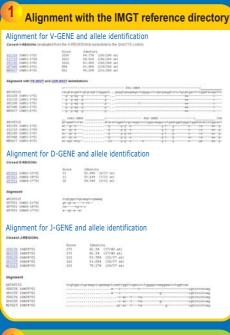
IMGT/V-QUEST and IMGT/JunctionAnalysis for antibody engineering

Véronique Giudicelli, Xavier Brochet, Gérard Lefranc, Marie-Paule Lefranc IMGT®, the international ImMunoGeneTics information system®, LIGM, Université Montpellier II, CNRS UPR1142, IGH 141 rue de la Cardonille, 34396 MONTPELLIER cedex 05, France Marie-Paule.Lefranc@igh.cnrs.fr



RESULTS FOR EACH SEQUENCE



2 IMGT numbering and translation

V-REGION	alignment according to the IMGT unique numbering
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IMGT/V-QUEST+JCTA QUERY PAGE

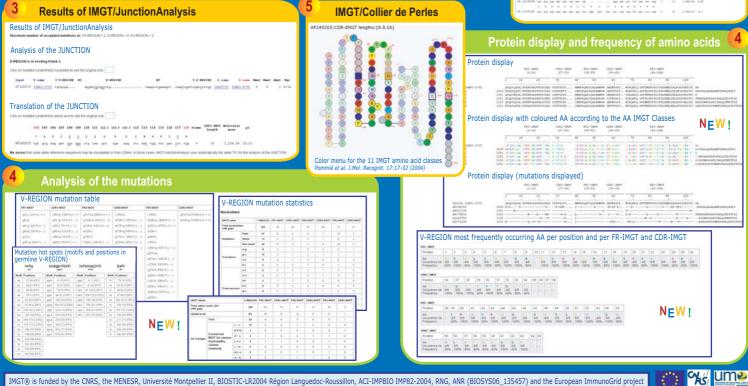
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IMGT/V-QUEST and **IMGT/JunctionAnalysis**, parts of IMGT®, the international ImMunoGeneTics information system®, are the first and so far unique online tools that provide a standardized and exhaustive characterization of recombinant antibodies, from 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)



SYNTHETIC VIEW PER ALLELE

Alignment of a batch of sequences with the closest germline allele

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IMGT numbering and translation

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Results of IMGT/JunctionAnalysis

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