

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, software resource, source code, data analysis 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: 20260817T040539+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 3837 mentions in open access literature.

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

Kong W, et al. (2026) Characterization of complete mitochondrial genome of *Hishimonus sellatus uhler* (Hemiptera: cicadellidae: deltocephalinae) and phylogeny of deltocephalinae. *BMC genomics*, 27(1).

Luo L, et al. (2026) Paternal genomic history and Y-chromosome phylogeny from the Chengdu Plain reveal multiple Indigenous East Asian farmer contributions to ancient Shu and their descendants. *BMC biology*, 24(1).

Fontes JT, et al. (2026) Phylogeography of the widely distributed John Dory (*Zeus faber*, Actinopterygii: Zeiformes) reaffirms the prevalence of at least two deeply divergent clades. *Journal of fish biology*, 108(1), 373.

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

Jeong YS, et al. (2026) *Dinopallor Comventus* n. gen., n. sp., a Novel Parasitoid of Marine Dinoflagellates Representing a Sister Lineage to Seagrass Parasites and Expanding the Host Range of *Phytomyxea* (Rhizaria, Endomyxa). *Microbial ecology*, 89(1), 57.

Zhang K, et al. (2026) De novo assembly of the first mitochondrial genome in *Benincasa* reveals structural dynamics and evolutionary insights in Cucurbitaceae. *BMC plant biology*, 26(1).

Zhou X, et al. (2026) Comparative genomic and phylogenetic analyses of the mitogenome of *Graptopetalum Paraguayense* (N. E. Br.) Walth. 1938. *Scientific reports*, 16(1), 4174.

Juma J, et al. (2026) Spatiotemporal patterns of Rift Valley fever virus in Africa: a retrospective genomic epidemiology and phylodynamic modelling study. *The Lancet. Microbe*, 7(3), 101251.

Song J, et al. (2026) Genome-wide identification of small GTPase gene family members in *Lentinula edodes* and the roles of *LeRho1* in biotic and abiotic stress responses. *Applied and environmental microbiology*, 92(4), e0196725.

Kolařík M, et al. (2026) The ambrosial mycobiota of *Treptoplatypus oxyurus* (Coleoptera, Platypodidae): a unique island of fungal diversity revealing *Wilhelmdebeerea oxyuri* gen.

et sp. nov. (Ophiostomatales), and two new yeast species *Blastobotrys sasensis* sp. nov., and *Sugiyamaella casensis* sp. nov. (Dipodascales). IMA fungus, 17, e177075.

He G, et al. (2026) Complex peopling history and expansion events inferred from large-scale modern and ancient Y chromosome sequences. Science advances, 12(14), eadu7935.

Liu S, et al. (2026) Complete chloroplast genome features and phylogenetic analysis of *Clematis cadmia*. Scientific reports, 16(1).

Tu B, et al. (2026) Phylogeny and Taxonomy of Spider-Pathogenic *Gibellula* (Cordycipitaceae, Hypocreales) from the Lancang-Mekong Biodiversity Hotspot: Four New Species and Five New National Records. Journal of fungi (Basel, Switzerland), 12(5).

An X, et al. (2026) Two Species of Wild Long-Fruited Jute (*Corchorus olitorius*) Characterization and Phylogenetic Analysis of the Complete Chloroplast Genomes. International journal of molecular sciences, 27(12).

Juárez-Cruz KJ, et al. (2026) Antifungal Activity of Native *Trichoderma afroharzianum* and *Arcopilus cupreus* Against *Neopestalotiopsis rosae* Causing Strawberry Root and Crown Rot in Mexico. Journal of fungi (Basel, Switzerland), 12(6).

Liu W, et al. (2026) A new species of *Pseudomphala* Heude, 1882 (Gastropoda, Truncatelloidea, Assimineidae) from Zhoushan of Zhejiang Province, East China Sea. ZooKeys, 1283, 79.

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.

Mungunkhuyag K, et al. (2026) Isolation and characterization of heavy metal tolerant microalgae from old mining areas of Saxony. Scientific reports, 16(1), 1337.

Pan W, et al. (2026) Analysis of chloroplast genomes and SSR classification and identification of *Agropyron* species and closely related species. Scientific reports, 16(1), 3579.

Deng Y, et al. (2026) Characterization of the Complete Mitochondrial Genome of *Pedicularis henryi* and Its Phylogenetic Implications in Lamiales. Biology, 15(7).