

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

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

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: 20260905T132752+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 4962 mentions in open access literature.

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

Rathore U, et al. (2026) Systematic discovery of pro- and anti-HIV host factors in primary human CD4+ T cells. *Cell*, 189(12), 3651.

Zeng L, et al. (2026) Functional genomics reveals key gene families and molecular pathways for extreme cold survival in the khapra beetle. *BMC biology*, 24(1).

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Nawae W, et al. (2026) Genome Assembly of Three Shrub Mangroves in the Genus *Acanthus* Reveals Two Polyploidy Events and Expansion of Genes Linked to Root Adaptation in Coastal Habitats. *GigaScience*, 15.

Bjornson S, et al. (2026) Stepwise evolutionary transitions in Cladophorales plastid genomes reveal origins of hairpin chromosomes. *Current biology : CB*, 36(7), 1659.

Li X, et al. (2026) INSIG1 parallel substitution drives lipid/sterol metabolic plasticity mediating desert adaptation in ungulates. *Communications biology*, 9(1), 245.

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.

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

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

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

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

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

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

Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). *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.

Qi Z, et al. (2025) Telomere-to-telomere genome assembly of *Electrophorus electricus* provides insights into the evolution of electric eels. *GigaScience*, 14.

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

Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.