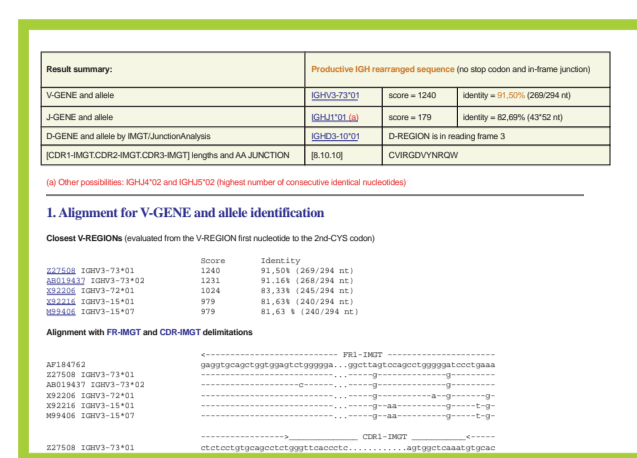


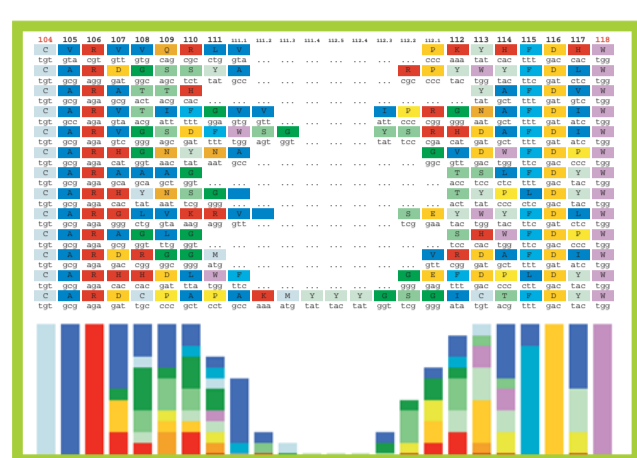
# IMGT® tools

## Sequence analysis



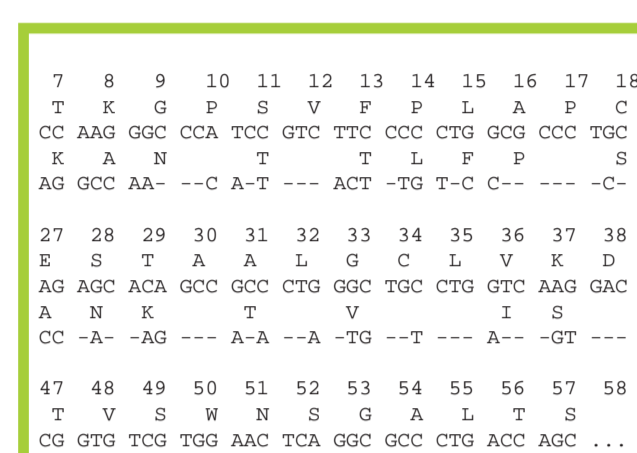
### IMGT/V-QUEST

LIGM (Montpellier)  
Brochet, X. et al.,  
*Nucleic Acids Res.*, 36, W503-W508 (2008)



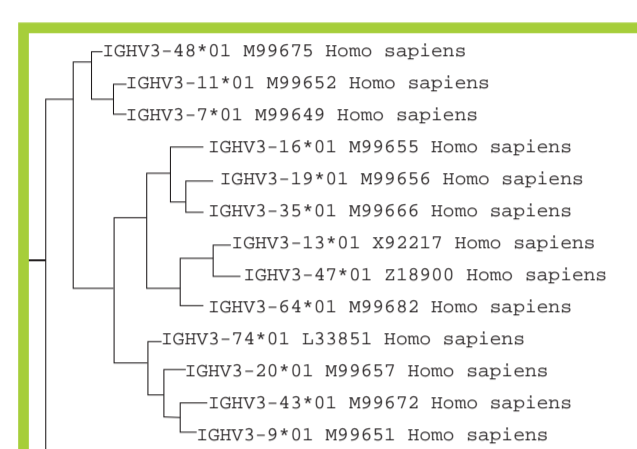
### IMGT/JunctionAnalysis

LIGM  
Yousfi Monod, M. et al.,  
*Bioinformatics*, 20, 1379-1385 (2004)



### IMGT/Allele-Align

LIGM  
Lefranc, M.-P.,  
*Immunome Res.*, 1:3 (2005)



### IMGT/PhyloGene

LIGM  
Elemento, O. and Lefranc, M.-P.,  
*Dev. Comp. Immunol.*, 27, 763-779 (2003)



### IMGT/DomainDisplay

LIGM  
Lefranc, M.-P. et al.,  
*Dev. Comp. Immunol.*, 29, 917-938 (2005)

**IMGT/V-QUEST** (V-QUery and STandardization) is a highly customized and integrated system for IG and TR standardized V-J and V-D-J sequence analysis. This tool analyses an input of up to fifty IG or TR germline or rearranged variable nucleotide sequences. IMGT/V-QUEST results comprise, for rearranged sequences, the identification of the V, D and J genes and alleles, nucleotide alignments by comparison with the IMGT/V-QUEST reference directory, delimitation of the FR-IMGT and CDR-IMGT, protein translation, result of IMGT/JunctionAnalysis, description of the mutations and IMGT Collier de Perles (2D representation) of the variable domain.

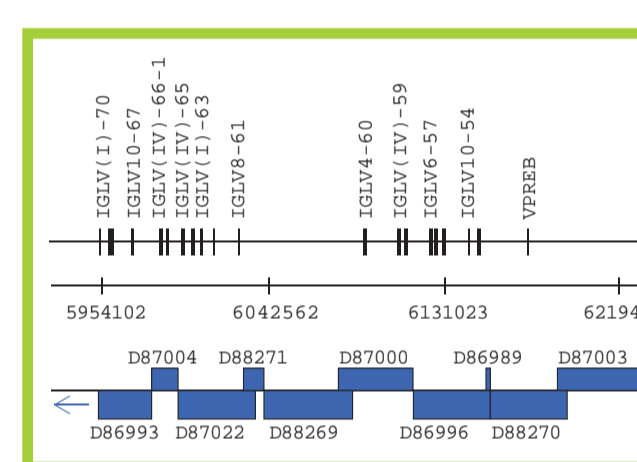
**IMGT/JunctionAnalysis** is a tool, complementary to IMGT/V-QUEST, which provides a thorough analysis of the V-J and V-D-J junctions of the IG and TR rearranged genes. In the case of V-D-J junctions (IGH, TRB and TRD), it identifies the D-GENE and allele involved in the rearrangements by comparison with the IMGT reference directory. IMGT/JunctionAnalysis delimits precisely the P and N regions of the V-J and V-D-J junctions.

**IMGT/Allele-Align** allows the comparison of two alleles highlighting the nucleotide and amino acid differences.

**IMGT/PhyloGene** is a tool for gene evolution analysis of the variable regions and constant domains of the IG and TR. This integrated software package computes and draws phylogenetic trees from nucleotide sequences with gaps according to the IMGT unique numbering.

**IMGT/DomainDisplay** allows queries for IMGT Alignments of domains of the IgSF and MhcSF superfamilies. Alignments are provided based on the IMGT unique numbering for V-DOMAIN and V-LIKE-DOMAIN, C-DOMAIN and C-LIKE-DOMAIN, G-DOMAIN and G-LIKE-DOMAIN.

## Genome analysis



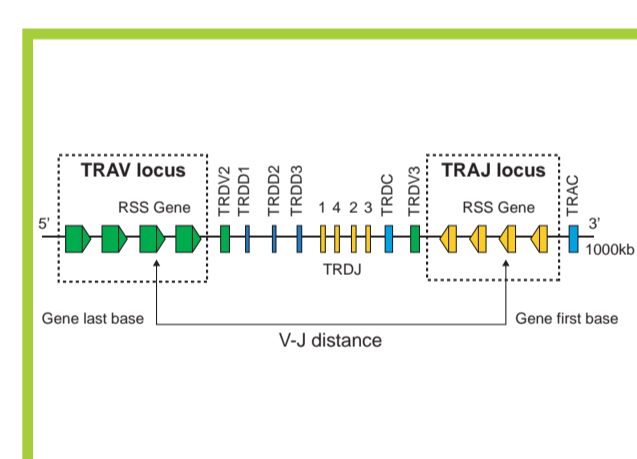
### IMGT/LocusView

### IMGT/GeneView

### IMGT/GeneSearch

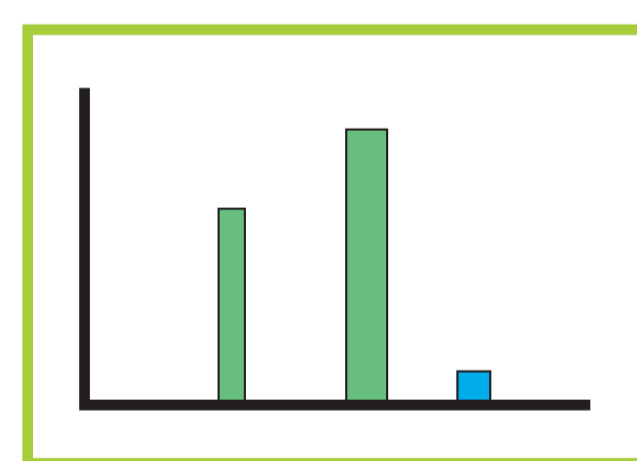
### IMGT/CloneSearch

LIGM  
Lefranc, M.-P.,  
*Immunome Res.*, 1:3 (2005)



### IMGT/GeneInfo

TIMC and ICH (Grenoble)  
Baum, T.P. et al.,  
*BMC Bioinformatics*, 7, 224 (2006)



### IMGT/GeneFrequency

LIGM  
Lefranc, M.-P. et al.,  
*In Silico Biology*, 5, 45-60 (2005)

IMGT® genome analysis tools manage the locus organization and gene location and provide the display of physical maps for the human and mouse IG, TR and MHC loci.

**IMGT/LocusView** allows to view a locus and to zoom on a given area.

**IMGT/GeneView** allows to view a given gene in a locus.

**IMGT/GeneSearch** allows to search for genes in a locus based on IMGT® gene names, functionality or localization on the chromosome.

**IMGT/CloneSearch** allows to search for clones corresponding to genes in IMGT/LocusView.

**IMGT/GeneInfo** provides information on data resulting from the mechanisms of V-J and V-D-J gene rearrangements in the T cell receptor (TR) loci of *Homo sapiens* and *Mus musculus*.

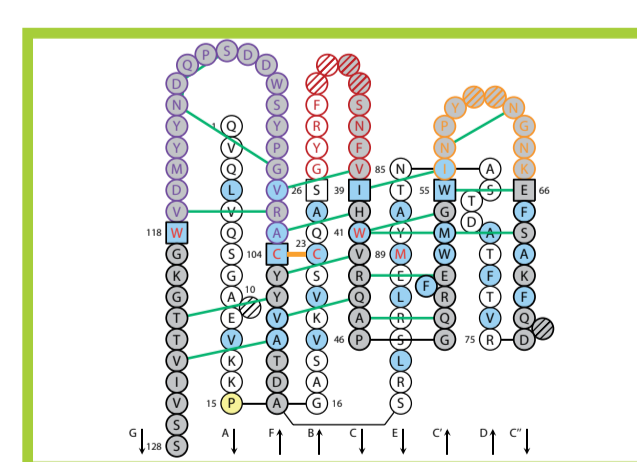
**IMGT/GeneFrequency** provides IG and TR gene histograms proportional to the number of IMGT/LIGM-DB gDNA and cDNA rearranged sequences and localized at the V, D and J gene positions along the loci. IMGT/GeneFrequency is available for human (*Homo sapiens*) and mouse (*Mus musculus*).

## 3D structure analysis



### IMGT/DomainGapAlign

LIGM  
Ehrenmann, F. et al.,  
*Nucleic Acids Res.*, 38, D301-307 (2010)



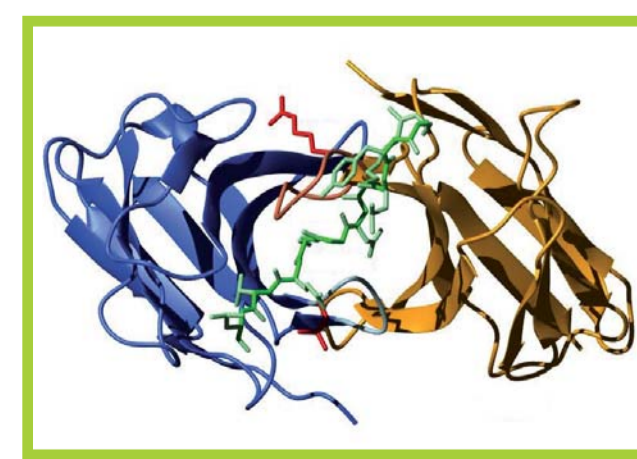
### IMGT/Collier-de-Perles

LIGM  
Kaas, Q. et al.,  
*Brief. Funct. Genomic Proteomic*, 6, 253-264 (2007)



### IMGT/DomainSuperimpose

LIGM  
Lefranc, M.-P. et al.,  
*Nucleic Acids Res.*, 33, D593-D597 (2005)



### IMGT/StructuralQuery

LIGM  
Kaas, Q. et al.,  
*Nucl. Acids. Res.*, 32, D208-D210 (2004)

**IMGT/DomainGapAlign** allows to align and "IMGT-gap" your domain amino acid sequence. The input sequence is displayed, aligned with the closest germline V-REGION or closest C-DOMAIN of the IMGT domain directory and with gaps according to the IMGT unique numbering for V-REGION, C-DOMAIN and C-LIKE-DOMAIN. It also allows to obtain IMGT Collier de Perles through the associated IMGT/Collier-de-Perles tool.

**IMGT/Collier-de-Perles** allows to make your own IMGT Collier de Perles starting from an amino acid sequence with gaps according to the IMGT unique numbering for V-DOMAIN and V-LIKE-DOMAIN, C-DOMAIN and C-LIKE-DOMAIN, G-DOMAIN and G-LIKE-DOMAIN. IMGT/Collier-de-Perles of V and C types can be displayed on one or two layers. This tool is also reached through IMGT/DomainGapAlign for amino acid sequences for which gaps need to be identified.

**IMGT/DomainSuperimpose** allows to superimpose two IMGT domain 3D structures from IMGT/3Dstructure-DB.

**IMGT/StructuralQuery** is a tool which allows to retrieve the IMGT/3Dstructure-DB entries per domain type and using amino acid structural criteria. The query can be performed using a form or writing a complex query.