

Resource Summary Report

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PhyloTreePruner

RRID:SCR_012069

Type: Tool

Proper Citation

PhyloTreePruner (RRID:SCR_012069)

Resource Information

URL: <http://sourceforge.net/projects/phylo tree pruner/>

Proper Citation: PhyloTreePruner (RRID:SCR_012069)

Description: A utility that uses a phylogenetic approach to refine orthology inferences made by graph-based (or other) methods.

Resource Type: software resource

Defining Citation: [PMID:24250218](#)

Keywords: applet

Resource Name: PhyloTreePruner

Resource ID: SCR_012069

Alternate IDs: OMICS_04250

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260808T190006+0000

Ratings and Alerts

No rating or validation information has been found for PhyloTreePruner.

No alerts have been found for PhyloTreePruner.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 34 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Liu YX, et al. (2026) HybSuite: An integrated pipeline for hybrid capture phylogenomics from reads to trees. *Applications in plant sciences*, 14(3), e70059.

Kan S, et al. (2024) Cytonuclear Interactions and Subgenome Dominance Shape the Evolution of Organelle-Targeted Genes in the Brassica Triangle of U. *Molecular biology and evolution*, 41(3).

Flury JM, et al. (2023) Potential Contribution of Ancient Introgression to the Evolution of a Derived Reproductive Strategy in Ricefishes. *Genome biology and evolution*, 15(8).

Sonoda GG, et al. (2023) Venomous Noodles: The Evolution of Toxins in Nemertea through Positive Selection and Gene Duplication. *Toxins*, 15(11).

Bilyk KT, et al. (2023) Positive and Relaxed Selective Pressures Have Both Strongly Influenced the Evolution of Cryonotothenioid Fishes during Their Radiation in the Freezing Southern Ocean. *Genome biology and evolution*, 15(4).

Iannello M, et al. (2023) Signatures of Extreme Longevity: A Perspective from Bivalve Molecular Evolution. *Genome biology and evolution*, 15(11).

Cortez T, et al. (2022) Molecular evolution and signatures of selective pressures on Bos, focusing on the Nelore breed (*Bos indicus*). *PloS one*, 17(12), e0279091.

Beric A, et al. (2021) Comparative phylogenetics of repetitive elements in a diverse order of flowering plants (Brassicales). *G3 (Bethesda, Md.)*, 11(7).

Bateman KS, et al. (2021) Identification and Full Characterisation of Two Novel Crustacean Infecting Members of the Family Nudiviridae Provides Support for Two Subfamilies. *Viruses*, 13(9).

Caurcel C, et al. (2021) MolluscDB: a genome and transcriptome database for molluscs. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 376(1825), 20200157.

Berger CA, et al. (2021) Shifts in morphology, gene expression, and selection underlie web loss in Hawaiian Tetragnatha spiders. *BMC ecology and evolution*, 21(1), 48.

Casasa S, et al. (2021) Polyphenism of a Novel Trait Integrated Rapidly Evolving Genes into Ancestrally Plastic Networks. *Molecular biology and evolution*, 38(2), 331.

Lu H, et al. (2021) Yeast metabolic innovations emerged via expanded metabolic network and gene positive selection. *Molecular systems biology*, 17(10), e10427.

Regan T, et al. (2021) Ancestral Physical Stress and Later Immune Gene Family Expansions Shaped Bivalve Mollusc Evolution. *Genome biology and evolution*, 13(8).

Stevens L, et al. (2020) The Genome of *Caenorhabditis bovis*. *Current biology : CB*, 30(6), 1023.

Meng R, et al. (2020) The Deep Evolutionary Relationships of the Morphologically Heterogeneous Nolinoideae (Asparagaceae) Revealed by Transcriptome Data. *Frontiers in plant science*, 11, 584981.

Mabry ME, et al. (2020) Phylogeny and multiple independent whole-genome duplication events in the Brassicales. *American journal of botany*, 107(8), 1148.

Shekhovtsov SV, et al. (2020) Species Delimitation of the *Eisenia nordenskioldi* Complex (Oligochaeta, Lumbricidae) Using Transcriptomic Data. *Frontiers in genetics*, 11, 598196.

DeBiasse MB, et al. (2020) Inferring Tunicate Relationships and the Evolution of the Tunicate Hox Cluster with the Genome of *Corella inflata*. *Genome biology and evolution*, 12(6), 948.

Smythe AB, et al. (2019) Improved phylogenomic sampling of free-living nematodes enhances resolution of higher-level nematode phylogeny. *BMC evolutionary biology*, 19(1), 121.