Resource Summary Report

Generated by NIF on May 24, 2025

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: service resource, data or information 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

Funding:

Availability: Free, Freely availalbe

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

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250523T054314+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 403 mentions in open access literature.

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

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.

Cai Z, et al. (2024) Selective deletion of E3 ubiquitin ligase FBW7 in VE-cadherin-positive cells instigates diffuse large B-cell lymphoma in mice in vivo. Cell death & disease, 15(3), 212.

Zhang Z, et al. (2024) The influences of ApoE isoforms on endothelial adherens junctions and actin cytoskeleton responding to mCRP. Angiogenesis, 27(4), 861.

Werren EA, et al. (2024) A de novo variant in PAK2 detected in an individual with Knobloch type 2 syndrome. bioRxiv : the preprint server for biology.

Dhungel S, et al. (2024) Nutrient Signaling-Dependent Quaternary Structure Remodeling Drives the Catalytic Activation of metazoan PASK. bioRxiv : the preprint server for biology.

Qian C, et al. (2024) The ?-Chain Mutation p.Arg17Stop Impairs Fibrinogen Synthesis and Secretion: A Nonsense Mutation Associated With Hypofibrinogenemia. Journal of clinical laboratory analysis, 38(24), e25123.

Khan ST, et al. (2024) Single-Cell Meta-Analysis Uncovers the Pancreatic Endothelial Cell Transcriptomic Signature and Reveals a Key Role for NKX2-3 in PLVAP Expression. Arteriosclerosis, thrombosis, and vascular biology, 44(12), 2596.

Jia Z, et al. (2024) Metabolic reprogramming and heterogeneity during the decidualization process of endometrial stromal cells. Cell communication and signaling : CCS, 22(1), 385.

O'Reilly ME, et al. (2024) linc-ADAIN, a human adipose lincRNA, regulates adipogenesis by modulating KLF5 and IL-8 mRNA stability. Cell reports, 43(5), 114240.

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.

Moraes B, et al. (2024) Aurora kinase as a putative target to tick control. Parasitology, 151(9), 983.

Sun Y, et al. (2024) Three Copies of zbed1 Specific in Chromosome W Are Essential for Female-Biased Sexual Size Dimorphism in Cynoglossus semilaevis. Biology, 13(3).

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.

Werren EA, et al. (2024) Biallelic variants in CSMD1 are implicated in a neurodevelopmental disorder with intellectual disability and variable cortical malformations. Cell death & disease, 15(5), 379.

Zhang K, et al. (2024) The spectrum of factor XI deficiency in Southeast China: four recurrent variants can explain most of the deficiencies. Orphanet journal of rare diseases, 19(1), 224.

Wang S, et al. (2024) Evolutionary conservation analysis of human sphingomyelin metabolism pathway genes. Heliyon, 10(23), e40810.

Chen Y, et al. (2024) Predicting novel biomarkers for early diagnosis and dynamic severity monitoring of human ulcerative colitis. Frontiers in genetics, 15, 1429482.

Zhang Y, et al. (2024) Predicting intercellular communication based on metabolite-related ligand-receptor interactions with MRCLinkdb. BMC biology, 22(1), 152.

Yang JC, et al. (2024) Enhanced Proteomic Coverage in Tissue Microenvironment by Immune Cell Subtype Library-Assisted DIA-MS. Molecular & cellular proteomics : MCP, 23(7), 100792.

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.