

IMGT/HighV-QUEST: A High-Throughput System and Web Portal for the Analysis of Rearranged Nucleotide Sequences of Antigen Receptors

- High-Throughput Version of IMGT/V-QUEST -

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IMGT/HighV-QUEST has been developed by IMGT®, the international ImMunoGeneTics Information System® to answer the problematic of the analysis of the antigen receptor data from Next-Generation Sequencing (NGS). The analysis of the expressed repertoires of antigen receptors - immunoglobulins (IG) or antibodies and T cell receptors - represents a crucial challenge for the study of the adaptive immune response in normal and disease-related situations because of the complexity and huge number of sequences (10^{12} IG and 10^{12} TR per individual). IMGT/HighV-QUEST, the high-throughput version of IMGT/V-QUEST, can analyse batches of more than 100,000 IG and TR rearranged sequences in one run, according to concepts of IMGT/ONTOLOGY. IMGT/HighV-QUEST is a secure system and a web portal. It requires user identification for data confidentiality and all data transactions are performed over a secure web connection provided by HTTPS technologies. It provides a simple user interface accessed via a classical web browser and which is similar to IMGT/V-QUEST.

Lefranc, Marie-Paule and al., Nucleic Acids Res., 37, 1006-1012, 2009.
Brochet, X. and al., Nucleic Acids Res., 36:W503-508, 2008.

Giudicelli, V. and Lefranc, M.-P., Bioinformatics, 15:1047-1054, 1999.
Duroux, P. and al., Biochimie, 90:570-583, 2008.

Analysis Submission

User must provide a title for the analysis and select the species and the receptor type of the sequences to be analysed. Sequences must be in FASTA format in a text file that will be uploaded. "Selection for results" and "Advanced parameters" options are similar to those of IMGT/V-QUEST.

Analysis title: (50 characters or less)

Species:

Receptor type: Immunoglobulin (IG) T cell Receptor (TR)

Sequences are from a single individual: Not indicated

Give the path access to a local file containing your sequences in FASTA format Browse...

Selection for results

A. Detailed View Nb of nucleotides per line in alignments: 60

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
7. V-REGION translation
8. V-REGION protein display
9. V-REGION mutation and AA change table
10. V-REGION mutation and AA change statistics
11. V-REGION mutation hotspots
12. Sequences of V-, V-J or V-D-REGION (nt and AA) with gaps in FASTA
13. Annotation by IMGT/Automat

B. Files in CSV

1. Summary
2. IMGT-gapped-nt-sequences
3. nt-sequences
4. IMGT-gapped-AA-sequences
5. AA-sequences
6. Junction
7. V-REGION-mutation-table
8. V-REGION-nt-mutation-statistics
9. V-REGION-AA-mutation-statistics
10. V-REGION-mutation-hot-spots
11. Parameters

C. Advanced parameters

Selection of IMGT reference directory set F+ORF+in-frame P With all alleles With allele *only*
Search for insertions and deletions Yes No
Parameters for IMGT/JunctionAnalysis Nb of accepted D-GENE in IGH JUNCTION default
Nb of accepted mutations: default in 3V-REGION
default in D-REGION
default in 5J-REGION
Parameters for "Detailed view":
Nb of nucleotides to exclude in 5' of the V-REGION for the evaluation of the nb of mutations (in results 9 and 10)
Nb of nucleotides to add (or exclude) in 3' of the V-REGION for the evaluation of the alignment score (in results 1)

