Resource Summary Report

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IMGT/GENE-DB

RRID:SCR_006964
Type: Tool

Proper Citation

IMGT/GENE-DB (RRID:SCR_006964)

Resource Information

URL: http://www.imgt.org/IMGTindex/IMGTgene-db.html

Proper Citation: IMGT/GENE-DB (RRID:SCR_006964)

Description: IMGT/GENE-DB is the comprehensive IMGT genome database for immunoglobulin (IG) and T cell receptor (TR) genes from human and mouse, and, in development, from other vertebrates. IMGT/GENE-DB is the international reference for the IG and TR gene nomenclature and works in close collaboration with the HUGO Nomenclature Committee, Mouse Genome Database and genome committees for other species. IMGT/GENE-DB allows a search of IG and TR genes by locus, group and subgroup, which are CLASSIFICATION concepts of IMGT-ONTOLOGY. Short cuts allow the retrieval gene information by gene name or clone name. Direct links with configurable URL give access to information usable by humans or programs. An IMGT/GENE-DB entry displays accurate gene data related to genome (gene localization), allelic polymorphisms (number of alleles, IMGT reference sequences, functionality, etc.) gene expression (known cDNAs), proteins and structures (Protein displays, IMGT Colliers de Perles). It provides internal links to the IMGT sequence databases and to the IMGT Repertoire Web resources, and external links to genome and generalist sequence databases. IMGT/GENE-DB manages the IMGT reference directory used by the IMGT tools for IG and TR gene and allele comparison and assignment, and by the IMGT databases for gene data annotation.

Abbreviations: IMGT/GENE-DB

Resource Type: narrative resource, database, international standard specification, data or information resource, standard specification

Defining Citation: PMID:15608191

Keywords: bio.tools

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Resource Name: IMGT/GENE-DB

Resource ID: SCR_006964

Alternate IDs: nif-0000-03012, biotools:IMGt_GENE-Db

Alternate URLs: https://bio.tools/IMGT_GENE-DB

Old URLs: http://imgt.cines.fr, http://imgt.cines.fr/cgi-bin/GENElect.jv

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250417T065259+0000

Ratings and Alerts

No rating or validation information has been found for IMGT/GENE-DB.

No alerts have been found for IMGT/GENE-DB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 74 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Deng W, et al. (2024) An allelic atlas of immunoglobulin heavy chain variable regions reveals antibody binding epitope preference resilient to SARS-CoV-2 mutation escape. Frontiers in immunology, 15, 1471396.

McIntire KM, et al. (2024) Maturation of germinal center B cells after influenza virus vaccination in humans. The Journal of experimental medicine, 221(8).

O'Brien H, et al. (2024) A modular protein language modelling approach to immunogenicity prediction. PLoS computational biology, 20(11), e1012511.

Jensen MF, et al. (2024) Enhancing TCR specificity predictions by combined pan- and peptide-specific training, loss-scaling, and sequence similarity integration. eLife, 12.

Gu W, et al. (2024) Single-Cell Antigen Receptor Sequencing in Pigs with Influenza. bioRxiv : the preprint server for biology.

Asashima H, et al. (2023) PD-1highCXCR5-CD4+ peripheral helper T cells promote CXCR3+ plasmablasts in human acute viral infection. Cell reports, 42(1), 111895.

Arnaud M, et al. (2022) Sensitive identification of neoantigens and cognate TCRs in human solid tumors. Nature biotechnology, 40(5), 656.

Unterman A, et al. (2022) Single-cell multi-omics reveals dyssynchrony of the innate and adaptive immune system in progressive COVID-19. Nature communications, 13(1), 440.

Kato T, et al. (2021) Peripheral T cell receptor repertoire features predict durable responses to anti-PD-1 inhibitor monotherapy in advanced renal cell carcinoma. Oncoimmunology, 10(1), 1862948.

Jiang R, et al. (2021) Single-cell immunophenotyping of the skin lesion erythema migrans identifies IgM memory B cells. JCI insight, 6(12).

Bai Y, et al. (2021) Improving the genome assembly of rabbits with long-read sequencing. Genomics, 113(5), 3216.

Hoehn KB, et al. (2021) Human B cell lineages associated with germinal centers following influenza vaccination are measurably evolving. eLife, 10.

Ma L, et al. (2021) Analysis of the heterogeneity of the BCR H-CDR3 repertoire in the bone marrow and spleen of 3-, 12-, and 20-month old mice. Immunity & ageing : I & A, 18(1), 17.

Lu Y, et al. (2021) CD4+ follicular regulatory T cells optimize the influenza virus-specific B cell response. The Journal of experimental medicine, 218(3).

Yang X, et al. (2021) Novel Allele Detection Tool Benchmark and Application With Antibody Repertoire Sequencing Dataset. Frontiers in immunology, 12, 739179.

Wei T, et al. (2021) Generation of neoantigen-specific T cells for adoptive cell transfer for treating head and neck squamous cell carcinoma. Oncoimmunology, 10(1), 1929726.

Fuchs T, et al. (2021) Trilineage Sequencing Reveals Complex TCR? Transcriptomes in Neutrophils and Monocytes Alongside T Cells. Genomics, proteomics & bioinformatics, 19(6), 926.

Kim W, et al. (2021) Germinal centre-driven maturation of B cell response to SARS-CoV-2

vaccination. bioRxiv : the preprint server for biology.

Turner JS, et al. (2020) Human germinal centres engage memory and naive B cells after influenza vaccination. Nature, 586(7827), 127.

Ye X, et al. (2020) High-Throughput Sequencing-Based Analysis of T Cell Repertoire in Lupus Nephritis. Frontiers in immunology, 11, 1618.