

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Phylogeny Programs

RRID:SCR_010797

Type: Tool

Proper Citation

Phylogeny Programs (RRID:SCR_010797)

Resource Information

URL: <http://evolution.genetics.washington.edu/phylip/software.html>

Proper Citation: Phylogeny Programs (RRID:SCR_010797)

Description: 392 phylogeny software packages and 54 free web servers describing all known software for inferring phylogenies (evolutionary trees). Submissions are welcome. Programs are listed by methods available, by computer systems on which they work, cross-referenced by method and by computer system, by ones which analyze particular kinds of data, to show the most recent listings, or to show ones most recently changed.

Abbreviations: Phylogeny Programs

Synonyms: Felsenstein's website

Resource Type: analysis service resource, data analysis service, data or information resource, portal, production service resource, service resource, software resource, topical portal

Keywords: phylogeny

Funding: NSF

Availability: Free, The community can contribute to this resource

Resource Name: Phylogeny Programs

Resource ID: SCR_010797

Alternate IDs: OMICS_00219

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260905T132647+0000

Ratings and Alerts

No rating or validation information has been found for Phylogeny Programs.

No alerts have been found for Phylogeny Programs.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Scossa F, et al. (2021) Ancestral sequence reconstruction - An underused approach to understand the evolution of gene function in plants? Computational and structural biotechnology journal, 19, 1579.

Posada D, et al. (2021) Felsenstein Phylogenetic Likelihood. Journal of molecular evolution, 89(3), 134.

Bester PA, et al. (2019) PhyloPi: An affordable, purpose built phylogenetic pipeline for the HIV drug resistance testing facility. PloS one, 14(3), e0213241.

Žiegytė R, et al. (2017) The widespread biting midge *Culicoides impunctatus* (Ceratopogonidae) is susceptible to infection with numerous *Haemoproteus* (Haemoproteidae) species. Parasites & vectors, 10(1), 397.

Duck G, et al. (2016) A Survey of Bioinformatics Database and Software Usage through Mining the Literature. PloS one, 11(6), e0157989.

Bukauskaitė D, et al. (2015) Biting midges (*Culicoides*, Diptera) transmit *Haemoproteus* parasites of owls: evidence from sporogony and molecular phylogeny. Parasites & vectors, 8, 303.

Hong SW, et al. (2011) Phylogeny and divergence times inferred from *rps16* sequence data analyses for *Tricyrtis* (Liliaceae), an endemic genus of north-east Asia. AoB PLANTS, 2011, plr025.

Cottam EM, et al. (2009) Full sequencing of viral genomes: practical strategies used for the amplification and characterization of foot-and-mouth disease virus. Methods in molecular biology (Clifton, N.J.), 551, 217.

Durand PM, et al. (2008) Evolutionary patterning: a novel approach to the identification of potential drug target sites in *Plasmodium falciparum*. PloS one, 3(11), e3685.

Tárraga J, et al. (2007) Phylemon: a suite of web tools for molecular evolution, phylogenetics and phylogenomics. Nucleic acids research, 35(Web Server issue), W38.

Kawakoshi A, et al. (2006) Identification of a natriuretic peptide (NP) in cyclostomes (lamprey and hagfish): CNP-4 is the ancestral gene of the NP family. *General and comparative endocrinology*, 148(1), 41.

Coller HA, et al. (2006) A new description of cellular quiescence. *PLoS biology*, 4(3), e83.

Maurer MH, et al. (2004) The path to enlightenment: making sense of genomic and proteomic information. *Genomics, proteomics & bioinformatics*, 2(2), 123.