Resource Summary Report

Generated by RRID on May 7, 2025

Tree families database

RRID:SCR_013401
Type: Tool

Proper Citation

Tree families database (RRID:SCR_013401)

Resource Information

URL: http://www.treefam.org

Proper Citation: Tree families database (RRID:SCR_013401)

Description: A database of phylogenetic trees of animal genes. It aims at developing a curated resource that gives reliable information about ortholog and paralog assignments, and evolutionary history of various gene families. TreeFam defines a gene family as a group of genes that evolved after the speciation of single-metazoan animals. It also tries to include outgroup genes like yeast (S. cerevisiae and S. pombe) and plant (A. thaliana) to reveal these distant members.TreeFam is also an ortholog database. Unlike other pairwise alignment based ones, TreeFam infers orthologs by means of gene trees. It fits a gene tree into the universal species tree and finds historical duplications, speciations and losses events. TreeFam uses this information to evaluate tree building, guide manual curation, and infer complex ortholog and paralog relations.The basic elements of TreeFam are gene families that can be divided into two parts: TreeFam-A and TreeFam-B families. TreeFam-B families are automatically created. They might contain errors given complex phylogenies. TreeFam-A families are manually curated from TreeFam-B ones. Family names and node names are assigned at the same time. The ultimate goal of TreeFam is to present a curated resource for all the families. phylogenetic tree, animal, vertebrate, invertebrate, gene, ortholog, paralog, evolutionary history, gene families, single-metazoan animals, outgroup genes like yeast (S. cerevisiae and S. pombe), plant (A. thaliana), historical duplications, speciations, losses, Human, Genome, comparative genomics

Synonyms: Tree families database, TreeFam

Resource Type: data or information resource, database

Keywords: evolutionary history, gene, gene families, genome, animal, comparative genomics, historical duplications, human, invertebrate, losses, ortholog, outgroup genes like yeast (s. cerevisiae and s. pombe), paralog, phylogenetic tree, plant (a. thaliana), single-metazoan animals, speciations, vertebrate, FASEB list

Funding:

Resource Name: Tree families database

Resource ID: SCR_013401

Alternate IDs: nif-0000-03588

Record Creation Time: 20220129T080315+0000

Record Last Update: 20250507T060915+0000

Ratings and Alerts

No rating or validation information has been found for Tree families database.

No alerts have been found for Tree families database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 82 mentions in open access literature.

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

Yan L, et al. (2025) Localization and Molecular Cloning of the ASMT Gene for Melatonin Synthesis in Pigs. International journal of molecular sciences, 26(2).

Ascanelli C, et al. (2024) Manipulating Myc for reparative regeneration. Frontiers in cell and developmental biology, 12, 1357589.

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

Martinez-Garcia M, et al. (2023) GRAS-1 is a novel regulator of early meiotic chromosome dynamics in C. elegans. PLoS genetics, 19(2), e1010666.

Deák G, et al. (2022) Missense Variants Reveal Functional Insights Into the Human ARID Family of Gene Regulators. Journal of molecular biology, 434(9), 167529.

Pan C, et al. (2022) A systematic pan-cancer study demonstrates the oncogenic function of

heterogeneous nuclear ribonucleoprotein C. Aging, 14(6), 2880.

Li ML, et al. (2022) Functional genomics analysis reveals the evolutionary adaptation and demographic history of pygmy lorises. Proceedings of the National Academy of Sciences of the United States of America, 119(40), e2123030119.

Oura S, et al. (2022) Trim41 is required to regulate chromosome axis protein dynamics and meiosis in male mice. PLoS genetics, 18(6), e1010241.

Xue DX, et al. (2022) A high-quality chromosome-level genome of the endangered roughskin sculpin provides insights into its evolution and adaptation. Molecular ecology resources, 22(5), 1892.

Lemonnier T, et al. (2021) The M-phase regulatory phosphatase PP2A-B55? opposes protein kinase A on Arpp19 to initiate meiotic division. Nature communications, 12(1), 1837.

Liu H, et al. (2021) A low dose of bisphenol A stimulates estradiol production by regulating ?-catenin-FOXL2-CYP19A1 pathway in human ovarian granulosa cells. Biochemical and biophysical research communications, 583, 192.

Zhang Y, et al. (2021) The genome of the naturally evolved obesity-prone Ossabaw miniature pig. iScience, 24(9), 103081.

Rudolph J, et al. (2021) HPF1 and nucleosomes mediate a dramatic switch in activity of PARP1 from polymerase to hydrolase. eLife, 10.

Fan HH, et al. (2021) Wdhd1 is essential for early mouse embryogenesis. Biochimica et biophysica acta. Molecular cell research, 1868(6), 119011.

Zhang Z, et al. (2021) The conserved transmembrane protein TMEM-39 coordinates with COPII to promote collagen secretion and regulate ER stress response. PLoS genetics, 17(2), e1009317.

Que T, et al. (2021) The reference genome and transcriptome of the limestone langur, Trachypithecus leucocephalus, reveal expansion of genes related to alkali tolerance. BMC biology, 19(1), 67.

Liu GH, et al. (2021) Dipylidium caninum draft genome - a new resource for comparative genomic and genetic explorations of flatworms. Genomics, 113(3), 1272.

Chen J, et al. (2021) Genome-wide analysis of intermuscular bone development reveals changes of key genes expression and signaling pathways in blunt snout bream (Megalobrama amblycephala). Genomics, 113(1 Pt 2), 654.

Li C, et al. (2021) Bicolor angelfish (Centropyge bicolor) provides the first chromosome-level genome of the Pomacanthidae family. GigaByte (Hong Kong, China), 2021, gigabyte32.

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.