

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 160 mentions in open access literature.

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

Nawae W, et al. (2026) Genome Assembly of Three Shrub Mangroves in the Genus *Acanthus* Reveals Two Polyploidy Events and Expansion of Genes Linked to Root Adaptation in Coastal Habitats. *GigaScience*, 15.

Martin SLF, et al. (2026) Haplotype-resolved chromosome-level genome assemblies of four *Diamesa* species reveal the genetic basis of cold tolerance and high-altitude adaptations in arctic chironomids. *GigaScience*, 15.

Brunner A, et al. (2026) Extensive mobilome dynamics in a widespread endosymbiont: long read metagenomics reveal dimeric plasmids and highly fragmented prophages in *Wolbachia* from *Culex pipiens*. *Research square*.

Chrudinová M, et al. (2026) Evolution of Insulin, Insulin-like Growth Factors, and Their Cognate Receptors in Vertebrates, Invertebrates, and Viruses. *Molecular biology and evolution*, 43(1).

Chopade A, et al. (2026) Shared biosynthetic architectures generate diverse γ -amino polyketide residues in cyanobacterial peptides. *bioRxiv : the preprint server for biology*.

Cassar O, et al. (2026) HTLV-1 genetic diversity of 52 complete sequences from 14 African countries reveals novel variants and a lack of typical P12/P8 and P30 accessory proteins in HTLV-1b, d, and f genotypes. *Emerging microbes & infections*, 15(1), 2651463.

Gastineau R, et al. (2026) Molecular characterisation of the invasive terrestrial nemertean *Geonemertes pelaensis*: long and complex mitogenome and presence of NUMTs. *Scientific reports*, 16(1), 3312.

Wang YY, et al. (2026) A Near Telomere-to-Telomere Genome of *Belamcanda chinensis* Provides Insights Into Genome Evolution and the Biosynthesis of Characteristic Isoflavones. *Plant biotechnology journal*, 24(6), 4285.

Choi N, et al. (2026) Novel mechanisms of chemosensory adaptation to the cave environment. *bioRxiv : the preprint server for biology*.

Jiu S, et al. (2026) Pangenome and resequencing analyses reveal flowering evolution and genetic control in *Cerasus*. *Nature communications*, 17(1).

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.

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

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.

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.

Chen HY, et al. (2025) Comprehensive species sampling reveals pervasive pseudogenization and recurrent complete loss of plastid *ndh* genes in the genus *Cymbidium* (Orchidaceae). *BMC plant biology*, 26(1), 181.

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).

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.

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.

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.