Resource Summary Report

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PhylomeDB

RRID:SCR_007850
Type: Tool

Proper Citation

PhylomeDB (RRID:SCR_007850)

Resource Information

URL: http://phylomedb.bioinfo.cipf.es

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Description: Database for phylomes, that is, complete collections of phylogenetic trees for all proteins encoded in a given genome. It aims at providing a repository of high-quality phylogenies and alignments for proteins encoded in model species. To derive a phylome, each protein encoded in a given genome is used as a seed to retrieve its homologs in other complete genomes. These sequences are aligned and processed to derive reliable phylogenies using several phylogenetic methods. Besides providing the evolutionary history of the gene families, phylomeDB includes phylogeny based predictions of orthology and paralogy relationships.

Synonyms: PhylomeDB

Resource Type: data or information resource, database

Defining Citation: PMID:17962297, PMID:21075798, PMID:24275491

Keywords: Genome-wide collections, gene phylogenies, phylogenetic trees collection, proteins encoded, genome, bio.tools, FASEB list

Funding:

Availability: Free, Freely Available

Resource Name: PhylomeDB

Resource ID: SCR_007850

Alternate IDs: nif-0000-03281, biotools:PhylomeDb

Alternate URLs: https://bio.tools/PhylomeDB

Record Creation Time: 20220129T080244+0000

Record Last Update: 20250410T065631+0000

Ratings and Alerts

No rating or validation information has been found for PhylomeDB.

No alerts have been found for PhylomeDB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 51 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Allio R, et al. (2024) OrthoMaM v12: a database of curated single-copy ortholog alignments and trees to study mammalian evolutionary genomics. Nucleic acids research, 52(D1), D529.

Menzies JAC, et al. (2024) A microRNA that controls the emergence of embryonic movement. eLife, 13.

Marcet-Houben M, et al. (2024) Genomics of the expanding pine pathogen Lecanosticta acicola reveals patterns of ongoing genetic admixture. mSystems, 9(3), e0092823.

Del Olmo V, et al. (2023) Origin of fungal hybrids with pathogenic potential from warm seawater environments. Nature communications, 14(1), 6919.

González-Lozano KJ, et al. (2023) Identification and Characterization of Dmct: A Cation Transporter in Yarrowia lipolytica Involved in Metal Tolerance. Journal of fungi (Basel, Switzerland), 9(6).

Smith ML, et al. (2022) Using all Gene Families Vastly Expands Data Available for Phylogenomic Inference. Molecular biology and evolution, 39(6).

Mixão V, et al. (2022) Genome analysis of five recently described species of the CUG-Ser clade uncovers Candida theae as a new hybrid lineage with pathogenic potential in the Candida parapsilosis species complex. DNA research : an international journal for rapid publication of reports on genes and genomes, 29(2).

Nevers Y, et al. (2022) The Quest for Orthologs orthology benchmark service in 2022. Nucleic acids research, 50(W1), W623.

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

Morel B, et al. (2022) SpeciesRax: A Tool for Maximum Likelihood Species Tree Inference from Gene Family Trees under Duplication, Transfer, and Loss. Molecular biology and evolution, 39(2).

Marcet-Houben M, et al. (2021) Comparative Genomics Used to Predict Virulence Factors and Metabolic Genes among Monilinia Species. Journal of fungi (Basel, Switzerland), 7(6).

Khvorykh G, et al. (2021) A Workflow for Selection of Single Nucleotide Polymorphic Markers for Studying of Genetics of Ischemic Stroke Outcomes. Genes, 12(3).

Mixão V, et al. (2021) Genome analysis of Candida subhashii reveals its hybrid nature and dual mitochondrial genome conformations. DNA research : an international journal for rapid publication of reports on genes and genomes, 28(3).

Lebovitz C, et al. (2021) Loss of Parkinson's susceptibility gene LRRK2 promotes carcinogen-induced lung tumorigenesis. Scientific reports, 11(1), 2097.

Reddy MR, et al. (2021) PAP90, a novel rice protein plays a critical role in regulation of D1 protein stability of PSII. Journal of advanced research, 30, 197.

Schall PZ, et al. (2021) Cross-species meta-analysis of transcriptome changes during the morula-to-blastocyst transition: metabolic and physiological changes take center stage. American journal of physiology. Cell physiology, 321(6), C913.

Chen Y, et al. (2020) Protein Interface Complementarity and Gene Duplication Improve Link Prediction of Protein-Protein Interaction Network. Frontiers in genetics, 11, 291.

Gerdol M, et al. (2020) Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. Genome biology, 21(1), 275.

van Leeuwen J, et al. (2020) Systematic analysis of bypass suppression of essential genes. Molecular systems biology, 16(9), e9828.

Fernández R, et al. (2020) Gene gain and loss across the metazoan tree of life. Nature ecology & evolution, 4(4), 524.