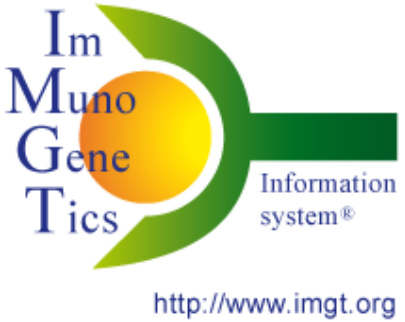
Immunotechnologie

Enseignements d'Immunoinformatique-
IMGT®, the international ImMunoGeneTics information system®

mardi 1er octobre 2013

Souphatta SASORITH



I. IMGT Bases de données et Outils

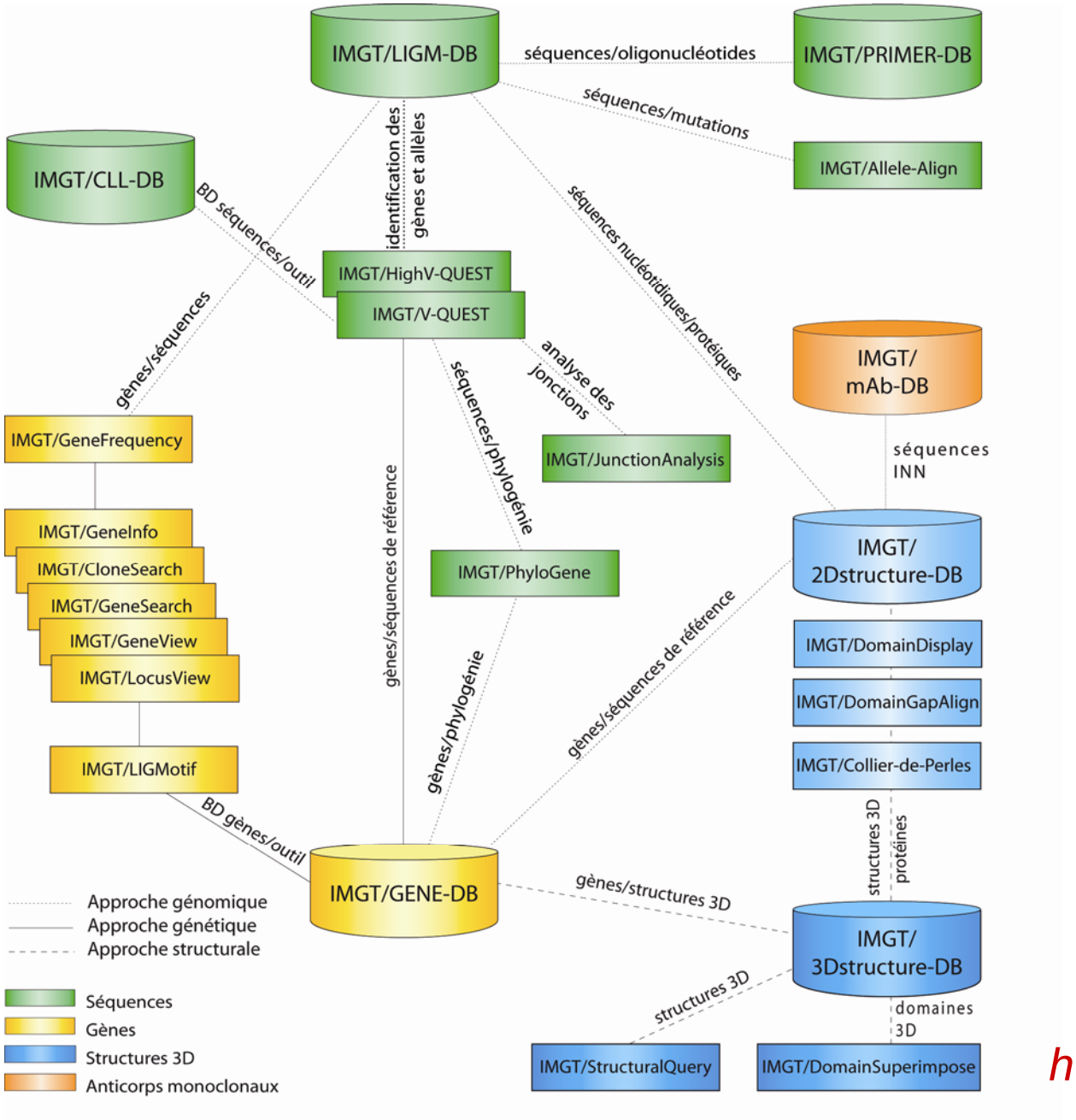
II. Les immunoglobulines:

- Structure générale des IG
- Chromosomes et locus
- Synthèse des IG (génétique moléculaire)

III. Structure des gènes :
V-GENE, D-GENE, J-GENE et C-GENE

IMGT bases de données et outils

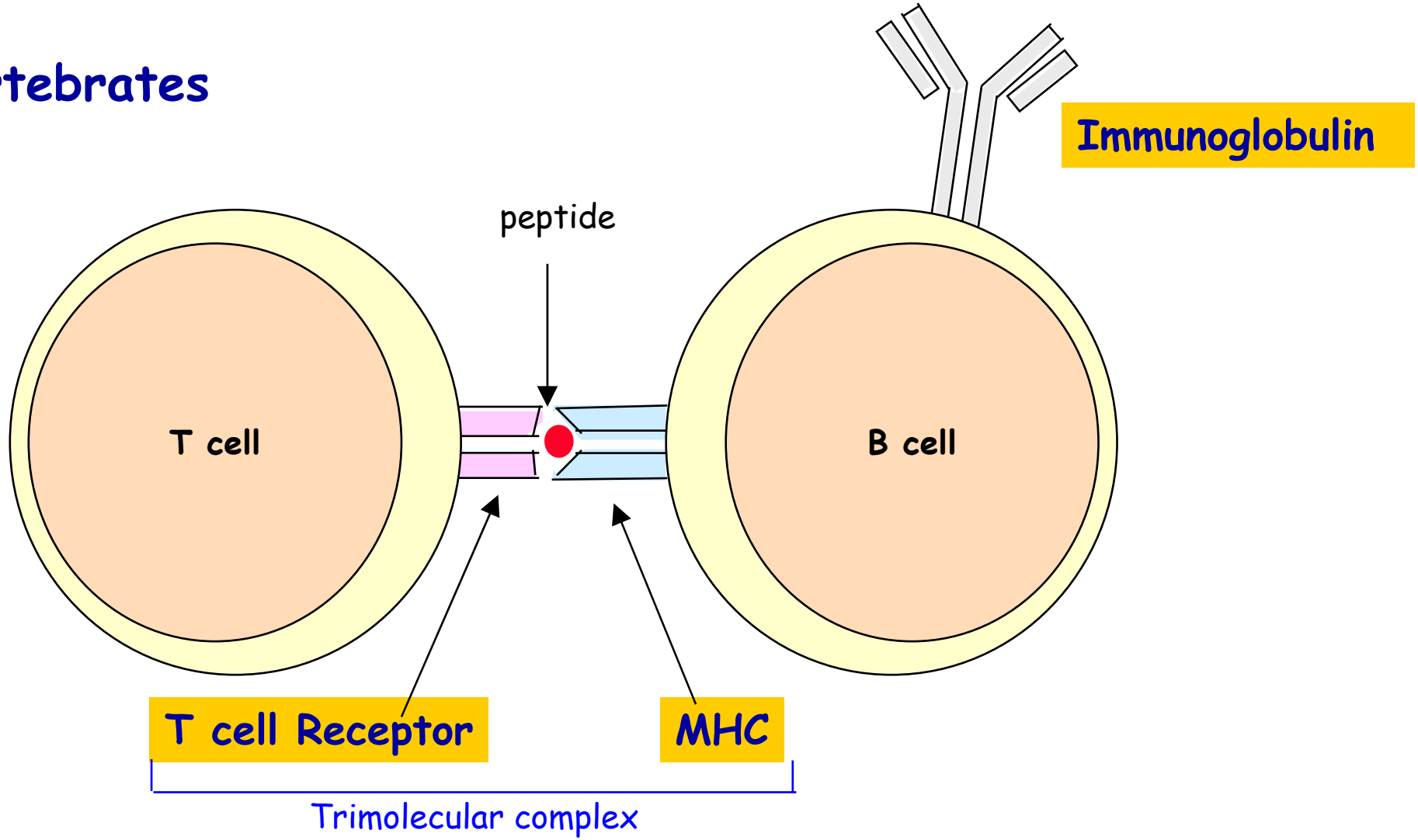
IMGT®, the international ImMunoGeneTics information system®



http://www.imgt.org

IMGT domain of research: the adaptive immune system

Vertebrates



Immunoglobuline membranaire (IGM)

receptor T (TR)

http://imgt.cines.fr

V-DOMAIN

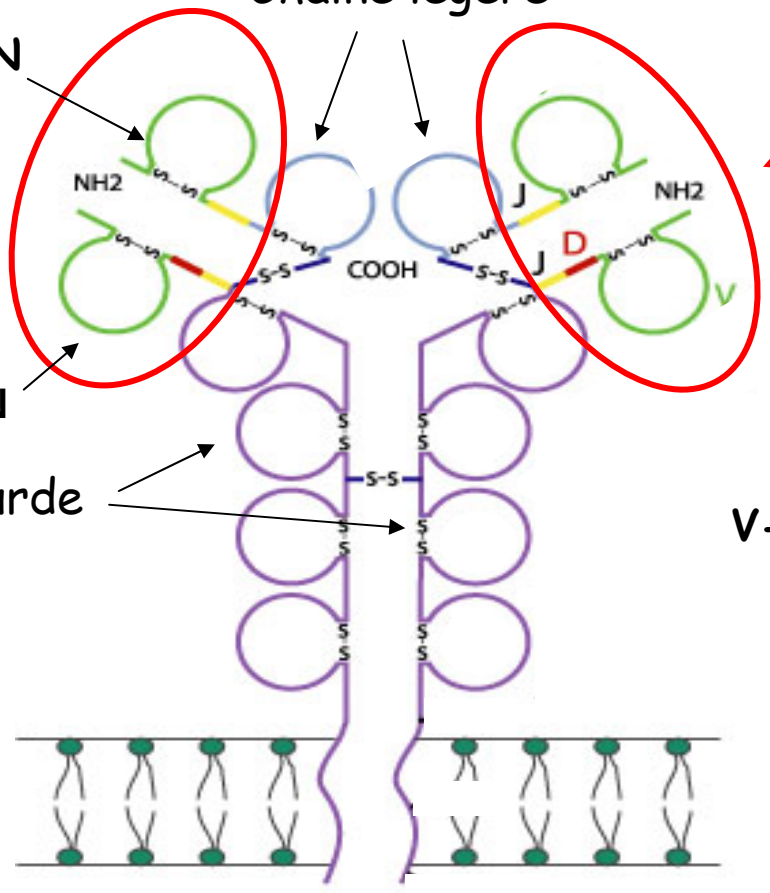
V-J-REGION

Chaîne légère

V-DOMAIN

V-D-J-REGION

Chaîne lourde



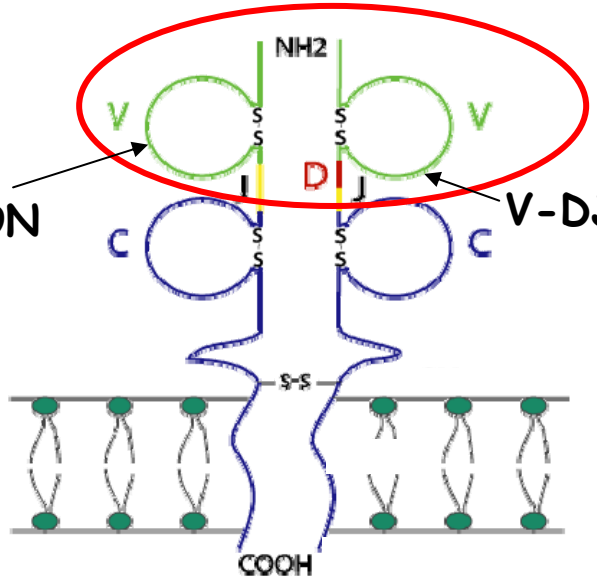
Contribution des 2

2 V-DOMAINs

Au site de fixation de l'antigène

Alpha - Beta

Gamma - Delta

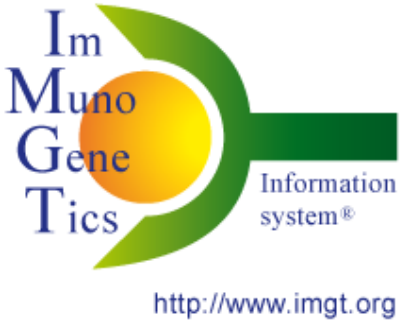


V-J-REGION

V-DJ-REGION

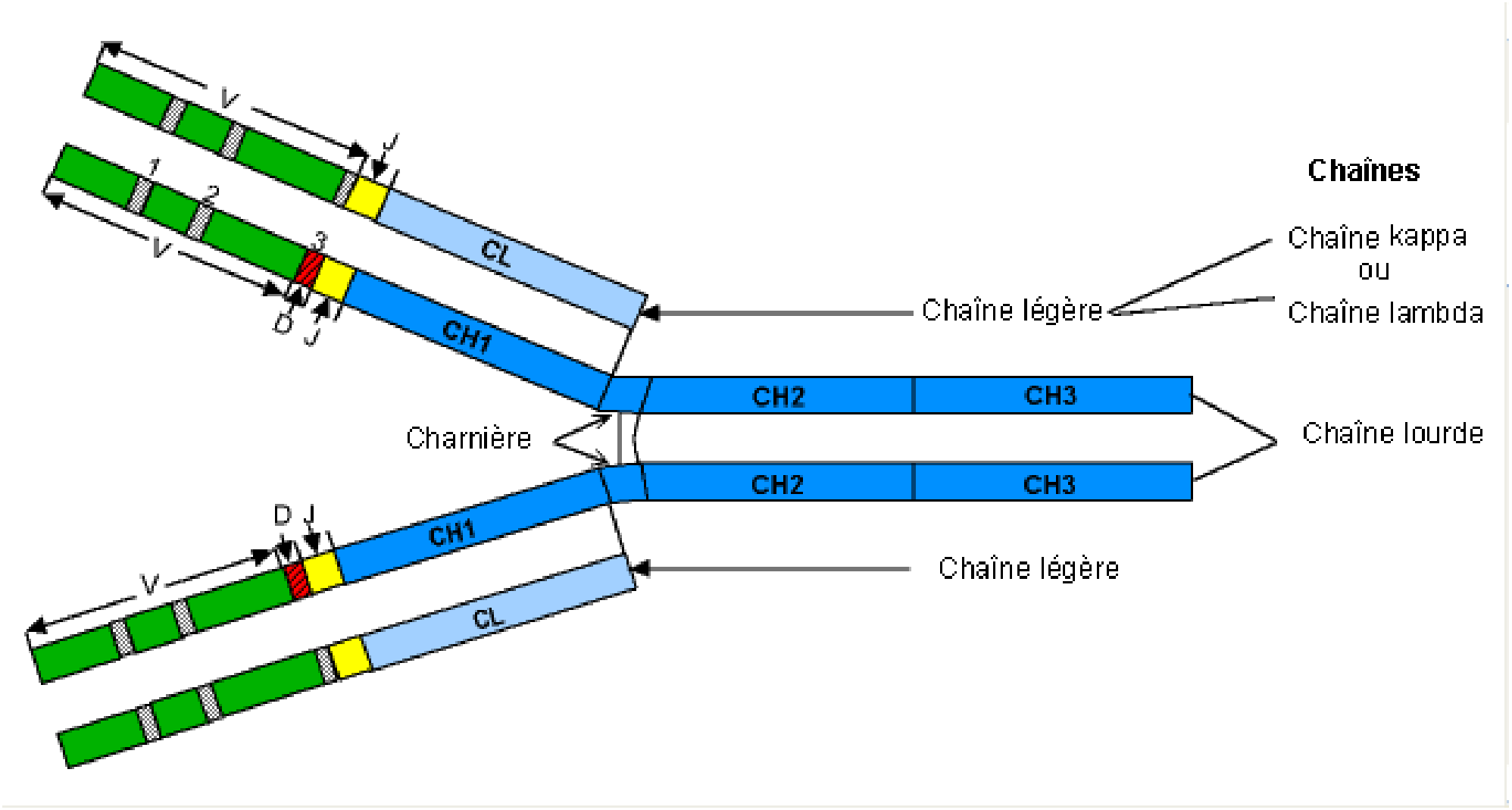
The Immunoglobulin FactsBook, 2001

Immunoglobulines



Immunoglobuline IgG

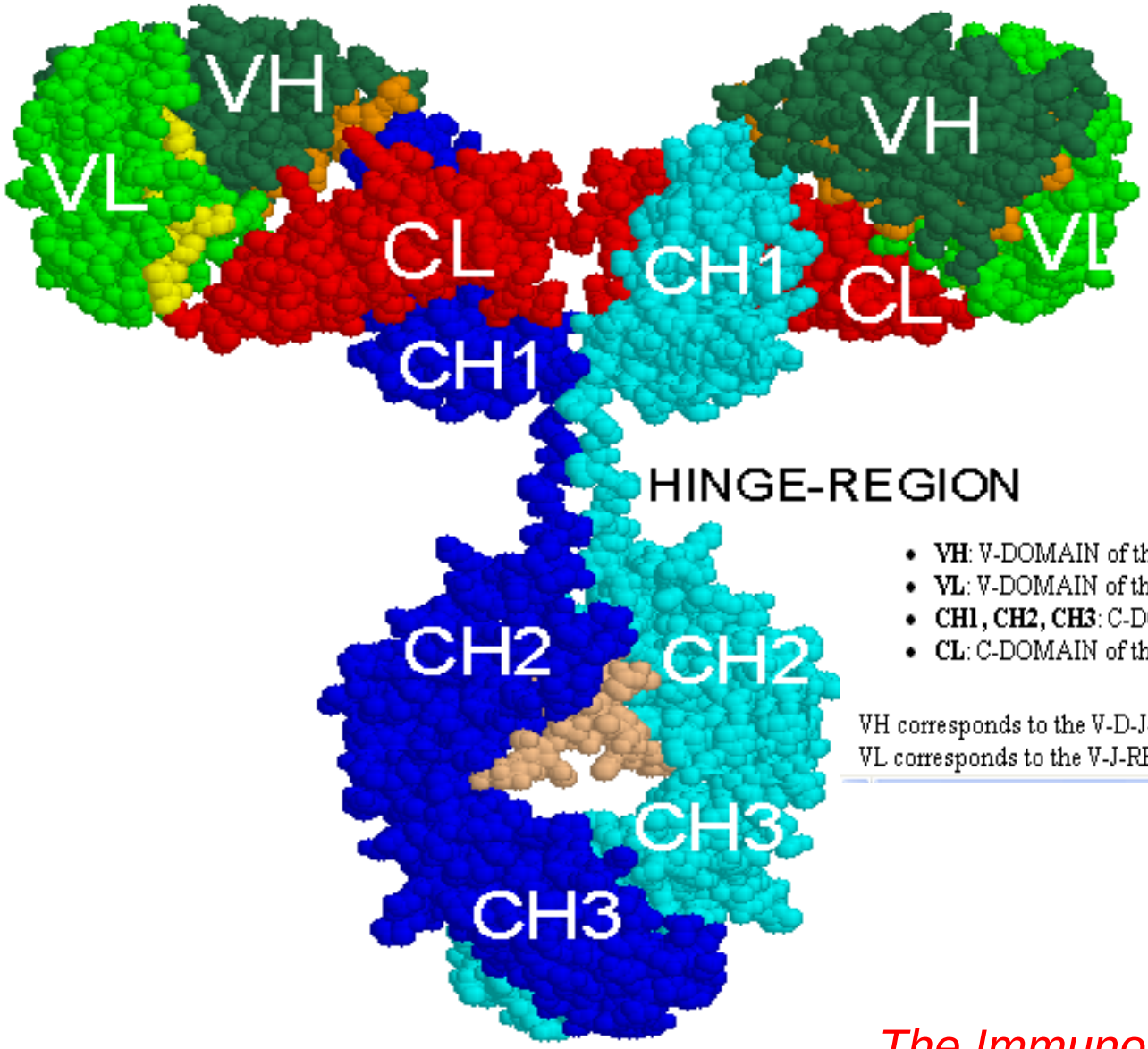
http://imgt.cines.fr



http://www.imgt.org

Spacefill 3D representation of an IgG

http://imgt.cines.fr



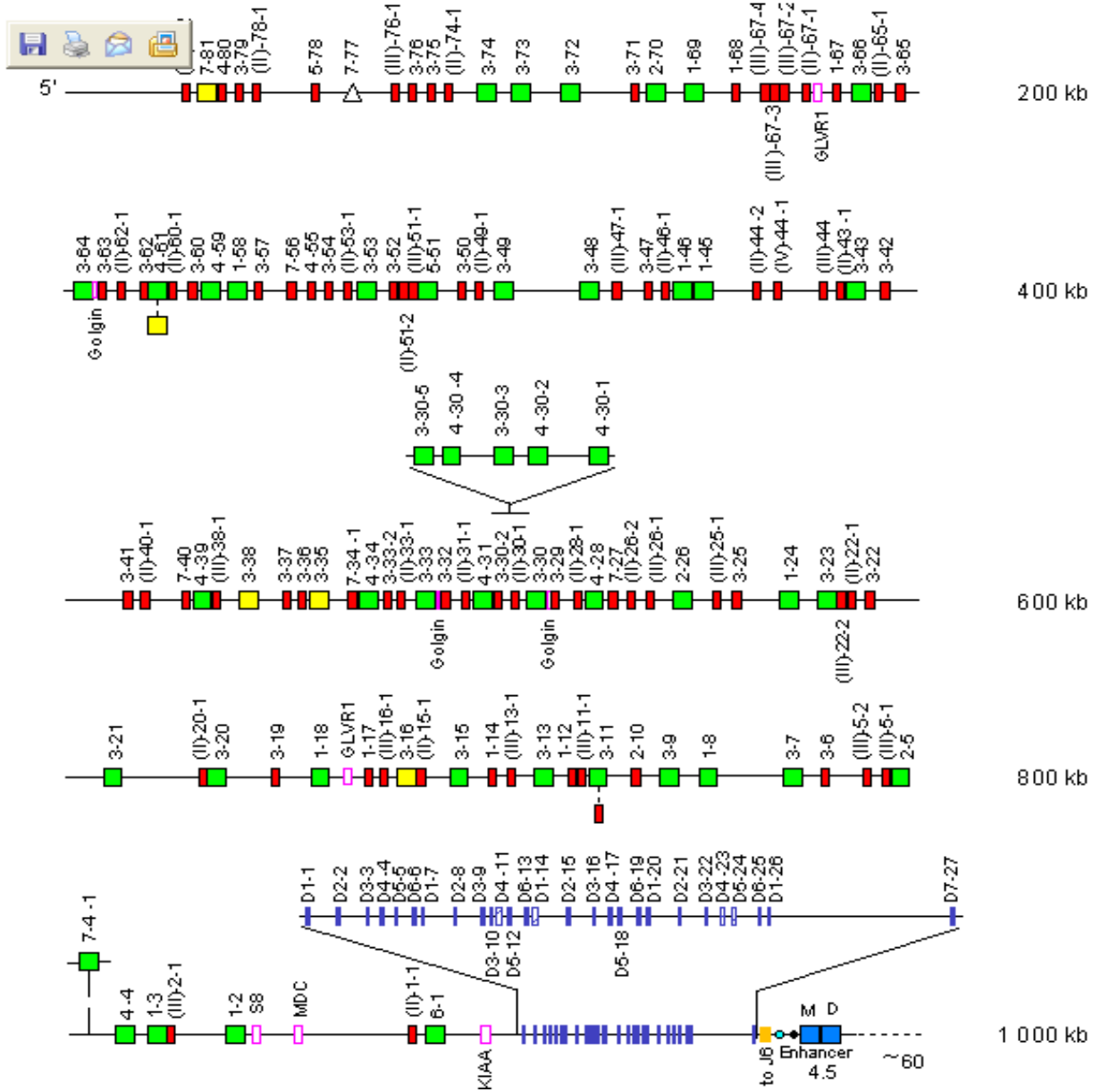
- **VH**: V-DOMAIN of the immunoglobulin heavy chain
- **VL**: V-DOMAIN of the immunoglobulin light chain
- **CH1, CH2, CH3**: C-DOMAIN of the immunoglobulin heavy chain
- **CL**: C-DOMAIN of the immunoglobulin light chain

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

The Immunoglobulin FactsBook, 2001

Human IGH locus

Chromosome 14q32.33



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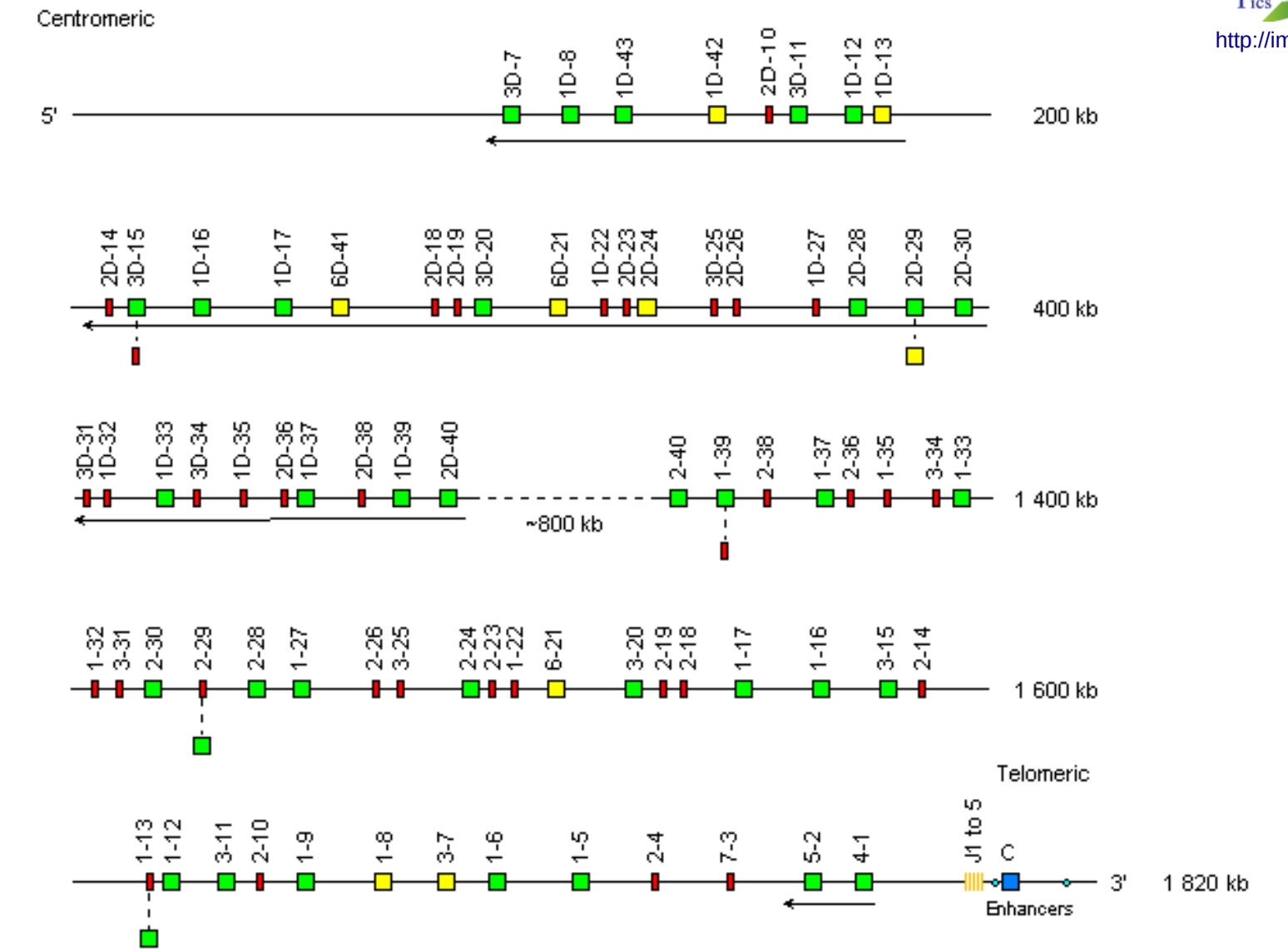
IMGT Repertoire, http://www.imgt.org

Human IGK locus

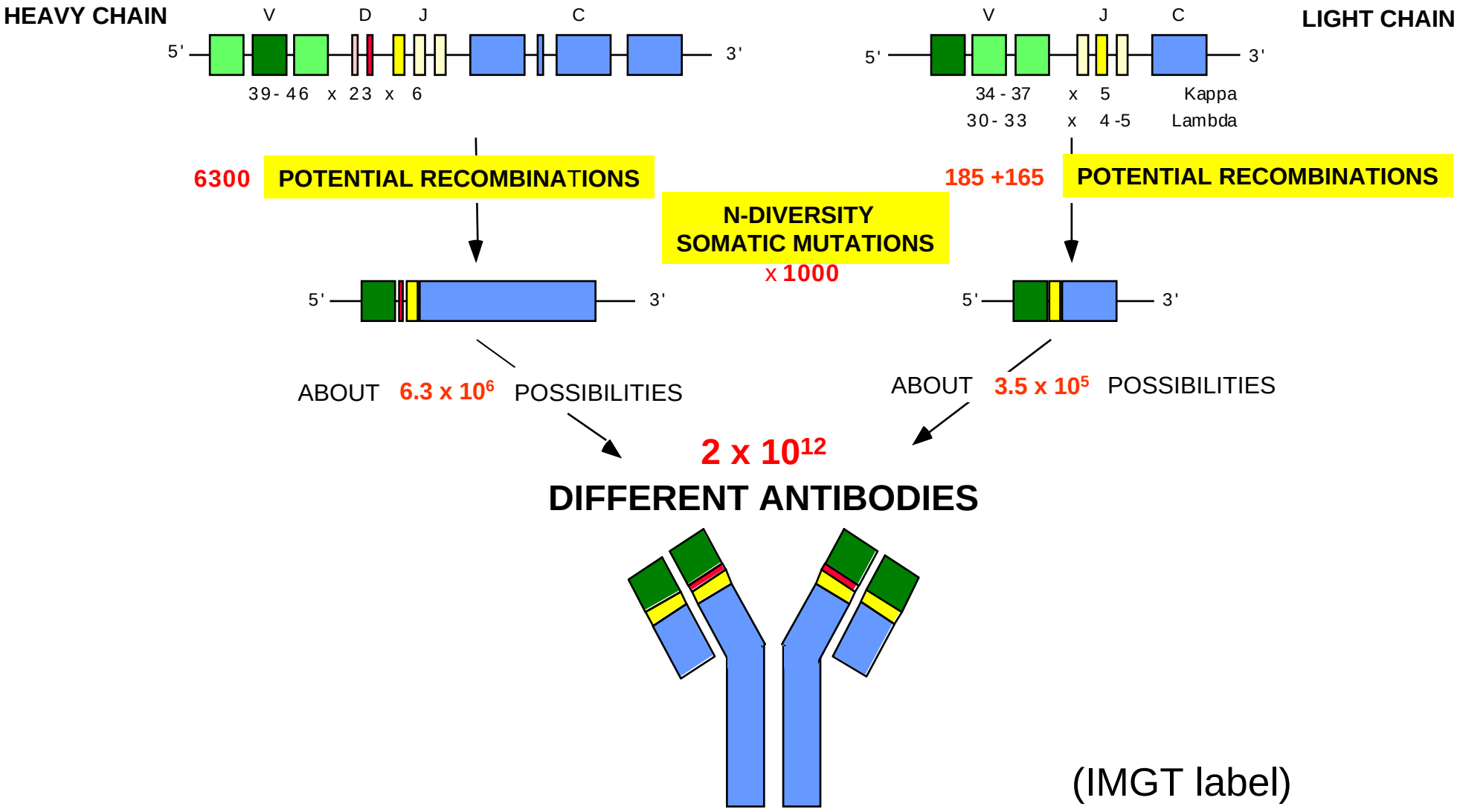
Chromosome 2p11.2



Immunoglobulin (IG) synthesis

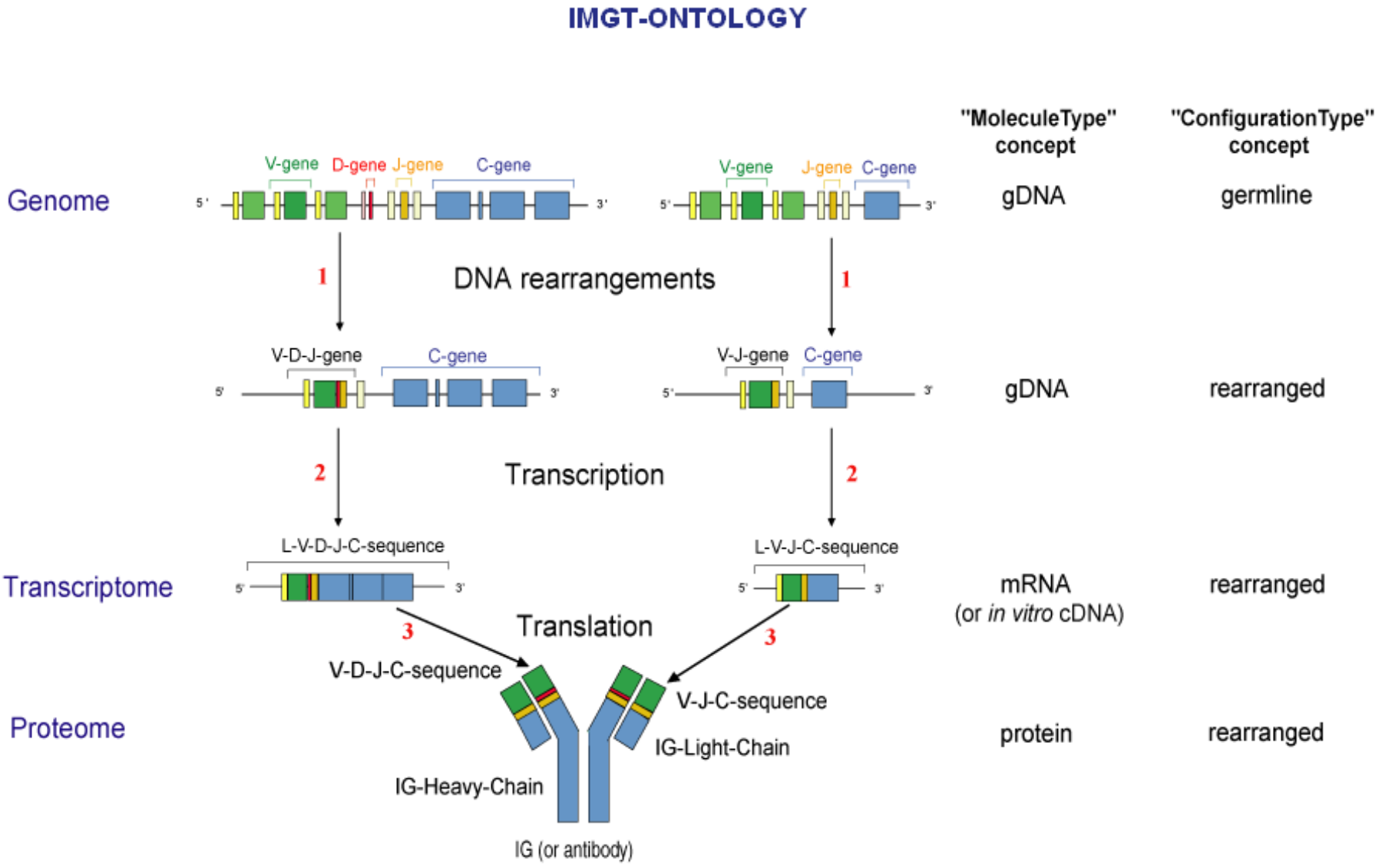
http://imgt.cines.fr

150
FUNCTIONAL IG GENES

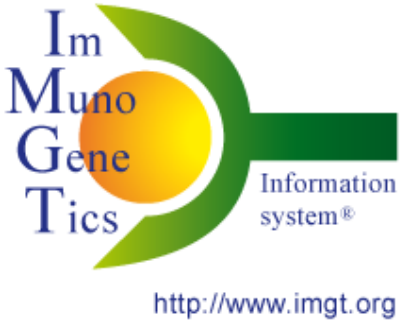


(IMGT label)

Immunoglobulin (IG) synthesis



Structure des Gènes



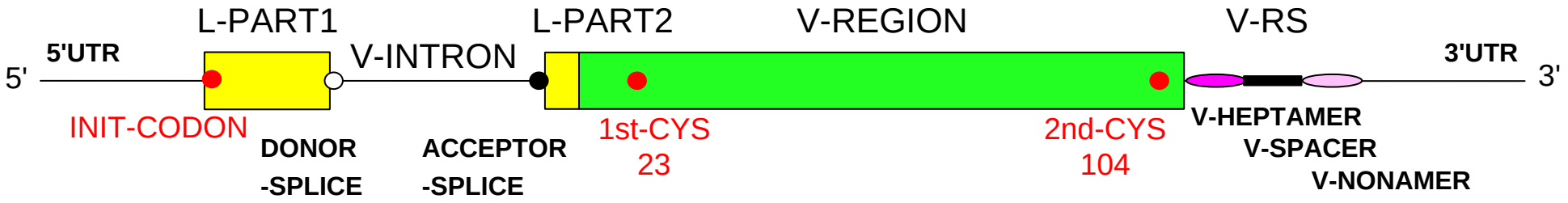
Genomic DNA in germline configuration

http://imgt.cines.fr

V-GENE

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

```
tgagagctcc gttcctcacc atggactgga cctggaggat cctcttcttg gtggcagcag      60
ccacaggtaa gaggctccct agtcccagtg atgagaaaga gattgagtcc agtccaggga     120
gatctcatcc acttctgtgt tctctccaca ggagcccact cccaggtgca gctggtgcag     180
tctggggctg aggtgaagaa gcctggggcc tcagtgaagg tctcctgcaa ggcttctgga     240
tacaccttca ccggctacta tatgcactgg gtgcgacagg cccctggaca agggcttgag     300
tggatgggat ggatcaaccc taacagtggt ggcacaaact atgcacagaa gtttcagggc     360
agggtcacca tgaccaggga cacgtccatc agcacagcct acatggagct gagcaggctg     420
agatctgacg acacggccgt gtattactgt gcgagagaca cagtgtgaaa acccacatcc     480
tgagggtgtc agaaacccaa gggaggaggc ag
```



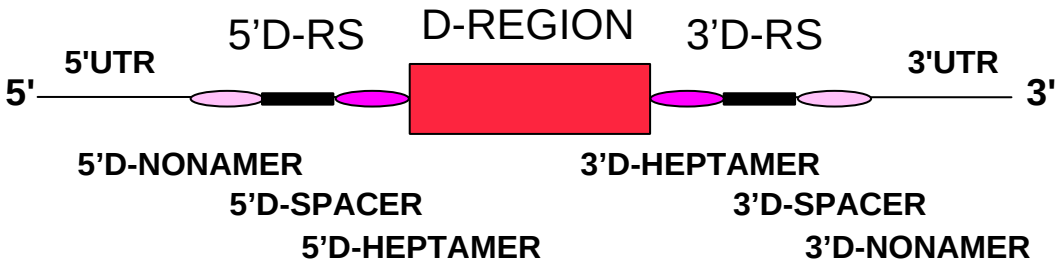
Genomic DNA in germline configuration

http://imgt.cines.fr

D-GENE

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

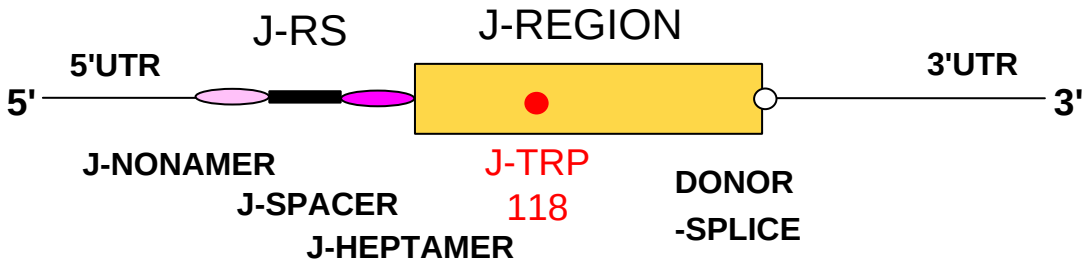
```
ccagccgcag ggtttttggc tgagctgaga accactgtgc taactgggga cacagtgatt      60
ggcagctcta caaaaaccat gctccccgg g
```



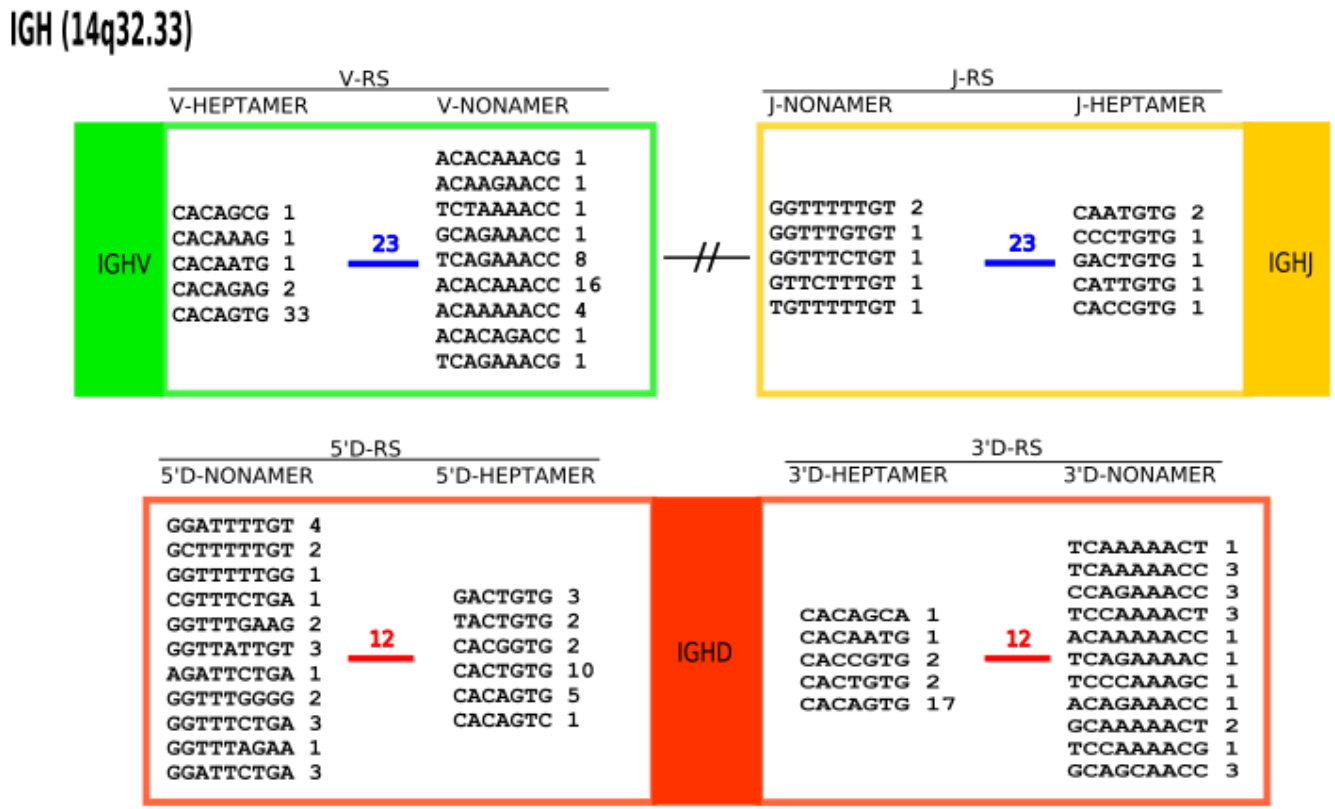
J-GENE

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

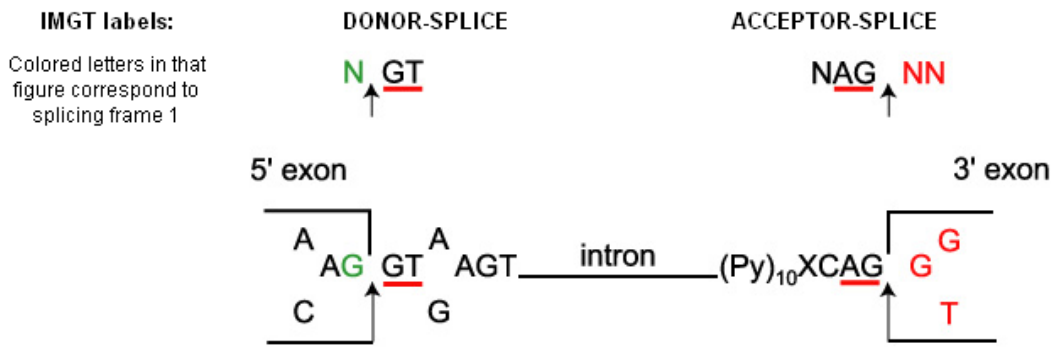
```
accccgggct gtgggtttct gtgcccctgg ctcagggctg actcaccgtg gctgaatact      60
tccagcactg gggccagggc accctggtca ccgtctcctc aggtgagtct gctgtactgg     120
ggatagcggg gagccatgtg tactgggcca agcaagggct ttggcttcag                170
```

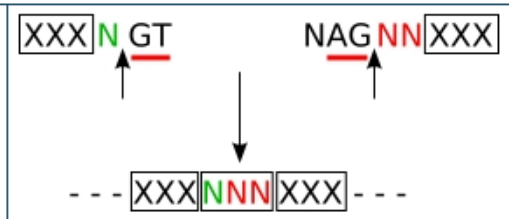
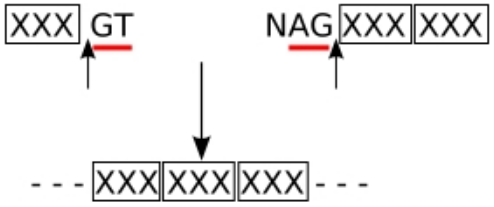
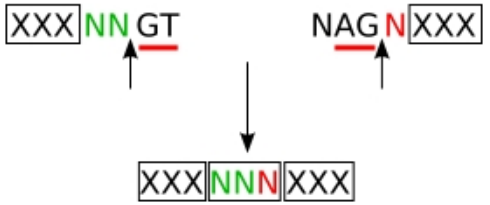


Signaux de recombinaison des IGH

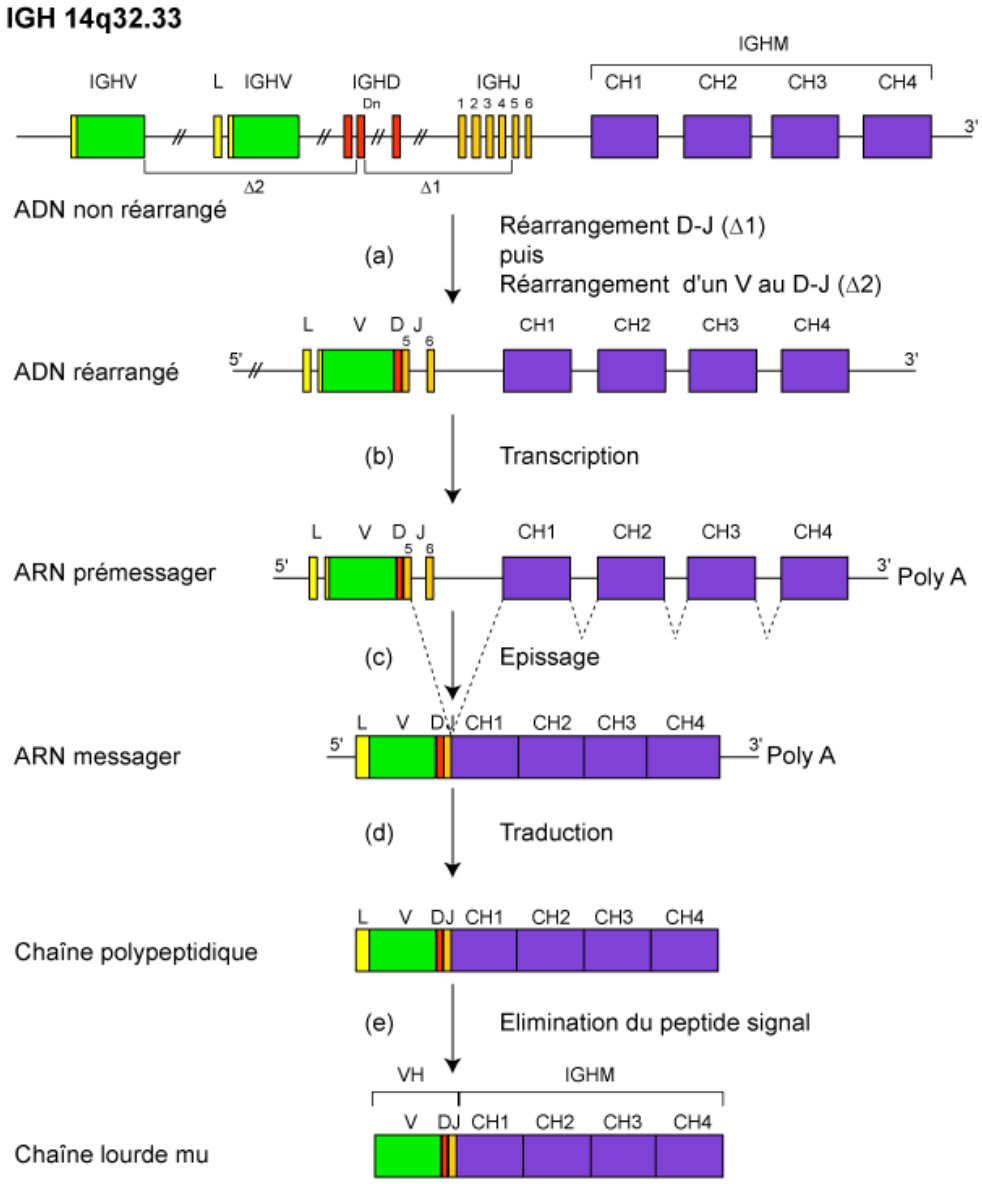


Sites d'épissage



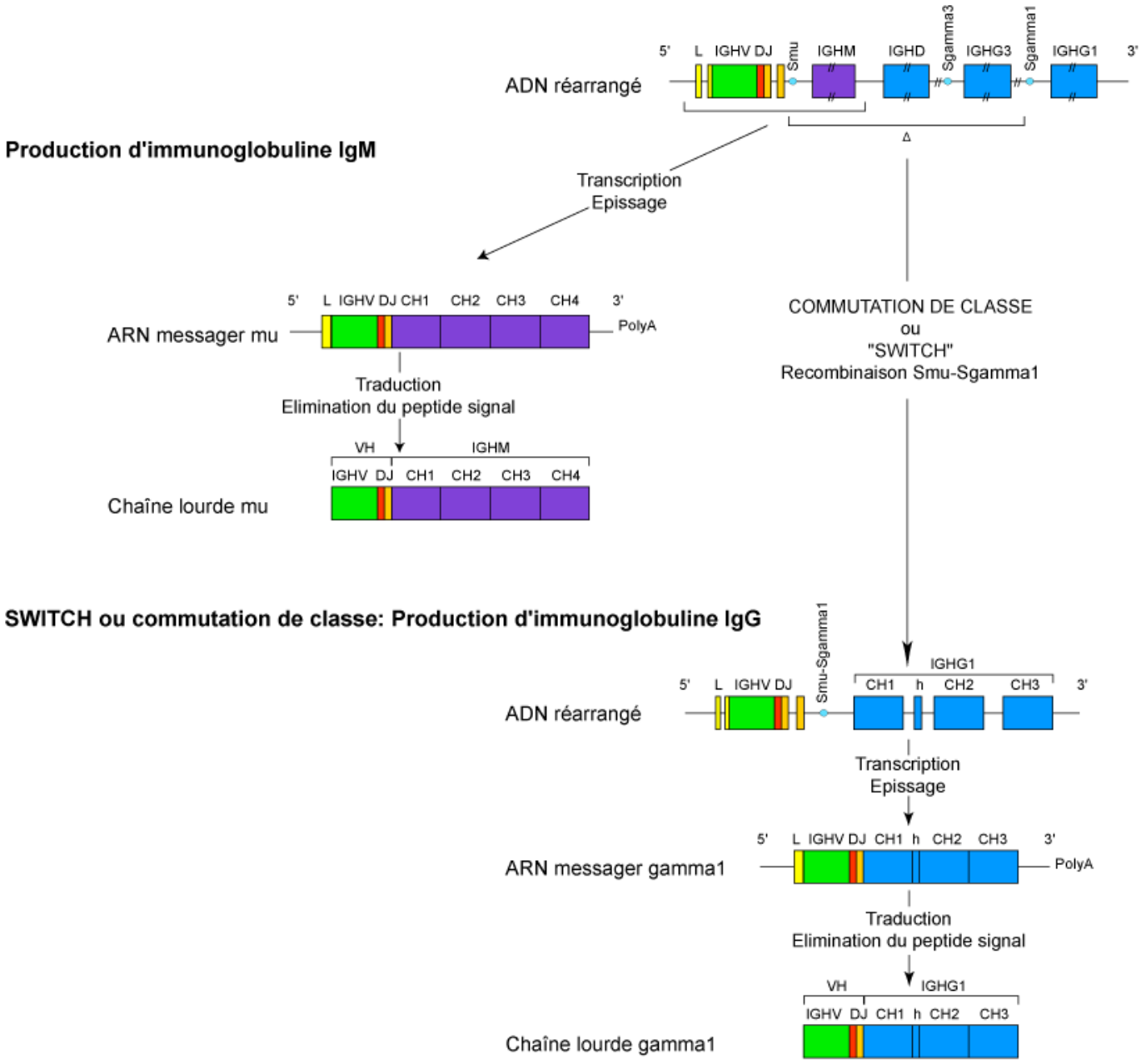
Splicing INTRON view			Splicing EXON view		
Different splicing types			In IMGT/LIGM-DB flat file for exon translation (1)	In IMGT/GENE-DB reference sequences of exons in FASTA format	
				Number of 'd' nucleotides (5)	
				added in 5' of the exon	deleted in 3' of the exon
Usual splicing for IG and TR (except M exons) (2)		splicing frame 1 (sf1)	codon_start3 (translation frame 3)	1	1
Splicing for M exons (3)		splicing frame 0 (sf0)	codon_start1 (translation frame 1)	0	0
Other splicing (4)		splicing frame 2 (sf2)	codon_start2 (translation frame 2)	2	2

Synthèse d'une chaîne lourde mu d'immunoglobuline



IMGT Tutorials, http://www.imgt.org

Commutation de classe IgM-IgG : recombinaison Smu-Sgamma



Sites de polyadenylation (ou Poly(A))

Poly(A) signal : POLYA_SIGNAL (IMGT label)

Motif conservé : AATAAA

Les signaux de polyadenylation sont localisés en aval des exons 3'.

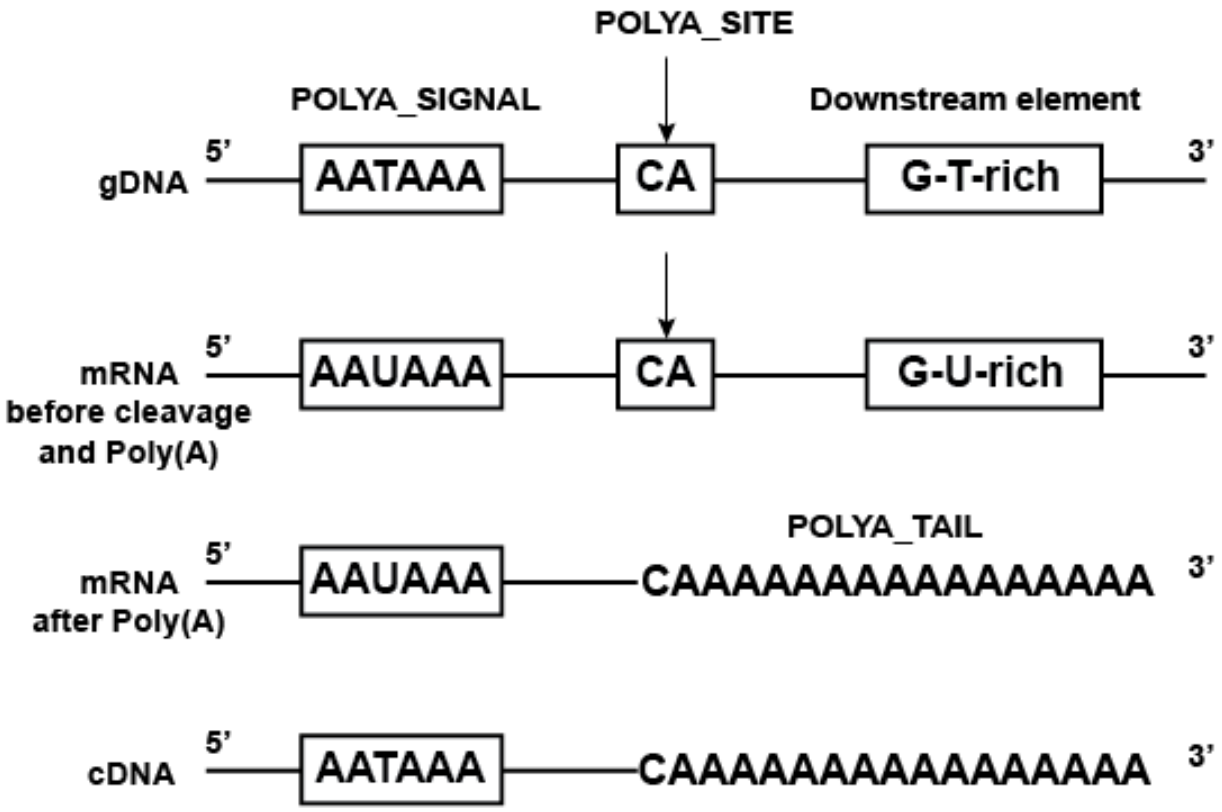
Poly(A) site : POLYA_SITE (IMGT label)

The POLYA_SITE est le site of clivage où le POLYA_TAIL is rajouté dans l'ARNm. Il peut être déterminé en comparant l'ADNc et l'ADNg.

La séquence en 5' du site de clivage sur l'ARNm est souvent CA.

Poly(A) queue : POLYA_TAIL (IMGT label)

Stretch d'adenosine monophosphate en 3'



Un POLYA_SIGNAL situé en aval de l'exon **CH3-CHS** de l' IGHG3 humain est utilisé pour la transcription des chaînes sécrétées.

Un POLYA_SIGNAL situé en aval de l'exon **M2** de l' IGHG3 humain est utilisé pour la transcription des chaînes membranaires.

Synthèse d'une chaîne lourde mu membranaire (lymphocyte B) et d'une chaîne lourde mu sécrétée (plasmocyte)