

Resource Summary Report

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DendroPy

RRID:SCR_024197

Type: Tool

Proper Citation

DendroPy (RRID:SCR_024197)

Resource Information

URL: <https://dendropy.org/>

Proper Citation: DendroPy (RRID:SCR_024197)

Description: Software Python library for phylogenetic computing. Provides classes and functions for simulation, processing, and manipulation of phylogenetic trees and character matrices, and supports the reading and writing of phylogenetic data in range of formats, such as NEXUS, NEWICK, NeXML, Phylip, FASTA., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: python-dendropy

Resource Type: software toolkit, software resource, software library

Defining Citation: [PMID:20421198](#)

Keywords: phylogenetic computing, manipulation of phylogenetic trees, reading and writing of phylogenetic data,

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: DendroPy

Resource ID: SCR_024197

Alternate IDs: OMICS_08877

Old URLs: <https://sources.debian.org/src/python3-dendropy/>

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260731T043145+0000

Ratings and Alerts

No rating or validation information has been found for DendroPy.

No alerts have been found for DendroPy.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Light-Maka I, et al. (2025) Bronze Age *Yersinia pestis* genome from sheep sheds light on hosts and evolution of a prehistoric plague lineage. *Cell*.

Thureborn O, et al. (2024) Plastid phylogenomics and cytonuclear discordance in Rubioideae, Rubiaceae. *PloS one*, 19(5), e0302365.

Stefan LM, et al. (2023) Diversity and structure of feather mite communities on seabirds from the north-east Atlantic and Mediterranean Sea. *Scientific reports*, 13(1), 4793.

Lescroart J, et al. (2023) Extensive Phylogenomic Discordance and the Complex Evolutionary History of the Neotropical Cat Genus *Leopardus*. *Molecular biology and evolution*, 40(12).

Derouiche L, et al. (2020) Deep mitochondrial DNA phylogeographic divergence in the threatened aoudad *Ammotragus lervia* (Bovidae, Caprini). *Gene*, 739, 144510.

Sanderson BJ, et al. (2020) A targeted sequence capture array for phylogenetics and population genomics in the Salicaceae. *Applications in plant sciences*, 8(10), e11394.

Guy AJ, et al. (2018) BioStructMap: a Python tool for integration of protein structure and sequence-based features. *Bioinformatics (Oxford, England)*, 34(22), 3942.

Rodriguez ZB, et al. (2018) Multiple origins of green blood in New Guinea lizards. *Science advances*, 4(5), eaao5017.

Castro-Severyn J, et al. (2017) Comparative Genomics Analysis of a New *Exiguobacterium* Strain from Salar de Huasco Reveals a Repertoire of Stress-Related Genes and Arsenic Resistance. *Frontiers in microbiology*, 8, 456.

Ngoc PC, et al. (2016) Complex Evolutionary Dynamics of Massively Expanded Chemosensory Receptor Families in an Extreme Generalist Chelicerate Herbivore. *Genome biology and evolution*, 8(11), 3323.

Larrañán J, et al. (2015) The resurrection of *Neohattoria* Kamim. (Jubulaceae, Marchantiophyta): a six decade systematic conflict resolved through a molecular perspective. *PhytoKeys*(50), 101.

Gumienny R, et al. (2015) Accurate transcriptome-wide prediction of microRNA targets and small interfering RNA off-targets with MIRZA-G. *Nucleic acids research*, 43(3), 1380.

Holzmeyer L, et al. (2015) Phylogeny of *Acronychia* (Rutaceae) and First Insights into Its Historical Biogeography and the Evolution of Fruit Characters. *PloS one*, 10(8), e0136296.

Novitsky V, et al. (2013) Phylogenetic relatedness of circulating HIV-1C variants in Mochudi, Botswana. *PloS one*, 8(12), e80589.

Tavera JJ, et al. (2012) Molecular phylogeny of grunts (Teleostei, Haemulidae), with an emphasis on the ecology, evolution, and speciation history of new world species. *BMC evolutionary biology*, 12, 57.