

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

Defining Citation: [PMID:15509596](#)

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

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NSF DEB-9996118;
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NIGMS R01

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: 20260729T044410+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 1497 mentions in open access literature.

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

Probst TS, et al. (2025) The first de novo genome assembly and annotation of a green-blooded skink (*Prasinohaema* aff. *flavipes*) from a historic museum sample. *The Journal of heredity*, 116(5), 653.

Sun B, et al. (2025) Genomic variants and molecular epidemiological characteristics of dengue virus in China revealed by genome-wide analysis. *Virus evolution*, 11(1), veaf013.

Kong W, et al. (2025) Identification and characterization of a novel reovirus strain isolated from grass carp (*Ctenopharyngodon idella*). *Virology journal*, 22(1), 92.

Bernard C, et al. (2025) Adaptive genomic plasticity in large-genome, broad-host-range vibrio phages. *The ISME journal*, 19(1).

Le Corf A, et al. (2025) Genomic and functional adaptations in guanylate-binding protein 5 (GBP5) highlight specificities of bat antiviral innate immunity. *bioRxiv : the preprint server for biology*.

Liu Y, et al. (2025) Molecular network analysis for detecting HIV transmission clusters: insights and implications. *Frontiers in public health*, 13, 1429464.

Lewitus E, et al. (2025) HIV-1 Vif global diversity and possible APOBEC-mediated response since 1980. *Virus evolution*, 11(1), veae108.

DeLeo DM, et al. (2025) Bioluminescence and environmental light drive the visual evolution of deep-sea shrimp (Oplophoroidea). *Communications biology*, 8(1), 213.

Saccone S, et al. (2025) Origin and Evolution of Genes in Eukaryotes: Mechanisms, Dynamics, and Functional Implications. *Genes*, 16(6).

Policarpo M, et al. (2025) Multiple Horizontal Transfers of Immune Genes Between Distantly Related Teleost Fishes. *Molecular biology and evolution*, 42(5).

Aggarwal SD, et al. (2025) Colonization dynamics of *Streptococcus pneumoniae* are determined by polymorphisms in the BlpAB transporter. *Infection and immunity*, 93(6), e0006125.

Liao H, et al. (2025) The complete chloroplast genomes of four *Aspidopterys* species and a comparison with other Malpighiaceae species. *Scientific reports*, 15(1), 17893.

Zhao TY, et al. (2025) Positive Selection Drives Mitochondrial Gene Rearrangement in Sternorrhyncha (Insecta: Hemiptera). *Ecology and evolution*, 15(7), e71789.

Cai L, et al. (2025) Altered Mitochondrial Respiration Is Associated With Loss of Nuclear-Encoded OXPHOS Genes in Parasitic Broomrapes. *Ecology and evolution*, 15(7), e71737.

Gong T, et al. (2025) Mutation profiling, evolution analysis, molecular dynamics simulation, and functional characterization of Omicron sub-strains. *Virus research*, 360, 199626.

Pospíšilová P, et al. (2025) Analysis of *Treponema pallidum* subsp. *pallidum* predicted outer membrane proteins (OMPeomes) in 21 clinical samples: variant sequences are predominantly surface-exposed. *mSphere*, 10(9), e0021325.

Wang WJ, et al. (2025) Genomic characterization of eight novel *Bartonella* species from bats and ectoparasites reveals phylogenetic diversity and host adaptation. *PLoS neglected tropical diseases*, 19(10), e0013646.

Morales-Saldaña S, et al. (2025) Comparative plastomes of five *Psittacanthus* species: genome organization, structural features, and patterns of pseudogenization and gene loss. *AoB PLANTS*, 17(4), plaf032.

Forni D, et al. (2025) Positive selection at core genes may underlie niche adaptation in *Fusobacterium animalis*. *Gut pathogens*, 17(1), 61.

O?uzo?lu TÇ, et al. (2025) Global Phylogenetic Analysis of the CDV Hemagglutinin Gene Reveals Positive Selection on Key Receptor-Binding Sites. *Viruses*, 17(9).