

Resource Summary Report

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jModelTest

RRID:SCR_015244

Type: Tool

Proper Citation

jModelTest (RRID:SCR_015244)

Resource Information

URL: <http://www.molecularrevolution.org/software/phylogenetics/jmodeltest>

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Description: Software tool used to carry out statistical selection of best-fit models of nucleotide substitution without the aid of PAUP*. It implements five different model selection strategies: hierarchical and dynamical likelihood ratio tests, Akaike and Bayesian information criteria, and a decision theory method. It also provides estimates of model selection uncertainty, parameter importances, and model-averaged parameter estimates.

Resource Type: software application, data processing software, source code, data analysis software, software resource

Defining Citation: [DOI:10.1038/nmeth.2109](https://doi.org/10.1038/nmeth.2109)

Keywords: best-fit model, nucleotide substitution, statistical analysis

Availability: Available for download

Resource Name: jModelTest

Resource ID: SCR_015244

Alternate IDs: OMICS_11546

Alternate URLs: <https://sources.debian.org/src/jmodeltest/>

Record Creation Time: 20220129T080324+0000

Record Last Update: 20260804T043550+0000

Ratings and Alerts

No rating or validation information has been found for jModelTest.

No alerts have been found for jModelTest.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3726 mentions in open access literature.

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

Shi M, et al. (2026) Genomic architecture and evolution of heterostyly: new insights from *Cordia subcordata* (Boraginaceae). *Molecular biology and evolution*, 43(1).

Zeng Y, et al. (2026) Endophyte *Acrocalymma vagum* establishes the holobiont with rice to attract beneficial microorganisms and promote disease resistance. *Journal of advanced research*, 79, 161.

Kim H, et al. (2025) Complete mitochondrial genome of the hybrid flounder *Paralichthys olivaceus* (?) × *Verasper variegatus* (?). *Mitochondrial DNA. Part B, Resources*, 10(6), 425.

Wang G, et al. (2025) Genomic evidence for hybridization and introgression between blue peafowl and endangered green peafowl and molecular foundation of leucistic plumage of blue peafowl. *GigaScience*, 14.

Kumar V, et al. (2025) Whole genome sequencing and assembly of the house sparrow, *Passer domesticus*. *GigaByte (Hong Kong, China)*, 2025, gigabyte161.

Coello Peralta RD, et al. (2025) Identification of *Ancylostoma caninum* in Domestic Dogs from Ecuador via Various Techniques. *Medical science monitor : international medical journal of experimental and clinical research*, 31, e947069.

Presswell B, et al. (2025) Size, spines, and primes: the drivers of collar spine numbers among echinostome trematodes. *Parasitology*, 152(1), 123.

?bi? O, et al. (2025) Mitogenomic Analysis of Glirids (Gliridae) and Squirrels (Sciuridae) From Türkiye: Evolutionary and Taxonomic Implications Within the Suborder Sciuromorpha. *Ecology and evolution*, 15(2), e70956.

Presswell B, et al. (2025) Two new species of kidney fluke (Trematoda: Renicolidae) from New Zealand penguins (Spheniscidae), with a description of *Renicola websterae* n. sp. *Systematic parasitology*, 102(2), 26.

Vieira Alves M, et al. (2025) Intratype variants and high genotypic diversity of human papillomavirus with polymorphisms in the antigenic hypervariable loops of the L1 protein from women living with human immunodeficiency virus in Northeastern Brazil. *Journal of*

medical microbiology, 74(3).

Ji SJ, et al. (2025) ?First record of *Morimotobathynella* Serban, 2000 (Bathynellacea, Bathynellidae) from subterranean waters of South Korea, with the description of a new species. *ZooKeys*, 1224, 109.

Richard PI, et al. (2025) Phylogenetic analysis of microbial CP-lyase cluster genes for bioremediation of phosphonate. *AMB Express*, 15(1), 42.

Martinez G, et al. (2025) Morphology and Molecular Phylogeny of Endosymbiotic Ciliates (Peritrichia, Mobilida) of Marine Invertebrates with Descriptions of Two Novel Species *Urceolaria clepsydra* n. sp. and *Urceolaria bratalia* n. sp. *The Journal of eukaryotic microbiology*, 72(2), e70003.

Gutiérrez-Liberato GA, et al. (2025) Leucocytozoon infections in tits (Aves, Paridae): blood and tissue stages investigated using an integrative approach. *Parasite (Paris, France)*, 32, 13.

Nair RR, et al. (2025) 'More tight-less tight' Patterns in the Climatic Niche Evolution of *Gymnocalycium* (Cactaceae): Were Pleistocene Glaciations a Prelude? *PloS one*, 20(5), e0323758.

Masaphy S, et al. (2025) Pezizales in Israel: Molecular Phylogenetic and ?13C?15N Stable Isotope Data Reveal New Records and Potential Discrepancies in Their Trophic Ecology. *Journal of fungi (Basel, Switzerland)*, 11(6).

Romano F, et al. (2025) Small Things that Make a Big Difference: Single-Cell Transcriptomic of Nanociliates Reveals Genes Potentially Involved in Mixotrophy. *Microbial ecology*, 88(1), 72.

Ngwe Tun MM, et al. (2025) Genomic analysis and molecular profiling of dengue viruses in Sabah, Malaysia during 2019-2020. *IJID regions*, 16, 100712.

Lee B, et al. (2025) Host niche partitioning and coexistence in *Amoebophrya* and *Parvilucifera* parasitoids infecting dinoflagellates. *ISME communications*, 5(1), ycaf126.

Belluardo F, et al. (2025) ?A new microendemic gecko from the small forest fragments of south-eastern Madagascar (Squamata, Gekkonidae, Paragehyra). *ZooKeys*, 1240, 1.