Resource Summary Report

Generated by RRID on Apr 8, 2025

InParanoid: Eukaryotic Ortholog Groups

RRID:SCR_006801
Type: Tool

Proper Citation

InParanoid: Eukaryotic Ortholog Groups (RRID:SCR_006801)

Resource Information

URL: http://inparanoid.sbc.su.se/cgi-bin/index.cgi

Proper Citation: InParanoid: Eukaryotic Ortholog Groups (RRID:SCR_006801)

Description: Collection of pairwise comparisons between 100 whole genomes generated by a fully automatic method for finding orthologs and in-paralogs between TWO species. Ortholog clusters in the InParanoid are seeded with a two-way best pairwise match, after which an algorithm for adding in-paralogs is applied. The method bypasses multiple alignments and phylogenetic trees, which can be slow and error-prone steps in classical ortholog detection. Still, it robustly detects complex orthologous relationships and assigns confidence values for in-paralogs. The original data sets can be downloaded.

Abbreviations: InParanoid

Synonyms: Inparanoid eukaryotic ortholog database

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

Defining Citation: PMID:19892828, PMID:18055500, PMID:15608241, PMID:11743721

Keywords: protein, ortholog, genome, drosophila pseudoobscura, duplication, entamoeba histolytica, escherichia colik12, eukaryotic, gasterosteus aculeatus, gene, aedes aegypti, apis mellifera, bos taurus, caenorhabditis remanei, candida glabrata, canis familiaris, ciona intestinalis, cryptococcus neoformans, debaromyces hansenii, dictyostelium discoideum, genomic, homolog, inparalog, kluyveromyces lactis, macaca mulatta, monodelphis domestica, orthology, oryza sativa, outparalog, proteome, tetraodon nigroviridis, xenopus tropicalis, blast, proteome, ortholog cluster, cluster, in-paralog, paralog, automatic clustering, genome comparison, FASEB list

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Karolinska Institutet; Stockholm; Sweden ;
Pfizer Corporation

Availability: Acknowledgement requested

Resource Name: InParanoid: Eukaryotic Ortholog Groups

Resource ID: SCR_006801

Alternate IDs: nif-0000-03024

Old URLs: http://www.cgb.ki.se/inparanoid/

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250407T215619+0000

Ratings and Alerts

No rating or validation information has been found for InParanoid: Eukaryotic Ortholog Groups.

No alerts have been found for InParanoid: Eukaryotic Ortholog Groups.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 185 mentions in open access literature.

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

Swapna LS, et al. (2024) ToxoNet: A high confidence map of protein-protein interactions in Toxoplasma gondii. PLoS computational biology, 20(6), e1012208.

Feng B, et al. (2024) Unique trajectory of gene family evolution from genomic analysis of nearly all known species in an ancient yeast lineage. bioRxiv : the preprint server for biology.

Yang J, et al. (2023) GelFAP v2.0: an improved platform for Gene functional analysis in Gastrodia elata. BMC genomics, 24(1), 164.

Meyer A, et al. (2023) New hypotheses of cell type diversity and novelty from orthology-driven comparative single cell and nuclei transcriptomics in echinoderms. eLife, 12.

Liu Q, et al. (2023) PhcX Is a LqsR-family response regulator that contributes to Ralstonia solanacearum virulence and regulates multiple virulence factors. mBio, 14(5), e0202823.

Naizabekov S, et al. (2023) Comparative genomic analysis of Methylocystis sp. MJC1 as a platform strain for polyhydroxybutyrate biosynthesis. PloS one, 18(5), e0284846.

Duan G, et al. (2023) HGD: an integrated homologous gene database across multiple species. Nucleic acids research, 51(D1), D994.

Foley S, et al. (2022) Evolutionary analyses of genes in Echinodermata offer insights towards the origin of metazoan phyla. Genomics, 114(4), 110431.

Shigenobu S, et al. (2022) Genomic and transcriptomic analyses of the subterranean termite Reticulitermes speratus: Gene duplication facilitates social evolution. Proceedings of the National Academy of Sciences of the United States of America, 119(3).

Wang J, et al. (2022) Computational methods, databases and tools for synthetic lethality prediction. Briefings in bioinformatics, 23(3).

Huang Z, et al. (2022) Comparative Genomic Analysis Reveals Potential Pathogenicity and Slow-Growth Characteristics of Genus Brevundimonas and Description of Brevundimonas pishanensis sp. nov. Microbiology spectrum, 10(2), e0246821.

Huan Y, et al. (2021) Label-Free Liquid Chromatography-Mass Spectrometry Proteomic Analysis of the Urinary Proteome for Measuring the Escitalopram Treatment Response From Major Depressive Disorder. Frontiers in psychiatry, 12, 700149.

Li MY, et al. (2021) Effects of Huangqin Decoction on ulcerative colitis by targeting estrogen receptor alpha and ameliorating endothelial dysfunction based on system pharmacology. Journal of ethnopharmacology, 271, 113886.

De Kegel B, et al. (2021) Comprehensive prediction of robust synthetic lethality between paralog pairs in cancer cell lines. Cell systems, 12(12), 1144.

Beatman TR, et al. (2021) A nomenclature for echinoderm genes. Database : the journal of biological databases and curation, 2021.

Sahu S, et al. (2021) Ongoing repair of migration-coupled DNA damage allows planarian adult stem cells to reach wound sites. eLife, 10.

Toren D, et al. (2021) Systems biology analysis of lung fibrosis-related genes in the bleomycin mouse model. Scientific reports, 11(1), 19269.

Gai Z, et al. (2021) Whole Genome Level Analysis of the Wnt and DIX Gene Families in Mice and Their Coordination Relationship in Regulating Cardiac Hypertrophy. Frontiers in genetics, 12, 608936.

Schartl M, et al. (2021) The Developmental and Genetic Architecture of the Sexually Selected Male Ornament of Swordtails. Current biology : CB, 31(5), 911.

Iqbal Z, et al. (2021) Toward Integrated Multi-Omics Intervention: Rice Trait Improvement and Stress Management. Frontiers in plant science, 12, 741419.