

Resource Summary Report

Generated by [RRID](#) on Apr 8, 2025

[PhyloBayes](#)

RRID:SCR_006402

Type: Tool

Proper Citation

PhyloBayes (RRID:SCR_006402)

Resource Information

URL: <http://megasun.bch.umontreal.ca/People/lartillot/www/>

Proper Citation: PhyloBayes (RRID:SCR_006402)

Description: A Bayesian Monte Carlo Markov Chain (MCMC) sampler software for phylogenetic reconstruction. Its main distinguishing feature is the underlying probabilistic model, CAT (Lartillot and Philippe, 2004). CAT is an infinite mixture model accounting for site-specific amino-acid or nucleotide preferences. It is well suited to phylogenomic studies using large multigene alignments.

Abbreviations: PhyloBayes

Synonyms: PhyloBayes - phylogenetic reconstruction using infinite mixtures

Resource Type: software resource

Defining Citation: [PMID:24318999](#)

Keywords: phylogenomic, multigene alignment, alignment, reconstruction

Funding:

Availability: Free, Public

Resource Name: PhyloBayes

Resource ID: SCR_006402

Alternate IDs: OMICS_02212

Record Creation Time: 20220129T080236+0000

Record Last Update: 20250214T183046+0000

Ratings and Alerts

No rating or validation information has been found for PhyloBayes.

No alerts have been found for PhyloBayes.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 473 mentions in open access literature.

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

Giacomelli M, et al. (2025) CAT-Posterior Mean Site Frequencies Improves Phylogenetic Modeling Under Maximum Likelihood and Resolves Tardigrada as the Sister of Arthropoda Plus Onychophora. *Genome biology and evolution*, 17(1).

Klirs Y, et al. (2024) Evolutionary Insights from the Mitochondrial Genome of *Oikopleura dioica*: Sequencing Challenges, RNA Editing, Gene Transfers to the Nucleus, and tRNA Loss. *Genome biology and evolution*, 16(9).

Petitgas C, et al. (2024) Metabolic and neurobehavioral disturbances induced by purine recycling deficiency in *Drosophila*. *eLife*, 12.

Boden JS, et al. (2024) Timing the evolution of phosphorus-cycling enzymes through geological time using phylogenomics. *Nature communications*, 15(1), 3703.

Dai J, et al. (2024) The First Two Complete Mitochondrial Genomes for the Subfamily Meligethinae (Coleoptera: Nitidulidae) and Implications for the Higher Phylogeny of Nitidulidae. *Insects*, 15(1).

Kaur T, et al. (2024) Discovery of a novel *Wolbachia* in Heterodera expands nematode host distribution. *Frontiers in microbiology*, 15, 1446506.

Hacker C, et al. (2024) Biogenesis, inheritance, and 3D ultrastructure of the microsporidian mitosome. *Life science alliance*, 7(1).

Bowles AMC, et al. (2024) Cryogenian Origins of Multicellularity in Archaeplastida. *Genome biology and evolution*, 16(2).

Iqbal Z, et al. (2024) A New Species of *Scymnus* (Coleoptera, Coccinellidae) from Pakistan with Mitochondrial Genome and Its Phylogenetic Implications. *Insects*, 15(5).

Dallagnol LC, et al. (2024) Evolutionary and phylogenetic insights from the mitochondrial genomic analysis of *Diceraeus melacanthus* and *D. furcatus* (Hemiptera: Pentatomidae). *Scientific reports*, 14(1), 12861.

Wu YF, et al. (2024) Complete mitochondrial genome data and phylogenetic analysis of *Papilio macilentus* Janson, 1877 (Lepidoptera: Papilionoidea: Papilionidae). *Mitochondrial DNA. Part B, Resources*, 9(5), 631.

Demura M, et al. (2024) New species and species diversity of *Desmodesmus* (Chlorophyceae, Chlorophyta) in Saga City, Japan. *Scientific reports*, 14(1), 18980.

Galindo LJ, et al. (2024) Transcriptomics of Diphyllatea (CRuMs) from South Pacific crater lakes confirm new cryptic clades. *The Journal of eukaryotic microbiology*, 71(6), e13060.

Rouzé H, et al. (2024) An integrative phylogeography for inferring cryptic speciation in the *Alpheus lottini* species complex, an important coral mutualist. *iScience*, 27(10), 111034.

Nishihara A, et al. (2024) Illuminating the coevolution of photosynthesis and Bacteria. *Proceedings of the National Academy of Sciences of the United States of America*, 121(25), e2322120121.

Wulansari D, et al. (2024) Identification and characterization of archaeal-type FAD synthase as a novel tractable drug target from the parasitic protozoa *Entamoeba histolytica*. *mSphere*, 9(9), e0034724.

Harada R, et al. (2024) Encyclopedia of Family A DNA Polymerases Localized in Organelles: Evolutionary Contribution of Bacteria Including the Proto-Mitochondrion. *Molecular biology and evolution*, 41(2).

Yu D, et al. (2024) Hagfish genome elucidates vertebrate whole-genome duplication events and their evolutionary consequences. *Nature ecology & evolution*, 8(3), 519.

Zhang D, et al. (2024) Phylogenetic placement and comparative analysis of the mitochondrial genomes of *Idiostoloidea* (Hemiptera: Heteroptera). *Ecology and evolution*, 14(5), e11328.

Hu Y, et al. (2024) Complete mitochondrial genome and phylogenetic analysis of *Dollfustrema vaneyi* (Trematoda: Bucephalidae). *BMC genomics*, 25(1), 862.