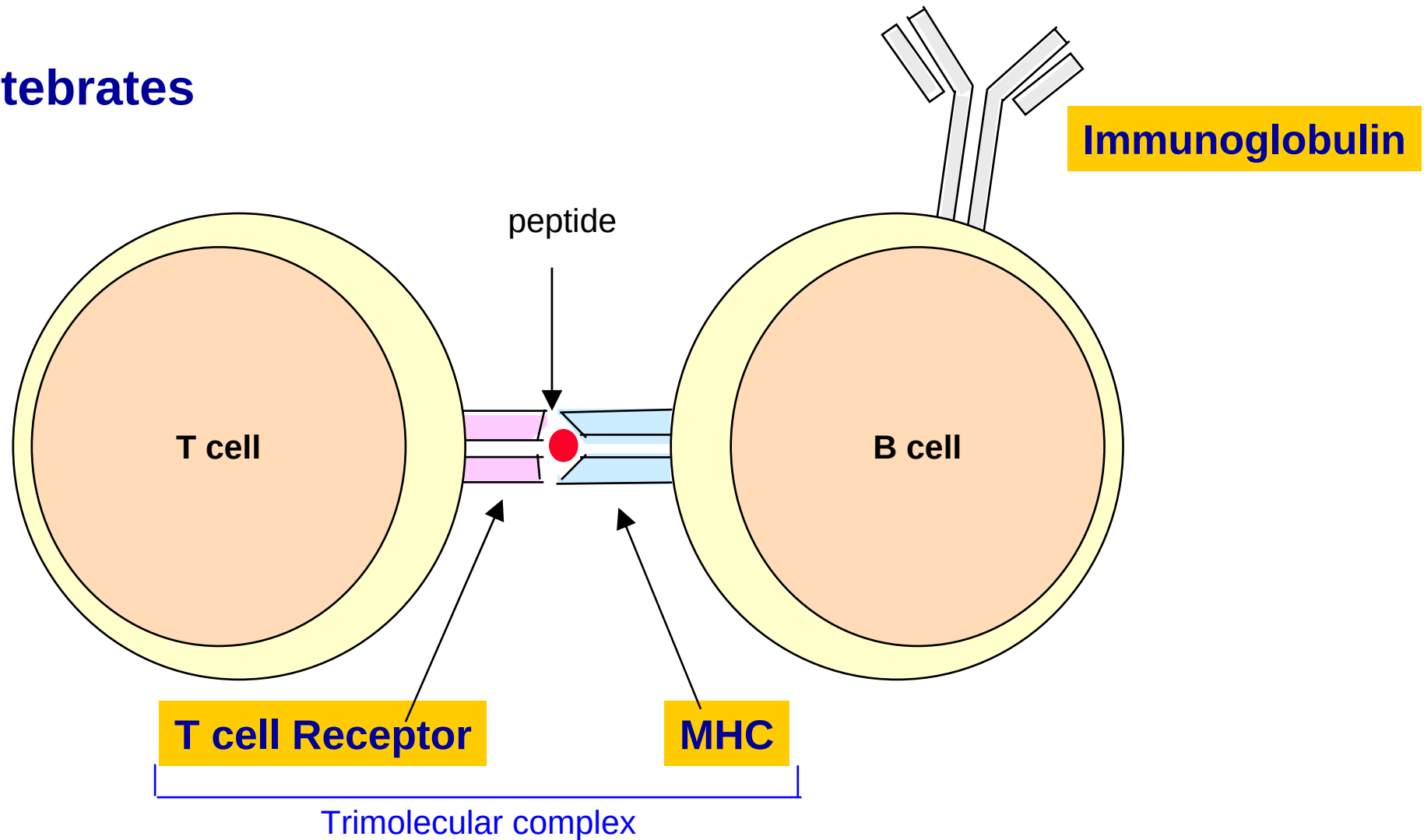


Analysis of the sequences, genes and
3D structures
of the immunoglobulins, T cell receptors and MHC
using the IMGT databases, tools and Web
resources
<http://imgt.cines.fr>

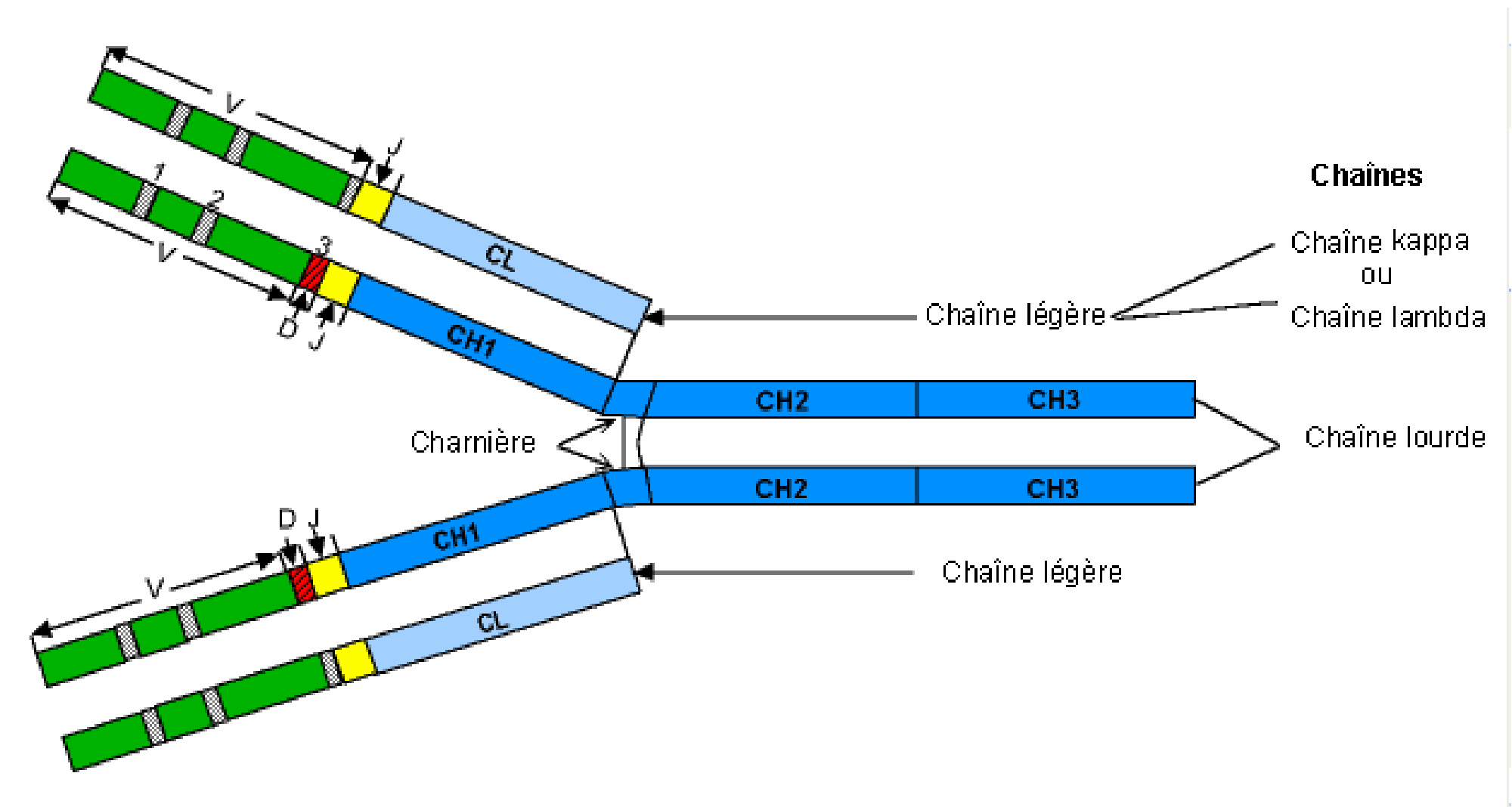
Marie-Paule Lefranc
Université Montpellier, CNRS
Institut Universitaire de France

IMGT domain of research: the adaptive immune system

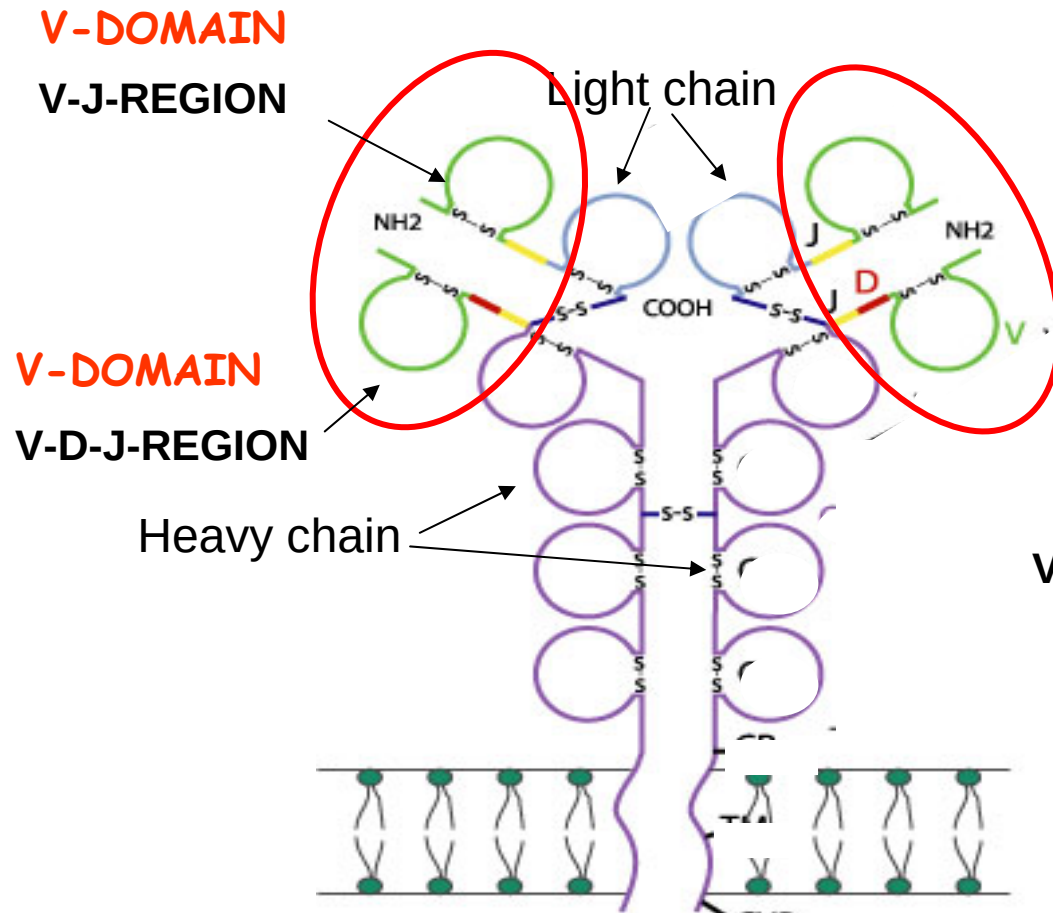
Vertebrates



Immunoglobulin IgG

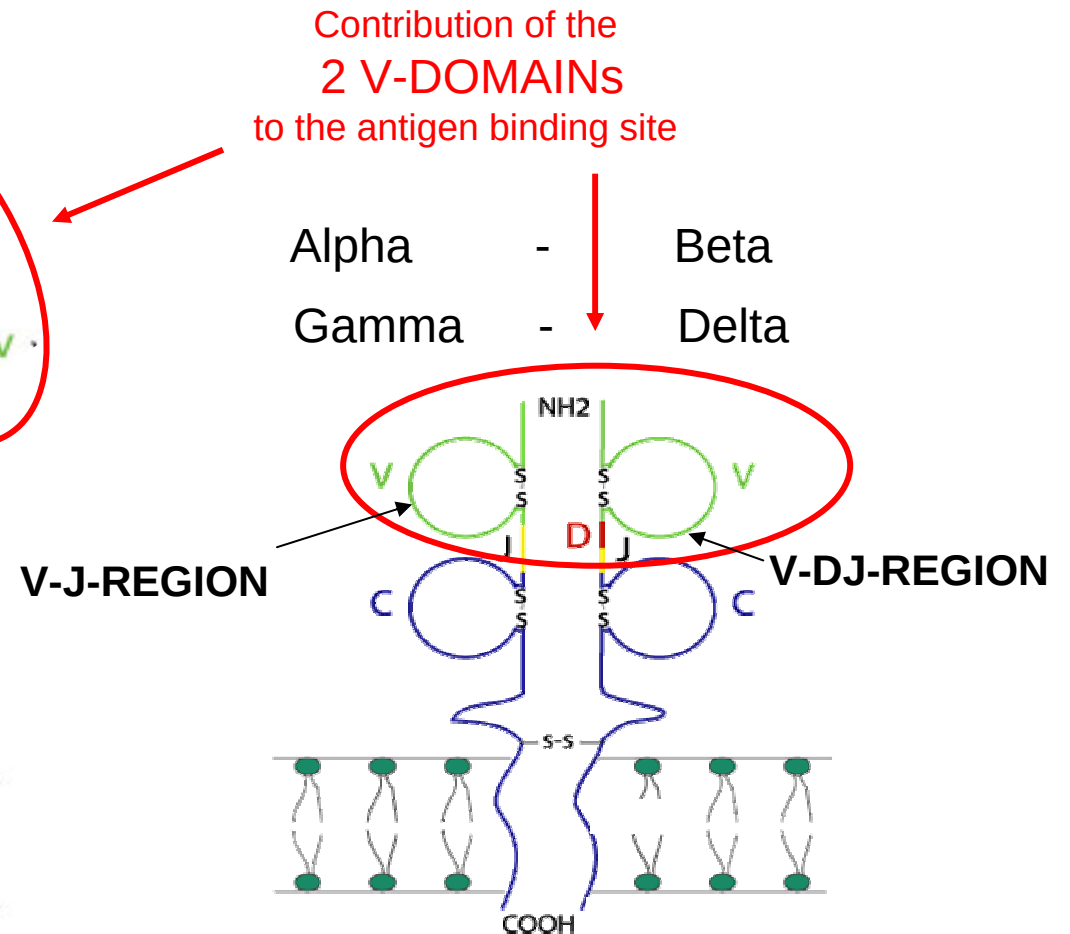


Immunoglobulin (IG)



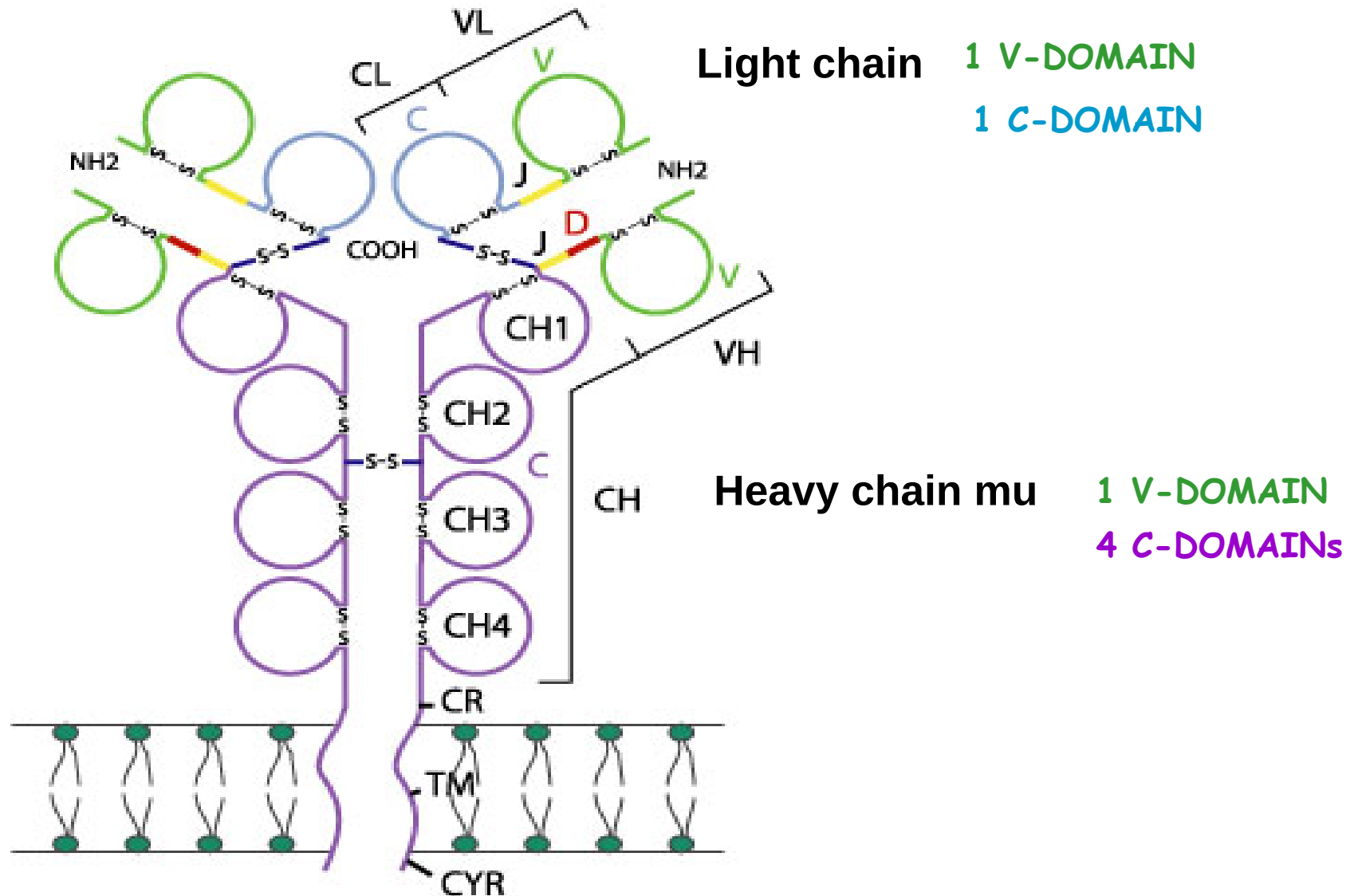
Membrane IgM

T cell receptor (TR)



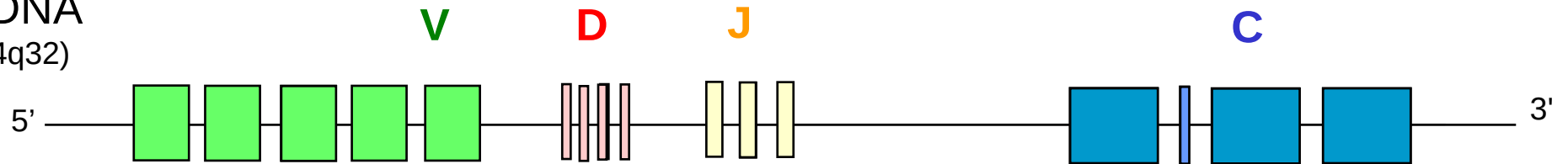
T cell receptor

Immunoglobulin IgM



Immunoglobulin synthesis

genomic DNA
(IGH Locus 14q32)



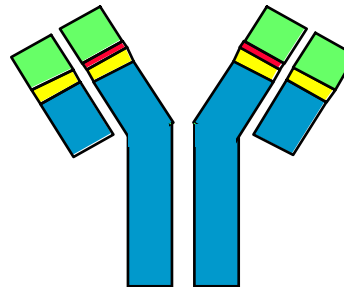
rearranged
DNA



mRNA

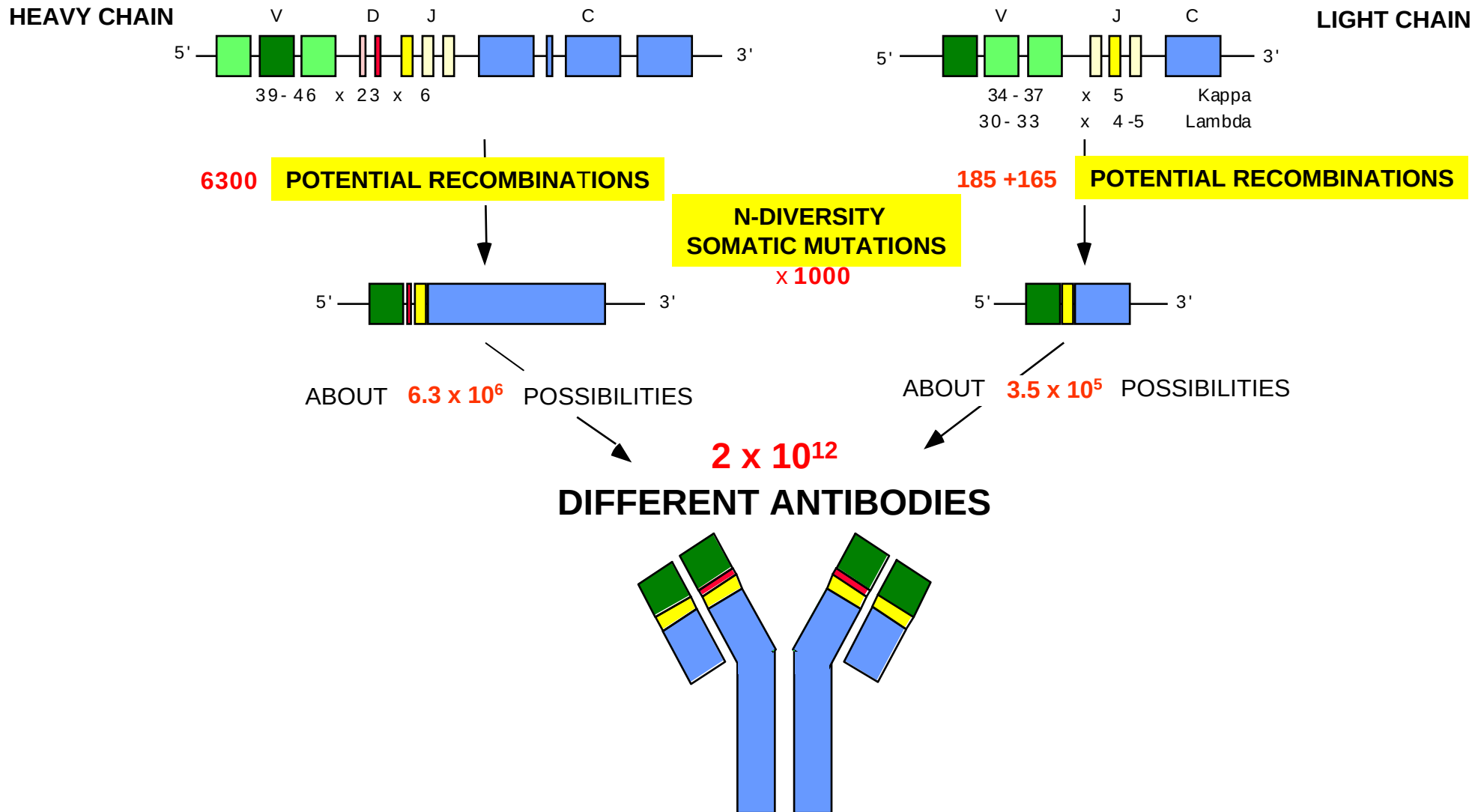


2×10^{12} different IG
per individual



Immunoglobulin (IG) synthesis

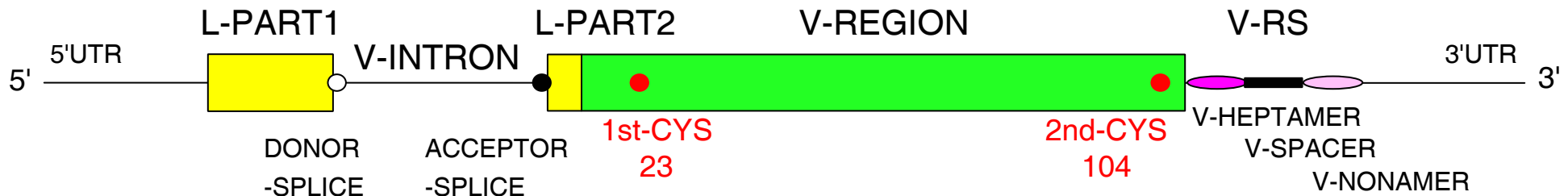
150 FUNCTIONAL IG GENES



An example of V-GENE

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

tgagagctcc	gttcctcacc	atggactgga	cctggaggat	cctcttcttg	gtggcagcag	60
ccacagggt	aa gaggctccct	agtcccagtg	atgagaaaga	gattgagtcc	agtccagggg	120
gatctcatcc	acttctgtgt	tctctccaca	ggagcccact	ccaggtgca	gctgggtgcag	180
tctggggctg	aggtgaagaa	gcctggggcc	tcagtgaagg	tctcctgcaa	ggcttctgga	240
tacaccttca	ccggctacta	tatgcactgg	gtgcgacagg	cccctggaca	agggcttgag	300
tggatgggat	ggatcaacc	taacagtgg	ggcacaaact	atgcacagaa	gtttcagggc	360
agggtcacca	tgaccaggga	cacgtccatc	agcacagcct	acatggagct	gagcaggctg	420
agatctgacg	acacggccgt	gtattactgt	gcgagagaca	cagtg	tgaaa accc	480
tgagggtg	tc agaaacc	caa gggaggaggc	ag			

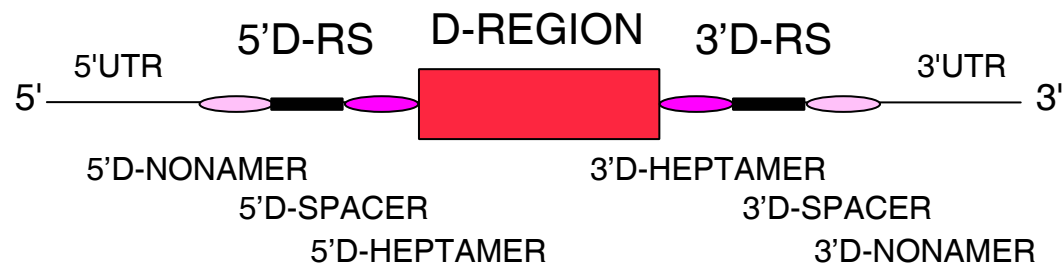


An example of D-GENE

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

```
ccagccgcag ggttttttggc tgagctgaga accactgtgc taactgggga cacagtgaatt  
ggcagctcta caaaaaccat gctcccccg g
```

60

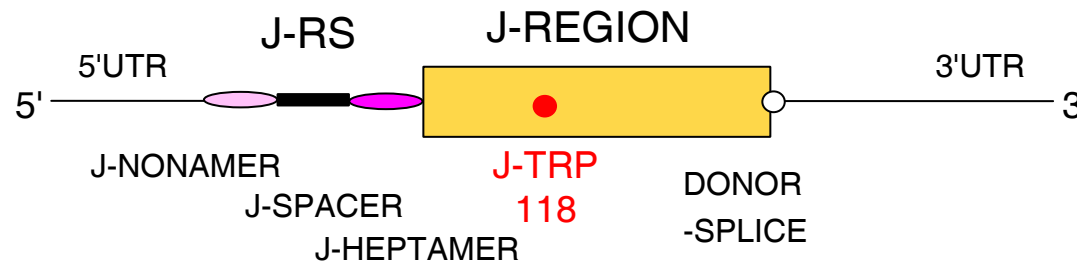


An example of J-GENE

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

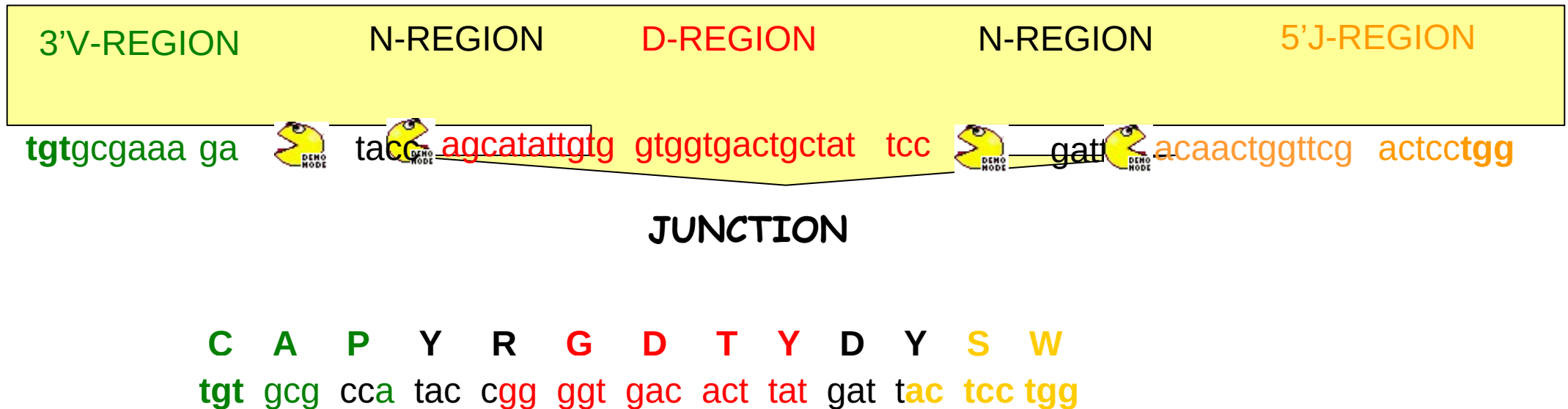
```

accccgggct gtgggtttct gtgcccctgg ctcagggctg actcaccgtg gctgaatact    60
tccagcactg gggccagggc accctgggtca ccgtctcctc aggtgagttc gctgtactgg    120
ggatagcggg gagccatgtg tactgggcc aagcaagggtc ttggcttcag    170
  
```



Heavy chain **WGXX** (J-TRP)
 Light chain **FGXX** (J-PHE)

Immunoglobulin V-D-J generation of sequence diversity



IMGT® Web Resources

IMGT Repertoire

8,000 HTML pages

HTML

Chromosomal localizations

Locus representations, ...

IMGT Bloc-notes

Interesting links

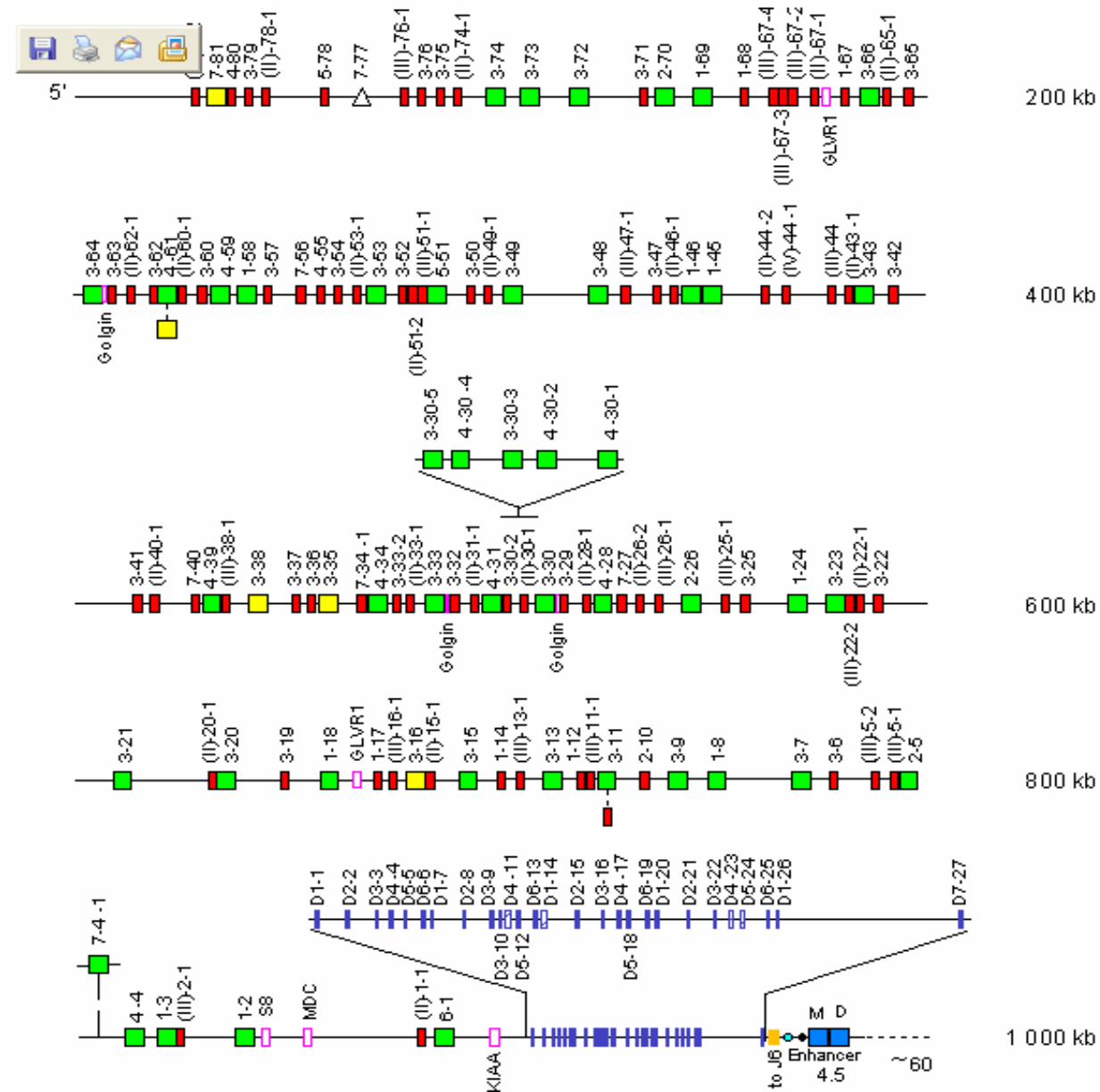
The IMGT Immunoinformatics page
(databases, tools, resources, ...)

IMGT Education

Tutorials, IMGT Lexique, ...

Human IGH locus

Chromosome
14q32.33



Human IGHV genes at chromosome 14q32.33

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

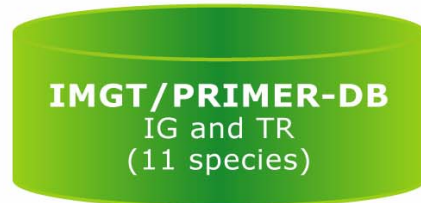
The eleven IMGT amino acid classes according to the physico-chemical properties

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

'Volume' classes		'Hydropathy' classes				
	in Å ³	Hydrophobic		Neutral	Hydrophilic	
Very large	189-228	F	W	Y		
Large	162-174	I L	M		H K R	
Medium	138-154	V				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		

IMGT databases and tools

Sequences



IMGT/V-QUEST

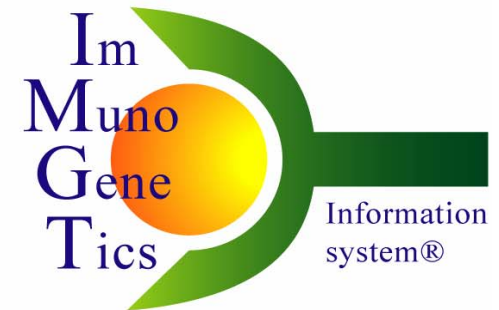
IMGT/JunctionAnalysis

IMGT/Allele-Align

IMGT/PhyloGene



IMGT/3Dstructure-DB
IG, TR and MHC



<http://imgt.cines.fr>

Genome

IMGT/GeneInfo

IMGT/LocusView

IMGT/GeneSearch

IMGT/GeneView

IMGT/StructuralQuery

2D and 3D structures

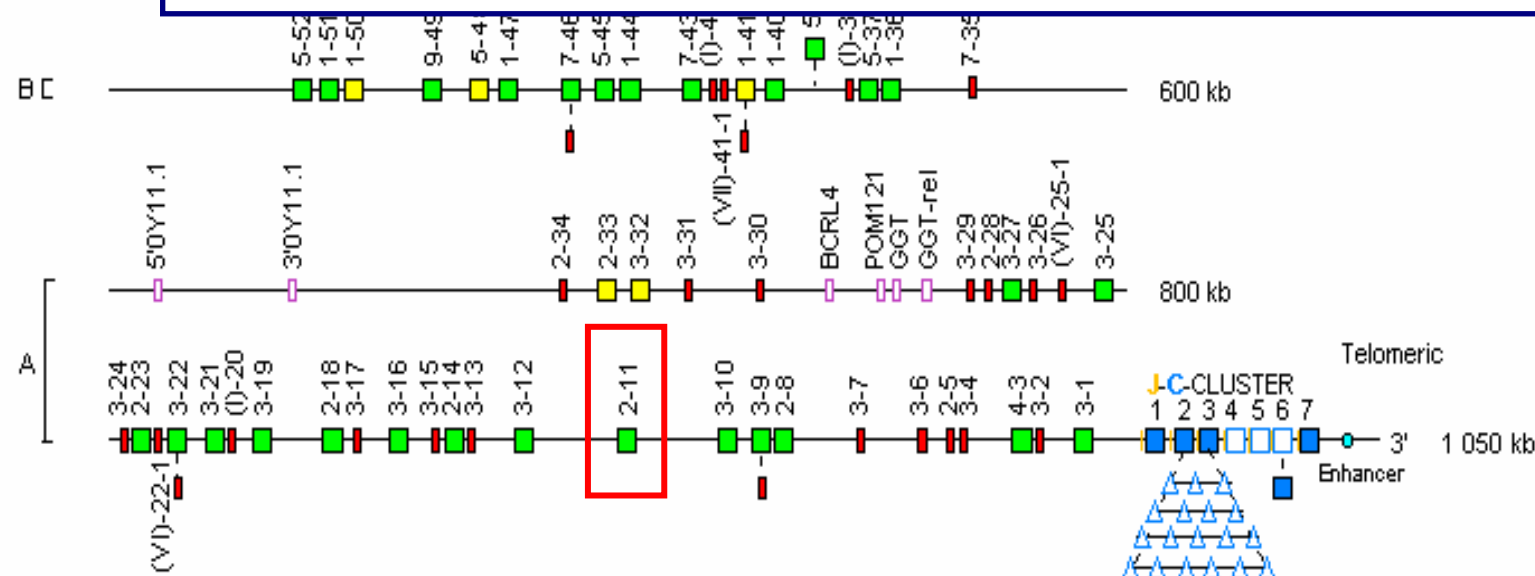
Human IGL 2

WELCOME !
to IMGT/GENE-DB

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IMMUNOGENETICS
INFORMATION SYSTEM®



<http://imgt.cines.fr>





IMGT/V-QUEST

Example of IMGT/V-QUEST results

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	181	_____.T.....T..T.....A.T.....T...G
<u>X86355</u>	IGHJ6*02	179	T.A.TACTACTACT...G.A.....
<u>X86355</u>	IGHJ3*02	172	_____.T.....T..TA.....A.T.....T...G



WELCOME ! to the IMGT/V-QUEST Search page

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INFORMATION SYSTEM®



<http://imgt.cines.fr>

Citing IMGT/V-QUEST: Giudicelli, V. et al. Nucl. Acids Res. 2004, 32, W435-440 [PMID: 15215425](https://pubmed.ncbi.nlm.nih.gov/15215425/) [PDF](#)

Analyse your Immunoglobulin nucleotide sequences

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

Analyse your T cell Receptor nucleotide sequences

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

IMGTV-QUEST - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

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

Analyse your Immunoglobulin sequences

Your selection: Human

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

☒ Include the analysis of the junction by IMGJunctionAnalysis

☐ Do not include the analysis of the junction by IMGJunctionAnalysis

Sequence

You may give your sequence a name (optional) :

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

```
gaggtgcagctgttgaggcgggggaggcttggtacagcctgggggggtccctgagactc
tctgtgcagcctctggattcacctttagcagctttgccatgagctgggtccgccaggct
cctgggaaggggctggactgggtctcagaaattagtggtagtggcggtaccacatattac
gcaggctccgtgaagggccggttcaccatctccagagacaactccaagaatacgtgttt
ctgcaaatgaatagcctgacagccgaagacacggccgtatattactgtgcgaagaggtt
```

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

Terminé

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...GGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACACCTTTAGCAGCTTTGCC...
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--...

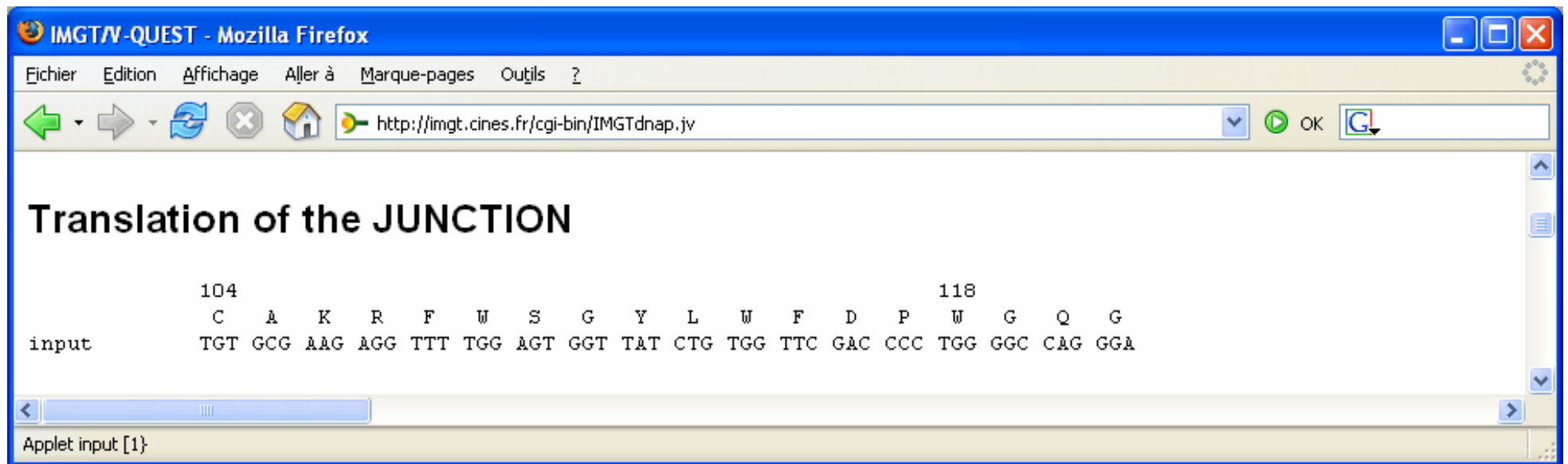
Alignment for D-GENE

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

Applet input [1}



IMGT/V-QUEST - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

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

Alignment for V-GENE

input		score	GAGGTGCAGCTGTTGGAGTCGGGGGGA...GGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACACCTTTAGCAGCTTTG
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--
M99675	IGHV3-48*01	1128	-----G-----T-----..-----C--T--A-A

Alignment for J-GENE

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

Results of IMGT/JunctionAnalysis

Analysis of the JUNCTION

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

Input Jmut Ngc

#1 input 0 2/3

Translation of the JUNCTION

	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	frame	length
#1 input	C	A	K	R	F	W	S	G	Y	L	W	F	D	P	W	+	13

Applet input [1]


IMGT/QUEST - Mozilla Firefox



Fichier Edition Affichage Aller à Marque-pages Outils ?


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

 OK

Alignment with FR-IMGT and CDR-IMGT delimitations

input

M99660 IGHV3-23*01

J00236 IGHV3-23*02

U29481 IGHV3-23*03

Z12358 IGHV3-48*03

M99675 IGHV3-48*01

```

<----- F R 1 - I M G T -----
1           5           10          15
GAG GTG CAG CTG TTG GAG TCG GGG GGA ... GGC TTG GTA CAG CCT GGG GGG TCC
--- --- --- --- --- --- --T --- --- --- --- --- --- --- ---
--- --- --- --- --- --- --T --- --- --- --- --- --- --- ---
--- --- --- --- --- --- --T --- --- --- --- --- --- --- ---
--- --- --- --- G--- --- --T --- --- --- --- --- --- --A ---
--- --- --- --- G--- --- --T --- --- --- --- --- --- --- ---

```

----->

input

M99660 IGHV3-23*01

J00236 IGHV3-23*02

U29481 IGHV3-23*03

Z12358 IGHV3-48*03

M99675 IGHV3-48*01

```

20           25           30           CDR1 - IMGT           35
CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTT AGC AGC TTT GCC ...
--- --- --- --- --- --- --- --- --- --- --- --- --- --A- --- ...
--- --- --- --- --- --- --- --- --- --- --- --- --- --A- --- ...
--- --- --- --- --- --- --- --- --- --- --- --- --- --A- --- ...
--- --- --- --- --- --- --- --- --- --- --C --T --T --A- --AA ...
--- --- --- --- --- --- --- --- --- --- --C --T --- --A- AG- ...

```

----->

input

M99660 IGHV3-23*01

J00236 IGHV3-23*02

U29481 IGHV3-23*03

Z12358 IGHV3-48*03

M99675 IGHV3-48*01

```

40           45           50
... ... ATG AGC TGG GTC CGC CAG GCT CCT GGG AAG GGG CTG GAC TGG GTC TCA
... ... --- --- --- --- --- --- --- --A --- --- --- --G --- ---
... ... --- --- --- --- --- --- --- --A --- --- --- --G --- ---
... ... --- --- --- --- --- --- --- --A --- --- --- --G --- ---
... ... --- --A- --- --- --- --- --- --A --- --- --- --G --- --T ---
... ... --- --A- --- --- --- --- --- --A --- --- --- --G --- --T ---

```

Applet input [1}

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
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           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 ...
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
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 S D
M99660 IGHV3-23*01
           -CT --- --- --- --- --T --- -G- --- ... --- --C --- --A- ---

```

Applet input [1]

IMGTV-QUEST - Mozilla Firefox

Eichier Edition Affichage Aller à Marque-pages Outils ?

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

"input" V-REGION

Nucleotidic sequence in FASTA format

```
>input
GAGGTGCAGCTGTTGGAGTCGGGGGGA...GGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG
GATTCACCTTTAGCAGCTTTGCC.....ATGAGCTGGGTCCGCCAGGCTCCTGGGAAGGGGCTGGACTGGGT
CTCAGAAAATTAGTGGTAGTGGCGGTACCACA.....TATTACGCAGGCTCCGTGAAG...GGCCGGTTCACCATCTCC
AGAGACAACCTCCAAGAATACGCTGTTTCTGCAAAATGAATAGCCTGACAGCCGAAGACACGGCCGTATATTACTGTGCGA
AGA
```

Analyse this sequence with IMGT/PhyloGene

Amino acid sequence

```
EVQLLESGG.GLVQPGGSLRLSCAASGFTFSSFA....MSWVRQAPGKGLDWVSEISGSGGTT..YYAGSVK.GRFTISRDN SKNTLFLQMNSLTAE DTAVYYCAKR
```

Applet input [1}

IMGT/V-QUEST - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

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

Collier de Perles

input

Diagram illustrating a sequence alignment or network structure, showing various amino acid residues (A, C, D, E, F, G, I, K, L, M, N, P, Q, R, S, T, V, W, Y) connected by lines, representing interactions or relationships between different sequences.

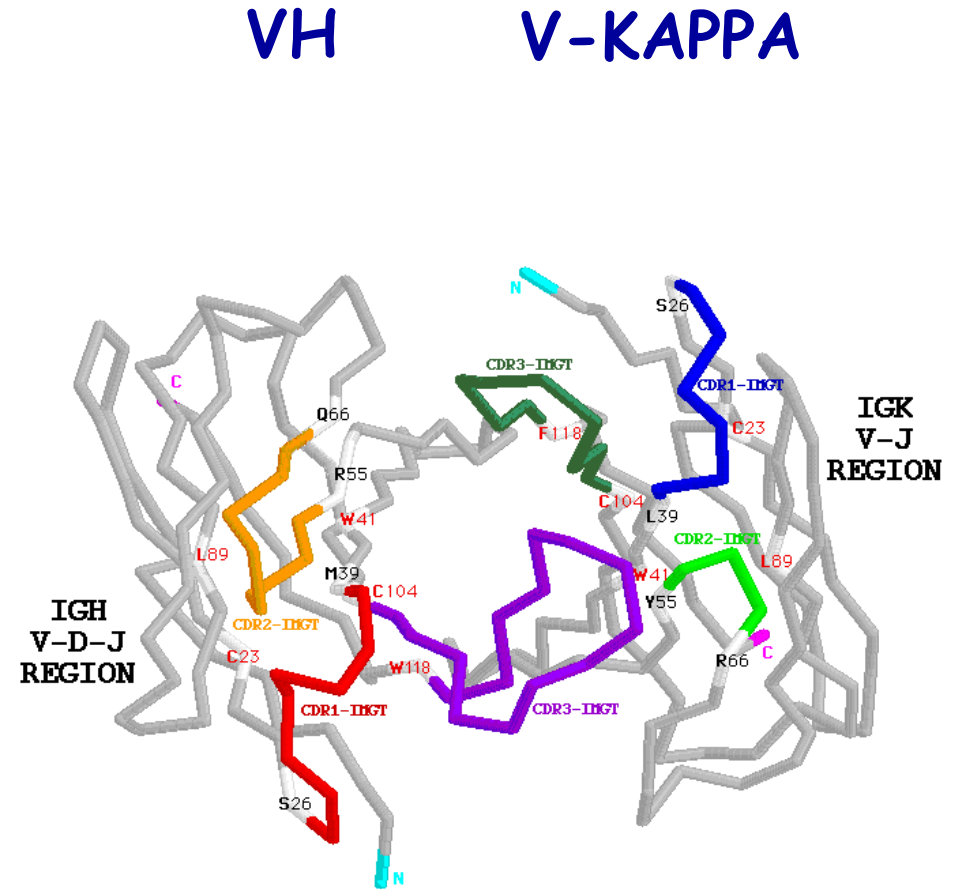
Legend for sequence alignment:

Sequence	Direction	Position
A	↓	1
B	↑	2
C	↓	3
C'	↑	3a
C''	↓	3b
D	↑	4
E	↓	5
F	↑	6

Applet input [1}

IMGT/JunctionAnalysis

<http://imgt.cines.fr>



View from above the CDRs

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

THANK YOU for using IMGT/JunctionAnalysis

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INFORMATION SYSTEM®



<http://imgt.cines.fr>

Analysis of the JUNCTIONS

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

Input	J-REGION	J name	D name	Vmut	Dmut	Jmut	Ngc
#1 M62724	tttaactactgg	IGHJ4*02	IGHD5-24*01	0	2	0	1/7
#2 Z47269	...actgggttcgacccctgg	IGHJ5*02	IGHD3-3*02	0	2	0	13/20

Translation of the JUNCTIONS

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

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

IMGT/JunctionAnalysis - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

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

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

IMGT/JunctionAnalysis Search page

Species :

Homo sapiens

Locus :

☒ IGH ☐ TRA
☐ IGK ☐ TRB
☐ IGL ☐ TRG
☐ TRD

Sequences

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

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

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

Parcourir...

Start Clear the form

Terminé

IMGT/JunctionAnalysis - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

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

Start Clear the form

Parameters for accepted mutations :

3'V-REGION and 5'J-REGION

☒ Default value

☐ Selected value

0 1 2 3 4 5 6

D-REGION

☒ Default value

☐ Selected value

0 1 2 3 4

Output options :

☒ Displayed ☐ Downloaded into a local file

Output order of the translation results :

☒ Input order ☐ Based on CDR3-IMGT length

Maximum number of characters per line :

☒ Unlimited ☐ 80 ☐ 100 ☐ 120

Terminé

THANK YOU
for using **IMGT/JunctionAnalysis**

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INFORMATION SYSTEM®



<http://imgt.cines.fr>

Analysis of the JUNCTIONs

Input	V name	V-REGION	N1	D-REGION	N2	J-REGION	J name
#1	M62724	IGHV7-4-1*02	tgtgcgagaga	aga .tagcaatggctacaa....	aata	tttgactactgg	IGHJ4*02
#2	Z47269	IGHV1-69*06	tgtgcgaga	gggggggctaaggtcgaatttttgagtggtt.....	tcattgggt	...actggttcgaccctctgg	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							
#1 M62724	Cgtg	Aaga	Rgaa	Egat	Sagc	Naat	Gggc			Ytac	Kaaa	Iata	Fttt	Dgac	Ytac	Wtg	+	13			
#2 Z47269	Cgtg	Aaga	Rggg	Eggg	Ggct	Aaag	Gtcgaa	Vttt	Ettg	Fgag	Htgg	Fttt	Gcat	Yggg	Wtac	Pttc	Wgac	ccc	tg	+	20

Terminé

IMGT/3Dstructure-DB and IMGT/StructuralQuery

Experimental technique	X-ray diffraction	Resolution	2.24	PDB release date	05-OCT-04
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Chain ID	1u8k_A	
IMGT chain description	L-KAPPA	
Chain amino acid sequence	[ALQLTQSPSSLSASVGDRIITITGRASQGVTSALAWYRQKPGSPQLLIYDASSLESQVPSRFSGSGSGTEFTLTISTLRPEDFATYYQQQ] [IGKV_1] [LHFYPHTFGGGTRVDVRRITVAAPSVFIFPPSDRQLKSGTASVWGLINNFYPREAKVQWKVINALQSGNSQESVTEQDSKDYSLSTLT] [IGK_1] LSKADYEKKHVEYGEVTHQGLSSPVTKSFNRGEC	
V-DOMAIN	IMGT domain description	V-KAPPA
	IGKV gene and allele name	IGKV1-13*02 (85.26%) Alignment details
	IGKJ gene and allele name	IGKJ4*01 (63.64%) , IGKJ4*02 (63.64%) Alignment details
	2D representation	Collier de Perles or Collier de Perles on 2 layers
	CDR-IMGT lengths	[6.3.9]
	Sheet composition	[A B D E] [C C' C' F G]
	[CDR1] [CDR2] ALQLTQSPSSLSASVGDRIITITGRASQGVTSAS...LAWYRQKPGSPQLLIYDAS...SLESQVPSRFSGSG...SGTEFTLT [CDR3] ISTLRPEDFATYYQQQLHF...YPHTFGGGTRVDVRR	
C-DOMAIN	IMGT domain description	C-KAPPA
	IGKC gene and allele name	IGKC*01 (98.13%) Alignment details
	2D representation	Collier de Perles or Collier de Perles on 2 layers
	Sheet composition	[A B D E] [C F G]
	...RTVAAPSVFIFPPSDRQLK...SGTASVWGLINNFYP...REARVQWKVINALQSGNSQESVTEQDSKDS...TYSLSSTLT LSKADY...EKHVEYGEVTHQGLSSPVTKSFNRGEC	

Chain ID	1u8k_C
IMGT chain description	Peptide
Chain amino acid sequence	LELDKWASL

From IMGT Colliers de Perles or from domain/chain sequence

41V - TRP (W)

chain : 1u8k_B

Secondary structure	Extended conformation
Phi	-122.64
Psi	137.12
ASA	0.0

Residue local structure

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

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

IMGT Collier de Perles

