

Resource Summary Report

Generated by [NIF](#) on Apr 21, 2025

[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, source code, software resource

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

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

Funding:

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: 20250420T015813+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

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7425 mentions in open access literature.

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

Cesaro S, et al. (2025) A crucial active site network of titratable residues guides catalysis and NAD⁺ binding in human succinic semialdehyde dehydrogenase. *Protein science : a publication of the Protein Society*, 34(1), e70024.

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 *Nippon spinosus* (Perciformes: Nipponidae): 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.

Yerlikaya Z, et al. (2025) Clade-1 Vap virulence proteins of *Rhodococcus equi* are associated with the cell surface and support intracellular growth in macrophages. *PloS one*, 20(1), e0316541.

Ortiz Martín I, et al. (2025) Using active learning methodologies to teach sequence analysis and molecular phylogeny. *Biochemistry and molecular biology education : a bimonthly publication of the International Union of Biochemistry and Molecular Biology*, 53(1), 21.

Oganesyan E, et al. (2025) Population Structure Based on Microsatellite Length Polymorphism, Antifungal Susceptibility Profile, and Enzymatic Activity of *Candida auris* Clinical Isolates in Russia. *Journal of fungi (Basel, Switzerland)*, 11(1).

Huang RY, et al. (2025) Ribotyping *Staphylococcus epidermidis* Using Probabilistic Sequence Analysis and Levenshtein Distance Algorithm. *Current microbiology*, 82(2), 78.

Koirala A, et al. (2025) Bacterial Isolation from Natural Grassland on Nitrogen-Free Agar Yields Many Strains Without Nitrogenase. *Microorganisms*, 13(1).

Kim BK, et al. (2025) Morphological and molecular identification of Particolored bat (*Vespertiliomurinus*) in South Korea: A first record. *Biodiversity data journal*, 13, e135293.

Zhang XL, et al. (2025) Research note: Genetically diverse avian hepatitis E virus identified in chickens with hepatitis-splenomegaly syndrome in Guangdong Province, China. *Poultry science*, 104(1), 104557.

Kamilari E, et al. (2025) *Bacillus safensis* APC 4099 has broad-spectrum antimicrobial activity against both bacteria and fungi and produces several antimicrobial peptides, including the novel circular bacteriocin safencin E. *Applied and environmental microbiology*, 91(1), e0194224.

Li N, et al. (2025) Chromosome-scale genome assembly of three-spotted seahorse (*Hippocampus trimaculatus*) with a unique karyotype. *Scientific data*, 12(1), 49.

Sánchez-Serna G, et al. (2025) Less, but More: New Insights From Appendicularians on Chordate Fgf Evolution and the Divergence of Tunicate Lifestyles. *Molecular biology and evolution*, 42(1).

Georgiev NFK, et al. (2025) Archaeal Signalling Networks-New Insights Into the Structure and Function of Histidine Kinases and Response Regulators of the Methanogenic Archaeon *Methanosarcina acetivorans*. *Environmental microbiology*, 27(2), e70047.

Zhou Q, et al. (2025) Phylogenetic analysis and detection of positive selection in the SIRT gene family across vertebrates. *Scientific reports*, 15(1), 848.

Cerqueira de Araujo A, et al. (2025) Genome sequences of four Ixodes species expands understanding of tick evolution. *BMC biology*, 23(1), 17.

Wang X, et al. (2025) The origin and transmission of HIV-1 CRF80_0107 among two major first-tier cities in China. *BMC infectious diseases*, 25(1), 104.

Vullien A, et al. (2025) The Rich Evolutionary History of the Reactive Oxygen Species Metabolic Arsenal Shapes Its Mechanistic Plasticity at the Onset of Metazoan Regeneration. *Molecular biology and evolution*, 42(1).