

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

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: 20260829T182458+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.

Osman AM, et al. (2026) First report of 'Candidatus *Anaplasma cameli*' and high molecular prevalence of *Anaplasma marginale* in dromedary camels (*Camelus dromedarius*) from Somalia. *Tropical animal health and production*, 58(2).

Arai N, et al. (2026) Transmission of *Salmonella* clones between different animal species in a horse and cattle breeding region in Japan. *Scientific reports*, 16(1).