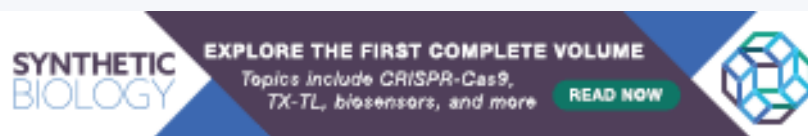


IMGT/V-QUEST, an integrated software program for immunoglobulin and T cell receptor V-J and V-D-J rearrangement analysis.

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IMGT/V-QUEST, an integrated software program for immunoglobulin and T cell receptor V-J and V-D-J rearrangement analysis



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Nucleic Acids Research, Volume 32, Issue suppl_2, 1 July 2004, Pages W435–W440, <https://doi.org/10.1093/nar/gkh412>

Published: 01 July 2004

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Abstract

IMGT/V-QUEST, for 'V-QUERy and STandardization', is an integrated software program which analyses the immunoglobulin (IG) and T cell receptor (TR) rearranged nucleotide sequences. The extraordinary diversity of the IG and TR repertoires (10^{12} antibodies and 10^{12} TR per individual) results from several mechanisms at the DNA level: the combinatorial diversity of the variable (V), diversity (D) and joining (J) genes, the N-diversity and, for IG, the somatic mutations. IMGT/V-QUEST identifies the V, D and J genes and alleles by alignment with the germline IG and TR gene and allele sequences of the IMGT reference directory. IMGT/V-QUEST delimits the structurally important features, frameworks and complementarity-determining regions (the last of these forming the antigen binding site), on the basis of the IMGT unique numbering. The tool localizes the somatic mutations of the IG rearranged sequences. IMGT/V-QUEST also dynamically displays a graphical two-dimensional representation, or IMGT Collier de Perles, of the IG and TR variable regions. Moreover, IMGT/V-QUEST can interact with IMGT/JunctionAnalysis for the detailed description of the V-J and V-D-J junctions, and with IMGT/PhyloGene for the construction of phylogenetic trees. IMGT/V-QUEST is currently available for human and mouse, and partly for non-human primates, sheep, chondrichthyes and teleostei. IMGT/V-QUEST is freely available at <http://imgt.cines.fr>.

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