

# IMGT®, the international ImMunoGeneTics information system®

<http://imgt.cines.fr>

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Educational sessions, Bioinformatics in immunogenetics  
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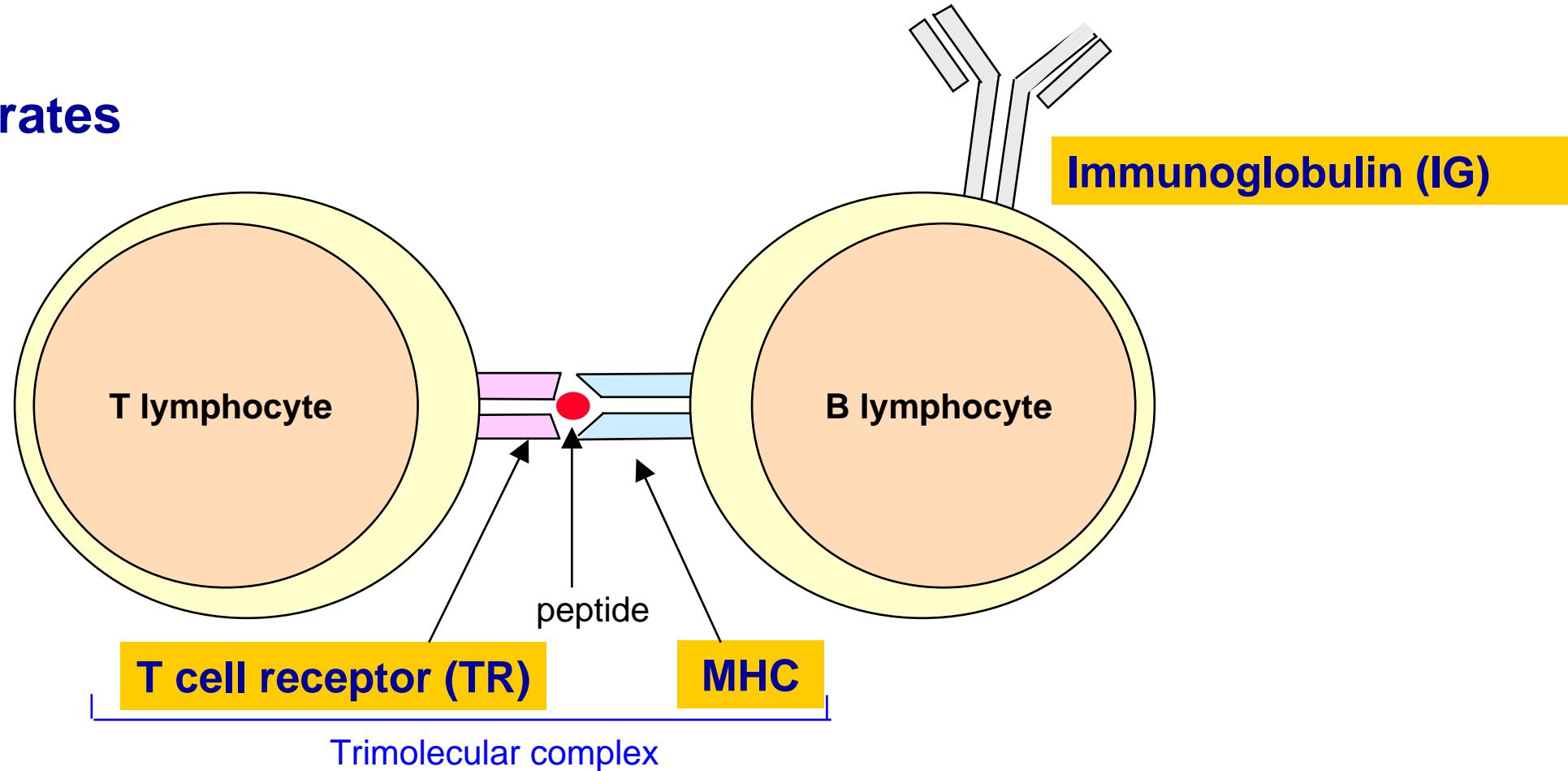


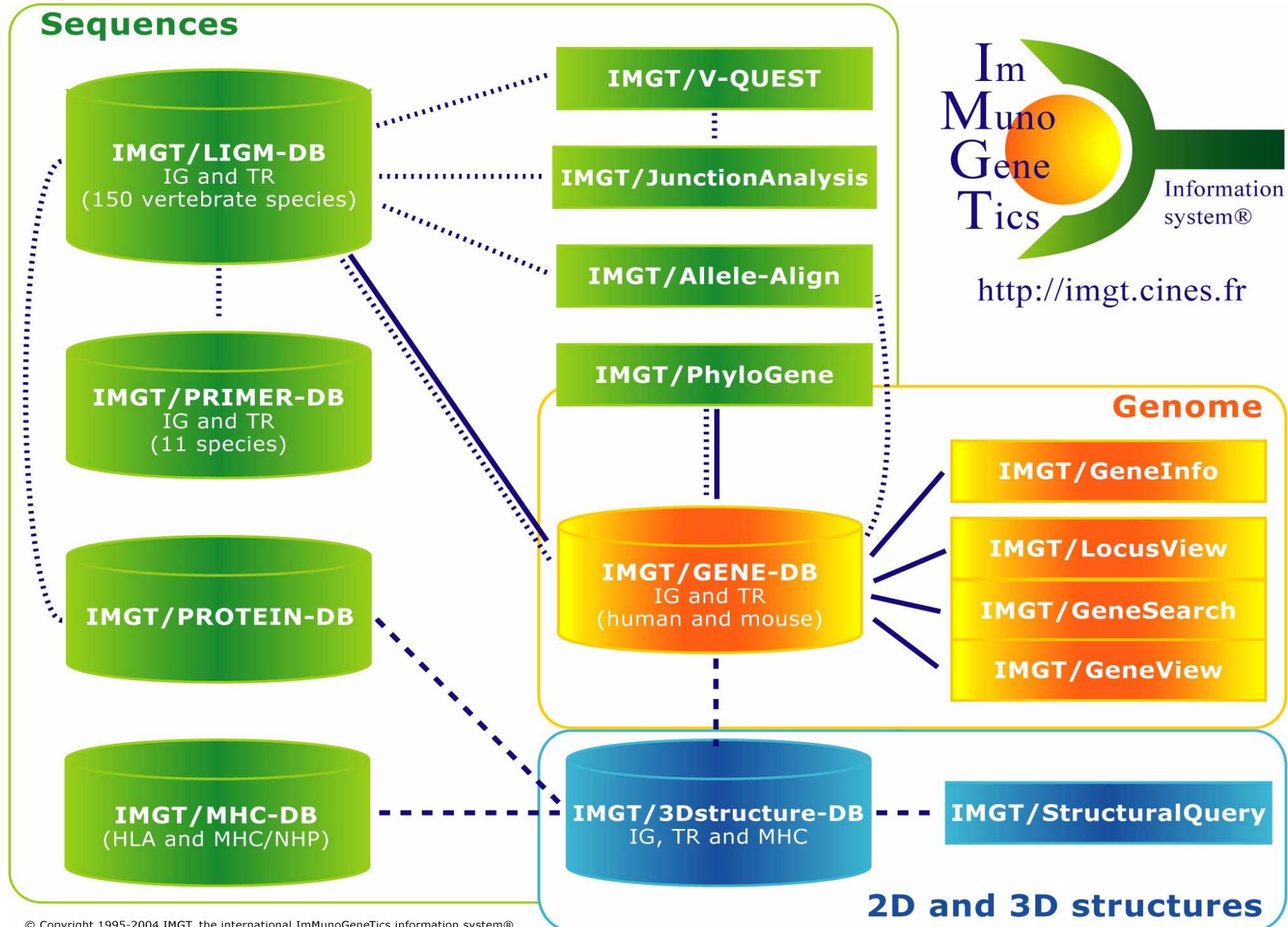
IMGT®, the international ImMunoGeneTics information system® Montpellier, France <http://imgt.cines.fr>  
IMGT founder and director: M.-P. Lefranc



# IMGT®, the international ImMunoGeneTics information system® <http://imgt.cines.fr>

## Vertebrates





# WELCOME !

## to the IMGT Home page

THE INTERNATIONAL  
IMMUNOGENETICS  
INFORMATION SYSTEM®



IMGT®, the international ImMunoGeneTics information system® <http://imgt.cines.fr>, is a high-quality integrated knowledge resource specialized in the immunoglobulins (IG), T cell receptors (TR), major histocompatibility complex (MHC), immunoglobulin superfamily (IgSF), major histocompatibility complex superfamily (MhcSF) and related proteins of the immune system (RPI) of human and other vertebrate species, created in 1989 by Marie-Paule Lefranc ([Université Montpellier 2, CNRS](#)). IMGT, a European project since 1992, works in close collaboration with EBI. IMGT consists of [sequence](#) databases (IMGT/LIGM-DB, a comprehensive database of IG and TR from human and other vertebrates, with translation for fully annotated sequences, IMGT/MHC-DB, IMGT/PRIMER-DB), [genome](#) database (IMGT/GENE-DB) and [structure](#) database (IMGT/3Dstructure-DB), [Web resources](#) (IMGT Marie-Paule page) and [interactive tools](#). The IMGT Home page <http://imgt.cines.fr> (Montpellier, France) provides a common access to all Immunogenetics data.

IMGT founder and director: [Marie-Paule Lefranc](mailto:Marie-Paule.Lefranc@igh.cnrs.fr) ([Marie-Paule.Lefranc@igh.cnrs.fr](mailto:Marie-Paule.Lefranc@igh.cnrs.fr)), Université Montpellier 2, CNRS, [LIGM](#), [IGH](#), [IFR3](#), Montpellier (France)

[IMGT Site Map](#)

[Information on IMGT® \(creations and updates, references, FAQ, citing IMGT, funding support...\)](#)



### IMGT databases

- [IMGT/LIGM-DB](#) (IG and TR from 221 species) (LIGM, Montpellier, France) (**122 084 entries**)
- [IMGT/MHC-DB](#) (IMGT/MHC-HLA, -NHP, -DLA, -FLA) (ANRI, BPRC, hosted at EBI)
- [IMGT/PRIMER-DB](#) (IG and TR from 11 species) (LIGM, Montpellier, France) (**1 864 entries**)
- [IMGT/GENE-DB](#) (IG and TR genes from human, mouse and rat) (LIGM, Montpellier, France) (**1 894 genes, 2 884 alleles**)
- [IMGT/3Dstructure-DB](#) (IG and TR, MHC and RPI gene and allele identification and IMGT Colliers de Perles) (**1 403 entries**)

### IMGT tools

- [IMGT/V-QUEST](#) (sequence alignment software for IG, TR and HLA)
- [IMGT/JunctionAnalysis](#) (for human and mouse IG and TR)
- [IMGT/Allele-Align](#)
- [IMGT/PhyloGene](#)
- [IMGT/DomainDisplay](#) (Amino acid sequences)
- [IMGT/LocusView](#), [IMGT/GeneView](#), [IMGT/GeneSearch](#), [IMGT/CloneSearch](#) (for human IGK, IGL, IGH, TRA/TRD, TRB, TRG, mouse TRA/TRD and human MHC)
- [IMGT/GenelInfo](#) (TIMC and ICH, Grenoble; LIGM, Montpellier)

### IMGT Web resources

- [IMGT Repertoire](#) (IG and TR, MHC and RPI)
- [IMGT Index](#) (FactsBook)
- [IMGT Scientific chart](#) (Sequence description, Numbering, Nomenclature, Representation rules)
- [IMGT Bloc-notes](#) (Interesting links, PubMed, Meeting announcements, Postdoctoral positions and jobs, Messages, Search engines...)
- [IMGT Education](#) (IMGT Lexique, Aide-mémoire, Tutorials, Questions and answers, Enseignements...)
- IMGT Medical page, IMGT Veterinary page, IMGT Biotechnology page
- IMGT Posters and diaporama
- [The IMGT Immunoinformatics page](#)

### IMGT other accesses

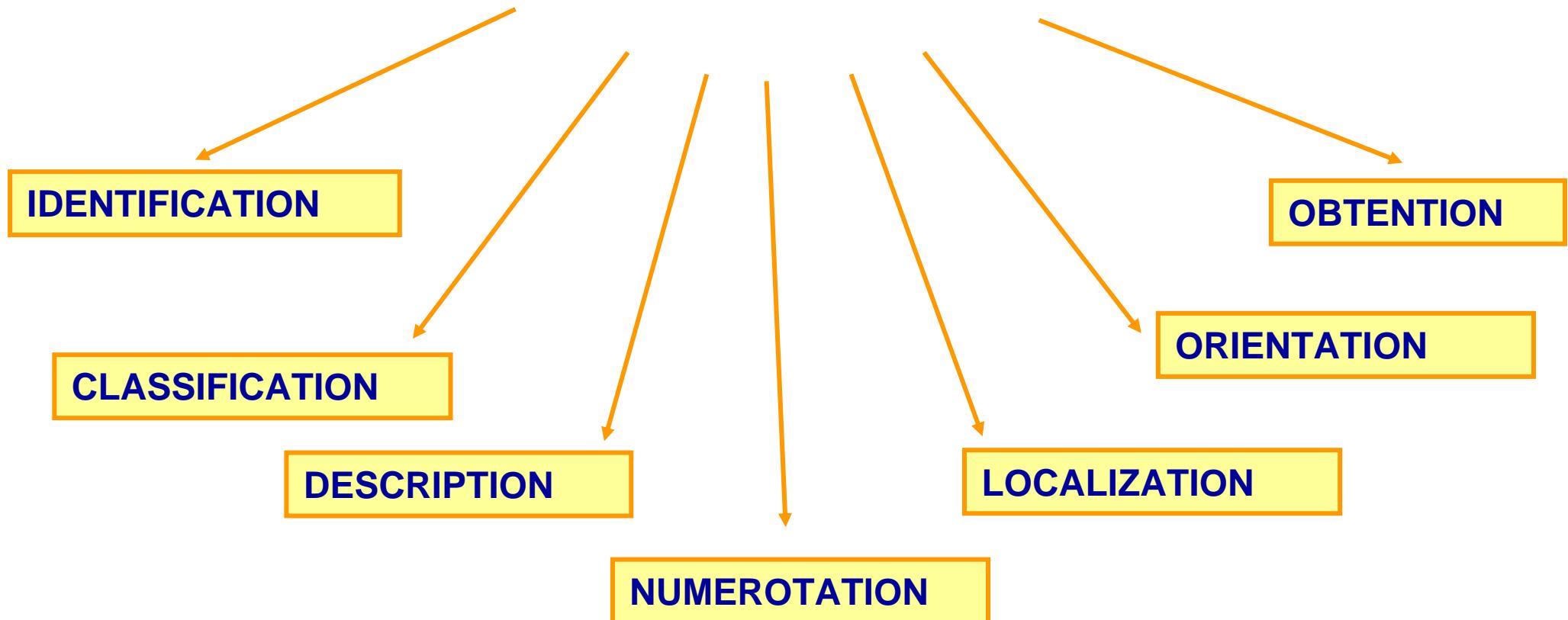
- IMGT Other accesses (SRS, FTP...)
- Compare your sequence against IMGT (BLAST, FASTA)
- IMGT/LIGM-DB Sequence submission
- IMGT flat file release information

Search

# IMGT-ONTOLOGY

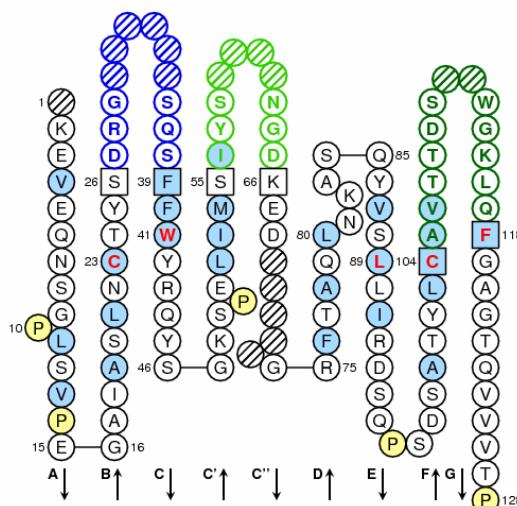
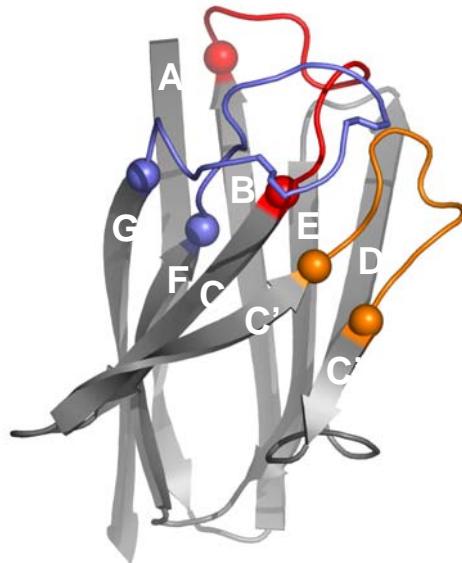
To standardize, to share, to reuse and to represent  
Immunogenetics knowledge

IMGT-ONTOLOGY relies on 7 axioms:

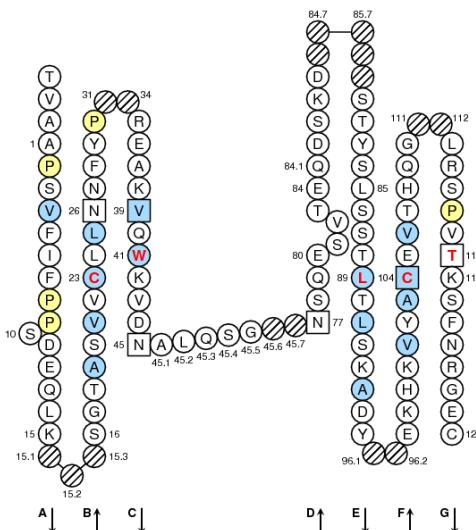
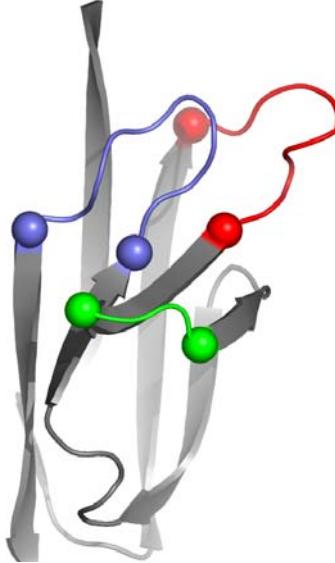


# IMGT unique numbering

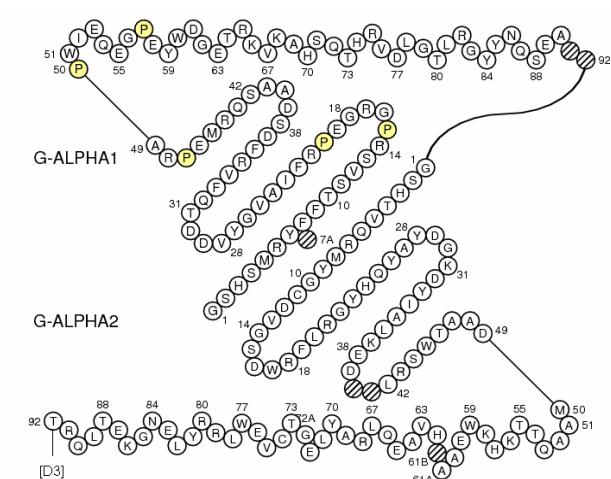
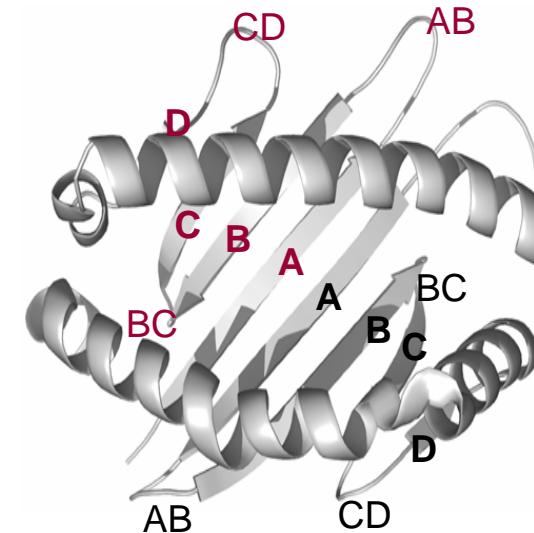
## V-DOMAIN (IG,TR)



## C-DOMAIN (IG,TR)



## G-DOMAIN (MHC)



Standardized description of the V-, C-, and G-DOMAINS, whatever the receptor, the chain type and the species.

# WELCOME !

## to IMGT/V-QUEST Search page

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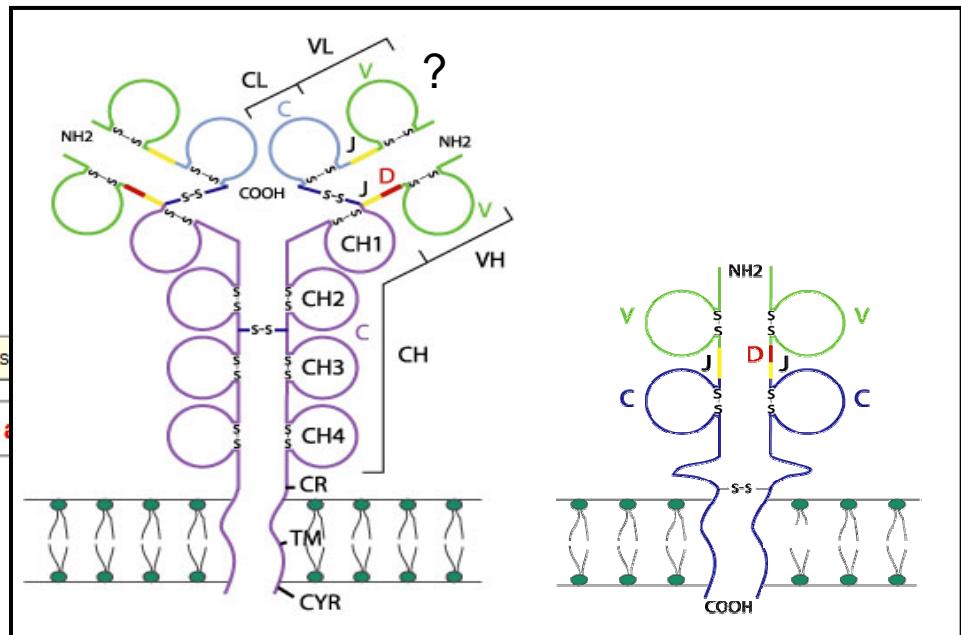
Citing IMGT/V-QUEST: Giudicelli, V. et al. Nucl. Acids Res.

From the Version 3.0.0 of IMGT/V-QUEST, gaps in CDR1-IMGT and CDR2-IMGT are indicated by question marks.

## 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 sets](#)



## Nucleotide sequences

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

Type (or copy/paste) your sequence(s) in **FASTA format**

```
>AF184762
atggagtttggctgagctgggtttcctgttctatttaaaagggtgtccactgttag
gtgcagctggggagtcggggggggcttagtccacgcctggggatccctgaaactctcc
tgtcagccctcggttccccctcgttggctcaatgtcactgggtccggcaggccccc
ggggaaagggtggagtggtgggtggcgatcaaaaggaaatgtcgtactgtgtggcggc
tatgtcgatggggcggctcaccatctccagatgttcaaaaggaaacacggcg
tttctgcataatgttcaacacggctgtggggatgttgcacggccatgttattttgtgtatccgg
ggagatgtttacaaccgcacagtggggccagggaaacctggtcacgtctccctcagcatcc
ccgaccagccccaaagggtttccctgtggcgttgcacgcacccaggccat
>AF069038
tcttcctccactgcacaagggtctctccctgtcatgttgcacgttgcacccatccat
```

Or give the path access to a local file containing your sequence(s) in **FASTA format**

Browse...

Done

# WELCOME ! to IMGT/V-QUEST Search page

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<http://imgt.cines.fr>

Citing IMGT/V-QUEST: Giudicelli, V. et al. Nucl. Acids Res. 32, W435-440 (2004). PMID: 15215425 [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 sets](#)

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](#)

```
>AF184762
atggagtttggctgagctgggtttcctgttctatttaaaagggtgtccactgtgag
gtgcagctggggagtctggggggaggcttagtccagcctggggatccctgaaactctcc
tgtcagccctcggttccccctcagtgctcaatgtcactggccggccaggccctcc
ggggaaagggtggagtggtgggtggccgtatcaaaaggatgtctgacgcacagca
tatgctgcgtcgatgagaggcaggctcaccatctccagagatgttcaaaagaacacggcg
tttctgc当地atgaaacagcctgaaaaggcgtatcacggccatgtattattgtgtatccgg
ggagatgtttacaaccgcacagtggggccagggaaacctggtcacogtctccatcgatcc
ccgaccagccccaaaggcttcccgtgacgcctctgcacgcacccagccat
>AF069038
tcttcctccactgcacaaggctctctcccggtcatgtgacgcaatccccctcta
```

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

[Browse...](#)

[Start](#) [Clear the form](#)

Done

**Selection for results display**

File Edit View History Bookmarks Tools Help

**Selection of results displays for 'Detailed view'**

**A. Detailed view**

Nb of nucleotides per line in alignments:

1.  Alignment for V-GENE  
 2.  Alignment for D-GENE  
 3.  Alignment for J-GENE  
 4.  Results of IMGT/JunctionAnalysis  
      with full list of eligible D-GENEs  
      without list of eligible D-GENEs  
 5.  Sequence of the JUNCTION ('nt' and 'AA')  
 6.  V-REGION alignment according to the IMGT numbering  
 7.  V-REGION translation  
 8.  V-REGION protein display  
 9.  V-REGION mutation table  
 10.  V-REGION mutation statistics  
 11.  V-REGION mutation hot spots  
 12. [IMGT Collier de Perles](#)  
      link to IMGT/Collier-de-Perles tool  
      IMGT Collier de Perles (for a nb of sequences < 5)  
      no IMGT Collier de Perles  
 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')  
 14.  Annotation by IMGT/Automat

**B. Synthesis view**

1.  Alignment for V-GENE  
 2.  V-REGION alignment according to the IMGT numbering  
 3.  V-REGION translation  
 4.  V-REGION protein display  
 5.  V-REGION protein display (with color)  
 6.  V-REGION protein display (only AA changes displayed)  
 7.  V-REGION most frequently occurring AA  
 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  
 Yes (slower, the nb of submitted sequences in a single run is limited to 10)

Search for insertions and deletions:  No

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 8 and 9)

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

Done

# A. 'Detailed view': Result summary

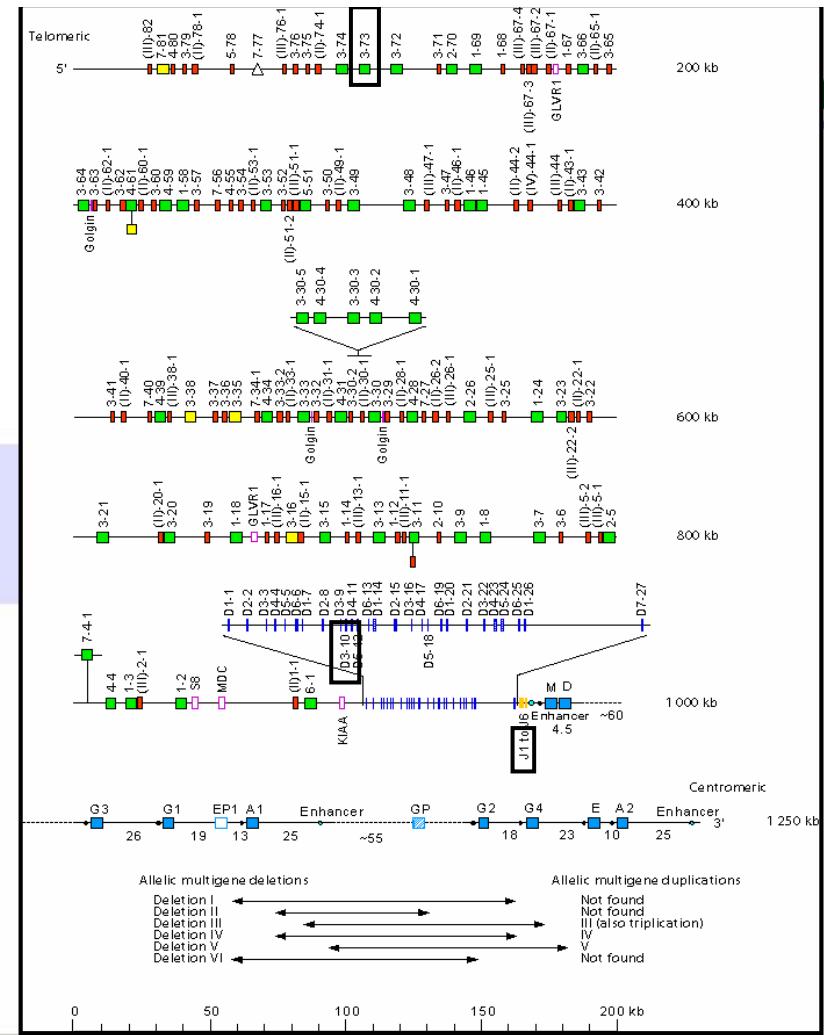
**Sequence number 1: AF184762**

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

```
>AF184762
atggagtttggctgagctgggtttccttgttgcattttaaaagggtgtccactgttag
gtcagctgtggagtctggggaggcttagtccagcctggggatccctgaaactctcc
tgtgcacccctctgggttcaccctcagtgcaatgtgcactgggtccggcaggcctcc
ggaaaagggtggagttgggtggcgatcaaaaggaatgtcgagtctgacgcacagca
tatgtcgctcgatgagagggcaggctcaccatctccagagatgattcaaagaacacggcg
tttctgcaaatgaacagcctgaaaagcgatgacacggccatgtattattgtgtatccgg
ggagatgttacaaccgacagtggggccagggAACCTGGTACCGTCTCCTCAGCATCC
ccgaccagccccaaaggcttcccctgagcctctgagcacccagccagat
```

Result summary:	Productive IGH rearranged sequence (no stop codon and in frame junction)		
V-GENE and allele	<a href="#">IGHV3-73*01</a>	score = 1240	identity = <b>91,50%</b> (269/294 nt)
J-GENE and allele	<a href="#">IGHJ1*01 (b)</a>	score = 179	identity = 82,69% (43/52 nt)
D-GENE and allele by IMGT/JunctionAnalysis	<a href="#">IGHD3-10*01</a>	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)



# A. 'Detailed view': Result summary

## Sequence number 1: AF184762

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

```
>AF184762
atggagtttggctgagctgggtttccttgtctatttaaaagggtgtccactgttag
gtcagctgtggagtctggggaggcttagtccagcctggggatccctgaaaactctcc
tgtgcagcctctgggttcaccctcagtgctcaaattgtgcactgggtccgcaggcctcc
ggaaagggtggagtgggtggcgatcaaaaggaatgctgagtgacgcacagca
tatgctgcgtcgatgagaggcaggctcaccatctccagagatgattcaaagaacacggcg
tttctgcaaatgaacacgcatacggcatgtattattgtgtatccgg
ggagatgttacaaccgacagtggggccagggAACCTGGTACCGTCTCCTCAGCATCC
ccgaccagccccaaaggcttcccgtgacgcctctgcagcacccagccagat
```

Result summary:	Productive IGH rearranged sequence (no stop codon and in frame junction)		
V-GENE and allele	<a href="#">IGHV3-73*01</a>	score = 1240	identity = <b>91,50%</b> (269/294 nt)
J-GENE and allele	<a href="#">IGHJ1*01 (b)</a>	score = 179	identity = 82,69% (43/52 nt)
D-GENE and allele by IMGT/JunctionAnalysis	<a href="#">IGHD3-10*01</a>	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)

# 1-3. 'Detailed view': 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-MGT delimitations

AF184762  
Z27508 IGHV3-73\*01  
AB019437 IGHV3-73\*02  
X92206 IGHV3-72\*01  
X92216 IGHV3-15\*01  
M99406 IGHV3-15\*07

AF184762  
Z27508 IGHV3-73\*02  
AB019437 IGHV3-73\*02  
X92206 IGHV3-72\*01  
X92216 IGHV3-15\*01  
M99406 IGHV3-15\*07

Score and nucleotide identity

```

<----- FR1-IMGT ----->
gagggtcagctggggagtcggggaa...ggcttagtccggcctggggatccctgaaa
.....-g-----q-----g-----
.....-c-----g-----g-----
.....-g-----g-----a-g-----g-
.....-g-----g-----aa-----g-----t-g-
.....-g-----aa-----g-----t-g-
.....-g-----aa-----g-----t-g-

```

```

-----<-----gtgcac----->
.....-t-----tgc-----a-
.....-a-----t-----a-cact-c.....-a-g-
.....-a-----tt-----aa-g-ctgg.....-a-ag-
.....-t-----tt-----aa-g-ctgg.....-a-a-

```

## 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

AF184762  
X13972 IGHD3-10\*01  
X93615 IGHD3-10\*02  
J00256 IGHD7-27\*01  
X97051 IGHD3-16\*02  
X93614 IGHD3-16\*01

```

gtgatccgggg
a--g-t----agtattataac
a--t--g---agtattataac
.ct-a-t----a
--t--a-c
ac-t-tg---agttatgctt

```

## 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 IG

#### Alignment

AF184762  
J00256 IGHJ1\*01  
X86355 IGHJ4\*02  
J00256 IGHJ4\*01  
X86355 IGHJ5\*02  
M25625 IGHJ4\*03

```

gtgatccggggagatgtttacaaccgacagtggggccagggaaacctggtcaccgtctcc
.....-c--aa---tt--ag--c-----c-
.....-ac---tttgact-c-----
.....ac---tttgact-c-----a-
.....caac-ggtt-gac-cc-----
.....gc---tttgact-c-----a-g-

```

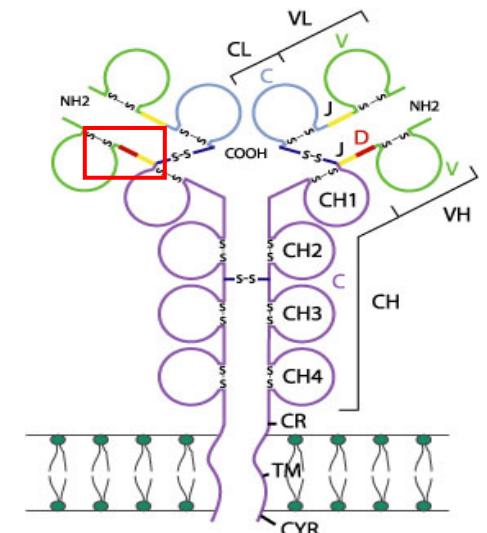
## 4. 'Detailed view': Results of IMGT/JunctionAnalysis

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	<a href="#">IGHV3-73*01</a>	tgt.....	g ..... <u>t</u> gat <u>c</u> gggg <u>g</u> at <u>g</u> tt.....	tacaaccga .....	.....cagtgg	<a href="#">IGHJ1*01</a>	<a href="#">IGHD3-10*01</a>	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>a</u> tc	cgg	gga	gat	gtt	tac	aac	cga	cag	tgg	+	10	1,508.72	9.24

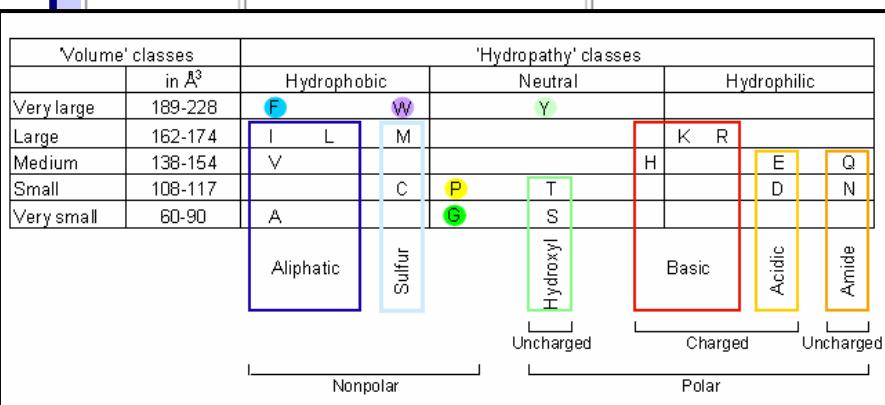
## 5. 'Detailed view': Sequence of the JUNCTION ('nt' and 'AA')

104 105 106 107 108 109 113 114 115 116 117 118  
C V I R G D V Y N R Q W  
tgt gtg atc cgg gga gat gtt tac aac cga cag tgg

# 9-11. 'Detailed view': mutation analysis

## 9. V-REGION mutation table

FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT
g36>a	t88>c, F30>L (+ -)	a115>g, M39>V (+ -)	t168>c	g211>a, V71>M (+ -)	a313>g, T105>V (- -)
g51>a	t99>a	t135>c	g170>a, R57>K (+ +)	a215>g, K72>R (+ +)	c314>t, T105>V (- -)
	g100>a, A34>N (- -)		c174>g, S58>R (- -)	t226>c, F76>L (+ -)	t315>g, T105>V (- -)
	c101>a, A34>N (- -)		a177>t, K59>N (+ -)	a263>t, Y88>F (- +)	g317>t, R106>I (- +)
			a181>g, N61>E (+ -)	c287>g, T96>S (+ +)	a318>c, R106>I (- +)
			c183>g, N61>E (+ -)	g291>t, E97>D (+ +)	
			a184>t	g301>a, V101>M (+ -)	
			g185>c	c309>t	
			t187>g, Y63>D (- -)		



# 9-11. 'Detailed view': mutation analysis

## 10. V-REGION mutation statistics

### Nucleotides

IMGT Label		V-REGION	FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT
<b>Total nucleotides with gaps</b>		<b>312 (318)</b>	78	36	51	30	117	0 (6)
Mutations	<b>Total</b>	<b>25 (30)</b>	2	4	2	9	8	0 (5)
	<b>Silent</b>	<b>8</b>	2	1	1	3	1	0
	<b>Non silent</b>	<b>17 (22)</b>	0	3	1	6	7	0 (5)
Transitions	<b>a&gt;g</b>	<b>3 (4)</b>	0	0	1	1	1	0 (1)
	<b>g&gt;a</b>	<b>6</b>	2	1				
	<b>c&gt;t</b>	<b>1 (2)</b>	0	0				
	<b>t&gt;c</b>	<b>4</b>	0	1				
Transversions	<b>a&gt;c</b>	<b>0 (1)</b>	0	0				
	<b>c&gt;a</b>	<b>1</b>	0	1				
	<b>a&gt;t</b>	<b>3</b>	0	0				
	<b>t&gt;a</b>	<b>1</b>	0	1				
	<b>g&gt;c</b>	<b>1</b>	0	0				
	<b>c&gt;g</b>	<b>3</b>	0	0				
	<b>g&gt;t</b>	<b>1 (2)</b>	0	0				
	<b>t&gt;g</b>	<b>1 (2)</b>	0	0				

### Amino acids

IMGT labels		V-REGION	FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT
<b>Total amino acids (AA) with gaps</b>		<b>104 (106)</b>	26	12	17	10	39	0 (2)
<b>Identical AA</b>		<b>89</b>	26	10	16	5	32	0
<b>Total</b>		<b>15 (17)</b>	0	2	1	5	7	0 (2)
AA changes	(---	3 (4)	0	1	0	2	0	0 (1)
	(++)	2	0	0	0	1	1	0
	(+ -)	7	0	1	1	2	3	0
	(- +)	1 (2)	0	0	0	0	1	0 (1)
	(-- +)	0	0	0	0	0	0	0
	(+ + -)	0	0	0	0	0	0	0
	(+ - +)	2	0	0	0	0	2	0

Conserved IMGT AA classes (hydropathy, volume, chemical)

# 9-11. 'Detailed view': mutation analysis

## 11. Mutation hot spots (in germline V-REGION)

(a/t) <u>a</u> <u>wa</u>		(a/g)g(c/t)(a/t) <u>rgyw</u>		(a/t)(a/g)c(c/t) <u>wrcy</u>		<u>t(a/t)</u> <u>tw</u>	
Motif	Positions	Motif	Positions	Motif	Positions	Motif	Positions
aa	58-59 (FR1)	agct	8-11 (FR1)	agct	8-11 (FR1)	tt	34-35 (FR1)
aa	142-143 (FR2)	ggct	31-34 (FR1)	agcc	41-44 (FR1)	tt	82-83 (CDR1)
ta	165-166 (FR2-CDR2)	ggtt	80-83 (CDR1)	aact	59-62 (FR1)	tt	88-89 (CDR1)
ta	168-169 (CDR2)	ggct	94-97 (CDR1)	agcc	72-75 (FR1)	tt	135-136 (FR2)
aa	171-172 (CDR2)	ggct	132-135 (FR2)	tgct	99-102 (CDR1)	tt	158-159 (FR2)
aa	175-176 (CDR2)	ggct	146-149 (FR2)	agct	177-180 (CDR2)	ta	165-166 (FR2-CDR2)
ta	180-181 (CDR2)	ggtt	156-159 (FR2)	tgct	201-204 (FR3)	tt	167-168 (CDR2)
ta	187-188 (CDR2)	agca	172-175 (CDR2)	agcc	277-280 (FR3)	ta	180-181 (CDR2)
ta	199-200 (FR3)	agct	177-180 (CDR2)	aacc	285-288 (FR3)	tt	186-187 (CDR2)
aa	214-215 (FR3)	agtt	184-187 (CDR2)	tact	307-310 (FR3)	ta	199-200 (FR3)
aa	249-250 (FR3)	agca	195-198 (CDR2)	tact	312-315 (FR3)	tt	226-227 (FR3)
aa	253-254 (FR3)	ggca	220-223 (FR3)			tt	246-247 (FR3)
ta	262-263 (FR3)	ggtt	224-227 (FR3)			ta	262-263 (FR3)
aa	269-270 (FR3)					ta	304-305 (FR3)
aa	274-275 (FR3)					tt	306-307 (FR3)
aa	283-284 (FR3)					ta	312-313 (FR3)
aa	285-286 (FR3)					ta	315-316 (CDR3)
ta	304-305 (FR3)						
ta	307-308 (FR3)						
ta	312-313 (FR3)						
ta	315-316 (CDR3)						

## 12. IMGT Collier de Perles

IMGT/Collier-de-Perles TOOL - Mozilla Firefox

Fichier Édition Affichage Historique Marque-pages Outils ?

http://imgt3d.igh.cnrs.fr/cgi/Collier-de-Perles.cgi

### Make Your Own IMGT Collier de Perles

Domain type: Variable (V)

Number of layers: 1

CDR-IMGT color type: 1 (RPJ, JGH, TRB, TRD)

Background color: 50% Hydrophobic positions

Domain sequence: EVQLVESGG . GLVQPGGSLKLSCAASGFTL . . . SGSNVHUVRQASGKGLEUWGRRIKRNAES

Domain sequence viewer with scroll bars.

Amino acid insertions: Position, Length, Numbering labels, ADD button.

CDR3-IMGT length: 10

Your domain title: [empty input field]

DRAW!

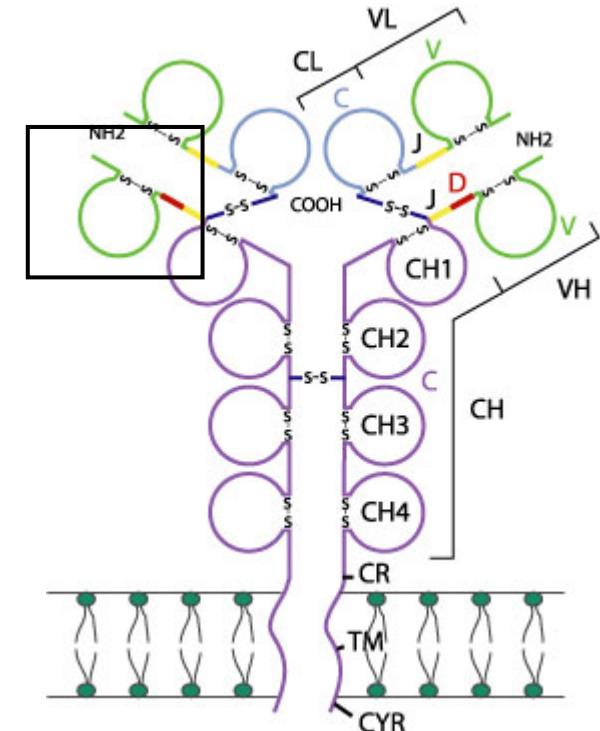
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The diagram shows a circular arrangement of amino acids (represented by colored circles) connected by lines, forming a loop. The amino acids are labeled with their one-letter codes and positions: 1(E), 10(G), 15(P), 23(C), 26(L), 39(V), 41(W), 46(S), 55(R), 66(A), 80(R), 85(N), 89(L), 104(C), 118(W), 128(S). Arrows at the bottom indicate CDR regions: A (down), B (up), C (down), C' (up), C'' (down), D (up), E (down), F (up), G (down).

Terminé

# 14. 'Detailed view': Annotation by IMGT/Automat

Label	Location/Qualifiers
<u>V-D-J-REGION</u>	<p>58..415</p> <p>/Nucleotide sequence</p> <pre>gaggtgcagctggaggctggggaggcttagtcagcctggggatccctgaaactc tcctgtcagcctctgggtcacccctcagtgctcaaattgtcactgggtccggcaggcc tccggaaaggctggaggctgggtggccgtatcaaaggaaatgtgagttcgacgcgaca gcatatgtcgatcgatggaggcggctcaccatccagagatgattcaaaaacacg gcgttctgcaaatgaacagcctgaaaaggcgtacacggccatgttattttgtgatc cggggagatgttacaaccacagtgggccaggaaacctgttaccgtctccctag</pre> <p>/Translation</p> <pre>EVQLVESGGGLVQPGGSLKLSCAASGFTLSGSNVHVRQASGKGLEWVGRIKRNAESDAT AYAASMRGRLTISRDDSNTAFLQMNSLKSDDTAMYCVIRGDVYNRQWGQGTLVTVSS</pre> <p>58..351</p> <p>/allele="IGHV3-73*01"</p> <p>/CDR_length="[8.10.10]"</p> <p>/gene="IGHV3-73"</p> <p>/Nucleotide sequence</p> <pre>gaggtgcagctggaggctggggaggcttagtcagcctggggatccctgaaactc tcctgtcagcctctgggtcacccctcagtgctcaaattgtcactgggtccggcaggcc tccggaaaggctggaggctgggtggccgtatcaaaggaaatgtgagttcgacgcgaca gcatatgtcgatcgatggaggcggctcaccatccagagatgattcaaaaacacg gcgttctgcaaatgaacagcctgaaaaggcgtacacggccatgttattttgt</pre> <p>/Translation</p> <pre>EVQLVESGGGLVQPGGSLKLSCAASGFTLSGSNVHVRQASGKGLEWVGRIKRNAESDAT AYAASMRGRLTISRDDSNTAFLQMNSLKSDDTAMYCVIRGDVYNRQWGQGTLVTVSS</pre> <p>58..132</p> <p>/AA_IMGT="AA 1 to 26, AA 10 is missing"</p> <p>/Nucleotide sequence</p> <pre>gaggtgcagctggaggctggggaggcttagtcagcctggggatccctgaaactc tcctgtcagcctct</pre> <p>/Translation</p> <pre>EVQLVESGGGLVQPGGSLKLSCAAS</pre> <p>121..123</p> <p>/Nucleotide sequence</p> <pre>tgt</pre> <p>/Translation</p> <pre>C</pre> <p>133..156</p> <p>/AA_IMGT="AA 27 to 34"</p> <p>/Nucleotide sequence</p> <pre>gggtcacccctcagtgctcaaatt</pre> <p>/Translation</p> <pre>GFTLSGN</pre> <p>157..207</p> <p>/AA_IMGT="AA 39 to 55"</p> <p>/Nucleotide sequence</p> <pre>gtgcactgggtccggcaggcctccggaaaggctggaggctgggtggccgt</pre> <p>/Translation</p> <pre>VHVRQASGKGLEWVG</pre> <p>163..165</p> <p>/Nucleotide sequence</p> <pre>tgg</pre> <p>/Translation</p> <pre>W</pre>
<u>V-REGION</u>	
<u>FRI-IMGT</u>	
<u>1st-CYS</u>	
<u>CDR1-IMGT</u>	
<u>FR2-IMGT</u>	
<u>CONSERVED-TRP</u>	



**IMGT/V-QUEST provides a full automatic annotation of the V-J-REGION or V-D-J-REGION.**



**Many thanks to the IMGT® team at Montpellier, France**