Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 17, 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: software resource, web application, source code

Defining Citation: DOI:10.1093/molbev/msq060

Keywords: phylogenic 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: 20250417T065458+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 FDI Lab - SciCrunch.org.

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 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.

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.

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

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.

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

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.

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).