IMGT® (http://imgt.cines.fr) standardization and tools for the analysis of immunoglobulin and T cell receptor repertoires and 3D structures

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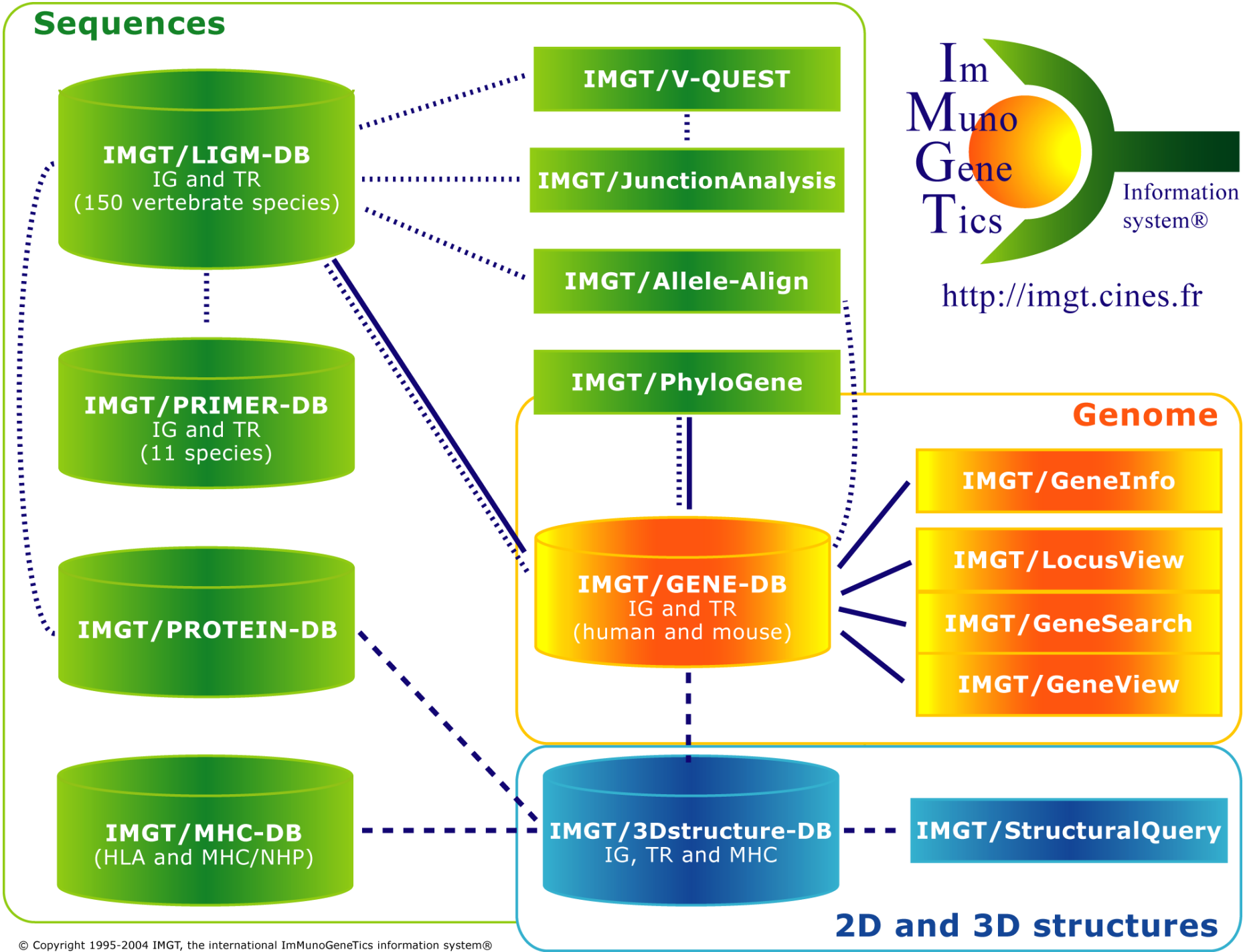
Université Montpellier, UPR CNRS 1142, IGH
Institut Universitaire de France

Tutorial ESF MARIE NETWORK on:
« BIOINFORMATICS AND AUTOIMMUNITY », October 11, 2006, Budapest, Hungary
Organizers: Vladimir Brusic, Marie-Paule Lefranc and Paolo Riccio



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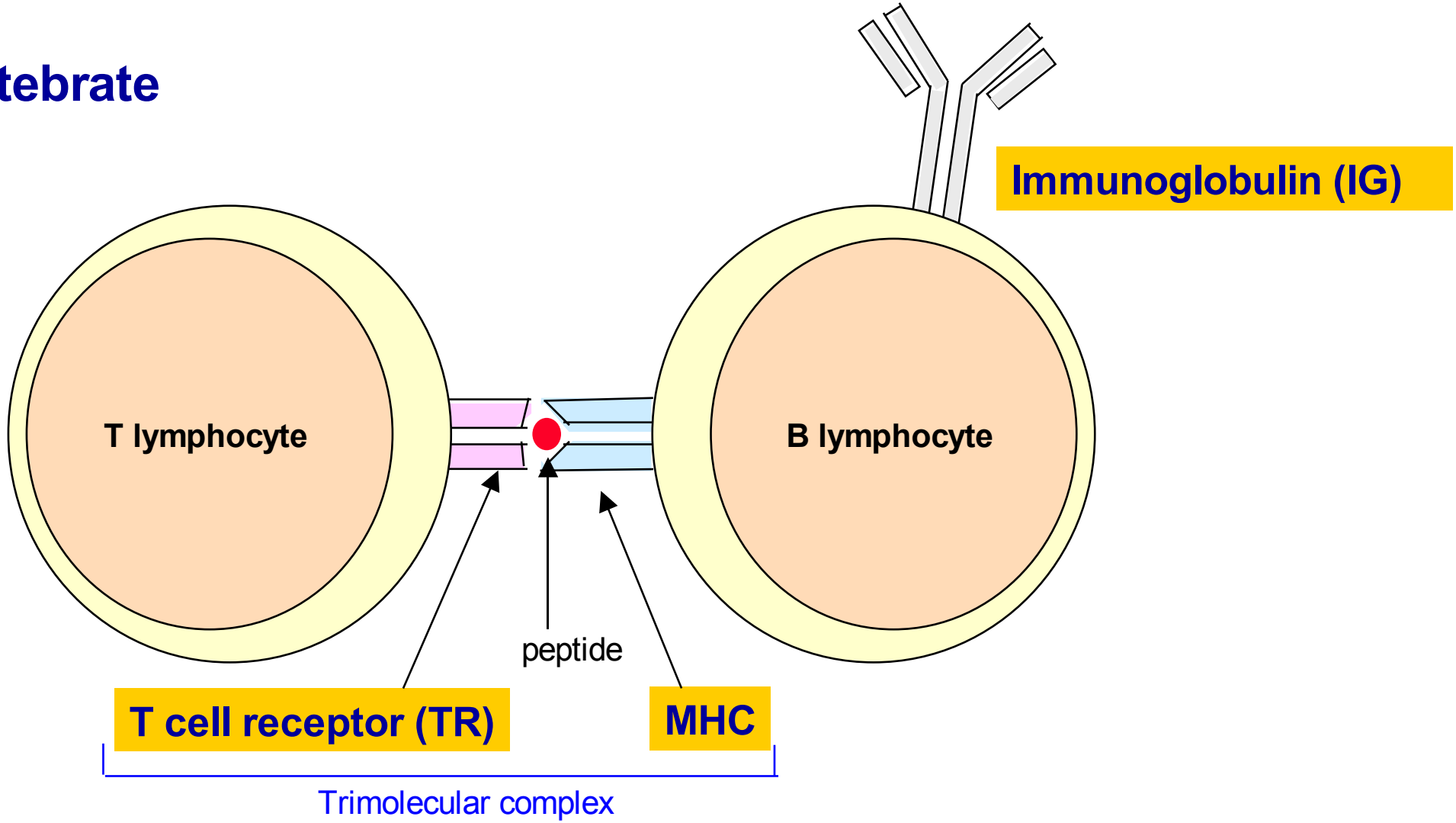
IMGT® domain: the adaptive immune response

http://imgt.cines.fr

Vertebrates



cDNA (in databases: mRNA!)

http://imgt.cines.fr

```
……..gagga ttcaccatgg aactggggct ccgctgggtt ttccttgttg ctttttaga 120
aggtgtccag tgtgaggtgc aactggtgga gtctggggga ggcctggtca agccgggggg 180
gtccctgaga ctctcctgtg cagcctctgg attaagcttc agtacctatg ccatgaactg 240
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```
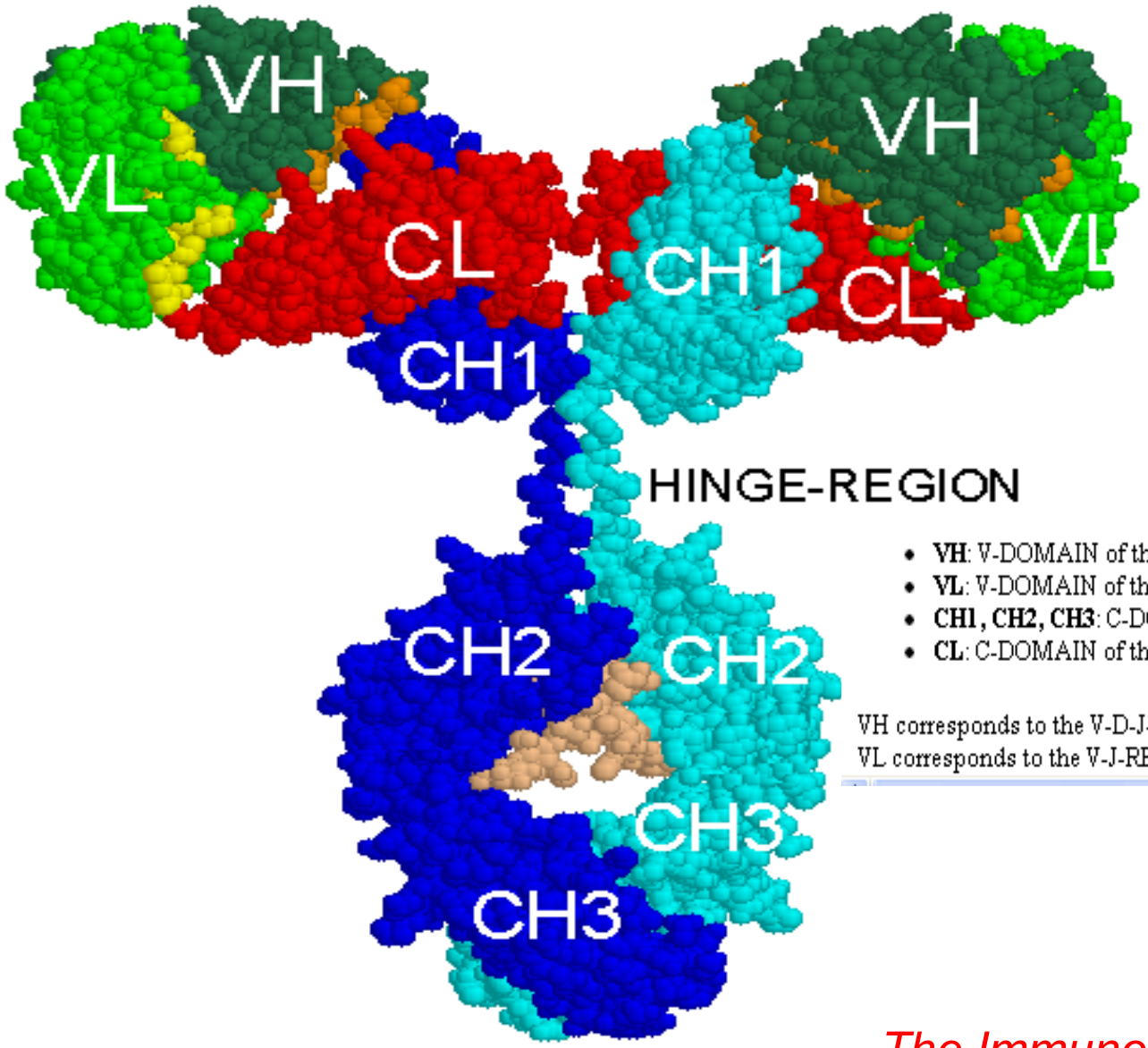

Spacefill 3D representation of an IgG

http://imgt.cines.fr



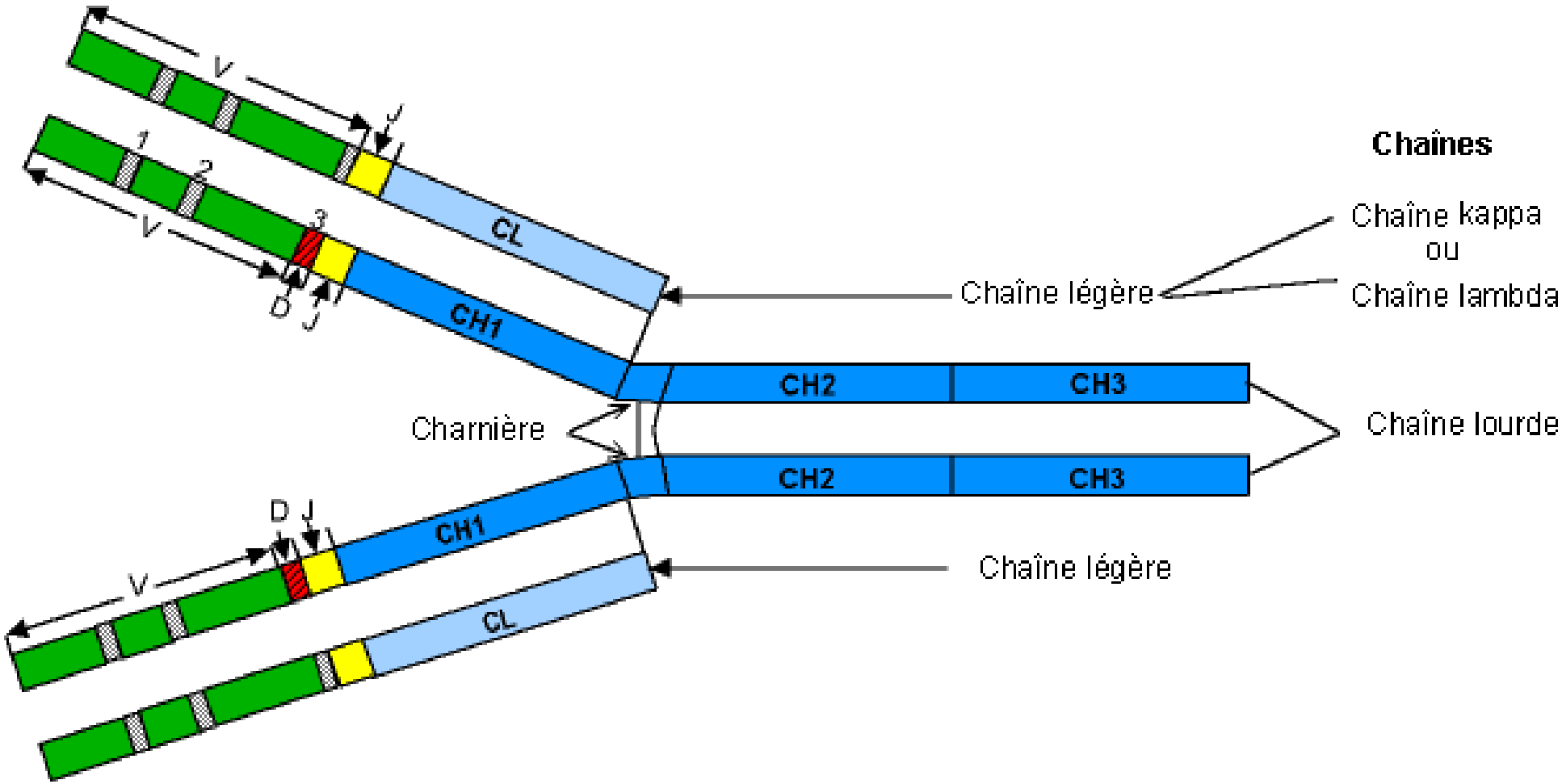
- **VH**: V-DOMAIN of the immunoglobulin heavy chain
- **VL**: V-DOMAIN of the immunoglobulin light chain
- **CH1, CH2, CH3**: C-DOMAIN of the immunoglobulin heavy chain
- **CL**: C-DOMAIN of the immunoglobulin light chain

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.

The Immunoglobulin FactsBook, 2001

Immunoglobulin IgG

http://imgt.cines.fr



cDNA

http://imgt.cines.fr

```
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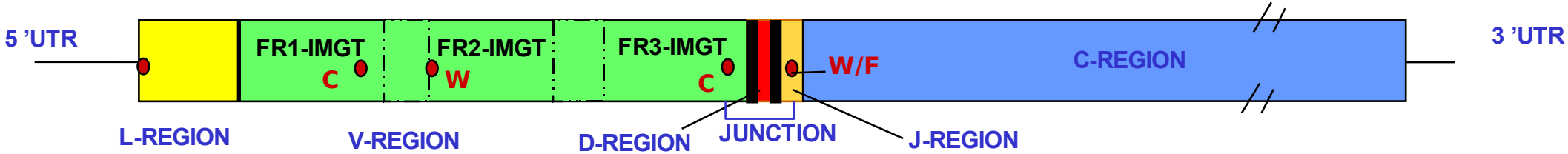
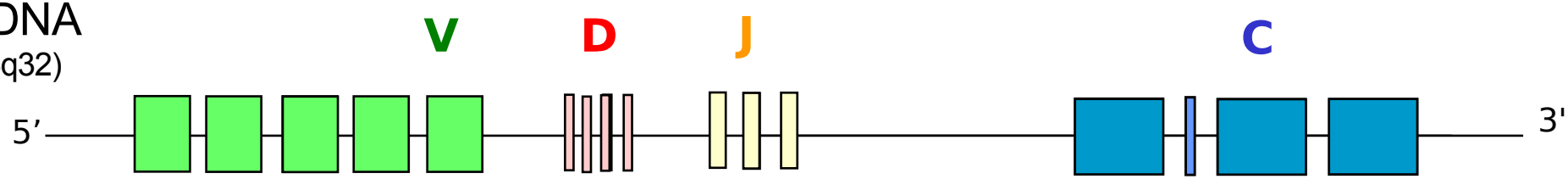


Immunoglobulin (IG) synthesis

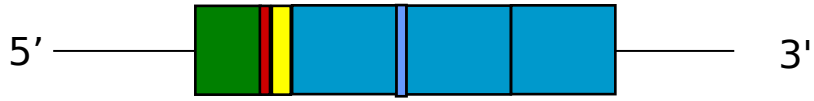
http://imgt.cines.fr

genomic DNA
(IGH Locus 14q32)

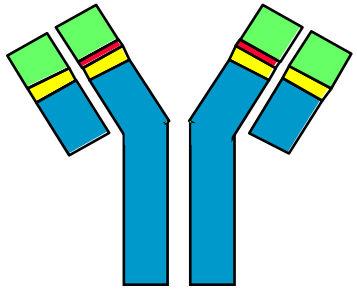


rearranged DNA

mRNA



2 x 10^{12} different IG per individual



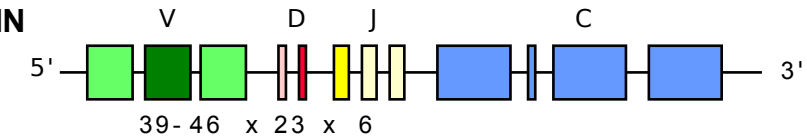
IMGT Repertoire, http://imgt.cines.fr

Immunoglobulin (IG) synthesis

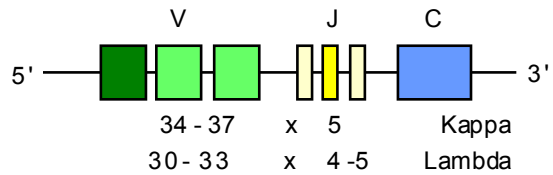
http://imgt.cines.fr

150
FUNCTIONAL IG GENES

HEAVY CHAIN



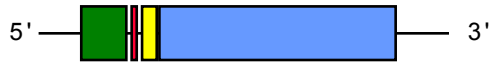
LIGHT CHAIN



6300 **POTENTIAL RECOMBINATIONS**

185 +165 **POTENTIAL RECOMBINATIONS**

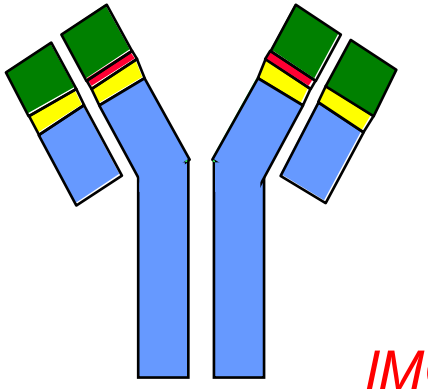
N-DIVERSITY
SOMATIC MUTATIONS
x 1000



ABOUT **6.3×10^6** POSSIBILITIES

ABOUT **3.5×10^5** POSSIBILITIES

2×10^{12}
DIFFERENT ANTIBODIES



IMGT Repertoire, http://imgt.cines.fr

Genomic DNA in germline configuration

http://imgt.cines.fr

V-GENE

```
>X62106.0|HSVI2|Homo sapiens VI-2 gene for immunoglobulin heavy chain
tgagagctcc gttcctcacc atggactgga cctggaggat cctcttcttg gtggcagcag      60
ccacaggtaa gaggctccct agtcccagtg atgagaaaga gattgagtcc agtccaggga     120
gatctcatcc acttctgtgt tctctccaca ggagcccact cccaggtgca gctggtgcag     180
tctggggctg aggtgaagaa gcctggggcc tcagtgaagg tctcctgcaa ggcttctgga     240
tacaccttca ccggctacta tatgcactgg gtgcgacagg cccctggaca agggcttgag     300
tggatgggat ggatcaaccc taacagtggt ggcacaaact atgcacagaa gtttcagggc     360
agggtcacca tgaccaggga cacgtccatc agcacagcct acatgggagct gaggagggctg   420
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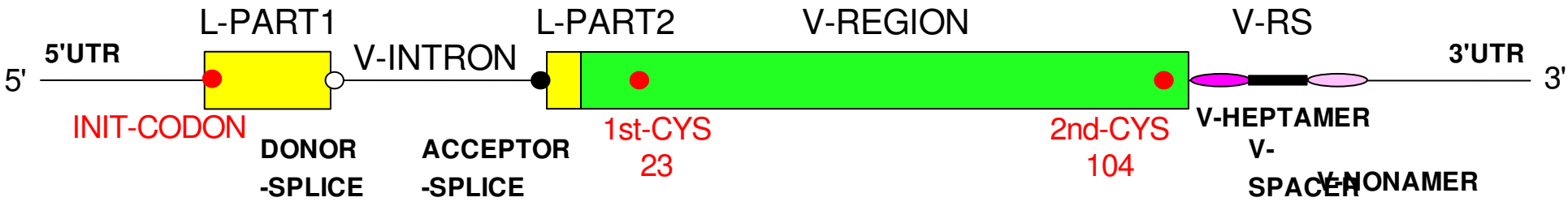
tgaaa
acccacatcc

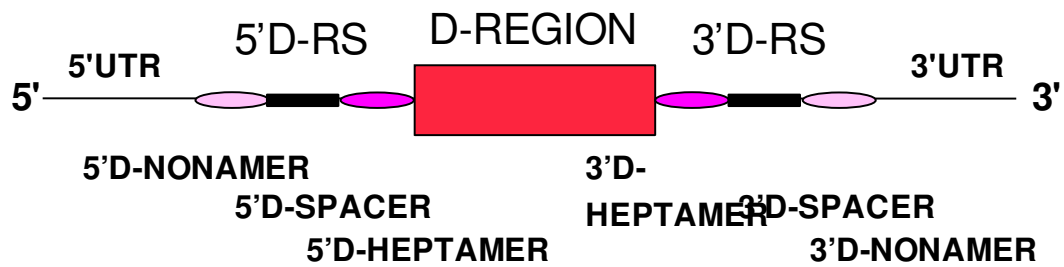


Genomic DNA in germline configuration

http://imgt.cines.fr

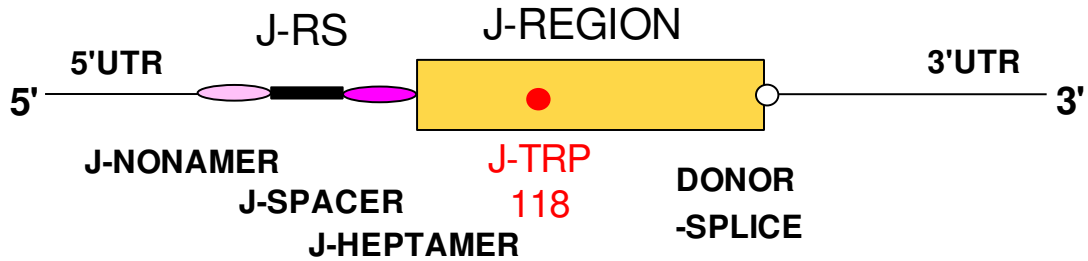
D-GENE

ggtttttggc tgagctgaga accactgtgc taactgggga cacagtcatt
ggcagctcta caaaaacca



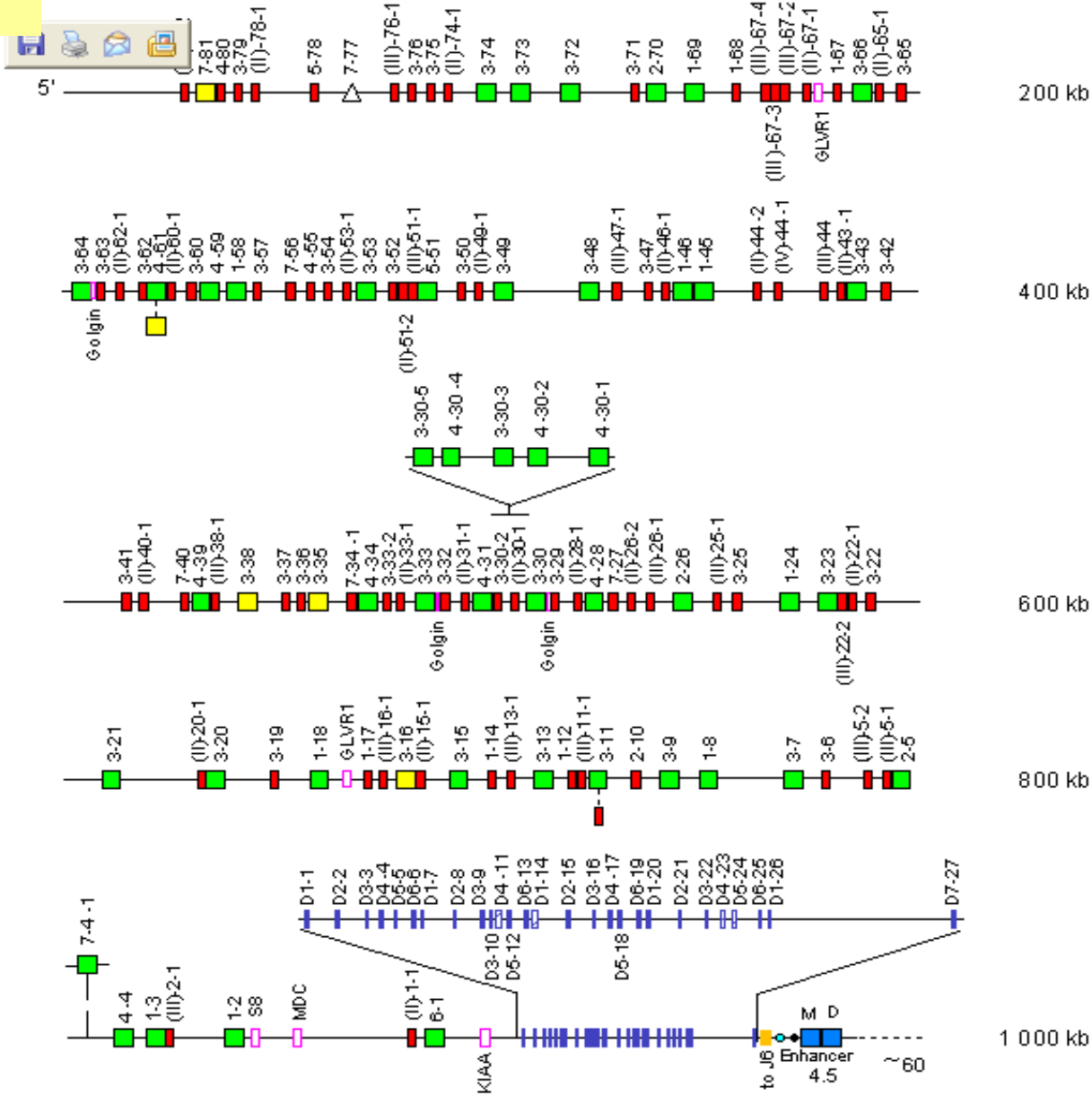
J-GENE

ggtttct gtgcccctgg ctcagggctg actcaccgtg gctgaatact
cccagcactg gggccagggc accctggtca ccgtctcctc ag



Human IGH locus

Chromosome 14q32.33



http://imgt.cines.fr

IMGT Marie-Paule page: IMGT repertoire - Netscape

Fichier Edition Afficher Aller Communicator Aide

Locus representation: Human IGL

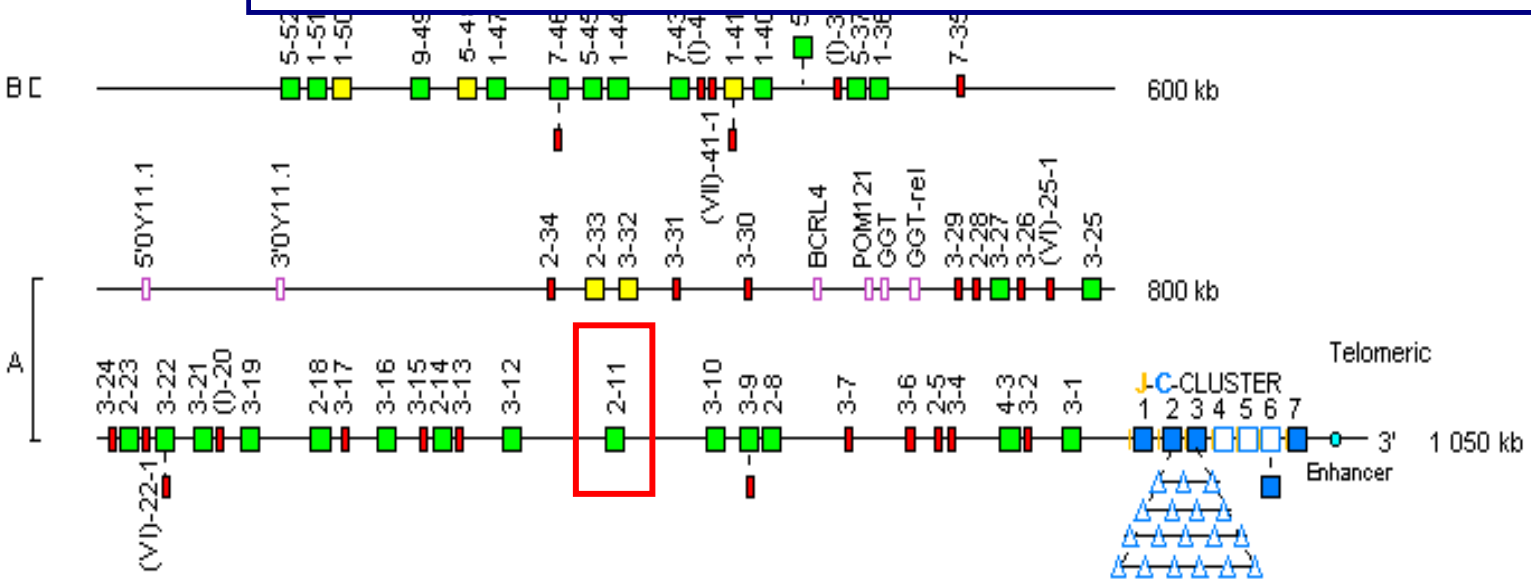
Human IGL 22q11.2

WELCOME !
to IMGT/GENE-DB

THE
INTERNATIONAL
IMMUNOGENETICS
INFORMATION SYSTEM®

ImMunoGeneTics
Information system®

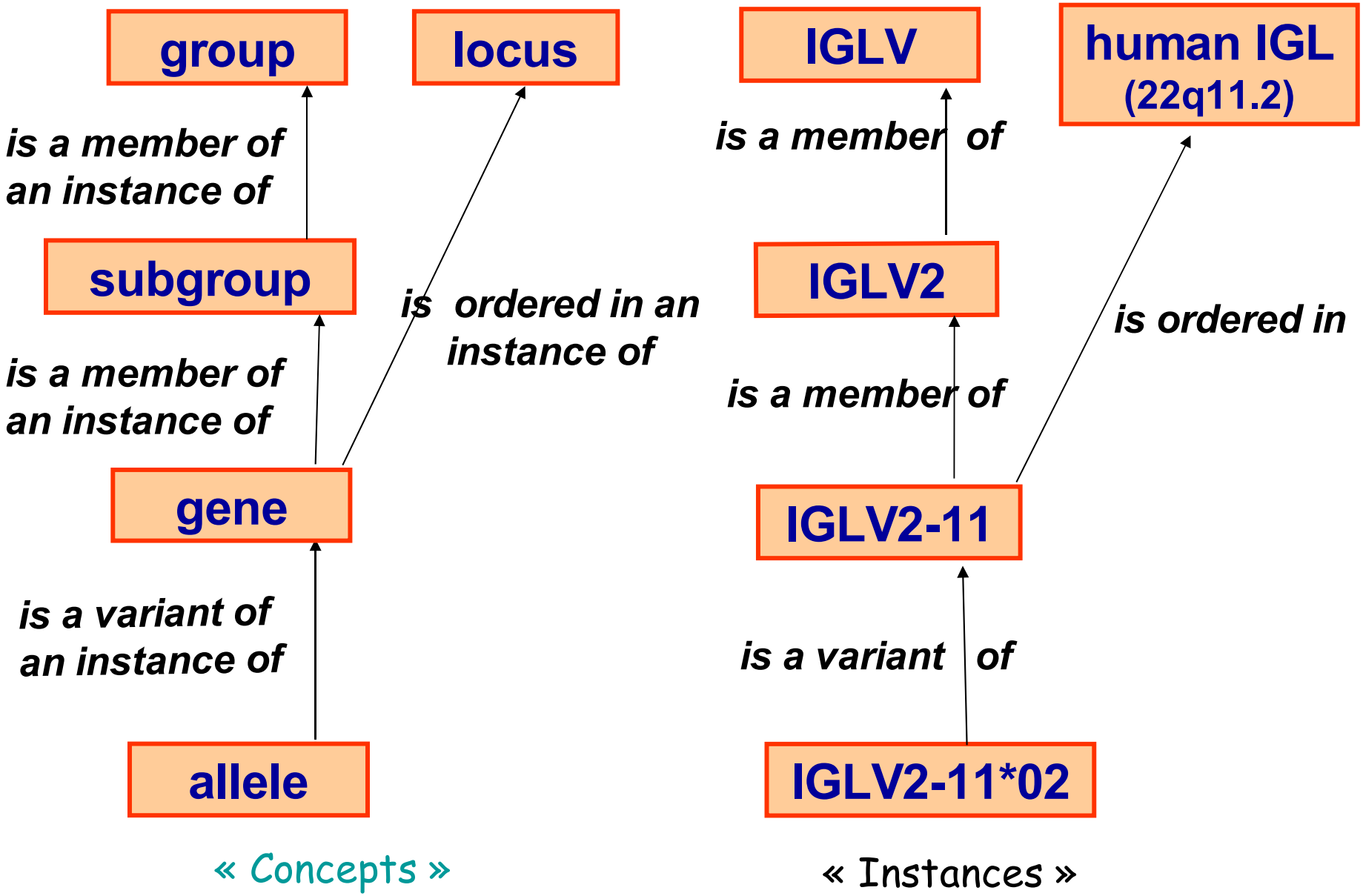
http://imgt.cines.fr



Giudicelli V. et al. Nucleic Acids Res. 33, D256-D261

"CLASSIFICATION" concept

http://imgt.cines.fr



1999
Entry of the 630 human IG and TR genes at NCBI

Cross-references between Entrez Gene and IMGT/GENE-DB

Gene - Mozilla Firefox

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NCBI Entrez Gene

My NCBI [Sign In] [Register]

All Databases PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books OMIM

Search Gene for Go Clear

Limits Preview/Index History Clipboard Details

Display Full Report Show 5 Send to

All: 1 Current Only: 1 Genes Genomes: 1 SNP GeneView: 1

1: **TRDV1 T cell receptor delta variable 1** [*Homo sapiens*]

GeneID: 28518 Primary source: HGNC:12262 updated 29-Aug-2006

Entrez Gene Home

Table Of Contents
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Genomic regions, transcripts...
Genomic context
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Related Sequences
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Links
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Nucleotide
Full text in PMC
Protein
PubMed
SNP
SNP: Genotype
SNP: GeneView
Taxonomy
AceView
Ensembl
Evidence Viewer
GDB
HGNC
IMGT/GENE-DB
ModelMaker
UCSC
UniGene
LinkOut

Entrez Gene Info
Feedback
Subscriptions

Summary

Official Symbol: TRDV1 **and Name**: T cell receptor delta variable 1 **provided by** HUGO Gene Nomenclature Committee
See related: IMGT/GENE-DB:TRDV1
Gene type: other
Gene name: TRDV1
Gene description: T cell receptor delta variable 1
RefSeq status: Reviewed
Organism: *Homo sapiens*
Lineage: *Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo*
Gene aliases: hDV101S1

Genomic regions, transcripts, and products

RefSeq below

NC_000014.7

[21634167 ▶ [21634736 ▶
5' 3'

Genomic context

See TRDV1 in MapViewer

chromosome: 14; **Location**: 14q11

[21159897 ▶ [22090915 ▶
TRA@
TRAV23DV6
TRAV22
TRDV1
TRAV24
TRAV25

Bibliography

Gene References into Function (GeneRIF): Submit

PubMed links

NCBI Reference Sequences (RefSeq)

Reference NG_001332

Related Sequences

Nucleotide		Protein
Genomic	AE000660 (100359..100928)	None
Genomic	M22198	AAA61104
mRNA	AF366516	AAK62930
mRNA	U91153	AAB62513

Terminé

IMGT/V-QUEST

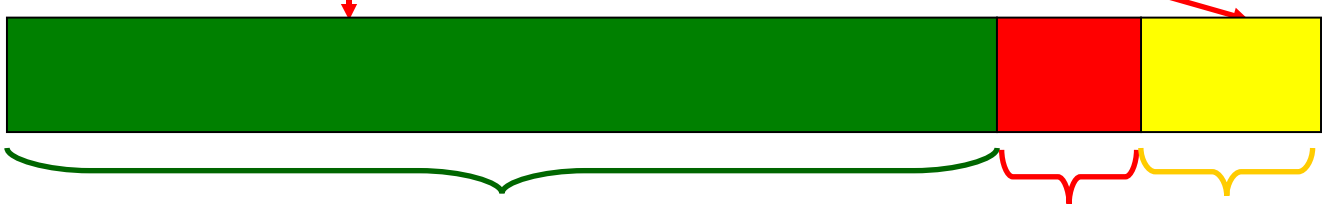
http://imgt.cines.fr

Alignment for V-GENE

```
AF402940                 score GTGCAGCTGCTCGAGCAGTCTGGGGCT___GAGGTGAGCAAGCCTGGGGCCTCAGTAAAGGTTTCCTGCA
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 CTTCACGGGGCGGGACGCTTTGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
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
```



Giudicelli et al. Nucleic Acids Res. 32, W435-W440 (2004)

IMGT/V-QUEST - Mozilla Firefox

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http://imgt.cines.fr/cgi-bin/IMGTdnap.jv?livret=0&Option=humanIg

OK

http://imgt.cines.fr

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 :

```
gaggtgcagctgttggagtcgggggggaggcttggtacagcctgggggggtccctgagactc
tcctgtgcagcctctggattcacctttagcagctttgccatgagctgggtccgccaggct
cctgggaaggggctggactgggtctcagaaattagtggtagtggcggtaccacatattac
gcaggctccgtgaagggccggttcaccatctccagagacaactccaagaatacgctgttt
ctgcaaatgaatagcctgacagccgaagacacggccgtatattactgtgcgaagaggttt
```

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

Parcourir...

Start Clear the form

Giudicelli et al. Nucleic Acids Res. 32, W435-W440 (2004)

IMGT/V-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 GAGGTGCAGCTGTTGGAGTCGGGGGGA...GGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTTTGCC....
M99660   IGHV3-23*01            1281 --------------------T------...------------------------------------------------------------A----....
J00236   IGHV3-23*02            1263 --------------------T------...------------------------------------------------------------A----....
U29481   IGHV3-23*03            1209 --------------------T------...------------------------------------------------------------A----....
Z12358   IGHV3-48*03            1128 ------------G-------T------...-----------------A--------------------------------------C--T--T-A--AA....
M99675   IGHV3-48*01            1128 ------------G-------T------...-------------------------------------------------------C--T----A-AG-....
```

Alignment for D-GENE

```
input                          score GTTTTGGAGTGGTT
X93618 IGHD3-3*02                 61 T-------------ATTATACC
X13972 IGHD3-3*01                 61 T-------------ATTATACC
X97051 IGHD6-19*01                34 --A-A-C-----C-GGTAC
X13972 IGHD3-9*01                 34 TA---T--C-----ATTATAAC
J00234 IGHD2-15*01                34 A-A---T------GGTAGCTGCTACTCC
```

Alignment for J-GENE

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

Applet input [1}

Giudicelli et al. Nucleic Acids Res. 32, W435-W440 (2004)

IMGT/V-QUEST

http://imgt.cines.fr

IMGT/V-QUEST - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

Alignment for J-GENE

Closest J-GENEs

		Score	Identity	
J00242	IGKJ4*01	152	94.11%	(32/34 nt)
AF103571	IGKJ4*02	143	91.17%	(31/34 nt)
J00242	IGKJ3*01	107	79.41%	(27/34 nt)
Z70260	IGKJ2*02	107	79.41%	(27/34 nt)
J00242	IGKJ2*01	107	79.41%	(27/34 nt)

Score and nucleotide identity

Alignment

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

Terminé

Giudicelli et al. Nucleic Acids Res. 32, W435-W440 (2004)

IMGT/V-QUEST - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

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

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 --- --- ... --- --- --- --- --- --- --- ---

                          ------------------------------>
                                                                  ___________________ CDR1 - IMGT ________
                              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 --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 ---
```

Applet input [1}

http://imgt.cines.fr

Giudicelli et al. Nucleic Acids Res. 32, W435-W440 (2004)

IMGT/V-QUEST - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

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

Translation

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

                          1               5                   10                  15
                           E   V   Q   L   L   E   S   G   G       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 --- --- ... --- --- --- --- --- --- --- ---

                          ------------------------------>
                                                          ___________________ CDR1 - IMGT ________
                              20                  25                  30                  35
                           L   R   L   S   C   A   A   S   G   F   T   F   S   S   F   A
input                     CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTT AGC AGC TTT GCC ... ...
                                                                                       Y
M99660 IGHV3-23*01        --- --- --- --- --- --- --- --- --- --- --- --- --- --- -A- --- ... ...

                                  <-------------------     F   R   2   -   I   M   G   T --------
_________
                                      40                  45                  50
                                   M   S   W   V   R   Q   A   P   G   K   G   L   D   W   V   S
input                     ... ... ATG AGC TGG GTC CGC CAG GCT CCT GGG AAG GGG CTG GAC TGG GTC TCA
                                                                                       E
M99660 IGHV3-23*01        ... ... --- --- --- --- --- --- --- --A --- --- --- --- --G --- --- ---

                          -->                                     <---------------------------
                              _____________ CDR2 - IMGT _______________
                          55                  60                  65                  70
                           E   I   S   G   S   G   G   T   T           Y   Y   A   G   S   V   K
input                     GAA ATT AGT GGT AGT GGC GGT ACC ACA ... ... TAT TAC GCA GGC TCC GTG AAG
                           A                           S                           D
M99660 IGHV3-23*01        -CT --- --- --- --- --T --- -G- --- ... ... --C --- --- -A- --- --- ---
```

Applet input [1}

Giudicelli et al. Nucleic Acids Res. 32, W435-W440 (2004)

IMGT/V-QUEST

http://imgt.cines.fr

IMGT/V-QUEST - Mozilla Firefox

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Case of complementary reverse sequences

Sequence number 1: test

Complementary reverse sequence compared with the human IG set from the IMGT reference directory

```
>test (complementary reverse)
caggtgcagctggtgcagtctgggggaggcgtagtccagcctgggaggtccttgagactc
tcctgtgcagagggcggattcactttcagttcctattctatgcactgggtccgccaggcg
ccaggcaagggcctggaatgggtggcggttatgtggtttgatggaactgaaaaatactct
gcagagtccgtgaagggccgattcaccatctccagagacaattccaagaacacattgttt
ttgcaaatgaacagcctgagagccgacgacacggctgtgtattactgtgcgagagagcct
gattggttattatgggggacaggggtgctctggacgtctggggccaagggaccacggtc
accgtctcctcagacatcgtgatgacccagtctccttccaccctgtctgcatctgtagga
gacagagtcaccatcacttgccgggccagtcagggcattagtagctggttggcctggtat
cagcagaaaccagggaaagcccctaagctcctgatgtatgaggcgtctagtttagaaagt
ggggtcccatcaaggttcagcggcagtggatccgggacagaattcactctcaccatcagc
agcctgcagcctgatgattttgcagcttattactgccaacattataacacttacccgtac
acttttggccagggaaccaagctggagataaaacgt
```

Terminé

Giudicelli et al. Nucleic Acids Res. 32, W435-W440 (2004)

IMGT/V-QUEST

IMGT/V-QUEST - Mozilla Firefox

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for using IMGT/V-QUEST

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Links to individual results

Number of analysed sequences: 50

AJ230234 AJ230235 AJ230236 AJ230237 AJ230238 AJ230239 AJ230240 AJ230241 AJ230242 AJ230243 AJ230244
AJ230245 AJ230246 AJ230247 AJ230248 AJ230249 AJ230250 AJ230251 AJ230252 AJ230253 AJ230254 AJ230255
AJ230257 AJ230258 AJ230259 AJ230260 AJ230261 AJ230262 AJ230263 AJ230264 AJ230265 AJ230266 AJ230267
AJ230268 AJ230269 AJ230270 AJ230271 AJ230272 AJ230273 AJ230274 AJ230275 AJ230276 AJ230278 AJ230279
AJ230280 AJ230281 AJ230282 AJ230283 AJ230284 AJ230285

This release of IMGT/V-QUEST uses IMGT/JunctionAnalysis for the analysis of the JUNCTION

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

Sequence number 1: AJ230234

Terminé

IMGT/V-QUEST

http://imgt.cines.fr

IMGT/V-QUEST - Mozilla Firefox

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IMGT/V-QUEST | Inversion-complémentation d'une sequenc...

V-REGION mutation statistics

Nucleotides

IMGT Label		V-REGION	FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT
Total nucleotides with gaps		333 (335)	78	36	51	30	117	21 (23)
Mutations	Total	36 (38)	11	3	9	3	9	1 (3)
	Silent	9 (11)	2	0	2	0	5	0 (2)
	Non silent	27	9	3	7	3	4	1
Transitions	a>g	3 (4)	0	0	2	0	1	0 (1)
	g>a	6	3	0	2	0	1	0
	c>t	9 (10)	2	1	2	2	2	0 (1)
	t>c	1	1	0	0	0	0	0
Transversions	a>c	4	1	1	0	0	1	1
	c>a	1	0	1	0	0	0	0
	a>t	2	0	0	2	0	0	0
	t>a	1	0	0	0	0	1	0
	g>c	6	2	0	0	1	3	0
	c>g	1	1	0	0	0	0	0
	g>t	1	0	0	1	0	0	0
	t>g	1	1	0	0	0	0	0

For CDR3-IMGT (and the V-REGION), the number of mutations is shown by comparison with the closest germline V-REGION, up to the 3' end deduced from the junction analysis, and between parentheses, up the 3' end of the complete germline V-REGION.

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

http://imgt.cines.fr

'Volume' classes		'Hydropathy' classes										
	in Å^3	Hydrophobic				Neutral				Hydrophilic		
Very large	189-228	F			W		Y					
Large	162-174	I	L		M					K	R	
Medium	138-154	V							H		E	Q
Small	108-117				C	P	T				D	N
Very small	60-90	A				G	S					
		Aliphatic			Sulfur		Hydroxyl		Basic		Acidic	Amide
							Uncharged		Charged			Uncharged
		Nonpolar					Polar					

Pommié et al. J. Mol Recognit. ***17****, 17-32, 2004*

IMGT/V-QUEST

http://imgt.cines.fr

V-REGION mutation table

FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT
a2>c, Q1>P (-)	c90>a, S30>R (-)	g132>a	g182>c, S61>T (++)	g197>c, S66>T (++)	a331>c, I111>L (+++)
c4>g, L2>V (++)	a91>c, S31>R (-)	c133>t, Q45>L (-)	c183>t, S61>T (++)	a200>g, K67>R (+++)	c334>t
t6>c, L2>V (++)	c93>t, S31>R (-)	a134>t, Q45>L (-)	c184>t, H62>Y (+)	c213>t	a335>g
g7>a, V3>M (+)		c136>t, P46>S (+)		a231>c	
t15>g		a140>g, E47>G (-)		g239>c, S80>T (++)	
g21>a		g153>t		g253>c, A85>P (-)	
g31>a, A11>I (++)		a155>t, Y52>F (+)		g291>a	
c32>t, A11>I (++)		a164>g, K55>R (+++)		t300>a	
c33>t, A11>I (++)		g165>a, K55>R (+++)		c303>t	
g60>c, K20>N (+)					
g77>c, S26>T (++)					

Immunoglobulin (IG) | T cell receptor (TR)

http://imgt.cines.fr

V-DOMAIN

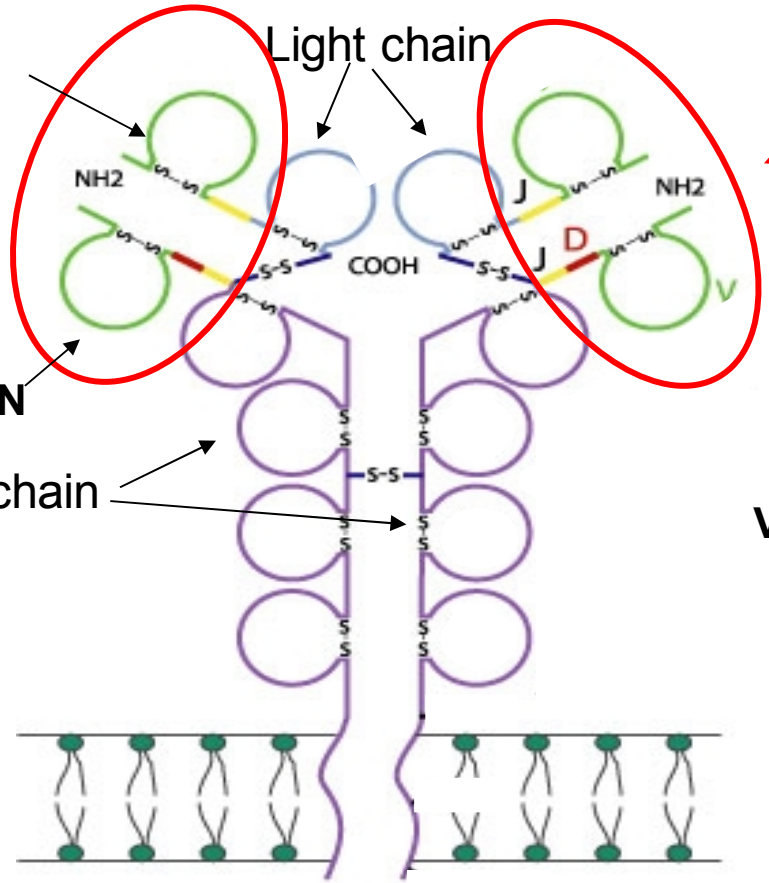
V-J-REGION

Light chain

V-DOMAIN

V-D-J-REGION

Heavy chain



Membrane IgM

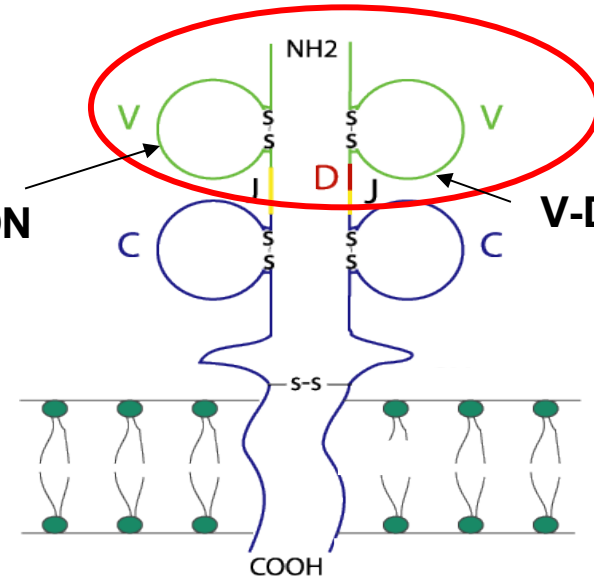
Contribution of the
2 V-DOMAINs
to the antigen binding site

Alpha - Beta

Gamma - Delta

V-J-REGION

V-DJ-REGION



T cell receptor

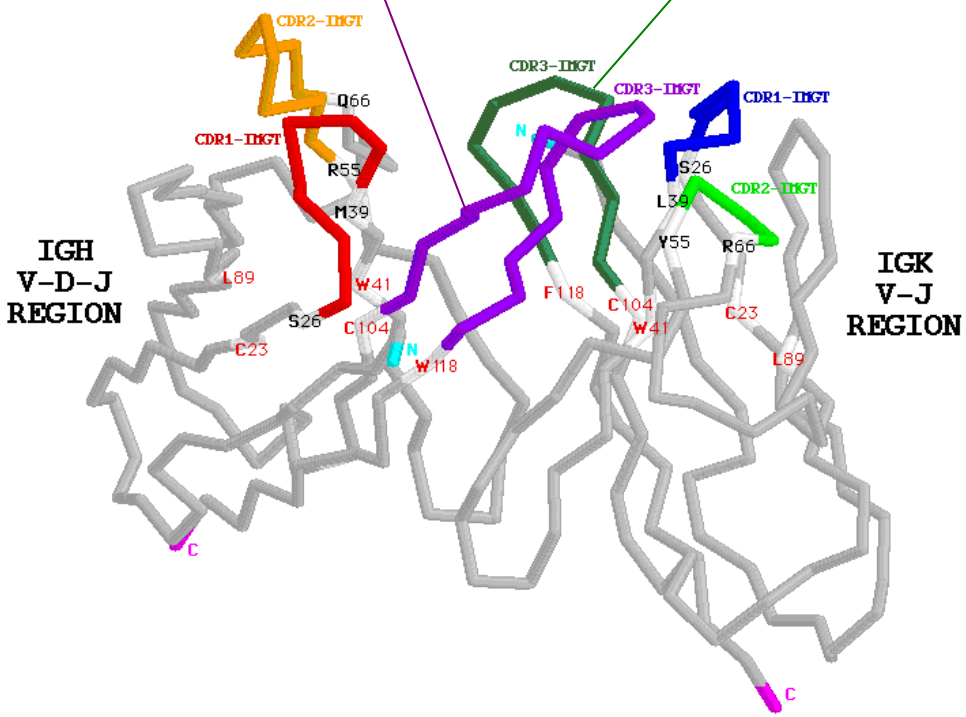
The Immunoglobulin FactsBook, 2001

Junctions of the V-DOMAINs

http://imgt.cines.fr

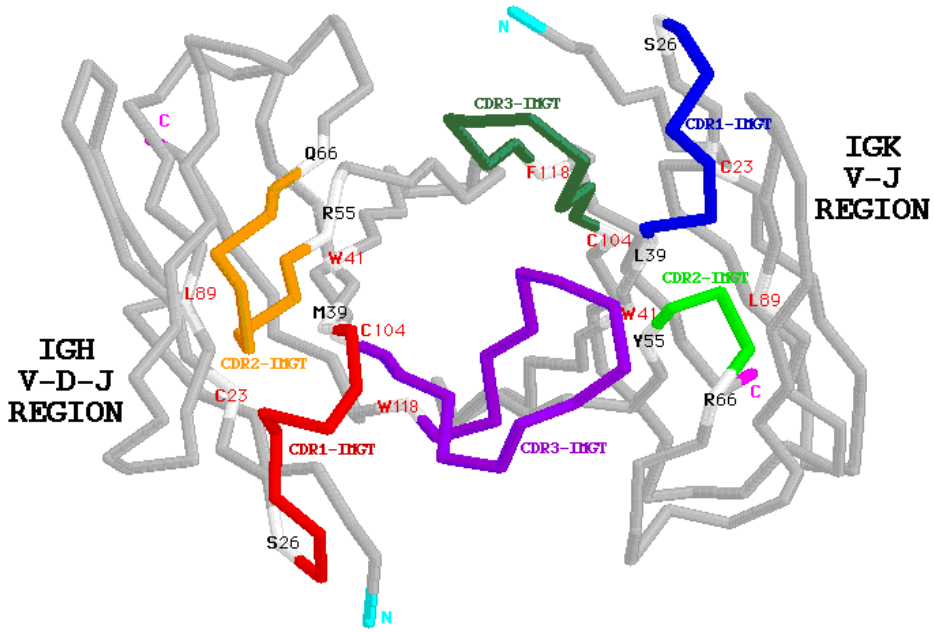
VH V-KAPPA

V-D-J junction V-J junction



Side view

VH V-KAPPA



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

http://imgt.cines.fr

3'V-REGION	N-REGION	D-REGION	N-REGION	5'J-REGION
tgtgcgaaaga	tacc agcatattgtg	gtggtgactgctat tcc	gat acaactggttcg	actcc**tgg**

JUNCTION

	C	**A**	**P**	**Y**	**R**	**G**	**D**	**T**	**Y**	**D**	**Y**	**S**
V	**tgt**	gcg	cca	tac	cgg	ggt	gac	act	tat	gat	tac	tcc tgg

IMGT/JunctionAnalysis

http://imgt.cines.fr

IMGT/JunctionAnalysis - Mozilla Firefox

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IMGT/JunctionAnalysis Results

Locus IGH
Species Homo sapiens
IMGTrepertoire link Locus representation

Maximum number of mutations :
V-REGION : 2; D-REGION : 4; J-REGION : 2
Deletion criterium : Using patterns
Best D gene choice for a same score : Less mutations

Description of the JUNCTIONs

Click on mutated (underscored) nucleotid to see the original one c

Addition

Addition

Mutation

Délétion

Délétion

Délétion

	Input	V name	V-REGION	P	N1	D-REGION	N2	P	J-REGION	J name	D name	Vmut	Dmut	Jmut	Ngc
#1	Z70256	IGHV2-26*01	tgtgtacg.....		tgttgt	.....gcagcgcctggtac	ccaaatatc		...actttgaccactgg	IGHJ4*02	IGHD6-13*01	1	2	1	5/15
#2	Z70257	IGHV3-7*02	tgtgcgag		ggatgg	.....cagctcttatgcc	cgccc		ctactggtacttcgatctctgg	IGHJ2*01	IGHD2-2*01	0	2	0	9/11
#3	Z70606	IGHV4-31*03			c	.gactacg.....	cact		..atgcttttgatgtctgg	IGHJ3*01	IGHD4-17*01	0	0	0	3/5
#4	Z70608	IGHV4-39*05			cagagta	.....acgatttttggagtggttatt.....	ccccgggggga		..atgcttttgatatctgg	IGHJ3*02	IGHD3-3*01	0	0	0	12/17
#5	Z70610	IGHV4-34*09	tgtgcgagag.		tcgggag	.....cgatttttggagtggttatt.....	cccga	ca	tgatgcttttgatatctgg	IGHJ3*02	IGHD3-3*01	0	0	0	9/12
#6	Z70611	IGHV4-59*01	tgtgcgaga..		ca	.....tggtaactataa.	tgccggcgttg		.. actggttcgacccctgg	IGHJ5*02	IGHD3-9*01	0	2	0	9/13
#7	Z70613	IGHV4-59*01				ctggtac	ctc		gactactgg	IGHJ4*02	IGHD6-13*01	0	0	0	4/6
#8	Z70614	IGHV4-59*01			actataa	acttat.....	ccc		gactactgg	IGHJ4*02	IGHD3-16*01	0	2	0	7/14
#9	Z70615	IGHV4-59*01	tgtgcgagag.		ggctg	gtaaagaggg.....	tttcggaa		.tactggtacttcgatctctgg	IGHJ2*01	IGHD5-24*01	0	2	0	7/13
#10	Z70616	IGHV4-34*01	tgtgcgagag.		cgg	.....gtttggg.....	ttccc		...actggttcgacccctgg	IGHJ5*02	IGHD3-16*01	0	0	0	6/8
#11	Z70620	IGHV4-30-4*01	tgtgcgagaga		cc	.....ggggcgggatggtt.....	cgg		.gatgcttttgatatctgg	IGHJ3*02	IGHD3-16*01	1	4	0	5/5
#12	Z70621	IGHV4-39*01	tgtgcgagaca		ccacgatttatgg	.....ttcggggagtt.....	tgaccccc		.....ttgactactgg	IGHJ4*02	IGHD3-16*01	0	1	0	12/21
#13	Z70622	IGHV4-39*06	tgtgcgagaga	t	tgccccgctcctgccaaaat	gtattactatggttcgggga.....	tatgtacg		.....tttgactactgg	IGHJ4*03	IGHD3-10*01	0	0	0	15/28

Terminé

IMGT/JunctionAnalysis - Mozilla Firefox

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

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
- ( ) 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 :

Parcourir...

Start Clear the form

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Yousfi Monod et al. Bioinformatics, 20, I379-I385 (2004)

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Analysis of the JUNCTIONs

```
   Input   V name        V-REGION          N1                  D-REGION                N2

#1 M62724  IGHV7-4-1*02 tgtgcgagaga      aga           .tagcaatggctacaa....          aata
#2 Z47269  IGHV1-69*06  tgtgcgagag.  gggggctaagg  ....tcgaatttttggagtggtt........ tcatgggt

   Input                J-REGION    J name       D name Vmut Dmut Jmut    Ngc

#1 M62724     .....tttgactactgg IGHJ4*02 IGHD5-24*01  0    2    0     1/7
#2 Z47269  ...actggttcgacccctgg IGHJ5*02  IGHD3-3*02  0    2    0   13/20
```

Translation of the JUNCTIONs

```
                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   F   F   L   F   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
```

-> IMGT/JunctionAnalysis Search page
-> IMGT/JunctionAnalysis Documentation

Yousfi Monod et al. Bioinformatics, 20, I379-I385 (2004)

IMGT/JunctionAnalysis

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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 ....tcgaatttttggagtggtt........ tcatgggt ...actggttcgacccctgg 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, I379-I385 (2004)

IMGT/JunctionAnalysis - Microsoft Internet Explorer

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Précédente Rechercher Favoris

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

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

IMGT/JunctionAnalysis Search page

Species :

Homo sapiens

Locus :

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

MBP 82-102- specific T cell junctions from MS patients

Sequences

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

```
>AB011247, TRBV28*01, TRBJ2-3*01
tgtgccagcagtagcgggggggacagatacgcagtatttt
>AB011248,TRBV28*01, TRBJ1-1*01
tgtgccagcagtatgggacagggggcttccactgaagctttcttt
>AB011249, TRBV27*01, TRBJ2-1*01
tgt gccagctctg gactaggcaa caatgagcagttcttc
```

Internet

IMGT/JunctionAnalysis - Microsoft Internet Explorer

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

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http://imgt.cines.fr

Analysis of the JUNCTIONs

```
   Input     V name     V-REGION          N1      D-REGION     N2                J-REGION     J name    D name Ngc

#1 AB011247 TRBV28*01 tgtgccagcagt.....     ......agcgggggg.      ...acagatacgcagtatttt TRBJ2-3*01 TRBD2*01 0/0
#2 AB011248 TRBV28*01 tgtgccagcagt..... at    gggacagggggc   ttc   ....cactgaagctttcttt TRBJ1-1*01 TRBD1*01 1/5
#3 AB011249 TRBV27*01 tgtgccagc........ tct .ggactag........ gca .....acaatgagcagttcttc TRBJ2-1*01 TRBD2*01 3/6
```

Translation of the JUNCTIONs

```
                 105     107     109     111     113     115     117            CDR3-IMGT
            104     106     108     110     112     114     116     118  frame  length

             C   A   S   S   S   G   G           T   D   T   Q   Y   F
#1 AB011247 tgt gcc agc agt agc ggg ggg         aca gat acg cag tat ttt    +      11
             C   A   S   S   M   G   Q   G   A   S   T   E   A   F   F
#2 AB011248 tgt gcc agc agt atg gga cag ggg gct tcc act gaa gct ttc ttt    +      13
             C   A   S   S   G   L   G           N   N   E   Q   F   F
#3 AB011249 tgt gcc agc tct gga cta ggc         aac aat gag cag ttc ttc    +      11
```

-> IMGT/JunctionAnalysis Search page
-> IMGT/JunctionAnalysis Documentation

MBP 82-102- specific T cell junctions from MS patients

IMGT Home page | IMGT Repertoire (IG and TR) | IMGT Repertoire (MHC) | IMGT Repertoire (RPI) | IMGT Index | IMGT Scientific chart | IMGT Education

Software material and data coming from IMGT server may be used for academic research only, provided that it is referred to IMGT, and cited as "IMGT, the international ImMunoGeneTics information system® http://imgt.cines.fr (founder and director: Marie-Paule Lefranc, Montpellier, France)." References to cite: Lefranc, M.-P. et al., Nucleic Acids Research, 27, 209-212 (1999) Cover of NAR; Ruiz, M. et al., Nucleic Acids Research, 28, 219-221 (2000); Lefranc, M.-P., Nucleic Acids Research, 29, 207-209 (2001); Lefranc, M.-P., Nucleic Acids Res., 31, 307-310 (2003); Lefranc, M.-P. et al., *In Silico* Biol., 5, 0006 (2004) [Epub], 5, 45-60 (2005); Lefranc, M.-P. et al., Nucleic Acids Res., 33, D593-D597 (2005) Full text.
For any other use please contact Marie-Paule Lefranc lefranc@ligm.igh.cnrs.fr.

IMGT/JunctionAnalysis - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

http://imgt.cines.fr

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
		C	V	R	V	V	Q	R	L	V								P	K	Y	H	F	D	H	W			
#1	Z70256	tgt	gta	cgt	gtt	gtg	cag	cgc	ctg	gta	...	...	...	...	...	...	...	ccc	aaa	tat	cac	ttt	gac	cac	tgg	+	15	2,438.76
		C	A	R	D	G	S	S	Y	A							R	P	Y	W	Y	F	D	L	W			
#2	Z70257	tgt	gcg	agg	gat	ggc	agc	tct	tat	gcc	...	...	...	...	...	...	cgc	ccc	tac	tgg	tac	ttc	gat	ctc	tgg	+	16	2,256.49
		C	A	R	A	T	T	H												Y	A	F	D	V	W			
#3	Z70606	tgt	gcg	aga	gcg	act	acg	cac	...	...	...	...	...	...	...	...	...	...	...	tat	gct	ttt	gat	gtc	tgg	+	11	1,604.77
		C	A	R	V	T	I	F	G	V	V					I	P	R	G	N	A	F	D	I	W			
#4	Z70608	tgt	gcc	aga	gta	acg	att	ttt	gga	gtg	gtt	...	...	...	...	att	ccc	cgg	ggg	aat	gct	ttt	gat	atc	tgg	+	18	2,426.78
		C	A	R	V	G	S	D	F	W	S	G				Y	S	R	H	D	A	F	D	I	W			
#5	Z70610	tgt	gcg	aga	gtc	ggg	agc	gat	ttt	tgg	agt	ggt	...	...	...	tat	tcc	cga	cat	gat	gct	ttt	gat	atc	tgg	+	19	2,539.73
		C	A	R	H	G	N	Y	N	A								G	V	D	W	F	D	P	W			
#6	Z70611	tgt	gcg	aga	cat	ggt	aac	tat	aat	gcc	...	...	...	...	...	...	...	ggc	gtt	gac	tgg	ttc	gac	ccc	tgg	+	15	2,072.21
		C	A	R	A	A	A	G											T	S	L	F	D	Y	W			
#7	Z70613	tgt	gcg	aga	gca	gca	gct	ggt	...	...	...	...	...	...	...	...	...	...	acc	tcc	ctc	ttt	gac	tac	tgg	+	12	1,531.71
		C	A	R	H	Y	N	S	G										T	Y	P	L	D	Y	W			
#8	Z70614	tgt	gcg	aga	cac	tat	aat	tcg	ggg	...	...	...	...	...	...	...	...	...	act	tat	ccc	ctc	gac	tac	tgg	+	13	1,846.01
		C	A	R	G	L	V	K	R	V							S	E	Y	W	Y	F	D	L	W			
#9	Z70615	tgt	gcg	aga	ggg	ctg	gta	aag	agg	gtt	...	...	...	...	...	...	tcg	gaa	tac	tgg	tac	ttc	gat	ctc	tgg	+	16	2,419.75
		C	A	R	A	G	L	G											S	H	W	F	D	P	W			
#10	Z70616	tgt	gcg	aga	gcg	ggt	ttg	ggt	...	...	...	...	...	...	...	...	...	...	tcc	cac	tgg	ttc	gac	ccc	tgg	+	12	1,602.8
		C	A	R	D	R	G	G	M									V	R	D	A	F	D	I	W			
#11	Z70620	tgt	gcg	aga	gac	cgg	ggc	ggg	atg	...	...	...	...	...	...	...	...	gtt	cgg	gat	gct	ttt	gat	atc	tgg	+	14	1,932.17
		C	A	R	H	H	D	L	W	F							G	E	F	D	P	L	D	Y	W			
#12	Z70621	tgt	gcg	aga	cac	cac	gat	tta	tgg	ttc	...	...	...	...	...	...	ggg	gag	ttt	gac	ccc	ctt	gac	tac	tgg	+	16	2,307.53
		C	A	R	D	C	P	A	P	A	K	M	Y	Y	Y	G	S	G	I	C	T	F	D	Y	W			

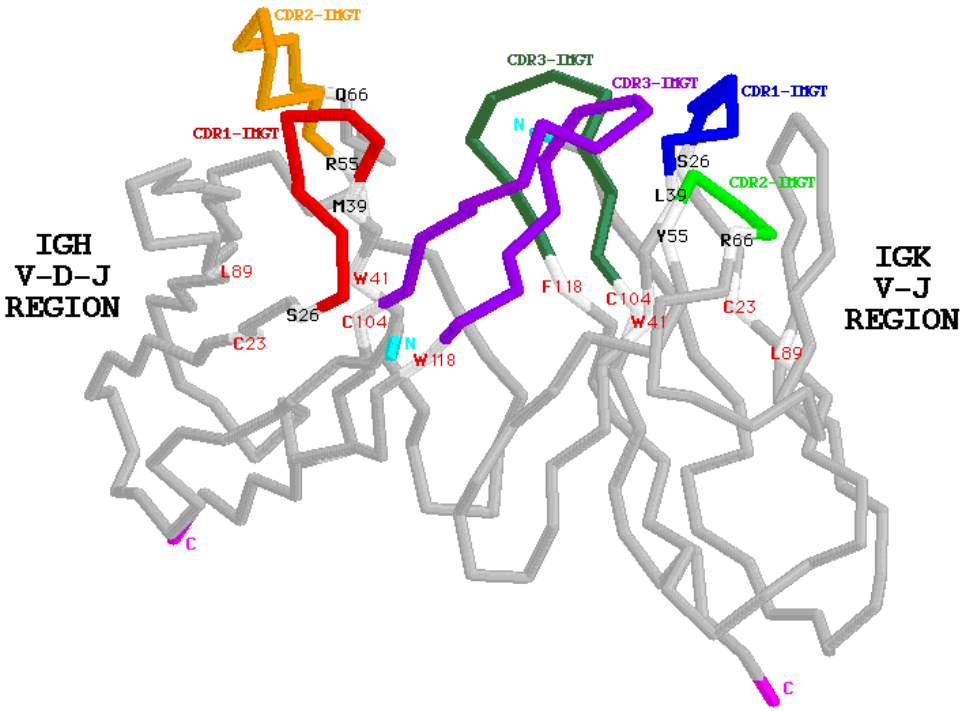
Terminé

*Pommié et al. J. Mol Recognit. **17**, 17-32, 2004*

V-DOMAINs

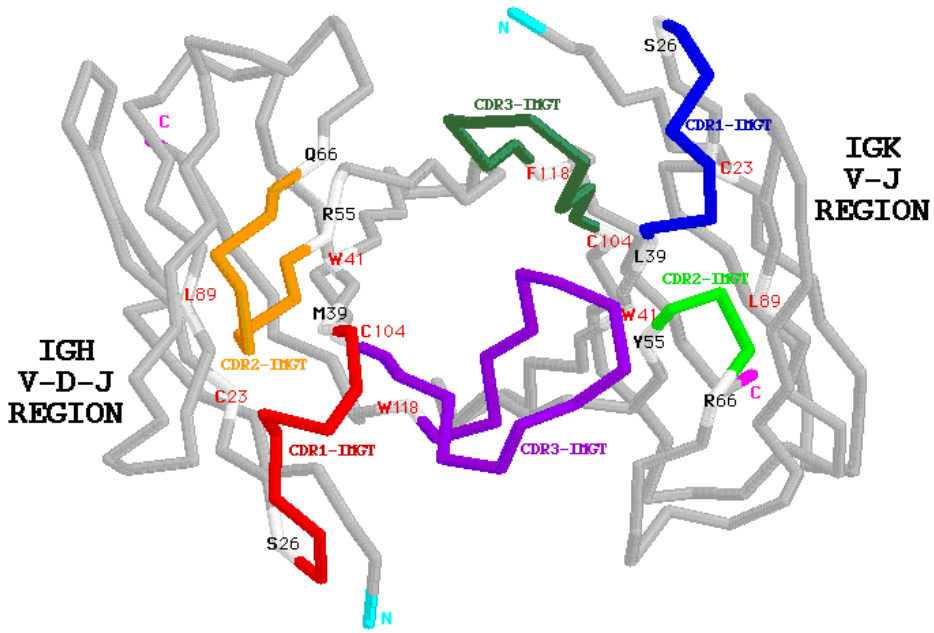
http://imgt.cines.fr

VH V-KAPPA



Side view

VH V-KAPPA



View from above

Mouse(Mus musculus) E5.2Fv

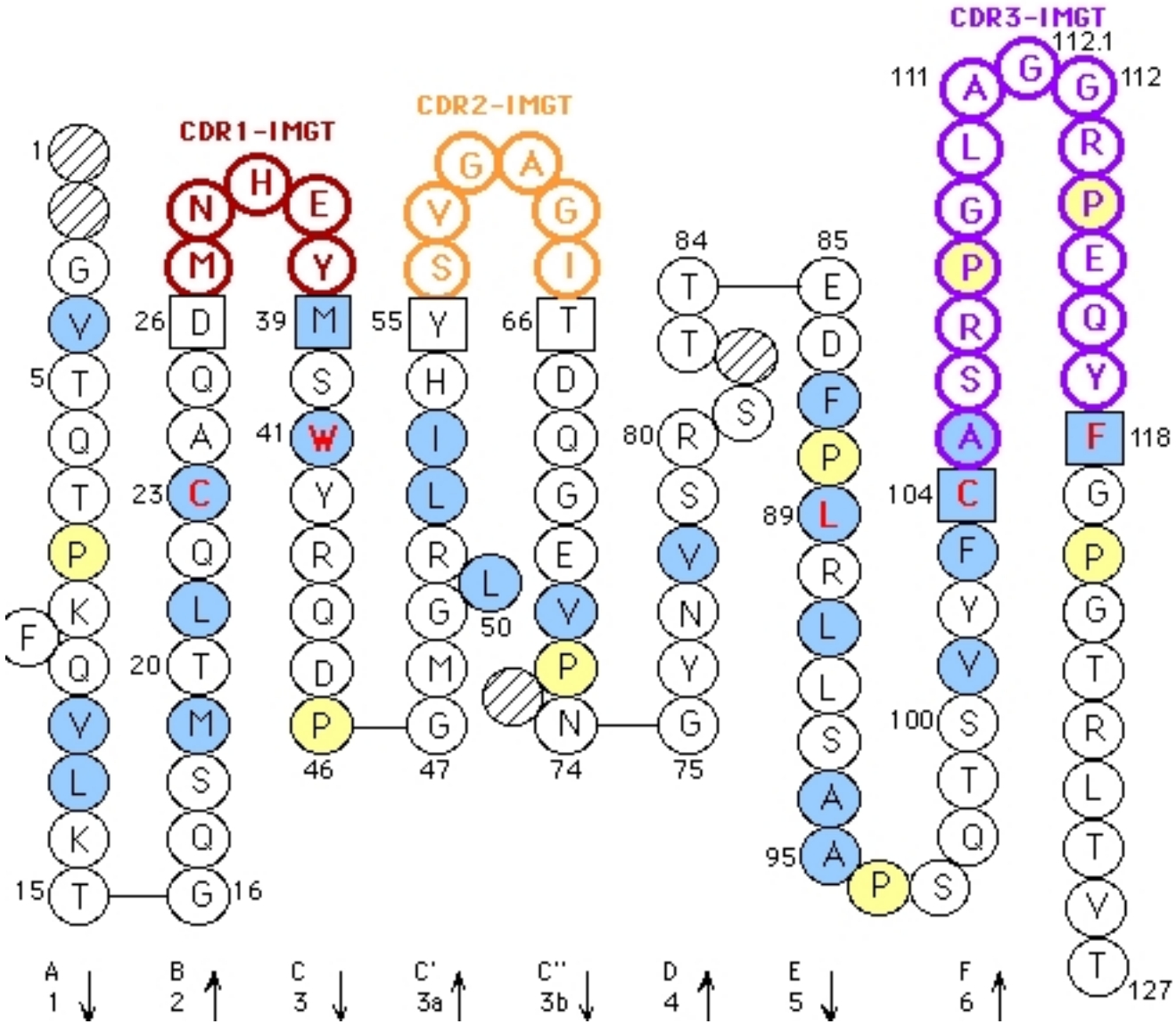
CDR3-IMGT= Complementarity determining region (105-117)

V-J junction (104-118)

V-D-J junction (104-118)

IMGT Collier de Perles

http://imgt.cines.fr



IMGT Repertoire, http://imgt.cines.fr

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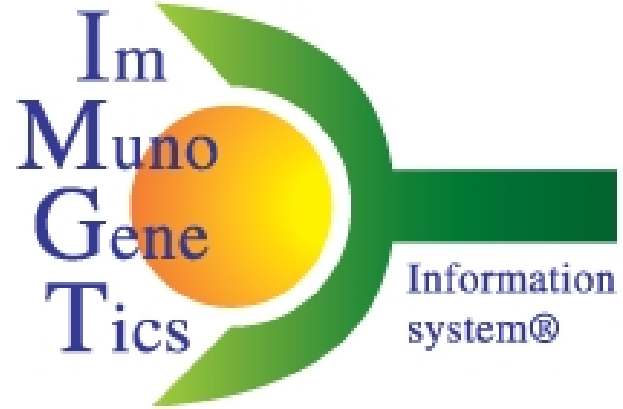
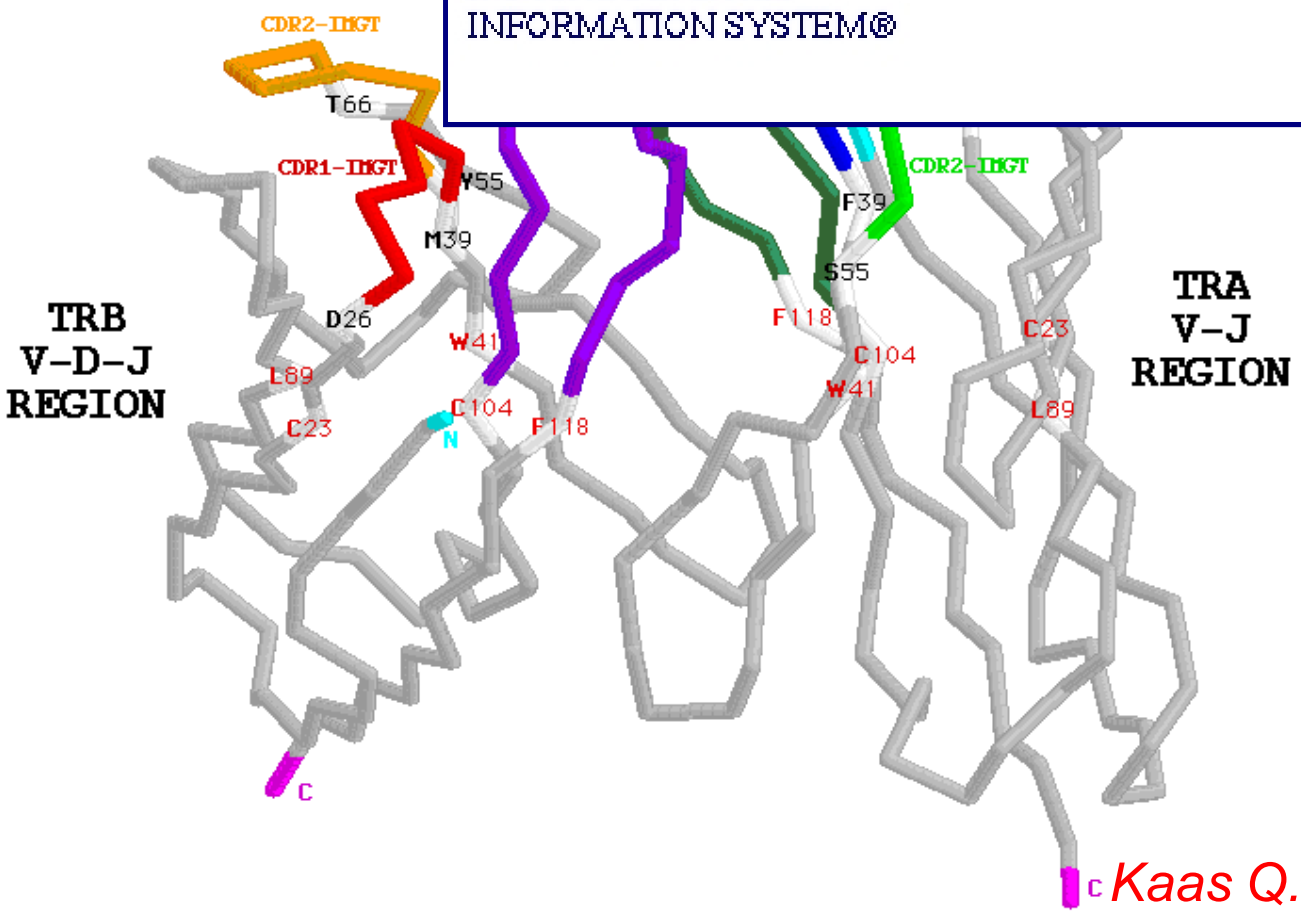
IMMUNOGENETICS
INFORMATION SYSTEM®



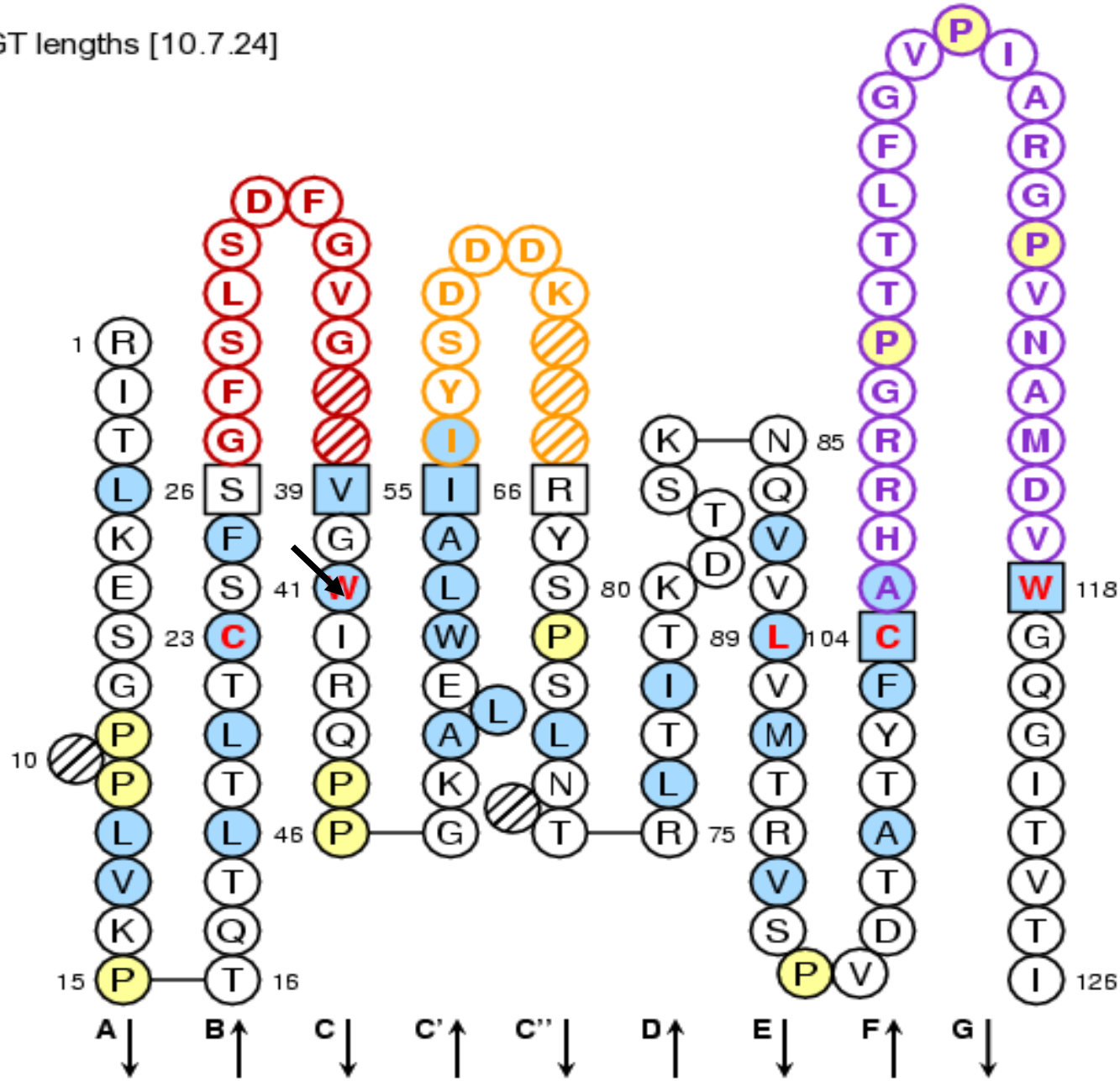
http://imgt.cines.fr



Kaas Q. et al. NAR 32, D208-D210 (2004)

IMGT Collier de Perles : *Homo sapiens* (Human) IGHV_1 V-DOMAIN from 2F5 (PDB: 1u8k_B)

CDR-IMGT lengths [10.7.24]



Kaas Q. et al. NAR 32, D208-D210 (2004)

Contact analysis

http://imgt.cines.fr

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

Kaas Q. et al. NAR 32, D208-D210 (2004)

IMGT Collier de Perles

http://imgt.cines.fr

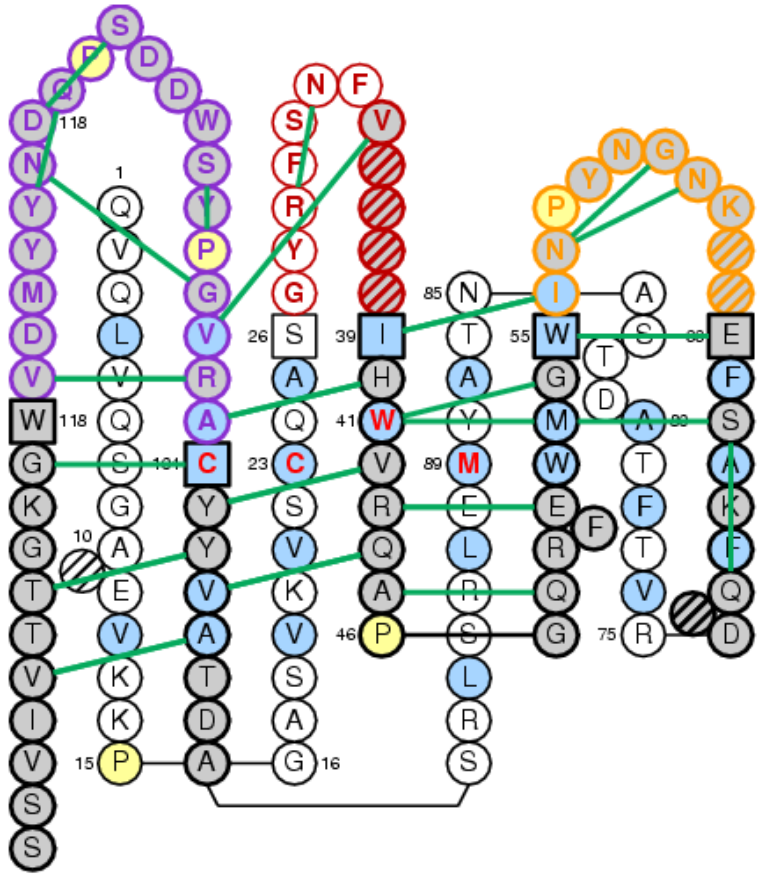
Collier de perles - Netscape

Fichier Edition Afficher Aller Communicator Aide

Signets Adresse : gt3d.igh.cnrs.fr/cgi-bin/collier_perles2P.cgi?domcode=1HZHHD00&name=B12&CDR1=8&CDR2=8&CDR3=20&species=HUMAN Infos connexes

Collier de Perles : HUMAN IGHV V-DOMAIN from B12 (PDB: 1hzh_H)

[8.8.20]



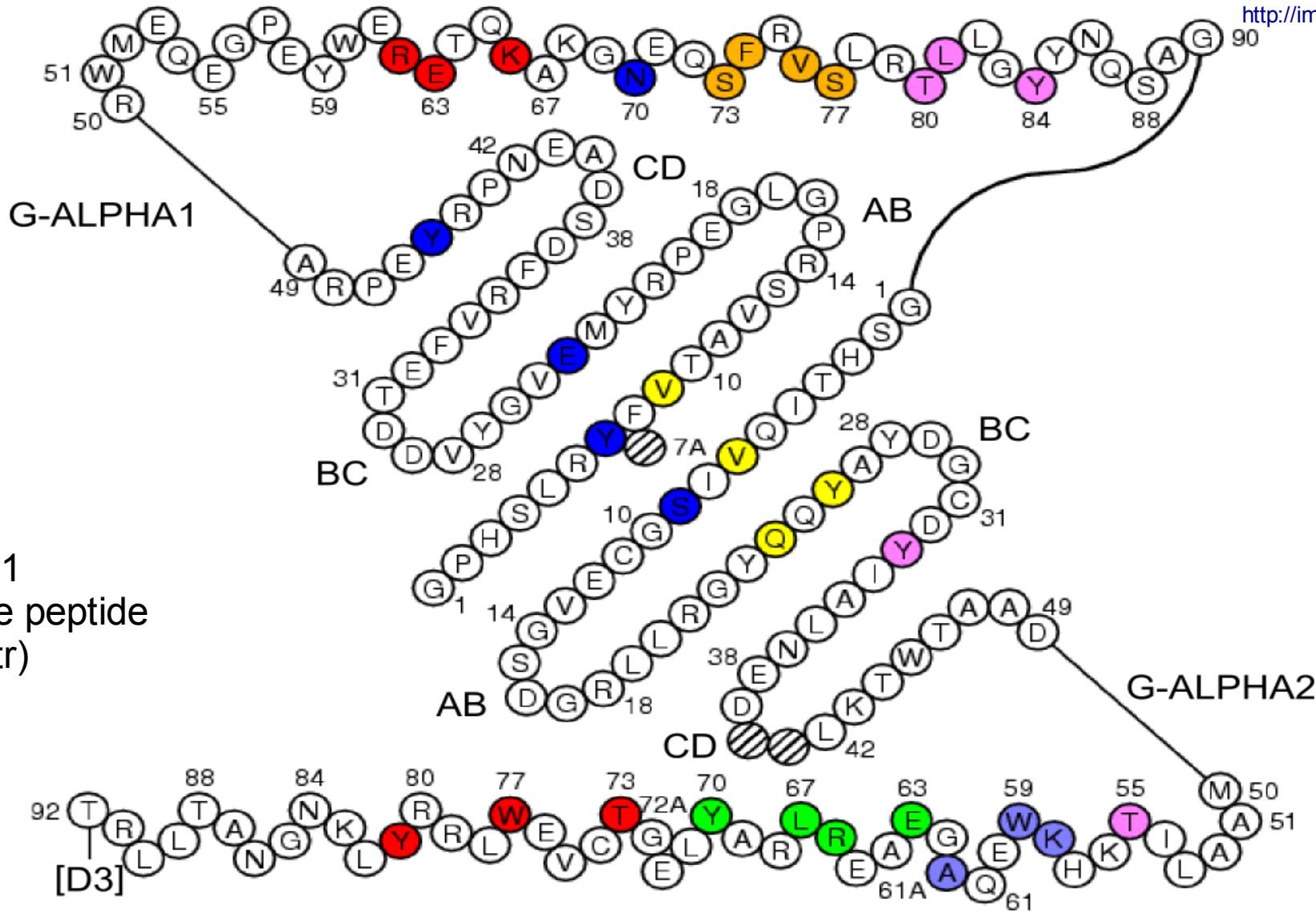
Document : chargé

Kaas Q. et al. NAR 32, D208-D210 (2004)

MHC class I IMGT contact sites

http://imgt.cines.fr

C1	1 E
C2	--
C3	2 Q
C4	3 Y
C5	(4 K)
C6	5 F
C7	--
C8	--
C9	6 Y
C10	7 S
C11	8 V



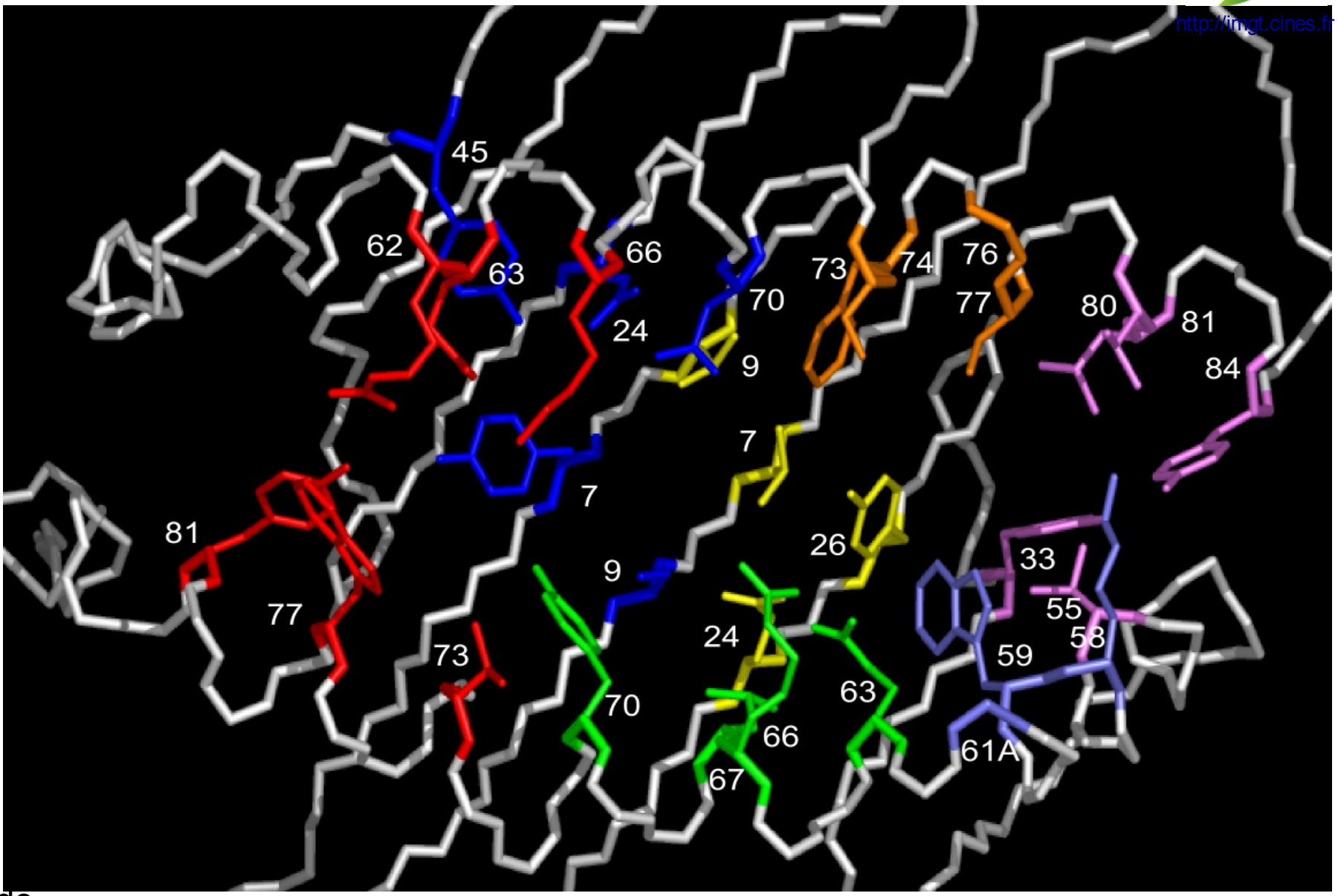
H2-K1*01
8 residue peptide
(code 1jtr)

Lefranc et al. Dev. Comp. Immunol. 29, 917-938 (2005)

IMGT pMHC contact sites

http://imgt.cines.fr

C1	1 E
C2	--
C3	2 Q
C4	3 Y
C5	(4 K)
C6	5 F
C7	--
C8	--
C9	6 Y
C10	7 S
C11	8 V



H2-K1*01
(code 1jtr)
8 residue peptide

Kaas and Lefranc In Silico Biology 2005

IMGT/3Dstructure-DB card - Microsoft Internet Explorer

Fichier Adresse http://imgt3d.igh.cnrs.fr/cgi/details.cgi?pdbcode=1BX2&Part=CONT&domcontcode=1BX2DC029 OK

THANK YOU

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IMGT/3Dstructure-DB card for : 1bx2

IMGT protein name	IMGT receptor type	IMGT receptor description	Ligand(s)	Species	CC	Chain ID
HLA-DR2	MHC	MHC-II-ALPHA_BETA		*Homo sapiens* (Human)	1	[1bx2_A1bx2_B]
	MHC	MHC-II-ALPHA_BETA		*Homo sapiens* (Human)	2	[1bx2_D1bx2_E]
		Peptide	Myelin basic protein MBP peptide 117-230 (P02686)	*Homo sapiens* (Human)	1	[1bx2_C]
		Peptide		*Homo sapiens* (Human)	2	[1bx2_F]
		Glucid	N-Acetyl-D-Glucosamine		2	[1bx2_1]
		Glucid			1	[1bx2_2]

Experimental technique X-ray diffraction Resolution (in angstrom) 2.60 PDB release date 22-DEC-99

Chain details | **Contact analysis** | 3D visualization Jmol or QuickPDB | Renumbered IMGT file | IMGT numbering comparison | References and links | Printable card

G-ALPHA (MHC class II)
with MBP peptide 117-230

Contact analysis:

IMGT/3Dstructure-DB Domain contacts

Contacts of Domain **G-ALPHA** Chain **1bx2_A** *with* Domain **(Ligand)** Chain **1bx2_C**

Atom contact types

- [ ] Non covalent
- [x] Polar
- [x] Hydrogen bond
- [ ] Non polar
- [ ] Covalent
- [ ] Disulfide

Check all
Uncheck all

Atom contact categories

- [ ] (BB) Backbone/backbone
- [ ] (SS) Side chain/side chain
- [ ] (BS) Backbone/side chain
- [ ] (SB) Side chain/backbone

Check all
Uncheck all

Show

Contacts summary:

IMGT/3Dstructure-DB card - Microsoft Internet Explorer

Fichier » Adresse http://imgt3d.igh.cnrs.fr/cgi/details.cgi?pdbcode=1BX2&Part=CONT&domcontcode=1BX2DC029 OK

IMGT/3Dstructure-DB Domain contacts

Contacts of Domain **G-ALPHA** Chain **1bx2_A** *with* Domain **(Ligand)** Chain **1bx2_C**

Atom contact types

- [ ] Non covalent
- [x] Polar
- [x] Hydrogen bond
- [ ] Non polar
- [ ] Covalent
- [ ] Disulfide

Check all
Uncheck all

Atom contact categories

- [ ] (BB) Backbone/backbone
- [ ] (SS) Side chain/side chain
- [ ] (BS) Backbone/side chain
- [ ] (SB) Side chain/backbone

Check all
Uncheck all

Show

Contacts summary:

Residue contacts	Number of residues			Atom contacts		
	Total	From 1	From 2	**Total**	**Polar**	**Hydrogen**
43	34	20	14	**360**	**58**	**9**

Residue@Position contacts:

Click 'R@P' for **IMGT/3Dstructure-DB Residue@Position contacts**

	Order						Order					Atom contacts		
	IMGT Num	Residue		Domain	Chain		IMGT Num	Residue		Domain	Chain	**Total**	**Polar**	**Hydrogen**
R@P	7	GLN	Q	G-ALPHA	1bx2_A	R@P	6	HIS	H		1bx2_C	**1**	**1**	**0**
R@P	7	GLN	Q	G-ALPHA	1bx2_A	R@P	7	PHE	F		1bx2_C	**9**	**0**	**0**
R@P	7	GLN	Q	G-ALPHA	1bx2_A	R@P	8	PHE	F		1bx2_C	**15**	**4**	**1**
R@P	9	GLU	E	G-ALPHA	1bx2_A	R@P	8	PHE	F		1bx2_C	**1**	**1**	**0**
R@P	9	GLU	E	G-ALPHA	1bx2_A	R@P	10	ASN	N		1bx2_C	**9**	**4**	**1**
R@P	24	PHE	F	G-ALPHA	1bx2_A	R@P	7	PHE	F		1bx2_C	**5**	**0**	**0**
R@P	26	PHE	F	G-ALPHA	1bx2_A	R@P	5	VAL	V		1bx2_C	**6**	**0**	**0**
R@P	26	PHE	F	G-ALPHA	1bx2_A	R@P	6	HIS	H		1bx2_C	**4**	**0**	**0**
R@P	26	PHE	F	G-ALPHA	1bx2_A	R@P	7	PHE	F		1bx2_C	**3**	**0**	**0**
R@P	34	PHE	F	G-ALPHA	1bx2_A	R@P	5	VAL	V		1bx2_C	**5**	**0**	**0**
R@P	47	TRP	W	G-ALPHA	1bx2_A	R@P	5	VAL	V		1bx2_C	**1**	**0**	**0**
R@P	53	GLY	G	G-ALPHA	1bx2_A	R@P	2	ASN	N		1bx2_C	**5**	**2**	**1**
R@P	54	ARG	R	G-ALPHA	1bx2_A	R@P	2	ASN	N		1bx2_C	**9**	**2**	**0**

Contacts of G-ALPHA (MHC class II) with MBP peptide 117-230

http://imgt.cines.fr

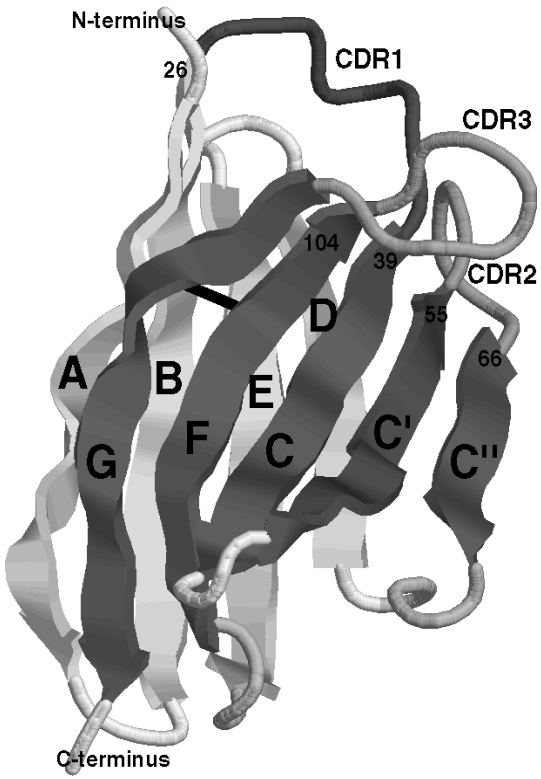
IMGT unique numbering

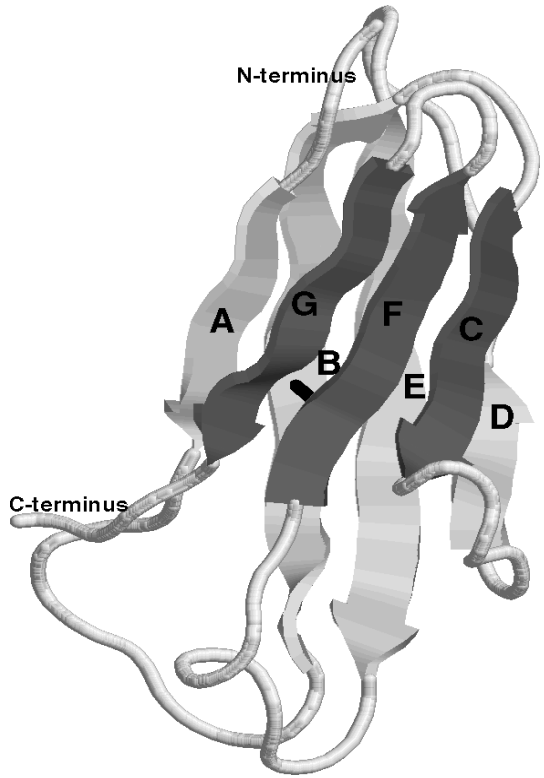
http://imgt.cines.fr

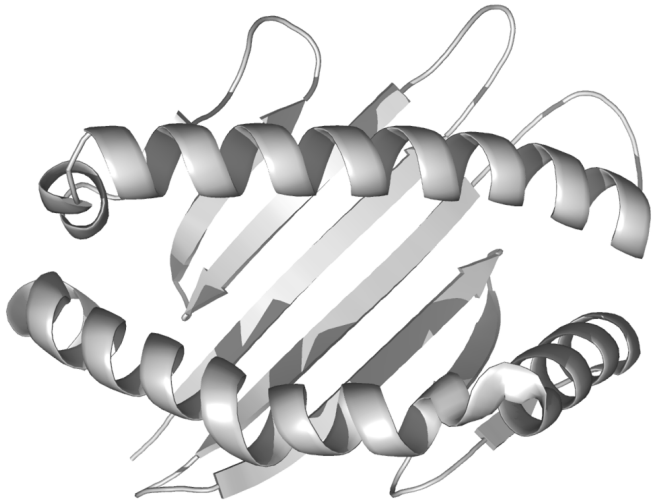
V-DOMAIN (IG,TR)
AND
V-LIKE-DOMAIN
(other than IG,TR)

C-DOMAIN (IG,TR)
AND
C-LIKE-DOMAIN
(other than IG,TR)

G-DOMAIN (MHC)
AND
G-LIKE-DOMAIN
(other than MHC)







Immunoglobulin superfamily (IgSF)

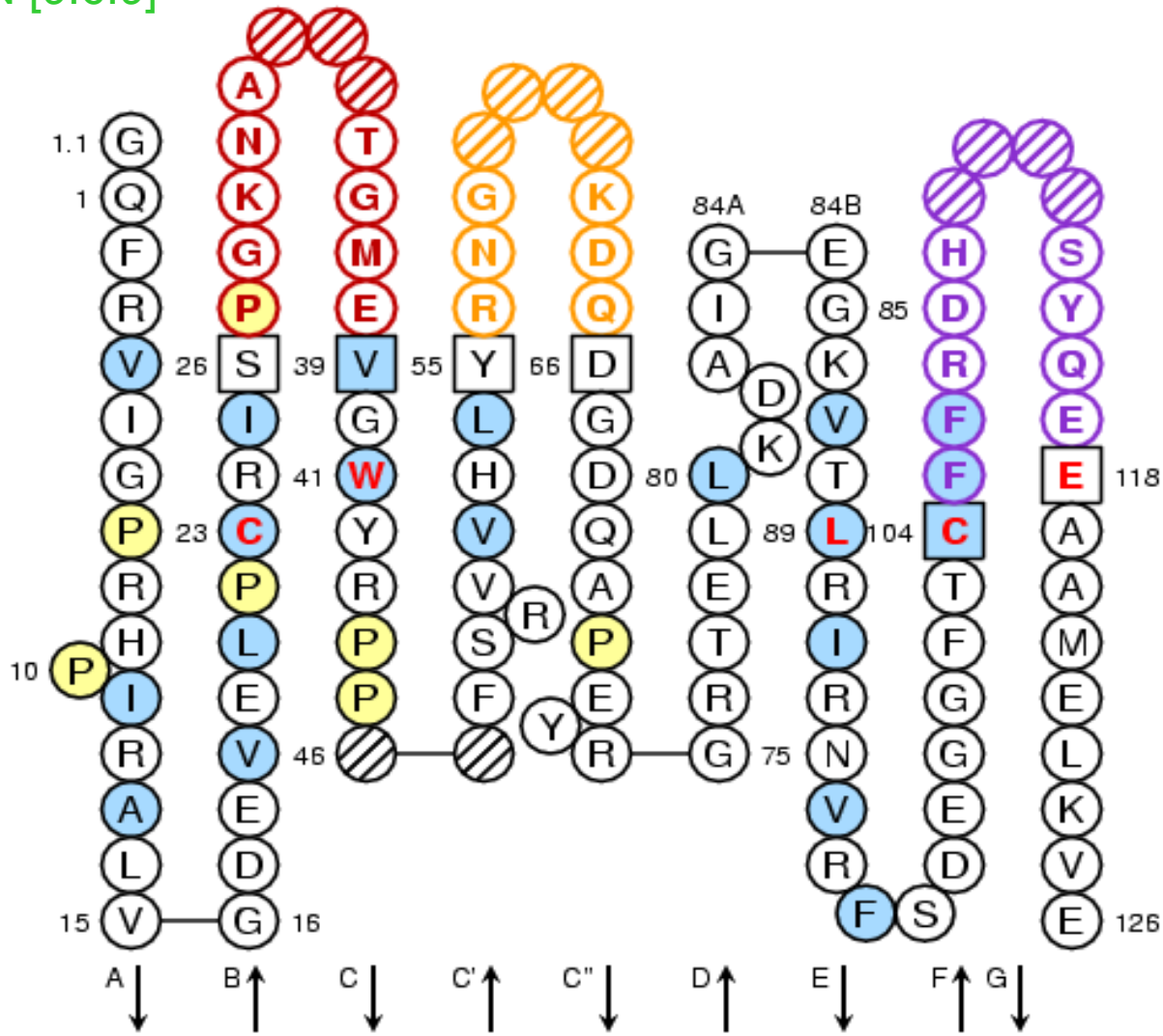
MHC superfamily (MhcSF)

IMGT Collier de Perles

http://imgt.cines.fr

Homo sapiens MOG (P13688)

V-LIKE-DOMAIN [9.6.9]



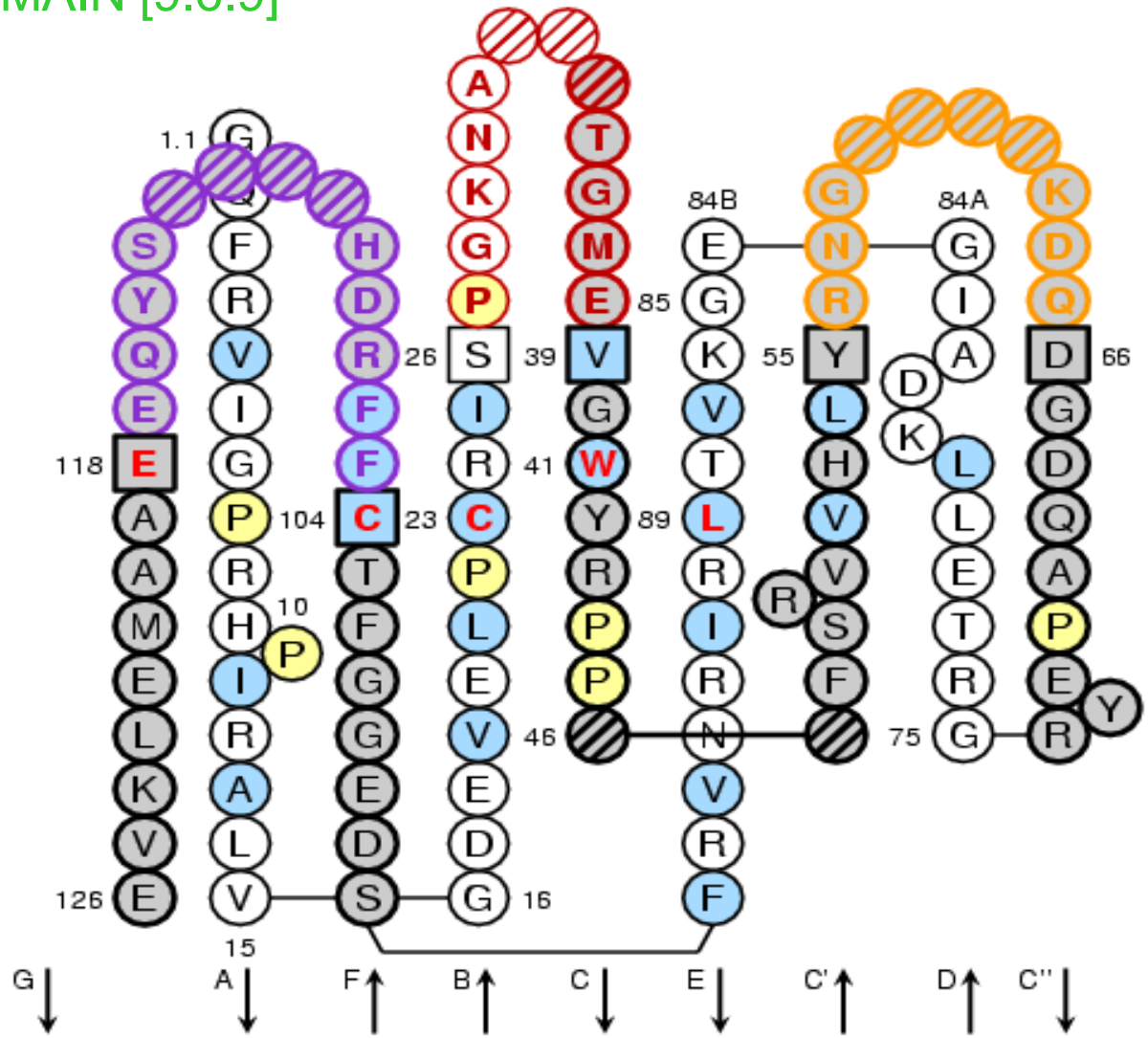
Duprat E. et al. Recent Res. Devel. Human Genet. 2, 111-136 (2004)

IMGT Collier de Perles

http://imgt.cines.fr

Homo sapiens MOG (P13688)

V-LIKE-DOMAIN [9.6.9]



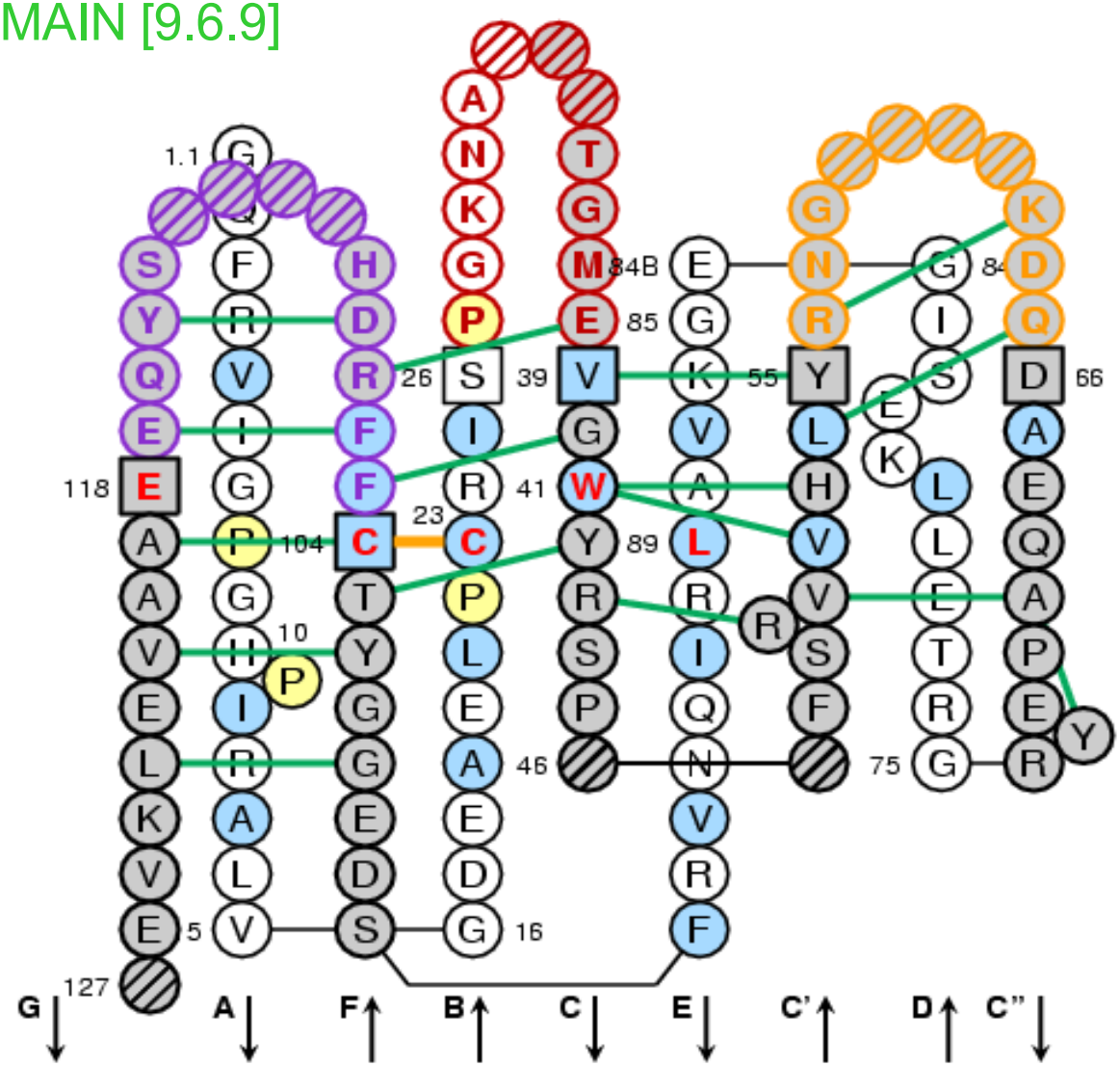
Duprat E. et al. Recent Res. Devel. Human Genet. 2, 111-136 (2004)

IMGT Collier de Perles

http://imgt.cines.fr

Rattus norvegicus MOG (1pkq_E)

V-LIKE-DOMAIN [9.6.9]



IMGT/3Dstructure-DB, http://imgt.cines.fr

IMGT Collier de Perles

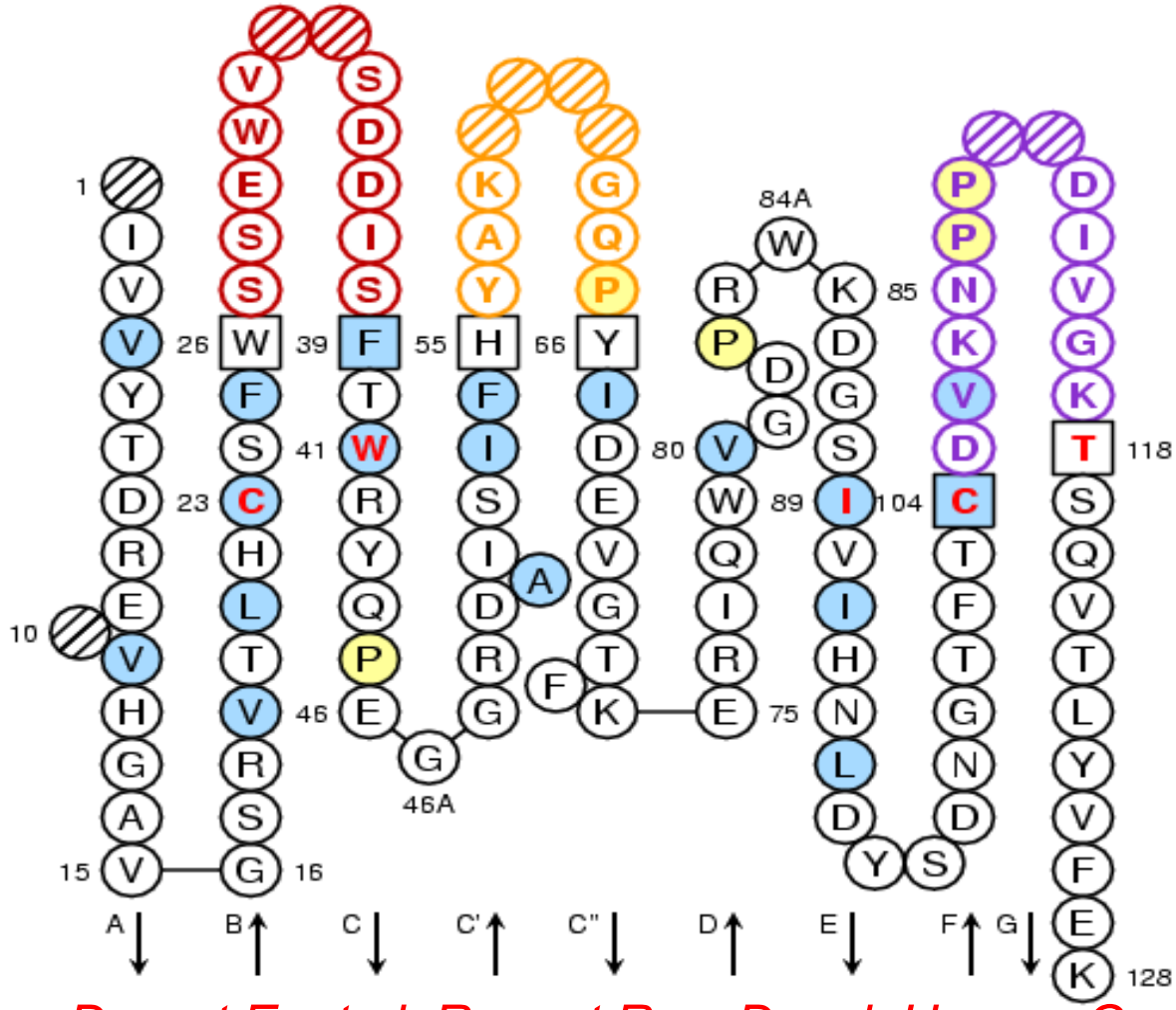
http://imgt.cines.fr

Homo sapiens MPZ (P25189)

V-LIKE-DOMAIN [10.6.11]

90 mutations in the V-LIKE-DOMAIN of MPZ (P0)

http://www.molgen.ua.ac.be/Datasource/Mutations.cfm



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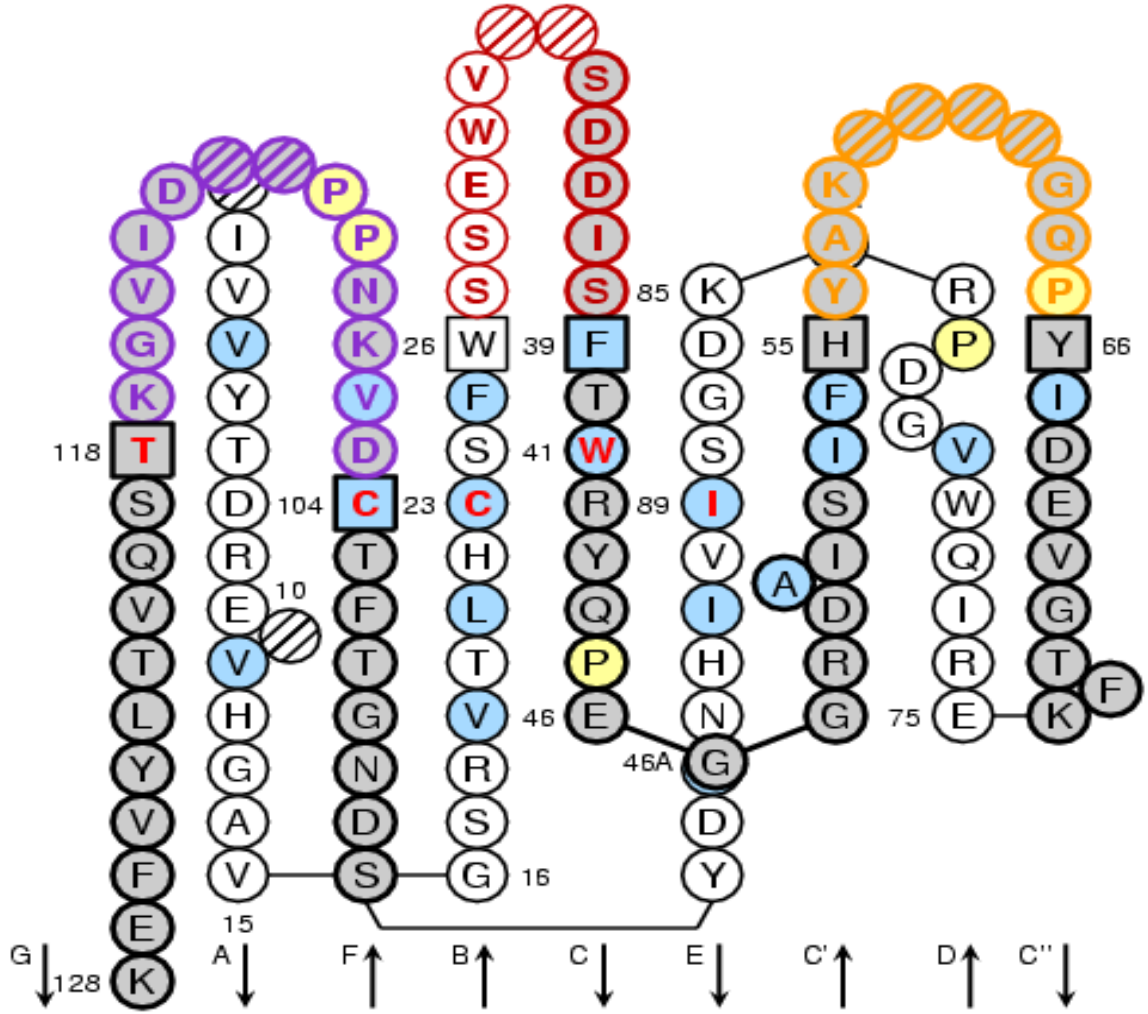
IMGT Collier de Perles

http://imgt.cines.fr

Homo sapiens MPZ (P25189)

V-LIKE-DOMAIN [10.6.11]



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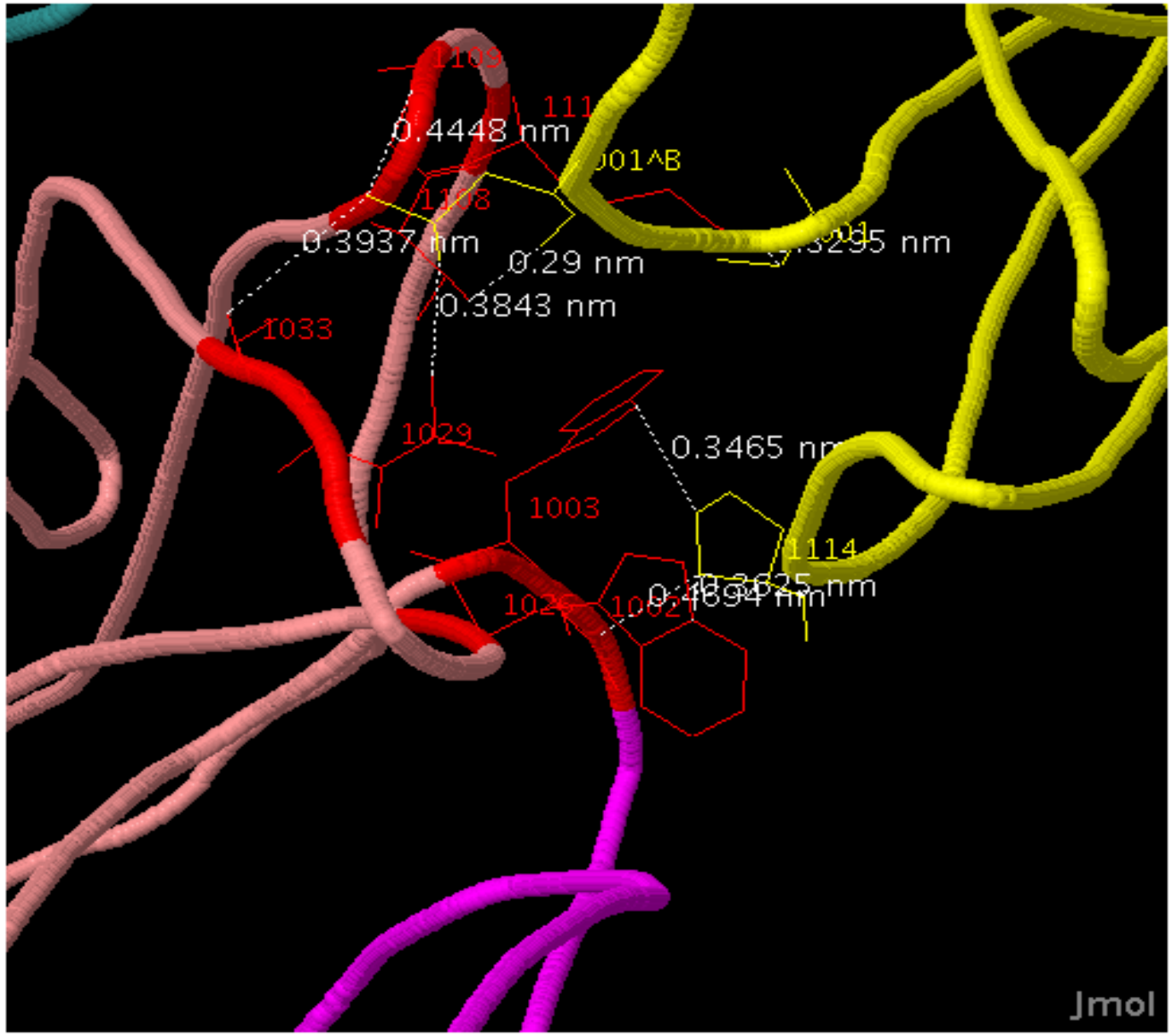
Interactions between domains

http://imgt.cines.fr

IGHG1
(FC-GAMMA1)

CH2
C-DOMAIN

FCGR3
B



[D2
d-LIKE-
DOMAIN

[D1] C-LIKE-DOMAIN

The IMGT team at Montpellier