

Resource Summary Report

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PAML

RRID:SCR_014932

Type: Tool

Proper Citation

PAML (RRID:SCR_014932)

Resource Information

URL: <http://abacus.gene.ucl.ac.uk/software/paml.html>

Proper Citation: PAML (RRID:SCR_014932)

Description: Package of programs for phylogenetic analyses of DNA or protein sequences using maximum likelihood. PAML estimates parameters and tests hypotheses to study the evolutionary process from a phylogenetic tree., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: PAML

Synonyms: Phylogenetic Analysis by Maximum Likelihood, Phylogenetic Analysis by Maximum Likelihood (PAML)

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

Defining Citation: [PMID:9367129](#), [DOI:10.1093/molbev/msm088](#)

Keywords: phylogenetic analysis, dna, protein sequences, evolutionary process, estimate parameters, test hypothesis, maximum likelihood, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: PAML

Resource ID: SCR_014932

Alternate IDs: OMICS_04238, biotools:paml

Alternate URLs: <https://bio.tools/paml>, <https://sources.debian.org/src/paml/>

License: GNU GPL v3

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260801T190510+0000

Ratings and Alerts

No rating or validation information has been found for PAML.

No alerts have been found for PAML.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4930 mentions in open access literature.

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

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. GigaScience, 14.

Liu C, et al. (2025) A chromosome-scale genome assembly of the pioneer plant *Stylosanthes angustifolia*: insights into genome evolution and drought adaptation. GigaScience, 14.

Bian C, et al. (2025) Telomere-to-telomere chromosome-scale genome assemblies of black and golden koi carp variants support construction of an ancient karyotype of Cypriniformes. GigaScience, 14.

Liang Y, et al. (2025) The molecular basis of octocoral calcification revealed by genome and skeletal proteome analyses. GigaScience, 14.

Chen M, et al. (2025) The genome of *Hippophae salicifolia* provides new insights into the sexual differentiation of sea buckthorn. GigaScience, 14.

, et al. (2025) Correction to: The telomere-to-telomere gapless genome of grass carp provides insights for genetic improvement. GigaScience, 14.

Cuevas Zuviría B, et al. (2025) Structural evolution of nitrogenase over 3 billion years. eLife, 14.

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. GigaScience, 14.

Bian C, et al. (2025) Chromosome-level genome assemblies of five *Sinocyclocheilus* species. GigaByte (Hong Kong, China), 2025, gigabyte155.

- Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.
- Qi Z, et al. (2025) Telomere-to-telomere genome assembly of *Electrophorus electricus* provides insights into the evolution of electric eels. *GigaScience*, 14.
- Mu W, et al. (2025) The haplotype-resolved T2T genome for *Bauhinia × blakeana* sheds light on the genetic basis of flower heterosis. *GigaScience*, 14.
- Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). *GigaScience*, 14.
- Liu F, et al. (2025) The telomere-to-telomere gapless genome of grass carp provides insights for genetic improvement. *GigaScience*, 14.
- Kudo SN, et al. (2025) Evolution of gene expression in seasonal environments. *eLife*, 14.
- Zhang G, et al. (2025) Genomic and transcriptomic analyses of *Heteropoda venatoria* reveal the expansion of P450 family for starvation resistance in spiders. *GigaScience*, 14.
- Yuan J, et al. (2025) A telomere-to-telomere genome assembly of koi carp (*Cyprinus carpio*) using long reads and Hi-C technology. *GigaScience*, 14.
- Xue HC, et al. (2025) A unified cell atlas of vascular plants reveals cell-type foundational genes and accelerates gene discovery. *Cell*.
- Xu ZM, et al. (2025) Genome-to-genome analysis reveals associations between human and mycobacterial genetic variation in tuberculosis patients from Tanzania. *BMC medical genomics*, 18(1), 99.
- Guo X, et al. (2025) Deciphering genetic adaptations of Old World camels through comparative genomic analyses across all camelid species. *iScience*, 28(5), 112477.