

Resource Summary Report

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

PAUP

RRID:SCR_014931

Type: Tool

Proper Citation

PAUP (RRID:SCR_014931)

Resource Information

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

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

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: 20260905T132752+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 2292 mentions in open access literature.

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

Ramassamy JL, et al. (2026) Adult T-cell leukemia/lymphoma in French Guiana (1990-2019): Epidemiology, clinical features, and HTLV-1 genetic diversity in the two main ethnic populations. *International journal of cancer*, 158(6), 1528.

Due??as M, et al. (2026) Revisiting the genus *Hyphodermella* (Basidiomycota, Polyporales) with descriptions of three new species. *MycKeys*, 128, 249.

de Abreu J, et al. (2026) High-Throughput Sequencing Supports Strong Geographical Patterns in the *Cladia aggregata* Complex (Ascomycota, Lecanorales) and Identifies the Asian Clade as an Independent Species. *Journal of fungi (Basel, Switzerland)*, 12(2).

Peng X, et al. (2026) A 5.3-million-year-old deep-sea whale necropolis in the Diamantina Zone. *Nature*, 654(8120), 978.

Cassar O, et al. (2026) HTLV-1 genetic diversity of 52 complete sequences from 14 African countries reveals novel variants and a lack of typical P12/P8 and P30 accessory proteins in HTLV-1b, d, and f genotypes. *Emerging microbes & infections*, 15(1), 2651463.

Sun X, et al. (2026) The Japanese Archipelago sheltered cave lions, not tigers, during the Late Pleistocene. *Proceedings of the National Academy of Sciences of the United States of America*, 123(6), e2523901123.

Sekandarpour P, et al. (2026) Emergence of *Stilbocrea gracilipes* associated with canker and dieback in pomegranate and eucalyptus trees and host-specific responses. *Microbiology spectrum*, 14(3), e0283925.

White RT, et al. (2026) Decentralized nanopore genomics reveals diverse *Klebsiella pneumoniae* and no evidence of patient-patient transmission in a New Zealand hospital. *Microbial genomics*, 12(4).

Camiletti BX, et al. (2026) Influence of fruit maturity and variety on seasonal postharvest fungal diseases and vascular streaking in California Avocados. *PloS one*, 21(6), e0351752.

Springer MS, et al. (2026) Molecular Evidence for the Parallel Evolution of Anosmia in Multiple Odontoceti (Toothed Whales) Clades. *Genes*, 17(6).

Wu XQ, et al. (2026) Two new species of *Pseudocosmospora* (Hypocreales) revealed through morphological and phylogenetic analyses. *MycKeys*, 128, 285.

Badry A, et al. (2026) DNA Barcoding and Phylogenetic Relationship of *Parabuthus liosoma* (Ehrenberg, 1828) (Scorpiones: Buthidae) in Saudi Arabia. *Biology*, 15(4).

Meng W, et al. (2026) Two new species of *Ceratostomella* and *Pararamichloridium* (Sordariomycetes) from Guangdong, China, based on morphological and phylogenetic evidence. *MycKeys*, 133, 259.

Astaraki S, et al. (2026) *Astragalus verus*, a miracle in de-desertification or a surprising niche for ecologically adaptable bacteria? *BMC plant biology*, 26(1).

Eduard J, et al. (2026) New species of *Kudoa* Meglitsch, 1947 (Cnidaria: Myxozoa) infecting the swim bladder musculature of *Batrachoides surinamensis* (Bloch & Shneider) (Batracoidiformes: Batrachoididae). *Systematic parasitology*, 103(2).

Sauerborn E, et al. (2026) Resolving plasmid-encoded carbapenem resistance dynamics and reservoirs in a hospital setting through nanopore sequencing. *Microbial genomics*, 12(2).

Kosushkin SA, et al. (2026) Genome sequencing uncovers the history of the Russian desman's gradual population decline and contributes to the evolutionary history of *Talpidae*. *BMC ecology and evolution*, 26(1), 12.

Kim M, et al. (2026) Molecular identification, phytochemical characterization, and bioactivity evaluation of the unexplored medicinal plant *Phedimus hybridus*. *Scientific reports*, 16(1), 4392.

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.

Butler CC, et al. (2026) Resolving widespread and endemic dinoflagellates (Symbiodiniaceae) mutualistic with Indo-Pacific octocorals reveals differences in specificity based on host phylogeny. *Journal of phycology*, 62(1), 191.