

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 2026

PhyML

RRID:SCR_014629

Type: Tool

Proper Citation

PhyML (RRID:SCR_014629)

Resource Information

URL: <http://www.atgc-montpellier.fr/phyml/>

Proper Citation: PhyML (RRID:SCR_014629)

Description: Web phylogeny server based on the maximum-likelihood principle.

Resource Type: software resource, web application, source code

Defining Citation: [DOI:10.1093/molbev/msq060](https://doi.org/10.1093/molbev/msq060)

Keywords: phylogenetic software, phylogeny, maximum likelihood, web server, bio.tools

Availability: Public server, Source code is available on request

Resource Name: PhyML

Resource ID: SCR_014629

Alternate IDs: biotools:phyml, OMICS_04241

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

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260731T042921+0000

Ratings and Alerts

No rating or validation information has been found for PhyML.

No alerts have been found for PhyML.

Data and Source Information

Usage and Citation Metrics

We found 7740 mentions in open access literature.

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

De Luca DG, et al. (2026) Phylogenomic analysis and genetic mechanisms of antifungal resistance in clinical isolates of *Candida glabrata* (*Nakaseomyces glabratus*) from across Canada, 2013-2020. *Microbiology spectrum*, 14(1), e0180325.

Lawson LP, et al. (2026) Whole-genome sequence of the African Common Reed Frog (*Hyperolius viridiflavus viridiflavus*) from Ethiopia. *G3 (Bethesda, Md.)*, 16(1).

Nisa S, et al. (2026) Genotyping Reveals Potential Sources of Human Leptospirosis Outbreaks in Aotearoa New Zealand. *Zoonoses and public health*, 73(1), 54.

De Coninck T, et al. (2025) OsAPSE modulates non-covalent interactions between arabinogalactan protein O-glycans and pectin in rice cell walls. *Frontiers in plant science*, 16, 1588802.

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.

Zilkha N, et al. (2025) Distinct oxytocin populations support seismic social communication and militant behaviors in a naturally solitary wild rodent. *iScience*, 28(12), 114151.

Mochales-Riaño G, et al. (2025) Chromosome-level reference genome for the medically important Arabian horned viper (*Cerastes gasperettii*). *GigaScience*, 14.

Bian C, et al. (2025) Chromosome-level genome assemblies of five *Sinocyclocheilus* species. *GigaByte (Hong Kong, China)*, 2025, gigabyte155.

Fierro Morales JC, et al. (2025) Reduced cell-substrate adhesion formation promotes cell migration in *Dictyostelium*. *Molecular biology of the cell*, 36(8), ar98.

Adams R, et al. (2025) A Tale of Too Many Trees: A Conundrum for Phylogenetic Regression. *Molecular biology and evolution*, 42(3).

Harding KJ, et al. (2025) Temporal and Spatial Dynamics of *Synechococcus* Clade II and Other Microbes in the Eutrophic Subtropical San Diego Bay. *Environmental microbiology*, 27(2), e70043.

Koffi ADK, et al. (2025) A barcode database for insects associated with the spread of the Cocoa Swollen Shoot Virus Disease in Côte d'Ivoire. *Biodiversity data journal*, 13, e144017.

Wardani RK, et al. (2025) Unraveling the Evolutionary Patterns of Genus *Frontonia*: An Integrative Approach with Morphological and Molecular Data. *Biology*, 14(3).

Yue H, et al. (2025) Enzyme Repertoires and Genomic Insights into *Lycium barbarum* Pectin Polysaccharide Biosynthesis. *Genomics, proteomics & bioinformatics*, 22(6).

Mukiibi R, et al. (2025) Integrated functional genomic analysis identifies regulatory variants underlying a major QTL for disease resistance in European sea bass. *BMC biology*, 23(1), 75.

Zealiyas K, et al. (2025) Viral Suppression and HIV Drug Resistance Among Patients on Second-Line Antiretroviral Therapy in Selected Health Facility in Ethiopia. *Viruses*, 17(2).

De Koch MD, et al. (2025) Diverse Anelloviruses Identified in Leporids from Arizona (USA). *Viruses*, 17(2).

Dufresnes C, et al. (2025) Speciation and historical invasions of the Asian black-spined toad (*Duttaphrynus melanostictus*). *Nature communications*, 16(1), 298.

Wang T, et al. (2025) ?*Liliumhuanglongense* (Liliaceae): a newly-discovered species in north-western Sichuan, China. *PhytoKeys*, 252, 9.

De Koch MD, et al. (2025) Novel lineage of anelloviruses with large genomes identified in dolphins. *Journal of virology*, 99(1), e0137024.