

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 5, 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: web application, software resource, 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: 20260805T044330+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 [SPARC SAWG](#) .

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.

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

Martin G, et al. (2025) Unravelling genomic drivers of speciation in *Musa* through genome assemblies of wild banana ancestors. *Nature communications*, 16(1), 961.

Patil MP, et al. (2025) Complete Mitochondrial Genome of *Niphon spinosus* (Perciformes: Niphonidae): Genome Characterization and Phylogenetic Analysis. *Biomolecules*, 15(1).

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

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

Veitova L, et al. (2025) European Brown hare (*Lepus europaeus*) as an accidental host of *Trypanosoma pestanai*. *International journal for parasitology. Parasites and wildlife*, 27, 101079.

Legrand A, et al. (2025) Ancient convergence with prokaryote defense and recent adaptations to lentiviruses in primates characterize the ancestral immune factors SAMD9s. *bioRxiv : the preprint server for biology*.

Lipp NF, et al. (2025) An origin for a eukaryotic lipid transfer protein fold in Asgard archaea. *bioRxiv : the preprint server for biology*.

Dias PJ, et al. (2025) Molecular evolution of the members of the Snq2/Pdr18 subfamily of Pdr transporters in the Hemiascomycete yeasts. *FEMS yeast research*, 25.

Fehér E, et al. (2025) Occurrence of Recombinant Canine Coronavirus, Picodistrovirus, and Circovirus in Red Foxes (*Vulpes vulpes*) Implies Frequent Virus Transmission Events Among Carnivores. *Transboundary and emerging diseases*, 2025, 6681119.

Rousseau C, et al. (2025) A Practical Comparison of Short- and Long-Read Metabarcoding Sequencing: Challenges and Solutions for Plastid Read Removal and Microbial Community Exploration of Seaweed Samples. *Molecular ecology resources*, 25(7), e14129.