

Resource Summary Report

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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. Database 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, service resource, database

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 available

Resource Name: HomoloGene

Resource ID: SCR_002924

Alternate IDs: nif-0000-02975, OMICS_01544

Alternate URLs: <http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=homologene>

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 385 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Beryozkin A, et al. (2024) Best Disease: Global Mutations Review, Genotype-Phenotype Correlation, and Prevalence Analysis in the Israeli Population. Investigative ophthalmology & visual science, 65(2), 39.

Chen Z, et al. (2024) Pan-cancer analysis revealing the multidimensional expression and prognostic and immunologic roles of TGFB1 in cancer. The Journal of international medical research, 52(1), 3000605231221361.

Petrova E, et al. (2024) Comparative analyses of Netherton syndrome patients and Spink5 conditional knock-out mice uncover disease-relevant pathways. Communications biology, 7(1), 152.

Mei H, et al. (2024) Multi-omics and pathway analyses of genome-wide associations implicate regulation and immunity in verbal declarative memory performance. Alzheimer's research & therapy, 16(1), 14.

Kilfeather P, et al. (2024) Single-cell spatial transcriptomic and translatomic profiling of dopaminergic neurons in health, aging, and disease. Cell reports, 43(3), 113784.

Jorstad NL, et al. (2023) Comparative transcriptomics reveals human-specific cortical features. Science (New York, N.Y.), 382(6667), eade9516.

Du ZH, et al. (2023) scPML: pathway-based multi-view learning for cell type annotation from single-cell RNA-seq data. Communications biology, 6(1), 1268.

Wang Q, et al. (2023) Two SOX11 variants cause Coffin-Siris syndrome with a new feature

of sensorineural hearing loss. American journal of medical genetics. Part A, 191(1), 183.

Løseth S, et al. (2023) Late-onset sensory-motor axonal neuropathy, a novel SLC12A6-related phenotype. Brain : a journal of neurology, 146(3), 912.

Wang L, et al. (2023) TimeTalk uses single-cell RNA-seq datasets to decipher cell-cell communication during early embryo development. Communications biology, 6(1), 901.

Lin Q, et al. (2023) Identification of genetic variants in two families with Keratoconus. BMC medical genomics, 16(1), 299.

Perazza LR, et al. (2023) Protectin DX as a therapeutic strategy against frailty in mice. GeroScience, 45(4), 2601.

Voelker P, et al. (2023) Molecular Mechanisms for Changing Brain Connectivity in Mice and Humans. International journal of molecular sciences, 24(21).

Li XF, et al. (2023) Macrophages promote anti-androgen resistance in prostate cancer bone disease. The Journal of experimental medicine, 220(4).

Zargar S, et al. (2023) An Insight into Wheat Germ Oil Nutrition, Identification of Its Bioactive Constituents and Computer-Aided Multidimensional Data Analysis of Its Potential Anti-Inflammatory Effect via Molecular Connections. Life (Basel, Switzerland), 13(2).

Tu KJ, et al. (2023) Mining cancer genomes for change-of-metabolic-function mutations. Communications biology, 6(1), 1143.

Zargar S, et al. (2023) Food Toxicity of Mycotoxin Citrinin and Molecular Mechanisms of Its Potential Toxicity Effects through the Implicated Targets Predicted by Computer-Aided Multidimensional Data Analysis. Life (Basel, Switzerland), 13(4).

Molendijk J, et al. (2023) urPTMdb/TeaProt: Upstream and Downstream Proteomics Analysis. Journal of proteome research, 22(2), 302.

Ma W, et al. (2023) Dermokine mutations contribute to epithelial-mesenchymal transition and advanced melanoma through ERK/MAPK pathways. PloS one, 18(7), e0285806.

Boeddrich A, et al. (2023) A proteomics analysis of 5xFAD mouse brain regions reveals the lysosome-associated protein Arl8b as a candidate biomarker for Alzheimer's disease. Genome medicine, 15(1), 50.