

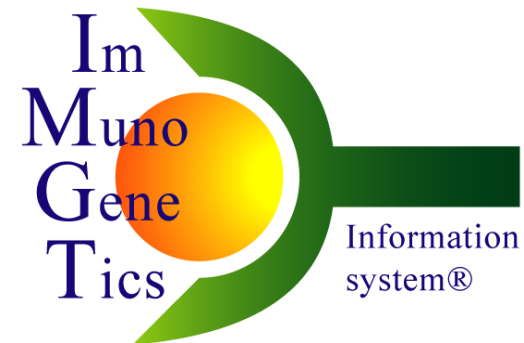
How is IMGT relevant to myelin diseases?

Marie-Paule Lefranc

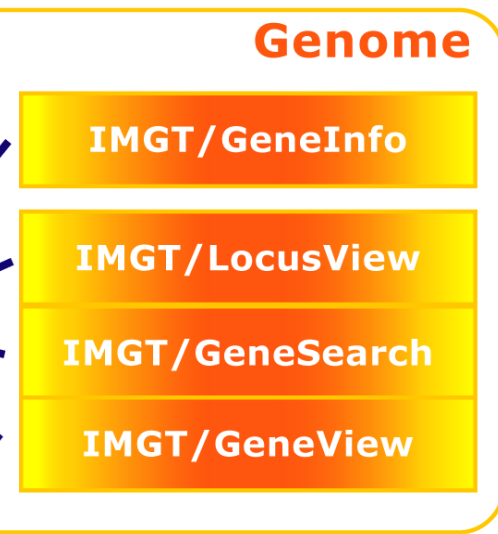
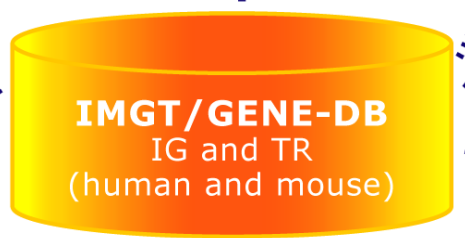
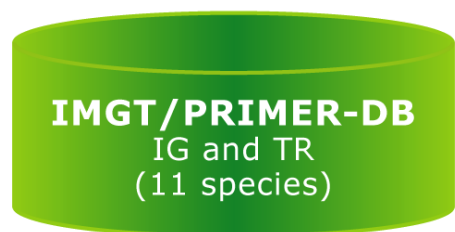
Laboratoire d'ImmunoGénétique Moléculaire
Université Montpellier, UPR CNRS 1142, IGH
Institut Universitaire de France

2006 Round table of the ESF MARIE Network on:
« MYELIN STRUCTURE AND ITS ROLE IN AUTOIMMUNITY »
28 September - 1 October 2006, Giovinazzo, Bari, Italy

Sequences

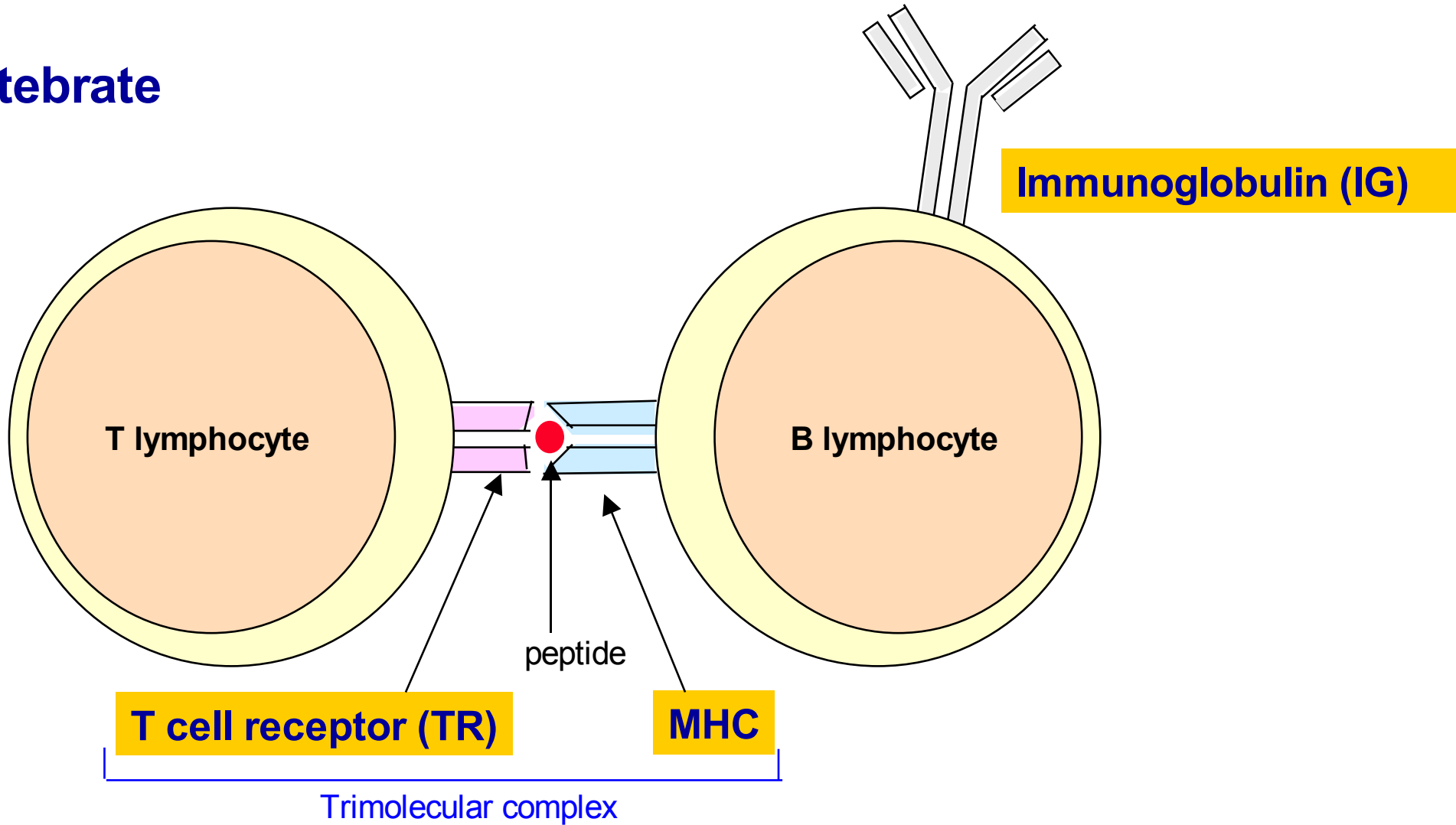


<http://imgt.cines.fr>



2D and 3D structures

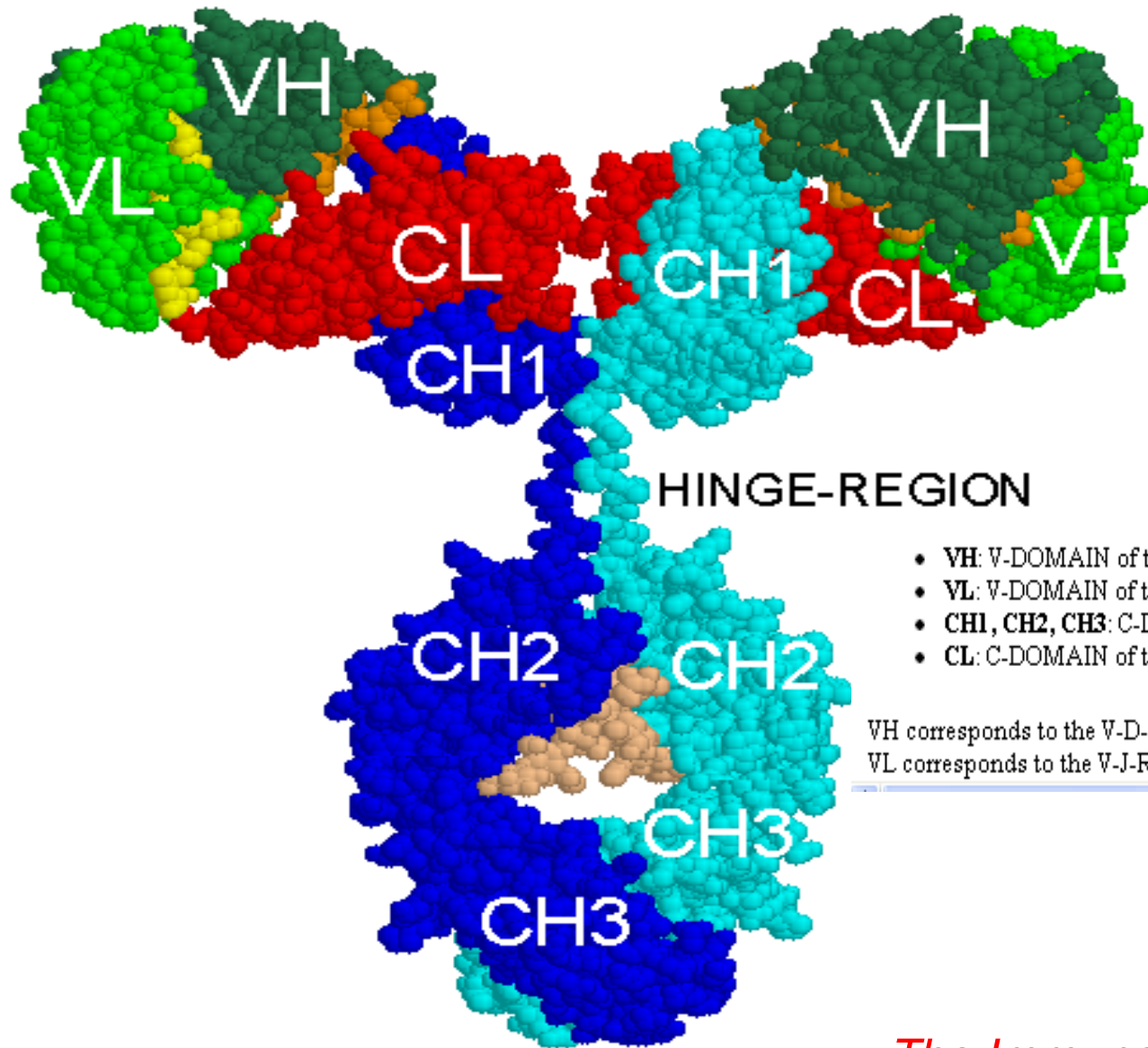
Vertebrate S



cDNA (in databases: mRNA!)

```
..... .gagga ttcacccatgg aactgggggct ccgctggggtt ttccttggtg cttttttaga 120
aggtgtccag tgtgaggtgc aactgggtgga gtctgggggga ggccctgggtca agccggggggg 180
gtccctgaga ctctcctgtg cagcctctgg attaagcttc agtacctatg ccatgaactg 240
ggtccgccag gctccagggga aggggctgga atgggtctca agtattagta gtagaagtga 300
ttacatatac tatagagact cagtgaaggg ccgattcacc atctccagag acaacgccaa 360
gaattcactg tatctgcaaa tgaatagcct gagagtcgac gacacggctg tctattactg 420
tgcgagagat tcttgtaatg gtgctatatg ttatggtttc agtccctggg gccagggaac 480
cctggtcacc gtctcctcag catccccgac cagccccaag gtcttcccgc tgagcctctg 540
cagcaccag ccagatggga acgtgggtcat cgcctgcctg gtccagggct tcttcccca 600
ggagccactc agtgtgacct ggagcgaaag cggacagggc gtgaccgcca gaaacttccc 660
accagccag gatgcctccg gggacctgta caccacgagc agccagctga ccctgcccgc 720
cacacagtgc ctagccggca agtccgtgac atgccacgtg aagcactaca cgaatcccag 780
ccaggatgtg actgtgcctt gccagttcc ctcaactcca cctaccccat ctccctcaac 840
tccacctacc ccattctcct catgctgccca cccccgactg tcaactgcacc gaccggcctt 900
cgaggacctg ctcttaggtt cagaagcgaa cctcacgtgc aactgaccg gectgagaga 960
tgcctcgggt gtcaccttca cctggacgcc ctcaagtggg aagagcgctg ttcaaggacc 1020
acctgagcgt gacctctgtg gctgctacag cgtgtccagt gtccctgcgg gctgtgcoga 1080
gccatggaac catggaaga ccttcaactg cactgctgcc taccctgagt ccaagacccc 1140
gctaaccgcc accctctcaa aatccggaaa cacattccgg cccgaggtcc acctgctgcc 1200
gccgccgtcg gaggagctgg ccctgaacga gctgggtgacg ctgacgtgcc tggcacgtgg 1260
cttcagccc aaggacgtgc tggttcgtg gctgcagggg tcacaggagc tgccccgcga 1320
gaagtacctg acttgggcat cccggcagga gccagccag ggcaccacca ccttoctgtt 1380
gaccagcata ctgctcgtgg cagccgagga ctggaagaag ggggacacct tctcctgcat 1440
ggtgggccac gaggcctgc cgctggcctt cacacagaag accatcgacc gcttggcggg 1500
taaaccacc catgtcaatg tgtctgttgt catggcggag gtggacggca cctgctactga 1560 ....
```

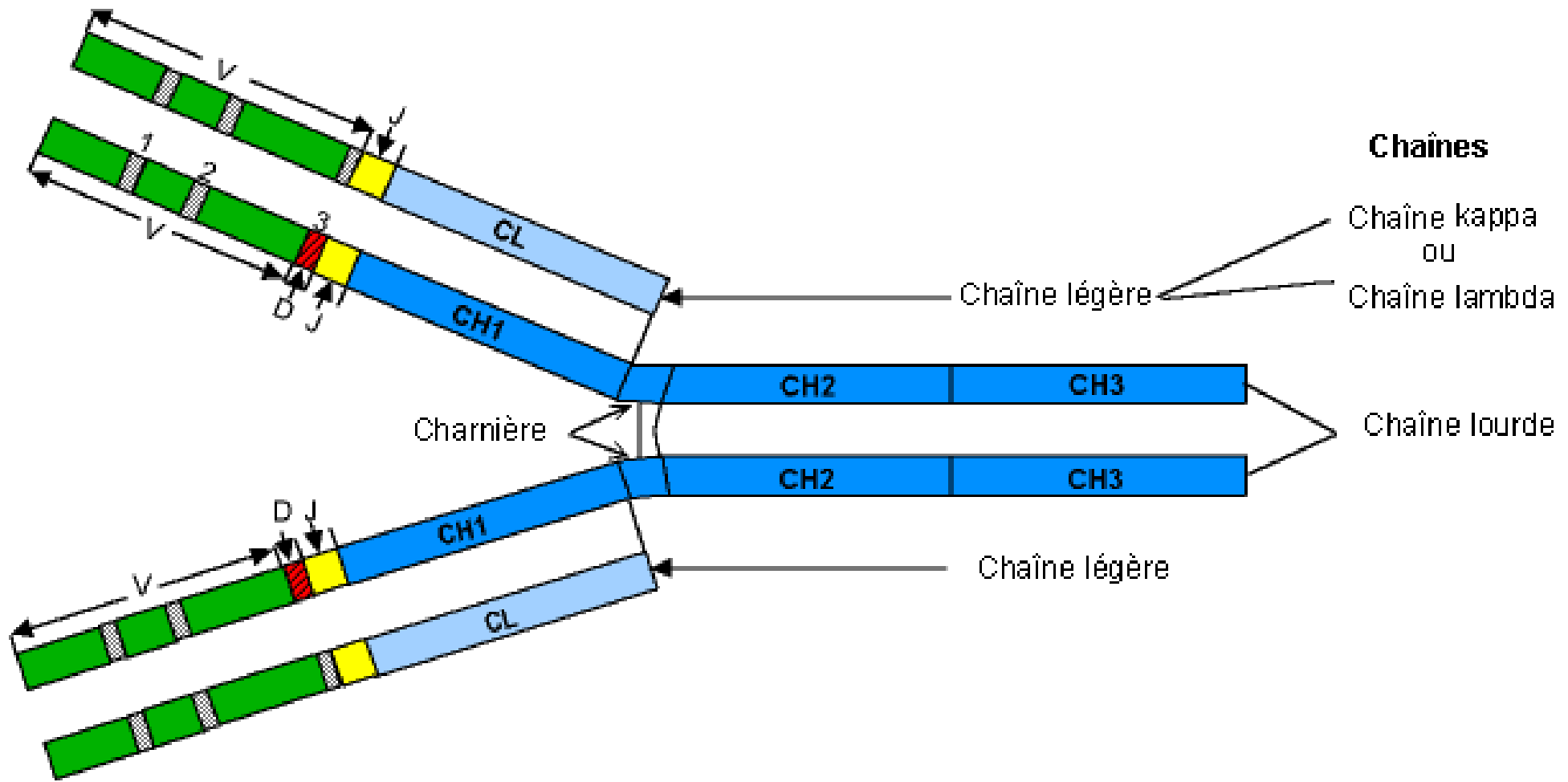
Spacefill 3D representation of an IgG



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

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

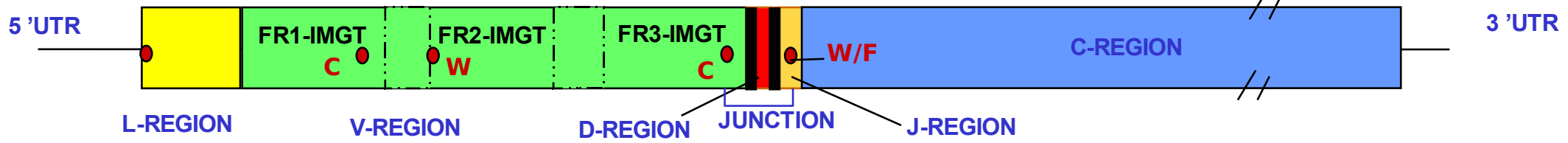
Immunoglobulin IgG



cDNA

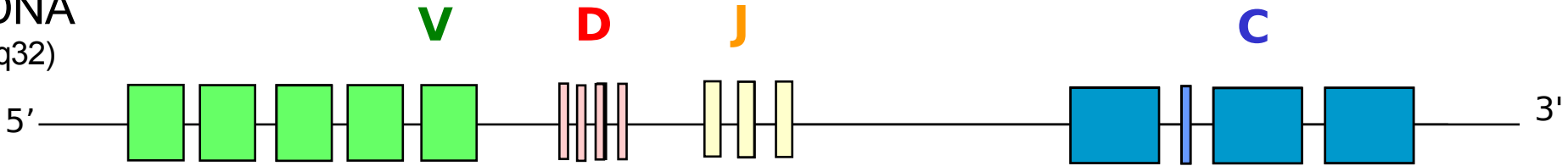
```

.....gagga ttcaccatgg aactggggct ccgctggggt ttcttggtg cttttttaga 120
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gtccctgaga ctctctgtg cagcctctgg attaagcttc agtacctatg ccatgaactg 240
gggccgag gtcaccagga aggggctgga atgggtctca agtattagta gtagaagtga 300
ttacatatac tatagagact cagtgaaggg ccgattcacc atctccagag acaacgccaa 360
gaattcactg tatctgcaaa tgaatagcct gagagtgcac gacacggctg tctattactg 420
tgcgagag tctcttgaatg gtgctatatg ttatggttcc agtccctggg gccagggaac 480
cctggtcacc gtctcctcag catccccgac cagccccaag gtcttcccgc tgagcctctg 540
cagcaccag ccagatggga acgtgggtcat cgctgcctg gtccagggct tcttcccca 600
ggagccactc agtgtgacct ggagcgaaag cggacagggc gtgaccgcca gaaacttcc 660
accagccag gatgcctccg gggacctgta caccacgagc agccagctga ccctgccggc 720
cacacagtgc ctagccggca agtccgtgac atgccacgtg aagcactaca cgaatcccag 780
ccaggatgtg actgtgccct gccagttcc ctcaactcca cctaccccat ctccctcaac 840
tccacctacc ccatctccct catgctgcca ccccgactg tcaactgcacc gaccggccct 900
cgaggacctg ctcttaggtt cagaagcgaa cctcacgtgc aactgaccg gcctgagaga 960
tgctcgggt gtcacctca cctggacgcc ctcaagtggg aagagcgctg ttcaaggacc 1020
acctgagcgt gacctctgtg gctgctacag cgtgtccagt gtctgcccgg gctgtgccga 1080
gcatggaac catggaaga ccttcaactg cactgctgcc taccgaggt ccaagacccc 1140
gctaaccgcc accctctcaa aatccggaaa cacattccgg cccgaggtcc acctgctgcc 1200
gccgccgtcg gaggagctgg ccctgaacga gctgggtgacg ctgacgtgcc tggcacgtgg 1260
ctcagcccc aaggacgtgc tggttcgctg gctgcagggg tcacaggagc tgccccgcga 1320
gaagtacctg acttgggcat cccggcagga gccagccag ggcaccacca ccttcgctgt 1380
gaccagcata ctgcgcgtgg cagccgagga ctggaagaag ggggacacct tctcctgcat 1440
ggtgggccac gaggccctgc cgctggcctt cacacagaag accatcgacc gcttggcggg 1500
taaaccacc catgtcaatg tgtctgttgt catggcggag gtggacggca cctgctactga 1560 ....
    
```



Immunoglobulin (IG) synthesis

genomic DNA
(IGH Locus 14q32)

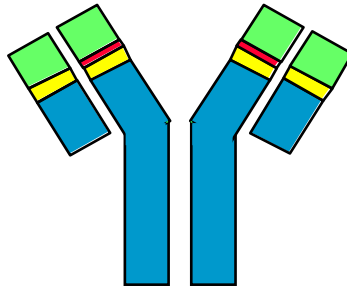


rearranged
DNA



mRNA

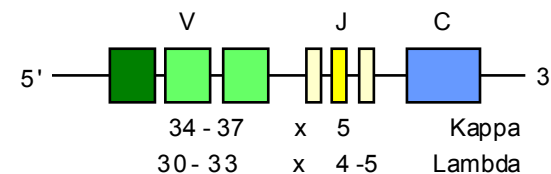
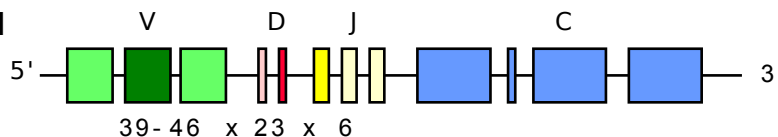
2×10^{12} different IG
per individual



Immunoglobulin (IG) synthesis

150 FUNCTIONAL IG GENES

HEAVY CHAIN



LIGHT CHAIN

6300

POTENTIAL RECOMBINATIONS

N-DIVERSITY
SOMATIC MUTATIONS

x 1000



ABOUT 6.3×10^6 POSSIBILITIES

185 + 165

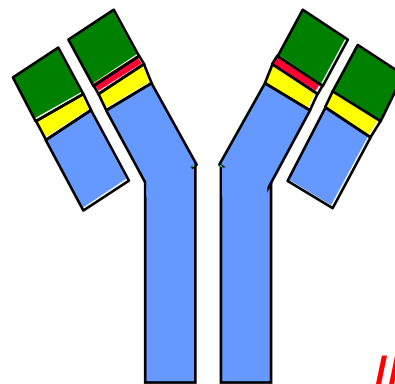
POTENTIAL RECOMBINATIONS



ABOUT 3.5×10^5 POSSIBILITIES

2×10^{12}

DIFFERENT ANTIBODIES

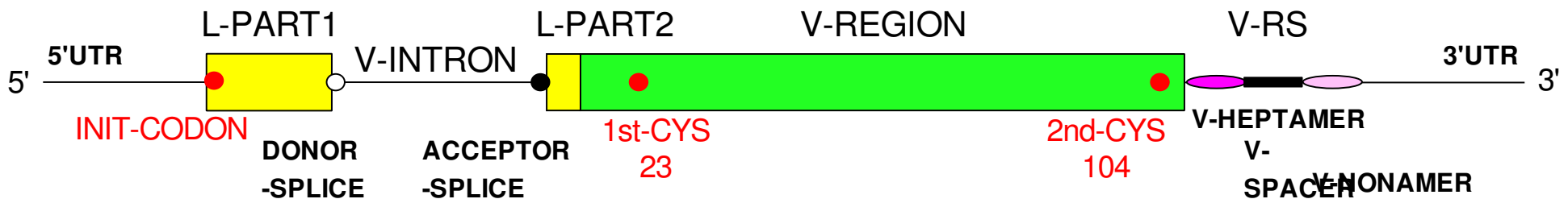


Genomic DNA in germline configuration

V-GENE

>X62106.0|HSV12|*Homo sapiens* VI-2 gene for immunoglobulin heavy chain

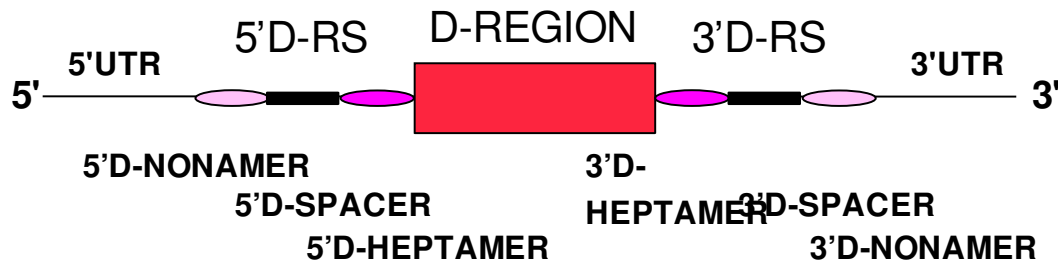
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gatctcatcc	acttctgtgt	tctctcca	caaggccact	cccaggtgca	gctgggtgcag	180
tctggggctg	aggtgaagaa	gcctggggcc	tcagtgaagg	tctcctgcaa	ggcttctgga	240
tacaccttca	ccggctacta	tatgcactgg	gtgcgacagg	cccctggaca	agggcttgag	300
tggatgggat	ggatcaacc	taacagtgg	ggcacaact	atgcacagaa	gtttcagggc	360
agggtcacca	tgaccagga	cacgtccatc	agcacagcct	acatgagct	gagagagctg	420
agatctgacg	acacggcctg	gtattactgt	gcgagagaca	cagtc	tgaaa	480
tgagggtg	tc agaaaccaa	gggaggaggc	ag		accacatcc	



Genomic DNA in germline configuration

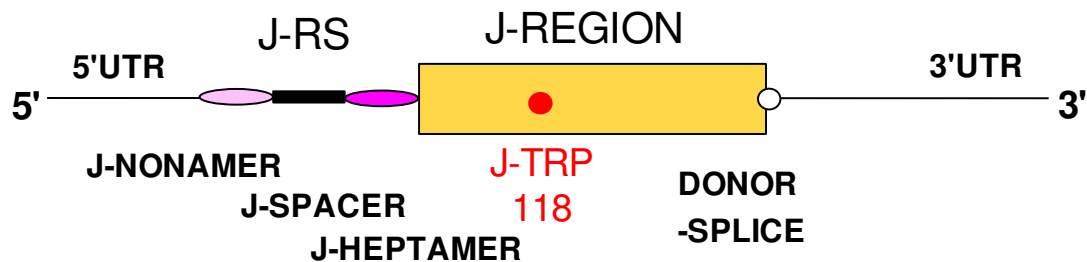
D-GENE

gggtttttgga c tgagctgaga ac cactgtgc taactgggga cacagtcatt
ggcagctctt caaaaacc

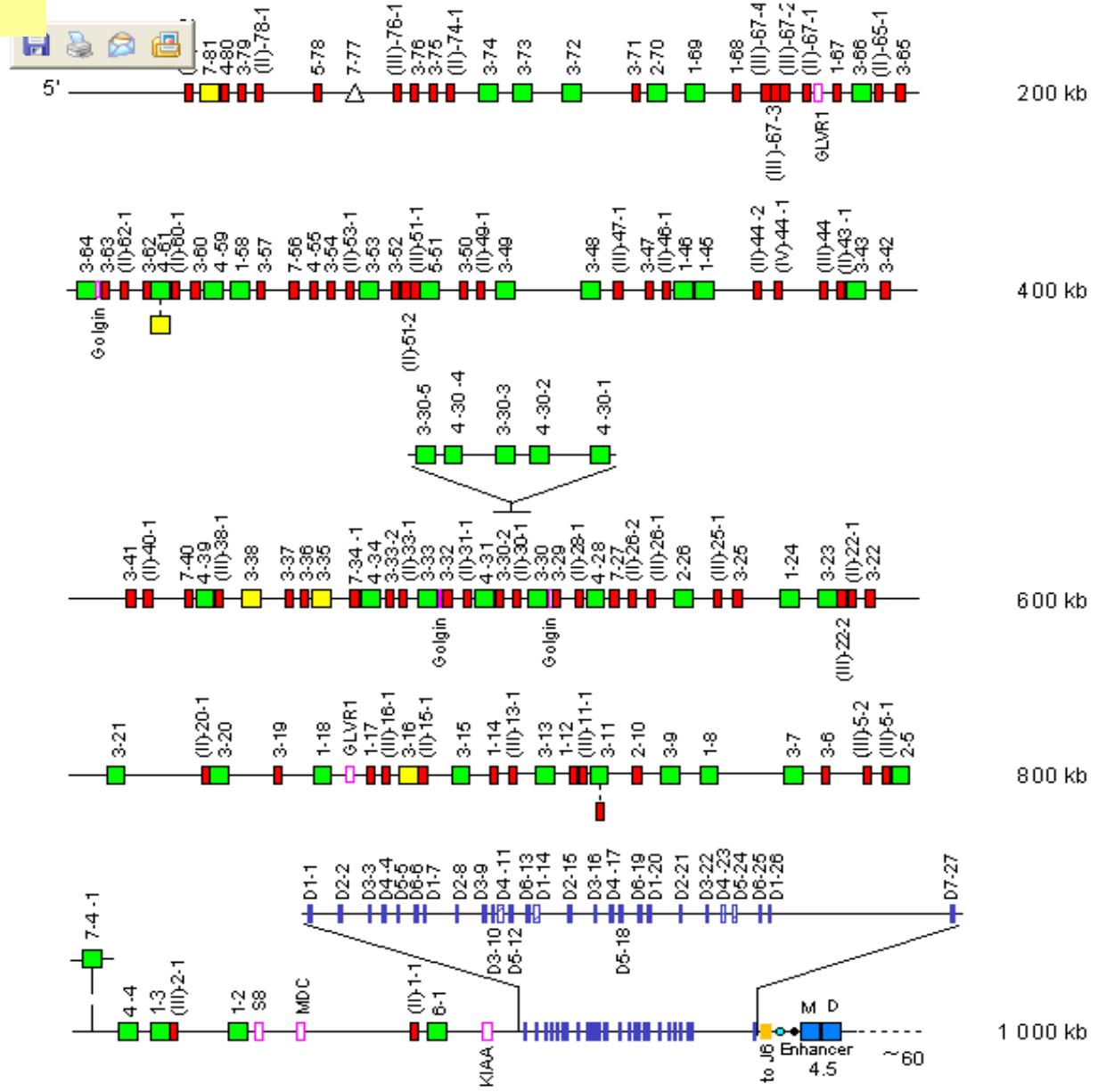


J-GENE

ggttttct gtgccctgg ctcagggtg actcaccgtg gctgaatact
ccagcactg ggccagggc acctggtca cgtctcctc ag



Chromosome 14q32.33



Locus representation: Human IGL

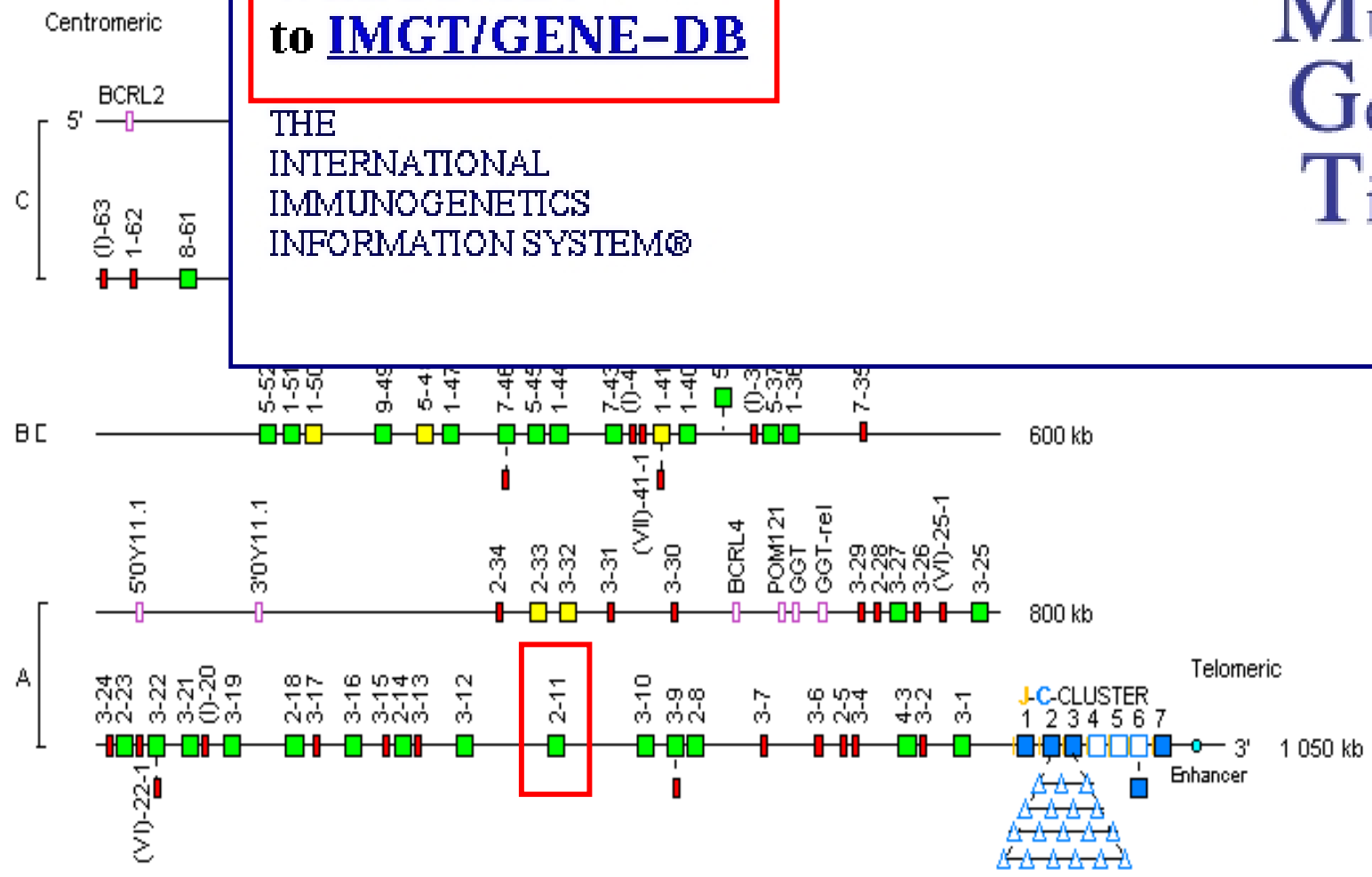
Human IGL 22q11.2

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

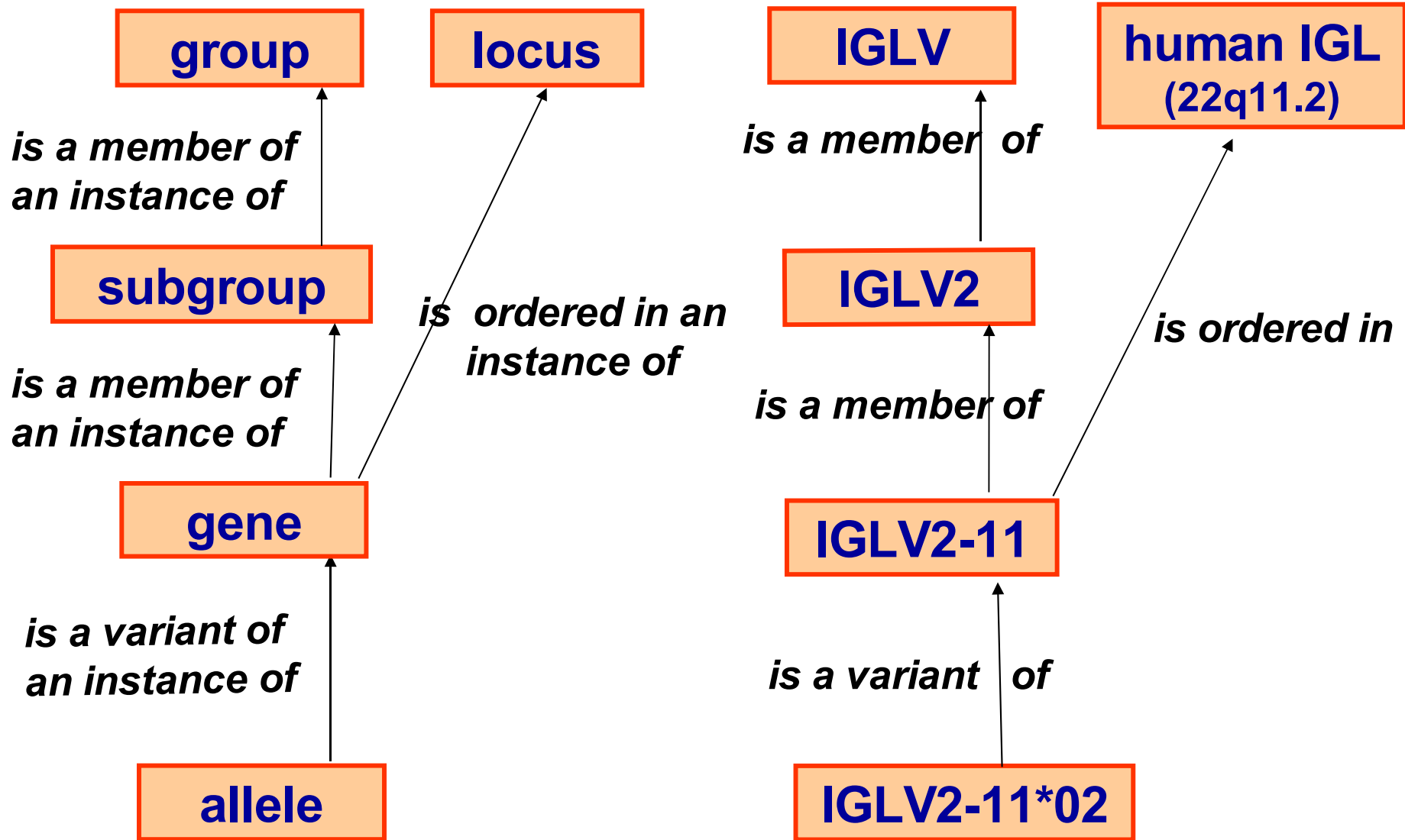
THE
INTERNATIONAL
IMMUNOGENETICS
INFORMATION SYSTEM®



<http://imgt.cines.fr>



"CLASSIFICATION" concept



« Concepts »

« Instances »

Since 2004
Entrez Gene
NCBI:
Direct links
to
IMGT/GENE-DB
entries

LocusLink Report - Netscape

Fichier Edition Afficher Aller Communicator Aide

NCBI

CGCTCAGGAT ACGCTCAGGAT ACGCTCAGGAT ACGCTCAGGAT ACGCTCAGGAT ACGCTCAGGAT ACGCTCAGGAT ACGCTCAGGAT ACGCTCAGGAT ACGCTCAGGAT
TTCTC TATA TATTCTCT TATA TATTCTCT TATA TATTCTCT TATA TATTCTCT TATA TATTCTCT TATA TATTCTCT TATA TATTCTCT TATA TATTCTCT
CCCCATCAGCACCCCCAT CCCCCATCAGCACCCCCAT CCCCCATCAGCACCCCCAT CCCCCATCAGCACCCCCAT CCCCCATCAGCACCCCCAT CCCCCATCAGCAC
CACAGACTGCACACAGACTGCACACAGACTGCACACAGACTGCACACAGACTGCACACAGACTGCACACAGACTGCACACAGACTGCACACAGACTGCACACAGACTGCAT

PubMed Entrez BLAST OMIM Map Viewer Taxonomy Structure

Search LocusLink Display Brief Organism: All

Query:

View One of 1 Loci

A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

PUB **ACEVIEW** **MAP** **VAR** **GDB**

Homo sapiens Official Gene Symbol and Name [HGNC]

IGLV2-11: immunoglobulin lambda variable 2-11

LocusID: 28816

Overview [Submit GeneRIF](#) ?

Locus Type: gene, segment

Alternate Symbols: V1-3, IGLV211

Map Information ?

Chromosome: 22 **mv**

Cytogenetic: 22q11.2 RefSeq

NCBI Reference Sequences (RefSeq) ?

Category: REVIEWED

Genomic: [NG_000002](#) **gb sv**

Category: NCBI Genome Annotation

Genomic Contig: [NT_011520](#) **gb sv mv ev mm**

Related Sequences ?

Nucleotide	Type	Protein	
D86998	g	BAA19994	BL
Z73657	g		

Additional Links ?

- [IMGT Repertoire for individual human immunoglobulin and T cell receptor genes](#)

IMGT/V-QUEST

Alignment for V-GENE

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

Alignment for J-GENE

<u>AF402940</u>		score	CTTCACGGGGCGGGACGCTTTGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
<u>J00256</u>	IGHJ3*01	181T.....T..T.....A.T.....T...G
<u>X86355</u>	IGHJ6*02	179	T.A.TACTACTACT...G.A.....
<u>X86355</u>	IGHJ3*02	172T.....T..TA.....A.T.....T...G



V-GENE

JUNCTION

J-GENE

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 :

```
gaggtgcagctggtggagtcggggggaggcttggtagcagcctgggggggtccctgagactc
tctgtgcagcctctggattcaccttagcagcttgccatgagctgggtccgccaggct
cctgggaaggggctggactgggtctcagaaatagtggtagtgggcggtaccacatatc
gcaggctccgtgaagggccgggtcaccatctccagagacaactccaagaatacgctggtt
ctgcaaatgaatagcctgacagccgaagacacggccgtatattactgtgcgaagaggtt
```

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

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

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

Alignment for V-GENE

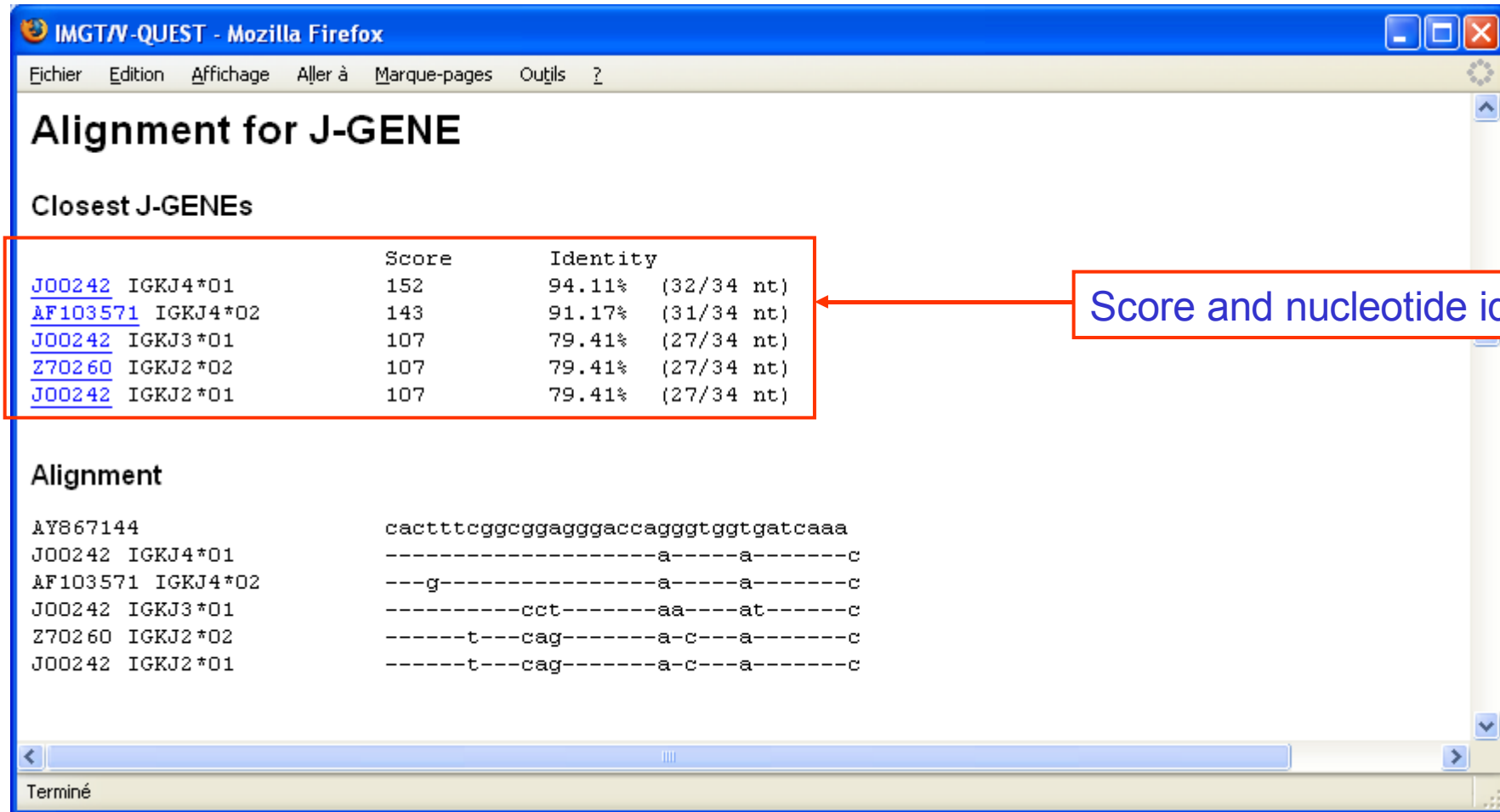
input		score	GAGGTGCAGCTGTTGGAGTCGGGGGA...GGCTTGGTACAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTAGCAGCTTTGCC...
M99660	IGHV3-23*01	1281	-----T-----A-----
J00236	IGHV3-23*02	1263	-----T-----A-----
U29481	IGHV3-23*03	1209	-----T-----A-----
Z12358	IGHV3-48*03	1128	-----G-----T-----A-----C--T--T-A--AA...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

Alignment for D-GENE

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



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)

Alignment

```
AY867144                cactttcggcggaggaccagggtggtgatcaaa
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

Score and nucleotide identity

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 --- --- --- --- --- --- --- ---
  
```

```

----->
      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 ---
  
```

Translation

```

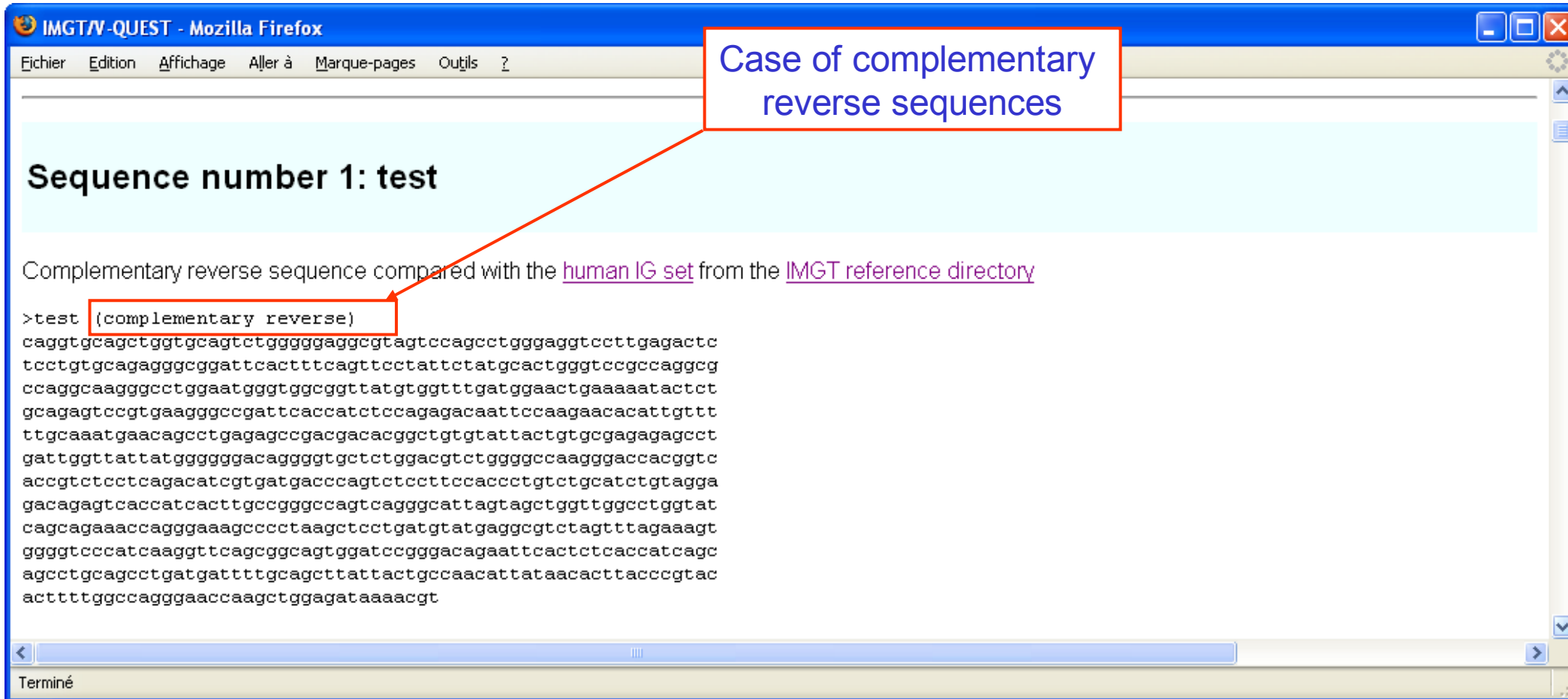
<----- F R 1 - I M G T -----
1           5           10           15
input      E V Q L L E S G G G L V Q P G G S
           GAG GTG CAG CTG TTG GAG TCG GGG GGA ... GGC TTG GTA CAG CCT GGG GGG TCC

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

----->
                20           25           30           CDR1 - IMGT           35
input      L R L S C A A S G F T F S S F A
           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
input      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
M99660 IGHV3-23*01 -----A-----G-----

-->                                     <-----
                CDR2 - IMGT
55           60           65           70
input      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                                     D
M99660 IGHV3-23*01 -CT-----T-----G-----... ..-C-----A-----
    
```



IMGT/V-QUEST - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

Sequence number 1: test

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

```
>test (complementary reverse)
caggtgcagctggtgcagctctgggggagggcgtagtcacagcctgggaggtccttgagactc
tctgtgcagagggcggattcactttcagttcctattctatgcactgggtccgcccaggcg
ccaggcaagggcctggaatgggtggcgggttatgtggtttgatggaactgaaaaatactct
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gacagagtcaccatcacttgccgggcccagtcagggcattagtagctgggtggcctggtat
cagcagaaaaccagggaaaagccctaaagctcctgatgtatgagggcgtctagtttagaaagt
gggggtcccataaggttcagcggcagtggtatccgggacagaattcactctcaccatcagc
agcctgcagcctgatgatttgcagcttattactgccaacattataaacacttacccgtac
acttttggccagggaaaccaagctggagataaaaact
```

Terminé

Case of complementary reverse sequences

IMGT/V-QUEST


IMGTV-QUEST - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

IMGTV-QUEST IMGTV-QUEST

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<http://imgt.cines.fr>

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](#)

Links to individual results

☞ **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

IMGT/V-QUEST - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

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	1 (3)
	Silent	9 (11)	2	0	2	0	0 (2)
	Non silent	27	9	3	7	3	1
Transitions	a>g	3 (4)	0	0	2	0	0 (1)
	g>a	6	3	0	2	0	0
	c>t	9 (10)	2	1	2	2	0 (1)
	t>c	1	1	0	0	0	0
Transversions	a>c	4	1	1	0	0	1
	c>a	1	0	1	0	0	0
	a>t	2	0	0	2	0	0
	t>a	1	0	0	0	0	1
	g>c	6	2	0	0	1	3
	c>g	1	1	0	0	0	0
	g>t	1	0	0	1	0	0
	t>g	1	1	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 IMG-T amino acid classes according to the physico-chemical properties

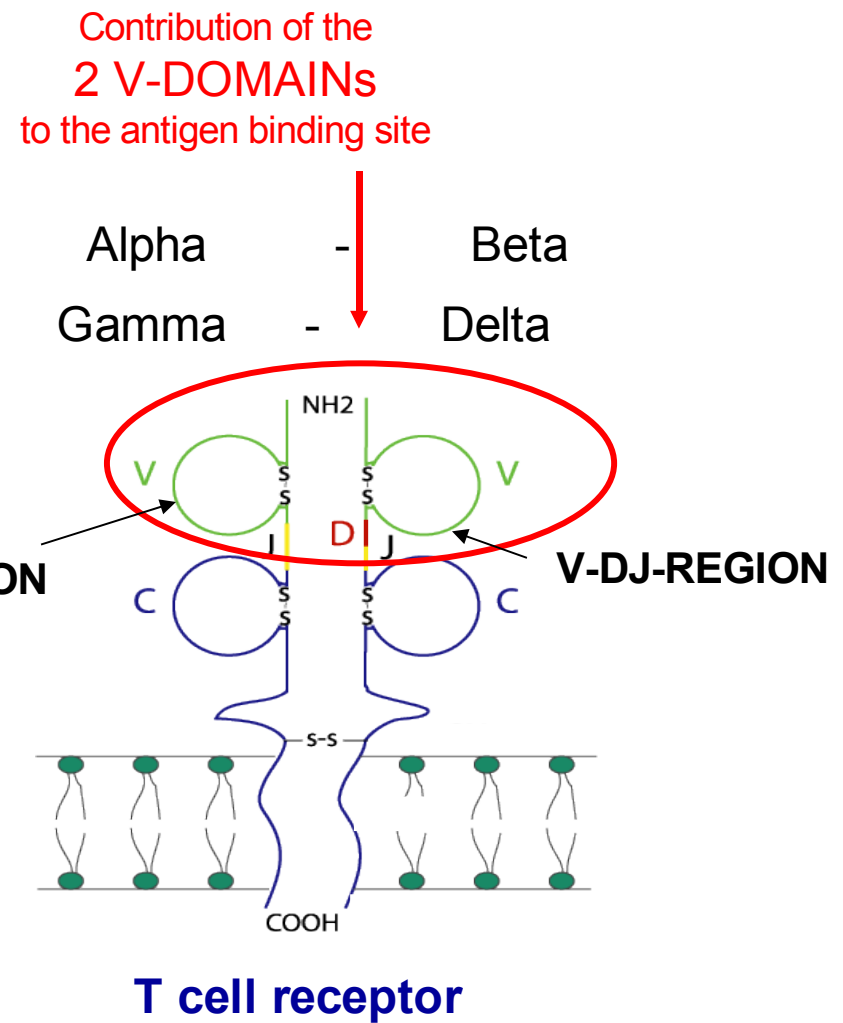
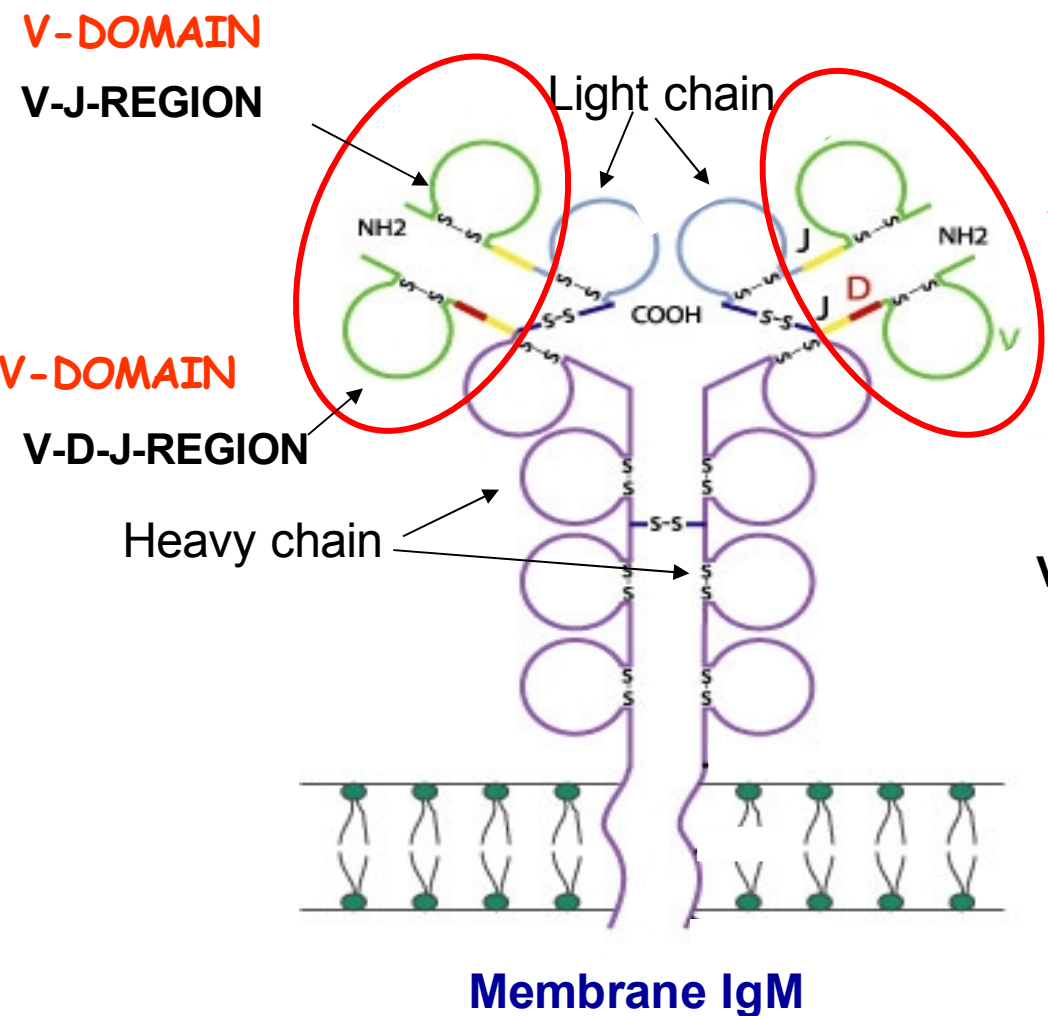
'Volume' classes		'Hydropathy' classes							
	in Å ³	Hydrophobic		Neutral		Hydrophilic			
Very large	189-228	F	W	Y					
Large	162-174	I	L	M	K		R		
Medium	138-154	V			H	E	Q		
Small	108-117		C	P	T	D	N		
Very small	60-90	A		G	S				
		Aliphatic		Sulfur	Hydroxyl	Basic		Acidic	Amide
						Charged			
				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

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 (++)					

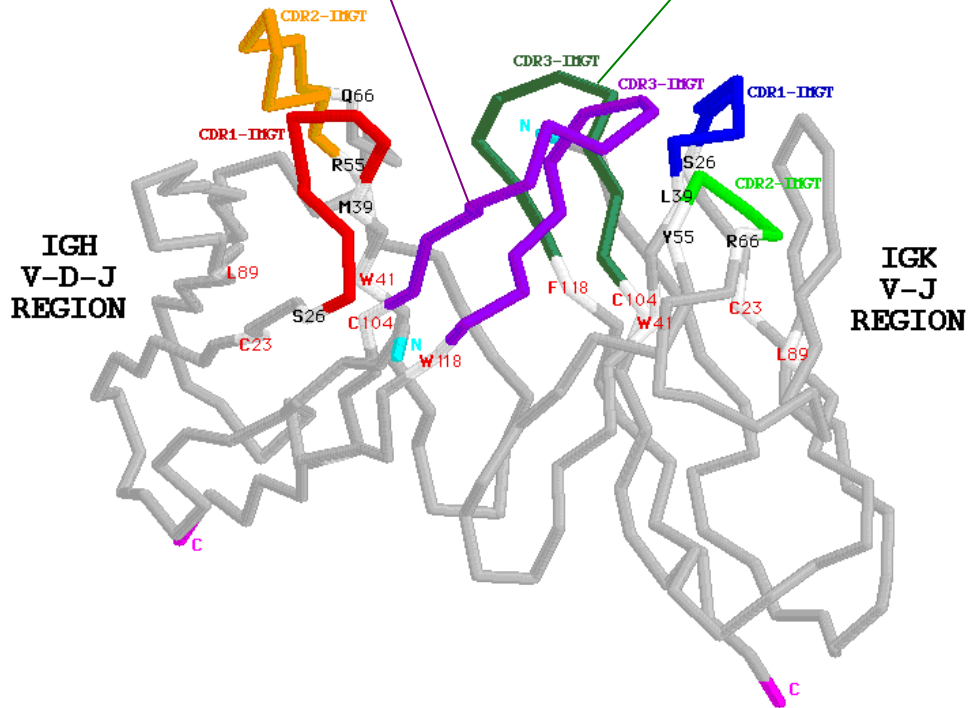
Immunoglobulin (IG)

T cell receptor (TR)



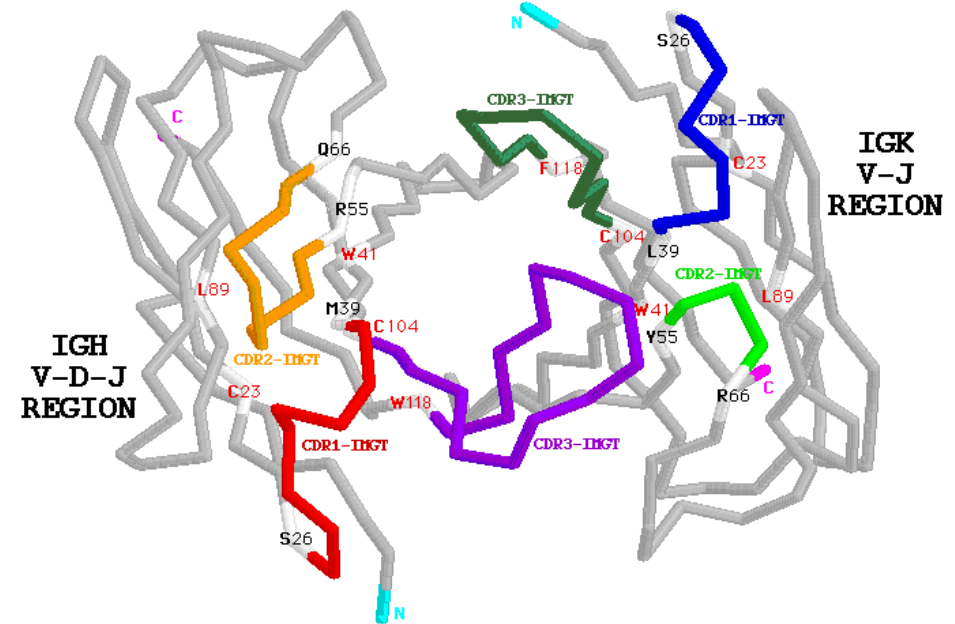
Junctions of the V-DOMAINS

VH V-D-J junction
V-KAPPA 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

3'V-REGION

N-REGION

D-REGION

N-REGION

5'J-REGION

tgtgcgaaaga



tacc



agcatattgtg

gtggtgactgctat

tcc



gat



acaactgggtcg actcctgg

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

IMGT/JunctionAnalysis Results

Locus IGH
Species Homo sapiens
IMGT repertoire link [Locus representation](#)

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

Description of the JUNCTIONS

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

#	Input	V name	V-REGION	P	N1	D-REGION	N2	P	J-REGION	J name	D name	Vmut	Dmut	Jmut	Ngc
#1	Z70256	IGHV2-26*01	tgtgtacg....		tgttgtgcagcgcctggtac	ccaaatac		...actttgaccactgg	IGHJ4*02	IGHD6-13*01	1	2	1	5/15
#2	Z70257	IGHV3-7*02	tgtgagag		ggatggcagctccttatgcc	cgcgcc		ctactggtacttcgatctctgg	IGHJ2*01	IGHD2-2*01	0	2	0	9/11
#3	Z70606	IGHV4-31*03	<u>c</u>		c	.gactacg.....	cact		..atgcttttgatgtctgg	IGHJ3*01	IGHD4-17*01	0	0	0	3/5
#4	Z70608	IGHV4-39*05	cagagta		cagagtaacgatttttgagtggttatt.....	ccccggggga		..atgcttttgatatctgg	IGHJ3*02	IGHD3-3*01	0	0	0	12/17
#5	Z70610	IGHV4-34*09	tgtgcgagag.		tcgggagcgatttttgagtggttatt.....	cccgga	ca	tgatgcttttgatatctgg	IGHJ3*02	IGHD3-3*01	0	0	0	9/12
#6	Z70611	IGHV4-59*01	tgtgcgaga..		catggttaactataa.	tgccggcgcttg		..actggttcgaccctgg	IGHJ5*02	IGHD3-9*01	0	2	0	9/13
#7	Z70613	IGHV4-59*01	actataa		actataactggatc	ctc		gactactgg	IGHJ4*02	IGHD6-13*01	0	0	0	4/6
#8	Z70614	IGHV4-59*01	actataa		actataaacttat.....	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.		cgggtttggg.....	ttccc		...actggttcgaccctgg	IGHJ5*02	IGHD3-16*01	0	0	0	6/8
#11	Z70620	IGHV4-30-4*01	tgtgcgagaga		ccggggcgggatggtt.....	cgg		.gatgctttgatctctgg	IGHJ3*02	IGHD3-16*01	1	4	0	5/5
#12	Z70621	IGHV4-39*01	tgtgcgagaca		ccacgattatggttcggggaggtt.....	tgaccccc	ttgactactgg	IGHJ4*02	IGHD3-16*01	0	1	0	12/21
#13	Z70622	IGHV4-39*06	tgtgcgagaga	t	tgccccgctcctgccaaaat	gtattactatggttcgggga.....	tatgtacg	ttgactactgg	IGHJ4*03	IGHD3-10*01	0	0	0	15/28

Addition

Addition

Mutation

Délétion

Délétion

Délétion

IMGJ/JunctionAnalysis - Mozilla Firefox

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

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

IMGJ/JunctionAnalysis Search page

Species :

Homo sapiens

Locus :

IGH 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
  
```

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Analysis of the JUNCTIONS

Input	V name	V-REGION	N1	D-REGION	N2
#1 M62724	IGHV7-4-1*02	tatgagagaga	aga	.tagcaatggctacaa....	aata
#2 Z47269	IGHV1-69*06	tgtgagagag.	gggggggctaaggtcgaattttggagtgggt.....	tcatgggt

Input	J-REGION	J name	D name	Vmut	Dmut	Jmut	Ngc
#1 M62724tttaactactag	IGHJ4*02	IGHD5-24*01	0	2	0	1/7
#2 Z47269	...actggttogaccctgg	IGHJ5*02	IGHD3-3*02	0	2	0	13/20

Translation of the JUNCTIONS

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

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....	aatatttgactactgg	IGHJ4*02
#2	Z47269	IGHV1-69*06	tgtgcgaga	gggggggctaaggtcgaatttttgagtggtt.....	tcatgggt	...actggttcgaccctgg	IGHJ5*02

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

Translation of the JUNCTIONS

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

IMGT/JunctionAnalysis - Microsoft Internet Explorer


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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 1:1379-1385 [PMID: 15262823](#) [IMGT/JunctionAnalysis](#)

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 :

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

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

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Analysis of the JUNCTIONS

Input	V name	V-REGION	M1	D-REGION	N2	J-REGION	J name	D name	Ngc		
#1	AB011247	TRBV28*01	tgtgccagcagct.....agcggggggg.	...acagatacgcagctat	ttt	TRBJ2-3*01	TRBD2*01	0/0		
#2	AB011248	TRBV28*01	tgtgccagcagct.....	at	gggacagggggc	ttccactgaagctttt	ttt	TRBJ1-1*01	TRBD1*01	1/5
#3	AB011249	TRBV27*01	tgtgccagc.....	tct	.ggactag.....	gcaacaatgagcagttt	ttc	TRBJ2-1*01	TRED2*01	3/6

Translation of the JUNCTIONS

	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	frame	length
#1	C	A	S	S	S	G	G			T	D	T	Q	Y	F	+	11
	tgt	gcc	agc	agt	agc	ggg	ggg			aca	gat	acg	cag	tat	ttt		
	C	A	S	S	M	G	Q	G	A	S	T	E	A	F	F	+	13
#2	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	tgt	gcc	agc	tct	gga	cta	ggc			aac	aat	gag	cag	ttc	ttc	+	11

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 For any other use please contact Marie-Paule Lefranc lefranc@ligm.igh.cnrs.fr.

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

JUNCTION alignments

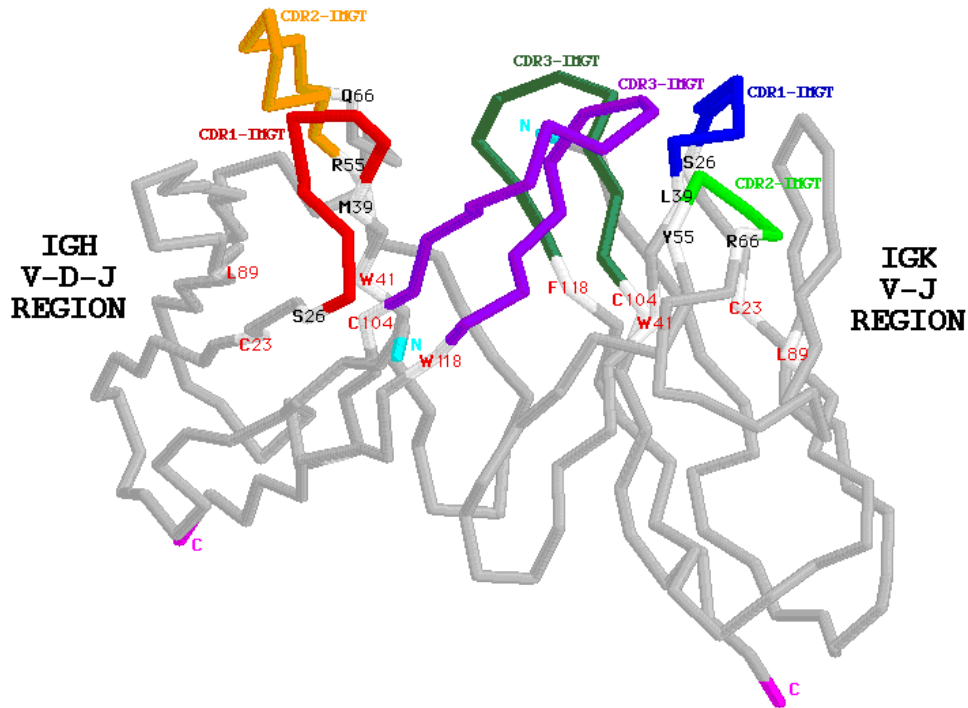
Click on mutated (underscored) amino acid to see the original one:

	104	105	106	107	108	109	110	111	111.1	111.2	111.3	111.4	112.5	112.4	112.3	112.2	112.1	112	113	114	115	116	117	118	Frame	CDR3-IMGT length	Molecular mass			
#1 Z70256	C	<u>V</u>	R	V	V	Q	<u>R</u>	L	V									P	K	Y	H	F	D	<u>H</u>	W	+	15	2,438.76		
#2 Z70257	C	A	R	D	G	S	<u>S</u>	Y	A									R	P	Y	W	Y	F	D	L	W	+	16	2,256.49	
#3 Z70606	C	A	R	A	T	T	H												Y	A	F	D	V	W	+	11	1,604.77			
#4 Z70608	C	A	R	V	T	I	F	G	V	V								I	P	R	G	N	A	F	D	I	W	+	18	2,426.78
#5 Z70610	C	A	R	V	G	S	D	F	<u>W</u>	S	G							Y	S	R	H	D	A	F	D	I	W	+	19	2,539.73
#6 Z70611	C	A	R	H	G	N	Y	N	A									G	V	D	W	F	D	P	W	+	15	2,072.21		
#7 Z70613	C	A	R	A	A	A	G											T	S	L	F	D	Y	W	+	12	1,531.71			
#8 Z70614	C	A	R	H	Y	N	<u>S</u>	G										T	Y	P	L	D	Y	W	+	13	1,846.01			
#9 Z70615	C	A	R	G	L	V	<u>K</u>	<u>R</u>	V									S	E	Y	W	Y	F	D	L	W	+	16	2,419.75	
#10 Z70616	C	A	R	A	G	L	G											S	H	W	F	D	P	W	+	12	1,602.8			
#11 Z70620	C	A	R	D	R	G	<u>G</u>	H										<u>V</u>	R	D	A	F	D	I	W	+	14	1,932.17		
#12 Z70621	C	A	R	H	H	D	L	W	F									G	E	F	D	P	L	D	Y	W	+	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	+					

V-DOMAINS

VH

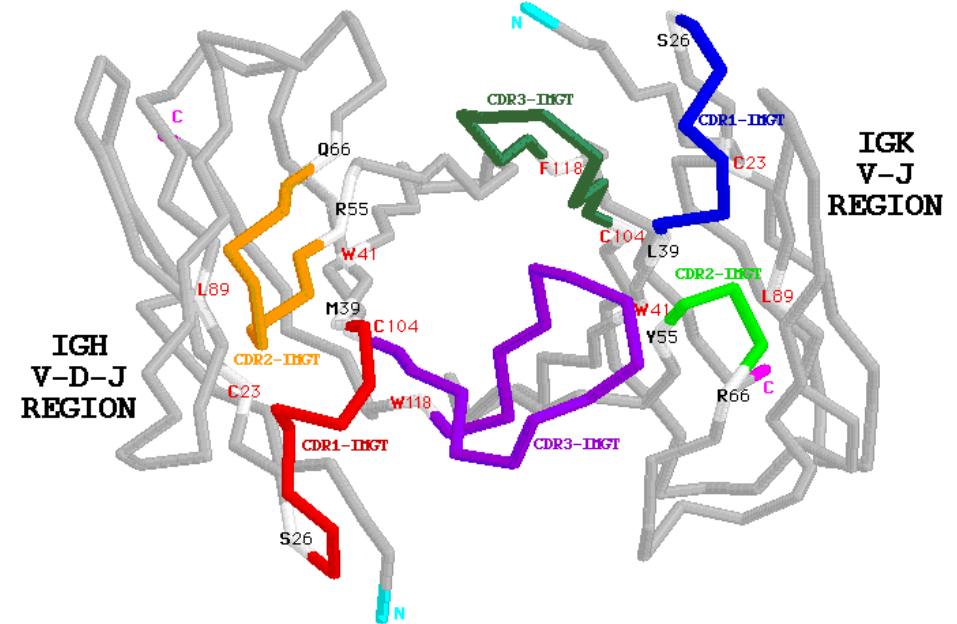
V-KAPPA



Side view

VH

V-KAPPA



View from above

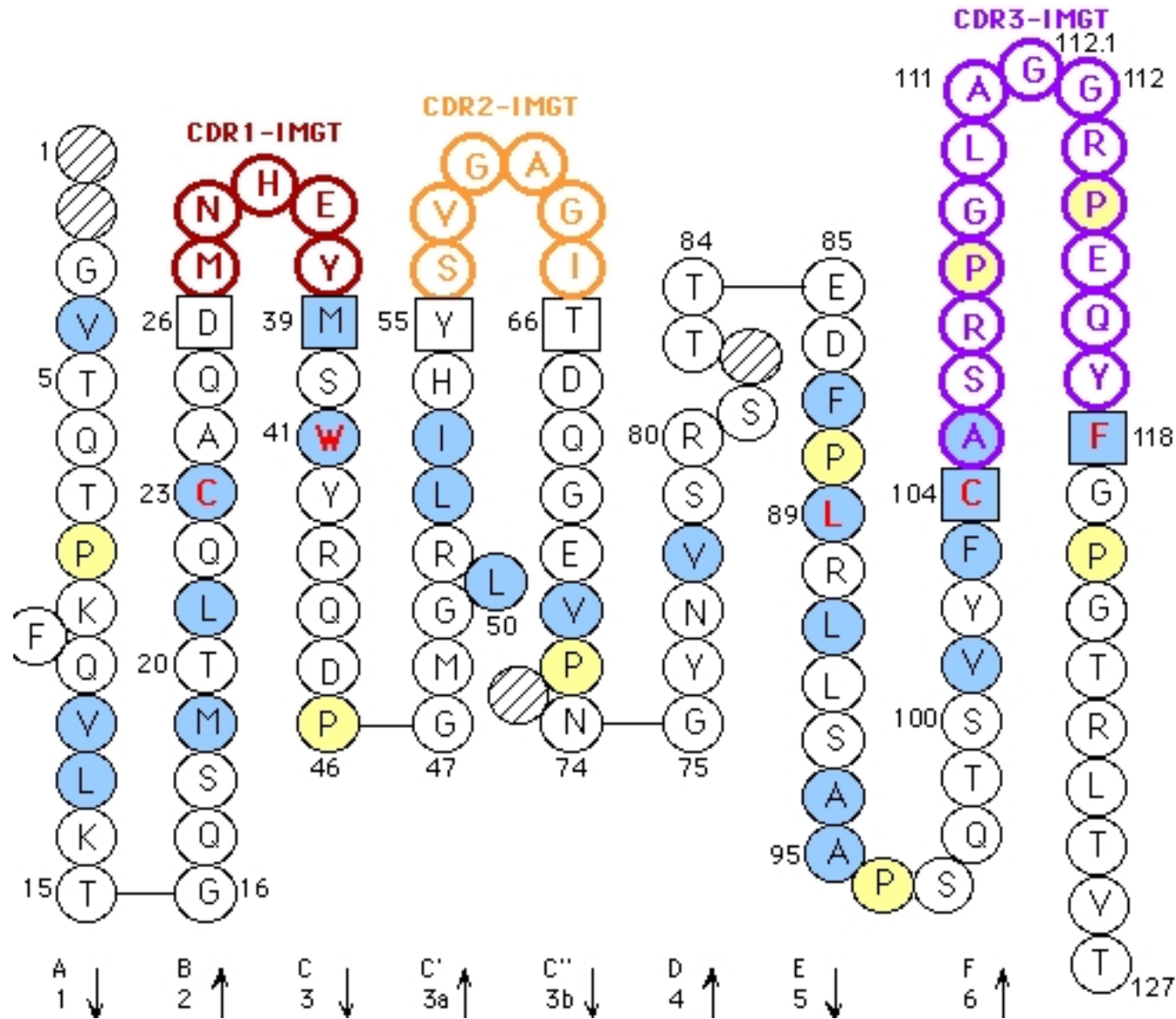
Mouse (*Mus musculus*) E5.2Fv

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

V-J junction (104-118)

V-D-J junction (104-118)

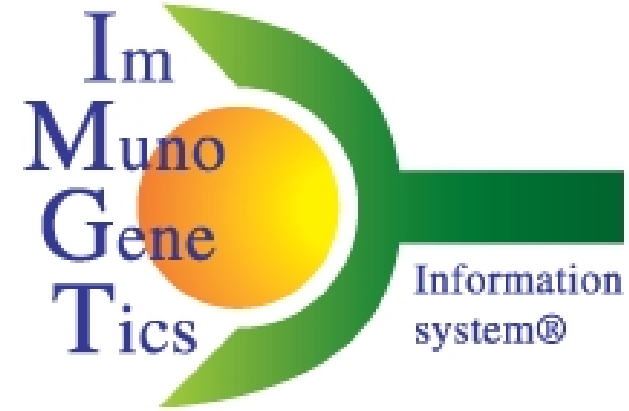
IMGT Collier de Perles



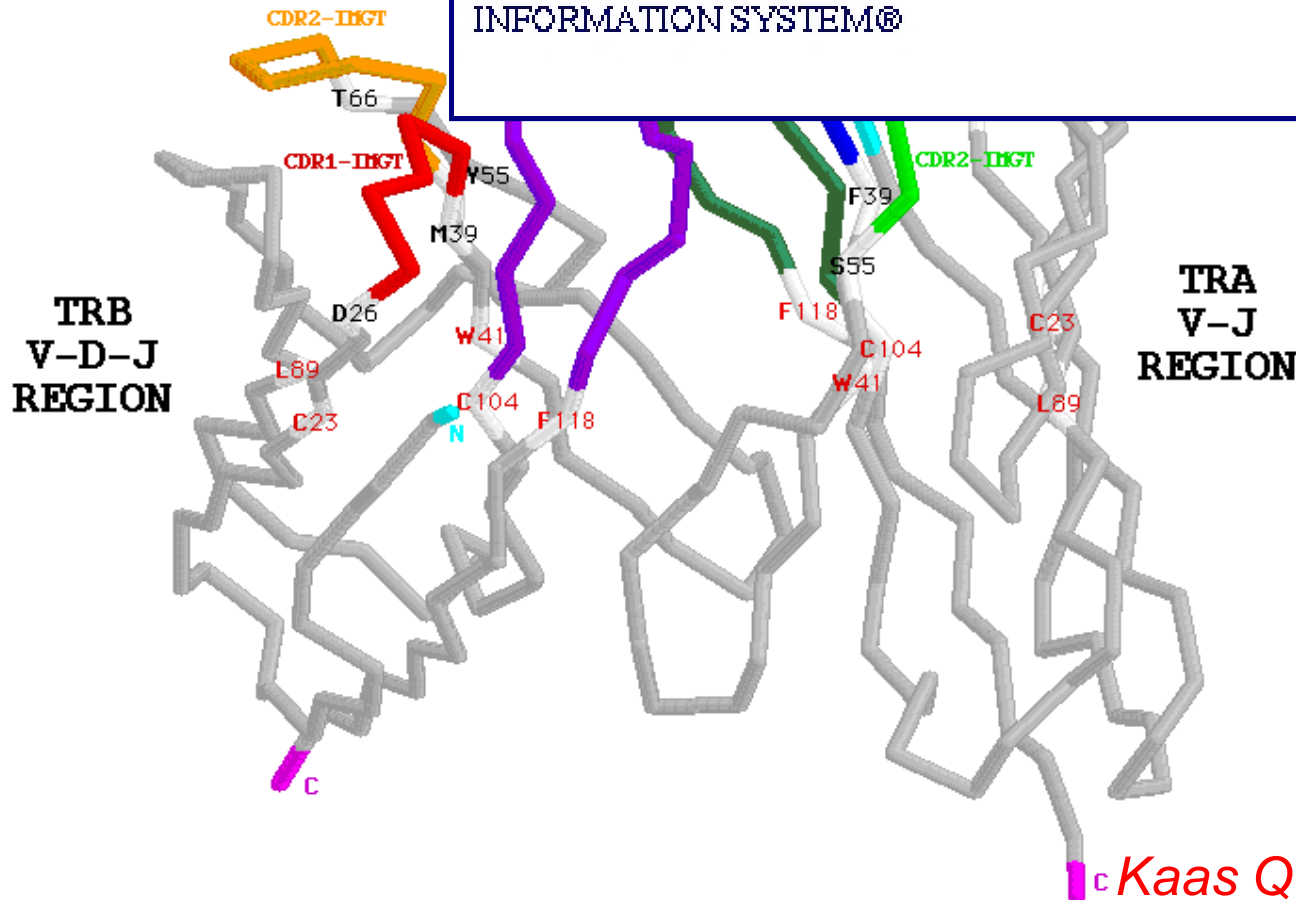
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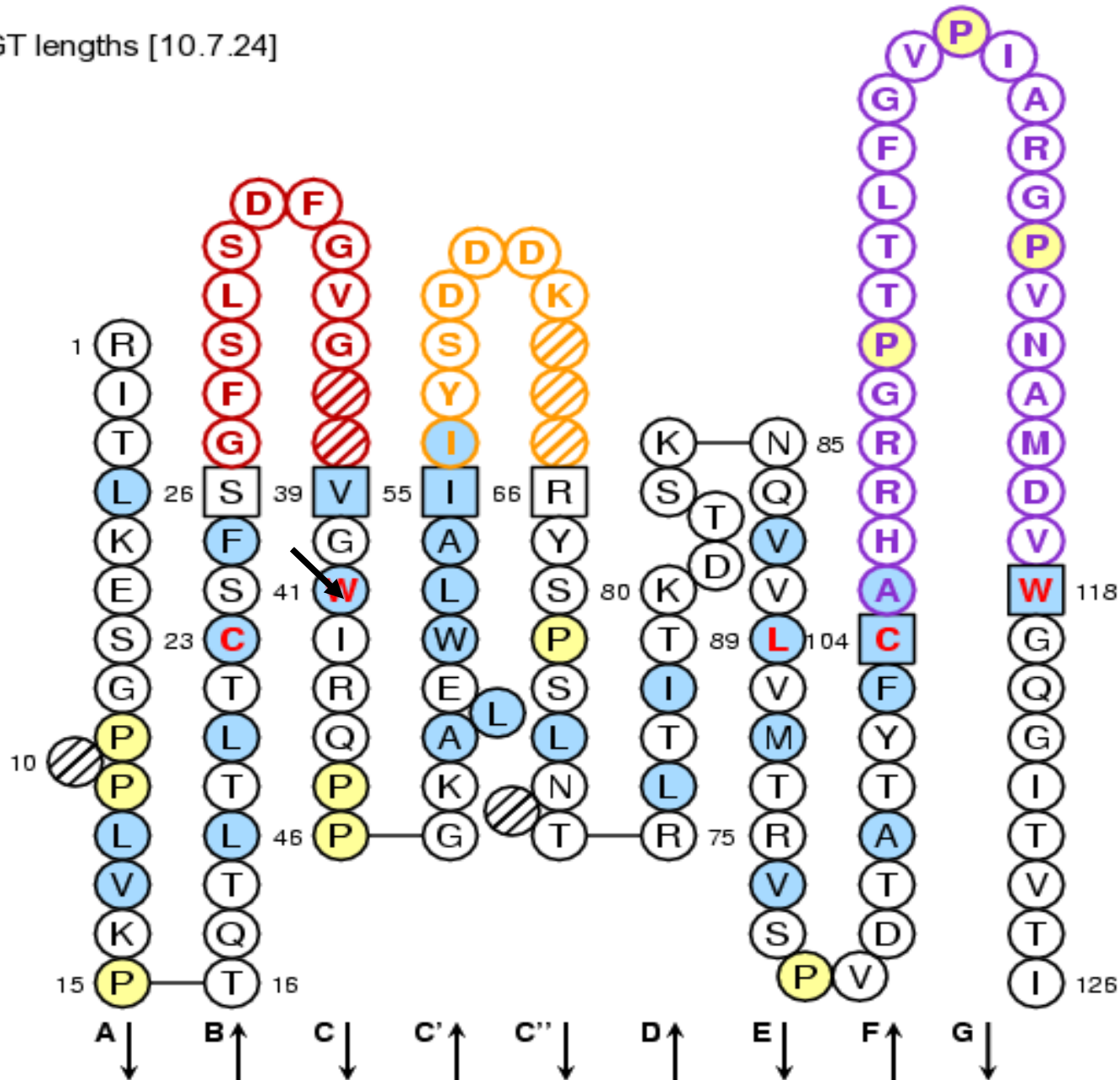


<http://imgt.cines.fr>



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

CDR-IMGT lengths [10.7.24]



Contact analysis

41V - TRP (W)

chain : 1u8k_B

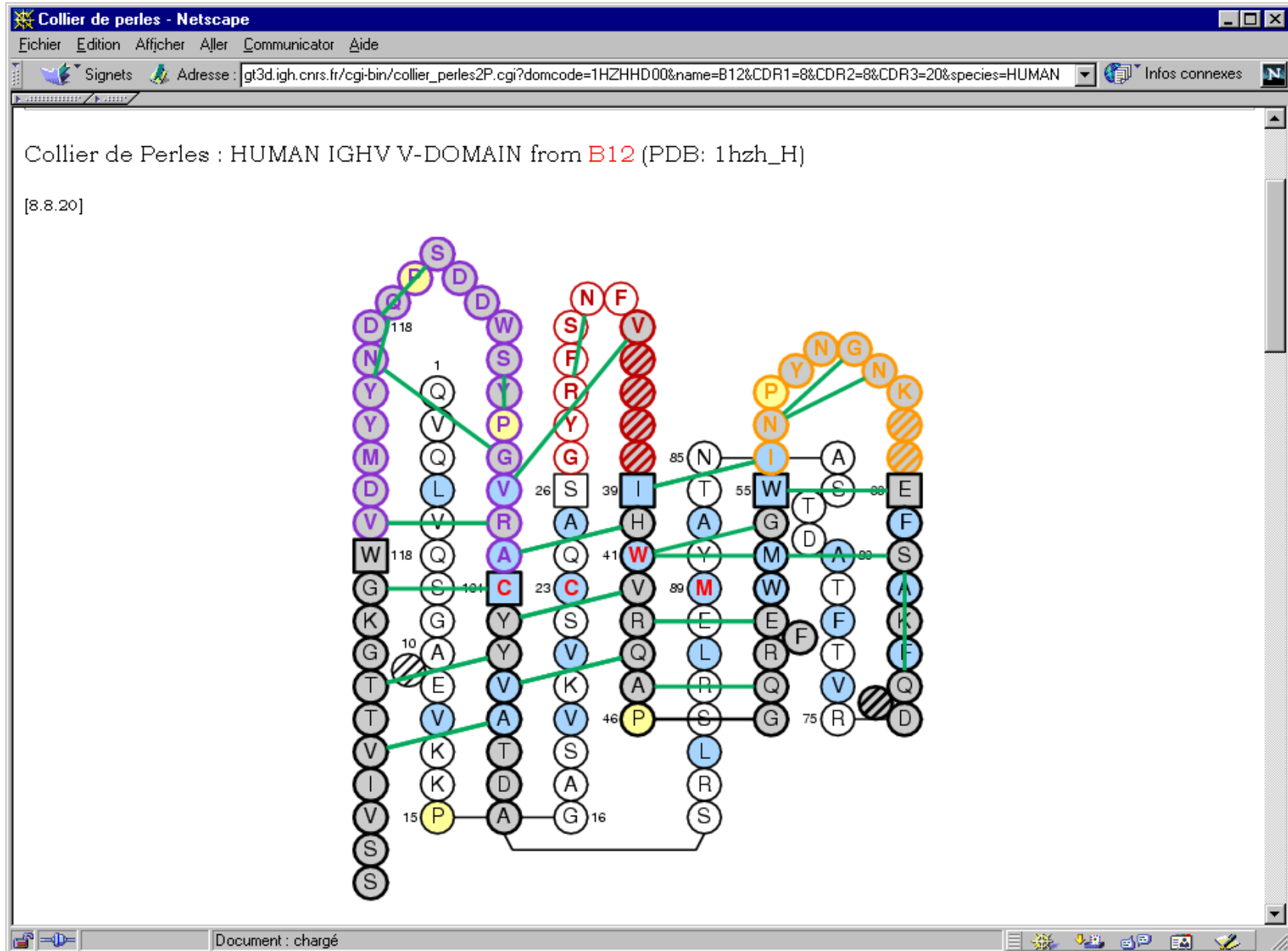
Secondary structure	Extended conformation
Phi	-122.64
Psi	137.12
ASA	0.0

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

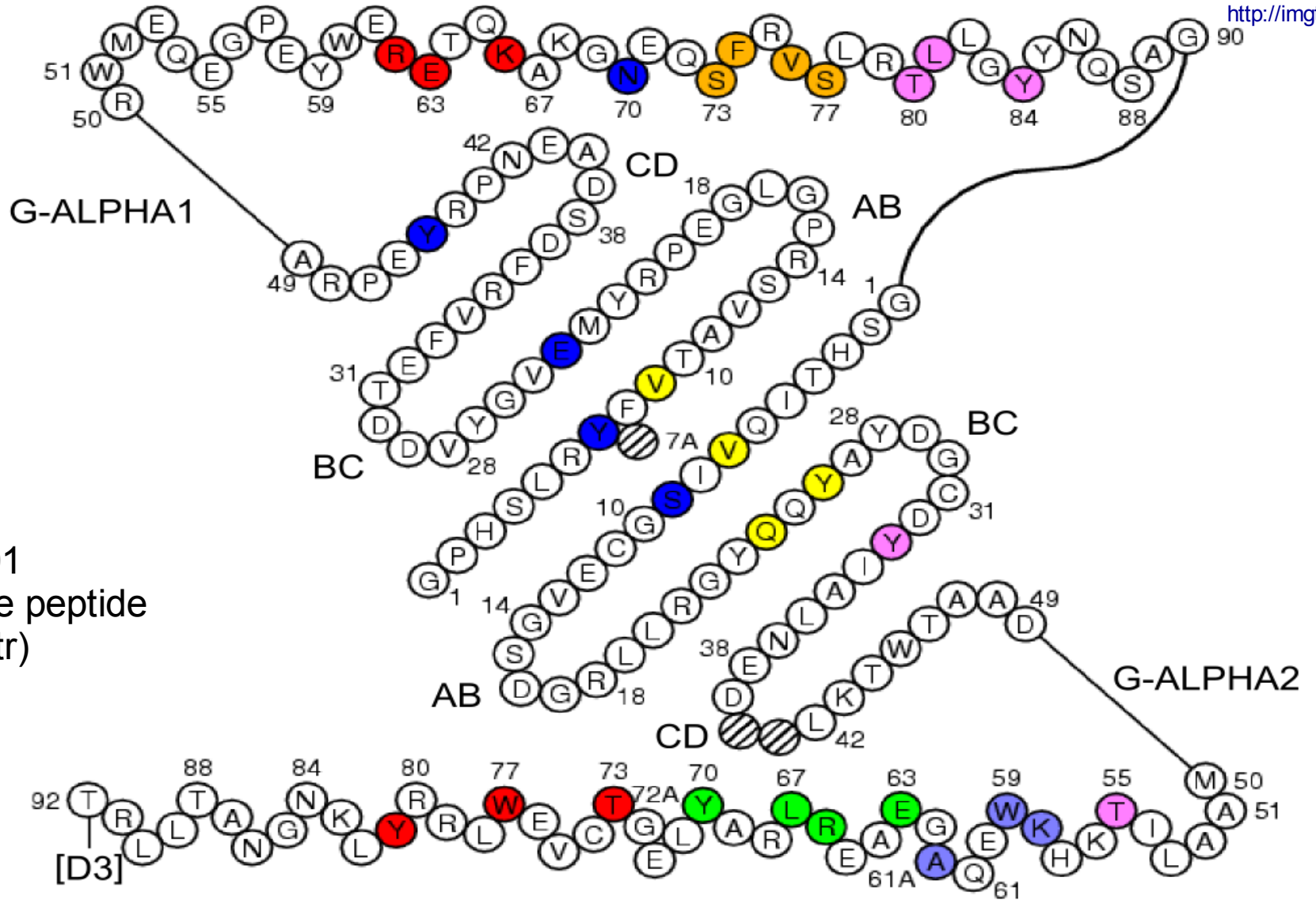
Tot	Total number of atomic pair contacts
NCov	Number of non covalent atomic
Pol	Number of polar atomic pair contacts
HB	Number of hydrogen bonds
NPol	Number of non polar atomic pair contacts
Cov	Number of covalent links (other than chain covalent links)
SS	Number of disulfide bridges

IMGT Collier de Perles



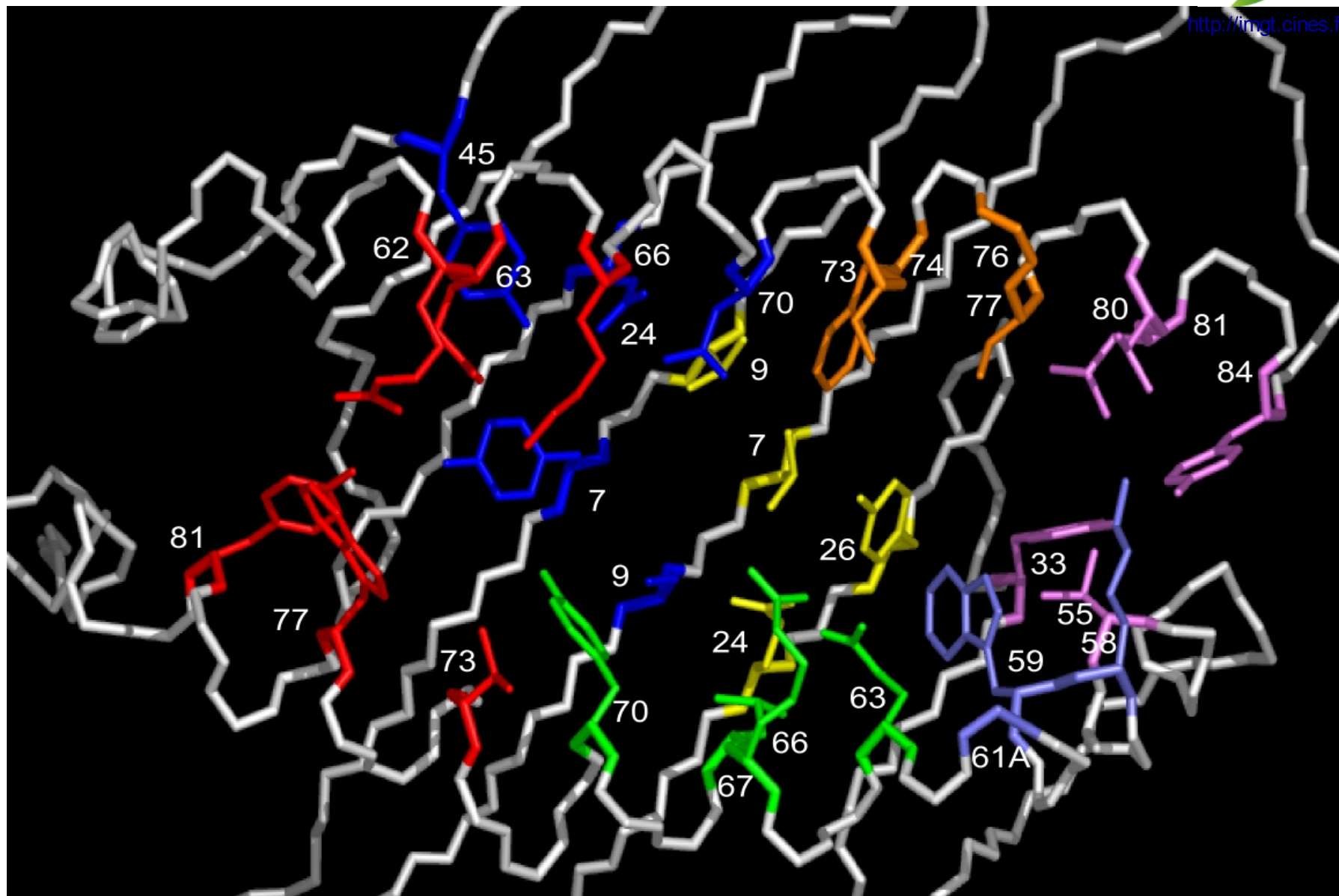
MHC class I IMGT contact sites

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)

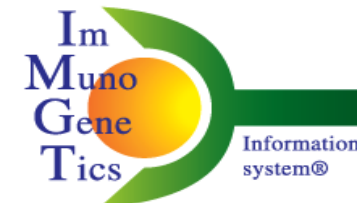
IMGT pMHC contact sites



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

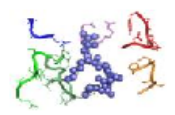
THANK YOU

for using [IMGT/3Dstructure-DB](#)



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IMMUNOGENETICS
INFORMATION SYSTEM®

<http://imgt.cines.fr>



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		<i>Homo sapiens</i> (Human)	1	[1bx2_A1bx2_B]
	MHC	MHC-II-ALPHA_BETA		<i>Homo sapiens</i> (Human)	2	[1bx2_D1bx2_E]
		Peptide	Myelin basic protein MBP peptide 117-230 (P02686)	<i>Homo sapiens</i> (Human)	1	[1bx2_C]
		Peptide		<i>Homo sapiens</i> (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
 - Polar
 - 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
-

Contacts summary:

IMGT/3Dstructure-DB Domain contacts

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

Atom contact types

Non covalent
 Polar
 Hydrogen bond
 Non polar

Covalent
 Disulfide

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

Check all
 Uncheck all

Check all
 Uncheck all

Contacts summary:

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

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

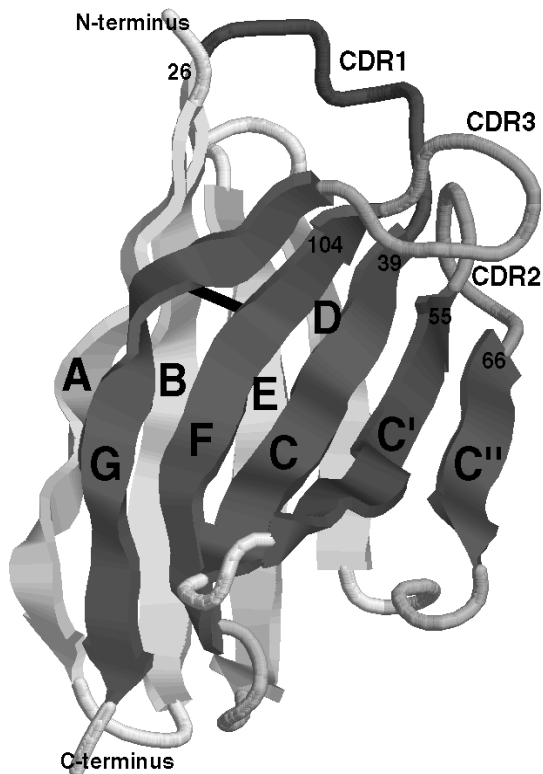
Residue@Position contacts:

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

<u>Order</u>					<u>Order</u>				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

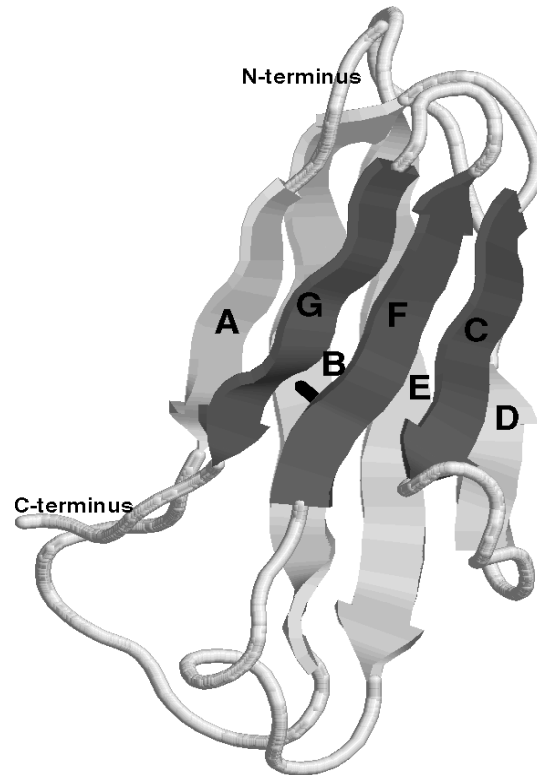
IMGT unique numbering

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

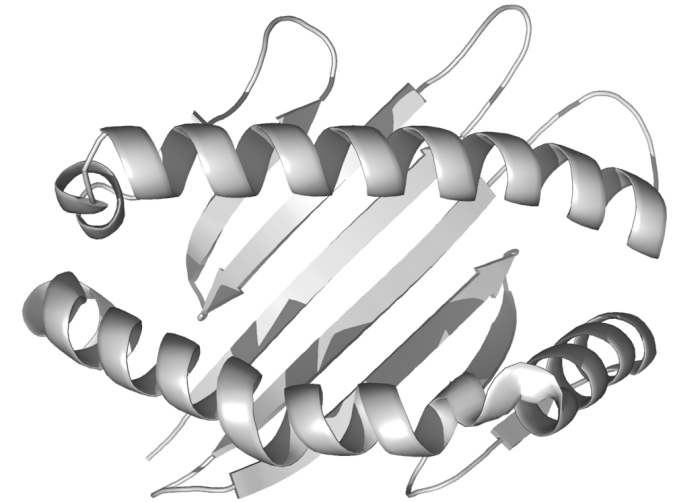


Immunoglobulin superfamily (IgSF)

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



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

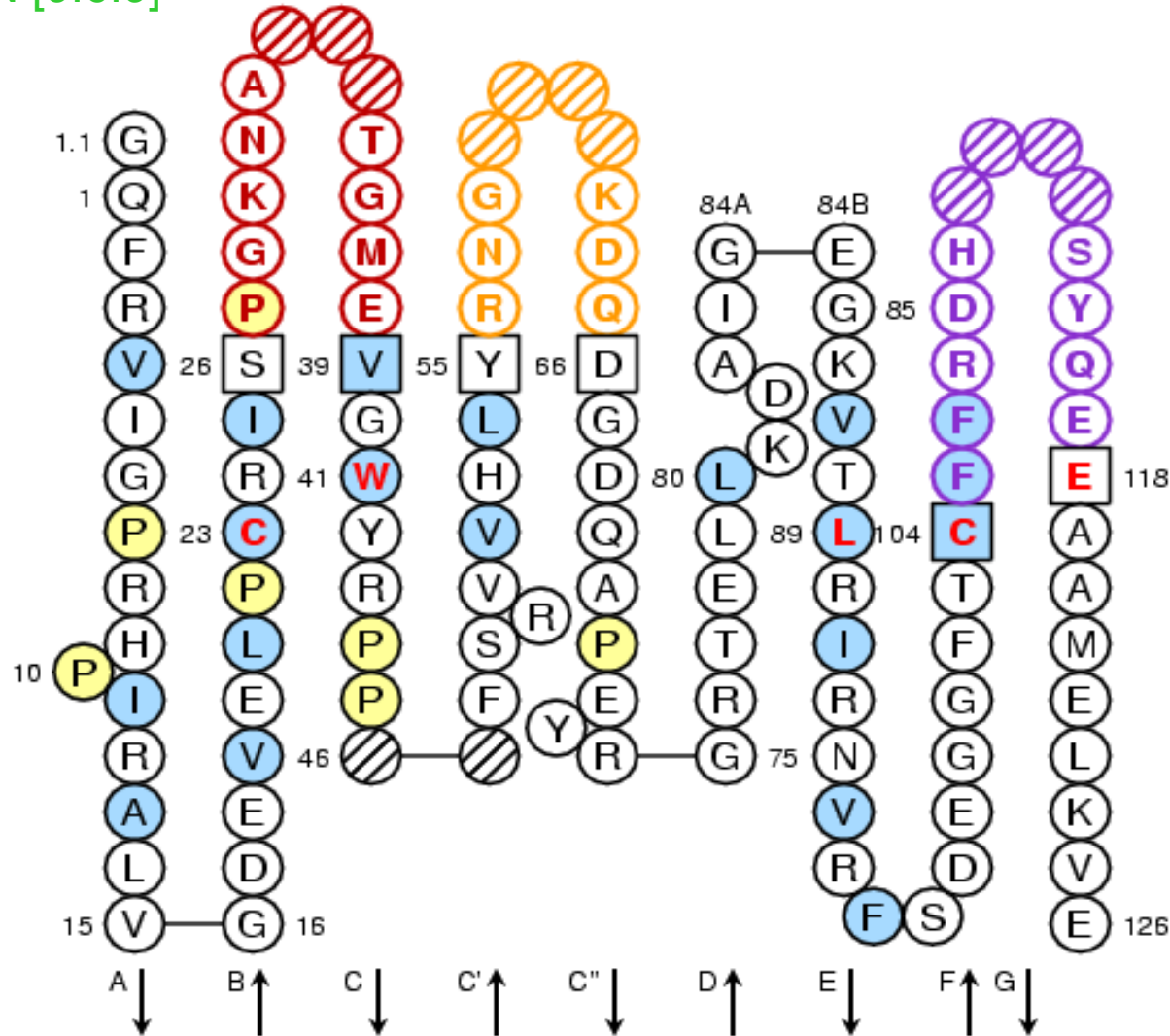


MHC superfamily (MhcSF)

IMGT Collier de Perles

Homo sapiens MOG (P13688)

V-LIKE-DOMAIN [9.6.9]

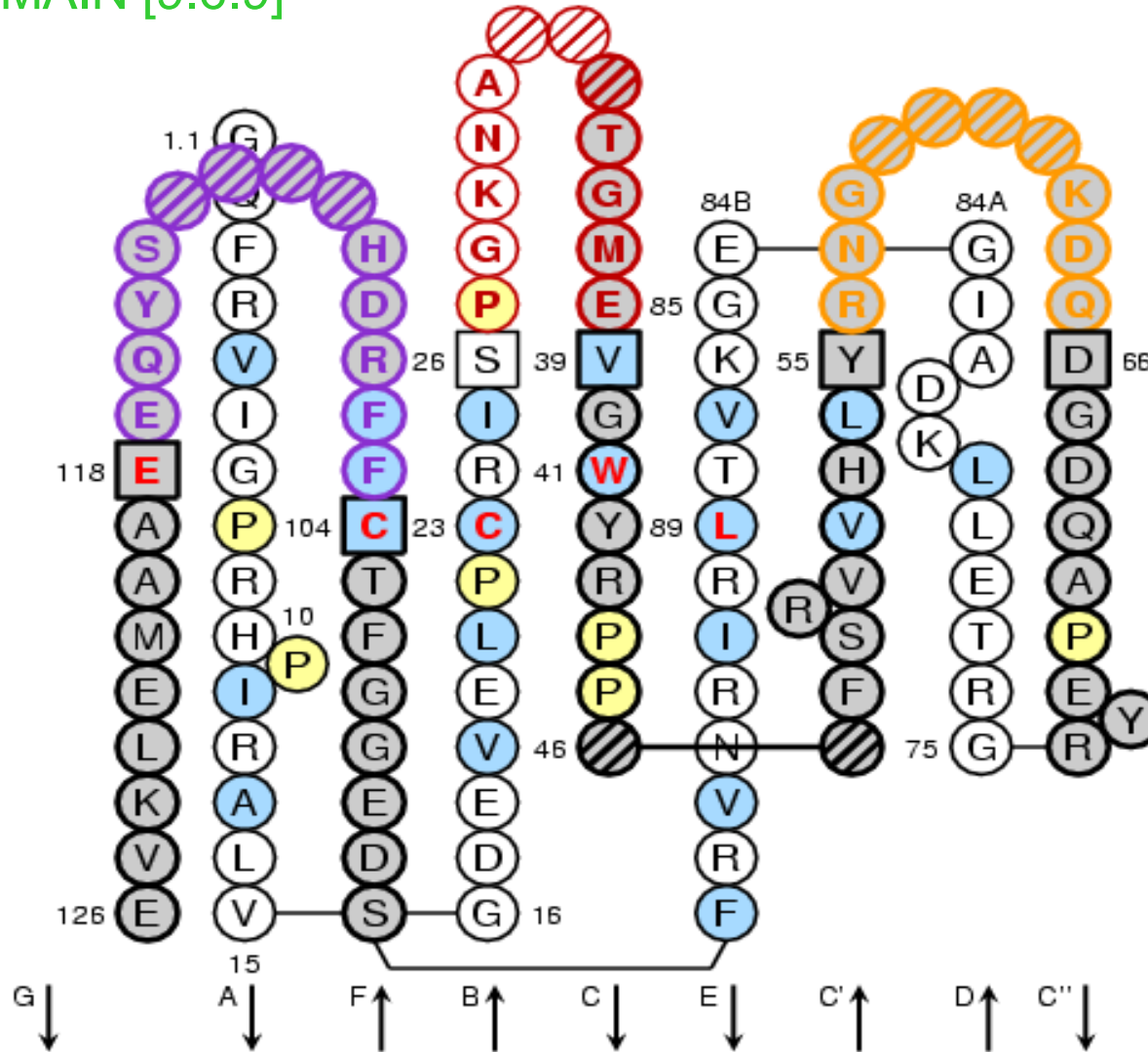


Duprat E. et al. Recent Res. Devel. Human Genet. 2, 111-136 (2004)

IMGT Collier de Perles

Homo sapiens MOG (P13688)

V-LIKE-DOMAIN [9.6.9]

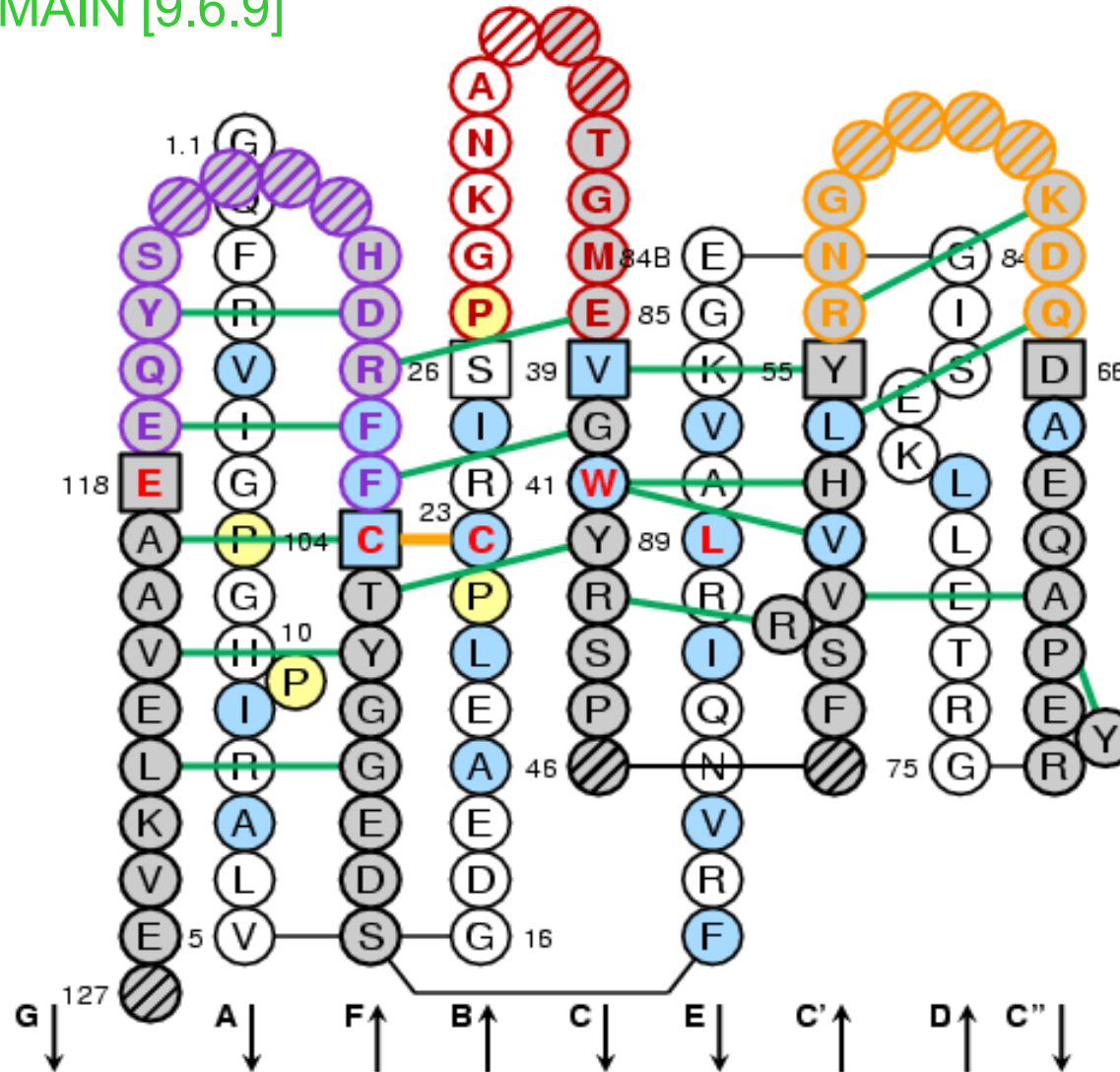


Duprat E. et al. Recent Res. Devel. Human Genet. 2, 111-136 (2004)

IMGT Collier de Perles

Rattus norvegicus MOG (1pkq_E)

V-LIKE-DOMAIN [9.6.9]



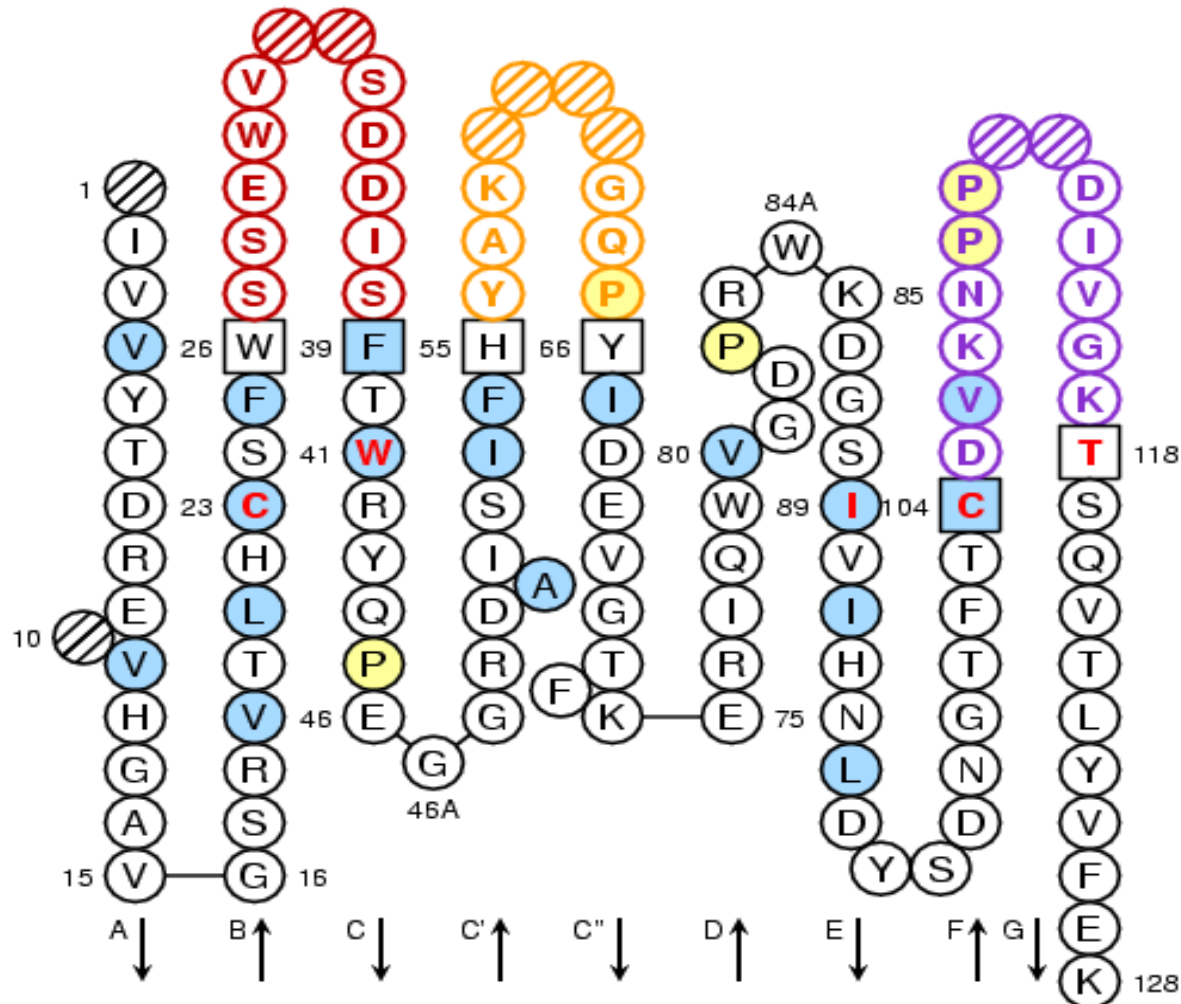
IMGT Collier de Perles

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>

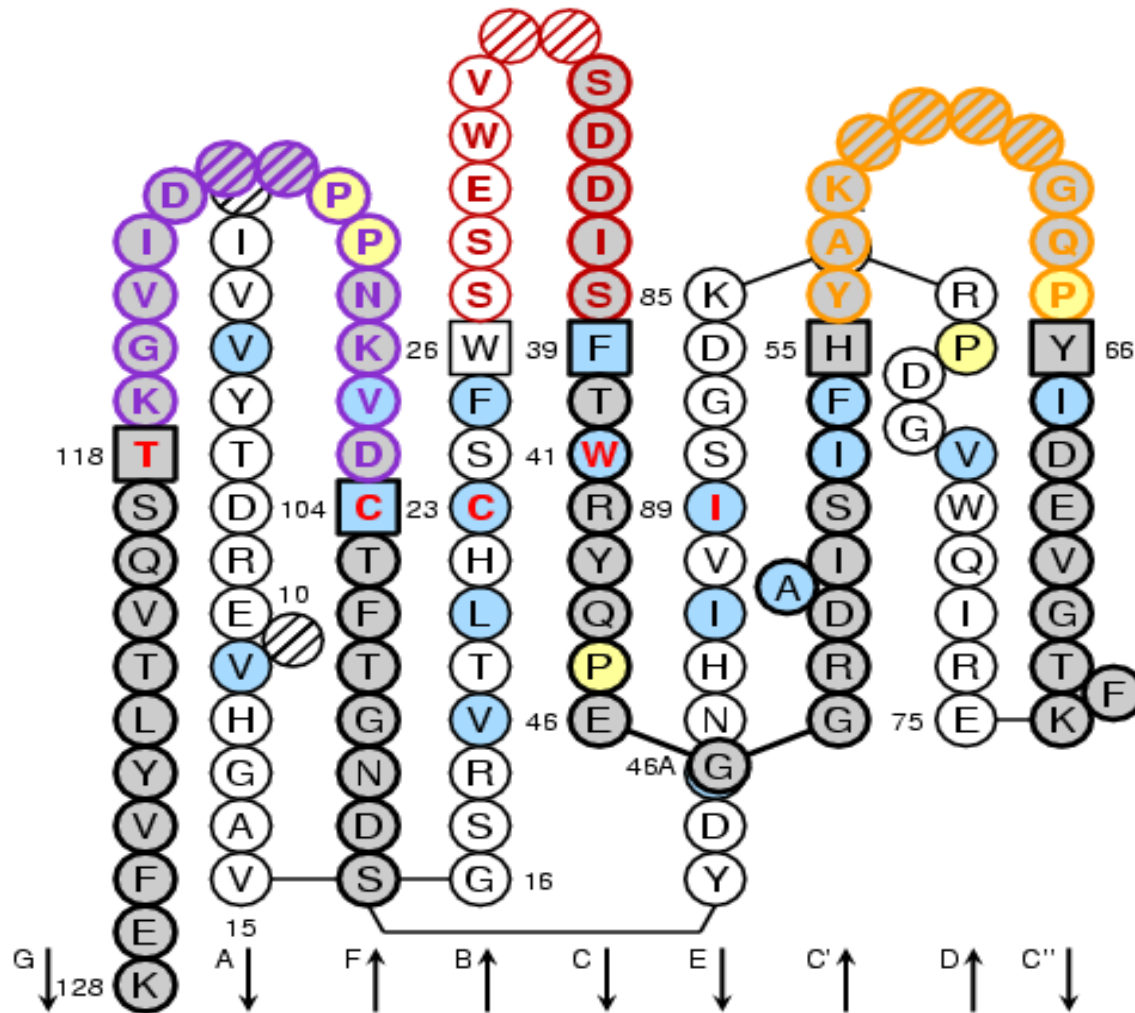


Duprat E. et al .Recent Res. Devel. Human Genet. 2, 111-136 (2004)

IMGT Collier de Perles

Homo sapiens MPZ (P25189)

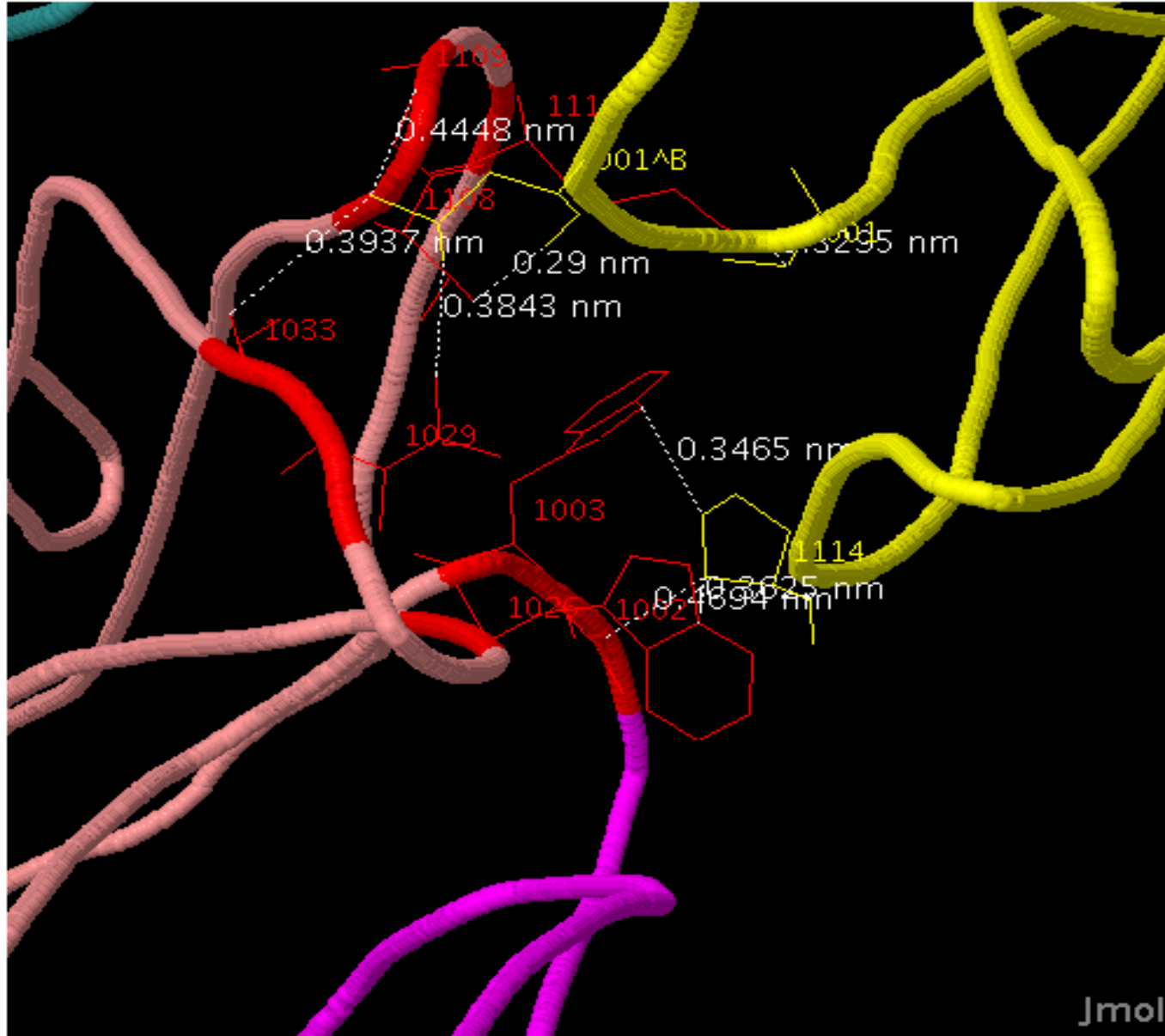
V-LIKE-DOMAIN [10.6.11]



Interactions between domains

FCGR3
B

[D2
D-LIKE-
DOMAIN



[D1] C-LIKE-DOMAIN

IGHG1
(FC-GAMMA1)

CH2
C-DOMAIN

What is available in the frame of the MARIE ESF network:

- IG and TR sequences
Databases: IMGT/LIGM-DB, IMGT/GENE-DB
Tools: IMGT/V-QUEST, IMGT/JunctionAnalysis
Web resources: IMGT Repertoire

- IG, TR, MHC, IgSF and MhcSF structures
based on the IMGT unique numbering
Database: IMGT/3Dstructure-DB
Tools: IMGT Collier de Perles, ...

- IMGT-ONTOLOGY

Perspectives:

19. Enhance query on interactions between epitopes and antigen receptors
20. Enhance query on specificities



The IMGT team at Montpellier