The use of IMGT/DomainGapAlign and IMGT/Collier-de-Perles (for amino acid sequences), IMGT/V-QUEST and IMGT/JunctionAnalysis (for nucleotide sequences) provides a standardized way to compare immunoglobulin sequences and to delimit the FR-IMGT and CDR-IMGT in the process of antibody humanization and engineering, whatever the chain type (heavy and light) and whatever the species (e.g. murine and human). Indeed these tools, like the IMGT databases and Web resources, are based on the IMGT-ONTOLOGY concepts of classification (IMGT gene and allele nomenclature approved by HGNC and WHO-IUIS [1,2]), of description (IMGT labels), and of numerotation (IMGT unique numbering for V-DOMAIN [3]). The comparison between V domain sequences include determination of the CDR-IMGT lengths (shown between brackets and separated with dots, e.g. [8.8.13]), percentage of identity between FR-IMGT calculated on 91 amino acids for VH (FR1-: 25, FR2-: 17, FR3-: 38, FR4-IMGT: 11) and 89 for V-KAPPA (FR1-: 26, FR2-: 17, FR3-: 36, FR4-IMGT: 10) and evaluation of the number of IMGT physicochemical classes changes [4,5].

The IMGT unique numbering and tools provide the delimitations of the FR-IMGT and CDR-IMGT for the analysis of antibody paratope or loop grafting in antibody engineering.

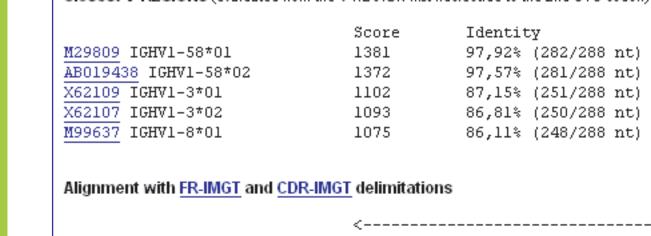
The IMGT unique numbering and tools based on the IMGT-ONTOLOGY concepts bridge the gap between sequences and 3D structures facilitating the analysis of antibody/antigen interactions.

[1] Lefranc and Lefranc. The Immunoglobulin FactsBook, Academic Press (2001) [2] Lefranc. WHO-IUIS report. Dev Comp Immunol (in press) [3] Lefranc et al. Dev Comp Immunol 27:55-77 (2003)

[4] Pommié et al. J Mol Recognit 17:17-32 (2004) [5] Magdelaine-Beuzelin et al. Crit Rev Oncol Hemat 64:210-225 (2007)

Analysis of antibody amino acid sequences:

Antibody amino acid	sequences are analysed per domain	using the IMGT/DomainGapAlign tool. S	Several sequences of the same		nainGapAlign displays your	•
-	nay be analysed simultaneously.	5 1 5		strands an	MGT, according to the IMG d loops, according to the IM	GT unique nu
IMGT/DomainG	apAlign QUERY				n the gene and allele name (omplete IMGT Collier de Per	
Select 'C' for sequence	•	for sequences of the variable domains and heavy chains. To delimit the domain les (in IMGT Repertoire).	• •	V	IGHV4-59*01	Species Homo sapiens Homo sapiens
Enter your sequ	ence(s) here (<u>FASTA format)</u>				FR1-IMGT	CDR1-IMGT
	<pre>KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ</pre>	Enter your sequence(s) here (FASTA format)			(1-26)	(27-38)
>alentuzumab_CH3 GQPREPQVYTLPPSRI >alentuzumab_CL	<pre>KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAF</pre>	>alemtuzumab_VH QVQLQESGPGLVRPSQTLSLTCTVSGFTFTDFYMNWVRQPPGRGI >alemtuzumab_VL DIQMTQSPSSLSASVGDRVTITCKASQNIDKYLNWYQQKPGKAPF		alemtuzumab_VH IGHV4-59*01 <i>(Homo sapiens)</i>	1 10 20 	
<				alemtuzumab_VL IGKV1-33*01 <i>(Homo sapiens)</i>	DIQMTQSPSSLSASVGDRVTITCKAS DIQMTQSPSSLSASVGDRVTITCQAS K	
Select a Domain t C Species Homo sapiens (Huma		Ciect a Domain type		С	IGHG1*01 or *02 IGHG1*01 or *02 or *03	Species Homo sapiens Homo sapiens Homo sapiens
English name	lign and IMGT-gap my sequence Clear the form	Homo sapiens (Human)			A AB (1-15)	B (16-26)
		Align and IMGT-gap my sequence Clea	r the form	alemtuzumab_CH1 IGHG1*01	1 10 87654321 123 ASTKGPSVFPLAPSSKSTS ASTKGPSVFPLAPSSKSTS	.GGTAALGCLVK
IMGT/DomainGa	apAlign RESULTS			(Homo sapiens) alemtuzumab CH2	APELLGGPSVFLFPPKPKDTLMI	SRTPENTCUUN
allele name of the close	sest sequence(s) from the IMGT referen	GION (for 'V') and the closest C-DOMAI nce directory is (are) provided with a perc e identified as having 73 % and 86.32 %	centage of identity.	IGHG1*01 (Homo sapiens)	APELLGGPSVFLFPPKPKDTLMI	SRTPEVTCVVV
IGHV4-59*01 and IGK The constant domain	V1-33*01, respectively. of the light chain has 100% identity wit	n <i>Homo sapiens</i> IGKC*01. The combine	d results of CH1 and CH3 of the	alemtuzumab_CH3 IGHG1*01 <i>(Homo sapiens)</i>	GQPREPQVYTLPPSRDELT	
IGHG1*03 would have	e been characterized by CH1: R120, CH	120, CH3: D12, L14) (there is no amino I3: E12, M14. m and concepts of IMGT-ONTOLOGY [²				Species Homo sapiens
were approved by the		NC) and by the WHO-IUIS Nomenclatur			A AB (1-15) <u>1 10</u>	B (16-26)
 [1] Lefranc et al., <i>In Silico</i> Biology [2] Lefranc. WHO-IUIS report. De [3] Lefranc et al., Dev Comp Imm [4] Lefranc et al., Dev Comp Imm 	unol 27:55-77 (2003)	 [5] Pommié et al. J Mol Recognit 17:17-32 (2 [6] Kaas et al. Nuc Acids Res 32:D208-D210 [7] Magdelaine-Neuzelin et al. Crit Rev Onco [8] Giudicelli et al. Nucl Acids Res 32:W435- [9] Yousfi Monod et al. Bioinformatics 20:i379) (2004) ol Hematol 64:210-225 (2007) W440 (2004)	alemtuzumab_CL IGKC*01 <i>(Homo sapiens)</i>	87654321 12 RTVAAPSVFIFPPSDEQLK RTVAAPSVFIFPPSDEQLK	3 .SGTASVVCLLN
	ysis of ant nces are analysed with IMGT/V-QUES ⁻	body nucle	eotide seq	uences		
 IMGT/V-QUEST and protein align IMGT/JunctionA 	identifies the sequences with the close ments according to the IMGT unique no nalysis analyses accurately the junction content, amino acid physicochemical p	st gene and allele in the IMGT reference umbering and provides an extensive analons of antibody rearranged sequences (I	ysis of the mutations [8].	Number of analyse	sults for the IMGT/V-(d sequences: 4 2 user_seq_33 user_seq_22	QUEST an
IMGT/V-QUEST		 synthesis view advanced parameters 			⁻ IMGT/V-QUEST uses <u>IMGT/Ju</u> ow nucleotide identity, dots (.	
Citing IMGT/V-QUEST: Giudicelli	Selection of parameters for the results	ı			•	
You are in the new IMG [*] Ew!	Display type : HTML 🛛 💌	Nb of nucleotides per line in alignment: 60 🛛 💌		Sequence number	1: user_seq_80	
The IMGT/V-QUEST now works o You therefore need to add ">" foll format) so the tool is able to sep rectangle "Selection of paramete You can also chose to see the "S batch of sequences expressing a	1. Alignment for V-GENE 5. Se 2. Alignment for D-GENE 6. V-F 3. Alignment for J-GENE 7. V-F 4. Results of IMGT/JunctionAnalysis 8. V-F	EGION alignment according to the IMGT numbering O EGION translation O EGION mutation table	<u>IMGT Collier de Perles</u> links to IMGT Collier de Perles IMGT Collier de Perles (PNG format, slow) no IMGT Collier de Perles	>user_seq_80 gaggtgcagctggtggagtct tcctgcaaggcttctggattc cgtggacaacgccttgagtgg gcacagaagttccaggaaaga	he <u>human IG set</u> from the <u>IMGT reference</u> gggcctgaggtgaagaagcctgggacctcagt acctttactagctctgctgtgcagtgggtgcg ataggacggatcgtcgttggcagtggtaacac gtcaccattaccagggacatgtccacaagtac tccgaggacacggccgtgtattactgtgcggc	gaaggtc acaggct aaactac agcctac
analyse your Immunogl	without list of eligible D-GENEs 10. □ V-F	EGION mutation statistics EGION mutation hot spots		caagggaccacggtcaccgtc	gagagcccttactactactggtatggacgt tcgagt	
our selection: Human	12. Sequences of V-, V-J- or V-D-J- R Access to IMGT/PhyloGe		Annotations by IMGT/Automat	V-GENE and allele		Productive IGH re IGHV1-58*01
our sequences are compared to	B. Synthesis view A second secon			J-GENE and allele		IGHJ6*02
Jucleotide sequences				D-GENE and allele by IMG		<u>IGHD3-10*01</u>
nter your sequence(s) in <u>FASTA</u> Type (or copy/paste) your sequence user_seq_80 aggtgcagctggtggagtctgggcc	 Alignment for V-GENEs V-REGION alignment according to the IMGT null V-REGION translation V-REGION protein display 	5. ⊻ <u>V-REGION protein dis</u> <u>nbering</u> 6. ⊻ <u>V-REGION protein dis</u> 7. ⊻ <u>V-REGION most frequ</u> 8. ⊻ <u>Results of IMGT/Junc</u>	splay (mutations diplayed) uently occurring AA	1. Alignment for V	CDR3-IMGT] lengths and AA JUNCTION	<u>on</u>
				Closest V-REGIONs (evaluat	ted from the V-REGION first nucleotide to the 2r	d-CYS codop)



_seq_80	gaggtgcagctggtggagtctgggcct
09 IGHV1-58*01	c-aacc
9438 IGHV1-58*02	c-aacc
09 IGHV1-3*01	cg
07 IGHV1-3*02	ctcg
37 IGHV1-8*01	cg
	-

	 New functionalities include: analysis of sequences by batch of 50 synthesis view
	 advanced parameters
IMGT/V-QUEST	QUERY
Citing IMCTALOUEST: Giudicolli	
citing initiativ-quest. olduitein	Selection of parameters for the results
■ You are in the new IMG	Display type : HTML 🔽 Nb of nucleotides per line in alignment: 60 🔽
NEW!	
The IMGT/V-QUEST now works o	O A. Detailed view
You therefore need to add ">" foll	
format) so the tool is able to sep rectangle "Selection of paramete	
You can also chose to see the "S	2. Alignment for D-GENE 6. V-REGION alignment according to the IMGT numbering
batch of sequences expressing a	3. ☑ Alignment for J-GENE 7. ☑ V-REGION translation ○ IMGT Collier de Perles (PNG format, slow) 4. ☑ Results of IMGT/JunctionAnalysis 8. ☑ V-REGION mutation table ○ no IMGT Collier de Perles
A n almaa mann Tuunuu a al	🔿 with full list of all within D. OFNICA 💦 0. 🔲 V. DEOLON wutsting statistics
Analyse your Immunogl	without list of eligible D-GENEs 10. <u>V-REGION mutation hot spots</u>
	12. 🔲 Sequences of V-, V-J- or V-D-J- REGION ('nt' and 'AA') with gaps in FASTA 13. 🔲 Annotations by IMGT/Automat
Your selection: Human	Access to IMGT/PhyloGene for V-REGION ('nt')
Your sequences are compared to	
Nucleotide sequences	
Enter your companyor(o) in EACTA	1. Image: Alignment for V-GENEs 5. Image: V-REGION protein display (with color)
Enter your sequence(s) in <u>FASTA</u>	
Type (or copy/paste) your see	3. ☑ V-REGION translation 7. ☑ V-REGION most frequently occurring AA 4. ☑ V-REGION protein display 8. ☑ Results of IMGT/JunctionAnalysis
>user_seq_80 gaggtgcagctggtggagtctgggcc	
>user_seq_42	Advanced parameters
caaatgcagctggtgcagtctgggcc >user_seq_33	
atggactggatttggaggatcctctt	Selection of IMGT reference F+ORF+ in frame P Selectory set
>user_seq_22 atggactggatttggaggatcctctt	directory set
	default 😒 in 3V-REGION
<	Selection of parameters for IMGT/JunctionAnalysis Nb of D-GENEs in IGH JUNCTIONS (default is 1) default Number of accepted mutations: default in D-REGION
	default 💟 in 5'J-REGION

Or give the path access to a l

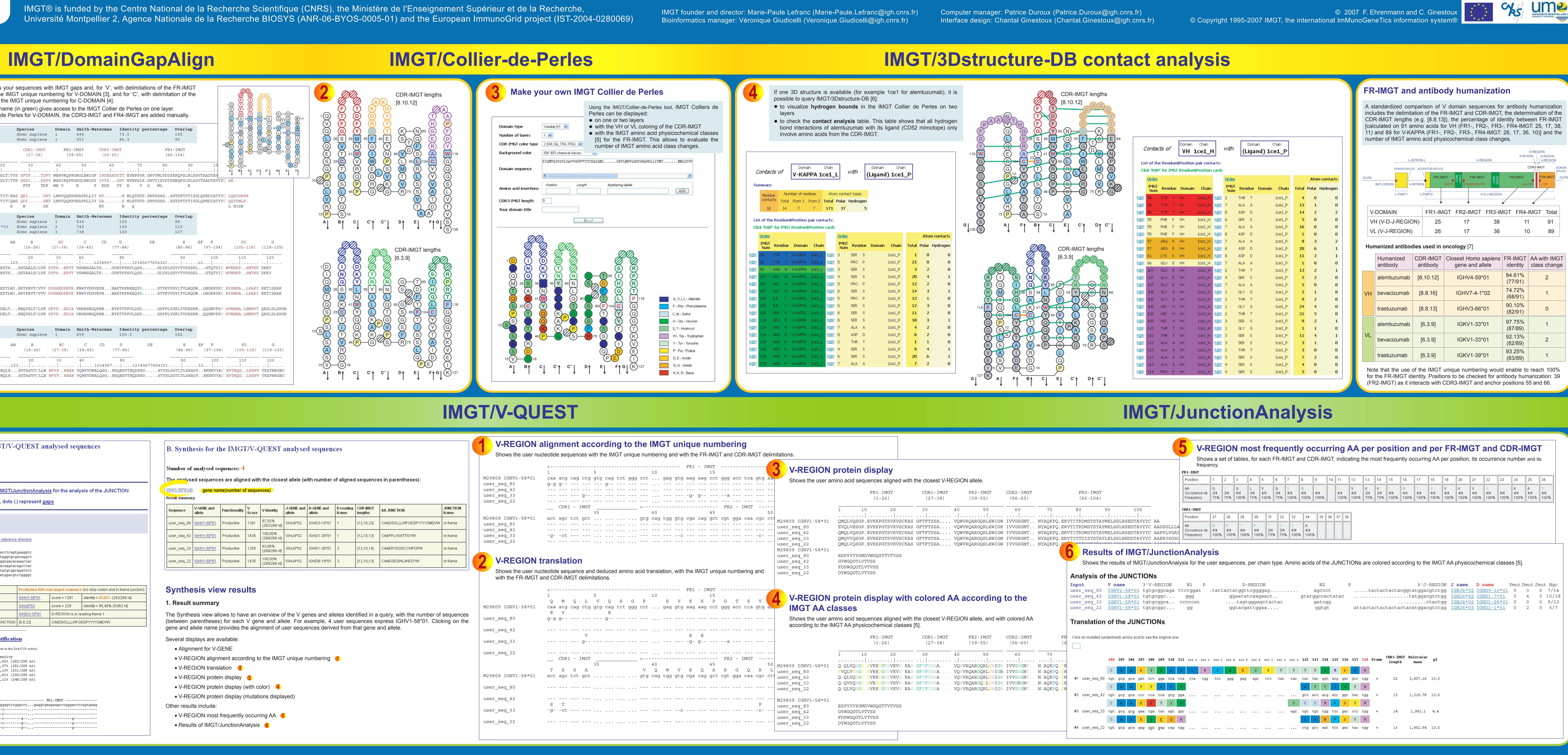
Start Clear the form

Nb of nucleotides to exclude in 5' of the V-REGION for the Nb of nucleotides to add (or exclude) in 3' of the V-REGION for the evaluation of the nb of mutations (in results 8 evaluation of the alignment score (in result 1) More options for Detailed view

IMGT unique numbering and tools for antibody humanization and engineering

Quentin Kaas, François Ehrenmann, Véronique Giudicelli, Patrice Duroux and Marie-Paule Lefranc

IMGT®, the international ImMunoGeneTics information system®, LIGM, Université Montpellier 2 CNRS UPR1142, IGH 141 rue de la Cardonille, 34396 MONTPELLIER cedex 05, France Marie-Paule.Lefranc@igh.cnrs.fr



ed sequences	B. Synth	esis for t	he IMG1	[/V-Q	QUEST	analyse	d sequen	ces				V-REGION a Shows the user number	-
he analysis of the JUNCTION		y: V-GENE and allele	es are aligne ne(number of Functionality	ed with <mark>f seque</mark>	nces) V Identity 97,92% (282/288 nt)	J-GENE and allele	ith number of allele	D reading	-	es in parentheses):	JUNCTION frame in frame	M29809 IGHV1-58*01 user_seq_80 user_seq_42 user_seq_33 user_seq_22 M29809 IGHV1-58*01 user_seq_80 user_seq_42	< 1 caa atg ca g-g g CDR1 act agc ta
	user_seq_42 user_seq_33	<u>IGHV1-58*01</u> <u>IGHV1-58*01</u>	Productive Productive	1435 1255	100,00% (288/288 nt) 93,06% (268/288 nt)		IGHD1-26*01 IGHD1-26*01	1 3	[12,10,13] [12,10,14]	CAAPPLVGATTIGYW CAAERYSGSCCWFDPW	in frame in frame	user_seq_33 user_seq_22	-gct -
d sequence(no stop codon and in frame junction)= 1381identity = 97,92% (282/288 nt)= 229identity = 85,48% (53/62 nt)	Synthe 1. Result	e <mark>sis vie</mark> summary		Ilts								Shows the user nue with the FR-IMGT a M29809 IGHV1-58*01	•
ON is in reading frame 1 GLLLWFGESPYYYYGMDVW	(between p gene and a Several dis • Alignr • V-REC	parentheses allele name splays are a ment for V-0 GION alignr	 for each provides th vailable: SENE ment accore 	V ger le aligr	ne and all nment of u	ele. For e iser seque	example, 4	user seq ed from t	uences ex	query, with the number of xpress IGHV1-58*01. Clic and allele.	•	1100r 000	E V g-g g CDR1
	• V-RE(• V-RE(GION trans GION prote GION prote GION prote	in display in display (with co		ayed)						M29809 IGHV1-58*01 user_seq_80 user_seq_42	T S S act agc to
g		lts include: GION most lts of IMGT/			•	5						user_seq_33 user_seq_22	S T -gct

http://imgt.cines.fr

system®

Information

Mun

(jene

	Humanized antibody	CDR-IMGT antibody	Closest <i>Homo sapiens</i> gene and allele	FR-IMGT identity	AA with IMGT class change
	alemtuzumab	[8.10.12]	IGHV4-59*01	84.61% (77/91)	2
VH	bevacizumab	[8.8.16]	IGHV7-4-1*02	74.72% (68/91)	1
	trastuzumab	[8.8.13]	IGHV3-66*01	90.10% (82/91)	0
	alemtuzumab	[6.3.9]	IGKV1-33*01	97.75% (87/89)	1
VL	bevacizumab	[6.3.9]	IGKV1-33*01	92.13% (82/89)	2
	trastuzumab	[6.3.9]	IGKV1-39*01	93.25% (83/89)	1

			ION et of tab			-							-				-								
	freque fraque			nes, 10		1 Г Г -11	IVIG I a			וו כו, ווו	luicatii	ig the i	1051 1	liequei		currin	у АА р		SILIOIT,	115 00	currer		unnder		5
Ĩ	Position	1	2 3	4	5	6	7	8	9	10 11	1 12	2 13	14	15	16	17	18	19	20	21	22	23	24	25	26
FR3-IMGT (66-104)	AA Occurence nb Frequency	Q 3/4 75%	M Q 3/4 4/4 75% 10	L 3/4 0% 75%	V 4/4 100%	Q 3/4 75%			P 4/4 100%		/4 4/ 00% 10		K 3/4 75%	P 4/4 100%	G 4/4 100%		S 4/4 100%		K 4/4 100%	V 4/4 100%		C 4/4 100%	K 4/4 100%	A 4/4 100%	S 4/4 100%
80 90 100	CDR1-IMGT								L	I							•	1	I		L				
	Position	27	28	29 3	0 3	31 32	33	34	35	36 37	7 38														
TRDMSTSTAYMELSSLRSEDTAVYYC AA TRDMSTSTAYMELSSLRSEDTAVYYC AADSGLLLW TRDMSTSTAYMELSSLRSEDTAVYYC AAPPLVGAT TTDISTSTAYLELSSLRNDDTAVYYC AAERYSGSC	AA Occurence nb Frequency	G 4/4 100%				- 8 3/4 3/4 75% 75	S 4 4/4 3% 1009	A 4/4 % 1009	%																
nput V name 3'V-REGION	N1 P		·	D-REG	SION				N2		P				-	5'J-	REGIO	N J I	name	Dn	ıame	V		mut Ji 0	
nalysis of the JUNCTIONsoputV name3'V-REGIONser_seq_80IGHV1-58*01tgtgcggcagattser_seq_42IGHV1-58*01tgtgcggctgtgcggcaser_seq_33IGHV1-58*01tgtgcggcacser_seq_22IGHV1-58*01tgtgcggcc		ISER S	tactatg ggaa	D-REG	FION gggag agaac jagcta	(t actac		gtate		t ctata g	P ac	Ns are	actac	ctacta	cggta ta	5'J- tggac tggac c	REGIO gtctg gtctg tactg	N J 1 g <u>IGH</u> g <u>IGH</u> g <u>IGH</u>	name HJ6*0 HJ6*0 HJ4*0	D n 02 IGH 02 IGH 02 IGH		V)*01 <u>*01</u> 5*01		omut Ji 0 4 0 2	0 7/ 0 10/ 0 9/
Analysis of the JUNCTIONSnputV name3'V-REGIONser_seq_80IGHV1-58*01tgtgcggcagattser_seq_42IGHV1-58*01tgtgcggctgtgcggcaser_seq_33IGHV1-58*01tgtgcggcacser_seq_22IGHV1-58*01tgtgcggcc	N1 P tctggat ggg ccccat	ISER S	tactatg ggaa	D-REG gttcgg tatcaa agtggg	FION gggag agaac jagcta	(t actac		gtate	N2 agccc ggccac gatcg	t ctata g	P ac	t	actac	ctacta	cggta ta	5'J- tggac tggac c	REGIO gtctg gtctg tactg	N J 1 g <u>IGH</u> g <u>IGH</u> g <u>IGH</u>	name HJ6*0 HJ6*0 HJ4*0	D n 02 IGH 02 IGH 02 IGH	1 ame ID3-10 ID1-7* ID1-26	V)*01 <u>*01</u> 5*01		0 4	0 7/3 0 10/ 0 9/3
Analysis of the JUNCTIONSnputV name3'V-REGIONser_seq_80IGHV1-58*01tgtgcggcagattser_seq_42IGHV1-58*01tgtgcggctgtgcggcaser_seq_33IGHV1-58*01tgtgcggcacser_seq_22IGHV1-58*01tgtgcggccranslation of the JUNCTIONS	N1 P tctggat ggg ccccat	ISER S	tactatg ggaa	D-REG gttcgg tatcaa agtggg	FION gggag agaac jagcta	(t actac		gtate	N2 agccc ggccac gatcg	t ctata g	P ac	t	actac	ctacta	cggta ta	5'J- tggac tggac c	REGIO gtctg gtctg tactg	N J 1 g <u>IGH</u> g <u>IGH</u> g <u>IGH</u>	name HJ6*0 HJ6*0 HJ4*0	D n 02 IGH 02 IGH 02 IGH	1 ame ID3-10 ID1-7* ID1-26	V)*01 <u>*01</u> 5*01		0 4	0 10/ 0 9/:
nalysis of the JUNCTIONSoputV name3'V-REGIONser_seq_80IGHV1-58*01tgtgcggcagattser_seq_42IGHV1-58*01tgtgcggctgtgcggcaser_seq_33IGHV1-58*01tgtgcggcacser_seq_22IGHV1-58*01tgtgcggctgtgcggcser_seq_22IGHV1-58*01tgtgcggccser_seq_22IGHV1-58*01tgtgcggcc	N1 P totggat ggg coccat gg	.tatt	ggaa ta ggta	D-REG gttcgg tatcaa agtggg cgattg	SION gggag agaac gagcta ggaa.	(t actac		gtat	N2 agccc ggccac gatcg ggtgt	t g c	P	t	actac	ctacta	cggta ta ctaca	5'J- tggac tggac C tggac	REGIO gtctg gtctg tactg gtctg	N J 1 g <u>IGH</u> g <u>IGH</u> g <u>IGH</u>	name HJ6*0 HJ6*0 HJ4*0	D n 02 IGH 02 IGH 02 IGH	1 ame ID3-10 ID1-7* ID1-26	V)*01 <u>*01</u> 5*01		0 4	0 7/: 0 10/ 0 9/:
put V name 3'V-REGION er_seq_80 IGHV1-58*01 tgtgcggcaga tt er_seq_42 IGHV1-58*01 tgtgcggca tgtgcggca c er_seq_33 IGHV1-58*01 tgtgcggca c er_seq_22 IGHV1-58*01 tgtgcggca c er_seq_22 IGHV1-58*01 tgtgcggca c cer_seq_22 IGHV1-58*01 tgtgcggca c cer_seq_23 IGHV1-58*01 tgtgcggca c cer_seq_23 IGHV1-58*01 tgtgcggca c cer_seq_33 IGHV1-58*01 tgtgcggca c cer_seq_34 IGHV1-58*01 tgtgcggca c cer_seq_35 IGHV1-58	N1 P totggat ggg coccat gg	.tatt	ggaa ta ggta	D-REG gttcgg tatcaa agtggg cgattg	SION gggag agaac gagcta ggaa.	(t actac		gtat	N2 agccc ggccac gatcg ggtgt	t g c	P	t	actac	ctacta 	cggta ta ctaca	5'J- tggac tggac tggac tggac	REGIO gtctg gtctg tactg gtctg	N J 1 g <u>IGH</u> g <u>IGH</u> g <u>IGH</u>	name HJ6*0 HJ6*0 HJ4*0	D n 02 IGH 02 IGH 02 IGH	1 ame ID3-10 ID1-7* ID1-26	V)*01 <u>*01</u> 5*01		0 4	0 7/3 0 10/ 0 9/3
malysis of the JUNCTIONS opt V name 3'V-REGION er_seq_80 IGHV1-58*01 tgtgcggcaga tt er_seq_42 IGHV1-58*01 tgtgcggca tgtgcggca td er_seq_33 IGHV1-58*01 tgtgcggca tgtgcggca td er_seq_22 IGHV1-58*01 tgtgcggca td td tdtscgcggc IGHV1-58*01 tgtgcggc td td Itck on mutated (underlined) amino acid to see the original one: I I I C A A D S <td>N1 P totggat ggg coccat gg</td> <td>.tatt</td> <td>ggaa ta ggta</td> <td>D-REG gttcgg tatcaa agtggg cgattg</td> <td>SION gggag agaac gagcta ggaa.</td> <td>(t actac</td> <td></td> <td>gtat</td> <td>N2 agccc ggccac gatcg ggtgt</td> <td>t g t 115</td> <td>P</td> <td>t</td> <td>actac</td> <td>ctacta </td> <td>cggta ta ctaca GT Mol</td> <td>5'J- tggac tggac tggac tggac</td> <td>REGIO gtctg gtctg gtctg gtctg</td> <td>N J 1 g <u>IGH</u> g <u>IGH</u> g <u>IGH</u></td> <td>name HJ6*0 HJ6*0 HJ4*0</td> <td>D n 02 IGH 02 IGH 02 IGH</td> <td>1ame ID3-10 ID1-7* ID1-26</td> <td>V)*01 <u>*01</u> 5*01</td> <td></td> <td>0 4</td> <td>0 7/1 0 10/ 0 9/1</td>	N1 P totggat ggg coccat gg	.tatt	ggaa ta ggta	D-REG gttcgg tatcaa agtggg cgattg	SION gggag agaac gagcta ggaa.	(t actac		gtat	N2 agccc ggccac gatcg ggtgt	t g t 115	P	t	actac	ctacta 	cggta ta ctaca GT Mol	5'J- tggac tggac tggac tggac	REGIO gtctg gtctg gtctg gtctg	N J 1 g <u>IGH</u> g <u>IGH</u> g <u>IGH</u>	name HJ6*0 HJ6*0 HJ4*0	D n 02 IGH 02 IGH 02 IGH	1 ame ID3-10 ID1-7* ID1-26	V)*01 <u>*01</u> 5*01		0 4	0 7/1 0 10/ 0 9/1
Analysis of the JUNCTIONS nput V name 3'V-REGION ser_seq_80 IGHV1-58*01 tgtgcggcaga tt ser_seq_42 IGHV1-58*01 tgtgcggca c ser_seq_33 IGHV1-58*01 tgtgcggca c ser_seq_22 IGHV1-58*01 tgtgcggca c franslation of the JUNCTIONS Idt 105 106 107 108 109 110 11 c A A D S G L L	N1 P totggat ggg coccat gg	.tatt	ggaa ta ggta	D-REG gttcgg tatcaa agtggg cgattg	SION gggag agaac gagcta ggaa.	(t actac		gtat	N2 agccc ggccac gatcg ggtgt	t g t 115	P aC 116 1: D gac g	t	actac	CDR3-IN lengt	cggta ta ctaca Ctaca	5'J- tggac tggac tggac tggac	REGIO gtctg gtctg gtctg gtctg 13.0	N J 1 g <u>IGH</u> g <u>IGH</u> g <u>IGH</u>	name HJ6*0 HJ6*0 HJ4*0	D n 02 IGH 02 IGH 02 IGH	1 ame ID3-10 ID1-7* ID1-26	V)*01 <u>*01</u> 5*01		0 4	0 7/ 0 10/ 0 9/