Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGRDVT ITCQASQDIS NYLNWYQQKP GKAPKLLIYY 50  
 TSLRHSQVPS RFSGSGSDTD YLTISSLPQ EDFATYFCQQ GNTLPLTFFG 100  
 GTKVEIKRTV AAPSIVFIPP SDEQLKSGTA SVVCLLNIFY PREAKVQMKV 150  
 DNALQSGNSQ ESVTEQDSKD STYSLSSITL LSKADYEKHK VYACEVTHQG 200  
 LSSPVTKSFN RGEK 214

## Post-translational modifications

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

Intra-H (C23-C104) 22-96 146-202 260-320 366-424  
 22"-96" 146"-202" 260"-320" 366"-424"

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

Inter-H-L (CH1 10-CL 126) 133-214" 133"-214"

Inter-H-H (h 8, h 11) 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-antennaires complexes fucosylés / glicanos de tipo CHO biantenaricos complejos fucosilados.

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

**survodutidum**

survodutide

L-histidyl-1-aminocyclobutanoyl-L-glutaminylglycyl-L-threonyl-L-phenylalanyl-L-threonyl-L-seryl-L- $\alpha$ -aspartyl-L-tyrosyl-L-seryl-L-lysyl-L-tyrosyl-L-leucyl-L- $\alpha$ -aspartyl-L- $\alpha$ -glutamyl-L-arginyl-L-alanyl-L-alanyl-L-lysyl-L- $\alpha$ -aspartyl-L-phenylalanyl-L-isoleucyl-N<sup>6</sup>-[N-(17-carboxyheptadecanoyl)-L- $\gamma$ -glutamylglycyl-L-serylglycyl-L-serylglycylglycyl]-L-lysyl-L-tryptophyl-L-leucyl-L- $\alpha$ -glutamyl-L-seryl-L-alaninamide  
*glucagon and glucagon-like peptide 1 (GLP-1) receptors agonist*

survodutide

L-histidyl-1-aminocyclobutanoyl-L-glutaminylglycyl-L-thréonyl-L-phénylalanyl-L-thréonyl-L-séryl-L- $\alpha$ -aspartyl-L-tyrosyl-L-séryl-L-lysyl-L-tyrosyl-L-leucyl-L- $\alpha$ -aspartyl-L- $\alpha$ -glutamyl-L-arginyl-L-alanyl-L-alanyl-L-lysyl-L- $\alpha$ -aspartyl-L-phénylalanyl-L-isoleucyl-N<sup>6</sup>-[N-(17-carboxyheptadécanoyl)-L- $\gamma$ -glutamylglycyl-L-sérylglycyl-L-sérylglycylglycyl]-L-lysyl-L-tryptophyl-L-leucyl-L- $\alpha$ -glutamyl-L-séryl-L-alaninamide  
*agoniste des récepteurs du glucagon et du peptide-1 similaire au glucagon (GLP-1)*

survodutida

L-histidil-1-aminociclobutanoil-L-glutaminilglicil-L-treonyl-L-fenilalanil-L-treonyl-L-seril-L- $\alpha$ -aspartil-L-tirosil-L-seril-L-lisil-L-tirosil-L-leucil-L- $\alpha$ -aspartil-L- $\alpha$ -glutamil-L-arginil-L-alanil-L-alanil-L-lisil-L- $\alpha$ -aspartil-L-fenilalanil-L-isoleucil-N<sup>6</sup>-[N-(17-carboxiheptadecanoil)-L- $\gamma$ -glutaminilglicil-L-serilglicil-L-serilglicilglicil]-L-lisil-L-triptofil-L-leucil-L- $\alpha$ -glutamil-L-seril-L-alaninamida  
*agonista de los receptores del glucagón y del péptido similar al glucagón (GLP-1)*

C<sub>192</sub>H<sub>289</sub>N<sub>47</sub>O<sub>61</sub>

2805997-46-8

Sequence I / Séquence I / Secuencia I

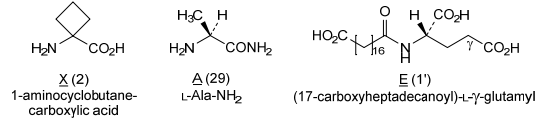
HXQGTFTSDY SKYLDERRAAK DFIKWLESA 29

Sequence II / Séquence II / Secuencia II

EGSGSGG 7'

Amide bridge location / Position du pont amide / Posición del puente amido  
7'-24 (Gly<sup>7</sup>-Lys<sup>6,24</sup>)

Modified residues / Résidus modifiés / Restos modificados



**suvemcitugum #**  
suvemcitug

immunoglobulin G1-kappa, anti-[*Homo sapiens* VEGFA (vascular endothelial growth factor A, VEGF-A, VEGF)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-452) [VH (*Homo sapiens* IGHV3-21\*01 (74.7%) -(IGHD) -IGHJ2\*01 (92.9%), CDR-IMGT [9.8.14] (26-34.52-59.98-111)) (1-122) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-219')-disulfide with kappa light chain humanized (1'-219') [V-KAPPA (*Homo sapiens* IGKV1-6\*01 (85.4%) -IGKJ4\*01 (100%), CDR-IMGT [8.3.12] (27-34.52-54.91-102)) (1'-112') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (158), V101 (196) (113'-219')]; dimer (231-231":234-234")-bisdisulfide; produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa  
*angiogenesis inhibitor*

suvemcitug

immunoglobuline G1-kappa, anti-[ *Homo sapiens* VEGFA facteur de croissance A de l'endothélium vasculaire, VEGF-A, VEGF)]; anticorps monoclonal humanisé chaîne lourde gamma1 humanisée (1-452) [VH (*Homo sapiens* IGHV3-21\*01 (74.7%) -(IGHD) -IGHJ2\*01 (92.9%), CDR-IMGT [9.8.14] (26-34.52-59.98-111)) (1-122) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-219')-disulfure avec la chaîne légère kappa humanisée (1'-219') [V-KAPPA (*Homo sapiens* IGKV1-6\*01 (85.4%) -IGKJ4\*01 (100%), CDR-IMGT [8.3.12] (27-34.52-54.91-102)) (1'-112') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (158), V101 (196) (113'-219')]; dimère (231-231":234-234")-bisdisulfure; produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa  
*inhibiteur de l'angiogénèse*

suvemcitug

immunoglobulina G1-kappa, anti-[ *Homo sapiens* VEGFA factor de crecimiento A de la endotelina vascular, VEGF-A, VEGF)]; anticuerpo monoclonal humanizado

cadena pesada gamma1 humanizada (1-452) [VH (*Homo sapiens* IGHV3-21\*01 (74.7%) -(IGHD)-IGHJ2\*01 (92.9%), CDR-IMGT [9.8.14] (26-34.52-59.98-111)) (1-122) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-219')-disulfuro con la cadena ligera kappa humanizada (1'-219') [V-KAPPA (*Homo sapiens* IGKV1-6\*01 (85.4%) -IGKJ4\*01 (100%), CDR-IMGT [8.3.12] (27-34.52-54.91-102)) (1'-112') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (158), V101 (196) (113'-219')]; dímero (231-231":234-234")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, forma glicosilada alfa  
*inhibidor de la angiogénesis*

1610010-57-5

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG	LVKFPGSLRL	SCAASGFSFS	NNDVMCWRQ	APGKGLEWIG	50
CIMTTDVVTE	YANWAKSRFT	VSRDSAKNSV	YLQMNSLRAE	DTAVYFCARD	100
SVGSPFLMSFD	LWGFGLVTV	SSASTKGPSV	FPLAPSSKST	SGGTAALGCL	150
VKDYFPEPVT	VSWSNGALTS	GVHTFFAVLQ	SSGLYSLSSV	VTVPSSSLGT	200
QTYICNVNHK	PSNTKVDKKV	EPKSDCKTHT	CPPCPAPELL	GGPSVFLFPP	250
KPKDTLMISR	TPEVTCVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTRVRSV	LTVLHQDNLN	GKEYKCKVSN	KALPAIEKT	ISKAKGQPRE	350
PQVYTLPPSR	DELTKNQVSL	TCLVKGFPYS	DIAVEWESNG	QPENNYKTFP	400
PVLDSGDSFF	LYSKLTVDKS	RWQQGNVFS	SVMHEALHNN	YTKSLSLSP	450
GR					452

Light chain / Chaîne légère / Cadena ligera

DIQMTPSPSS	LSASVGRVTV	INCQASQSIY	NNNELSWYQQ	KPGKPPKLLI	50
YRASTLASGV	PSRFSGSGSG	TDFTLTISSL	QPEDVATYYC	GGYKSYSDNG	100
NGFGGGTRVE	IKRTVAAPS	FIFPPSDEQL	KSGTASVIVCL	LNNFYYPREAK	150
VQWVKVDNALQ	SGNSQESVTE	QDSKDYSTYSL	SSTLTLSKAD	YEKHKVYACE	200
VTHQGLSSPV	TKSFRNGEC				219

**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)	23-90	139-199		
	23"-90"	139"-199"		

Inter-H-L (h 5-CL 126) 225-219" 225"-219"

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

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

H CH2 N84.4; 302, 302"

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal  
H CHS K2: 452, 452"**suvutresgenum autoleucelum #**

suvutresgene autoleucel

autologous T lymphocytes obtained from peripheral blood lymphocytes by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector encoding an affinity-enhanced cancer testis antigen (NY-ESO-1<sup>6259</sup>) specific T-cell receptor (TCR) and co-expressing a dominant-negative transforming growth factor beta (TGF-β) type II cell surface receptor (dnTGF-βRII; truncated non-signalling TGF-βRII). The TCR is based on *letetresgene autoleucel* and specifically recognises a peptide (SLLMWITQC), which is shared by the cancer antigens NY-ESO-1 (CTAG1B) and LAGE-1a (CTAG2) presented on human leukocyte antigen HLA-A\*02. The expressed transgene comprises dnTGF-βRII joined by the foot-

and-mouth disease virus ribosome skipping sequence (F2A) to the TCR  $\alpha$  chain, joined by the porcine teschovirus-1 ribosome skipping sequence (P2A) to the TCR  $\beta$  chain and is under control of the elongation factor 1 alpha (EF1 $\alpha$ ) promoter. The construct is flanked by long terminal repeats (LTR) that have a deletion in the U3 part of the LTR, and also contains a  $\psi$  packaging signal, Rev response element (RRE), central polypurine tract (cPPT) and a central termination sequence (CTS). The vector is pseudotyped with vesicular stomatitis virus (VSV) G glycoprotein. The leukapheresis material is enriched for CD4/CD8 T lymphocytes by positive immunoselection, activated by CD3 and CD28 agonists and transduced with the lentiviral vector. The cells are then expanded initially in media supplemented with AB serum and interleukin 2 (IL-2), and then in media supplemented with only IL-2. The T lymphocytes ( $\geq 95\%$ ) are positive for the transgene ( $\geq 10\%$  CAR positive), and are cytotoxic to T2 cells loaded with the target peptide *cell-based gene therapy (antineoplastic)*

suvutresgène autoleucel

lymphocytes T autologues obtenus à partir de lymphocytes de sang périphérique par leucaphérèse, transduits avec un vecteur lentiviral auto-inactif et non répliquant codant un récepteur de cellules T (TCR) spécifique de l'antigène du cancer du testicule à affinité renforcée (NY-ESO-1<sup>ct259</sup>) et co-exprimant un récepteur de surface cellulaire dominant-négatif du facteur de croissance transformant bêta (TGF- $\beta$ ) de type II (dnTGF- $\beta$ RII; TGF- $\beta$ RII tronqué non signalant). Le TCR est basé sur le *lététresgène autoleucel* et reconnaît spécifiquement un peptide (SLLMWITQC) qui est partagé par les antigènes de cancer NY-ESO-1 (CTAG1B) et LAGE-1a (CTAG2) présentés sur l'antigène leucocytaire humain HLA-A\*02. Le transgène exprimé comprend dnTGF- $\beta$ RII lié par la séquence de saut d'exon du ribosome du virus de la fièvre aphteuse (F2A) à la chaîne TCR  $\alpha$ , lié par la séquence de saut d'exon du ribosome du teschovirus-1 de porc (P2A) à la chaîne TCR  $\beta$  et est sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF1 $\alpha$ ). La construction est flanquée de longues répétitions terminales (LTR) qui présentent une délétion dans la partie U3 de la LTR, et contient également un signal d'encapsulation  $\psi$ , un élément de réponse Rev (RRE), un tractus polypurine central (cPPT) et une séquence de terminaison centrale (CTS). Le vecteur est pseudotypé avec la glycoprotéine G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est enrichi en lymphocytes T CD4/CD8 par immunosélection positive, activé par des agonistes CD3 et CD28 et transduit avec le vecteur lentiviral. Les cellules sont ensuite développées dans un premier temps dans un milieu complété par du sérum AB et de l'interleukine 2 (IL-2), puis dans un milieu complété uniquement par de l'IL-2. Les lymphocytes T ( $\geq 95\%$ ) sont positifs pour le transgène ( $\geq 10\%$  CAR positif), et sont cytotoxiques pour les cellules T2 chargées avec le peptide cible *thérapie génique à base de cellules (antinéoplasique)*

suvutresgén autoleucel

linfocitos T autólogos obtenidos de linfocitos de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica para un receptor de linfocitos T (TCR) con afinidad aumentada, específico para el antígeno de cáncer de testículo (NY-ESO-1<sup>c259</sup>) y que coexpresa un receptor de superficie celular dominante negativo del factor de crecimiento transformante beta (TGF-β) tipo II (dnTGF-βRII; TGF-βRII truncado, no señalizante). El TCR está basado en *letetresgén autoleucel* y reconoce específicamente un péptido (SLLMWITQC), compartido por los antígenos de cáncer NY-ESO-1 (CTAG1B) y LAGE-1a (CTAG2), presentado en el antígeno común leucocitario HLA-A\*02. El transgén expresado contiene dnTGF-βRII unido, mediante la secuencia de salto ribosómico del virus de la fiebre aftosa (F2A), a la cadena TCRα, unida, mediante la secuencia de salto ribosómico del teschovirus 1 porcino (P2A), a la cadena TCRβ y está bajo el control del promotor del factor de elongación 1 alfa (EF1α). El constructo está flanqueado por repeticiones terminales largas (LTR) que tienen una delección en la parte U3 del LTR, y también contiene una señal de empaquetamiento ψ, un elemento de respuesta Rev (RRE), una secuencia de tracto de polipurina central (cPPT) y una secuencia de terminación central (CTS). El vector está seudotipado con la glicoproteína G del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se enriquece para linfocitos T CD4/CD8 mediante inmunoselección positiva, se activa mediante agonistas de CD3 y CD28 y se transduce con el vector lentiviral. Las células son después expandidas inicialmente en medio suplementado con suero AB e interleuquina 2 (IL-2), y después en medio suplementado sólo con IL-2. Los linfocitos T (≥95%) son positivos para el transgén (≥10% positivos para el CAR) y son citotóxicos frente a células T2 cargadas con el péptido diana

*terapia génica basada en células (antineoplásico)*

**suzetriginum**

suzetrigine

4-[(2R,3S,4S,5R)-3-(3,4-difluoro-2-methoxyphenyl)-4,5-dimethyl-5-(trifluoromethyl)oxolane-2-carboxamido]pyridine-2-carboxamide  
*sodium channel protein type 10 subunit alpha blocker, analgesic*

suzétrigine

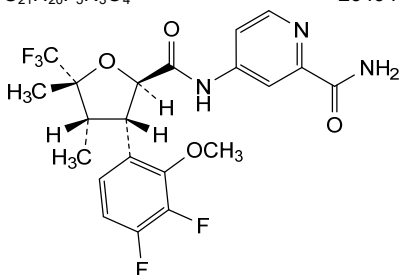
4-[(2R,3S,4S,5R)-3-(3,4-difluoro-2-méthoxyphényl)-4,5-diméthyl-5-(trifluorométhyl)oxolane-2-carboxamido]pyridine-2-carboxamide  
*bloqueur de la sous-unité alpha type 10 de la protéine des canaux sodiques, analgésique*

suzetrigina

4-[(2R,3S,4S,5R)-3-(3,4-difluoro-2-metoxifenil)-4,5-dimetil-5-(trifluorometil)oxolano-2-carboxamido]piridina-2-carboxamida  
*bloqueante del subunidad alfa tipo 10 de la proteína de los canales del sodio, analgésico*



$C_{21}H_{20}F_5N_3O_4$  2649467-58-1

**tamuzimodum**

tamuzimod

(5*R*)-5-(2,5-dichloro-4-{5-[8-chloro-6-(trifluoromethyl)imidazo[1,2-*a*]pyridin-2-yl]-1,2,4-oxadiazol-3-yl}phenoxy)piperidin-2-one  
*immunomodulator*

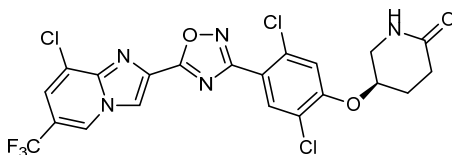
tamuzimod

(5*R*)-5-(2,5-dichloro-4-{5-[8-chloro-6-(trifluorométhyl)imidazo[1,2-*a*]pyridin-2-yl]-1,2,4-oxadiazol-3-yl}phénoxy)pipéridin-2-one  
*immunomodulateur*

tamuzimod

(5*R*)-5-(2,5-dicloro-4-{5-[8-cloro-6-(trifluorometil)imidazo[1,2-*a*]piridin-2-il]-1,2,4-oxadiazol-3-il}fenoxi)piperidin-2-ona  
*immunomodulador*

$C_{21}H_{13}Cl_3F_3N_5O_3$  2097854-81-2

**taplucainium chloride**

taplucainium chloride

1-benzyl-1-[2-(2,6-dimethylanilino)-2-oxoethyl]azepan-1-ium chloride  
*sodium channel blocker, analgesic*

chlorure de taplucaïnum

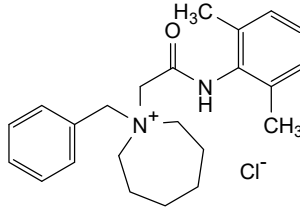
chlorure de 1-benzyl-1-[2-(2,6-diméthylanilino)-2-oxoéthyl]azépan-1-ium  
*bloqueur des canaux sodiques, analgésique*

cloruro de taplucaínio

cloruro de 1-bencil-1-[2-(2,6-dimetilanilino)-2-oxoetil]azepan-1-ium  
*bloqueante de los canales del sodio, analgésico*

C<sub>23</sub>H<sub>31</sub>ClN<sub>2</sub>O

2489565-37-7



**tegoprubartum #**  
tegoprubart

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD40LG (CD40 ligand, CD40L, tumor necrosis factor ligand superfamily member 5, TNFSF5, tumor necrosis factor related activation protein, TRAP, CD154)], chimeric monoclonal antibody; gamma1 heavy chain chimeric (1-448) [VH Musmus/Homsap (*Mus musculus* IGHV1S81\*02 (84.5%) -(IGHD) -IGHJ3\*01 (90.9%) A128>S (118)/*Homo sapiens* IGHV1-46\*01 (76.5%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1\*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v37 h S5, G1v61 h S11, G1v62 h S14, G1v63 CH2 S2 (CH1 K120 (215) (119-216), hinge 1-15 C5>S (221), C11>S (227), C14>S (230) (217-231), CH2 P2>S (239) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], non covalently paired to the kappa light chain chimeric (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-7\*01 (87.9%) -IGKJ1\*02 (100%)/*Homo sapiens* IGKV3-11\*01 (75.5%) -IGKJ4\*01 (90.9%) V124>L (108), 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 non covalent, produced in Chinese hamster ovary (CHO) cells, glycoform alfa  
*immunosuppressant*

tégoprubart

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD40LG (CD40 ligand, CD40L, membre 5 de la superfamille des ligands facteurs de nécrose tumorale, TNFSF5, protéine d'activation apparentée au facteur de nécrose tumorale, TRAP, CD154)], anticorps monoclonal chimérique; chaîne lourde gamma1 chimérique (1-448) [VH Musmus/Homsap (*Mus musculus* IGHV1S81\*02 (84.5%) -(IGHD) -IGHJ3\*01 (90.9%) A128>S (118)/*Homo sapiens* IGHV1-46\*01 (76.5%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1\*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v37 h S5, G1v61 h S11, G1v62 h S14, G1v63 CH2 S2 (CH1 K120 (215) (119-216), charnière 1-15 C5>S (221), C11>S (227), C14>S (230) (217-231), CH2 P2>S (239) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], apparée de manière non covalente à la chaîne légère kappa chimérique (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-7\*01 (87.9%) -IGKJ1\*02 (100%)/*Homo sapiens* IGKV3-11\*01 (75.5%) -IGKJ4\*01 (90.9%) V124>L (108), 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 non covalent, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa  
*immunosuppresseur*

tegoprubart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD40LG (CD40 ligando, CD40L, miembro 5 de la superfamilia de los ligandos factores de necrosis tumoral, TNFSF5, proteína de activación con el factor de necrosis tumoral, TRAP, CD154)], anticuerpo monoclonal quimérico;  
 cadena pesada gamma1 quimérica (1-448) [VH Musmus/Homsap (*Mus musculus* IGHV1S81\*02 (84.5%) -(IGHD) -IGHJ3\*01 (90.9%) A128>S (118)/*Homo sapiens* IGHV1-46\*01 (76.5%) -(IGHD) -IGHJ1\*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1\*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v37 h S5, G1v61 h S11, G1v62 h S14, G1v63 CH2 S2 (CH1 K120 (215) (119-216), bisagra 1-15 C5>S (221), C11>S (227), C14>S (230) (217-231), CH2 P2>S (239) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], manera emparejada no covalente a la cadena ligera kappa quimérica (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-7\*01 (87.9%) -IGKJ1\*02 (100%)/*Homo sapiens* IGKV3-11\*01 (75.5%) -IGKJ4\*01 (90.9%) V124>L (108), 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 no covalente, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa  
*inmunosupresor*

2628092-47-5

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VVKPGASVKL SCKASGYIFT SYMYWVKQA PGQGLEWIGE 50  
 INPSNGDTNF NEKFKSKATL TVDKSASTAY MELSLRSED TAVYVCTRSD 100  
 GRNDMDSWGQ GTLVTVSSAS TKGPSVFLPA PSSKSTSGGT AALGCLVKDY 150  
 FEPVPTVSNW SGALTSVGHV FFAVLQSSGL YSLSSVTVTP SSSLGTQYI 200  
 CNVNHKFSNT KVDKKVEPKS SDKHTSPSPS PAPELLGGSS VFLFPPKPKD 250  
 TLMISRTPEV TCWVVDVSHS DPEVKFNMYV DGVEVHNKAT KPREEQYNST 300  
 YRVVSVLTVL HQDWLNGKEY KCKVSNKALP ARIEKTISKA KGQPREPQVY 350  
 TLPDSRDELTKNQVSLTCLV KGFVPSDIAV EWESNGQPEN NYKTTTPVPLD 400  
 SDGSFFLYSK LTVDKSRWQQ GNVFPCSVMH EALHNHYTQK SLSLSPGK 448

## Light chain / Chaîne légère / Cadena ligera

DIVLTQSPAT LSVSPGERAT ISCRASQVRS SSTYSYMHVY QQKPGQPPKL 50  
 LIKYASNLES GVPARFSGSG SGTDFTLTIS SVEPEDFATY YCQHSWEIPP 100  
 TFGGGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREARV 150  
 QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKYACEV 200  
 THQGLSSPVT KSFNRGEC 218

## Post-translational modifications

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

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

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

Inter-H-L (h 5-CL 126)\* h 5 S (G1v37), CL 126 C h 5" S (G1v37), CL 126" C

Inter-H-H (h 11, h 14)\* h 11 S (G1v61), h 14 S (G1v62) h 11" S (G1v61), h 14" S (G1v62)

\*No H-L and H-H interchain disulfide bridges

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

Q &gt; pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxopropililo)

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 / glycans 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"

**temtokibartum #**  
temtokibart

immunoglobulin G1-lambda2, anti-[*Homo sapiens* IL22RA1 interleukin 22 receptor subunit alpha 1, IL22R)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV3-NL1\*01 (89.8%) -(IGHD) -IGHJ5\*01 (92.3%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1\*01, G1m17,1 CH1 K120, CH3 D12, L14, IGHG1v36 CH2 Q84.4 (CH1 K120 (217) (121-218), hinge 1-15 (219-233), CH2 N84.4>Q (300) (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-208')-disulfide with lambda light chain humanized (1'-209') [V-LAMBDA (*Homo sapiens* IGLV3-9\*02 (80.9%) -IGLJ2\*01 (100%), CDR-IMGT [2.3.10] (26-27.45-47.84-93)) (1'-103') -*Homo sapiens* IGLC2\*01 (100%) (104'-209')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, non-glycosylated  
*anti-inflammatory*

temtokibart

immunoglobuline G1-lambda2, anti-[*Homo sapiens* IL-22RA1 (sous-unité alpha 1 du récepteur de l'interleukine 22, IL22R)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-450) [VH (*Homo sapiens* IGHV3-NL1\*01 (89.8%) -(IGHD) - IGHJ5\*01 (92.3%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1\*01 G1m17,1 CH1 K120, CH3 D12, L14, IGHG1v36 CH2 Q84.4 (CH1 K120 (217) (121-218), charnière 1-15 (219-233), CH2 N84.4>Q (300) (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-208')-disulfure avec la chaîne légère lambda humanisée (1'-209') [V-LAMBDA (*Homo sapiens* IGLV3-9\*02 (80.9%) -IGLJ2\*01 (100%), CDR-IMGT [2.3.10] (26-27.45-47.84-93)) (1'-103') -*Homo sapiens* IGLC2\*01 (100%) (104'-209')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV ne présentant pas le gène de la glutamine synthétase (GS-KO), non-glycosylé  
*anti-inflammatoire*

temtokibart

inmunoglobulina G1-lambda2, anti-[*Homo sapiens* IL-22RA1 (subunidad alfa 1 del receptor de la interleukina 22, IL22R)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-450) [VH (*Homo sapiens* IGHV3-NL1\*01 (89.8%) -(IGHD) - IGHJ5\*01 (92.3%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1\*01 G1m17,1 CH1 K120, CH3 D12, L14, IGHG1v36 CH2 Q84.4 (CH1 K120 (217) (121-218), bisagra 1-15 (219-233), CH2 N84.4>Q (300) (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-208')-disulfuro con la cadena ligera lambda humanizada (1'-209') [V-LAMBDA (*Homo sapiens* IGLV3-9\*02 (80.9%) -IGLJ2\*01 (100%), CDR-IMGT [2.3.10] (26-27.45-47.84-93)) (1'-103') -*Homo sapiens* IGLC2\*01 (100%) (104'-209')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GS-KO), no glicosilado  
*antiinflamatorio*

2639874-57-8

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLVESGGG LVQFGGSLRL SCAASGFTFS SYDMNWVROA PFKGLEWVSS 50  
 IYNDASNTAY SDSVKGRTTI SRDNKNTLY LQMNLSRAED TAVYYCAKVG 100  
 FSGTYYESWV CQGTLVTVYSS ASTKGPSVVF LAPSSKSTSG GTAALGCLVK 150  
 DFFPEPVTVS WNSGALTSVY HTPFAVLQSS GLYSLSVSVT VPSSSLGTQT 200  
 YICNVNHPKS NTKVDKVEP KSCDKHTCF FCPAPELGG PSVFLFPKP 250  
 KDTLMLSRTP EVTCVVVDVSD HEDPEVFNW YVDGVEVHNA KTKPREEQYQ 300  
 STYRVVSVLT VLRHGDWLNK EYKCKVSNKA LPAPIERTIS KAKGQPREPQ 350  
 VYTLPPSRDE LTRNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTTPV 400  
 LDDSGSFFLY SKLTVDKSRW QQGNVFPSCSV MHEALHNHYT QRSLSLSPEK 450

## Light chain / Chaîne légère / Cadena ligera

SYELTQPSSV SVALGQTARI TCQGGYIAHW YQQKPGQAPV LVIYQNNRP 50  
 SGIPERFSGS GAGNTATLTI SRAQAEDEAD YYCQSGSSSS NAVFGGGTKL 100  
 TVLGQPKAAP SVTLFPPSSE ELQANKATLV CLISDFYFGA VTVAWKADSS 150  
 PVKAGVETTT PSKQSNKKA ASSYLSLTPE QWKSHRSYSC QVTHEGSTVE 200  
 KTVAPTECS 209

## 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'-83' 131'-190'  
 22"-83" 131"-190"

Inter-H-L (h 5-CL 126) 223-208" 223"-208"

Inter-H-H (h 11, h 14) 229-229" 232-232"

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

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxopropilo)

H VH Q1: 1, 1"

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

H CH2 N84.4>Q (G1v36): 300, 300"

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

H CHS K2: 450, 450"

**timdarpaceptum #**  
timdarpacept

human signal-regulatory protein alpha (SIRP $\alpha$ , tyrosine-protein phosphatase non-receptor type substrate 1) receptor domain 1 fragment (1-133) natural variant V2 (SIRP $\alpha$  V2; L<sup>14</sup>>S, T<sup>20</sup>>S, T<sup>22</sup>>I, R<sup>24</sup>>H, A<sup>27</sup>>V, G<sup>45</sup>>A, D<sup>65</sup>>E, L<sup>66</sup>>S, N<sup>70</sup>>E, R<sup>77</sup>>S, G<sup>79</sup>>S, D<sup>100</sup>>del, V<sup>102</sup>>T<sup>101</sup>) engineered variant (N<sup>80</sup>>A), fused to a human immunoglobulin G1 C-terminal Fc fragment (134-365) [*Homo sapiens* IGHG1\*01; hinge: 134-148; CH2: 149-258; CH3: 259-363; CHS: 364-365]), disulfide bridged dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa *antineoplastic*

timdarpacept

protéine humaine de régulation du signal alpha (SIRP $\alpha$ , substrat 1 de la tyrosine-protéine-phosphatase de type non-récepteur), fragment du domaine 1 du récepteur (1-133) variant modifié (N<sup>80</sup>>A) du variant naturel V2 (SIRP $\alpha$  V2; L<sup>14</sup>>S, T<sup>20</sup>>S, T<sup>22</sup>>I, R<sup>24</sup>>H, A<sup>27</sup>>V, G<sup>45</sup>>A, D<sup>65</sup>>E, L<sup>66</sup>>S, N<sup>70</sup>>E, R<sup>77</sup>>S, G<sup>79</sup>>S, D<sup>100</sup>>del, V<sup>102</sup>>T<sup>101</sup>), fusionné à un fragment Fc en C-terminal de l'immunoglobuline G1 humaine (134-365) [*Homo sapiens* IGHG1\*01; charnière: 134-148; CH2: 149-258; CH3: 259-363; CHS: 364-365]), dimère à pont disulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa *antineoplasique*

timdarpacept

proteína alfa reguladora de la señal humana (SIRP $\alpha$ , sustrato 1 de tipo no receptor de tirosina-proteína fosfatasa), fragmento del dominio receptor 1 (1-133) variante natural V2 (SIRP $\alpha$  V2; L<sup>14</sup>>S, T<sup>20</sup>>S, T<sup>22</sup>>I, R<sup>24</sup>>H, A<sup>27</sup>>V, G<sup>45</sup>>A, D<sup>65</sup>>E, L<sup>66</sup>>S, N<sup>70</sup>>E, R<sup>77</sup>>S, G<sup>79</sup>>S, D<sup>100</sup>>del, V<sup>102</sup>>T<sup>101</sup>) variante diseñada (N<sup>80</sup>>A), fusionada al fragmento Fc C-terminal de la inmunoglobulina humana G1 (134-365) [*Homo sapiens* IGHG1\*01; bisagra: 134-148; CH2: 149-258; CH3: 259-363; CHS: 364-365]], dímero con puente disulfuro, producido en células ováricas de hámster Chino (CHO), forma glicosilada alfa  
*antineoplásico*

2749520-17-8

## Sequence / Séquence / Secuencia

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EELQVIQPD KSVSVAAGES AILHCTVTSL IPVGPIQWFR GAGPARELIY 50
NQKEGHFPRV TTVESETKRE NMDFSISISA ITPADAGTY Y CVKFRKGSFD 100
TEFKSGAGTE LSVRAKPSAP VVSGFAARAT PQHEPKSCDK THTCPPCPAP 150
ELLGSPSVFL FPPKPKDTLM ISRTPEVTCV VVDVSHEDPE VKFNWIVDGV 200
EVHNAKTQPR EEQYNSTYRV VSVLTVLHQD WLNKGEYKCK VSNKALPAPI 250
EKTISKAKGQ PREPQVYTLF PSRDELTKNQ VSLTCLVKG F YPSDIAVEWE 300
SNQQPENNYK TTPPVLDSDG SFFLYSKLTV DKSRWQQGNV FSCSVMEHAL 350
HNHYTQKSL S LSPGK 365

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## Natural variant / Variante naturelle / Variante natural

L<sup>14</sup>>S, T<sup>20</sup>>S, T<sup>22</sup>>I, R<sup>24</sup>>H, A<sup>27</sup>>V, G<sup>45</sup>>A, D<sup>65</sup>>E, L<sup>66</sup>>S, N<sup>70</sup>>E, R<sup>77</sup>>S, G<sup>79</sup>>S, D<sup>100</sup>>del, V<sup>102</sup>>T<sup>101</sup>

## Mutation / Mutation / Mutación

N<sup>80</sup>>A

## Post-translational modifications

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

Intra-chain: 25-91, 179-239, 285-343

25'-91', 179'-239', 285'-343'

Inter-chain: 138-138', 144-144', 147-147'

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

N215, N215'

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

H CHS K2: K363, K365'

**tinocabtagenum autoleucelum #**

tinocabtagene autoleucel

autologous T lymphocytes obtained from peripheral blood lymphocytes by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector, encoding a bispecific chimeric antigen receptor targeting CD19 and CD22 (Siglec-2). The expressed transgene comprises a CD8 $\alpha$  leader sequence, an anti-CD19 and anti-CD22 fully human single chain fragment variable (scFv), a CD8 $\alpha$  hinge and transmembrane region, and a 4-1BB and CD3 $\zeta$  signalling domain and is under control of the elongation factor 1 alpha (EF1 $\alpha$ ) promoter. The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a  $\psi$  packaging signal, a Rev response element (RRE), a central polypurine tract (cPPT) sequence and a mutated Woodchuck hepatitis virus posttranscriptional regulatory element (WPRE). The vector is pseudotyped with vesicular stomatitis virus (VSV) G envelope protein. The leukapheresis material is enriched for CD4/CD8 T lymphocytes by positive immunoselection, activated by CD3 and CD28 agonists and transduced with the vector. The cells are then expanded in optimized serum-free cell culture media with serum replacement and interleukin 2 (IL-2). The T lymphocytes ( $\geq 90\%$ ; with  $< 5\%$  CD19+/CD22+ B cell impurity) are positive for the transgene ( $\geq 10\%$  CAR positive) and secrete interferon gamma (IFN- $\gamma$ )  
*cell-based gene therapy (antineoplastic)*

tinocabtagène autoleucel

lymphocytes T autologues obtenus à partir de lymphocytes de sang périphérique par leucaphérèse, transduits avec un vecteur lentiviral auto-inactivant et non répliquant, codant un récepteur antigénique chimérique bispécifique ciblant CD19 et CD22 (Siglec-2). Le transgène exprimé comprend une séquence de tête CD8 $\alpha$ , un fragment variable entièrement humain à chaîne unique (scFv) anti-CD19 et anti-CD22, une charnière CD8 $\alpha$  et une région transmembranaire, ainsi qu'un domaine de signalisation 4-1BB et CD3 $\zeta$  et est sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF1 $\alpha$ ). La construction est flanquée de répétitions longues terminales (LTR) en 5' et 3' et contient également un signal d'encapsidation  $\psi$ , un élément de réponse Rev (RRE), une séquence de tractus polypurine central (cPPT) et un élément régulateur post-transcriptionnel (WPRE) muté du virus de l'hépatite de Woodchuck. Le vecteur est pseudotypé avec la protéine d'enveloppe G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est enrichi en lymphocytes T CD4/CD8 par immunosélection positive, activé par des agonistes CD3 et CD28 et transduit avec le vecteur. Les cellules sont ensuite amplifiées dans un milieu de culture cellulaire optimisé sans sérum avec remplacement de sérum et interleukine 2 (IL-2). Les lymphocytes T ( $\geq 90\%$ ; avec  $< 5\%$  d'impuretés de cellules B CD19+/CD22+) sont positifs pour le transgène ( $\geq 10\%$  CAR positif) et sécrètent de l'interféron gamma (IFN- $\gamma$ )  
*thérapie génique à base de cellules (antineoplasique)*

tinocabtagén autoleucel

linfocitos T autólogos obtenidos de linfocitos de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica para un receptor de antígenos quimérico biespecífico dirigido a CD19 y CD22 (Siglec-2). El transgén expresado contiene una secuencia líder de CD8 $\alpha$ , un fragmento variable de cadena sencilla (scFv) totalmente humano anti-CD19 y otro anti-CD22, una región bisagra y transmembrana de CD8 $\alpha$ , y un dominio de señalización 4-1BB y CD3 $\zeta$ , y está bajo el control del promotor del factor de elongación 1 alfa (EF1 $\alpha$ ). El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento  $\psi$ , un elemento de respuesta Rev (RRE), una secuencia de tracto de polipurina central (cPPT) y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE) mutado. El vector está seudotipado con la proteína G de la envuelta del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se enriquece para linfocitos T CD4/CD8 mediante inmunoselección positiva, se activa mediante agonistas de CD3 y CD28 y se transduce con el vector. Las células son después expandidas en medio de cultivo celular optimizado sin suero, con sustituto de suero e interleuquina 2 (IL-2). Los linfocitos T ( $\geq 90\%$ ; con  $< 5\%$  de impureza de linfocitos B CD19+/CD22+) son positivos para el transgén ( $\geq 10\%$  positivos para el CAR) y secretan interferón gamma (IFN- $\gamma$ )  
*terapia génica basada en células (antineoplásico)*

**tinodasertibum**

tinodasertib

4-{6-[4-(morpholine-4-carbonyl)phenyl]imidazo[1,2-a]pyridin-3-yl}benzotrile  
*serine/ threonine kinase inhibitor, antineoplastic*

tinodasertib

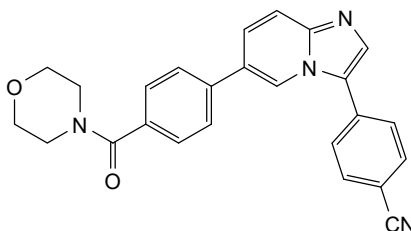
4-{6-[4-(morpholine-4-carbonyl)phényl]imidazo[1,2-a]pyridin-3-yl}benzotrile  
*inhibiteur de sérine/ thréonine kinase, antinéoplasique*

tinodasertib

4-{6-[4-(morfolina-4-carbonil)fenil]imidazo[1,2-a]piridin-3-il}benzotrilo  
*inhibidor de serina/ treonina kinasa, antineoplásico*

C<sub>25</sub>H<sub>20</sub>N<sub>4</sub>O<sub>2</sub>

1464151-33-4

**tividenofuspum alfa #**

tividenofusp alfa

human iduronate 2-sulfatase (IDS,  $\alpha$ -L-iduronate sulfate sulfatase, EC:3.1.6.13) pro-protein (1-525), fused via the peptide linker <sup>526</sup>GGGG<sup>530</sup> to a human immunoglobulin G1 C-terminal Fc fragment (531-757) variant (L<sup>544</sup>>A, L<sup>545</sup>>A, T<sup>676</sup>>S, L<sup>678</sup>>A, Y<sup>717</sup>>V), disulfide bridged to an engineered human immunoglobulin G1 anti-(human type 1 transferrin receptor (TfR1)) C-terminal Fc fragment (1'-227'), variant (L<sup>14</sup>>A, L<sup>15</sup>>A, T<sup>146</sup>>W, N<sup>164</sup>>Y, Q<sup>166</sup>>T, P<sup>167</sup>>E, E<sup>168</sup>>W, N<sup>169</sup>>A, D<sup>193</sup>>T, S<sup>195</sup>>E, R<sup>196</sup>>E, N<sup>201</sup>>F), heterodimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa;  
 human iduronate 2-sulfatase (IDS,  $\alpha$ -L-iduronate sulfate sulfatase, idursulfase, EC:3.1.6.13, UniProt:P22304), pro-protein (1-525), fused via the peptidic linker G<sub>4</sub>S (526-530) with a human immunoglobulin G1 hinge-CH2-CH3 Fc fragment [*Homo sapiens* IGHG1\*01 (531-757) (hinge (531-540, N-terminal hinge residues EPKSC deleted), CH2 L<sup>544</sup>>A, L<sup>545</sup>>A (541-650), CH3 T<sup>676</sup>>S, L<sup>678</sup>>A, Y<sup>717</sup>>V (651-755), CHS (756-757))], (536-6':539-9')-bisdisulfide with a human immunoglobulin G1 hinge-CH2-CH3 Fc fragment [*Homo sapiens* IGHG1\*01 (1'-227') (hinge (1-10), CH2 L<sup>14</sup>>A, L<sup>15</sup>>A (11-120), CH3 T<sup>146</sup>>W, N<sup>164</sup>>Y, Q<sup>166</sup>>T, P<sup>167</sup>>E, E<sup>168</sup>>W, N<sup>169</sup>>A, D<sup>193</sup>>T, S<sup>195</sup>>E, R<sup>196</sup>>E, N<sup>201</sup>>F engineered for binding to the human type 1 transferrin receptor (TfR1) (121-225), CHS (226-227))], produced in Chinese hamster ovary (CHO) cells, glycoform alfa  
*enzyme replacement therapy (mucopolysaccharidosis type 2)*



tividénofuscus alfa

iduronate 2-sulfatase humaine (IDS, α-L-iduronate sulfate sulfatase, EC:3.1.6.13) pro-protéine (1-525), fusionnée via la liaison peptidique <sup>526</sup>GGGGS<sup>530</sup> à une variante du fragment Fc C-terminal de l'immunoglobuline G1 humaine (531-757) (L<sup>544</sup>>A, L<sup>545</sup>>A, T<sup>676</sup>>S, L<sup>678</sup>>A, Y<sup>717</sup>>V), attachée par pont disulfure à un fragment Fc C-terminal (1'-227') de l'immunoglobuline G1 humaine modifiée anti-(récepteur de la transferrine de type 1 humaine (TfR1)), variant (L<sup>14</sup>>A, L<sup>15</sup>>A, T<sup>146</sup>>W, N<sup>164</sup>>Y, Q<sup>166</sup>>T, P<sup>167</sup>>E, E<sup>168</sup>>W, N<sup>169</sup>>A, D<sup>193</sup>>T, S<sup>195</sup>>E, R<sup>196</sup>>E, N<sup>201</sup>>F), hétérodimère, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa;

iduronate 2-sulfatase humaine (IDS, α-L-iduronate sulfate sulfatase, idursulfase, EC:3.1.6.13, UniProt:P22304), pro-protéine (1-525), fusionnée via la liaison peptidique G<sub>4</sub>S (526-530) avec un fragment charnière-CH2-CH3 (Fc) de l'immunoglobuline G1 humaine [*Homo sapiens* IGHG1\*01 (531-757) (charnière (531-540), fragment N-terminal EPKSC supprimé), CH2 L<sup>544</sup>>A, L<sup>545</sup>>A (541-650), CH3 T<sup>676</sup>>S, L<sup>678</sup>>A, Y<sup>717</sup>>V (651-755), CHS (756-757))], (536-6':539-9')-bisdisulfure avec un fragment charnière-CH2-CH3 (Fc) de l'immunoglobuline G1 humaine [*Homo sapiens* IGHG1\*01 (1'-227') (charnière (1-10), CH2 L<sup>14</sup>>A, L<sup>15</sup>>A (11-120), CH3 T<sup>146</sup>>W, N<sup>164</sup>>Y, Q<sup>166</sup>>T, P<sup>167</sup>>E, E<sup>168</sup>>W, N<sup>169</sup>>A, D<sup>193</sup>>T, S<sup>195</sup>>E, R<sup>196</sup>>E, N<sup>201</sup>>F modifiés dans le domaine CH3 pour lier au récepteur de la transferrine de type 1 humaine (TfR1), (121-225), CHS (226-227))], produit dans les cellules ovariennes de hamster chinois (CHO), glycoforme alfa

*traitement enzymatique substitutif (mucopolysaccharidoses de type 2)*

tividénofuscus alfa

iduronato 2-sulfatasa humana (IDS, α-L-iduronato sulfato sulfatasa, EC:3.1.6.13) proproteína (1-525), fusionada a través de un enlace peptídico <sup>526</sup>GGGGS<sup>530</sup> a una inmunoglobulina G1 humana con un fragmento Fc C-terminal (531-757) variante (L<sup>544</sup>>A, L<sup>545</sup>>A, T<sup>676</sup>>S, L<sup>678</sup>>A, Y<sup>717</sup>>V), disulfuro unido a una inmunoglobulina humana diseñada G1 anti-(receptor de la transferrina de tipo 1 humano (TfR1)) fragmento Fc C-terminal (1'-227'), variante (L<sup>14</sup>>A, L<sup>15</sup>>A, T<sup>146</sup>>W, N<sup>164</sup>>Y, Q<sup>166</sup>>T, P<sup>167</sup>>E, E<sup>168</sup>>W, N<sup>169</sup>>A, D<sup>193</sup>>T, S<sup>195</sup>>E, R<sup>196</sup>>E, N<sup>201</sup>>F), heterodímero, producido en células ováricas de hámster Chino, glicofoma alfa;

iduronato 2-sulfatasa humana (IDS, α-L-iduronato sulfato sulfatasa, idursulfasa, EC:3.1.6.13, UniProt:P22304), proproteína (1-525), fusionada mediante el enlace peptídico G<sub>4</sub>S (526-530) con un fragmento bisagra-CH2-CH3 (Fc) de inmunoglobulina G1 humana (531-757), [*Homo sapiens* IGHG1\*01 (531-757) (bisagra (531-540), fragmento N-terminal EPKSC suprimido), CH2 L<sup>544</sup>>A, L<sup>545</sup>>A (541-650), CH3 T<sup>676</sup>>S, L<sup>678</sup>>A, Y<sup>717</sup>>V (651-755), CHS (756-757))], (536-6':539-9')-bisdisulfuro con un fragmento bisagra-CH2-CH3 (Fc) de inmunoglobulina G1 humana [*Homo sapiens* IGHG1\*01 (1'-227') (bisagra (1-10), CH2 L<sup>14</sup>>A, L<sup>15</sup>>A (11-120), CH3 T<sup>146</sup>>W, N<sup>164</sup>>Y, Q<sup>166</sup>>T, P<sup>167</sup>>E, E<sup>168</sup>>W, N<sup>169</sup>>A, D<sup>193</sup>>T, S<sup>195</sup>>E, R<sup>196</sup>>E, N<sup>201</sup>>F) diseñados en el dominio CH3 para unirse al receptor de transferrina de tipo 1 humano (TfR1), (121-225), CHS (226-227))], producido en células ováricas de hámster Chino (CHO), glicofoma alfa

*tratamiento enzimático de sustitución (mucopolisacaridosis tipo 2)*

2641020-57-5

## Sequences / Séquences / Secuencias

## IDS × Fc

```

SETQANSTTD ALNVLIIVD DLRPSLGCYQ DKLVRSPNID QLASHSLLFQ 50
NAFAQQAVCA PSRVSELTGR RPDTRLYDF NSYWRVHAGN FSTIPQYFKE 100
NGYVTMSVGK VFHFGISSNH TDDSPYSWSF PPYHPSSEKY ENTKTCRGPD 150
GELHANLLCP VDVLDVPEGT LPDKQSTEQA IQLLEKMKTS ASPFFLAAGY 200
HKPHIFFRYP KEFQKLYPLE NITLAPDPEV PDGLPPVAYN FWMDIRQRED 250
VQALNISVPY GPIPVDFQRK IRQSYFASVS YLDTQVGRLL SALDDLQLAN 300
STIIAFTSDH GWALGEHGEW AKYSNFDVAT HVPLIFYVPG RTASLPEAGE 350
KLFFYLDPFD SASQLMEPGR QSMDLVELVS LFPTLAGLAG LQVPPRCVPV 400
SFHVLCREG KNLLKHFRRR DLEEDPYLPG NPRELIAYSQ YPRPSDIPQW 450
NSDKPSLKDI KIMGYSIRTI DYRYTVWVGF NPDEFLANFS DIHAGELYFV 500
DSDPLQDHNH YNDSQGGDLF QLLMPGGGGS DKTHTCPPCP APEAAAGGPSV 550
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK 600
PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK 650
GQPREPQVYT LPPSRDELTK NQVSLSCAVK GFYPSDIAVE WESNGQPENN 700
YKTTFPVLDS DGSFFLVSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS 750
LSLSPGK 757

```

## anti-TfR1 Fc

```

DKTHTCPPCP APEAAAGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED 50
PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK 100
CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK NQVSLWCLVK 150
GFYPSDIAVE WESYCTEWAAN YKTTFPVLDS DGSFFLYSKL TVTKREWQQG 200
EVFSCSVMHE ALHNHYTQKS LSLSPGK 227

```

## Mutation / Mutation / Mutación

L<sup>544</sup>>A, L<sup>545</sup>>A, T<sup>676</sup>>S, L<sup>678</sup>>A, Y<sup>717</sup>>Y, L<sup>14</sup>>A, L<sup>15</sup>>A, T<sup>146</sup>>W, N<sup>164</sup>>Y, Q<sup>166</sup>>I, p<sup>167</sup>>E, E<sup>168</sup>>W, N<sup>169</sup>>A, D<sup>193</sup>>I, S<sup>193</sup>>E, R<sup>196</sup>>E, N<sup>201</sup>>F

## Peptide linker / Peptide liant / Péptido de unión

526-530 GGGG

## Post-translational modifications

Disulfide bridge locations / Positions de pont disulfure / Posiciones del puentes disulfuro

Intra-chain 146-159, 397-407, 571-631, 677-735

41'-101', 147'-205'

Inter-chain 536-6', 539-9'

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

N6, N90, N300, N488, N512, N607; N77

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

H CHS K2: K757, K227

Other modification / Autre modification / Otra modificación

C59: Cys → 3-OxoAla (formylGly)

## tivumecirnonum

tivumecirnon

2-[(3R)-3-(1-{1-[(1R)-1-(2,4-dichlorophenyl)ethyl]-3-(trifluoromethyl)-1H-pyrazolo[3,4-b]pyrazin-6-yl}azetidín-3-yl)piperidin-1-yl]ethan-1-ol  
*chemokine receptor 4 (CCR4) antagonist, antineoplastic*

tivumécirnon

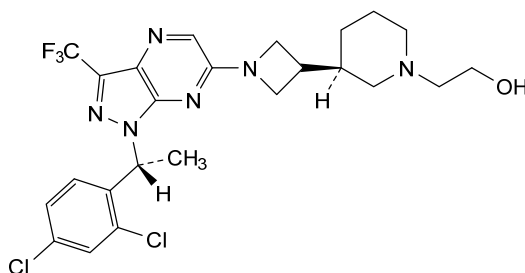
2-[(3R)-3-(1-{1-[(1R)-1-(2,4-dichlorophényl)éthyl]-3-(trifluorométhyl)-1H-pyrazolo[3,4-b]pyrazin-6-yl}azétidín-3-yl)pipéridin-1-yl]éthan-1-ol  
*antagoniste du récepteur 4 de la chimiokine (CCR4), antinéoplasique*

tivumecirnon

2-[(3R)-3-(1-{1-[(1R)-1-(2,4-diclorofenil)etil]-3-(trifluorometil)-1H-pirazolo[3,4-b]pirazin-6-il}azetidín-3-il)piperidin-1-il]etan-1-ol  
*antagonista del receptor de quimiocina 4 (CCR4), antineoplásico*

C<sub>24</sub>H<sub>27</sub>Cl<sub>2</sub>F<sub>3</sub>N<sub>6</sub>O

2174938-78-2



**trabikibartum #**  
trabikibart

immunoglobulin G4-kappa, anti-[*Homo sapiens* CSF2RB (colony stimulating factor 2 (granulocyte-macrophage) receptor beta chain, granulocyte-macrophage colony stimulating factor (GM-CSF) receptor beta chain, IL3RB, IL5RB)], *Homo sapiens* monoclonal antibody; gamma4 heavy chain *Homo sapiens* (1-444) [VH (*Homo sapiens*IGHV3-23\*02 (85.7%) -(IGHD) -IGHJ3\*02 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens*IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (118-215), hinge 1-12 S10>P (225) (216-227), CH2 L92 (306) (228-337), CH3 (338-442), CHS (443-444)) (118-444)], (131-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-12\*01 (100%) -IGKJ5\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC\*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (223-223":226-226")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1SV, glycoform alfa  
*anti-inflammatory*

trabikibart

immunoglobuline G4-kappa, anti-[*Homo sapiens* CSF2RB (chaîne bêta du récepteur du facteur 2 stimulant les colonies (granulocyte-macrophage), chaîne bêta du récepteur du facteur stimulant des colonies de granulocytes et macrophages (GM-CSF), IL3RB, IL5RB)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma4 *Homo sapiens* (1-444) [VH (*Homo sapiens*IGHV3-23\*02 (85.7%) -(IGHD) -IGHJ3\*02 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens*IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (118-215), charnière 1-12 S10>P (225) (216-227), CH2 L92 (306) (228-337), CH3 (338-442), CHS (443-444)) (118-444)], (131-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-12\*01 (100%) -IGKJ5\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC\*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (223-223":226-226")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1SV, glycoforme alfa  
*anti-inflammatoire*

trabikibart

inmunoglobulina G4-kappa, anti-[*Homo sapiens* CSF2RB (cadena beta del receptor del factor 2 estimulante de las colonias (granulocito-macrófago, cadena beta del receptor del factor estimulante de las colonias de granulocitos y macrófagos (GM-CSF), IL3RB, IL5RB)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma4 *Homo sapiens* (1-444) [VH (*Homo sapiens* IGHV3-23\*02 (85.7%) -(IGHD) -IGHJ3\*02 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG4\*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (118-215), bisagra 1-12 S10>P (225) (216-227), CH2 L92 (306) (228-337), CH3 (338-442), CHS (443-444)) (118-444)], (131-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12\*01 (100%) -IGKJ5\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (223-223":226-226")-bisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1SV, forma glicosilada alfa *antiinflamatorio*

2643974-98-3

## Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGTFPP WYRVHWVRQA PGKLEWVSS 50
IRSSGGFPYY NYKVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARFY 100
DSFFDIWQQG TMVTVSSAST KGPSVFLAP CSRSTSESTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVTVPS SSLGTRKTYTC 200
NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF PPKPKDTLMI 250
SRTEPVTCTVV VDVQSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV 300
SVLTVLHQDW LNKKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP 350
SQEEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TTPVLDSDGS 400
FFLYSRLTVD KSRWQEGNVF SCSVMHEALH NHYTQKLSLSL SLGK 444
```

## Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS VSASVGRVT ITCRASQGIS SWLAWYQKPK GKAPKLLIYA 50
ASSLQSGVPS RFGSGSGGTD FTLTISLQEP EDFATYYCQP ANSFPITFGQ 100
GTRLEIKRTY AAPSVFIFPP SDEQLKSGTA SVVCLLNFFY PREAKVQWVK 150
DNALQSGNSQ ESVTEQDSKD STYLSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEK 214
```

## Post-translational modifications

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

Intra-H (C23-C104) 22-96 144-200 258-318 364-422  
22-96" 144"-200" 258"-318" 364"-422"

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

Inter-H-L (CH1 10-CL 126) 131-214' 131"-214"

Inter-H-H (h 8, h 11) 223-223" 226-226"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación  
H CH2 N84.4: 294, 294"

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal  
H CHS K2: 444, 444"

**trastuzumabum botidotinum #**

trastuzumab botidotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor tyrosine-protein kinase erbB-2, epidermal growth factor receptor 2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], humanized monoclonal antibody; conjugated to duostatin-5 (Duo-5) via a cleavable linker;  
gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV3-66\*01 (81.6%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA

- (*Homo sapiens* IGKV1-39\*01 (86.3%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214'); dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa; 188', 188'''-lysine diamide conjugated to duostatin-5 (Duo-5) via a cleavable linker, in a drug-antibody ratio (DAR) of 2  
*antineoplastic*
- trastuzumab botidotine immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB2 (récepteur tyrosine-protéine kinase erbB-2, récepteur 2 du facteur de croissance épidermique, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticorps monoclonal humanisé; conjugué à la duostatine-5 (Duo-5) via un linker clivable;  
chaîne lourde gamma1 humanisée (1-450) [VH (*Homo sapiens*IGHV3-66\*01 (81.6%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens*IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-39\*01 (86.3%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214'); dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa; 188', 188'''- lysine diamide conjuguée à la duostatine-5 (Duo-5) via un linker clivable, dans un rapport principe actif - anticorps de 2  
*antineoplasique*
- trastuzumab botidotina inmunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor tirosina-proteína kinasa erbB-2, receptor 2 del factor de crecimiento epidérmico, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticuerpo monoclonal humanizado; conjugado con la duostatina-5 (Duo-5) a través de un enlace escindible;  
cadena pesada gamma1 humanizada (1-450) [VH (*Homo sapiens*IGHV3-66\*01 (81.6%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens*IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-39\*01 (86.3%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC\*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214'); dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa; 188', 188'''- lisina diamia conjugada con la duostatina-5 (Duo-5) a través de un enlace escindible, en un ratio de principio activo-anticuerpo de 2  
*antineoplásico*

## Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG LVQPGGSLRL SCAASGFNIK DTYIHWVRQA PGKGLEWVAR 50  
 IYPTNGYTRY ADSVKGRFTI SADTSKNTAY LQMNSLRAD TAVYYCSRWG 100  
 GDGFYAMDYV GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150  
 DYFPEPVTVS WNSGALTSKV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200  
 YICNVNHKPS NTKVDKKEVP KSCDKTHTCP PCPAPPELLGG PSVFLFPPKP 250  
 KDTLMIKSRTP EVTQVVDVDS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300  
 STYRVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIIS KAKGQPREPQ 350  
 VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEVESNGQP ENNYKTPFPV 400  
 LDSGGFFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450

## Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGRDVT ITCRASQDVN TAVAWYQQKPK GKAPKLLIYS 50  
 ASFLYSGVPS RFGSRSRGTG FTLTISLQEP EDFATYCYCQ HYTPPTFFGQ 100  
 GTKVEIKRVT AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQMKV 150  
 DNALQSGNSQ ESVTEQDSKD STYLSLSSTLT LSKADYEKHK VYACEVTHQG 200  
 LSSPVTKSEN RGEK 214

## Post-translational modifications

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

Intra-H (C23-C104) 22-96 147-203 264-324 370-428  
 22"-96" 147"-203" 264"-324" 370"-428"

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

Inter-H-L (h 5-CL 126) 223-214' 223"-214"

Inter-H-H (h 11, h 14) 229-229\* 232-232"

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

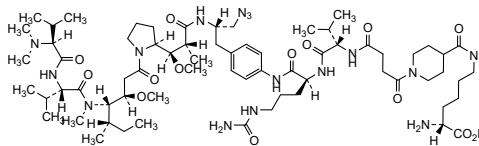
H CH2 N84.4: 300, 300"

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

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

## Modified residues / Résidus modifiés / Restos modificados

K (188', 188")  
 N<sup>6</sup>-R-L-Lys



**trastuzumabum vedotinum #**  
 trastuzumab vedotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor tyrosine-protein kinase erbB-2, epidermal growth factor receptor 2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], humanized monoclonal antibody; conjugated to auristatin E; gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV3-66\*01 (81.6%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (86.3%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa; conjugated, on an average of 3-4 cysteinyl, to monomethylauristatin E (MMAE), via a cleavable maleimidocaproyl-valylcitrullinyl-p-aminobenzyloxycarbonyl (mc-val-cit-PABC) type linker

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

antineoplastic

trastuzumab védotíne

immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB2 (récepteur tyrosine-protéine kinase erbB-2, récepteur 2 du facteur de croissance épidermique, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticorps monoclonal humanisé; conjugué à l'auristatine E;

chaîne lourde gamma1 humanisée (1-450) [VH (*Homo sapiens* IGHV3-66\*01 (81.6%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (86.3%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa; conjugué, sur 3-4 résidus cystéinyles en moyenne, à la monométhylauristatine E (MMAE), via un linker clivable de type maléimidocaproyl-valylcitrullinyl-p-aminobenzoyloxycarbonyl (mc-val-cit-PABC)

Pour la partie *védotíne*, veuillez-vous référer au document '*INN for pharmaceutical substances: Names for radicals, groups and others\** *antineoplasique*

trastuzumab vedotina

immunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor tirosina-proteína kinasa erbB-2, receptor 2 del factor de crecimiento epidérmico, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticuerpo monoclonal humanizado; conjugado con la auristatina E;

cadena pesada gamma1 humanizada (1-450) [VH (*Homo sapiens* IGHV3-66\*01 (81.6%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1\*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (86.3%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, forma glicosilada alfa; conjugado, en 3-4 restos cisteinil por término medio, a la monometilauristatina E (MMAE), a través de un enlace escindible de tipo maléimidocaproyl-valilcitrulinil-p-aminobenciloxicarbonil (mc-val-cit-PABC)

Para la fracción *vedotina*, se pueda referirse al documento '*INN for pharmaceutical substances: Names for radicals, groups and others\** *antineoplásico*

2740607-04-7

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG	LVQPGGSLRL	SCAASGFNIK	DTYIHVVQRQ	PGKGLEWVAR	50
IYPTNGYTRY	ADSVKGRFTI	SADTSKNTAY	LQMSLRRAED	TAVYYCSRWG	100
GDGFYAMDYW	GGTTLVTVSS	ASTKGFSPVF	LAFSSKSTSG	GTAALGCLVK	150
DYFPEPVTVS	WNSGALTSGV	HTFFAVLQSS	GLYSLSSVVT	VPSSSLGTQT	200
YICNVNHPKS	NTKVDKKEPE	KSCDKTHTCP	PCPAPELLGG	PSVFLFPPKP	250
KDTLMISRTP	EVTCAVVVDVS	HEDPEVKFNW	YVDGVEVHNA	KTKPREEQYN	300
STYRVVSVLT	VLHQDWLNGK	EYKCKVSNKA	LPAPIEKTIS	KAKGQPREPQ	350
VYTLPPSREE	MTRKQVSLTC	LVKGFYPSDI	AVEWESNGQP	ENNYKTTFPV	400
LDSGGSFFLY	SKLTVDKSRW	QQGNVFCSCV	MHEALHNHYT	QKSLSLSPGK	450

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS	LSASVGDRTV	ITCRASQDVN	TAVAWYQQKQ	GKAPKLLIYS	50
ASFLYSGVPS	RFGSGRSGTD	FTLTISLSLPQ	EDFATYYCQQ	HYTTPPTFGQ	100
GTKVEIKRIV	AAPSVEFIFPP	SDEQLKSGTA	SVVCLLNIFY	PREAKVQWKV	150
DNALQSGNSQ	ESVTEQDSKD	STYLSLSTLT	LSKADYEKHK	VYACEVTHQG	200
LSSPVTKSFN	RGEC				214

**Post-translational modifications**

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

Intra-H (C23-C104)	22-96	147-203	264-324	370-428
	22"-96"	147"-203"	264"-324"	370"-428"

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

Inter-H-L\* (h 5-CL 126) 223-214" 223"-214"

Inter-H-H\* (h 11, h 14) 229-229" 232-232"

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

\*Au moins deux des quatre ponts disulfures inter-chaînes ne sont pas présents, 4 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif.

\*Al menos dos de los cuatro puentes disulfuro inter-catenarios no estan presentes, una media de 4 cisteinil está conjugada a conectores de principio activo.

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

H CH2 N84.4: 300, 300"

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

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

**trovocabtagenum autoleucelum #**  
trovocabtagene autoleucel

autologous T lymphocytes obtained from peripheral blood mononuclear cells by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector encoding a chimeric antigen receptor (CAR) targeting human B cell maturation antigen (BCMA). The expressed transgene comprises a CD8 $\alpha$  leader sequence, an anti-BCMA single chain variable fragment (scFv), a CD8 $\alpha$  hinge and transmembrane domain, and a 4-1BB (CD137) and CD3 $\zeta$  signal domain, under control of the human elongation factor 1 $\alpha$  (EF-1 $\alpha$ ) short promoter. The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a  $\psi$  packaging signal, a Rev response element (RRE), a central polypurine tract (cPPT) sequence and a mutated Woodchuck hepatitis virus posttranscriptional regulatory element (WPRE). The vector is pseudotyped with vesicular stomatitis virus (VSV) glycoprotein G. The leukapheresis material is enriched for CD4/8+ T lymphocytes by positive immunoselection, activated by CD3 and CD28 agonists and transduced with the lentiviral vector before further culture and expansion in serum free growth media containing interleukin 2 (IL-2). The cell suspension consists of T lymphocytes (>90%; CD3+/CD45+), with  $\geq$ 10% of the T lymphocytes expressing the CAR-BCMA transgene. The T lymphocytes secrete interferon gamma (IFN- $\gamma$ ) following co-culture with BCMA-expressing cells  
*cell-based gene therapy (antineoplastic)*



trovocabtagène autoleucel

lymphocytes T autologues obtenus à partir de cellules mononucléaires de sang périphérique par leucaphérèse, transduits avec un vecteur lentiviral auto-inactivant et non répliquant codant un récepteur antigénique chimérique (CAR) ciblant l'antigène de maturation des cellules B humaines (BCMA). Le transgène exprimé comprend une séquence de tête CD8 $\alpha$ , un fragment variable à chaîne unique (scFv) anti-BCMA, un domaine charnière et transmembranaire CD8 $\alpha$ , et un domaine de signalisation 4-1BB (CD137) et CD3 $\zeta$ , sous le contrôle du promoteur court du facteur d'élongation humain 1 $\alpha$  (EF-1 $\alpha$ ). La construction est flanquée de répétitions longues terminales (LTR) en 5' et 3' et contient également un signal d'encapsulation  $\psi$ , un élément de réponse Rev (RRE), une séquence du tractus polypurine central (cPPT) et un élément régulateur post-transcriptionnel (WPRE) muté du virus de l'hépatite de Woodchuck. Le vecteur est pseudotypé avec la glycoprotéine G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est enrichi en lymphocytes T CD4/8+ par immunosélection positive, activé par des agonistes CD3 et CD28 et transduit avec le vecteur lentiviral avant une nouvelle culture et une expansion dans un milieu de croissance sans sérum contenant de l'interleukine 2 (IL-2). La suspension cellulaire est composée de lymphocytes T (>90%; CD3+/CD45+), avec  $\geq$ 10% des lymphocytes T exprimant le transgène CAR-BCMA. Les lymphocytes T sécrètent de l'interféron gamma (IFN- $\gamma$ ) après co-culture avec les cellules exprimant BCMA  
*thérapie génique à base de cellules (antinéoplasique)*

trovocabtagén autoleucel

linfocitos T autólogos obtenidos de células mononucleares de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica para un receptor de antígenos quimérico (CAR) dirigido al antígeno de maduración de células B (BCMA). El transgén expresado contiene una secuencia líder de CD8 $\alpha$ , un fragmento variable de cadena sencilla (scFv) anti-BCMA, un dominio bisagra y transmembrana de CD8 $\alpha$ , y un dominio de señalización 4-1BB (CD137) y CD3 $\zeta$ , bajo el control del promotor corto del factor de elongación 1 alfa (EF1 $\alpha$ ) humano. El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento  $\psi$ , un elemento de respuesta Rev (RRE), una secuencia de tracto de polipurina central (cPPT) y una secuencia y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE) mutado. El vector está seudotipado con la glicoproteína G del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se enriquece para linfocitos T CD4/8+ mediante inmunoselección positiva, se activa mediante agonistas de CD3 y CD28 y se transduce con el vector lentiviral antes del cultivo y expansión adicional en medio de crecimiento sin suero que contiene interleuquina 2 (IL-2). La suspensión celular consiste en linfocitos T (>90%; CD3+/CD45+), con  $\geq$ 10% de linfocitos T que expresan el transgén CAR-BCMA. Los linfocitos T secretan interferón gamma (IFN- $\gamma$ ) tras el cocultivo con células que expresan BCMA  
*terapia génica basada en células (antineoplásico)*

**udifitimodum**

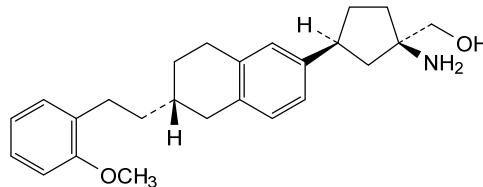
udifitimod [[ (1*R*,3*S*)-1-amino-3-{{(6*S*)-6-[2-(2-methoxyphenyl)ethyl]-5,6,7,8-tetrahydronaphthalen-2-yl}cyclopentyl]methanol  
*immunomodulator*

udifitimod [[ (1*R*,3*S*)-1-amino-3-{{(6*S*)-6-[2-(2-méthoxyphényl)éthyl]-5,6,7,8-tétrahydronaphthalén-2-yl}cyclopentyl]méthanol  
*immunomodulateur*

udifitimod [[ (1*R*,3*S*)-1-amino-3-{{(6*S*)-6-[2-(2-metoxifenil)etil]-5,6,7,8-tetrahidronaftalén-2-il}ciclopentil]metanol  
*immunomodulador*

C<sub>25</sub>H<sub>33</sub>NO<sub>2</sub>

1883345-06-9



**umedaptanibum pegolum**

umedaptanib pegol

5'-[{{6-[[{{(2*RS*)-2,3-bis[ω-methoxypoly(oxyethylene)-α-yl]propxoy}carbonyl)amino]hexanyl)oxy}(hydroxy)phosphoryl]-2'-O-methylguanylyl-(3'→5')-2'-O-methylguanylyl-(3'→5')-2'-O-methylguanylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-2'-O-methyluridylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-2'-O-methylcytidylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-2'-O-methylguanylyl-(3'→5')-2'-O-methylguanylyl-(3'→5')-guanylyl-(3'→5')-2'-O-methylcytidylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-2'-O-methyluridylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-2'-O-methyluridylyl-(3'→5')-2'-O-methylguanylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-O-methyluridylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-2'-O-methylcytidylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-guanylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-2'-O-methylguanylyl-(3'→5')-2'-O-methyluridylyl-(3'→5')-2'-O-methylcytidylyl-(3'→5')-2'-O-methylcytidylyl-(3'→3')-thymidine  
*angiogenesis inhibitor*

umédaptanib pégol

5'-[{{6-[[{{(2*RS*)-2,3-bis[ω-méthoxypoly(oxyéthylène)-α-yl]propxoy}carbonyl)amino]hexanyl)oxy}(hydroxy)phosphoryl]-2'-O-méthylguanylyl-(3'→5')-2'-O-méthylguanylyl-(3'→5')-2'-O-méthylguanylyl-(3'→5')-2'-O-méthyladénylyl-(3'→5')-2'-O-méthyluridylyl-(3'→5')-2'-O-méthyladénylyl-(3'→5')-2'-O-méthylcytidylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-O-méthyladénylyl-(3'→5')-2'-O-méthylguanylyl-(3'→5')-2'-O-méthylguanylyl-(3'→5')-guanylyl-(3'→5')-2'-O-méthylcytidylyl-(3'→5')-2'-O-méthyladénylyl-(3'→5')-2'-O-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-O-méthyladénylyl-(3'→5')-2'-O-méthyluridylyl-(3'→5')-2'-O-méthyladénylyl-(3'→5')-2'-O-méthylcytidylyl-(3'→5')-2'-O-méthyladénylyl-(3'→5')-guanylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-O-méthyladénylyl-(3'→5')-2'-O-méthylguanylyl-(3'→5')-2'-O-méthyluridylyl-(3'→5')-2'-O-méthylcytidylyl-(3'→3')-thymidine



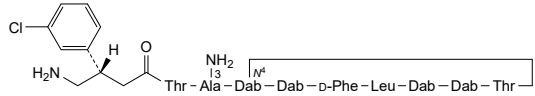
upleganán

$N^{4,3}$ ,9-anhidro{*N*-[[*(3S)*-4-amino-3-(3-clorofenil)butanoil]-*L*-treonil-3-amino-*L*-alanil-(*2S*)-2,4-diaminobutanoil-(*2S*)-2,4-diaminobutanoil-*D*-fenilalanil-*L*-leucil-(*2S*)-2,4-diaminobutanoil-(*2S*)-2,4-diaminobutanoil-*L*-treonina}

*antibacteriano*

C<sub>52</sub>H<sub>82</sub>ClN<sub>15</sub>O<sub>12</sub>

2407717-17-1



Dab = (*2S*)-2,4-diaminobutanoic acid  
 = acide (*2S*)-2,4-diaminobutanoïque  
 = ácido (*2S*)-2,4-diaminobutanoico

**vabametkibum**

vabametkib

(*4*<sup>2</sup>*S*)-1<sup>1</sup>,8<sup>4</sup>-dimethyl-2(6,1)-[1,2,3]triazolo[4,5-*b*]pyrazine-4(2,4)-morpholina-5(2,5)-pyrimidina-8(1)-piperazina-1(4)-pyrazola-6(1,4)-benzenaoctaphane  
*hepatocyte growth factor receptor inhibitor, antineoplastic*

vabametkib

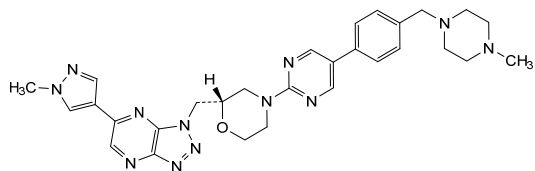
(*4*<sup>2</sup>*S*)-1<sup>1</sup>,8<sup>4</sup>-diméthyl-2(6,1)-[1,2,3]triazolo[4,5-*b*]pyrazine-4(2,4)-morpholina-5(2,5)-pyrimidina-8(1)-pipérazina-1(4)-pyrazola-6(1,4)-benzénaoctaphane  
*inhibiteur du récepteur du facteur de croissance des hépatocytes, antinéoplasique*

vabametkib

(*4*<sup>2</sup>*S*)-1<sup>1</sup>,8<sup>4</sup>-dimetil-2(6,1)-[1,2,3]triazolo[4,5-*b*]pirazina-4(2,4)-morfolina-5(2,5)-pirimidina-8(1)-piperazina-1(4)-pirazola-6(1,4)-bencenaoctafano  
*inhibidor del receptor del factor de crecimiento de los hepatocitos, antineoplásico*

C<sub>29</sub>H<sub>34</sub>N<sub>12</sub>O

1571903-56-4

**vamikibartum #**

vamikibart

immunoglobulin G2-kappa, anti-[*Homo sapiens* IL6 (interleukin 6)], humanized and chimeric monoclonal antibody;  
 gamma2 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV1-69\*11 (86.7%) -(IGHD) -IGHJ5\*02 (90.9%) L123>T (117), CDR-IMGT [8.8.15] (26-33,51-58,97-111)) (1-122) -*Homo sapiens* IGHG2\*01, G2m.. CH2 V45.1, G2v8 CH2 A93 (CH1 (123-220), hinge 1-12 (221-232), CH2 V45.1 (283), H93>A (311) (233-341), CH3 (342-446), CHS (447-448)) (123-448)],

- (136-218')-disulfide with kappa light chain chimeric (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-2\*01 (79.8%) -IGKJ2\*03 (90.9%) S120>Q (104)/*Homo sapiens* IGKV4-1\*01 (79.2%) -IGKJ2\*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC\*01, Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (224-224":225-225":228-228":231-231")-tetrakisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1M, glycoform alfa  
*anti-inflammatory*
- vamikibart immunoglobuline G2-kappa, anti-[*Homo sapiens* IL6 (interleukine 6)], anticorps monoclonal humanisé et chimérique;  
chaîne lourde gamma2 humanisée (1-448) [VH (*Homo sapiens* IGHV1-69\*11 (86.7%) -(IGHD) -IGHJ5\*02 (90.9%) L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG2\*01, G2m.. CH2 V45.1, G2v8 CH2 A93 (CH1 (123-220), charnière 1-12 (221-232), CH2 V45.1 (283), H93>A (311) (233-341), CH3 (342-446), CHS (447-448)) (123-448)], (136-218')-disulfure avec la chaîne légère kappa chimérique (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-2\*01 (79.8%) -IGKJ2\*03 (90.9%) S120>Q (104)/*Homo sapiens* IGKV4-1\*01 (79.2%) -IGKJ2\*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC\*01, Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (224-224":225-225":228-228":231-231")- tétrakisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1M, glycoforme alfa  
*anti-inflammatoire*
- vamikibart immunoglobulina G2-kappa, anti-[*Homo sapiens* IL6 (interleukina 6)], anticuerpo monoclonal humanizado y quimérico;  
cadena pesada gamma2 humanizada (1-448) [VH (*Homo sapiens* IGHV1-69\*11 (86.7%) -(IGHD) -IGHJ5\*02 (90.9%) L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG2\*01, G2m.. CH2 V45.1, G2v8 CH2 A93 (CH1 (123-220), bisagra 1-12 (221-232), CH2 V45.1 (283), H93>A (311) (233-341), CH3 (342-446), CHS (447-448)) (123-448)], (136-218')-disulfuro con la cadena ligera kappa quimérica (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-2\*01 (79.8%) -IGKJ2\*03 (90.9%) S120>Q (104)/*Homo sapiens* IGKV4-1\*01 (79.2%) -IGKJ2\*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC\*01, Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (224-224":225-225":228-228":231-231")- tetrakisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1M, forma glicosilada alfa  
*antiinflamatorio*

2744320-12-3

## Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VKKPGSSVKV SCKASGYVLP NYLIEWVRQA PGQGLEWMGV 50  
 TTPGGGTINY AOKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARSR 100  
 WDP LYYALE YWGGT TVTV SSASTKGPSV FPLAPCSRST SESTAALGCL 150  
 VKDYFFPEPVT VSWNSGALTS GVHTFPAVLQ SGLYLSLSSV VTPSSNFGT 200  
 QTYTCNVDPHK PSNTKVDKTV ERKCCVCEPP CPAPFVAGPS VFLFPKPKD 250  
 TLMISRTPEV TCVVVDVSHS DPEVQFNWYV DGEVHNAKT KPREEQFNST 300  
 FRVVSVLFVY AQDWLNGKEY KCKVSNKGLP APIEKTISKT KGPREPQVY 350  
 TLPFSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTTPMLD 400  
 SDGSFFLYSK LTVDKSRWQQ GNVFCSVMH EALHNNHYTK SLSLSPGK 448

## Light chain / Chaîne légère / Cadena ligera

DIVMTQSPDS LAVSLGERAT INCRASEVD NYGIPFMNRY QOKPGQPPKL 50  
 LIYAASNRGS GVPDRFSGSG SGTDFLTLSI SLQAEDVAVY YCQQSEEVPL 100  
 TFGQGTKEII KRTVAAPSVF IFPPSDEQLK SGTASVCLL NNFYPREAKV 150  
 QRKVDNALQS GNSQESVTEQ DSRDSTYSLS 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) 22-96 149-205 262-322 368-426  
 22-96<sup>a</sup> 149-205<sup>a</sup> 262-322<sup>a</sup> 368-426<sup>a</sup>  
 Intra-L (C23-C104) 23-92<sup>b</sup> 138-198<sup>b</sup>  
 23-92<sup>b</sup> 138-198<sup>b</sup>

Inter-H-L (CH1 10-CL 126) 136-218<sup>c</sup> 136-218<sup>c</sup>Inter-H-H (h 4, h 5, h 8, h11) 224-224<sup>d</sup> 225-225<sup>d</sup> 228-228<sup>d</sup> 231-231<sup>d</sup>

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

Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolyle)  
 H VH Q1: 1, 1<sup>e</sup>

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

H CH2 N84.4: 298, 298<sup>e</sup>

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal  
 H CHS K2: 448, 448<sup>f</sup>veligrotugum #  
veligrotug

immunoglobulin G1-kappa, anti-[*Homo sapiens* IGF1R (insulin-like growth factor 1 receptor, IGF1-R, IGF-1R, CD221)], chimeric monoclonal antibody; gamma1 heavy chain chimeric (1-454) [VH (*Mus musculus* IGHV1S81\*02 (91.8%) -(IGHD) -IGHJ1\*01 (93.8%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, D12, L14 (CH1 K120 (221) (125-222), hinge 1-15 (223-237), CH2 (238-347), CH3 D12 (363), L14 (365) (348-452), CHS (453-454)) (125-454)], (227-219')-disulfide with kappa light chain chimeric (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117\*01 (93.0%) -IGKJ1\*02 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (233-233":236-236")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa  
*insulin-like growth factor 1 receptor (IGF-1R) antagonist*

## véligrotug

immunoglobuline G1-kappa, anti-[*Homo sapiens* IGF1R (récepteur du facteur de croissance 1 analogue à l'insuline, IGF1-R, IGF-1R, CD221)], anticorps monoclonal chimérique; chaîne lourde gamma1 chimérique (1-454) [VH (*Mus musculus* IGHV1S81\*02 (91.8%) -(IGHD) -IGHJ1\*01 (93.8%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, D12, L14 (CH1 K120 (221) (125-222), charnière

1-15 (223-237), CH2 (238-347), CH3 D12 (363), L14 (365) (348-452), CHS (453-454) (125-454)], (227-219')-disulfure avec la chaîne légère kappa chimérique (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117\*01 (93.0%) -IGKJ1\*02 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (233-233":236-236")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa  
*antagoniste du récepteur du facteur de croissance de type 1 apparenté à l'insuline (IGF-1R)*

veligrotug

immunoglobulina G1-kappa, anti-[*Homo sapiens* IGF1R (receptor del factor de crecimiento 1 análogo a la insulina, IGF1-R, IGF-1R, CD221)], anticuerpo monoclonal quimérico;  
 cadena pesada gamma1 quimérica (1-454) [VH (*Mus musculus* IGHV1S81\*02 (91.8%) -(IGHD) -IGHJ1\*01 (93.8%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, D12, L14 (CH1 K120 (221) (125-222), bisagra 1-15 (223-237), CH2 (238-347), CH3 D12 (363), L14 (365) (348-452), CHS (453-454) (125-454)], (227-219')-disulfuro con la cadena ligera kappa quimérica (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117\*01 (93.0%) -IGKJ1\*02 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (233-233":236-236")-bisdisulfuro, producido en las células ováricas de hamster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa  
*antagonista del receptor del factor de crecimiento 1 similar a la insulina (IGF-1R)*

2728655-31-8

## Heavy chain / Chaîne lourde / Cadena pesada

```

QVQLVQSGAE VVKPGASVKL SCKASGYTFT SYWMHWVKQR PGQGLEWIGE 50
INPSNGRNTNY NQKFGQKATL TVDKSSSTAY MQLSSLTSED SAVVYFARGR 100
PDYVYSSKMWY FDVWGQGTTV TVSSASTKGP SVFPLAPSSK STSGGTAALG 150
CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS SVVTVPSSSL 200
GTQTYICNVN HKPSNTKVDK KVEPKSCDKT HCCPCPAPE LLGGPSVFLF 250
PKPKDTLMI SRTEPEVTCV VDVSHEDPEV KFNWYVDGVE VHNARTKPRE 300
EQYNSTYRVV SVLTVLHQDW LMGKEYKCKV SNKALPAPIE KTISKARGQP 350
REPQVYTLFP SRDELTKNQV SLTCLVKGFY PSDIAVEWES NQPFENNYKT 400
TFPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKLSL 450
SPGK 454

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## Light chain / Chaîne légère / Cadena ligera

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DVMVTQTPLS LPVSLGDPAS ISCRSSQSIV HSNVNTYLEW YLQKPGQSPR 50
LLIYKVSNRV SGVPRDFSGS GAGTDFTLRI SRVEAEDLGI YYCFQGSHPV 100
PTFGGGTRLE IKRTVAAPSV FIFPPSDEQL KSGTASVVL LNNFYPREAK 150
VQWVKVDNALQ SGNSQESVTE QDSKDYSTSL SSSLTSLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFRNGEC 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, F96 151-207 268-328 374-432  
 22", F96" 151"-207" 268"-328" 374"-432"

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

Inter-H-L (h 5-CL 126) 227-219" 227"-219"

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

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

glutamínilo N-terminal

Q &gt; pyrroglutamyl (pE, 5-oxoprolyl) / pyrroglutamyle (pE, 5-oxoprolyle) / piroglutamilo

(pE, 5-oxoprolyle)

H VH Q1: 1, 1"

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

H CH2 N84.4: 304, 304"

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

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

H CHS K2: 454, 454"

**ventoberantum**

ventoberant

1-ethyl-3-[(3*R*)-3-((2*S*)-2-hydroxy-3-[3-(methanesulfonyl)phenoxy]propyl)amino]-1-oxa-8-azaspiro[4.5]decane-8-sulfonyl]quinolin-4(1*H*)-one  
*beta-3 adrenoceptor antagonist*

ventobérant

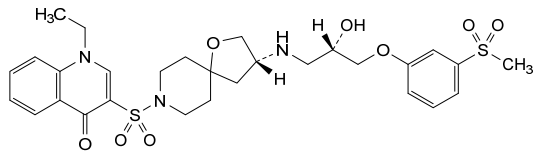
1-éthyl-3-[(3*R*)-3-((2*S*)-2-hydroxy-3-[3-(méthanesulfonyl)phénoxy]propyl)amino]-1-oxa-8-azaspiro[4.5]décane-8-sulfonyl]quinoléin-4(1*H*)-one  
*antagoniste des récepteurs bêta-3 adrénergiques*

ventoberant

1-etil-3-[(3*R*)-3-((2*S*)-2-hidroxi-3-[3-(metanosulfonyl)fenoxi]propil)amino]-1-oxa-8-azaspiro[4.5]decano-8-sulfonyl]quinolein-4(1*H*)-ona  
*antagonista de los receptores beta-3 adrenérgicos*

C<sub>29</sub>H<sub>37</sub>N<sub>3</sub>O<sub>8</sub>S<sub>2</sub>

2169905-68-2

**vensobafuspum alfa #**

vensobafusp alfa

humanized immunoglobulin G4-kappa, anti-(human complement factor C5) engineered heavy chain variant (S<sup>233</sup>>P, M<sup>433</sup>>L, N<sup>439</sup>>A), fused at the C-terminus of the heavy chain (1-452) to a human complement factor H (CFH, H factor 1, HF1) functional domain fragment (1-306, 453-758 in the current sequence), variant (V<sup>44</sup>>I<sup>496</sup>), disulfide bridged dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa; humanized monoclonal antibody fusion with human complement factor H; type: IgG4-kappa; antigen: human complement C5, CPAMD4 (C5); CDR source: *Mus musculus* (humanized by CDR grafting); heavy chain class: gamma 4; HV germline: *Homo sapiens* IGHV1-18\*01; HJ germline: *Homo sapiens* IGHJ3\*01; HC germline: *Homo sapiens* IGHG4\*01; VH: 1-125; CH1: 126-223; hinge: 224-235 (S233P hinge stabilization); CH2: 236-345; CH3: 346-450 (M433L, N439A; enhance FcRn binding); CHS: 451-452; LV germline: *Homo sapiens* IGKV1-9\*01; LJ germline: *Homo sapiens* IGKJ2\*01; LC germline: *Homo sapiens* IGKC\*01; VL: 1-107; CL: 108-214; CDR Kabat H1: DYHFD (31-35); CDR Kabat H2: DISMNYGYHIYNQKFKD (50-66); CDR Kabat H3: RDIRYSGNSYKWFYFDE (99-114); CDR Kabat L1: RTSKSIKHLA (24-34); CDR Kabat L2: SGSTLQS (50-56); CDR Kabat L3: QQHNEYPYT (89-97); fusion protein heavy: 453-758; human complement factor H residues 1-306 (CFH)  
*immunomodulator*



vensobafusp alfa

immunoglobuline G4-kappa humanisée, anti-(facteur du complément humain C5), variant modifié de la chaîne lourde (S<sup>233</sup>>P, M<sup>433</sup>>L, N<sup>439</sup>>A), fusionné à l'extrémité C-terminale de la chaîne lourde (1-452) à un fragment du domaine fonctionnel du facteur du complément humain H (CFH, factor 1 H, HF1) (1-306, 453-758 dans la séquence actuelle), variant (V<sup>44</sup>>I<sup>496</sup>), dimère à pont disulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa; fusion d'un anticorps monoclonal humanisé avec le facteur H du complément humain; type: IgG4-kappa; antigène: complément humain C5, CPAMD4 (C5); Source CDR: *Mus musculus* (humanisé par greffe de CDR); classe de la chaîne lourde: gamma 4; HV lignée germinale: *Homo sapiens* IGHV1-18\*01; HJ lignée germinale: *Homo sapiens* IGHJ3\*01; HC lignée germinale: *Homo sapiens* IGHG4\*01; VH: 1-125; CH1: 126-223; charnière: 224-235 (stabilisation de la charnière S233P); CH2: 236-345; CH3: 346-450 (M433L, N439A; améliorant la liaison FcRn); CHS: 451-452; LV lignée germinale: *Homo sapiens* IGKV1-9\*01; LJ lignée germinale: *Homo sapiens* IGKJ2\*01; LC lignée germinale: *Homo sapiens* IGKC\*01; VL: 1-107; CL: 108-214; CDR Kabat H1: DYHFD (31-35); CDR Kabat H2: DISMNYGYHIYNQKFKD (50-66); CDR Kabat H3: RDIRYSGNSYKWFDE (99-114); CDR Kabat L1: RTSKSISKHLA (24-34); CDR Kabat L2: SGSTLQS (50-56); CDR Kabat L3: QQHNEYPYT (89-97); protéine de fusion lourde: 453-758; résidus 1-306 du facteur du complément H humain (CFH)  
*immunomodulateur*

vensobafusp alfa

inmoglobulina humanizada G4-kappa, anti-(factor de complemento humano C5) diseñado con la variante de cadena pesada (S<sup>233</sup>>P, M<sup>433</sup>>L, N<sup>439</sup>>A), fusionado en la terminal C de la cadena pesada (1-452) a un factor H de complemento humano (CFH, H factor 1, HF1) fragmento de dominio funcional (1-306, 453-758 en la secuencia actual), variante (V<sup>44</sup>>I<sup>496</sup>), dímero con puente disulfuro, producido en células ováricas de hámster Chino (CHO), forma glicosilada alfa; anticuerpo monoclonal humanizado de fusion con factor H del complemento humano; tipo: IgG4-kappa; antígeno: complemento humano C5, CPAMD4 (C5); fuente CDR: *Mus musculus* (humanizado por injerto CDR); clase cadena pesada: gamma 4; línea germinal HV: *Homo sapiens* IGHV1-18\*01; línea germinal HJ: *Homo sapiens* IGHJ3\*01; línea germinal HC: *Homo sapiens* IGHG4\*01; VH: 1-125; CH1: 126-223; bisagra: 2 24-235 (S233P estabilización de bisagra); CH2: 236-345; CH3: 346-450 (M433L, N439A; promover union FcRn); CHS: 451-452; línea germinal LV: *Homo sapiens* IGKV1-9\*01; línea germinal LJ: *Homo sapiens* IGKJ2\*01; línea germinal LC: *Homo sapiens* IGKC\*01; VL: 1-107; CL: 108-214; CDR Kabat H1: DYHFD (31-35); CDR Kabat H2: DISMNYGYHIYNQKFKD (50-66); CDR Kabat H3: RDIRYSGNSYKWFDE (99-114); CDR Kabat L1: RTSKSISKHLA (24-34); CDR Kabat L2: SGSTLQS (50-56); CDR Kabat L3: QQHNEYPYT (89-97); proteína de fusión pesada: 453-758; residuos del factor H del complemento humano 1-306 (CFH)  
*immunomodulador*

2724922-85-2

## Sequence / Séquence / Secuencia

## Heavy chain / Chaîne lourde / Cadena pesada: IgG4-CFH

VVQLVQSGAE VKKPGASVKV SCKASGYTIT DYHFDWVRQA PGQGLEWMDG 50  
 ISMNYGYHIY NQKFKDRVTM TDTSTSTAY MELRSLRSD TAVYCARRD 100  
 IRYSGNSYKW YFDEWQGTMT VTSSASTKG PSVFLPAPCS RSTSESTAAL 150  
 GCLVKDYFPE PVTVSWNSGA LTVSGVHTFPA VLQSSGLYSL SSVVTVFSSS 200  
 LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPFCPAPEFL GGPSVFLFPP 250  
 KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ 300  
 FNSTYRVVVS LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE 350  
 PQVYTLPPSQ EEMTRNQVSL TCLVKGKFSN DIAVEWESNG QPENNYKTFP 400  
 PVLDSGDSGF LYSRLTVDKS RWQEGNVFSC SVLHEALHAH YTKRSLSLSL 450  
 GRKEDCNELPP RRNTEILTGS WSDQTYPEGT QAIYKCRPGY RSLGNIMVC 500  
 RKGWVALNP LRKCKRRCFG HPGDTPFGFT TLTGGNVFEY GVKAVYTCNE 550  
 GYQLLGEINY RECDTGWNT DIPICEVVKC LPVTAPENGK IVSASMEPDR 600  
 EYHFGQAVRF VCNISGKIEG DEEMHCSDDG FWSKEKPKCV EISCKSPDVI 650  
 NGSPIISQKII YKENERFOYK CNMGYEYSER GDAVCTESGW RPLPSCSEKS 700  
 CDRNFIYPNGD YSPLRIKHRT GDEITYQCRN GFYPATRGNT AKCTSTGWIP 750  
 APCRCTLKP 758

## Light chains / Chaînes légères / Cadenas ligeras

DIQLTQSPSF LSASVGDRTV TTRCTSKSIS KHLAWYQQKP GKAPKLLIYS 50  
 GSTLQSGVPS RFSGSGSGTE FTLTISLQF EDFATYCCQ HNEYPTFFGQ 100  
 GTKLEIKRTV AAPSVEIFPP SDEQLKSGTA SVVCLLNNEY PREAKVQWIKV 150  
 DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200  
 LSSPVTKSFN RGEIC 214

## Mutation / Mutation / Mutación

IgG1 Heavy chain: S<sup>233</sup>>P, M<sup>333</sup>>L, N<sup>439</sup>>A, S<sup>233</sup>>P, M<sup>433</sup>>L, N<sup>439</sup>>A

## Natural variant / Variante naturelle / Variante natural

CHF: V<sup>44</sup>>I<sup>496</sup>, V<sup>44</sup>>I<sup>496</sup>

## Post-translational modifications

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

Intra-H: 22 - 96, 152 - 208, 226 - 326, 372 - 430  
 22<sup>o</sup>-96<sup>o</sup>, 152<sup>o</sup>-208<sup>o</sup>, 226<sup>o</sup>-326<sup>o</sup>, 372<sup>o</sup>-430<sup>o</sup>  
 Intra-CFH: 455 - 500, 486 - 514, 519 - 563, 548 - 575, 580 - 626, 612 - 639, 644 - 685,  
 671 - 696, 701 - 743, 728 - 754  
 455<sup>o</sup>-500<sup>o</sup>, 486<sup>o</sup>-514<sup>o</sup>, 519<sup>o</sup>-563<sup>o</sup>, 548<sup>o</sup>-575<sup>o</sup>, 580<sup>o</sup>-626<sup>o</sup>, 612<sup>o</sup>-639<sup>o</sup>, 644<sup>o</sup>-685<sup>o</sup>,  
 671<sup>o</sup>-696<sup>o</sup>, 701<sup>o</sup>-743<sup>o</sup>, 728<sup>o</sup>-754<sup>o</sup>  
 Intra-L: 23<sup>o</sup> - 88<sup>o</sup>, 134<sup>o</sup> - 194<sup>o</sup>  
 23<sup>o</sup>-92<sup>o</sup>, 134<sup>o</sup>-194<sup>o</sup>  
 Inter-H-L: 139-214<sup>o</sup>, 139<sup>o</sup>-214<sup>o</sup>  
 Inter-H-H: 231-231<sup>o</sup>, 234-234<sup>o</sup>

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

N302, N302<sup>o</sup>

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

H VH Q1> pyroglutamyl (pE, 5-oxoprolyl): 1, 1<sup>o</sup>

**verzistobartum #**  
verzistobart

immunoglobulin G1-kappa, anti-[*Homo sapiens* HAVCR2 (hepatitis A virus cellular receptor 2, T cell immunoglobulin and mucin domains family member 3, TIM3, TIM-3, TIMD3, CD366)], *Homo sapiens* monoclonal antibody;  
 gamma1 heavy chain *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV3-23\*04 (94.9%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1\*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, IGHG1v29 CH2 A84.4 (CH1 R120 (217) (121-218), hinge 1-15 (219-233), CH2 N84.4>A (300) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K2>del (449)) (121-449)], (223-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V- KAPPA (*Homo sapiens* IGKV3D-11\*02 (96.7%) -IGKJ4\*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, non-glycosylated immunostimulant, antineoplastic



**vididencelum**

vididencel

cell-cycle arrested (gamma-irradiated) dendritic cells (DCs) derived from the cell line DCOne, which originated from MUTZ-3 cells that arose from mononuclear blasts isolated from a 29-year-old male patient with acute myelomonocytic leukaemia. The cells are initially grown in media containing granulocyte-macrophage colony-stimulating factor (GM-CSF), followed by differentiation in the presence of granulocyte-macrophage colony-stimulating factor (GM-CSF), tumour necrosis factor alpha (TNF- $\alpha$ ), interleukin 4 (IL-4) and *mitoxantrone*. Finally, the cells are matured in the presence of media containing prostaglandin-E2 (PGE2), TNF- $\alpha$ , and IL-1 $\beta$ . After cryopreservation the cells are gamma-irradiated to induce cell-cycle arrest, leaving >70% of the cells viable.

The final cell suspension contains  $\geq$ 70% dendritic cells (HLA-DR) which express CD1a (DC differentiation marker >30%), CD83 (DC maturation marker; >30%), CD40 (>60%), CD80 (>50%) and CD86 (co-stimulatory molecules, highly expressed by mature DC; >70%), HLA-ABC (>70%) and HLA-DP/DQ/DR >70%). The preparation also stimulates T lymphocytes in a mixed lymphocyte reaction (MLR) and can induce migration. *cell therapy (antineoplastic)*

vididencel

cellules dendritiques (DC) au cycle cellulaire arrêté (irradiées aux rayons gamma) dérivées de la lignée cellulaire DCOne, qui provient de cellules MUTZ-3 issues de blastes mononucléaires isolés d'un patient masculin de 29 ans atteint de leucémie myélomonocytaire aiguë. Les cellules sont initialement cultivées dans un milieu contenant le facteur de stimulation des colonies de granulocytes-macrophages (GM-CSF), puis elles sont différenciées en présence du facteur de stimulation des colonies de granulocytes-macrophages (GM-CSF), du facteur de nécrose tumorale alpha (TNF- $\alpha$ ), de l'interleukine 4 (IL-4) et de la *mitoxantrone*. Enfin, les cellules sont maturées en présence d'un milieu contenant de la prostaglandine-E2 (PGE2), du TNF- $\alpha$  et de l'IL-1 $\beta$ . Après la cryoconservation, les cellules sont irradiées aux rayons gamma pour induire un arrêt du cycle cellulaire, laissant >70% des cellules viables. La suspension cellulaire contient  $\geq$ 70% de cellules dendritiques (HLA-DR) qui expriment CD1a (marqueur de différenciation des DC >30%), CD83 (marqueur de maturation des DC; >30%), CD40 (>60%), CD80 (>50%) et CD86 (molécules de co-stimulation, hautement exprimées par les DC matures; >70%), HLA-ABC (>70%) et HLA-DP/DQ/DR >70%). La préparation stimule également les lymphocytes T dans une réaction lymphocytaire mixte (MLR) et peut induire la migration. *thérapie cellulaire (antinéoplasique)*

vididencel

células dendríticas (DCs) con el ciclo celular detenido (sometidas a radiación gamma) derivadas de la línea celular DCOne, que se originaron a partir de células MUTZ-3 que a su vez surgieron de blastos mononucleares aislados de un paciente varón de 29 años con leucemia mielomonocítica aguda. Las células se crecen inicialmente en medio que contiene factor estimulador de colonias de monocitos-macrófagos (GM-CSF), seguido de diferenciación en presencia de factor estimulador de colonias de monocitos-macrófagos (GM-CSF), factor de necrosis tumoral alfa (TNF- $\alpha$ ), interleuquina 4 (IL-4) y *mitoxantrona*. Finalmente, las células se maduran en presencia de medio que contiene prostaglandina E2 (PGE2), TNF- $\alpha$  e IL-1 $\beta$ . Después de la criopreservación, las células se someten a radiación gamma para inducir la detención del ciclo celular, dejando >70% de las células viables. La suspensión celular contiene  $\geq$ 70% de células dendríticas (HLA-DR) que expresan CD1a (marcador de diferenciación de DC; >30%), CD83 (marcador de maduración de DC; >30%), CD40 (>60%), CD80 (>50%) y CD86 (moléculas coestimuladoras que se expresan mucho en DC maduras; >70%), HLA-ABC (>70%) y HLA-DP/DQ/DR >70%). La preparación también estimula a los linfocitos T en una reacción mixta de linfocitos (MLR) y puede inducir migración

*terapia celular (antineoplásico)*

**vonifimodum**

vonifimod

2-amino-2-[2-(1-decyl-1*H*-1,2,3-triazol-4-yl)ethyl]propane-1,3-diol  
*immunomodulator*

vonifimod

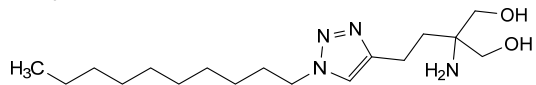
2-amino-2-[2-(1-décyl-1*H*-1,2,3-triazol-4-yl)éthyl]propane-1,3-diol  
*immunomodulateur*

vonifimod

2-amino-2-[2-(1-decil-1*H*-1,2,3-triazol-4-il)etil]propano-1,3-diol  
*immunomodulador*

C<sub>17</sub>H<sub>34</sub>N<sub>4</sub>O<sub>2</sub>

2118903-18-5

**vonsetamigum #**

vonsetamig

immunoglobulin G4-kappa, anti-[*Homo sapiens* TNFRSF17 (TNF receptor superfamily member 17, BCMA, TNFRSF13A, CD269) and CD3E (CD3 epsilon)], *Homo sapiens* monoclonal antibody, bispecific, bivalent; gamma4 heavy chain anti-TNFRSF17 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-7\*01 (93.9%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.18] (26-33.51-58.97-114)) (1-125) -*Homo sapiens*

- IGHG4\*01, G4v5 h P10, nG4m(a) CH2 L92, IGHG4v7 CH2 delE1.4, P1.3, V1.2, A1.1 (CH1 (126-223), hinge 1-12 S10>P (233) (224-235), CH2 E1.4>del, F1.3>P (238), L1.2>V (239), G1.1>A (240), L92 (313) (236-344), CH3 (345-449), CHS (450-451)) (126-451)], (139-215')-disulfide with kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (100%) -IGKJ5\*01 (100%), CDR-IMGT [6.3.10] (27-32.50-52.89-98)) (1'-108') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')];  
 gamma4 heavy chain anti-CD3E *Homo sapiens* (1"-450") [VH (*Homo sapiens* IGHV3-9\*01 (99.0%) -(IGHD) -IGHJ6\*01 (94.7%), CDR-IMGT [8.8.17] (26-33.51-58.96-113)) (1"-124") -*Homo sapiens* IGHG4\*01, G4v5 h P10, nG4m(a) CH2 L92, IGHG4v7 CH2 delE1.4, P1.3, V1.2, A1.1, IGHG4v8 CH3 R115, F116, P125 (CH1 (125"-222"), hinge 1-12 S10>P (232) (223"-234"), CH2 E1.4>del, F1.3>P (237), L1.2>V (238), G1.1>A (239), L92 (312) (235"-343"), CH3 H115>R (438), Y116>F (439), L125>P (448) (344"-448"), CHS (449"-450")) (125"-450")], (138"-215'")-disulfide with kappa light chain *Homo sapiens* (1'"-215'") [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (100%) -IGKJ5\*01 (100%), CDR-IMGT [6.3.10] (27-32.50-52.89-98)) (1'"-108'") -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (154), V101 (192) (109'"-215'")]; dimer (231-230":234-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa  
*antineoplastica*
- vonsétamig immunoglobuline G4-kappa, anti-[*Homo sapiens* TNFRSF17 (membre 17 de la superfamille des récepteurs du TNF, BCMA, TNFRSF13A, CD269) and CD3E (CD3 epsilon)], anticorps monoclonal *Homo sapiens*, bispécifique, bivalent;  
 chaîne lourde gamma4 anti-TNFRSF17 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-7\*01 (93.9%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.18] (26-33.51-58.97-114)) (1-125) -*Homo sapiens* IGHG4\*01, G4v5 h P10, nG4m(a) CH2 L92, IGHG4v7 CH2 delE1.4, P1.3, V1.2, A1.1 (CH1 (126-223), charnière 1-12 S10>P (233) (224-235), CH2 E1.4>del, F1.3>P (237), L1.2>V (238), G1.1>A (239), L92 (313) (236-344), CH3 (345-449), CHS (450-451)) (126-451)], (139-215')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (100%) -IGKJ5\*01 (100%), CDR-IMGT [6.3.10] (27-32.50-52.89-98)) (1'-108') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')];  
 chaîne lourde gamma4 anti-CD3E *Homo sapiens* (1"-450") [VH (*Homo sapiens* IGHV3-9\*01 (99.0%) -(IGHD) -IGHJ6\*01 (94.7%), CDR-IMGT [8.8.17] (26-33.51-58.96-113)) (1"-124") -*Homo sapiens* IGHG4\*01, G4v5 h P10, nG4m(a) CH2 L92, IGHG4v7 CH2 delE1.4, P1.3, V1.2, A1.1, IGHG4v8 CH3 R115, F116, P125 (CH1 (125"-222"), charnière 1-12 S10>P (232) (223"-234"), CH2 E1.4>del, F1.3>P (237), L1.2>V (238), G1.1>A (239), L92 (312) (235"-343"), CH3 H115>R (438), Y116>F (439), L125>P (448) (344"-448"), CHS (449"-450")) (125"-450")], (138"-215'")-disulfure avec la chaîne légère kappa *Homo sapiens* (1'"-215'") [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (100%) -IGKJ5\*01 (100%), CDR-IMGT [6.3.10] (27-32.50-52.89-98)) (1'"-108'") -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (154), V101 (192) (109'"-215'")]; dimère (231-230":234-233")-bisdisulfure, produit dans des cellules ovariennees de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa  
*antineoplastique*
- vonsetamig immunoglobulina G4-kappa, anti-[*Homo sapiens* TNFRSF17 (miembro 17 de la superfamilia de los receptores del TNF, BCMA, TNFRSF13A, CD269) y CD3E (CD3 épsilon)], anticuerpo monoclonal *Homo sapiens*, biespecifico, bivalente;

cadena pesada gamma4 anti-TNFRSF17 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-7\*01 (93.9%) -(IGHD) -IGHJ4\*01 (100%), CDR-IMGT [8.8.18] (26-33.51-58.97-114)) (1-125) -*Homo sapiens* IGHG4\*01, G4v5 h P10, nG4m(a) CH2 L92, IGHG4v7 CH2 delE1.4, P1.3, V1.2, A1.1 (CH1 (126-223), bisagra 1-12 S10>P (233) (224-235), CH2 E1.4>del, F1.3>P (237), L1.2>V (238), G1.1>A (239), L92 (313) (236-344), CH3 (345-449), CHS (450-451)) (126-451)], (139-215')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (100%) -IGKJ5\*01 (100%), CDR-IMGT [6.3.10] (27-32.50-52.89-98)) (1'-108') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')];

cadena pesada gamma4 anti-CD3E *Homo sapiens* (1"-450") [VH (*Homo sapiens* IGHV3-9\*01 (99.0%) -(IGHD) -IGHJ6\*01 (94.7%), CDR-IMGT [8.8.17] (26-33.51-58.96-113)) (1"-124") -*Homo sapiens* IGHG4\*01, G4v5 h P10, nG4m(a) CH2 L92, IGHG4v7 CH2 delE1.4, P1.3, V1.2, A1.1, IGHG4v8 CH3 R115, F116, P125 (CH1 (125"-222"), bisagra 1-12 S10>P (232) (223"-234"), CH2 E1.4>del, F1.3>P (237), L1.2>V (238), G1.1>A (239), L92 (312) (235"-343"), CH3 H115>R (438), Y116>F (439), L125>P (448) (344"-448"), CHS (449"-450")) (125"-450"), (138"-215'")-disulfuro con la cadena ligera kappa *Homo sapiens* (1'"-215'") [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (100%) -IGKJ5\*01 (100%), CDR-IMGT [6.3.10] (27-32.50-52.89-98)) (1'"-108'") -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (154), V101 (192) (109'"-215'"); dímero (231-230":234-233'")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa antineoplásico

2408319-33-3

## Heavy chain / Chaîne lourde / Cadena pesada: anti-TNFRSF17 (H)

```
EVQLVESGGG LVQFPGSLRL SCAASGFTFS NFWMTVVRQA PGKLEWVAN 50
MNQDGSSEKYY VDSVKGFRFTI SRDNAKSSLY LQMNSLRAED TAVYYCARDR 100
EYCIKSTCYD DFDYWGQGTLL VTVSSASTKG PSVFLAPCS RSTSESTAAL 150
GCLVKDYFPE PVTVSWNSGA LTVSGVHTFPA VLQSSGLYSL SSVTVFSS 200
LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPFCAPPVA GPSVFLFPPK 250
PKDTLMISRT PEVTCVVDV SQEDPEVQFN WYVDGVEVHN AKTKPREEQF 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK GLPSSIEKTI SKAKGQPREP 350
QYVTLPPSQE EMTKNQVSLT CLVKGFPYPSD IAVEWESNGQ PENNYKTTTP 400
VLDSGDSFPL YSRLTVDKSR WQEGNVFSCS VMHEALHNHY TQKSLSLSLG 450
K 451
```

## Heavy chain / Chaîne lourde / Cadena pesada: anti-CD3E (H')

```
EVQLVESGGG LVQFGRSLRL SCAASGFTFD DYSMHWVRQA PGKLEWVSG 50
ISWNSGKIGY ADSVKGFRFTI SRDNAKNSLY LQMNSLRAED TALIYCAKYG 100
SGYKGFYYG MDVWGQGTTV TVSSASTKGP SVFPLAPCSR STSESTAALG 150
CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSL SVTVFSSSL 200
GKTKTYTCNV DHKPSNTKVDK RVESKYGPPC PFCAPPVAG PSVFLFPPK 250
KDTLMISRTPEVTCVVDV SQEDPEVQFNW YVDGVEVHNA KTKPREEQFN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKG LPSSIEKTIS KAKGQPREPQ 350
VYTLPPSQEE MTRKNQVSLTCLVKGFPYPSDI AVEWESNGQP ENNYKTTTPV 400
LDSGDSFPLY SRLTVDKSRW QEGNVFSCSV MHEALHNRT QKSLSLSPGK 450
```

## Light chain / Chaîne légère / Cadena ligera (L', L'')

```
DIQMTQSPSS LSASVGRVIT ITCRASQSI SYLNWYQQKPK GKAPKLLIYA 50
ASSLQSGVPS RFGSGSGSDT FTLTISLQPF EDFATYYCQQ SYSTPPIITFG 100
QGTREIKRRT VAAQPSVFIFF PSDEQLKSGT ASVCLLNFF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGECC 215
```

## Post-translational modifications

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

Intra-H (C23-C104) 22-96 152-208 265-325 371-429  
22"-96" 151"-207" 264"-324" 370"-428"

Intra-H CDR3 (C111-C112.1) 103-108

Intra-L (C23-C104) 23'-88' 135'-195'

23'"-88'" 135'"-195'"

Inter-H-L (CH1 10-CL 126) 139-215' 138"-215"

Inter-H-H (h 8, h 11) 231-230" 234-233'

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

H CH2 N84.4: 301, 300"

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

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

H CHS K2: 451, 450"

**vopikitungum #**

vopikitung

immunoglobulin G1-kappa, anti-[*Homo sapiens* IL2RA (interleukin 2 receptor alpha subunit, IL-2RA, TAC, p55, CD25)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-452) [VH (*Homo sapiens*IGHV1-69\*01 (99.0%) -(IGHD) -IGHJ3\*02 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens*IGHG1\*01 (100%), G1m17,1 CH1 K120, D12, L14 (CH1 K120 (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-5\*03 (98.9%) -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 (231-231":234-234")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa *antineoplastic*

vopikitung

immunoglobuline G1-kappa, anti-[*Homo sapiens* IL2RA (sous-unité alpha du récepteur de l'interleukine 2, IL-2RA, TAC, p55, CD25)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens*IGHV1-69\*01 (99.0%) -(IGHD) -IGHJ3\*02 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens*IGHG1\*01 (100%), G1m17,1CH1 K120, D12, L14 (CH1 K120 (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-5\*03 (98.9%) -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 (231-231":234-234")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa *antinéoplasique*

vopikitung

immunoglobulina G1-kappa, anti-[*Homo sapiens* IL2RA (subunidad alfa del receptor de la interleukina 2, IL-2RA, TAC, p55, CD25)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens*IGHV1-69\*01 (99.0%) -(IGHD) -IGHJ3\*02 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens*IGHG1\*01 (100%), G1m17,1 CH1 K120, D12, L14 (CH1 K120 (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-5\*03 (98.9%) -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 (231-231":234-234")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa *antineoplásico*



2733581-99-0

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE	VKKPGSSVKV	SCKASGGTFS	SLAISWVRQA	PGQGLEWMGG	50
IIPFGTANY	AQKFGQGRVTI	TADESTSTAY	MELSSLRSED	TAVYVCARGG	100
SVSGTLVDVD	IWGQGTMTVTV	SSASTKGPSV	FPLAPSSKST	SGGTAALGCL	150
VKDYFFPEVPT	VSWSNGALTS	GVHTFPAVLQ	SSGLYSLSSV	VTVPSSSLGT	200
QTYICNVNHK	PSNTKVDKVK	EPKSCDKTHT	CPPCPAPELL	GGPSVFLFPP	250
KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTPREEEQ	300
YNSTYRVVSV	LTVLHQDNLN	GKEYKCKVSN	KALPAPIEKT	ISKAKGQPRE	350
PQVYTLPPSR	DELTKNQVSL	TCLVKGFPYS	DIAVEWESNG	QPENNYKTPP	400
PVLDSDGSFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	450
GK					452

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPST	LSASVGDRTV	ITCRASQGIS	SWLAWYQQKP	GKAPKLLIYK	50
ASSLESQVPS	RFGSGSGSTE	FTLTISLSLP	DDFATYYCQQ	YNIYPIITFGG	100
GTKVEIKRTV	AAPSVFIFPP	SDEQLKSGTA	SUVCLLNIFY	PREAKVQMKV	150
DNALQSGNSQ	ESVTEQDSKD	STYLSLSTLT	LSKADYEKHK	VYACEVTHQG	200
LSSPVTKSFN	RGEC				214

**Post-translational modifications**  
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro  
 Intra-H (C23-C104) 22-96 149-205 266-326 372-430  
 22"-96" 149"-205" 266"-326" 372"-430"  
 Intra-L (C23-C104) 23"-88" 134"-194"  
 23"-88" 134"-194"  
 Inter-H-L (h 5-CL 126) 225-214" 225"-214"  
 Inter-H-H (h 11, h 14) 231-231" 234-234"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal  
 Q > pyrroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)  
 H VH Q1: 1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación  
 H CH2 N84.4: 302, 302"

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

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

**vorumotidum**  
 vorumotide

human Wilms tumor protein (WT33)-(328-349)-peptide;  
 L-prolylglycyl-L-cysteinyl-L-asparaginyl-L-lysyl-L-arginyl-L-tyrosyl-L-phenylalanyl-L-lysyl-L-leucyl-L-seryl-L-histidyl-L-leucyl-L-glutaminyll-L-methionyl-L-histidyl-L-seryl-L-arginyl-L-lysyl-L-histidyl-L-threonylglycine  
*immunological agent for active immunization (antineoplastic)*

vorumotide

protéine humaine de la tumeur de Wilms (WT33)-(328-349)-peptide;  
 L-prolylglycyl-L-cystéinyl-L-asparaginyl-L-lysyl-L-arginyl-L-tyrosyl-L-phénylalanyl-L-lysyl-L-leucyl-L-séryl-L-histidyl-L-leucyl-L-glutaminyll-L-méthionyl-L-histidyl-L-séryl-L-arginyl-L-lysyl-L-histidyl-L-thréonylglycine  
*agent immunologique d'immunisation active (antineoplasique)*

vorumotida

proteína humana del tumor de Wilms (WT33)-(328-349)-péptido;  
 L-prolilglicil-L-cisteinil-L-asparaginil-L-lisil-L-arginil-L-tirosil-L-fenilalanil-L-lisil-L-leucil-L-seril-L-histidil-L-leucil-L-glutaminiil-L-metionil-L-histidil-L-seril-L-argnil-L-lisil-L-histidil-L-treonilglicina  
*agente inmunológico para inmunización activa (antineoplásico)*

## PGCNKRYFKL SHLQMHSRKH TG 22

**zasocitinibum**

zasocitinib

*N*-[(1*R*,2*R*)-2-methoxycyclobutyl]-7-(methylamino)-5-[[2-oxo[1(2*H*),2'-bipyridin]-3-yl]amino]-pyrazolo[1,5-*a*]pyrimidine-3-carboxamide  
*Janus kinase inhibitor, anti-inflammatory*

zasocitinib

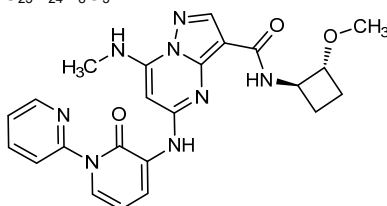
*N*-[(1*R*,2*R*)-2-méthoxycyclobutyl]-7-(méthylamino)-5-[[2-oxo[1(2*H*),2'-bipyridin]-3-yl]amino]-pyrazolo[1,5-*a*]pyrimidine-3-carboxamide  
*inhibiteur de la kinase de Janus, anti-inflammatoire*

zasocitinib

*N*-[(1*R*,2*R*)-2-metoxiciclobutil]-7-(metilamino)-5-[[2-oxo[1(2*H*),2'-bipiridin]-3-il]amino]-pirazolo[1,5-*a*]pirimidina-3-carboxamida  
*inhibidor de la kinasa de Janus, antiinflamatorio*

C<sub>23</sub>H<sub>24</sub>N<sub>8</sub>O<sub>3</sub>

2272904-53-5

**zatonacaftorum**

zatonacaftor

1-[5-ethyl-2-(propan-2-yloxy)pyridin-3-yl]-*N*-[(2-methylquinolin-5-yl)sulfonyl]-cyclopropanecarboxamide  
*cystic fibrosis transmembrane regulator (CFTR) protein modulator*

zatonacaftor

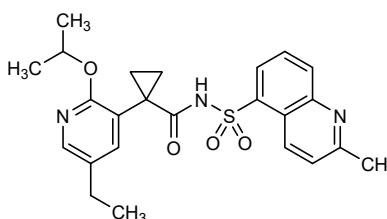
1-[5-éthyl-2-(propan-2-yloxy)pyridin-3-yl]-*N*-[(2-méthylquinolin-5-yl)sulfonyl]-cyclopropanecarboxamide  
*modulateur de la protéine régulatrice de la perméabilité transmembranaire impliquée dans la mucoviscidose (CFTR)*

zatonacaftor

1-[5-etil-2-(propan-2-iloxi)piridin-3-il]-*N*-[(2-metilquinolin-5-il)sulfonyl]-ciclopropanecarboxamida  
*modulador de la proteína reguladora de la conductancia transmembrana de la fibrosis quística (CFTR)*

C<sub>24</sub>H<sub>27</sub>N<sub>3</sub>O<sub>4</sub>S

2301945-38-8



**zavondemstatum**

zavondemstat

3-[[[(4*R*)-7-[*N*-methyl-4-(propan-2-yl)anilino]-3,4-dihydro-2*H*-1-benzopyran-4-yl]methyl]amino]pyridine-4-carboxylic acid  
*lysine-specific histone demethylase 4 (KDM4) inhibitor, antineoplastic*

zavondemstat

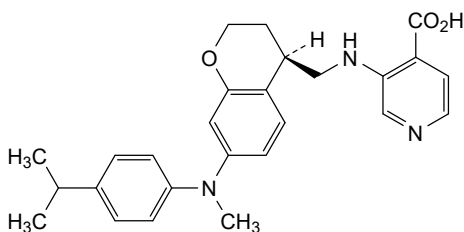
acide 3-[[[(4*R*)-7-[*N*-méthyl-4-(propan-2-yl)anilino]-3,4-dihydro-2*H*-1-benzopyran-4-yl]méthyl]amino]pyridine-4-carboxylique  
*inhibiteur de l'histone déméthylase-4 spécifique de la lysine (KDM4), antinéoplasique*

zavondemstat

ácido 3-[[[(4*R*)-7-[*N*-metil-4-(propan-2-il)anilino]-3,4-dihidro-2*H*-1-benzopiran-4-il]metil]amino]piridina-4-carboxílico  
*inhibidor de la histona demetilasa-4 específica de la lisina (KDM4), antineoplásico*

C<sub>26</sub>H<sub>29</sub>N<sub>3</sub>O<sub>3</sub>

1851412-93-5

**zelasudilum**

zelasudil

4-{5-[(4-cyclopropyl-1*H*-indazol-5-yl)amino]-1-methyl-1*H*-1,2,4-triazol-3-yl}-*N*-(2,2-difluoroethyl)benzamide  
*Rho-associated (ROCK) kinase inhibitor*

zélasudil

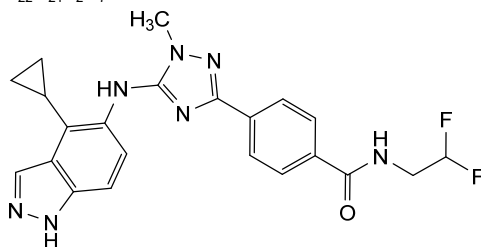
4-{5-[(4-cyclopropyl-1*H*-indazol-5-yl)amino]-1-méthyl-1*H*-1,2,4-triazol-3-yl}-*N*-(2,2-difluoroéthyl)benzamide  
*inhibiteur de la protéine kinase associée à Rho (ROCK)*

zelasudil

4-{5-[(4-ciclopropil-1*H*-indazol-5-il)amino]-1-metil-1*H*-1,2,4-triazol-3-il}-*N*-(2,2-difluoroetil)benzamida  
*inhibidor de la proteína kinasa asociada al Rho (ROCK)*

C<sub>22</sub>H<sub>21</sub>F<sub>2</sub>N<sub>7</sub>O

2365193-22-0



**zelnecirnonum**

zelnecirnon

(1<sup>1r</sup>,1<sup>3r</sup>,2<sup>3R</sup>,6R)-4<sup>5</sup>,7<sup>2</sup>,7<sup>4</sup>-trichloro-4<sup>6</sup>,6-dimethyl-5-aza-4(2,4)-pyrimidina-2(1,3)-piperidina-3(3,1)-azetidina-7(1)-benzena-1(1)-cyclobutanaheptaphane-3-carboxylic acid

*chemokine receptor 4 (CCR4) antagonist, anti-inflammatory*

zelnécirnon

acide (1<sup>1r</sup>,1<sup>3r</sup>,2<sup>3R</sup>,6R)-4<sup>5</sup>,7<sup>2</sup>,7<sup>4</sup>-trichloro-4<sup>6</sup>,6-diméthyl-5-aza-4(2,4)-pyrimidina-2(1,3)-pipéridina-3(3,1)-azétidina-7(1)-benzéna-1(1)-cyclobutanaheptaphane-3-carboxylique

*antagoniste du récepteur 4 de la chimiokine (CCR4), anti-inflammatoire*

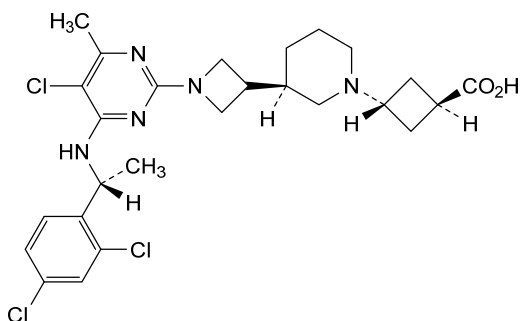
zelnecirón

ácido (1<sup>1r</sup>,1<sup>3r</sup>,2<sup>3R</sup>,6R)-4<sup>5</sup>,7<sup>2</sup>,7<sup>4</sup>-triclóro-4<sup>6</sup>,6-dimetil-5-aza-4(2,4)-pirimidina-2(1,3)-piperidina-3(3,1)-azetidina-7(1)-bencena-1(1)-ciclobutanaheptafano-3-carboxílico

*antagonista del receptor de quimiocina 4 (CCR4), antiinflamatorio*

C<sub>27</sub>H<sub>34</sub>Cl<sub>3</sub>N<sub>5</sub>O<sub>2</sub>

2366152-15-8

**zenidololum**

zenidolol

*rac-(2R,3R)-1-[(7-methyl-2,3-dihydro-1H-inden-4-yl)oxy]-3-[(propan-2-yl)amino]butan-2-ol*  
*beta-2 adrenoceptor antagonist*

zénidolol

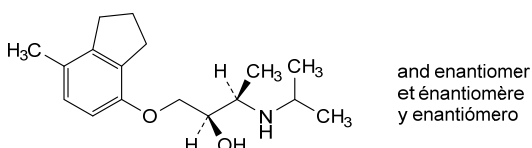
*rac-(2R,3R)-1-[(7-méthyl-2,3-dihydro-1H-indén-4-yl)oxy]-3-[(propan-2-yl)amino]butan-2-ol*  
*antagoniste des récepteurs bêta-2 adrénergiques*

zenidolol

*rac-(2R,3R)-1-[(7-metil-2,3-dihidro-1H-inden-4-il)oxi]-3-[(propan-2-il)amino]butan-2-ol*  
*antagonista de los receptores beta-2 adrenérgicos*

C<sub>17</sub>H<sub>27</sub>NO<sub>2</sub>

91021-57-7



**zidesamtinibum**

zidesamtinib

(6*R*)-2<sup>2</sup>-ethyl-5<sup>4</sup>-fluoro-4<sup>2</sup>,6-dimethyl-2<sup>2</sup>*H*,4<sup>2</sup>*H*-7-oxa-1(3,5)-pyridina-2(3,4)-pyrazola-4(4,5)-[1,2,3]triazola-5(1,2)-benzenacycloheptaphan-1<sup>6</sup>-amine  
*tyrosine kinase inhibitor, antineoplastic*

zidésamtinib

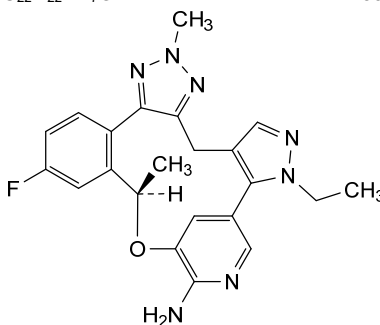
(6*R*)-2<sup>2</sup>-éthyl-5<sup>4</sup>-fluoro-4<sup>2</sup>,6-diméthyl-2<sup>2</sup>*H*,4<sup>2</sup>*H*-7-oxa-1(3,5)-pyridina-2(3,4)-pyrazola-4(4,5)-[1,2,3]triazola-5(1,2)-benzénacycloheptaphan-1<sup>6</sup>-amine  
*inhibiteur de tyrosine kinase, antinéoplasique*

zidesamtinib

(6*R*)-2<sup>2</sup>-etil-5<sup>4</sup>-fluoro-4<sup>2</sup>,6-dimetil-2<sup>2</sup>*H*,4<sup>2</sup>*H*-7-oxa-1(3,5)-piridina-2(3,4)-pirazola-4(4,5)-[1,2,3]triazola-5(1,2)-bencenacycloheptafan-1<sup>6</sup>-amina  
*inhibidor de tirosina kinasa, antineoplásico*

C<sub>22</sub>H<sub>22</sub>FN<sub>7</sub>O

2739829-00-4

**zongertinibum**

zongertinib

*N*-[1-(8-{3-methyl-4-[(1-methyl-1*H*-1,3-benzimidazol-5-yl)oxy]anilino}pyrimido[5,4-*d*]pyrimidin-2-yl)piperidin-4-yl]prop-2-enamide  
*tyrosine kinase inhibitor, antineoplastic*

zongertinib

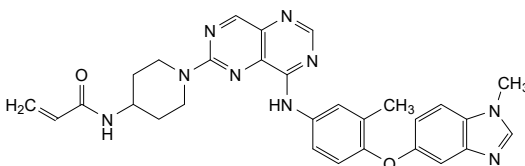
*N*-[1-(8-{3-méthyl-4-[(1-méthyl-1*H*-1,3-benzimidazol-5-yl)oxy]anilino}pyrimido[5,4-*d*]pyrimidin-2-yl)pipéridin-4-yl]prop-2-énamide  
*inhibiteur de tyrosine kinase, antinéoplasique*

zongertinib

*N*-[1-(8-{3-metil-4-[(1-metil-1*H*-1,3-benzimidazol-5-il)oxi]anilino}pirimido[5,4-*d*]pirimidin-2-il)piperidin-4-il]prop-2-enamida  
*inhibidor de tirosina kinasa, antineoplásico*

C<sub>29</sub>H<sub>29</sub>N<sub>9</sub>O<sub>2</sub>

2728667-27-2



**zotizalkibum**

zotizalkib

(1<sup>3</sup>S)-1<sup>3</sup>-(difluoromethyl)-3<sup>5</sup>-fluoro-6,6-dimethyl-1<sup>2</sup>,1<sup>3</sup>-dihydro-4-oxa-7-aza-1(4,6)-pyrazolo[1',5':1,2]pyrimido[5,4-b][1,4]oxazina-3(1,2)-benzenacyclooctaphan-8-one  
*anaplastic lymphoma kinase (ALK) tyrosine kinase receptor inhibitor, antineoplastic*

zotizalkib

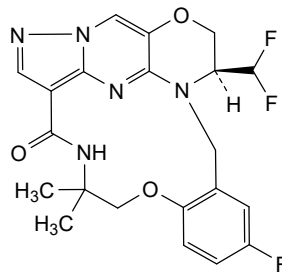
(1<sup>3</sup>S)-1<sup>3</sup>-(difluorométhyl)-3<sup>5</sup>-fluoro-6,6-diméthyl-1<sup>2</sup>,1<sup>3</sup>-dihydro-4-oxa-7-aza-1(4,6)-pyrazolo[1',5':1,2]pyrimido[5,4-b][1,4]oxazina-3(1,2)-benzénacyclooctaphan-8-one  
*inhibiteur du récepteur de la tyrosine kinase du lymphome anaplasique (ALK), antinéoplasique*

zotizalkib

(1<sup>3</sup>S)-1<sup>3</sup>-(difluorometil)-3<sup>5</sup>-fluoro-6,6-dimetil-1<sup>2</sup>,1<sup>3</sup>-dihidro-4-oxa-7-aza-1(4,6)-pirazolo[1',5':1,2]pirimido[5,4-b][1,4]oxazina-3(1,2)-bencenacilooctafan-8-ona  
*inhibidor del receptor de la tirosina kinasa del linfoma anaplásico (ALK), antineoplásico*

C<sub>21</sub>H<sub>20</sub>F<sub>3</sub>N<sub>5</sub>O<sub>3</sub>

2648641-36-3

**zovostotugum #**

zovostotug

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD163 (scavenger receptor cysteine-rich (SRCR) type 1 M130)], *Homo sapiens* monoclonal antibody;  
 gamma1 heavy chain *Homo sapiens* (1-463) [VH (*Homo sapiens* IGHV3-30\*01 (99.0%) -(IGHD) -IGHJ6\*01 (100%), CDR-IMGT [8.8.26] (26-33.51-58.97-122)) (1-133) -*Homo sapiens* IGHG1\*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (230) (134-231), hinge 1-15 (232-246), CH2 (247-356), CH3 E12 (372), M14 (374) (357-461), CHS (462-463)) (134-463)], (236-215')-disulfide with kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (100%) -IGKJ1\*01 (100%), CDR-IMGT [6.3.10] (27-32.50-52.89-98)) (1'-108') -*Homo sapiens* IGKC\*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (242-242":245-245")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1 lacking the glutamine synthetase (GS-KO) gene, glycoform alfa  
*immunostimulant, antineoplastic*

zovostotug

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD163 (récepteur éboueur riche en cystéines (SRCR) de type 1 M130)], anticorps monoclonal *Homo sapiens*;

chaîne lourde gamma1 *Homo sapiens* (1-463) [VH (*Homo sapiens* IGHV3-30\*01 (99.0%) -(IGHD) -IGHJ6\*01 (100%), CDR-IMGT [8.8.26] (26-33.51-58.97-122)) (1-133) -*Homo sapiens* IGHG1\*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (230) (134-231), charnière 1-15 (232-246), CH2 (247-356), CH3 E12 (372), M14 (374) (357-461), CHS (462-463)) (134-463)], (236-215')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (100%) -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 (154), V101 (192) (109'-215')]; dimère (242-242":245-245")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1 ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa  
*immunostimulant, antinéoplasique*

zovostotug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD163 (receptor desactivador rico en cisteína (SFCR) de tipo 1 M130)], anticuerpo monoclonal *Homo sapiens*;  
cadena pesada gamma1 *Homo sapiens* (1-463) [VH (*Homo sapiens* IGHV3-30\*01 (99.0%) -(IGHD) -IGHJ6\*01 (100%), CDR-IMGT [8.8.26] (26-33.51-58.97-122)) (1-133) -*Homo sapiens* IGHG1\*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (230) (134-231), bisagra 1-15 (232-246), CH2 (247-356), CH3 E12 (372), M14 (374) (357-461), CHS (462-463)) (134-463)], (236-215')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39\*01 (100%) -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 (154), V101 (192) (109'-215')]; dímero (242-242":245-245")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1 en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa  
*inmunoestimulante, antineoplásico*

2756228-84-7

## Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG VQPGKSLRL SCAASGFTFS SYAMHWVRQA PGKGLEWVAV 50
ISYDGNKYY ADSVGRFTI SRDNSKNTLY LQMNSLRAED TAVYVCAREN 100
VRPYDFWFSG YSESYYYGM DVMGQGTWT VSSASTKGPS VFPLAPSSKS 150
TSGGTAALCG LVKDYFPEPV TVSNNSGALT SGVHTFPAVL QSSGLYSLSS 200
VVTVPSSSLG TQTYICNVNH KPSNPKVDRK VEPKSCDPTH TCPPCPAPEL 250
LGGPSVFLFP FPKKDTLMIS RTPEVTCVVV DVSHEDEPEK FMYVVDGVEV 300
HNAKTKPREE QYNSTRVRS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK 350
TISKAKGQPR EPQVYTLPPS REEMTRKQVS LTCLVKGFPY SDIAVEWESN 400
GQPENNYKTT PVLVDSGDSF FLYSKLTVDK SRWQQGNVFS CSMVHEALHN 450
HYTQKSLSLG FGR 463
```

## Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGRVIT ITCRASQGIS SYLWVYQQKPK GKAPKLLIYA 50
ASSLQSGVPS RFGSGSGGTD FTLTISLQPF EDFATYYCQQ SYSTPRGTFG 100
QGTKEVTKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNPF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYLSSTLT TSLKADYEKH KVVYACEVTHQ 200
GLSSPVTKSF NRGEK 215
```

## Post-translational modifications

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

Intra-H (C23-C104) 22-96 160-216 277-337 383-441  
22"-96" 160"-216" 277"-337" 383"-441"  
Intra-L (C23-C104) 23"-88" 135"-195"  
23"-88" 135"-195"

Inter-H-L (h 5-CL 126) 236-215' 236"-215"

Inter-H-H (h 11, h 14) 242-242" 245-245"

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

H CH2 N84.4: 313, 313"

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

N-terminal L-kappa end clipping at serine S9 / Coupure de l'extrémité N-terminale de L-kappa

à la sérine S9 / Recorte del extremo N de L-kappa en la serina S9

1'-9', 1"-9" (1%)

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

H CHS K2: 463, 463"

**zurletrectinibum**

zurletrectinib

(2<sup>2</sup>R,2<sup>4</sup>S,5S)-3<sup>5</sup>,2<sup>4</sup>-difluoro-5-methyl-4-oxa-7,9-diaza-1(5,3)-pyrazolo[1,5-*a*]pyrimidina-3(3,2)-pyridina-2(1,2)-pyrrolidinacyclononaphan-8-one  
*tyrosine kinase inhibitor, antineoplastic*

zurlérectinib

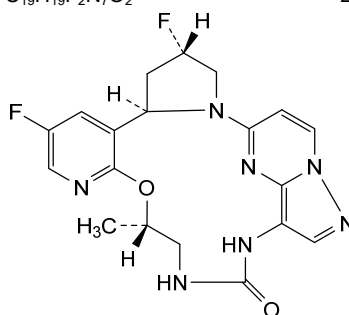
(2<sup>2</sup>R,2<sup>4</sup>S,5S)-3<sup>5</sup>,2<sup>4</sup>-difluoro-5-méthyl-4-oxa-7,9-diaza-1(5,3)-pyrazolo[1,5-*a*]pyrimidina-3(3,2)-pyridina-2(1,2)-pyrrolidinacyclononaphan-8-one  
*inhibiteur de tyrosine kinase, antinéoplasique*

zurletrectinib

(2<sup>2</sup>R,2<sup>4</sup>S,5S)-3<sup>5</sup>,2<sup>4</sup>-difluoro-5-metil-4-oxa-7,9-diaza-1(5,3)-pirazolo[1,5-*a*]pirimidina-3(3,2)-piridina-2(1,2)-pirrolidinaciclonoanfan-8-ona  
*inhibidor de tirosina kinasa, antineoplásico*

C<sub>19</sub>H<sub>19</sub>F<sub>2</sub>N<sub>7</sub>O<sub>2</sub>

2403703-30-8



# Electronic structure available on Mednet: <https://extranet.who.int/soinn/>

# Structure électronique disponible sur Mednet: <https://extranet.who.int/soinn/>

# Estructura electrónica disponible en Mednet: <https://extranet.who.int/soinn/>



**Names for chemical modifications of INN (substituent groups, counterions, adduct partners, etc.):**

Many pharmaceutical substances for which an International Nonproprietary Name (INN) has been established are used as modified derivatives (salts, esters, protein-drug conjugates, solvates, etc.). The chemical modification (including counterions) involved may be of complex nature and it is then inconvenient to use its systematic chemical name. Consequently, shorter nonproprietary names for such modifications have been devised, and these are recommended for creating modified International Nonproprietary Names (INN).

**Dénominations applicables aux modifications chimiques des DCI (groupes substituants, contre-ions, adduits, etc.) :**

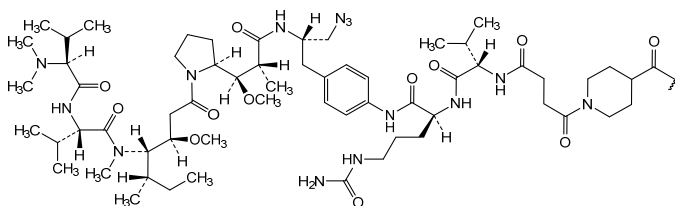
Certaines substances pour lesquelles une dénomination commune internationale proposée a été établie sont parfois utilisées comme dérivés modifiés (sels, esters, médicaments conjugués à des protéines, produits de solvatation, etc.). Les modifications chimiques (incluant les contre-ions) sont alors quelques fois si complexes qu'il est malcommode de les désigner conformément à la nomenclature chimique systématique. Des dénominations communes abrégées ont donc été formées ou choisies pour certaines d'entre elles et il est suggéré de les employer pour créer les dénominations communes internationales modifiées (DCIM).

**Denominaciones aplicables a modificaciones químicas de las DCI (grupos sustituyentes, contraiones, aductos, etc.):**

Muchas sustancias farmacéuticas para las cuales hay establecidas una denominación común internacional (DCI) pueden usarse como derivados modificados (sales, ésteres, medicamentos conjugados con proteínas, solvatos, etc.). Las modificaciones químicas (incluidos los contraiones) implicadas pueden ser de naturaleza compleja y por tanto es inapropiado utilizar su nombre químico sistemático. Como consecuencia, se han diseñado denominaciones abreviadas para estas modificaciones y se recomiendan para la creación de Denominaciones Comunes Internacionales modificadas (DCIM).

**botidotinum**

botidotin	1-(4-[[[(2S)-1-[[[(2S)-1-{4-[(2R)-3-azido-2-[(2R,3R)-3-[(2S)-1-[(3R,4S,5S)-4-[(N,N-diméthyl-L-valyl-L-valyl)(méthyl)amino]-3-méthoxy-5-méthylheptanoyl]pyrrolidin-2-yl]-3-méthoxy-2-méthylpropanamido}propyl]anilino]-5-(carbamoylamino)-1-oxopentan-2-yl]amino]-3-méthyl-1-oxobutan-2-yl]amino]-4-oxobutanoyl]piperidine-4-carbonyl
botidotine	1-(4-[[[(2S)-1-[[[(2S)-1-{4-[(2R)-3-azido-2-[(2R,3R)-3-[(2S)-1-[(3R,4S,5S)-4-[(N,N-diméthyl-L-valyl-L-valyl)(méthyl)amino]-3-méthoxy-5-méthylheptanoyl]pyrrolidin-2-yl]-3-méthoxy-2-méthylpropanamido}propyl]anilino]-5-(carbamoylamino)-1-oxopentan-2-yl]amino]-3-méthyl-1-oxobutan-2-yl]amino]-4-oxobutanoyl]pipéridine-4-carbonyle
botidotina	1-(4-[[[(2S)-1-[[[(2S)-1-{4-[(2R)-3-azido-2-[(2R,3R)-3-[(2S)-1-[(3R,4S,5S)-4-[(N,N-diméthyl-L-valil-L-valil)(méthyl)amino]-3-méthoxy-5-méthylheptanoil]pirrolidin-2-il]-3-méthoxy-2-méthylpropanamido}propil]anilino]-5-(carbamoylamino)-1-oxopentan-2-il]amino]-3-méthyl-1-oxobutan-2-il]amino]-4-oxobutanoyl]piperidina-4-carbonilo
	$C_{61}H_{101}N_{14}O_{12}$ *



**cafraglutidum**  
cafraglutide

L-histidyl-2-methylalanyl-L- $\alpha$ -glutamylglycyl-L-threonyl-L-phenylalanyl-L-threonyl-L-seryl-L- $\alpha$ -aspartyl-L-tyrosyl-L-seryl-L-seryl-L-tyrosyl-L-leucyl-L- $\alpha$ -glutamyl-L- $\alpha$ -glutamyl-L-glutamyl-L-alanyl-L-alanyl-L-lysyl-L- $\alpha$ -glutamyl-L-phenylalanyl-L-isoleucyl-L-alanyl-L-tryptophyl-L-leucyl-L-valyl-L-lysylglycylglycylglycylglycylglycylglycylglycyl-L-serylglycylglycylglycylglycyl-L-serylglycylglycylglycylglycyl-L-seryl-N<sup>6</sup>-(sulfanylacetyl)-L-lysynamide

cafraglutide

L-histidyl-2-méthylalanyl-L- $\alpha$ -glutamylglycyl-L-thréonyl-L-phénylalanyl-L-thréonyl-L-séryl-L- $\alpha$ -aspartyl-L-tyrosyl-L-séryl-L-séryl-L-tyrosyl-L-leucyl-L- $\alpha$ -glutamyl-L- $\alpha$ -glutamyl-L-glutamyl-L-alanyl-L-alanyl-L-lysyl-L- $\alpha$ -glutamyl-L-phénylalanyl-L-isoleucyl-L-alanyl-L-tryptophyl-L-leucyl-L-valyl-L-lysylglycylglycylglycylglycylglycylglycylglycyl-L-sérylglycylglycylglycylglycyl-L-sérylglycylglycylglycylglycyl-L-séryl-N<sup>6</sup>-(sulfanylacétyl)-L-lysynamide

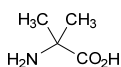
cafraglutide

L-histidil-2-metilalanil-L- $\alpha$ -glutamilglicil-L-treonil-L-fenilalanil-L-treonil-L-seril-L- $\alpha$ -aspartil-L-tirosil-L-seril-L-seril-L-tirosil-L-leucil-L- $\alpha$ -glutamil-L- $\alpha$ -glutamil-L-glutaminiil-L-alanil-L-alanil-L-lisil-L- $\alpha$ -glutamil-L-fenilalanil-L-isoleucil-L-alanil-L-triptofil-L-leucil-L-valil-L-lisilglicilglicilglicilglicilglicilglicilglicilglicil-L-serilglicilglicilglicilglicil-L-serilglicilglicilglicilglicil-L-seril-N<sup>6</sup>-(sulfanilacetil)-L-lisynamida

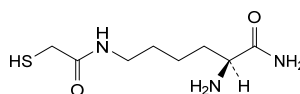
HAEGTFTSDY SSYLEEQAAK EFIAWLVKGG GGGGGSGGGG SGGGGSK 47

Modified residues / Résidus modifiés / Restos modificados

A (2)  
2-methyl-Ala, Aib  
aminoisobutyric acid



K (47)  
N<sup>6</sup>-(sulfanylacetyl)-L-lysynamide



**samrotecanum**  
samrotecan

1-[(2*S*,5*S*)-1-[[*(9S)*-9-ethyl-9-hydroxy-10,13-dioxo-2,3,9,10,13,15-hexahydro-1*H*,12*H*-benzo[*de*]pyrano[3',4':6,7]indolizino[1,2-*b*]quinolin-4-yl]amino]-2-methyl-1,4,7,35-tetraoxo-5-(propan-2-yl)-10,13,16,19,22,25,28,31-octaoxa-3,6,34-triazaheptatriacontan-37-yl]-2,5-dioxopyrrolidin-3-yl

samrotécàn

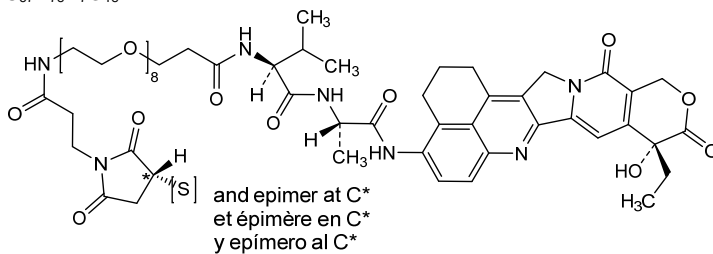
1-[(2*S*,5*S*)-1-[[*(9S)*-9-éthyl-9-hydroxi-10,13-dioxo-2,3,9,10,13,15-hexahydro-1*H*,12*H*-benzo[*de*]pyrano[3',4':6,7]indolizino[1,2-*b*]quinolin-4-yl]amino]-2-méthyl-1,4,7,35-tétraoxo-5-(propan-2-yl)-10,13,16,19,22,25,28,31-octaoxa-3,6,34-triazaheptatriacontan-37-yl]-2,5-dioxopyrrolidin-3-yle

samrotecàn

1-[(2*S*,5*S*)-1-[[*(9S)*-9-etil-9-hidroxi-10,13-dioxo-2,3,9,10,13,15-hexahydro-1*H*,12*H*-benzo[*de*]pirano[3',4':6,7]indolizino[1,2-*b*]quinolin-4-il]amino]-2-

metil-1,4,7,35-tetraoxo-5-(propan-2-il)-10,13,16,19,22,25,28,31-octaoxa-3,6,34-triazaheptatriacontan-37-il]-2,5-dioxopirrolidin-3-ilo

$C_{57}H_{78}N_7O_{18}S^{\bullet}$



**tomilopilum**

tomilopil

3-ethoxy-2,2-dimethyl-3-oxopropan-1-yl

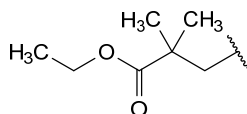
tomilopil

3-éthoxy-2,2-diméthyl-3-oxopropan-1-yle

tomilopilo

3-etoxi-2,2-dimetil-3-oxopropan-1-ilo

$C_7H_{13}O_2^{\bullet}$



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

**Proposed International Nonproprietary Names (Prop. INN): List 120**  
**Dénominations communes internationales proposées (DCI Prop.): Liste 120**  
**Denominaciones Comunes Internacionales Propuestas (DCI Prop.): Lista 120**  
*(WHO Drug Information, Vol. 32, No. 4, 2018)*

p.595	<i>supprimer</i> étranacogène dezaparovec	<i>insérer</i> étranacogène dézaparovec
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p.664	<i>suprimáse</i> volrubigèn ralaparovec	<i>insertase</i> volrubigén ralaparovec
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**Proposed International Nonproprietary Names (Prop. INN): List 121**  
**Dénominations communes internationales proposées (DCI Prop.): Liste 121**  
**Denominaciones Comunes Internacionales Propuestas (DCI Prop.): Lista 121**  
*(WHO Drug Information, Vol. 33, No. 2, 2019)*

p.286	<i>suprimáse</i> letetresgèn autoleucel	<i>insertase</i> letetresgén autoleucel
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**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. 4, 2019)*

p.811	<b>belzupacapum sarotalocanum</b> belzupacap sarotalocan	<i>remplacer la description par la suivante</i>
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**nanoparticule** vide dérivée du virus du papillomavirus humain 16 (HPV) modifié, 55 nm de diamètre, conjuguée à approximativement 200 molécules d'un photosensibilisant à base de **phtalocyanine** (groupe *sarotalocan*). Chaque particule est composée de 72 capsomères, faits de 5 molécules de protéine de capsid virale L1 modifiée [P<sup>78</sup>>R, T<sup>176</sup>>N, D<sup>273</sup>>T, N<sup>285</sup>>T, S<sup>288</sup>>N, T<sup>353</sup>>P, T<sup>389</sup>>S] et d'une molécule de protéine de capsid virale L2; capsid du virus du papillomavirus humain 16 (HPV16), une coquille sphérique de 72 unités de capsomère pentagonal (L1)<sub>5</sub>(L2)<sub>1</sub>, s'auto-assemblant comprenant les protéines recombinantes de capsid virale L1 ([P<sup>78</sup>>R, T<sup>176</sup>>N, D<sup>273</sup>>T, N<sup>285</sup>>T, S<sup>288</sup>>N, T<sup>353</sup>>P, T<sup>389</sup>>S]-modifiée) et L2, conjuguées à environ 200 groupes *sarotalocan* (colorant absorbant les proches **infrarouges**) en N<sup>6</sup> des résidus lysine; produite par des cellules rénales embryonnaires humaines (HEK293)

p.903 -904	<i>delete/supprimer/suprimáse</i> <b>upifitamabum</b> upifitamab upifitamab upifitamab	<i>insert/insérer/insertese</i> <b>upinitatugum</b> upinitatug upinitatug upinitatug
---------------	--	--



p.972  
-973

*delete/supprimer/suprimáse*  
**encukalnerum**  
 encukalner  
 encukalner  
 encukalner

*insert/insérer/insertese*  
**azetukalnerum**  
 azetukalner  
 azetukalner  
 azetukalner

p.983

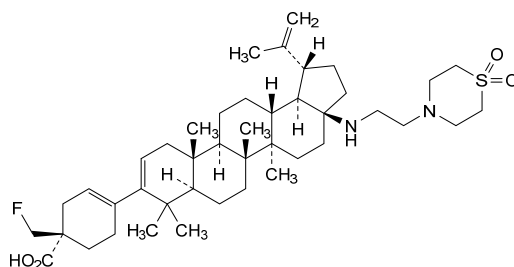
**fipravirimum**  
 fipravirimat  
 fipravirimat  
 fipravirimat

*replace the chemical name and structure by the following ones*  
*remplacer le nom chimique et la structure par les suivants*  
*sustitúyase el nombre químico y la estructura por los siguientes*

(1*R*)-4-(17 $\beta$ -[[2-(1,1-dioxo-1 $\lambda^6$ -thiomorpholin-4-yl)ethyl]amino]-28-norlupa-2,20(29)-dien-3-yl)-1-(fluoromethyl)cyclohex-3-ene-1-carboxylic acid

acide (1*R*)-4-(17 $\beta$ -[[2-(1,1-dioxo-1 $\lambda^6$ -thiomorpholin-4-yl)éthyl]amino]-28-norlupa-2,20(29)-dién-3-yl)-1-(fluorométhyl)cyclohex-3-ène-1-carboxylique

ácido (1*R*)-4-(17 $\beta$ -[[2-(1,1-dioxo-1 $\lambda^6$ -tiomorfolin-4-il)etil]amino]-28-norlupa-2,20(29)-dien-3-il)-1-(fluorometil)ciclohex-3-eno-1-carboxílico



p.1152

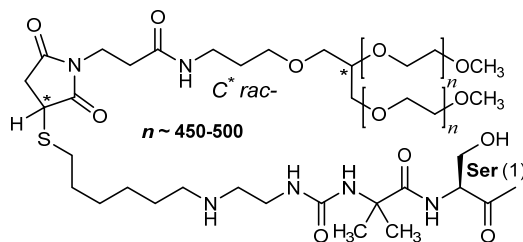
**palopegteriparatidum**  
 palopegteriparatide  
 palopegtériparatide  
 palopegteriparatida

*replace the structure by the following one*  
*remplacer la structure par la suivante*  
*sustitúyase la estructura por la siguiente*

Sequence / Séquence / Secuencia

SVSEIQLMHN LGKHLNSMER VEWLRKKLQD VHNF 34

Modified residue / Résidu modifié / Resto modificado



**Proposed International Nonproprietary Names (Prop. INN): List 127**  
**Dénominations communes internationales proposées (DCI Prop.): Liste 127**  
**Denominaciones Comunes Internacionales Propuestas (DCI Prop.): Lista 127**  
**(WHO Drug Information, Vol. 36, No. 2, 2022)**

p.332 **bezeparsenum**

bezeparsen

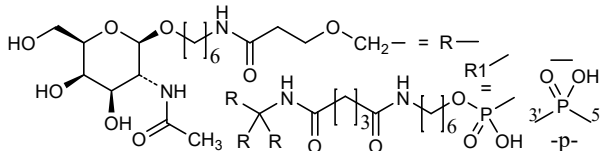
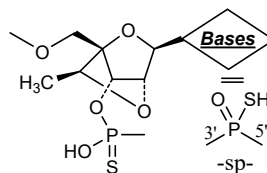
bézéparsen

bezeparsén

*replace the structure by the following one**remplacer la structure par la suivante**sustitúyase la estructura por la siguiente*(3'-5') R1-A=A=U=d (A=A=T=C=T=C=A=T=G=T=) C=A=GLegend:

A, G &amp; T : deoxynucleoside

C : 2'-deoxy-5-methylcytidine

A & G : 2'-O,4'-C-[(S)-ethylidene] nucleosideC & U : 2'-O,4'-C-[(S)-ethylidene]-5-methylnucleosidep.365 **denecimigum #**

denecimig

dénécimig

denecimig

*replace the structure by the following one**remplacer la structure par la suivante**sustitúyase la estructura por la siguiente*

## Heavy chain / Chaîne lourde / Cadena pesada : anti-F9 (H)

EVQLVESGGG LVQGRSLRL SCAASGFTFH DYAMHWVRQV PGKGLEWVSG 50  
 ISWRGDIGGY VKSVKGRFTI SRDNAKNSLY LQMNSLRAED TALYYCVKSY 100  
 GSGSFYNAPD SWGQGLTVTV SSASTKGPSV FPLAPCSRST SESTAALGCL 150  
 VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVFSSSLGT 200  
 KTYTCNVDPK PSNTKVDKRV ESKYGPCCPP CPAPEFLGGP SVFLFPKPKF 250  
 DTLMSRTP E VTCVVVDVQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS 300  
 TYRVVSVLTV LHQDNLNGKE YKCKVSNKGL PSSIEKTIK AKGQPREPQV 350  
 YTLFPQSQEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTTPVL 400  
 DSDGSFFLYS RLTVDKSRWQ EGNVFSQSV MHEALHNHYTQ KSLSLSLG 448

## Light chain / Chaîne légère / Cadena ligera : anti-F9 (L)

DIQMTQSPST LSASVGRVIT ITCRASQSI SWLAWYQQK GKAPKFLIYK 50  
 ASKLERGTPS RFSGSGSGTE FSLTISLQPD DDFATYYCLE YSSYIRTPGQ 100  
 TYRVVSVLTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY BREAKVQWKV 150  
 DNALQSGNSQ ESVTEQDSKD STYSLSLT LSKADYKHKH VYACEVTHQG 200  
 LSSPVTKSFN RGE C 214

Heavy chain / Chaîne lourde / Cadena pesada : anti-F10 (H<sup>1</sup>)

EVQLVQSGAE VVKPAGESLRI SCKGSGYSFS TSWIVWVRQM PGKGLEWVMG 50  
 IDPDSDFTSY SPSFQGHVIT SADKSI STAY LQWSSLKASD TAMYYCARLH 100  
 YINSEEFDVW GQGLTVTVSS ASTKGPSVFP LAPCSRSTSE STAALGLCVK 150  
 DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTKT 200  
 YTCNVDPKPS NTKVDKRVES KYGPPCCPSP APEFLGGPSV FLFPKPKD 250  
 LMSRTPPEVT CVVVDVQED PEVQFNWYD GVEVHNAKTK PREEQFNSTY 300  
 RVVSVLTVLH QDNLNGKEYK CKVSNKGLPS SIEKTIKAK QPREPQVYT 350  
 LPFSQEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTPPVLD 400  
 DGSFLLYSKL TVDKSRWQEG NVFSCVMHE ALHNHYTQKS LSLSLG 446

Light chain / Chaîne légère / Cadena ligera : anti-F10 (L<sup>1</sup>)

EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSVLAWYQQK PGQAPRLLIY 50  
 GQSSRTRGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QFGDSQLFTF 100  
 GQGTKLEIKR TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAVQW 150  
 KVDNALQSGN SQESVTEQDS KDSTYSLST LTLKADYK HKVYACEVTH 200  
 QGLSSPVTKS FNRGEC 216

## Post-translational modifications

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

Intra-H (C23-C104) 22-96 149-205 263-323 369-427  
 22"-96" 147"-203" 261"-321" 367"-425"

Intra-L (C23-C104) 23"-88" 134"-194"  
 23"-89" 136"-196"

Inter-H-L (CH1 10-CL 126) 136-214 134"-216"

Inter-H-H (h 8, h 11) 228-226" 231-229"

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

H CH2 N84.4: 299, 297"

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

p.383 **erepdekinrum**  
 erepdekinra  
 érepdékinra  
 erepdekinra

*replace the mechanism of action by the following one*  
*remplacer le mécanisme d'action par le suivant*  
*sustitúyase el mecanismo de acción por el siguiente*

*interleukin-17A antagonist*  
*antagoniste de l'interleukine 17A*  
*antagonista de la interleukina-17A*

p.435 **nexiguranum**  
 -436 nexiguran  
 néxiguran  
 nexigurán

*replace the chemical name and structure by the following ones*  
*remplacer le nom chimique et la structure par les suivants*  
*sustitúyase el nombre químico y la estructura por los siguientes*

*all-P-ambo-2'-O-methyl-P-thioadenylyl-(3'→5')-2'-O-methyl-P-thioadenylyl-(3'→5')-2'-O-methyl-P-thioadenylyl-(3'→5')-guanylyl-(3'→5')-guanylyl-(3'→5')-cytidylyl-(3'→5')-uridylyl-(3'→5')-guanylyl-(3'→5')-cytidylyl-(3'→5')-uridylyl-(3'→5')-guanylyl-(3'→5')-adenylyl-(3'→5')-uridylyl-(3'→5')-guanylyl-(3'→5')-adenylyl-(3'→5')-cytidylyl-(3'→5')-adenylyl-(3'→5')-cytidylyl-(3'→5')-cytidylyl-(3'→5')-uridylyl-(3'→5')-guanylyl-(3'→5')-uridylyl-(3'→5')-uridylyl-(3'→5')-uridylyl-(3'→5')-uridylyl-(3'→5')-uridylyl-(3'→5')-adenylyl-(3'→5')-guanylyl-(3'→5')-adenylyl-2'-O-*







**Proposed International Nonproprietary Names (Prop. INN): List 127-COVID-19 (special edition)- addendum****Dénominations communes internationales proposées (DCI Prop.): Liste 127-COVID-19 (édition spéciale)- addendum****Denominaciones Comunes Internacionales Propuestas (DCI Prop.): Lista 127-COVID-19 (edición especial)- addendum****(WHO Drug Information, Vol. 36, No. 2, 2022)**p.557  
-558**carocovateinum**  
carocovatein  
carocovatéine  
carocovateína*replace the chemical name and structure by the following ones  
remplacer le nom chimique et la structure par les suivants  
sustitúyase el nombre químico i la estructura por los siguientes*

severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) Spike (S) glycoprotein (S glycoprotein, UniProt P0DTC2), stable prefusion conformation variant (R<sup>669</sup>>G, R<sup>670</sup>>S, R<sup>672</sup>>S, K<sup>973</sup>>P, V<sup>974</sup>>P), C-terminal transmembrane domain (1196-1260) deleted and replaced with the

<sup>1196</sup>GSGYIPEAPRDGQAYVRKDG EWVLLSTFLGRSLEVL FQ<sup>1233</sup> peptide containing the enterobacteria phage **T4** fibrin C-terminal foldon domain fragment

<sup>458</sup>GYIPEAPRDGQAYVRKDG EWVLLSTFL<sup>484</sup>, followed by the remnant of a human rhinovirus (HRV) 3C protease cleavage sequence (<sup>1228</sup>LEVL FQ<sup>1233</sup>), trimer, produced in Chinese hamster ovary (CHO) cells, cell line CHO-S, glycoform alfa

glycoprotéine de la spicule (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SRAS-CoV-2) (glycoprotéine S, UniProt P0DTC2), variante de conformation de préfusion stable (R<sup>669</sup>>G, R<sup>670</sup>>S, R<sup>672</sup>>S, K<sup>973</sup>>P, V<sup>974</sup>>P), domaine transmembranaire C-terminal (1196-1260) supprimé et remplacé par le peptide

<sup>1196</sup>GSGYIPEAPRDGQAYVRKDG EWVLLSTFLGRSLEVL FQ<sup>1233</sup> contenant le fragment <sup>458</sup>GYIPEAPRDGQAYVRKDG EWVLLSTFL<sup>484</sup> du domaine foldon C-terminal de la fibratine du phage **T4** des entérobactéries, suivi du reste d'une séquence de clivage par la protéase d'un rhinovirus humain (HRV) 3C (<sup>1228</sup>LEVL FQ<sup>1233</sup>), trimère, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-S, glycoforme alfa

**glicoproteína de la espícula (S)** del síndrome respiratorio severo agudo del coronavirus 2 (SARS-CoV-2) (glicoproteína S, UniProt P0DTC2), variante de conformación estable de perfusión (R<sup>669</sup>>G, R<sup>670</sup>>S, R<sup>672</sup>>S, K<sup>973</sup>>P, V<sup>974</sup>>P), dominio transmembrana C-terminal (1196-1260) eliminado y reemplazado con el péptido <sup>1196</sup>GSGYIPEAPRDGQAYVRKDG EWVLLSTFLGRSLEVL FQ<sup>1233</sup> que contiene el fragmento del **dominio foldon C-terminal de la fibratina del fago T4 de las enterobacterias**, seguido del resto de una **secuencia de escisión de la proteasa de uno rinovirus humano** (HRV) 3C (<sup>1228</sup>LEVL FQ<sup>1233</sup>), trímero, producido en células ováricas de hámster Chino (CHO), línea celular CHO-S, glicoforma alfa

## Monomer / Monomère / Monómero

QCVNLTRTRQ	LPPAYTNSFT	RGVYYPDKVF	RSSVLHSTQD	LFLPFFSNVT	50
WFHAIHVSQT	NGTKRFDNVP	LPFNDGVYFA	STEKSNIRG	WIFGTTLDSK	100
TQSLLIYNNA	TNVVIKVFCEP	QFCNDPFLGV	YYHKNNKSWM	ESEFRVYSSA	150
NNCTFEYVSQ	PFLMDLEGKQ	GNFKNLREFV	FKNIDGYFKI	YSKHTPINLV	200
RDLPQGFSAI	EPLVDLPIGI	NITRFQTLA	LHRSYLTPGD	SSSGWTAGAA	250
AYYVGYLQPR	TFLLYKNENG	TITDAVDCAL	DPLSETKCTL	KSFTVEKGIY	300
QTSNFRVQPT	ESIVRFPNIT	NLCPFGEVFN	ATRFASVYAW	NRKRISNCVA	350
DYSVLYNSAS	FSTFKCYGVS	PTKLNLDLCT	NVYADSFVIR	GDEVRQIAPG	400
QTGKIADYNY	KLPDDFTGCV	IAWNSNNLDS	KVGGNYNYLY	RLFRKSNLKP	450
FERDISTEYI	QAGSTPCNGV	EGFNCFPLQ	SYGFQPTNGV	GYQPYRVVVL	500
SPELLHAPAT	VCGPKKSTNL	VKNKCVNMFN	NGLTGTGVLT	ESNKKFLFPQ	550
QFGRDIADTT	DAVRDPQTL	ILDITPCSFG	GVSVITPGTN	TSNQVAVLYQ	600
DVNCTEVPVA	IHADQLTPTW	RVYSTGNSVF	QTRAGCLIGA	EHVNNSYECD	650
IPIGAGICAS	YQTQTNSP <u>GS</u>	<u>ASS</u> VASQSII	AYTMSLGAEN	SVAYSNNNSIA	700
IPNFTISVT	TEILPVSMTK	TSVDCMTYIC	GDSTECNLL	LQYGSFCTQL	750
NRALTGIAVE	QDKNTQEVFA	QVKQIYKTPP	IKDFGGFNFS	QILPDPSPKPS	800
KRSFIEDLLF	NKVTLADAGF	IKQYGDCLGD	IAARDLICAQ	KFNGLTVLPP	850
LLTDEMIQY	TSALLAGTIT	SGWTFGAGAA	LQIPFAMQMA	YRFNGIGVTO	900
NVLYENQKLI	ANQFNSAIGK	IQDSLSSSTAS	ALGKQLQDVVN	QNAQALNLTQ	950
KQLSSNFGAI	SSVLNDILSR	LD <u>PE</u> AEVQI	DRLITGRLOS	LQTIVTQQLI	1000
RAAEIRASAN	LAATKMSECV	LGQSKRVDFC	GKGYHLSMFP	QSAPHGVVFL	1050
HVTYVPAQEK	NFTTAPAICH	DGKAHFPPREG	VFVSNGTWHF	VTQRNFVEPQ	1100
IITTDNTEFVS	GNCDDVIGIV	NNTVYDPLQP	ELDSFKEELD	KYFKNHTSPD	1150
VDLGDISGIN	ASVVNIQKEI	DRLNEVAKNL	NESLIDLQEL	KGYEQSG <u>GYI</u>	1200
<u>PEAPRDQAY</u>	<u>VRKDGEWVLL</u>	<u>STFLGRS</u> <u>LEV</u>	<u>LFO</u>		1233

## Mutation / Mutation / Mutación

R<sup>669</sup>>G, R<sup>670</sup>>S, R<sup>672</sup>>S, K<sup>973</sup>>P, V<sup>974</sup>>P

## Peptide linker / Peptide liant / Péptido de unión

GS 1196-1197 GRS 1225-1227

## Foldon domain / Foldon domaine / Foldon dominio

GYIPEAPRDG QAYVRKDGEW VLLSTFL 1198-1224

## Post-translational modifications

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

Intra-chain: 2-123, 118-153, 278-288, 323-348, 366-419, 378-512, 467-475, 525-577,  
604-636, 649-658, 725-747, 730-736, 827-838, 1019-1030, 1069-1113

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

N4, N48, N61, N109, N136, N152, N221, N269, N318, N330, N590, N603, N644, N696,  
N704, N788, N1061, N1085, N1121, N1145, N1160, N1181

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

Q1 &gt; pyroglutamyl (pE, 5-oxoprolyl)

p.575

**nulabeglogenum autogedtemcelum**

nulabeglogene autogedtemcel

nulabéglogène autogedtemcel

nulabeglogén autogedtemcel

*replace the description by the following one**remplacer la description par la suivante**sustitúyase la descripción por la siguiente*

autologous CD34+ hematopoietic stem and progenitor cells (HSPCs) obtained by apheresis from sickle cell patients, genetically modified *ex vivo* by CRISPR/Cas9 (clustered regularly interspaced short palindromic repeats/CRISPR-associated protein 9)-mediated gene editing consisting of a single guide RNA (sgRNA) targeting the first exon of the human  $\beta$ -globin (HBB) gene, and using a homology-directed repair mechanism to correct the nucleic acid sequence encoding the glutamic acid to valine mutation at position 6 in the HBB protein via an adeno-associated

virus serotype 6 (AAV6) vector in which the **sgRNA targeting corrective** sequence is located between two HBB homology arms. Following genetic modification, each cell can have one of six combinations of HBB allele (WT/WT, INDEL/WT, INDEL/INDEL, INDEL/HR, WT/HR, HR/HR, where WT refers to the wild type sickle cell disease allele, INDEL refers to an insertion/deletion event but no correction of the HBB gene, and HR refers to a corrected HBB allele). **On average 56% of the cells have at least one corrected HBB allele (HR). The final substance consists of cells with  $\geq 20\%$  alleles that are corrected of the E6V mutation, measured by the frequency of homologous recombination events.** The cell suspension is enriched for CD34+ cells using magnetic bead separation. The substance consists of cells with the CD45+ and CD34+ phenotype, with  $\geq 80\%$  CD34+ purity. The functional characterization of the cells is based on the ability to form erythroid and myeloid colonies on semisolid methylcellulose-based medium

Cellules souches et progénitrices hématopoïétiques CD34+ autologues (HSPC) obtenues par aphérese à partir de patients atteints de drépanocytose, génétiquement modifiées *ex vivo* par édition génique médiée par CRISPR/Cas9 (courtes répétitions palindromiques groupées et régulièrement espacées / protéine 9 associée à CRISPR) consistant d'un ARN guide unique (sgRNA) ciblant le premier exon du gène de la  $\beta$ -globine humaine (HBB), et en utilisant un mécanisme de réparation dirigé par homologie pour corriger la séquence d'acide nucléique codant la mutation en position 6 de l'acide glutamique en valine dans la protéine HBB via un vecteur du virus adéno-associé de sérotype 6 (AAV6) dans lequel la **séquence correctrice** est située entre deux bras d'homologie HBB. Après modification génétique, chaque cellule peut présenter l'une des six combinaisons de l'allèle HBB (WT/WT, INDEL/WT, INDEL/INDEL, INDEL/HR, WT/HR, HR/HR, où WT désigne l'allèle sauvage de la drépanocytose, INDEL désigne un événement d'insertion/délétion mais sans correction du gène HBB, et HR désigne un allèle HBB corrigé). **La substance finale est constituée de cellules avec  $\geq 20\%$  d'allèles corrigés de la mutation E6V, mesurée par la fréquence des événements de recombinaison homologue.** La suspension cellulaire est enrichie en cellules CD34+ à l'aide d'une séparation par billes magnétiques. La substance est constituée de cellules présentant les phénotype CD45+ et CD34+, avec une pureté CD34+ de  $\geq 80\%$ . La caractérisation fonctionnelle des cellules est basée sur la capacité à former des colonies érythroïdes et myéloïdes sur un milieu semi-solide à base de méthylcellulose.

Células madre y progenitoras hematopoyéticas (HSPCs) autólogas CD34+ obtenidas por aféresis de pacientes con anemia falciforme, modificadas genéticamente *ex vivo* mediante edición génica mediada por CRISPR/Cas9 (repeticiones palindrómicas cortas agrupadas y espaciadas regularmente / proteína asociada a CRISPR 9) consistente en un único RNA guía (sgRNA) dirigido al primer exón del gen de la  $\beta$ -globina humana (HBB) y usando un mecanismo de reparación dirigida por homología para corregir la mutación de ácido glutámico a valina en la posición 6 del gen HBB por medio de un vector de virus adenoasociado de serotipo 6 (AAV6) en el que la **secuencia correctora** se localiza entre dos brazos de homología en el HBB.

Tras la modificación genética, cada célula puede tener una de seis combinaciones de alelos HBB (WT/WT, INDEL/WT, INDEL/INDEL, INDEL/HR, WT/HR, HR/HR, donde WT se refiere al alelo del tipo silvestre de la anemia falciforme, INDEL se refiere a un evento de inserción/delección, pero no corrección, del gen HBB, y HR se refiere a un alelo de HBB corregido). **La substancia final consiste en células con  $\geq 20\%$  de los alelos corregidos de la mutación E6V, medido por la frecuencia de eventos de recombinación homóloga.**

La suspensión celular se enriquece en células CD34+ usando una separación con bolas magnéticas. La substancia consiste en células con el fenotipo CD45+ y CD34+, con  $\geq 70\%$  de pureza. La caracterización funcional de las células se basa en la capacidad de formar colonias eritroides y mieloides en medio semisólido basado en metilcelulosa.

## Proposed International Nonproprietary Names: List 128 – COVID-19 (special edition)

Comments on, or formal objections to, the proposed names may be forwarded by any person to the INN Programme of the World Health Organization within two weeks of the date of their publication on *WHO INN Programme website*, i.e., for **List 128 – COVID-19 (special edition) of Proposed INN not later than 22 August 2022, exceptionally for this special edition. Publication date: 08/08/2022**

## Dénominations communes internationales proposées: Liste 128 - COVID-19 (édition spéciale)

Des observations ou des objections formelles à l'égard des dénominations proposées peuvent être adressées par toute personne au Programme des Dénominations communes internationales de l'Organisation mondiale de la Santé dans un délai de deux semaines à compter de la date de leur publication sur le *site Internet du Programme des DCI de l'OMS*, c'est à dire pour la **Liste 128 - COVID-19 (édition spéciale) de DCI Proposées le 22 août 2022 au plus tard, exceptionnellement pour cette édition spéciale. Date de publication : 08/08/2022**

## Denominaciones Comunes Internacionales Propuestas: Lista 128 - COVID-19 (edición especial)

Cualquier persona puede dirigir observaciones u objeciones respecto de las denominaciones propuestas, al Programa de Comunes Internacionales de la Organización Mundial de la Salud, en un plazo de dos semanas, contados desde la fecha de su publicación en el *sitio web del Programa de las DCI de la OMS*, es decir, para **la Lista 128 - COVID-19 (edición especial) de DCI Propuestas el 22 de agosto de 2022 a más tardar, excepcionalmente para esta edición especial. Fecha de publicación: 08/08/2022**

<i>Proposed INN (Latin, English, French, Spanish)</i>	<i>Chemical name or description: Action and use: Molecular formula, Chemical Abstracts Service (CAS) registry number: Graphic formula</i>
<i>DCI Proposée</i>	<i>Nom chimique ou description: Propriétés et indications: Formule brute, Numéro dans le registre du CAS: Formule développée</i>
<i>DCI Propuesta</i>	<i>Nombre químico o descripción: Acción y uso: Fórmula molecular, Número de registro del CAS: Fórmula desarrollada</i>

**secelasomeranum #**

- secelasomeran messenger RNA (mRNA), 5'-capped, encoding a full-length, codon-optimised pre-fusion stabilised conformation variant (K983P and V984P) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) spike (S) glycoprotein (Beta variant, B.1.351; based upon GISAID No. EPI\_ISL\_2689878), further optimized by two additional stop codons, flanked by an artificial 5' untranslated region (UTR) and a 3' UTR derived from the human alpha globin gene (HBA1) and terminated by a 3' poly(A) tail; contains N<sup>1</sup>-methylpseudouridine instead of uridine (*all-U>m<sup>1</sup>Ψ*).  
*immunological agent for active immunization (anti-SARS-CoV-2)*
- sécélasoméran ARN messenger (ARNm), protégé d'une coiffe en 5', codant la séquence entière d'un variant de la glycoprotéine de spicule (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère; Beta variant, B.1.351; basé sur GISAID No. EPI\_ISL\_2689878) à la conformation stabilisée par pré-fusion (K983P et V984P) et aux codons optimisés, optimisation renforcée par l'ajout de deux codons stop, flanqué d'une région non traduite (UTR) en 5' artificielle et d'une UTR en 3' dérivée du gène de l'alpha-globine humaine (HBA1) et terminé par une queue poly(A) en 3'; contient de la N<sup>1</sup>-méthylpseudouridine au lieu de l'uridine (*tout-U>m<sup>1</sup>Ψ*).  
*agent immunologique pour immunisation active (anti-SARS-CoV-2)*
- secelasomerán ARN mensajero (ARNm), protegido en 5', que codifica para una variante estabilizada en conformación pre-fusión (K983P and V984P) de la glicoproteína de la espícula (S) del SARS-Cov-2 (coronavirus 2 del síndrome respiratorio agudo severo; Beta variant, B.1.351; basada en GISAID No. EPI\_ISL\_2689878) completa, con codones optimizados y dos codones de terminación adicionales, flanqueado por una región 5' no traducida (UTR) artificial y una UTR en 3' derivada del gen de la globina alfa humana (HBA1) y terminado por una cola poly(A) en 3'; contiene N<sup>1</sup>-metilpseudouridina en lugar de uridina (*todo-U>m<sup>1</sup>Ψ*).  
*agente inmunológico para inmunización activa (anti-SARS-CoV-2)*

2642373-67-7

- # Electronic structure available on Mednet: <https://extranet.who.int/soinn/>  
# Structure électronique disponible sur Mednet: <https://extranet.who.int/soinn/>  
# Estructura electrónica disponible en Mednet: <https://extranet.who.int/soinn/>

Please note that due to exceptional pandemic circumstances, this Proposed INN was open for public consultation for a period of two weeks only (instead of four months) and the publication date to be retained is the date of web publication on the WHO INN website. The procedure "INN for Variant COVID-19 Vaccine Active Substances" can be found at <https://www.who.int/publications/i/item/inn-21-520>.

Veillez noter qu'en raison de circonstances pandémiques exceptionnelles, cette DCI Proposée a été ouverte à la consultation publique pour une période de deux semaines seulement (au lieu de quatre mois) et la date de publication à retenir est la date de publication sur le site Internet du Programme des DCI de l'OMS. La procédure "INN for Variant COVID-19 Vaccine Active Substances" peut être trouvée à <https://www.who.int/publications/i/item/inn-21-520>.

Tenga en cuenta que debido a circunstancias excepcionales de la pandemia, esta DCI Propuesta estaba abierta a la consulta pública durante un periodo de sólo dos semanas (en lugar de cuatro meses) y la fecha de publicación que debe conservarse es la fecha de publicación en el sitio web del Programa de las DCI de la OMS. Se puede encontrar la procedura "INN for Variant COVID-19 Vaccine Active Substances" en nuestro sitio web <https://www.who.int/publications/i/item/inn-21-520>.



**Proposed International Nonproprietary Names: List 128 – COVID-19 (special edition – ADDENDUM 1)**

Comments on, or formal objections to, the proposed names may be forwarded by any person to the INN Programme of the World Health Organization within two weeks of the date of their publication on *WHO INN Programme website*, i.e., for **List 128 – COVID-19 (special edition – ADDENDUM 1) of Proposed INN not later than 29 September 2022, exceptionally for this special edition. Publication date: 15/09/2022**

**Dénominations communes internationales proposées: Liste 128 - COVID-19 (édition spéciale – ADDENDUM 1)**

Des observations ou des objections formelles à l'égard des dénominations proposées peuvent être adressées par toute personne au Programme des Dénominations communes internationales de l'Organisation mondiale de la Santé dans un délai de deux semaines à compter de la date de leur publication sur le *site Internet du Programme des DCI de l'OMS*, c'est à dire pour la **Liste 128 - COVID-19 (édition spéciale – ADDENDUM 1) de DCI Proposées le 29 septembre 2022 au plus tard, exceptionnellement pour cette édition spéciale. Date de publication : 15/09/2022**

**Denominaciones Comunes Internacionales Propuestas: Lista 128 - COVID-19 (edición especial – ADDENDUM 1)**

Cualquier persona puede dirigir observaciones u objeciones respecto de las denominaciones propuestas, al Programa de Comunes Internacionales de la Organización Mundial de la Salud, en un plazo de dos semanas, contados desde la fecha de su publicación en el *sitio web del Programa de las DCI de la OMS*, es decir, para **la Lista 128 - COVID-19 (edición especial – ADDENDUM 1) de DCI Propuestas el 29 de septiembre de 2022 a más tardar, excepcionalmente para esta edición especial. Fecha de publicación: 15/09/2022**

<i>Proposed INN (Latin, English, French, Spanish)</i>	<i>Chemical name or description: Action and use: Molecular formula, Chemical Abstracts Service (CAS) registry number: Graphic formula</i>
<i>DCI Proposée</i>	<i>Nom chimique ou description: Propriétés et indications: Formule brute, Numéro dans le registre du CAS: Formule développée</i>
<i>DCI Propuesta</i>	<i>Nombre químico o descripción: Acción y uso: Fórmula molecular, Número de registro del CAS: Fórmula desarrollada</i>

**davesomeranum #**

davesomeran

messenger RNA (mRNA), 5'-capped, encoding a full-length, codon-optimised pre-fusion stabilised conformation variant (K981P and V982P) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) spike (S) glycoprotein (Omicron variants B.1.1.529.4 and B.1.1.529.5; also known as BA.4 and BA.5; based upon GISAID No. EPI\_ISL\_12548717) further optimized by two additional stop codons, flanked by an artificial 5' untranslated region (UTR) and a 3' UTR derived from the human alpha globin gene (HBA1) modified to contain an identification and ratio (IDR) sequence to enable identification and relative ratio determination of individual RNA components in a multivalent mRNA vaccine, and terminated by a 3' poly(A) tail; contains N<sup>1</sup>-methylpseudouridine instead of uridine (*all-U>m<sup>1</sup>Ψ*).  
*immunological agent for active immunization (anti-SARS-CoV-2)*

davésoméran

ARN messenger (ARNm), protégé d'une coiffe en 5', codant la séquence entière optimisée au niveau des codons d'un variant de conformation stabilisée avant fusion (K981P et V982P) de la glycoprotéine de spicule (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère) (variants Omicron B.1.1.529.4 et B.1.1.529.5; également connus sous les noms de BA.4 et BA.5; basé sur le numéro GISAID EPI\_ISL\_12548717), dont l'optimisation a été renforcée par deux codons stop supplémentaires, flanqué d'une région non traduite (UTR) artificielle en 5' et d'une UTR en 3' dérivée du gène de l'alpha-globine humaine (HBA1) modifiée pour contenir une séquence d'identification et de ratio (IDR) afin de permettre l'identification et la détermination du ratio relatif de chaque composant d'ARN dans un vaccin ARNm multivalent, et terminé par une queue poly(A) en 3'; contient de la N<sup>1</sup>-méthylpseudouridine à la place de l'uridine (*tout-U>m<sup>1</sup>Ψ*).  
*agent immunologique pour immunisation active (anti-SARS-CoV-2)*

davesomerán

ARN mensajero (ARNm), protegido en 5', que codifica para la secuencia completa, con codones optimizados, de una variante estabilizada en conformación pre-fusión (K981P y V982P) de la glicoproteína de la espícula (S) del SARS-Cov-2 (coronavirus 2 del síndrome respiratorio agudo severo (variantes Omicron B.1.1.529.4 y B.1.1.529.5; también conocidas como BA.4 y BA.5; basadas en GISAID No. EPI\_ISL\_12548717) con dos codones de terminación adicionales, flanqueado por una región 5' no traducida (UTR) artificial y una UTR en 3' derivada del gen de la globina alfa humana (HBA1) modificada para incluir una secuencia de identificación y ratio (IDR) para permitir la identificación y la determinación el ratio relativo de los componentes individuales de ARN en una vacuna de ARNm multivalente, y terminado por una cola poli(A) en 3'; contiene N<sup>1</sup>-metilpseudouridina en lugar de uridina (*todo-U>m<sup>1</sup>Ψ*).  
*agente inmunológico para inmunización activa (anti-SARS-CoV-2)*

2798905-80-1

**famtozinameranum #**

famtozinameran messenger RNA (mRNA), 5'-capped, encoding a full-length, codon-optimised pre-fusion stabilised conformation variant (K981P and V982P) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) spike (S) glycoprotein (Omicron sub-lineages B.1.1.529.4 and B.1.1.529.5 also referred to as BA.4 and BA.5; based upon GISAID: EPI\_ISL\_13017830), flanked by 5' and 3' untranslated regions and a 3' poly(A) tail; contains N<sup>1</sup>-methylpseudouridine instead of uridine (*all-U>m<sup>1</sup>Ψ*).  
*immunological agent for active immunization (anti-SARS-CoV-2)*

famtozinaméran ARN messenger (ARNm), protégé d'une coiffe en 5', codant la séquence entière aux codons optimisés d'un variant à la conformation stabilisée avant fusion (K981P et V982P) de la glycoprotéine de spicule (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère) (sous-lignées Omicron B.1.1.529.4 et B.1.1.529.5; également connues sous les noms de BA.4 et BA.5; d'après GISAID : EPI\_ISL\_13017830), flanqué de régions non traduites en 5' et 3' et d'une queue poly(A) en 3'; contient de la N<sup>1</sup>-méthylpseudouridine à la place de l'uridine (*tout-U>m<sup>1</sup>Ψ*).  
*agent immunologique pour immunisation active (anti-SARS-CoV-2)*

famtozinamerán ARN mensajero (ARNm), protegido en 5', que codifica para la secuencia completa, con codones optimizados, de una variante estabilizada en conformación pre-fusión (K981P y V982P) de la glicoproteína de la espícula (S) del SARS-Cov-2 (coronavirus 2 del síndrome respiratorio agudo severo) (sublinajes B.1.1.529.4 and B.1.1.529.5 de Omicron, también conocidas como BA.4 y BA.5; basadas en GISAID: EPI\_ISL\_13017830), flanqueada por regiones 5' y 3' no traducidas y una cola poli(A) en 3'; contiene N<sup>1</sup>-metilpseudouridina en lugar de uridina (*todo-U>m<sup>1</sup>Ψ*).  
*agente inmunológico para inmunización activa (anti-SARS-CoV-2)*

2785347-58-0

# Electronic structure available on Mednet: <https://extranet.who.int/soinn/>

# Structure électronique disponible sur Mednet: <https://extranet.who.int/soinn/>

# Estructura electrónica disponible en Mednet: <https://extranet.who.int/soinn/>

*Please note that due to exceptional pandemic circumstances, this Proposed INN was open for public consultation for a period of two weeks only (instead of four months) and the publication date to be retained is the date of web publication on the WHO INN website. The procedure "INN for Variant COVID-19 Vaccine Active Substances" can be found at <https://www.who.int/publications/i/item/inn-21-520>.*

*Veillez noter qu'en raison de circonstances pandémiques exceptionnelles, cette DCI Proposée a été ouverte à la consultation publique pour une période de deux semaines seulement (au lieu de quatre mois) et la date de publication à retenir est la date de publication sur le site Internet du Programme des DCI de l'OMS. La procédure "INN for Variant COVID-19 Vaccine Active Substances" peut être trouvée à <https://www.who.int/publications/i/item/inn-21-520>.*

*Tenga en cuenta que debido a circunstancias excepcionales de la pandemia, esta DCI Propuesta estaba abierta a la consulta pública durante un período de sólo dos semanas (en lugar de cuatro meses) y la fecha de publicación que debe conservarse es la fecha de publicación en el sitio web del Programa de las DCI de la OMS. Se puede encontrar la procedura "INN for Variant COVID-19 Vaccine Active Substances" en nuestro sitio web <https://www.who.int/publications/i/item/inn-21-520>.*

## Proposed International Nonproprietary Names: List 128 – COVID-19 (special edition – ADDENDUM 2)

Comments on, or formal objections to, the proposed names may be forwarded by any person to the INN Programme of the World Health Organization within four months of the date of their publication in *WHO Drug Information*, i.e., for **List 128 – COVID-19 (special edition – ADDENDUM 2) Proposed INN not later than 19 May 2023**.

**Publication date: 20.01.2023.**

## Dénominations communes internationales proposées: Liste 128 – COVID-19 (édition spéciale – ADDENDUM 2)

Des observations ou des objections formelles à l'égard des dénominations proposées peuvent être adressées par toute personne au Programme des Dénominations communes internationales de l'Organisation mondiale de la Santé dans un délai de quatre mois à compter de la date de leur publication dans *WHO Drug Information*, c'est à dire pour la **Liste 128 – COVID-19 (édition spéciale – ADDENDUM 2) de DCI Proposées le 19 mai 2023 au plus tard**.

**Date de publication: 20.01.2023**

## Denominaciones Comunes Internacionales Propuestas: Lista 128 – COVID-19 (edición especial – ADDENDUM 2)

Cualquier persona puede dirigir observaciones u objeciones respecto de las denominaciones propuestas, al Programa de Denominaciones Comunes Internacionales de la Organización Mundial de la Salud, en un plazo de cuatro meses, contados desde la fecha de su publicación en *WHO Drug Information*, es decir, para la **Lista 128 – COVID-19 (edición especial – ADDENDUM 2) de DCI Propuestas el 19 de Mayo de 2023 a más tardar**.

**Fecha de publicación: 20.01.2023**

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*Proposed INN  
(Latin, English, French,  
Spanish)*

*Chemical name or description: Action and use: Molecular  
formula, Chemical Abstracts Service (CAS) registry number:  
Graphic formula*

*DCI Proposée*

*Nom chimique ou description: Propriétés et indications:  
Formule brute: Numéro dans le registre du CAS: Formule  
développée*

*DCI Propuesta*

*Nombre químico o descripción: Acción y uso: Fórmula  
molecular: Número de registro del CAS: Fórmula desarrollada*

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**aderamastatum**  
aderamastat

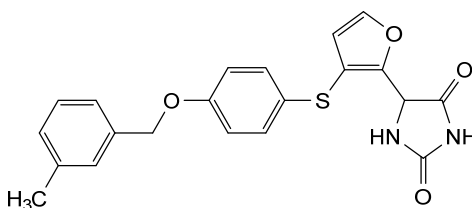
(1<sup>4</sup>Ξ)-7<sup>3</sup>-methyl-5-oxa-3-thia-1(4)-imidazolidina-2(2,3)-  
furana-4(1,4),7(1)-dibenzenaheptaphane-1<sup>2</sup>,1<sup>5</sup>-dione  
*matrix metalloproteinase inhibitor*

adéramastat (1<sup>4</sup>Ξ)-7<sup>3</sup>-méthyl-5-oxa-3-thia-1(4)-imidazolidina-2(2,3)-furana-4(1,4),7(1)-dibzenaheptaphane-1<sup>2</sup>,1<sup>5</sup>-dione  
*inhibiteur de la métalloprotéinase de la matrice*

aderamastat (1<sup>4</sup>Ξ)-7<sup>3</sup>-metil-5-oxa-3-tia-1(4)-imidazolidina-2(2,3)-furana-4(1,4),7(1)-dibcenaheptafano-1<sup>2</sup>,1<sup>5</sup>-diona  
*inhibidor de la metaloproteínasa de matriz*

C<sub>21</sub>H<sub>18</sub>N<sub>2</sub>O<sub>4</sub>S

877176-23-3



**alsecovateinum #**  
alsecovatein

severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) glycoprotein (S glycoprotein, UniProt P0DTC2, strain Wuhan-Hu-1) (1-1260), stable prefusion conformation variant (R<sup>669</sup>>Q, R<sup>670</sup>>Q, R<sup>672</sup>>Q, K<sup>973</sup>>P, V<sup>974</sup>>P), trimer, produced in *Spodoptera frugiperda* (Sf9) insect cells, glycoform alfa  
*immunological agent for active immunization (anti-SARS-CoV-2)*

alsécovatéine

glycoprotéine du spicule (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2) (glycoprotéine S, UniProt P0DTC2, souche Wuhan-Hu-1) (1-1260), variante de conformation stable par pré-fusion (R<sup>669</sup>>Q, R<sup>670</sup>>Q, R<sup>672</sup>>Q, K<sup>973</sup>>P, V<sup>974</sup>>P), trimère, produits dans des cellules d'insecte *Spodoptera frugiperda* (Sf9), glycoforme alfa  
*agent immunologique d'immunisation active (anti-SARS-CoV-2)*

alsecovateína

glicoproteína de la espícula (S) del coronavirus 2 del síndrome respiratorio severo agudo (SARS-CoV-2) (glicoproteína S, UniProt P0DTC2, cepa Wuhan-Hu-1) (1-1260), variante de conformación de prefusión estable (R<sup>669</sup>>Q, R<sup>670</sup>>Q, R<sup>672</sup>>Q, K<sup>973</sup>>P, V<sup>974</sup>>P), trimero, producido en células de insecto de *Spodoptera frugiperda* (Sf9), glicoforma alfa  
*agente inmunológico para inmunización activa (anti-SARS-CoV-2)*

Monomer sequence / Séquence du monomère / Secuencia del monómero

QCYNLITRTRQ LPPAYTNSFT RGVYYPKPVF RSSLVHSTQD LFLPFFSNVT	50
WFHAIHVSQT NGTKRFDNFV LFPNDGVYFA STEKSNIIIRG WIFGTTLDSK	100
TQSLILVNNNA TNVVIKVECF QFCNDPFLGV YHKNNKSWM ESEFRVYSSA	150
NNCTFEYVSQ PFLMDLEGKQ GNFKNLRE FV FKNIDGYFKI YSKHTPINLV	200
RDLPQGGFSAL EPLVDLFIGI NITRFQTLA LHRSYLTPGD SSSGWTAGAA	250
AYYVGYLQPR TELLYNENG TITDAVDCAL DPLSETKCTL KSFTEKGIY	300
QTSNFRVQPT ESIVRFENIT NLCPPFGEVFN ATRFASVYAW NRKRISNCVA	350
DYSVLYNSAS FSTFKCYGVS PTKLNDLCFT NVYADSEVIR GDEVQRQIAPG	400
QTGKIADYNY KLPDDFTGCV IAWNSNLDL KVGGNYNLYL RLFKRSNLKP	450
FERDISTEILY QAGSTPCNGV EGFNCYFPLQ SYGFQPTNGV GYQPYRVVVL	500
SFELLHAPAT VCGPKKSTNL VKNKCVNFWF NGLTGTGVLV ESNKKFLPFPQ	550
QFGRDIADTT DAVRDPQTEI ILDITPCSPG GVSIVTPTGN TSNQVAVLYQ	600
DVNCTEVPVA IHADQLTPTW RVYSTGSNVF QTRAGCLIGA EHVNSYECD	650
IPIGAGICAS YQTQTNSPQQ AQSVASQSI IAYTMSLGAEN SVAYSNNISIA	700
IPTNFTISVT TEILPVSMTK TSVDCMTYIC GDSTECSNLL LQYGSFCTQL	750
NRALTGIAVE QDKNTQEVFA QVKQIYKTPP IKDFGGFNFS QILPDPSPKPS	800
KRSFIEDLLF NKVTLADAGF IKQYGDCLGD IAARDLICAQ KFNGLTVLPP	850
LLTDEMIQYQ TSALLAGTIT SGWTFGAGAA LQIPFAMQMA YRNFNGVGTQ	900
NVLYENQKLI ANQFNSAIGK IQDLSLSTAS ALGKLQOVVN QNAQALNTLV	950
KQLSSNFAGI SSVLNDILSR LDPFAAEVQI DRLITGRLOS LQTYVYQQLI	1000
RAAEIRASAN LAATKMSQCV LGQSKRVDFC KGYHLMSPF QSAPHGVVFL	1050
HVTYVPAQEK NFFTAPAICH DGKAHFPREG VEVSNQTHWF VTQRNFYEQP	1100
IITTDNTEFVS GNCDVYVIGV NNTVYDPLQP ELDSFKEELD KYFKNHTSPD	1150
VDLGDISGIN ASVVNIQKEI DRLNEVAKNL NESLIDLQEL GKYEQYIKWP	1200
WYIWLGFYAG LIAIVMVTIM LCCMTSCCSC LKGCSCGSC CKFDEDDSEF	1250
VLKGVKLIHYT	1260

Mutation / Mutation / Mutación  
R<sup>669</sup>->Q, R<sup>670</sup>->Q, R<sup>672</sup>->Q, K<sup>973</sup>->P, V<sup>974</sup>->P

**Post-translational modifications**

Disulfide location / Position des ponts disulfure / Posiciones de los puentes disulfuro  
Intra-chain: 2-123, 118-153, 278-288, 323-348, 366-419, 378-512, 467-475, 525-577, 604-636, 649-658, 725-747, 730-736, 827-838, 1019-1030, 1069-1113

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación  
N48, N61, N109, N136, N152, N221, N269, N318, N330, N590, N603, N644, N788, N1061, N1085, N1121, N1145, N1160

O-glycosylation / O-glycosylation / O-glicosilación  
O-glycosylation is experimentally confirmed with uncertainty on precise Ser and Thr glycosylated residues

**canrivitugum #**  
canrivitug

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* (1-451) [VH (*Homo sapiens* IGHV4-59\*11 (97.9%)-(IGHD) -IGHJ5\*02 (93.8%), CDR-IMGT [8.7.15] (26-33.51-57.96-110)) (1-121) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (218) (122-219), hinge 1-15 (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-217')-disulfide with lambda light chain *Homo sapiens* (1'-218') [V- LAMBDA (*Homo sapiens* IGLV1-40\*01 (94.9%) -IGLJ1\*01 (100%), CDR-IMGT [9.3.12] (26-34.52-54.91-102)) (1'-112') -*Homo sapiens* IGLC2\*01 (100%) (113'-218')]; dimer (230-230'':233-233'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa *antiviral*

canrivitug

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

chaîne lourde gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV4-59\*11 (97.9%) -(IGHD) -IGHJ5\*02 (93.8%), CDR-IMGT [8.7.15] (26-33.51-57.96-110)) (1-121) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (218) (122-219), charnière 1-15 (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-217')-disulfure avec la chaîne légère lambda *Homo sapiens* (1'-218') [V-LAMBDA (*Homo sapiens* IGLV1-40\*01 (94.9%) -IGLJ1\*01 (100%), CDR-IMGT [9.3.12] (26-34.52-54.91-102)) (1'-112') -*Homo sapiens* IGLC2\*01 (100%) (113'-218')]; dimère (230-230":233-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa *antiviral*

canrivitug

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

cadena pesada gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV4-59\*11 (97.9%) -(IGHD) -IGHJ5\*02 (93.8%), CDR-IMGT [8.7.15] (26-33.51-57.96-110)) (1-121) -*Homo sapiens* IGHG1\*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (218) (122-219), bisagra 1-15 (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-217')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-218') [V-LAMBDA (*Homo sapiens* IGLV1-40\*01 (94.9%) -IGLJ1\*01 (100%), CDR-IMGT [9.3.12] (26-34.52-54.91-102)) (1'-112') -*Homo sapiens* IGLC2\*01 (100%) (113'-218')]; dímero (230-230":233-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa *antiviral*

2663616-93-9

Heavy chain / Chaîne lourde / Cadena pesada

QVQLQESGPG LVKPSETLSL TCTVSGGSIS SHYWSWIRQP PGKGLEWIGY 50  
IYYSGSSNYS PSLKSRVTIS VDTSKNQFSL KLNSVTAADT AVYICARHYD 100  
ILTGFDFWDF WQGGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150  
KDYFFPEPVTV SNMGSALTSV VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200  
TYICNVMHNP SNTKVDKKEV PKSCDKTHTC PFCPAPELLG GPSVLFPPK 250  
PKDTLIMISRT PEVTCVVVDV SHEDPEVKFN WYWDGVEVHN AKTKPREEQY 300  
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350  
QVYTLPPSRD ELTKNQVSLT CLVKGFIYPSD IAVEWESNGQ FENNYKTTTP 400  
VLDSDGSSFFL YSKLTVDKSR WQGGNVSFCS VMHEALHNNY TQKSLSLSPG 450  
K 451

Light chain / Chaîne légère / Cadena ligera

QSVLTQPPFSV SGAPGQRVTI SCTGSSSNIG THYDVHWYQQ LPGTAPKLLI 50  
YGNNSRPFSGV PDRFSGRSG TSASLAITGL QAEDEADYIC QSFNLSLTPA 100  
YVFGTGKTVT VLGQPKAAPS VTLFPPSSEE LQANKATLVC LISDFYPGAV 150  
TVAWKADSSP VKAGVETTPP SKQSNNKYAA SSVLSLTPAQ WKSHRSYSQC 200  
VTHEGSTVEK TVAPTECS 218

**Post-translational modifications**

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

Intra-H (C23-C104) 22-95 148-204 265-325 371-429  
22"-95" 148"-204" 265"-325" 371"-429"

Intra-L (C23-C104) 22'-90' 140'-199'  
22"'-90"" 140"'-199""

Inter-H-L (h 5-CL 126) 224-217' 224"-217""

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

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

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxoprolilo)

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: 301, 301"  
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantennarios complejos fucosilados

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

H CHS K2: 451, 451"

**enlicovateinum #**

enlicovatein

severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) glycoprotein (UniProt P0DTC2, strain Wuhan-Hu-1) fragment (3-1260, 1-1258 in the current sequence), stable prefusion conformation variant (R<sup>669</sup>>G<sup>667</sup>, R<sup>670</sup>>S<sup>668</sup>, R<sup>672</sup>>S<sup>670</sup>, K<sup>973</sup>>P<sup>971</sup>, V<sup>974</sup>>P<sup>972</sup>) fused to a C-terminal hexahistidine tag (1259-1264), trimer, produced in *Trichoplusia ni* (derivative of TnT4) insect cells, glycoform alfa immunological agent for active immunization (anti-SARS-CoV-2)

enlicovateine

fragment (3-1260, 1-1258 dans la séquence actuelle) de la glycoprotéine du spicule (S) du coronavirus 2 du syndrome respiratoire aigu sévère (UniProt P0DTC2, souche Wuhan-Hu-1), variant de conformation stable par pré-fusion (R<sup>669</sup>>G<sup>667</sup>, R<sup>670</sup>>S<sup>668</sup>, R<sup>672</sup>>S<sup>670</sup>, K<sup>973</sup>>P<sup>971</sup>, V<sup>974</sup>>P<sup>972</sup>) fusionné à une étiquette hexahistidine en C-terminal (1259-1264), trimère, produit dans des cellules d'insecte *Trichoplusia ni* (derivant de TnT4), glycoforme alfa agent immunologique d'immunisation active (anti-SARS-CoV-2)

enlicovateína

glicoproteína de la espícula (S) del coronavirus 2 del síndrome respiratorio severo agudo (SARS-CoV-2) (UniProt P0DTC2, cepa Wuhan-Hu-1) fragmento (3-1260, 1-1258 en la secuencia actual), variante de conformación de prefusión estable (R<sup>669</sup>>G<sup>667</sup>, R<sup>670</sup>>S<sup>668</sup>, R<sup>672</sup>>S<sup>670</sup>, K<sup>973</sup>>P<sup>971</sup>, V<sup>974</sup>>P<sup>972</sup>) fusionada a la etiqueta de hexahistidina del terminal C (1259-1264), trímero, producido en células de insectos de *Trichoplusia ni* (derivada de TnT4), glicoforma alfa agente inmunológico para inmunización activa (anti-SARS-CoV-2)

2769989-44-6

Monomer sequence / Séquence du monomère / Secuencia del monómero

VNLTTRTQLP	PAYTNSFTRG	VYYPDKVFRS	SVLHSTQDLF	LPFFSNVTFW	50
HAIHVSQTNG	TKRFDNPVLP	FNDGVYFAST	EKSNIIRGWI	FGTTLDSKTQ	100
SLLLVNNTAT	VVIKVCBFQF	CNDPFLGVY	HKNKSNWMS	EFRVYSSANN	150
CTFEVVSQPF	LMDLGKQGN	FKNLREFVFK	NDGYFKIYS	KHTPINLVRD	200
LPQGFSALEP	LVDLPIGINI	TRFQTLALH	RSYLTFGDSS	SGWTAGAAAY	250
VYGYLQPRTF	LLKYNENGTI	TDAVDCALDF	LSETKCTKLS	FTVEKGIYQT	300
SNFRVQPTES	IVRFNINL	CPFGEVFNAT	RFASVYAMNR	KRISNCVADY	350
SVLYNSASFS	TRFCYGVSP	KLNDLCFTNV	YADSFVIRGD	EVRQIAPGQT	400
GKIADNYKL	PDDFTGCVIA	WNSNLDLSDV	GGNYNYLYRL	FRKSNLKPFE	450
RDISTEIIYA	GSTPCNGVEG	FNCYFPLQSY	GFQPTNGVGY	QPYRVVLSF	500
ELLHAPATVC	GPKKSTNLVK	NKCVNFNFG	LTGTGVLTES	NKKFLPQQF	550
GRDIADTTDA	VRDPQTEIL	DITPCSFGV	SVITPGTNTS	NQVAVLYQDV	600
NCTEVPVAIH	ADQLPPTWRV	YSTGNSVFTQ	RAGCLIGAEH	VNNSYEDCIP	650
IGAGICASYQ	TQTNSPGSA	SVASQSIAY	TMSLGAENSV	AYSNSIAIP	700
TNFTISVTE	ILPVSMTKTS	VDCTMFCGD	STECSNLLQ	YGSFCTQLNR	750
ALTGIAVEQD	KNTQEVFAQV	KQIYKTPPIK	DFGGFNFSQI	LPDPSKFSKR	800
SFIEDLLEFNK	VTLADAGFIK	QYGDCLGDI	ARDLICAQFK	NGLTVLPELL	850
TDEMIAQYTS	ALLAGTITSG	WTFGAGAAQ	IPFAMQAYR	FNGIGVTQNV	900
LYENQKLIAN	QFNSAIKGIQ	DSLSTASAL	GKLQDVVQNV	AQALNTLVKQ	950
LSSNFGAISS	VLNDILSRDL	PPEAEVQIDR	LITGRQLSLQ	TYVTQQLIRA	1000
AEIRASANLA	ATKMESECVLQ	QSKRVDFCGK	GYHLMSFPQS	APHGVVFLHV	1050
TYVPAQEKNF	TTAPAICHGD	KAHFPREGVF	VSNGTHFVFT	QRNFYEPQII	1100
TDNTDFVSGN	CDVIVIGVNN	TVYDPLQPEL	DSEKELDKY	FRNHTSPDWD	1150
LGDISGINAS	VVNIQKEIDR	LNEVAKNLNE	SLIDLQELGK	YEQYIKWPMY	1200
IWLGFIAGLI	AIVMVTIMLC	CMTSCCSCLK	GCCSCGSCCK	FDEDDSEPVL	1250
KGVKLHYTH	HHHHH				1264

Mutation / Mutation / Mutación

R<sup>669</sup>>G<sup>667</sup>, R<sup>670</sup>>S<sup>668</sup>, R<sup>672</sup>>S<sup>670</sup>, K<sup>973</sup>>P<sup>971</sup>, V<sup>974</sup>>P<sup>972</sup>

Hexahistidine tag / Marqueur hexahistidine / Etiqueta de hexahistidina

HHHHHH 1259-1264

Post-translational modifications

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

Intra-chain: 116-151, 276-286, 321-346, 364-417, 376-510, 465-473, 523-575, 602-634, 647-656, 723-745, 728-734, 825-836, 1017-1028, 1067-1111

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

N2, N46, N59, N107, N134, N150, N219, N267, N316, N328, N588, N601, N642, N694, N702, N786, N1059, N1083, N1119, N1143, N1158, N1179

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación (predicted)

T308, S310, T661, T663



**laricovateinum #**

laricovatein severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) alpha lineage B.1.1.7 (Gisaid: EPI\_ISL\_764238) spike (S) glycoprotein fragment (1-1192), stable prefusion conformation variant (R<sup>666</sup>G, R<sup>667</sup>>S, R<sup>669</sup>>S, F<sup>801</sup>>P, A<sup>876</sup>>P, A<sup>883</sup>>P, A<sup>926</sup>>P, K<sup>970</sup>>P, V<sup>971</sup>>P) fused to the enterobacteria phage T4 fibritin foldon domain fragment (458-484, 1193-1219 in the current sequence), trimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa *immunological agent for active immunization (anti-SARS-CoV-2)*

laricovatéine fragment de la glycoprotéine du spicule (S) (1-1192) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2), lignée alpha B.1.1.7 (Gisaid: EPI\_ISL\_764238), variant de conformation stable par pré-fusion (R<sup>666</sup>G, R<sup>667</sup>>S, R<sup>669</sup>>S, F<sup>801</sup>>P, A<sup>876</sup>>P, A<sup>883</sup>>P, A<sup>926</sup>>P, K<sup>970</sup>>P, V<sup>971</sup>>P) fusionné au fragment du domaine foldon de la fibritine de phage T4 d'entérobactéries (458-484, 1193-1219 dans la séquence actuelle), trimère, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa *agent immunologique d'immunisation active (anti-SARS-CoV-2)*

laricovateína fragmento de la glicoproteína de la espícula (S) (1-1192) del coronavirus 2 del síndrome respiratorio severo agudo (SARS-CoV-2) linaje alfa B.1.1.7 (Gisaid: EPI\_ISL\_764238), variante de conformación de prefusión estable (R<sup>666</sup>G, R<sup>667</sup>>S, R<sup>669</sup>>S, F<sup>801</sup>>P, A<sup>876</sup>>P, A<sup>883</sup>>P, A<sup>926</sup>>P, K<sup>970</sup>>P, V<sup>971</sup>>P) fusionada al fragmento de dominio de foldón de fibritina del fago T4 de enterobacterias (458-484, 1193-1219 en la secuencia actual), trímero, producido en células ováricas de hámster Chino (CHO), glicofoma alfa *agente inmunológico para inmunización activa (anti-SARS-CoV-2)*

2777034-67-8

Monomer sequence / Séquence du monomère / Secuencia del monómero

QCYNLTTTRQ	LPPAYTNSFT	RGVYYPKVF	RSSVLHSTQD	LFLPFSNVT	50
WFHAISCTNG	TKRFDMNPLV	FNDGVYFAS	EKSNLIIRGM	FCTTLDSTKQ	100
SLLIIVNNATN	VVIKVFCEPQ	CNDPFLGVVH	KNNKSMWSE	FRVYSSANNC	150
TFEYVYQPF	MDLEGKQGNF	KNLREFVFNK	IDGYFKIYSK	HTFINLVRGL	200
PQGFSALEP	VDLPIGINIT	RFQTLALHR	SYLTPGDSSS	GWTAGAAYY	250
VGVLPQRTFL	LKYNENGTIT	DAVDCALDEL	SETKCTLKS	FVEKGIYQTS	300
NFRVQPTESI	VREFNITNLC	PGFGEVFNTR	FASVYAWNRK	RISNCVADYS	350
VLYNSASFST	FKCYGVSPK	LNDLCFTNVY	ADSEVIRGDE	VRQIAPGQTG	400
KIADVNYKLF	DDFTGCVIAM	NSNNLDSKVG	GNYNYLYRFL	RKSNLKPFFER	450
DISTEIYQAG	STPCNGVEGF	NCYFFLQSYG	FQPTYGVGVQ	PYRVVLSFE	500
LLHAPATVCG	PKKSTNLVKN	KCVNFNENGL	TGTGVLTESN	KKFLPQQFG	550
RDIDDTDAV	RDPQTEILD	ITFCFSGGVS	VITPGTNTSN	QVAVLYQGVN	600
CTEVPAVIAH	DQLFTTRVRY	STGSNVFOQR	AGCLIGAETH	NNSYECDIPI	650
GAGICASYQT	QNSPQASAS	VASQSIAYT	MSLGAENSWA	YSNNSIAIFI	700
NFTISVTEIE	LPVSMTKTSV	DCMTYICGDS	TECSNLLLQY	GSFCTQLNRA	750
LTGIAVEQDK	NTQEVFAQVK	QIYKTPPIKD	PGGFNFSQIL	PDFSKPSKRS	800
<b>P</b> IEDLLFNK	TLADAGFIKQ	YDGLDGDIAA	RDLCIAQKFN	GLTVLPLLLT	850
DEMIAQY TSA	LLAGTITSGW	TFGAG <b>P</b> ALQI	<b>P</b> FP <b>M</b> QMA YRF	NGIGVTPQNVL	900
YENQKLIANQ	FNSAIGKIQD	SLS <b>T</b> <b>P</b> SALG	KLQDVVNQNA	QALNTLVKQL	950
SSNFGAIVSV	LNDILARL <b>P</b>	<b>P</b> EA <b>E</b> VQIDRL	ITGRLQSLQT	YVTQQLIRAA	1000
EIRASANLAA	TKMSECVLGG	SKRVDFCGKG	YHLSMFPQSA	PHGVVPLHVT	1050
YVPAQEKNT	TAPAICHGDK	AHFPREGVVF	SNGTHWFVTQ	RNFVEPQIIT	1100
THNTFVSGNC	DVVIQIVNNT	VYDPLQFELD	SPKEELDKYF	KNHTSPDVDL	1150
GDISGINASV	VNIQEKIDRL	NEVAKNLNES	LIDLQELGRY	<b>EQ</b> <b>QYI</b> <b>PEA</b> <b>P</b>	1200
<u>DQQA YVRKDG</u>	<u>EWVLLSTFL</u>				1219

Mutation / Mutation / Mutación  
H<sup>665</sup>>P, R<sup>666</sup>>G, R<sup>667</sup>>S, R<sup>669</sup>>S, F<sup>801</sup>>P, A<sup>876</sup>>P, A<sup>883</sup>>P, A<sup>926</sup>>P, K<sup>970</sup>>P, V<sup>971</sup>>P

Foldon domain / Foldon domaine / Foldon dominio  
G Y I P E A P R D G Q A Y V R K D G E W V L L S T F L 1193-1219

Post-translational modifications  
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro  
Intra-chain: 2-121, 116-150, 275-285, 320-345, 363-416, 375-509, 464-472, 522-574, 601-633, 646-655, 722-744, 727-733, 824-835, 1016-1027, 1066-1110

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación (predicted)  
N4, N48, N59, N107, N133, N149, N218, N266, N315, N327, N587, N600, N641, N693, N701, N785, N1058, N1082, N1118, N1142, N1157, N1178

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación (predicted)  
T307, S309

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

**mindeudesivirum**

mindeudesivir

(2*R*,3*R*,4*R*,5*R*)-2-(4-amino-(5-<sup>2</sup>H)pyrrolo[2,1-*f*][1,2,4]triazin-7-yl)-2-cyano-5-(((2-methylpropanoyl)oxy)methyl)oxolane-3,4-diyl bis(2-methylpropanoate)  
*antiviral*

mindeudésivir

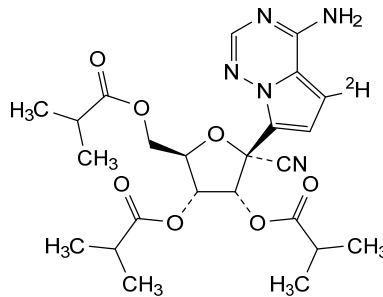
bis(2-méthylpropanoate) de (2*R*,3*R*,4*R*,5*R*)-2-(4-amino-(5-<sup>2</sup>H)pyrrolo[2,1-*f*][1,2,4]triazin-7-yl)-2-cyano-5-(((2-méthylpropanoyl)oxy)méthyl)oxolane-3,4-diyle  
*antiviral*

mindeudesivir

bis(2-metilpropanoato) de (2*R*,3*R*,4*R*,5*R*)-2-(4-amino-(5-<sup>2</sup>H)pirrolo[2,1-*f*][1,2,4]triazin-7-il)-2-ciano-5-(((2-metilpropanoil)oxi)metil)oxolano-3,4-diilo  
*antiviral*

C<sub>24</sub>H<sub>30</sub><sup>2</sup>NN<sub>5</sub>O<sub>7</sub>

1887069-10-4



**riticovateinum #**

riticovatein

severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) delta lineage B.1.617.2 (Gisaid: EPI\_ISL\_1999775) spike (S) glycoprotein fragment (1-1193), stable prefusion conformation variant (R<sup>666</sup>>P, R<sup>667</sup>>G, R<sup>668</sup>>S, R<sup>670</sup>>S, F<sup>802</sup>>P, A<sup>877</sup>>P, A<sup>884</sup>>P, A<sup>927</sup>>P, K<sup>971</sup>>P, V<sup>972</sup>>P) fused to the enterobacteria phage T4 fibrin foldon domain fragment (458-484, 1194-1220 in the current sequence), trimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa  
*immunological agent for active immunization (anti-SARS-CoV-2)*

riticovatéine

fragment de la glycoprotéine du spicule (S) (1-1193) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2), lignée delta B.1.617.2 (Gisaid: EPI\_ISL\_1999775), variant de conformation stable par pré-fusion (R<sup>666</sup>>P, R<sup>667</sup>>G, R<sup>668</sup>>S, R<sup>670</sup>>S, F<sup>802</sup>>P, A<sup>877</sup>>P, A<sup>884</sup>>P, A<sup>927</sup>>P, K<sup>971</sup>>P, V<sup>972</sup>>P) fusionné au fragment du domaine foldon de la fibratine du phage T4 d'entérobactéries (458-484, 1194-1220 dans la séquence actuelle), trimère, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa  
*agent immunologique d'immunisation active (anti-SARS-CoV-2)*

riticovateína

fragmento de la glicoproteína de la espícula (S) (1-1193) del coronavirus 2 del síndrome respiratorio severo agudo (SARS-CoV-2) linaje delta B.1.617.2 (Gisaid: EPI\_ISL\_1999775), variante de conformación de refusión estable ( $R^{666}>P$ ,  $R^{667}>G$ ,  $R^{668}>S$ ,  $R^{670}>S$ ,  $F^{802}>P$ ,  $A^{877}>P$ ,  $A^{884}>P$ ,  $A^{927}>P$ ,  $K^{971}>P$ ,  $V^{972}>P$ ) fusionada al fragmento de dominio de foldón de fibritina del fago T4 de enterobacterias (458-484, 1194-1220 en la secuencia actual), trímero, producido en células ováricas de hámster Chino (CHO), glicofórmula alfa  
*agente inmunológico para inmunización activa (anti-SARS-CoV-2)*

2777034-69-0

Monomer sequence / Séquence du monomère / Secuencia del monómero

QCYNLRTRTG	LPPAYTNSFT	RGVYYPDKVF	RSSVLHSTQD	LFLPFFSNVT	50
WFHAIHVSQT	NGTKRFDNPV	LPFNDGVYFA	STEKSNIIIRG	WIFGTTLDSE	100
TQSLLLVNNNA	TNVVIVKVECF	QFCNDPFLGV	YHKNKNSWM	ESGVSSANN	150
CTFEVYSQPF	LMDLEKQGN	FKNLREVFVK	NIDGYFKIYS	KHTPINLVRD	200
LPQGSALPE	LVDLPIGINI	TRFQTLALH	RSYLTPGDS	SGWTAGAAAY	250
YVGYLQPRTF	LLKYNENGTI	TDAVDCALDP	LSEKTKLKS	FVTEKGIYQT	300
SNRFVQPTES	IVRFPNITNL	CPFGEVFNAT	RFASVYAWN	KRISNCVADY	350
SVLYNSASF	TFKCYGVSPT	KLNDLCFTNV	YADSFVIRGD	EVRQIAPGQT	400
GKIADYNYKL	PDDFTGCVIA	WNSNNLDSKV	GGNYMYRYL	FRKSNLKFPE	450
RDISTEIIYA	GSKPCNGVEG	FNCYFPLQSY	GFOPTNGVGY	QYRVVVLVSF	500
ELLHAPATVC	GPKKSTNLVK	NKCVNFMFNG	LTGTGVLTES	NKKFLFPQQF	550
GRDIADTTDA	VRDPQTELEI	DITPCSEFGV	SVITPFGTMS	NQVAVLYQGV	600
NCTEVFVAIH	ADQLTPTWRV	YSTGSNVFQT	RAGCLIGAEH	VNNSYECDDP	650
IGAGICASYQ	TQTNSPGSAS	SVASQSI IAY	TMSLGAENSV	AYSNNSIATP	700
TNFTISVTE	ILPVSMTKTS	VDCTMYICGD	STECSNLLQ	YGSFCTQLNR	750
ALGTIAVEQD	KNTQEVFAQV	KQIYKTPPIK	DFGGNFQSI	LPDPSKPSKR	800
SPIEDLLFNK	VTLADAGFIK	QYGDCLGDIA	ARDLLCAQKF	NGLTVLPPLL	850
TDEMQAQT	ALLAGTITSG	WTFGAGPALQ	IPFPMQMARY	FNGIGVTQNV	900
LYENQKLIAN	QFNSAIGKIQ	DSLSTPSAL	GKLNQVNVQN	AQALNLTLVKQ	950
LSSNFGAISS	VLNDILSRLD	PEAEVQIDR	LITGRLLQSLQ	TYVTQQLIRA	1000
AEIRASANLA	ATKMSSECVLG	QSKRVDFCGK	GYHLMSPQOS	APHGVVFLHV	1050
TYVPAQEKNF	TTAPAICHGD	KAHFPRGQV	VSNGTHWFVT	QRNFYEPQII	1100
TTDNTFVSGN	CDVVIGIVNN	TVYDPLQPEL	DSFKEELDKY	FRNHTSPDVD	1150
LGDISGINAS	VVNIQKEIDR	LNEVAKNLNE	SLIDLQELGK	YEQGYIFEAP	1200
RDGQAYVRKD	GEWVLLSTFL				1220

Mutation / Mutation / Mutación  
 $R^{666}>P$ ,  $R^{667}>G$ ,  $R^{668}>S$ ,  $R^{670}>S$ ,  $F^{802}>P$ ,  $A^{877}>P$ ,  $A^{884}>P$ ,  $A^{927}>P$ ,  $R^{971}>P$ ,  $V^{972}>P$

Foldon domain / Foldon domaine / Foldon dominio  
GYIFEAPRDC QAYVRKDGWE VLLSTFL 1194-1220

Post-translational modifications  
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro  
Intra-chain: 2-123, 118-151, 276-286, 321-346, 364-417, 376-510, 465-473, 523-575,  
602-634, 647-656, 723-745, 728-734, 825-836, 1017-1028, 1067-1111

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación (predicted)  
N48, N61, N109, N136, N150, N219, N267, N316, N328, N588, N601, N642, N694,  
N702, N786, N1059, N1083, N1119, N1143, N1158, N1179

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación (predicted)  
T308, S310

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

**selvacovateinum #**  
selvacovatein

severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), beta lineage (B.1.351) spike (S) glycoprotein (natural variant  $K^{404}>N^{99}$ ,  $E^{471}>K^{166}$ ,  $N^{488}>Y^{183}$ ) receptor binding domain (RBD) fragment (306-524, 1-219 in the current sequence), fused to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), alpha lineage (B.1.1.7) spike (S) glycoprotein (natural variant  $N^{488}>Y^{402}$ ), receptor binding domain (RBD) fragment (306-524, 220-438 in the current sequence), produced in Chinese hamster ovary (CHO)-K1 cells, glycoform alfa  
*immunological agent for active immunization (anti-SARS-CoV-2)*

**selvacovatéine** fragment (306-524, 1-219 dans la séquence actuelle) du domaine de liaison au récepteur (RBD) de la glycoprotéine du spicule (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2) de la lignée bêta (B.1.351) (variant naturel (K<sup>404</sup>>N<sup>99</sup>, E<sup>471</sup>>K<sup>166</sup>, N<sup>488</sup>>Y<sup>183</sup>), fusionné au fragment (306-524, 220-438 dans la séquence actuelle) du domaine de liaison au récepteur (RBD) de la glycoprotéine de la spicule (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2) de la lignée alpha (B.1.1.7) (variant naturel (N<sup>488</sup>>Y<sup>402</sup>), produit dans des cellules ovariennes de hamster chinois (CHO)-K1, glycoforme alfa *agent immunologique d'immunisation active (anti-SARS-CoV-2)*

**selvacovateína** fragmento del dominio de unión al receptor (RBD) (306-524, 1-219 en la secuencia actual) de la glicoproteína de la espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SARS-CoV-2), linaje beta (B.1.351) (variante natural K<sup>404</sup>>N<sup>99</sup>, E<sup>471</sup>>K<sup>166</sup>, N<sup>488</sup>>Y<sup>183</sup>), fusionado al fragmento del dominio de unión al receptor (RBD) (306-524, 220-438 en la secuencia actual) de la glicoproteína de la espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SARS-CoV-2), linaje alfa (B.1.1.7) (variante natural N<sup>488</sup>>Y<sup>402</sup>), producido en células ováricas de hámster Chino (CHO)-K1, glicoforma alfa *agente inmunológico para inmunización activa (anti-SARS-CoV-2)*

2750241-84-8

Sequence / Séquence / Secuencia

<b>RVQPTESIVR FPNITNLCPPF GEVFNATREA SVYAWNRKRI SMCVADYSVL</b>	50
<b>YNSASFSTFK CYGVSPTKLN DLCFTNVYAD SFVIRGDEVR QIAPGQTGNI</b>	100
<b>ADYNYKLPDD FTGCVIAWNS NNLDISKVGGN YNYLYRFRK SNLKPFRDI</b>	150
<b>STEIYQAGST PCNGV<sub>2</sub>GFNC YFPLQSYGFQ PT<sub>2</sub>GVGYQPY RVVLSFELL</b>	200
<b>HAPATVCGPK KSTNLVKNKR VQPTESIVRF PNI<sub>2</sub>TNLCPPF EVFNATRFAS</b>	250
<b>VYAWNRKRIS NCVADYSVLY NSASFSTFK YGVSFPTKLN LCFTNVYADS</b>	300
<b>FVIRGDEVRQ IAPGQTGKIA DYNKLPDDF TGCVIAWNS NNLDISKVGGNY</b>	350
<b>NYLYRFRKS NLKPFERDIS TEIYQAGSTP CNGVEGFNCY FPLQSYGFQP</b>	400
<b>TYGVGYQPYR VVLSFELLH APATVCGPKK STNLVKNK</b>	438

Natural variant / Variante naturelle / Variante natural

K<sup>404</sup>>N<sup>99</sup>, E<sup>471</sup>>K<sup>166</sup>, N<sup>488</sup>>Y<sup>183</sup>, N<sup>488</sup>>Y<sup>402</sup>

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro  
18-43, 61-114, 73-207, 162-70, 237-262, 280-333, 292-426, 381-389

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación  
N13, N25, N232, N244

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación  
T5, T224

C-terminal lysine clipping / Coupeure de la lysine C-terminale / Recorte de lisina C-terminal  
K438

**sorimcovateinum #**  
sorimcovatein

severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), omicron lineage B.1.1.529 (Gisaid: EPI\_ISL\_6640917) spike (S) glycoprotein fragment (1-1192), stable prefusion conformation variant (H<sup>665</sup>>P, R<sup>666</sup>>G, R<sup>667</sup>>S, R<sup>669</sup>>S, F<sup>801</sup>>P, A<sup>876</sup>>P, A<sup>883</sup>>P, A<sup>926</sup>>P, K<sup>970</sup>>P, V<sup>971</sup>>P) fused to the enterobacteria phage T4 fibrin foldon domain fragment (458-484, 1193-1219 in the current sequence), trimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa *immunological agent for active immunization (anti-SARS-CoV-2)*

sorimcovatéine

fragment de la glycoprotéine du spicule (S) (1-1192) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2), lignée omicron B.1.1.529 (Gisaid: EPI\_ISL\_6640917), variant de conformation stable par pré-fusion (H<sup>665</sup>>P, R<sup>666</sup>>G, R<sup>667</sup>>S, R<sup>669</sup>>S, F<sup>801</sup>>P, A<sup>876</sup>>P, A<sup>883</sup>>P, A<sup>926</sup>>P, K<sup>970</sup>>P, V<sup>971</sup>>P) fusionné au fragment du domaine foldon de la fibratine du phage T4 d'entérobactéries (458-484, 1193-1219 dans la séquence actuelle), trimère, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa  
*agent immunologique d'immunisation active (anti-SARS-CoV-2)*

sorimcovatefina

fragmento de la glicoproteína de la espícula (S) (1-1192) del coronavirus 2 del síndrome respiratorio agudo severo (SARS-CoV-2), linaje omicron B.1.1.529 (Gisaid: EPI\_ISL\_6640917), variante de conformación de prefusión estable (H<sup>665</sup>>P, R<sup>666</sup>>G, R<sup>667</sup>>S, R<sup>669</sup>>S, F<sup>801</sup>>P, A<sup>876</sup>>P, A<sup>883</sup>>P, A<sup>926</sup>>P, K<sup>970</sup>>P, V<sup>971</sup>>P) fusionado al fragmento de dominio de foldón de fibratina del fago T4 de enterobacterias (458-484, 1193-1219 en la secuencia actual), trímero, producido en células ováricas de hámster Chino (CHO), glicofoma alfa  
*agente inmunológico para inmunización activa (anti-SARS-CoV-2)*

2777034-70-3

Monomer sequence / Séquence du monomère / Secuencia del monómero	
QCENLTTTRTQ	LPPAYTNSFT RGVYYPDKVF RSSLVHSTQD LFLPFFSNVT 50
WFHVISGTNG	TKRFDNFVLP FNDGVYFASI EKSNIIRGWI FGTLDSKTQ 100
SLLIYVNNATN	VVIKVCDFQF CNDPFLDHNK NKSWMSESEFR VYSSANNCTF 150
EYVSQPFLLM	LEGKQGNFRN LRFVFKNID GYFKIYSKHT PIIVREPEDL 200
PQGFSALEPL	VDLPIGINIT RFQTLALALHR SYLTPGDSSS GWTAGAAAYY 250
VGYLQPRTEFL	LKYNENGTIT DAVDCALDEL SETRCTLKSF TVEKGIYQTS 300
NFRVQPTESI	VRFPNITNLC PFDEVFNATR FASVIAMNRK RISNCVADYS 350
VLYNLAPFFT	FKCYGVSPK LNDLCFTNVY ADSEVIRGDE VRQIAPGQTG 400
NIADYNYKPL	DDFTGCVIAW NSNKLDSKVS GNYNYLRLF RKSNLKPFER 450
DISTEIQVAG	NKPCNGVAGF NCYFPLRSYS FRPTYGVGHQ PYRVVLSFE 500
LLHAPATVCG	PKKSTNLVKN KCVNFNGL KGTGVLTESN KKFLPFQFQG 550
RDIADTDAV	RDFQTEILD ITPCSFGGVS VITPGTNTSN QVAVLYQGVN 600
CTEVEPVAIHA	DQLTPTWRVY STGSNVFQTR AGCLIGAEVY NNSYECDFPI 650
GAGICASYQT	QTKSPGASAS VASQSIIAYT MSLGAENVA YSNNSIAIPT 700
NFTISVTTEI	LPVSMTKTSS DCTMYICGDS TECSNLLQY GFSCFTQKRA 750
LTGIAVEQDK	NTQEVFAQVK QIYKTPPIKY FGGNFQSIL PDPSPKSKRS 800
PIEDLLENKV	TLADAGFIKQ YGDCIGDIAA RDLICAQKFK GLTVLPPLLT 850
DEMIQYNTSA	LLAGIITSGW TFGAGPALQI PPEMQMAYRF NGIGVTQNVL 900
YENQKLIANQ	FNSAIGKIQD SLSSTPSALG KLQDVVNHNA QALNTLVKQL 950
SSKFGAIVSS	LNDIFSRLLP PEAEVQIDRL ITGRQLQSLQ YVTQQLIRAA 1000
EIRASANLAA	TKMSECVLQK SKRVDFCGKG YHLSMFPQSA PHGVVFLHVT 1050
YVPAQEKNEF	TAPAICHHDG AHFPREGVVF SNGTHWFVQT RNFVPEQIIT 1100
TDNTEFVSGN	DVVIGIVNNT VYDPLQPELD SFKEELDKYF KNHTSPDVL 1150
GDISGINASV	VNIQKEIDRL NEVAKNLNES LIDLQELGKY EQGYIPEAPR 1200
<u>DGQAYVRKDG</u>	<u>EWVLLSTFL</u> 1219

Mutation / Mutation / Mutación  
H<sup>665</sup>>P, R<sup>666</sup>>G, R<sup>667</sup>>S, R<sup>669</sup>>S, F<sup>801</sup>>P, A<sup>876</sup>>P, A<sup>883</sup>>P, A<sup>926</sup>>P, K<sup>970</sup>>P, V<sup>971</sup>>P

Foldon domain / Foldon domaine / Foldon dominio  
GYIPEAPRDG QAYVRKDG EWVLLSTFL 1193-1219

**Post-translational modifications**

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro  
Intra-chain: 2-121, 116-148, 275-285, 320-345, 363-416, 375-509, 464-472, 522-574,  
601-633, 646-655, 722-744, 727-733, 824-835, 1016-1027, 1066-1110

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación (predicted)  
N4, N48, N59, N107, N131, N147, N218, N266, N315, N327, N587, N600, N641, N693,  
N701, N785, N1058, N1082, N1118, N1142, N1157, N1178

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación (predicted)  
T307, S309

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

**talfirastidum**

talfirastide

angiotensin-(1-7)-peptide;  
L- $\alpha$ -aspartyl-L-arginyl-L-valyl-L-tyrosyl-L-isoleucyl-L-histidyl-L-proline  
*angiotensin 1-7, anti-inflammatory*

talfirastide

angiotensine-(1-7)-peptide;  
L- $\alpha$ -aspartyl-L-arginyl-L-valyl-L-tyrosyl-L-isoleucyl-L-histidyl-L-proline  
*angiotensine 1-7, anti-inflammatoire*

talfirastida

angiotensina-(1-7)-péptido;  
L- $\alpha$ -aspartil-L-arginil-L-valil-L-tirosil-L-isoleucil-L-histidil-L-prolina  
*angiotensina 1-7, antiinflamatorio*

C<sub>41</sub>H<sub>62</sub>N<sub>12</sub>O<sub>11</sub>

51833-78-4

H— Asp – Arg – Val – Tyr – Ile – His – Pro — OH

**tibrecoவைினம் #**

tibrecoவைின

severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), beta lineage B.1.351 (Gisaid: EPI\_ISL\_736940) Spike (S) glycoprotein fragment (1-1192), stable prefusion conformation variant (R<sup>666</sup>>G, R<sup>667</sup>>S, R<sup>669</sup>>S, F<sup>801</sup>>P, A<sup>876</sup>>P, A<sup>883</sup>>P, A<sup>926</sup>>P, K<sup>970</sup>>P, V<sup>971</sup>>P) fused to the enterobacteria phage T4 fibrin foldon domain fragment (458-484, 1193-1219 in the current sequence), trimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa  
*immunological agent for active immunization (anti-SARS-CoV-2)*

tibrécovateïne

fragment de glycoprotéine du spicule (S) (1-1192) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2), lignée bêta B.1.351 (Gisaid: EPI\_ISL\_736940), variant de conformation stable par pré-fusion (R<sup>666</sup>>G, R<sup>667</sup>>S, R<sup>669</sup>>S, F<sup>801</sup>>P, A<sup>876</sup>>P, A<sup>883</sup>>P, A<sup>926</sup>>P, K<sup>970</sup>>P, V<sup>971</sup>>P) fusionné au fragment du domaine foldon de la fibratine du phage T4 d'entérobactéries (458-484, 1193-1219 dans la séquence actuelle), trimère, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa  
*agent immunologique d'immunisation active (anti-SARS-CoV-2)*

tibrecoவைீனா

fragmento de la glicoproteína de la espícula (S) (1-1192) del coronavirus 2 del síndrome respiratorio agudo severo (SARS-CoV-2), linaje beta B.1.351 (Gisaid: EPI\_ISL\_736940), variante de conformación de prefusión estable (R<sup>666</sup>>G, R<sup>667</sup>>S, R<sup>669</sup>>S, F<sup>801</sup>>P, A<sup>876</sup>>P, A<sup>883</sup>>P, A<sup>926</sup>>P, K<sup>970</sup>>P, V<sup>971</sup>>P) fusionado al fragmento de dominio de foldón de fibratina del fago T4 de enterobacterias (458-484, 1193-1219 en la secuencia actual), trímero, producido en células ováricas de hámster Chino (CHO), glicoforma alfa  
*agente inmunológico para inmunización activa (anti-SARS-CoV-2)*

2777034-68-9

## Monomer sequence / Séquence du monomère / Secuencia del monómero

QCVNFTTRTQ LPPAYTNSFT RGVYYPDKVF RSSVLHSTQD LFLPFPSNVT 50  
 WFHAIHVSQT NGTKRFANPV LPFNDGVYFA STEKSNLIRG WIFGTTLDGK 100  
 TQSLLIYNNA TNVVIKVCVF QFCNDPFLGV YYHKNNKSWM ESEFRVYSSA 150  
 NNCTFEYVSQ PFLMDLEGKQ GNFKNLREFV FKNIDGYFKI YSKHTPIINLV 200  
 RGLFPQGFSAE EPLVDLPIGI NITRFQTLHI SYLTPGDSST GWTAGAAAYY 250  
 VGYLQPTFLL LKYNENGTIT DAVDCALDPL SETKCTLKSF TVERGIYQTS 300  
 NFRVQPTESI VRFPNITNLC PFGVEFNATR FASVYAWNRK RISNCVADYS 350  
 VLYNSASFST FKCYGVSPTK LNDLCFTNIV ADSFVIRGDE VRQIAPGQTG 400  
 NIADYNYKLP DDFTCGVIAW NSNNLDSKVG GNYNYLYRLF RRSNLRKPFER 450  
 DISTEYIYQAG STPCNGVKGK NCFYPLQSYG FQPTGYGVGYG PYRVVVLSEF 500  
 LLHAPATVCG PPKSTNLVKN KCVNFENGL TGTGVLTESN KKFLLPQQFG 550  
 RDIADTTDAV RDPQTLLELD ITPCSFGGVS VITPGTNTSN QVAVLYQGVN 600  
 CTEVPVAIHA DQLTPTRWVY STGSNVFQTR AGCLIGAEHV NNSYECDIPI 650  
 GAGICASYQT QTNSPGSASS VASQSIATY MSLGVENSVA YSNNIAIPT 700  
 NFTISVTEI LPVSMTKTSV DCTMYICGDS TECSNLLQY GSFCTQLNRA 750  
 LTGIAVEQDK NTQEVFAQVK QIYKTPPIKD FGGFNFSQIL PDPKSPKRS 800  
**P**IEDLLFNKV TLADAGFIKQ YGDCGLDIAA RDLICAQKFN GLTVLPLLT 850  
 DEMIAQY TSA LLAGTITSCW TFGAGP~~AL~~QI **P**EPQ~~MA~~YRF NGIGVTQNVL 900  
 YENQKLIANQ FNSAIGKIQD SLSST~~ES~~ALG KLQDVVNQNA QALNTLVKQL 950  
 SSNFGA~~ISSV~~ LNDILSR~~LD~~**P**EA~~EV~~QIDRL ITGR~~LQ~~SLQT YVTQQLIRAA 1000  
 EIRASANLAA TKMSECVLGG SKRVDFCGKG YHLMSPQSA PHGVVFLHVT 1050  
 YVPAQEK~~NFT~~ TAPAICHGDK AHFPREGVVF SNGTHWFVQT RNFYEPQIIT 1100  
 TDNTFVSGNC DVVIGIVMNT VYDPLQPELD SFKEELDKYF KNHTSPD~~VLD~~ 1150  
 GDISGINASV VNIQKEIDRL NEVARNLNES LIDLQELGKY EQGYIPEAPR 1200  
DGQAYVRKDG EWVLLSTFL 1219

## Mutation / Mutation / Mutación

~~R~~<sup>666</sup>-~~G~~, ~~R~~<sup>667</sup>-~~S~~, ~~R~~<sup>669</sup>-~~S~~, ~~F~~<sup>801</sup>-~~P~~, ~~A~~<sup>876</sup>-~~P~~, ~~A~~<sup>885</sup>-~~P~~, ~~A~~<sup>926</sup>-~~P~~, ~~K~~<sup>970</sup>-~~P~~, ~~V~~<sup>971</sup>-~~P~~

## Foldon domain / Foldon domaine / Foldon dominio

GYIPEAPRDG QAYVRKDGW VLLSTFL 1193-1219

## Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro  
 Intra-chain: 2-123, 118-153, 275-285, 320-345, 363-416, 375-509, 464-472, 522-574,  
 601-633, 646-655, 722-744, 727-733, 824-835, 1016-1027, 1066-1110

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación (predicted)  
 N4, N48, N61, N109, N136, N152, N221, N266, N315, N327, N587, N600, N641, N693,  
 N701, N785, N1058, N1082, N1118, N1142, N1157, N1178

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación (predicted)  
 T307, S309

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del  
 glutamino N-terminal  
 Q1 >pyroglutamyl (pE, 5-oxoprolyl)

# Electronic structure available on Mednet: <https://extranet.who.int/soinn/>

# Structure électronique disponible sur Mednet: <https://extranet.who.int/soinn/>

# Estructura electrónica disponible en Mednet: <https://extranet.who.int/soinn/>

## ANNEX 1

# PROCEDURE FOR THE SELECTION OF RECOMMENDED INTERNATIONAL NONPROPRIETARY NAMES FOR PHARMACEUTICAL SUBSTANCES<sup>1</sup>

The following procedure shall be followed by the World Health Organization (hereinafter also referred to as “WHO”) in the selection of recommended international nonproprietary names for pharmaceutical substances, in accordance with resolution WHA3.11 of the World Health Assembly, and in the substitution of such names.

*Article 1* - Proposals for recommended international nonproprietary names and proposals for substitution of such names shall be submitted to WHO on the form provided therefore. The consideration of such proposals shall be subject to the payment of an administrative fee designed only to cover the corresponding costs of the Secretariat of WHO (“the Secretariat”). The amount of this fee shall be determined by the Secretariat and may, from time to time, be adjusted.

*Article 2* - Such proposals shall be submitted by the Secretariat to the members of the Expert Advisory Panel on the International Pharmacopoeia and Pharmaceutical Preparations designated for this purpose, such designated members hereinafter referred to as “the INN Expert Group”, for consideration in accordance with the “General principles for guidance in devising International Nonproprietary Names for Pharmaceutical Substances”, annexed to this procedure<sup>2</sup>. The name used by the person discovering or first developing and marketing a pharmaceutical substance shall be accepted, unless there are compelling reasons to the contrary.

*Article 3* - Subsequent to the examination provided for in article 2, the Secretariat shall give notice that a proposed international nonproprietary name is being considered.

a) Such notice shall be given by publication in *WHO Drug Information*<sup>3</sup> and by letter to Member States and to national and regional pharmacopoeia commissions or other bodies designated by Member States.

i) Notice shall also be sent to the person who submitted the proposal (“the original applicant”) and other persons known to be concerned with a name under consideration.

b) Such notice shall:

i) set forth the name under consideration;

ii) identify the person who submitted the proposal for naming the substance, if so requested by such person;

iii) identify the substance for which a name is being considered;

iv) set forth the time within which comments and objections will be received and the person and place to whom they should be directed;

v) state the authority under which WHO is acting and refer to these rules of procedure.

c) In forwarding the notice, the Secretariat shall request that Member States take such steps as are necessary to prevent the acquisition of proprietary rights in the proposed name during the period it is under consideration by WHO.

*Article 4* - Comments on the proposed name may be forwarded by any person to WHO within four months of the date of publication, under article 3, of the name in *WHO Drug Information*.

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<sup>1</sup> See Annex 1 in WHO Technical Report Series, No. 581, 1975. The original text was adopted by the Executive Board in resolution EB15.R7 and amended in resolutions EB43.R9 and EB115.R4.

<sup>2</sup> See Annex 2.

<sup>3</sup> Before 1987, lists of international nonproprietary names were published in the *Chronicle of the World Health Organization*.



*Article 5* - A formal objection to a proposed name may be filed by any interested person within four months of the date of publication, under article 3, of the name in *WHO Drug Information*.

Such objection shall:

- i) identify the person objecting;
- ii) state his or her interest in the name;
- iii) set forth the reasons for his or her objection to the name proposed.

*Article 6* - Where there is a formal objection under article 5, WHO may either reconsider the proposed name or use its good offices to attempt to obtain withdrawal of the objection. Without prejudice to the consideration by WHO of a substitute name or names, a name shall not be selected by WHO as a recommended international nonproprietary name while there exists a formal objection thereto filed under article 5 which has not been withdrawn.

*Article 7* - Where no objection has been filed under article 5, or all objections previously filed have been withdrawn, the Secretariat shall give notice in accordance with subsection (a) of article 3 that the name has been selected by WHO as a recommended international nonproprietary name.

*Article 8* - In forwarding a recommended international nonproprietary name to Member States under article 7, the Secretariat shall:

- a) request that it be recognized as the nonproprietary name for the substance; and
- b) request that Member States take such steps as are necessary to prevent the acquisition of proprietary rights in the name and to prohibit registration of the name as a trademark or trade name.

*Article 9*

a) In the extraordinary circumstance that a previously recommended international nonproprietary name gives rise to errors in medication, prescription or distribution, or a demonstrable risk thereof, because of similarity with another name in pharmaceutical and/or prescription practices, and it appears that such errors or potential errors cannot readily be resolved through other interventions than a possible substitution of a previously recommended international nonproprietary name, or in the event that a previously recommended international nonproprietary name differs substantially from the nonproprietary name approved in a significant number of Member States, or in other such extraordinary circumstances that justify a substitution of a recommended international nonproprietary name, proposals to that effect may be filed by any interested person. Such proposals shall be submitted on the form provided therefore and shall:

- i) identify the person making the proposal;
- ii) state his or her interest in the proposed substitution; and
- iii) set forth the reasons for the proposal; and
- iv) describe, and provide documentary evidence regarding the other interventions undertaken in an effort to resolve the situation, and the reasons why these other interventions were inadequate.

Such proposals may include a proposal for a new substitute international nonproprietary name, devised in accordance with the General principles, which takes into account the pharmaceutical substance for which the new substitute international nonproprietary name is being proposed.

The Secretariat shall forward a copy of the proposal, for consideration in accordance with the procedure described in subsection (b) below, to the INN Expert Group and the original applicant or its successor (if different from the person bringing the proposal for substitution and provided that the original applicant or its successor is known or can be found through diligent effort, including contacts with industry associations).

In addition, the Secretariat shall request comments on the proposal from:

- i) Member States and national and regional pharmacopoeia commissions or other bodies designated by Member States (by including a notice to that effect in the letter referred to in article 3(a), and
- ii) any other persons known to be concerned by the proposed substitution.

The request for comments shall:

- i) state the recommended international nonproprietary name that is being proposed for substitution (and the proposed substitute name, if provided);
- ii) identify the person who submitted the proposal for substitution (if so requested by such person);
- iii) identify the substance to which the proposed substitution relates and reasons put forward for substitution;
- iv) set forth the time within which comments will be received and the person and place to whom they should be directed; and
- v) state the authority under which WHO is acting and refer to these rules of procedure.

Comments on the proposed substitution may be forwarded by any person to WHO within four months of the date of the request for comments.

b) After the time period for comments referred to above has elapsed, the Secretariat shall forward any comments received to the INN Expert Group, the original applicant or its successor and the person bringing the proposal for substitution. If, after consideration of the proposal for substitution and the comments received, the INN Expert Group, the person bringing the proposal for substitution and the original applicant or its successor all agree that there is a need to substitute the previously recommended international nonproprietary name, the Secretariat shall submit the proposal for substitution to the INN Expert Group for further processing. Notwithstanding the foregoing, the original applicant or its successor shall not be entitled to withhold agreement to a proposal for substitution in the event the original applicant or its successor has no demonstrable continuing interest in the recommended international nonproprietary name proposed for substitution.

In the event that a proposal for substitution shall be submitted to the INN Expert Group for further processing, the INN Expert Group will select a new international nonproprietary name in accordance with the General principles referred to in article 2 and the procedure set forth in articles 3 to 8 inclusive. The notices to be given by the Secretariat under article 3 and article 7, respectively, including to the original applicant or its successor (if not the same as the person proposing the substitution, and provided that the original applicant or its successor is known or can be found through diligent effort, including contacts with industry associations), shall in such event indicate that the new name is a substitute for a previously recommended international nonproprietary name and that Member States may wish to make transitional arrangements in order to accommodate existing products that use the previously recommended international nonproprietary name on their label in accordance with national legislation.

If, after consideration of the proposal for substitution and the comments received in accordance with the procedure described above, the INN Expert Group, the original applicant or its successor and the person bringing the proposal for substitution do not agree that there are compelling reasons for substitution of a previously recommended international nonproprietary name, this name shall be retained (provided always that the original applicant or its successor shall not be entitled to withhold agreement to a proposal for substitution in the event that the original applicant or its successor has no demonstrable continuing interest in the recommended international nonproprietary name proposed to be substituted). In such an event, the Secretariat shall advise the person having proposed the substitution, as well as the original applicant or its

successor (if not the same as the person proposing the substitution, and provided that the original applicant or its successor is known or can be found through diligent effort, including contacts with industry associations), Member States, national and regional pharmacopoeia commissions, other bodies designated by Member States, and any other persons known to be concerned by the proposed substitution that, despite a proposal for substitution, it has been decided to retain the previously recommended international nonproprietary name (with a description of the reason(s) why the proposal for substitution was not considered sufficiently compelling).

## ANNEX 2

### GENERAL PRINCIPLES FOR GUIDANCE IN DEVISING INTERNATIONAL NONPROPRIETARY NAMES FOR PHARMACEUTICAL SUBSTANCES<sup>1</sup>

1. International Nonproprietary Names (INN) should be distinctive in sound and spelling. They should not be inconveniently long and should not be liable to confusion with names in common use.

2. The INN for a substance belonging to a group of pharmacologically related substances should, where appropriate, show this relationship. Names that are likely to convey to a patient an anatomical, physiological, pathological or therapeutic suggestion should be avoided.

*These primary principles are to be implemented by using the following secondary principles:*

3. In devising the INN of the first substance in a new pharmacological group, consideration should be given to the possibility of devising suitable INN for related substances, belonging to the new group.

4. In devising INN for acids, one-word names are preferred; their salts should be named without modifying the acid name, e.g. "oxacillin" and "oxacillin sodium", "ibufenac" and "ibufenac sodium".

5. INN for substances which are used as salts should in general apply to the active base or the active acid. Names for different salts or esters of the same active substance should differ only in respect of the name of the inactive acid or the inactive base. For quaternary ammonium substances, the cation and anion should be named appropriately as separate components of a quaternary substance and not in the amine-salt style.

6. The use of an isolated letter or number should be avoided; hyphenated construction is also undesirable.

7. To facilitate the translation and pronunciation of INN, "f" should be used instead of "ph", "t" instead of "th", "e" instead of "ae" or "oe", and "i" instead of "y"; the use of the letters "h" and "k" should be avoided.

8. Provided that the names suggested are in accordance with these principles, names proposed by the person discovering or first developing and marketing a pharmaceutical preparation, or names already officially in use in any country, should receive preferential consideration.

9. Group relationship in INN (see General principle 2) should if possible be shown by using a common stem. The following list contains examples of stems for groups of substances, particularly for new groups. There are many other stems in active use.<sup>2</sup> Where a stem is shown without any hyphens it may be used anywhere in the name.

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<sup>1</sup> In its Twentieth report (WHO Technical Report Series, No. 581, 1975), the WHO Expert committee on Nonproprietary Names for Pharmaceutical Substances reviewed the general principles for devising, and the procedures for selecting, INN in the light of developments in pharmaceutical compounds in recent years. The most significant change has been the extension to the naming of synthetic chemical substances of the practice previously used for substances originating in or derived from natural products. This practice involves the use of a characteristic "stem" indicative of a common property of the members of a group. The reason for, and the implications of, the change are fully discussed.

The guiding principles were updated during the 13<sup>th</sup> consultation on nonproprietary names for pharmaceutical substances (Geneva, 27-29 April 1983) (PHARM S/NOM 928 13 May 1983, revised 18 August 1983).

<sup>2</sup> A more extensive listing of stems is contained in the working document WHO/EMP/RHT/TSN/2018.1 which is regularly updated and can be requested from the INN Programme, WHO, Geneva.

<b>Latin</b>	<b>English</b>	
-acum	-ac	anti-inflammatory agents, ibufenac derivatives
-adolom	-adol }	analgesics
-adol-	-adol-}	
-astum	-ast	antiasthmatic, antiallergic substances not acting primarily as antihistaminics
-astinum	-astine	antihistaminics
-azepamum	-azepam	diazepam derivatives
bol	bol	steroids, anabolic
-cain-	-cain-	class I antiarrhythmics, procainamide and lidocaine derivatives
-cainum	-caine	local anaesthetics
cef-	cef-	antibiotics, cephalosporanic acid derivatives
-cillinum	-cillin	antibiotics, 6-aminopenicillanic acid derivatives
-conazolom	-conazole	systemic antifungal agents, miconazole derivatives
cort	cort	corticosteroids, except prednisolone derivatives
-coxibum	-coxib	selective cyclo-oxygenase inhibitors
-entanum	-entan	endothelin receptor antagonists
gab	gab	gabamimetic agents
gado-	gado-	diagnostic agents, gadolinium derivatives
-gatrانum	-gatrان	thrombin inhibitors, antithrombotic agents
gest	gest	steroids, progestogens
gli	gli	antihyperglycaemics
io-	io-	iodine-containing contrast media
-metacinum	-metacin	anti-inflammatory, indometacin derivatives
-mycinum	-mycin	antibiotics, produced by <i>Streptomyces</i> strains
-nidazolom	-nidazole	antiprotozoal substances, metronidazole derivatives
-ololom	-olol	β-adrenoreceptor antagonists
-oxacinum	-oxacin	antibacterial agents, nalidixic acid derivatives
-platinum	-platin	antineoplastic agents, platinum derivatives
-poetinum	-poetin	erythropoietin type blood factors
-pril(at)um	-pril(at)	angiotensin-converting enzyme inhibitors
-profenum	-profen	anti-inflammatory substances, ibuprofen derivatives
prost	prost	prostaglandins
-relinum	-relin	pituitary hormone release-stimulating peptides
-sartanum	-sartan	angiotensin II receptor antagonists, antihypertensive (non-peptidic)
-vaptanum	-vaptan	vasopressin receptor antagonists
vin-	vin- }	vinca-type alkaloids
-vin-	-vin-}	

## ANNEXE 1

### PROCEDURE A SUIVRE EN VUE DU CHOIX DE DENOMINATIONS COMMUNES INTERNATIONALES RECOMMANDEES POUR LES SUBSTANCES PHARMACEUTIQUES<sup>1</sup>

L'Organisation mondiale de la Santé (également désignée ci-après sous l'appellation « OMS ») observe la procédure exposée ci-dessous pour l'attribution de dénominations communes internationales recommandées pour les substances pharmaceutiques, conformément à la résolution WHA3.11 de l'Assemblée mondiale de la Santé, et pour le remplacement de telles dénominations.

**Article 1** - Les propositions de dénominations communes internationales recommandées et les propositions de remplacement de telles dénominations sont soumises à l'OMS sur la formule prévue à cet effet. L'examen de telles propositions est soumis au paiement d'une taxe administrative destinée uniquement à couvrir les coûts correspondants assumés par le Secrétariat de l'OMS (« le Secrétariat »). Le montant de cette taxe est déterminé par le Secrétariat et peut être modifié de temps à autre.

<sup>1</sup> Voir annexe 1 dans OMS, Série de Rapports techniques, N° 581, 1975. Le texte original a été adopté par le Conseil exécutif dans sa résolution EB15.R7 et amendé dans ses résolutions EB43.R9 et EB115.R4.

**Article 2** - Ces propositions sont soumises par le Secrétariat aux experts désignés à cette fin parmi les personnalités inscrites au Tableau d'experts de la Pharmacopée internationale et des Préparations pharmaceutiques, ci-après désignés sous l'appellation « le Groupe d'experts des DCI » ; elles sont examinées par les experts conformément aux « Directives générales pour la formation de dénominations communes internationales pour les substances pharmaceutiques » reproduites ci-après<sup>1</sup>. La dénomination acceptée est la dénomination employée par la personne qui découvre ou qui, la première, fabrique et lance sur le marché une substance pharmaceutique, à moins que des raisons majeures n'obligent à s'écarter de cette règle.

**Article 3** - Après l'examen prévu à l'article 2, le Secrétariat notifie qu'un projet de dénomination commune internationale est à l'étude.

a) Cette notification est faite par une insertion dans *WHO Drug Information*<sup>2</sup> et par l'envoi d'une lettre aux Etats Membres et aux commissions nationales et régionales de pharmacopée ou autres organismes désignés par les Etats Membres.

i) Notification est également faite à la personne qui a soumis la proposition (« le demandeur initial ») et à d'autres personnes portant à la dénomination mise à l'étude un intérêt notoire.

b) Cette notification contient les indications suivantes :

i) dénomination mise à l'étude;

ii) nom de l'auteur de la proposition tendant à attribuer une dénomination à la substance, si cette personne le demande ;

iii) définition de la substance dont la dénomination est mise à l'étude ;

iv) délai pendant lequel seront reçues les observations et les objections à l'égard de cette dénomination ; nom et adresse de la personne habilitée à recevoir ces observations et objections ;

v) mention des pouvoirs en vertu desquels agit l'OMS et référence au présent règlement.

c) En envoyant cette notification, le Secrétariat demande aux Etats Membres de prendre les mesures nécessaires pour prévenir l'acquisition de droits de propriété sur la dénomination proposée pendant la période au cours de laquelle cette dénomination est mise à l'étude par l'OMS.

**Article 4** - Des observations sur la dénomination proposée peuvent être adressées à l'OMS par toute personne, dans les quatre mois qui suivent la date de publication de la dénomination dans *WHO Drug Information* (voir l'article 3).

**Article 5** - Toute personne intéressée peut formuler une objection formelle contre la dénomination proposée dans les quatre mois qui suivent la date de publication de la dénomination dans *WHO Drug Information* (voir l'article 3).

Cette objection doit s'accompagner des indications suivantes :

i) nom de l'auteur de l'objection ;

ii) intérêt qu'il ou elle porte à la dénomination en cause ;

iii) raisons motivant l'objection contre la dénomination proposée.

**Article 6** - Lorsqu'une objection formelle est formulée en vertu de l'article 5, l'OMS peut soit soumettre la dénomination proposée à un nouvel examen, soit intervenir pour tenter d'obtenir le retrait de l'objection. Sans préjudice de l'examen par l'OMS d'une ou de plusieurs appellations de

<sup>1</sup> Voir annexe 2.

<sup>2</sup> Avant 1987, les listes de dénominations communes internationales étaient publiées dans la *Chronique de l'Organisation mondiale de la Santé*.

remplacement, l'OMS n'adopte pas d'appellation comme dénomination commune internationale recommandée tant qu'une objection formelle présentée conformément à l'article 5 n'est pas levée.

*Article 7* - Lorsqu'il n'est formulé aucune objection en vertu de l'article 5, ou que toutes les objections présentées ont été levées, le Secrétariat fait une notification conformément aux dispositions du paragraphe a) de l'article 3, en indiquant que la dénomination a été choisie par l'OMS en tant que dénomination commune internationale recommandée.

*Article 8* - En communiquant aux Etats Membres, conformément à l'article 7, une dénomination commune internationale recommandée, le Secrétariat :

- a) demande que cette dénomination soit reconnue comme dénomination commune de la substance considérée ; et
- b) demande aux Etats Membres de prendre les mesures nécessaires pour prévenir l'acquisition de droits de propriété sur cette dénomination et interdire le dépôt de cette dénomination comme marque ou appellation commerciale.

*Article 9* -

a) Dans le cas exceptionnel où une dénomination commune internationale déjà recommandée donne lieu à des erreurs de médication, de prescription ou de distribution ou en comporte un risque démontrable, en raison d'une similitude avec une autre appellation dans la pratique pharmaceutique et/ou de prescription, et où il apparaît que ces erreurs ou ces risques d'erreur ne peuvent être facilement évités par d'autres interventions que le remplacement éventuel d'une dénomination commune internationale déjà recommandée, ou dans le cas où une dénomination commune internationale déjà recommandée diffère sensiblement de la dénomination commune approuvée dans un nombre important d'Etats Membres, ou dans d'autres circonstances exceptionnelles qui justifient le remplacement d'une dénomination commune internationale recommandée, toute personne intéressée peut formuler une proposition dans ce sens. Cette proposition est présentée sur la formule prévue à cet effet et doit s'accompagner des indications suivantes :

- i) nom de l'auteur de la proposition ;
- ii) intérêt qu'il ou elle porte au remplacement proposé ;
- iii) raisons motivant la proposition ; et
- iv) description, faits à l'appui, des autres interventions entreprises pour tenter de régler le problème et exposé des raisons pour lesquelles ces interventions ont échoué.

Les propositions peuvent comprendre une proposition de nouvelle dénomination commune internationale de remplacement, établie conformément aux Directives générales, compte tenu de la substance pharmaceutique pour laquelle la nouvelle dénomination commune internationale de remplacement est proposée.

Le Secrétariat transmet une copie de la proposition pour examen, conformément à la procédure exposée plus loin au paragraphe b), au Groupe d'experts des DCI et au demandeur initial ou à son successeur (s'il s'agit d'une personne différente de celle qui a formulé la proposition de remplacement et pour autant que le demandeur initial ou son successeur soit connu ou puisse être retrouvé moyennant des efforts diligents, notamment des contacts avec les associations industrielles).

De plus, le Secrétariat demande aux entités et personnes ci-après de formuler des observations sur la proposition :

- i) les Etats Membres et les commissions nationales et régionales de pharmacopée ou d'autres organismes désignés par les Etats Membres (en insérant une note à cet effet dans la lettre mentionnée à l'article 3.a), et
- ii) toutes autres personnes portant au remplacement proposé un intérêt notoire.

La demande d'observations contient les indications suivantes :

i) dénomination commune internationale recommandée pour laquelle un remplacement est proposé (et la dénomination de remplacement proposée, si elle est fournie) ;

ii) nom de l'auteur de la proposition de remplacement (si cette personne le demande) ;

iii) définition de la substance faisant l'objet du remplacement proposé et raisons avancées pour le remplacement ;

iv) délai pendant lequel seront reçus les commentaires et nom et adresse de la personne habilitée à recevoir ces commentaires ; et

v) mention des pouvoirs en vertu desquels agit l'OMS et référence au présent règlement.

Des observations sur la proposition de remplacement peuvent être communiquées par toute personne à l'OMS dans les quatre mois qui suivent la date de la demande d'observations.

b) Une fois échu le délai prévu ci-dessus pour la communication d'observations, le Secrétariat transmet les observations reçues au Groupe d'experts des DCI, au demandeur initial ou à son successeur et à l'auteur de la proposition de remplacement. Si, après avoir examiné la proposition de remplacement et les observations reçues, le Groupe d'experts des DCI, l'auteur de la proposition de remplacement et le demandeur initial ou son successeur reconnaissent tous qu'il est nécessaire de remplacer la dénomination commune internationale déjà recommandée, le Secrétariat soumet la proposition de remplacement au Groupe d'experts des DCI pour qu'il y donne suite.

Nonobstant ce qui précède, le demandeur initial ou son successeur n'est pas habilité à refuser son accord à une proposition de remplacement au cas où il ne peut être démontré qu'il porte un intérêt durable à la dénomination commune internationale recommandée qu'il est proposé de remplacer.

Dans le cas où une proposition de remplacement est soumise au Groupe d'experts des DCI pour qu'il y donne suite, le Groupe choisit une nouvelle dénomination commune internationale conformément aux Directives générales mentionnées à l'article 2 et selon la procédure décrite dans les articles 3 à 8 inclus. La notification faite par le Secrétariat en vertu de l'article 3 et de l'article 7, respectivement, y compris au demandeur initial ou à son successeur (si ce n'est pas la même personne que celle qui a proposé le remplacement et pour autant que le demandeur initial ou son successeur soit connu ou puisse être retrouvé moyennant des efforts diligents, notamment des contacts avec les associations industrielles), doit dans un tel cas indiquer que la nouvelle dénomination remplace une dénomination commune internationale déjà recommandée et que les Etats Membres peuvent souhaiter prendre des mesures transitoires pour les produits existants qui utilisent la dénomination commune internationale déjà recommandée sur leur étiquette conformément à la législation nationale.

Si, après examen de la proposition de remplacement et des observations communiquées conformément à la procédure exposée plus haut, le Groupe d'experts des DCI, le demandeur initial ou son successeur et l'auteur de la proposition de remplacement ne s'accordent pas sur le fait qu'il y a des raisons impératives de remplacer une dénomination commune internationale déjà recommandée, cette dernière est conservée (étant entendu toujours que le demandeur initial ou son successeur n'est pas habilité à refuser son accord à une proposition de remplacement au cas où il ne peut être démontré qu'il porte un intérêt durable à la dénomination commune internationale recommandée qu'il est proposé de remplacer). Dans un tel cas, le Secrétariat informe l'auteur de la proposition de remplacement, ainsi que le demandeur initial ou son successeur (s'il s'agit d'une personne différente de celle qui a formulé la proposition de remplacement et pour autant que le demandeur initial ou son successeur soit connu ou puisse être retrouvé moyennant des efforts diligents, notamment des contacts avec les associations industrielles), les Etats Membres, les commissions nationales et régionales de pharmacopée, les autres organismes désignés par les Etats Membres et toutes autres personnes portant un intérêt notoire au remplacement proposé que, malgré une proposition de remplacement, il a été décidé de conserver la dénomination commune internationale déjà recommandée (avec une brève description de la ou des raisons pour lesquelles la proposition de remplacement n'a pas été jugée suffisamment impérative).

## ANNEXE 2

# DIRECTIVES GÉNÉRALES POUR LA FORMATION DE DENOMINATIONS COMMUNES INTERNATIONALES APPLICABLES AUX SUBSTANCES PHARMACEUTIQUES<sup>1</sup>

1. Les dénominations communes internationales (DCI) devront se distinguer les unes des autres par leur consonance et leur orthographe. Elles ne devront pas être d'une longueur excessive, ni prêter à confusion avec des appellations déjà couramment employées.

2. La DCI de chaque substance devra, si possible, indiquer sa parenté pharmacologique. Les dénominations susceptibles d'évoquer pour les malades des considérations anatomiques, physiologiques, pathologiques ou thérapeutiques devront être évitées dans la mesure du possible.

*Outre ces deux principes fondamentaux, on respectera les principes secondaires suivants :*

3. Lorsqu'on formera la DCI de la première substance d'un nouveau groupe pharmacologique, on tiendra compte de la possibilité de former ultérieurement d'autres DCI appropriées pour les substances apparentées du même groupe.

4. Pour former des DCI des acides, on utilisera de préférence un seul mot. Leurs sels devront être désignés par un terme qui ne modifie pas le nom de l'acide d'origine : par exemple «oxacilline» et «oxacilline sodique», «ibufénac» et «ibufénac sodique».

5. Les DCI pour les substances utilisées sous forme de sels devront en général s'appliquer à la base active (ou à l'acide actif). Les dénominations pour différents sels ou esters d'une même substance active ne différeront que par le nom de l'acide inactif (ou de la base inactif). En ce qui concerne les substances à base d'ammonium quaternaire, la dénomination s'appliquera de façon appropriée au cation et à l'anion en tant qu'éléments distincts d'une substance quaternaire. On évitera de choisir une désignation évoquant un sel aminé.

6. On évitera d'ajouter une lettre ou un chiffre isolé ; en outre, on renoncera de préférence au trait d'union.

7. Pour simplifier la traduction et la prononciation des DCI, la lettre « f » sera utilisée à la place de « ph », « t » à la place de « th », « e » à la place de « ae » ou « oe », et « i » à la place de « y » ; l'usage des lettres « h » et « k » sera aussi évité.

8. On retiendra de préférence, pour autant qu'elles respectent les principes énoncés ici, les dénominations proposées par les personnes qui ont découvert ou qui, les premières, ont fabriqué et lancé sur le marché les préparations pharmaceutiques considérées, ou les dénominations déjà officiellement adoptées par un pays.

9. La parenté entre substances d'un même groupe (voir Directive générale 2) sera si possible indiquée dans les DCI par l'emploi de segments-clés communs. La liste ci-après contient des exemples de segments-clés pour des groupes de substances, surtout pour des groupes récents. Il y a beaucoup d'autres segments-clés en utilisation active.<sup>2</sup> Les segments-clés indiqués sans trait d'union pourront être insérés n'importe où dans une dénomination.

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<sup>1</sup> Dans son vingtième rapport (OMS, Série de Rapports techniques, N° 581, 1975), le Comité OMS d'experts des Dénominations communes pour les Substances pharmaceutiques a examiné les directives générales pour la formation des dénominations communes internationales et la procédure à suivre en vue de leur choix, compte tenu de l'évolution du secteur pharmaceutique au cours des dernières années. La modification la plus importante a été l'extension aux substances de synthèse de la pratique normalement suivie pour désigner les substances tirées ou dérivées de produits naturels. Cette pratique consiste à employer des syllabes communes ou groupes de syllabes communes (segments-clés) qui sont caractéristiques et indiquent une propriété commune aux membres du groupe des substances pour lequel ces segments-clés ont été retenus. Les raisons et les conséquences de cette modification ont fait l'objet de discussions approfondies.

Les directives ont été mises à jour lors de la treizième consultation sur les dénominations communes pour les substances pharmaceutiques (Genève, 27-29 avril 1983) (PHARM S/NOM 928, 13 mai 1983, révision en date du 18 août 1983).

<sup>2</sup> Une liste plus complète de segments-clés est contenue dans le document de travail WHO/EMP/RHT/TSN/2018.1 qui est régulièrement mis à jour et qui peut être demandé auprès du programme des DCI, OMS, Genève



Latin	Français	
-acum	-ac	substances anti-inflammatoires du groupe de l'ibufénac analgésiques
-adolum	-adol }	
-adol-	-adol- }	
-astum	-ast	
-astinum	-astine	antiasthmatiques, antiallergiques n'agissant pas principalement en tant qu'antihistaminiques
-azepamum	-azéпам	antihistaminiques
bol	bol	substances du groupe du diazépam
-cain-	-cain-	stéroïdes anabolisants
-cainum	-caïne	antiarythmiques de classe I, dérivés du procaïnamide et de la lidocaïne
cef-	céf-	anesthésiques locaux
-cillinum	-cilline	antibiotiques, dérivés de l'acide céphalosporanique
-conazolium	-conazole	antibiotiques, dérivés de l'acide 6-aminopénicillanique
cort	cort	agents antifongiques systémiques du groupe du miconazole
-coxibum	-coxib	corticostéroïdes, autres que les dérivés de la prednisolone
-entanum	-entan	inhibiteurs sélectifs de la cyclo-oxygénase
gab	gab	antagonistes du récepteur de l'endothéline
gado-	gado-	gabamimétiques
-gatranum	-gatran	agents diagnostiques, dérivés du gadolinium
gest	gest	antithrombines, antithrombotiques
gli	gli	stéroïdes progestogènes
io-	io-	antihyperglycémiant
-metacinum	-métacine	produits de contraste iodés
-mycinum	-mycine	substances anti-inflammatoires du groupe de l'indométacine
-nidazolium	-nidazole	antibiotiques produits par des souches de <i>Streptomyces</i>
-ololum	-olol	substances antiprotozoaires du groupe du métronidazole
-oxacinum	-oxacine	antagonistes des récepteurs β-adrénergiques
-platinum	-platine	substances antibactériennes du groupe de l'acide nalidixique
-poetinum	-poétine	antinéoplasiques, dérivés du platine
-pril(at)um	-pril(ate)	facteurs sanguins de type érythro-poétine
-profenum	-profène	inhibiteurs de l'enzyme de conversion de l'angiotensine
prost	prost	substances anti-inflammatoires du groupe de l'ibuprofène
-relinum	-réline	prostaglandines
-sartanum	-sartan	peptides stimulant la libération d'hormones hypophysaires
-vaptanum	-vaptan	antagonistes d'un récepteur de l'angiotensine II,
vin-	vin- }	antihypertenseurs (non peptidiques)
-vin-	-vin- }	antagonistes du récepteur de la vasopressine
		alcaloïdes du type vinca

## ANEXO 1

# PROCEDIMIENTO DE SELECCIÓN DE DENOMINACIONES COMUNES INTERNACIONALES RECOMENDADAS PARA SUSTANCIAS FARMACÉUTICAS<sup>1</sup>

La Organización Mundial de la Salud (OMS) seguirá el procedimiento que se expone a continuación tanto para seleccionar denominaciones comunes internacionales recomendadas para las sustancias farmacéuticas, de conformidad con lo dispuesto en la resolución WHA3.11, como para sustituir esas denominaciones.

*Artículo 1* - Las propuestas de denominaciones comunes internacionales recomendadas y las propuestas de sustitución de esas denominaciones se presentarán a la OMS en los formularios que se proporcionen a estos efectos. El estudio de estas propuestas estará sujeto al pago de una tasa destinada a sufragar los costos de administración que ello suponga para la Secretaría de la OMS («la Secretaría»). La Secretaría establecerá la cuantía de esa tasa y podrá ajustarla periódicamente.

*Artículo 2* - Estas propuestas serán sometidas por la Secretaría a los miembros del Cuadro de Expertos en Farmacopea Internacional y Preparaciones Farmacéuticas encargados de su estudio, en adelante designados como «el Grupo de Expertos en DCI», para que las examinen de conformidad con los «Principios generales de orientación para formar denominaciones comunes internacionales para sustancias farmacéuticas», anexos a este procedimiento.<sup>2</sup> A menos que haya poderosas razones en contra, la denominación aceptada será la empleada por la persona que haya descubierto o fabricado y comercializado por primera vez esa sustancia farmacéutica.

*Artículo 3* - Tras el examen al que se refiere el artículo 2, la Secretaría notificará que está en estudio un proyecto de denominación internacional.

a) Esa notificación se hará mediante una publicación en *Información Farmacéutica OMS*<sup>3</sup> y el envío de una carta a los Estados Miembros y a las comisiones nacionales y regionales de las farmacopeas u otros organismos designados por los Estados Miembros.

i) La notificación será enviada también a la persona que haya presentado la propuesta («el solicitante inicial») y a otras personas que tengan un interés especial en una denominación objeto de estudio.

b) En esa notificación se incluirán los siguientes datos:

i) la denominación sometida a estudio;

ii) la identidad de la persona que ha presentado la propuesta de denominación de la sustancia, si lo pide esa persona;

iii) la identidad de la sustancia cuya denominación está en estudio;

iv) el plazo fijado para recibir observaciones y objeciones, así como el nombre y la dirección de la persona a quien deban dirigirse; y

v) los poderes conferidos para el caso a la OMS y una referencia al presente procedimiento.

<sup>1</sup> Véase el anexo 1 en OMS, Serie de Informes Técnicos, N° 581, 1975. El texto vigente fue adoptado por el Consejo Ejecutivo en su resolución EB15.R7 y modificado en las resoluciones EB43.R9 y EB115.R4..

<sup>2</sup> Véase el anexo 2.

<sup>3</sup> Hasta 1987 las listas de DCI se publicaban en la *Crónica de la Organización Mundial de la Salud*.

c) Al enviar esa notificación, la Secretaría solicitará de los Estados Miembros la adopción de todas las medidas necesarias para impedir la adquisición de derechos de patente sobre la denominación propuesta, durante el periodo en que la OMS la tenga en estudio.

*Artículo 4* - Toda persona puede formular a la OMS observaciones sobre la denominación propuesta dentro de los cuatro meses siguientes a su publicación en *Información Farmacéutica OMS*, conforme a lo dispuesto en el artículo 3.

*Artículo 5* - Toda persona interesada puede presentar una objeción formal a una denominación propuesta dentro de los cuatro meses siguientes a su publicación en *Información Farmacéutica OMS*, conforme a lo dispuesto en el artículo 3.

Esa objeción deberá acompañarse de los siguientes datos:

- i) la identidad de la persona que formula la objeción;
- ii) las causas que motivan su interés por la denominación; y
- iii) las causas que motivan su objeción a la denominación propuesta.

*Artículo 6* - Cuando se haya presentado una objeción formal en la forma prevista en el artículo 5, la OMS podrá reconsiderar el nombre propuesto o utilizar sus buenos oficios para intentar lograr que se retire la objeción. La OMS no seleccionará como denominación común internacional una denominación a la que se haya hecho una objeción formal, presentada según lo previsto en el artículo 5, que no haya sido retirada, todo ello sin perjuicio de que la Organización examine otra denominación o denominaciones sustitutivas.

*Artículo 7* - Cuando no se haya formulado ninguna objeción en la forma prevista en el artículo 5, o cuando todas las objeciones presentadas hayan sido retiradas, la Secretaría notificará, conforme a lo dispuesto en el párrafo a) del artículo 3, que la denominación ha sido seleccionada por la OMS como denominación común internacional recomendada.

*Artículo 8* - Al comunicar a los Estados Miembros una denominación común internacional, conforme a lo previsto en el artículo 7, la Secretaría:

a) solicitará que esta denominación sea reconocida como denominación común para la sustancia de que se trate; y

b) solicitará a los Estados Miembros que adopten todas las medidas necesarias para impedir la adquisición de derechos de patente sobre la denominación, y prohíban que sea registrada como marca de fábrica o como nombre comercial.

#### *Artículo 9*

a) En el caso excepcional de que, debido a su semejanza con otra denominación utilizada en las prácticas farmacéuticas y/o de prescripción, una denominación común internacional recomendada anteriormente ocasione errores de medicación, prescripción o distribución, o suponga un riesgo manifiesto de que esto ocurra, y parezca que tales errores o potenciales errores no sean fácilmente subsanables con otras medidas que no sean la posible sustitución de esa denominación común internacional recomendada anteriormente; en el caso de que una denominación común internacional recomendada anteriormente difiera considerablemente de la denominación común aprobada en un número importante de Estados Miembros, o en otras circunstancias excepcionales que justifiquen el cambio de una denominación común internacional recomendada, cualquier persona interesada puede presentar propuestas en este sentido. Esas propuestas se presentarán en los formularios que se proporcionen a estos efectos e incluirán los siguientes datos:

- i) la identidad de la persona que presenta la propuesta;
- ii) las causas que motivan su interés en la sustitución propuesta;
- iii) las causas que motivan la propuesta; y

iv) una descripción, acompañada de pruebas documentales, de las otras medidas que se hayan adoptado con el fin de resolver la situación y de los motivos por los cuales dichas medidas no han sido suficientes.

Entre esas propuestas podrá figurar una relativa a una nueva denominación común internacional sustitutiva, formulada con arreglo a los Principios generales y que tenga en cuenta la sustancia farmacéutica para la que se proponga la nueva denominación común internacional sustitutiva.

La Secretaría enviará al Grupo de Expertos en DCI y al solicitante inicial o a su sucesor (en el caso de que sea una persona diferente de la que ha presentado la propuesta de sustitución y siempre que el solicitante inicial o su sucesor sean conocidos o puedan ser encontrados mediante esfuerzos diligentes, como el contacto con las asociaciones industriales) una copia de la propuesta, para que sea examinada de conformidad con el procedimiento descrito en el párrafo *b) infra*.

Además, la Secretaría solicitará observaciones sobre la propuesta:

i) a los Estados Miembros y a las comisiones nacionales y regionales de las farmacopeas u otros organismos designados por los Estados Miembros (ello se hará incluyendo una notificación a tal efecto en la carta a la que se refiere el párrafo *a)* del artículo 3), y

ii) a cualquier persona que tenga un interés especial en la sustitución propuesta.

Al solicitar que se formulen estas observaciones se facilitarán los siguientes datos:

i) la denominación común internacional recomendada que se propone sustituir (y la denominación sustitutiva propuesta, si se ha facilitado);

ii) la identidad de la persona que ha presentado la propuesta de sustitución (si lo pide esa persona);

iii) la identidad de la sustancia a la que se refiere la sustitución propuesta y las razones para presentar la propuesta de sustitución;

iv) el plazo fijado para recibir observaciones, así como el nombre y la dirección de la persona a quien deban dirigirse; y

v) los poderes conferidos para el caso a la OMS y una referencia al presente procedimiento.

Toda persona puede formular a la OMS observaciones sobre la sustitución propuesta dentro de los cuatro meses siguientes a la fecha en que se realizó la solicitud de observaciones.

*b)* Una vez agotado el mencionado plazo para la formulación de observaciones, la Secretaría enviará todos los comentarios recibidos al Grupo de Expertos en DCI, al solicitante inicial o a su sucesor, y a la persona que haya presentado la propuesta de sustitución. Si después de examinar la propuesta de sustitución y las observaciones recibidas, el Grupo de Expertos en DCI, la persona que haya presentado la propuesta de sustitución y el solicitante inicial, o su sucesor, están de acuerdo en la necesidad de sustituir la denominación común internacional recomendada anteriormente, la Secretaría remitirá la propuesta de sustitución al Grupo de Expertos en DCI para que la tramite.

No obstante lo anterior, el solicitante inicial o su sucesor no tendrán derecho a impedir el acuerdo sobre una propuesta de sustitución en el caso de que hayan dejado de tener un interés demostrable en la denominación común internacional cuya sustitución se propone.

En caso de que la propuesta de sustitución sea presentada al Grupo de Expertos en DCI para que la tramite, este grupo seleccionará una nueva denominación común internacional de conformidad con los Principios generales a los que se refiere el artículo 2 y al procedimiento establecido en los artículos 3 a 8 inclusive. En ese caso, en las notificaciones que la Secretaría ha de enviar con arreglo a los artículos 3 y 7, respectivamente, incluida la notificación al solicitante

inicial o a su sucesor (en el caso de que no sea la misma persona que propuso la sustitución y siempre que el solicitante inicial o su sucesor sean conocidos o puedan ser encontrados mediante esfuerzos diligentes, como el contacto con las asociaciones industriales), se indicará que la nueva denominación sustituye a una denominación común internacional recomendada anteriormente y que los Estados Miembros podrán, si lo estiman oportuno, adoptar disposiciones transitorias aplicables a los productos existentes en cuya etiqueta se utilice, con arreglo a la legislación nacional, la denominación común internacional recomendada anteriormente que se haya sustituido.

En caso de que, después de haber estudiado la propuesta de sustitución y los comentarios recibidos de conformidad con el procedimiento descrito anteriormente, el Grupo de Expertos en DCI, el solicitante inicial o su sucesor y la persona que haya presentado la propuesta de sustitución no lleguen a un acuerdo sobre la existencia de razones poderosas para sustituir una denominación común internacional recomendada anteriormente, esta denominación se mantendrá (siempre en el entendimiento de que el solicitante inicial o su sucesor no tendrán derecho a impedir el acuerdo sobre una propuesta de sustitución en el caso de que hayan dejado de tener un interés demostrable en la denominación común internacional cuya sustitución se propone). En ese caso, la Secretaría comunicará a la persona que haya propuesto la sustitución, así como al solicitante inicial o a su sucesor (en el caso de que no sea la misma persona que propuso la sustitución y siempre que el solicitante inicial o su sucesor sean conocidos o puedan ser encontrados mediante esfuerzos diligentes, como el contacto con las asociaciones industriales), a los Estados Miembros, a las comisiones nacionales y regionales de las farmacopeas o a otros organismos designados por los Estados Miembros y a cualquier otra persona que tenga interés en la sustitución propuesta, que, pese a la presentación de una propuesta de sustitución, se ha decidido mantener la denominación común internacional recomendada anteriormente (con una descripción de la o las razones por las que se ha considerado que la propuesta de sustitución no estaba respaldada por razones suficientemente poderosas).

## ANEXO 2

### PRINCIPIOS GENERALES DE ORIENTACIÓN PARA FORMAR DENOMINACIONES COMUNES INTERNACIONALES PARA SUSTANCIAS FARMACÉUTICAS<sup>1</sup>

1. Las denominaciones comunes internacionales (DCI) deberán diferenciarse tanto fonética como ortográficamente. No deberán ser incómodamente largas, ni dar lugar a confusión con denominaciones de uso común.

2. La DCI de una sustancia que pertenezca a un grupo de sustancias farmacológicamente emparentadas deberá mostrar apropiadamente este parentesco. Deberán evitarse las denominaciones que puedan tener connotaciones anatómicas, fisiológicas, patológicas o terapéuticas para el paciente.

*Estos principios primarios se pondrán en práctica utilizando los siguientes principios secundarios:*

3. Al idear la DCI de la primera sustancia de un nuevo grupo farmacológico, deberá tenerse en cuenta la posibilidad de poder formar DCI convenientes para las sustancias emparentadas que se agreguen al nuevo grupo.

4. Al idear DCI para ácidos, se preferirán las de una sola palabra; sus sales deberán denominarse sin modificar el nombre del ácido: p. ej. «oxacilina» y «oxacilina sódica», «ibufenaco» y «ibufenaco sódico».

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<sup>1</sup> En su 20º informe (OMS, Serie de Informes Técnicos, Nº 581, 1975), el Comité de Expertos de la OMS en Denominaciones Comunes para las Sustancias Farmacéuticas revisó los Principios generales para formar denominaciones comunes internacionales (DCI), y su procedimiento de selección, a la luz de las novedades registradas en los últimos años en materia de compuestos farmacéuticos. El cambio más importante había consistido en hacer extensivo a la denominación de sustancias químicas sintéticas el método utilizado hasta entonces para las sustancias originadas en productos naturales o derivadas de éstos. Dicho método conlleva la utilización de una «partícula» característica que indica una propiedad común a los miembros de un grupo. En el citado informe se examinan en detalle las razones y consecuencias de este cambio. Los Principios generales de orientación se actualizaron durante la 13ª consulta sobre denominaciones comunes para sustancias farmacéuticas (Ginebra, 27 a 29 de abril de 1983) (PHARM S/NOM 928, 13 de mayo de 1983, revisado el 18 de agosto de 1983).

5. Las DCI para las sustancias que se usan en forma de sal deberán en general aplicarse a la base activa o al ácido activo. Las denominaciones para diferentes sales o ésteres de la misma sustancia activa solamente deberán diferir en el nombre del ácido o de la base inactivos. En los compuestos de amonio cuaternario, el catión y el anión deberán denominarse adecuadamente por separado, como componentes independientes de una sustancia cuaternaria y no como sales de una amina.
6. Deberá evitarse el empleo de letras o números aislados; también es indeseable el empleo de guiones.
7. Para facilitar la traducción y la pronunciación, se emplearán de preferencia las letras «f» en lugar de «ph», «t» en lugar de «th», «e» en lugar de «ae» u «oe», e «i» en lugar de «y»; se deberá evitar el empleo de las letras «h» y «k».
8. Siempre que las denominaciones propuestas estén de acuerdo con estos principios, recibirán una consideración preferente las denominaciones propuestas por la persona que haya descubierto las sustancias, o que fabrique y comercialice por primera vez una sustancia farmacéutica, así como las denominaciones ya adoptadas oficialmente en cualquier país.
9. El parentesco entre sustancias del mismo grupo se pondrá de manifiesto en las DCI (véase el Principio 2) utilizando una partícula común. En la lista que figura a continuación se indican ejemplos de partículas para grupos de sustancias, en particular para grupos nuevos. Existen muchas otras partículas que se usan habitualmente.<sup>1</sup> Cuando una partícula aparece sin guión alguno, puede utilizarse en cualquier lugar de la palabra.

Latín	Español	
- <i>acum</i>	- <i>aco</i>	antiinflamatorios derivados del ibufenaco
- <i>adolum</i>	- <i>adol</i> )	analgésicos
- <i>adol-</i>	- <i>adol-</i> )	
- <i>astum</i>	- <i>ast</i>	antiasmáticos, sustancias antialérgicas cuya acción principal no es la antihistamínica
- <i>astinum</i>	- <i>astina</i>	antihistamínicos
- <i>azepamum</i>	- <i>azepam</i>	derivados del diazepam
<i>bol</i>	<i>bol</i>	esteroides anabolizantes
- <i>cain-</i>	- <i>caína-</i>	antiarrítmicos de clase I, derivados de procainamida y lidocaína
- <i>cainum</i>	- <i>caína-</i>	
<i>cef-</i>	<i>cef-</i>	antibióticos, derivados del ácido cefalosporánico
- <i>cillinum</i>	- <i>cilina</i>	antibióticos derivados del ácido 6-aminopenicilánico
- <i>conazolium</i>	- <i>conazol</i>	antifúngicos sistémicos derivados del miconazol
<i>cort</i>	<i>cort</i>	corticosteroides, excepto derivados de prednisolona
- <i>coxibum</i>	- <i>coxib</i>	inhibidores selectivos de ciclooxigenasa
- <i>entanum</i>	- <i>entán</i>	antagonistas del receptor de endotelina
<i>gab</i>	<i>gab</i>	gabamiméticos
<i>gado-</i>	<i>gado-</i>	agentes para diagnóstico derivados de gadolinio
- <i>gartranum</i>	- <i>gastrán</i>	inhibidores de la trombina antitrombóticos
<i>gest</i>	<i>gest</i>	esteroides progestágenos
<i>gli</i>	<i>gli</i>	hipoglucemiantes, antihiper glucémicos
<i>io-</i>	<i>io-</i>	medios de contraste iodados
- <i>metacinum</i>	- <i>metacina</i>	antiinflamatorios derivados de indometacina
- <i>mycinum</i>	- <i>micina</i>	antibióticos producidos por cepas de <i>Streptomyces</i>
- <i>nidazolium</i>	- <i>nidazol</i>	antiprotozoarios derivados de metronidazol
- <i>ololum</i>	- <i>olol</i>	antagonistas de receptores β-adrenérgicos

<sup>1</sup> En el documento de trabajo WHO/EMP/RHT/TSN/2018.1, que se actualiza periódicamente y puede solicitarse al Programa sobre Denominaciones Comunes Internacionales, OMS, Ginebra, figura una lista más amplia de partículas.

<i>-oxacinum</i>	<i>-oxacino</i>	antibacterianos derivados del ácido nalidíxico
<i>-platinum</i>	<i>-platino</i>	antineoplásicos derivados del platino
<i>-poetinum</i>	<i>-poetina</i>	factores sanguíneos similares a la eritropoyetina
<i>-pril(at)um</i>	<i>-pril(at)</i>	inhibidores de la enzima convertora de la angiotensina
<i>-profenum</i>	<i>-profeno</i>	antiinflamatorios derivados del ibuprofeno
<i>prost</i>	<i>prost</i>	prostaglandinas
<i>-relinum</i>	<i>-relina</i>	péptidos estimulantes de la liberación de hormonas hipofisarias
<i>-sartanum</i>	<i>-sartán</i>	antihipertensivos (no peptídicos) antagonistas del receptor de angiotensina II
<i>-vaptanum</i>	<i>-vaptán</i>	antagonistas del receptor de vasopresina
<i>vin-</i>	<i>vin-</i> )	alcaloides de la vinca
<i>-vin-</i>	<i>-vin-</i> )	

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## Selected WHO publications of related interest

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**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)**

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