

IMGT-ONTOLOGY

et analyse des répertoires immunitaires

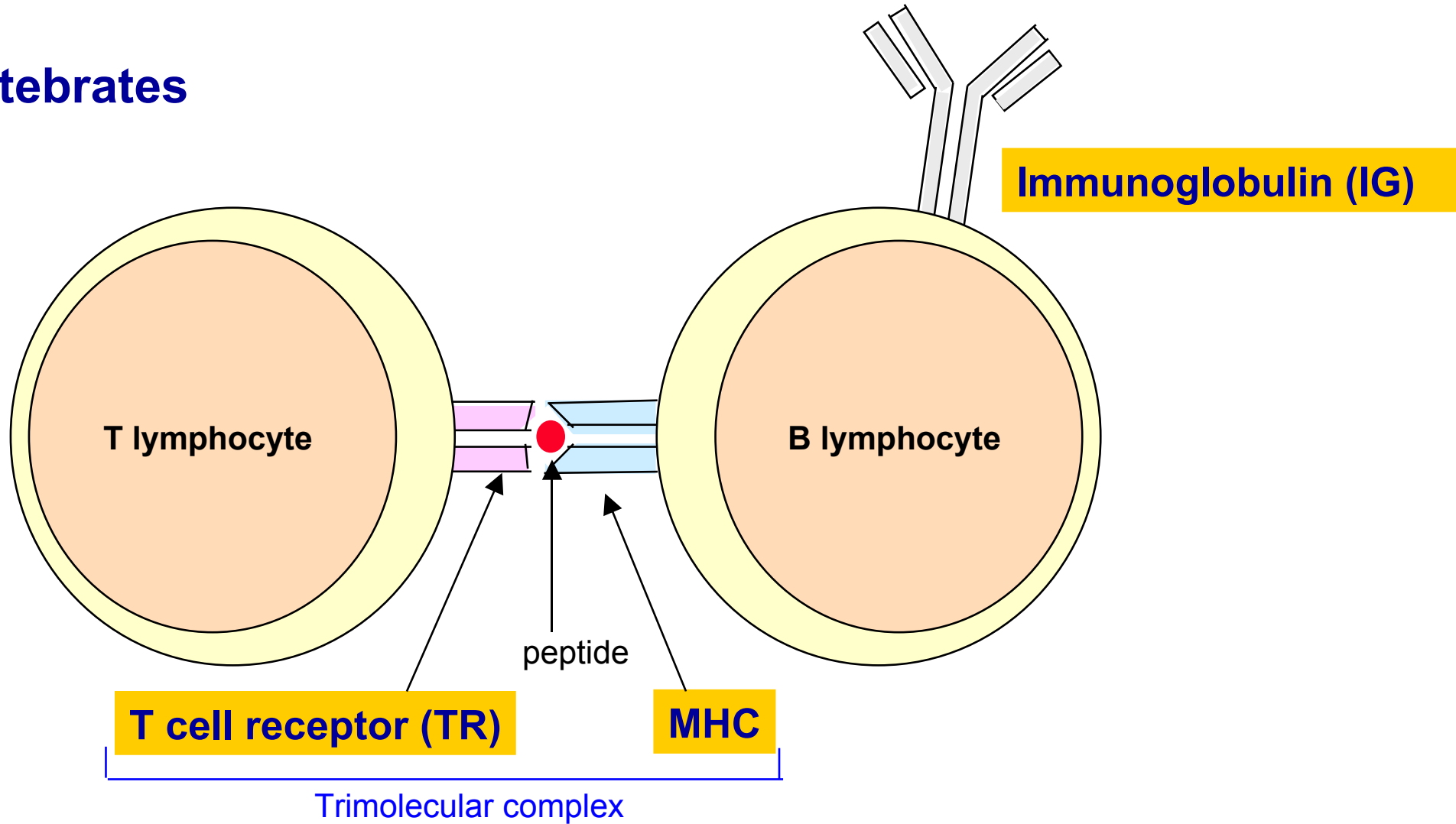
Marie-Paule Lefranc

Université Montpellier 2, IGH, UPR CNRS 1142

Institut Universitaire de France

24 ème Atelier Technologique de la Société Française d'Immunologie
Lyon, 26 novembre 2007

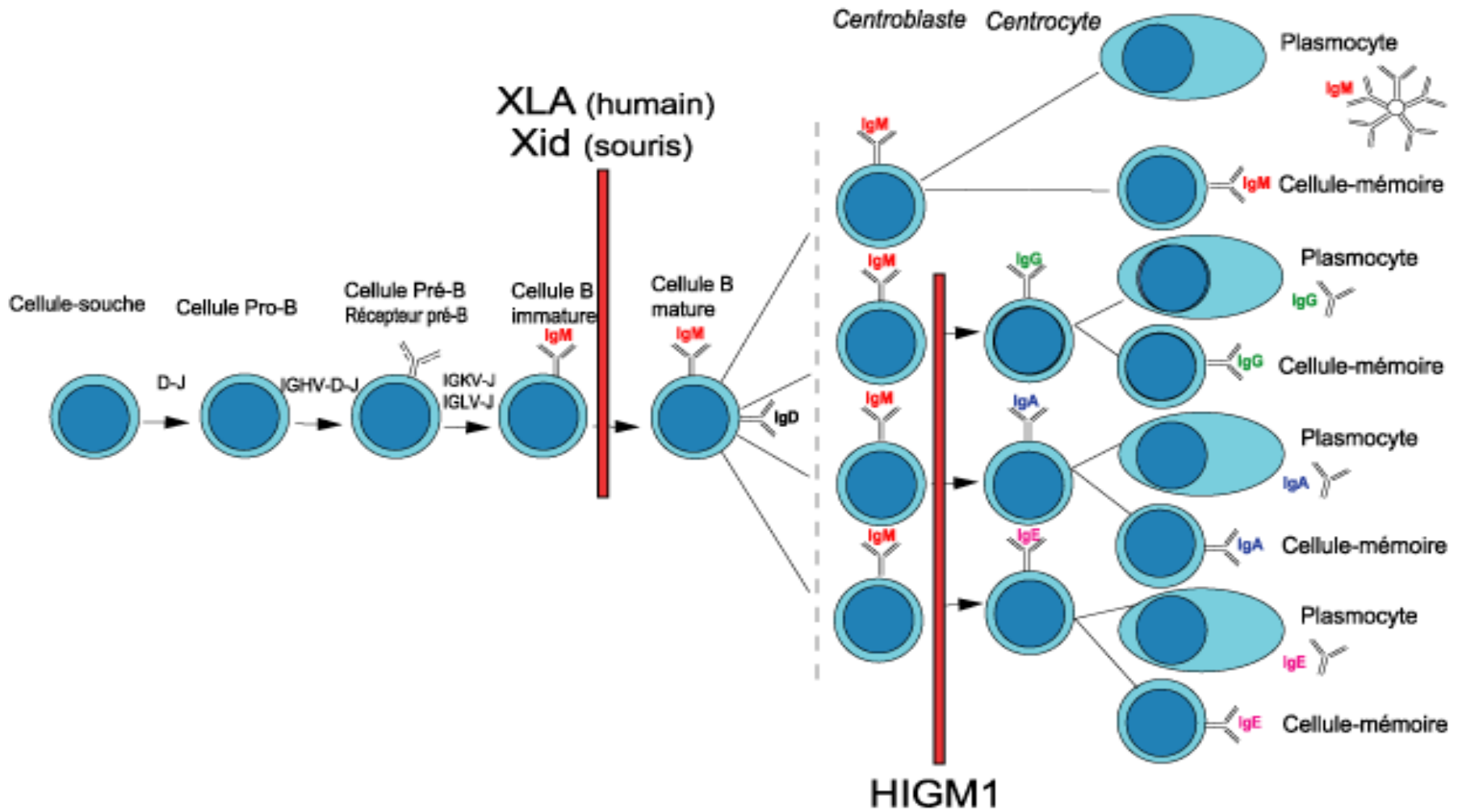
Vertebrates



Bone marrow

Blood

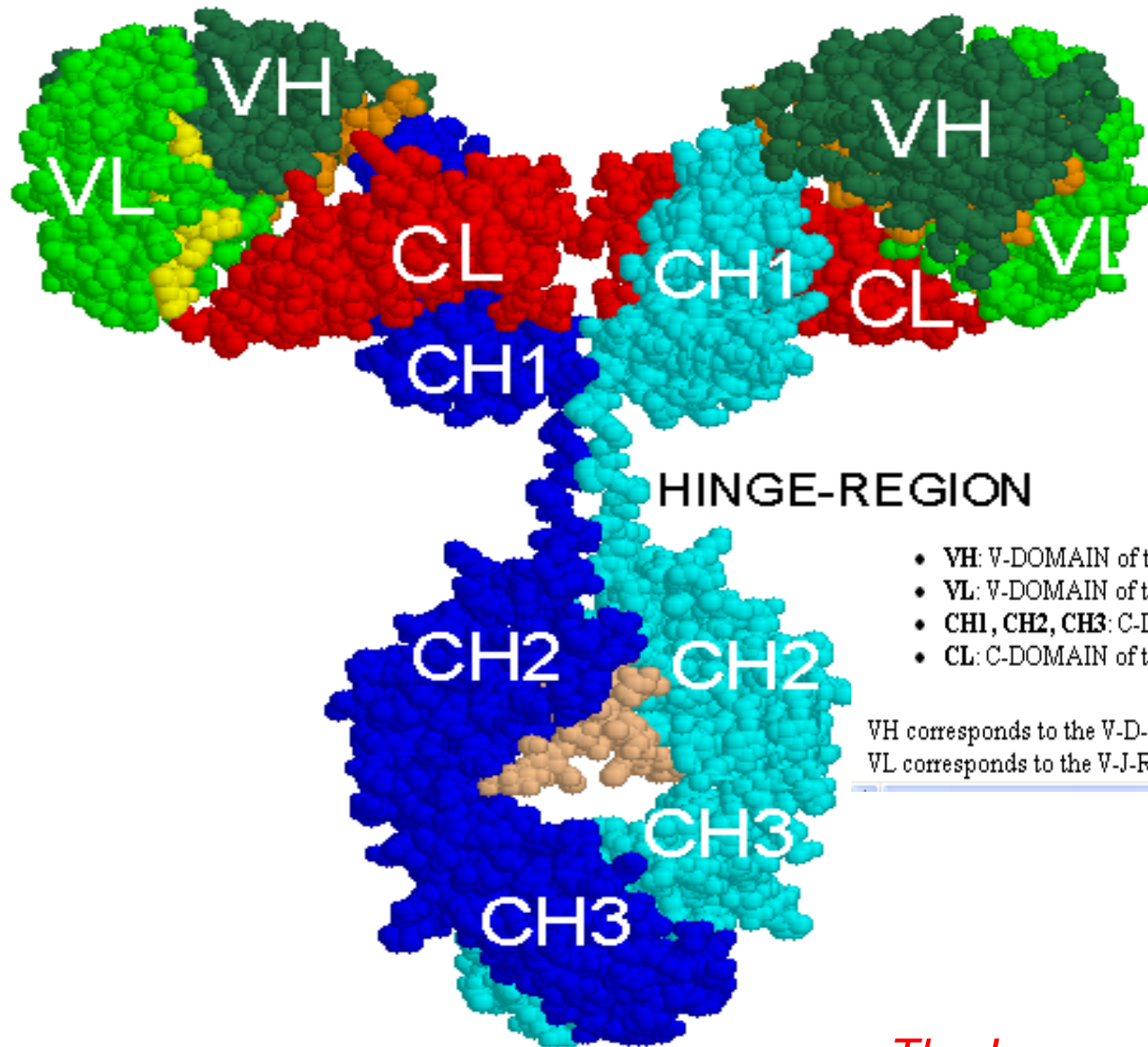
Lymph nodes, spleen



V-D-J and V-J
rearrangements

Hypermutations,
selection

Spacefill 3D representation of an IgG



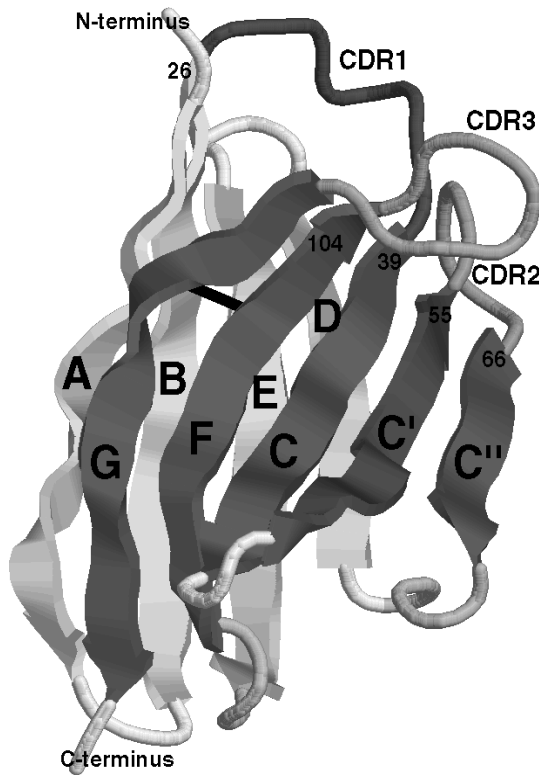
- **VH**: V-DOMAIN of the immunoglobulin heavy chain
- **VL**: V-DOMAIN of the immunoglobulin light chain
- **CH1, CH2, CH3**: C-DOMAIN of the immunoglobulin heavy chain
- **CL**: C-DOMAIN of the immunoglobulin light chain

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.

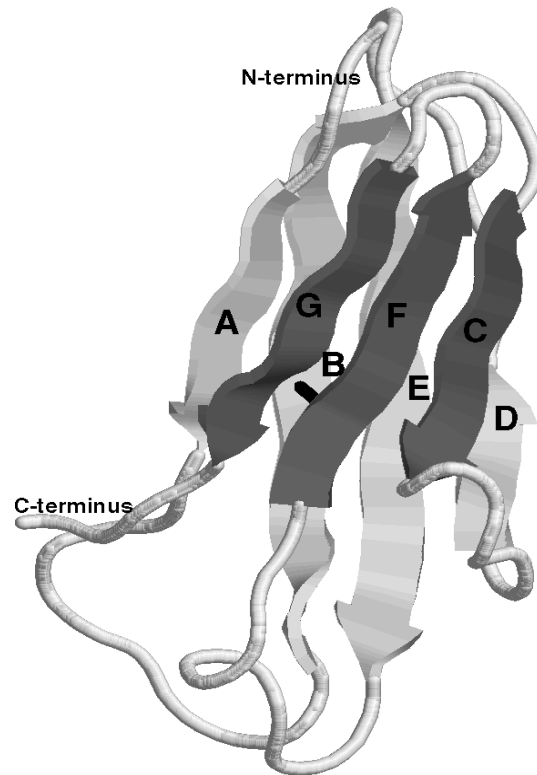
Structural domains

IG and TR

V-DOMAIN



C-DOMAIN



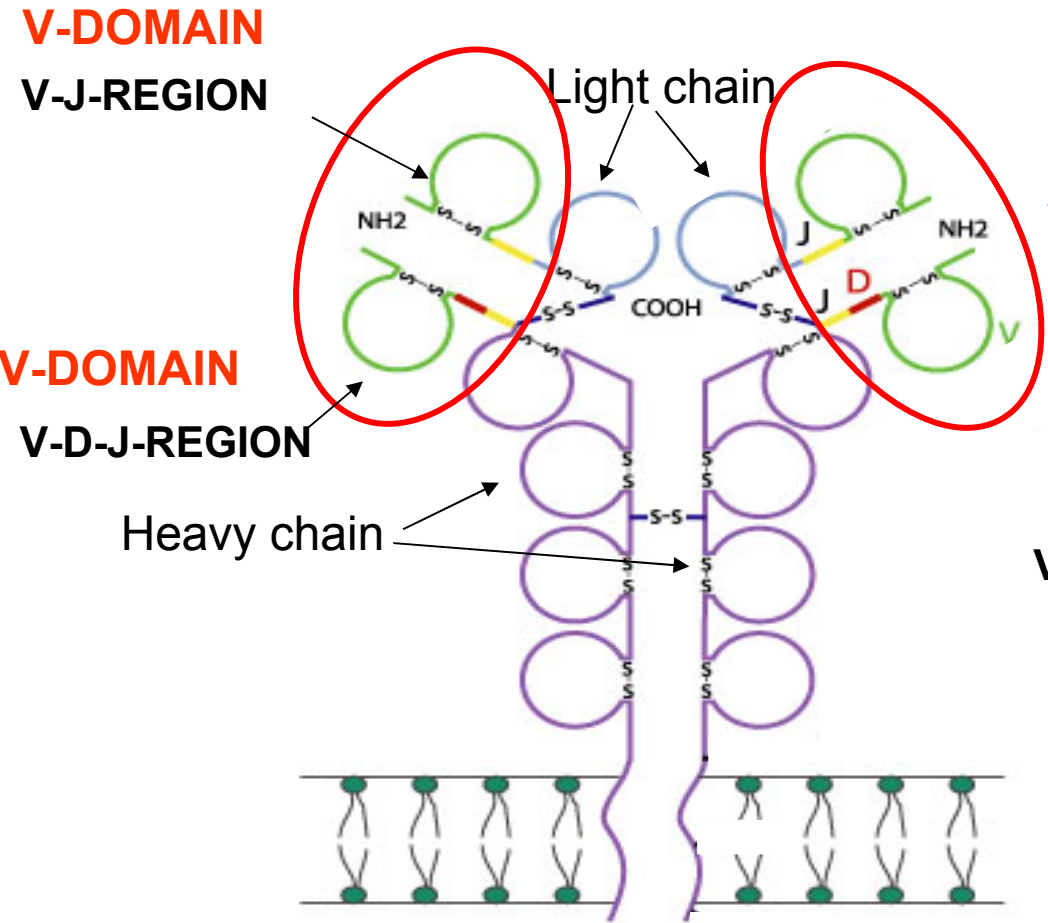
MHC

G-DOMAINS

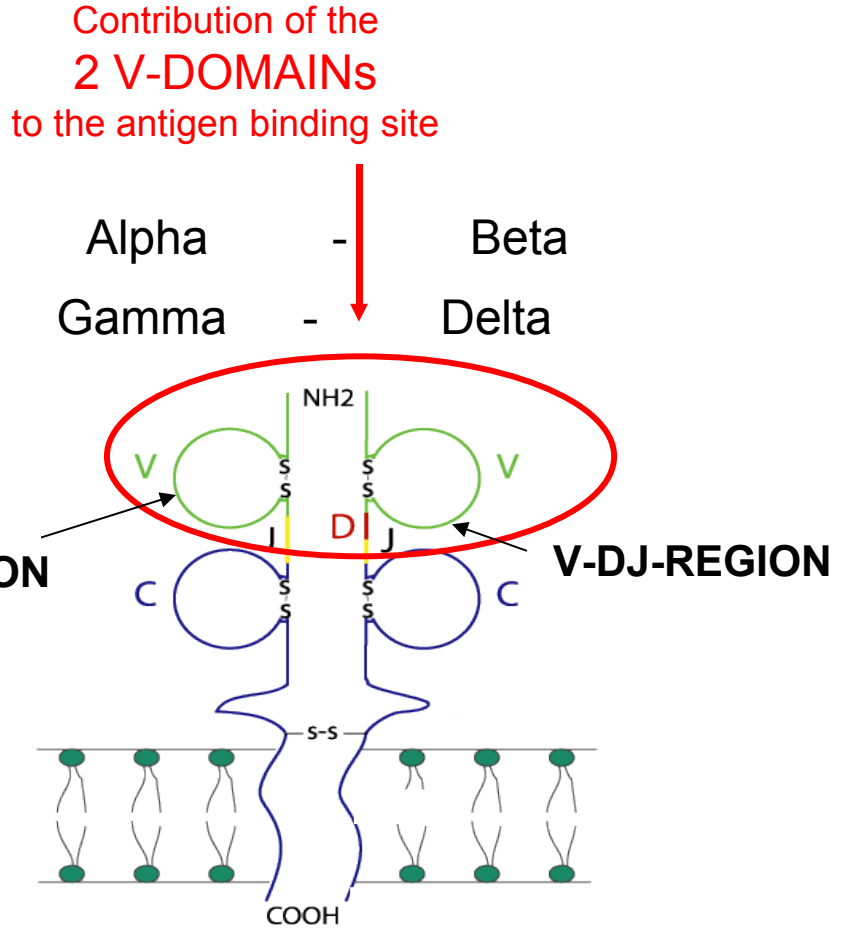


Immunoglobulin (IG)

T cell receptor (TR)

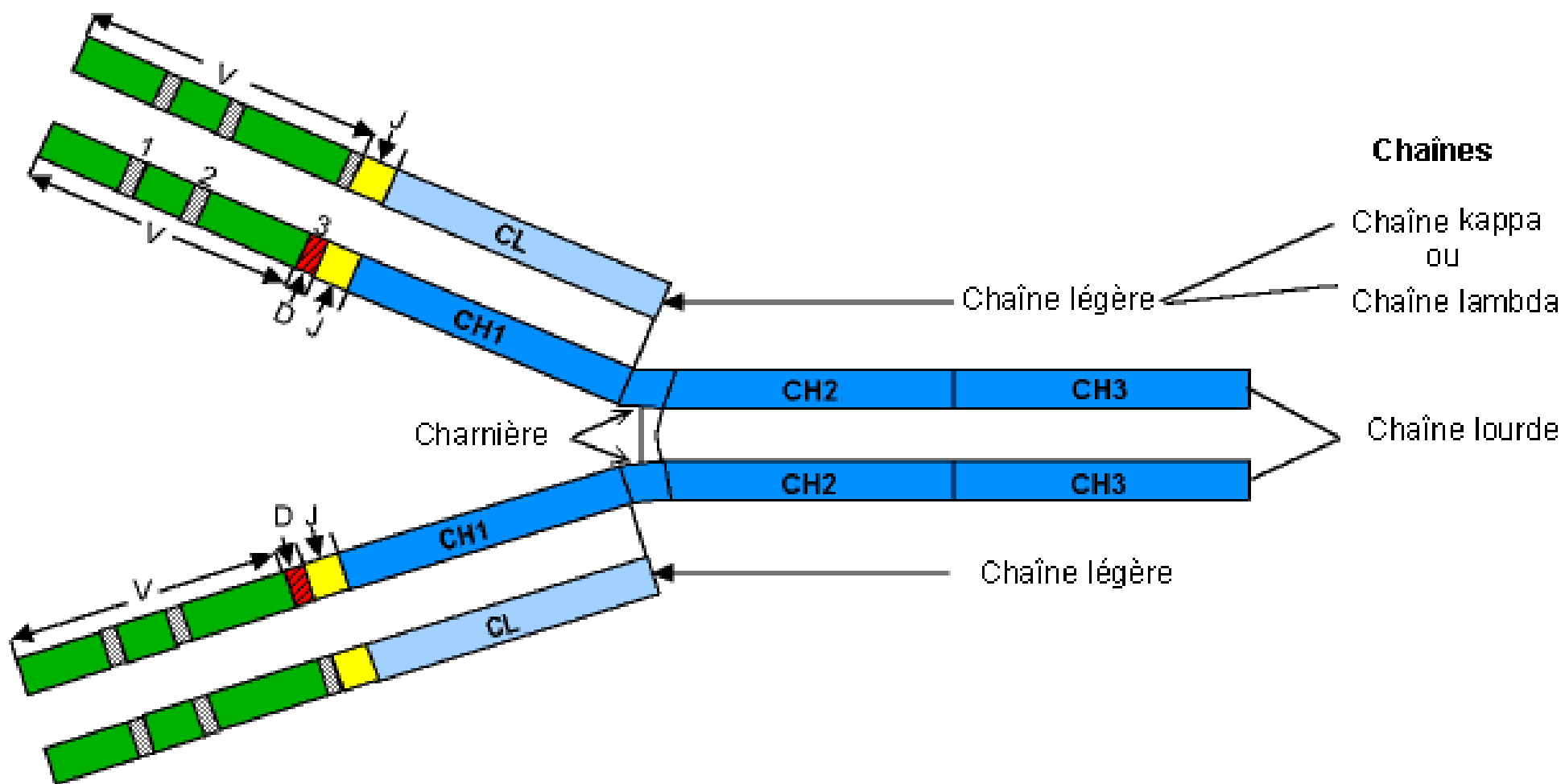


Membrane IgM



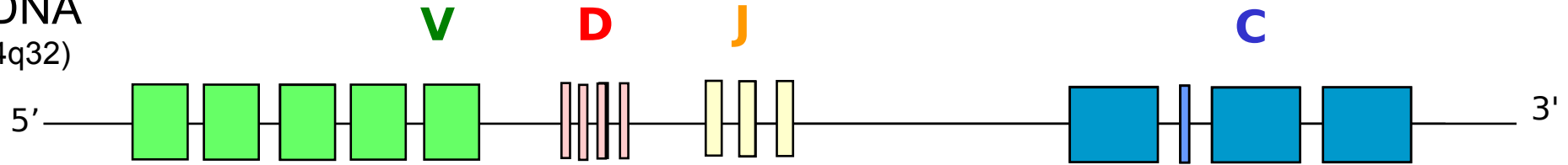
T cell receptor

Immunoglobulin IgG

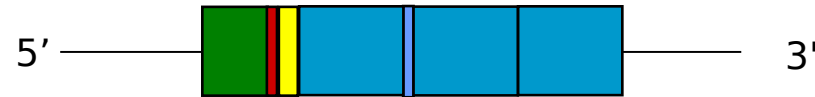


Immunoglobulin (IG) synthesis

genomic DNA
(IGH Locus 14q32)

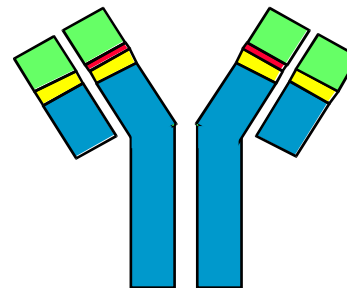


rearranged
DNA



mRNA

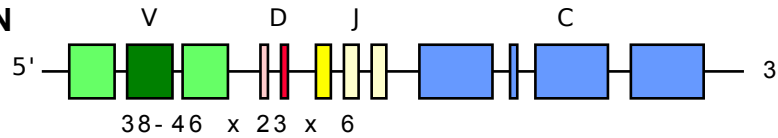
2×10^{12} different IG
per individual



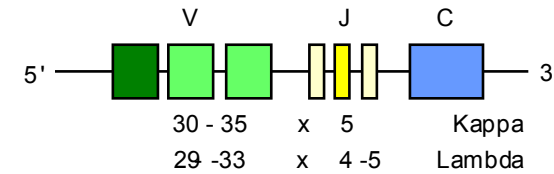
Immunoglobulin (IG) synthesis

150 FUNCTIONAL IG GENES

HEAVY CHAIN



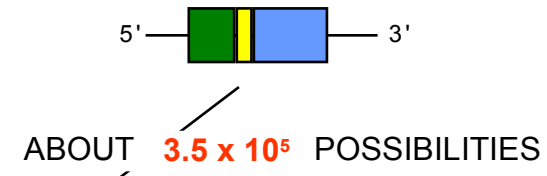
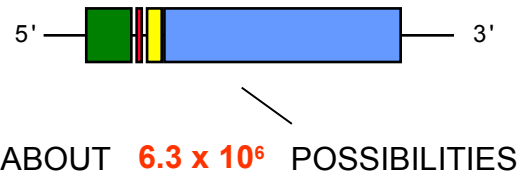
LIGHT CHAIN



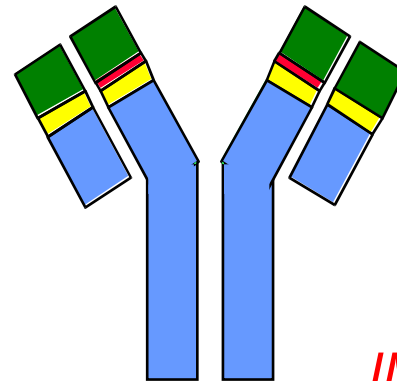
6300 POTENTIAL RECOMBINATIONS

185 + 165 POTENTIAL RECOMBINATIONS

N-DIVERSITY
SOMATIC MUTATIONS
x 1000



2×10^{12}
DIFFERENT ANTIBODIES

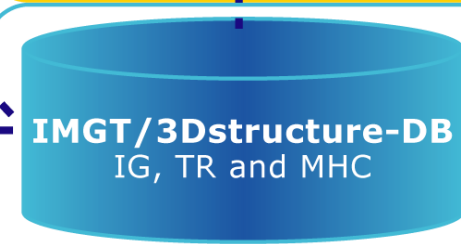
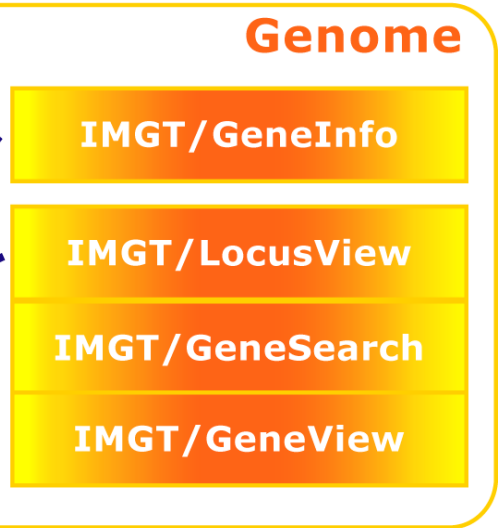
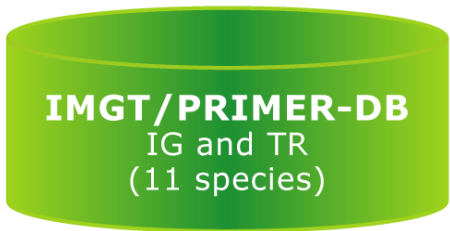


IMGT databases and tools

Sequences



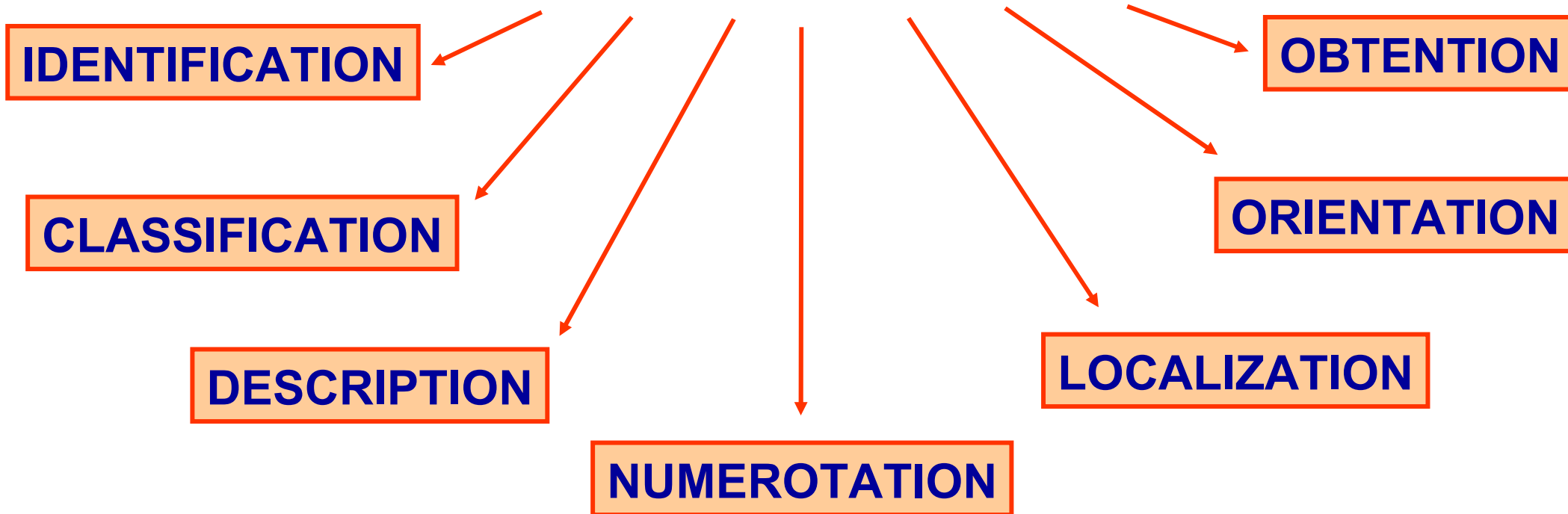
<http://imgt.cines.fr>



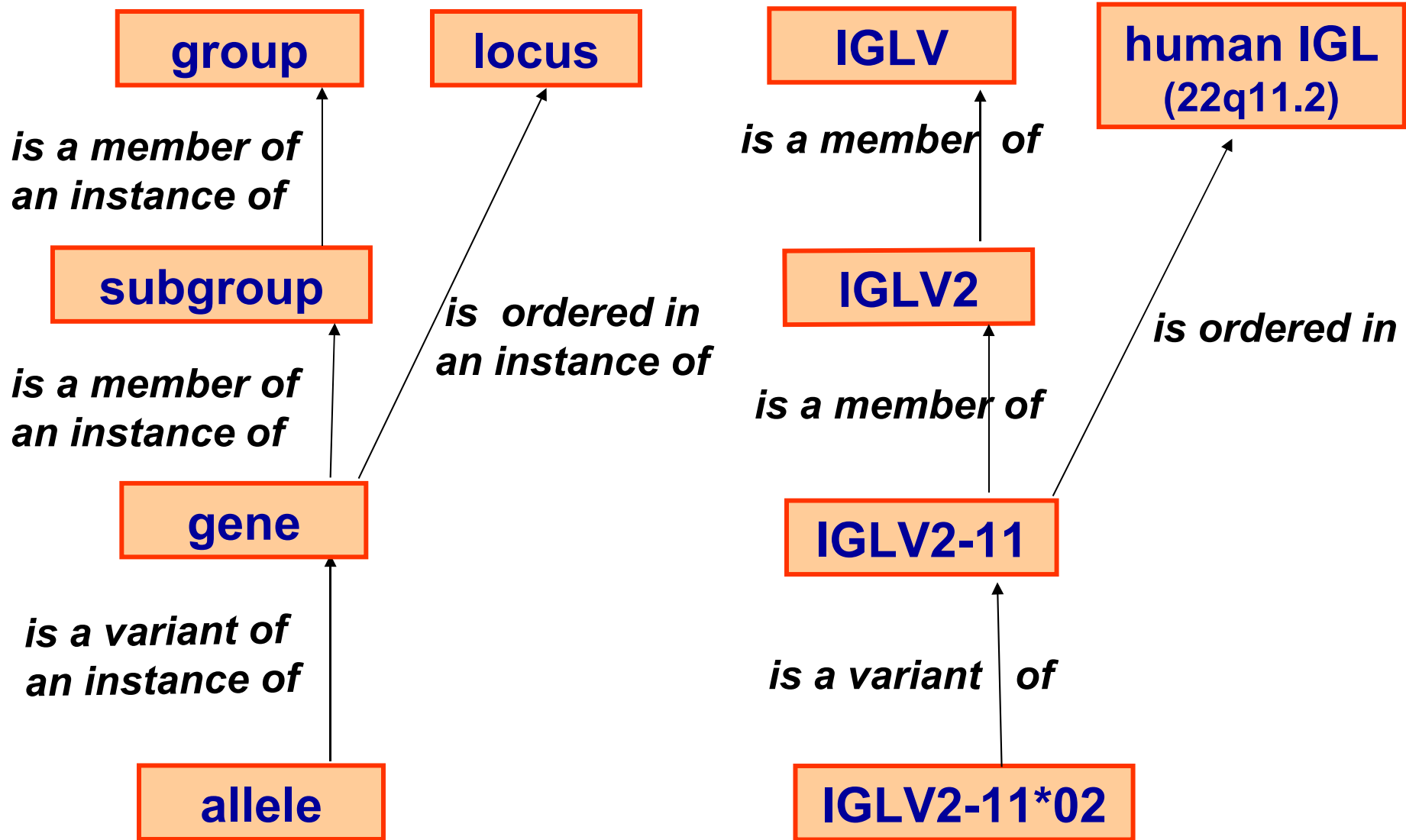
2D and 3D structures

IMGT-ONTOLOGY seven axioms:

To share, reuse and represent knowledge
in Immunogenetics and Life Sciences



CLASSIFICATION axiom

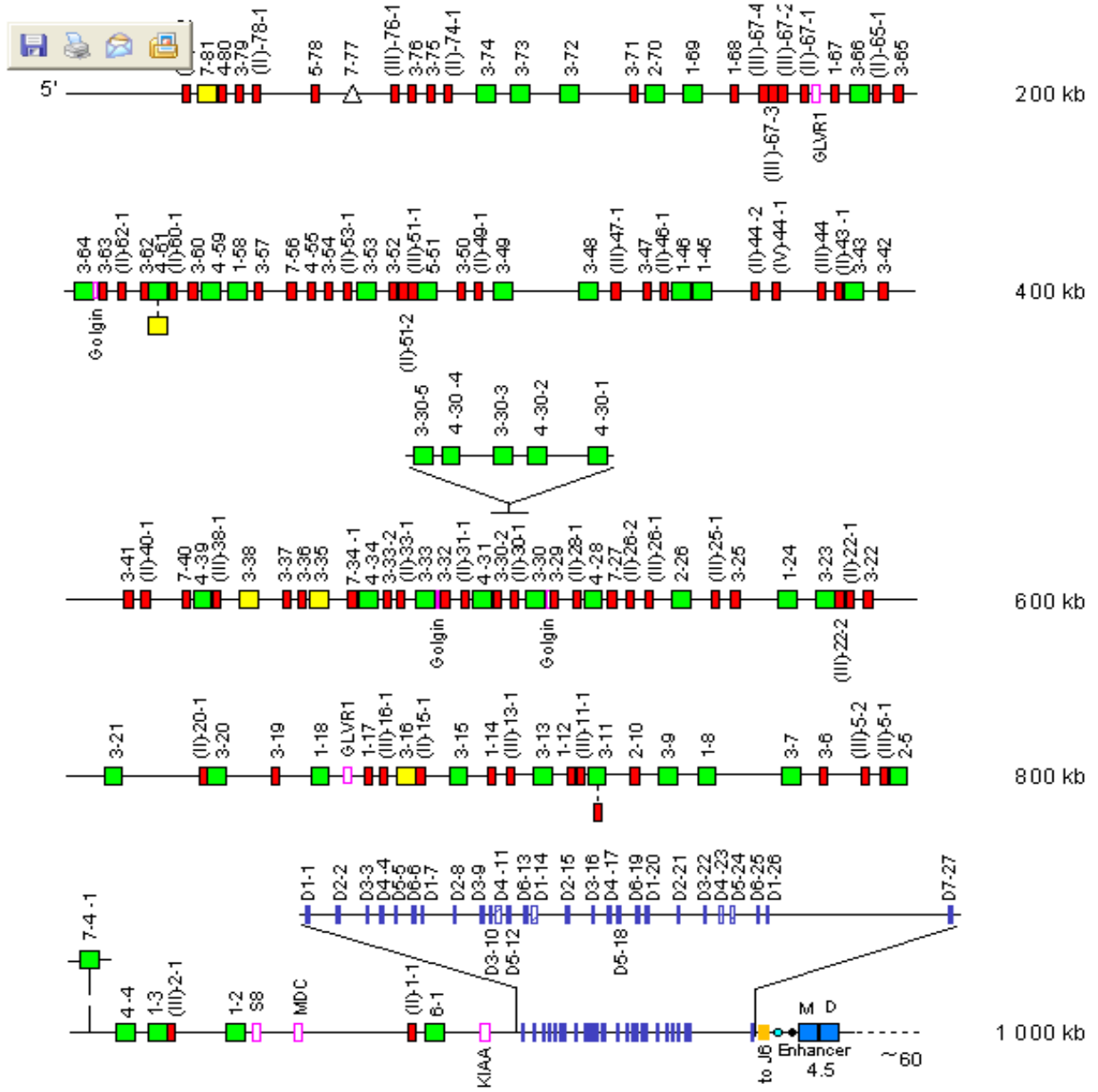


« Concepts »

« Instances »

Human IGH locus

Chromosome 14q32.33



Locus representation: Human IGL

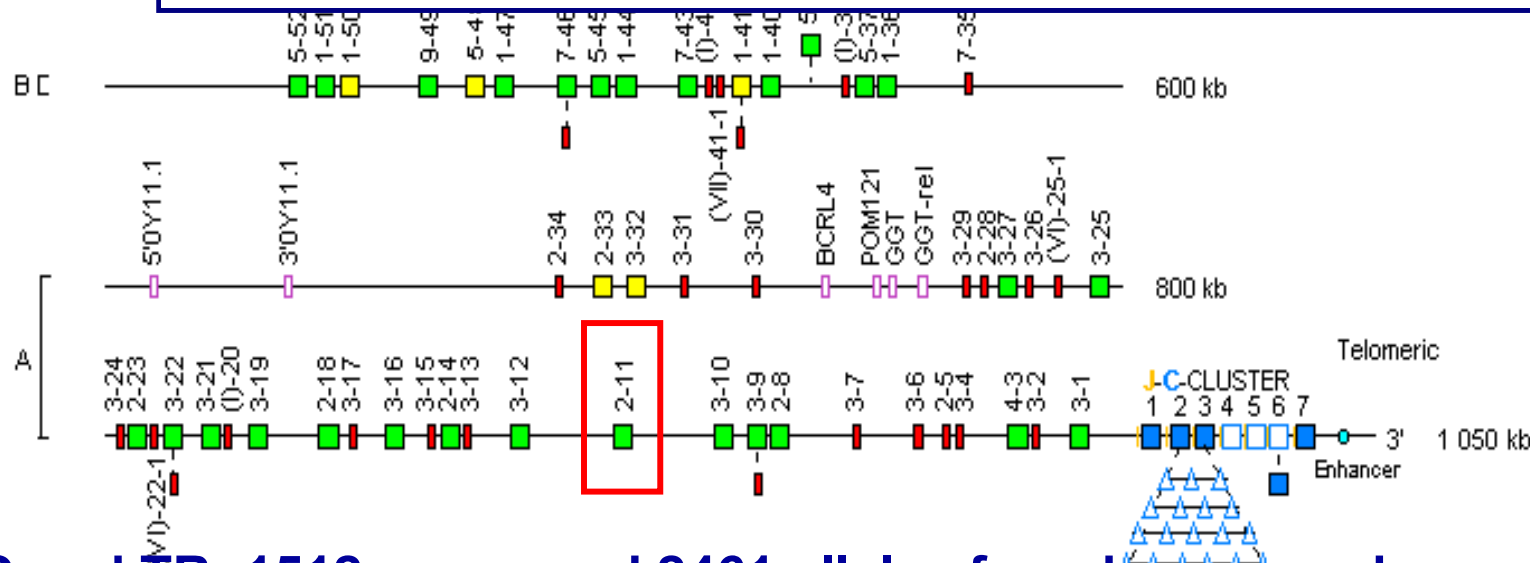
Human IGL 2

WELCOME ! to IMGT/GENE-DB

THE
INTERNATIONAL
IMMUNOGENETICS
INFORMATION SYSTEM®



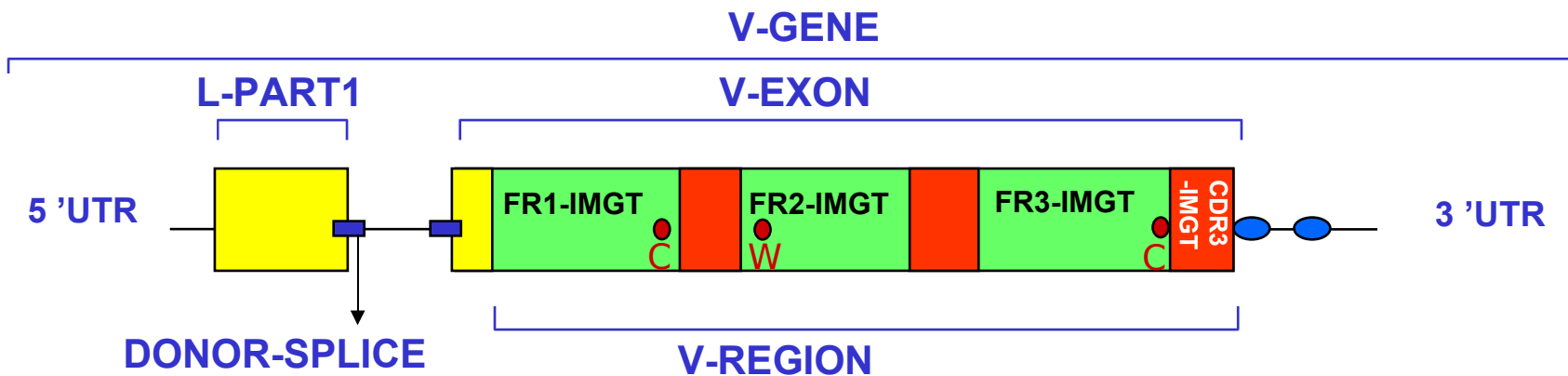
<http://imgt.cines.fr>



IG and TR: 1512 genes and 2461 alleles from human and mouse

DESCRIPTION axiom

PROTOTYPE for a V-GENE



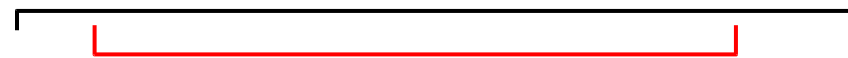
Label 1

Label 2

Relations entre Labels

V-GENE

V-EXON



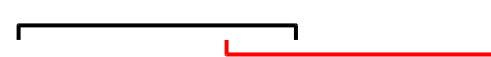
FR3-IMGT

CDR3-IMGT



L-PART1

DONOR-SPLICE



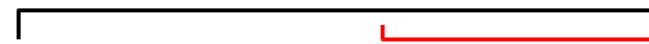
V-REGION

FR1-IMGT



V-REGION

CDR3-IMGT

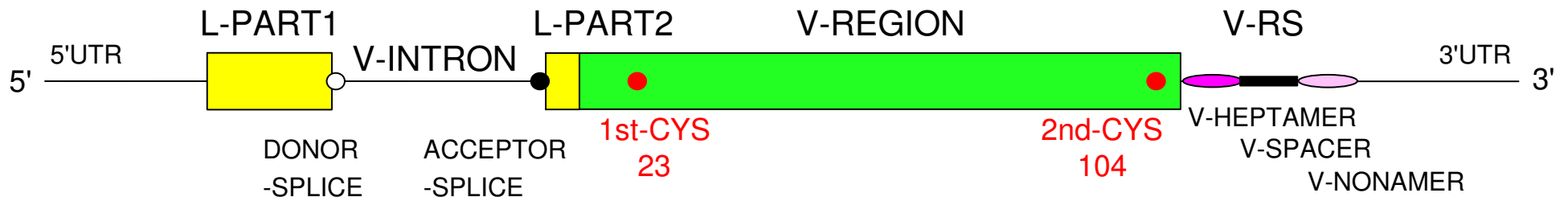


An example of V-GENE

>X62106.0|HSMV2|*Homo sapiens* VI-2 gene for immunoglobulin heavy chain

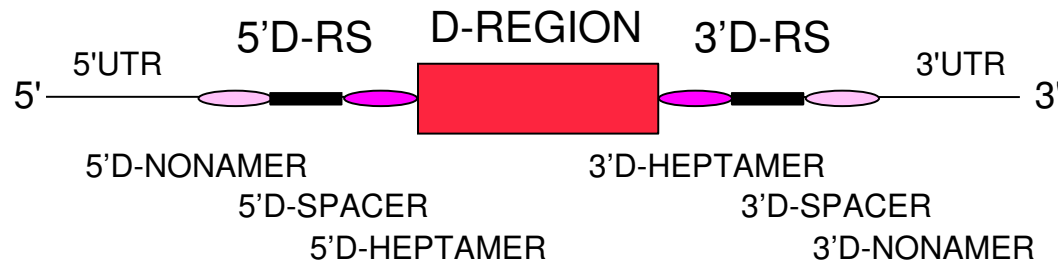
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ccacagggttaa gaggctccct agtcccagtg atgagaaaga gattgagtcc agtccagggg      120
gatctcatcc acttctgtgt tctctcca ca ggagcccact ccaggtgca gctggtgcag      180
tctggggctg aggtgaagaa gcctggggcc tcagtgaagg tctctgcaa ggcttctgga      240
tacaccttca ccggctacta tatgcaactg gtgacgacagg ccctggaca agggcttgag      300
tggatgggat ggatcaacc taacagtggg ggcacaaact atgcacagaa gtttcagggc      360
agggtcacca tgaccagggg cacgtccatc agcacagcct acatggagct gagcaggctg      420
agatctgacg acacggccgt gtattactgt gcgagagaca cagtgtgaaa acccacaatcc      480
tgagggtgtc agaaacccaa gggaggaggc ag
  
```



An example of D-GENE

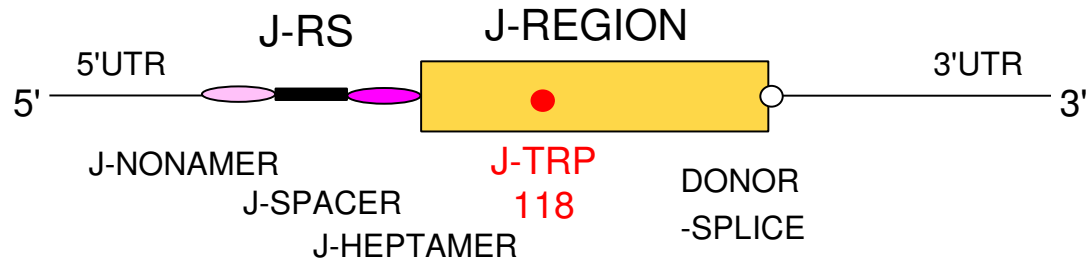
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ggcagctcta caaaaacc



An example of J-GENE

```

ggtttct gtgccctgg ctcagggctg actcaccgtg gctgaatact
tccagcactg ggccagggc accctggtea cegtctctc ag
  
```



Heavy chain **WG**XG (J-TRP)
 Light chain **FG**XG (J-PHE)

IMGT/LIGM-DB

**D
E
S
C
R
I
P
T
I
O
N**

IMGT/LIGM-DB Consultation module v3 - Mozilla Firefox

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

Done

114 238 sequences from 209 species

IMGT-ONTOLOGY:

277 IMGT labels for sequences

285 IMGT labels for 3D structures

SO (Sequence ontology):

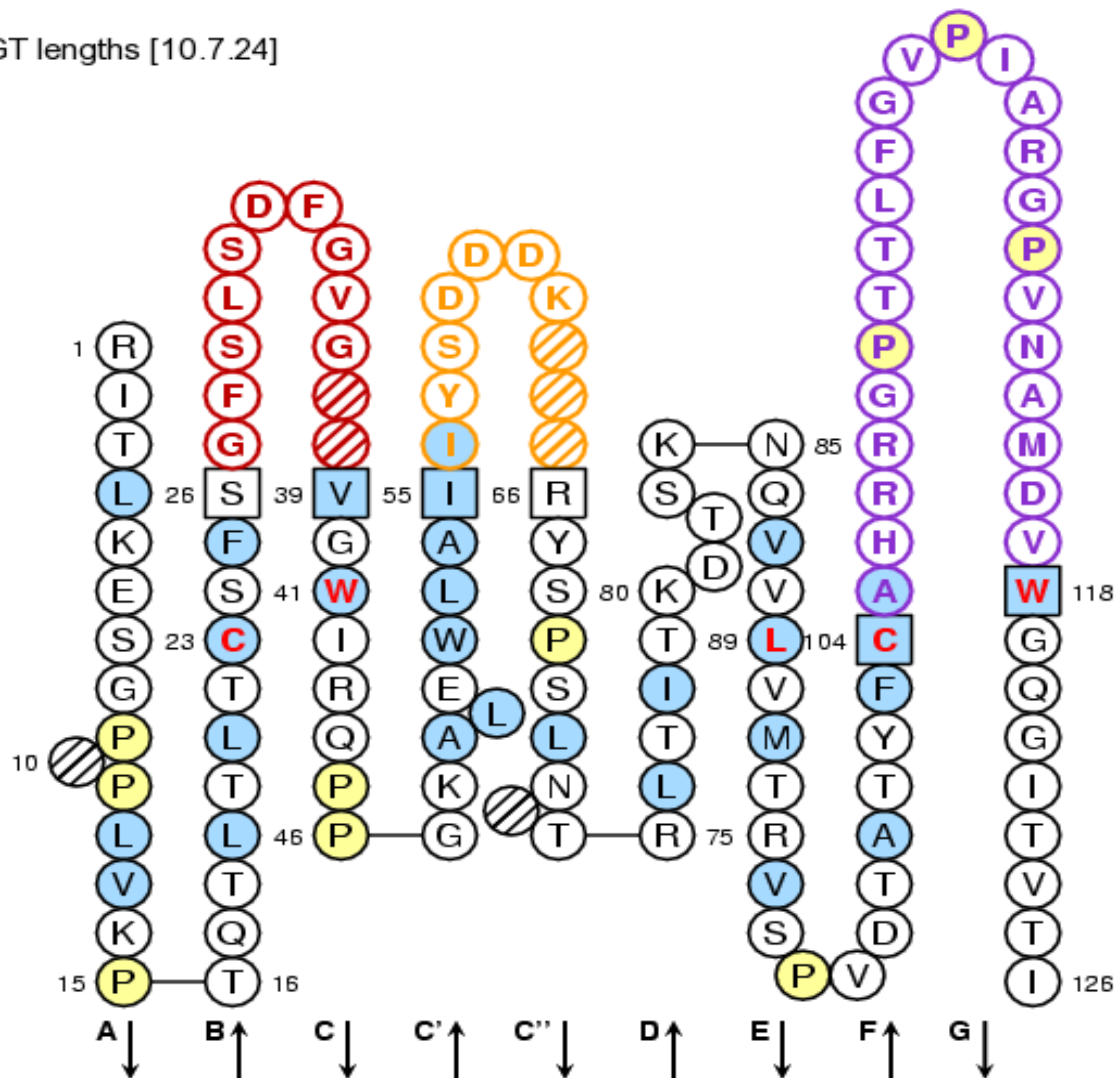
67 IMGT labels

NUMEROTATION axiom

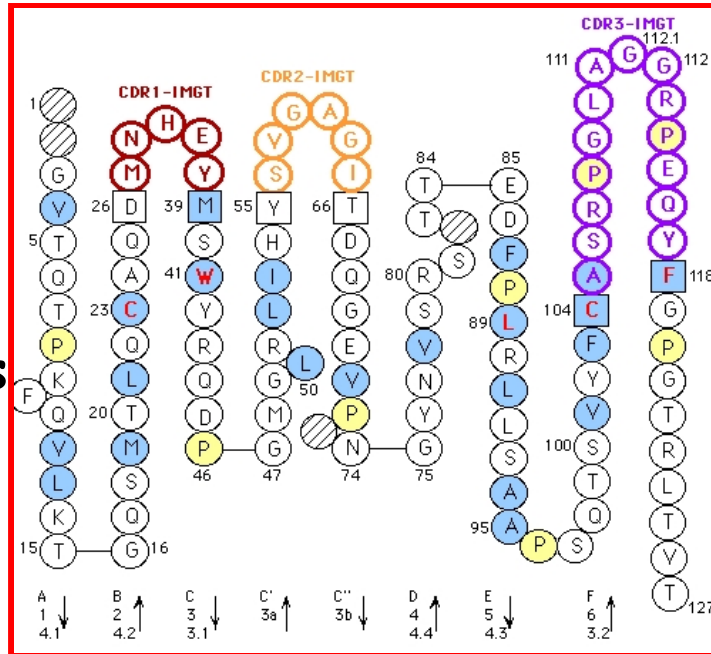
IMGT Collier de Perles : *Homo sapiens* (Human) IGHV_1 V-DOMAIN from 2F5 (PDB: 1u8k_B)

CDR-IMGT lengths [10.7.24]

IMGT
Collier
de
Perles



IMGT Web resources: 8 000 pages HTML



X02850 ,TRAV8-6*01	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20			
AE000659,TRAV8-6*02	A	Q	S	V	T	Q	L	D	S	Q	V	P	V	F	E	E	A	P	V	E			
M86361 ,TRAV8-6*02	GC	CG	TCT	GTG	ACC	CRG	CTT	GAC	ASC	CAR	GTC	CCT	TTT	GAR	GAR	GCC	CCT	GTG	GAG				

X02850 ,TRAV8-6*01	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40			
AE000659,TRAV8-6*02	L	R	C	N	V	S	S	V	S	V	V	V	V	V	L	F	L	F	L	F			
M86361 ,TRAV8-6*02	CTG	AGG	TGC	ARC	TAC	TCA	TGG	TCT	GTT	TCA	GTG	TAT			

X02850 ,TRAV8-6*01	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60			
AE000659,TRAV8-6*02	T	L	V	V	Q	V	P	N	Q	G	L	Q	L	L	L	K	V	L	S	G	S		
M86361 ,TRAV8-6*02	TGG	TAT	GTG	CAR	TAC	CCC	ARC	CAR	GGA	CTC	CAG	CTT	CTC	CTG	AAQ	TAT	TTA	TCA	GGA	TCC			

X02850 ,TRAV8-6*01	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80			
AE000659,TRAV8-6*02	T	L	L	V	V	E	S	I	N			
M86361 ,TRAV8-6*02	ACC	CTG	GTT	GAA	AGC	ATC	ARC			

X02850 ,TRAV8-6*01	81	82	83	84	84A	84B	84c	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
AE000659,TRAV8-6*02	A	E	F	H	K	S	Q	T	S	F	H	L	R	K	P	S	V	H	I	S	D	T	A
M86361 ,TRAV8-6*02	GCT	GAA	TTT	ARC	ARG	AGT	CAA	ACT	TCC	TTC	CAC	TTG	AGG	AAA	CCC	TCA	CTC	CAT	ATA	AGC	GAC	ACG	GCT

X02850 ,TRAV8-6*01	101	102	103	104	105	106	107	108
AE000659,TRAV8-6*02	E	Y	F	C	A	V	S
M86361 ,TRAV8-6*02	GAG	TAC	TTT	TGT	GCT	GTG	AGT	GA

X02850 ,TRAV8-6*01	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127
AE000659,TRAV8-6*02	A	G	R	G	P	E	Q	Y	A	F	C	F	Y	V	T	R	L	T	Y	T
M86361 ,TRAV8-6*02	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG

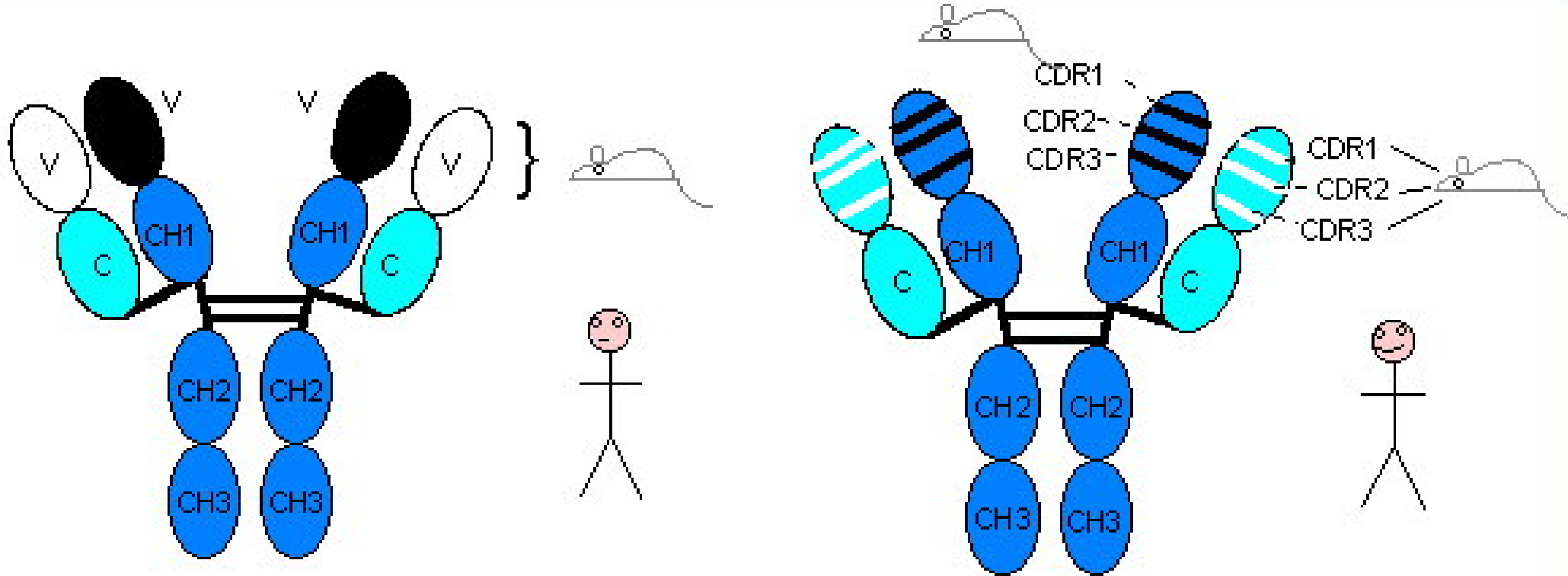
IMGT Alignment of alleles

IMGT Collier de Perles

IMGT Protein Display

TRAV gene	FR1-IMGT (1-26)	CDR1-IMGT (27-38)	FR2-IMGT (39-55)	CDR2-IMGT (56-65)	FR3-IMGT (66-104)	CDR3-IMGT (105-115)
AE000658, TRAV1-1	GQSLEQ.PSEVTAVEGAIQINCTYQ	TSGFYG.....	LSWYQQHGGAPTFLSY	NALDG.....	LEETG.....	RFSSFLSRSDSYGYLLLQELQMKDSASYFC
AE000658, TRAV1-2	GQNIDQ.PTEMTATEGAIQINCTYQ	TSGFNG.....	LFWYQQHAGEAPTFLSY	NVLDG.....	LEEKG.....	RFSSFLSRSGYSYLLLKELQMKDSASYLC
AE000658, TRAV2	KDQVFQ.PSTVASSEGAIVVEIFCNHS	VSNAYN.....	PFWYLFHPGCAPIRLLVK	GSK.....	PSQQG.....	RYNMTYER.FSSSLLILQVREADAAVYFC
AE000658, TRAV3	AQSVAQPEDQVNAEAGNPLTVKCTYS	VSGNPY.....	LFWYVQYPNRLQLFLLK	YITGDNL.....	VKGSY.....	GFEAEFNKSQTSFHLKPKSALVSDSALYFC
AE000658, TRAV4	LAKITQ.PISMDSYEGQEVNITOSH	NIATNDY.....	ITWYQQFSPQGRFIIQ	GYKT.....	KVINE.....	VASFLIPADRKSFTLSLPRVSLSDTAVYFC
AE000659, TRAV5	GEDVEQS.LFLSVREGDSSVINCTYT	DSSSTY.....	LYWYKQEPGAGLQLLTY	IFSNMD.....	MKQDQ.....	RLTLLNKKDKHLSRIADTQTGDSAIYFC
AE000659, TRAV6	SQKIEQNSALNIQEGKTATLTCNYT	NYSPAY.....	LQWYRQDPGRGPVFLLL	IRENEK.....	EKRKE.....	RLKVTFTDITLQKSLFHIITASQPADSATYFC
AE000659, TRAV7	ENQVEHSPHFLGPQQGDVASMCTYS	VSRFNN.....	LQWYRQNTGMGPKHLLS	MYSAGY.....	EKQKG.....	RLNATLLK.NGSSLYITAVQPEDSATYFC
AE000659, TRAV8-1	AQSVSQHNHHVILSEASLELLGCNYS	YGGTVM.....	LFWYVQYPGQHLQLLLK	YFSGDPL.....	VKGIK.....	GFEAEFIKSKFSPNLRKPSVQVSDTAEYFC
AE000659, TRAV8-2	AQSVTQLDSHVSVSEGTVPVLLRCNYS	SSYSPS.....	LFWYVQHPNKGQLQLLLK	YTSAAITL.....	VKGIN.....	GFEAEFKKSETSPHLTKPSAHMSDAAEYFC
AE000659, TRAV8-3	AQSVTQPDIIHITVSEGASLELLRCNYS	YGATPY.....	LFWYVQSPGQGLQLLLK	YFSGDITL.....	VQGIK.....	GFEAEFKRSQSSFNLRKPSVHWSDAAEYFC
AE000659, TRAV8-4	AQSVTQLGSHVSVSEGALVLLRCNYS	SSVPPY.....	LFWYVQYPNQLQLLLK	YTSAAITL.....	VKGIN.....	GFEAEFKKSETSPHLTKPSAHMSDAAEYFC
X02850 ,TRAV8-6	AQSVTQLDSQVPVFEAAPVELRCNYS	SSVSVY.....	LFWYVQYPNQLQLLLK	YLSGSL.....	VESIN.....	GFEAEFNKSQTSFHLRKPSTVHISDTAEYFC
AE000660, TRAV8-7	TQSVTQLDGHITVSEEAPELRCNYS	YSGVPS.....	LFWYVQYSSQSLQLLLK	DLTEATQ.....	VKGIK.....	GFEAEFKKSETSPYLRKPSVHWSDAAEYFC
AE000659, TRAV9-1	GDSVVTQEGQVLPSEFGSLIYVCSYF	TTQVPS.....	LFWYVQYVPGEGPOLH.K	AMKAND.....	KGRNK.....	GFEAMYRKFSTSPHLKPKSVQFSDSAVYFC

Chimeric and humanized antibodies



chimeric antibody

humanized antibody

Humanized CAMPATH-1H mutant 1

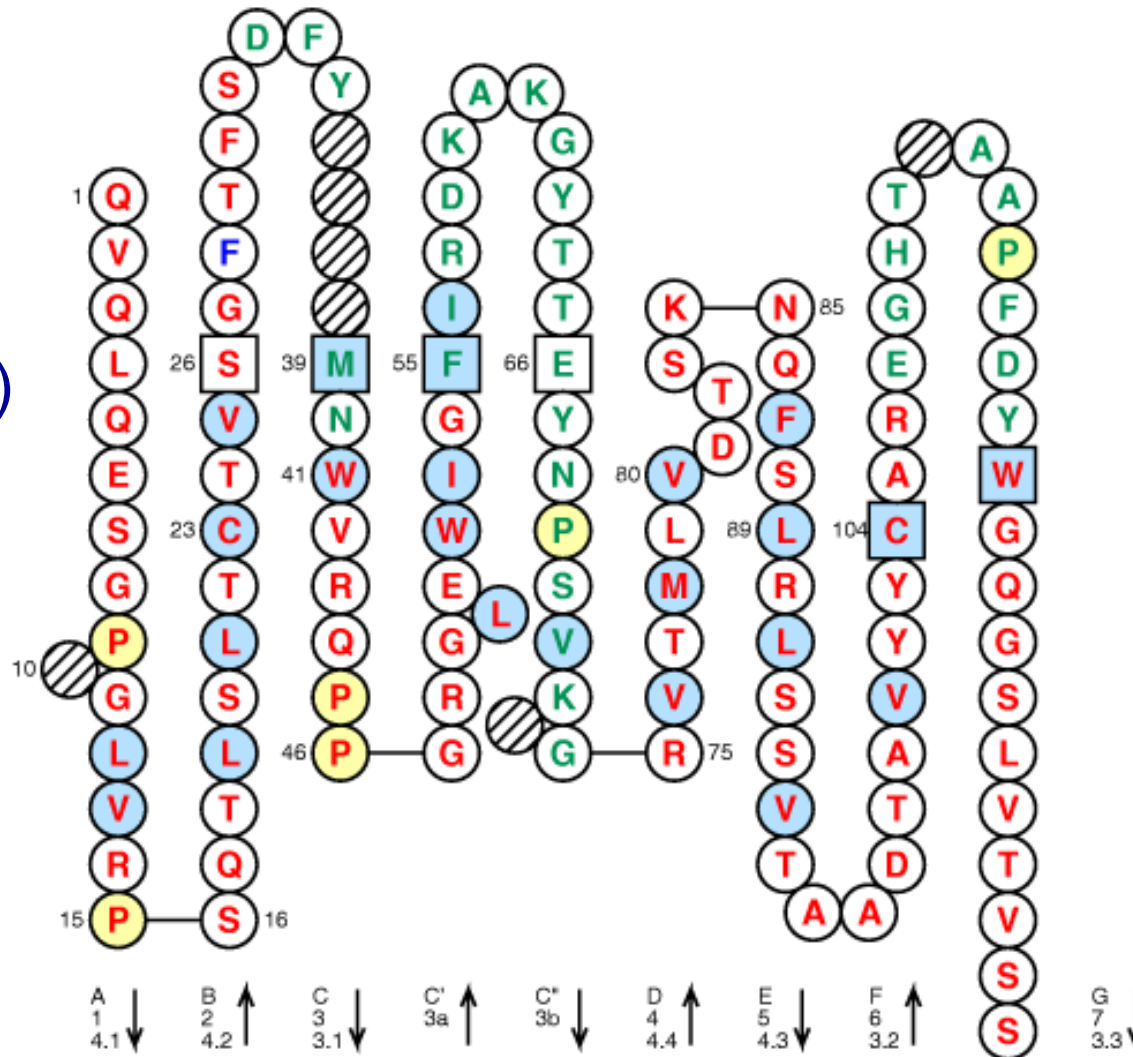
Mutant 1: **S28>F**

Mutant 2:
alemtuzumab
S31>T

VH domain
(V-D-J-REGION)

[8.10.12]

■ human
■ rat



IMGTV-QUEST


WELCOME ! to the IMGT/V-QUEST Search page

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INFORMATION SYSTEM®



<http://imgt.cines.fr>

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

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

Analyse your Immunoglobulin nucleotide sequences

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

Analyse your T cell Receptor nucleotide sequences

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

Analyse your Immunoglobulin sequences

Your selection: Human

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

Nucleotide sequences

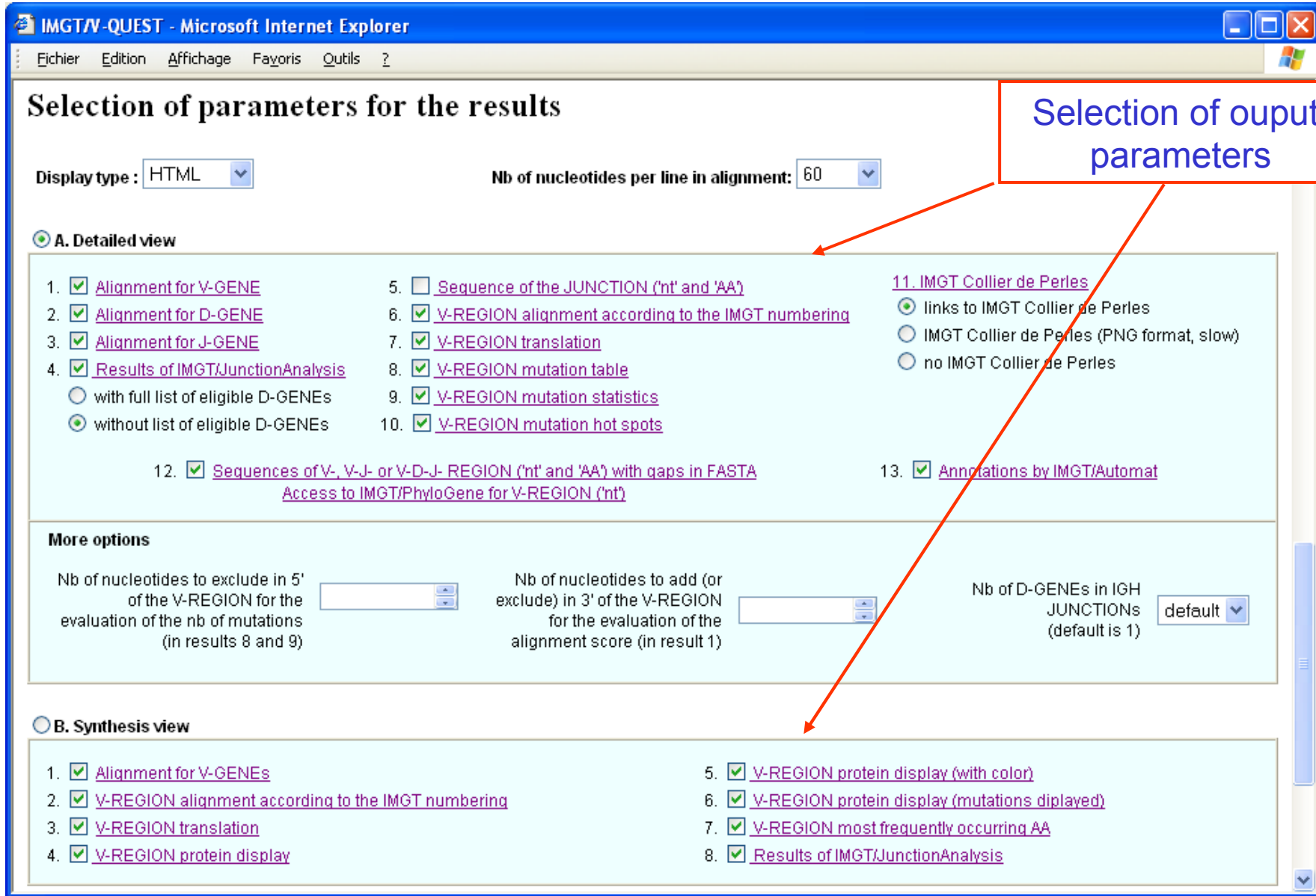
Enter your sequence(s) in [FASTA format](#) (FASTA format is required):

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

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>AY393054
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>AY393055
gctgggttttccttgttgctatttcaaaaggtgtccagtgtgaggtgcagctggtggagactggaggaggcttgatccagcctggggg
tccttgagactctcctgtgcagcctctgggttcaccgtcagtagcaactacatgagctgggtccgccaggctccaggaaggggctgga
```

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

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



Selection of parameters for the results

Display type : Nb of nucleotides per line in alignment:

A. Detailed view

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

More options

Nb of nucleotides to exclude in 5' of the V-REGION for the evaluation of the nb of mutations (in results 8 and 9)

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

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

B. Synthesis view

- 1. [Alignment for V-GENEs](#)
- 2. [V-REGION alignment according to the IMGT numbering](#)
- 3. [V-REGION translation](#)
- 4. [V-REGION protein display](#)
- 5. [V-REGION protein display \(with color\)](#)
- 6. [V-REGION protein display \(mutations displayed\)](#)
- 7. [V-REGION most frequently occurring AA](#)
- 8. [Results of IMGT/JunctionAnalysis](#)

Selection of output parameters

Sequences aligned with IGHV5-51*03

1. Alignment for V-GENE

```

<-----FR1-IMGT-----
X56368 IGHV5-51*03 gaggtgcagctggtgcagctctggagca...gaggtgaaaaagccgggggagtcctctgaag
AY393084 1327 -----gc-----
AY393088 1309 -----gc-----
AY393089 1255 ---g-----a-----a-----a---
AY393091 1237 -----
AY393092 1255 ---g-----a-----a-----a---
AY393094 1300 -----gc--t-----
----->-----CDR1-IMGT-----<-----
X56368 IGHV5-51*03 atctcctgtaagggttctggatacagctttaccagctactgg.....atcggc
AY393084 1327 ----t-----c-----ta-----
AY393088 1309 -----g-c-----tc-----
AY393089 1255 -----c-----c-g-----
AY393091 1237 -----t-tt-c---aa-----
AY393092 1255 -----c-----c-g-----
AY393094 1300 -----c-----t---ta-----
-----FR2-IMGT----->-----CDR
X56368 IGHV5-51*03 tgggtgcccagatgccccgggaaaggcctggagtgatggggatcatctatcctggtgac
AY393084 1327 -----t-----
AY393088 1309 -----t-----
AY393089 1255 -----g---a---g-g---
AY393091 1237 -----a---c-----g---c---a---a---t
AY393092 1255 -----g---a---g-g---
AY393094 1300 -----t-----t-----

```

IMGT/QUEST - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

6. Protein display (mutations displayed)

		FR1-IMGT (1-26)	CDR1-IMGT (27-38)	FR2-IMGT (39-55)	CD (
		1 10 20	30	40 50	
	
X56368 IGHV5-51*03		EVQLVQSGA.EVKKPGESLKISCKGS	GYSFTSYW....	IGWVRQMPGKGLEWMI	IY
AY393084	1327	--R-----,-----A-	-----N-....	-----	-F
AY393088	1309	--R-----,-----RA-	-----H-....	-----	-F
AY393089	1255	-G--E----,-----A-	--T-A-....	-----V--	V-
AY393091	1237	-----,-----	--I--K-....	-----I-----VA-	-N
AY393092	1255	-G--E----,-----A-	--T-A-....	-----V--	V-
AY393094	1300	--R-----,-----A-	-----N-....	-----I--	-F
		R2-IMGT 56-65)	FR3-IMGT (66-104)		
		60 70 80 90 100			
			
X56368 IGHV5-51*03		PGDSDT..	RYSPSFQ.GQVTISADKSISTAYLQWSSLKASDTAMYIC	AR	
AY393084	1327	-----..	I-----V-----I---	--QNPPEYSGA	
AY393088	1309	-----..	I-----E-----T-S-----	--QNPPEYSGA	
AY393089	1255	---F---..	K-----H---V-R-----F---	--EMLYGSGGY	
AY393091	1237	-D-----..	--NT---,-----V-----T-----	--QNPPEYSGA	
AY393092	1255	---F---..	K-----H---R-T-----VI---	--EMLYGSGGY	
AY393094	1300	-----..	I-----V---N-----T-----	--QNPPEYSGA	

IMGT/V-QUEST - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

3. V-REGION translation

```

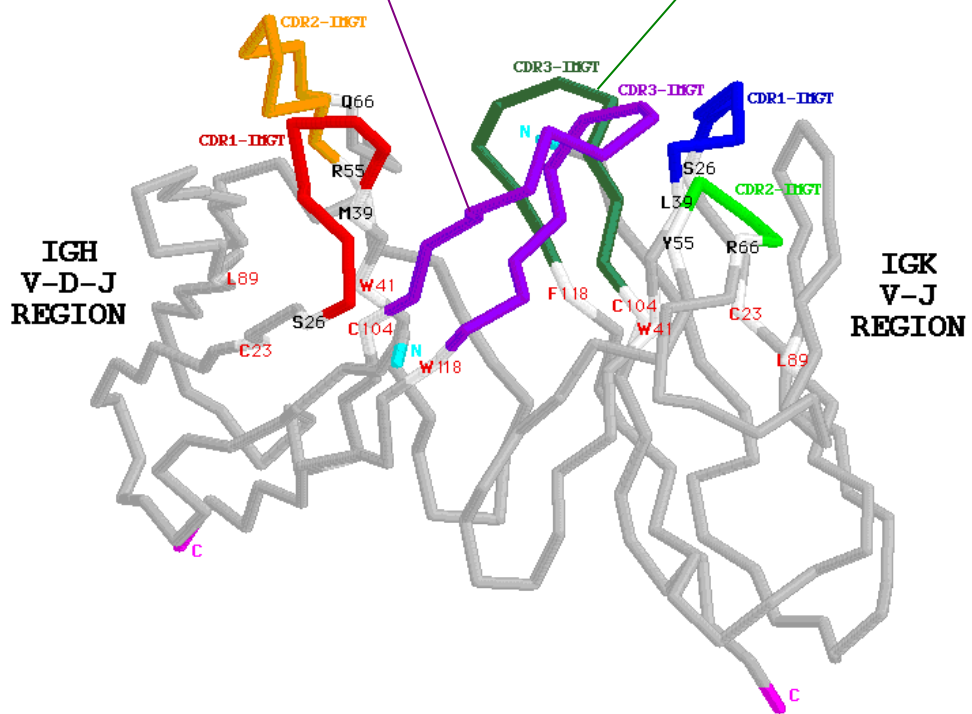
<-----FR1 - IMGT
1           5           10           15
E   V   Q   L   V   Q   S   G   A   E   V   K   K   P
X56368 IGHV5-51*03 gag gtg cag ctg gtg cag tct gga gca ... gag gtg aaa aag ccg
                                     R
AY393084 1327 --- --gc --- -- -- -- -- -- -- -- -- -- -- -- -- -- -- --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

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

```

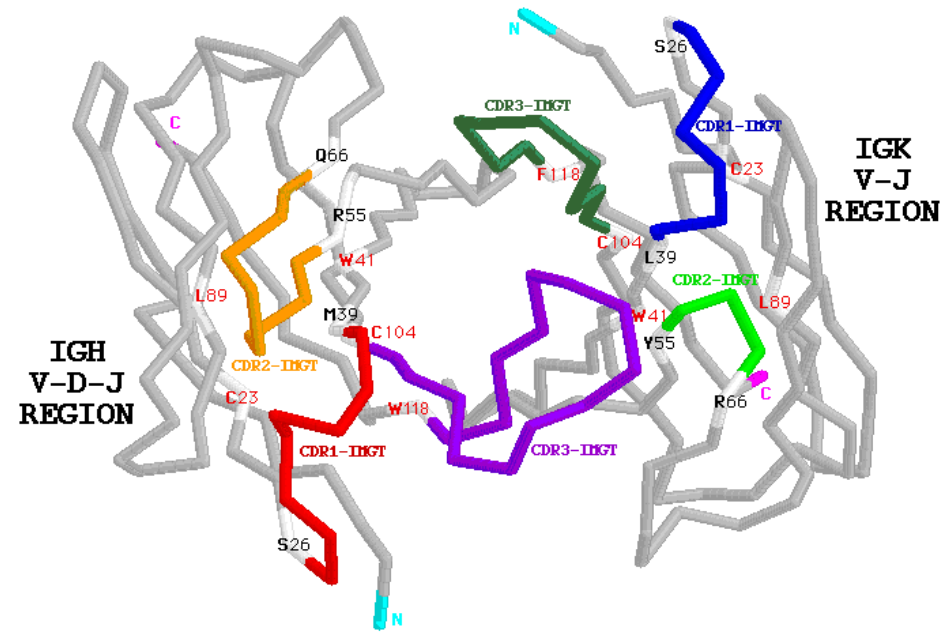
V-DOMAINS: VH and V-KAPPA

VH **V-KAPPA**
V-D-J junction **V-J junction**



Side view of the V-DOMAINS

VH **V-KAPPA**



View from above the CDRs

Mouse (Mus musculus) E5.2Fv

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

Immunoglobulin V-D-J generation of sequence diversity

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 W

tgt gcg cca tac cgg ggt gac act tat gat tac tcc tgg

IMGT/JunctionAnalysis

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

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INTERNATIONAL
IMMUNOGENETICS
INFORMATION SYSTEM®



<http://imgt.cines.fr>

Analysis of the JUNCTIONS

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

Input	J-REGION	J name	D name	Vmut	Dmut	Jmut	Ngc
#1 M62724tttaactactgg	IGHJ4*02	IGHD5-24*01	0	2	0	1/7
#2 Z47269	...actggttegaccctgg	IGHJ5*02	IGHD3-3*02	0	2	0	13/20

Translation of the JUNCTIONS

	104	105	106	107	108	109	110	111	111.1	111.2	111.3	112.4	112.2	112.3	112.1	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	Y	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		

WELCOME ! to IMGT/JunctionAnalysis

THE INTERNATIONAL
IMMUNOGENETICS
INFORMATION SYSTEM®



<http://imgt.cines.fr>

Analyse the JUNCTION of your IG and TR nucleotide sequences

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

Species:

Homo sapiens

Locus:

IGH IGK IGL

 TRA TRB TRG TRD

JUNCTION nucleotide sequences

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

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


IMGT/JunctionAnalysis Results



<http://imgt.cines.fr>

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		tgtgtggcagc <u>gc</u> ctgttac	ccaaatac		...actttgacc <u>act</u> gg	IGHJ4*02	IGHD6-13*01	1	2	1	5/15
#2	Z70257	IGHV3-7*02		ggatggcagc <u>ct</u> ttatgcc	cgccc		ctactgg <u>tact</u> tcgatctctgg	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		cagagtaacgatttttgagtggttatt.....	ccccggggga		..atgcttttgatctctgg	IGHJ3*02	IGHD3-3*01	0	0	0	12/17
#5	Z70610	IGHV4-34*09		tcgggagcgatttttgagtggttatt.....	cccgca	ca	tgatgcttttgatctctgg	IGHJ3*02	IGHD3-3*01	0	0	0	9/12
#6	Z70611	IGHV4-59*01		catggt <u>aact</u> ataa.	tgccggcggtg		...actggttcgaccctgg	IGHJ5*02	IGHD3-9*01	0	2	0	9/13
#7	Z70613	IGHV4-59*01		cagcagctgttac	ctccct		...ctttgactactgg	IGHJ4*02	IGHD6-13*01	0	0	0	4/6
#8	Z70614	IGHV4-59*01		cactataattcggggacttat.....	cccctc	gactactgg	IGHJ4*02	IGHD3-16*01	0	2	0	7/14
#9	Z70615	IGHV4-59*01		ggctg	gtaaagaggg.....	tttcggaa		.tactgg <u>tact</u> tcgatctctgg	IGHJ2*01	IGHD5-24*01	0	2	0	7/13
#10	Z70616	IGHV4-34*01		cgggtttggg.....	tccc		...actggttcgaccctgg	IGHJ5*02	IGHD3-16*01	0	0	0	6/8
#11	Z70620	IGHV4-30-4*01		ccggggcgggatggtt.....	cgg		.gatgcttttgatctctgg	IGHJ3*02	IGHD3-16*01	1	4	0	5/5
#12	Z70621	IGHV4-39*01		ccacgatttatggttcggggagtt.....	tgaccccc	ttgactactgg	IGHJ4*02	IGHD3-16*01	0	1	0	12/21
#13	Z70622	IGHV4-39*06	t	tgccccgctcctgccccaaat	gtattactatggttcgggga.....	tatgtacg	tttactactgg	IGHJ4*03	IGHD3-10*01	0	0	0	15/28

The eleven IMGT 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
					Uncharged	Charged		Uncharged	
		Nonpolar		Polar					

IMGJ/JunctionAnalysis: analysis of the IG and TR junctions

JUNCTION alignments with translation and IMGJ AA classes

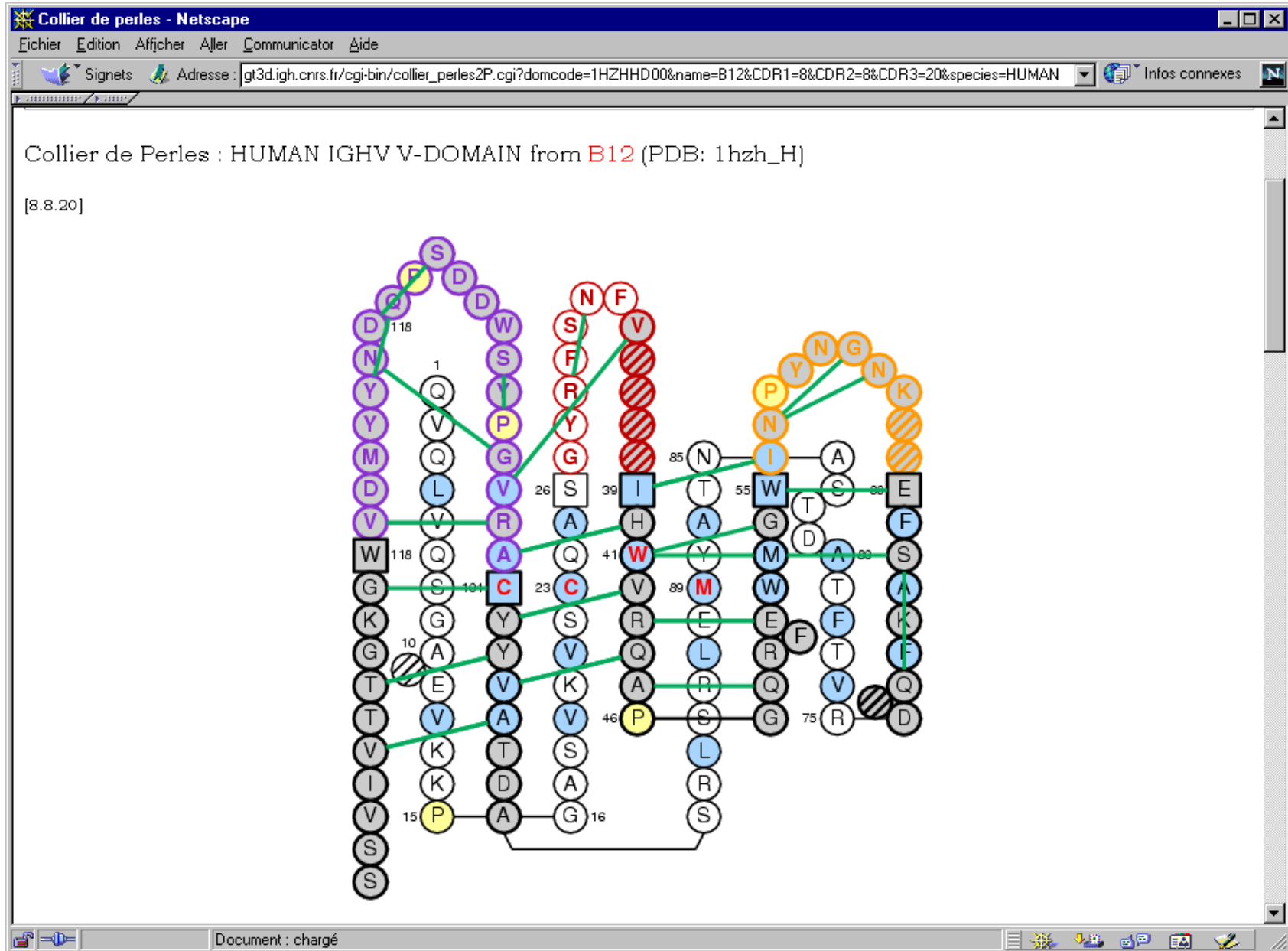
Click on mutated (underlined) amino acid to see the original one:

	104	105	106	107	108	109	110	111	111.1	111.2	111.3	112.3	112.2	112.1	112	113	114	115	116	117	118
#1 AY393054	C	S	P	G	G	S	<u>A</u>	Y						Y	<u>H</u>	E	<u>H</u>	F	Q	<u>Q</u>	W
	tgt	agt	ccc	ggg	ggt	agt	<u>gct</u>	tat	tac	<u>cac</u>	gaa	<u>cac</u>	ttc	cag	<u>cag</u>	tgg
#2 AY393055	C	<u>V</u>	K	P	T	D	D	D	G				<u>H</u>	R	A	E	Y	F	Q	<u>Y</u>	W
	tgt	<u>gtg</u>	aaa	ccc	acg	gat	gat	gat	ggc	<u>cac</u>	cgg	gct	gaa	tac	ttc	cag	<u>tac</u>	tgg
#3 AY393058	C	S	P	G	G	S	<u>A</u>	Y						Y	<u>H</u>	E	<u>D</u>	F	Q	<u>Q</u>	W
	tgt	agt	ccc	ggg	ggt	<u>agc</u>	<u>gct</u>	tat	tac	<u>cac</u>	gaa	<u>gac</u>	ttc	cag	<u>cag</u>	tgg
#4 AY393072	C	S	P	G	G	S	<u>A</u>	Y						Y	<u>H</u>	E	<u>H</u>	F	Q	<u>Q</u>	W
	tgt	agt	ccc	ggg	ggt	agt	<u>gct</u>	tat	tac	<u>cac</u>	gaa	<u>cac</u>	ttc	cag	<u>cag</u>	tgg
#5 AY393088	C	A	R	Q	N	P	P	E	Y	S	G	A	Y	<u>H</u>	<u>D</u>	G	W	F	D	P	W
	tgt	gcg	aga	caa	aac	ccc	ccc	gag	tat	agt	ggc	gca	tat	<u>cat</u>	<u>gat</u>	ggg	tgg	ttc	gac	ccc	tgg
#6 AY393089	C	A	R	E	M	L	Y	G	S	G	<u>G</u>	Y	Y	P	P	D	A	F	<u>E</u>	<u>L</u>	W
	tgt	gcg	aga	gag	atg	ctc	tat	ggt	tcg	ggg	<u>ggt</u>	tat	tac	ccc	cct	gat	gca	ttt	<u>gag</u>	<u>ctc</u>	tgg
#7 AY393091	C	A	R	Q	N	P	P	E	Y	S	G	A	Y	<u>H</u>	<u>D</u>	G	W	F	D	P	W
	tgt	gcg	aga	cag	aat	ccc	ccc	gag	tat	agt	ggc	gca	tat	<u>cat</u>	<u>gat</u>	ggg	tgg	ttc	gac	ccc	tgg
#8 AY393092	C	A	R	E	M	L	Y	G	S	G	<u>G</u>	Y	Y	P	P	D	A	F	<u>E</u>	<u>V</u>	W
	tgt	gcg	aga	gag	atg	ctc	tat	ggt	tcg	ggg	<u>ggt</u>	tat	tac	ccc	cct	gat	<u>gca</u>	ttt	<u>gag</u>	<u>gtc</u>	tgg
#9 AY393094	C	A	R	Q	N	P	P	E	Y	S	G	A	Y	<u>H</u>	<u>D</u>	G	W	F	D	P	W
	tgt	gcg	aga	cag	aac	ccc	ccc	gag	tat	agt	ggc	gca	tat	<u>cat</u>	<u>gat</u>	ggg	tgg	ttc	gac	ccc	tgg

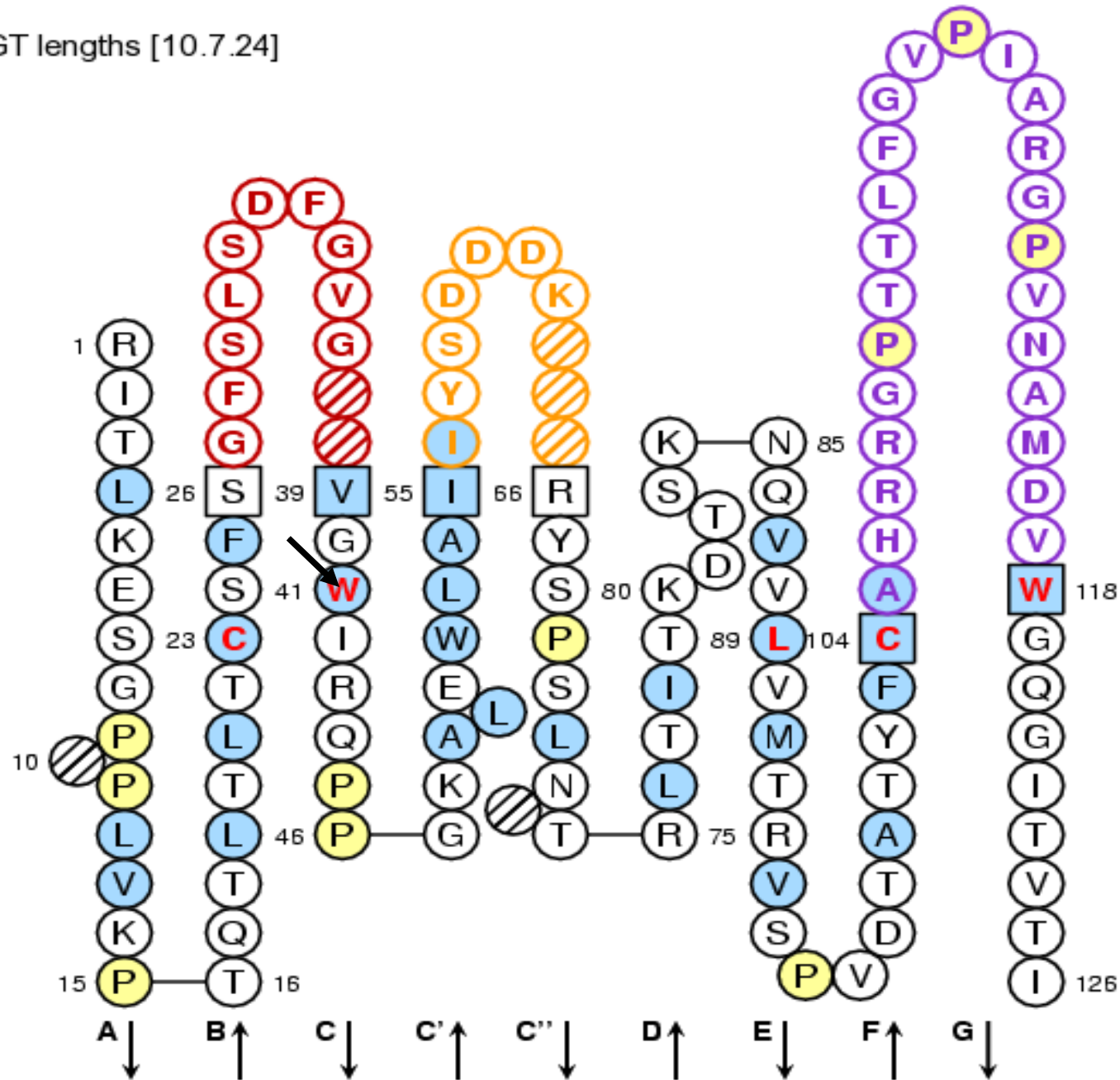
Yousfi Monod et al. Bioinformatics 20, i379-i385 (2004)

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

IMGT/3Dstructure-DB: analysis of 3D structures



CDR-IMGT lengths [10.7.24]



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

Who is using IMGT?

Medical research:

allergies
autoimmune diseases
AIDS
leukemias
lymphomas
myelomas
translocations
detection of residual diseases

Biotechnology related to antibody engineering:

chimeric
humanized
human antibodies
scFv
combinatorial libraries
intrabodies

Veterinary research:

IG and TR repertoire
domestic and farm species
wild species

Comparative and developmental immunology:

evolution of the adaptive immune system



Many thanks to the IMGT® team at Montpellier, France