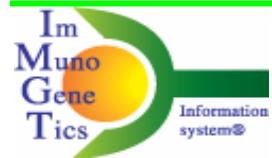


Analysis of the sequences, genes and 3D structures of the immunoglobulins, T cell receptors and MHC using the IMGT databases, tools and Web resources

<http://imgt.cines.fr>

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

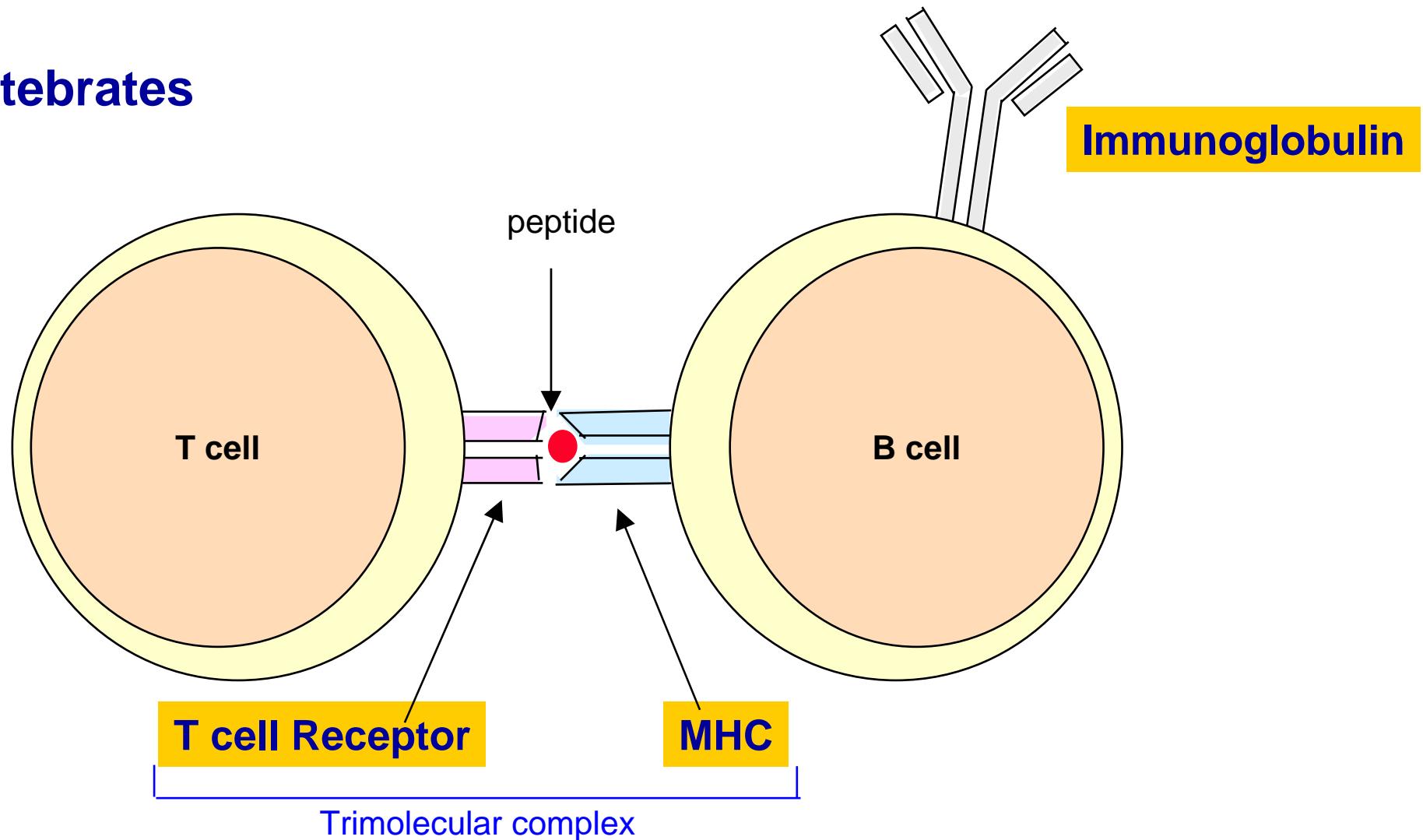


The international ImMunoGeneTics information system®
Coordinator: M.-P. Lefranc, Montpellier, France <http://imgt.cines.fr>

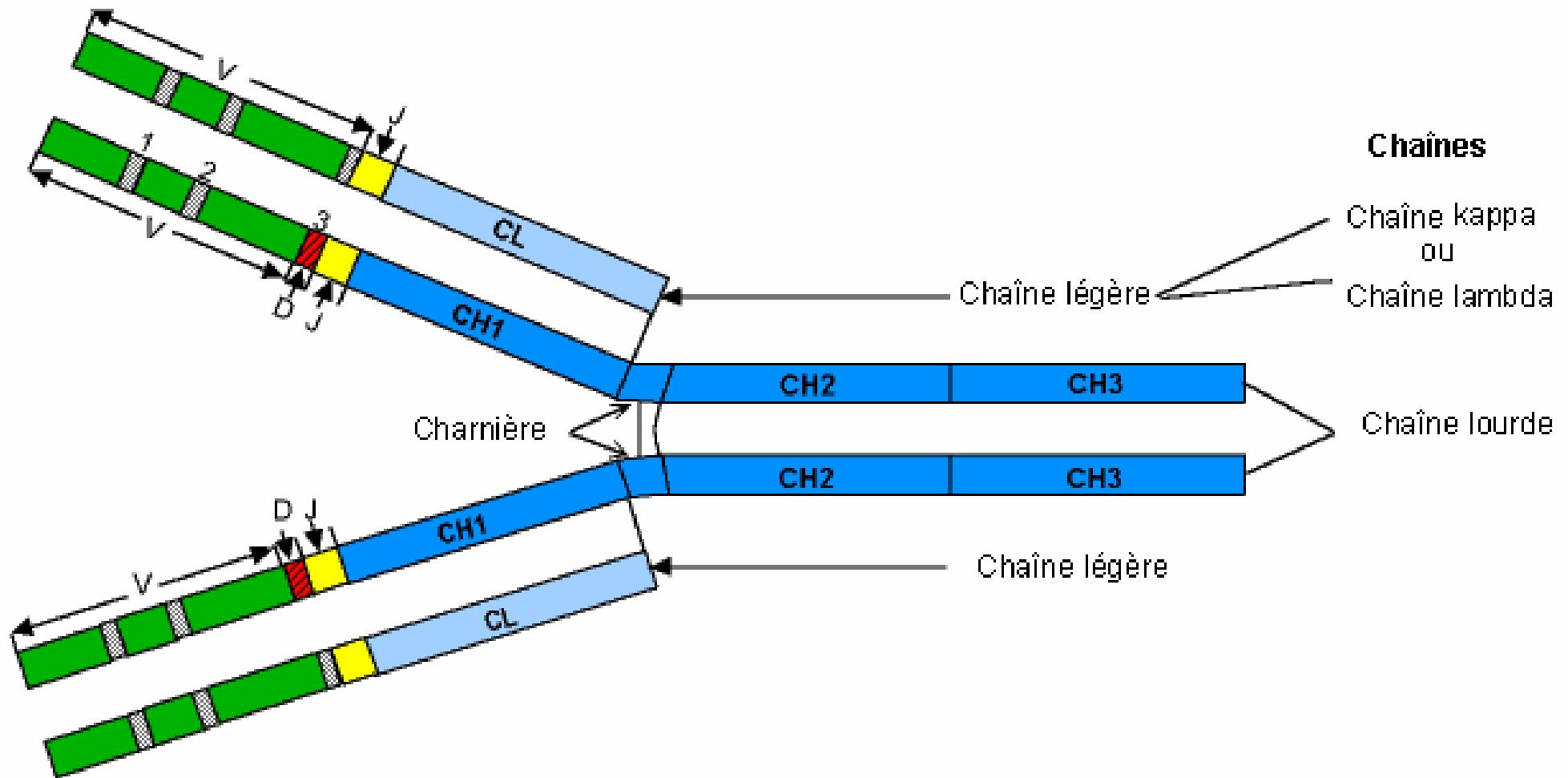


IMGT domain of research: the adaptive immune system

Vertebrates



Immunoglobulin IgG



Immunoglobulin (IG)

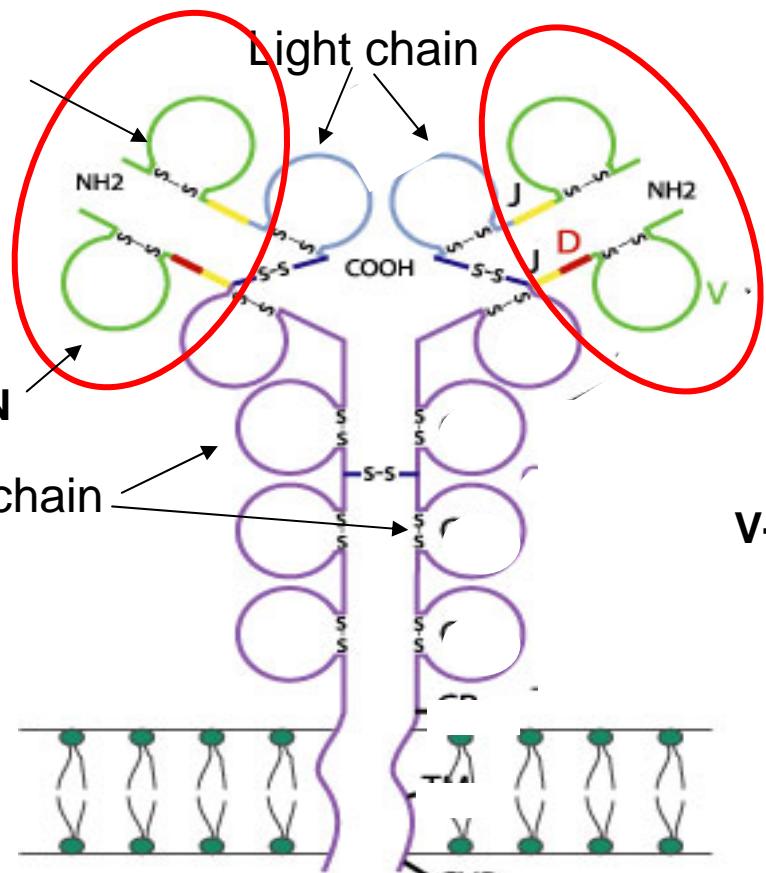
V-DOMAIN

V-J-REGION

V-DOMAIN

V-D-J-REGION

Heavy chain



Membrane IgM

T cell receptor (TR)

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

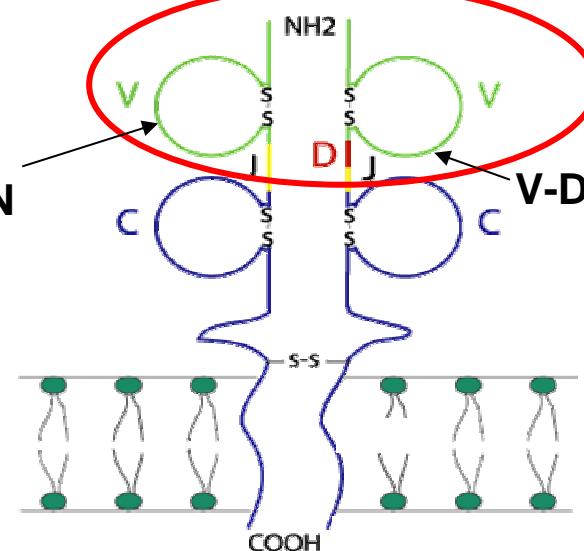
Alpha

Gamma

Beta

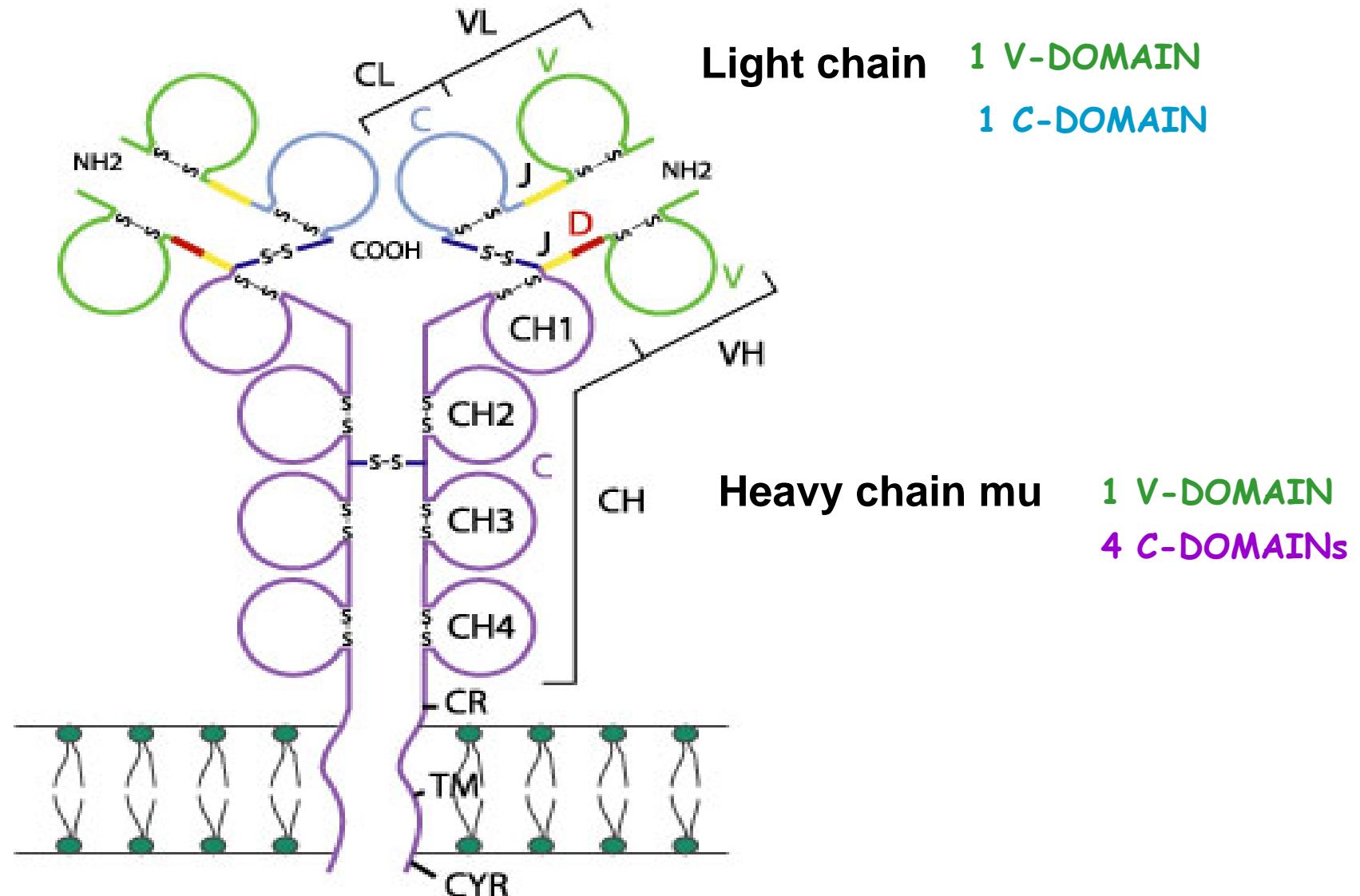
Delta

V-J-REGION



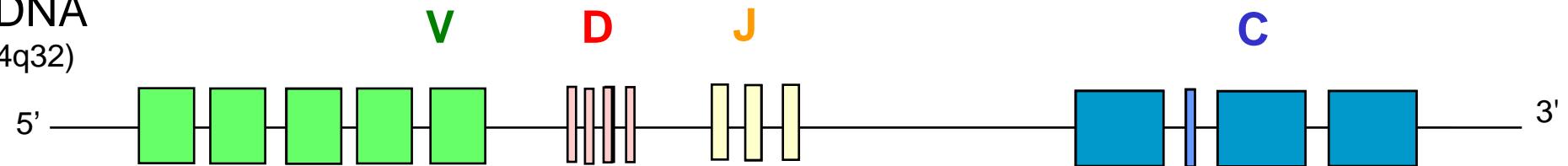
T cell receptor

Immunoglobulin IgM



Immunoglobulin synthesis

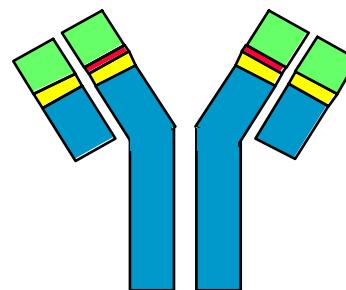
genomic DNA
(IGH Locus 14q32)



rearranged
DNA

mRNA

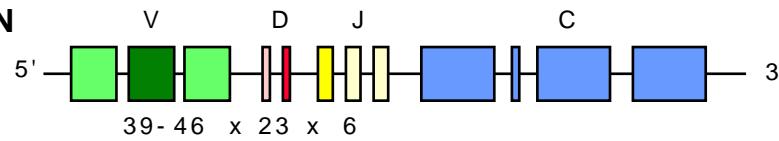
2×10^{12} different IG
per individual



Immunoglobulin (IG) synthesis

150
FUNCTIONAL IG GENES

HEAVY CHAIN



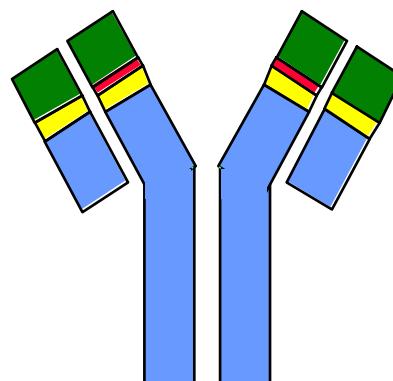
6300 POTENTIAL RECOMBINATIONS



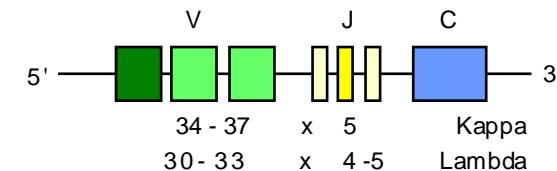
ABOUT 6.3×10^6 POSSIBILITIES

2×10^{12}

DIFFERENT ANTIBODIES



LIGHT CHAIN



185 + 165 POTENTIAL RECOMBINATIONS

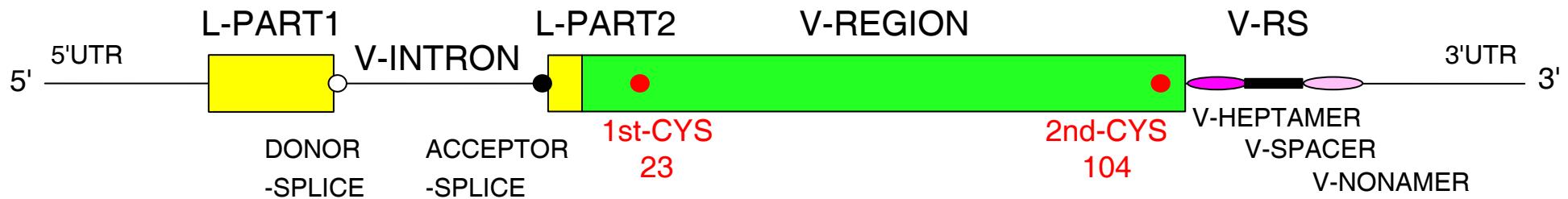


ABOUT 3.5×10^5 POSSIBILITIES

An example of V-GENE

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

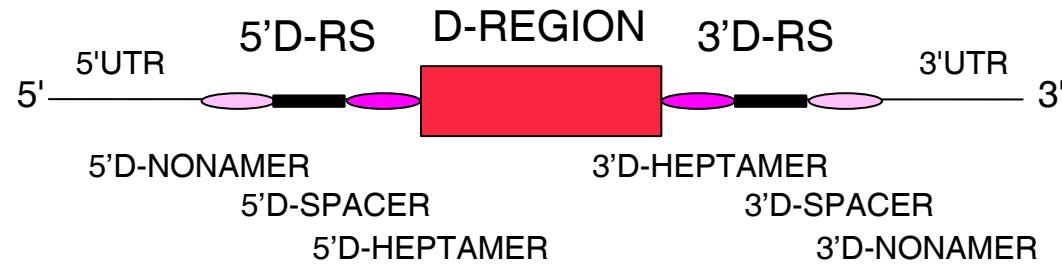
| | | | | | | |
|------------|-------------|------------|-------------|------------|-------------|-----|
| tgagagctcc | gttcctcacc | atggactgga | cctggaggat | cctcttcttg | gtggcagcag | 60 |
| ccacaggtaa | gaggctccct | agtcccagtg | atgagaaaaga | gattgagtcc | agtccaggga | 120 |
| gatctcatcc | acttctgtgt | tctctccca | ggagccccact | cccaggtgca | gctgggtgcag | 180 |
| tctggggctg | aggtgaagaa | gcctggggcc | tcaagtgaagg | tctcctgcaa | ggcttctgga | 240 |
| tacaccttca | ccggctacta | tatgcactgg | gtgcgacagg | cccctggaca | agggcttgag | 300 |
| tggatggat | gatatcaaccc | taacagtgg | ggcacaaaact | atgcacagaa | gtttcagggc | 360 |
| agggtcacca | tgaccaggg | cacgtccatc | agcacagcct | acatggagct | gagcaggctg | 420 |
| agatctgacg | acacggccgt | gtattactgt | gcgagagaca | cagtgtgaaa | acccacatcc | 480 |
| tgagggtgtc | agaaacccaa | gggaggaggc | ag | | | |



An example of D-GENE

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

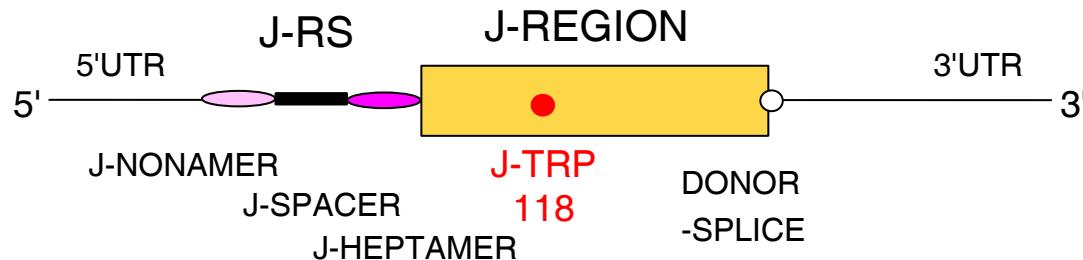
ccagccgcag gg_{5'D-NONAMER}ttttggc tgagctgaga acc_{5'D-SPACER}actgtgc taactgggga cacagtgatt
ggcagctcta caaaaaccat gctccccgg g 60



An example of J-GENE

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

| | |
|--|-----|
| accccgggct gtgggtttct gtgcgcctgg ctcagggctg actcaccgtg gctgaatact | 60 |
| tccagcactg ggccagggc accctggtca ccgtctcctc algtgagtct gctgtactgg | 120 |
| ggatagcggg gagccatgtg tactggcca agcaaggct ttggcttcag | 170 |



Heavy chain **WGXG** (J-TRP)
Light chain **FGXG** (J-PHE)

Immunoglobulin V-D-J generation of sequence diversity

3'V-REGION

N-REGION

D-REGION

N-REGION

5'J-REGION

tgtgcgaaa ga  tac agcatatttg  gtggactgctat tcc  gat acaactggttcg actcctgg

JUNCTION

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

IMGT® Web Resources

IMGT Repertoire
HTML

8,000 HTML pages

Chromosomal localizations
Locus representations, ...

IMGT Bloc-notes

Interesting links
The IMGT Immunoinformatics page
(databases, tools, resources, ...)

IMGT Education

Tutorials, IMGT Lexique, ...

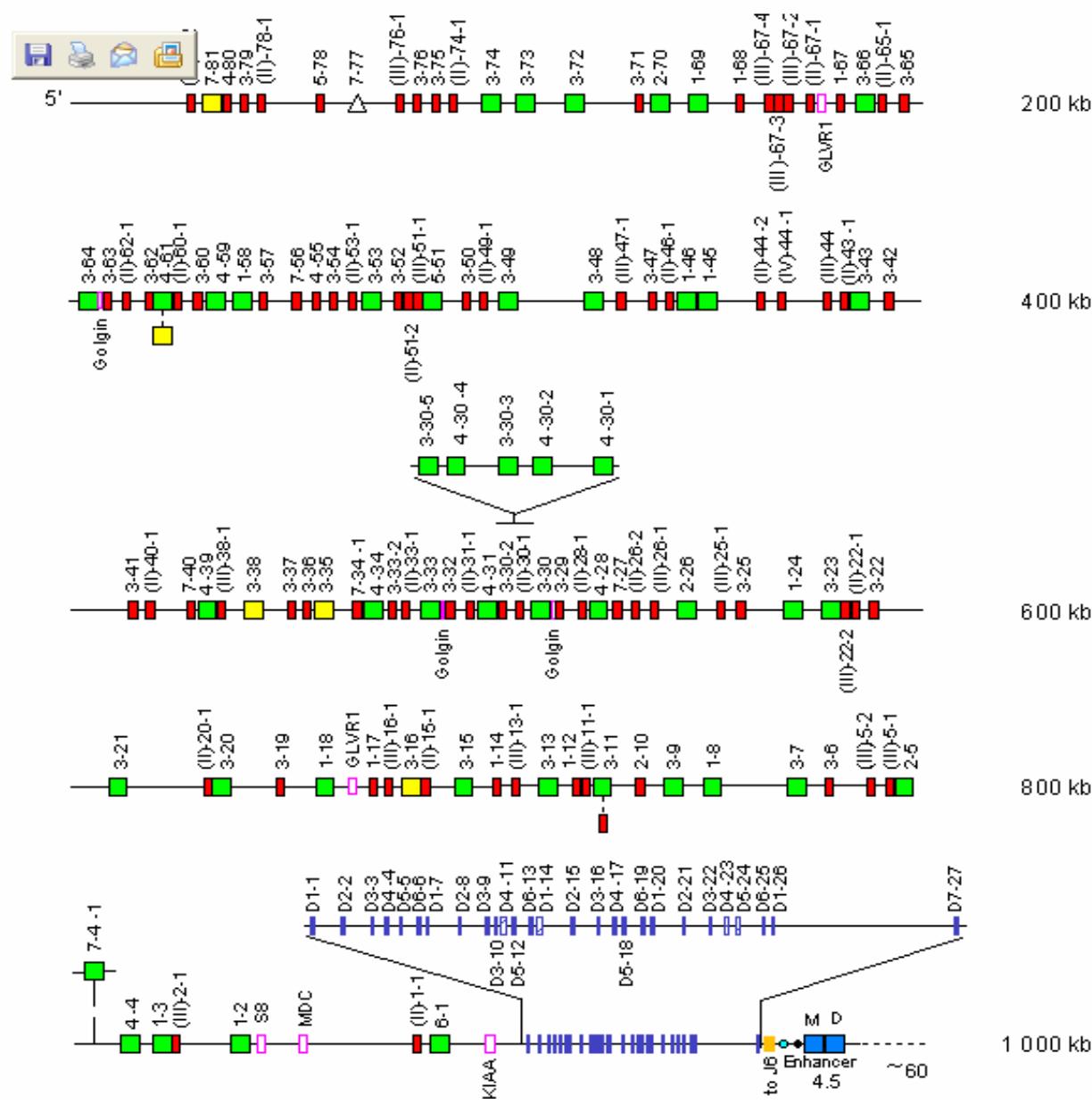


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Human IGH locus

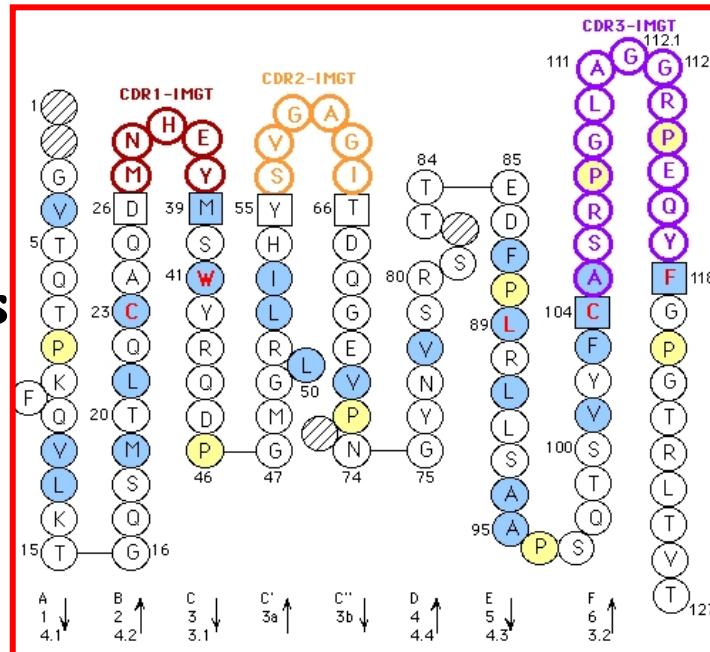
Chromosome
14q32.33



Human IGHV genes at chromosome 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(I) | - | - | 22 | 22 |
| IGHV(II) | - | - | 18 | 18 |
| IGHV(IV) | - | - | 1 | 1 |
| Total | 38-44(+2)* | 4(+1)* | 79(+2)* | 123-129*** |

Collier de Perles



| | | | | | | | | | | | | | | | | | | | | | | | | |
|----------|--------------|-----------|------|-------|------|------|------|------|------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-----|-----|-----|-----|-----|
| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | | | |
| X02850 | , TRAV8-6*01 | R | O | S | V | T | O | L | D | S | O | V | P | F | E | A | P | V | E | | | | | |
| | | GCC | CRC | TCT | GTG | RCC | CAG | CTT | GAC | RGC | AAA | GTC | CCT | GTC | TTT | GAR | GAR | GCC | CCT | GTG | GRG | | | |
| AE000659 | , TRAV8-6*02 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | | | |
| M86361 | , TRAV8-6*02 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | | | |
| | | CDR1-IMGT | | | | | | | | | | | | | | | | | | | | | | |
| | | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | | | |
| X02850 | , TRAV8-6*01 | L | R | C | N | Y | S | S | S | V | S | V | S | V | Y | | | | | L | F | | | |
| | | CTG | A GG | T GCG | A RC | T AC | TCA | T CG | T CT | G TT | T CA | G TG | T AT | | | | | | | CTG | TTC | | | |
| AE000659 | , TRAV8-6*02 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | | | |
| M86361 | , TRAV8-6*02 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | | | |
| | | CDR2- | | | | | | | | | | | | | | | | | | | | | | |
| | | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | | | |
| X02850 | , TRAV8-6*01 | W | Y | Y | Y | P | Y | P | Y | P | L | L | L | X | Y | L | Y | L | Y | W | S | | | |
| | | TGG | TAT | GTG | CAA | TAC | CCC | ARC | CAA | GGG | CTC | CAG | CTT | CTG | CTG | ARG | TAT | TTT | TCA | GRG | TTC | | | |
| AE000659 | , TRAV8-6*02 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | | | |
| M86361 | , TRAV8-6*02 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | | | |
| | | IMGT | | | | | | | | | | | | | | | | | | | | | | |
| | | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | | | |
| X02850 | , TRAV8-6*01 | T | L | S | V | E | S | I | H | | | | | | | | | | | 6 | F | E | | |
| | | ACC | CTG | | | | | | | | | | | | | | | | | 66T | TTT | GRG | | |
| AE000659 | , TRAV8-6*02 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | | |
| M86361 | , TRAV8-6*02 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | | |
| | | 81 | 82 | 83 | 84 | 84R | 84G | 84C | 85 | 86 | 87 | 88 | 89 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 100 |
| X02850 | , TRAV8-6*01 | A | E | F | N | K | S | Q | T | S | F | H | | R | K | P | S | V | H | I | S | D | T | R |
| | | GCT | GRG | TTT | ARC | ARC | ACT | CRA | ACT | TCC | TTC | GAC | TTG | AGG | AAA | CCC | TCA | GTC | ATR | AGC | GAC | GCT | CTC | |
| AE000659 | , TRAV8-6*02 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | |
| M86361 | , TRAV8-6*02 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | |
| | | CDR3-IMGT | | | | | | | | | | | | | | | | | | | | | | |
| | | 101 | 102 | 103 | 104 | 105 | 106 | 107 | 108 | | | | | | | | | | | | | | | |
| X02850 | , TRAV8-6*01 | E | Y | F | C | R | V | S | | | | | | | | | | | | | | | | |
| | | GRG | TAC | TTC | TGT | GCT | GTC | AGT | GRG | | | | | | | | | | | | | | | |
| AE000659 | , TRAV8-6*02 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | | |
| M86361 | , TRAV8-6*02 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --G | #c | --- | --- | --- | | | | |

Alignment of alleles

| TRAV gene | FR1-IMGT (1-26) | CDR1-IMGT (27-38) | FR2-IMGT (39-55) | CDR2-IMGT (56-65) | FR3-IMGT (66-104) | CDR3-IMGT (105-115) | | |
|-------------------|-------------------------------|----------------------|----------------------|----------------------|----------------------|-----------------------------------|-----------------------|------|
| | 1 10 20 | 30 | 40 50 | 60 | 70 | 80 84ABC 90 | 100 | 110 |
| AE000658, TRAV1-1 | GQSLEQ PSEVTAVEGAIQVINCTYQ | TSGFYC | L SWYQQHDGGAPTFLSY | NALDG. | LEETG. | RFSFLSRSDSYCGYLLQELQMKDSAS YFC | AVR. | |
| AE000658, TRAV1-2 | GQNIDQ PTEMTATEGAIQVINCTYQ | TSGFNG | L FWYQQHAGEAPTFLSY | NWLDG. | LEEKG. | RFSFLSRSKGYSYLLKELQMKDSAS YLC | AVR. | |
| AE000658, TRAV2 | KDQVFQ PSTVASSEGAVVIEFCNHS | VSMAYN | FFWYLHFPGCAPRLLVK | GSK. | PSQGQ. | RYNMTYER. | FSSSLILQVREADAAVYC | AVE. |
| AE000658, TRAV3 | AQSVAQPEDQVNVAEGGNPLTVKCTYS | VSGNPY | L FWYVQYPNRQLQFLLK | YTGDNL. | VKGSY. | GFEAEFNKSQTSHLKKPSALVSDSAL YFC | AVRD. | |
| AE000658, TRAV4 | LAKITQ PISMDSYEGQE VNITCSHN | NIATNDY | I TWYQQFPSQGQPRFIQ | GYKT. | KVTNE. | VASLFIPADRKSSTLSPRVSLS DTA VYYC | LVGD. | |
| AE000659, TRAV5 | GEDVEQS LFLSVREGDSSV INCTYT | DSSSTY | L WYKQKEPQAGLQLLTY | IFSNMD. | MKQDQ. | RLTVLLNKKDKHLSLRIADT QTGDS AYFC | AES. | |
| AE000659, TRAV6 | SQKIEQNSEALNIQEGKTATLTCNYT | NYSPAY | L QWYRQDPGRGPVFL LL | IRENEK. | EKRKE. | RLKVTFDTT LKQSLFHITASQPADSAT YLC | ALD. | |
| AE000659, TRAV7 | ENQVEHSPHFLGPQQGDV ASMSCTYS | VSRFNN | L QWYRQNTGMGPKHL LS | MYSAGY. | EKQKG. | RLNATLLK. | NGSSLYITAVQPEDSAT YFC | AVD. |
| AE000659, TRAV8-1 | AQS VSQHHHVILSEAASLELG CNYS | YGGTVN | L FWYVQYPGQHQLQLLLK | YFGCDPL. | VKGIK. | GFEAEFIKSFKSFMLRKPSVQWS DTA EYFC | AVN. | |
| AE000659, TRAV8-2 | AQS VTQLD SHVSVS EGT VLLRCNYS | SSYSPS | L FWYVQHPNKQLQLLLK | YTSAATL. | VKGIN. | GFEAEFKKSETSFH LT KPSAHMS DAAEYFC | VVS. | |
| AE000659, TRAV8-3 | AQS VTQPDHIITVSEGASLELRCNYS | YGATPY | L FWYVQSPGQGQLQLLLK | YFGCDTL. | VQGIK. | GFEAEFKRSQSSFMRLRKP SVHWS DAAEYFC | AVG. | |
| AE000659, TRAV8-4 | AQS VTQLGS HVSVSE GALVLLRCNYS | SSVPPY | L FWYVQYPNQGLQLLLK | YTSAATL. | VKGIN. | GFEAEFKKSETSFH LT KPSAHMS DAAEYFC | AVS. | |
| X02850, TRAV8-6 | AQS VTQLDSQVPV FEEAPVLRCNYS | SSVSVY | L FWYVQYPNQGLQLLLK | YLSGSTL. | YESIN. | GFEAEFNKSQTSHLKKPSVHIS DTA EYFC | AVS. | |
| AE000660, TRAV8-7 | TQSVTQLDGHITVSEAPLELKC NYS | YSGVPS | L FWYVQYSSQQLQLLLK | DLTAEATQ. | VKGIR. | GFEAEFKKSETSFYLRKP STHVS DAAEYFC | AVGDR. | |
| AE000659, TRAV9-1 | QDSWVQTCQWVLPSEGDLSIYWCNSYV | TTMVP S | L FWYVQYSPGQGQLQLLLK | AMKAND. | KGRNK. | GFEAFMRYKFTTSPHFLKD DSVOFSIS AYFC | ALS. | |

Protein Display

The eleven IMGT amino acid classes according to the physico-chemical properties

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

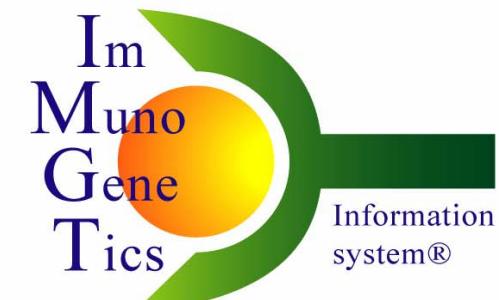
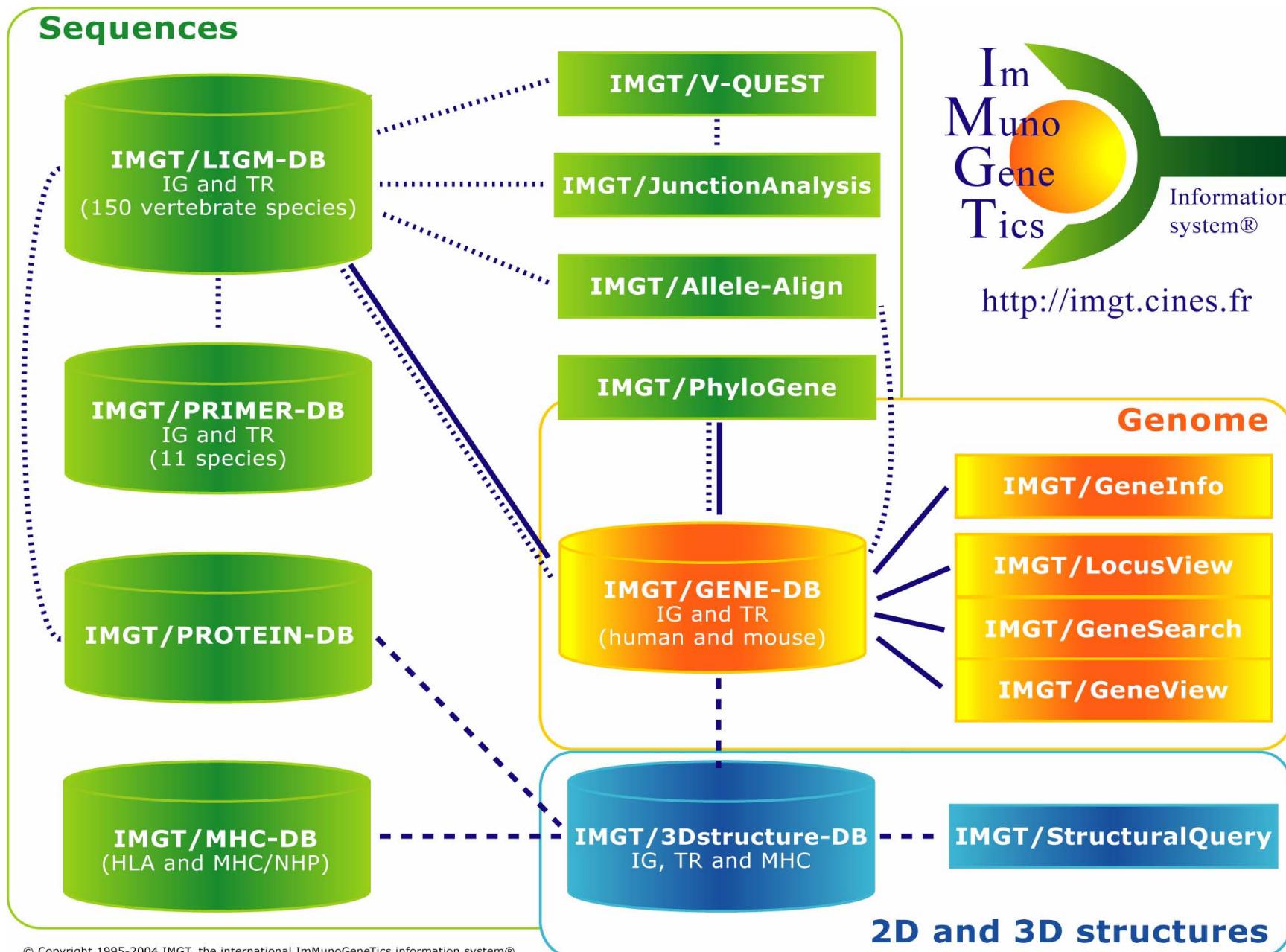
| 'Volume' classes | | 'Hydropathy' classes | | | | | | | | |
|------------------|---------|----------------------|---|---|----------|---|---|-------------|---|--|
| | in Å³ | Hydrophobic | | | Neutral | | | Hydrophilic | | |
| Very large | 189-228 | F | | W | | Y | | | | |
| Large | 162-174 | I | L | M | | | K | R | | |
| Medium | 138-154 | V | | | | H | | E | Q | |
| Small | 108-117 | | C | P | T | | D | | N | |
| Very small | 60-90 | A | G | S | | | | | | |
| | | Aliphatic | | | Sulfur | | | Basic | | |
| | | Uncharged | | | Hydroxyl | | | Charged | | |
| | | Nonpolar | | | Polar | | | Uncharged | | |
| | | Uncharged | | | Charged | | | Uncharged | | |
| | | Nonpolar | | | Polar | | | Uncharged | | |

IMGT databases and tools



The international ImMunoGeneTics information system®
Coordinator: M.-P. Lefranc, Montpellier, France <http://imgt.cines.fr>





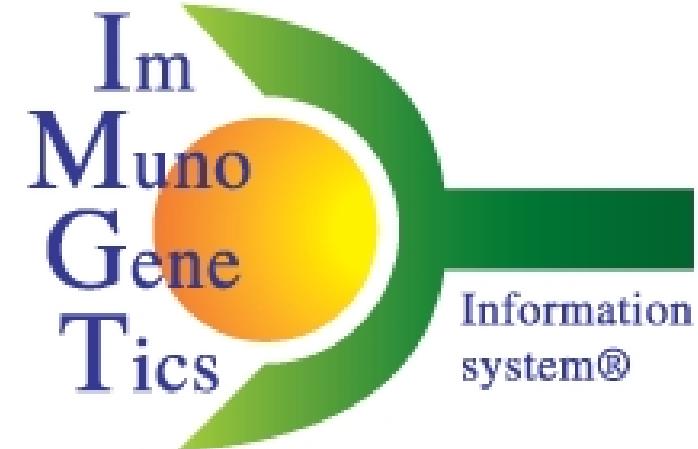
Locus representation: Human IGL

Human IGL 2

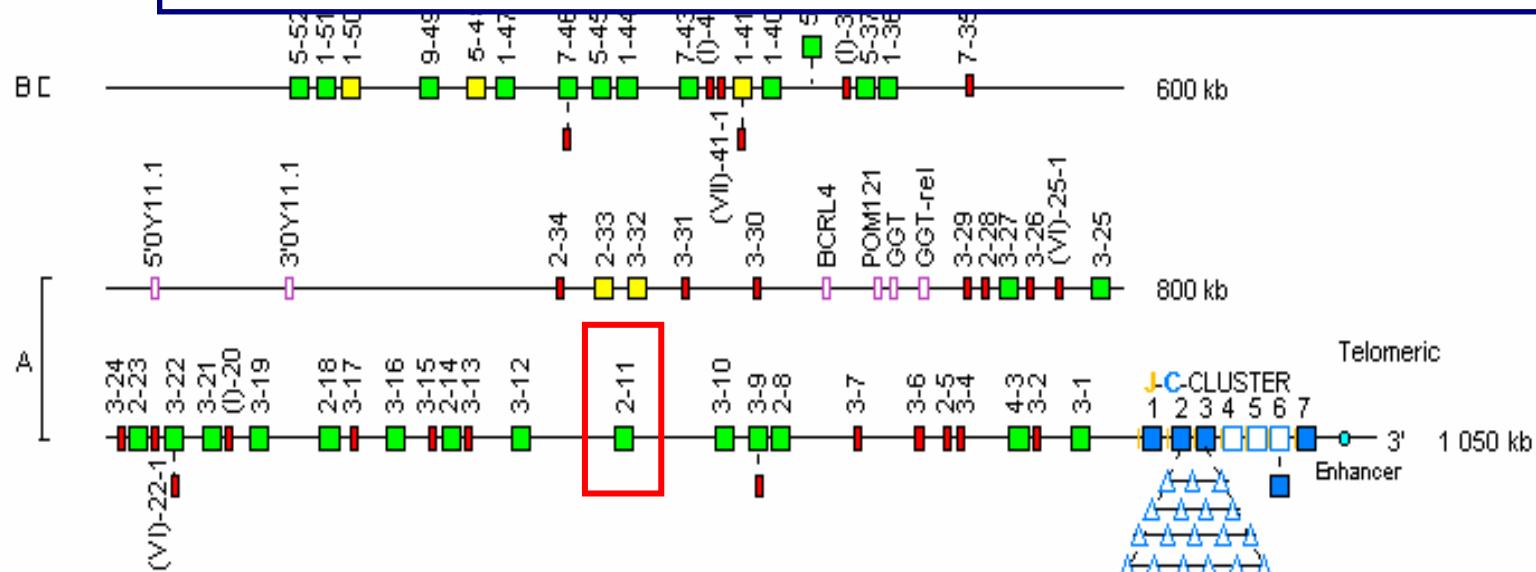
Centromere
BCR
5' →
C
0-63
1-62

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Fichier Edition Afficher Ailler Communicator Aide

Signets Adresse : <http://ligm.igh.cnrs.fr:8104/cgi-bin/IMGTlect.jv> Infos connexes [N](#)

V-GENE <1..297> /partiel

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Created by Marie-Paule Lefranc (CNRS, Montpellier II University, France)
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Catalogue

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

FR1-IMGT
1st-CYS
CDR1-IMGT
FR2-IMGT
CONSERVED-TRP
CDR2-IMGT
FR3-IMGT
2nd-CYS
CDR3-IMGT

103..153
/AA_IMGT="39 to 55"
/translation="VSWYQQHPGKAPKLMIY"
109..111
154..162
/AA_IMGT="56 to 58"
/translation="DVS"
163..270
/AA_IMGT="66 to 104, AA 73, 81, 82 missing"
/translation="KRPSGVPDFSGSKSGNTASLTISGLQAEADYYC"
268..270
271..297
/AA_IMGT="105 to 113"
/translation="CSYAGSYTF"

SQ Sequence 297 BP; 60 A; 93 C; 71 G; 73 T; 0 other;
cagtcgtcccc tggactcggcc tggctcgatgt tccgggtctc ctggacatgc agtcaccatc
tccttcactca caaccacccaa tttatattatg ctttataact atatcttcctt ctaccaacaa

60
120



Document chargé

IMGT/V-QUEST



The international ImMunoGeneTics information system®
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Example of IMGT/V-QUEST results

Alignment for V-GENE

| | | | | |
|--------------------------|-------------|-----------------------------------|-------|---------------------------------------|
| AF402940 | | score GTGCAGCTGCTCGAGCAGTCTGGGGCT | _____ | GAGGTGAGCAAGCCTGGGGCTCAGTAAAGGTTCTGCA |
| X62109 | IGHV1-3*01 | 1146 CA.GTC.A...T.T..... | |AG.....G..... |
| X62107 | IGHV1-3*02 | 1110 CA.GTT.A...G.T..... | |AG.....G..... |
| M99637 | IGHV1-8*01 | 957 CA.GT..A...G.T..... | |AG.....G....C..... |
| L06612 | IGHV1-46*03 | 948 CA.GT..A...G.T..... | |AG.....G..... |
| X92343 | IGHV1-46*01 | 948 CA.GT..A...G.T..... | |AG.....G..... |

Alignment for J-GENE

| | | | |
|--------------------------|----------|---|---------------|
| AF402940 | | score CTTCACGGGGCGGGACGCTTGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA | |
| J00256 | IGHJ3*01 | 181 _____T.....T..T..... | A.T.....T...G |
| X86355 | IGHJ6*02 | 179 T.A.TACTACTACT...G.A..... | |
| X86355 | IGHJ3*02 | 172 _____T.....T..TA..... | A.T.....T...G |





WELCOME ! to the IMGT/V-QUEST Search page

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IMMUNOGENETICS
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http://imgt.cines.fr

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

Analyse your Immunoglobulin nucleotide sequences

- [Human](#)
- [Mouse](#)
- [Chondrichthyes](#)
- [Teleostei](#) (contains now 19 species)
 - [Atlantic cod](#)
 - [Channel catfish](#)
 - [Rainbow trout](#)
- [Sheep](#)

Analyse your T cell Receptor nucleotide sequences

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

[Fichier](#) [Edition](#) [Affichage](#) [Aller à](#) [Marque-pages](#) [Outils](#) [?](#)<http://imgt.cines.fr/cgi-bin/IMGTdnap.jv?livret=0&Option=humanIg>[OK](#)

Analyse your Immunoglobulin sequences

Your selection: Human

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

- Include the analysis of the junction by IMGT/JunctionAnalysis
- Do not include the analysis of the junction by IMGT/JunctionAnalysis

Sequence

You may give your sequence a name (optional) :

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

```
gaggtgcagctgttggagtggggggggggctggtaacaggctgggggtccctgagactc
tcctgtgcagccctggattcaccttagcagctttggcatgagctgggtccggcaggct
cctggaaaggggctggactgggtctcagaaatttagtggtagtggcggtaccacatattac
gcaggctcgtgaaggggcggttaccatctccagagacaactccaagaatacgctgttt
ctgcaaatgaatagctgacagccgaagacacggccgtatattactgtgcgaagaggttt
```

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

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

IMGT/QUEST - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

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

Sequence compared with the Human IG set from the IMGT reference directory

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

Alignment for V-GENE

| input | score | sequence |
|--------------------|-------|-------------------------|
| M99660 IGHV3-23*01 | 1281 | -----T----- |
| J00236 IGHV3-23*02 | 1263 | -----T----- |
| U29481 IGHV3-23*03 | 1209 | -----T----- |
| Z12358 IGHV3-48*03 | 1128 | -----G-----T-----A----- |
| M99675 IGHV3-48*01 | 1128 | -----G-----T----- |

Alignment for D-GENE

| input | score | sequence |
|-------------------|-------|-----------------------------|
| X93618IGHD3-3*02 | 61 | T-----ATTATAACC |
| X13972IGHD3-3*01 | 61 | T-----ATTATAACC |
| X97051IGHD6-19*01 | 34 | --A-A-C----C-GGTAC |
| X13972IGHD3-9*01 | 34 | TA---T--C----ATTATAAC |
| J00234IGHD2-15*01 | 34 | A-A---T-----GGTAGCTGCTACTCC |

Alignment for J-GENE

| input | score | sequence |
|----------------|-------|-----------------------------|
| X86355IGHJ5*02 | 219 |-CAAC----- |
| J00256IGHJ5*01 | 201 |-CAAC-----T-----A----- |
| X86355IGHJ4*02 | 177 |AC-AC---TA----- |

Applet input [1]

IMGT/V-QUEST - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

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

OK G

Translation of the JUNCTION

| | |
|-------|--|
| input | C A K R F W S G Y L W F D P W G Q G |
| | TGT GCG AAG AGG TTT TGG AGT GGT TAT CTG TGG TTC GAC CCC TGG GGC CAG GGA |

Applet input [1]

IMGT/QUEST - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

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

Alignment for V-GENE

| input | score | IGHV3-23*01 | IGHV3-23*02 | IGHV3-23*03 | IGHV3-48*03 | IGHV3-48*01 |
|--------|-------|--------------------|--------------|--------------|--------------------------------|--------------------------------|
| M99660 | 1281 | -----T-----. | -----T-----. | -----T-----. | -----G-----T-----. | -----G-----T-----. |
| J00236 | 1263 | -----T-----. | -----T-----. | -----T-----. | -----A-----. | -----A-----. |
| U29481 | 1209 | -----T-----. | -----T-----. | -----T-----. | -----A-----. | -----A-----. |
| Z12358 | 1128 | -----G-----T-----. | -----T-----. | -----A-----. | -----C-----T-----T-----A-----. | -----C-----T-----A-----A-----. |
| M99675 | 1128 | -----G-----T-----. | -----T-----. | -----A-----. | -----C-----T-----A-----A-----. | -----C-----T-----A-----A-----. |

Alignment for J-GENE

| input | score | IGHJ5*02 | IGHJ5*01 | IGHJ4*02 |
|--------|-------|-----------------------------|-----------------------------|------------------------|
| X86355 | 219 |-CAAC----- |-CAAC----- |AC-AC-T---TA----- |
| J00256 | 201 |-CAAC-----T-----A----- |-CAAC-----T-----A----- |AC-AC-T---TA----- |
| X86355 | 177 | | | |

Results of IMGT/JunctionAnalysis

Analysis of the JUNCTION

| Input V name | V-REGION | D-REGION | N2 | J-REGION | J name | D name | Vmut | Dmut |
|----------------------|---------------|------------------------------|-----|---------------------|----------|-------------------|------|------|
| #1 input IGHV3-23*01 | tgtgcgaa..... |gaggtttggagtggttat..... | ctg |tggttcgaccctgg | IGHJ5*02 | IGHD3-3*02 | 0 | 3 |

Input Jmut Ngc

#1 input 0 2/3

Translation of the JUNCTION

| 105 | 107 | 109 | 111 | 113 | 115 | 117 | CDR3-IMGT | | | | | | | |
|---|-----|-----|-----|-----|-----|-----|------------------|---|---|---|---|---|---|---|
| 104 | 106 | 108 | 110 | 112 | 114 | 116 | 118 frame length | | | | | | | |
| C | A | K | R | F | W | S | G | Y | L | W | F | D | P | W |
| #1 input tgt gcg aag agg ttt tgg agt ggt tat ctg tgg ttc gac ccc tgg + 13 | | | | | | | | | | | | | | |

Applet input [1]

Alignment with FR-IMGT and CDR-IMGT delimitations

<----- F R 1 - I M G T -----

| | | | | | | | | | | | | | | | | | | |
|--------|-------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 1 | 5 | 10 | 15 | | | | | | | | | | | | | | |
| input | GAG | GTG | CAG | CTG | TTG | GAG | TCG | GGG | GGA | ... | GGC | TTG | GTA | CAG | CCT | GGG | GGG | TCC |
| M99660 | IGHV3-23*01 | --- | --- | --- | --- | -T | --- | --- | ... | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| J00236 | IGHV3-23*02 | --- | --- | --- | --- | -T | --- | --- | ... | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| U29481 | IGHV3-23*03 | --- | --- | --- | --- | -T | --- | --- | ... | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Z12358 | IGHV3-48*03 | --- | --- | --- | --- | G | --- | -T | --- | ... | --- | --- | --- | -A | --- | --- | --- | --- |
| M99675 | IGHV3-48*01 | --- | --- | --- | --- | G | --- | -T | --- | ... | --- | --- | --- | A | --- | --- | --- | --- |

----->

| | | | | | | | | | | | | | | | | | | |
|--------|-------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 20 | 25 | 30 | 35 | | | | | | | | | | | | | | |
| input | CTG | AGA | CTC | TCC | TGT | GCA | GCC | TCT | GGA | TTC | ACC | TTT | AGC | AGC | TTT | GCC | ... | ... |
| M99660 | IGHV3-23*01 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | -A | --- | --- | --- | ... | ... |
| J00236 | IGHV3-23*02 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | -A | --- | --- | --- | ... | ... |
| U29481 | IGHV3-23*03 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | -A | --- | --- | --- | ... | ... |
| Z12358 | IGHV3-48*03 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | -C | -T | -A | -AA | ... | ... |
| M99675 | IGHV3-48*01 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | -C | -T | -A | AG- | ... | ... |

<----- F R 2 - I M G T -----

| | | | | | | | | | | | | | | | | | | |
|--------|-------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 40 | 45 | 50 | | | | | | | | | | | | | | | |
| input | ... | ... | ATG | AGC | TGG | GTC | CGC | CAG | GCT | CCT | GGG | AAG | GGG | CTG | GAC | TGG | GTC | TCA |
| M99660 | IGHV3-23*01 | ... | ... | --- | --- | --- | --- | --- | --- | --- | --- | -A | --- | --- | --- | -G | --- | --- |
| J00236 | IGHV3-23*02 | ... | ... | --- | --- | --- | --- | --- | --- | --- | --- | -A | --- | --- | --- | -G | --- | --- |
| U29481 | IGHV3-23*03 | ... | ... | --- | --- | --- | --- | --- | --- | --- | --- | -A | --- | --- | --- | -G | --- | --- |
| Z12358 | IGHV3-48*03 | ... | ... | --- | -A- | --- | --- | --- | --- | --- | --- | -A | --- | --- | --- | -G | --- | -T |
| M99675 | IGHV3-48*01 | ... | ... | --- | -A- | --- | --- | --- | --- | --- | --- | -A | --- | --- | --- | -G | --- | -T |

IMGT/V-QUEST - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

A set of small, semi-transparent navigation icons located at the bottom right of the screen. From left to right, they include: a green arrow pointing left, a grey arrow pointing right, a blue circular arrow indicating refresh or redo, a grey octagonal icon with a red 'X' inside, and a yellow house-like icon.

| | <----- | | | | F | R | I | M | G | T | ----- | | | | | | | |
|-------|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|-----|-----|-----|
| 1 | E | V | Q | L | 5 | E | S | G | G | 10 | G | L | V | Q | P | G | G | S |
| input | GAG | GTG | CAG | CTG | TTG | GAG | TCG | GGG | GGA | ... | GGC | TTG | GTA | CAG | CCT | GGG | GGG | TCC |

M99660 IGHV3-23*01 --- --- --- --- --- -T --- --- --- --- --- --- ---

M99660 IGHV3-23*01 --- --- --- --- --- --- --- --- --- --- --- -A- --- . . .

| <----- | | | | | F | R | Z | - | I | M | G | T | ----- | | | |
|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------|-----|-----|-----|
| | | | | | 40 | 45 | | | 50 | | | | | | | |
| M | S | W | V | R | Q | A | P | G | K | G | L | D | W | V | S | |
| | ATG | AGC | TGG | GTC | CGC | CAG | GCT | CCT | GGG | AAG | GGG | CTG | GAC | TGG | GTC | TCA |
| | | | | | | | | | | | | | E | | | |

```
-->                               <-----  

      CDR2 - IMGT  

55   60   65   70  

E   I   S   G   S   G   G   T   T   Y   Y   A   G   S   V   K  

GAA ATT AGT GGT AGT GGC GGT ACC ACA ... ... TAT TAC GCA GGC TCC GTG AAG  

A           S           D  

CT          T          C          G          A
```

M99660 IGHV3-23*01 -CT --- --- --- --- --T --- -G- --- --C --- --- -A- --- --- ---

IMGT/V-QUEST - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

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

"input" V-REGION

Nucleotidic sequence in FASTA format

```
>input
GAGGTGCAGCTGTTGGAGTCGGGGGA...GGCTTGGTACAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG
GATTACACCTTAGCAGCTTGCC.....ATGAGCTGGGTCCGCCAGGCTCCTGGGAAGGGGCTGGACTGGGT
CTCAGAAATTAGTGGTAGTGGCGGTACCACA.....TATTACGCAGGCTCCGTGAAG...GGCCGGTTAACCATCTCC
AGAGACAACCTCCAAGAACATCGCTGTTCTGCAAATGAATAGCCTGACAGCCGAAGACACGGCCGTATATTACTGTGCGA
AGA
```

Analyse this sequence with IMGT/PhyloGene

Amino acid sequence

```
EVQLLESGG.GLVQPGGSLRLSCAASGFTFSSFA....MSWVRQAPGKGLDWVSEISGSGGTT..YYAGSVK.GRFTISRDNSKNTLFLQMNSLTAEDETAVYYCAKR
```

Applet input [1]

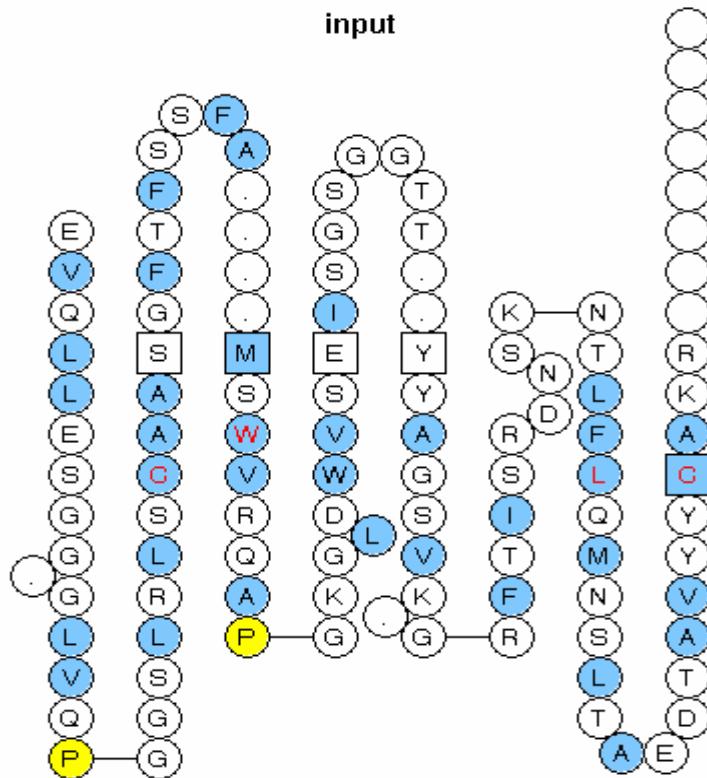


http://imgt.cines.fr/cgi-bin/IMGTdnap.jv



Collier de Perles

input



A 1 4.1 ↓ B 2 4.2 ↑ C 3 3.1 ↓ C' 3a ↑ C'' 3b ↓ D 4 4.4 ↑ E 5 4.3 ↓ F 6 3.2 ↑

Applet input [1]

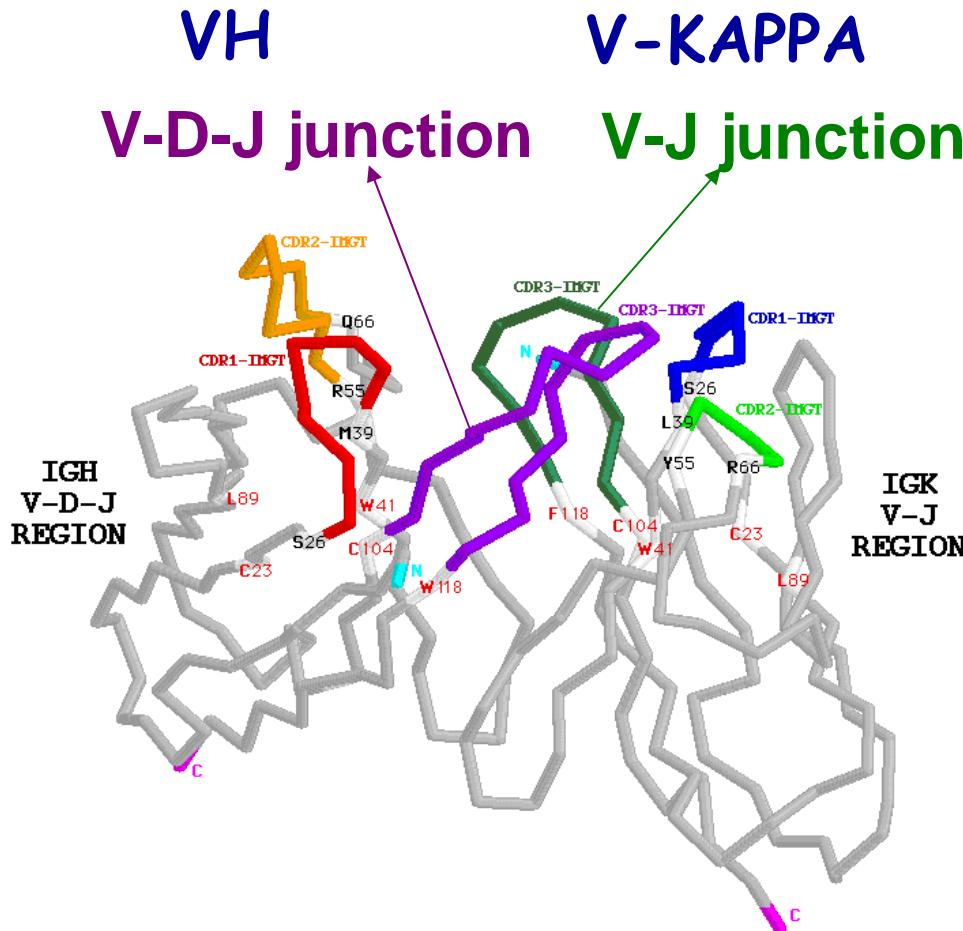
IMGT/JunctionAnalysis



The international ImMunoGeneTics information system®
Coordinator: M.-P. Lefranc, Montpellier, France <http://imgt.cines.fr>



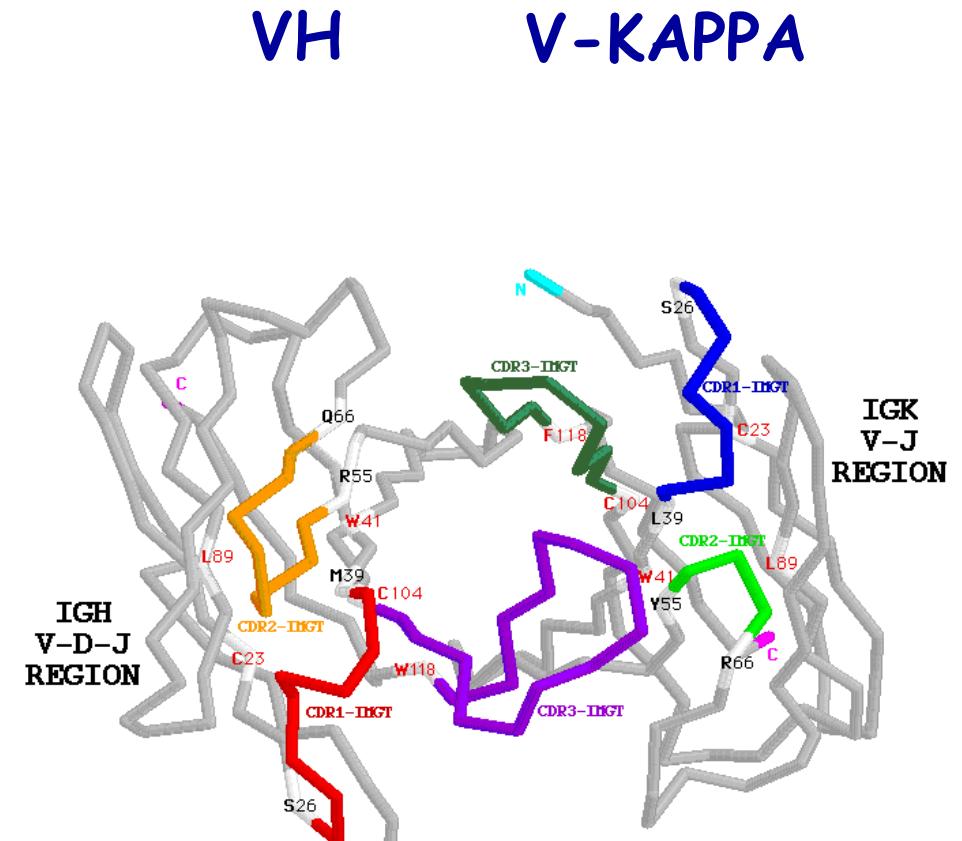
V-DOMAINs: VH and V-KAPPA



Side view of the V-DOMAINs

Mouse (*Mus musculus*) E5.2Fv

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



View from above the CDRs

THANK YOU for using IMGT/JunctionAnalysis

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INFORMATION SYSTEM®



<http://imgt.cines.fr>

Analysis of the JUNCTIONS

| Input | V name | V-REGION | N1 | D-REGION | | | N2 |
|-----------|--------------|-------------|---------------|------------------------------|--|--|----------|
| #1 M62724 | IGHV7-4-1*02 | tgtgcgagaga | aga |taqcaatqqctacaa.... | | | aata |
| #2 Z47269 | IGHV1-69*06 | tgtgcgagag. | ggggggcttaagg |tcgaattttggagtggtt..... | | | tcatgggt |

| Input | J-REGION | J name | D name | Vmut | Dmut | Jmut | Ngc |
|-----------|---------------------|----------|-------------|------|------|------|-------|
| #1 M62724 |tttactactaa | 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

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

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

[-> IMGT/JunctionAnalysis Documentation](#)

IMGT/JunctionAnalysis - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

http://imgt.cines.fr/cgi-bin/IMGTjcta.jv?livret=0 OK G

Citing IMGT/JunctionAnalysis: Yousfi Monod, M. et al. Bioinformatics 2004, 20 Supplement 1:I379-I385 PMID: 15262823

IMGT/JunctionAnalysis Search page

Species :

Homo sapiens

Locus :

IGH TRA
 IGK TRB
 IGL 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 :

Parcourir...

Terminé

Fichier Edition Affichage Aller à Marque-pages Outils ?



http://imgt.cines.fr/cgi-bin/IMGTjcta.jv?livret=0



Parameters for accepted mutations :

3'V-REGION and 5'J-REGION

 Default value
1
2
3
4
5
6 Selected value

D-REGION

 Default value
1
2
3
4 Selected value

Output options :

 Displayed Downloaded into a local file

Output order of the translation results :

 Input order Based on CDR3-IMGT length

Maximum number of characters per line :

 Unlimited 80 100 120

IMGT/JunctionAnalysis - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

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

**THANK YOU
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Muno
Gene
Tics**
Information system®
<http://imgt.cines.fr>

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 |tcgaattttggagtggtt..... | 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

| 104 | 105 | 106 | 107 | 108 | 109 | 110 | 111 | 111.1 | 111.2 | 112.3 | 112.4 | 112.1 | 112.2 | 113 | 114 | 115 | 116 | 117 | 118 | CDR3-IMGT frame length | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-------|-------|-------|-------|-------|-------|-----|-----|-----|-----|-----|-----|---------------------------|-----|-----|----|----|
| C | A | R | E | D | S | N | G | | | | | | | | Y | K | I | F | D | Y | W | | | |
| #1 M62724 | tgt | gct | 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 | gct | aga | ggg | ggg | gct | aag | gtc | gaa | ttt | ttg | gag | tgg | ttt | cat | ggg | tac | tgg | ttc | gac | ccc | tgg | + | 20 |

Terminé

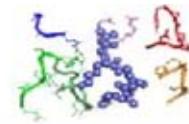
IMGT/3Dstructure-DB and IMGT/StructuralQuery



The international ImMunoGeneTics information system®
Coordinator: M.-P. Lefranc, Montpellier, France <http://imgt.cines.fr>



IMGT/3Dstructure-DB card for : 1u8k



| IMGT protein name | IMGT receptor description | Type | Ligand(s) | Species | CC | Chain ID |
|-------------------|---------------------------|------|-----------|-----------------------------|----|-----------------|
| 2F5 | FAB-GAMMA-3_KAPPA | IG | GP41 | <i>Homo sapiens</i> (Human) | 1 | [1u8k_A 1u8k_B] |
| | Peptide | | | | 1 | [1u8k_C] |

Experimental technique X-ray diffraction

Resolution 2.24

PDB release date 05-OCT-04

| 1u8k_B | | 1u8k_A | | 1u8k_C | |
|---------------------------|--|--|---|--|--|
| Chain ID | VH-CH1 | Chain ID | L-KAPPA | Chain ID | |
| IMGT chain description | | IMGT chain description | IGKV_1 | IMGT chain description | |
| Chain amino acid sequence | [RITLKESGPPLVKPTQTLTLCFSFGSLSDFGVGVWIRQPPGKALEWLAIYSDDDKRYSPSINTRLTIKDTSINQVVLVMTRSPV [] [D] [IGHJ_1] [IGHV_1] [DTATYFCAHRRGPTTLFGV/PIARGPVNANDVWQQGITVTISSTSTKGPSVPLAPCSASTAGGTAALGCL/KDYFPEPVTVSWNSGALT HC_1] [GVHTFPAAVLQSSGLYSLSSVTVPPSSLGTQTYTCNVNHNKPNTKV/DIKRVEPKS] | Chain amino acid sequence | [ALQLTQSPSSLSASVGDRITITCGRASQGVTSALAWYRQKPGSPQQLLIYDASSLESV/PSRFSGSGSGTEFTLTISTLRPEDFATYYQQQ [] [IGKJ_1] [LHFYPHTFGGGTRVDV/RTVAAPSVF/PPPSDRQLKSGTASV/CLINNFYPREAK/QWKVINALQSGNSQESVTEQDSKDKSTYSLSTLT LSKADYEKKHVYECEVTHQGLSSPVTKSFNRGECL] | IMGT domain description | V-KAPPA |
| V-DOMAIN | IMGT domain description IGHV gene and allele name IGHJ gene and allele name 2D representation CDR-IMGT lengths Sheet composition | IMGT domain description IGHV1-13*02 (85.26%) Alignment details IGHV1-13*01 (63.64%) , IGKV4*01 (63.64%) Alignment details V-DOMAIN [10.7.24] [A B D E] [C C" C' F G] | IGKV gene and allele name IGKV4*01 (63.64%) , IGKV1-13*02 (85.26%) Alignment details | 2D representation Collier de Perles or Collier de Perles on 2 layers CDR-IMGT lengths [6.3.9] Sheet composition [A B D E] [C C" C' F G] | IGKV domain description IGKV1-13*02 (85.26%) Alignment details IGKV1-13*01 (63.64%) , IGKV4*01 (63.64%) Alignment details V-DOMAIN [CDR1] [CDR2] [ALQLTQSPSSLSASVGDRITITCGRASQGVTSALAWYRQKPGSPQQLLIYDASSLESV/PSRFSGSGSGTEFTLTISTLRPEDFATYYQQQ [CDR3] [ISTRPDTEDATYYQQQLHF...YPHTFGGGTRVDV] |
| C-DOMAIN | IMGT domain description IGHC gene and allele name 2D representation Sheet composition | IMGT domain description IGHG3*01 (97.94%), IGHG3*03 (97.94%), IGHG3*04 (97.94%), IGHG3*05 (97.94%), IGHG3*06 (97.94%), IGHG3*07 (97.94%), IGHG3*08 (97.94%), IGHG3*09 (97.94%), IGHG3*10 (97.94%), IGHG3*11 (97.94%), IGHG3*12 (97.94%), IGHG3*13 (97.94%), IGHG3*14 (97.94%), IGHG3*15 (97.94%), IGHG3*16 (97.94%), IGHG3*17 (97.94%), IGHG3*20 (97.94%), Alignment details 2D representation Collier de Perles or Collier de Perles on 2 layers Sheet composition [A B D E] [C F G]STKGPSVPLAPCSKSTA...GGTAALGCLVKDYFPP..EP/TVSWNSGALT....GVHTFPAAVLQSS.....GLYSLSSVTV PSSSL...GTQTYTCNVNHNKP..SNTRV/DIKRVEPKS] | 2D representation Collier de Perles or Collier de Perles on 2 layers Sheet composition [A B D E] [C F G] | 2D representation Collier de Perles or Collier de Perles on 2 layers Sheet composition [A B D E] [C F G] | IGKC gene and allele name IGKC*01 (98.13%) Alignment details C-DOMAIN [CDR1] [CDR2] [....RTVAAPSVF/PPPSDRQLK...SGTASV/CLINNFYP..REAIWQKVINALQSGNSQESVTEQDSKDS.....TYSLSSTLT SKADY..EKHKHVYECEVTHQG...LSSPVTKSFNRGECL] |
| | | Chain ID | | Chain ID | 1u8k_C |
| | | IMGT chain description | Peptide | IMGT chain description | |
| | | Chain amino acid sequence | LELDKWASL | Chain amino acid sequence | |

From IMGT Colliers de Perles or from domain/chain sequence

41V - TRP (W)

chain : 1u8k_B

| | Secondary structure | Extended conformation |
|-----|---------------------|-----------------------|
| Phi | -122.64 | |
| Psi | 137.12 | |
| ASA | 0.0 | |

Residue local structure

| | IMGT Num | Code 1C | Code 3C | Chain | Domain | Tot | NCov | Pol | HB | NPol | Cov | SS |
|----------------------|----------|---------|---------|--------|--------|-----|------|-----|----|------|-----|----|
| Info | 6V1 | E | GLU | 1u8k_B | VH | 6 | 6 | 0 | 0 | 6 | 0 | 0 |
| Info | 21V1 | L | LEU | 1u8k_B | VH | 17 | 17 | 0 | 0 | 17 | 0 | 0 |
| Info | 22V1 | T | THR | 1u8k_B | VH | 8 | 8 | 0 | 0 | 8 | 0 | 0 |
| Info | 23V1 | C | CYS | 1u8k_B | VH | 10 | 10 | 0 | 0 | 10 | 0 | 0 |
| Info | 39V1 | V | VAL | 1u8k_B | VH | 2 | 2 | 1 | 0 | 1 | 0 | 0 |
| Info | 43V1 | R | ARG | 1u8k_B | VH | 2 | 2 | 1 | 0 | 1 | 0 | 0 |
| Info | 51V1 | E | GLU | 1u8k_B | VH | 2 | 2 | 1 | 0 | 1 | 0 | 0 |
| Info | 52V1 | W | TRP | 1u8k_B | VH | 11 | 11 | 3 | 0 | 8 | 0 | 0 |
| Info | 53V1 | L | LEU | 1u8k_B | VH | 15 | 15 | 1 | 1 | 14 | 0 | 0 |
| Info | 54V1 | A | ALA | 1u8k_B | VH | 18 | 18 | 4 | 2 | 14 | 0 | 0 |
| Info | 55V1 | I | ILE | 1u8k_B | VH | 2 | 2 | 1 | 0 | 1 | 0 | 0 |
| Info | 78V1 | I | ILE | 1u8k_B | VH | 5 | 5 | 0 | 0 | 5 | 0 | 0 |
| Info | 87V1 | V | VAL | 1u8k_B | VH | 11 | 11 | 1 | 0 | 10 | 0 | 0 |
| Info | 88V1 | V | VAL | 1u8k_B | VH | 6 | 6 | 2 | 0 | 4 | 0 | 0 |
| Info | 89V1 | L | LEU | 1u8k_B | VH | 33 | 33 | 1 | 0 | 32 | 0 | 0 |
| Info | 102V1 | Y | TYR | 1u8k_B | VH | 5 | 5 | 0 | 0 | 5 | 0 | 0 |
| Info | 103V1 | F | PHE | 1u8k_B | VH | 18 | 18 | 2 | 0 | 16 | 0 | 0 |
| Info | 104V1 | C | CYS | 1u8k_B | VH | 26 | 26 | 0 | 0 | 26 | 0 | 0 |
| Info | 105V1 | A | ALA | 1u8k_B | VH | 1 | 1 | 1 | 0 | 0 | 0 | 0 |

| | |
|-------------|--|
| Tot | Total number of atomic pair contacts |
| NCo | Number of non covalent atomic |
| Pol | Number of polar atomic pair contacts |
| HB | Number of hydrogen bonds |
| NPol | Number of non polar atomic pair contacts |
| Cov | Number of covalent links (other than chain covalent links) |
| SS | Number of disulfide bridges |

IMGT Collier de Perles

