http://imgt.cines.fr

Immunoglobulin gene databases and on-line resources

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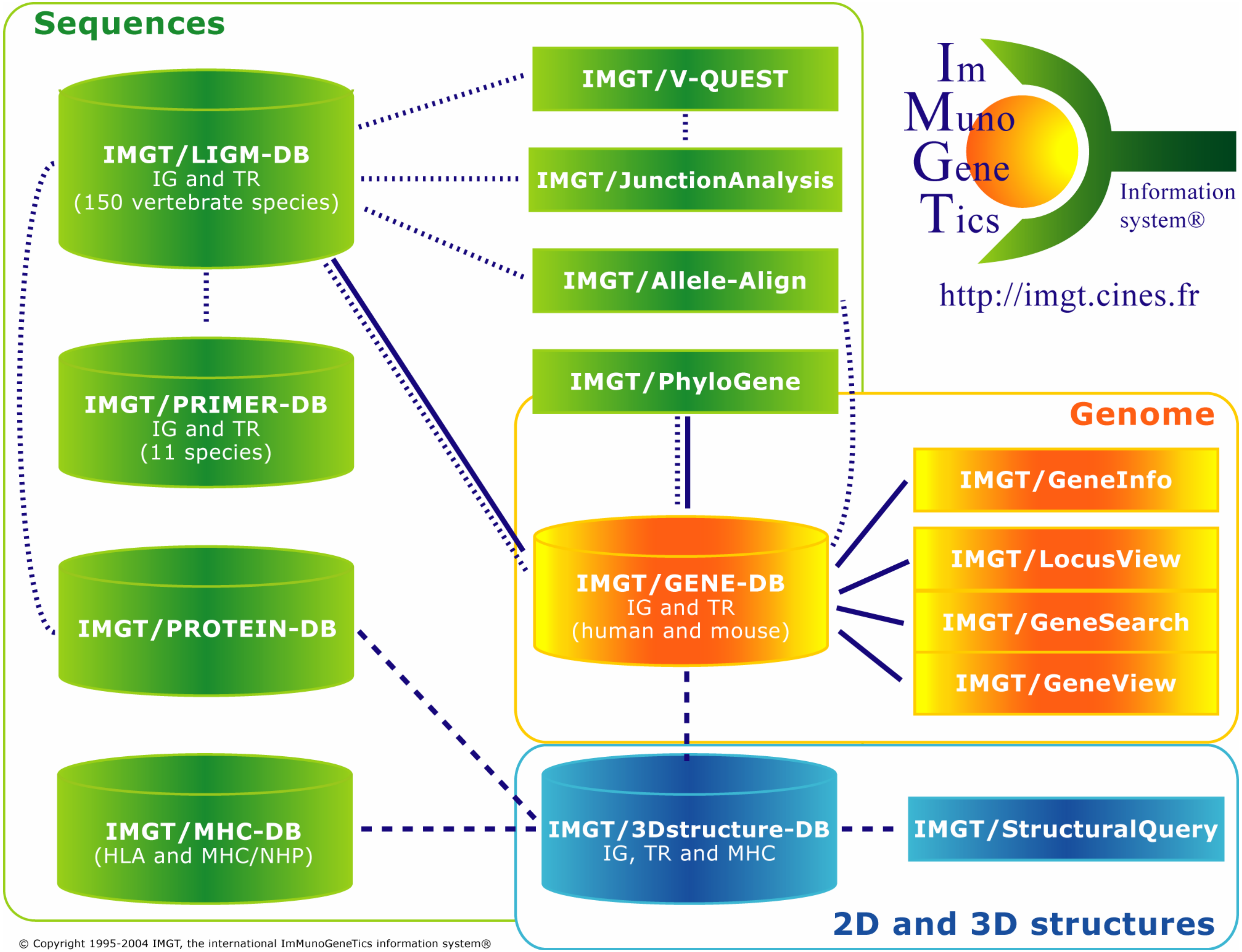
Université Montpellier, CNRS
Institut Universitaire de France

Educational Workshop on
Immunoglobulin Gene Analysis in Chronic Lymphocytic Leukemia
Uppsala, June 14-15, 2007

IMGT databases and tools



Sequences

IMGT/LIGM-DB
IG and TR
(150 vertebrate species)

IMGT/PRIMER-DB
IG and TR
(11 species)

IMGT/PROTEIN-DB

IMGT/MHC-DB
(HLA and MHC/NHP)

IMGT/V-QUEST

IMGT/JunctionAnalysis

IMGT/Allele-Align

IMGT/PhyloGene

ImMunoGeneTics
Information system®

http://imgt.cines.fr

Genome

IMGT/GENE-DB
IG and TR
(human and mouse)

IMGT/GeneInfo

IMGT/LocusView

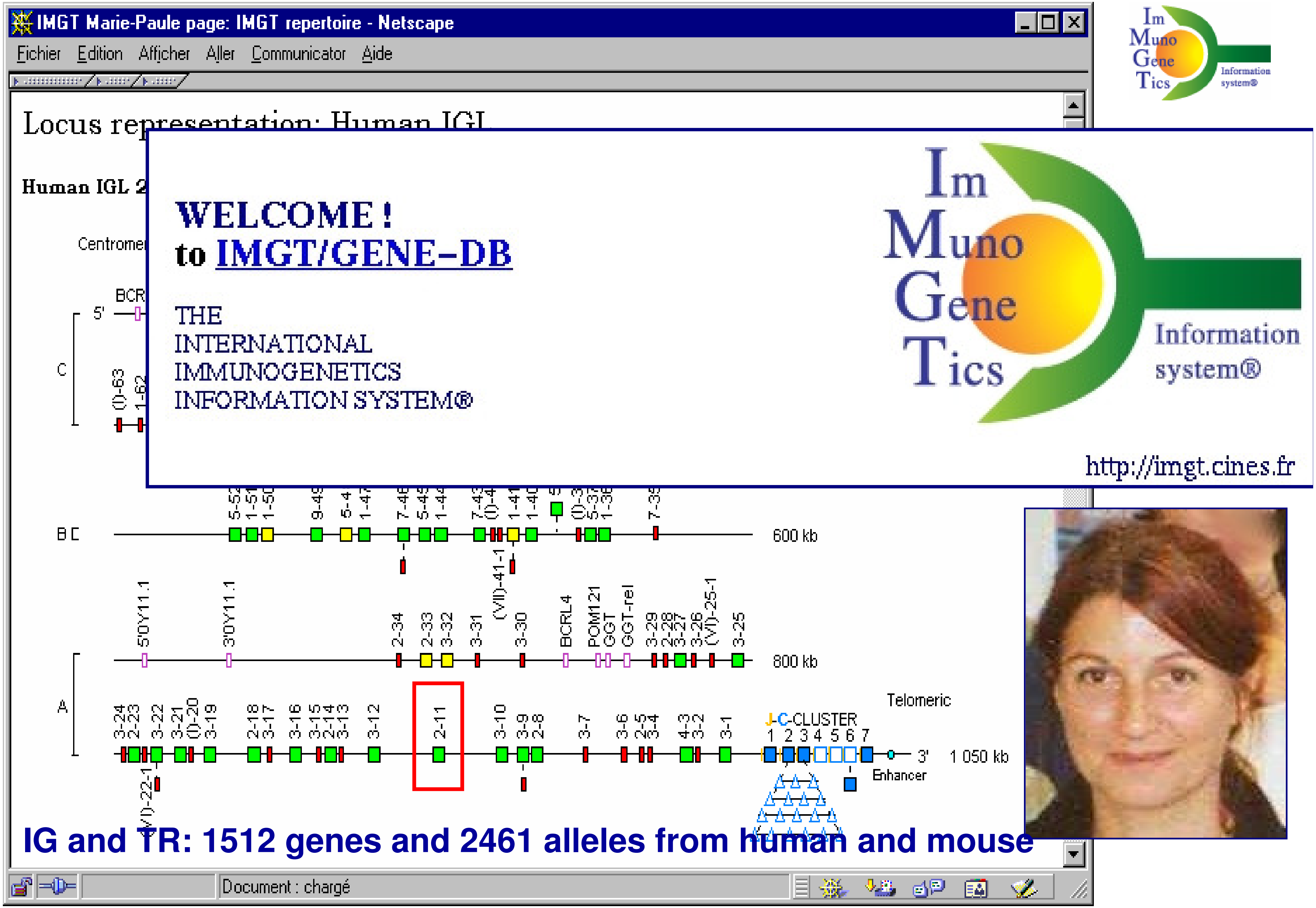
IMGT/GeneSearch

IMGT/GeneView

IMGT/3Dstructure-DB
IG, TR and MHC

IMGT/StructuralQuery

2D and 3D structures



Locus representation: Human IGL

Human IGL 2

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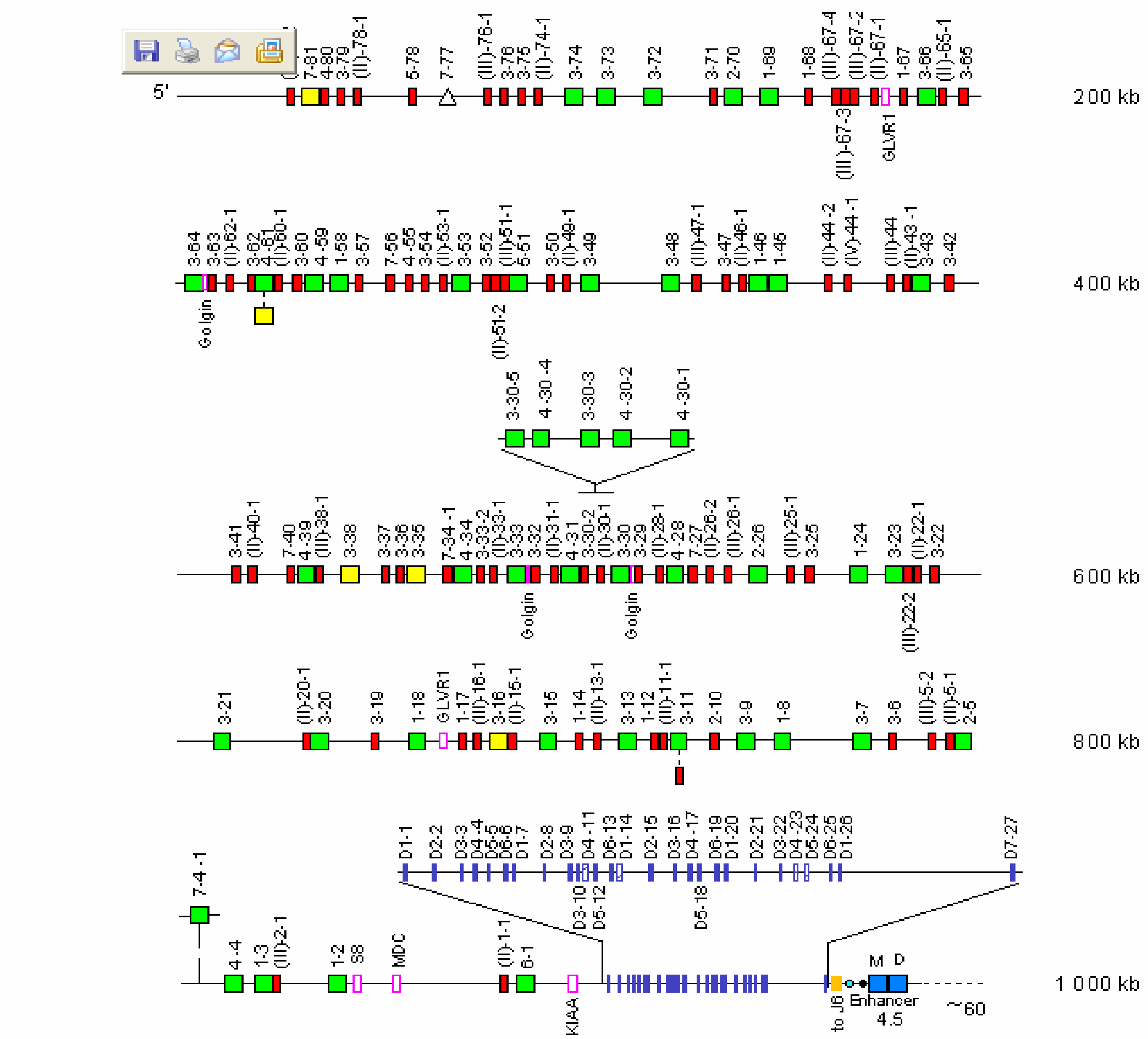
IG and TR: 1512 genes and 2461 alleles from human and mouse

Human IGH locus

http://imgt.cines.fr

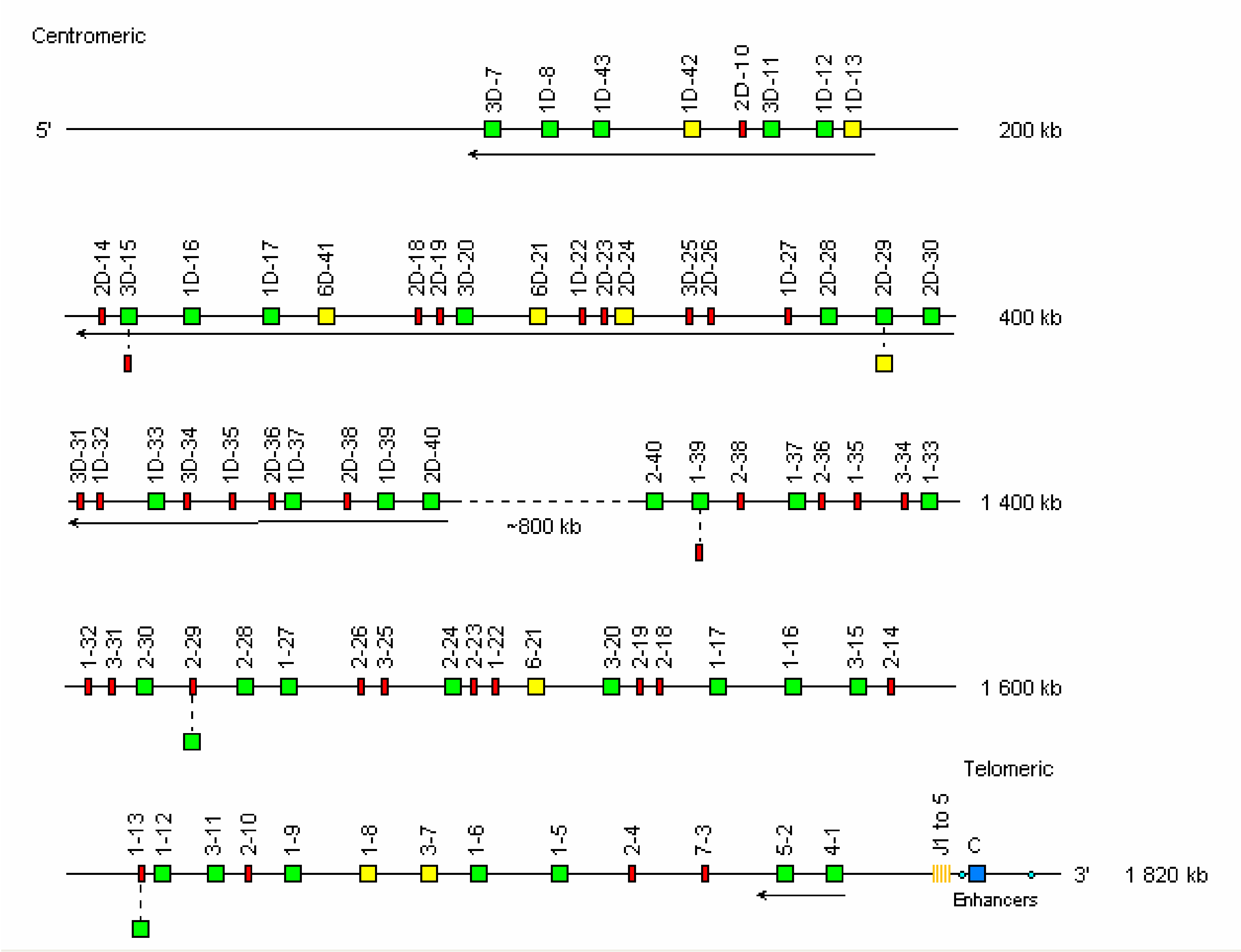
Chromosome 14q32.33



Human IGK locus

http://imgt.cines.fr

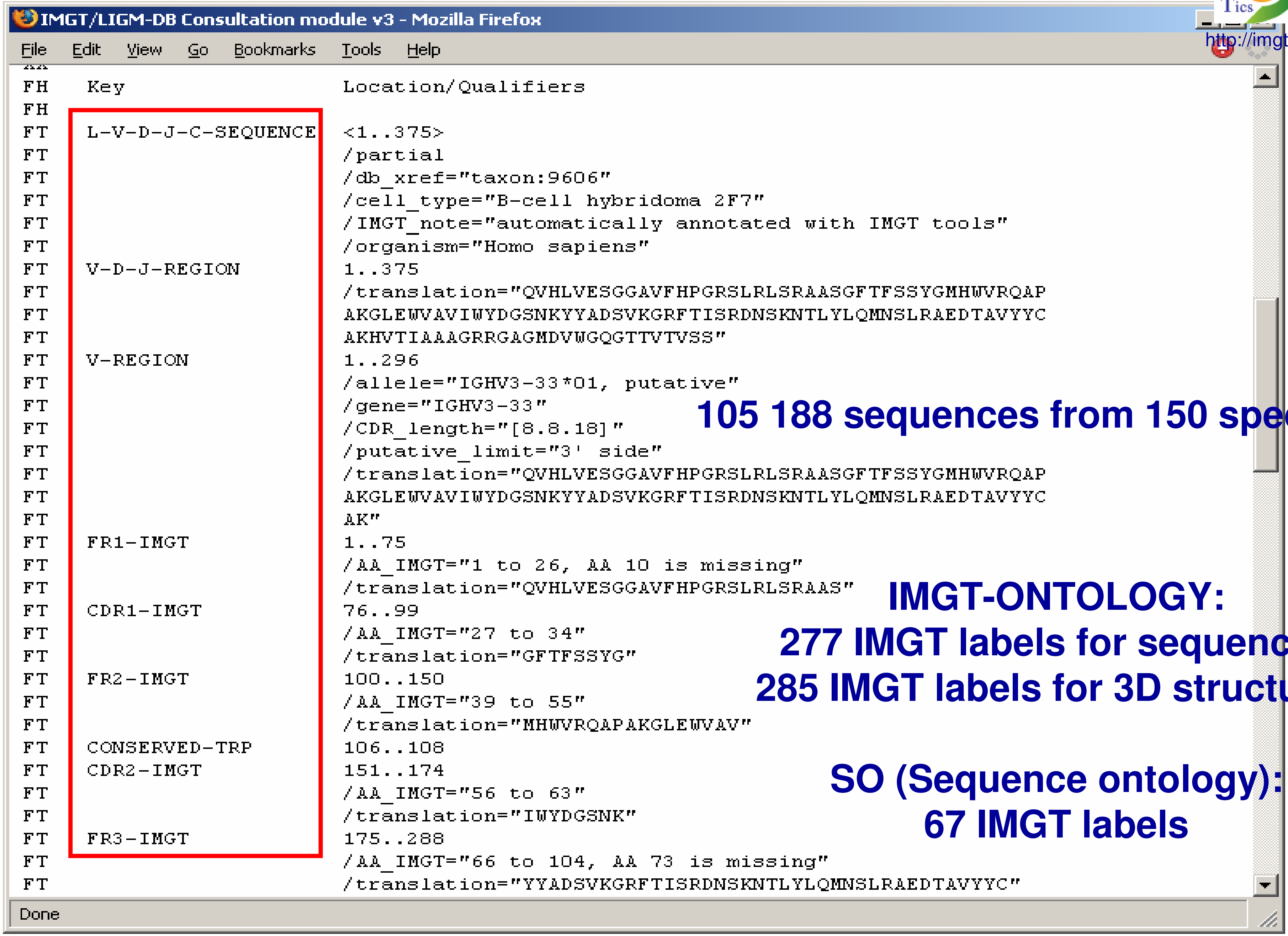
Chromosome 2p11.2



IMGT/LIGM-DB

http://imgt.cines.fr

DESCRIPTION



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FH   Key                 Location/Qualifiers
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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"
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FT                       AKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC
FT                       AKHVTIAAAGRRGAGMDVWGQGTTVTVSS"
FT   V-REGION            1..296
FT                       /allele="IGHV3-33*01, putative"
FT                       /gene="IGHV3-33"
FT                       /CDR_length="[8.8.18]"
FT                       /putative_limit="3' side"
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FT                       AKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC
FT                       AK"
FT   FR1-IMGT            1..75
FT                       /AA_IMGT="1 to 26, AA 10 is missing"
FT                       /translation="QVHLVESGGAVFHPGRSLRLSRAAS"
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="YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC"
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105 188 sequences from 150 species

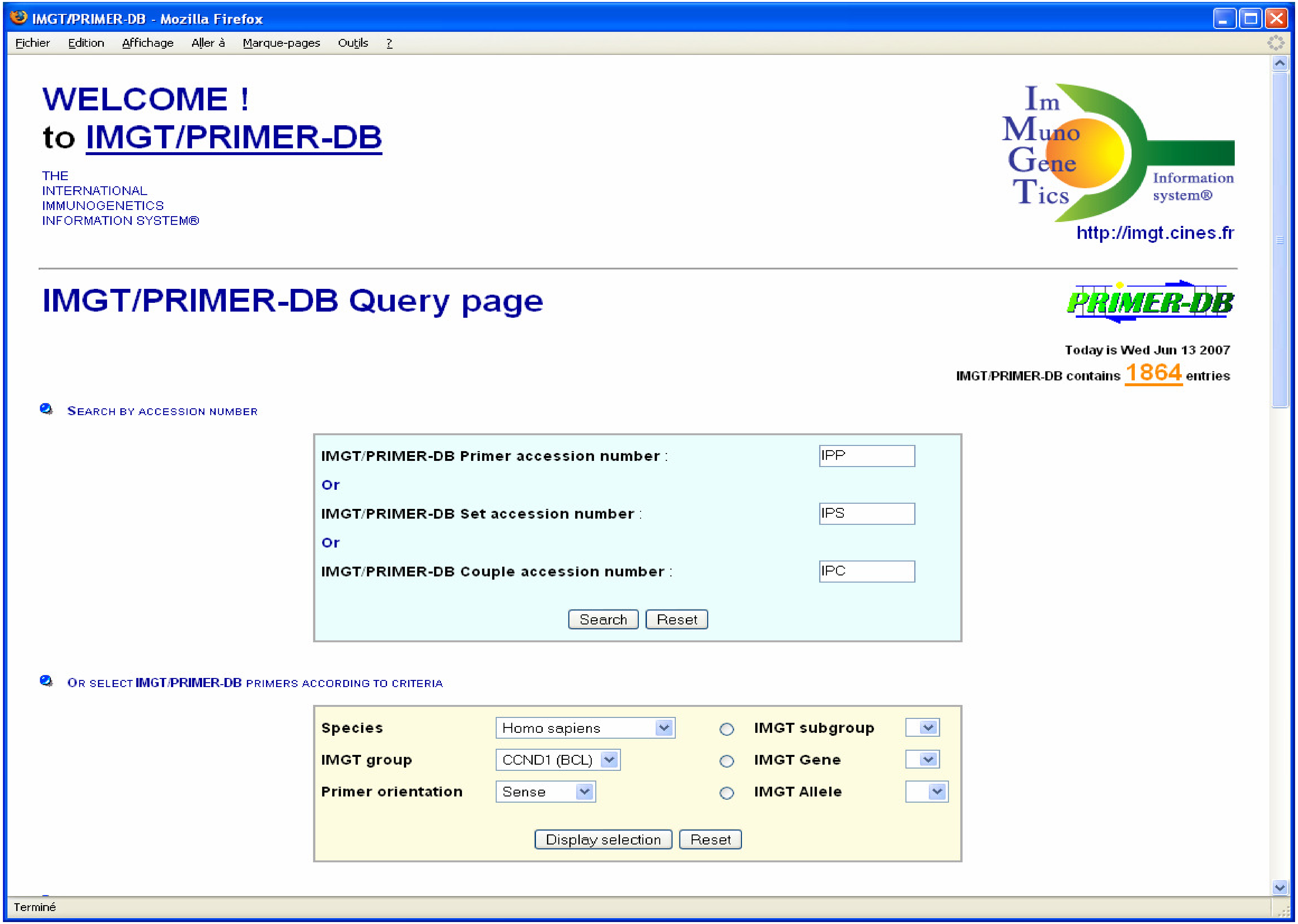
IMGT-ONTOLOGY:

277 IMGT labels for sequences

285 IMGT labels for 3D structures

SO (Sequence ontology):

67 IMGT labels



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IMGT/PRIMER-DB Query page

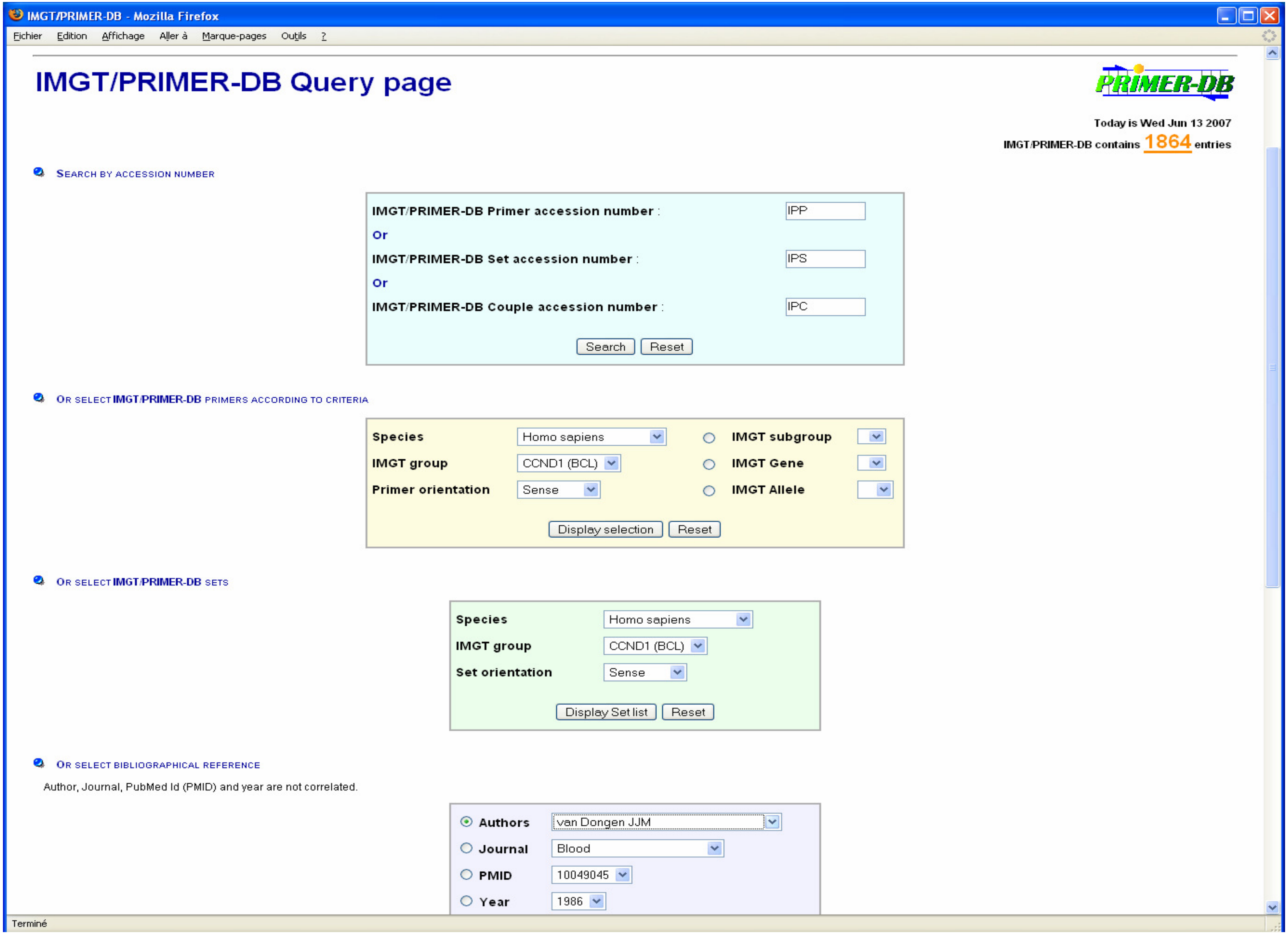
Today is Wed Jun 13 2007
IMGT/PRIMER-DB contains 1864 entries

SEARCH BY ACCESSION NUMBER

IMGT/PRIMER-DB Primer accession number : IPP
Or
IMGT/PRIMER-DB Set accession number : IPS
Or
IMGT/PRIMER-DB Couple accession number : IPC

OR SELECT IMGT/PRIMER-DB PRIMERS ACCORDING TO CRITERIA

Species	Homo sapiens	○	**IMGT subgroup**	
IMGT group	CCND1 (BCL)	○	**IMGT Gene**	
Primer orientation	Sense	○	**IMGT Allele**	



IMGT/PRIMER-DB Query page

Today is Wed Jun 13 2007

IMGT/PRIMER-DB contains 1864 entries

SEARCH BY ACCESSION NUMBER

IMGT/PRIMER-DB Primer accession number : IPP

Or

IMGT/PRIMER-DB Set accession number : IPS

Or

IMGT/PRIMER-DB Couple accession number : IPC

OR SELECT IMGT/PRIMER-DB PRIMERS ACCORDING TO CRITERIA

Species: Homo sapiens
IMGT group: CCND1 (BCL)
Primer orientation: Sense
○ **IMGT subgroup**
○ **IMGT Gene**
○ **IMGT Allele**

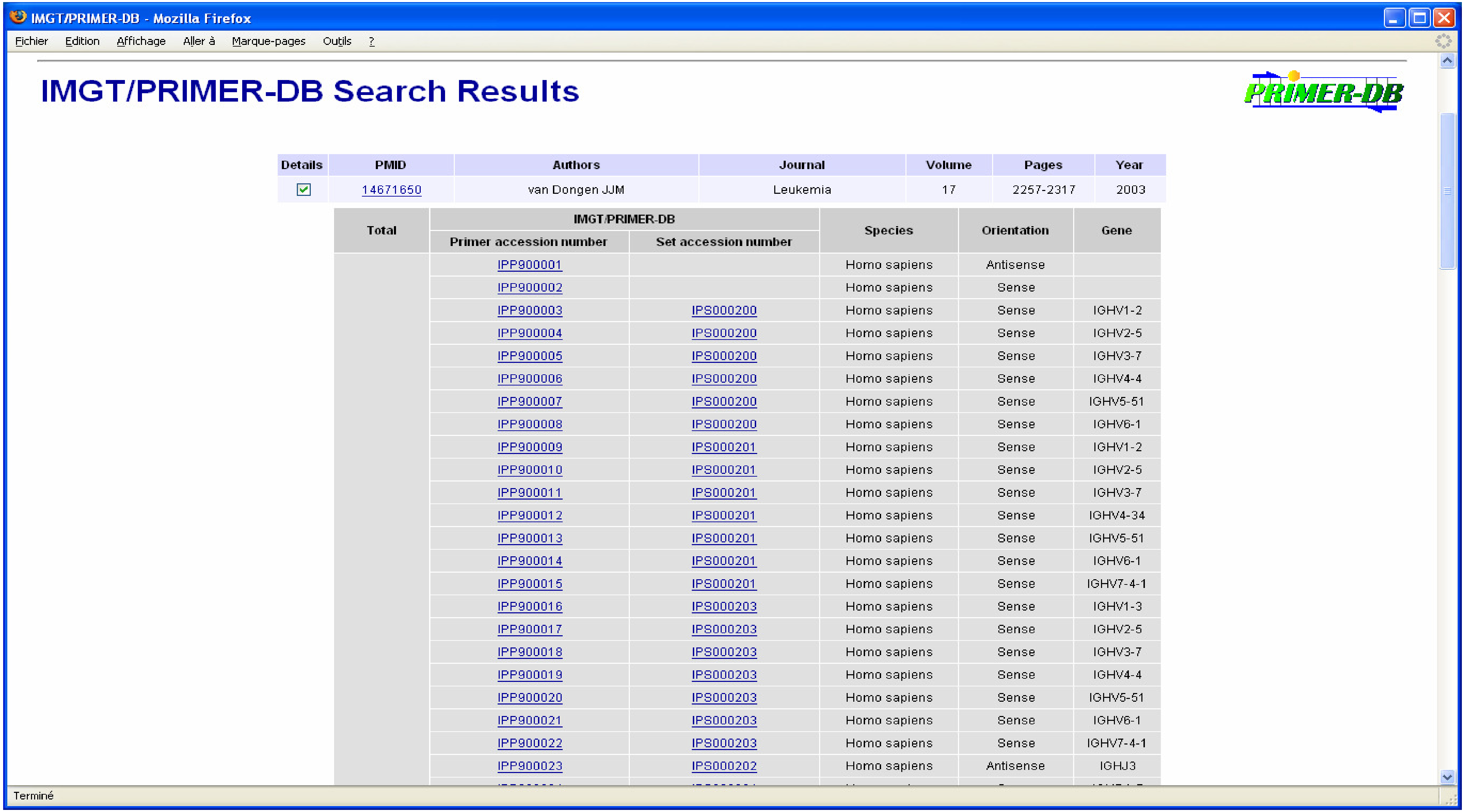
OR SELECT IMGT/PRIMER-DB SETS

Species: Homo sapiens
IMGT group: CCND1 (BCL)
Set orientation: Sense

OR SELECT BIBLIOGRAPHICAL REFERENCE

Author, Journal, PubMed Id (PMID) and year are not correlated.

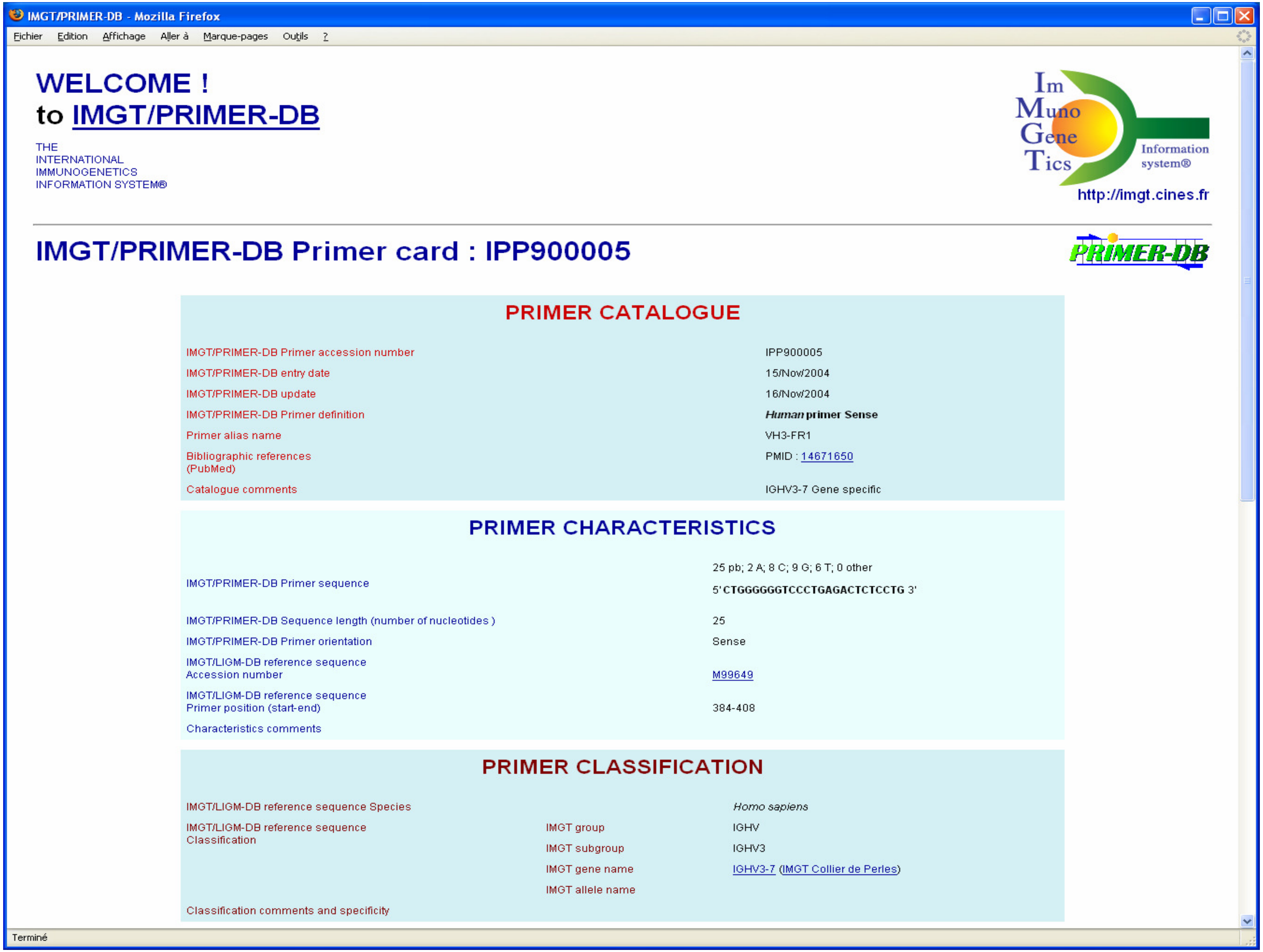
● **Authors**: van Dongen JJM
○ **Journal**: Blood
○ **PMID**: 10049045
○ **Year**: 1986



IMGT/PRIMER-DB Search Results

Details	PMID	Authors	Journal	Volume	Pages	Year
☑	14671650	van Dongen JJM	Leukemia	17	2257-2317	2003

Total	IMGT/PRIMER-DB		Species	Orientation	Gene
	Primer accession number	Set accession number			
	IPP900001		Homo sapiens	Antisense	
	IPP900002		Homo sapiens	Sense	
	IPP900003	IPS000200	Homo sapiens	Sense	IGHV1-2
	IPP900004	IPS000200	Homo sapiens	Sense	IGHV2-5
	IPP900005	IPS000200	Homo sapiens	Sense	IGHV3-7
	IPP900006	IPS000200	Homo sapiens	Sense	IGHV4-4
	IPP900007	IPS000200	Homo sapiens	Sense	IGHV5-51
	IPP900008	IPS000200	Homo sapiens	Sense	IGHV6-1
	IPP900009	IPS000201	Homo sapiens	Sense	IGHV1-2
	IPP900010	IPS000201	Homo sapiens	Sense	IGHV2-5
	IPP900011	IPS000201	Homo sapiens	Sense	IGHV3-7
	IPP900012	IPS000201	Homo sapiens	Sense	IGHV4-34
	IPP900013	IPS000201	Homo sapiens	Sense	IGHV5-51
	IPP900014	IPS000201	Homo sapiens	Sense	IGHV6-1
	IPP900015	IPS000201	Homo sapiens	Sense	IGHV7-4-1
	IPP900016	IPS000203	Homo sapiens	Sense	IGHV1-3
	IPP900017	IPS000203	Homo sapiens	Sense	IGHV2-5
	IPP900018	IPS000203	Homo sapiens	Sense	IGHV3-7
	IPP900019	IPS000203	Homo sapiens	Sense	IGHV4-4
	IPP900020	IPS000203	Homo sapiens	Sense	IGHV5-51
	IPP900021	IPS000203	Homo sapiens	Sense	IGHV6-1
	IPP900022	IPS000203	Homo sapiens	Sense	IGHV7-4-1
	IPP900023	IPS000202	Homo sapiens	Antisense	IGHJ3



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IMGT/PRIMER-DB Primer card : IPP900005

PRIMER CATALOGUE

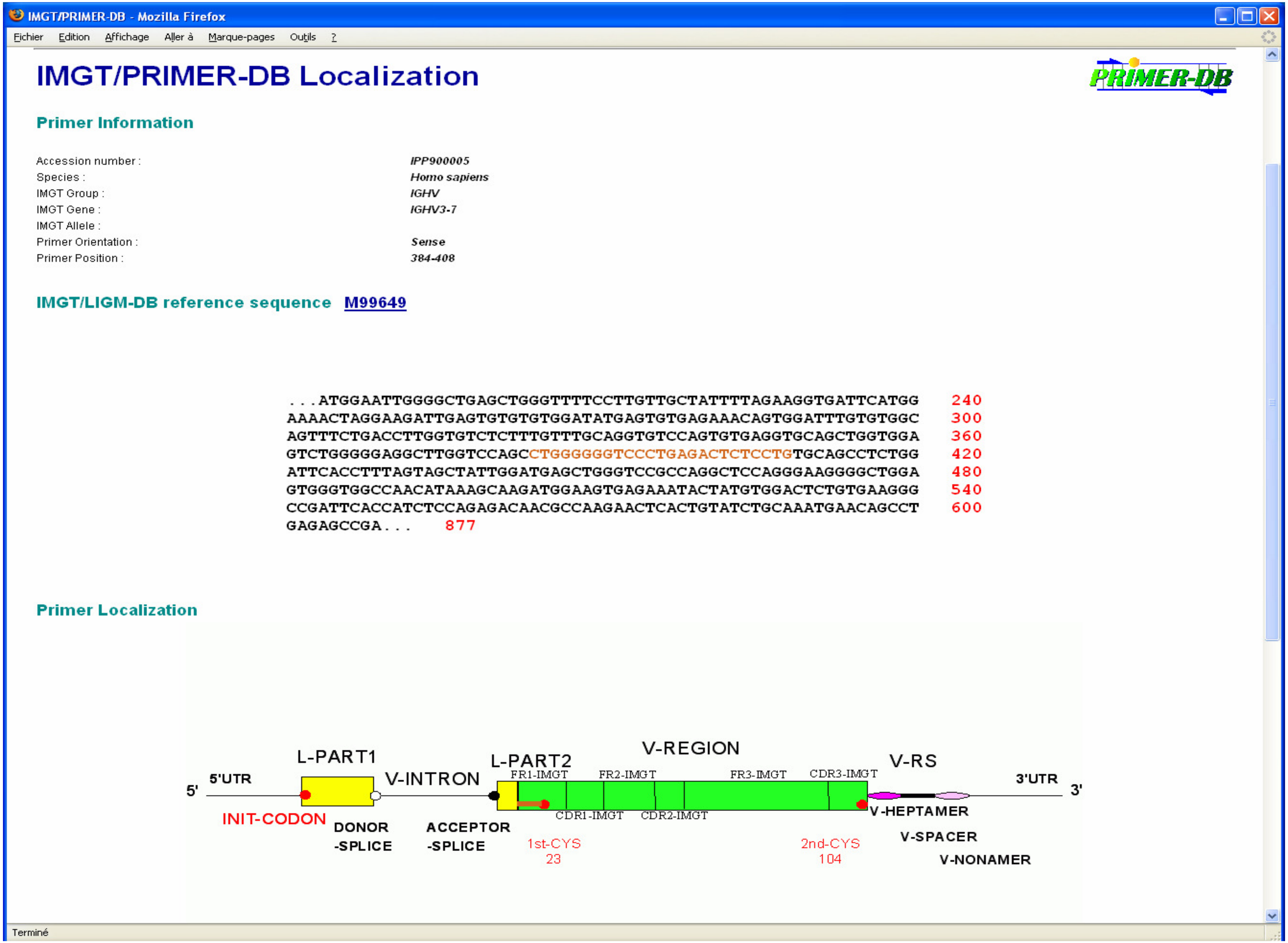
IMGT/PRIMER-DB Primer accession number	IPP900005
IMGT/PRIMER-DB entry date	15/Nov/2004
IMGT/PRIMER-DB update	16/Nov/2004
IMGT/PRIMER-DB Primer definition	***Human* primer Sense**
Primer alias name	VH3-FR1
Bibliographic references (PubMed)	PMID : 14671650
Catalogue comments	IGHV3-7 Gene specific

PRIMER CHARACTERISTICS

IMGT/PRIMER-DB Primer sequence	25 pb; 2 A; 8 C; 9 G; 6 T; 0 other 5' **CTGGGGGGTCCCTGAGACTCTCCTG** 3'
IMGT/PRIMER-DB Sequence length (number of nucleotides)	25
IMGT/PRIMER-DB Primer orientation	Sense
IMGT/LIGM-DB reference sequence Accession number	M99649
IMGT/LIGM-DB reference sequence Primer position (start-end)	384-408
Characteristics comments	

PRIMER CLASSIFICATION

IMGT/LIGM-DB reference sequence Species		*Homo sapiens*
IMGT/LIGM-DB reference sequence Classification	IMGT group	IGHV
	IMGT subgroup	IGHV3
	IMGT gene name	IGHV3-7 (IMGT Collier de Perles)
	IMGT allele name	
Classification comments and specificity		



IMGT/PRIMER-DB Localization

Primer Information

Accession number :	*IPP900005*
Species :	*Homo sapiens*
IMGT Group :	*IGHV*
IMGT Gene :	*IGHV3-7*
IMGT Allele :	
Primer Orientation :	*Sense*
Primer Position :	*384-408*

IMGT/LIGM-DB reference sequence M99649

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AAAACTAGGAAGATTGAGTGTGTGTGGATATGAGTGTGAGAAACAGTGGATTTGTGTGGC   300
AGTTTCTGACCTTGGTGTCTCTTTGTTTGCAGGTGTCCAGTGTGAGGTGCAGCTGGTGGA   360
GTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGG   420
ATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA   480
GTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTGGACTCTGTGAAGGG   540
CCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCT   600
GAGAGCCGA...    877
```

Primer Localization

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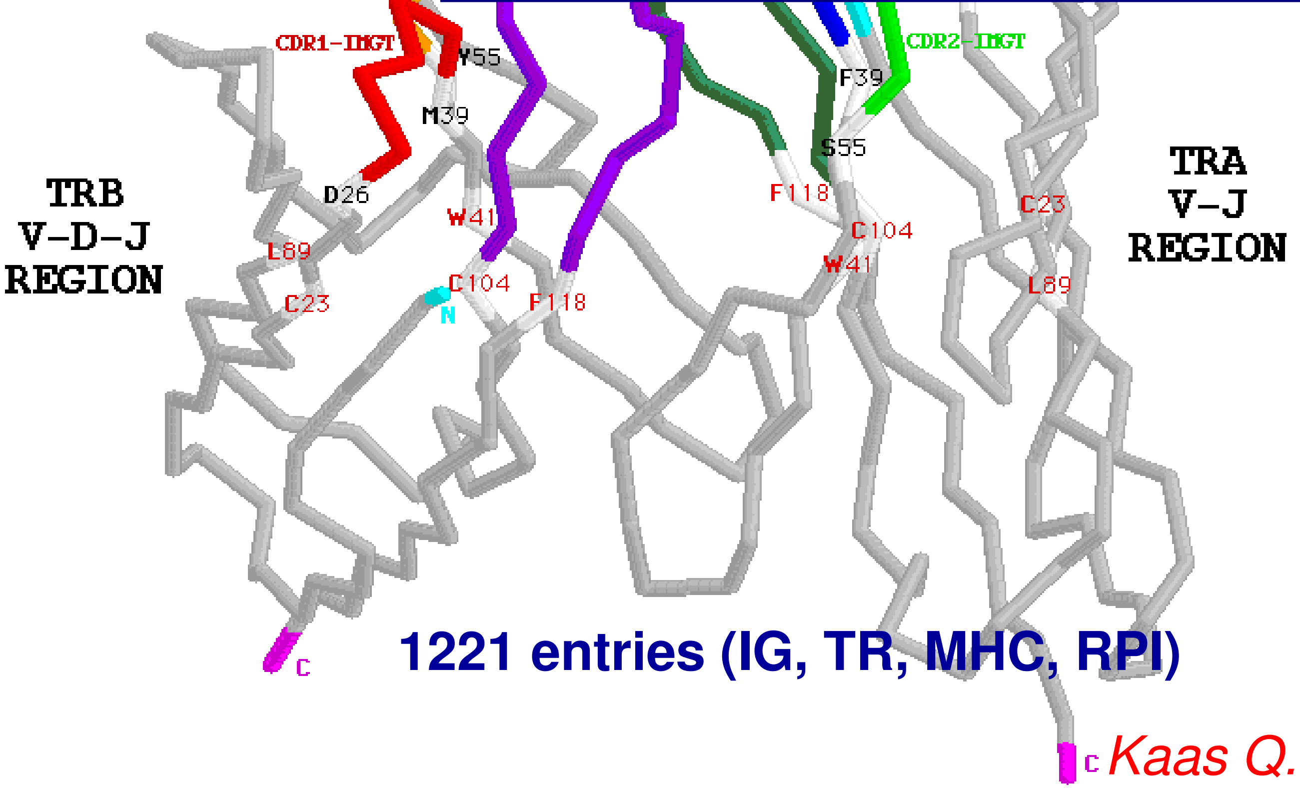

1221 entries (IG, TR, MHC, RPI)

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

IMGT/3Dstructure-DB card for : 1u8k

IMGT protein name	IMGT receptor description	Type	Ligand(s)	Species	CC	Chain ID
2F5	FAB-GAMMA-3_KAPPA	IG		*Homo sapiens* (Human)	1	[1u8k_A 1u8k_B]
	Peptide		GP41		1	[1u8k_C]

Experimental technique X-ray diffraction Resolution 2.24 PDB release date 05-OCT-04

Chain ID		1u8k_B
IMGT chain description		VH-CH1
Chain amino acid sequence		[IGHV_1 RITLKESGPPLVKPTQTLTLTCSFSGFSLSDFGVGVGWIRQPPGKALEWLAIIYSDDDKRYSPSLNTRLTITKDTSKNQVVLVMTRVSPV][D][IGHJ_1] [IG DTATYFCAHRRGPTTLFGVPIARGPVNAMDVWGQGITVTISSTSTKGPSVFPLAPCS*KSTAGG*TAALGCLVKDYFPEPVTVSWNSGALTS HC_1] GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVEPKS
V-DOMAIN	IMGT domain description	VH
	IGHV gene and allele name	IGHV2-5*05 (85.00%), IGHV2-5*06 (85.00%), *Alignment details*
	IGHJ gene and allele name	IGHJ6*01 (83.33%), IGHJ6*02 (83.33%), *Alignment details*
	2D representation	Collier de Perles or Collier de Perles on 2 layers
	CDR-IMGT lengths	[10.7.24]
	Sheet composition	[A B D E] [C C" C' F G]
		[CDR1] [CDR2] RITLKESGP.PLVKPTQTLTLTCSFSGFSLSDFGVG..VGWIRQPPGKALEWLAIIYSDDDK...RYSPSLN.TRLTITKDTSKNQVVLV [CDR3] MTRVSPVDTATYFCAHRRGPTTLFGVPIARGPVNAMDVWGQGITVTI
C-DOMAIN	IMGT domain description	CH1
	IGHC gene and allele name	IGHG3*01 (97.94%), IGHG3*03 (97.94%), IGHG3*04 (97.94%), IGHG3*05 (97.94%), IGHG3*06 (97.94%), IGHG3*07 (97.94%), IGHG3*08 (97.94%), IGHG3*09 (97.94%), IGHG3*10 (97.94%), IGHG3*11 (97.94%), IGHG3*12 (97.94%), IGHG3*13 (97.94%), IGHG3*14 (97.94%), IGHG3*15 (97.94%), IGHG3*16 (97.94%), IGHG3*17 (97.94%), IGHG3*20 (97.94%), *Alignment details*
	2D representation	Collier de Perles or Collier de Perles on 2 layers
	Sheet composition	[A B D E] [C F G]
		.....STKGPSVFPLAPCS*KSTA*...*GG*TAALGCLVKDYFP..EPVTVSWNSGALTS....GVHTFPAVLQSS......GLYSLSSVVTV PSSSL...GTQTYTCNVNHKP..SNTKVDKRV

Chain ID		1u8k_A
IMGT chain description		L-KAPPA
Chain amino acid sequence		[IGKV_1 ALQLTQSPSSLSASVGDRITITCRASQGVTSALAWYRQKPGSPPQLLIYDASSLESGVPSRFSGSGSGTEFTLTISTLRPEDFATYYCQQ] [IGKJ_1][IGKC_1 LHFYPHTFGGGTRVDVRRTVAAPSVFIFPPSDRQLKSGTASVVCLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT] LSKADYEKHKVYECEVTHQGLSSPVTKSFNRGEC
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] ALQLTQSPSSLSASVGDRITITCRASQGVTSA......LAWYRQKPGSPPQLLIYDAS.......SLESGVP.SRFSGSG..SGTEFTLT [CDR3] ISTLRPEDFATYYCQQLHF....YPHTFGGGTRVDVR
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...SGTASVVCLINNFYP..REAKVQWKVDNALQSGNSQESVTEQDSKDS.......TYSLSSTLTL SKADY..EKHKVYECEVTHQG..LSSPVTKSFNRGEC

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

<table>
<tr><td>Chain ID</td><td colspan="2">1u8k_B</td></tr>
<tr><td>IMGT chain description</td><td colspan="2">VH-CH1</td></tr>
<tr><td>Chain amino acid sequence</td><td colspan="2">[IGHV_1
RITLKESGPPLVKPTQTLTLTCSFSGFSLSDFGVGVGWIRQPPGKALEWLAIIYSDDDKRYSPSLNTRLTITKDTSKNQVVLVMTRVSPV
][D][IGHJ_1] [IG
DTATYFCAHRRGPTTLFGVPIARGPVNAMDVWGQGITVTISSTSTKGPSVFPLAPCS<i>KSTAGG</i>TAALGCLVKDYFPEPVTVSWNSGALTS
HC_1]
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVEPKS</td></tr>
<tr><td rowspan="7">V-DOMAIN</td><td>IMGT domain description</td><td>VH</td></tr>
<tr><td>IGHV gene and allele name</td><td>IGHV2-5*05 (85.00%), IGHV2-5*06 (85.00%), <i>Alignment details</i></td></tr>
<tr><td>IGHJ gene and allele name</td><td>IGHJ6*01 (83.33%), IGHJ6*02 (83.33%), <i>Alignment details</i></td></tr>
<tr><td>2D representation</td><td>Collier de Perles or Collier de Perles on 2 layers</td></tr>
<tr><td>CDR-IMGT lengths</td><td>[10.7.24]</td></tr>
<tr><td>Sheet composition</td><td>[A B D E] [C C" C' F G]</td></tr>
<tr><td colspan="2">[CDR1] [CDR2]
RITLKESGP.PLVKPTQTLTLTCSFSGFSLSDFGVG..VGWIRQPPGKALEWLAIIYSDDDK...RYSPSLN.TRLTITKDTSKNQVVLV
[CDR3]
MTRVSPVDTATYFCAHRRGPTTLFGVPIARGPVNAMDVWGQGITVTI</td></tr>
<tr><td rowspan="5">C-DOMAIN</td><td>IMGT domain description</td><td>CH1</td></tr>
<tr><td>IGHC gene and allele name</td><td>IGHG3*01 (97.94%), IGHG3*03 (97.94%), IGHG3*04 (97.94%), IGHG3*05 (97.94%), IGHG3*06 (97.94%), IGHG3*07 (97.94%), IGHG3*08 (97.94%), IGHG3*09 (97.94%), IGHG3*10 (97.94%), IGHG3*11 (97.94%), IGHG3*12 (97.94%), IGHG3*13 (97.94%), IGHG3*14 (97.94%), IGHG3*15 (97.94%), IGHG3*16 (97.94%), IGHG3*17 (97.94%), IGHG3*20 (97.94%), <i>Alignment details</i></td></tr>
<tr><td>2D representation</td><td>Collier de Perles or Collier de Perles on 2 layers</td></tr>
<tr><td>Sheet composition</td><td>[A B D E] [C F G]</td></tr>
<tr><td colspan="2">.....STKGPSVFPLAPCS<i>KSTA</i>...<i>GG</i>TAALGCLVKDYFP..EPVTVSWNSGALTS....GVHTFPAVLQSS......GLYSLSSVVTV
PSSSL...GTQTYTCNVNHKP..SNTKVDKRV</td></tr>
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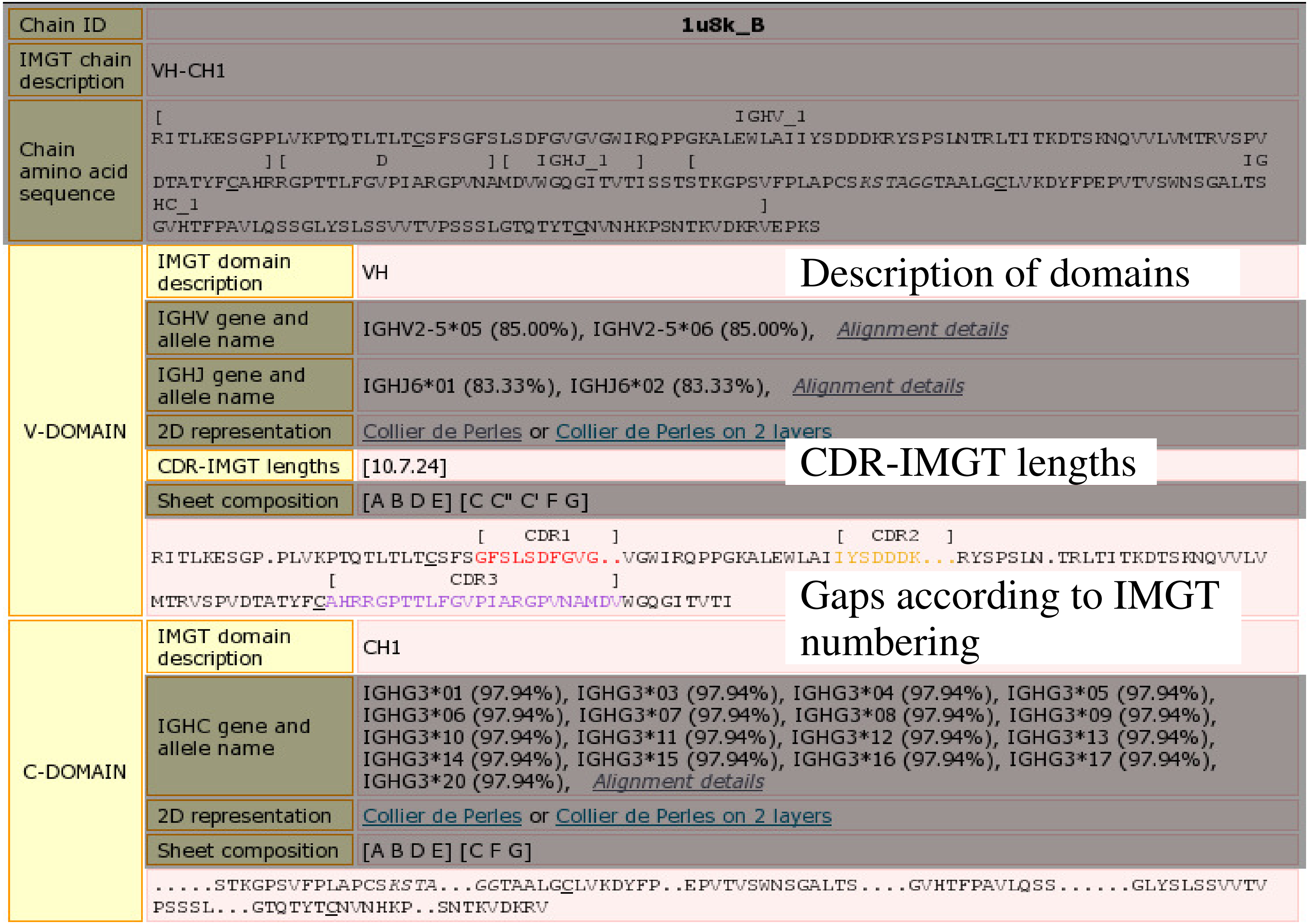


Chain ID	1u8k_B
IMGT chain description	VH-CH1
Chain amino acid sequence	see below

```
[                                              IGHV_1
RITLKESGPPLVKPTQTLTLTCSFSGFSLSDFGVGVGWIRQPPGKALEWLAIIYSDDDKRYSPSLNTRLTITKDTSKNQVVLVMTRVSPV
         ][        D        ][   IGHJ_1    ]   [                                            IG
DTATYFCAHRRGPTTLFGVPIARGPVNAMDVWGQGITVTISSTSTKGPSVFPLAPCSKSTAGGTAALGCLVKDYFPEPVTVSWNSGALTS
HC_1                                             ]
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVEPKS
```

V-DOMAIN

IMGT domain description	VH
IGHV gene and allele name	IGHV2-5*05 (85.00%), IGHV2-5*06 (85.00%), Alignment details
IGHJ gene and allele name	IGHJ6*01 (83.33%), IGHJ6*02 (83.33%), Alignment details
2D representation	Collier de Perles or Collier de Perles on 2 layers
CDR-IMGT lengths	[10.7.24]
Sheet composition	[A B D E] [C C" C' F G]

```
                          [   CDR1    ]                 [  CDR2   ]
RITLKESGP.PLVKPTQTLTLTCSFSGFSLSDFGVG..VGWIRQPPGKALEWLAIIYSDDDK...RYSPSLN.TRLTITKDTSKNQVVLV
              [         CDR3         ]
MTRVSPVDTATYFCAHRRGPTTLFGVPIARGPVNAMDVWGQGITVTI
```

C-DOMAIN

IMGT domain description	CH1
IGHC gene and allele name	IGHG3*01 (97.94%), IGHG3*03 (97.94%), IGHG3*04 (97.94%), IGHG3*05 (97.94%), IGHG3*06 (97.94%), IGHG3*07 (97.94%), IGHG3*08 (97.94%), IGHG3*09 (97.94%), IGHG3*10 (97.94%), IGHG3*11 (97.94%), IGHG3*12 (97.94%), IGHG3*13 (97.94%), IGHG3*14 (97.94%), IGHG3*15 (97.94%), IGHG3*16 (97.94%), IGHG3*17 (97.94%), IGHG3*20 (97.94%), Alignment details
2D representation	Collier de Perles or Collier de Perles on 2 layers
Sheet composition	[A B D E] [C F G]

```
.....STKGPSVFPLAPCSKSTA...GGTAALGCLVKDYFP..EPVTVSWNSGALTS....GVHTFPAVLQSS......GLYSLSSVVTV
PSSSL...GTQTYTCNVNHKP..SNTKVDKRV
```

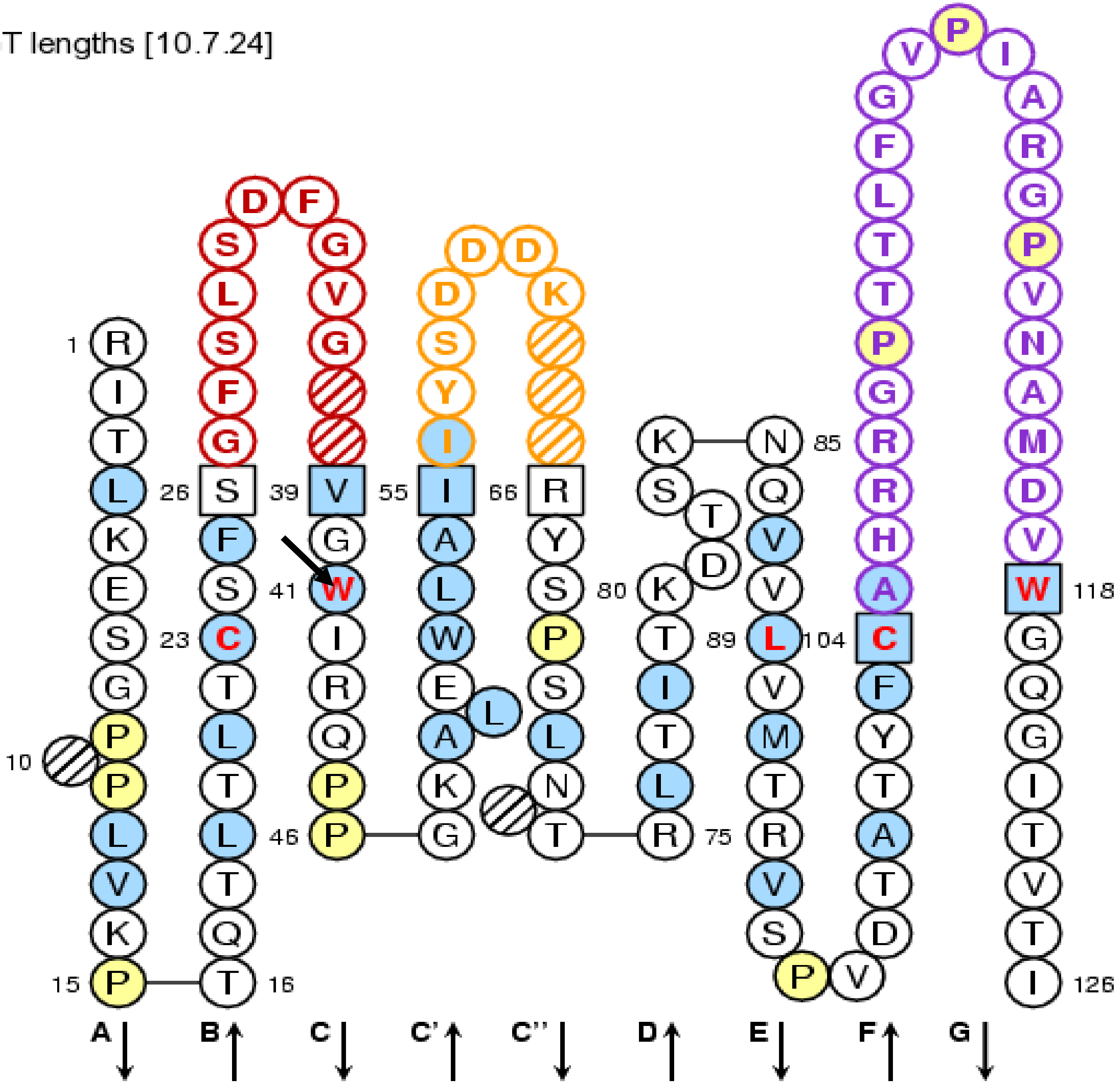
Description of domains

CDR-IMGT lengths

Gaps according to IMGT numbering

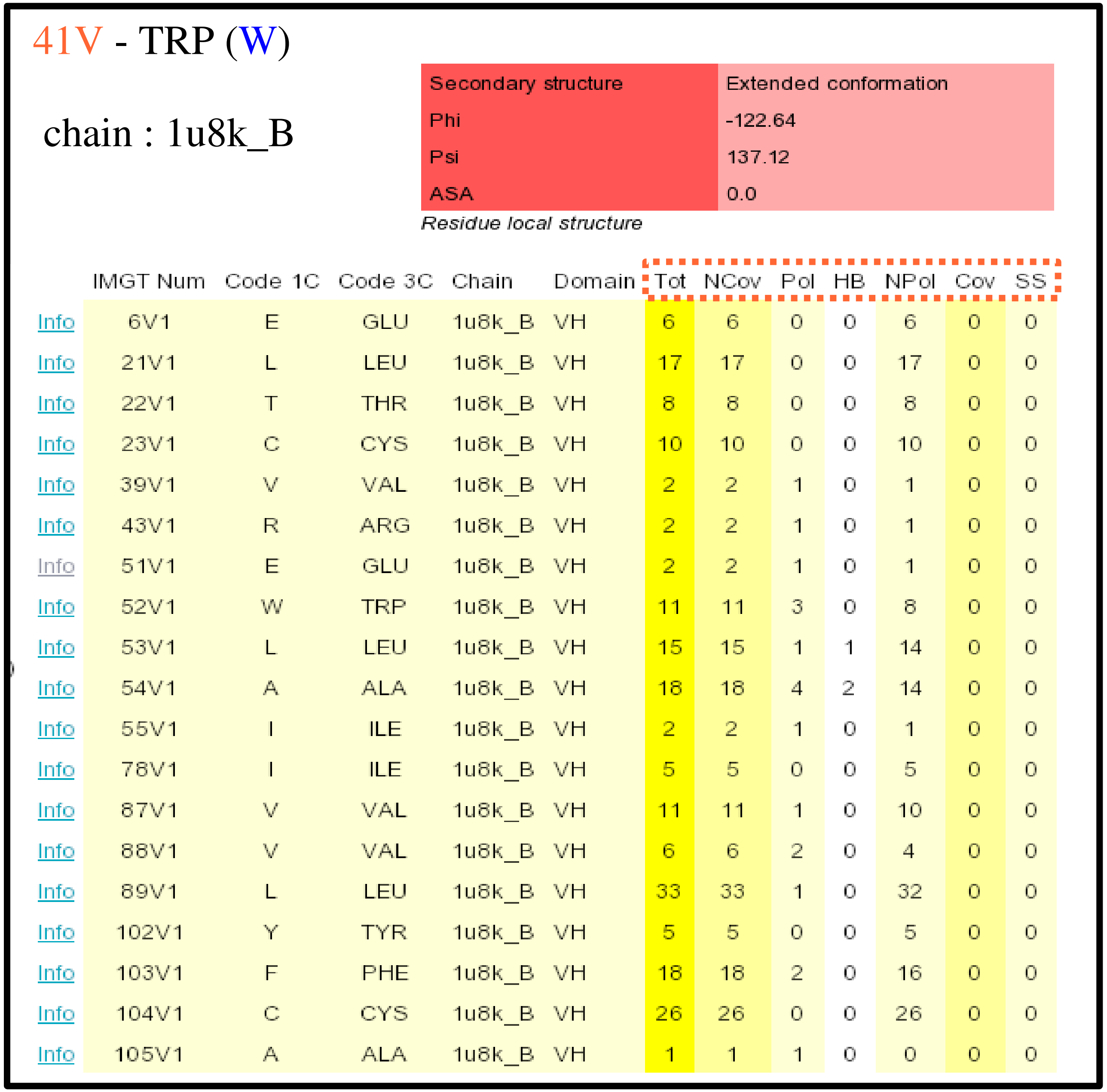
IMGT Collier de Perles : *Homo sapiens* (Human) IGHV_1 V-DOMAIN from 2F5 (PDB: 1u8k_B)

CDR-IMGT lengths [10.7.24]



From IMGT Colliers de Perles or from domain/chain sequen

http://imgt.cines.fr



41V - TRP (W)

chain : 1u8k_B

Secondary structure	Extended conformation
Phi	-122.64
Psi	137.12
ASA	0.0

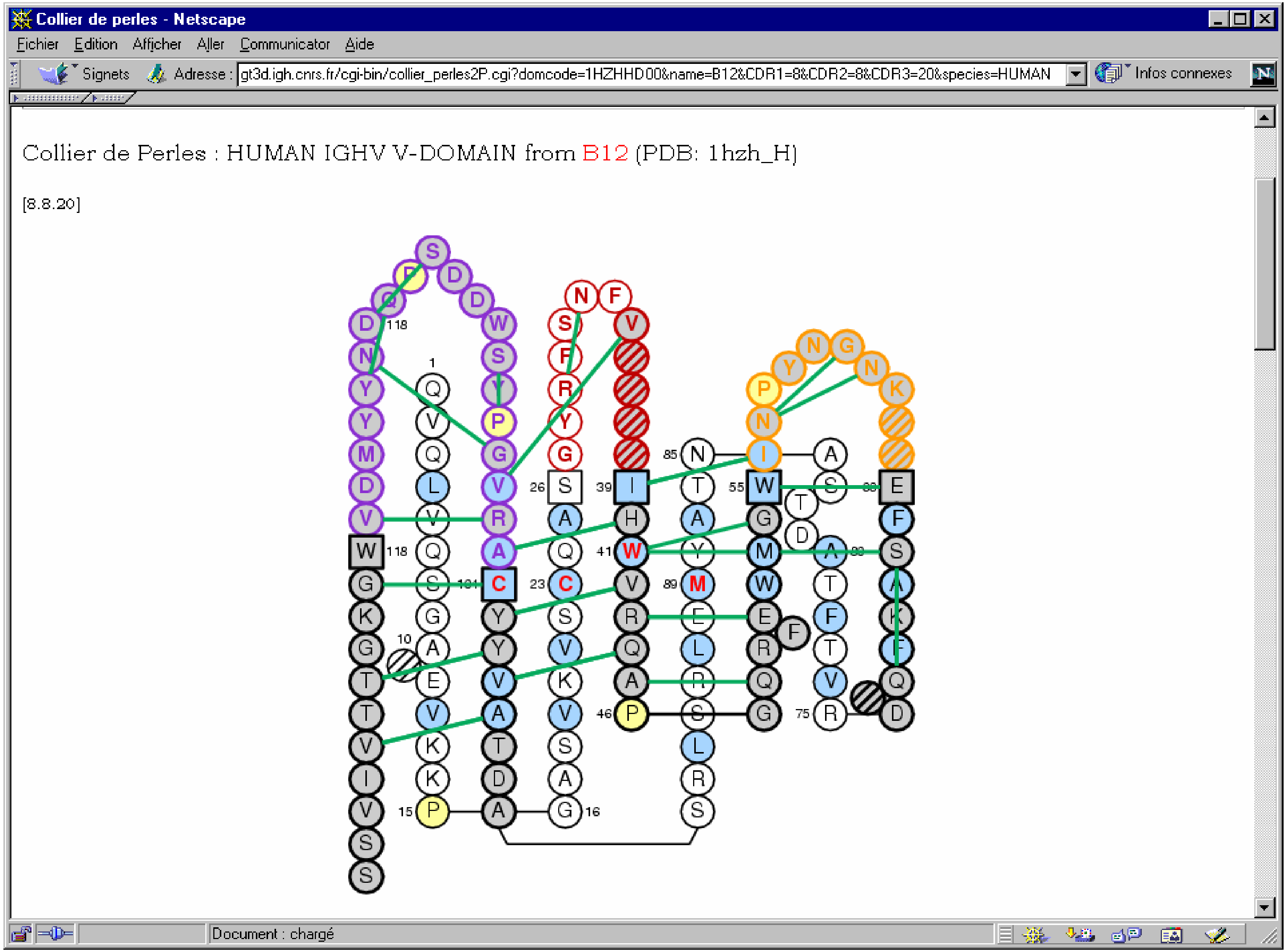
Residue local structure

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

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

IMGT Collier de Perles on two layers

http://imgt.cines.fr



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

[8.8.20]

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

IMGT® Ressources Web

http://imgt.cines.fr

IMGT Repertoire

8.000 pages HTML

Chromosomal localizations
Locus representations, …

IMGT Bloc-notes

Interesting links

The IMGT Immunoinformatics page

Links to external databases and tools: Kabat, VBase/DNAPLOT, JoinSolver, IgBlast, SoDa,…

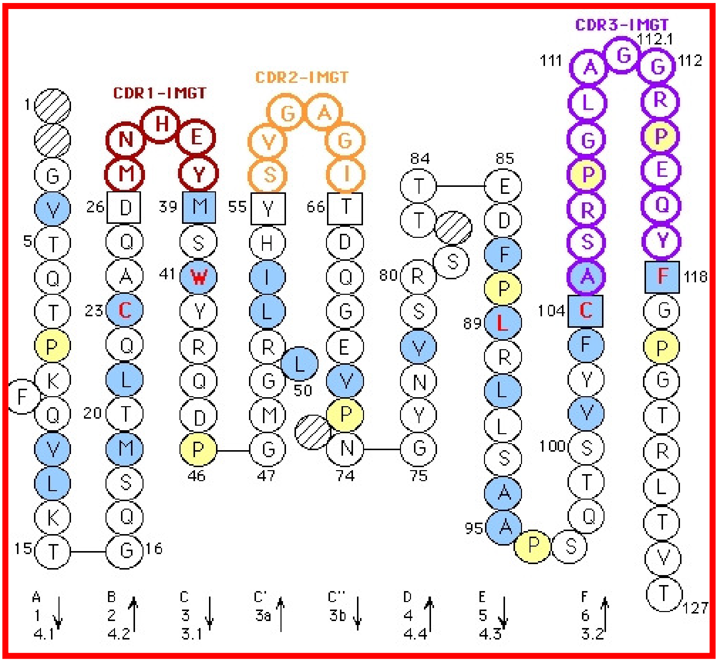
IMGT Education

Tutorials, IMGT Lexique, …

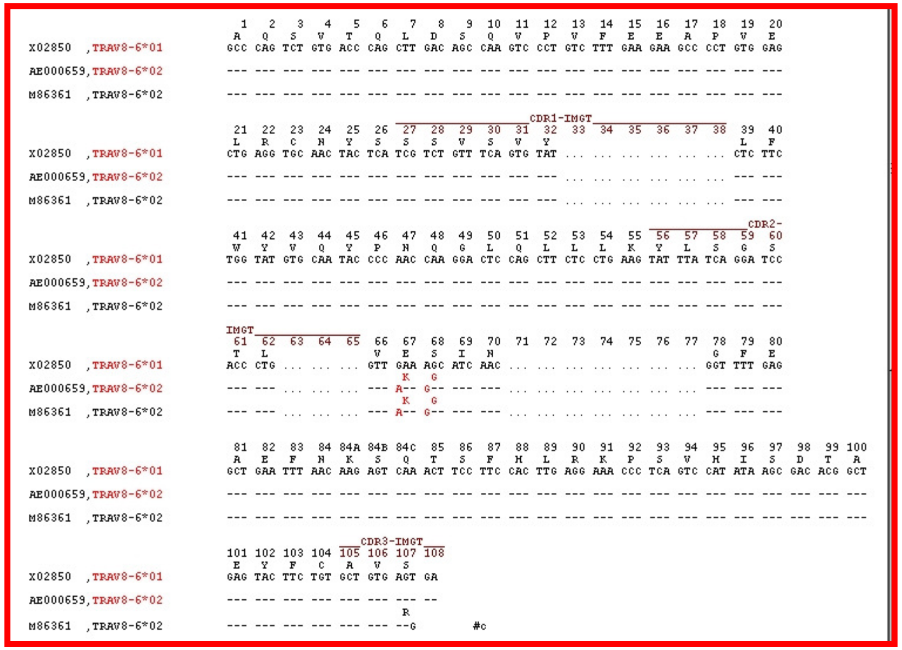
IMGT Web resources: 8 000 pages HTML

http://imgt.cines.fr

IMGT Collier de Perles



IMGT Alignment of alleles



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

                                           CDR1-IMGT
                   21  22  23  24  25  26  27  28  29  30  31  32  33  34  35  36  37  38  39  40
                    L   R   C   N   Y   S   S   S   V   S   V   Y                           L   F
X02850  ,TRAV8-6*01 CTG AGG TGC AAC TAC TCA TCG TCT GTT TCA GTG TAT ... ... ... ... ... ... CTC TTC
AE000659,TRAV8-6*02 --- --- --- --- --- --- --- --- --- --- --- --- ... ... ... ... ... ... --- ---
M86361  ,TRAV8-6*02 --- --- --- --- --- --- --- --- --- --- --- --- ... ... ... ... ... ... --- ---

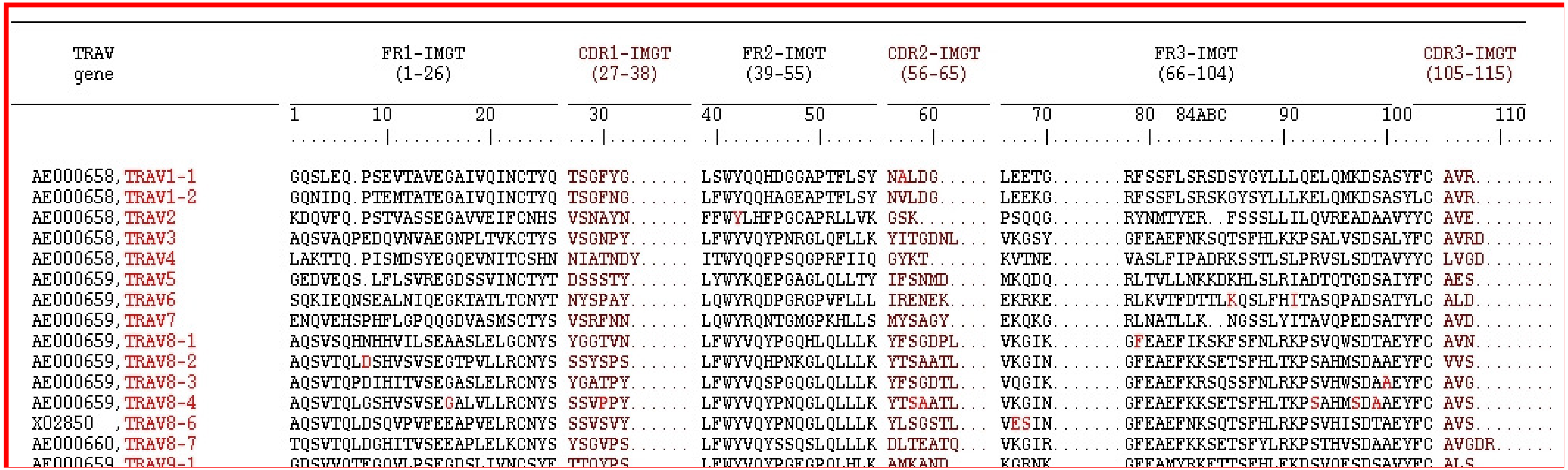
                                                                                        CDR2-
                   41  42  43  44  45  46  47  48  49  50  51  52  53  54  55  56  57  58  59  60
                    W   Y   V   Q   Y   P   N   Q   G   L   Q   L   L   L   K   Y   L   S   G   S
X02850  ,TRAV8-6*01 TGG TAT GTG CAA TAC CCC AAC CAA GGA CTC CAG CTT CTC CTG AAG TAT TTA TCA GGA TCC
AE000659,TRAV8-6*02 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
M86361  ,TRAV8-6*02 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

                   IMGT
                   61  62  63  64  65  66  67  68  69  70  71  72  73  74  75  76  77  78  79  80
                    T   L                   V   E   S   I   N                           G   F   E
X02850  ,TRAV8-6*01 ACC CTG ... ... ... GTT GAA AGC ATC AAC ... ... ... ... ... ... ... GGT TTT GAG
                                            K   G
AE000659,TRAV8-6*02 --- --- ... ... ... --- A-- G-- --- --- ... ... ... ... ... ... ... --- --- ---
                                            K   G
M86361  ,TRAV8-6*02 --- --- ... ... ... --- A-- G-- --- --- ... ... ... ... ... ... ... --- --- ---

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

                                   CDR3-IMGT
                   101 102 103 104 105 106 107 108
                    E   Y   F   C   A   V   S
X02850  ,TRAV8-6*01 GAG TAC TTC TGT GCT GTG AGT GA
AE000659,TRAV8-6*02 --- --- --- --- --- --- --- --
                                            R
M86361  ,TRAV8-6*02 --- --- --- --- --- --- --G          #c
```

IMGT Protein Display



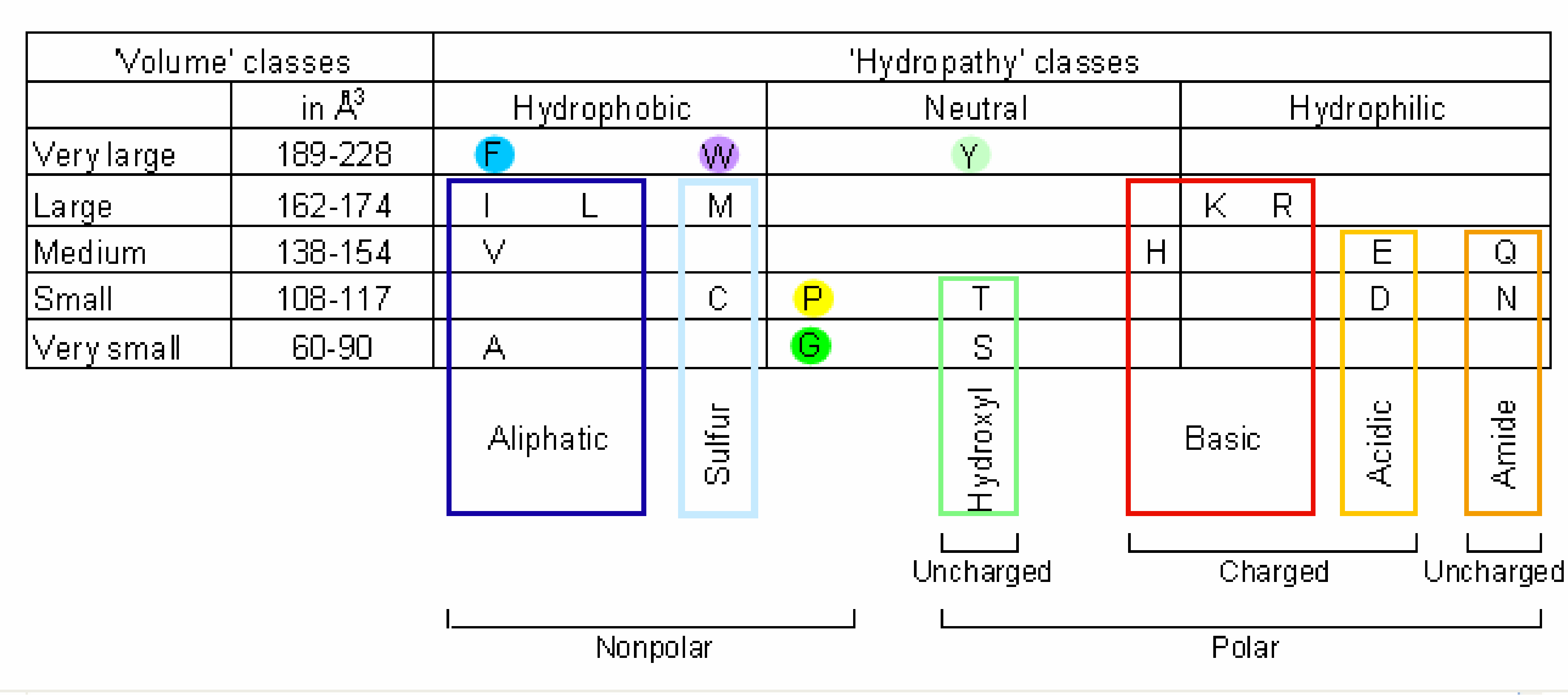
```
       TRAV                   FR1-IMGT              CDR1-IMGT     FR2-IMGT        CDR2-IMGT            FR3-IMGT                      CDR3-IMGT
       gene                    (1-26)                (27-38)       (39-55)         (56-65)             (66-104)                      (105-115)

                         1        10        20         30        40        50        60        70       80  84ABC    90        100       110
                         .........|.........|......  ...|.........  .|.........|.....  ....|.....  ....|.........|.............|.........|....  .....|.....

AE000658,TRAV1-1   GQSLEQ.PSEVTAVEGAIVQINCTYQ TSGFYG...... LSWYQQHDGGAPTFLSY NALDG..... LEETG.......RFSSFLSRSDSYGYLLLQELQMKDSASYFC AVR........
AE000658,TRAV1-2   GQNIDQ.PTEMTATEGAIVQINCTYQ TSGFNG...... LFWYQQHAGEAPTFLSY NVLDG..... LEEKG.......RFSSFLSRSKGYSYLLLKELQMKDSASYLC AVR........
AE000658,TRAV2     KDQVFQ.PSTVASSEGAVVEIFCNHS VSNAYN...... FFWYLHFPGCAPRLLVK GSK....... PSQQG.......RYNMTYER..FSSSLLILQVREADAAVYYC AVE........
AE000658,TRAV3     AQSVAQPEDQVNVAEGNPLTVKCTYS VSGNPY...... LFWYVQYPNRGLQFLLK YITGDNL... VKGSY.......GFEAEFNKSQTSFHLKKPSALVSDSALYFC AVRD.......
AE000658,TRAV4     LAKTTQ.PISMDSYEGQEVNITCSHN NIATNDY..... ITWYQQFPSQGPRFIIQ GYKT...... KVTNE.......VASLFIPADRKSSTLSLPRVSLSDTAVYYC LVGD.......
AE000659,TRAV5     GEDVEQS.LFLSVREGDSSVINCTYT DSSSTY...... LYWYKQEPGAGLQLLTY IFSNMD.... MKQDQ.......RLTVLLNKKDKHLSLRIADTQTGDSAIYFC AES........
AE000659,TRAV6     SQKIEQNSEALNIQEGKTATLTCNYT NYSPAY...... LQWYRQDPGRGPVFLLL IRENEK.... EKRKE.......RLKVTFDTTLKQSLFHITASQPADSATYLC ALD........
AE000659,TRAV7     ENQVEHSPHFLGPQQGDVASMSCTYS VSRFNN...... LQWYRQNTGMGPKHLLS MYSAGY.... EKQKG.......RLNATLLK..NGSSLYITAVQPEDSATYFC AVD........
AE000659,TRAV8-1   AQSVSQHNHHVILSEAASLELGCNYS YGGTVN...... LFWYVQYPGQHLQLLLK YFSGDPL... VKGIK.......GFEAEFIKSKFSFNLRKPSVQWSDTAEYFC AVN........
AE000659,TRAV8-2   AQSVTQLDSHVSVSEGTPVLLRCNYS SSYSPS...... LFWYVQHPNKGLQLLLK YTSAATL... VKGIN.......GFEAEFKKSETSFHLTKPSAHMSDAAEYFC VVS........
AE000659,TRAV8-3   AQSVTQPDIHITVSEGASLELRCNYS YGATPY...... LFWYVQSPGQGLQLLLK YFSGDTL... VQGIK.......GFEAEFKRSQSSFNLRKPSVHWSDAAEYFC AVG........
AE000659,TRAV8-4   AQSVTQLGSHVSVSEGALVLLRCNYS SSVPPY...... LFWYVQYPNQGLQLLLK YTSAATL... VKGIN.......GFEAEFKKSETSFHLTKPSAHMSDAAEYFC AVS........
X02850  ,TRAV8-6   AQSVTQLDSQVPVFEEAPVELRCNYS SSVSVY...... LFWYVQYPNQGLQLLLK YLSGSTL... VESIN.......GFEAEFNKSQTSFHLRKPSVHISDTAEYFC AVS........
AE000660,TRAV8-7   TQSVTQLDGHITVSEEAPLELKCNYS YSGVPS...... LFWYVQYSSQSLQLLLK DLTEATQ... VKGIR.......GFEAEFKKSETSFYLRKPSTHVSDAAEYFC AVGDR......
AE000659,TRAV9-1   GDSVVQTEGQVLPSEGDSLIVNCSYE TTQYPS       LFWYVQYPGEGPQLHLK AMKAND     KGRNK       GFEAMYRKETTSFHLEKDSVQESDSAVYFC ALS
```

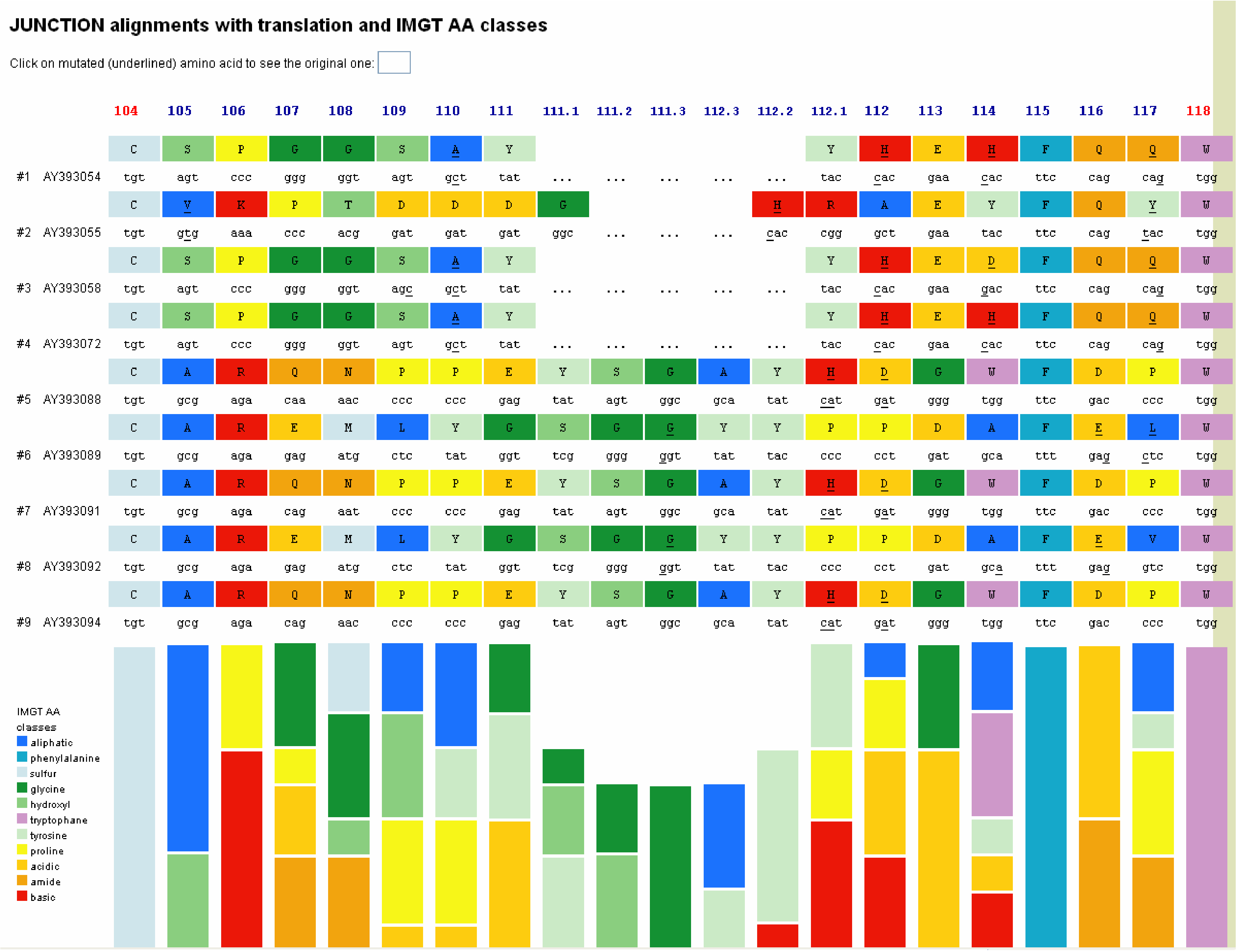
The eleven IMGT amino acid classes according to the physico-chemical properties

http://imgt.cines.fr



'Volume' classes		'Hydropathy' classes		
	in Å³	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	

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



JUNCTION alignments with translation and IMGT 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
		C	S	P	G	G	S	A	Y						Y	H	E	H	F	Q	Q	W
#1	AY393054	tgt	agt	ccc	ggg	ggt	agt	gct	tat	...	...	...	...	...	tac	cac	gaa	cac	ttc	cag	cag	tgg
		C	V	K	P	T	D	D	D	G				H	R	A	E	Y	F	Q	Y	W
#2	AY393055	tgt	gtg	aaa	ccc	acg	gat	gat	gat	ggc	...	...	...	cac	cgg	gct	gaa	tac	ttc	cag	tac	tgg
		C	S	P	G	G	S	A	Y						Y	H	E	D	F	Q	Q	W
#3	AY393058	tgt	agt	ccc	ggg	ggt	agc	gct	tat	...	...	...	...	...	tac	cac	gaa	gac	ttc	cag	cag	tgg
		C	S	P	G	G	S	A	Y						Y	H	E	H	F	Q	Q	W
#4	AY393072	tgt	agt	ccc	ggg	ggt	agt	gct	tat	...	...	...	...	...	tac	cac	gaa	cac	ttc	cag	cag	tgg
		C	A	R	Q	N	P	P	E	Y	S	G	A	Y	H	D	G	W	F	D	P	W
#5	AY393088	tgt	gcg	aga	caa	aac	ccc	ccc	gag	tat	agt	ggc	gca	tat	cat	gat	ggg	tgg	ttc	gac	ccc	tgg
		C	A	R	E	M	L	Y	G	S	G	G	Y	Y	P	P	D	A	F	E	L	W
#6	AY393089	tgt	gcg	aga	gag	atg	ctc	tat	ggt	tcg	ggg	ggt	tat	tac	ccc	cct	gat	gca	ttt	gag	ctc	tgg
		C	A	R	Q	N	P	P	E	Y	S	G	A	Y	H	D	G	W	F	D	P	W
#7	AY393091	tgt	gcg	aga	cag	aat	ccc	ccc	gag	tat	agt	ggc	gca	tat	cat	gat	ggg	tgg	ttc	gac	ccc	tgg
		C	A	R	E	M	L	Y	G	S	G	G	Y	Y	P	P	D	A	F	E	V	W
#8	AY393092	tgt	gcg	aga	gag	atg	ctc	tat	ggt	tcg	ggg	ggt	tat	tac	ccc	cct	gat	gca	ttt	gag	gtc	tgg
		C	A	R	Q	N	P	P	E	Y	S	G	A	Y	H	D	G	W	F	D	P	W
#9	AY393094	tgt	gcg	aga	cag	aac	ccc	ccc	gag	tat	agt	ggc	gca	tat	cat	gat	ggg	tgg	ttc	gac	ccc	tgg

Improvements IMGT/V-QUEST version 3

http://imgt.cines.fr

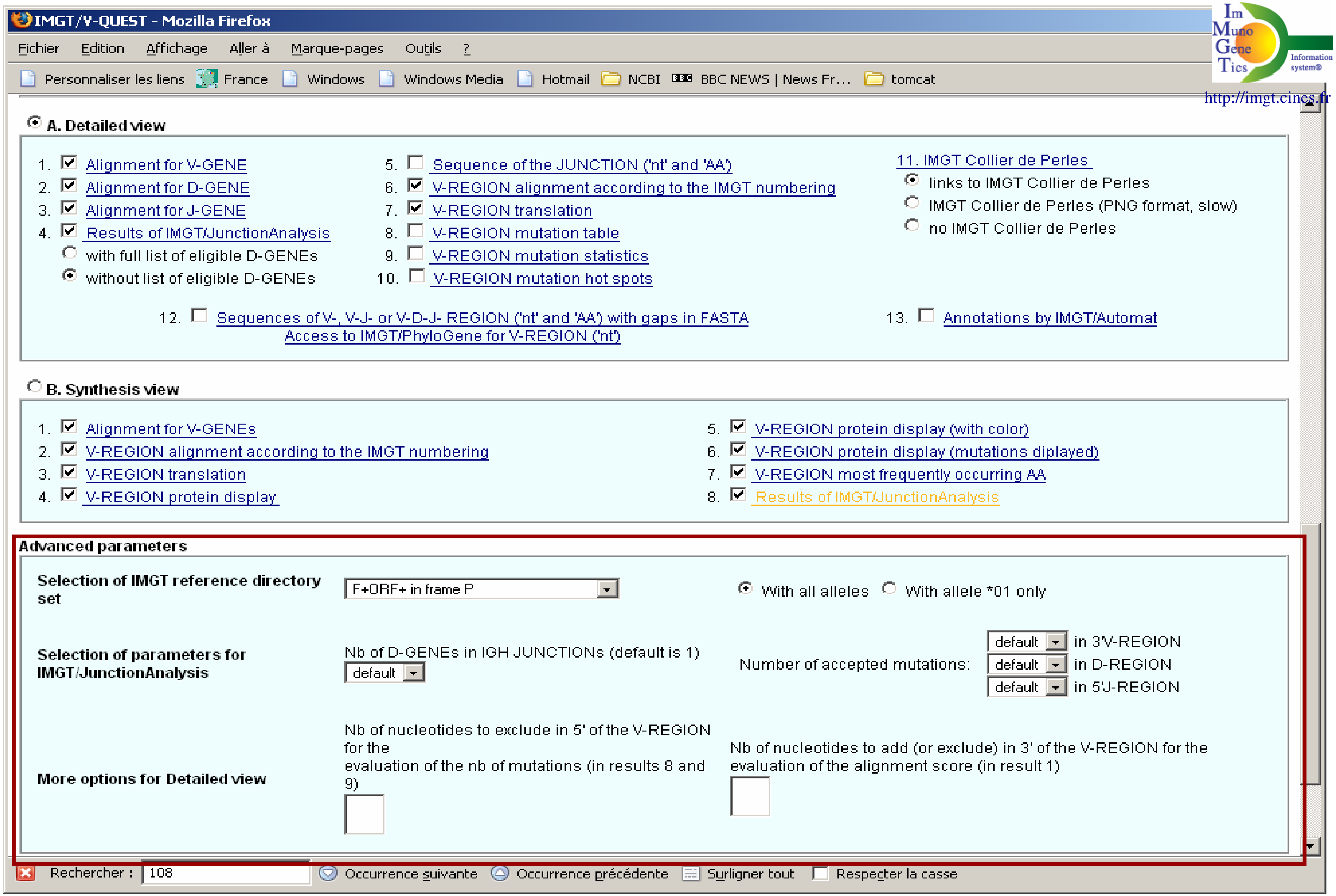
IMGT/V-QUEST query page:

- 4 options are available for the IMGT reference directory
    - F+ORF *(only functional and ORF genes)*
    - F+ORF+in frame P **(default)** *(functional, ORF genes and in frame pseudogenes)*
    - F+ORF including orphons *(only functional and ORF genes, including orphons)*
    - F+ORF+in frame P including orphons *(functional, ORF genes and in frame pseudognes, including orphons)*

- The analysis can be performed by comparison with only the alleles *01 of the IMGT reference directory or with all alleles **(default)**.

- The number of accepted mutations for IMGT/JunctionAnalysis can be modified

- The maximun number of sequences for a single run is 100 (instead of 50)



● **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

○ **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 diplayed)
7. ☑ V-REGION most frequently occurring AA
8. ☑ Results of IMGT/JunctionAnalysis

Advanced parameters

Selection of IMGT reference directory set: F+ORF+ in frame P; ● With all alleles ○ With allele *01 only

Selection of parameters for IMGT/JunctionAnalysis: Nb of D-GENEs in IGH JUNCTIONs (default is 1): default

Number of accepted mutations:
default in 3'V-REGION
default in D-REGION
default in 5'J-REGION

More options for Detailed view

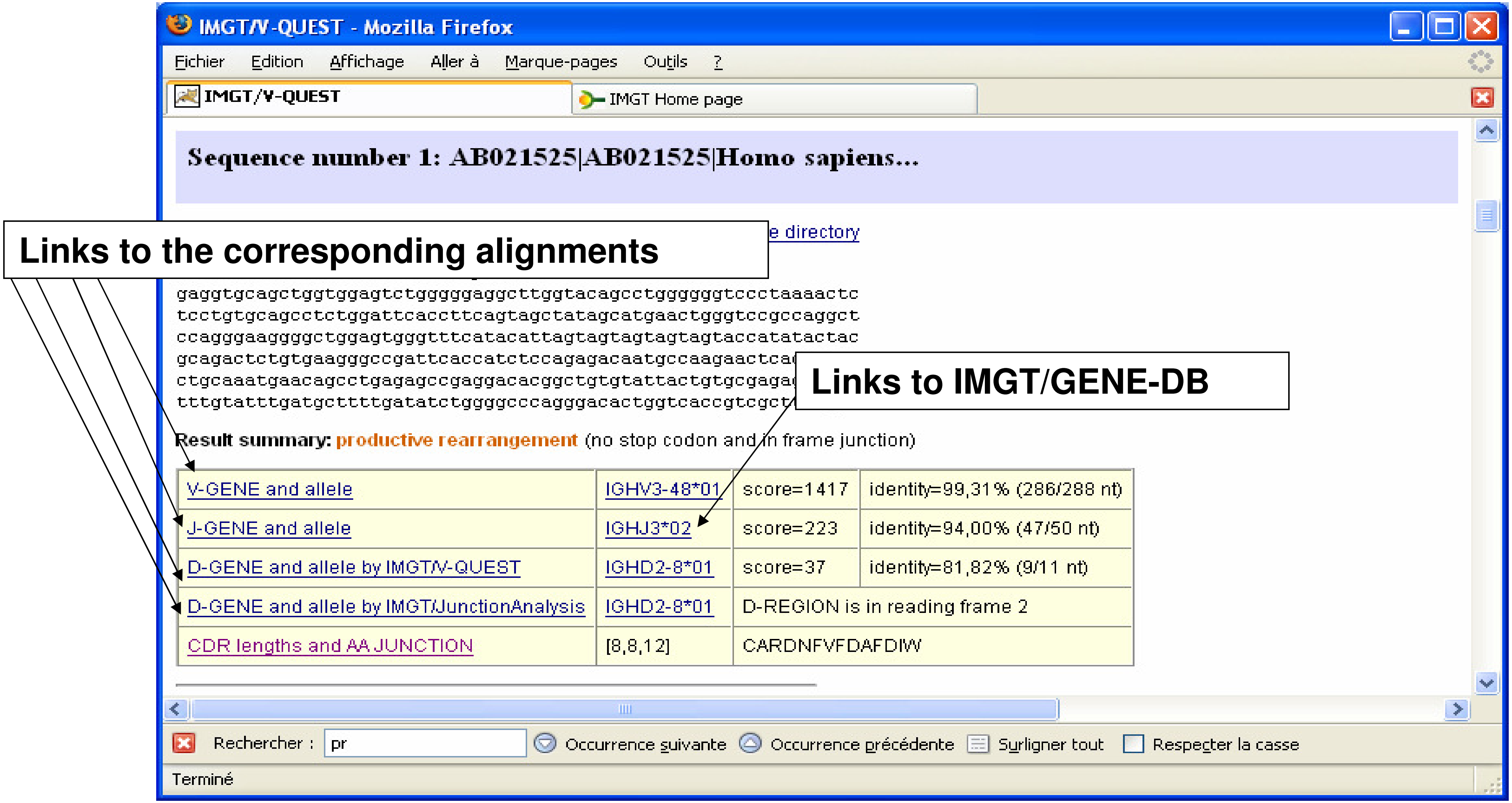
Nb of nucleotides to exclude in 5' of the V-REGION for the evaluation of the nb of mutations (in results 8 and 9):

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

http://imgt.cines.fr

A. Detailed results: Result summary

http://imgt.cines.fr



Sequence number 1: AB021525|AB021525|Homo sapiens...

Links to the corresponding alignments

e directory

```
gaggtgcagctggtggagtctgggggaggcttggtacagcctggggggtccctaaaactc
tcctgtgcagcctctggattcaccttcagtagctatagcatgaactgggtccgccaggct
ccagggaagggctggagtgggtttcatacattagtagtagtagtagtaccatatactac
gcagactctgtgaagggccgattcaccatctccagagacaatgccaagaactca
ctgcaaatgaacagcctgagagccgaggacacggctgtgtattactgtgcgaga
tttgtatttgatgcttttgatatctggggcccagggacactggtcaccgtcgct
```

Links to IMGT/GENE-DB

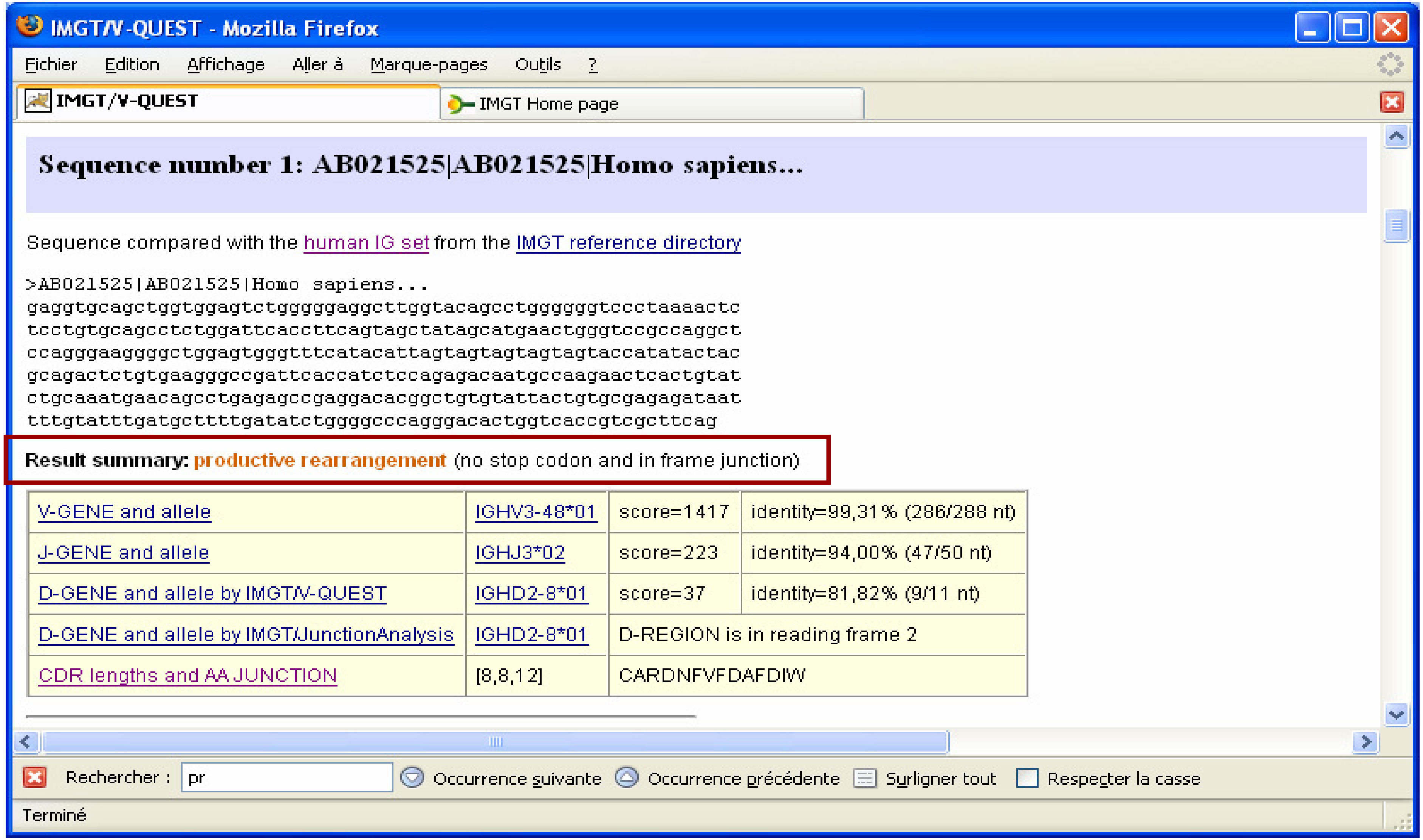
Result summary: productive rearrangement (no stop codon and in frame junction)

V-GENE and allele	IGHV3-48*01	score=1417	identity=99,31% (286/288 nt)
J-GENE and allele	IGHJ3*02	score=223	identity=94,00% (47/50 nt)
D-GENE and allele by IMGT/V-QUEST	IGHD2-8*01	score=37	identity=81,82% (9/11 nt)
D-GENE and allele by IMGT/JunctionAnalysis	IGHD2-8*01	D-REGION is in reading frame 2	
CDR lengths and AA JUNCTION	[8,8,12]	CARDNFVFDAFDIW	

A. Detailed results: Evaluation of the rearrangement

http://imgt.cines.fr

Example: productive rearrangement (no stop codon and in frame junction)



Sequence number 1: AB021525|AB021525|Homo sapiens...

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

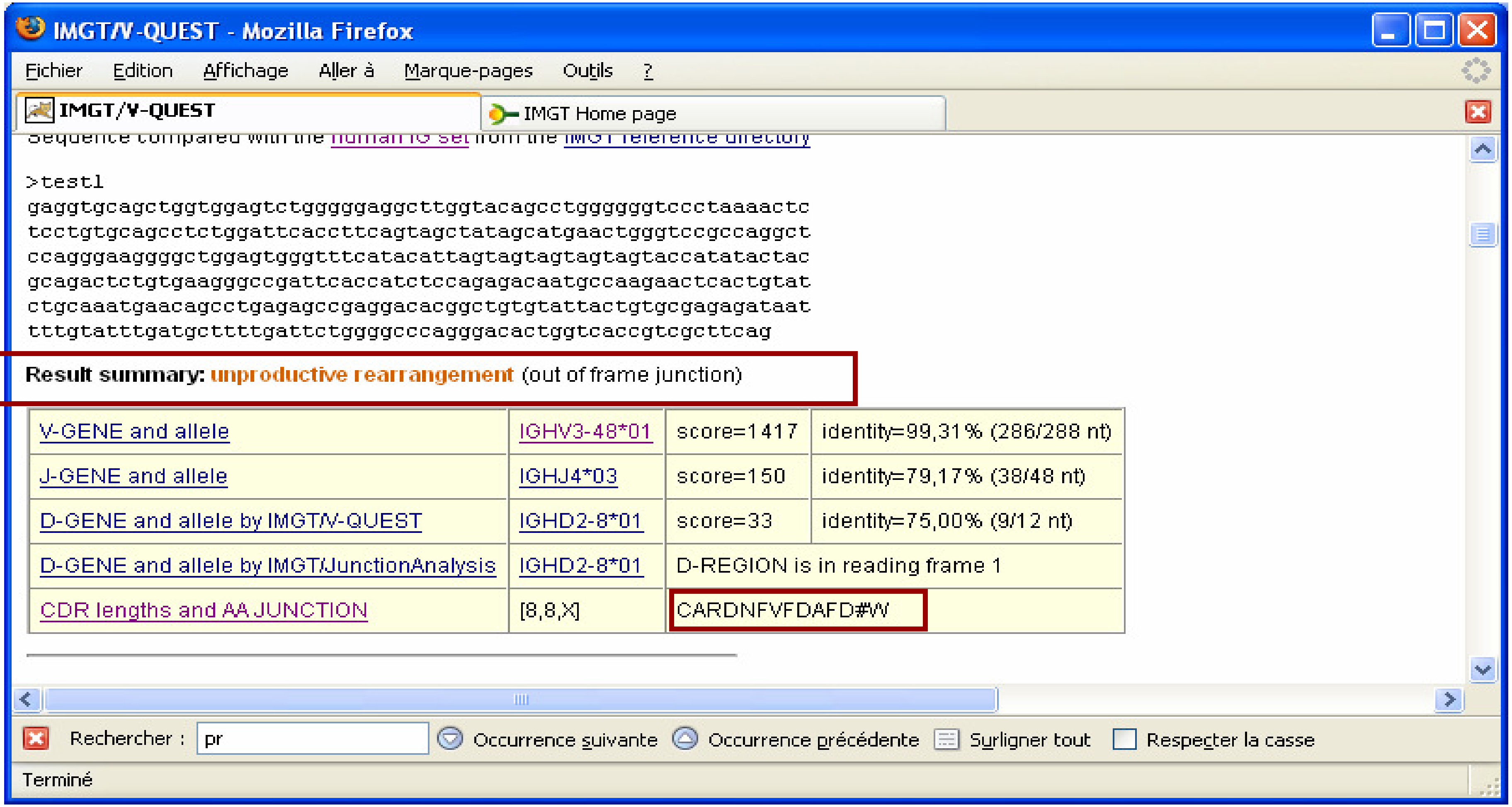
```
>AB021525|AB021525|Homo sapiens...
gaggtgcagctggtggagtctgggggaggcttggtacagcctggggggtccctaaaactc
tcctgtgcagcctctggattcaccttcagtagctatagcatgaactgggtccgccaggct
ccagggaaggggctggagtgggtttcatacattagtagtagtagtagtaccatatactac
gcagactctgtgaagggccgattcaccatctccagagacaatgccaagaactcactgtat
ctgcaaatgaacagcctgagagccgaggacacggctgtgtattactgtgcgagagataat
tttgtatttgatgcttttgatatctggggcccagggacactggtcaccgtcgcttcag
```

Result summary: productive rearrangement (no stop codon and in frame junction)

V-GENE and allele	IGHV3-48*01	score=1417	identity=99,31% (286/288 nt)
J-GENE and allele	IGHJ3*02	score=223	identity=94,00% (47/50 nt)
D-GENE and allele by IMGT/V-QUEST	IGHD2-8*01	score=37	identity=81,82% (9/11 nt)
D-GENE and allele by IMGT/JunctionAnalysis	IGHD2-8*01	D-REGION is in reading frame 2	
CDR lengths and AA JUNCTION	[8,8,12]	CARDNFVFDAFDIW	

A. Detailed results: Evaluation of the rearrangement

Example: unproductive rearrangement (out of frame junction)



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

```
>testl
gaggtgcagctggtggagtctgggggaggcttggtacagcctggggggtccctaaaactc
tcctgtgcagcctctggattcaccttcagtagctatagcatgaactgggtccgccaggct
ccagggaaggggctggagtgggtttcatacattagtagtagtagtagtaccatatactac
gcagactctgtgaagggccgattcaccatctccagagacaatgccaagaactcactgtat
ctgcaaatgaacagcctgagagccgaggacacggctgtgtattactgtgcgagagataat
tttgtatttgatgcttttgattctggggcccagggacactggtcaccgtcgcttcag
```

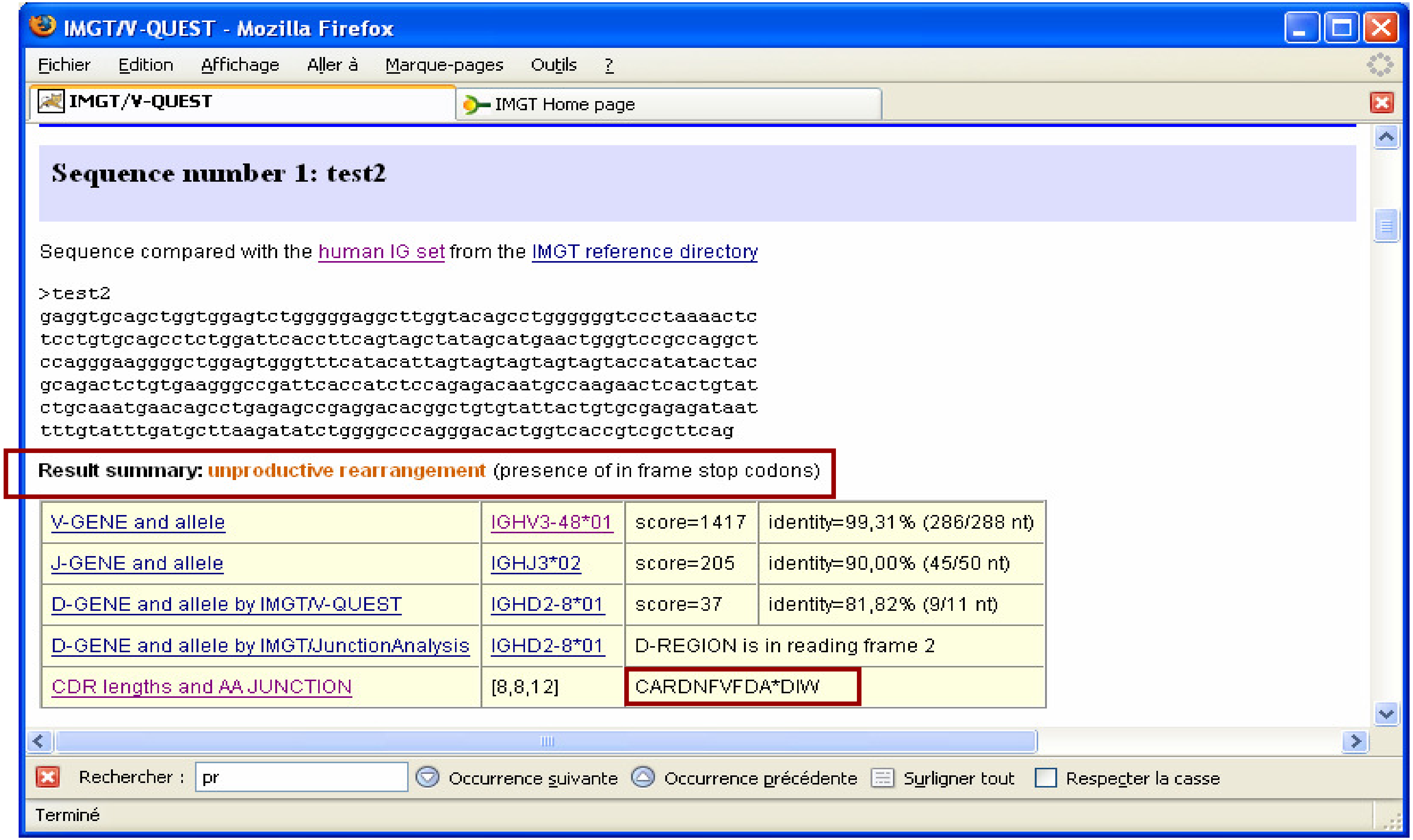
Result summary: unproductive rearrangement (out of frame junction)

V-GENE and allele	IGHV3-48*01	score=1417	identity=99,31% (286/288 nt)
J-GENE and allele	IGHJ4*03	score=150	identity=79,17% (38/48 nt)
D-GENE and allele by IMGT/V-QUEST	IGHD2-8*01	score=33	identity=75,00% (9/12 nt)
D-GENE and allele by IMGT/JunctionAnalysis	IGHD2-8*01	D-REGION is in reading frame 1	
CDR lengths and AA JUNCTION	[8,8,X]	CARDNFVFDAFD#W	

A. Detailed results: Evaluation of the rearrangement

Example: unproductive rearrangement (presence of in frame stop codons)

http://imgt.cines.fr



Sequence number 1: test2

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

```
>test2
gaggtgcagctggtggagtctgggggaggcttggtacagcctggggggtccctaaaactc
tcctgtgcagcctctggattcaccttcagtagctatagcatgaactgggtccgccaggct
ccagggaaggggctggagtgggtttcatacattagtagtagtagtagtaccatatactac
gcagactctgtgaagggccgattcaccatctccagagacaatgccaagaactcactgtat
ctgcaaatgaacagcctgagagccgaggacacggctgtgtattactgtgcgagagataat
tttgtatttgatgcttaagatatctggggcccagggacactggtcaccgtcgcttcag
```

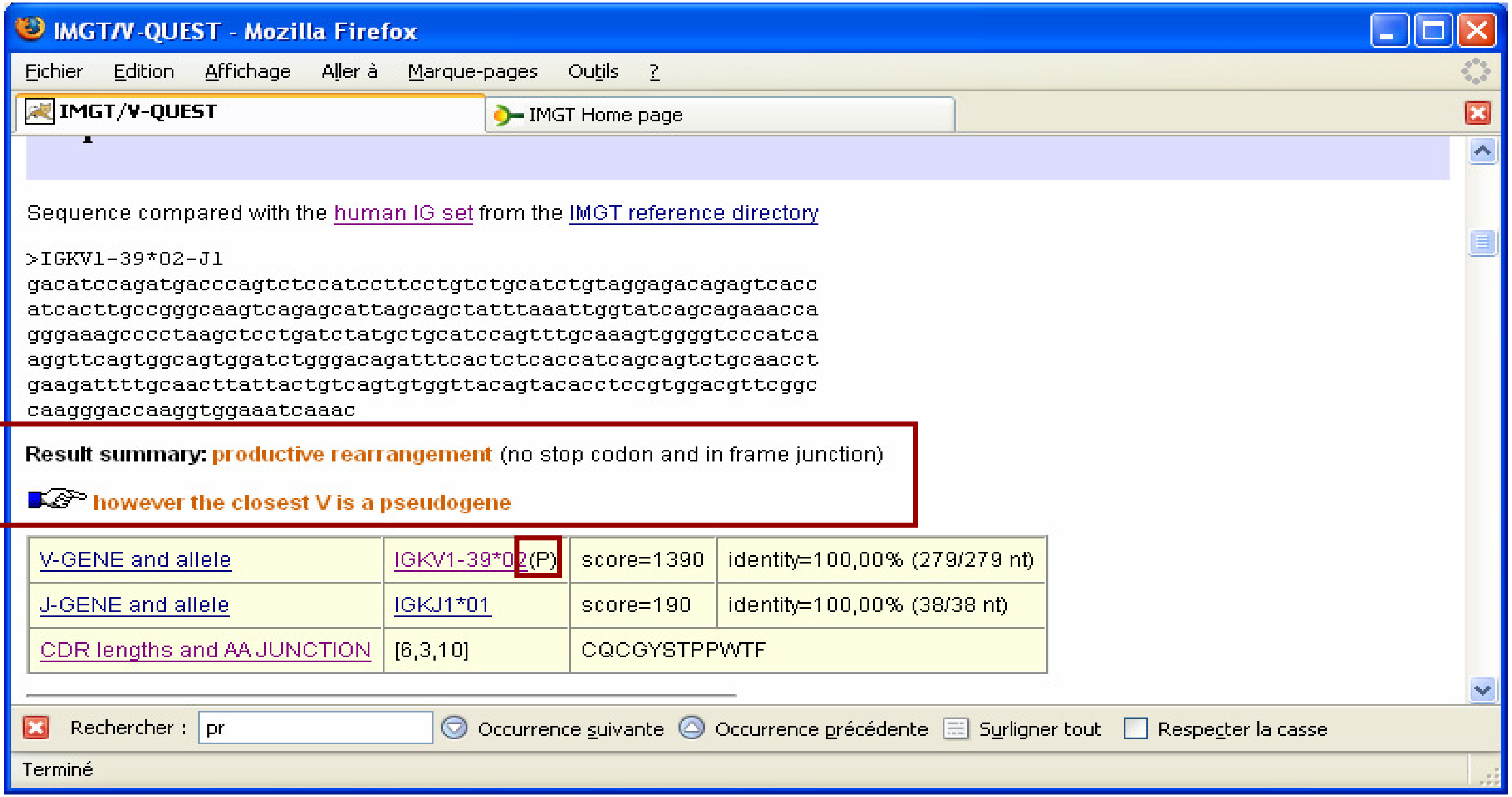
Result summary: unproductive rearrangement (presence of in frame stop codons)

V-GENE and allele	IGHV3-48*01	score=1417	identity=99,31% (286/288 nt)
J-GENE and allele	IGHJ3*02	score=205	identity=90,00% (45/50 nt)
D-GENE and allele by IMGT/V-QUEST	IGHD2-8*01	score=37	identity=81,82% (9/11 nt)
D-GENE and allele by IMGT/JunctionAnalysis	IGHD2-8*01	D-REGION is in reading frame 2	
CDR lengths and AA JUNCTION	[8,8,12]	CARDNFVFDA*DIW	

A. Detailed results: Evaluation of the rearrangement

Example: the closest V gene is a pseudogene

http://imgt.cines.fr



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

```
>IGKV1-39*02-J1
gacatccagatgacccagtctccatccttcctgtctgcatctgtaggagacagagtcacc
atcacttgccgggcaagtcagagcattagcagctatttaaattggtatcagcagaaacca
gggaaagcccctaagctcctgatctatgctgcatccagtttgcaaagtggggtcccatca
aggttcagtggcagtggatctgggacagatttcactctcaccatcagcagtctgcaacct
gaagattttgcaacttattactgtcagtgtggttacagtacacctccgtggacgttcggc
caagggaccaaggtggaaatcaaac
```

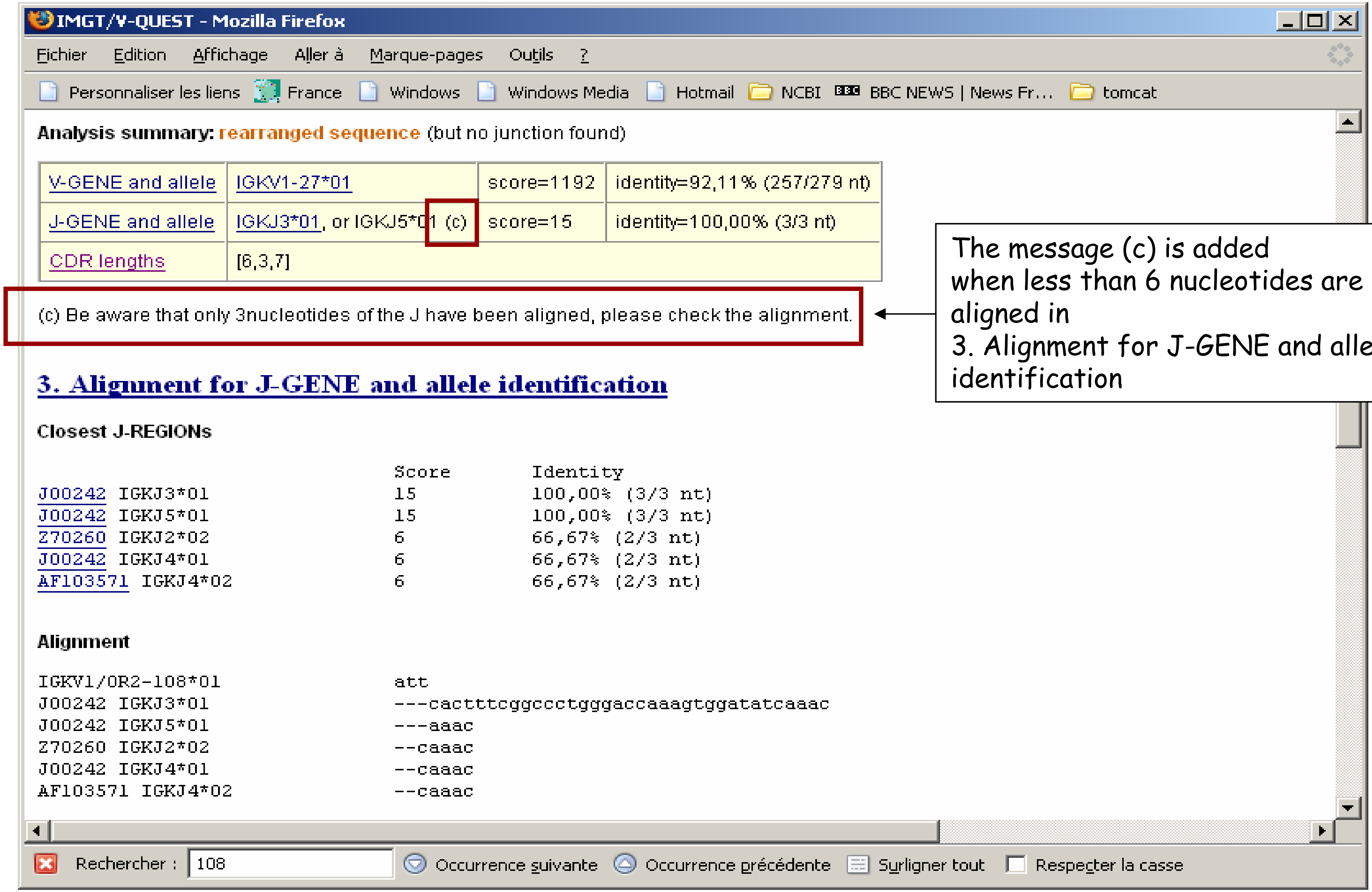
Result summary: productive rearrangement (no stop codon and in frame junction)

☞ however the closest V is a pseudogene

V-GENE and allele	IGKV1-39*02(P)	score=1390	identity=100,00% (279/279 nt)
J-GENE and allele	IGKJ1*01	score=190	identity=100,00% (38/38 nt)
CDR lengths and AA JUNCTION	[6,3,10]	CQCGYSTPPWTF	

A. Detailed results: Quality evaluation of the results

http://imgt.cines.fr



Analysis summary: rearranged sequence (but no junction found)

V-GENE and allele	IGKV1-27*01	score=1192	identity=92,11% (257/279 nt)
J-GENE and allele	IGKJ3*01, or IGKJ5*01 (c)	score=15	identity=100,00% (3/3 nt)
CDR lengths	[6,3,7]		

(c) Be aware that only 3nucleotides of the J have been aligned, please check the alignment.

3. Alignment for J-GENE and allele identification

Closest J-REGIONs

```
                                   Score        Identity
J00242 IGKJ3*01                    15           100,00% (3/3 nt)
J00242 IGKJ5*01                    15           100,00% (3/3 nt)
Z70260 IGKJ2*02                    6            66,67% (2/3 nt)
J00242 IGKJ4*01                    6            66,67% (2/3 nt)
AF103571 IGKJ4*02                  6            66,67% (2/3 nt)
```

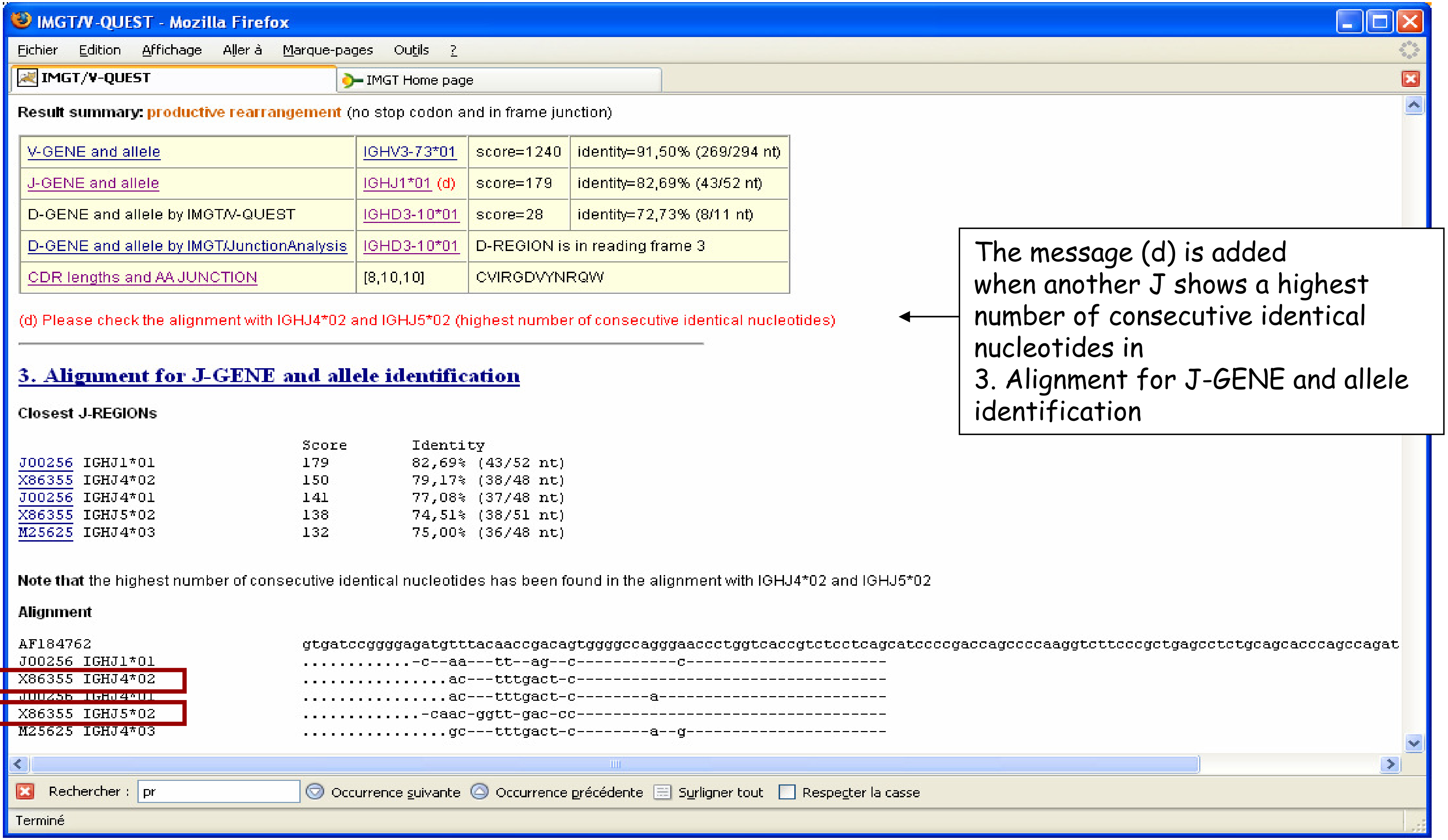
Alignment

```
IGKV1/OR2-108*01                   att
J00242 IGKJ3*01                    ---cactttcggccctgggaccaaagtggatatcaaac
J00242 IGKJ5*01                    ---aaac
Z70260 IGKJ2*02                    --caaac
J00242 IGKJ4*01                    --caaac
AF103571 IGKJ4*02                  --caaac
```

The message (c) is added when less than 6 nucleotides are aligned in
3. Alignment for J-GENE and allele identification

A. Detailed results: Quality evaluation of the results

http://imgt.cines.fr



Result summary: productive rearrangement (no stop codon and in frame junction)

V-GENE and allele	IGHV3-73*01	score=1240	identity=91,50% (269/294 nt)
J-GENE and allele	IGHJ1*01 (d)	score=179	identity=82,69% (43/52 nt)
D-GENE and allele by IMGT/V-QUEST	IGHD3-10*01	score=28	identity=72,73% (8/11 nt)
D-GENE and allele by IMGT/JunctionAnalysis	IGHD3-10*01	D-REGION is in reading frame 3	
CDR lengths and AA JUNCTION	[8,10,10]	CVIRGDVYNRQW	

(d) Please check the alignment with IGHJ4*02 and IGHJ5*02 (highest number of consecutive identical nucleotides)

The message (d) is added when another J shows a highest number of consecutive identical nucleotides in
3. Alignment for J-GENE and allele identification

3. Alignment for J-GENE and allele identification

Closest J-REGIONs

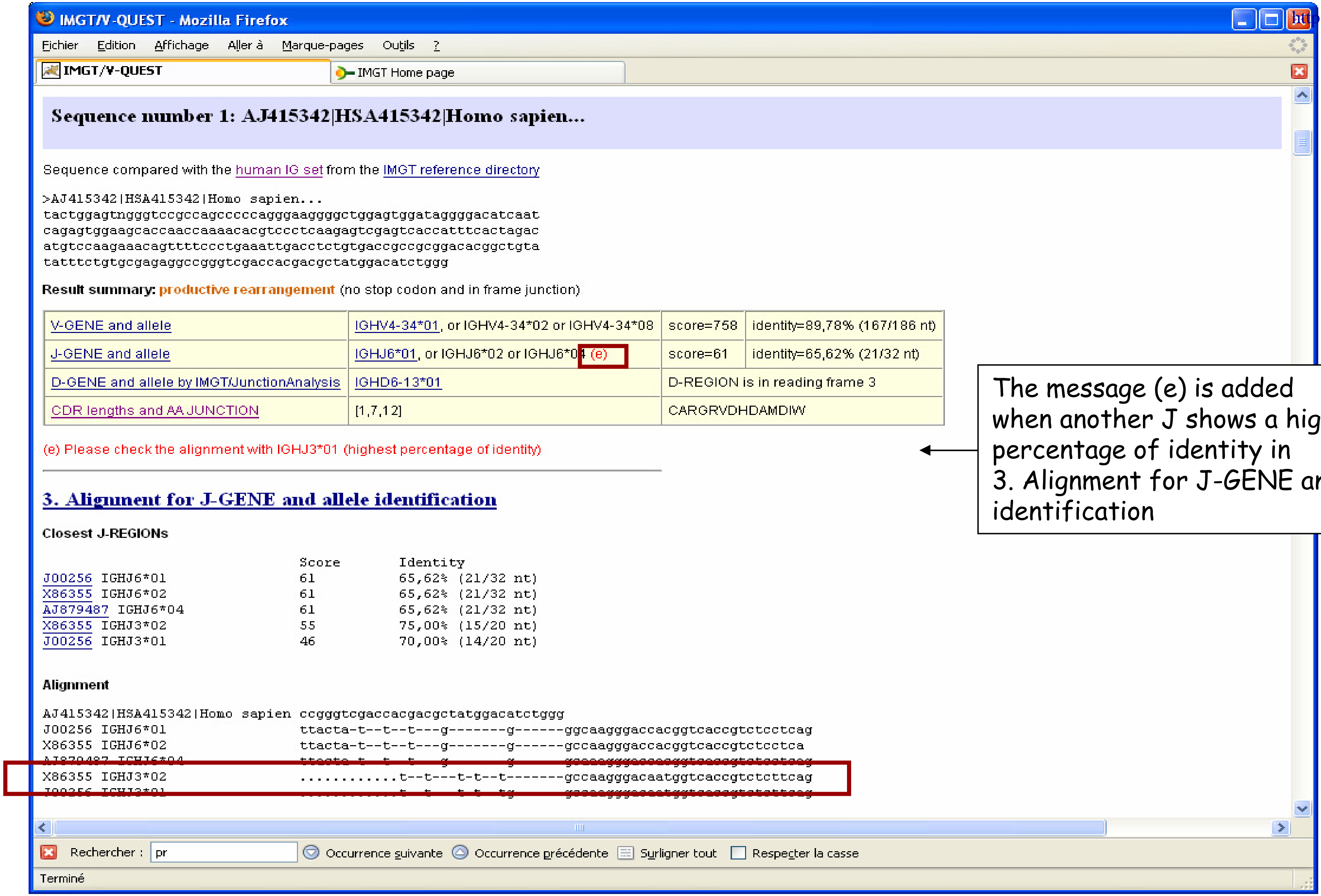
```
                               Score       Identity
J00256 IGHJ1*01                179         82,69% (43/52 nt)
X86355 IGHJ4*02                150         79,17% (38/48 nt)
J00256 IGHJ4*01                141         77,08% (37/48 nt)
X86355 IGHJ5*02                138         74,51% (38/51 nt)
M25625 IGHJ4*03                132         75,00% (36/48 nt)
```

Note that the highest number of consecutive identical nucleotides has been found in the alignment with IGHJ4*02 and IGHJ5*02

Alignment

```
AF184762                       gtgatccggggagatgtttacaaccgacagtggggccagggaaccctggtcaccgtctcctcagcatccccgaccagccccaaggtcttcccgctgagcctctgcagcacccagccagat
J00256 IGHJ1*01                ............-c--aa---tt--ag--c-----------c----------------------
X86355 IGHJ4*02                ................ac---tttgact-c----------------------------------
J00256 IGHJ4*01                ................ac---tttgact-c--------a-------------------------
X86355 IGHJ5*02                .............-caac-ggtt-gac-cc----------------------------------
M25625 IGHJ4*03                ................gc---tttgact-c--------a--g----------------------
```

A. Detailed results: Quality evaluation of the results



Sequence number 1: AJ415342|HSA415342|Homo sapien...

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

```
>AJ415342|HSA415342|Homo sapien...
tactggagtngggtccgccagcccccagggaaggggctggagtggataggggacatcaat
cagagtggaagcaccaaccaaaacacgtccctcaagagtcgagtcaccatttcactagac
atgtccaagaaacagttttccctgaaattgacctctgtgaccgccgcggacacggctgta
tatttctgtgcgagaggccgggtcgaccacgacgctatggacatctggg
```

Result summary: productive rearrangement (no stop codon and in frame junction)

V-GENE and allele	IGHV4-34*01, or IGHV4-34*02 or IGHV4-34*08	score=758	identity=89,78% (167/186 nt)
J-GENE and allele	IGHJ6*01, or IGHJ6*02 or IGHJ6*04 (e)	score=61	identity=65,62% (21/32 nt)
D-GENE and allele by IMGT/JunctionAnalysis	IGHD6-13*01	D-REGION is in reading frame 3	
CDR lengths and AA JUNCTION	[1,7,12]	CARGRVDHDAMDIW	

(e) Please check the alignment with IGHJ3*01 (highest percentage of identity)

3. Alignment for J-GENE and allele identification

Closest J-REGIONs

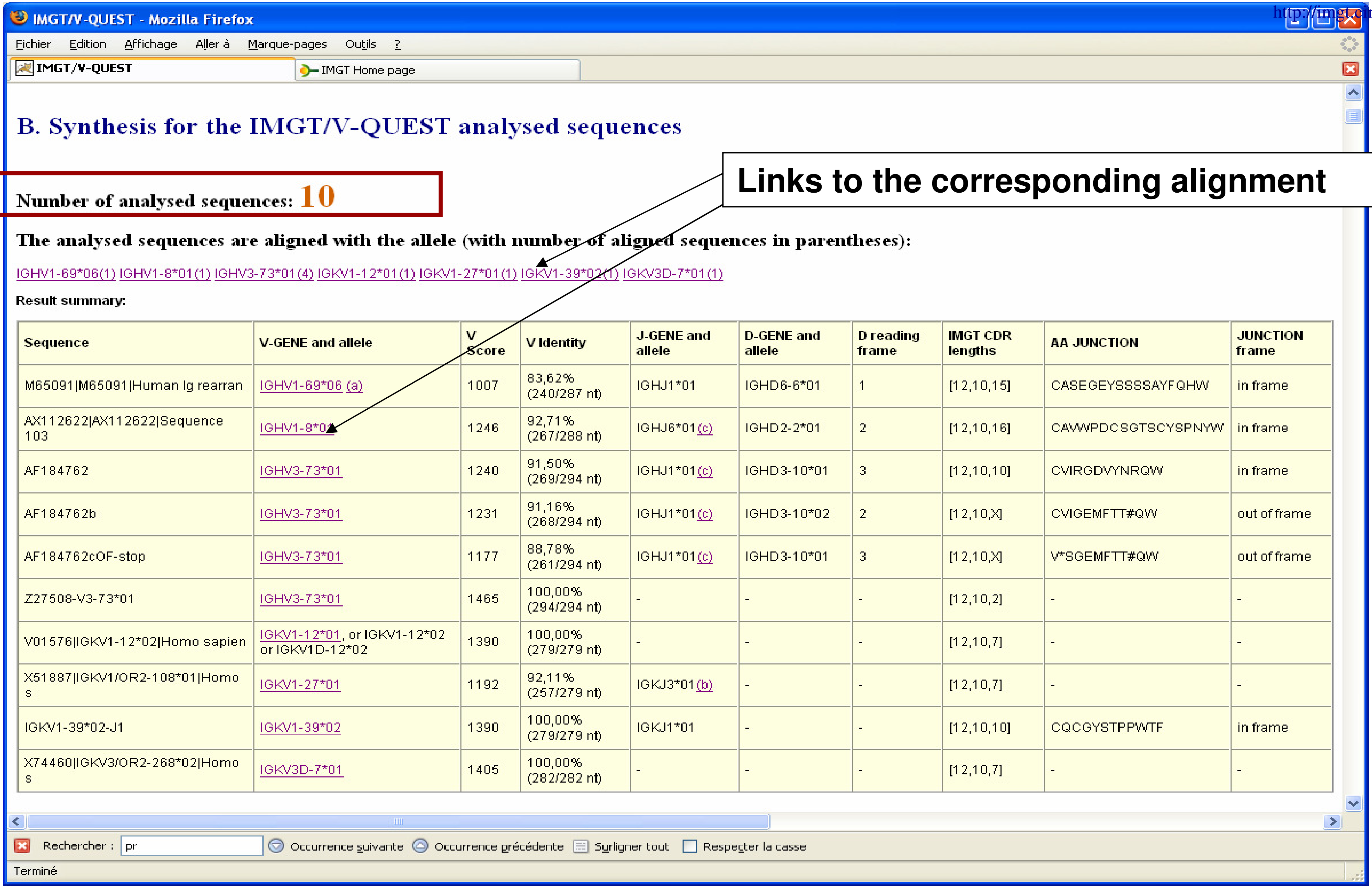
```
                               Score       Identity
J00256 IGHJ6*01                61          65,62% (21/32 nt)
X86355 IGHJ6*02                61          65,62% (21/32 nt)
AJ879487 IGHJ6*04              61          65,62% (21/32 nt)
X86355 IGHJ3*02                55          75,00% (15/20 nt)
J00256 IGHJ3*01                46          70,00% (14/20 nt)
```

Alignment

```
AJ415342|HSA415342|Homo sapien ccgggtcgaccacgacgctatggacatctggg
J00256 IGHJ6*01                ttacta-t--t--t---g-------g------ggcaagggaccacggtcaccgtctcctcag
X86355 IGHJ6*02                ttacta-t--t--t---g-------g------gccaagggaccacggtcaccgtctcctca
AJ879487 IGHJ6*04              ttacta-t--t--t---g-------g------ggcaagggaccacggtcaccgtctcctcag
X86355 IGHJ3*02                ............t--t---t-t--t-------gccaagggacaatggtcaccgtctcttcag
J00256 IGHJ3*01                ............t--t---t-t--tg------gccaagggacaatggtcaccgtctcttcag
```

The message (e) is added when another J shows a highest percentage of identity in 3. Alignment for J-GENE and allele identification

B. Synthesis results: Result summary



B. Synthesis for the IMGT/V-QUEST analysed sequences

Number of analysed sequences: 10

The analysed sequences are aligned with the allele (with number of aligned sequences in parentheses):

IGHV1-69*06(1) IGHV1-8*01(1) IGHV3-73*01(4) IGKV1-12*01(1) IGKV1-27*01(1) IGKV1-39*02(1) IGKV3D-7*01(1)

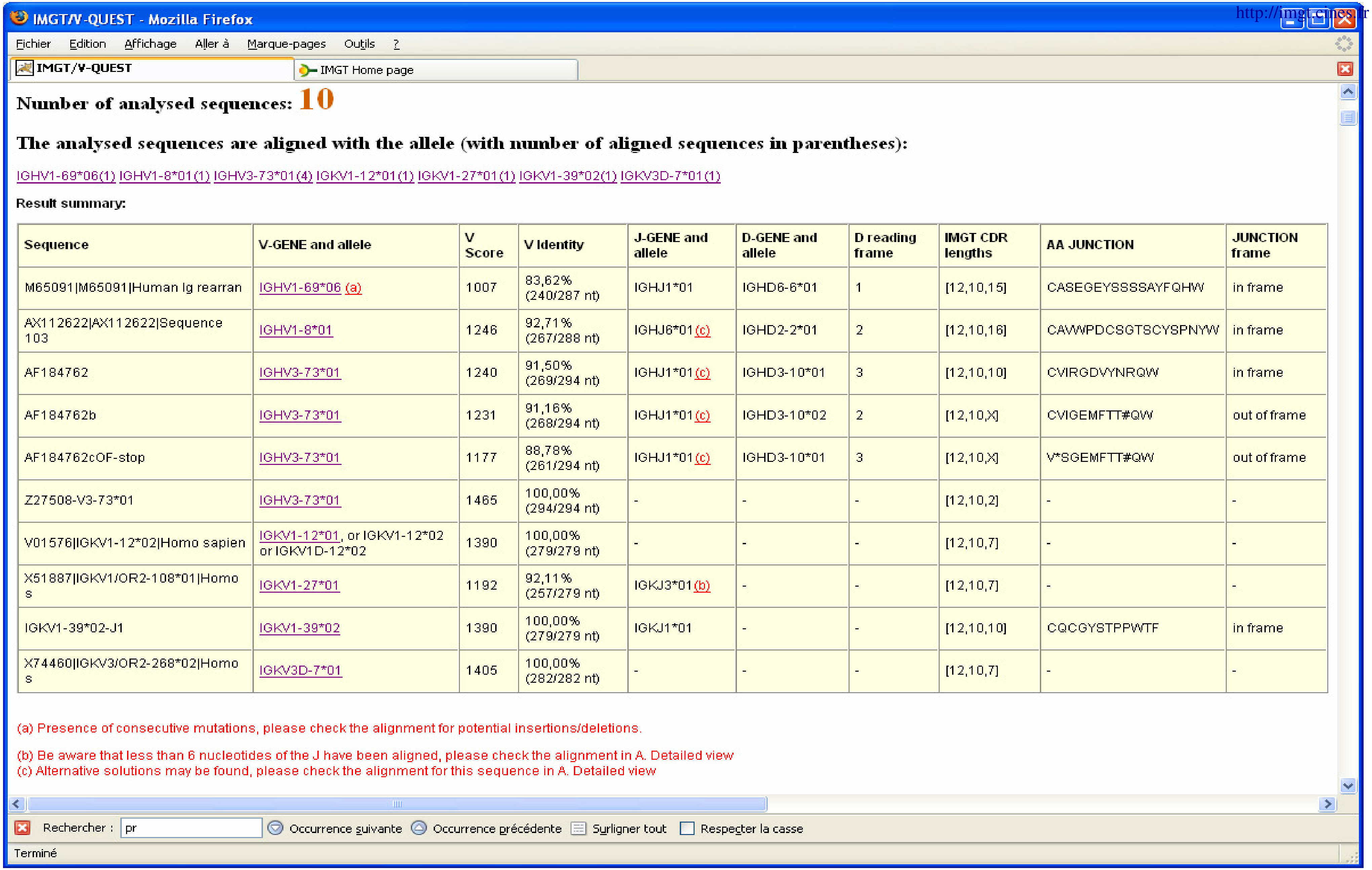
Result summary:

Sequence	V-GENE and allele	V Score	V Identity	J-GENE and allele	D-GENE and allele	D reading frame	IMGT CDR lengths	AA JUNCTION	JUNCTION frame
M65091|M65091|Human Ig rearran	IGHV1-69*06 (a)	1007	83,62% (240/287 nt)	IGHJ1*01	IGHD6-6*01	1	[12,10,15]	CASEGEYSSSSAYFQHW	in frame
AX112622|AX112622|Sequence 103	IGHV1-8*01	1246	92,71% (267/288 nt)	IGHJ6*01 (c)	IGHD2-2*01	2	[12,10,16]	CAVWPDCSGTSCYSPNYW	in frame
AF184762	IGHV3-73*01	1240	91,50% (269/294 nt)	IGHJ1*01 (c)	IGHD3-10*01	3	[12,10,10]	CVIRGDVYNRQW	in frame
AF184762b	IGHV3-73*01	1231	91,16% (268/294 nt)	IGHJ1*01 (c)	IGHD3-10*02	2	[12,10,X]	CVIGEMFTT#QW	out of frame
AF184762cOF-stop	IGHV3-73*01	1177	88,78% (261/294 nt)	IGHJ1*01 (c)	IGHD3-10*01	3	[12,10,X]	V*SGEMFTT#QW	out of frame
Z27508-V3-73*01	IGHV3-73*01	1465	100,00% (294/294 nt)	-	-	-	[12,10,2]	-	-
V01576|IGKV1-12*02|Homo sapien	IGKV1-12*01, or IGKV1-12*02 or IGKV1D-12*02	1390	100,00% (279/279 nt)	-	-	-	[12,10,7]	-	-
X51887|IGKV1/OR2-108*01|Homo s	IGKV1-27*01	1192	92,11% (257/279 nt)	IGKJ3*01 (b)	-	-	[12,10,7]	-	-
IGKV1-39*02-J1	IGKV1-39*02	1390	100,00% (279/279 nt)	IGKJ1*01	-	-	[12,10,10]	CQCGYSTPPWTF	in frame
X74460|IGKV3/OR2-268*02|Homo s	IGKV3D-7*01	1405	100,00% (282/282 nt)	-	-	-	[12,10,7]	-	-

Links to the corresponding alignment

B. Synthesis results: Quality evaluation of the results

http://imgt.cines.fr



Number of analysed sequences: 10

The analysed sequences are aligned with the allele (with number of aligned sequences in parentheses):

IGHV1-69*06(1) IGHV1-8*01(1) IGHV3-73*01(4) IGKV1-12*01(1) IGKV1-27*01(1) IGKV1-39*02(1) IGKV3D-7*01(1)

Result summary:

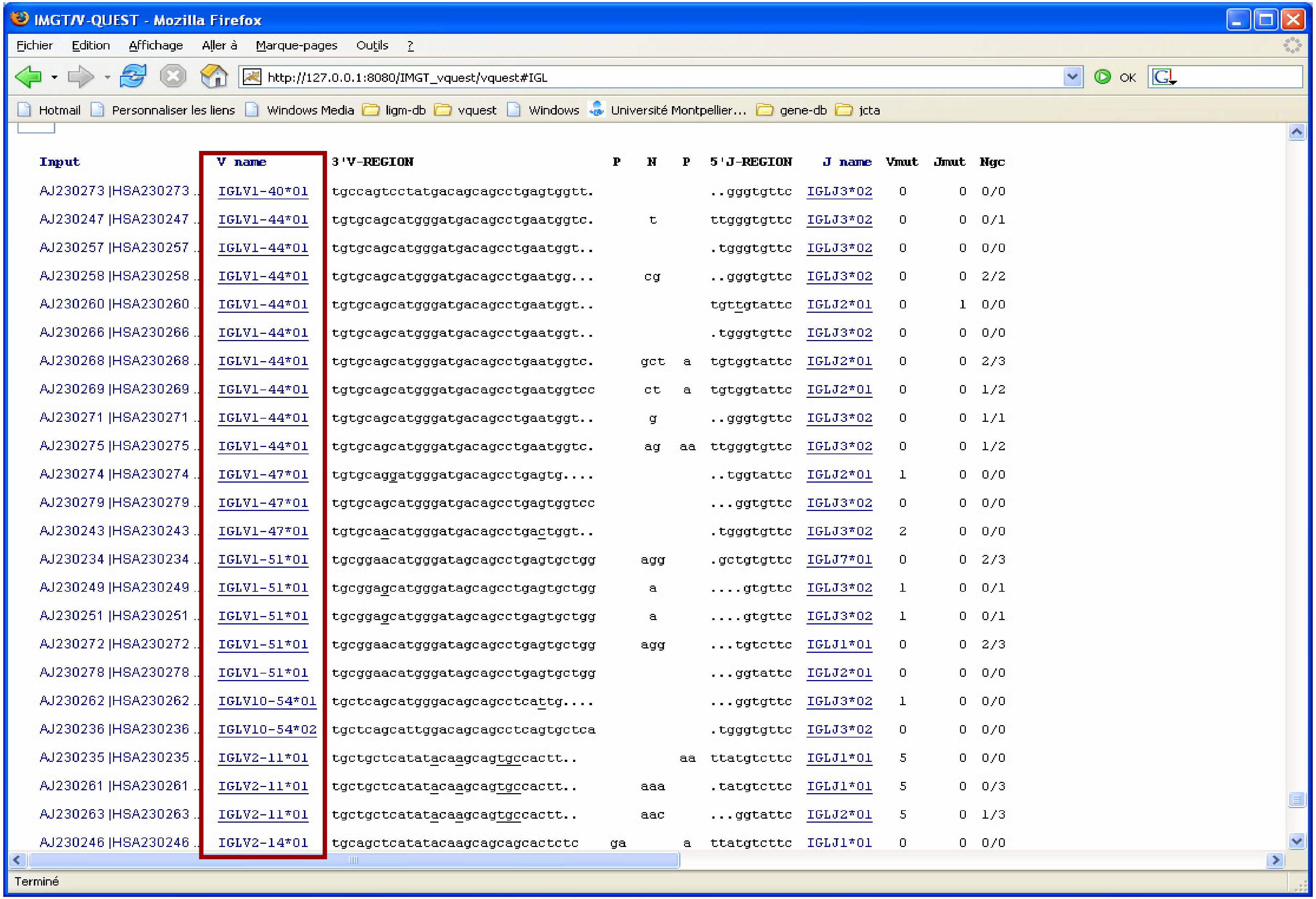
Sequence	V-GENE and allele	V Score	V Identity	J-GENE and allele	D-GENE and allele	D reading frame	IMGT CDR lengths	AA JUNCTION	JUNCTION frame
M65091|M65091|Human Ig rearran	IGHV1-69*06 (a)	1007	83,62% (240/287 nt)	IGHJ1*01	IGHD6-6*01	1	[12,10,15]	CASEGEYSSSSAYFQHW	in frame
AX112622|AX112622|Sequence 103	IGHV1-8*01	1246	92,71% (267/288 nt)	IGHJ6*01 (c)	IGHD2-2*01	2	[12,10,16]	CAWWPDCSGTSCYSPNYW	in frame
AF184762	IGHV3-73*01	1240	91,50% (269/294 nt)	IGHJ1*01 (c)	IGHD3-10*01	3	[12,10,10]	CVIRGDVYNRQW	in frame
AF184762b	IGHV3-73*01	1231	91,16% (268/294 nt)	IGHJ1*01 (c)	IGHD3-10*02	2	[12,10,X]	CVIGEMFTT#QW	out of frame
AF184762cOF-stop	IGHV3-73*01	1177	88,78% (261/294 nt)	IGHJ1*01 (c)	IGHD3-10*01	3	[12,10,X]	V*SGEMFTT#QW	out of frame
Z27508-V3-73*01	IGHV3-73*01	1465	100,00% (294/294 nt)	-	-	-	[12,10,2]	-	-
V01576|IGKV1-12*02|Homo sapien	IGKV1-12*01, or IGKV1-12*02 or IGKV1D-12*02	1390	100,00% (279/279 nt)	-	-	-	[12,10,7]	-	-
X51887|IGKV1/OR2-108*01|Homo s	IGKV1-27*01	1192	92,11% (257/279 nt)	IGKJ3*01 (b)	-	-	[12,10,7]	-	-
IGKV1-39*02-J1	IGKV1-39*02	1390	100,00% (279/279 nt)	IGKJ1*01	-	-	[12,10,10]	CQCGYSTPPWTF	in frame
X74460|IGKV3/OR2-268*02|Homo s	IGKV3D-7*01	1405	100,00% (282/282 nt)	-	-	-	[12,10,7]	-	-

(a) Presence of consecutive mutations, please check the alignment for potential insertions/deletions.

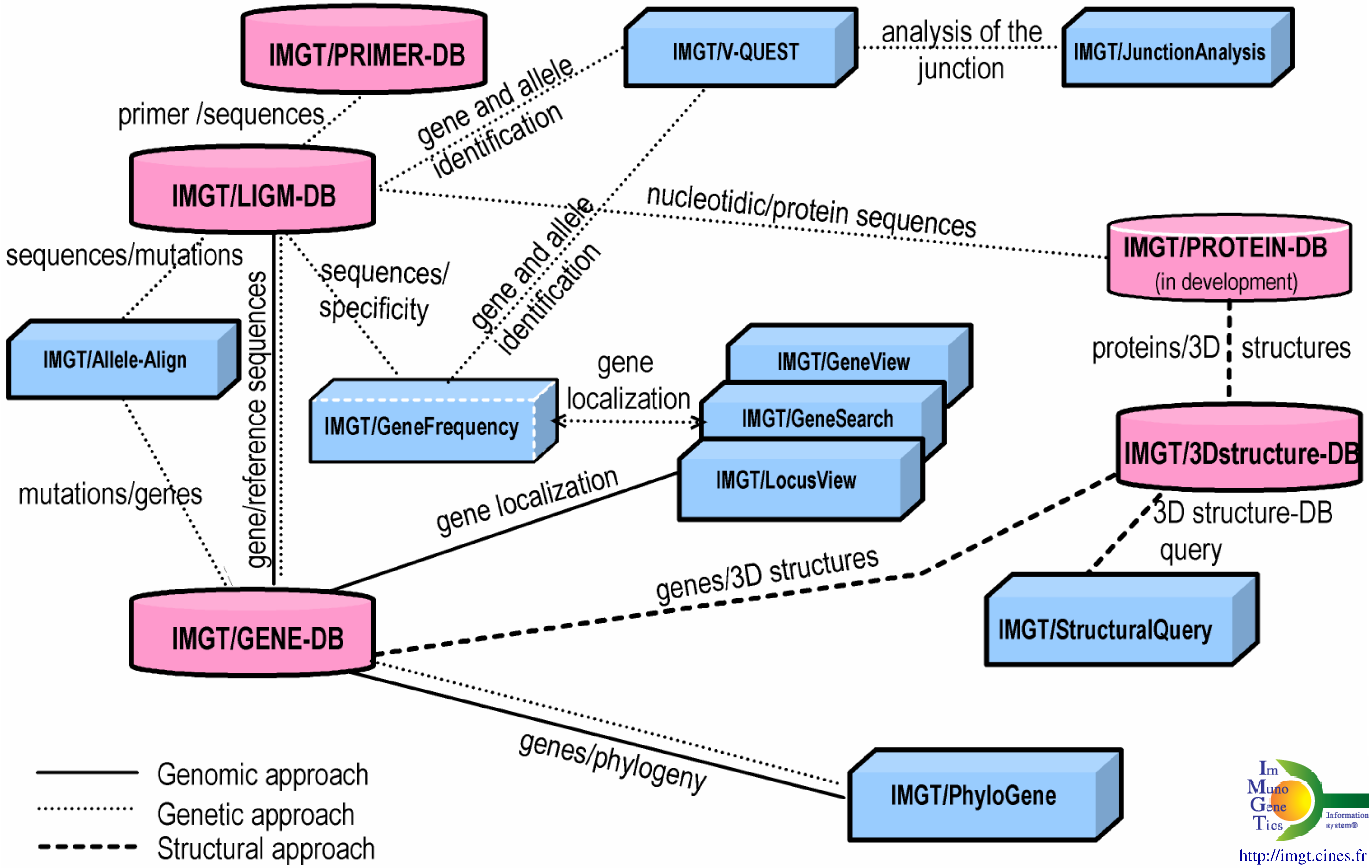
(b) Be aware that less than 6 nucleotides of the J have been aligned, please check the alignment in A. Detailed view
(c) Alternative solutions may be found, please check the alignment for this sequence in A. Detailed view

B. Synthesis results: Junction are sorted per V gene

http://imgt.cines.fr



Input	V name	3'V-REGION	P	N	P	5'J-REGION	J name	Vmut	Jmut	Ngc
AJ230273 |HSA230273 .	IGLV1-40*01	tgccagtcctatgacagcagcctgagtggtt.				..gggtgttc	IGLJ3*02	0	0	0/0
AJ230247 |HSA230247 .	IGLV1-44*01	tgtgcagcatgggatgacagcctgaatggtc.		t		ttgggtgttc	IGLJ3*02	0	0	0/1
AJ230257 |HSA230257 .	IGLV1-44*01	tgtgcagcatgggatgacagcctgaatggt..				.tgggtgttc	IGLJ3*02	0	0	0/0
AJ230258 |HSA230258 .	IGLV1-44*01	tgtgcagcatgggatgacagcctgaatgg...		cg		..gggtgttc	IGLJ3*02	0	0	2/2
AJ230260 |HSA230260 .	IGLV1-44*01	tgtgcagcatgggatgacagcctgaatggt..				tgttgtattc	IGLJ2*01	0	1	0/0
AJ230266 |HSA230266 .	IGLV1-44*01	tgtgcagcatgggatgacagcctgaatggt..				.tgggtgttc	IGLJ3*02	0	0	0/0
AJ230268 |HSA230268 .	IGLV1-44*01	tgtgcagcatgggatgacagcctgaatggtc.		gct	a	tgtggtattc	IGLJ2*01	0	0	2/3
AJ230269 |HSA230269 .	IGLV1-44*01	tgtgcagcatgggatgacagcctgaatggtcc		ct	a	tgtggtattc	IGLJ2*01	0	0	1/2
AJ230271 |HSA230271 .	IGLV1-44*01	tgtgcagcatgggatgacagcctgaatggt..		g		..gggtgttc	IGLJ3*02	0	0	1/1
AJ230275 |HSA230275 .	IGLV1-44*01	tgtgcagcatgggatgacagcctgaatggtc.		ag	aa	ttgggtgttc	IGLJ3*02	0	0	1/2
AJ230274 |HSA230274 .	IGLV1-47*01	tgtgcaggatgggatgacagcctgagtg....				..tggtattc	IGLJ2*01	1	0	0/0
AJ230279 |HSA230279 .	IGLV1-47*01	tgtgcagcatgggatgacagcctgagtggtcc				...ggtgttc	IGLJ3*02	0	0	0/0
AJ230243 |HSA230243 .	IGLV1-47*01	tgtgcaacatgggatgacagcctgactggt..				.tgggtgttc	IGLJ3*02	2	0	0/0
AJ230234 |HSA230234 .	IGLV1-51*01	tgcggaacatgggatagcagcctgagtgctgg		agg		.gctgtgttc	IGLJ7*01	0	0	2/3
AJ230249 |HSA230249 .	IGLV1-51*01	tgcggagcatgggatagcagcctgagtgctgg		a		....gtgttc	IGLJ3*02	1	0	0/1
AJ230251 |HSA230251 .	IGLV1-51*01	tgcggagcatgggatagcagcctgagtgctgg		a		....gtgttc	IGLJ3*02	1	0	0/1
AJ230272 |HSA230272 .	IGLV1-51*01	tgcggaacatgggatagcagcctgagtgctgg		agg		...tgtcttc	IGLJ1*01	0	0	2/3
AJ230278 |HSA230278 .	IGLV1-51*01	tgcggaacatgggatagcagcctgagtgctgg				...ggtattc	IGLJ2*01	0	0	0/0
AJ230262 |HSA230262 .	IGLV10-54*01	tgctcagcatgggacagcagcctcattg....				...ggtgttc	IGLJ3*02	1	0	0/0
AJ230236 |HSA230236 .	IGLV10-54*02	tgctcagcattggacagcagcctcagtgctca				.tgggtgttc	IGLJ3*02	0	0	0/0
AJ230235 |HSA230235 .	IGLV2-11*01	tgctgctcatatacaagcagtgccactt..			aa	ttatgtcttc	IGLJ1*01	5	0	0/0
AJ230261 |HSA230261 .	IGLV2-11*01	tgctgctcatatacaagcagtgccactt..		aaa		.tatgtcttc	IGLJ1*01	5	0	0/3
AJ230263 |HSA230263 .	IGLV2-11*01	tgctgctcatatacaagcagtgccactt..		aac		...ggtattc	IGLJ2*01	5	0	1/3
AJ230246 |HSA230246 .	IGLV2-14*01	tgcagctcatatacaagcagcagcactctc	ga		a	ttatgtcttc	IGLJ1*01	0	0	0/0



IMGT/PRIMER-DB

IMGT/V-QUEST

analysis of the junction

IMGT/JunctionAnalysis

primer /sequences

gene and allele identification

IMGT/LIGM-DB

nucleotidic/protein sequences

IMGT/PROTEIN-DB
(in development)

sequences/mutations

sequences/ specificity

gene and allele identification

gene/reference sequences

IMGT/Allele-Align

proteins/3D structures

gene localization

IMGT/GeneView

IMGT/GeneSearch

IMGT/GeneFrequency

IMGT/LocusView

IMGT/3Dstructure-DB

mutations/genes

gene localization

3D structure-DB query

genes/3D structures

IMGT/StructuralQuery

IMGT/GENE-DB

genes/phylogeny

IMGT/PhyloGene

Genomic approach

Genetic approach

Structural approach

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Who is using IMGT?

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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