Resource Summary Report

Generated by NIF on Apr 22, 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

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: 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 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.

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.

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.

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.

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

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

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.

Skórzewski G, et al. (2025) Contact zone of slow worms Anguis fragilis Linnaeus, 1758 and Anguis colchica (Nordmann, 1840) in Poland. PeerJ, 13, e18563.

Curantz C, et al. (2025) A positive feedback loop between germ cells and gonads induces and maintains sexual reproduction in a cnidarian. Science advances, 11(2), eadq8220.

Halfmann PJ, et al. (2025) Multivalent S2 subunit vaccines provide broad protection against Clade 1 sarbecoviruses in female mice. Nature communications, 16(1), 462.