

# Immuno-informatique

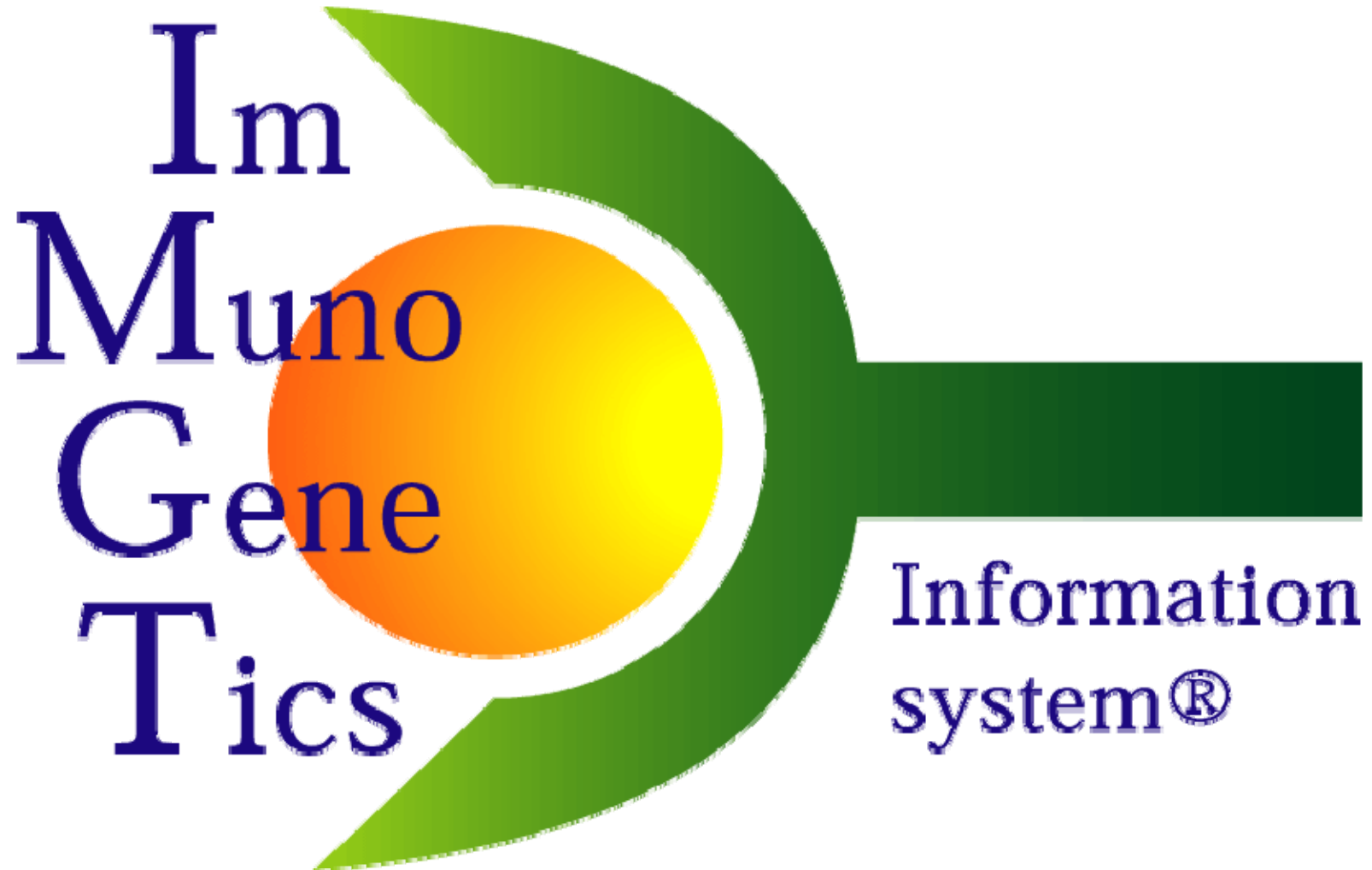
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FMBS312, Master recherche 2 Bio-Med, TC3,  
Universités Montpellier 1 et 2, ENSCM  
30 septembre 2013

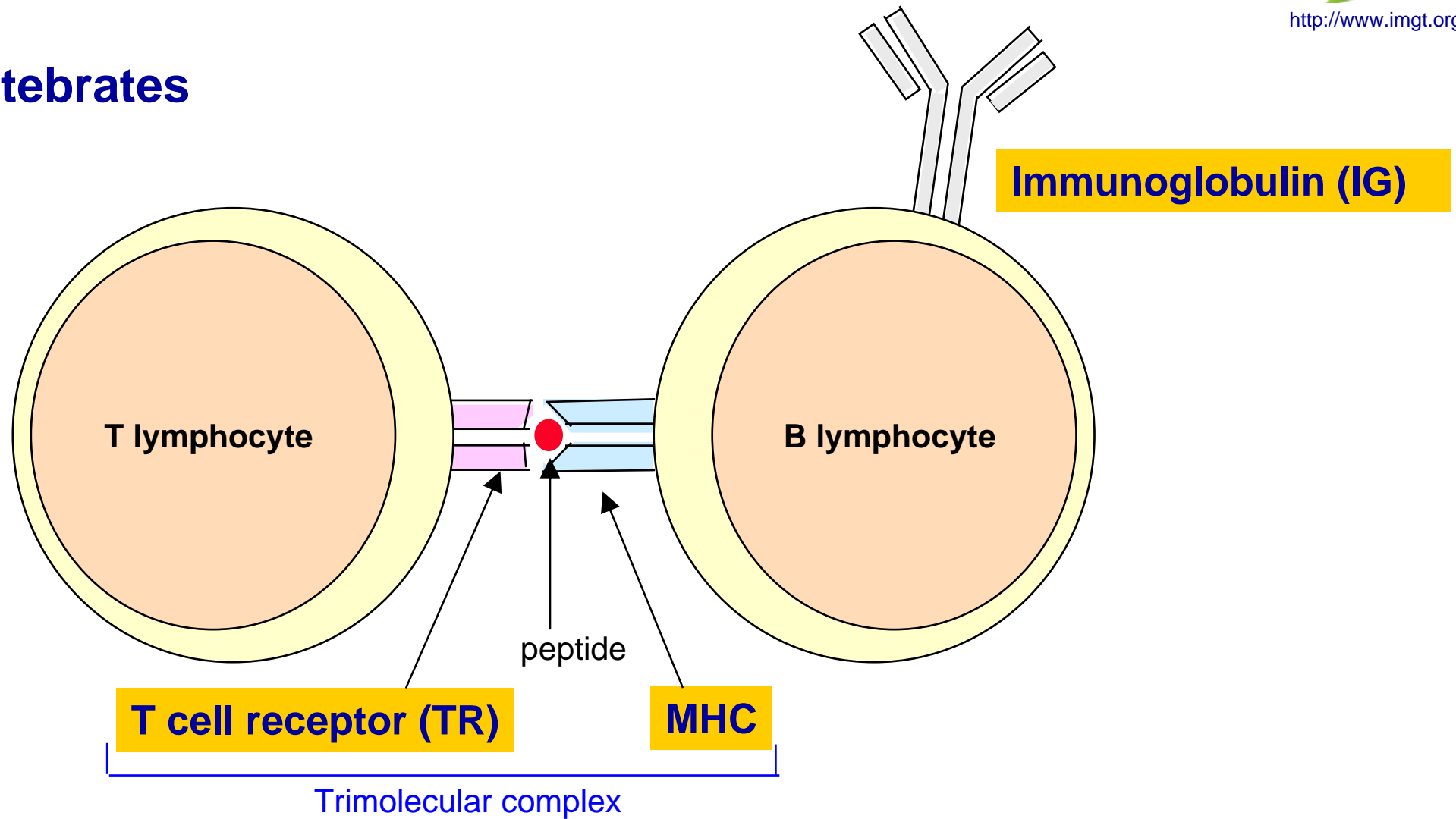
IMGT<sup>®</sup>, the international ImMunoGeneTics information system<sup>®</sup>

<http://www.imgt.org>



# IMGT® domain: the adaptive immune response

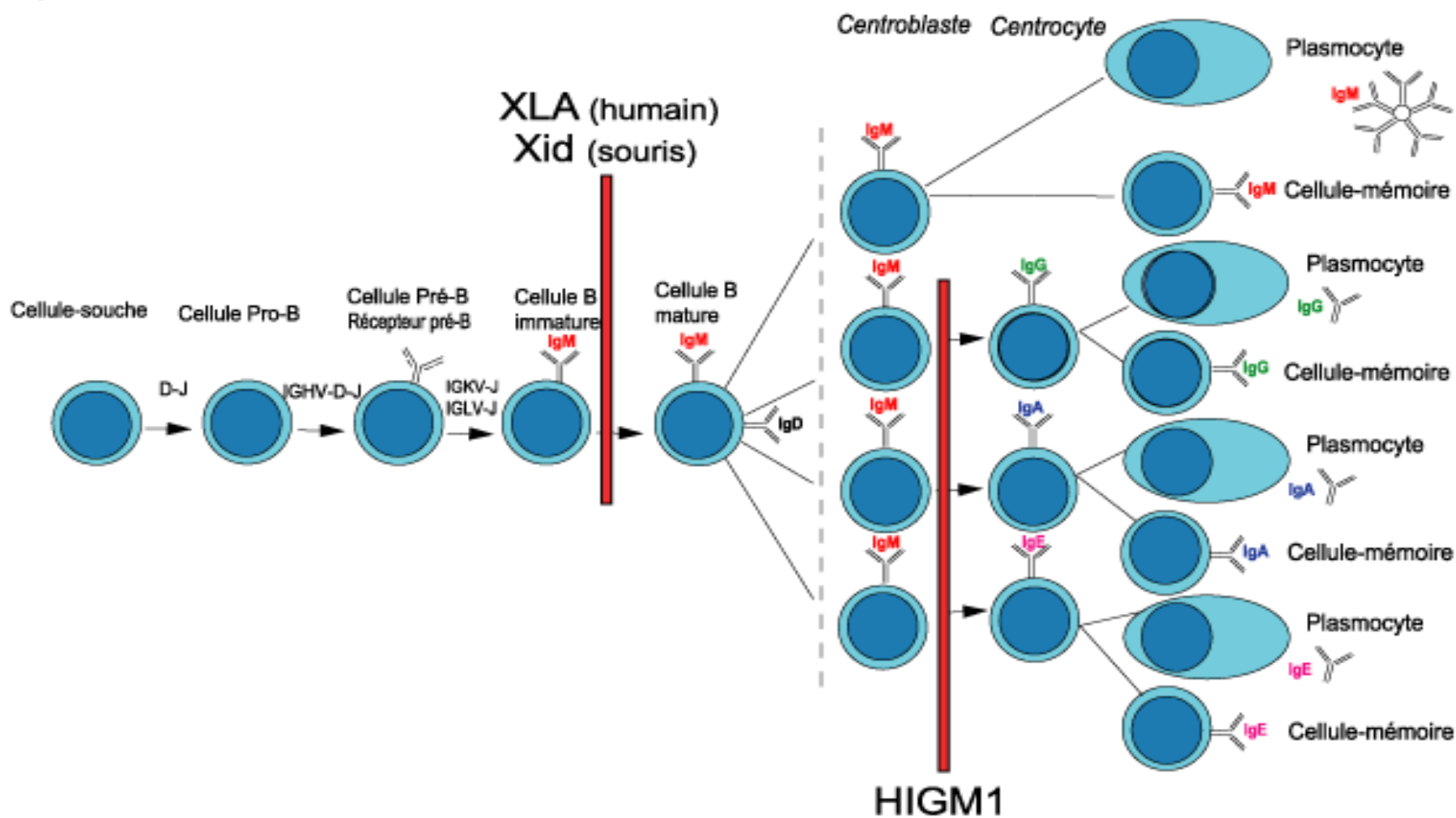
## Vertebrates



Bone marrow

Blood

Lymph nodes, spleen



V-D-J and V-J rearrangements

Hypermutations, selection

When and why was IMGT  
created?

# IMGT birth and objectives

IMGT was created in June 1989, following the Human Genome Meeting HGM, at New Haven, USA.

- \* Thomas Shows and Ken Kidd, meeting organizers*
- \* Lap Chee Tsui, chromosome 7 responsable*
- \* Claude Boucheix (CD nomenclature)*

1. At New haven, entry of the 16 human T cell receptor gamma genes (**TRG**) in the genome database, Genome Database (GDB).
2. IMGT was created to answer the need to manage the T cell receptor (**TR**) and immunoglobulin (**IG**) genes and to enter them in the generalist databases.

# Why was IMGT necessary?

1. Unique structure of the immunoglobulin (IG) and T cell receptor (TR) genes.

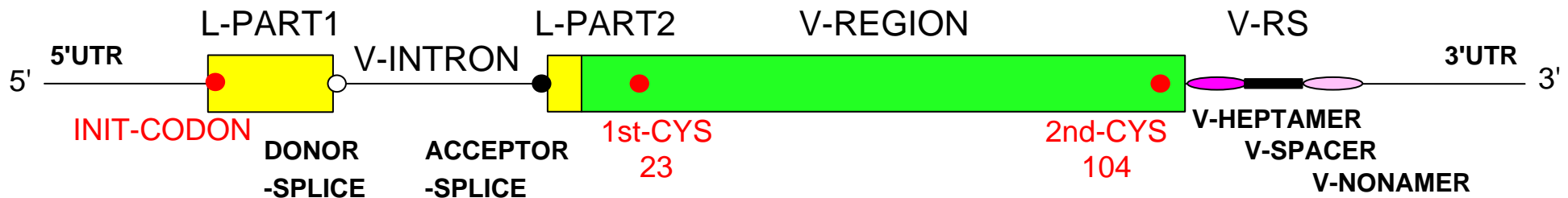
# Genomic DNA in germline configuration

## V-GENE

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

```

tgagagctcc gttcctcacc atggactgga cctggaggat cctcttcttg gtggcagcag      60
ccacaggaa gaggctccct agtcccagtg atgagaaaga gattgagtcc agtccagggg      120
gatctcatcc acttctgtgt tctctccaca ggagcccact cccaggtgca gctgggtgcag      180
tctggggctg aggtgaagaa gcctggggcc tcagtgaagg tctcctgcaa ggcttctgga      240
tacaccttca ccggctacta tatgcactgg gtgcgacagg cccttgaca agggcttgag      300
tggatgggat ggatcaacc taacagtggg ggcacaaact atgcacagaa gtttcagggc      360
agggtcacca tgaccagggg cacgtccatc agcacagcct acatggagct gagcaggctg      420
agatctgacg acacggccgt gtattactgt gcgagagaca cagtgtgaaa acccacatcc      480
tgagggtgtc agaaacccaa gggaggaggc ag
    
```





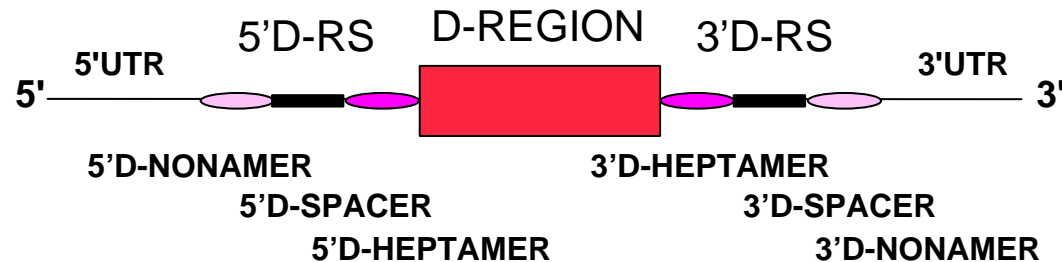
# Genomic DNA in germline configuration

## D-GENE

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

```
ccagccgcag ggTTTTTggc tgagctgaga ac cactgtgc taactgggga cacagtgatt
ggcagctcta caaaaaccat gctccccgg g
```

60



## J-GENE

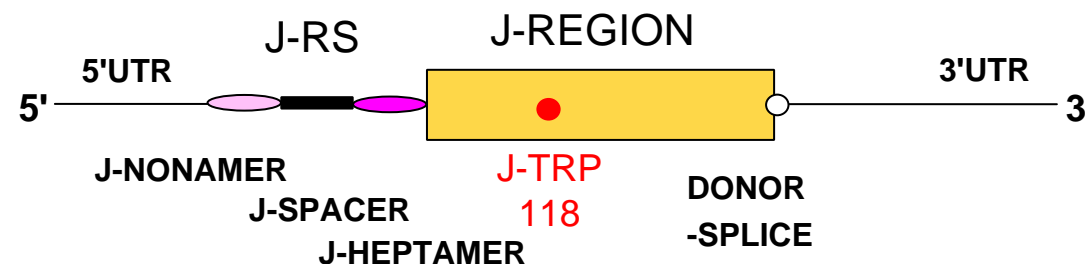
>J00256|IGHJ1\*01|*Homo sapiens* J-GENE

```
accccgggct gtgggtttct gtgcccctgg ctcagggtg actcaccgtg gctgaatact
tccagcactg gggccagggc accctgggtca ccgtctcctc aggtgagtct gctgtactgg
ggatagcggg gagccatgtg tactgggcca agcaagggtc ttggcttcag
```

60

120

170

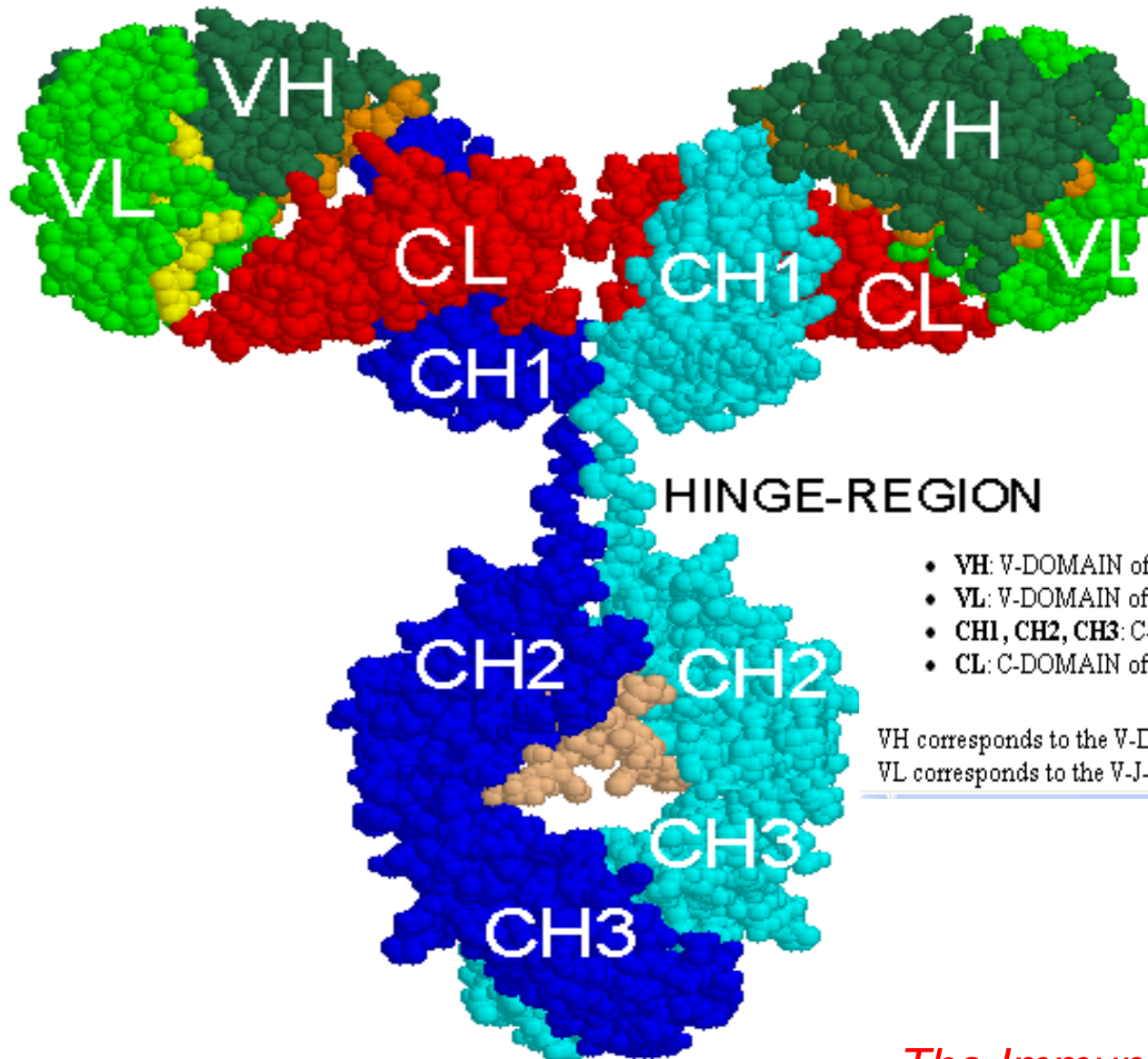


## Why was IMGT necessary?

2. Huge diversity of the immunoglobulin and T cell receptor repertoires.

IMGT is at the origin of Immunoinformatics

# Spacefill 3D representation of an IgG

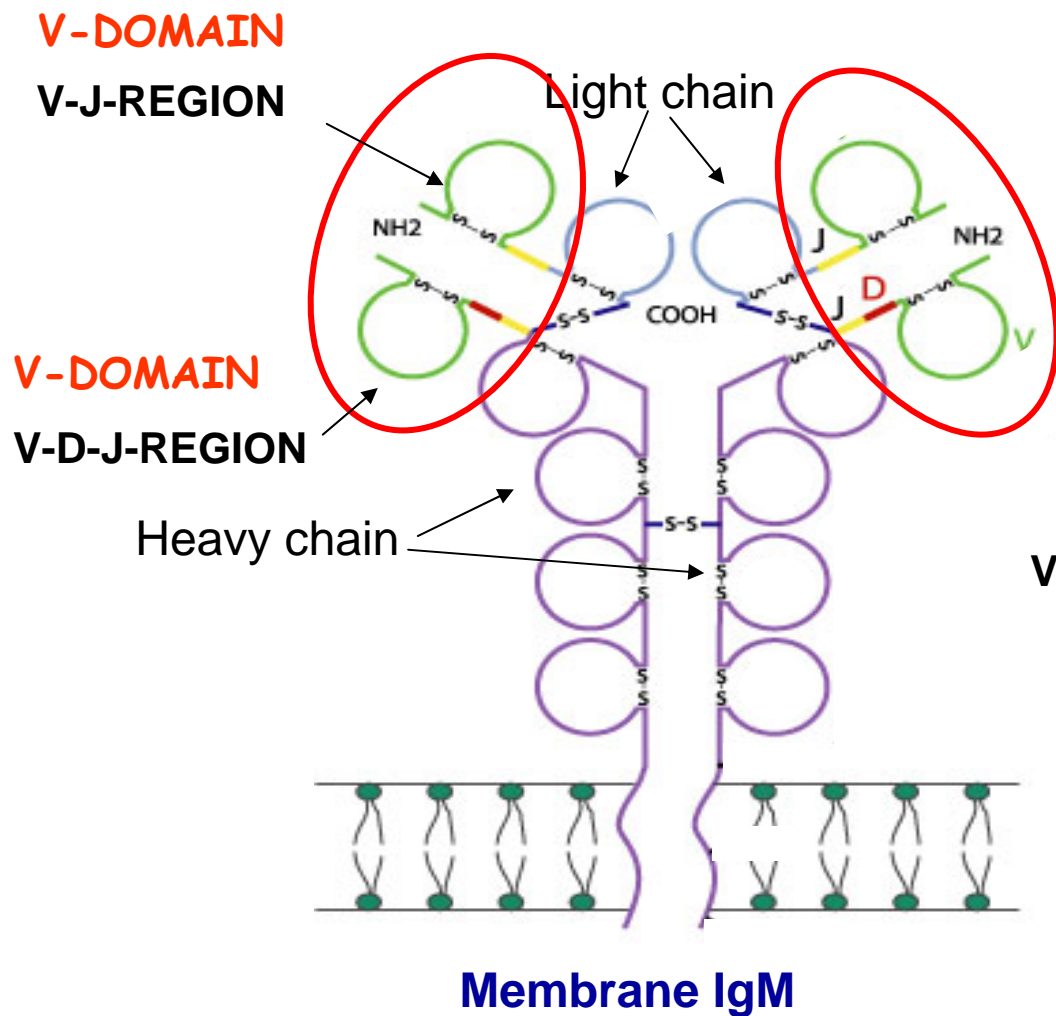


- VH: V-DOMAIN of the immunoglobulin heavy chain
- VL: V-DOMAIN of the immunoglobulin light chain
- CH1, CH2, CH3: C-DOMAIN of the immunoglobulin heavy chain
- CL: C-DOMAIN of the immunoglobulin light chain

VH corresponds to the V-D-J-REGION (in green (V), orange (DJ)) of the heavy chain.  
VL corresponds to the V-J-REGION (in green (V) and yellow (J)) of the light chain.

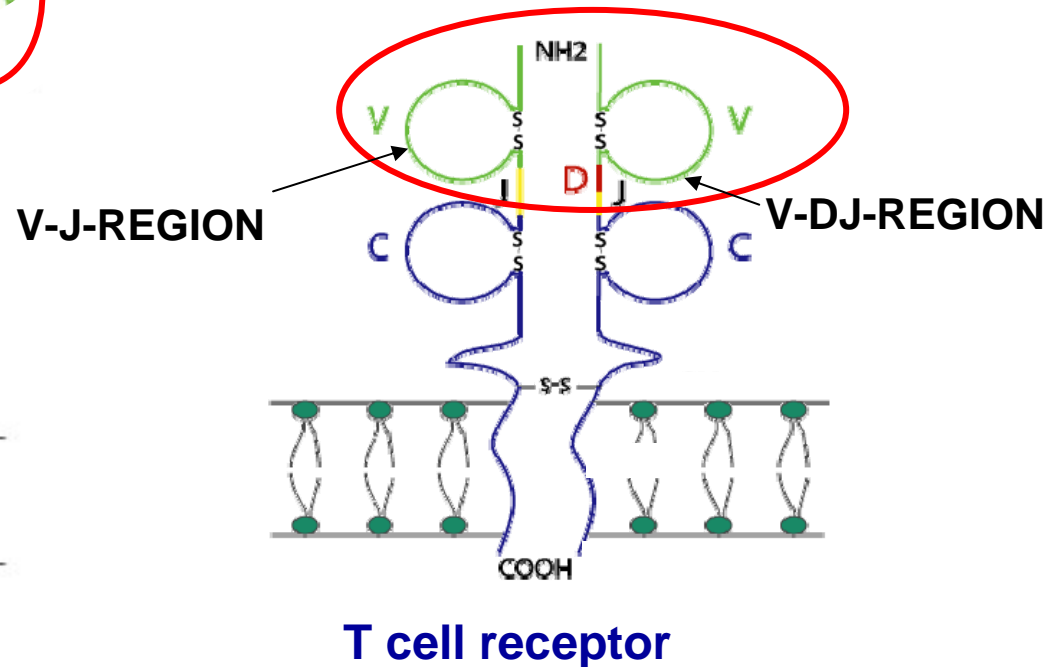
# Immunoglobulin (IG)

# T cell receptor (TR)

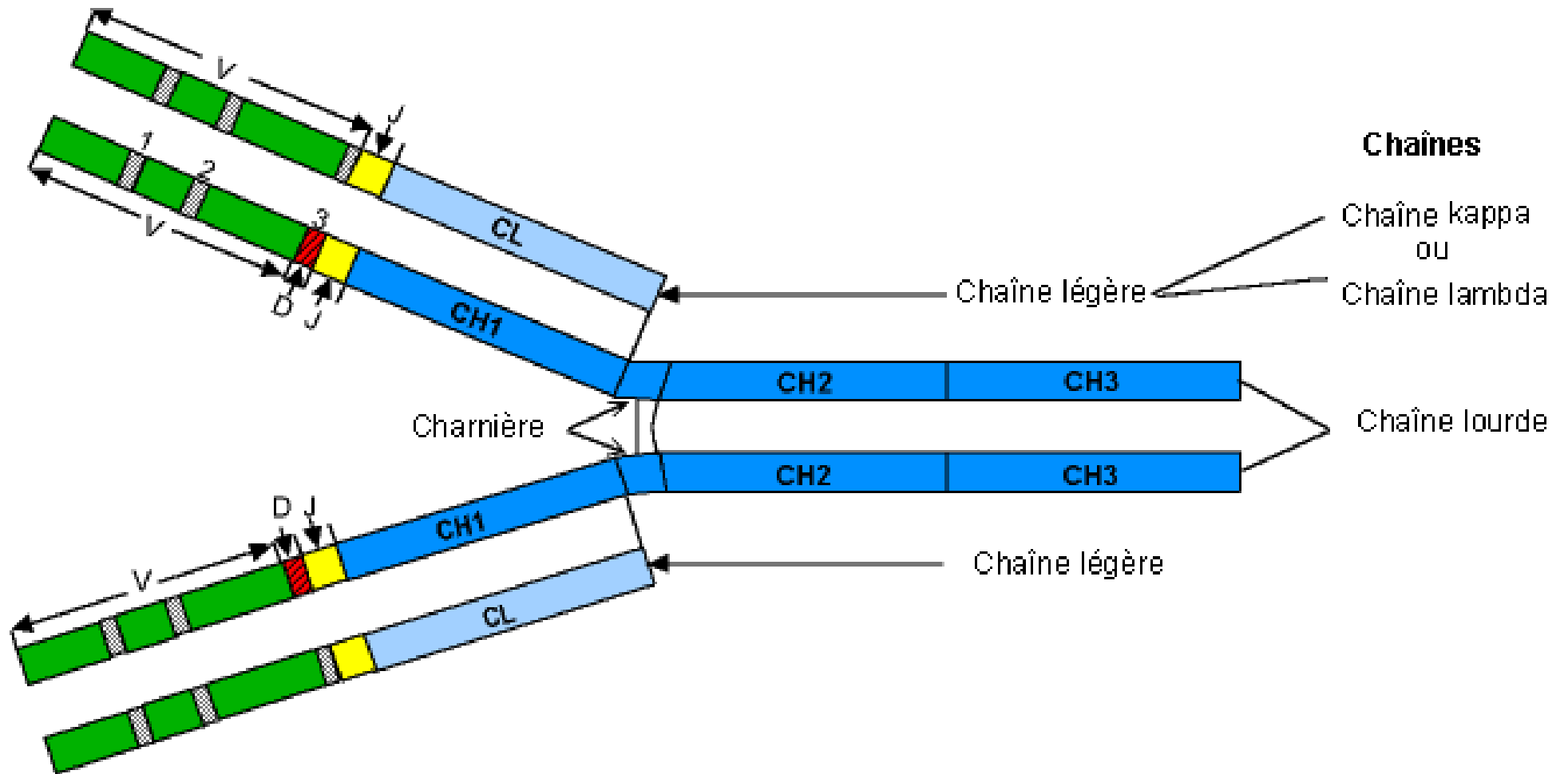


Contribution of the  
2 V-DOMAINS  
to the antigen binding site

Alpha - Beta  
Gamma - Delta

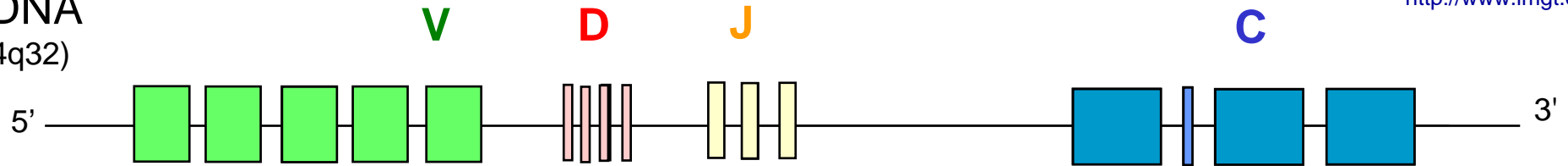


# Immunoglobulin IgG



# Immunoglobulin (IG) synthesis

genomic DNA  
(IGH Locus 14q32)

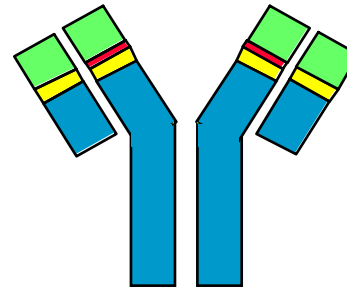


rearranged  
DNA



mRNA

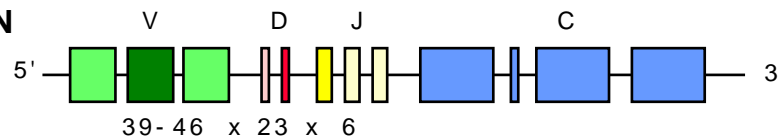
$2 \times 10^{12}$  different IG  
per individual



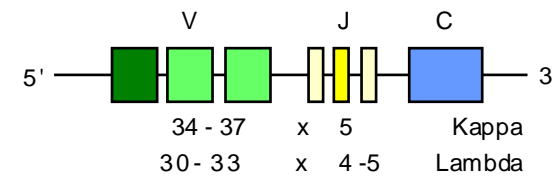
# Immunoglobulin (IG) synthesis

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

**HEAVY CHAIN**



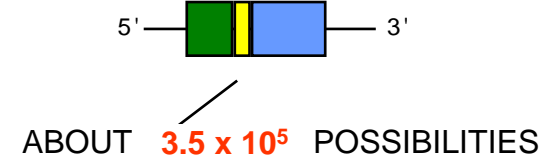
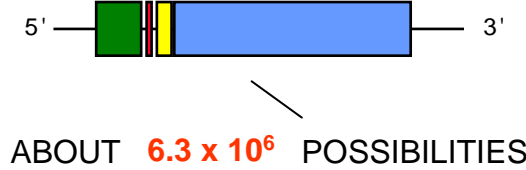
**LIGHT CHAIN**



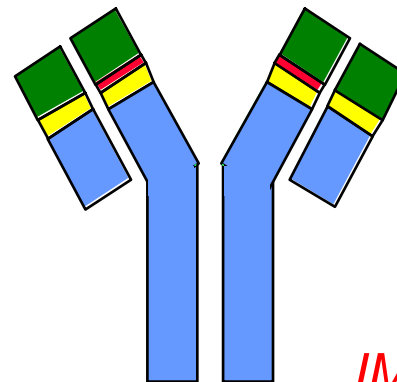
**6300** **POTENTIAL RECOMBINATIONS**

**185 + 165** **POTENTIAL RECOMBINATIONS**

**N-DIVERSITY  
SOMATIC MUTATIONS  
x 1000**



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



# What was the first goal?

## CONTENT

1. Immunoglobulins **AND** T cell receptors
2. Human **AND** other vertebrate species

## DATA

1. Genes **AND** alleles
2. Sequences (germline **AND** rearranged)
3. Polymorphisms: genomic **AND** somatic hypermutations
4. 3D structures



# IMGT® Web resources

IMGT Repertoire **10,000 pages HTML**

Chromosomal localizations

Locus representations

Genes tables

Potential repertoire

Alignments of alleles

Protein displays

IMGT Colliers de Perles...

IMGT Index

IMGT Bloc-notes

Interesting links, PubMed,

Meeting announcements

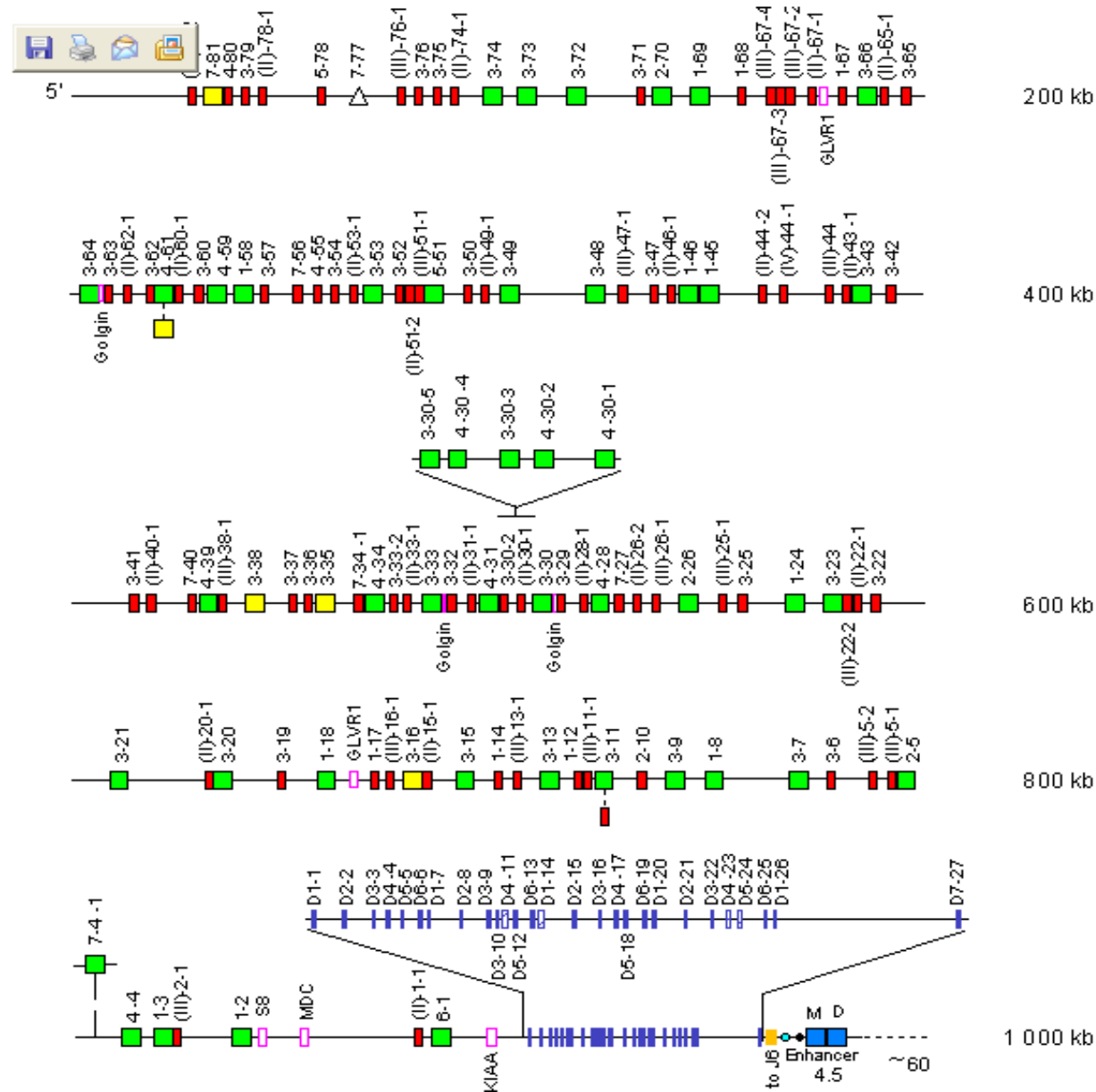
IMGT Immunoinformatics page,...

IMGT Education

Tutorials, IMGT Lexique, ...

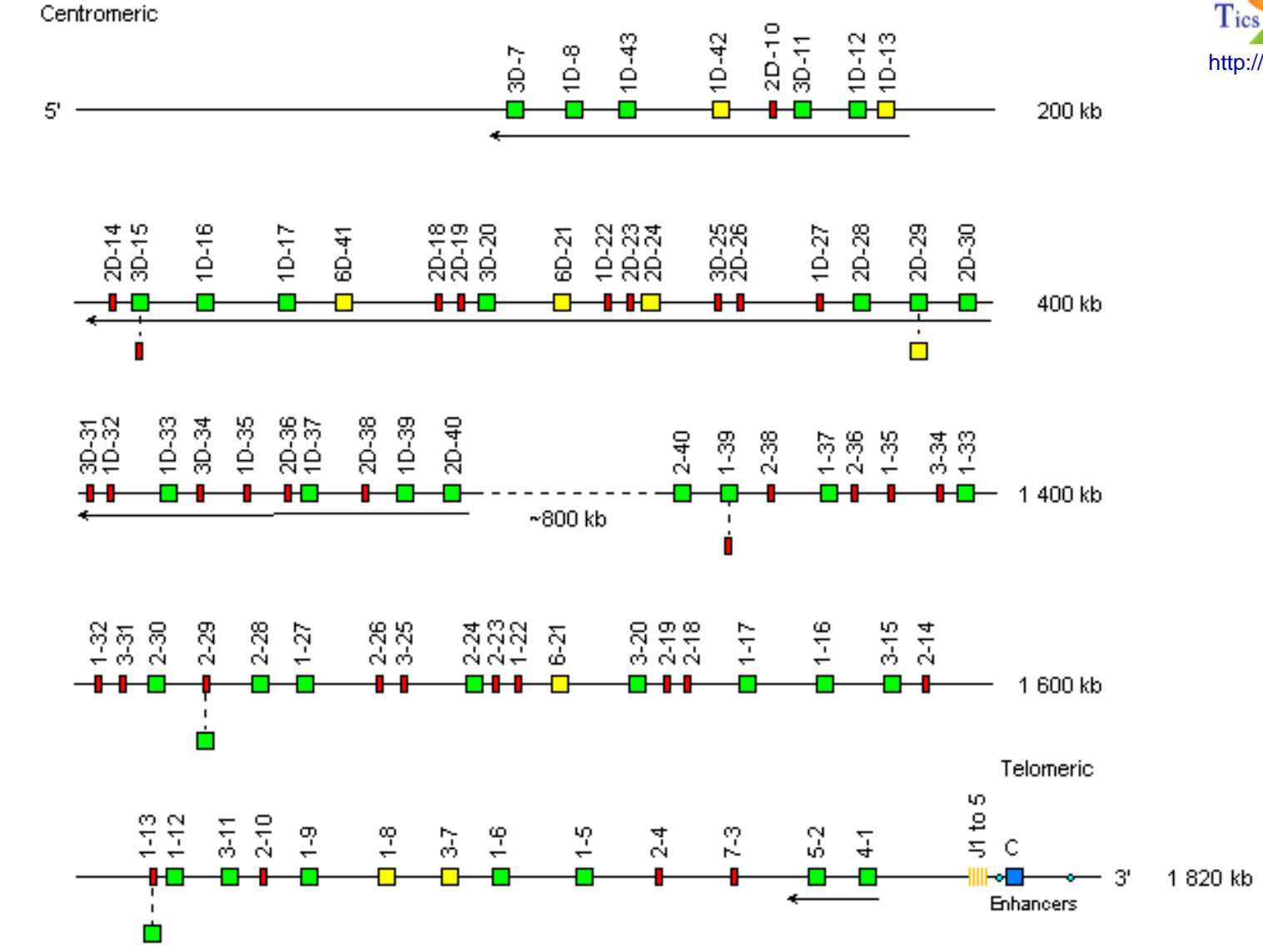
# Human IGH locus

Chromosome  
14q32.33



# Human IGK locus

## Chromosome 2p11.2



# Human IGHV genes on chromosome 14 at 14q32.33

| Subgroup  | Functional   | ORF    | Pseudogene | Total     |
|-----------|--------------|--------|------------|-----------|
| IGHV1     | 9            | -      | 5          | 14        |
| IGHV2     | 3            | -      | 1          | 4         |
| IGHV3     | 18-20**(+1)* | 3      | 25(+1)*    | 47-49**   |
| IGHV4     | 6-9**(+1)*   | (+1)*  | 2          | 9-12**    |
| IGHV5     | 1            | -      | 1          | 2         |
| IGHV6     | 1            | -      | -          | 1         |
| IGHV7     | 0-1**        | 1      | 4          | 5-6**     |
| IGHV(II)  | -            | -      | 22         | 22        |
| IGHV(III) | -            | -      | 18         | 18        |
| IGHV(IV)  | -            | -      | 1          | 1         |
| Total     | 38-44(+2)*   | 4(+1)* | 79(+2)*    | 123-129** |

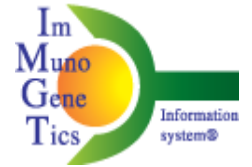
# IMGT Alignment of alleles



<http://www.imgt.org>

|                      |           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----------------------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| X02850 , TRAV8-6*01  | 1         | 2   | 3   | 4   | 5   | 6   | 7   | 8   | 9   | 10  | 11  | 12  | 13  | 14  | 15  | 16  | 17  | 18  | 19  | 20  |     |     |     |
|                      | A         | Q   | S   | V   | T   | Q   | L   | D   | S   | Q   | V   | P   | V   | F   | E   | E   | A   | P   | V   | E   |     |     |     |
|                      | GCC       | CAG | TCT | GTG | ACC | CAG | CTT | GAC | AGC | CAA | GTC | CCT | GTC | TTT | GAA | GAA | GCC | CCT | GTG | GAG |     |     |     |
| AE000659, TRAV8-6*02 | ---       | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |     |     |     |
| M86361 , TRAV8-6*02  | ---       | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |     |     |     |
|                      | CDR1-IMGT |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| X02850 , TRAV8-6*01  | 21        | 22  | 23  | 24  | 25  | 26  | 27  | 28  | 29  | 30  | 31  | 32  | 33  | 34  | 35  | 36  | 37  | 38  | 39  | 40  |     |     |     |
|                      | L         | R   | C   | N   | Y   | S   | S   | S   | V   | S   | V   | Y   |     |     |     |     |     |     | L   | F   |     |     |     |
|                      | CTG       | AGG | TGC | ARC | TAC | TCA | TCG | TCT | GTT | TCA | GTG | TAT | ... | ... | ... | ... | ... | ... | CTC | TTC |     |     |     |
| AE000659, TRAV8-6*02 | ---       | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |     |     |     |
| M86361 , TRAV8-6*02  | ---       | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |     |     |     |
|                      | CDR2-     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| X02850 , TRAV8-6*01  | 41        | 42  | 43  | 44  | 45  | 46  | 47  | 48  | 49  | 50  | 51  | 52  | 53  | 54  | 55  | 56  | 57  | 58  | 59  | 60  |     |     |     |
|                      | W         | Y   | V   | Q   | Y   | P   | N   | Q   | G   | L   | Q   | L   | L   | L   | K   | Y   | L   | S   | G   | S   |     |     |     |
|                      | TGG       | TAT | GTG | CAA | TAC | CCC | ARC | CAA | GGA | CTC | CAG | CTT | CTC | CTG | AGG | TAT | TTA | TCA | GGA | TCC |     |     |     |
| AE000659, TRAV8-6*02 | ---       | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |     |     |     |
| M86361 , TRAV8-6*02  | ---       | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |     |     |     |
|                      | IMGT      |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| X02850 , TRAV8-6*01  | 61        | 62  | 63  | 64  | 65  | 66  | 67  | 68  | 69  | 70  | 71  | 72  | 73  | 74  | 75  | 76  | 77  | 78  | 79  | 80  |     |     |     |
|                      | T         | L   |     |     |     | V   | E   | S   | I   | N   |     |     |     |     |     |     | G   | F   | E   |     |     |     |     |
|                      | ACC       | CTG | ... | ... | ... | GTT | GAA | AGC | ATC | ACC | ... | ... | ... | ... | ... | ... | GGT | TTT | GAG |     |     |     |     |
| AE000659, TRAV8-6*02 | ---       | --- | --- | --- | --- | --- | R   | G   | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |     |     |     |
| M86361 , TRAV8-6*02  | ---       | --- | --- | --- | --- | --- | R   | G   | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |     |     |     |
|                      | 81        | 82  | 83  | 84  | 84A | 84B | 84C | 85  | 86  | 87  | 88  | 89  | 90  | 91  | 92  | 93  | 94  | 95  | 96  | 97  | 98  | 99  | 100 |
|                      | A         | E   | F   | N   | K   | S   | Q   | T   | S   | F   | H   | L   | R   | K   | P   | S   | V   | H   | I   | S   | D   | T   | A   |
|                      | GCT       | GAA | TTT | AAC | AAG | AGT | CAA | ACT | TCC | TTC | CAC | TTG | AGG | AAA | CCC | TCA | GTC | CAT | ATA | AGC | GAC | ACG | GCT |
| AE000659, TRAV8-6*02 | ---       | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| M86361 , TRAV8-6*02  | ---       | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|                      | CDR3-IMGT |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| X02850 , TRAV8-6*01  | 101       | 102 | 103 | 104 | 105 | 106 | 107 | 108 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|                      | E         | Y   | F   | C   | A   | V   | S   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|                      | GAG       | TAC | TTC | TGT | GCT | GTG | AGT | GA  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| AE000659, TRAV8-6*02 | ---       | --- | --- | --- | --- | --- | --- | --- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| M86361 , TRAV8-6*02  | ---       | --- | --- | --- | --- | --- | R   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|                      |           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|                      |           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

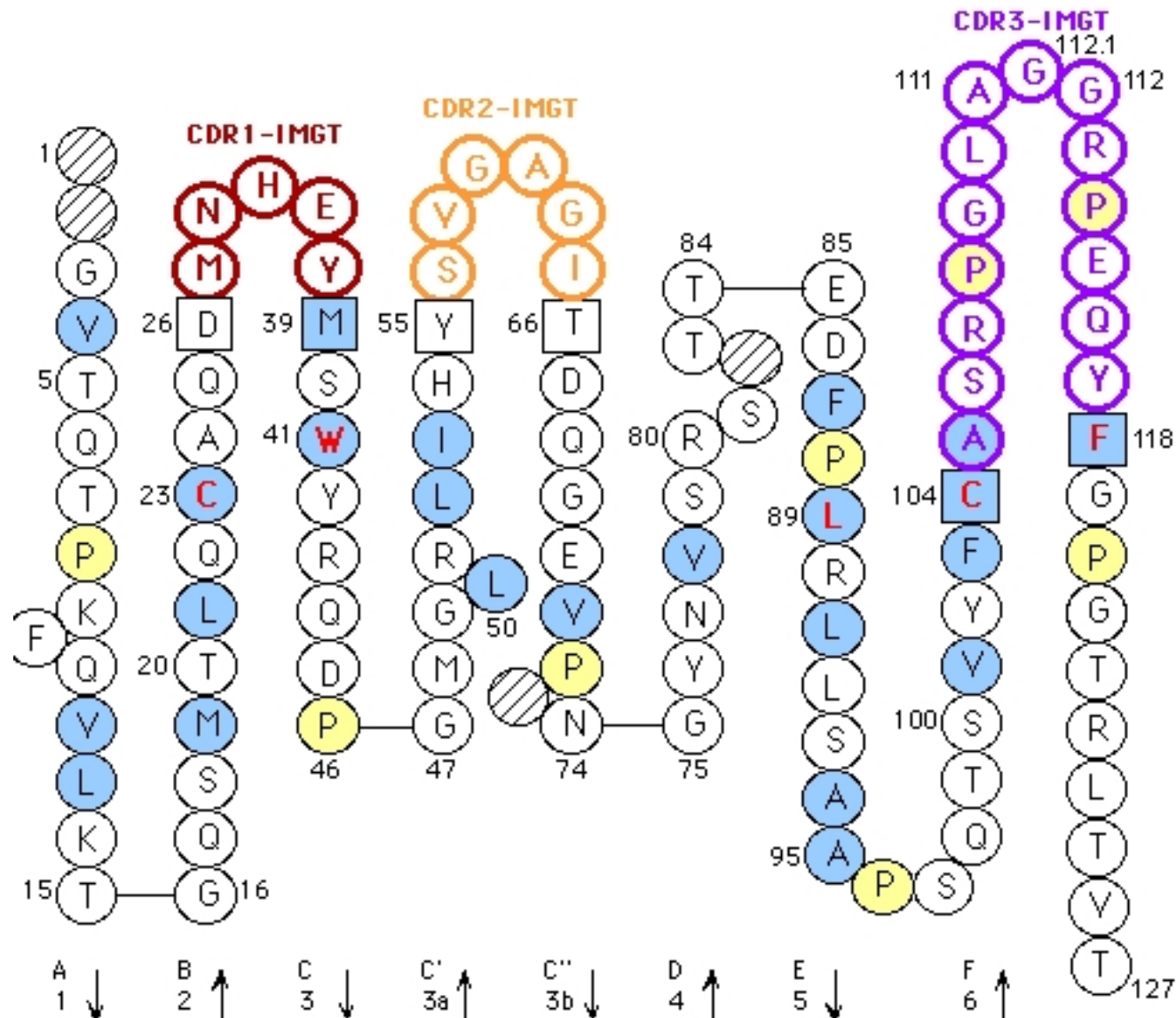
# IMGT Protein display



<http://www.imgt.org>

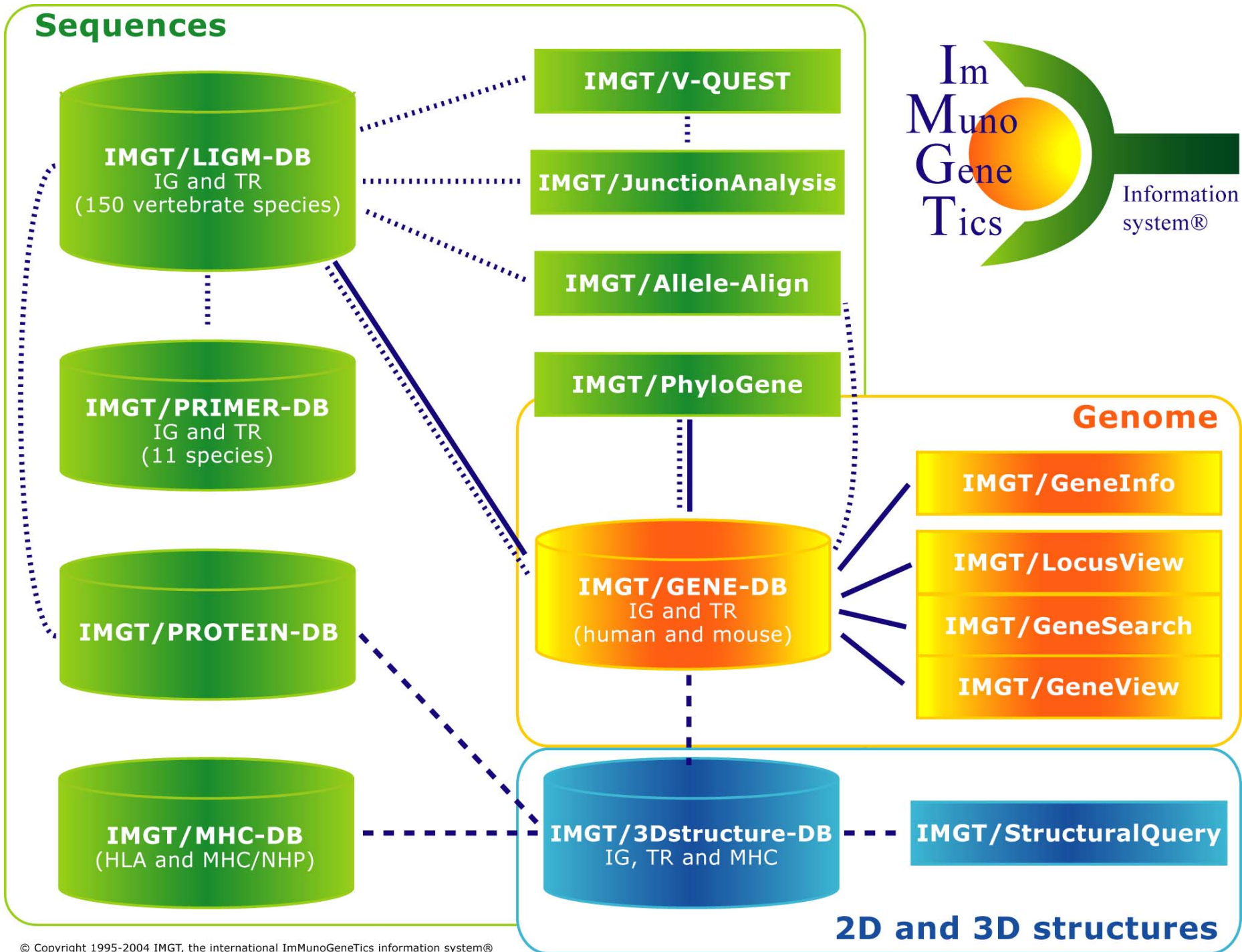
| TRAV<br>gene      | FR1-IMGT<br>(1-26) |             |                | CDR1-IMGT<br>(27-38) |         |             | FR2-IMGT<br>(39-55) |       |          | CDR2-IMGT<br>(56-65) |          |             | FR3-IMGT<br>(66-104) |  |  | CDR3-IMGT<br>(105-115) |  |  |
|-------------------|--------------------|-------------|----------------|----------------------|---------|-------------|---------------------|-------|----------|----------------------|----------|-------------|----------------------|--|--|------------------------|--|--|
|                   | 1                  | 10          | 20             | 30                   | 40      | 50          | 60                  | 70    | 80       | 84ABC                | 90       | 100         | 110                  |  |  |                        |  |  |
| AE000658, TRAV1-1 | GQSLEQ             | PSEVTAVEGAI | VQINCTYQ       | TSGFYG               | LSWYQQH | DGGAPITFLSY | NADG                | LEETG | RFSSFLSR | SDSYGYLL             | QELQMKDS | SASYFC      | AVR                  |  |  |                        |  |  |
| AE000658, TRAV1-2 | GQNIDQ             | PTEMTATEGAI | VQINCTYQ       | TSGFNG               | LFWYQQH | AGEAPITFLSY | NVLDG               | LEEKG | RFSSFLSR | SKGYSYLL             | KKELQMKD | SASYLC      | AVR                  |  |  |                        |  |  |
| AE000658, TRAV2   | KDQVFQ             | PSTVASSEGAV | VEIFCNHS       | VSNAVY               | FFWYLHF | PGCAPRLLVK  | GSK                 | PSQQG | RYNMTYER | FSSLLILQ             | VREADAAV | YVC         | AVE                  |  |  |                        |  |  |
| AE000658, TRAV3   | AQSVAQPEDQ         | VNVAEGNPL   | TVKCTYS        | VSGMPY               | LFWYVQY | PNRGLQFLK   | YITGDNL             | VKGSY | GFEAEFNK | SQTSFHLK             | KPSALVSD | SALYFC      | AVRD                 |  |  |                        |  |  |
| AE000658, TRAV4   | LAKTTQ             | PISMSYEGQ   | EVNITCSHN      | NIATNDY              | ITWYQQF | PSQGRFIIQ   | GYKT                | KVTNE | VASLFI   | PADRKSST             | LSLPRVSL | SDTAVYYC    | LVGD                 |  |  |                        |  |  |
| AE000659, TRAV5   | GEDVEQS            | LFLSVREGD   | SSVINCTYT      | DSSSTY               | LYWYKQ  | EPGAGLQLLTY | IFSNMD              | MKQDQ | RLTVLLN  | KKDKHL               | SLRIADTQ | TGDSAIYFC   | AES                  |  |  |                        |  |  |
| AE000659, TRAV6   | SQKIEQNSE          | ALNIQEGKT   | TATLTCNYT      | NYSPAY               | LQWYRQ  | DPRGPVFLLL  | IRENEK              | EKRKE | RLKVTFD  | TTKISLF              | ILASQP   | ADSATYLC    | ALD                  |  |  |                        |  |  |
| AE000659, TRAV7   | ENQVEHSP           | HFLGPQQG    | DVASMSCTYS     | VSRFNN               | LQWYRQ  | NTGMGPKLLS  | MYSAGY              | EKQKG | RLNATLLK | NGSSLYI              | TAVQPED  | SATYFC      | AVD                  |  |  |                        |  |  |
| AE000659, TRAV8-1 | AQSVSQHN           | HVILSEAAS   | LELGCNYS       | YGGTVN               | LFWYVQY | PGQLQLLLK   | YFSGDPL             | VKGIK | GFEAEF   | IKSKFSF              | NLRKPSV  | QWSDTAEYFC  | AVN                  |  |  |                        |  |  |
| AE000659, TRAV8-2 | AQSVTQ             | DSHVS       | VSECTPVLLRCNYS | SSYSPS               | LFWYVQ  | HPNKGLQLLLK | YFSAATL             | VKGIN | GFEAEFK  | KSETSF               | HLLTKPSA | HMSDAAEYFC  | VVS                  |  |  |                        |  |  |
| AE000659, TRAV8-3 | AQSVTQ             | PDIHITV     | SEGASLELRCNYS  | YGATPY               | LFWYVQ  | SPGQLQLLLK  | YFSGDTL             | VQGIK | GFEAEFK  | RQSQSF               | NLRKPSV  | HWSDAEYFC   | AVG                  |  |  |                        |  |  |
| AE000659, TRAV8-4 | AQSVTQ             | LGSHVSV     | IGAVLLRCNYS    | SSVPPY               | LFWYVQY | PNQGLQLLLK  | YFSAATL             | VKGIN | GFEAEFK  | KSETSF               | HLLTKPSA | HMSDAAEYFC  | AVS                  |  |  |                        |  |  |
| X02850, TRAV8-6   | AQSVTQ             | LDQVQV      | FEEAPVELRCNYS  | SSVSVY               | LFWYVQY | PNQGLQLLLK  | YLSGSTL             | VEGIN | GFEAEFNK | SQTSFHL              | RKPSVHIS | SDTAEYFC    | AVS                  |  |  |                        |  |  |
| AE000660, TRAV8-7 | TQSVTQ             | LDGHITV     | SEEAPLELRCNYS  | YSGVPS               | LFWYVQY | SSQLQLLLK   | DLTEATQ             | VKGIR | GFEAEFK  | KSETSF               | YLRKPS   | THVSDAAEYFC | AVGDR                |  |  |                        |  |  |
| AE000659, TRAV9-1 | GDSWQTE            | GQWLPS      | EGDSLIVNCSYF   | TTQVPS               | LFWYVQY | PGGRLHLK    | AMKAMD              | KGRNK | GFEAMY   | RKETTSE              | HLEKDS   | WQSDSAVYFC  | ALS                  |  |  |                        |  |  |

# IMGT Collier de Perles



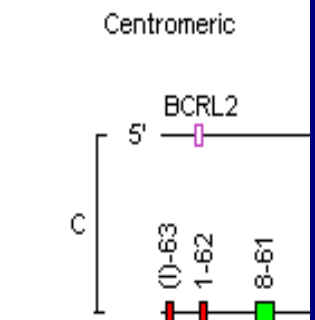
# IMGT databases and tools





Locus representation: Human IGL

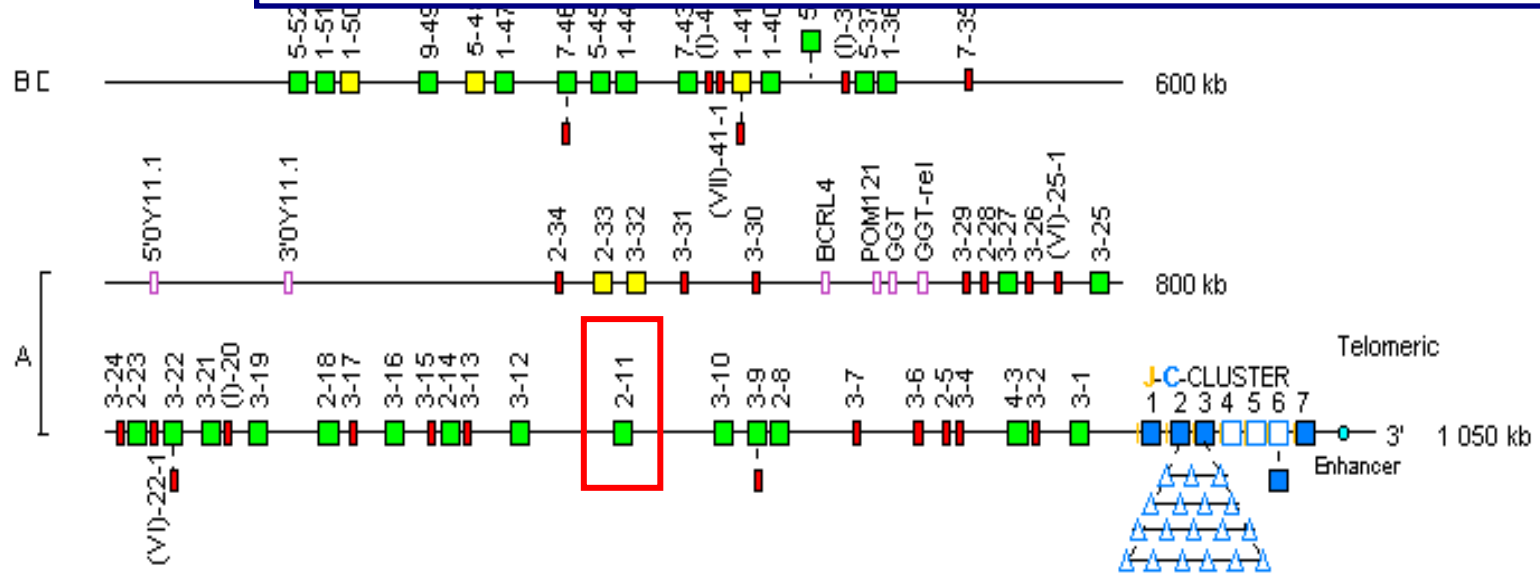
Human IGL 22q11.2



**WELCOME !**  
**to IMGT/GENE-DB**

THE  
 INTERNATIONAL  
 IMMUNOGENETICS  
 INFORMATION SYSTEM®

Information system®



*Giudicelli V. et al. Nucleic Acids Res. 33, D256-D261 (2005)*

[Help](#)
[IMGT Home page](#)
[IMGT Marie-Paule page](#)
[New search](#)

Created by Marie-Paule Lefranc (CNRS, Montpellier II University, France)  
<http://imgt.cines.fr>

**IMGT/LIGM-DB ON LINE, HERE YOU ARE !**

Five types of search are available : select one by clicking on the button

● accession number, mnemonic, definition, creation date, length, [annotation level](#)

```

FT V-GENE <1..297>
FT /p
FT /c
FT /c
FT /a
FT /m
FT /g
FT /o
FT V-REGION 1.
FT /a
FT /g
FT /t
FT PGI
FT YTI
FT FR1-IMGT 1.
FT /A
FT /t
FT 1st-CYS 64..102
FT CDR1-IMGT 76..102
FT /AA_IMGT="27 to 35"
FT /translation="SSDVGGYNY"
FT FR2-IMGT 103..153
FT /AA_IMGT="39 to 55"
FT /translation="VSWYQQHPGKAPKLMYI"
FT CONSERVED-TRP 109..111
FT CDR2-IMGT 154..162
FT /AA_IMGT="56 to 58"
FT /translation="DVS"
FT FR3-IMGT 163..270
FT /AA_IMGT="66 to 104, AA 73, 81, 82 missing"
FT /translation="KRPSGVPDFRFSGSKSGNTASLTISGLQAEDEADYYC"
FT 2nd-CYS 268..270
FT CDR3-IMGT 271..297
FT /AA_IMGT="105 to 113"
FT /translation="CSYAGSYTF"
XX
SQ Sequence 297 BP; 60 A; 93 C; 71 G; 73 T; 0 other;
cagtctgcc tgactcagcc tcgtccagtg tccgggtctc ctggacagtc agtcaccatc 60
tctacacta gaaccacaa taatattaat atttataact atatctctca ataccaacaa 120
  
```

Document : chargé



# IMGT/LIGM-DB

DESCRIPTION

| Key                | Location/Qualifiers  |
|--------------------|--|
| L-V-D-J-C-SEQUENCE | <1..375><br>/partial<br>/db_xref="taxon:9606"<br>/cell_type="B-cell hybridoma 2F7"<br>/IMGT_note="automatically annotated with IMGT tools"<br>/organism="Homo sapiens"   |
| V-D-J-REGION       | 1..375<br>/translation="QVHLVESGGAVFHPGRSLRLSRAASGFTFSSYGMHWVRQAP<br>AKGLEWVAVIWDGSKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC<br>AKHVITIAAAGRRGAGMDVWGQGTITVTVSS"  |
| V-REGION           | 1..296<br>/allele="IGHV3-33*01, putative"<br>/gene="IGHV3-33"<br>/CDR_length="[8.8.18]"<br>/putative_limit="3' side"<br>/translation="QVHLVESGGAVFHPGRSLRLSRAASGFTFSSYGMHWVRQAP<br>AKGLEWVAVIWDGSKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC<br>AK" |
| FR1-IMGT           | 1..75<br>/AA_IMGT="1 to 26, AA 10 is missing"<br>/translation="QVHLVESGGAVFHPGRSLRLSRAAS"  |
| CDR1-IMGT          | 76..99<br>/AA_IMGT="27 to 34"<br>/translation="GFTFSSYG"   |
| FR2-IMGT           | 100..150<br>/AA_IMGT="39 to 55"<br>/translation="MHWVRQAPAKGLEWVAV"  |
| CONSERVED-TRP      | 106..108   |
| CDR2-IMGT          | 151..174<br>/AA_IMGT="56 to 63"<br>/translation="IWDGSKN"  |
| FR3-IMGT           | 175..288<br>/AA_IMGT="66 to 104, AA 73 is missing"<br>/translation="YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC"   |

173.206 sequences from 343 species

IMGT-ONTOLOGY:

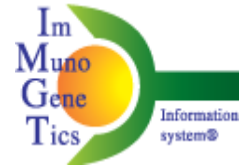
277 IMGT labels for sequences

285 IMGT labels for 3D structures

SO (Sequence ontology):

67 IMGT labels

# cDNA (in databases: mRNA!)



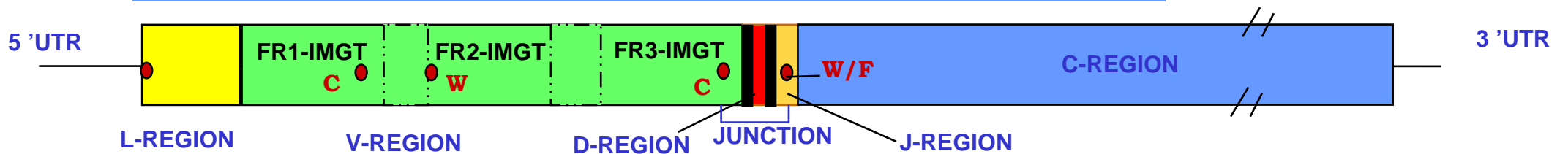
<http://www.imgt.org>

```
..... .gagga ttcacccatgg aactggggcct ccgctggggtt ttccttggtg cttttttaga 120
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gtccctgaga ctctcctgtg cagcctctgg attaagcttc agtacctatg ccatgaactg 240
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cctggtcacc gtctcctcag catccccgac cagccccaag gtcttcccgc tgagcctctg 540
cagcaccag ccagatggga acgtgggtcat cgctgcctg gtccagggct tcttcccca 600
ggagccactc agtgtgacct ggagcgaaag cggacagggc gtgaccgcca gaaacttccc 660
accagccag gatgcctccg gggacctgta caccacgagc agccagctga ccctgccggc 720
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cgaggacctg ctcttaggtt cagaagcgaa cctcacgtgc aactgaccg gcctgagaga 960
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ggtgggccac gaggccctgc cgctggcctt cacacagaag accatcgacc gcttggcggg 1500
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```

# cDNA

```

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aggtgtccag tgtgaggtgc aactgggtgga gtctggggga ggctgggtca agccgggggg 180
gtccctgaga ctctctgtg cagcctctgg attaagcttc agtacctatg cdatgaadtg 240
gggccgag gtcaccagga aggggctgga atgggtctca agtattagta gtagaagtga 300
ttacatatac tatagagact cagtgaaggg ccgattcacc atctccagag acaacgccaa 360
gaattcactg tatctgcaaa tgaatagcct gagagtcgac gacacggctg tctattactg 420
tgcgagagat tctttgtaatg gtgctatatg ttatggtttc agtccctggg gccagggaac 480
cctggtcacc gtctctcag catccccgac cagccccaaag gtcttcccgc tgagcctctg 540
cagcaccag ccagatggga acgtgggtcat cgctgcctg gtccagggtc tcttcccca 600
ggagccactc agtgtgacct ggagcgaaag cggacagggc gtgaccgcca gaaacttccc 660
accagccag gatgcctccg gggacctgta caccacgagc agccagctga ccctgccggc 720
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ccaggatgtg actgtgccct gccagttcc ctcaactcca cctaccccat ctccctcaac 840
tccacctacc ccatctccct catgctgcc accccgactg tcaactgacc gaccggccct 900
cgaggacctg ctcttaggtt cagaagcgaa cctcacgtgc aactgaccg gcctgagaga 960
tgcctcgggt gtcaccttca cctggacgcc ctcaagtggg aagagcgctg ttcaaggacc 1020
acctgagcgt gacctctgtg gctgctacag cgtgtccagt gtctgcccgg gctgtgccga 1080
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gctaaccgcc accctctcaa aatccgaaa cacattccgg cccgagggtc acctgctgcc 1200
gccgccgtcg gaggagctgg ccctgaacga gctgggtgacg ctgacgtgcc tggcacgtgg 1260
cttcagcccc aaggacgtgc tggttcgtg gctgcagggg tcacaggagc tgccccgcga 1320
gaagtacctg acttgggcat cccggcagga gccagccag ggcaccacca ccttcgctgt 1380
gaccagcata ctgcgcgtgg cagccgagga ctggaagaag ggggacacct tctcctgcat 1440
gggtggccac gaggccctgc cgtggcctt cacacagaag accatcgacc gcttggcggg 1500
taaaccacc catgtcaatg tgtctgttgt catggcggag gtggacggca cctgctactga 1560 ...
  
```



# The IMGT-ONTOLOGY concepts

I  
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IMGT/LIGM-DB Consultation module v3 - Netscape

Fichier Edition Afficher Aller Communicator Aide

ID HSCOMFRAA IMGT/LIGM annotation : automatic; RNA HUM; 375 BP.

XX

AC L39956;

XX

DT 28-SEP-2001 (Rel. 200139-5, arrived in LIGM-DB )

DT 13-NOV-2001 (Rel. 200146-2, Last updated, Version 2)

XX

DE Homo sapiens monospecific anti-ssDNA antibody heavy chain variable region

DE mRNA, complementarity determining regions 1-3 and framework regions 1-4.

DE ;

DE RNA; rearranged configuration; Ig-Heavy; regular; functionality

DE productive; group IGHV; subgroup HV3; specificity anti-DNA single-stranded

DE (ss) [human].

XX

KW antigen receptor; immunoglobulin superfamily; Ig; Ig-Heavy; variable;

KW diversity; joining; hybridoma; immunoglobulin.

XX

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates;

OC Catarrhini; Hominidae; Homo.

XX

RN [1]

RP 1-375

RX MEDLINE; 96195158.

RA Mitamura K., Suenaga R., Wilson K.B., Abdou N.I.;

RT "V gene sequences of human anti-ssDNA antibodies secreted by lupus-derived

RT CD5-negative B cell hybridomas";

RL Clin. Immunol. Immunopathol. 78(2):152-160(1996).

XX

DR EMBL; L39956.

XX

FH Key Location/Qualifiers

FH

FT L-V-D-J-C-SEQUENCE <1..375>

FT /partial

Document : chargé



# The IMGT-ONTOLOGY concepts

**D  
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```
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="QVHLVESGGAVFHPGRSLRLSRAASGFTESYCNHHTDQAP
FT AKGLEWVAVIWDGSKYYADSVKGRFTISRDNKNTLYL
FT AKHVTIAAAGRRGAGMDVWGQTTVTVSS"
FT V-REGION 1..296
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FT /gene="IGHV3-33"
FT /CDR_lengths="[8,8,18]"
FT /putative_limit="3' side"
FT /translation="QVHLVESGGAVFHPGRSLRLSRA
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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="IWDGSKN"
FT FR3-IMGT 175..288
FT /AA_IMGT="66 to 104, AA 73 is missing"
FT /translation="YYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYC"
Done
```

**OBTENTION**

**CLASSIFICATION**

**NUMEROTATION**



# IMGT/V-QUEST

# IMGT/V-QUEST

## 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                            |



# WELCOME ! to IMGT/V-QUEST

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

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


Current version: 3.1.2 (18 July 2008)

## Analyse your Immunoglobulin nucleotide sequences

 [Human](#)

 [Mouse](#)

 [Rat](#)


 [Chondrichthyes](#)

 [Teleostei](#)

- [Atlantic cod](#)
- [Channel catfish](#)
- [Rainbow trout](#)

 [Sheep](#)

## Analyse your T cell Receptor nucleotide sequences

 [Human](#)

 [Nonhuman primates](#)

## Analyse your Immunoglobulin sequences

### Your selection: Human

Your sequences are compared to the **Human IG set** from the [IMGTV-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
gctgggttttccttgttgctatTTTAAAAGGTgtccaatgtgaggtgcagctggtggagtctgggggaggcttggtagcagccagggcgg
tccttgagactctcctgtgcagcttctggattgaccttgggtgattactttatgagctggttccgccaggctccaggaagggactgga
gtgggtaggtttcattaagagcgaacttatggtgggacaacagaatacggcgcgtctgtgaaaggcagattcatcatctcgagagatg
attccaaaagcatcgctatTTTGCAAATgaacagcctggaaccgaggacacagccatatattactgtagtcgggggggtagtgcttat
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accctcctccaagagcacctctgggggcacagcggccctgggctgcttggcaaggactacttcccc
>AY393055
gctgggttttccttgttgctatTTTCAAAGGTgtccagtgtgaggtgcagctggtggagactggaggaggcttgatccagcctgggggg
tccttgagactctcctgtgcagcctctgggttcaccgtcagtagcaactacatgagctgggtccgccaggctccaggaaggggctgga
```

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

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

Selection of results displays for 'Detailed view'

## Selection of parameters for the results

Display type : HTML

Nb of nucleotides per line in alignment: 60

### A. Detailed view

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

### B. Synthesis view

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

### Advanced parameters

Selection of IMGT reference directory set: F+ORF+ in frame P

With all alleles  With allele \*01 only

Selection of parameters for IMGT/JunctionAnalysis

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

Number of accepted mutations: default  in 3'-V-REGION

default  in D-REGION

default  in 5'-J-REGION

More options 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):

## Selection of parameters for the results

Display type : HTML

Nb of nucleotides per line in alignment: 60

### A. Detailed view

- |  |   |
|--|---|
| 1. <input checked="" type="checkbox"/> Alignment for V-GENE  | 5. <input type="checkbox"/> Sequence of the JUNCTION ('nt' and 'AA')                      |
| 2. <input checked="" type="checkbox"/> Alignment for D-GENE  | 6. <input checked="" type="checkbox"/> V-REGION alignment according to the IMGT numbering |
| 3. <input checked="" type="checkbox"/> Alignment for J-GENE  | 7. <input checked="" type="checkbox"/> V-REGION translation                               |
| 4. <input checked="" type="checkbox"/> Results of IMGT/JunctionAnalysis  | 8. <input type="checkbox"/> V-REGION mutation table                                       |
| <input type="radio"/> with full list of eligible D-GENES   | 9. <input type="checkbox"/> V-REGION mutation statistics                                  |
| <input checked="" type="radio"/> without list of eligible D-GENES  | 10. <input type="checkbox"/> V-REGION mutation hot spots                                  |
| 12. <input type="checkbox"/> Sequences of V-, V-J- or V-D-J- REGION ('nt' and 'AA') with gaps in FASTA<br>Access to IMGT/PhyloGene for V-REGION ('nt') | 13. <input type="checkbox"/> Annotations by IMGT/Automat                                  |

Selection of results displays for 'Synthesis view'

### B. Synthesis view

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

### Advanced parameters

Selection of IMGT reference directory set: F+ORF+ in frame P  With all alleles  With allele \*01 only

Selection of parameters for IMGT/JunctionAnalysis: Nb of D-GENES in IGH JUNCTIONs (default is 1) default in 3'-REGION; Number of accepted mutations: default in D-REGION; default in 5'-REGION

More options 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)



## Selection of parameters for the results

Display type : HTML [dropdown]

Nb of nucleotides per line in alignment: 60 [dropdown]

### A. Detailed view

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

Advanced parameters

### B. Synthesis view

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

### Advanced parameters

Selection of IMGT reference directory set: F+ORF+ in frame P [dropdown]  With all alleles  With allele \*01 only

Selection of parameters for IMGT/JunctionAnalysis: Nb of D-GENES in IGH JUNCTIONs (default is 1) [dropdown] Number of accepted mutations: [dropdown] in 3V-REGION, [dropdown] in D-REGION, [dropdown] in 5J-REGION

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

# A. 'Detailed view': Result summary

## Sequence number 1: AF184762

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

>AF184762

```
atggagtttgggctgagctggggttttcttggctattttaaagggtgccactgtgag
gtgcagctggaggagctctggggaggcttagtccagcctgggggatccctgaaactctc
tgtgcagcctctgggttcaccctcagtggtcctcaaatgtgcactgggtccgccaggcctc
gggaaagggctggagtggttggccgatcaaaaggaatgctgagctctgacgcgacagca
tatgctgctgatgagaggcaggctcaccatctccagagatgattcaaagaacacggcg
tttctgcaaatgaacagcctgaaaagcgatgacacggccatgtattattgtgtgatccg
ggagatgtttacaaccgacagtggggcccagggaaaccctggtcaccgtctcctcagcatcc
ccgaccagccccaaggtcttcccgtgagcctctgcagcaccagccagat
```

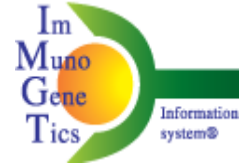
Automatic evaluation

| 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 IMG T/JunctionAnalysis                | <a href="#">IGHD3-10*01</a>  | D-REGION is in reading frame 3 |                                       |
| [CDR1-IMG T.CDR2-IMG T.CDR3-IMG T] 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



<http://www.imgt.org>

## 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            |
|--------------------------------------|-------|---------------------|
| <a href="#">Z27508</a> IGHV3-73*01   | 1240  | 91,50% (269/294 nt) |
| <a href="#">AB019437</a> IGHV3-73*02 | 1231  | 91,16% (268/294 nt) |
| <a href="#">X92206</a> IGHV3-72*01   | 1024  | 83,33% (245/294 nt) |
| <a href="#">X92216</a> IGHV3-15*01   | 979   | 81,63% (240/294 nt) |
| <a href="#">M99406</a> IGHV3-15*07   | 979   | 81,63% (240/294 nt) |

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

```

AF184762          <----- FRL-IMGT ----->
Z27508 IGHV3-73*01  gaggtgcagctggtggagtctggggga...ggcttagtccagcctgggggatccctgaaa
AB019437 IGHV3-73*02  .....-g-----g-----g-----
X92206 IGHV3-72*01  .....-g-----a-g-----g-----
X92216 IGHV3-15*01  .....-g--aa-----g---t-g-----
M99406 IGHV3-15*07  .....-g--aa-----g---t-g-----
    
```

Score and nucleotide identity

```

AF184762          <----->
Z27508 IGHV3-73*01  .....gtgcac.....a-----
AB019437 IGHV3-73*02  .....t-----tgc-----a-----
X92206 IGHV3-72*01  .....a-----t-----a-cact-c-----a-g--
X92216 IGHV3-15*01  .....a-----tt-----aa-g-ctgg-----a-ag-
M99406 IGHV3-15*07  .....t-----tt-----aa-g-ctgg-----a-a-
    
```

## D-GENE

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

Closest D-REGIONS

|                                    | Score | Identity         |
|------------------------------------|-------|------------------|
| <a href="#">X13972</a> IGHD3-10*01 | 28    | 72,73% (8/11 nt) |
| <a href="#">X93615</a> IGHD3-10*02 | 19    | 63,64% (7/11 nt) |
| <a href="#">J00256</a> IGHD7-27*01 | 14    | 60,00% (6/10 nt) |
| <a href="#">X97051</a> IGHD3-16*02 | 13    | 62,50% (5/8 nt)  |
| <a href="#">X93614</a> IGHD3-16*01 | 10    | 54,55% (6/11 nt) |

Alignment

```

AF184762          gtgatccgggg
X13972 IGHD3-10*01  a--g-t-----agttattataac
X93615 IGHD3-10*02  a--t--g---agttattataac
J00256 IGHD7-27*01  .ct-a-t-----a
X97051 IGHD3-16*02  --t--a-c
X93614 IGHD3-16*01  ac-t-tg---agttatgctt-----
    
```

### 3. Alignment for J-GENE and allele identification

Closest J-REGIONS

|                                 | Score | Identity          |
|---------------------------------|-------|-------------------|
| <a href="#">J00256</a> IGHJ1*01 | 179   | 82,69% (43/52 nt) |
| <a href="#">X86355</a> IGHJ4*02 | 150   | 79,17% (38/48 nt) |
| <a href="#">J00256</a> IGHJ4*01 | 141   | 77,08% (37/48 nt) |
| <a href="#">X86355</a> IGHJ5*02 | 138   | 74,51% (38/51 nt) |
| <a href="#">M25625</a> 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

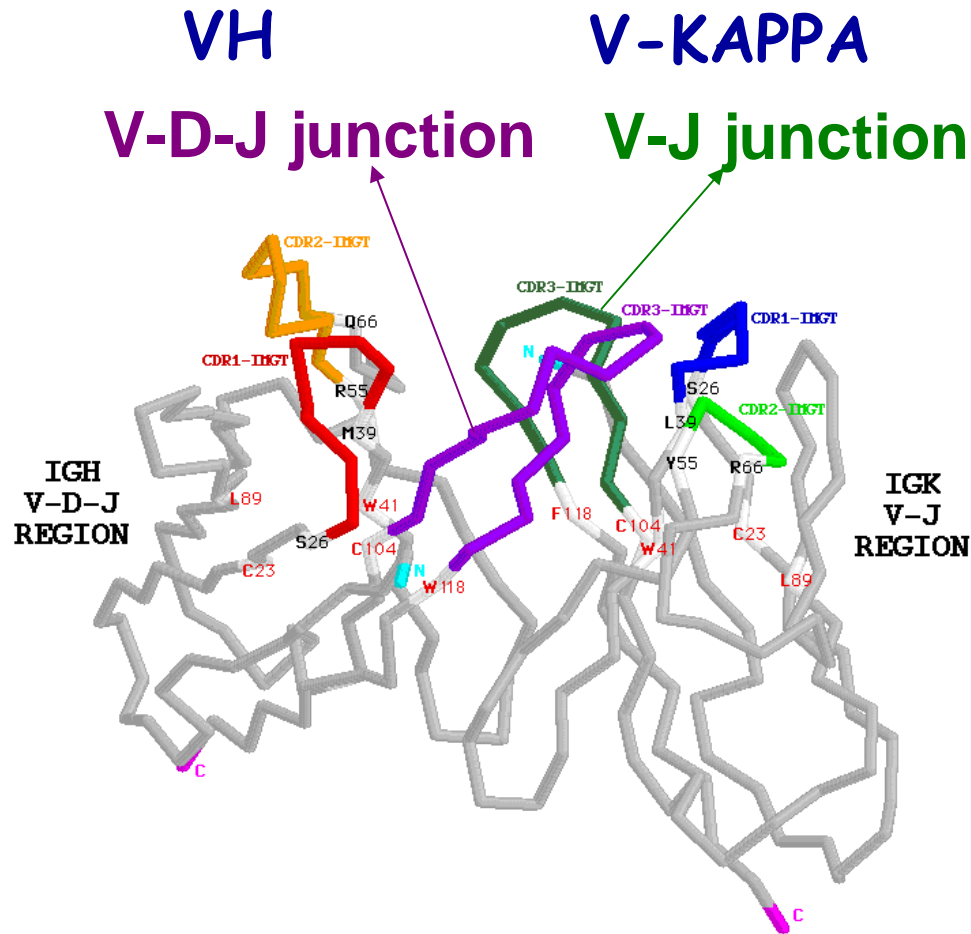
Alignment

```

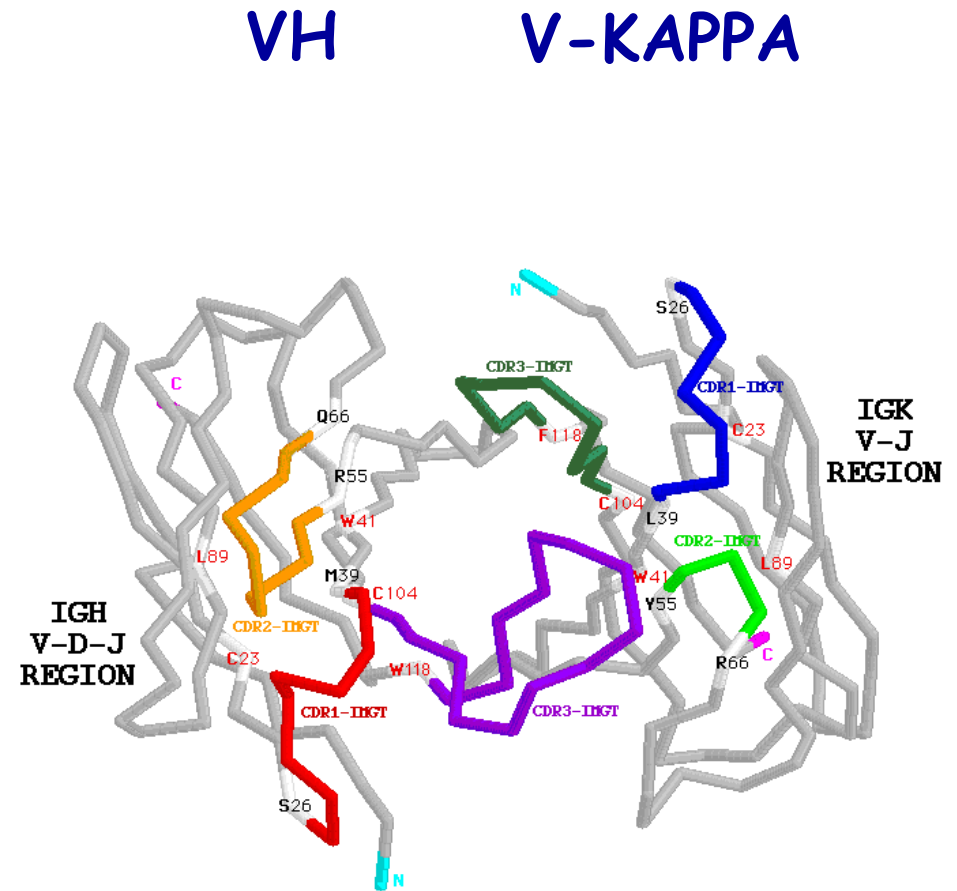
AF184762          gtgatccggggagatggtttacaaccgacagtggggccagggaacctggcaccgtctcc
J00256 IGHJ1*01  .....c--aa---tt--ag--c-----c-----
X86355 IGHJ4*02  .....ac---tttgact-c-----
J00256 IGHJ4*01  .....ac---tttgact-c-----a-----
X86355 IGHJ5*02  .....-caac-ggtt-gac-cc-----
M25625 IGHJ4*03  .....gc---tttgact-c-----a--g-----
    
```

## J-GENE

# Junctions of the V-DOMAINS



**Side view**



**View from above**

*Mouse (Mus musculus) E5.2Fv*

CDR3-IMGT= Complementarity determining region (105-117)

V-J junction (104-118)

V-D-J junction (104-118)

# Generation of the JUNCTION diversity

3'V-REGION

N-REGION

D-REGION

N-REGION

5'J-REGION

tgtgcgaaa ga



tacc

agcatattgig

gtggtgactgctat

tcc



gatt



acaactgggtcg

actcctgg

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

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

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IMMUNOGENETICS  
INFORMATION SYSTEM®



## 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 | ....tcgaatttttggagtggtt..... | 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   | F     | F     | L     | F     | W     | F     | H   | G   | V   | W   | F   | D   | P   | W     | +                | 20 |

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

*Yousfi Monod et al. Bioinformatics, 20, 1379-1385 (2004)*

Citing IMGJ/JunctionAnalysis: Yousfi Monod, M. et al. Bioinformatics 2004, 20 Supplement 1:1379-1385 PMID: 15262823

## IMGJ/JunctionAnalysis Search page

### Species :

Homo sapiens ▾

### Locus :

- IGH
- IGK
- IGL
- TRA
- TRB
- TRG
- TRD

### Sequences

- Type (or copy/paste) required information and nucleotide sequences into the box below :

```
>M62724, IGHV7-4-1*02, IGHJ4*02  
TGT GCG AGA GAA GAT AGC AAT GGC TAC AAA ATA TTT GAC TAC TGG  
>Z47269, IGHV1-69*06, IGHJ5*02  
TGT GCG AGA GGG GGG GCT AAG GTC GAA TTT TTG GAG TGG TTT CAT GGG TAC TGG  
TTC GAC CCC TGG
```

- Or give the path access to a local file containing your sequences :


IMGJ/JunctionAnalysis - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

http://imgt.cines.fr/cgi-bin/IMGJjcta.jv

**THANK YOU**  
for using **IMGJ/JunctionAnalysis**

THE  
INTERNATIONAL  
IMMUNOGENETICS  
INFORMATION SYSTEM®



**Analysis of the JUNCTIONS**

| Input | V name | V-REGION     | N1          | D-REGION      | N2                         | J-REGION | J name                       |
|-------|--------|--------------|-------------|---------------|----------------------------|----------|------------------------------|
| #1    | M62724 | IGHV7-4-1*02 | tgtgcgagaga | aga           | .tagcaatggctacaa....       | aata     | .....tttgactactgg IGHJ4*02   |
| #2    | Z47269 | IGHV1-69*06  | tgtgcgaga   | gggggggctaagg | ....tcgaatttttgagtggt..... | tcatgggt | ...actggttcgaccctgg IGHJ5*02 |

| Input | D name | Vmut        | Dmut | Jmut | Ngc |       |
|-------|--------|-------------|------|------|-----|-------|
| #1    | M62724 | IGHD5-24*01 | 0    | 2    | 0   | 1/7   |
| #2    | Z47269 | IGHD3-3*02  | 0    | 2    | 0   | 14/21 |

**Translation of the JUNCTIONS**

|    | 105    | 107 | 109 | 111 | 111.2 | 112.4 | 112.2 | 112   | 114 | 116 | 118 | CDR3-IMGT |        |     |     |     |     |     |     |     |     |     |     |   |    |
|----|--------|-----|-----|-----|-------|-------|-------|-------|-----|-----|-----|-----------|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|----|
|    | 104    | 106 | 108 | 110 | 111.1 | 111.3 | 112.3 | 112.1 | 113 | 115 | 117 | frame     | length |     |     |     |     |     |     |     |     |     |     |   |    |
|    | C      | A   | R   | E   | D     | S     | N     | G     |     | Y   | K   | I         | F      | D   | Y   | W   |     |     |     |     |     |     |     |   |    |
| #1 | M62724 | tgt | gcg | aga | gaa   | gat   | agc   | aat   | ggc |     | tac | aaa       | ata    | ttt | gac | tac | tgg | +   | 13  |     |     |     |     |   |    |
|    | C      | A   | R   | G   | G     | A     | K     | V     | E   | F   | L   | E         | W      | F   | H   | G   | Y   | W   | F   | D   | P   | W   |     |   |    |
| #2 | Z47269 | tgt | gcg | aga | ggg   | ggg   | gct   | aag   | gtc | gaa | ttt | ttg       | gag    | tgg | ttt | cat | ggg | tac | tgg | ttc | gac | ccc | tgg | + | 20 |

*Yousfi Monod et al. Bioinformatics, 20, 1379-1385 (2004)*



# 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) nucleotide to see the original one:

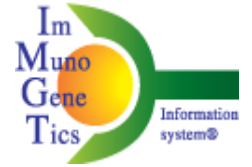
| Input | V name | V-REGION                      | P | N1                   | D-REGION                      | N2          | P  | J-REGION               | J name                   | D name                      | Vmut | Dmut | Jmut | Ngc   |
|-------|--------|-------------------------------|---|----------------------|-------------------------------|-------------|----|------------------------|--------------------------|-----------------------------|------|------|------|-------|
| #1    | Z70256 | <a href="#">IGHV2-26*01</a>   |   | tgttgt               | .....gcagcgcctggtac           | ccaaatatac  |    | ...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               | .....cagctcttatgcc            | cgccc       |    | ctactggactctcgatctctgg | <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..... | ccccggggga  |    | ..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..... | cccgga      | ca | tgatgcttttgatctctgg    | <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                   | .....tggttaactataa.           | tgccggcggtg |    | ...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.....       | ccctc       |    | .....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                | gtaaagaggg.....               | tttcggaa    |    | .tactggactctcgatctctgg | <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         |    | .gatgcttttgatctctgg    | <a href="#">IGHJ3*02</a> | <a href="#">IGHD3-16*01</a> | 1    | 4    | 0    | 5/5   |
| #12   | Z70621 | <a href="#">IGHV4-39*01</a>   |   | ccacgatttatgg        | .....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 | tgccccgctctgccccaaat | gtattactatggttcgggga.....     | tatgtacg    |    | .....ttgactactgg       | <a href="#">IGHJ4*03</a> | <a href="#">IGHD3-10*01</a> | 0    | 0    | 0    | 15/28 |

# The eleven IMG-T amino acid classes according to the physico-chemical properties

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



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



<http://www.imgt.org>

## 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 | <a href="#">IGHV3-73*01</a> | tgt.....   | g  | ..... <u>tgat</u> <u>cggggagat</u> ggtt..... | tacaaccga | .....cagtg | <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   | <u>D</u> | <u>V</u> | Y   | N   | R   | Q   | W   |       |                  |                |          |      |
| AF184762 | tgt | gtg | <u>atc</u> | cg  | gga | gat      | g        | tt  | tac | aac | cga | cag | tgg   | +                | 10             | 1,508.72 | 9.24 |

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

## 5. 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
```

## JUNCTION alignments

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

|            | 104 | 105      | 106 | 107 | 108 | 109      | 110      | 111      | 111.1 | 111.2 | 111.3 | 111.4 | 112.5 | 112.4 | 112.3 | 112.2 | 112.1 | 112 | 113      | 114 | 115 | 116 | 117 | 118      | Frame | CDR3-IMGT Length | Molecular mass |          |          |          |
|------------|-----|----------|-----|-----|-----|----------|----------|----------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-----|----------|-----|-----|-----|-----|----------|-------|------------------|----------------|----------|----------|----------|
| #1 Z70256  | C   | <u>V</u> | R   | V   | V   | Q        | <u>R</u> | L        | V     |       |       |       |       |       |       |       |       | P   | K        | Y   | H   | F   | D   | <u>H</u> | W     | +                | 15             | 2,438.76 |          |          |
|            | tgt | gta      | cgt | gtt | gtg | cag      | cgc      | ctg      | gta   | ...   | ...   | ...   | ...   | ...   | ...   | ...   | ccc   | aaa | tat      | cac | ttt | gac | cac | tgg      |       |                  |                |          |          |          |
| #2 Z70257  | C   | A        | R   | D   | G   | S        | <u>S</u> | Y        | A     |       |       |       |       |       |       | R     | P     | Y   | W        | Y   | F   | D   | L   | W        | +     | 16               | 2,256.49       |          |          |          |
|            | tgt | gcg      | agg | gat | ggc | agc      | tct      | tat      | gcc   | ...   | ...   | ...   | ...   | ...   | ...   | cgc   | ccc   | tac | tgg      | tac | ttc | gat | ctc | tgg      |       |                  |                |          |          |          |
| #3 Z70606  | C   | A        | R   | A   | T   | T        | H        |          |       |       |       |       |       |       |       |       |       |     | Y        | A   | F   | D   | V   | W        | +     | 11               | 1,604.77       |          |          |          |
|            | tgt | gcg      | aga | gcg | act | acg      | cac      | ...      | ...   | ...   | ...   | ...   | ...   | ...   | ...   | ...   | ...   | ... | tat      | gct | ttt | gat | gtc | tgg      |       |                  |                |          |          |          |
| #4 Z70608  | C   | A        | R   | V   | T   | I        | F        | G        | V     | V     |       |       |       |       |       | I     | P     | R   | G        | N   | A   | F   | D   | I        | W     | +                | 18             | 2,426.78 |          |          |
|            | tgt | gcc      | aga | gta | acg | att      | ttt      | gga      | gtg   | gtt   | ...   | ...   | ...   | ...   | att   | ccc   | cgg   | ggg | aat      | gct | ttt | gat | atc | tgg      |       |                  |                |          |          |          |
| #5 Z70610  | C   | A        | R   | V   | G   | S        | D        | F        | W     | S     | G     |       |       |       |       | Y     | S     | R   | H        | D   | A   | F   | D   | I        | W     | +                | 19             | 2,539.73 |          |          |
|            | tgt | gcg      | aga | gtc | ggg | agc      | gat      | ttt      | tgg   | agt   | ggt   | ...   | ...   | ...   | tat   | tcc   | cga   | cat | gat      | gct | ttt | gat | atc | tgg      |       |                  |                |          |          |          |
| #6 Z70611  | C   | A        | R   | H   | G   | <u>N</u> | Y        | N        | A     |       |       |       |       |       |       |       |       | G   | V        | D   | W   | F   | D   | P        | W     | +                | 15             | 2,072.21 |          |          |
|            | tgt | gcg      | aga | cat | ggt | aac      | tat      | aat      | gcc   | ...   | ...   | ...   | ...   | ...   | ...   | ...   | ...   | ggc | gtt      | gac | tgg | ttc | gac | ccc      | tgg   |                  |                |          |          |          |
| #7 Z70613  | C   | A        | R   | A   | A   | A        | G        |          |       |       |       |       |       |       |       |       |       |     | T        | S   | L   | F   | D   | Y        | W     | +                | 12             | 1,531.71 |          |          |
|            | tgt | gcg      | aga | gca | gca | gct      | ggt      | ...      | ...   | ...   | ...   | ...   | ...   | ...   | ...   | ...   | ...   | acc | tcc      | ctc | ttt | gac | tac | tgg      |       |                  |                |          |          |          |
| #8 Z70614  | C   | A        | R   | H   | Y   | N        | <u>S</u> | G        |       |       |       |       |       |       |       |       |       |     | <u>I</u> | Y   | P   | L   | D   | Y        | W     | +                | 13             | 1,846.01 |          |          |
|            | tgt | gcg      | aga | cac | tat | aat      | tcg      | ggg      | ...   | ...   | ...   | ...   | ...   | ...   | ...   | ...   | ...   | act | tat      | ccc | ctc | gac | tac | tgg      |       |                  |                |          |          |          |
| #9 Z70615  | C   | A        | R   | G   | L   | V        | <u>K</u> | <u>R</u> | V     |       |       |       |       |       |       |       |       | S   | E        | Y   | W   | Y   | F   | D        | L     | W                | +              | 16       | 2,419.75 |          |
|            | tgt | gcg      | aga | ggg | ctg | gta      | aag      | agg      | gtt   | ...   | ...   | ...   | ...   | ...   | ...   | tcg   | gaa   | tac | tgg      | tac | ttc | gat | ctc | tgg      |       |                  |                |          |          |          |
| #10 Z70616 | C   | A        | R   | A   | G   | L        | G        |          |       |       |       |       |       |       |       |       |       |     | S        | H   | W   | F   | D   | P        | W     | +                | 12             | 1,602.8  |          |          |
|            | tgt | gcg      | aga | gcg | ggt | ttg      | ggt      | ...      | ...   | ...   | ...   | ...   | ...   | ...   | ...   | ...   | ...   | tcc | cac      | tgg | ttc | gac | ccc | tgg      |       |                  |                |          |          |          |
| #11 Z70620 | C   | A        | R   | D   | R   | G        | <u>G</u> | M        |       |       |       |       |       |       |       |       |       |     | <u>V</u> | R   | D   | A   | F   | D        | I     | W                | +              | 14       | 1,932.17 |          |
|            | tgt | gcg      | aga | gac | cgg | ggc      | ggg      | atg      | ...   | ...   | ...   | ...   | ...   | ...   | ...   | ...   | ...   | gtt | cgg      | gat | gct | ttt | gat | atc      | tgg   |                  |                |          |          |          |
| #12 Z70621 | C   | A        | R   | H   | H   | D        | L        | W        | F     |       |       |       |       |       |       |       |       |     | G        | E   | F   | D   | P   | L        | D     | Y                | W              | +        | 16       | 2,307.53 |
|            | tgt | gcg      | aga | cac | cac | gat      | tta      | tgg      | ttc   | ...   | ...   | ...   | ...   | ...   | ...   | ggg   | gag   | ttt | gac      | ccc | ctt | gac | tac | tgg      |       |                  |                |          |          |          |
|            | C   | A        | R   | D   | C   | P        | A        | P        | A     | K     | M     | Y     | Y     | Y     | G     | S     | G     | I   | C        | T   | F   | D   | Y   | W        |       |                  |                |          |          |          |

## 6. 'Detailed view': V-REGION alignment

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

```
<----- FR1 - IMGT
1           5           10           15
AF184762    gag gtg cag ctg gtg gag tct ggg gga ... ggc tta gtc cag cct
Z27508 IGHV3-73*01  --- --- --- --- --- --- --- --- ---g --- --- ---
AB019437 IGHV3-73*02  --- --- --- --- ---c --- --- --- ---g --- --- ---
X92206 IGHV3-72*01  --- --- --- --- --- --- --- --- ---g --- --- ---
X92216 IGHV3-15*01  --- --- --- --- --- --- --- --- ---g --a a-- ---
M99406 IGHV3-15*07  --- --- --- --- --- --- --- --- ---g --a a-- ---

----->
                20           25           30
AF184762    ggg gga tcc ctg aaa ctc tcc tgt gca gcc tct ggg ttc acc ctc
Z27508 IGHV3-73*01  --- --g --- --- --- --- --- --- --- --- --- ---t--
AB019437 IGHV3-73*02  --- --g --- --- --- --- --- --- --- --- --- ---t--
X92206 IGHV3-72*01  --a --g --- --- -g- --- --- --- --- --a --- ---t--
X92216 IGHV3-15*01  --- --g --- --t -g- --- --- --- --- --a --- --t t--
M99406 IGHV3-15*07  --- --g --- --t -g- --- --- --- --- --t --- --t t--
```

## 7. 'Detailed view': V-REGION translation

### 7. V-REGION translation

```
<----- FR1 - IMGT
1           5           10           15
AF184762    E V Q L V E S G G G L V Q P
gag gtg cag ctg gtg gag tct ggg gga ... ggc tta gtc cag cct

Z27508 IGHV3-73*01  --- --- --- --- --- --- --- --- ---g --- --- ---

----->
                20           25           30
AF184762    G G S L K L S C A A S G F T L
ggg gga tcc ctg aaa ctc tcc tgt gca gcc tct ggg ttc acc ctc
F
Z27508 IGHV3-73*01  --- --g --- --- --- --- --- --- --- --- ---t--
```

## 8-10. 'Detailed view': mutation analysis

### 8. 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 (- - -) |                        |                        |

# 8-10. 'Detailed view': mutation analysis

## 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> | <b>312 (318)</b>  | <b>78</b>      | <b>36</b> | <b>51</b> | <b>30</b> | <b>117</b> | <b>0 (6)</b> |
| <b>Mutations</b>                   | <b>Total</b>      | <b>25 (30)</b> | <b>2</b>  | <b>4</b>  | <b>2</b>  | <b>9</b>   | <b>0 (5)</b> |
|                                    | <b>Silent</b>     | <b>8</b>       | <b>2</b>  | <b>1</b>  | <b>1</b>  | <b>3</b>   | <b>0</b>     |
|                                    | <b>Non silent</b> | <b>17 (22)</b> | <b>0</b>  | <b>3</b>  | <b>1</b>  | <b>6</b>   | <b>0 (5)</b> |
| <b>Transitions</b>                 | <b>a&gt;g</b>     | <b>3 (4)</b>   | <b>0</b>  | <b>0</b>  | <b>1</b>  | <b>1</b>   | <b>0 (1)</b> |
|                                    | <b>g&gt;a</b>     | <b>6</b>       | <b>2</b>  | <b>1</b>  |           |            |              |
|                                    | <b>c&gt;t</b>     | <b>1 (2)</b>   | <b>0</b>  | <b>0</b>  |           |            |              |
|                                    | <b>t&gt;c</b>     | <b>4</b>       | <b>0</b>  | <b>1</b>  |           |            |              |
| <b>Transversions</b>               | <b>a&gt;c</b>     | <b>0 (1)</b>   | <b>0</b>  | <b>0</b>  |           |            |              |
|                                    | <b>c&gt;a</b>     | <b>1</b>       | <b>0</b>  | <b>1</b>  |           |            |              |
|                                    | <b>a&gt;t</b>     | <b>3</b>       | <b>0</b>  | <b>0</b>  |           |            |              |
|                                    | <b>t&gt;a</b>     | <b>1</b>       | <b>0</b>  | <b>1</b>  |           |            |              |
|                                    | <b>g&gt;c</b>     | <b>1</b>       | <b>0</b>  | <b>0</b>  |           |            |              |
|                                    | <b>c&gt;g</b>     | <b>3</b>       | <b>0</b>  | <b>0</b>  |           |            |              |
|                                    | <b>g&gt;t</b>     | <b>1 (2)</b>   | <b>0</b>  | <b>0</b>  |           |            |              |
|                                    | <b>t&gt;g</b>     | <b>1 (2)</b>   | <b>0</b>  | <b>0</b>  |           |            |              |

### Amino acids

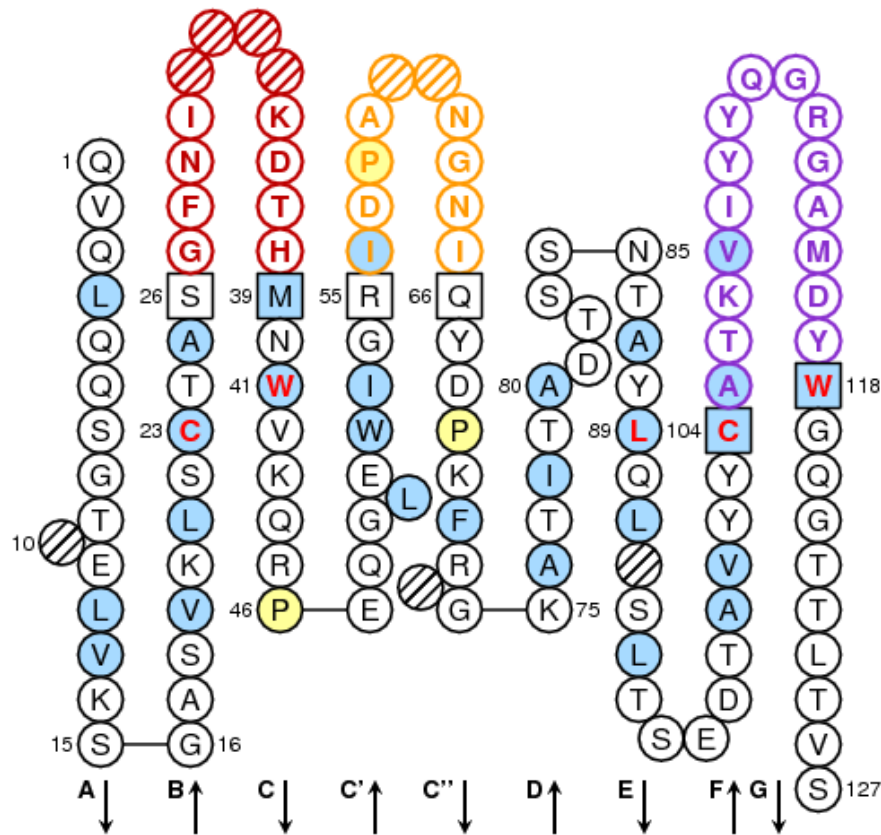
| IMGT labels                             | V-REGION  | FR1-IMGT       | CDR1-IMGT    | FR2-IMGT  | CDR2-IMGT | FR3-IMGT  | CDR3-IMGT    |              |
|---|---|----------------|--------------|-----------|-----------|-----------|--------------|--------------|
| <b>Total amino acids (AA) with gaps</b>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

# 8-10. 'Detailed view': mutation analysis

## 10. Mutation hot spots (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          |
| 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) | ggct                            | 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)     | ggct                            | 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)      | ggct                            | 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)     |                                 |                |                                 |                |                     |                    |

# 11. IMGT Collier de Perles



## IMGT unique numbering rules

- maintain conserved AA, and therefore codons, at the same positions
- standardize the delimitations of FR-IMGT and CDR-IMGT

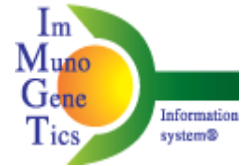
CDR-IMGT lengths are in themselves a crucial information.

[8.8.15]

**Standardized description of the V-DOMAIN, whatever the antigen receptor, the chain type and the species.**



# 13. 'Detailed view': Annotation by IMG/Automat



<http://www.imgt.org>

## 13. Annotations by IMG/Automat

| Label                         | Location/Qualifiers  |
|-------------------------------|--|
| <a href="#">V-D-J-REGION</a>  | 58..415<br>/Nucleotide sequence<br>gaggtgcagctggtggagtctggggaggccttagtccagcctgggggatccctgaaactc<br>tcctgtgcagcctctgggttcaccctcagtggtcaaatgtgcaactgggcccaggcc<br>tccgggaaaggctggagtgggtggccgtatcaaaaggaatgctgagctgacgcgaca<br>gcatatgctgcgtcgatgagaggcaggctcaccatctccagagatgattcaaagaacacg<br>gcgtttctgcaaatgaacagcctgaaaagcgtgacacggccatgtattattgtgatc<br>cggggagatgtttacaaccgacagtggggccagggaaacctggtcaccgtctcctcag<br>/Translation<br>EVQLVESGGGLVQPGGSLKLSCAASGFTLSGSNVHWVRQASGKGLEWVGRIKRNAESDAT<br>AYAASMRGRLTISRDDSKNTAFLQMNSLKSDDTAMYYCVIRGDVYNRQWQGTLVTVSS |
| <a href="#">V-REGION</a>      | 58..351<br>/allele="IGHV3-73*01"<br>/CDR_length="[8.10.10]"<br>/gene="IGHV3-73"<br>/Nucleotide sequence<br>gaggtgcagctggtggagtctggggaggccttagtccagcctgggggatccctgaaactc<br>tcctgtgcagcctctgggttcaccctcagtggtcaaatgtgcaactgggcccaggcc<br>tccgggaaaggctggagtgggtggccgtatcaaaaggaatgctgagctgacgcgaca<br>gcatatgctgcgtcgatgagaggcaggctcaccatctccagagatgattcaaagaacacg<br>gcgtttctgcaaatgaacagcctgaaaagcgtgacacggccatgtattattgtgatc<br>/Translation<br>EVQLVESGGGLVQPGGSLKLSCAASGFTLSGSNVHWVRQASGKGLEWVGRIKRNAESDAT<br>AYAASMRGRLTISRDDSKNTAFLQMNSLKSDDTAMYYC           |
| <a href="#">FR1-IMG</a>       | 58..132<br>/AA IMG="AA 1 to 26, AA 10 is missing"<br>/Nucleotide sequence<br>gaggtgcagctggtggagtctggggaggccttagtccagcctgggggatccctgaaactc<br>tcctgtgcagcctct<br>/Translation<br>EVQLVESGGGLVQPGGSLKLSCAAS  |
| <a href="#">1st-CYS</a>       | 121..123<br>/Nucleotide sequence<br>tgt<br>/Translation<br>C   |
| <a href="#">CDR1-IMG</a>      | 133..156<br>/AA IMG="AA 27 to 34"<br>/Nucleotide sequence<br>gggttcaccctcagtggtcaaat<br>/Translation<br>GFTLSGSN   |
| <a href="#">FR2-IMG</a>       | 157..207<br>/AA IMG="AA 39 to 55"<br>/Nucleotide sequence<br>gtgcaactgggtccgccaaggcctccgggaaaggctggagtgggtggccgt<br>/Translation<br>VHWVRQASGKLEWVGR   |
| <a href="#">CONSERVED-TRP</a> | 163..165<br>/Nucleotide sequence<br>tgg<br>/Translation<br>W   |

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





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