

Resource Summary Report

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modeltest

RRID:SCR_026633

Type: Tool

Proper Citation

modeltest (RRID:SCR_026633)

Resource Information

URL: <https://github.com/ddarriba/modeltest>

Proper Citation: modeltest (RRID:SCR_026633)

Description: Software tool for selecting the best-fit model of evolution for DNA and protein alignments. Used for selection of DNA and Protein evolutionary models.

Synonyms: ModelTest-NG

Resource Type: software application, software resource

Defining Citation: [PMID:31432070](#)

Keywords: selecting the best-fit model of evolution, DNA and protein alignments, selection of DNA and Protein evolutionary models,

Funding: Ministry of Economy and Competitiveness of Spain ;
FEDER funds of the EU ;
Galician Government ;
Klaus Tschira Foundation

Availability: Free, Available for download, Freely available

Resource Name: modeltest

Resource ID: SCR_026633

License: GNU GPL v3.0

Record Creation Time: 20250326T060329+0000

Record Last Update: 20260805T044602+0000

Ratings and Alerts

No rating or validation information has been found for modeltest.

No alerts have been found for modeltest.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 145 mentions in open access literature.

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

Debnath SC, et al. (2025) Seasonal dynamics and factors shaping microbiomes in freshwater finfish earthen aquaculture ponds in Bangladesh. *Environmental microbiome*, 20(1), 38.

Zeng Z, et al. (2025) Diversity of Gracilariaceae (Gracilariales, Rhodophyta) Across Distinct Ecosystems in Zhanjiang, China: A Foundation for Screening Potential Cultivable Species in Southern China. *Ecology and evolution*, 15(7), e71748.

Zupfer K, et al. (2025) Evolutionary conservation of ubiquitin-like protein urmylation as revealed by URM1 gene shuffle from archaea to yeast. *Communications biology*, 8(1), 1637.

Gorospe JM, et al. (2025) Historical introgression as a driver of diversification of diploid *Picris* (Compositae) in the Mediterranean Basin. *The Plant journal : for cell and molecular biology*, 124(3), e70565.

Ezzedine JA, et al. (2025) Snow- and ice-ecosystem cleaning capability of the pucciniomycotinous yeast *Phenoliferia psychrophenolica*. *Communications biology*, 8(1), 1084.

Li Y, et al. (2025) Genetic characterization on the nucleoprotein and fusion gene of wild-type measles virus circulating in Shanghai, 2001-2022. *Journal of virus eradication*, 11(1), 100589.

Li B, et al. (2025) A Reassessment of Phylogenetic Relationships in Class Oligohymenophorea (Protista, Ciliophora) Based on Updated Multigene Data. *Ecology and evolution*, 15(2), e70950.

Qiu S, et al. (2025) Functional evolution and diversification of CYP82D subfamily members have shaped flavonoid diversification in the genus *Scutellaria*. *Plant communications*, 6(1), 101134.

La Torre R, et al. (2025) A chromosome-level genome assembly of the Peruvian Algarrobo (*Neltuma pallida*) provides insights on its adaptation to its unique ecological niche. *G3 (Bethesda, Md.)*, 15(2).

- Peng JC, et al. (2025) Standing genetic variation and introgression shape the cryptic radiation of *Aquilegia* in the mountains of Southwest China. *Communications biology*, 8(1), 684.
- Rosa F, et al. (2025) Morphological and genetic polymorphisms in *Rhipicephalus sanguineus* (Latreille 1806) from the Iberian Peninsula. *Parasitology research*, 124(9), 105.
- Naktang C, et al. (2025) Chromosome-level assemblies of two hexaploid bamboos, *Thyrsostachys oliveri* and *Thyrsostachys siamensis*, provide a foundation for functional and comparative genomics studies. *GigaScience*, 14.
- Wang C, et al. (2025) Taxonomic status and spatial genetic pattern of *Taxus* in northern and central China: insights from integrative taxonomy, ecology and phylogeography. *BMC plant biology*, 25(1), 181.
- Hisatsune J, et al. (2025) *Staphylococcus aureus* ST764-SCCmecII high-risk clone in bloodstream infections revealed through national genomic surveillance integrating clinical data. *Nature communications*, 16(1), 2698.
- Zhou W, et al. (2025) *Pternopetalumshunhuangensis* (Apiaceae), a new species from Hunan, China. *PhytoKeys*, 253, 261.
- Morey-León G, et al. (2025) Global epidemiology of *Mycobacterium tuberculosis* lineage 4 insights from Ecuadorian genomic data. *Scientific reports*, 15(1), 3823.
- Diaz OL, et al. (2025) Identification of enterobacteriaceae causing septicemia in the axolotl *Ambystoma mexicanum*. *Antonie van Leeuwenhoek*, 118(3), 56.
- Marik T, et al. (2025) Novel peptaibiotics identified from *Trichoderma* clade Viride. *Natural products and bioprospecting*, 15(1), 48.
- Peterse IF, et al. (2025) Hydrogen Oxidation Benefits Alphaproteobacterial Methanotrophs Under Severe Methane Limitation. *Environmental microbiology*, 27(8), e70163.
- Rodríguez-Herrera J, et al. (2025) A computational Evo-Devo approach for elucidating the roles of PLETHORA transcription factors in regulating root development. *PloS one*, 20(7), e0327511.