

Resource Summary Report

Generated by T1D on Aug 2, 2026

PAUP

RRID:SCR_014931

Type: Tool

Proper Citation

PAUP (RRID:SCR_014931)

Resource Information

URL: <http://paup.sc.fsu.edu>

Proper Citation: PAUP (RRID:SCR_014931)

Description: Software which creates phylogenetic trees from molecular, morphological and/or behavioral data through high speed computer analysis.

Abbreviations: PAUP

Synonyms: Phylogenetic Analysis Using Parsimony

Resource Type: software resource, data visualization software, data processing software, software application, data analysis software

Keywords: phylogenetic tree, phylogeny, evolutionary tree, molecular data, morphological data, behavioral data

Availability: Free

Resource Name: PAUP

Resource ID: SCR_014931

Alternate URLs: http://people.sc.fsu.edu/~dswofford/paup_test/

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260803T040647+0000

Ratings and Alerts

No rating or validation information has been found for PAUP.

No alerts have been found for PAUP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2266 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Frajman B, et al. (2026) Multiple long-distance dispersals accompanied by reduction of body size shaped the evolutionary history of four spurges (*Euphorbia*) endemic to Mediterranean islands. *Plant biology (Stuttgart, Germany)*, 28(1), 178.

Strausfeld NJ, et al. (2025) Cambrian origin of the arachnid brain. *Current biology : CB*, 35(15), 3777.

Zhu Y, et al. (2025) ?New species and records of *Phaeobotryon* (Botryosphaeriales, Botryosphaeriaceae) from *Larix* in China. *MycoKeys*, 112, 1.

White WT, et al. (2025) Reallocation of the magnificent catshark *Proscyllium magnificum* Last & Vongpanich, 2004 to the genus *Ctenacis* Compagno, 1973 (Carcharhiniformes: Proscylliidae). *Journal of fish biology*, 106(2), 523.

Ahmadpour A, et al. (2025) Morphological and Molecular Characterization of a New Section and Two New Species of *Alternaria* from Iran. *Life (Basel, Switzerland)*, 15(6).

Lavrov DV, et al. (2025) Pervasive Mitochondrial tRNA Gene Loss in Clade B of Haplosclerid Sponges (Porifera, Demospongiae). *Genome biology and evolution*, 17(3).

White RT, et al. (2025) 20 years later: unravelling the genomic success of New Zealand's home-grown AK3 community-associated methicillin-resistant *Staphylococcus aureus*. *Microbial genomics*, 11(7).

Chen T, et al. (2025) Deciphering the evolutionary imprints of *Camellia oleifera* Abel.: delineating its distinct phylogeographic structure and demographic history through microsatellite and plastid fragment. *BMC plant biology*, 25(1), 526.

Zhang ZY, et al. (2025) ?Discover hidden taxa of *Erysiphe* section *Erysiphe* fungi (Ascomycota, Erysiphaceae) based on morphology and multilocus phylogeny in China. *MycoKeys*, 118, 119.

Pfordt A, et al. (2025) Phylogenetic analysis of plant-pathogenic and non-pathogenic *Trichoderma* isolates on maize from plants, soil, and commercial bio-products. *Applied and environmental microbiology*, 91(3), e0193124.

Alda F, et al. (2025) Geography is a stronger predictor of diversification of monogenean parasites (Platyhelminthes) than host relatedness in characin fishes of Middle America. *PloS one*, 20(4), e0316974.

Gutiérrez-Escobar AJ, et al. (2025) Global diversity of integrating conjugative elements (ICEs) in *Helicobacter pylori* and their influence on genome architecture. *bioRxiv : the preprint server for biology*.

Sangthong D, et al. (2025) Molecular characterization of *Rhipicephalus microplus* and *Haemaphysalis bispinosa* ticks from cattle across Thailand: Regional identification and evidence of different genetic sub-structures between mainland and peninsular populations. *PloS one*, 20(11), e0337052.

Sigeman H, et al. (2025) The loss of a supergene in obligately polygynous *Formica* wood ant species. *Molecular biology and evolution*, 42(12).

Klimov PB, et al. (2025) The evolutionary history and timeline of mites in ancient soils. *Scientific reports*, 15(1), 13555.

Wu D, et al. (2025) Phylogeographic history of *Parthenocissus* (Vitaceae) in North America based on chloroplast and nuclear DNA sequences. *Frontiers in plant science*, 16, 1521784.

Ahmadpour A, et al. (2025) Diversity of *Alternaria* Section *Nimbya* in Iran, with the Description of Eight New Species. *Journal of fungi* (Basel, Switzerland), 11(3).

Gao W, et al. (2025) Characterization and phylogenetic analysis of the complete mitochondrial genome of *Fomitopsis palustris* (Berk. & M.A. Curtis) Gilb. & Ryvarden, 1985 (Polyporales: Fomitopsidaceae). *Mitochondrial DNA. Part B, Resources*, 10(6), 532.

Tokiwa T, et al. (2025) A vascular filarial nematode in sika deer (*Cervus nippon*): Morphological and molecular characterization of *Elaeophora* (Nematoda: Onchocercidae) in Japan. *International journal for parasitology. Parasites and wildlife*, 27, 101068.

Jamshed S, et al. (2025) Elucidating time divergence and biogeography of *Euonymus hamiltonianus* complex using complete plastome analysis. *Scientific reports*, 15(1), 29905.