Resource Summary Report

Generated by Kravitz on Sep 10, 2026

HomoloGene

RRID:SCR_002924
Type: Tool

Proper Citation

HomoloGene (RRID:SCR_002924)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/homologene

Proper Citation: HomoloGene (RRID:SCR_002924)

Description: Automated system for constructing putative homology groups from complete gene sets of wide range of eukaryotic species. Databse that provides system for automatic detection of homologs, including paralogs and orthologs, among annotated genes of sequenced eukaryotic genomes. HomoloGene processing uses proteins from input organisms to compare and sequence homologs, mapping back to corresponding DNA sequences. Reports include homology and phenotype information drawn from Online Mendelian Inheritance in Man, Mouse Genome Informatics, Zebrafish Information Network, Saccharomyces Genome Database and FlyBase.

Abbreviations: HomoloGene

Synonyms: NCBI HomoloGene

Resource Type: data or information resource, database, service resource

Defining Citation: PMID:23193264

Keywords: homolog, paralog, ortholog, genome, gene, protein, protein alignment, phenotype, conserved domain, homology, amino acid sequence, cell, dna, gold standard

Availability: Free, Freely availalbe

Resource Name: HomoloGene

Resource ID: SCR_002924

Alternate IDs: nif-0000-02975, r3d100010781, OMICS_01544

Alternate URLs: http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=homologene, https://doi.org/10.17616/R3889F

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260905T133119+0000

Ratings and Alerts

No rating or validation information has been found for HomoloGene.

No alerts have been found for HomoloGene.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 459 mentions in open access literature.

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

Guo Y, et al. (2026) Analysis of the Phenotype and Gene Mutations of Two Families With Combined Mutations of Anticoagulant Protein Genes. Molecular genetics & genomic medicine, 14(4), e70191.

Xu F, et al. (2026) SERPINC1 mutations and thrombotic events in inherited antithrombin deficiency: a study on the han population of East China. Orphanet journal of rare diseases, 21(1).

Corkish C, et al. (2026) Plasmacytoid Dendritic Cells Exhibit High Transferrin Receptor Expression Without Iron Accumulation. European journal of immunology, 56(6), e70219.

Guo YL, et al. (2026) [Clinical and genetic analysis of two families with combined defect in antithrombin and protein C genes]. Zhonghua xue ye xue za zhi = Zhonghua xueyexue zazhi, 47(2), 166.

Wang M, et al. (2026) Exploration of the Pathogenic Mechanism of the Factor XIII A Subunit in a Patient With Congenital Factor XIII Deficiency. Molecular genetics & genomic medicine, 14(1), e70193.

Xu C, et al. (2026) A Novel LMX1A Frameshift Variant Underlies Familial Phenotypic Heterogeneity in DFNA7. Human mutation, 2026, 9930672.

Queeno SR, et al. (2026) Profiling the epigenomic landscape of late embryonic and adult mouse hind limb muscles. Scientific reports, 16(1).

Liu Y, et al. (2026) Electrostatic tuning of the pyridoxal-5'-phosphate cofactor site defines pH dependence in type I cystathionine ??-lyases. The Journal of biological chemistry, 302(6), 111469.

Smith GA, et al. (2026) Murine osteosarcoma recapitulates the driver landscape and genomic complexity of osteosarcoma evolution in humans. bioRxiv : the preprint server for biology.

Weigel C, et al. (2026) SPNS2 exports sphingosine-1-phosphate and imports glucose. Nature communications, 17(1).

Chen Y, et al. (2026) DL-GapFilling: a novel deep learning framework for improved plant genome gap filling. Briefings in bioinformatics, 27(1).

Peyton M, et al. (2026) Single-cell analysis reveals neuroprotective histone deacetylase inhibitor pathways. Alzheimer's & dementia : the journal of the Alzheimer's Association, 22(2), e71108.

Chen T, et al. (2026) Identification and Experimental Validation of Biomarkers Associated with PI3K/AKT Signaling Pathway in Spinal Cord Injury. Molecular neurobiology, 63(1).

Ma K, et al. (2026) Multilabel prediction of virus target proteins via multimodal graph representation learning. PLoS computational biology, 22(5), e1014320.

Oesinghaus L, et al. (2026) Transforming the cytokine literature into a resource for experimental analysis and discovery. bioRxiv : the preprint server for biology.

Chen X, et al. (2025) dentification and characterization of novel PAX4 variants in patients with suspected MODY9. BMJ open diabetes research & care, 13(6).

Yoon JW, et al. (2025) Th1-poised naive CD4 T cell subpopulation reflects anti-tumor immunity and autoimmune disease. Nature communications, 16(1), 1962.

Dhungel S, et al. (2025) Structural assembly of the PAS domain drives the catalytic activation of metazoan PASK. Proceedings of the National Academy of Sciences of the United States of America, 122(12), e2409685122.

Wu K, et al. (2025) Cytosolic WPRa4 and Plastoskeletal PMI4 Proteins Mediate Touch Response in a Model Organism Arabidopsis. Molecular & cellular proteomics : MCP, 24(7), 101015.

Sun Q, et al. (2025) Identification of a novel missense variant in the LMX1B gene associated with nail-patella syndrome in a Chinese family. Frontiers in genetics, 16, 1574076.