

Resource Summary Report

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PHYLIP

RRID:SCR_006244

Type: Tool

Proper Citation

PHYLIP (RRID:SCR_006244)

Resource Information

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

Proper Citation: PHYLIP (RRID:SCR_006244)

Description: A free package of software programs for inferring phylogenies (evolutionary trees). The source code is distributed (in C), and executables are also distributed. In particular, already-compiled executables are available for Windows (95/98/NT/2000/me/xp/Vista), Mac OS X, and Linux systems. Older executables are also available for Mac OS 8 or 9 systems.

Abbreviations: PHYLIP

Synonyms: PHYLogeny Inference Package

Resource Type: data processing software, source code, software resource, software application

Keywords: phylogeny prediction, evolutionary tree, bio.tools

Funding: NSF ;
NIGMS ;
DOE

Availability: Free

Resource Name: PHYLIP

Resource ID: SCR_006244

Alternate IDs: nif-0000-06708, OMICS_04240, biotools:phylip

Alternate URLs: <https://bio.tools/phylip>, <https://sources.debian.org/src/phylip/>

Record Creation Time: 20220129T080235+0000

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Ratings and Alerts

No rating or validation information has been found for PHYLIP.

No alerts have been found for PHYLIP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3511 mentions in open access literature.

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

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

Okane I, et al. (2025) *Xylaria iriomotensis* sp. nov. from termite nests and notes on *X. angulosa*. *Botanical studies*, 66(1), 4.

Zhong H, et al. (2025) Benchmarking cross-species single-cell RNA-seq data integration methods: towards a cell type tree of life. *Nucleic acids research*, 53(1).

Li J, et al. (2025) SoyOD: An Integrated Soybean Multi-omics Database for Mining Genes and Biological Research. *Genomics, proteomics & bioinformatics*, 22(6).

Wei F, et al. (2025) Identification of Taihang-chicken-specific genetic markers using genome-wide SNPs and machine learning: BREED-SPECIFIC SNPS OF TAIHANG CHICKEN. *Poultry science*, 104(1), 104585.

Dodd GK, et al. (2025) In silico functional analysis of the human, chimpanzee, and gorilla MHC-A repertoires. *Immunogenetics*, 77(1), 12.

Mendonça P, et al. (2025) The influence of the forest corridors to the north of the Andes on the diversification of the bright-rumped Attila, *Attila spadiceus* (Passeriformes, Tyrannidae), during the climatic oscillations of the middle Pleistocene. *Ecology and evolution*, 15(1),

e70331.

Cho MS, et al. (2024) Phylogenetic relationships and genetic diversity of the Korean endemic *Phedimus latiovalifolius* (Crassulaceae) and its close relatives. *Scientific reports*, 14(1), 16255.

Cui J, et al. (2024) Does coevolution in refugia drive mimicry in bumble bees? Insights from a South Asian mimicry group. *Science advances*, 10(24), eadl2286.

Chen H, et al. (2024) Deciphering the Genetic Landscape: Insights Into the Genomic Signatures of Changle Goose. *Evolutionary applications*, 17(8), e13768.

Hugall AF, et al. (2024) Genetic variation in the brooding brittle-star: a global hybrid polyploid complex? *Royal Society open science*, 11(8), 240428.

Zhu S, et al. (2024) The jacktree genome and population genomics provides insights for the mechanisms of the germination obstacle and the conservation of endangered ornamental plants. *Horticulture research*, 11(8), uhae166.

Knief U, et al. (2024) Evolution of Chromosomal Inversions across an Avian Radiation. *Molecular biology and evolution*, 41(6).

Gàlvez-Morante A, et al. (2024) Dollo Parsimony Overestimates Ancestral Gene Content Reconstructions. *Genome biology and evolution*, 16(4).

Harrison PM, et al. (2024) Intrinsically Disordered Compositional Bias in Proteins: Sequence Traits, Region Clustering, and Generation of Hypothetical Functional Associations. *Bioinformatics and biology insights*, 18, 11779322241287485.

Jácome R, et al. (2024) Structural and Evolutionary Analysis of Proteins Endowed with a Nucleotidyltransferase, or Non-canonical Palm, Catalytic Domain. *Journal of molecular evolution*, 92(6), 799.

Hung SW, et al. (2024) A cyclic dipeptide for salinity stress alleviation and the trophic flexibility of endophyte provide insights into saltmarsh plant-microbe interactions. *ISME communications*, 4(1), ycae041.

Yang FS, et al. (2024) Signatures of Adaptation and Purifying Selection in Highland Populations of *Dasiphora fruticosa*. *Molecular biology and evolution*, 41(6).

Zunino L, et al. (2024) Genomic evidence of genuine wild versus admixed olive populations evolving in the same natural environments in western Mediterranean Basin. *PloS one*, 19(1), e0295043.

Chu L, et al. (2024) Chromosome-level reference genome and resequencing of 322 accessions reveal evolution, genomic imprint and key agronomic traits in adzuki bean. *Plant biotechnology journal*, 22(8), 2173.