

Resource Summary Report

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HyPhy

RRID:SCR_016162

Type: Tool

Proper Citation

HyPhy (RRID:SCR_016162)

Resource Information

URL: <http://hyphy.org/>

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Description: Open source software package for comparative sequence analysis using stochastic evolutionary models. Used for analysis of genetic sequence data in particular the inference of natural selection using techniques in phylogenetics, molecular evolution, and machine learning.

Synonyms: HyPhy:Hypothesis Testing using Phylogenies, Hyphy-pt

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource, software toolkit

Defining Citation: [PMID:15509596](#)

Keywords: analysis, genetic, sequence, multiply, alignment, rate, pattern, data, evolution, platform, python, r, bio.tools

Funding: NIGMS R01 ;

NIH R01 AI47745;

NIH U01 AI43638;

NSF DBI-0096033;

NSF DEB-9996118;

University of California Universitywide AIDS Research Program IS02-SD-701;

University of California ;

San Diego Center for AIDS Research/NIAID Developmental Award 2 P30 AI36214

Availability: Free, Available for download, Freely available

Resource Name: HyPhy

Resource ID: SCR_016162

Alternate IDs: SCR_016271, biotools:HyPhy, OMICS_04235

Alternate URLs: <https://sources.debian.org/src/hyphy-pt/>, <https://veg.github.io/hyphy-site/>, <https://github.com/veg/hyphy>, <https://bio.tools/HyPhy>,

License: GNU

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260912T195836+0000

Ratings and Alerts

No rating or validation information has been found for HyPhy.

No alerts have been found for HyPhy.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1586 mentions in open access literature.

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

Wu J, et al. (2026) Pathogenicity of a Canine-Derived Feline Panleukopenia Virus in Cats and NS1 Evolution Associated with Adaptation to Dogs. *Animals : an open access journal from MDPI*, 16(7).

Douglas AJ, et al. (2026) The *Rana sylvatica* skin-secreted antimicrobial peptide (AMP) gene repertoire highlights broader patterns in anuran AMP evolution. *Scientific reports*, 16(1).

Ceballos EG, et al. (2026) Organization of neuropeptide systems in the human brain. *Nature neuroscience*, 29(5), 1212.

Christensen KE, et al. (2026) Signatures of Innovation and Selection in the Extremotolerant Yeast *Kluyveromyces marxianus*. *Genome biology and evolution*, 18(3).

DeSalle R, et al. (2026) Natural selection and language genes in humans. *Scientific reports*, 16(1).

de Siqueira E Silva MC, et al. (2026) Mitochondrial genomes from RNA-Seq reveal phylogeny and selection in *Mepraia* (Hemiptera: Reduviidae). *Molecular genetics and genomics : MGG*, 301(1).

Chen Y, et al. (2026) Delineating the "who-where-how" of persistent HIV epidemics: a 23-year longitudinal genetic network, phylodynamic, and spatial analysis for precise

intervention in rural China. *Emerging microbes & infections*, 15(1), 2671470.

Thompson MG, et al. (2026) Quantitative Dissection of *Agrobacterium* Virulence to Generate a Synthetic Ti Plasmid. *ACS synthetic biology*, 15(4), 1640.

Brcko IC, et al. (2026) Phylodynamic reconstruction of H1N1pdm09 influenza virus transmission in Brazil: a decade of evolutionary dynamics. *Emerging microbes & infections*, 15(1), 2620237.

Kaul A, et al. (2026) Novel genes arise from genomic deletions across the bacterial tree of life. *bioRxiv* : the preprint server for biology.

Fogg LG, et al. (2026) The visual system of the longest-living vertebrate, the Greenland shark. *Nature communications*, 17(1), 39.

Thomas WR, et al. (2026) Genomic comparisons and the adaptive basis of brain size plasticity and chromosomal instability in the Eurasian common shrew. *Molecular biology and evolution*, 43(2).

Kobakhidze S, et al. (2026) Codon usage optimization contributes to evolutionary dynamics of TetM following its acquisition via interspecies and intergeneric recombination events in recipient bacteria. *BMC microbiology*, 26(1).

Helsen J, et al. (2026) Progressive coevolution of the yeast centromere and kinetochore. *Nature*, 651(8107), 1012.

Chen W, et al. (2026) Rapid detection and genomic characterisation of feline chaphamaparvovirus in southwestern China. *Journal of feline medicine and surgery*, 28(1), 1098612X251407164.

Park S, et al. (2026) Structural variation and evolutionary dynamics of plastid genomes in the subgenus *Lychnis* (*Silene*, *Caryophyllaceae*): insights from genome rearrangements and substitution rates. *BMC plant biology*, 26(1), 266.

Hao L, et al. (2026) *Imagin*: An Integrase-Like Gene Conserved Across Malacostracan Crustaceans Derived From a *Ginger1* DNA Transposon. *Genome biology and evolution*, 18(2).

Martin KR, et al. (2026) Major Histocompatibility Complex Immunogenetic Diversity Differs Substantially Across Sea Turtle Species and Genomic Regions. *Genome biology and evolution*, 18(2).

Shi H, et al. (2026) Emergence and evolution of HoBi-like pestivirus clades a and c in sheep from central China. *BMC veterinary research*, 22(1), 82.

Kuang Z, et al. (2026) Genomic insights into chromosomal fusion and its evolutionary implications for zokors. *Molecular biology and evolution*, 43(2).