

# Interpretation of IG gene sequences

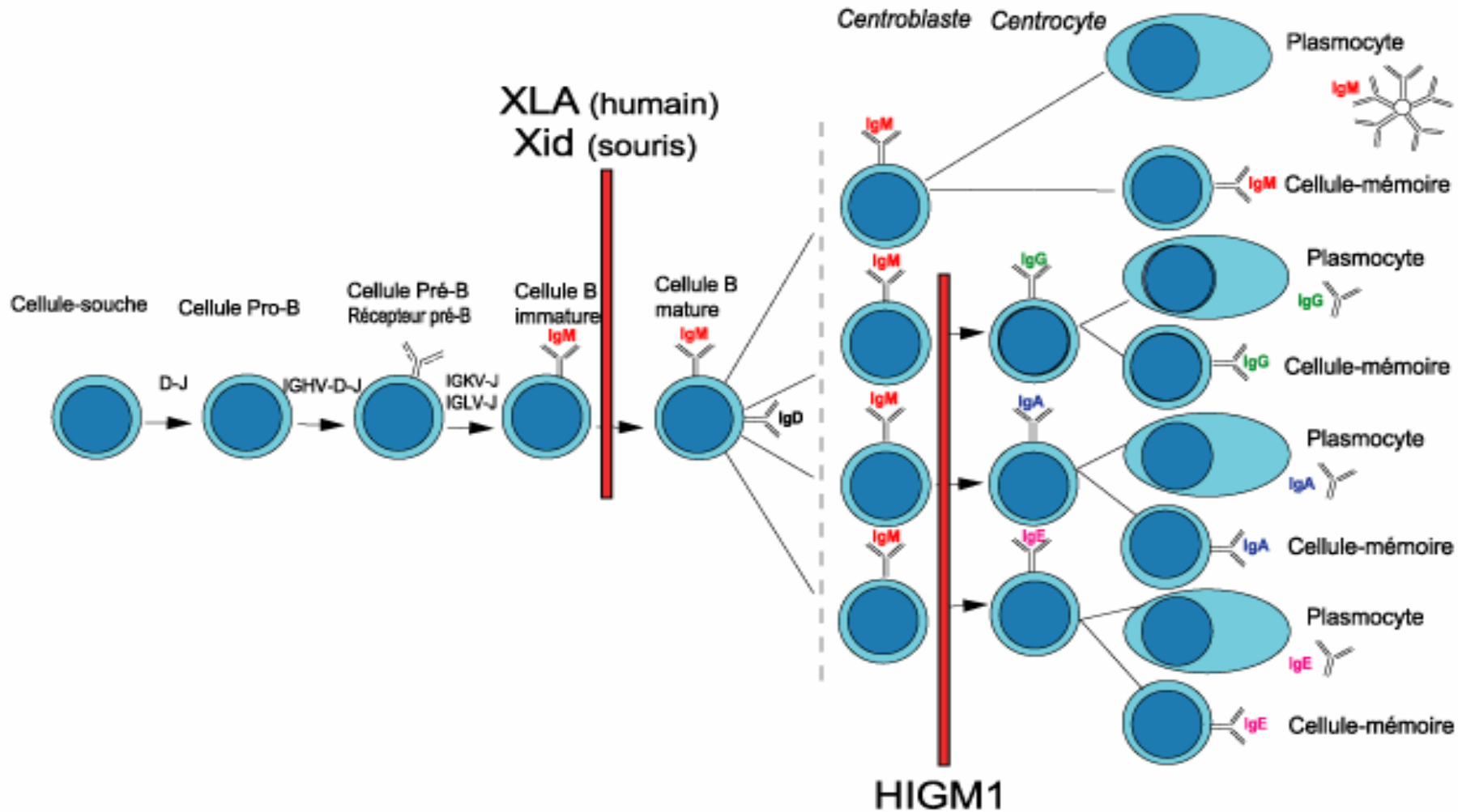
**Marie-Paule Lefranc**  
Université Montpellier, CNRS  
Institut Universitaire de France

Educational Workshop on  
Immunoglobulin Gene Analysis in Chronic Lymphocytic Leukemia  
Uppsala, June 14-15, 2007

Bone marrow

Blood

Lymph nodes, spleen

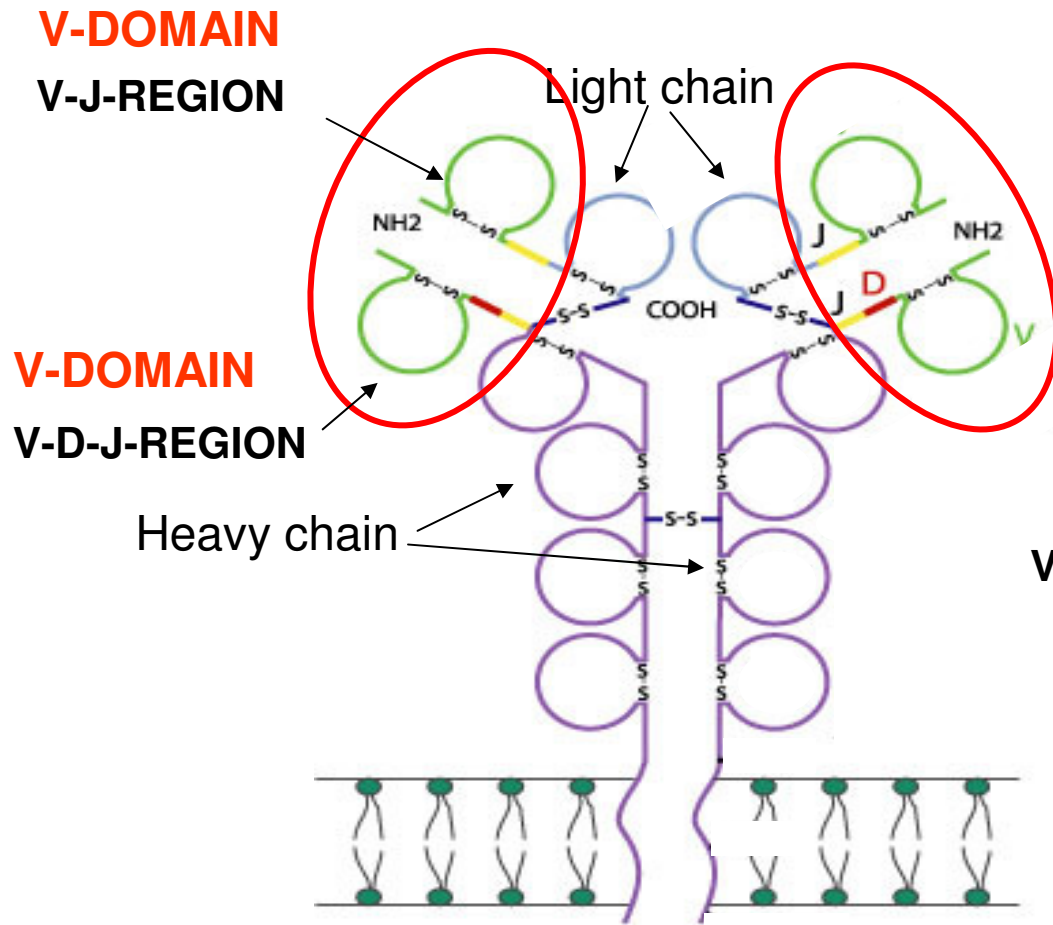


V-D-J and V-J rearrangements

Hypermutations, selection

# Immunoglobulin (IG)

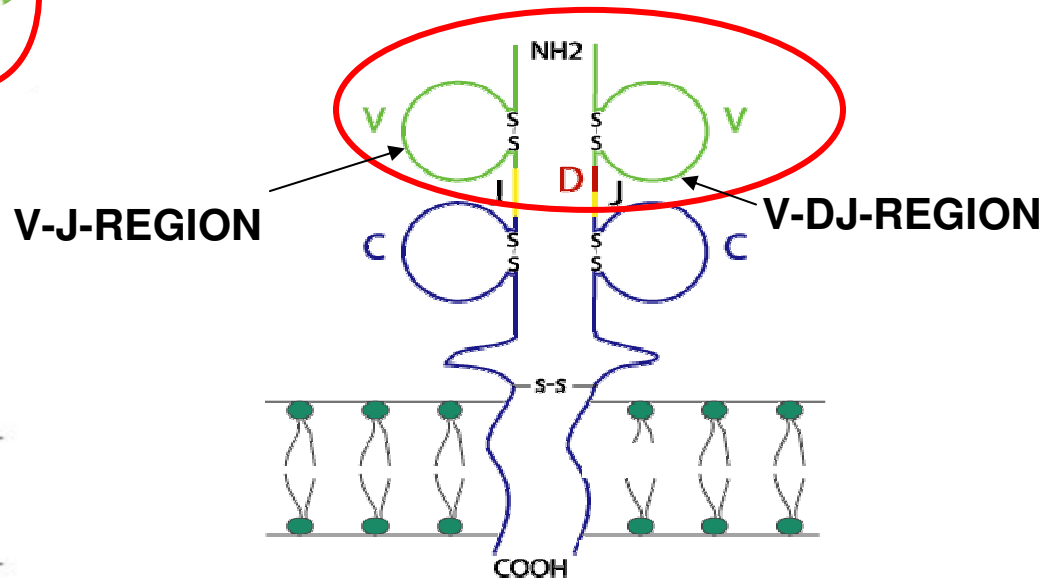
# T cell receptor (TR)



**Membrane IgM**

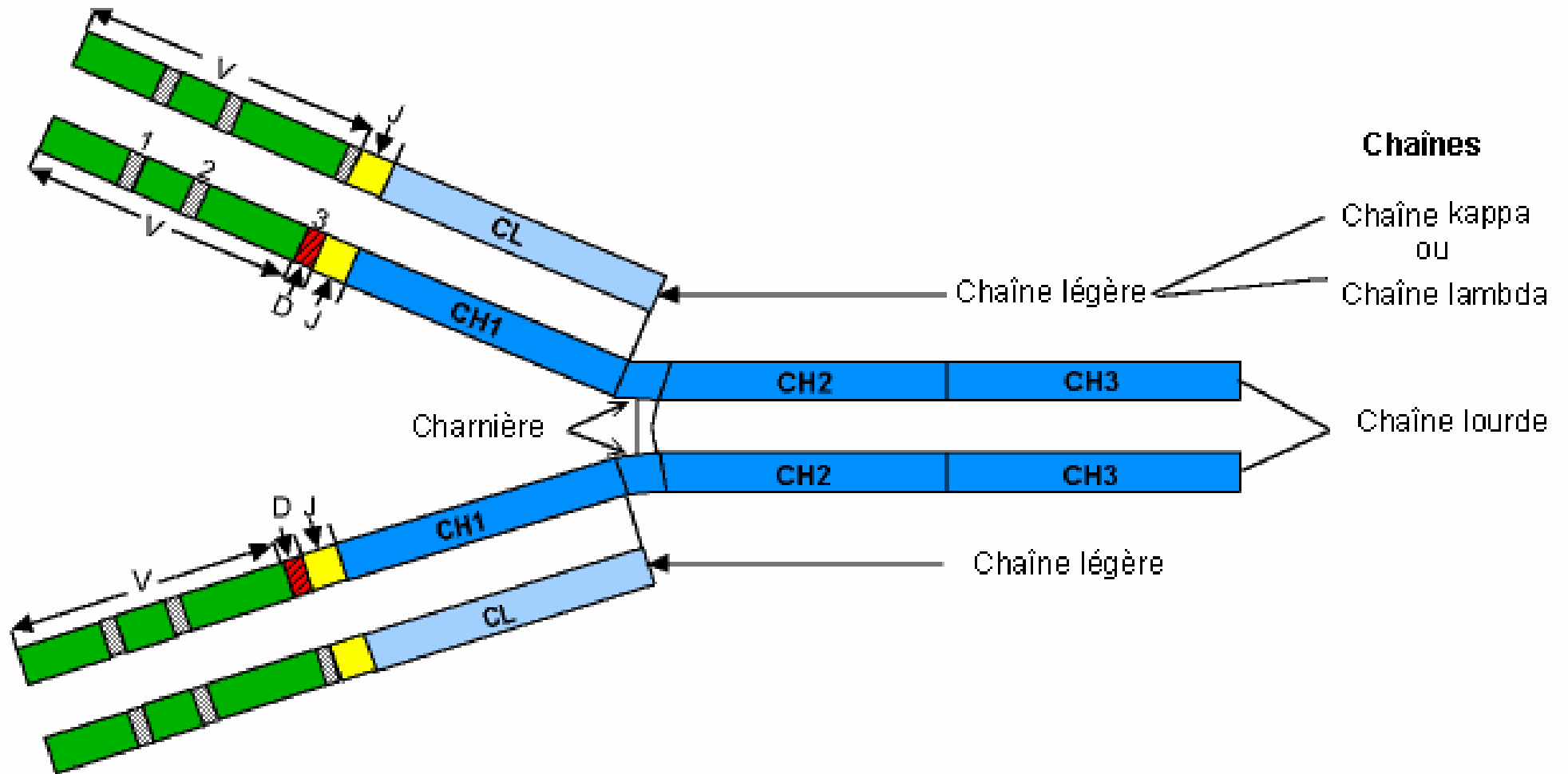
Contribution of the  
**2 V-DOMAINS**  
to the antigen binding site

Alpha - Beta  
Gamma - Delta



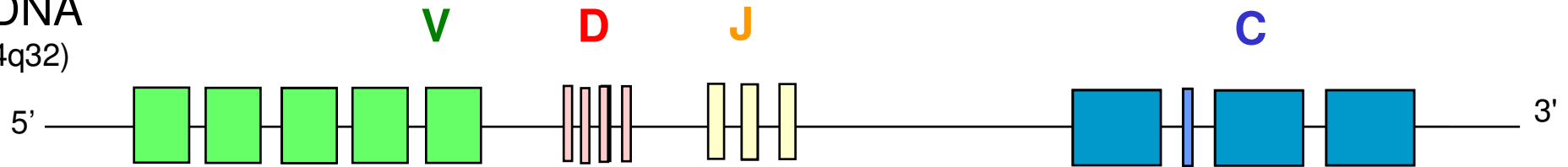
**T cell receptor**

# Immunoglobulin IgG



# Immunoglobulin (IG) synthesis

genomic DNA  
(IGH Locus 14q32)

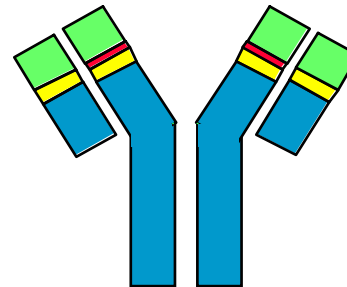


rearranged  
DNA



mRNA

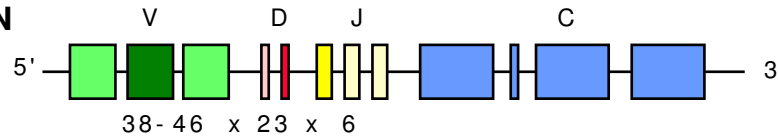
$2 \times 10^{12}$  different IG  
per individual



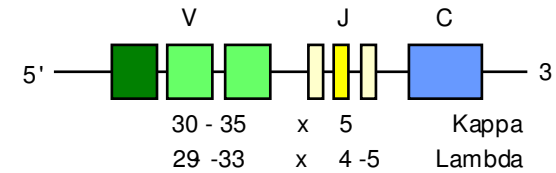
# Immunoglobulin (IG) synthesis

**150**  
**FUNCTIONAL IG GENES**

**HEAVY CHAIN**



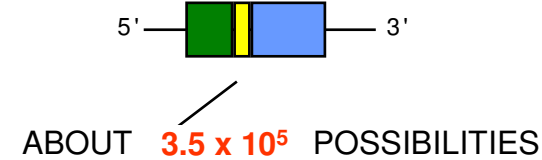
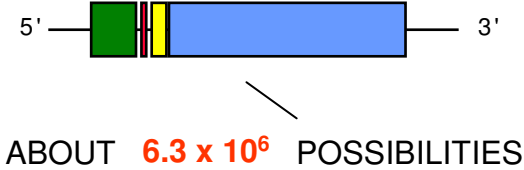
**LIGHT CHAIN**



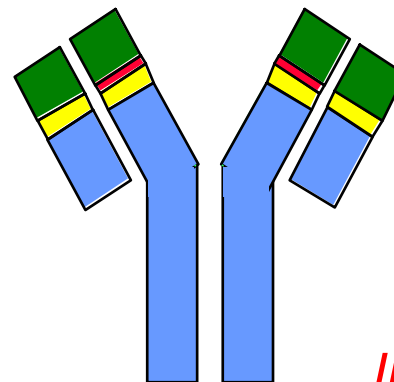
**6300** POTENTIAL RECOMBINATIONS

**185 + 165** POTENTIAL RECOMBINATIONS

**N-DIVERSITY  
SOMATIC MUTATIONS  
x 1000**



**$2 \times 10^{12}$**   
**DIFFERENT ANTIBODIES**



# IMGT®, the international ImMunoGeneTics information system®

Created in 1989 (Université Montpellier II and CNRS)

## 1) IMGT domains of research:

Immunogenetics -Immunoinformatics

\* *Immunoglobulins (IG), T cell receptors (TR), major histocompatibility complex (MHC) of human and other vertebrates,*

\* *Immunoglobulin superfamily IgSF and MhcSF,*

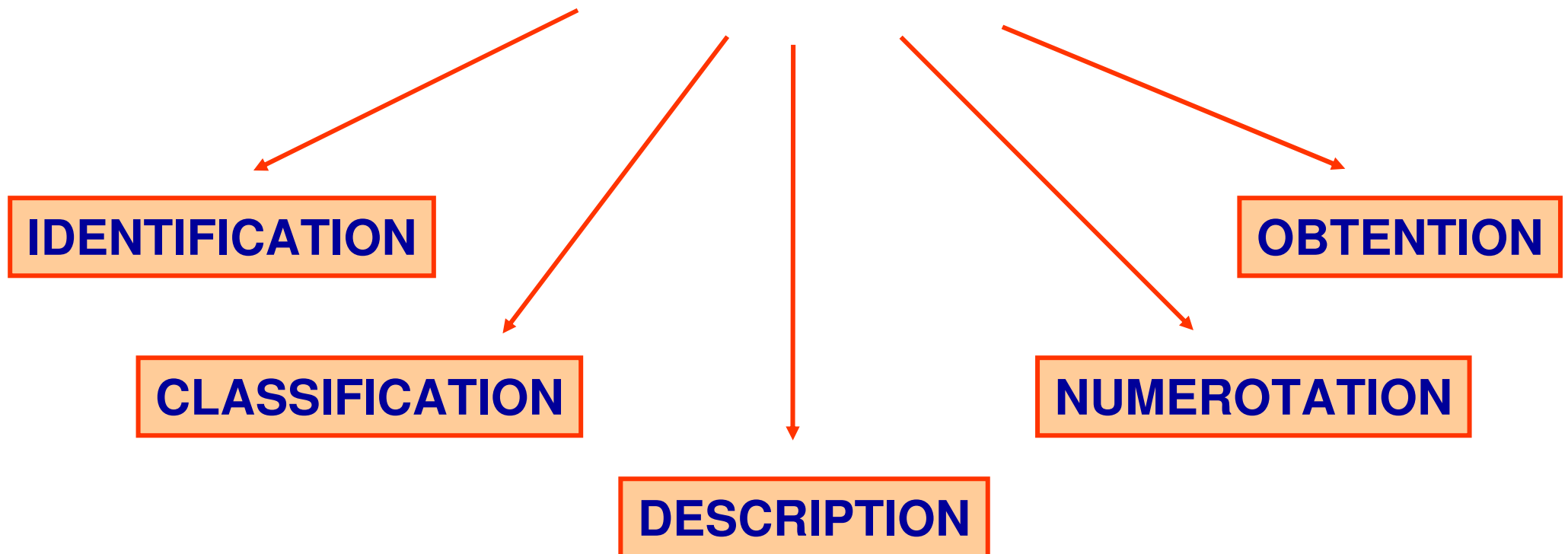
\* *Related proteins of the immune system (RPI)*

## 2) IMGT-ONTOLOGY axioms

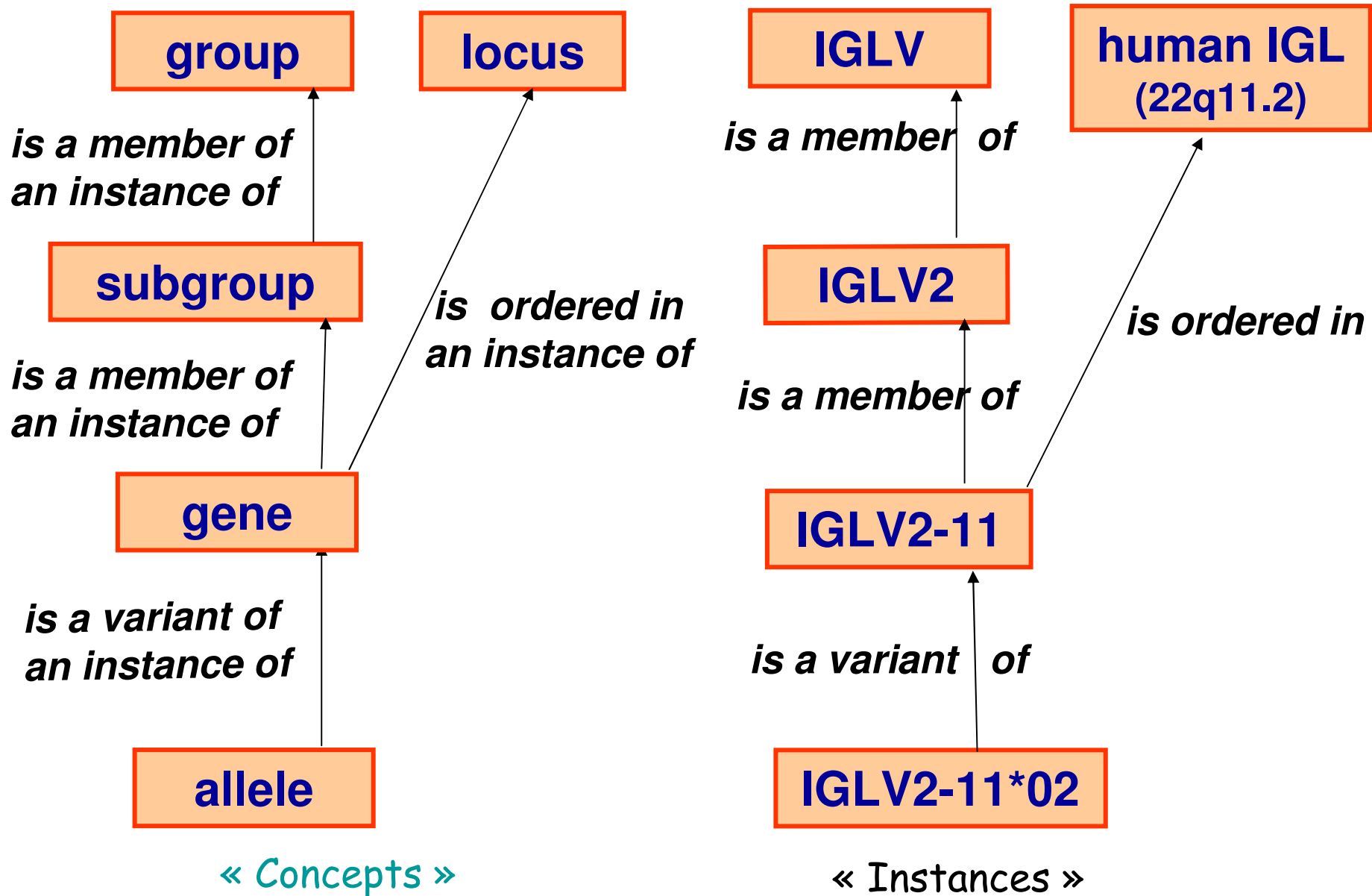
## 3) IMGT-Choreography: *Dynamic knowledge management*

## IMGT-ONTOLOGY five main axioms

to share, reuse and represent knowledge  
in immunogenetics

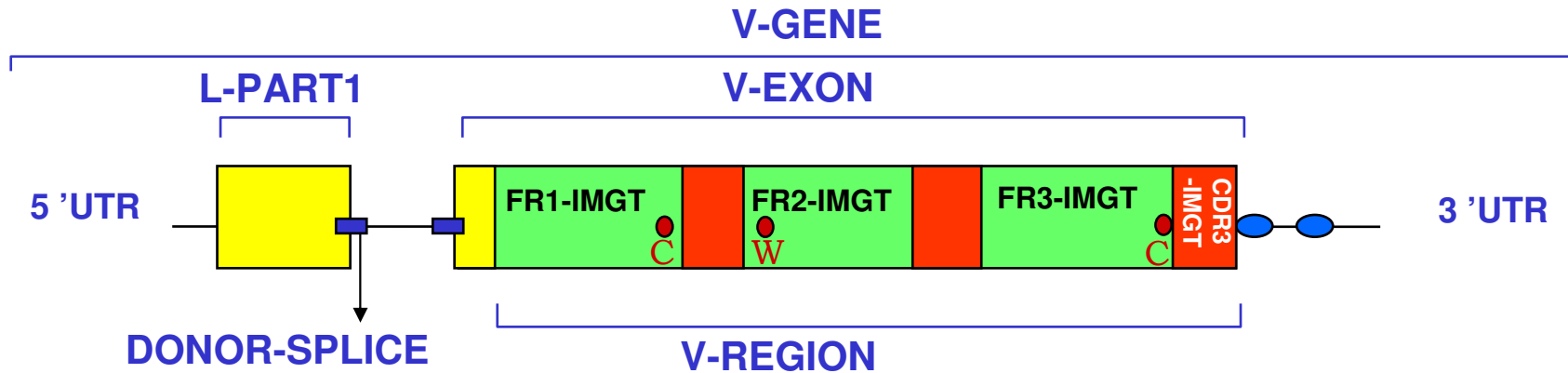


# "CLASSIFICATION" axiom



# "DESCRIPTION" axiom

## PROTOTYPE for a V-GENE



Label 1

Label 2

V-GENE

V-EXON

FR3-IMGT

CDR3-IMGT

L-PART1

DONOR-SPLICE

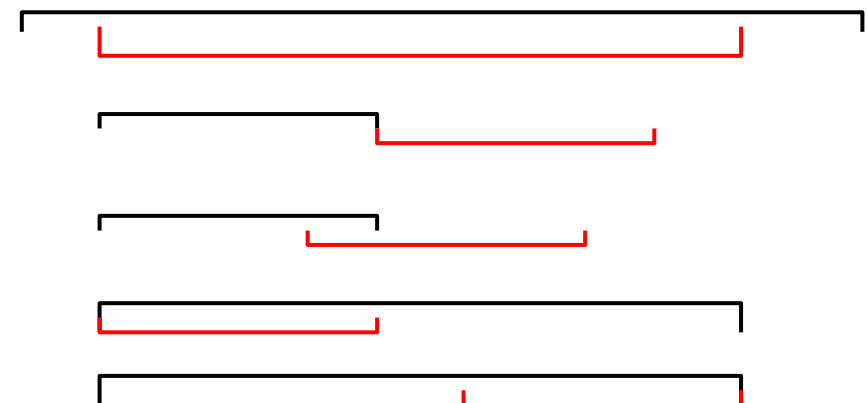
V-REGION

FR1-IMGT

V-REGION

CDR3-IMGT

Relations entre Labels

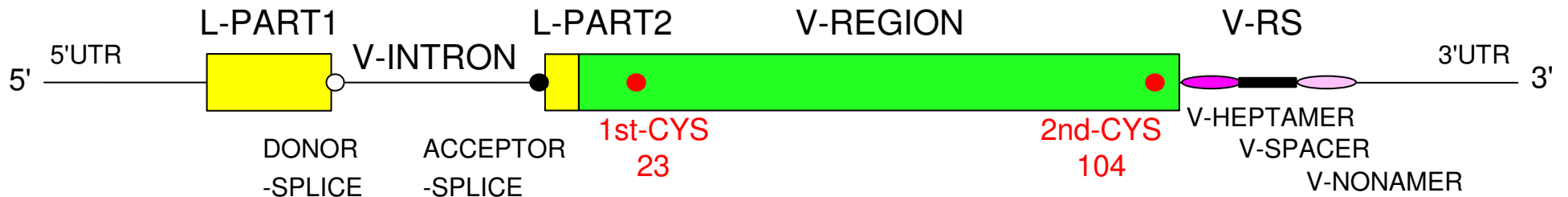


# An example of V-GENE

>X62106.0|HSVI2|*Homo sapiens* VI-2 gene for immunoglobulin heavy chain

```

tgagagctcc gttcctcacc atggactgga cctggaggat cctcttcttg gtggcagcag      60
ccacaggtaa gaggctccct agtcccagtg atgagaaaga gattgagtcc agtccagggg      120
gatctcatcc acttctgtgt tctctccaca ggagccact ccaggtgca gctggtgcag      180
tctggggctg aggtgaagaa gcttggggcc tcagtgaagg tctctgcaa ggcttctgga      240
tacaccttca ccggtacta tatgcactgg gtgcgacagg ccctggaca agggcttgag      300
tggatgggat ggatcaacc taacagtggg ggcacaaact atgcacagaa gtttcagggc      360
agggtcacca tgaccagga cacgtccatc agcacagcct acatggagct gagcaggctg      420
agatctgacg acacggccgt gtattactgt gcgagagaca cagtgtgaaa acccatcc      480
tgagggtgtc agaaacccaa gggaggaggc ag
  
```

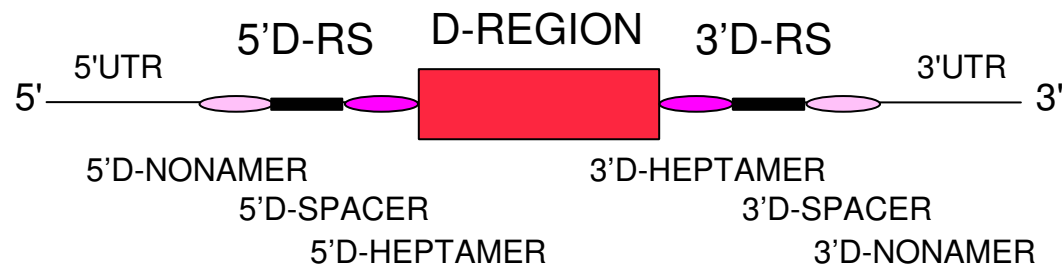


## An example of D-GENE

>J00256|IGHD7-27\*01|*Homo sapiens* D-GENE

```
ccagccgcag ggTTTTTggc tgagctgaga accactgtgc taactgggga cacagtgatt
ggcagctcta caaaaaccat gctcccccg g
```

60

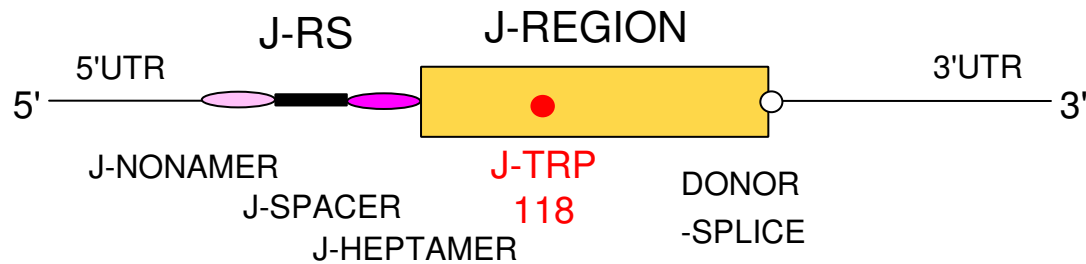


# An example of J-GENE

>J00256 | IGHJ1\*01 | *Homo sapiens* J-GENE

```

accccgggct gtgggtttct gtgcccctgg ctcagggctg actcaccgtg gctgaatact      60
tccagcactg gggccagggc acctgggtca cegtctctc aggtgagtct gctgtactgg      120
ggatagcggg gagccatgtg tactggggcca agcaagggct ttggcttcag      170
  
```

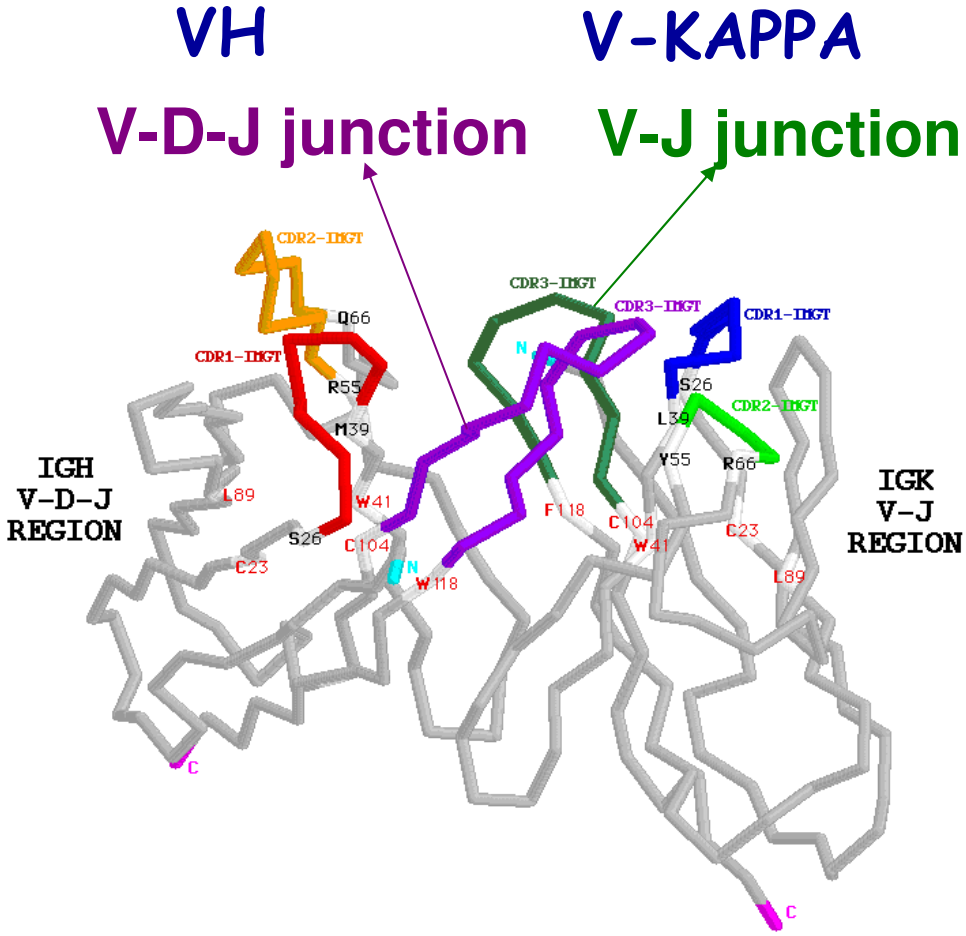


Heavy chain      **WG**XG (J-TRP)

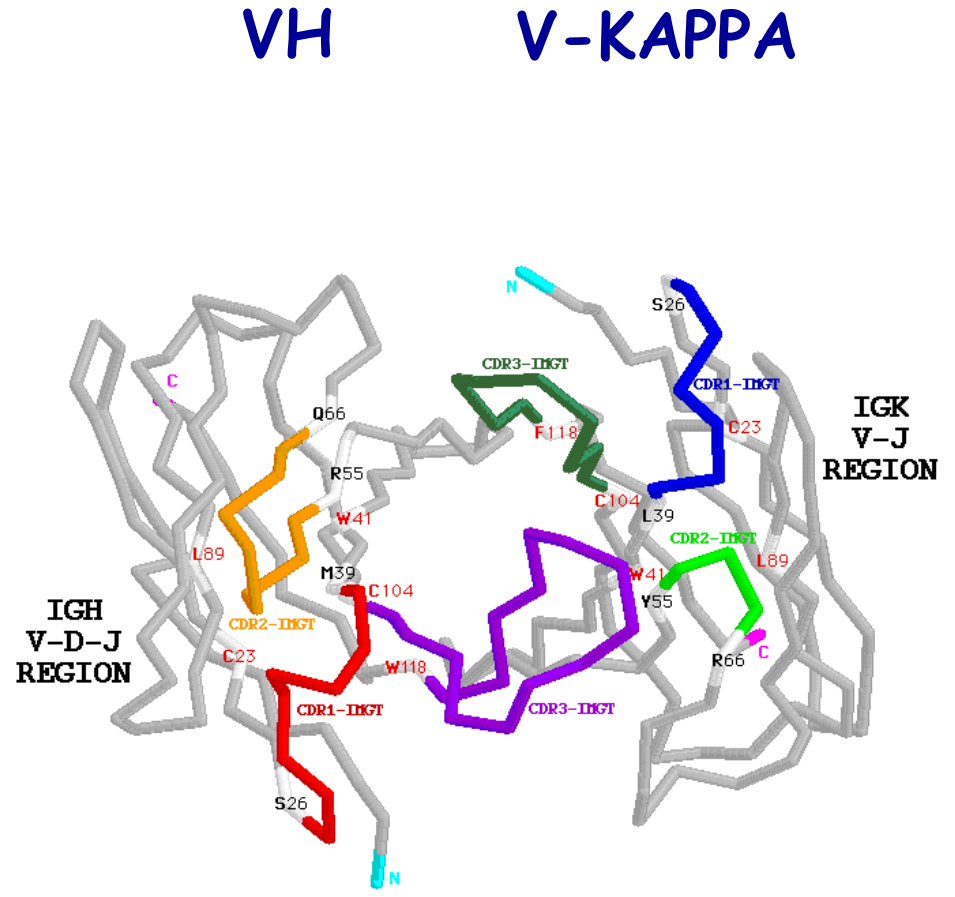
Light chain      **FG**XG (J-PHE)



# V-DOMAINS: VH and V-KAPPA



**Side view of the V-DOMAINS**



**View from above the CDRs**

*Mouse (Mus musculus) E5.2Fv*

CDR3-IMGT= Complementarity determining region (105-117)  
**V-J junction (104-118)**  
**V-D-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 W**  
**tgt gcg cca tac cgg ggt gac act tat gat tac tcc tgg**

# IMGT/JunctionAnalysis

# 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 | tgttccgagaga | aga           | .tagcaatggctacaa....         | aata     |
| #2 Z47269 | IGHV1-69*06  | tgtgcgagag.  | gggggggctaagg | ....togaatttttggagtggtt..... | tcatgggt |

| Input     | J-REGION            | J name   | D name      | Vmut | Dmut | Jmut | Ngc   |
|-----------|---------------------|----------|-------------|------|------|------|-------|
| #1 M62724 | .....tttaactactag   | IGHJ4*02 | IGHD5-24*01 | 0    | 2    | 0    | 1/7   |
| #2 Z47269 | ...actggttcgaccctgg | 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 | frame | CDR3-IMGT length |    |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-------|-------|-------|-------|-------|-------|-----|-----|-----|-----|-----|-----|-----|-------|------------------|----|
| #1 M62724 | C   | A   | R   | E   | D   | S   | N   | G   |       |       |       |       |       |       | Y   | K   | I   | F   | D   | Y   | W   | +     | 13               |    |
| #2 Z47269 | C   | A   | R   | G   | G   | A   | K   | V   | E     | F     | L     | E     | W     | F     | H   | G   | V   | W   | F   | D   | P   | W     | +                | 20 |

-> [IMGT/JunctionAnalysis Search page](#)  
-> [IMGT/JunctionAnalysis Documentation](#)

# WELCOME ! to IMGJ/JunctionAnalysis

THE INTERNATIONAL  
IMMUNOGENETICS  
INFORMATION SYSTEM®



<http://imgt.cines.fr>

## Analyse the JUNCTION of your IG and TR nucleotide sequences

Reference: Yousfi Monod, M. et al., Bioinformatics, 20, i379-i385 (2004). [PMID: 15262823](#). [PDF](#)

### Species:

Homo sapiens

### Locus:

IGH IGK IGL  
     
TRA TRB TRG TRD

### JUNCTION nucleotide sequences

Type (or copy/paste) your JUNCTION nucleotide sequence(s) into the box below (click [here](#) for required format):

```
>AY393054, IGHV3-49*03, IGHJ1*01  
tgtagtccccggggtagtgcttattaccacgaacacttccagcagtgg  
>AY393055, IGHV3-53*02, IGHJ1*01  
tgtgtgaaacccacggatgatgatggccaccgggctgaatacttccagtaactgg
```

## 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 | N         | D-REGION                | 5'J-REGION              | J name          | D name             | Vmut | Dmut | Jmut | Ngc |
|----------|--------------------|------------|-----------|-------------------------|-------------------------|-----------------|--------------------|------|------|------|-----|
| AY393054 | <u>IGHV3-49*03</u> | tgta.....  | gtcccgggg | .....gtagtggttattaccgac | ...gaagacttccagcagtggtg | <u>IGHJ1*01</u> | <u>IGHD3-22*01</u> | 0    | 2    | 2    | 8/9 |

### Translation of the JUNCTION

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

|          | 104 | 105 | 106 | 107 | 108 | 109 | 110      | 111 | 112 | 113        | 114 | 115        | 116 | 117 | 118 | Frame | CDR3<br>-<br>IMGT<br>length | Molecular<br>mass | pI       |     |
|----------|-----|-----|-----|-----|-----|-----|----------|-----|-----|------------|-----|------------|-----|-----|-----|-------|-----------------------------|-------------------|----------|-----|
|          | C   | S   | P   | G   | G   | S   | <u>A</u> | Y   | Y   | <u>H</u>   | E   | <u>H</u>   | F   | Q   | Q   | W     |                             |                   |          |     |
| AY393054 | tgt | agt | ccc | ggg | ggt | agt | ggt      | tat | tac | <u>gac</u> | gaa | <u>gac</u> | ttc | cag | cag | tgg   | +                           | 14                | 1,897.02 | 6.5 |

**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.



# 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 | <a href="#">IGHV2-26*01</a>   |   | tgtgtgt              | .....gcagc <u>gc</u> cctgttac | ccaaatc     |    | ...actttgaccactgg      | <a href="#">IGHJ4*02</a> | <a href="#">IGHD6-13*01</a> | 1    | 2    | 1    | 5/15  |
| #2    | Z70257 | <a href="#">IGHV3-7*02</a>    |   | ggatgg               | .....cagc <u>ct</u> tattgcc   | cgccc       |    | ctactggtacttcgatctctgg | <a href="#">IGHJ2*01</a> | <a href="#">IGHD2-2*01</a>  | 0    | 2    | 0    | 9/11  |
| #3    | Z70606 | <a href="#">IGHV4-31*03</a>   |   | c                    | .gactacg.....                 | cact        |    | ..atgcttttgatgtctgg    | <a href="#">IGHJ3*01</a> | <a href="#">IGHD4-17*01</a> | 0    | 0    | 0    | 3/5   |
| #4    | Z70608 | <a href="#">IGHV4-39*05</a>   |   | cagagta              | ....acgatttttgagtggttatt....  | ccccgggga   |    | ..atgcttttgatctctgg    | <a href="#">IGHJ3*02</a> | <a href="#">IGHD3-3*01</a>  | 0    | 0    | 0    | 12/17 |
| #5    | Z70610 | <a href="#">IGHV4-34*09</a>   |   | tcgggag              | .....cgatttttgagtggttatt....  | cccga       | ca | tgatgctttgatctctgg     | <a href="#">IGHJ3*02</a> | <a href="#">IGHD3-3*01</a>  | 0    | 0    | 0    | 9/12  |
| #6    | Z70611 | <a href="#">IGHV4-59*01</a>   |   | ca                   | .....tggt <u>aa</u> ctataa.   | tgccggcgttg |    | ...actggttcgaccctgg    | <a href="#">IGHJ5*02</a> | <a href="#">IGHD3-9*01</a>  | 0    | 2    | 0    | 9/13  |
| #7    | Z70613 | <a href="#">IGHV4-59*01</a>   |   |                      | .....cagcagctggtac            | ctccct      |    | ...ctttgactactgg       | <a href="#">IGHJ4*02</a> | <a href="#">IGHD6-13*01</a> | 0    | 0    | 0    | 4/6   |
| #8    | Z70614 | <a href="#">IGHV4-59*01</a>   |   | cactataa             | .....ttcggggacttat.....       | cccctc      |    | .....gactactgg         | <a href="#">IGHJ4*02</a> | <a href="#">IGHD3-16*01</a> | 0    | 2    | 0    | 7/14  |
| #9    | Z70615 | <a href="#">IGHV4-59*01</a>   |   | ggctg                | gta <u>aa</u> gaggg.....      | tttcggaa    |    | .tactggtacttcgatctctgg | <a href="#">IGHJ2*01</a> | <a href="#">IGHD5-24*01</a> | 0    | 2    | 0    | 7/13  |
| #10   | Z70616 | <a href="#">IGHV4-34*01</a>   |   | cgg                  | .....gtttggg.....             | ttccc       |    | ...actggttcgaccctgg    | <a href="#">IGHJ5*02</a> | <a href="#">IGHD3-16*01</a> | 0    | 0    | 0    | 6/8   |
| #11   | Z70620 | <a href="#">IGHV4-30-4*01</a> |   | cc                   | .....ggggcgggatggtt....       | cgg         |    | .gatgctttgatctctgg     | <a href="#">IGHJ3*02</a> | <a href="#">IGHD3-16*01</a> | 1    | 4    | 0    | 5/5   |
| #12   | Z70621 | <a href="#">IGHV4-39*01</a>   |   | ccacgattatgg         | .....ttcggggagtt.....         | tgaccccc    |    | .....ttgactactgg       | <a href="#">IGHJ4*02</a> | <a href="#">IGHD3-16*01</a> | 0    | 1    | 0    | 12/21 |
| #13   | Z70622 | <a href="#">IGHV4-39*06</a>   | t | tgccccgcctcctccaaaat | gtattactatggttcgggga.....     | tatgtacg    |    | .....ttgactactgg       | <a href="#">IGHJ4*03</a> | <a href="#">IGHD3-10*01</a> | 0    | 0    | 0    | 15/28 |

# IMGT/V-QUEST


# WELCOME ! to the IMGT/V-QUEST Search page

THE  
INTERNATIONAL  
IMMUNOGENETICS  
INFORMATION SYSTEM®




<http://imgt.cines.fr>


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

 You are in the new IMGT/V-QUEST, upgraded for multiple sequences and with new functionalities. **NEW!**

## Analyse your Immunoglobulin nucleotide sequences

-  [Human](#)
-  [Mouse](#)
-  [Chondrichthyes](#)
-  [Teleostei](#)
  - [Atlantic cod](#)
  - [Channel catfish](#)
  - [Rainbow trout](#)
-  [Sheep](#)

## Analyse your T cell Receptor nucleotide sequences

-  [Human](#)
-  [Mouse](#)
-  [Non-human primates](#)

# Analyse your Immunoglobulin sequences

## Your selection: Human

Your sequences are compared to the **Human IG set** from the [IMGTM-QUEST reference directory sets](#)

## Nucleotide sequences

Enter your sequence(s) in [FASTA format](#) (FASTA format is required):

Type (or copy/paste) your sequence(s) into the box below :

```
>AY393054
gctgggttttccttgttgctatTTTAAAAGGTgtccaatgtgaggtgcagctggtggagtctggggaggcttggtagaccagggcgg
tccttgagactctcctgtgcagcttctggattgaccttgggtgattactttatgagctggttccgccaggctccaggaagggactgga
gtgggtaggtttcattaagagcgaacttatggtgggacaacagaatacggcgcgtctgtgaaaggcagattcatcatctcgagagatg
attccaaaagcatcgctatTTTgcaaatgaacagcctggaaccgaggacacagccatatattactgtagtccccggggtagtgcttat
taccacgaacacttccagcagtggggcccgggaccatggtcacctctcctcagcctccaccaagggcccatcggtcttccccctggc
accctcctccaagagcacctctgggggcacagcggccctgggctgcttggtaaggactacttcccc
>AY393055
gctgggttttccttgttgctatTTTCAAAGGTgtccagtgtgaggtgcagctggtggagactggaggaggcttgatccagcctgggggg
tccttgagactctcctgtgcagcctctgggttcaccgtcagtagcaactacatgagctgggtccgccaggctccaggaaggggctgga
```

Analysis of several sequences (in FASTA format) in a single run

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



IMGT/V-QUEST - Microsoft Internet Explorer

Fichier Edition Affichage Favoris Outils ?

## Selection of parameters for the results

Display type : HTML      Nb of nucleotides per line in alignment: 60

**A. Detailed view**

- 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 mutation table
- 9.  V-REGION mutation statistics
- 10.  V-REGION mutation hot spots
- 11. IMGT Collier de Perles
  - links to IMGT Collier de Perles
  - IMGT Collier de Perles (PNG format, slow)
  - no IMGT Collier de Perles
- 12.  Sequences of V-, V-J- or V-D-J- REGION ('nt' and 'AA') with gaps in FASTA  
Access to IMGT/PhyloGene for V-REGION ('nt')
- 13.  Annotations by IMGT/Automat

**More options**

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)

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

**B. Synthesis view**

- 1.  Alignment for V-GENEs
- 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 (mutations displayed)
- 7.  V-REGION most frequently occurring AA
- 8.  Results of IMGT/JunctionAnalysis

Selection of output parameters



IMGT/V-QUEST - Microsoft Internet Explorer

Fichier Edition Affichage Favoris Outils ?

Adresse [http://imgt.cines.fr/IMGT\\_vquest/vquest](http://imgt.cines.fr/IMGT_vquest/vquest) OK

# THANK YOU for using IMGT/V-QUEST



Im  
Muno  
Gene  
Tics  
Information  
system@

<http://imgt.cines.fr>

THE  
INTERNATIONAL  
IMMUNOGENETICS  
INFORMATION SYSTEM@

 You are in the new IMGT/V-QUEST, *upgraded for multiple sequences and with new functionalities.* **NEW!**

---

## A. Detailed results for the IMGT/V-QUEST analysed sequences

Number of analysed sequences: **10**

[AY393054](#) [AY393055](#) [AY393058](#) [AY393072](#) [AY393084](#) [AY393088](#) [AY393089](#) [AY393091](#) [AY393092](#) [AY393094](#)

---

 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: AY393054

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

```
>AY393054
gctgggttttccttctgtgctatctttaaagggtgtccaatgtgaggtgcagctggaggat
ctgggggaggcttggtagcagccagggcgggtccctgagactctctgtgcagcttctggat
tgaccttgggtgattactttatgagctgggtccgccaggtccagggaaaggactggagt
gggtaggtttcattaaagagcgaacttatggtgggacaacagaatacggcgcgtctgtga
aaggcagattcatcatctcgagagatgattccaaaagcatcgctatttgcaaatgaaca
gcctgaaaaccgaggacacagccatatactctgtagtccccggggtagtgcttattacc
acgaacacttccagcagtgggccggccaccatggtcaccgtctcctcagcctccacca
aqqqcccatcggctctccccctqccaccctcctccaaqacacctctqqqqccacagcqq
```

Case of complementary reverse sequences

## Sequence number 1: test

Complementary reverse sequence compared with the [human IG set](#) from the [IMGT reference directory](#)

```
>test (complementary reverse)
caggtgcagctggtgcagctctgggggaggcgtagtccagcctgggaggtccttgagactc
tctgtgcagaggggggattcactttcagttcctattctatgcactgggtccgccaggcg
ccaggcaagggcctggaatgggtggcggttatgtggtttgatggaactgaaaaatactct
gcagagtccgtgaagggccgattcaccatctccagagacaattccaagaacacattgttt
ttgcaaatgaacagcctgagagccgacgacacggctgtgtattactgtgcgagagagcct
gattggttattatggggggacaggggtgctctggacgtctggggccaagggaccacggtc
accgtctcctcagacatcgtgatgaccagtcctcctccaccctgtctgcacatctgtagga
gacagagtaccatcacttgccggggccagtcagggcatagtagctgggtggcctggtat
cagcagaaaccagggaaagcccctaagtcctgatgtatgagggcgtctagtttagaaagt
ggggtcccatcaaggttcagcgggcagtggtccgggacagaattcactctcaccatcagc
agcctgcagcctgatgattttgcagcttattactgccaacattataaacacttacccgta
acttttggccagggaaaccaagctggagataaaaacgt
```

Terminé

IMGT/V-QUEST - Microsoft Internet Explorer

Fichier Edition Affichage Favoris Outils ?

Score and nucleotide identity

## 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            |
|--------------------------------------|-------|---------------------|
| <a href="#">AB019438</a> IGHV3-49*03 | 1321  | 94.55% (278/294 nt) |
| <a href="#">M99676</a> IGHV3-49*01   | 1303  | 93.87% (276/294 nt) |
| <a href="#">M99401</a> IGHV3-49*02   | 1285  | 93.19% (274/294 nt) |
| <a href="#">X92216</a> IGHV3-15*01   | 1078  | 85.37% (251/294 nt) |
| <a href="#">M99404</a> IGHV3-15*06   | 1069  | 85.03% (250/294 nt) |

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

```

AY393054
AB019438 IGHV3-49*03
M99676 IGHV3-49*01
M99401 IGHV3-49*02
X92216 IGHV3-15*01
M99404 IGHV3-15*06

<-----FR1-IMGT-----
gaggtgcagctggtggagtctggggga...ggcttggtacagccagggcggtcctgaga
-----
-----
-----
-----a---t---g-----t---
-----a---t---g-----t---

----->_____CDR1-IMGT_____<-----
ctctcctgtgcagcttctggattgaccttgggtgattacttt.....atgagc
-----a-----c-----tgc-----
-----a-----c-----tgc-----
-----a-----c-----gt---tcc-----
-----c-----c---t---ca---a-cgc---gg-----
  
```

IMGT/V-QUEST - Microsoft Internet Explorer

Fichier Edition Affichage Favoris Outils ?

## 2. Alignment for D-GENE and allele identification

**Closest D-REGIONS**

|                                    | Score | Identity          |
|------------------------------------|-------|-------------------|
| <a href="#">X93614</a> IGHD3-16*01 | 29    | 59.09% (13/22 nt) |
| <a href="#">X93616</a> IGHD3-22*01 | 29    | 59.09% (13/22 nt) |
| <a href="#">J00234</a> IGHD2-15*01 | 20    | 54.54% (12/22 nt) |
| <a href="#">X93618</a> IGHD3-3*02  | 20    | 54.54% (12/22 nt) |
| <a href="#">X97051</a> IGHD5-24*01 | 20    | 61.53% (8/13 nt)  |

**Alignment**

```

AY393054          gtcccgggggtagtgcttatta
X93614 IGHD3-16*01 t-tgg---a--ta-----acc
X93616 IGHD3-22*01 actat-ata-----g-----ctac
J00234 IGHD2-15*01 --agt--t-----ctgc--c--cc
X93618 IGHD3-3*02  ag-attttt-g---g-----tacc
X97051 IGHD5-24*01 .....-----a-a-ggc--caattac
  
```

IMGITV-QUEST - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

## Alignment for J-GENE and allele identification

### Closest J-GENES

|                                   | Score | Identity          |
|-----------------------------------|-------|-------------------|
| <a href="#">J00242</a> IGKJ4*01   | 152   | 94.11% (32/34 nt) |
| <a href="#">AF103571</a> IGKJ4*02 | 143   | 91.17% (31/34 nt) |
| <a href="#">J00242</a> IGKJ3*01   | 107   | 79.41% (27/34 nt) |
| <a href="#">Z70260</a> IGKJ2*02   | 107   | 79.41% (27/34 nt) |
| <a href="#">J00242</a> IGKJ2*01   | 107   | 79.41% (27/34 nt) |

Score and nucleotide identity

### Alignment

```
AY867144          cactttcggcgggagggaccaggggtggtgatcaaa
J00242 IGKJ4*01  -----a-----a-----c
AF103571 IGKJ4*02 ---g-----a-----a-----c
J00242 IGKJ3*01  -----cct-----aa----at-----c
Z70260 IGKJ2*02  -----t--cag-----a-c--a-----c
J00242 IGKJ2*01  -----t--cag-----a-c--a-----c
```

Terminé

IMGT/V-QUEST - Microsoft Internet Explorer

Fichier Edition Affichage Favoris Outils ?

## 6. V-REGION alignment according to the IMGT unique numbering

```

<-----FR1 - IMGT
1          5          10          15
AY393054   gag gtg cag ctg gtg gag tct ggg gga ... ggc ttg gta cag cca
AB019438 IGHV3-49*03 --- --- --- --- --- --- --- --- --- --- --- ---
M99676 IGHV3-49*01 --- --- --- --- --- --- --- --- --- --- --- ---
M99401 IGHV3-49*02 --- --- --- --- --- --- --- --- --- --- --- ---
X92216 IGHV3-15*01 --- --- --- --- --- --- --- --- --- a-- --t
M99404 IGHV3-15*06 --- --- --- --- --- --- --- --- --- a-- --t

----->
          20          25          30
AY393054   ggg cgg tcc ctg aga ctc tcc tgt gca gct tct gga ttg acc ttt
AB019438 IGHV3-49*03 --- --- --- --- --- --- --- a-- --- --- --c --- ---
M99676 IGHV3-49*01 --- --- --- --- --- --- --- a-- --- --- --c --- ---
M99401 IGHV3-49*02 --- -c- --- --- --- --- --- a-- --- --- --c --- ---
X92216 IGHV3-15*01 --- g-- --- --t --- --- --- --- --c --- --- --c --t --c
M99404 IGHV3-15*06 --- g-- --- --t --- --- --- --- --c --- --- --c --t --c

___ CDR1 - IMGT _____<-----
          35          40          45
AY393054   ggt gat tac ttt ... .. atg agc tgg ttc cgc cag gct
AB019438 IGHV3-49*03 --- --- --t gc- ... .. --- --- --- --- --- ---
M99676 IGHV3-49*01 --- --- --t gc- ... .. --- --- --- --- --- ---
M99401 IGHV3-49*02 --g t-- --t cc- ... .. --- --- --- --- --- ---
X92216 IGHV3-15*01 a-- a-c gc- -gg ... .. --- --- --- --- --- ---
M99404 IGHV3-15*06 a-- a-c gc- -gg ... .. --- --- --- --- --- ---

FR2 - IMGT -----> _____ CDR2
          50          55          60
AY393054   cca ggg aag gga ctg gag tgg gta ggt ttc att aag agc gaa act
AB019438 IGHV3-49*03 --- --- --g --- --- --- --- --- --- -ga --- a-- g--
M99676 IGHV3-49*01 --- --- --g --- --- --- --- --- --- -ga --- a-- g--
M99401 IGHV3-49*02 --- --- --g --- --- --- --- --- --- -ga --- a-- g--
X92216 IGHV3-15*01 --- --- --g --- --- --t --c cgt --- --a --- a-- ---
M99404 IGHV3-15*06 --- --- --g --- --- --c --c cgt --- --a --- a-- ---

```

IMGTV-QUEST - Microsoft Internet Explorer

Fichier Edition Affichage Favoris Outils ?

## 7. V-REGION translation

```

<----- FR1 - IMGT
1           5           10           15
E V Q L V E S G G           G L V Q P
AY393054 gag gtg cag ctg gtg gag tct ggg gga ... ggc ttg gta cag cca
AB019438 IGHV3-49*03 ----- ... -----

----->
                20           25           30
G R S L R L S C A A S G L T F
AY393054 ggg cgg tcc ctg aga ctc tcc tgt gca gct tct gga ttg acc ttt
AB019438 IGHV3-49*03 ----- a-----c-----
                T           F

___ CDR1 - IMGT _____<-----
                35           40           45
G D Y F           M S W F R Q A
AY393054 ggt gat tac ttt ... .. atg agc tgg ttc cgc cag gct
AB019438 IGHV3-49*03 ----- A-----
                A

FR2 - IMGT -----> _____ CDR2
                50           55           60
P G K G L E W V G F I K S E T
AY393054 cca ggg aag gga ctg gag tgg gta ggt ttc att aag agc gaa act
AB019438 IGHV3-49*03 ----- g-----ga---a--g--
                R           K A

- IMGT _____<-----
                65           70           75
Y G G T T E Y A A S V K           G R
AY393054 tat ggt ggg aca aca gaa tac gcc gcg tct gtg aaa ... ggc aga
AB019438 IGHV3-49*03 ----- ... -----

```

IMGT/V-QUEST - Microsoft Internet Explorer

Fichier Edition Affichage Favoris Outils ?

## 8. V-REGION mutation table

| FR1-IMGT                | CDR1-IMGT  | FR2-IMGT | CDR2-IMGT  | FR3-IMGT   | CDR3-IMGT  |
|-------------------------|--|----------|--|--|--|
| a70>g, T24>A<br>(- - -) | c84>g, F28>L<br>(+ - -)<br><br>t99>c<br><br>g100>t, A34>F<br>(+ - -)<br><br>c101>t, A34>F<br>(+ - -) | g147>a   | g170>a, R57>K<br>(+ + +)<br><br>a171>g, R57>K<br>(+ + +)<br><br>a175>g, K59>E<br>(+ - -)<br><br>g178>a, A60>T (-<br>- -) | c230>t, T77>I (- -<br>-)<br><br>a237>g<br><br>c265>t<br><br>a283>g, K95>E<br>(+ - -)<br><br>g301>a, V101>I<br>(+ - +)<br><br>g303>a, V101>I<br>(+ - +) | c314>g, T105>S<br>(+ - +)<br><br>a316>c, R106>P<br>(- - -)<br><br>g317>c, R106>P<br>(- - -)<br><br>a318>c, R106>P<br>(- - -)<br><br>a320>g |

IMGT/V-QUEST - Microsoft Internet Explorer

Fichier Edition Affichage Favoris Outils ?

## 9. 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> |                   | 313 (320) | 78       | 36        | 51       | 30        | 117      | 1 (8)     |
| <b>Mutations</b>                   | <b>Total</b>      | 16 (21)   | 1        | 4         | 1        | 4         | 6        | 0 (5)     |
|                                    | <b>Silent</b>     | 4 (5)     | 0        | 1         | 1        | 0         | 2        | 0 (1)     |
|                                    | <b>Non silent</b> | 12 (16)   | 1        | 3         | 0        | 4         | 4        | 0 (4)     |
| <b>Transitions</b>                 | <b>a&gt;g</b>     | 5 (6)     | 1        | 0         | 0        | 2         | 2        | 0 (1)     |
|                                    | <b>g&gt;a</b>     | 5         | 0        | 0         | 1        | 2         | 2        | 0         |
|                                    | <b>c&gt;t</b>     | 3         | 0        | 1         | 0        | 0         | 2        | 0         |
|                                    | <b>t&gt;c</b>     | 1         | 0        | 1         | 0        | 0         | 0        | 0         |
| <b>Transversions</b>               | <b>a&gt;c</b>     | 0 (2)     | 0        | 0         | 0        | 0         | 0        | 0 (2)     |
|                                    | <b>c&gt;a</b>     | 0         | 0        | 0         | 0        | 0         | 0        | 0         |
|                                    | <b>a&gt;t</b>     | 0         | 0        | 0         | 0        | 0         | 0        | 0         |
|                                    | <b>t&gt;a</b>     | 0         | 0        | 0         | 0        | 0         | 0        | 0         |
|                                    | <b>g&gt;c</b>     | 0 (1)     | 0        | 0         | 0        | 0         | 0        | 0 (1)     |
|                                    | <b>c&gt;g</b>     | 1 (2)     | 0        | 1         | 0        | 0         | 0        | 0 (1)     |
|                                    | <b>g&gt;t</b>     | 1         | 0        | 1         | 0        | 0         | 0        | 0         |
|                                    | <b>t&gt;g</b>     | 0         | 0        | 0         | 0        | 0         | 0        | 0         |

IMGT/V-QUEST - Microsoft Internet Explorer

Eichier Edition Affichage Favoris Outils ?

### Amino acids

| IMGT labels                      |  | V-REGION  | FR1-IMGT | CDR1-IMGT | FR2-IMGT | CDR2-IMGT | FR3-IMGT | CDR3-IMGT |       |
|----------------------------------|--|-----------|----------|-----------|----------|-----------|----------|-----------|-------|
| Total amino acids (AA) with gaps |  | 105 (106) | 26       | 12        | 17       | 10        | 39       | 1 (2)     |       |
| Identical AA                     |  | 95        | 25       | 10        | 17       | 7         | 36       | 0         |       |
| AA changes                       | Total  | 10 (11)   | 1        | 2         | 0        | 3         | 3        | 1 (2)     |       |
|                                  | Conserved IMGT AA classes (hydropathy, volume, chemical) | (- - -)   | 3 (4)    | 1         | 0        | 0         | 1        | 1         | 0 (1) |
|                                  |  | (+ + +)   | 1        | 0         | 0        | 0         | 1        | 0         | 0     |
|                                  |  | (+ - -)   | 4        | 0         | 2        | 0         | 1        | 1         | 0     |
|                                  |  | (- + -)   | 0        | 0         | 0        | 0         | 0        | 0         | 0     |
|                                  |  | (- - +)   | 0        | 0         | 0        | 0         | 0        | 0         | 0     |
|                                  |  | (+ + -)   | 0        | 0         | 0        | 0         | 0        | 0         | 0     |
|                                  |  | (+ - +)   | 2        | 0         | 0        | 0         | 0        | 1         | 1     |

IMGT/V-QUEST - Microsoft Internet Explorer

Fichier Edition Affichage Favoris Outils ?

## 10. Mutation hot spots (motifs and positions in germline V-REGION)

| <b>(a/t)a</b><br>wa |                | <b>(a/g)g(c/t)(a/t)</b><br>rgyw |                | <b>(a/t)(a/g)c(c/t)</b><br>wrcy |                | <b>t(a/t)</b><br>tw |                |
|---------------------|----------------|---------------------------------|----------------|---------------------------------|----------------|---------------------|----------------|
| Motif               | Positions      | Motif                           | Positions      | Motif                           | Positions      | Motif               | Positions      |
| ta                  | 38-39 (FR1)    | agct                            | 8-11 (FR1)     | agct                            | 8-11 (FR1)     | tt                  | 34-35 (FR1)    |
| ta                  | 69-70 (FR1)    | ggct                            | 31-34 (FR1)    | agcc                            | 41-44 (FR1)    | ta                  | 38-39 (FR1)    |
| ta                  | 97-98 (CDR1)   | ggta                            | 36-39 (FR1)    | agct                            | 72-75 (FR1)    | ta                  | 69-70 (FR1)    |
| aa                  | 142-143 (FR2)  | agct                            | 72-75 (FR1)    | tgct                            | 99-102 (CDR1)  | tt                  | 75-76 (FR1)    |
| ta                  | 158-159 (FR2)  | agct                            | 118-121 (FR2)  | agct                            | 118-121 (FR2)  | tt                  | 82-83 (CDR1)   |
| ta                  | 168-169 (CDR2) | ggtt                            | 122-125 (FR2)  | agct                            | 177-180 (CDR2) | tt                  | 88-89 (CDR1)   |
| aa                  | 171-172 (CDR2) | ggct                            | 132-135 (FR2)  | agcc                            | 277-280 (FR3)  | tt                  | 96-97 (CDR1)   |
| aa                  | 175-176 (CDR2) | ggct                            | 146-149 (FR2)  | aacc                            | 285-288 (FR3)  | tt                  | 124-125 (FR2)  |
| ta                  | 181-182 (CDR2) | ggta                            | 156-159 (FR2)  | agcc                            | 297-300 (FR3)  | ta                  | 158-159 (FR2)  |
| aa                  | 192-193 (CDR2) | ggtt                            | 160-163 (FR2)  | tact                            | 307-310 (FR3)  | tt                  | 162-163 (FR2)  |
| aa                  | 197-198 (FR3)  | agca                            | 172-175 (CDR2) | tact                            | 312-315 (FR3)  | tt                  | 167-168 (CDR2) |
| ta                  | 199-200 (FR3)  | agct                            | 177-180 (CDR2) |                                 |                | tt                  | 180-181 (CDR2) |

## 11. IMGT Collier de Perles for AY393058

[IMGT Collier de Perles \(Perl\)](#)

[IMGT Collier de Perles in PNG format](#) (Java applet)

[IMGT Collier de Perles in interactive SVG format on one layer](#) (Java applet)

[IMGT Collier de Perles in interactive SVG format on two layers](#) (Java applet)

## 12. 'AY393058' V-REGION and V-D-J-REGION

### V-REGION nucleotide sequence in FASTA format

```
>AY393058
gaggtgcagctggtggagtctggggga...gccttggtacagccagggcgggtccctgaca
ctctcctgcacatcttctggattgacctttgatgattacttt.....atgagc
tggttccgccaggctccaggaaggactggagtgggtaggtttcattaggagcaaaact
tatggtgggacaacagaatacgcgcgtctgtgcaa...ggcagattcaccatctcaaga
gatgattccaaaagcatcgctatctgcaaatgaacagcctgaaaaccgaggacacagcc
atatattactgta
```

Analyse this sequence with IMGT/PhyloGene

### V-REGION amino acid sequence in FASTA format

```
>AY393058
EVQLVESGG.ALVQPGRSLTLSCTSSGLTFDDYF...MSWFRQAPGKGLEWVGFIRSKT
YGGTTEYAASVQ.GRFTISRDDSKSIAYLQMNSLKTEDTAIYYC
```

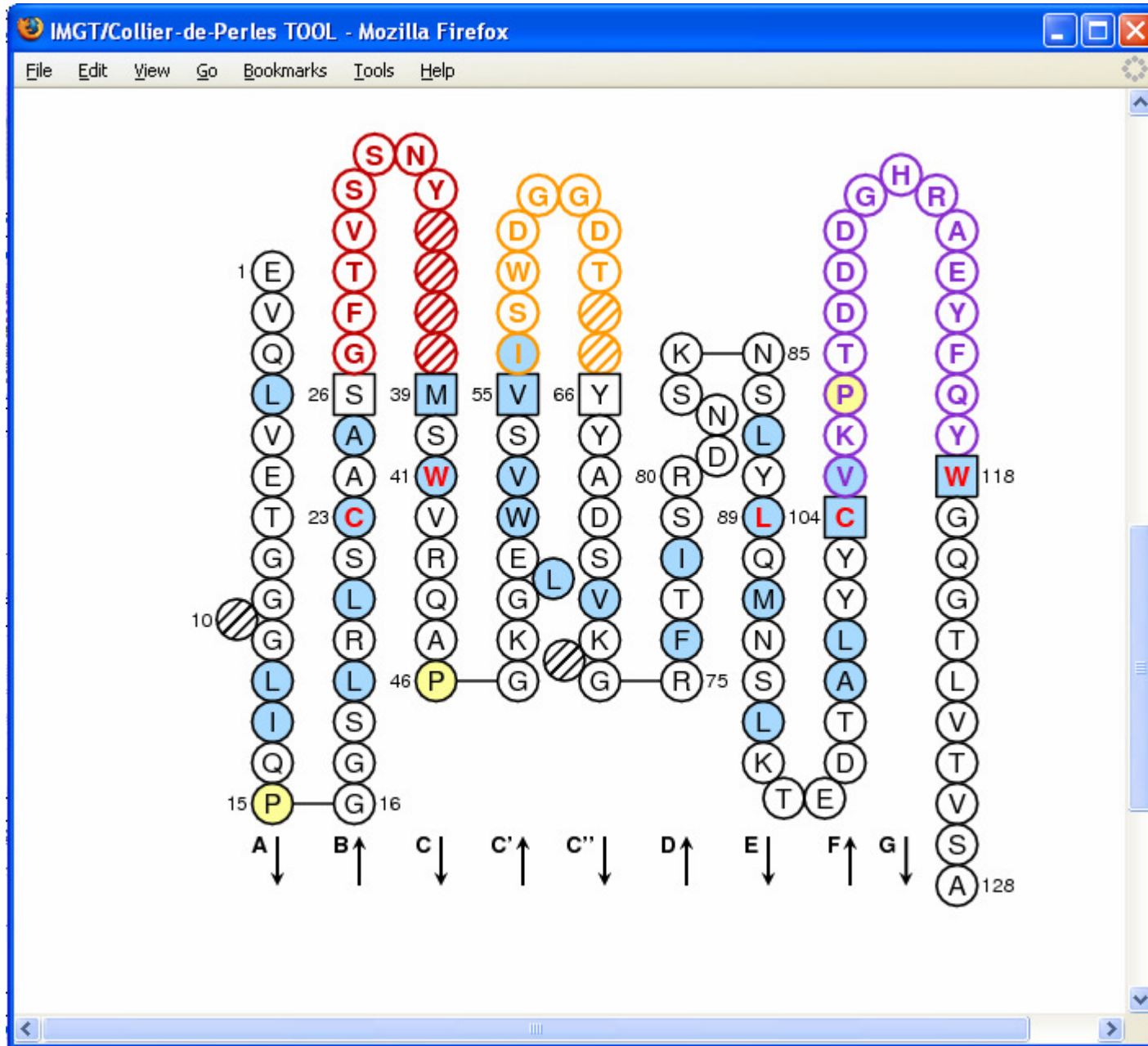
### V-REGION amino acid sequence on one line

```
>AY393058
EVQLVESGG.ALVQPGRSLTLSCTSSGLTFDDYF...MSWFRQAPGKGLEWVGFIRSKTYGGTTEYAASVQ.GRFTISRDDSKSIAYLQMNSLKTEDTAIYYC
```

### V-D-J-REGION nucleotide sequence in FASTA format

```
>AY393058
gaggtgcagctggtggagtctggggga...gccttggtacagccagggcgggtccctgaca
ctctcctgcacatcttctggattgacctttgatgattacttt.....atgagc
tggttccgccaggctccaggaaggactggagtgggtaggtttcattaggagcaaaact
tatggtgggacaacagaatacgcgcgtctgtgcaa...ggcagattcaccatctcaaga
gatgattccaaaagcatcgctatctgcaaatgaacagcctgaaaaccgaggacacagcc
atatattactgtagtcccggggtagcgttattaccacgaagacttcagcagtgggggc
cgggcaccatggtcaccgtctcctcag
```





## Annotations by IMGT/Automat

| Label                        | Location/Qualifiers   |
|------------------------------|---|
| <a href="#">V-D-J-REGION</a> | 42..411<br>/Nucleotide sequence<br>gaggtgcagctggtggagctctgggggagccttggtacagccagggcgggtccctgacactc<br>tcctgcacatcttctggattgacctttgatgattactttatgagctggttccgccaggct<br>ccaggaagggactggagtggttaggtttcattaggagcaaaacttatggtgggacaaca<br>gaatacgcgcgctctgtgcaaggcagattcaccatctcaagagatgattccaaaagcatc<br>gcctatctgcaaatgaacagcctgaaaaccgaggacacagccatatattactgtagtccc<br>ggggtagcgcttattaccacgaagacttccagcagtggggcccgggcaccatggtcacc<br>gtctcctcag<br>/Translation<br>EVQLVESGGALVQPGRSLTSLCTSSGLTFDDYFMSWFRQAPGKGLEWVGFIRSKTYGGTT<br>EYAASVQGRFTISRDDSKSIAYLQMNSLKTEDTAIYYCSPGGSAYYHEDFQWGPQTMVT<br>VSS |
| <a href="#">V-REGION</a>     | 42..336<br>/allele="IGHV3-49*03"<br>/CDR_length="[8,10,14]"<br>/gene="IGHV3-49"<br>/Nucleotide sequence<br>gaggtgcagctggtggagctctgggggagccttggtacagccagggcgggtccctgacactc<br>tcctgcacatcttctggattgacctttgatgattactttatgagctggttccgccaggct<br>ccaggaagggactggagtggttaggtttcattaggagcaaaacttatggtgggacaaca<br>gaatacgcgcgctctgtgcaaggcagattcaccatctcaagagatgattccaaaagcatc<br>gcctatctgcaaatgaacagcctgaaaaccgaggacacagccatatattactgta<br>/Translation<br>EVQLVESGGALVQPGRSLTSLCTSSGLTFDDYFMSWFRQAPGKGLEWVGFIRSKTYGGTT<br>EYAASVQGRFTISRDDSKSIAYLQMNSLKTEDTAIYYC                                       |
| <a href="#">FR1-IMGT</a>     | 42..116<br>/AA_IMGT="AA 1 to 26, AA 10 is missing"<br>/Nucleotide sequence<br>gaggtgcagctggtggagctctgggggagccttggtacagccagggcgggtccctgacactc<br>tcctgcacatcttct<br>/Translation<br>EVQLVESGGALVQPGRSLTSLCTSS  |
| <a href="#">1st-CYS</a>      | 105..107<br>/Nucleotide sequence<br>tgc<br>/Translation<br>C  |
| <a href="#">CDR1-IMGT</a>    | 117..140<br>/AA_IMGT="AA 27 to 34"<br>/Nucleotide sequence<br>ggattgacctttgatgattacttt  |

IMGT/V-QUEST - Microsoft Internet Explorer

Fichier Edition Affichage Favoris Outils ?

## Selection of parameters for the results

Display type :       Nb of nucleotides per line in alignment:

**A. Detailed view**

|   |   |   |
|---|---|---|
| 1. <input checked="" type="checkbox"/> <a href="#">Alignment for V-GENE</a>   | 5. <input type="checkbox"/> <a href="#">Sequence of the JUNCTION ('nt' and 'AA')</a>                      | 11. <a href="#">IMGT Collier de Perles</a>  |
| 2. <input checked="" type="checkbox"/> <a href="#">Alignment for D-GENE</a>   | 6. <input checked="" type="checkbox"/> <a href="#">V-REGION alignment according to the IMGT numbering</a> | <input checked="" type="radio"/> links to IMGT Collier de Perles                    |
| 3. <input checked="" type="checkbox"/> <a href="#">Alignment for J-GENE</a>   | 7. <input checked="" type="checkbox"/> <a href="#">V-REGION translation</a>                               | <input type="radio"/> IMGT Collier de Perles (PNG format, slow)                     |
| 4. <input checked="" type="checkbox"/> <a href="#">Results of IMGT/JunctionAnalysis</a>   | 8. <input checked="" type="checkbox"/> <a href="#">V-REGION mutation table</a>                            | <input type="radio"/> no IMGT Collier de Perles                                     |
| <input type="radio"/> with full list of eligible D-GENES  | 9. <input checked="" type="checkbox"/> <a href="#">V-REGION mutation statistics</a>                       |   |
| <input checked="" type="radio"/> without list of eligible D-GENES   | 10. <input checked="" type="checkbox"/> <a href="#">V-REGION mutation hot spots</a>                       |   |
| 12. <input checked="" type="checkbox"/> <a href="#">Sequences of V-, V-J- or V-D-J- REGION ('nt' and 'AA') with gaps in FASTA</a><br><a href="#">Access to IMGT/PhyloGene for V-REGION ('nt')</a> |   | 13. <input checked="" type="checkbox"/> <a href="#">Annotations by IMGT/Automat</a> |

**More options**

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)

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

**B. Synthesis view**

|   |   |
|---|---|
| 1. <input checked="" type="checkbox"/> <a href="#">Alignment for V-GENES</a>                              | 5. <input checked="" type="checkbox"/> <a href="#">V-REGION protein display (with color)</a>          |
| 2. <input checked="" type="checkbox"/> <a href="#">V-REGION alignment according to the IMGT numbering</a> | 6. <input checked="" type="checkbox"/> <a href="#">V-REGION protein display (mutations displayed)</a> |
| 3. <input checked="" type="checkbox"/> <a href="#">V-REGION translation</a>                               | 7. <input checked="" type="checkbox"/> <a href="#">V-REGION most frequently occurring AA</a>          |
| 4. <input checked="" type="checkbox"/> <a href="#">V-REGION protein display</a>                           | 8. <input checked="" type="checkbox"/> <a href="#">Results of IMGT/JunctionAnalysis</a>               |

Selection of output parameters



# THANK YOU for using IMGT/V-QUEST

THE  
INTERNATIONAL  
IMMUNOGENETICS  
INFORMATION SYSTEM®



<http://imgt.cines.fr>

👉 You are in the new IMGT/V-QUEST, *upgraded for multiple sequences and with new functionalities.* **NEW!**

## B. Synthesis for the IMGT/V-QUEST analysed sequences

The analysed sequences are aligned with the allele(s):

[IGHV3-49\\*03](#) [IGHV3-53\\*02](#) [IGHV5-51\\*03](#)

Results of IMGT/JunctionAnalysis for : IGH junctions

### Sequences aligned with IGHV3-49\*03

#### 1. Alignement for V-GENE

```

<----- FRI-IMGT -----
AB019438 IGHV3-49*03      gaggtgcagctggtggagctctggggga...ggcttggtacagccagggcggtccctgaga
AY393054                  1321 -----
AY393058                  1330 -----c-----c-
AY393072                  1258 -----g-----c-----g...-----t--ag-----
----->----- CDR1-IMGT -----<-----
AB019438 IGHV3-49*03      ctctcctgtacagcttctggattcaccttgggtgattatgct.....atgagc
AY393054                  1321 -----g-----g-----ctt-----
AY393058                  1330 -----c--t-----g-----a-----ctt-----
AY393072                  1258 -----g-----c-----g-----ctt-----
    
```

IMGT/QUEST - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

## Sequences aligned with IGHV5-51\*03

### 1. Alignement for V-GENE

```

<-----FR1-IMGT-----
X56368 IGHV5-51*03      gaggtgcagctggtgcagctctggagca...gaggtgaaaaagccgggggagtcctctgaag
AY393084                1327 -----gc-----
AY393088                1309 -----gc-----a
AY393089                1255 ---g-----a-----a-----a---
AY393091                1237 -----
AY393092                1255 ---g-----a-----a-----a---
AY393094                1300 -----gc--t-----
----->_____CDR1-IMGT_____<-----
X56368 IGHV5-51*03      atctctctgtaagggttctggatacagctttaccagctactgg.....atcggc
AY393084                1327 ----t-----c-----ta-----
AY393088                1309 -----g-c-----tc-----
AY393089                1255 -----c-----c--g-----
AY393091                1237 -----t-tt-c--aa-----
AY393092                1255 -----c-----c--g-----
AY393094                1300 -----c-----t-----ta-----
-----FR2-IMGT----->_____CDR
X56368 IGHV5-51*03      tgggtgcgccagatgcccgggaaaggcctggagtggatggggatcatctatcctggtgac
AY393084                1327 -----t-----
AY393088                1309 -----t-----
AY393089                1255 -----g--a--g-g-----
AY393091                1237 -----a--c-----g--c-----a--a--t
AY393092                1255 -----g--a--g-g-----
AY393094                1300 -----t-----t-----

```

IMGT/V-QUEST - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

### 3. V-REGION translation

```

<-----FR1 - IMGT
      1       5       10       15
      E   V   Q   L   V   Q   S   G   A   ...   E   V   K   K   P
X56368 IGHV5-51*03   gag gtg cag ctg gtg cag tct gga gca ... gag gtg aaa aag ccg
                        R
AY393084           1327 --- --- -gc --- --- --- --- --- ... --- --- --- ---
                        R
AY393088           1309 --- --- -gc --- --- --- --- --- ... --- --- --- ---
                        G           E
AY393089           1255 --- -g- --- --- -a- --- --- --- --- ... --a --- --- ---
AY393091           1237 --- --- --- --- --- --- --- --- --- ... --- --- --- ---
                        G           E
AY393092           1255 --- -g- --- --- -a- --- --- --- --- ... --a --- --- ---
                        R
AY393094           1300 --- --- -gc --t --- --- --- --- --- ... --- --- --- ---

----->
      20       25       30
      G   E   S   L   K   I   S   C   K   G   S   G   Y   S   F
X56368 IGHV5-51*03   ggg gag tct ctg aag atc tcc tgt aag ggt tct gga tac agc ttt
                        A
AY393084           1327 --- --- --- --- --- --- --t --- --- -c- --- --- --- ---
                        R   A
AY393088           1309 --- --- --- --- --a --- --- --- -g- -c- --- --- --- ---
                        A           T
AY393089           1255 --- --- --- --a --- --- --- --- -c- --- --- --- -c- ---
                        I
AY393091           1237 --- --- --- --- --- --- --- --- --- --- -t -tt --c
                        A           T
AY393092           1255 --- --- --- --a --- --- --- --- --- -c- --- --- --- -c- ---
                        A
AY393094           1300 --- --- --- --- --- --- --- --- --- -c- --- --- --- -t ---

```

IMGT/V-QUEST - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

### 5. Protein display with coloured AA according to the AA IMGT Classes

|                    | FR1-IMGT<br>(1-26)         | CDR1-IMGT<br>(27-38) | FR2-IMGT<br>(39-55) | CD |
|--------------------|----------------------------|----------------------|---------------------|----|
|                    | 1 10 20                    | 30                   | 40 50               |    |
| X56368 IGHV5-51*03 | EVQLVQSGA.EVKKPGESLKI      | CKGS GYSFTSYW...     | IGUVRQMPGKGLEWVGI   | IY |
| AY393084           | 1327 EVRLVQSGA.EVKKPGESLKI | CKAS GYSFTSNW...     | IGUVRQMPGKGLEWVGI   | IF |
| AY393088           | 1309 EVRLVQSGA.EVKKPGESLKI | CRAS GYSFTSHW...     | IGUVRQMPGKGLEWVGI   | IF |
| AY393089           | 1255 EGQLEQSGA.EVKKPGESLKI | CKAS GYTFASYW...     | IGUVRQMPGKGLEWVGI   | VY |
| AY393091           | 1237 EVQLVQSGA.EVKKPGESLKI | CKGS GYIFTKYW...     | IGUVRQIPGKGLEWVAI   | IN |
| AY393092           | 1255 EGQLEQSGA.EVKKPGESLKI | CKAS GYTFASYW...     | IGUVRQMPGKGLEWVGI   | VY |
| AY393094           | 1300 EVRLVQSGA.EVKKPGESLKI | CKAS GYSFTSNW...     | IGUVRQMPGKGLEWIGI   | IF |

|                    | R2-IMGT<br>(56-65)                | FR3-IMGT<br>(66-104)              |
|--------------------|-----------------------------------|-----------------------------------|
|                    | 60 70 80 90 100                   |                                   |
| X56368 IGHV5-51*03 | PGDSDT.. RYSPSFQ.GQVTISADKSI      | STAYLQWSSLKASDTAMYYC AR           |
| AY393084           | 1327 PGDSDT.. IYSPSFQ.GQVTISVDKSI | STAYLQWSSLKASDTAIYYC ARQNPPEYSGA  |
| AY393088           | 1309 PGDSDT.. IYSPSFE.GQVTISADKSI | STAYLQWSSLKATDSAMYYC ARQNPPEYSGA  |
| AY393089           | 1255 PGDFDT.. KYSPSFQ.GHVTISVDRS  | ISTAYLQWSSLKASDTAFYYC AREMLYGSGGY |
| AY393091           | 1237 PDDSDT.. RYNTSFQ.GQVTISVDKSI | STAYLQWSSLKATDTAMYYC ARQNPPEYSGA  |
| AY393092           | 1255 PGDFDT.. KYSPSFQ.GHVTISADRST | STAYLQWSSLKASDTVIYYC AREMLYGSGGY  |
| AY393094           | 1300 PGDSDT.. IYSPSFQ.GQVTISVDKSI | NTAYLQWSSLKATDTAMYYC ARQNPPEYSGA  |

IMGTV-QUEST - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

### 6. Protein display (mutations displayed)

|                    | FR1-IMGT<br>(1-26) | CDR1-IMGT<br>(27-38) | FR2-IMGT<br>(39-55) | CD<br>(          |    |
|--------------------|--------------------|----------------------|---------------------|------------------|----|
|                    | 1 10 20            | 30                   | 40 50               |                  |    |
| X56368 IGHV5-51*03 | EVQLVQSGA          | EVKPKGESLKISCKGS     | GYSFTSYW...         | IGWVRQMPGKGLEWMI | IY |
| AY393084           | 1327 --R-----      | -----A-              | -----N-....         | -----            | -F |
| AY393088           | 1309 --R-----      | -----RA-             | -----H-....         | -----            | -F |
| AY393089           | 1255 -G--E----     | -----A-              | --T-A-....          | -----V--         | V- |
| AY393091           | 1237 -----         | -----                | --I--K-....         | -----I-----VA-   | -N |
| AY393092           | 1255 -G--E----     | -----A-              | --T-A-....          | -----V--         | V- |
| AY393094           | 1300 --R-----      | -----A-              | -----N-....         | -----I--         | -F |

|                    | R2-IMGT<br>(56-65) | FR3-IMGT<br>(66-104)                       |
|--------------------|--------------------|--|
|                    | 60                 | 70 80 90 100                               |
| X56368 IGHV5-51*03 | PGDSDT..           | RYSPSFQ.GQVTISADKSISTAYLQWSSLKASDTAMYIC AR |
| AY393084           | 1327 -----..       | I-----V-----I--- --QNPPEYSGA               |
| AY393088           | 1309 -----..       | I----E-----T-S----- --QNPPEYSGA            |
| AY393089           | 1255 ---F---..     | K-----H---V-R-----F--- --EMLYGSGGY         |
| AY393091           | 1237 -D-----..     | --NT-----V-----T----- --QNPPEYSGA          |
| AY393092           | 1255 ---F---..     | K-----H---R-T-----VI--- --EMLYGSGGY        |
| AY393094           | 1300 -----..       | I-----V---N-----T----- --QNPPEYSGA         |



# IMGT/V-QUEST and IMGT/JunctionAnalysis

## Alignment for V-GENE

|                          |             |       |   |
|--------------------------|-------------|-------|---|
| <a href="#">AF402940</a> |             | score | GTGCAGCTGCTCGAGCAGTCTGGGGCT__GAGGTGAGCAAGCCTGGGGCCTCAGTAAAGGTTTCCTGCA |
| <a href="#">X62109</a>   | IGHV1-3*01  | 1146  | CA.GTC.A...T.T.....AG.....G.....                                      |
| <a href="#">X62107</a>   | IGHV1-3*02  | 1110  | CA.GTT.A...G.T.....AG.....G.....                                      |
| <a href="#">M99637</a>   | IGHV1-8*01  | 957   | CA.GT..A...G.T.....AG.....G...C.....                                  |
| <a href="#">L06612</a>   | IGHV1-46*03 | 948   | CA.GT..A...G.T.....AG.....G.....                                      |
| <a href="#">X92343</a>   | IGHV1-46*01 | 948   | CA.GT..A...G.T.....AG.....G.....                                      |

## Alignment for J-GENE

|                          |          |       |   |
|--------------------------|----------|-------|---|
| <a href="#">AF402940</a> |          | score | CTTCACGGGGCGGGACGCTTTGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA |
| <a href="#">J00256</a>   | IGHJ3*01 | 181   | .....T.....T..T.....A.T.....T...G                             |
| <a href="#">X86355</a>   | IGHJ6*02 | 179   | T.A.TACTACTACT...G.A.....                                     |
| <a href="#">X86355</a>   | IGHJ3*02 | 172   | .....T.....T..TA.....A.T.....T...G                            |

