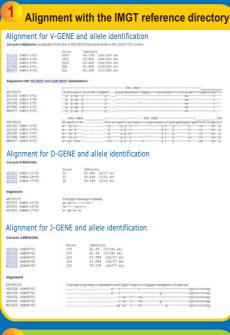# IMGT/V-QUEST and IMGT/JunctionAnalysis for antibody engineering

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http://imgt.cines.fr

Im Muno Gene Tics Information system®

RESULTS FOR EACH SEQUENCE

1 Alignment with the IMGT reference directory

Alignment for V-GENE and allele identification

Closest V-REGIONs (evaluated from the V-REGION first nucleotide to the 2nd-CYS codon)

Alignment with FR-IMGT and CDR-IMGT delimitations

Alignment for D-GENE and allele identification

Closest D-REGIONs

Alignment for J-GENE and allele identification

Closest J-REGIONs

2 IMGT numbering and translation

V-REGION alignment according to the IMGT unique numbering

V-REGION translation

3 Results of IMGT/JunctionAnalysis

Results of IMGT/JunctionAnalysis

Maximum number of accepted mutations in: 3'V-REGION = 2, D-REGION = 4, 5'J-REGION = 2

Analysis of the JUNCTION

D-REGION is in reading frame 3.

Click on mutated (underlined) nucleotide to see the original one

Translation of the JUNCTION

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

Be aware that some allele reference sequences may be incomplete or from cDNAs. In those cases, IMGT/JunctionAnalysis users automatically the allele *01 for the analysis of the JUNCTION

4 Analysis of the mutations

V-REGION mutation table

V-REGION mutation statistics

Mutation hot spots (motifs and positions in germline V-REGION)

NEW!

IMGT/V-QUEST+JCTA QUERY PAGE

WELCOME ! to IMGT/V-QUEST

RESULTS FOR EACH SEQUENCE

SYNTHETIC VIEW PER ALLELE

NEW!

IMGT/V-QUEST and IMGT/JunctionAnalysis, parts of IMGT®, the international ImMunoGeneTics information system®, are the first and so far unique online tools that provide a standardized and exhaustive characterization of recombinant antibodies, from nucleotide sequences to graphical amino acid sequence 2D representations (IMGT Colliers de Perles).

• IMGT/V-QUEST compares the sequences with the IMGT reference directory, displays the nucleotide and protein alignments according to the IMGT unique numbering and provides an extensive analysis of the mutations.

• IMGT/JunctionAnalysis analyses accurately the junctions of antibody rearranged sequences (IGHD genes and alleles, N- and P-REGION, "gc" content, amino acid physicochemical properties, pI).

Giudicelli et al. Nucleic Acids Res 32:435-440 (2004).
Yousfi Monod et al. Bioinformatics 20:379-385 (2004).

5 IMGT/Collier de Perles

AF245315;CDR-IMGT lengths:[8.8.16]

Color menu for the 11 IMGT amino acid classes
Pommié et al. J.Mol. Recognit. 17:17-32 (2004)

SYNTHETIC VIEW PER ALLELE

1 Alignment of a batch of sequences with the closest germline allele

Alignment for V-GENE

NEW!

2 IMGT numbering and translation

V-REGION alignment according to the IMGT unique numbering

V-REGION translation

NEW!

3 Results of IMGT/JunctionAnalysis

Analysis of the JUNCTIONs

Translation of the JUNCTIONs

NEW!

4 Protein display and frequency of amino acids

Protein display

Protein display with coloured AA according to the AA IMGT Classes

NEW!

Protein display (mutations displayed)

V-REGION most frequently occurring AA per position and per FR-IMGT and CDR-IMGT

NEW!