

Online tools for interpretation of IG sequences

Marie-Paule Lefranc

**3rd Educational Workshop on Immunoglobulin Gene Analysis
in Chronic Lymphocytic Leukemia**

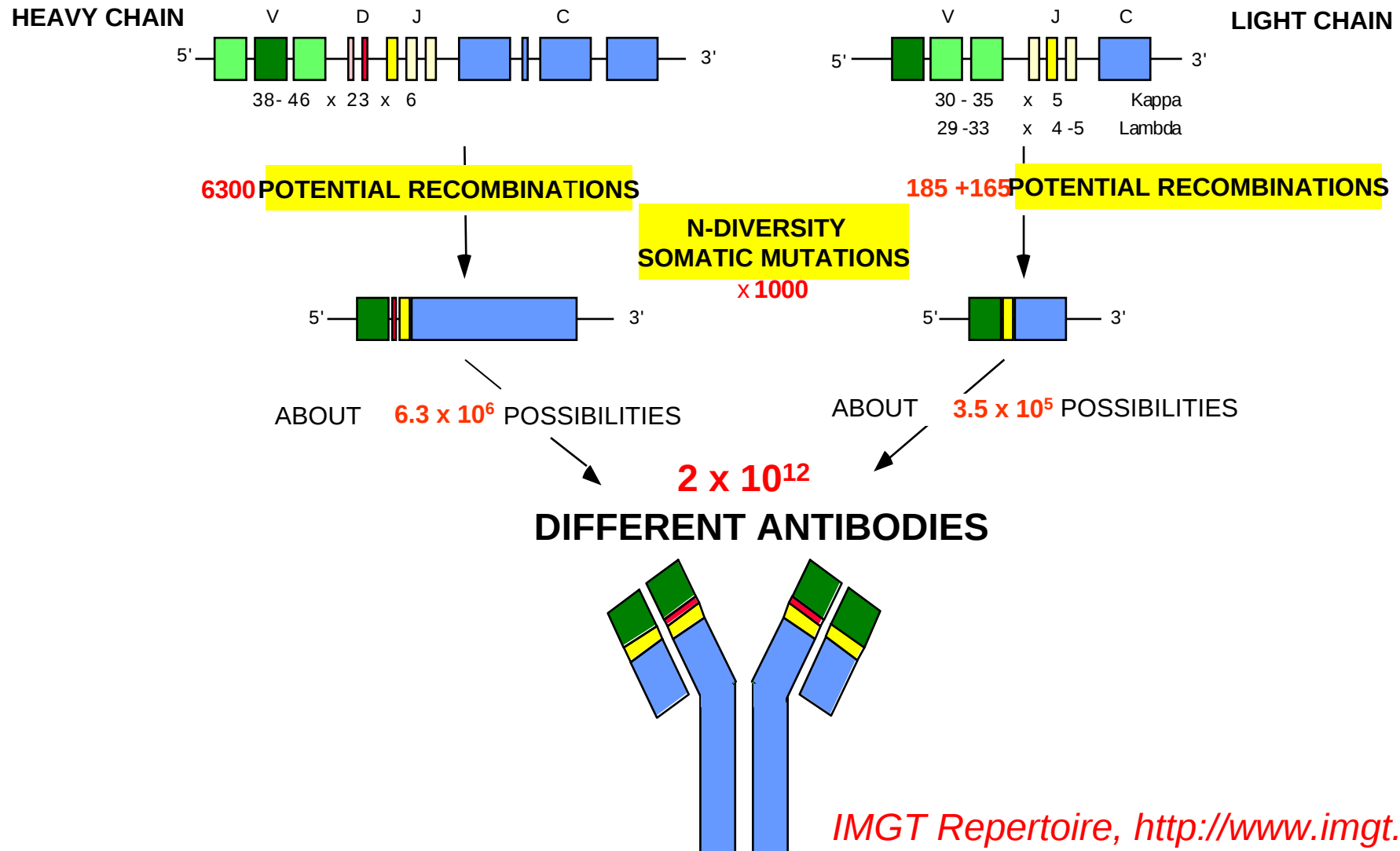
24-25 September 2009 - Thessaloniki, Greece

Outline

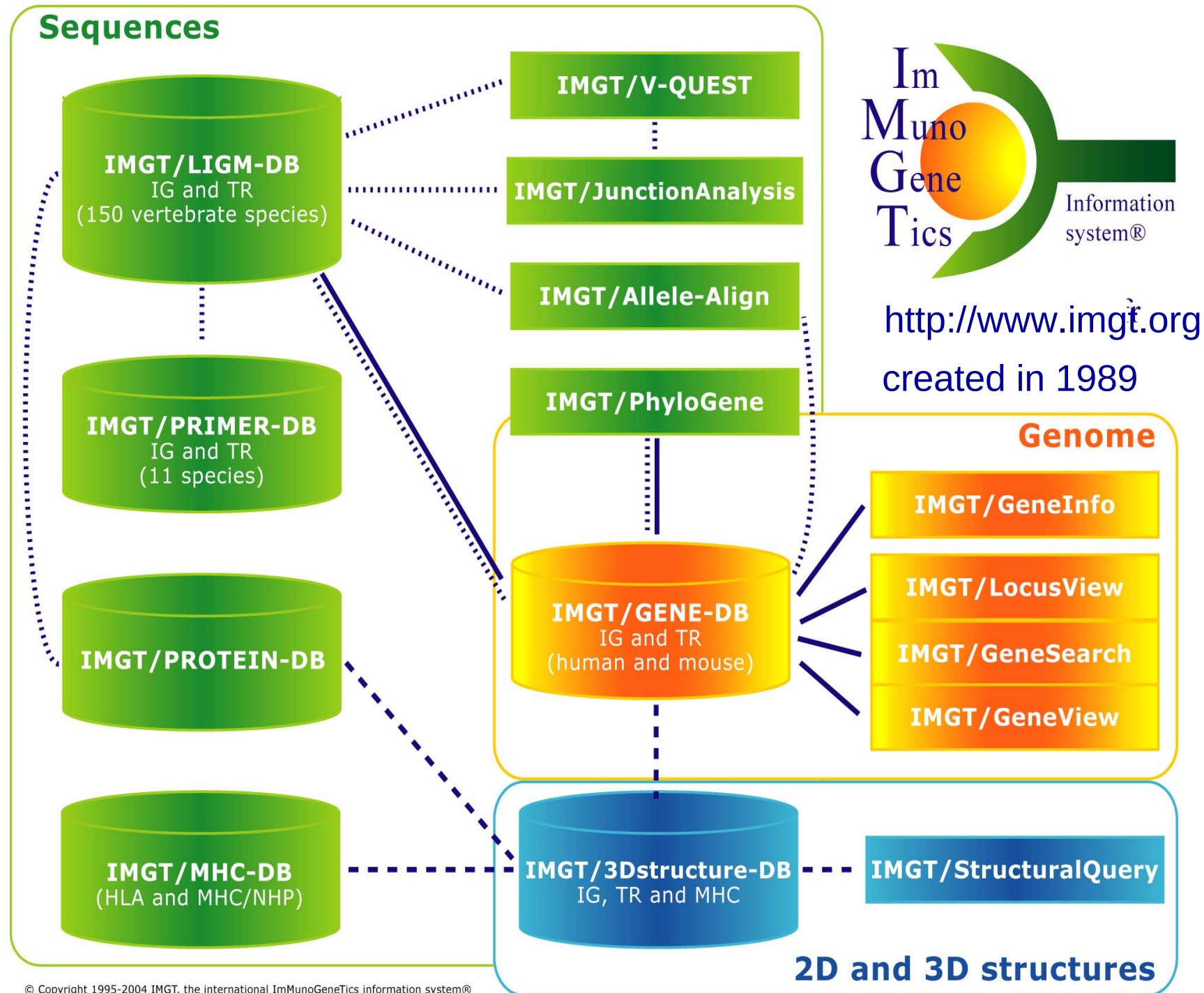
- IMGT® standards based on IMGT-ONTOLOGY
 - classification: gene nomenclature
 - description: labels et prototypes
 - numerotation: IMGT unique numberingIMGT Collier de Perles
- IMGT/JunctionAnalysis
IMGT/V-QUEST
IMGT/Collier-de-Perles
IMGT/DomainGapAlign
IMGT/3Dstructure-DB

Immunoglobulin (IG) synthesis

150 FUNCTIONAL IG GENES



Sequences

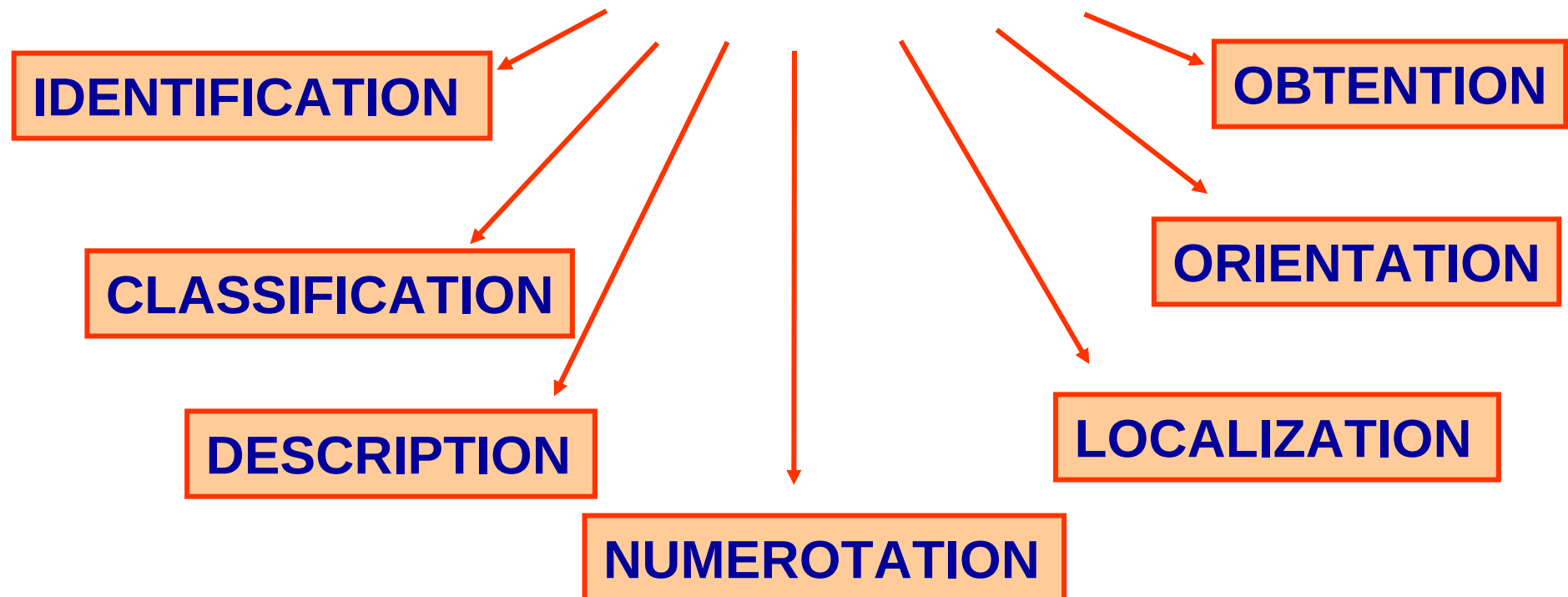


IMGT-ONTOLOGY

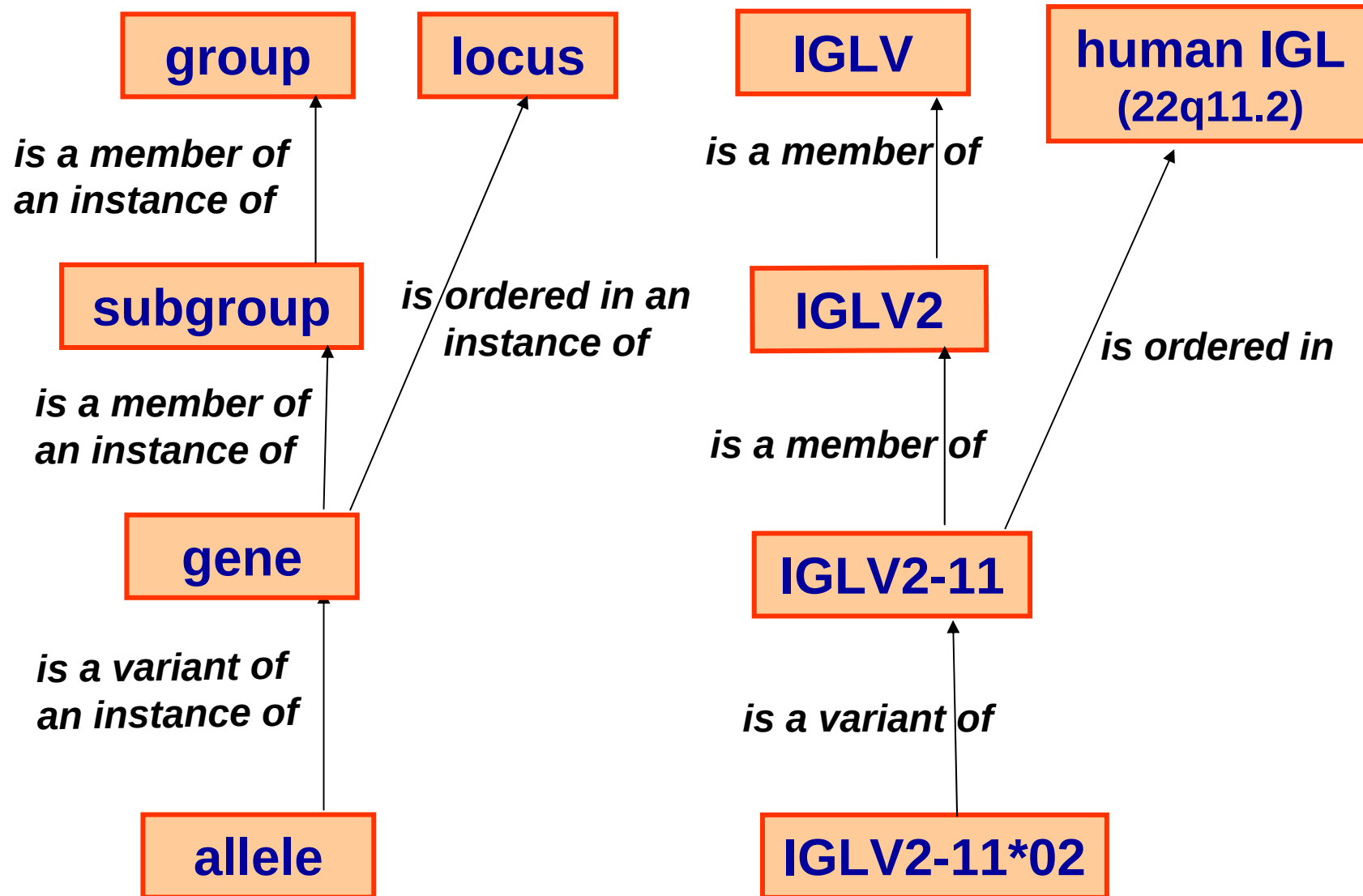
axioms and concepts

IMGT-ONTOLOGY seven axioms:

To share, reuse and represent knowledge
in Immunogenetics and Life Sciences



CLASSIFICATION axiom



« Concepts »

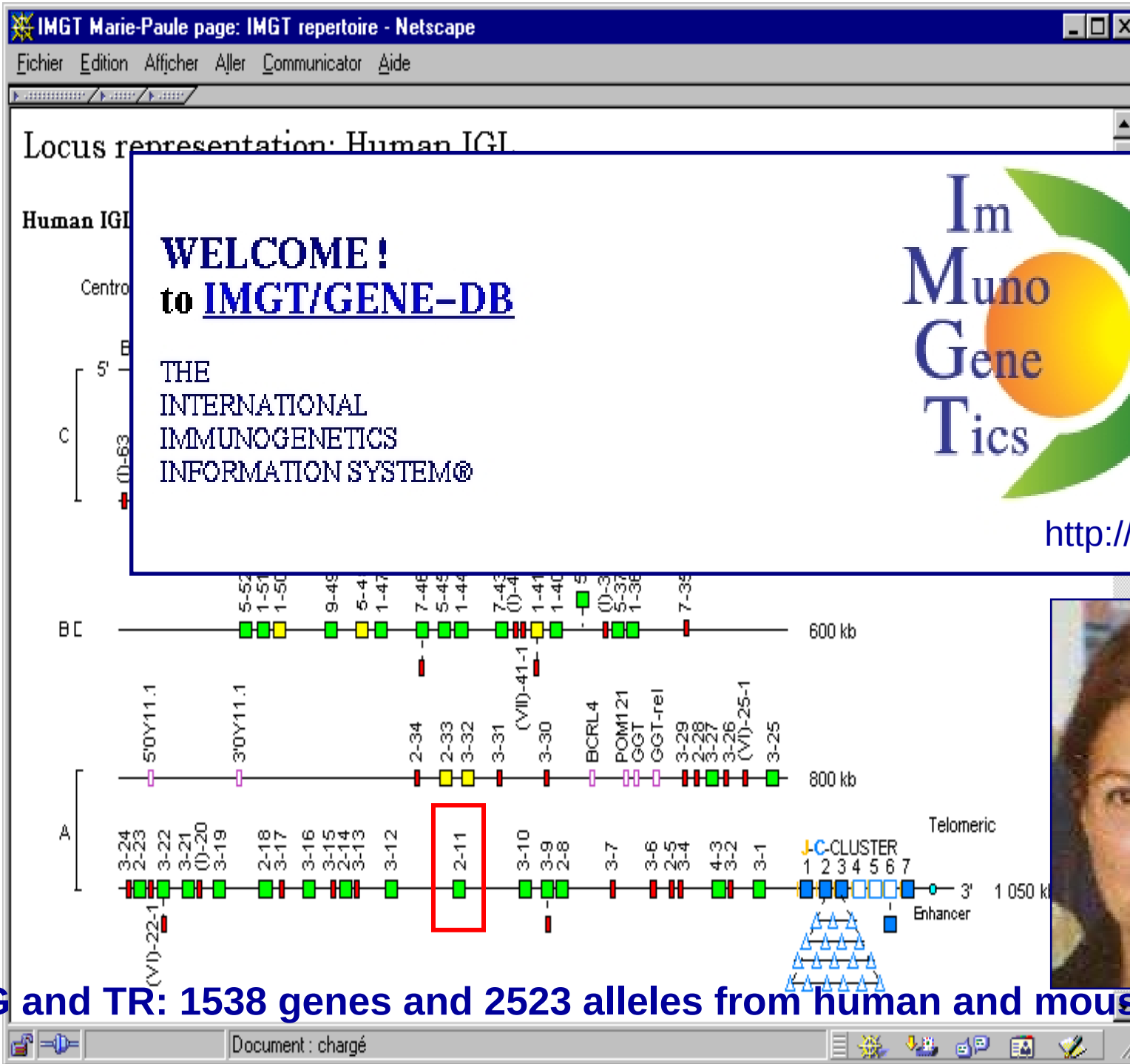
« Instances »

CLASSIFICATION axiom

1. The IMGT-ONTOLOGY main concepts of classification
 - include 'group', 'subgroup', 'gene', 'allele'.
 - have allowed to set up the nomenclature of the immunoglobulin (IG) genes (V, D, J, C genes).
2. IMGT gene names have been approved by the HUGO Nomenclature Committee (HGNC) in 1999.
3. New alleles are validated by the WHO-IUIS/IMGT nomenclature committee and entered in IMGT/GENE-DB.
4. IMGT/GENE-DB is the international reference database for IG genes (direct links from NCBI Entrez Gene) and alleles.

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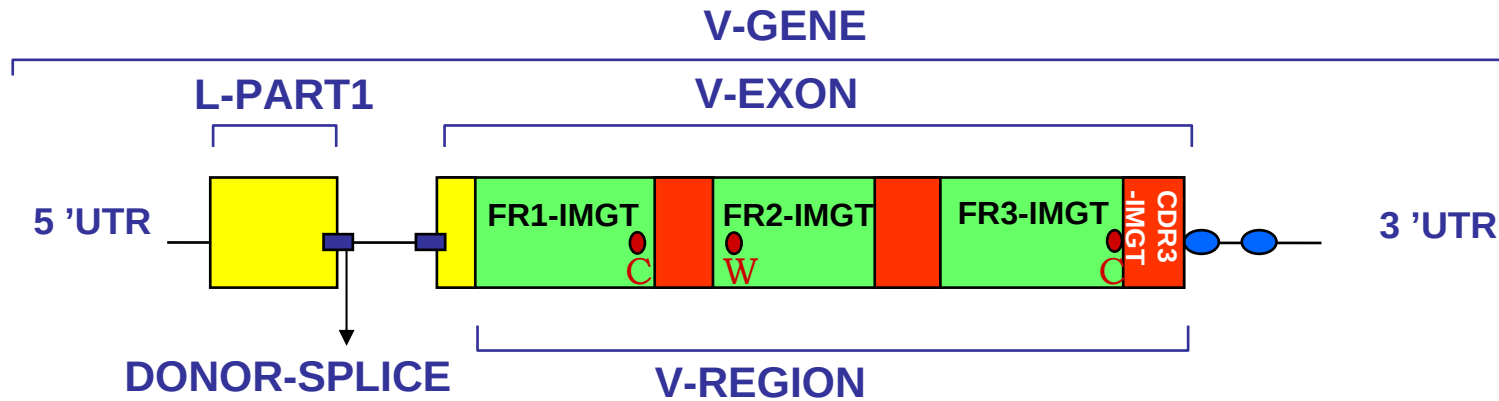
<http://www.imgt.org>



IG and TR: 1538 genes and 2523 alleles from human and mouse

DESCRIPTION axiom

PROTOTYPE for a V-GENE



Label 1

Label 2

Relations entre Labels

V-GENE

V-EXON



FR3-IMGT

CDR3-IMGT



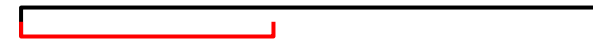
L-PART1

DONOR-SPLICE



V-REGION

FR1-IMGT



V-REGION

CDR3-IMGT



DESCRIPTION axiom

1. The IMGT-ONTOLOGY concepts of description:
 - comprise the **standardized IMGT labels** and their **relations**.
 - have allowed **to describe** the IG (or antibody) sequences and structures, **whatever the chain type or the species**.
2. **IMGT labels** are used in all IMGT® databases and tools for the description of:
 - **nucleotide** and **amino acid** sequences (IMGT/LIGM-DB...)
 - **2D** and **3D** structures (IMGT/3Dstructure-DB...).
3. Sequence Ontology (**SO**) includes **IMGT labels**.
4. **IMGT® databases** can be queried **using labels** (a big 'plus' compared to generalist databases).

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IMGT/LIGM-DB



<http://www.imgt.org>

**D
E
S
C
R
I
P
T
I
O
N**

IMGT/LIGM-DB Consultation module v3 - Mozilla Firefox		
File	Edit	View
Go	Bookmarks	Tools
Help		
FH	Key	Location/Qualifiers
FH		
FT	L-V-D-J-C-SEQUENCE	<1..375>
FT		/partial
FT		/db_xref="taxon:9606"
FT		/cell_type="B-cell hybridoma 2F7"
FT		/IMGT_note="automatically annotated with IMGT tools"
FT		/organism="Homo sapiens"
FT	V-D-J-REGION	1..375
FT		/translation="QVHLVESGGAVFHPGRSLRLSRAASGFTTFSSYGMHWVRQAP
FT		AKGLEWVAVIWDGSKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC
FT		AKHVTIAAAGRRGAGMDVWGQGTITVTVSS"
FT	V-REGION	1..296
FT		/allele="IGHV3-33*01, putative"
FT		/gene="IGHV3-33"
FT		/CDR_length="[8.8.18]"
FT		/putative_limit="3' side"
FT		/translation="QVHLVESGGAVFHPGRSLRLSRAASGFTTFSSYGMHWVRQAP
FT		AKGLEWVAVIWDGSKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC
FT		AK"
FT	FR1-IMGT	1..75
FT		/AA_IMGT="1 to 26, AA 10 is missing"
FT		/translation="QVHLVESGGAVFHPGRSLRLSRAAS"
FT	CDR1-IMGT	76..99
FT		/AA_IMGT="27 to 34"
FT		/translation="GFTTFSSYG"
FT	FR2-IMGT	100..150
FT		/AA_IMGT="39 to 55"
FT		/translation="MHWVRQAPAKGLEWVAV"
FT	CONSERVED-TRP	106..108
FT	CDR2-IMGT	151..174
FT		/AA_IMGT="56 to 63"
FT		/translation="IWYDGSNK"
FT	FR3-IMGT	175..288
FT		/AA_IMGT="66 to 104, AA 73 is missing"
FT		/translation="YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC"
FT		

137 753 sequences from 236 species

IMGT-ONTOLOGY:

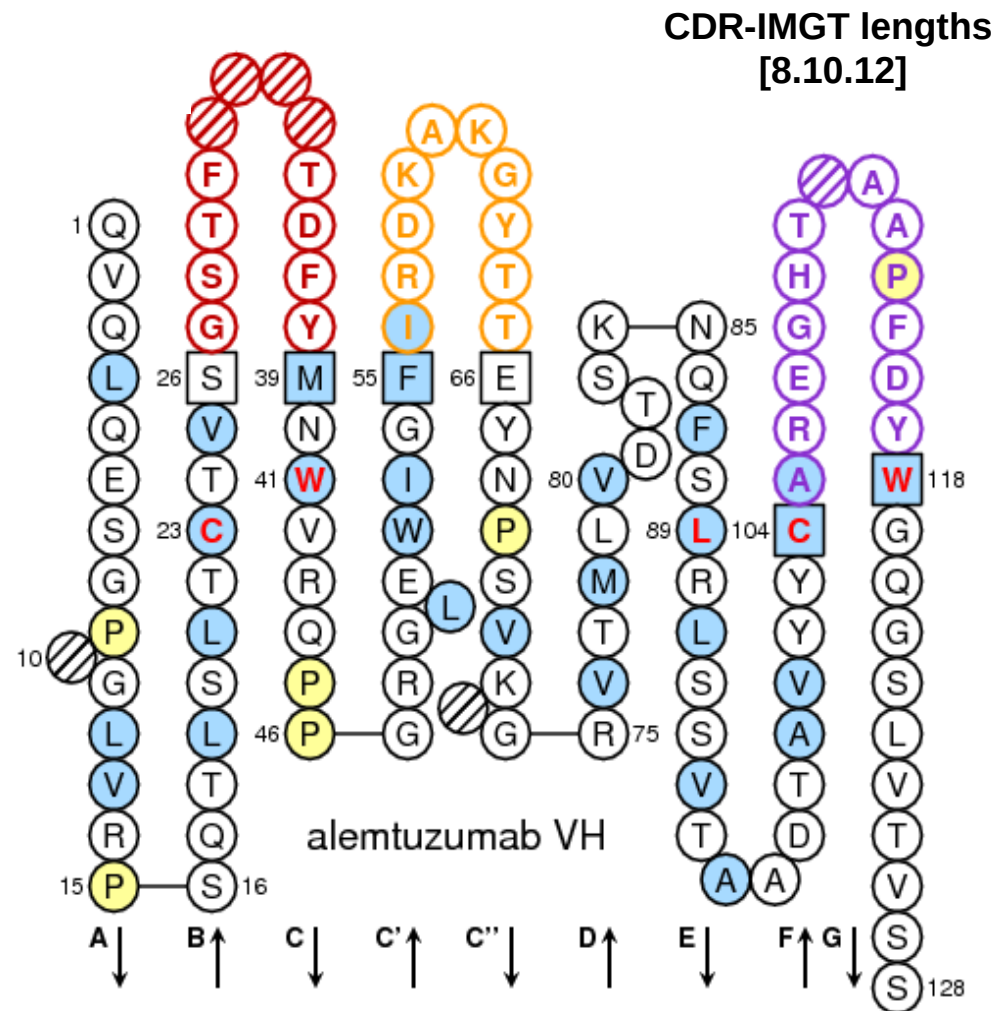
277 IMGT labels for sequences

285 IMGT labels for 3D structures

SO (Sequence ontology):

67 IMGT labels

NUMEROTATION axiom



Lefranc et al. Dev. Comp. Immunol. 27, 55-77 (2003)

NUMEROTATION axiom

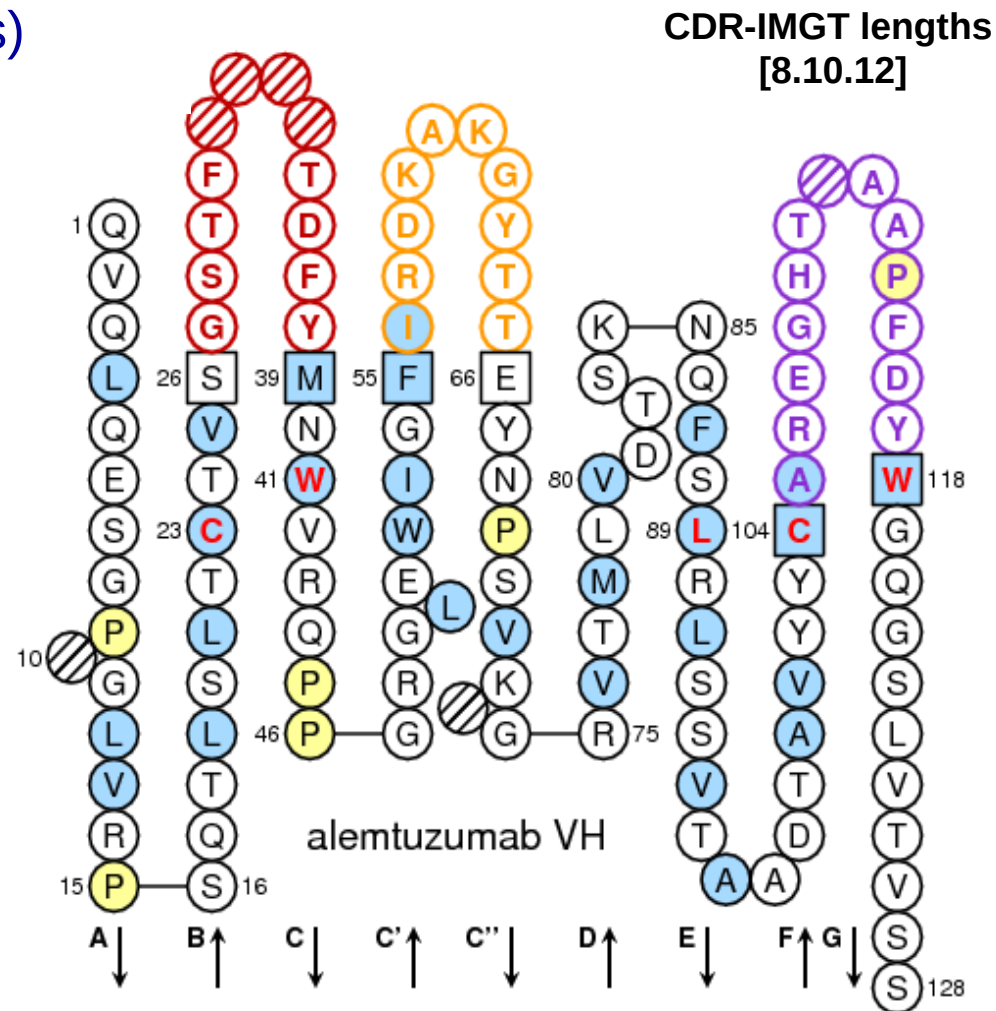
1. IMGT unique numbering

- conserved AA (and codons)
at the same positions:

1st-CYS **23**

2nd-CYS **104**

J-PHE, J-TRP **118**



NUMEROTATION axiom

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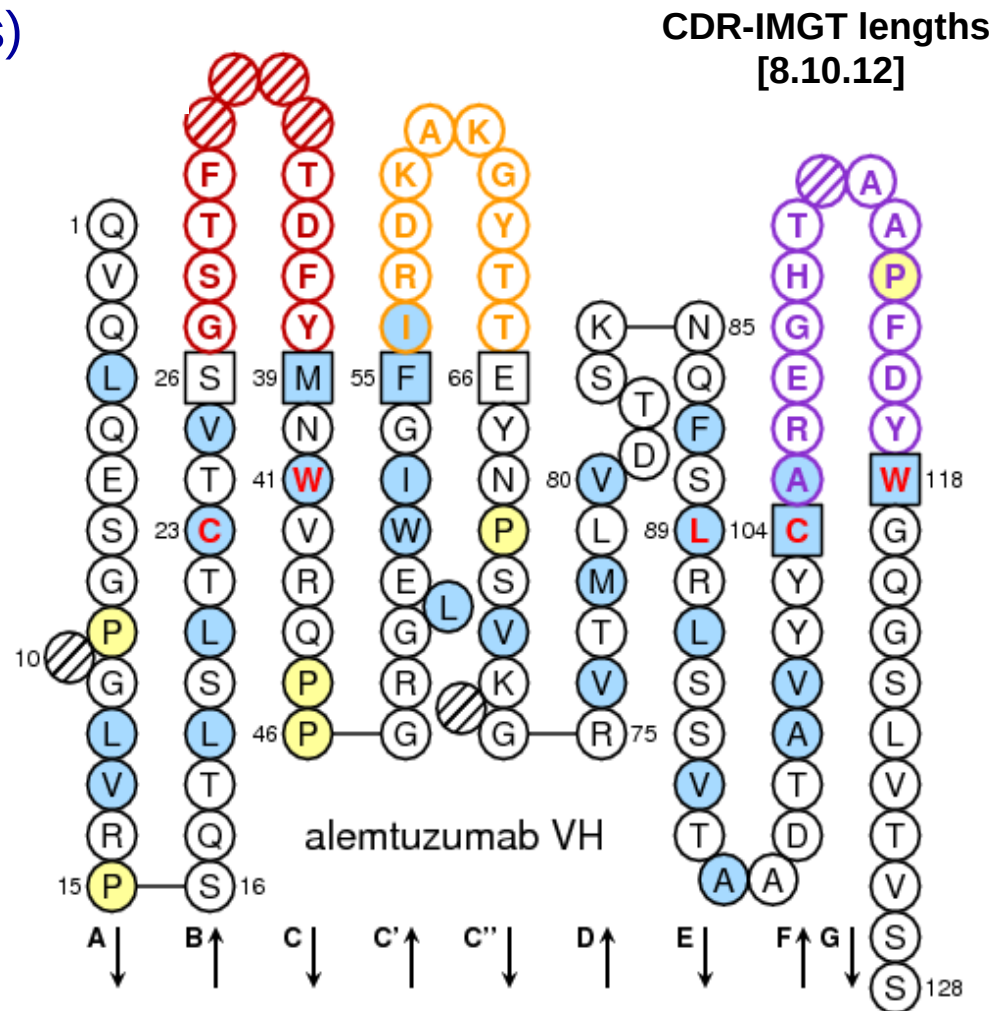
1st-CYS **23**

2nd-CYS **104**

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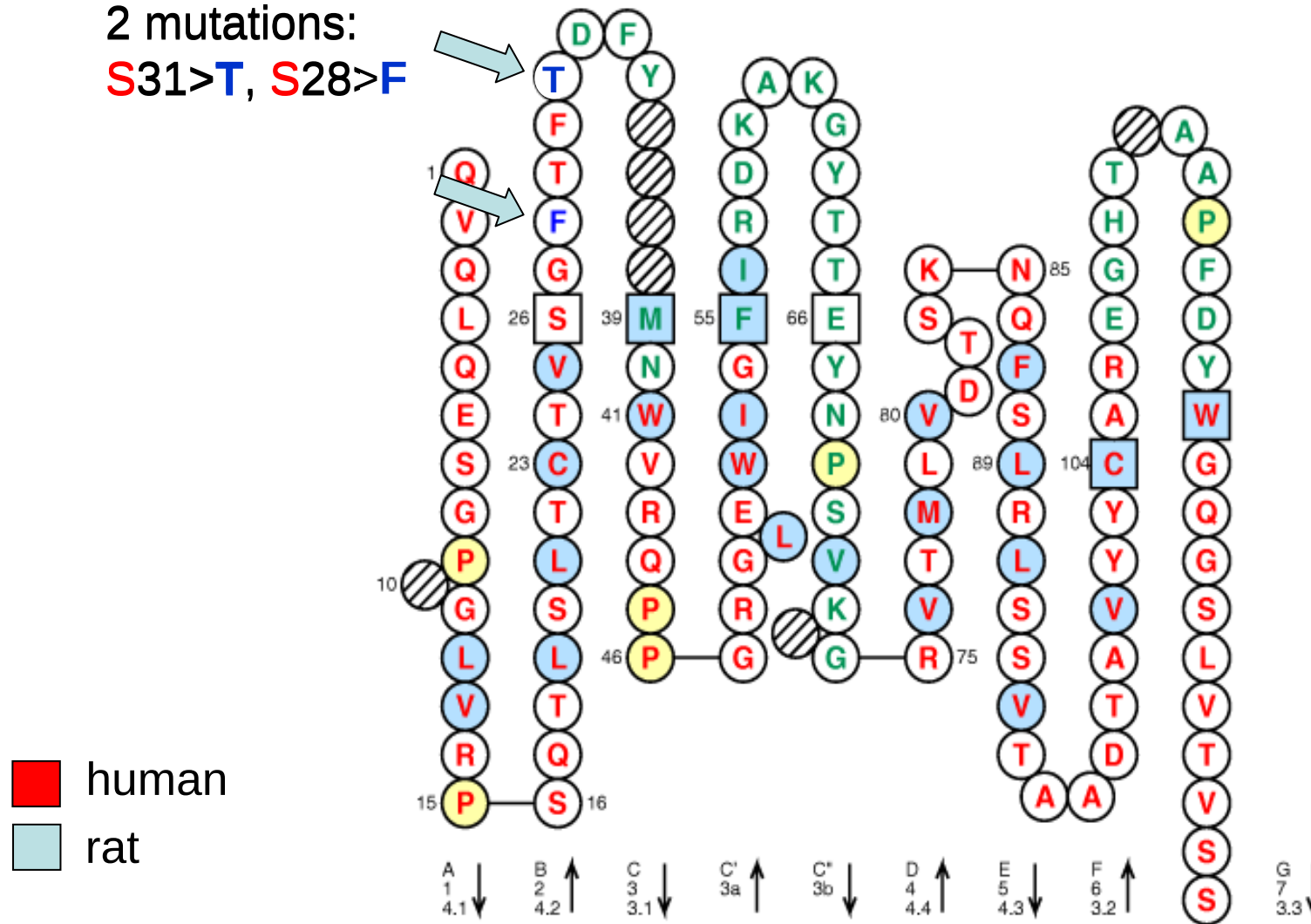
2. IMGT Collier de Perles

- standardized delimitation of
the FR-IMGT and CDR-IMGT.
- CDR-IMGT lengths.



Alemtuzumab

2 mutations:
S31>T, **S28>F**



VH domain
[8.10.12]

NUMEROTATION axiom

1. The IMGT-ONTOLOGY concepts of numerotation include:

- IMGT unique numbering
- IMGT Collier de Perles.

2. The concepts bridge the gap between sequences and 3D structures, at the amino acid (codon) level, for:

- the variable domains (V-DOMAIN)
- the constant domains (C-DOMAIN).

4. The concepts are used for:

- Mutations, polymorphisms
- CDR-IMGT lengths
- contact analysis, paratope definition.

5. WHO-INN programme requires the CDR-IMGT lengths for antibody.

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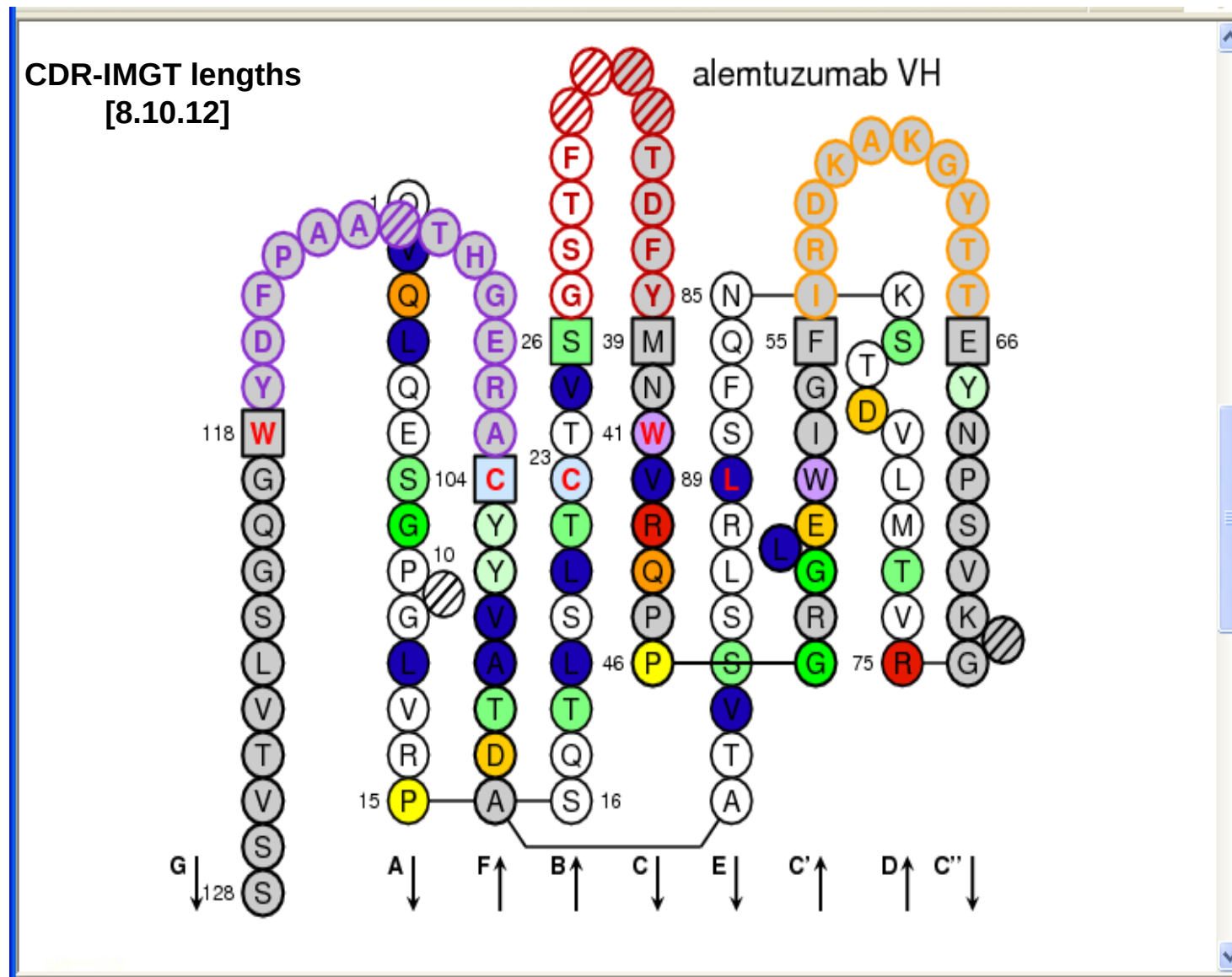
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The eleven IMGT amino acid classes according to the physicochemical properties

'Volume' classes		'Hydropathy' classes			
	in Å ³	Hydrophobic		Neutral	Hydrophilic
Very large	189-228	F	W	Y	
Large	162-174	I L	M		K R
Medium	138-154	V			H E Q
Small	108-117		C	P T	D N
Very small	60-90	A		G S	
		Aliphatic		Hydroxyl	Basic
		Sulfur			Acidic
					Amide
				Uncharged	Charged
					Uncharged
		Nonpolar		Polar	

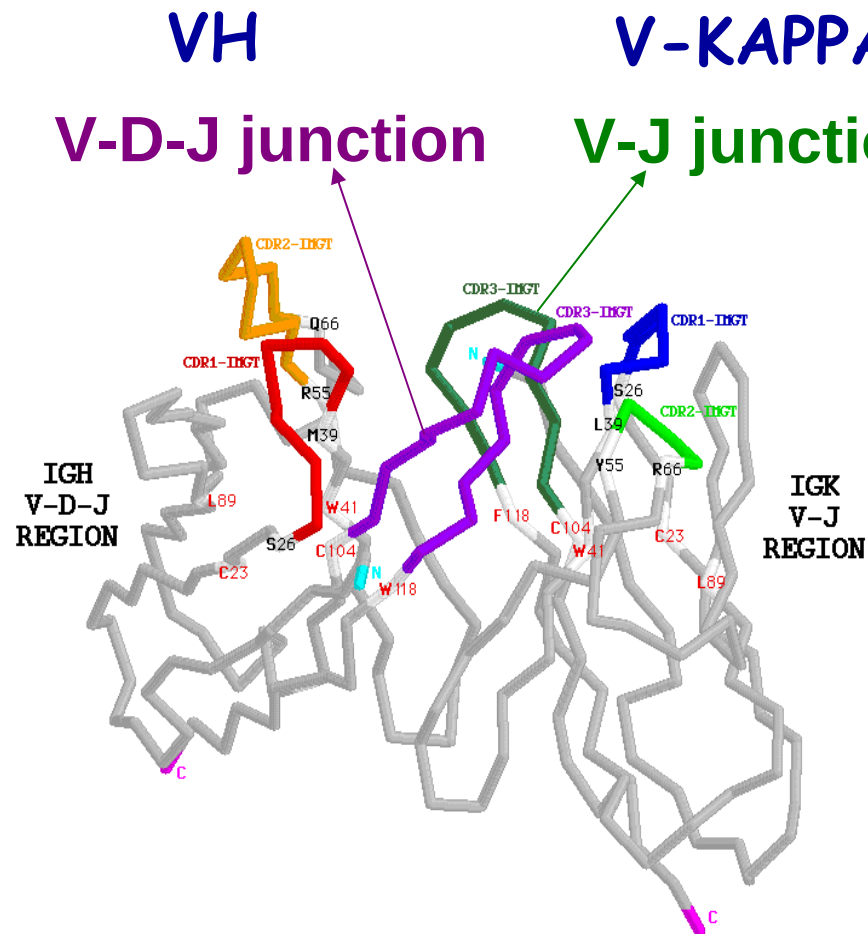
IMGT Collier de Perles amino acid profile

<http://www.imgt.org>

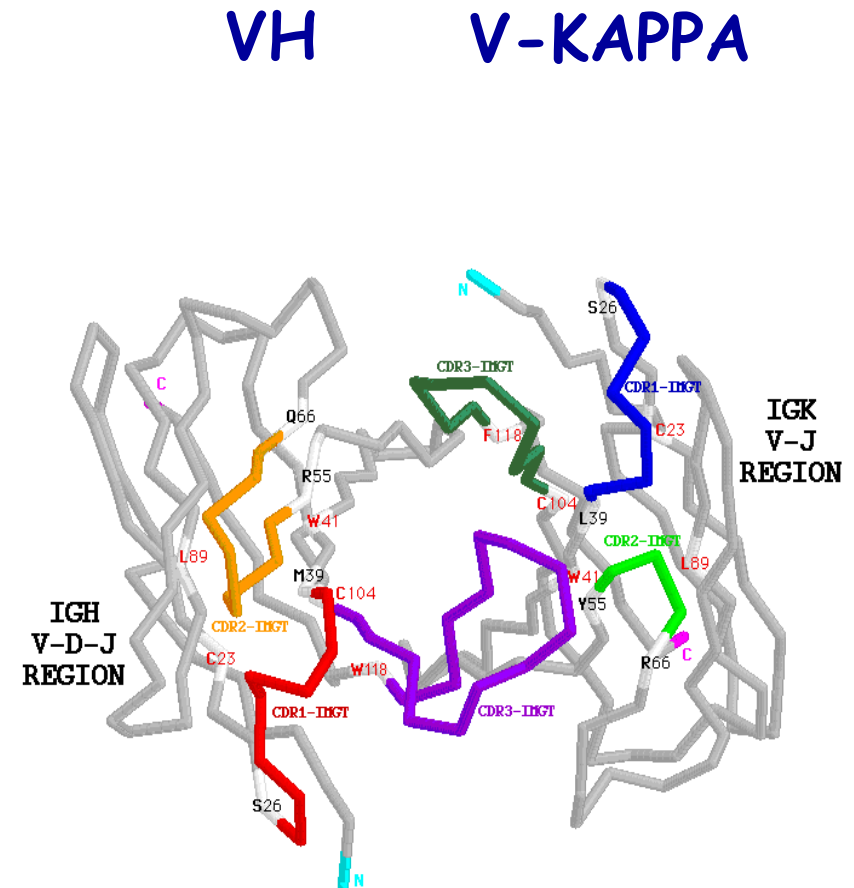


Pommié et al. J. Mol Recognit. 17, 17-32 (2004)

V-DOMAIN: VH and V-KAPPA



Side view of the V-DOMAIN



View from above the CDR-IMGT

CDR3-IMGT= Complementarity determining region (105-117)
V-D-J junction (104-118), V-J junction (104-118)

Immunoglobulin V-D-J generation of sequence diversity



JUNCTION

C A P Y R G D T Y D Y
 S tgt gcg cca tac cgg ggt gac act tat gat tac
 tcc tgg

IMGT/JunctionAnalysis: analysis of the IG and TR junctions

THANK YOU
for using [IMGT/JunctionAnalysis](#)

THE
INTERNATIONAL
IMMUNOGENETICS
INFORMATION SYSTEM®



Analysis of the JUNCTIONS

Input	V name	V-REGION	N1	D-REGION	N2
#1 M62724	IGHV7-4-1*02	tgtgcgagaga	aga	.tagcaatggctacaa....	aata
#2 Z47269	IGHV1-69*06	tgtgcgagag.	ggggggctaagg	tcgaatttttgagtggt.....	tcatgggt

Input	J-REGION	J name	D name	Vmut	Dmut	Jmut	Ngc
#1 M62724	tttgactactgg	IGHJ4*02	IGHD5-24*01	0	2	0	1/7
#2 Z47269	...actggttcgacccctgg	IGHJ5*02	IGHD3-3*02	0	2	0	13/20

Translation of the JUNCTIONS

	104	105	106	107	108	109	110	111	111.1	111.2	111.3	112.4	112.2	112.1	112	113	114	115	116	117	118	CDR3-IMGT frame	length	
#1 M62724	C	A	R	E	D	S	N	G							Y	K	I	F	D	Y	W	+	13	
	tgt	g	c	a	a	a	a	a							tac	aaa	ata	ttt	gac	tac	tgg			
	C	A	R	G	G	A	K	V							G	Y	W	F	D	P	W			
#2 Z47269	tgt	g	c	a	a	a	a	a							cat	ggg	tac	tgg	ttc	gac	ccc	tgg	+	20

IMGT/JunctionAnalysis: analysis of the IG and TR junctions



<http://www.imgt.org>

IMGT/JunctionAnalysis Results

Locus IGH
Species Homo sapiens
IMGTrepertoire link [Locus representation](#)

Maximum number of mutations :
V-REGION : 2; D-REGION : 4; J-REGION : 2
Deletion criterium : Using patterns
Best D gene choice for a same score : Less mutations

Description of the JUNCTIONS

Click on mutated (underscored) nucleotid to see the original one:

Input	V name	V-REGION	P	N1	D-REGION	N2	P	J-REGION	J name	D name	Vmut	Dmut	Jmut	Ngc
#1	Z70256	IGHV2-26*01		tgttgt	gcagcgcctggtac	ccaaatattc		...actttgaccactgg	IGHJ4*02	IGHD6-13*01	1	2	1	5/15
#2	Z70257	IGHV3-7*02		ggatgg	cagctcttatgcc	cgccc		ctactgggtacttcgatctctgg	IGHJ2*01	IGHD2-2*01	0	2	0	9/11
#3	Z70606	IGHV4-31*03		c	.gactacg.....	cact		..atgcttttgatgtctgg	IGHJ3*01	IGHD4-17*01	0	0	0	3/5
#4	Z70608	IGHV4-39*05		cagagta	acgatttttgagtggttatt.....	ccccggggga		..atgcttttgatatactgg	IGHJ3*02	IGHD3-3*01	0	0	0	12/17
#5	Z70610	IGHV4-34*09		tcgggag	cgatttttgagtggttatt.....	cccga	ca	tgatgcttttgatatactgg	IGHJ3*02	IGHD3-3*01	0	0	0	9/12
#6	Z70611	IGHV4-59*01		ca	tggttaactataa.	tgccggcggtg		...actggttcgaccctgg	IGHJ5*02	IGHD3-9*01	0	2	0	9/13
#7	Z70613	IGHV4-59*01			cagcagctggtac	ctccct		...ctttgactactgg	IGHJ4*02	IGHD6-13*01	0	0	0	4/6
#8	Z70614	IGHV4-59*01		cactataa	ttcggggacttat.....	ccctc		gactactgg	IGHJ4*02	IGHD3-16*01	0	2	0	7/14
#9	Z70615	IGHV4-59*01		ggctg	gtaaagaggg.....	tttcggaa		.tactgggtacttcgatctctgg	IGHJ2*01	IGHD5-24*01	0	2	0	7/13
#10	Z70616	IGHV4-34*01		cgg	gtttggg.....	ttccc		...actggttcgaccctgg	IGHJ5*02	IGHD3-16*01	0	0	0	6/8
#11	Z70620	IGHV4-30-4*01		cc	ggggcgggatggtt.....	cgg		.gatgcttttgatatactgg	IGHJ3*02	IGHD3-16*01	1	4	0	5/5
#12	Z70621	IGHV4-39*01		ccacgatttatgg	ttcggggagtt.....	tgaccccc		ttgactactgg	IGHJ4*02	IGHD3-16*01	0	1	0	12/21
#13	Z70622	IGHV4-39*06	t	tgccccgtctctgccaaaat	gtattactatggttcgggga.....	tatgtacg		tttgactactgg	IGHJ4*03	IGHD3-10*01	0	0	0	15/28

IMGT/JunctionAnalysis: analysis of the IG and TR junctions



<http://www.imgt.org>

JUNCTION alignments with translation and IMGT AA classes

Click on mutated (underlined) amino acid to see the original one:

	104	105	106	107	108	109	110	111	111.1	111.2	111.3	112.3	112.2	112.1	112	113	114	115	116	117	118
	C	S	P	G	G	S	<u>A</u>	Y						Y	<u>H</u>	E	<u>H</u>	F	Q	<u>Q</u>	W
#1 AY393054	tgt	agt	ccc	ggg	ggt	agt	gct	tat	...	...	...	...	...	tac	<u>cac</u>	gaa	<u>cac</u>	ttc	cag	cag	tgg
	C	<u>V</u>	K	P	T	D	D	D	G				<u>H</u>	R	A	E	Y	F	Q	<u>Y</u>	W
#2 AY393055	tgt	gtg	aaa	ccc	acg	gat	gat	gat	ggc	...	...	...	<u>cac</u>	cgg	gct	gaa	tac	ttc	cag	<u>tac</u>	tgg
	C	S	P	G	G	S	<u>A</u>	Y						Y	<u>H</u>	E	<u>D</u>	F	Q	<u>Q</u>	W
#3 AY393058	tgt	agt	ccc	ggg	ggt	agc	gct	tat	...	...	...	...	...	tac	<u>cac</u>	gaa	<u>gac</u>	ttc	cag	cag	tgg
	C	S	P	G	G	S	<u>A</u>	Y						Y	<u>H</u>	E	<u>H</u>	F	Q	<u>Q</u>	W
#4 AY393072	tgt	agt	ccc	ggg	ggt	agt	gct	tat	...	...	...	...	...	tac	<u>cac</u>	gaa	<u>cac</u>	ttc	cag	cag	tgg
	C	A	R	Q	N	P	P	E	Y	S	G	A	Y	<u>H</u>	<u>D</u>	G	W	F	D	P	W
#5 AY393088	tgt	gcg	aga	caa	aac	ccc	ccc	gag	tat	agt	ggc	gca	tat	<u>cat</u>	<u>gat</u>	ggg	tgg	ttc	gac	ccc	tgg
	C	A	R	E	M	L	Y	G	S	G	<u>G</u>	Y	Y	P	P	D	A	F	<u>E</u>	<u>L</u>	W
#6 AY393089	tgt	gcg	aga	gag	atg	ctc	tat	ggt	tcg	ggg	<u>ggt</u>	tat	tac	ccc	cct	gat	gca	ttt	gag	<u>ctc</u>	tgg
	C	A	R	Q	N	P	P	E	Y	S	G	A	Y	<u>H</u>	<u>D</u>	G	W	F	D	P	W
#7 AY393091	tgt	gcg	aga	cag	aat	ccc	ccc	gag	tat	agt	ggc	gca	tat	<u>cat</u>	<u>gat</u>	ggg	tgg	ttc	gac	ccc	tgg
	C	A	R	E	M	L	Y	G	S	G	<u>G</u>	Y	Y	P	P	D	A	F	<u>E</u>	V	W
#8 AY393092	tgt	gcg	aga	gag	atg	ctc	tat	ggt	tcg	ggg	<u>ggt</u>	tat	tac	ccc	cct	gat	gca	ttt	gag	gtc	tgg
	C	A	R	Q	N	P	P	E	Y	S	G	A	Y	<u>H</u>	<u>D</u>	G	W	F	D	P	W
#9 AY393094	tgt	gcg	aga	cag	aac	ccc	ccc	gag	tat	agt	ggc	gca	tat	<u>cat</u>	<u>gat</u>	ggg	tgg	ttc	gac	ccc	tgg

Yousfi Monod et al. Bioinformatics **20**, i379-i385 (2004)
Pommié et al. J. Mol Recognit. **17**, 17-32 (2004)

IMGT/V-QUEST 'Synthesis view':

8. Results of IMGT/JunctionAnalysis



<http://www.imgt.org>

8. Results of IMGT/JunctionAnalysis

Results for the IGH junctions

Analysis of the JUNCTIONS

Click on mutated (underlined) nucleotide to see the original one:

☐

Input	V name	3'V-REGION	P	N1	P	D-REGION	N2	5'J-REGION	J name	D name	Vmut	Dmut	Jmut	Ngc
seq1	IGHV1-18*01	tgtgcgagaga		gcactcctcggc		...ctacagta.....	tgcggcggaagggt	ctttgagtactgg	IGHJ4*02	IGHD4-4*01	0	0	2	20/28
seq2	IGHV3-30*04	tgtgcgagaga		tcgga		..gtatagcagtgcc.....	ccagt	actactttgactactgg	IGHJ4*02	IGHD6-19*01	0	0	0	6/10
seq3	IGHV3-30*04	tgtgcgagag.		gaaggacgaag		ggttcggggag.....	accggc	tacttcagcactgg	IGHJ1*01	IGHD3-10*01	0	0	0	12/18
seq4	IGHV3-30*04	tgtgcgagaga	t	tcctcctaccc	ccc	gggtatagcagcagctgg...	ag	ttgagtactgg	IGHJ4*02	IGHD6-13*01	0	0	1	8/13

Translation of the JUNCTIONS

Click on mutated (underlined) amino acid to see the original one:

☐

		104	105	106	107	108	109	110	111	111.1	111.2	112.3	112.2	112.1	112	113	114	115	116	117	118	Frame	CDR3-IMGT length	Molecular mass	pI
		C	A	R	E	H	S	S	A	Y	S	M	R	R	K	G	V	F	H	Y	W				
#1	seq1	tgt	gcg	aga	gag	cac	tcc	tcg	gcc	tac	agt	atg	cgg	cgg	aaa	ggg	gtc	ttt	<u>cat</u>	tac	tgg	+	18	2,471.81	10.28
		C	A	R	D	R	S	I	A	V				A	Q	Y	Y	F	D	Y	W				
#2	seq2	tgt	gcg	aga	gat	cgg	agt	ata	gca	gtg	...	...	...	gcc	cag	tac	tac	ttt	gac	tac	tgg	+	15	2,127.37	6.58
		C	A	R	G	R	T	K	G	S			G	R	P	G	Y	F	Q	H	W				
#3	seq3	tgt	gcg	aga	gga	agg	acg	aag	ggt	tcg	...	...	ggg	aga	ccc	ggc	tac	ttc	cag	cac	tgg	+	16	2,064.32	11.72
		C	A	R	D	S	S	Y	P	P	G		I	A	A	A	G	V	X	Y	W				
#4	seq4	tgt	gcg	aga	gat	tcc	tcc	tac	ccc	ccg	ggt	...	ata	gca	gca	gct	gga	gtt	<u>gan</u>	tac	tgg	+	17	1,884.1	6.44

Done

IMGT/V-QUEST <http://www.imgt.org>

V-QUEST Search Page - Mozilla Firefox

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http://imgt.cines.fr/IMGT_vquest/share/textes/

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WELCOME ! to IMGT/V-QUEST

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Citing IMGT/V-QUEST: Brochet, X. et al., Nucl. Acids Res. 36, W503-508 (2008). [PMID: 18503082](#) [PDF](#)

From the Version 3.0.0 of IMGT/V-QUEST, gaps in CDR1-IMGT and CDR2-IMGT are placed at the top of the loops

Current version: 3.1.2 (18 July 2008)

Analyse your Immunoglobulin nucleotide sequences

 Human	 Teleostei
 Mouse	 - Atlantic cod
	 - Channel catfish
	 - Rainbow trout
 Rat	
 Chondrichthyes	 Sheep

Analyse your T cell Receptor nucleotide sequences

 Human	 Nonhuman primates
 Mouse	

Done

IMGT/V-QUEST Search page

WELCOME ! to IMGT/V-QUEST Search page

THE
INTERNATIONAL
IMMUNOGENETICS
INFORMATION SYSTEM®



Citing IMGT/V-QUEST: Brochet, X. et al., Nucl. Acids Res. 36, W503-508 (2008). [PMID: 18503082](#) [PDF](#)

From the Version 3.0.0 of IMGT/V-QUEST, gaps in CDR1-IMGT and CDR2-IMGT are placed at the top of the loops

Analyse your Immunoglobulin sequences

Your selection: **Human**

Your sequences are compared to the Human (*Homo sapiens*) IG set from the [IMGT/V-QUEST reference directory](#)

Analysis by batches of up to
50 sequences in a single run

Nucleotide sequences

Sequence sets to test IMGT/V-QUEST are available [here](#)

☒ Type (or copy/paste) your sequence(s) in [FASTA format](#)

```
>seq1
caggtgcagctggtgcagctctggagctgaggtgaagaagcctggggcctcagtgaaggtc
tcctgcaaggcttctggttacaccttaccagctatggtatcagctgggtgcgacaggcc
cctggacaaggccttgagtggatgggatggatcagcgttacaatggtaacacaaactat
gcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctac
atggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgagagtata
cgtgcttttgatatctggggccaagggaacacgggtcacccgtctcgagc
>seq1
caggtgcagctggtgcagctctggggctgaagtgaagaagcctgggtcctcggtgaaggtc
tcctgcaaggcttttgagtcaccttcagtagttacgctatcagctgggtgcgacaggcc
cctggacaaggccttgagtggatgggagggatcatcccttggttcggaaaggcaactac
```

☐ Or give the path access to a local file containing your sequence(s) in [FASTA format](#)

Done

IMGT/V-QUEST Selection for results display

```
>seq2  
caggtgcagctggtgcagtcctgggctgaagtgaagaagcctgggtcctcggtgaaggtc  
tcctgcaaggcttttgagtcaccttcagtagttacgctatcagctgggtgcgacaggcc  
cctggacaaggccctgagtggtggaggatcatcccttctggtcggaaaggcaaaactac
```

☐ Or give the path access to a local file containing your sequence(s) in [FASTA format](#)

Selection for results display

CLASSIFICATION

Export in text ☐

Nb of nucleotides per line in alignments:

☒ A. Detailed view

- | | | |
|---|---|---|
| 1. ☒ Alignment for V-GENE | 6. ☒ V-REGION alignment | 12. IMGT Collier de Perles |
| 2. ☒ Alignment for D-GENE | 7. ☒ V-REGION translation | ☒ link to IMGT/Collier-de-Perles tool |
| 3. ☒ Alignment for J-GENE | 8. ☒ V-REGION protein display | ☐ IMGT Collier de Perles (for a nb of sequences < 5) |
| 4. ☒ Results of IMGT/JunctionAnalysis | 9. ☐ V-REGION mutation table | ☐ no IMGT Collier de Perles |
| ☐ with full list of eligible D-GENEs | 10. ☐ V-REGION mutation statistics | 13. ☐ Sequences of V-, V-J- or V-D-J- REGION ('nt' and 'AA') with gaps in FASTA and access to IMGT/PhyloGene for V-REGION ('nt') |
| ☒ without list of eligible D-GENEs | 11. ☐ V-REGION mutation hot spots | 14. ☐ Annotation by IMGT/Automat |
| 5. ☐ Sequence of the JUNCTION ('nt' and 'AA') | | |

☐ B. Synthesis view

- | | |
|---|---|
| 1. ☒ Alignment for V-GENE | 5. ☒ V-REGION protein display (with AA class colors) |
| 2. ☒ V-REGION alignment | 6. ☒ V-REGION protein display (only AA changes displayed) |
| 3. ☒ V-REGION translation | 7. ☒ V-REGION most frequently occurring AA |
| 4. ☒ V-REGION protein display | 8. ☒ Results of IMGT/JunctionAnalysis |

Advanced parameters

Selection of IMGT reference directory set

[Search for insertions and deletions](#)

☒ No

☒ With all alleles ☐ With allele *01 only

☐ Yes (slower, the nb of submitted sequences in a single run is limited to 10)

Parameters for IMGT/JunctionAnalysis

Nb of D-GENEs in IGH JUNCTIONs (default is 1)

Nb of accepted mutations:

in 3'V-REGION

in D-REGION

in 5'J-REGION

Done

IMGT/V-QUEST Selection for results display



<http://www.imgt.org>

```
>seq2
caggtgcagctggtgcagtcctggggctgaagtgaagaagcctgggtcctcggtgaaggtc
tcctgcaaggcttttgagtcaccttcagtagttacgctatcagctgggtgcgacagggc
cctggacaaggccctgagtgatgggagggatcatccctttgttcggaaaggcaactac
```

☐ Or give the path access to a local file containing your sequence(s) in [FASTA format](#)

Selection for results display

DESCRIPTION

Export in text ☐

Nb of nucleotides per line in alignments:

☒ A. Detailed view

- | | | |
|--|--|--|
| <ul style="list-style-type: none">1. ☒ Alignment for V-GENE2. ☒ Alignment for D-GENE3. ☒ Alignment for J-GENE4. ☒ Results of IMGT/JunctionAnalysis<ul style="list-style-type: none">☐ with full list of eligible D-GENES☒ without list of eligible D-GENES5. ☐ Sequence of the JUNCTION ('nt' and 'AA') | <ul style="list-style-type: none">6. ☒ V-REGION alignment7. ☒ V-REGION translation8. ☒ V-REGION protein display9. ☐ V-REGION mutation table10. ☐ V-REGION mutation statistics11. ☐ V-REGION mutation hot spots | <ul style="list-style-type: none">12. IMGT Collier de Perles<ul style="list-style-type: none">☒ link to IMGT/Collier-de-Perles tool☐ IMGT Collier de Perles (for a nb of sequences < 5)☐ no IMGT Collier de Perles13. ☐ Sequences of V-, V-J- or V-D-J- REGION ('nt' and 'AA') with gaps in FASTA and access to IMGT/PhyloGene for V-REGION ('nt')14. ☐ Annotation by IMGT/Automat |
|--|--|--|

☐ B. Synthesis view

- | | |
|---|---|
| <ul style="list-style-type: none">1. ☒ Alignment for V-GENE2. ☒ V-REGION alignment3. ☒ V-REGION translation4. ☒ V-REGION protein display | <ul style="list-style-type: none">5. ☒ V-REGION protein display (with AA class colors)6. ☒ V-REGION protein display (only AA changes displayed)7. ☒ V-REGION most frequently occurring AA8. ☒ Results of IMGT/JunctionAnalysis |
|---|---|

Advanced parameters

- | | |
|--|---|
| <p>Selection of IMGT reference directory set <input type="text" value="F+ORF+ in-frame P"/></p> <p>Search for insertions and deletions ☒ No</p> <p>Parameters for IMGT/JunctionAnalysis</p> | <p>☒ With all alleles ☐ With allele *01 only</p> <p>☐ Yes (slower, the nb of submitted sequences in a single run is limited to 10)</p> <p>Nb of D-GENES in IGH JUNCTIONS (default is 1) <input type="text" value="default"/></p> <p>Nb of accepted mutations: <input type="text" value="default"/> in 3'-REGION
<input type="text" value="default"/> in D-REGION
<input type="text" value="default"/> in 5'-REGION</p> |
|--|---|

Done

IMGT/V-QUEST Selection for results display



<http://www.imgt.org>

```
>seq2
caggtgcagctggtgcagtcctctggggctgaagtgaagaagcctgggtcctcggtgaaggtc
tcctgcaaggcttttgagtcaccttcagtagttacgctatcagctgggtgcgacaggcc
cctggacaaggccctgagtgatgggagggatcatccctttgttcggaaaggcaactac
```

☐ Or give the path access to a local file containing your sequence(s) in [FASTA format](#)

Selection for results display

NUMEROTATION

Export in text ☐

Nb of nucleotides per line in alignments:

☒ A. Detailed view

- | | | |
|---|---|---|
| 1. ☒ Alignment for V-GENE | 6. ☒ V-REGION alignment | 12. IMGT Collier de Perles |
| 2. ☒ Alignment for D-GENE | 7. ☒ V-REGION translation | ☒ link to IMGT/Collier-de-Perles tool |
| 3. ☒ Alignment for J-GENE | 8. ☒ V-REGION protein display | ☐ IMGT Collier de Perles (for a nb of sequences < 5) |
| 4. ☒ Results of IMGT/JunctionAnalysis | 9. ☐ V-REGION mutation table | ☐ no IMGT Collier de Perles |
| ☐ with full list of eligible D-GENES | 10. ☐ V-REGION mutation statistics | 13. ☐ Sequences of V-, V-J- or V-D-J- REGION ('nt' and 'AA') with gaps in FASTA and access to IMGT/PhyloGene for V-REGION ('nt') |
| ☒ without list of eligible D-GENES | 11. ☐ V-REGION mutation hot spots | 14. ☐ Annotation by IMGT/Automat |
| 5. ☐ Sequence of the JUNCTION ('nt' and 'AA') | | |

☐ B. Synthesis view

- | | |
|---|---|
| 1. ☒ Alignment for V-GENE | 5. ☒ V-REGION protein display (with AA class colors) |
| 2. ☒ V-REGION alignment | 6. ☒ V-REGION protein display (only AA changes displayed) |
| 3. ☒ V-REGION translation | 7. ☒ V-REGION most frequently occurring AA |
| 4. ☒ V-REGION protein display | 8. ☒ Results of IMGT/JunctionAnalysis |

Advanced parameters

- | | | | | | | | | |
|---|---|---|--------------------------------------|---------------|--------------------------------------|-------------|--------------------------------------|---------------|
| Selection of IMGT reference directory set | <input type="text" value="F+ORF+ in-frame P"/> | ☒ With all alleles ☐ With allele *01 only | | | | | | |
| Search for insertions and deletions | ☒ No | ☐ Yes (slower, the nb of submitted sequences in a single run is limited to 10) | | | | | | |
| Parameters for IMGT/JunctionAnalysis | Nb of D-GENES in IGH JUNCTIONS (default is 1)
<input type="text" value="default"/> | Nb of accepted mutations:
<table border="0"><tr><td><input type="text" value="default"/></td><td>in 3'V-REGION</td></tr><tr><td><input type="text" value="default"/></td><td>in D-REGION</td></tr><tr><td><input type="text" value="default"/></td><td>in 5'J-REGION</td></tr></table> | <input type="text" value="default"/> | in 3'V-REGION | <input type="text" value="default"/> | in D-REGION | <input type="text" value="default"/> | in 5'J-REGION |
| <input type="text" value="default"/> | in 3'V-REGION | | | | | | | |
| <input type="text" value="default"/> | in D-REGION | | | | | | | |
| <input type="text" value="default"/> | in 5'J-REGION | | | | | | | |

Done

IMGT/V-QUEST 'Detailed view': Result summary

Sequence number 1: AF184762

Sequence compared with the [human IG set](#) from the [IMGT reference directory](#)

>AF184762

```
atggagtgtggctgagctgggttttctgttgctattttaaaagggtgccactgtgag
gtgcagctggtggagctctggggaggccttagtccagcctggggatccctgaaactctc
tgtgcagcctctgggttcacccctcagtggtcctcaaatgtgcactgggtccgccaggcctc
gggaaagggttgagtggttgccgtatcaaaagggaatgtgagctgacgcgacagca
tatgtctcgctgatgagaggcaggctcaccatctccagagatgattcaagaacacggcg
tttctgcaaatgaacagcctgaaaagcgatgacacggccatgtattattgtgtgatccg
ggagatgtttacaaccgacagtggggccagggaacctggtcaccgtctctcagcatcc
ccgaccagccccaagggtcttccgctgagcctctgcagcaccagccagat
```

Automatic evaluation

Result summary:	Productive IGH rearranged sequence (no stop codon and in frame junction)		
V-GENE and allele	IGHV3-73*01	score = 1240	identity = 91,50% (269/294 nt)
J-GENE and allele	IGHJ1*01 (b)	score = 179	identity = 82,69% (43/52 nt)
D-GENE and allele by IMGT/JunctionAnalysis	IGHD3-10*01	D-REGION is in reading frame 3	
[CDR1-IMGT.CDR2-IMGT.CDR3-IMGT] lengths and AA JUNCTION	[8.10.10]	CVIRGDVYNRQW	

(b) Other possibilities: IGHJ4*02 and IGHJ5*02 (highest number of consecutive identical nucleotides)

IMGT/V-QUEST provides **22 different output results** (analysis of IG nucleotide sequences and of their translation)

IMGT/V-QUEST 'Detailed view':

Result summary table

Number of analysed sequences: 4

[seq1](#) [seq2](#) [seq3](#) [seq4](#)

☞ This release of IMGT/V-QUEST uses [IMGT/JunctionAnalysis](#) for the analysis of the JUNCTION

☞ Hyphens (-) show nucleotide identity, dots (.) represent gaps

Sequence number 1: seq1

Sequence compared with the [human IG set](#) from the [IMGT reference directory](#)

```
>seq1
caggtgcagctggtgcagctctggagctgaggtgaagaagcctggggcctcagtgaaggtc
tcctgcaaggtctctggttacacctttaccagctatggtatcagctgggtgcgacaggcc
cctggacaagggtctgagtggtggatggatcagcgcttacaatggtaacacaaactat
gcacagaagctccagggcagagtcacccatgaccacagacacatccacgagcacagcctac
atggagctgaggagcctgagatctgacgacacggcgtgtattactgtgcgagaggtata
cgtgcttttgatatctggggccaaggaccacggtcaccgtctcgcagc
```

CLASSIFICATION

Result summary:	Productive IGH rearranged sequence (no stop codon and in-frame junction)		
V-GENE and allele	IGHV1-18*01	score = 1426	identity = 99,65% (287/288 nt)
J-GENE and allele	IGHJ3*02 (a)	score = 164	identity = 81,63% (40/49 nt)
D-GENE and allele by IMGT/JunctionAnalysis	IGHD2-2*02	D-REGION is in reading frame 3	
[CDR1-IMGT.CDR2-IMGT.CDR3-IMGT] lengths and AA JUNCTION	[8.8.9]	CARGIRAFDIW	

(a) Other possibilities: IGHJ6*02 (highest number of consecutive identical nucleotides)

Done

IMGT/V-QUEST 'Detailed view': Result summary table

Number of analysed sequences: 4

[seq1](#) [seq2](#) [seq3](#) [seq4](#)

☞ This release of IMGT/V-QUEST uses [IMGT/JunctionAnalysis](#) for the analysis of the JUNCTION

☞ Hyphens (-) show nucleotide identity, dots (.) represent gaps

Sequence number 1: seq1

Sequence compared with the [human IG set](#) from the [IMGT reference directory](#)

```
>seq1
caggtgcagctgggtgcagctctggagctgaggtgaagaagcctggggcctcagtgaaggtc
tcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgacacaggcc
cctggacaagggtctgagtggtatggatggatcagcgcttacaatggtaacacaaactat
gcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctac
atggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgagaggtata
cgtgcttttgatatctggggccaagggaaccacggtcaccgtctctgagc
```

For D-GENE,
- other potential D
- mutation parameter
- amino acid sequence

Result summary:	Productive IGH rearranged sequence (no stop codon and in-frame junction)		
V-GENE and allele	IGHV1-18*01	score = 1426	identity = 99,65% (287/288 nt)
J-GENE and allele	IGHJ3*02 (a)	score = 164	identity = 81.63% (40/49 nt)
D-GENE and allele by IMGT/JunctionAnalysis	IGHD2-2*02	D-REGION is in reading frame 3	
[CDR1-IMGT.CDR2-IMGT.CDR3-IMGT] lengths and AA JUNCTION	[8.8.9]	CARGIRAFDIW	

(a) Other possibilities: IGHJ6*02 (highest number of consecutive identical nucleotides)

Done

IMGT/V-QUEST 'Detailed view':

Result summary table

Number of analysed sequences: 4

[seq1](#) [seq2](#) [seq3](#) [seq4](#)

☞ This release of IMGT/V-QUEST uses [IMGT/JunctionAnalysis](#) for the analysis of the JUNCTION

☞ Hyphens (-) show nucleotide identity, dots (.) represent gaps

Sequence number 1: seq1

Sequence compared with the [human IG set](#) from the [IMGT reference directory](#)

```
>seq1
caggtgcagctggtgcagctctggagctgaggtgaagaagcctggggcctcagtgaaggtc
tcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcc
cctggacaaggccttgagtggatgggatggatcagcgcttacaatggtaacacaaactat
gcacagaagctccagggcagagtcacccatgaccacagacacatccacgagcacagcctac
atggagctgaggagcctgagatctgacgacacggcgtgtattactgtgcgagaggtata
cgtgcttttgatatctggggccaagggaaccacggtcaccgtctcgcagc
```

DESCRIPTION

NUMEROTATION

Result summary:	Productive IGH rearranged sequence (no stop codon and in-frame junction)		
V-GENE and allele	IGHV1-18*01	score = 1426	identity = 99,65% (287/288 nt)
J-GENE and allele	IGHJ3*02 (a)	score = 164	identity = 81,63% (40/49 nt)
D-GENE and allele by IMGT/JunctionAnalysis	IGHD2-2*02	D-REGION is in reading frame 3	
[CDR1-IMGT.CDR2-IMGT.CDR3-IMGT] lengths and AA JUNCTION	[8.8.9]	CARGIRAFDIW	

(a) Other possibilities: IGHJ6*02 (highest number of consecutive identical nucleotides)

Done

IMGT/V-QUEST 'Synthesis view': Summary table



<http://www.imgt.org>

Number of analysed sequences: 7

CLASSIFICATION

Sequences compared with the [human IG set](#) from the [IMGT reference directory](#)

Summary table:

DESCRIPTION

NUMEROTATION

Sequence ID	V-GENE and allele	Functionality	V-REGION score	V-REGION identity % (nt)	J-GENE and allele	D-GENE and allele	D-REGION reading frame	CDR-IMGT lengths	AA JUNCTION	JUNCTION frame
seq1	IGHV1-69*06	Productive	1050	95,63% (219/229 nt)	IGHJ3*02	IGHD3-16*02	2	[8.8.21]	CARGGDYDIWGSYRASDAFDIW	in-frame
seq2	IGHV1-69*06	Productive	1300	94,79% (273/288 nt)	IGHJ4*01	IGHD6-13*01	1	[8.8.21]	CARERVGAYTSSWYGDYVSFDYW	in-frame
seq3	IGHV4-34*01	Productive	1411	99,30% (283/285 nt)	IGHJ6*02	IGHD2-2*02	3	[8.7.20]	CWIVVPAIVPNYYYYGMDWW	in-frame
seq4	IGHV4-34*01	Productive	1294	95,09% (271/285 nt)	IGHJ6*02	IGHD3-10*01	2	[8.7.20]	CARDFSPSPPGHYDARNDMDWW	in-frame
seq5	IGHV4-34*01	Productive	1285	94,74% (270/285 nt)	IGHJ6*03	IGHD3-22*01	2	[8.7.21]	CARWYFDTSGYYPRNFYYMDWW	in-frame
seq6	IGHV4-34*01	Productive	1258	93,68% (267/285 nt)	IGHJ6*02	IGHD2-2*02	3	[8.7.25]	CARGHKTAIREPPTIGPIYYSYDMDWW	in-frame
seq7	IGHV4-34*01	Productive	1420	100,00% (285/285 nt)	IGHJ5*02	IGHD2-2*01	3	[8.7.25]	CARGDWRIWVPAAVDTAMAANWFDPW	in-frame

Results of IMGT/JunctionAnalysis for : [IGH](#) junctions

Alignment with the closest alleles:

The analysed sequences are aligned with the closest allele (with number of aligned sequences in parentheses):

[IGHV1-69*06\(2\)](#) [IGHV4-34*01\(5\)](#)

IMGT/V-QUEST 'Detailed view':

7. V-REGION translation



<http://www.imgt.org>

IMGT/V-QUEST - Mozilla Firefox

Fichier Édition Affichage Historique Marque-pages Outils ?

7. V-REGION translation

```
<----- FR1 - IMGT ----->
1      5      10      15      20
Q V Q L V Q S G A E V K K P G S S V K V S C
cag gtg cag ctg gtg cag tct ggg gct ... gaa gtg aag aag cct ggg tcc tcg gtg aag gtc tcc tg

L22582 IGHV1-69*01
-----g-----

-----> CDR1 - IMGT <----->
25      30      35      40      45
K A F G V T F S S Y A I S W V R Q A
c aag gct ttt gga gtc acc ttc ... agt agt tac gct atc agc tgg gtg cga cag gcc

L22582 IGHV1-69*01
-----c-----g-----c-----t-----

FR2 - IMGT -----> CDR2 - IMGT <----->
50      55      60      65
P G Q G P E W M G G I I P L F G K A N Y A
cct gga caa ggg cct gag tgg atg gga ggg atc atc cct ttg ... ttc gga aag gca aac tac gc

L22582 IGHV1-69*01
-----t-----a-c-----t-----ca-----

FR3 - IMGT ----->
70      75      80      85      90
Q K F Q G R V T I T A D A S T S T V Y M E
a cag aag ttc cag ... ggc aga gtc acg att acc gcg gac gca tcc acg agc acg gtc tac atg gag

L22582 IGHV1-69*01
-----a-----c-----

-----> CDR3 - IMGT -----
95      100      104
V S S L R S E D T A V Y Y C A R Q Y G S S G Y
gtg agc agc ctg aga tct gag gac acg gcc gtg tat tat tgt gcg aga caa tat ggt agt agt ggt ta

L22582 IGHV1-69*01
c-----c-----g-----

Y A Y W G H G T L V T V
t tac gcc tac tgg ggc cac gga acc ctg gtc acc gtc t

L22582 IGHV1-69*01
```

Terminé

zotero

IMGT/V-QUEST 'Detailed view':

9. V-REGION mutation table

Nucleotide substitution

Amino acid change

9. V-REGION mutation table

FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT
g33>a c77>t, S26>F (- - -)	g83>t, G28>V (- - -) c105>t c108>t t111>c	t149>c, L50>P (- - -)	a175>t, I59>L (+ + +) c177>g, I59>L (+ + +) t186>c t189>a c191>a, T64>K (- - -) a192>g, T64>K (- - -)	a245>c, E82>K (- - -) a258>g c260>t, A87>V (+ - +) c271>g, L91>V (+ - +) c309>t	g319>c



Terminé



zotero

IMGT/V-QUEST 'Detailed view':

9. V-REGION mutation table

Nucleotide substitution

Amino acid change

9. V-REGION mutation table

FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT
g33>a c77>t, S26>F (- -)	g83>t, G28>V (- - -) c105>t c108>t t111>c	t149>c, L50>P (- - -)	a175>t, I59>L (+ + +) c177>g, I59>L (+ + +) t186>c t189>a c191>a, T64>K (- - -) a192>g, T64>K (- - -)	a245>c, E82>K (- - -) a258>g c260>t, A87>V (+ - +) c271>g, L91>V (+ + +) c309>t	g319>c

Terminé

zotero

Hydropathy

Volume

Physicochemical properties (+ : conserved classes)

(+ : conserved classes)

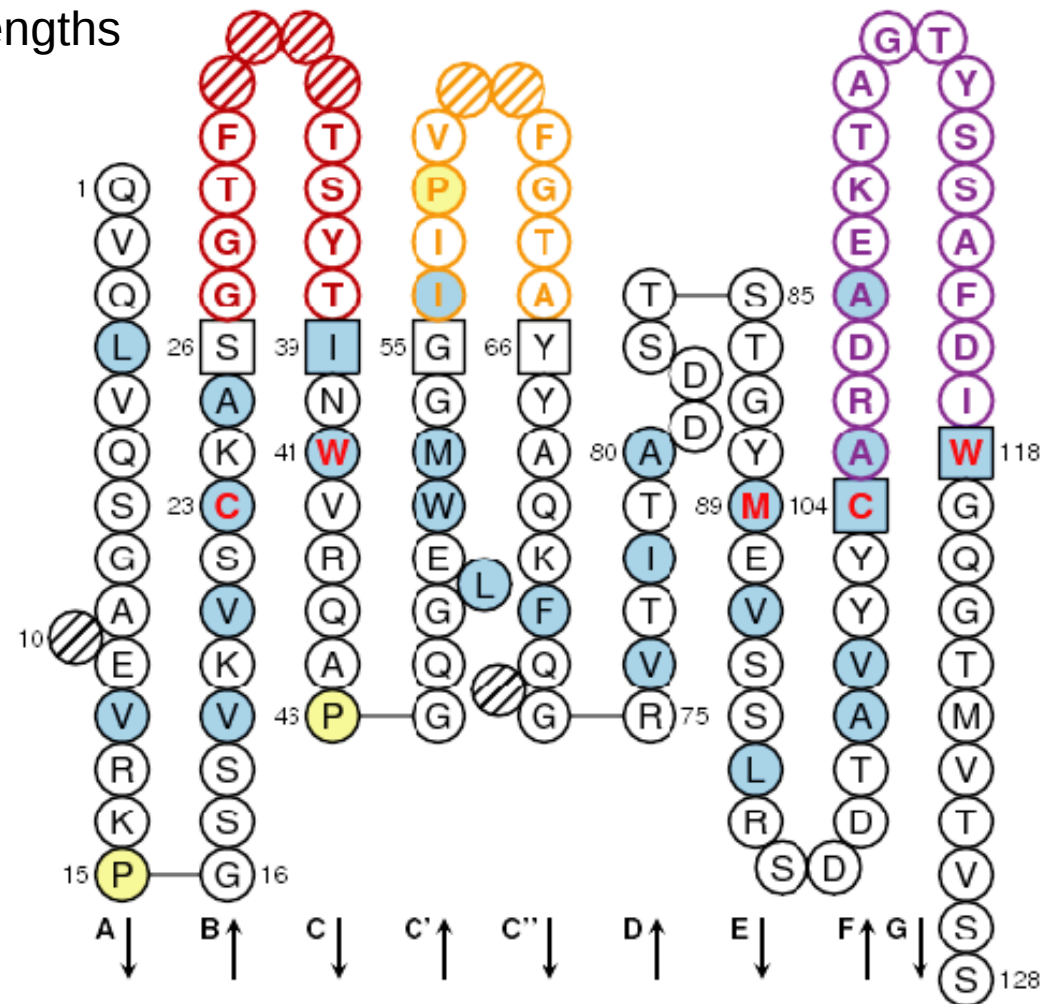
(- : different classes)

(+ : conserved classes)

IMGT/V-QUEST 'Detailed view':

12. Link to the IMGT/Collier-de-Perles tool

CDR-IMGT lengths
[8.8.17]



IMGT Collier de Perles for V-DOMAIN

IMGT/DomainGapAlign



<http://www.imgt.org>

Sequence name: ALEMTUZUMAB

V-REGION
identity percent

Closest reference gene and allele(s) from the IMGT domain directory

V gene and allele	Species	Domain	Smith-Waterman Score	Identity percentage	Overlap	
<u>IGHV4-59*01</u>	Homo sapiens	1	494	73.0	100	
J gene and allele	Species	Domain	Smith-Waterman Score	Identity percentage	Overlap	Align your sequence with
<u>IGHJ4*01</u>	Homo sapiens	1	94	92.9	14	☒
<u>IGHJ4*02</u>	Homo sapiens	1	94	92.9	14	☐
<u>IGHJ4*03</u>	Homo sapiens	1	94	92.9	14	☐

Alignment with the closest V gene and allele from the IMGT domain directory

FR1-IMGT (1-26)				CDR1-IMGT (27-38)			FR2-IMGT (39-55)				CDR2-IMGT (56-65)			FR3-IMGT (66-104)					CDR3-IMGT (105-117)									
A (1-15)		B (16-26)			BC (27-38)			C (39-46)		C' (47-55)		C'C'' (56-65)			C'' (66-74)		D (75-84)		E (85-96)			F (97-104)		FG				
1		10	15	16	23	26	27	38	39	41	46	47	55	56	65	66	74	75	80	84	85	89	96	97	104	105		
.....					..				.																..			
ALEMTUZUMAB		QVQLQESGP.GLVRP SQTLSLTCTVS				GFTF...TDFY			MNVWRQPP			GRGLEWIGF			IRDKAKGYTT			EYNPSVK.G		RVITMLVDTSK			NQFSLRSSVTA			ADTAVYYC		AR
IGHV4-59*01		QVQLQESGP.GLVKP SETLSLTCTVS				GGSI...SSYY			WSWIRQPP			GKGLEWIGY			IYYS...GST			NYNPSLK.S		RVITISVDTSK			NQFSLRSSVTA			ADTAVYYC		AR
(Homo sapiens)		R Q				FTF TDF			MN V R F			RDK YT			E V G ML			R										

Alignment with the closest J gene and allele from the IMGT domain directory

ALEMTUZUMAB	.FDYWGGGSLVTSS	J-REGION
IGHJ4*01	YFDYWGGGTLVTSS	S
(Homo sapiens)		

14 / 91 FR-IMGT AA differences

IMGT/DomainGapAlign provides analysis of IG amino acid sequences, per domain (V, C)

Towards «Potential immunogenicity evaluation »

Comparison with the closest human germline genes:

		V-REGION identity percent	FR-IMGT AA differences
VH	alemtuzumab	73 %	14 /91
	bevacizumab	72.40 %	23
	trastuzumab	81.63 %	9
V-KAPPA	alemtuzumab	86.32 %	2 /89
	bevacizumab	87.40 %	7
	trastuzumab	86.32 %	6

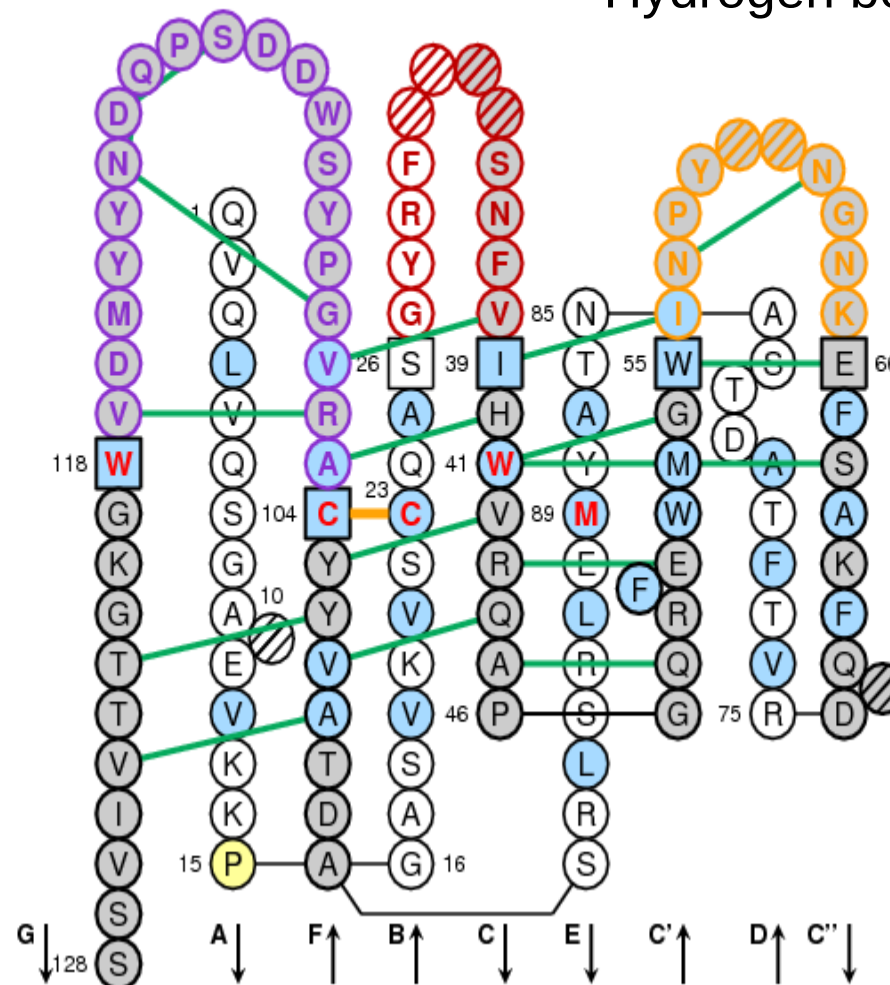
IMGT/3Dstructure-DB

<http://www.imgt.org>

IMGT Collier de Perles : *Homo sapiens* (Human) IGHV V-DOMAIN from b12 (1hzh_H)

CDR-IMGT lengths [8.8.20]

Hydrogen bonds



Contacts VH-(Ligand), V-KAPPA-(Ligand)

IMGT molecule name	IMGT description	Chain ID	IMGT chain description	Domain number	IMGT domain description
CAMPATH-1H, alemtuzumab , MABCAMPATH®	FAB-GAMMA-1_KAPPA	1ce1_H	VH-CH1	[D1]	VH
				[D2]	CH1
		1ce1_L	L-KAPPA	[D1]	V-KAPPA
				[D2]	C-KAPPA
CD52 (synthetic peptide)	Peptide	1ce1_P	Peptide		

	Unit 1		Unit 2		Residue contacts	Number of residues			Atom contact types		
	Domain	Chain	Domain	Chain		Total	From 1	From 2	Total	Polar	Hydrogen
DomPair	VH	1ce1_H	CH1	1ce1_H	19	17	8	9	125	9	1
DomPair			V-KAPPA	1ce1_L	63	45	24	21	532	61	6
DomPair			(Ligand)	1ce1_P	25	19	12	7	216	40	9
DomPair	CH1	1ce1_H	VH	1ce1_H	19	17	9	8	125	9	1
DomPair			C-KAPPA	1ce1_L	68	58	28	30	498	40	6
DomPair	V-KAPPA	1ce1_L	VH	1ce1_H	63	45	21	24	532	61	6
DomPair			C-KAPPA	1ce1_L	18	18	8	10	137	19	2
DomPair			(Ligand)	1ce1_P	16	14	7	7	171	37	5
DomPair	C-KAPPA	1ce1_L	CH1	1ce1_H	68	58	30	28	498	40	6
DomPair			V-KAPPA	1ce1_L	18	18	10	8	137	19	2

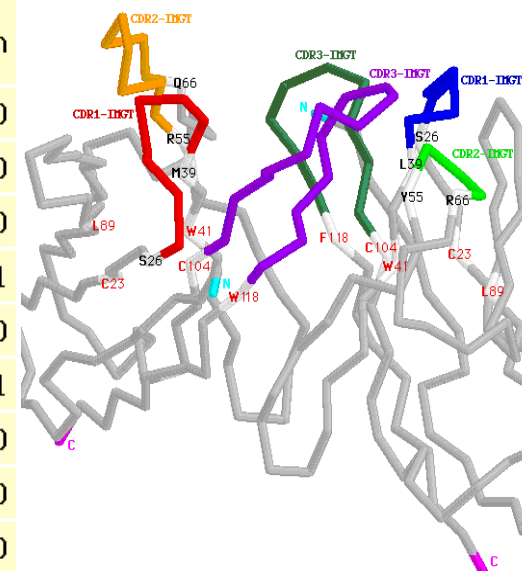
Contacts V-KAPPA-(Ligand)

Residue contacts	Number of residues			Atom contact types		
	Total	From 1	From 2	Total	Polar	Hydrogen
16	14	7	7	171	37	5

List of the Residue@Position pair contacts:

Click 'R@P' for IMGT Residue@Position cards

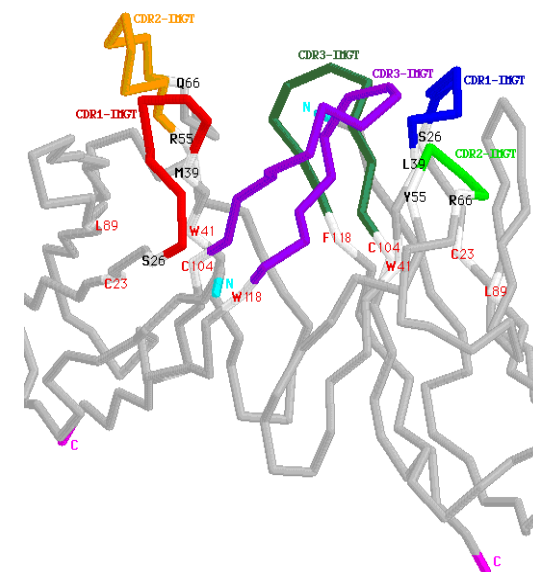
Order					Order					Atom contacts		
IMGT Num	Residue	Domain	Chain		IMGT Num	Residue	Domain	Chain		Total	Polar	Hydrogen
R@P 38	TYR	Y	V-KAPPA	1ce1_L	R@P 3	SER	S	1ce1_P		1	0	0
R@P 38	TYR	Y	V-KAPPA	1ce1_L	R@P 5	PRO	P	1ce1_P		21	0	0
R@P 56	ASN	N	V-KAPPA	1ce1_L	R@P 3	SER	S	1ce1_P		3	2	0
R@P 107	HIS	H	V-KAPPA	1ce1_L	R@P 4	SER	S	1ce1_P		20	4	1
R@P 107	HIS	H	V-KAPPA	1ce1_L	R@P 5	PRO	P	1ce1_P		12	2	0
R@P 107	HIS	H	V-KAPPA	1ce1_L	R@P 6	SER	S	1ce1_P		14	3	1
R@P 108	ILE	I	V-KAPPA	1ce1_L	R@P 5	PRO	P	1ce1_P		12	1	0
R@P 108	ILE	I	V-KAPPA	1ce1_L	R@P 6	SER	S	1ce1_P		12	3	0
R@P 109	SER	S	V-KAPPA	1ce1_L	R@P 6	SER	S	1ce1_P		11	2	0
R@P 114	ARG	R	V-KAPPA	1ce1_L	R@P 6	SER	S	1ce1_P		18	3	1
R@P 114	ARG	R	V-KAPPA	1ce1_L	R@P 7	ALA	A	1ce1_P		4	2	0
R@P 114	ARG	R	V-KAPPA	1ce1_L	R@P 8	ASP	D	1ce1_P		6	2	0
R@P 116	ARG	R	V-KAPPA	1ce1_L	R@P 2	THR	T	1ce1_P		1	1	0
R@P 116	ARG	R	V-KAPPA	1ce1_L	R@P 4	SER	S	1ce1_P		9	4	1
R@P 116	ARG	R	V-KAPPA	1ce1_L	R@P 6	SER	S	1ce1_P		20	6	1
R@P 116	ARG	R	V-KAPPA	1ce1_L	R@P 7	ALA	A	1ce1_P		7	2	0



Kaas Q. et al. 2004

Contacts VH-(Ligand)

	IMGT Num	Residue		Domain	Chain		IMGT Num	Residue		Domain	Chain	Total	Polar	Hydrogen
R@P	38	TYR	Y	VH	1ce1_H	R@P	2	THR	T		1ce1_P	4	0	0
R@P	38	TYR	Y	VH	1ce1_H	R@P	7	ALA	A		1ce1_P	13	1	0
R@P	38	TYR	Y	VH	1ce1_H	R@P	8	ASP	D		1ce1_P	14	2	2
R@P	55	PHE	F	VH	1ce1_H	R@P	6	SER	S		1ce1_P	5	0	0
R@P	55	PHE	F	VH	1ce1_H	R@P	7	ALA	A		1ce1_P	16	0	0
R@P	55	PHE	F	VH	1ce1_H	R@P	8	ASP	D		1ce1_P	1	0	0
R@P	57	ARG	R	VH	1ce1_H	R@P	7	ALA	A		1ce1_P	9	3	2
R@P	57	ARG	R	VH	1ce1_H	R@P	8	ASP	D		1ce1_P	20	6	1
R@P	61	LYS	K	VH	1ce1_H	R@P	8	ASP	D		1ce1_P	11	2	1
R@P	66	GLU	E	VH	1ce1_H	R@P	7	ALA	A		1ce1_P	1	0	0
R@P	107	GLU	E	VH	1ce1_H	R@P	2	THR	T		1ce1_P	13	2	1
R@P	107	GLU	E	VH	1ce1_H	R@P	4	SER	S		1ce1_P	5	2	0
R@P	107	GLU	E	VH	1ce1_H	R@P	7	ALA	A		1ce1_P	5	0	0
R@P	108	GLY	G	VH	1ce1_H	R@P	1	GLY	G		1ce1_P	2	1	0
R@P	108	GLY	G	VH	1ce1_H	R@P	2	THR	T		1ce1_P	9	2	0
R@P	109	HIS	H	VH	1ce1_H	R@P	1	GLY	G		1ce1_P	24	4	0
R@P	109	HIS	H	VH	1ce1_H	R@P	2	THR	T		1ce1_P	21	5	0
R@P	109	HIS	H	VH	1ce1_H	R@P	3	SER	S		1ce1_P	9	2	1
R@P	110	THR	T	VH	1ce1_H	R@P	1	GLY	G		1ce1_P	1	1	0
R@P	110	THR	T	VH	1ce1_H	R@P	3	SER	S		1ce1_P	11	4	1
R@P	112	ALA	A	VH	1ce1_H	R@P	3	SER	S		1ce1_P	3	1	0
R@P	113	ALA	A	VH	1ce1_H	R@P	2	THR	T		1ce1_P	3	0	0
R@P	113	ALA	A	VH	1ce1_H	R@P	3	SER	S		1ce1_P	7	2	0
R@P	113	ALA	A	VH	1ce1_H	R@P	4	SER	S		1ce1_P	4	0	0
R@P	114	PRO	P	VH	1ce1_H	R@P	4	SER	S		1ce1_P	5	0	0





Many thanks to the IMGT® team at Montpellier, France

