

On-line tools for interpretation of IG sequences

Marie-Paule Lefranc

How to use the IMGT/V-QUEST tool

Véronique Giudicelli

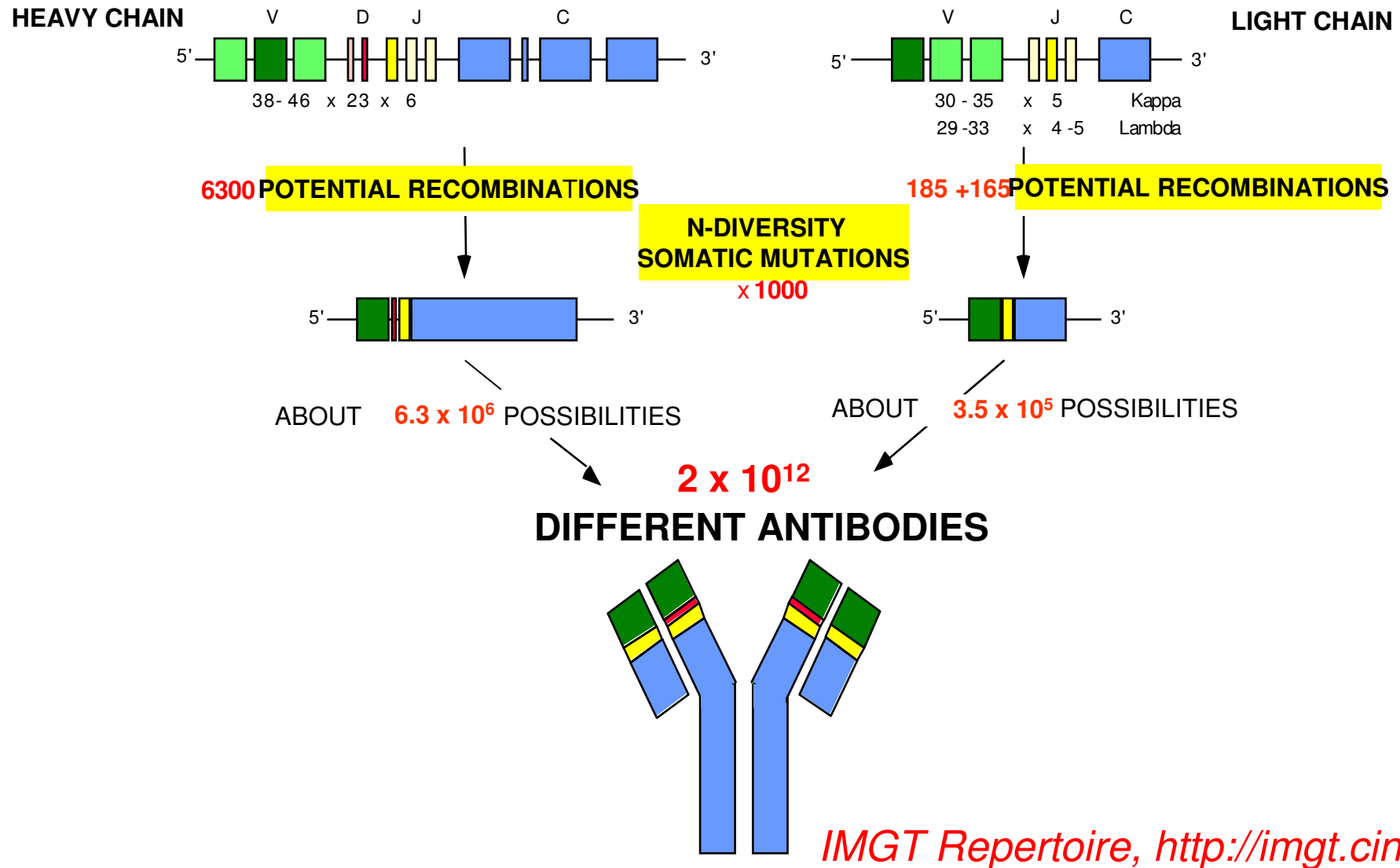
**2nd Educational Workshop on Immunoglobulin Gene Analysis
in Chronic Lymphocytic Leukemia**
9-10 October 2008 - Paris, France

Outline

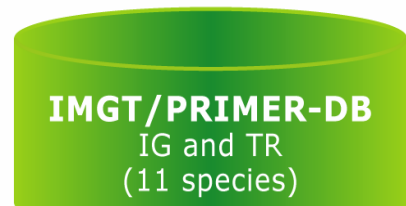
1. IMGT® standards based on IMGT-ONTOLOGY
 - classification: gene nomenclature (WHO/IUIS, NCBI)
 - description: Antibody Society
 - numerotation: IMGT unique numbering
IMGT Colliers de Perles
2. IMGT/V-QUEST
3. IMGT/JunctionAnalysis
4. IMGT/Collier-de-Perles

Immunoglobulin (IG) synthesis

150 FUNCTIONAL IG GENES



Sequences



IMGT/V-QUEST

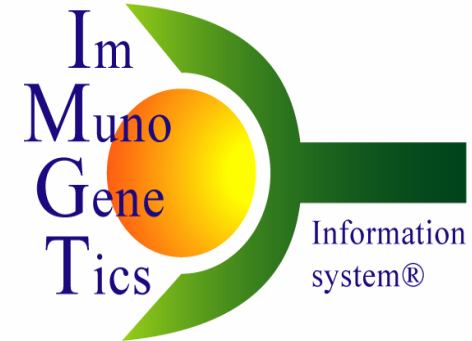
IMGT/JunctionAnalysis

IMGT/Allele-Align

IMGT/PhyloGene

IMGT/GENE-DB
IG and TR
(human and mouse)

IMGT/3Dstructure-DB
IG, TR and MHC



<http://imgt.cines.fr>

Genome

IMGT/GeneInfo

IMGT/LocusView

IMGT/GeneSearch

IMGT/GeneView

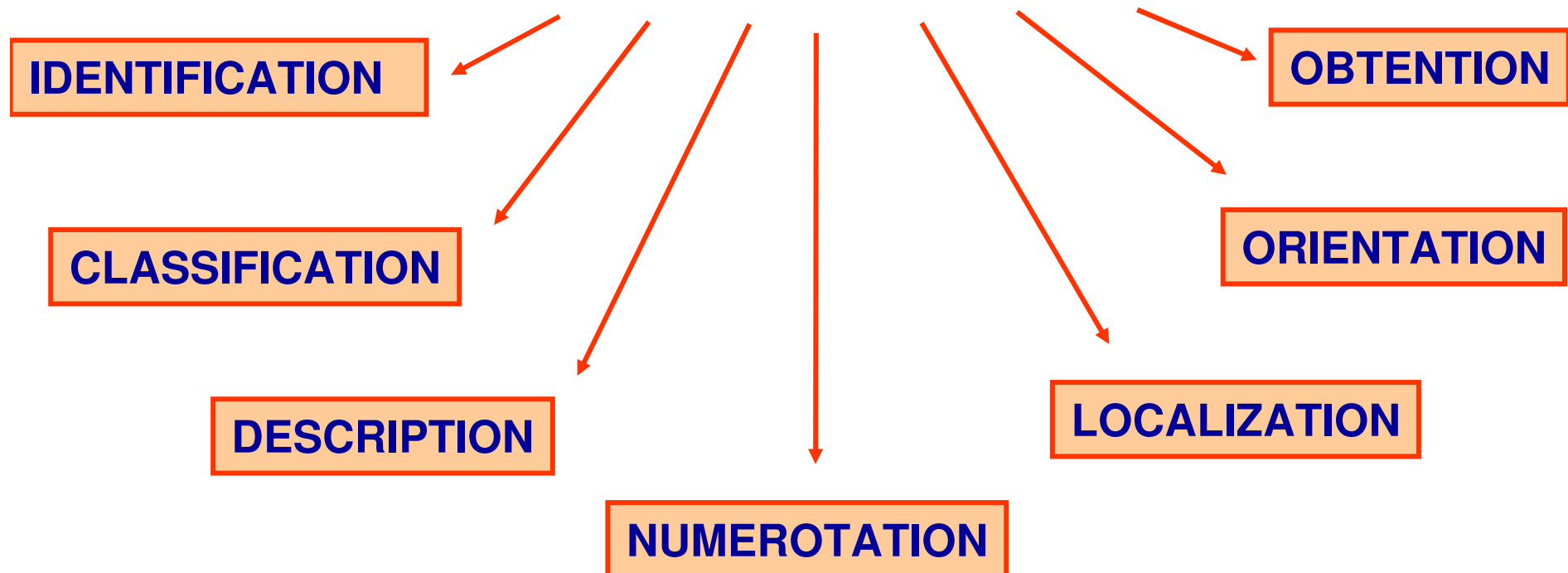
2D and 3D structures

IMGT-ONTOLOGY

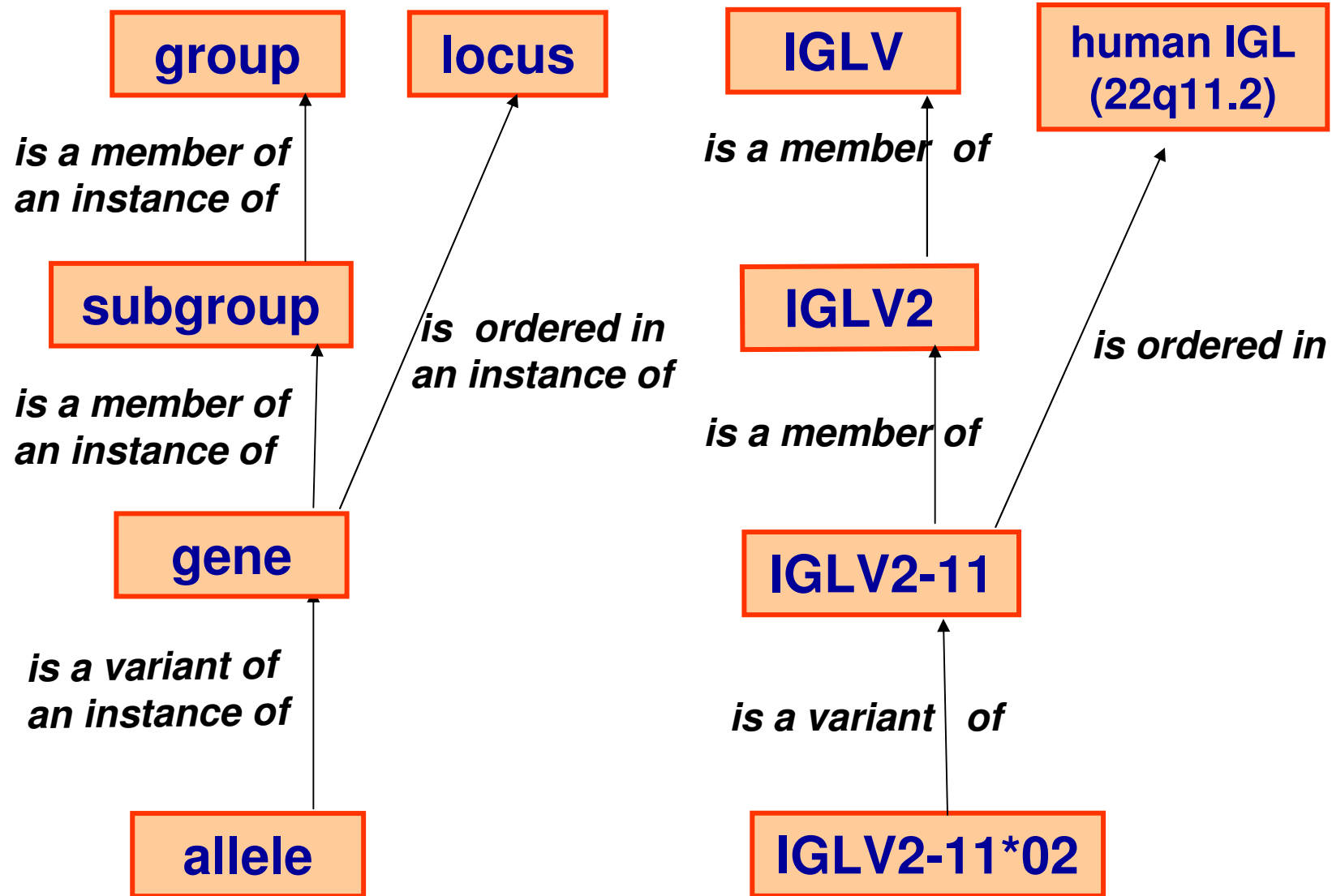
axioms and concepts

IMGT-ONTOLOGY seven axioms:

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



CLASSIFICATION axiom



« Concepts »

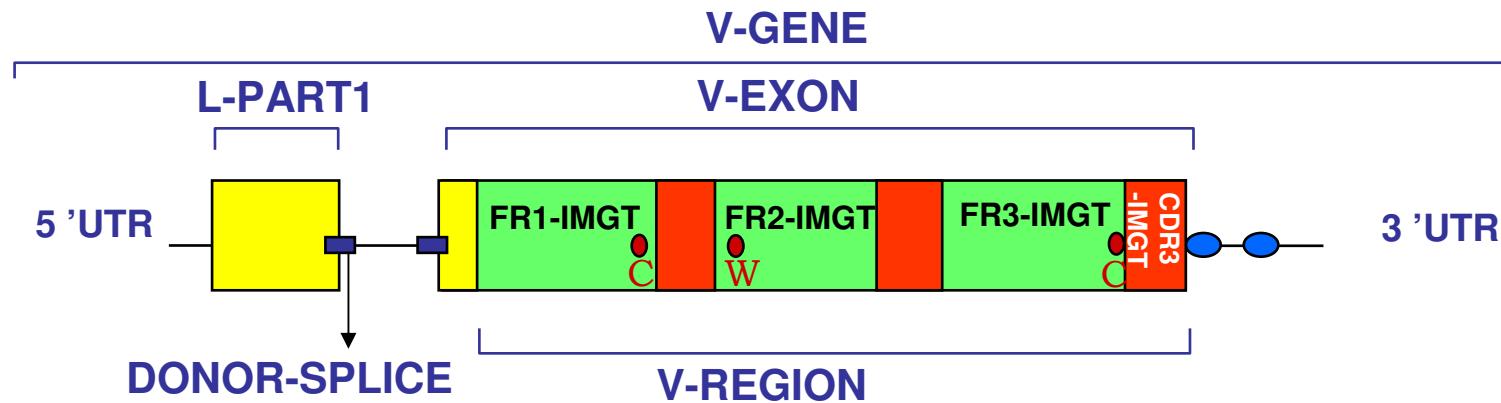
« Instances »

CLASSIFICATION axiom

- The IMGT-ONTOLOGY main concepts of classification include 'group', 'subgroup', 'gene', 'allele'.
- They allowed to set up the **nomenclature** for IG and TR genes (V, D, J, C genes).
- IMGT gene names were approved by **HGNC** in 1999 and entered in GDB, LocusLink and **Entrez Gene (NCBI)**.
- **IMGT/GENE-DB** is the **international reference database** for IG and TR genes (direct links from Entrez Gene NCBI).
- **WHO-IUIS/IMGT** 2007 report (*Dev. Comp. Immunol., Immunogenetics*).

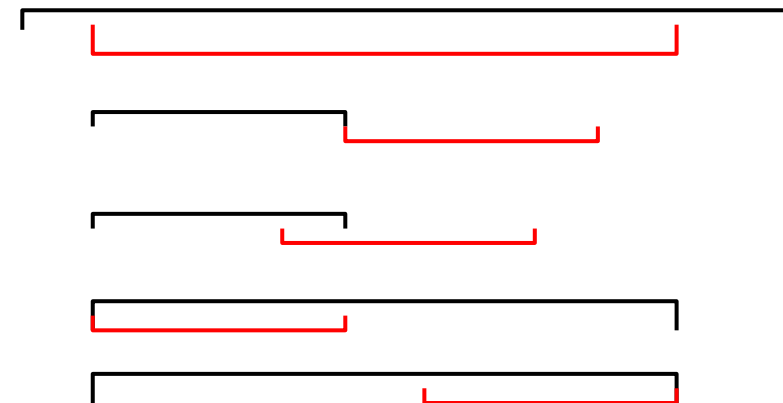
DESCRIPTION axiom

PROTOTYPE for a V-GENE



Label 1	Label 2
V-GENE	V-EXON
FR3-IMGT	CDR3-IMGT
L-PART1	DONOR-SPLICE
V-REGION	FR1-IMGT
V-REGION	CDR3-IMGT

Relations entre Labels



IMGT/LIGM-DB



http://imgt.cines.fr

**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="QVHLVESGGAVFHPGRSLRLSRAASGFTFSSYGMHWVRQAP
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="QVHLVESGGAVFHPGRSLRLSRAASGFTFSSYGMHWVRQAP
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="GFTFSSYG"
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		

126 667 sequences from 223 species

IMGT-ONTOLOGY:

277 IMGT labels for sequences

285 IMGT labels for 3D structures

SO (Sequence ontology):

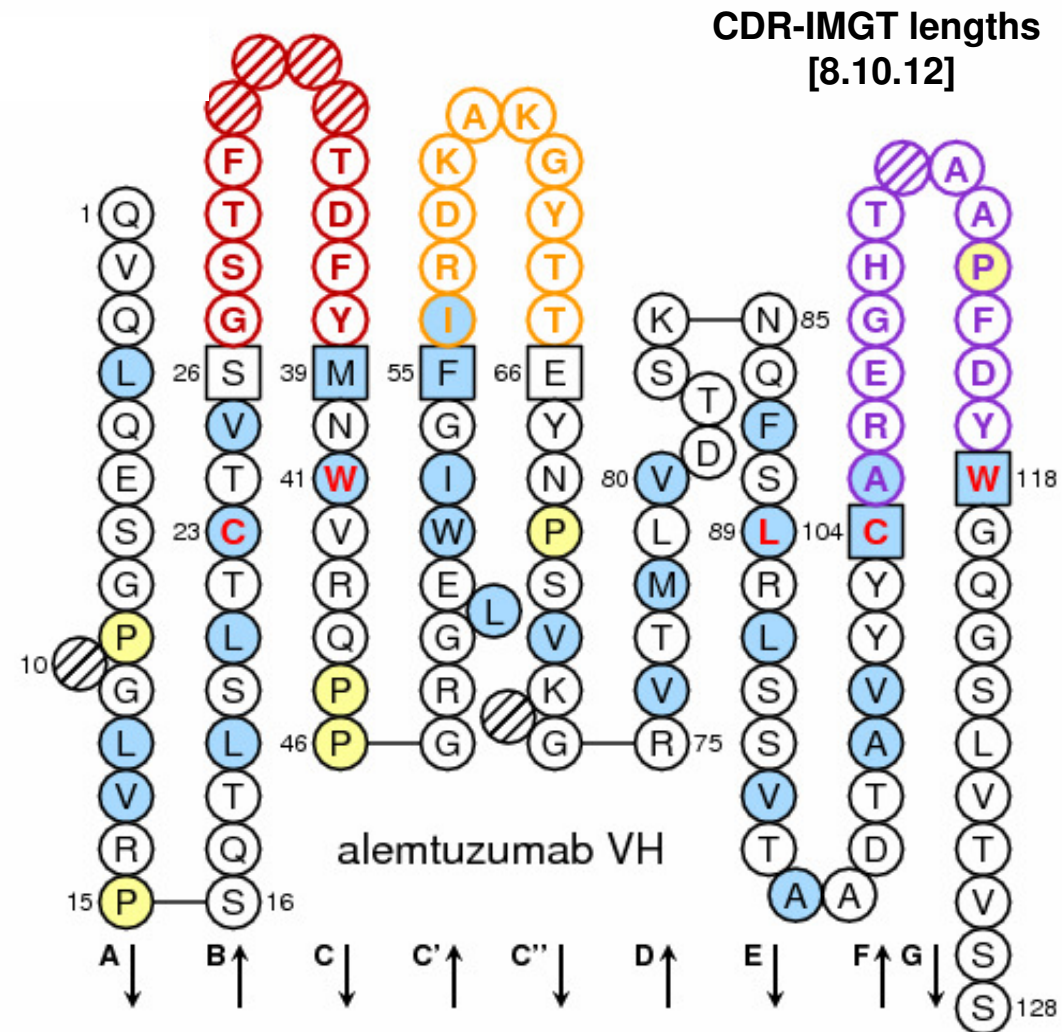
67 IMGT labels

DESCRIPTION axiom

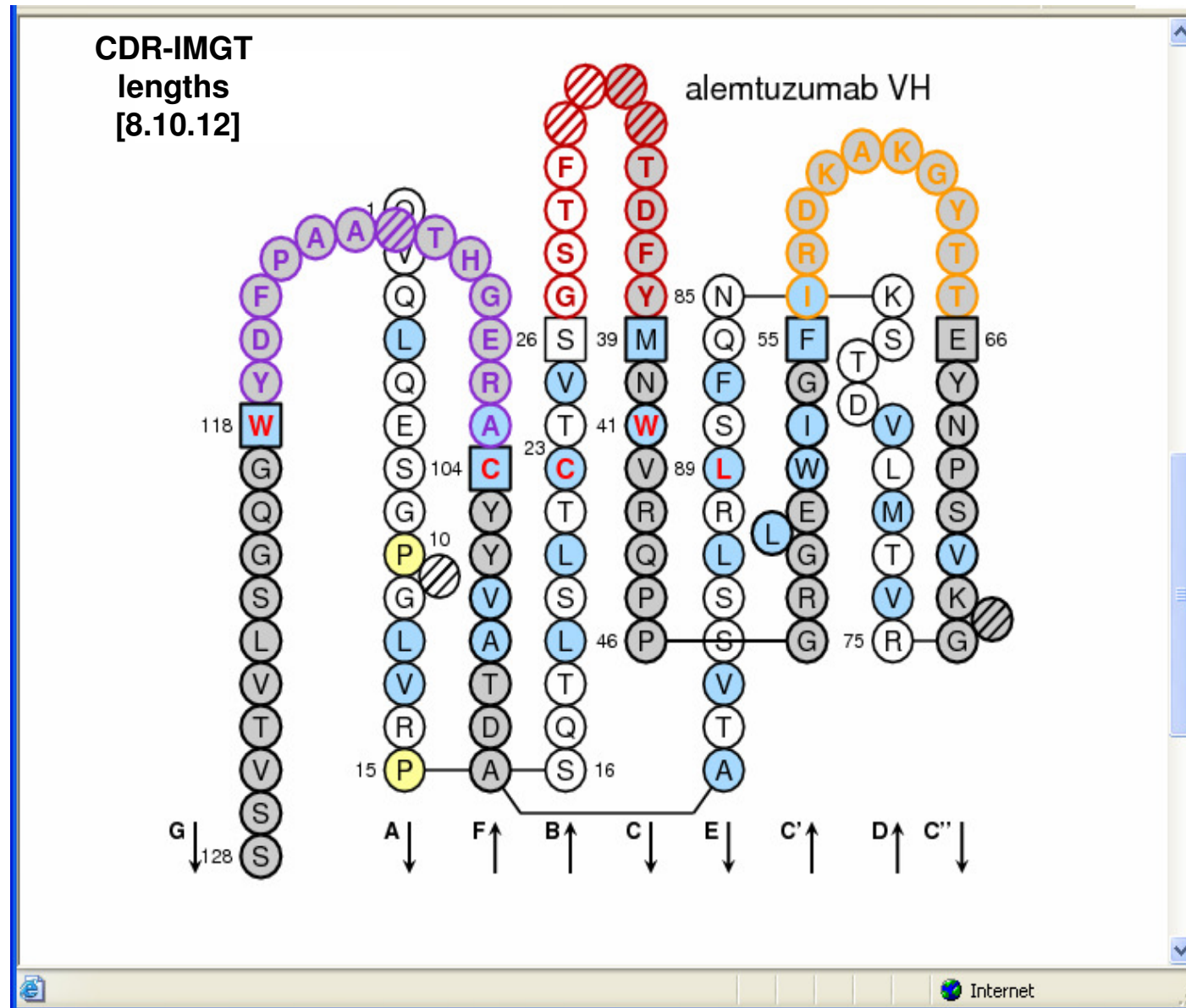
- The IMGT-ONTOLOGY concepts of description comprise the standardized **IMGT labels** and relations.
- The IMGT-ONTOLOGY concepts of description allow **to describe** the IG, TR and MHC sequences and 3D structures, **whatever the receptor type, the chain type, or the species.**
- It is possible **to query** the IMGT® databases (**IMGT/LIGM-DB** for sequences, **IMGT/3Dstructure-DB** for 3D structures) with IMGT labels.
- They are particularly useful to describe IG, TR, and MHC and their complexes (**IG/antigen, TR/pMHC**).
- Sequence Ontology (SO) includes IMGT labels.

NUMEROTATION axiom

IMGT
Collier
de
Perles



IMGT Collier de Perles on two layers



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

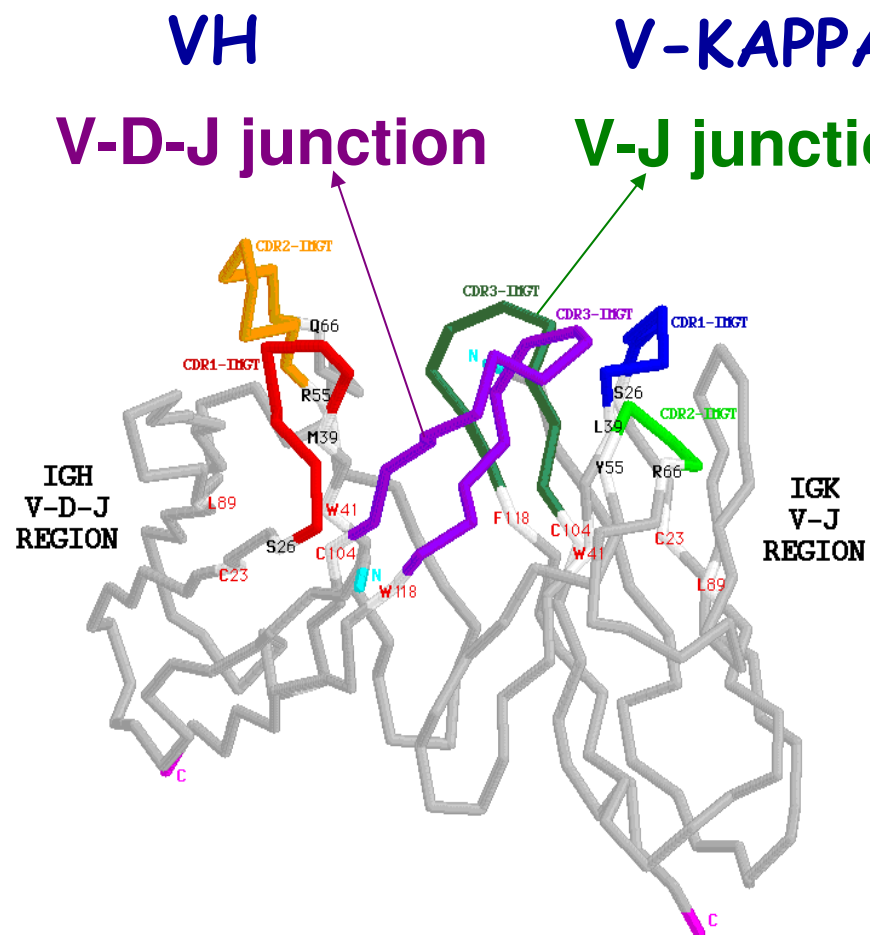
The eleven IMGT amino acid classes according to the physicochemical properties

'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		P T		D N
Very small	60-90	A	G S		
		Aliphatic	Sulfur	Hydroxyl	Basic
					Acidic
					Amide
		Uncharged		Charged	Uncharged
		Nonpolar		Polar	

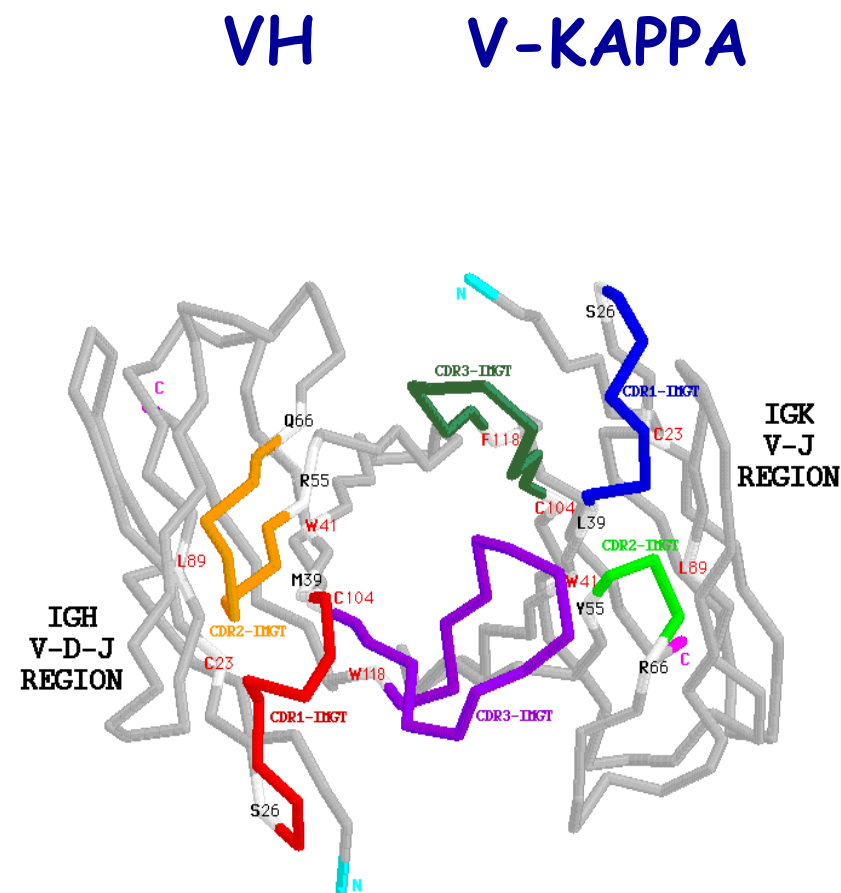
NUMEROTATION axiom

- The IMGT-ONTOLOGY concepts of numerotation include **IMGT unique numbering** and **IMGT Collier de Perles** for V-DOMAIN (**IG** and **TR**).
- The IMGT-ONTOLOGY concepts of numerotation allow to bridge the gap between sequences and 3D structures.
- They allow to define the **CDR-IMGT** lengths.
- They have been extended to the C-DOMAIN (**IG** and **TR**) and G-DOMAIN (**MHC**).
- They are used for mutations, polymorphisms, contact analysis, potential immunogenicity evaluation and paratope definition.

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
 § 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®



<http://imgt.cines.fr>

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	tcgaatttttgagtggtt.....	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	gcg	aga	gaa	gat	agc	aat	ggc							tac	aaa	ata	ttt	gac	tac	tgg			
#2 Z47269	C	A	R	G	G	A	K	V	E	F	L	E	W	F	H	G	Y	W	F	D	P	W	+	20
	tgt	gcg	aga	ggg	ggg	gct	aag	gtc	gaa	ttt	ttg	gag	tgg	ttt	cat	ggg	tac	tgg	ttc	gac	ccc	tgg		

IMGT/JunctionAnalysis: analysis of the IG and TR junctions



<http://imgt.cines.fr>

IMGT/JunctionAnalysis Results

Locus IGH
Species Homo sapiens
IMGT repertoire 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	tgtgtacg.....		tgttgt	gcagcgccctggtag	ccaaatatc		...actttgaccactgg	IGHJ4*02	IGHD6-13*01	1	2	1	5/15
#2	Z70257	IGHV3-7*02	tgtgcgag.		ggatgg	cagctccttatgcc	cgccc		ctactgggtacttcgatctctgg	IGHJ2*01	IGHD2-2*01	0	2	0	9/11
#3	Z70606	IGHV4-31*03	tgtgcgagag.		c	.gactacg.....	cact		..atgcctttgatgtctgg	IGHJ3*01	IGHD4-17*01	0	0	0	3/5
#4	Z70608	IGHV4-39*05	tgtgc.		cagagta	acgatttttgagtggttatt.....	ccccggggga		..atgcctttgatctctgg	IGHJ3*02	IGHD3-3*01	0	0	0	12/17
#5	Z70610	IGHV4-34*09	tgtgcgagag.		tcgggag	cgatttttgagtggttatt.....	cccga	ca	tgatgcctttgatctctgg	IGHJ3*02	IGHD3-3*01	0	0	0	9/12
#6	Z70611	IGHV4-59*01	tgtgcgaga..		ca	tggttaactataa.	tgccggcggttg		...actgggtcgaccctgg	IGHJ5*02	IGHD3-9*01	0	2	0	9/13
#7	Z70613	IGHV4-59*01	tgtgcgagag.			cagcagctggtag	ctccct		ctttgactactgg	IGHJ4*02	IGHD6-13*01	0	0	0	4/6
#8	Z70614	IGHV4-59*01	tgtgcgaga..		cactataa	ttcgggggacttat.....	cccctc		gactactgg	IGHJ4*02	IGHD3-16*01	0	2	0	7/14
#9	Z70615	IGHV4-59*01	tgtgcgagag.		ggctg	gtaaagaggg.....	tttcggaa		.tactgggtacttcgatctctgg	IGHJ2*01	IGHD5-24*01	0	2	0	7/13
#10	Z70616	IGHV4-34*01	tgtgcgagag.		cgg	gtttggg.....	ttccc		...actgggtcgaccctgg	IGHJ5*02	IGHD3-16*01	0	0	0	6/8
#11	Z70620	IGHV4-30-4*01	tgtgcgagaga		cc	gggggggagtggtt.....	cgg		.gatgcctttgatctctgg	IGHJ3*02	IGHD3-16*01	1	4	0	5/5
#12	Z70621	IGHV4-39*01	tgtgcgagaca		ccacgatttatgg	ttcgggggagtt.....	tgaccccc		ttgactactgg	IGHJ4*02	IGHD3-16*01	0	1	0	12/21
#13	Z70622	IGHV4-39*06	tgtgcgagaga	t	tgccccgcctctgcacaaat	gtattactatggttcgggga.....	tatgtacg		tttgactactgg	IGHJ4*03	IGHD3-10*01	0	0	0	15/28

IMGT/JunctionAnalysis: analysis of the IG and TR junctions



<http://imgt.cines.fr>

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	<u>gag</u>	<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	<u>gag</u>	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 <http://imgt.cines.fr>

V-QUEST Search Page - Mozilla Firefox

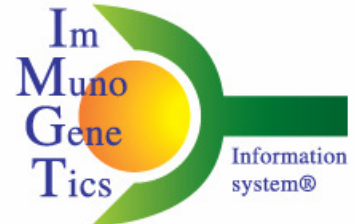
File Edit View History Bookmarks Tools Help

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

Most Visited Getting Started Latest Headlines tomcat Outils linguistiques

WELCOME ! to IMGT/V-QUEST

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<http://imgt.cines.fr>

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
 Rat	 Channel catfish
 Chondrichthyes	 Rainbow trout
	 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

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<http://imgt.cines.fr>

Citing IMGT/V-QUEST: Brochet, X. et al., Nucl. Acids Res. 36, W503-508 (2008). [PMID: 18503082](https://pubmed.ncbi.nlm.nih.gov/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
tcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcc
cctggacaagggttgagtggatgggatggatcagcgttacaatggtaacacaaactat
gcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctac
atggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgagaggtata
cgtgcttttgatatctggggccaagggaacacgggtcacccgtctcgcagc
>seq1
caggtgcagctggtgcagctctggggctgaagtgaagaagcctgggtcctcgtgaaggtc
tcctgcaaggcttttgagtcaccttcagtagttacgctatcagctgggtgcgacaggcc
cctggacaagggttgagtggatgggatgggatcatccctttgttcggaaaggcaaaactac
```

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

Done

IMGT/V-QUEST Selection for results display



<http://imgt.cines.fr>

```
>seq2
caggtgcagctggtgcagctctggggctgaagtgaagaagcctgggtcctcggtgaaggtc
tcctgcaaggcttttggagtcaccttcagtagttacgctatcagctgggtgcgacaggcc
cctggacaagggcctgagtggaaggaggatcacccttctgttcggaaaggcaactac
```

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

Selection for results display

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

Selection for
results
displays

IMGT/V-QUEST Advanced parameters



<http://imgt.cines.fr>

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

Selection for results display

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

☒ 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)

Nb of accepted mutations:

in 3'-V-REGION

in D-REGION

in 5'-J-REGION

Parameters for "Detailed view"

Nb of nucleotides to exclude in 5' of the V-REGION for the evaluation of the nb of mutations (in results 9 and 10)

Nb of nucleotides to add (or exclude) in 3' of the V-REGION for the evaluation of the alignment score (in results 1)

Done

IMGT/V-QUEST 'Detailed view':

Result summary table



<http://imgt.cines.fr>

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
caggtgcagctggtgcagctctggagctgaggtgaagaagcctggggcctcagtgaaagtc
tcctgcaaggcttctggttacacctttaccagctatggtatcagctgggtgcgacaggcc
cctggacaagggttgagtggatggatggatcagcgcttacaatggttaacacaaactat
gcacagaagctccagggcagagtcacacatgaccacagacacatccacgagcacagcctac
atggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgagaggtata
cgtgcttttgatatctggggccaagggaaccacggtcacggtctcagc
```

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
caggtgcagctgggtcagctctggagctgaggtgaagaagcctggggcctcagtgaaggtc
tcctgcaaggcttctgttacacctttaccagctatggtatcagctgggtgacacaggcc
cctggacaagggcttgatggatggatggatcagcgcttacaatggttaacacaaactat
gcacagaagctccagggcagagtcacccatgaccacagacacatccacgagcacagcctac
atggagctgaggagcctgagatctgacgacacggcgtgtattactgtgcgagaggtata
cgtgcttttgatatctggggccaagggaccacgggtcacgcgtctcgagc
```

Automatic evaluation

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



<http://imgt.cines.fr>

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
caggtgcagctggtgcagctctggagctgaggtgaagaagcctggggcctcagtgaggctc
tcctgcaaggctctctggttacacctttaccagctatggtatcagctgggtgacagggcc
cctggacaagggtctgagtggtggatggatgagcgttacatggtaacacaaactat
gcacagaagctccagggcagagtcacccatgaccacagacacatccacgagcacagcctac
atggagctgaggagcctgagatctgacgacacggccgtgtattactgtgagaggtata
cgtgcttttgatatctggggccaagggaaccacggtcaccgtctcgagc
```

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



<http://imgt.cines.fr>

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
tcctgcaaggcttctgttacacctttaccagctatggtatcagctgggtgacacaggcc
cctggacaaggccttgatggatggatggatcagcgttacaatggaacacaaactat
gcacagaagctccagggcagagtcaccatgaccacagacacatccacgagcacagcctac
atggagctgaggagcctgagatctgacgacacggcgtgtattactgtgcgagaggtata
cgtgcttttgatatctggggccaagggaaccacgggtcacgcgtctcgagc
```

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



<http://imgt.cines.fr>

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
caggtgcagctgggtgcagctctggagctgaggtgaagaagcctggggcctcagtgaaagtc
tcctgcaaggcttctctgttacacctttaccagctatggtatcagctgggtgacacaggcc
cctggacaagggcttgatggatggatggatcagcgttacaatggaacacaaactat
gcacagaagctccagggcagagtcacccatgaccacagacacatccacgagcacagcctac
atggagctgaggagcctgagatctgacgacacggccgtgtattactgtgcgagaggtata
cgtgcttttgatatctggggccaagggaccacggtcacccgtctcgagc
```

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



<http://imgt.cines.fr>

Sequence number 2: seq_2

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

```
>seq_2
gaggtgcagctggtggagtctgggggaggcttggtaaagccgggggggtccctgagactc
tcccggtgcagcctctggattcaccttcagtgaactactacatgaactgggtccgccaggct
ccagggaaggggctggagtggggctcatccattactagtagtagtactatatattacgca
gactctgtgaagggccgattcaccatctccagagacaacgccaagaactaactgtatctg
caaatgaagagcctgagagttgaggacacggctgtgcattactgttcgagagataaggtc
gagtaggtattacgatttttggagtgggtatttttacgaagaaactggttcgacccctggg
gccagggaacccctggtcaccgtctcctcag
```

Result summary:	Unproductive IGH rearranged sequence (stop codons, out-of-frame junction)		
V-GENE and allele	IGHV3-h*01(P)	score = 1321	identity = 96.14% (274/285 nt)
J-GENE and allele	IGHJ5*02	score = 237	identity = 96.08% (49/51 nt)
D-GENE and allele by IMGT/JunctionAnalysis	IGHD3-3*01	D-REGION is in reading frame 3	
[CDR1-IMGT.CDR2-IMGT.CDR3-IMGT] lengths and AA JUNCTION	[8.7.X]	CSRDKVE*VLRFLFWLFYE#NWFDPW	

Done

IMGT/V-QUEST 'Detailed view': selections



<http://imgt.cines.fr>

Nucleotide sequences

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

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

```
>seq1
caggtgcagctggtgcagctctggggctgaagtgaagaagcctgggtcctcggggaaggtc
tcctgcaagccttttggagtcaccttcagtagttacgtatcagctgggtgcgacaggcc
cctggacaaggcctgagtggtggaggatcatcccttgggtcgaaaggcaaaactac
gcacagaagtccaggggcagagtcacgattaccgcggaagcgcacacgagcaggtctac
atggaggtgagcagcctgagatctgaggacacggcctgtattattgtgcgagacaatat
ggtagtagtggttattacgcctactggggccacggaaccctggtcacogtct
>seq 2
gaggtgcagctggtggagtcctgggggagggccttggtaaagccgggggggtccctgagactc
tcccgtagcgcctctggattcaccttcagtgactactacatgaactgggtccggcaggct
ccagggaaggggctggagtggggctcatccattactagtagtagtactatatattacgca
```

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

Selection for results display

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 |

Done

IMGT/V-QUEST 'Detailed view':

1. Alignments for V-, D-, and J-GENE

V-GENE

1. Alignment for V-GENE and allele identification

Closest V-REGIONS (evaluated from the V-REGION first nucleotide to the 2nd-CYS codon)

	Score	Identity
Z27508 IGHV3-73*01	1240	91.50% (269/294 nt)
AB019437 IGHV3-73*02	1231	91.16% (268/294 nt)
X92206 IGHV3-72*01	1024	83.33% (245/294 nt)
X92216 IGHV3-15*01	979	81.63% (240/294 nt)
M99406 IGHV3-15*07	979	81.63% (240/294 nt)

Alignment with FR-IMGT and CDR-IMGT delimitations

```
seq1
Z27508 IGHV3-73*01
AB019437 IGHV3-73*02
X92206 IGHV3-72*01
X92216 IGHV3-15*01
M99406 IGHV3-15*07

<-----FR1-IMGT-----
gaggtgcagctggtggagtctggggga...ggcttagtccagcctg
-----g-----
-----c-----g-----
-----g-----
-----g-aa-----
-----g-aa-----

----->-----CDR1-IMGT-----
ctctcctgtgcagcctctgggttcaccctc.....agtg
-----t-----
-----t-----
-----a-----t-----
-----a-----tt-----a
-----t-----tt-----a
```

Score and nucleotide identity

D-GENE

2. Alignment for D-GENE and allele identification

Closest D-REGIONS

	Score	Identity
X13972 IGHD3-10*01	28	72.73% (8/11 nt)
X93615 IGHD3-10*02	19	63.64% (7/11 nt)
J00256 IGHD7-27*01	14	60.00% (6/10 nt)
X97051 IGHD3-16*02	13	62.50% (5/8 nt)
X93614 IGHD3-16*01	10	54.55% (6/11 nt)

Alignment

```
seq1
X13972 IGHD3-10*01
X93615 IGHD3-10*02
J00256 IGHD7-27*01
X97051 IGHD3-16*02
X93614 IGHD3-16*01

gtgatccgggg
a--g-t-----agttattataac
a--t--g---agttattataac
.ct-a-t-----a
--t--a-c
ac-t-tg---agttatgcttatacc
```

J-GENE

3. Alignment for J-GENE and allele identification

Closest J-REGIONS

	Score	Identity
J00256 IGHJ1*01	179	82.69% (43/52 nt)
X86355 IGHJ4*02	150	79.17% (38/48 nt)
J00256 IGHJ4*01	141	77.08% (37/48 nt)
X86355 IGHJ5*02	138	74.51% (38/51 nt)
M25625 IGHJ4*03	132	75.00% (36/48 nt)

Note that the highest number of consecutive identical nucleotides has been found in the alignment with IGHJ4*02 and IGHJ5*02

Alignment

```
seq1
J00256 IGHJ1*01
X86355 IGHJ4*02
J00256 IGHJ4*01
X86355 IGHJ5*02
M25625 IGHJ4*03

gtgatccgggggagatgtttacaaccgacagtggggccaggaa
.....-c--aa--tt--ag--c-----c-
.....ac---tttgact-c-----
.....ac---tttgact-c-----a---
.....-caac-gggt-gac-cc-----
.....gc---tttgact-c-----a--g-
```

IMGT/V-QUEST 'Detailed view':

4. Results of IMGT/JunctionAnalysis



<http://imgt.cines.fr>

4. Results of IMGT/JunctionAnalysis

Maximum number of accepted mutations in: 3'V-REGION = 2, D-REGION = 4, 5'J-REGION = 2

Analysis of the JUNCTION

D-REGION is in reading frame 3.

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



Input	V name	3'V-REGION	N1	D-REGION	N2	5'J-REGION	J name	D name	Vmut	Dmut	Jmut	Ngc
AF184762	IGHV3-73*01	tgt <u>.....</u> g		tgatcgcgggagatggt.....	tacaaccga	cagtg	IGHJ1*01	IGHD3-10*01	0	4	1	5/10

Translation of the JUNCTION

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



	104	105	106	107	108	109	113	114	115	116	117	118	Frame	CDR3-IMGT length	Molecular mass	pI
	C	V	I	R	G	D	V	Y	N	R	Q	W				
AF184762	tgt	gtg	<u>atc</u>	cgg	gga	<u>gat</u>	ggt	tac	aac	cga	cag	tgg	+	10	1,508.72	9.24

IMGT/V-QUEST 'Detailed view':

4. Results of IMGT/JunctionAnalysis



<http://imgt.cines.fr>

4. Results of IMGT/JunctionAnalysis

Maximum number of accepted mutations in: 3'V-REGION = 2, D-REGION = 4, 5'J-REGION = 2

Analysis of the JUNCTION

D-REGION is in reading frame 2.

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



Input	V name	3'V-REGION	N1	D-REGION	N2	5'J-REGION	J name	D name	Vmut	Dmut	Jmut	Ngc
seq1	IGHV1-69*01	tgtgcgaga..	caa	tatggtagtagtggtattac...	gc	ctactgg	IGHJ4*01	IGHD3-22*01	0	1	0	3/5

Translation of the JUNCTION

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



	104	105	106	107	108	109	110	112	113	114	115	116	117	118	Frame	CDR3-IMGT length	Molecular mass	pI
	C	A	R	Q	Y	G	S	S	G	Y	Y	A	Y	W				
seq1	tgt	gcg	aga	caa	tat	ggt	agt	agt	ggt	tat	tac	gcc	tac	tgg	+	12	1,674.81	8.89

Be aware that some allele reference sequences may be incomplete or from cDNAs. In those cases, IMGT/JunctionAnalysis uses automatically the allele *01 for the analysis of the JUNCTION.

Terminé

zotero

IMGT/V-QUEST 'Detailed view':

7. V-REGION translation



<http://imgt.cines.fr>

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 -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 -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

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>A (- - -) a258>g c260>t, A87>V (+ - +) c271>g, L91>V (+ - +) c309>t	g319>c



Terminé



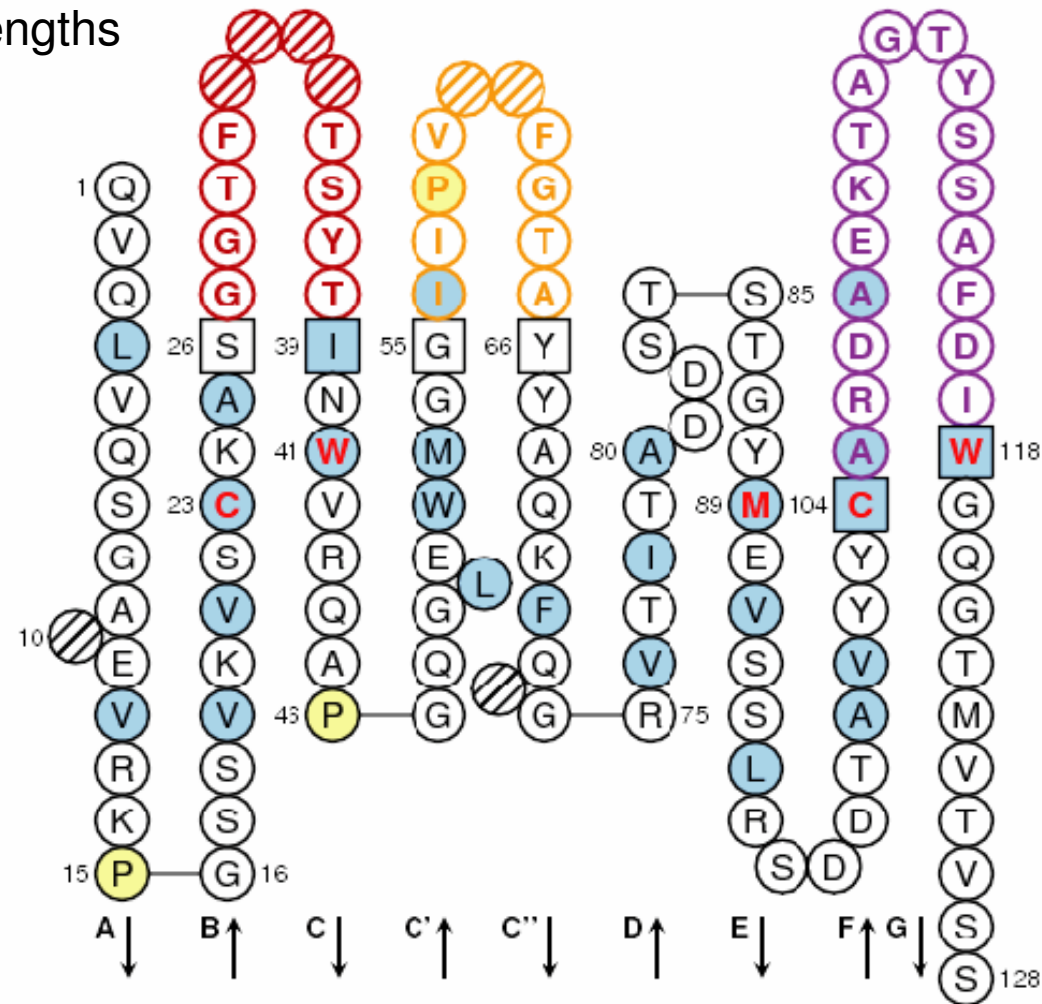
zotero

Hydropathy (+ : conserved)
Volume (- : different)
Physicochemical properties (+ : conserved)

IMGT/V-QUEST 'Detailed view':

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

CDR-IMGT lengths
[8.8.17]



IMGT/V-QUEST Advanced parameters: Search for insertions and deletions



<http://imgt.cines.fr>

IMGT/V-QUEST - Mozilla Firefox

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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: 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) default	Nb of accepted mutations: <table border="0"><tr><td> default </td><td>in 3'V-REGION</td></tr><tr><td> default </td><td>in D-REGION</td></tr><tr><td> default </td><td>in 5'J-REGION</td></tr></table>	default	in 3'V-REGION	default	in D-REGION	default	in 5'J-REGION
default	in 3'V-REGION							
default	in D-REGION							
default	in 5'J-REGION							
Parameters for "Detailed view"	Nb of nucleotides to exclude in 5' of the V-REGION for the evaluation of the nb of mutations (in results 9 and 10) 	Nb of nucleotides to add (or exclude) in 3' of the V-REGION for the evaluation of the alignment score (in results 1) 						

Done

IMGT/V-QUEST Advanced parameters:

Result summary for sequences with insertions



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Sequence number 1: seq1

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

```
>seq1
gaggtgaaggtggtcagtcctggagcagaggtgaaaaagcccgaggagtctctgcacatc
tcctgtcagatttcGCAGACGGTcagacgactttaccactctctggatcggtgggtg
cgccagatgcccgggaaagggtggagtggatggggatcatctggcctggtgactctgat
accacatacagtcctccttccaaggccagctctccatttcagccgacaagtccaccagt
accgcctaccttcagtgagcagcctgaaggcctcggactccgccatgtattactgtgcg
accaacagtggttattaccccggggatggccttgattactggggccagggaaccctgac
attgtctcctca
```

Result summary:

Nucleotide insertions have been detected and automatically removed for this analysis: they are displayed as capital letters in the user submitted sequence above.

localization in V-REGION	nb of inserted nt	inserted nt	causing frameshift	from V-REGION codon	from nt position in user submitted sequence
CDR1-IMGT	9	GCAGACGGT	no	27	76

IMGT/V-QUEST results after removal of the insertion(s):

Potentially productive IGH rearranged sequence: no stop codon and in-frame junction

(Check also your sequence with [BLAST](#) against IMGT/GENE-DB reference sequences to eventually identify out-of-frame pseudogenes)

V-GENE and allele	IGHV5-51*01	score = 1201	identity = 90.97% (262/288 nt)
J-GENE and allele	IGHJ4*02	score = 172	identity = 85.11% (40/47 nt)
D-GENE and allele by IMGT/JunctionAnalysis	IGHD3-22*01	D-REGION is in reading frame 2	
[CDR1-IMGT.CDR2-IMGT.CDR3-IMGT] lengths and AA JUNCTION	[8.8.14]	CATNSGYYPGDGFDYW	

Done

IMGT/V-QUEST Advanced parameters:

Result summary for sequences with deletions



<http://imgt.cines.fr>

Result summary:	Nucleotide deletions have been detected (shown by dots in the alignments):			
	localization	nb of deleted nt	causing frame shift	from V-REGION codon
	CDR2-IMGT	3	no	64
from nt position in user submitted sequence 226				
IMGT/V-QUEST results after filling the deletion(s) gap(s): Potentially productive IGH rearranged sequence: no stop codon and in-frame junction (Check also your sequence with BLAST against IMGT/GENE-DB reference sequences to eventually identify out-of-frame pseudogenes)				
V-GENE and allele	IGHV1-46*01, or IGHV1-46*02 or IGHV1-46*03		score = 1186	identity = 90.88% (259/285 nt)
J-GENE and allele	IGHJ4*02		score = 145	identity = 78.72% (37/47 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	[8.7.12]		CAGVQGVARPLGDW	

1. Alignment for V-GENE and allele identification

Closest V-REGIONS (evaluated from the V-REGION first nucleotide to the 2nd-CYS codon)

	Score	Identity
X92343 IGHV1-46*01	1186	90.88% (259/285 nt)
J00240 IGHV1-46*02	1186	90.88% (259/285 nt)
L06612 IGHV1-46*03	1186	90.88% (259/285 nt)
X62106 IGHV1-2*02	1051	85.61% (244/285 nt)
Z12310 IGHV1-2*04	1042	85.26% (243/285 nt)

Alignment with [FR-IMGT](#) and [CDR-IMGT](#) delimitations

	FR1-IMGT	CDR1-IMGT
seq1	caggtgcagctgctgcagctctggggct...gaggtgaggaagcctggggcctcagtgaaaaattctcctgcaagccatctggcttctccttc.....atcacctactattttcac	
X92343 IGHV1-46*01	-----g-----a-----gg-----g-----a-a-a-----C-g-----a-g-----	
J00240 IGHV1-46*02	-----g-----a-----gg-----g-----a-a-a-----a-g-----a-g-----	
L06612 IGHV1-46*03	-----g-----a-----gg-----g-----a-a-a-----C-g-----a-g-----	
X62106 IGHV1-2*02	-----g-----a-----gg-c-----g-t-----a-a-a-----c-gg-----a-g-----	
Z12310 IGHV1-2*04	-----g-----a-----gg-c-----g-t-----a-a-a-----C-gg-----a-g-----	
	FR2-IMGT	CDR2-IMGT
seq1	tgggtgcgacaggcccccggacaggggcttgagtgagtgaggagtaatcaaccctagt.....ggtggc...caacctactcacagaagtccag...ggcagagtcgcatgaccagg	
X92343 IGHV1-46*01	-----t-----a-----a-----tagc-----g-----g-----a-----	
J00240 IGHV1-46*02	-----t-----a-----a-----tagc-----g-----g-----a-----	
L06612 IGHV1-46*03	-----t-----a-----a-----tagc-----g-----g-----a-----	
X62106 IGHV1-2*02	-----t-----tgg-----ac-----a-----tggc-----a-----tg-----g-----a-----	
Z12310 IGHV1-2*04	-----t-----tgg-----ac-----a-----tggc-----a-----tg-----t-----g-----a-----	

Done

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



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Number of analysed sequences: 7

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

Summary table:

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]	CARGGDYDYIWGSYRASDAFDIW	in-frame
seq2	IGHV1-69*06	Productive	1300	94,79% (273/288 nt)	IGHJ4*01	IGHD6-13*01	1	[8.8.21]	CARERVGAYTSSWYG DYVSFDYW	in-frame
seq3	IGHV4-34*01	Productive	1411	99,30% (283/285 nt)	IGHJ6*02	IGHD2-2*02	3	[8.7.20]	CWIVVPA AIVPNYYYYGMDVW	in-frame
seq4	IGHV4-34*01	Productive	1294	95,09% (271/285 nt)	IGHJ6*02	IGHD3-10*01	2	[8.7.20]	CARDFSPSPPGHYDARNDMDVW	in-frame
seq5	IGHV4-34*01	Productive	1285	94,74% (270/285 nt)	IGHJ6*03	IGHD3-22*01	2	[8.7.21]	CARWYYFDTSGYYPRNFYYMDVW	in-frame
seq6	IGHV4-34*01	Productive	1258	93,68% (267/285 nt)	IGHJ6*02	IGHD2-2*02	3	[8.7.25]	CARGHKTAIREPPTIGPIIYSDMDVW	in-frame
seq7	IGHV4-34*01	Productive	1420	100,00% (285/285 nt)	IGHJ5*02	IGHD2-2*01	3	[8.7.25]	CARGDWRIVVPAAVDTAMAANWFDPW	in-frame

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

Alignment with the closest alleles:

The analysed sequences are aligned with the closest allele (with

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

Alignments of the 5 sequences with IGHV4-34*01

Terminé

zotero

‘Synthesis view’:

1. Alignment for V-GENE

Sequences aligned with IGHV4-34*01

1. Alignment for V-GENE

X92278 IGHV4-34*01
seq3
seq4
seq5
seq6
seq7

-----FRL-IMGT----->
cagggtgcagctacagcaggtggggcgca...ggactgttgaagccttcggagaccctgtccctcaccctgcgcctgtctatgtgtgggtcctc
-----cg-a-----
-----g-----c-----t-----t-----

X92278 IGHV4-34*01
seq3
seq4
seq5
seq6
seq7

CDR1-IMGT	<	FR2-IMGT	>	CDR2
.....	agtggttactactggagctggatccgccagcccccagggaaggggctggagtggaattgggggaatcaatcatagt.			
.....	-c-	-c-	-c-	-t
.....	-t-	-g-	-c-	-t-
.....	-a-	-c-	-a-	-g-a-g-

X92278 IGHV4-34*01
seq3
seq4
seq5
seq6
seq7

```

2-IMGT          <                                     FR3-IMGT
..... ggaagcaccacaactacaacccgctccctcaag... agtcgagtcaccatatcagtagacacgtccaagaaccagttctccctgaag
.....
..... -g-t-      -t-          -c-      -t-          -t-a-      -t-
..... -t--t--c-      -gt-      -gc-...          -g-      -a-          -g-

```

X92278 IGHV4-34*01
seq3
seq4
seq5
seq6
seq7

-----> CDR3-IMGT
 ctgagcctctgtgaccgccgcggacacggctgtgtattactgtgcgagagg
 -----ctg--tt-tagtagtaccagctgctatagtaccacactactactactac
 g--c-----at-ttttgcgcctcgccccgggacactatgatgcgaggagaac
 -----t-----gt-gtattactttgatactagtgtgtattaccocccgaacttc
 -a-----c-----ccataagaccgcgaatcagagaaccactactatagggcct
 -----t-----cgattgcgcatttgttaactaccagctactctggatatac

X92278 IGHV4-34*01
seq3
seq4
seq5
seq6
seq7

ggtatggagcgtctggggccaagggaccacggtcacccgtctctctca
 gatatggagcgtctggggccacgggaccacggtcactgtctctctca
 tactacatggagcgtctggggccaaggggaccccggtcacccgtctctctca
 atttattactctctacgatggacgtctggggccaagggaccacggtcacccgtctctctca
 ggtatggcccttaactgtgttcaccccttgaggacacggaacctgttcaccgtctctctcaag

IGHJ6*02
IGHJ6*02
IGHJ6*03
IGHJ6*02
IGHJ5*02

IMGT/V-QUEST 'Synthesis view':

8. Results of IMGT/JunctionAnalysis

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.....	tgcgcggaaggggt	ctttgagtactgg	IGHJ4*02	IGHD4-4*01	0	0	2	20/28
seq2	IGHV3-30*04	tgtgcgagaga		tcgga		..gtatagcagtggc.....	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

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