

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

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: 20260801T190522+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 [T1D](#).

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.

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).

Roy A, et al. (2025) Insights into the genome of *Azotobacter* sp. strain CWF10, isolated from an agricultural field in Central India. *Access microbiology*, 7(1).

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

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.

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.

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.

Carvalho ITS, et al. (2025) *Plasmodium* species infecting lizards in the Brazilian Cerrado: Identification and description of a novel species, *Plasmodium brasiliensis* n. sp. *PloS one*, 20(4), e0319402.

Duong B, et al. (2025) Zoogonids (trematoda) infecting Indo-West Pacific damselfishes (Pomacentridae), including the proposal of a new genus and two new species. *Parasitology*, 152(4), 436.

Andrade-Gómez L, et al. (2025) *Sinistroporomonorchis bolini* n. sp. (Trematoda: Monorchiidae) from the Ocellated killifish, *Floridichthys polyommus* (Cyprinodontidae) in the Yucatán Peninsula, Mexico based on an integrative taxonomy analysis. *Parasitology*, 152(1), 106.

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

Yao Y, et al. (2025) *Bacillus velezensis* A-27 as a potential biocontrol agent against *Meloidogyne incognita* and effects on rhizosphere communities of celery in field. *Scientific reports*, 15(1), 1057.

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.

Markakis G, et al. (2025) First Investigation of Haemosporidian Species and Record of Novel Genetic Lineages in Eurasian Griffon Vultures (*Gyps fulvus*) in Greece. *Veterinary sciences*, 12(10).

Azzena I, et al. (2025) Conservation hints for *Pinna nobilis* from a century-old genetic time capsule. *Scientific reports*, 15(1), 37660.