

Resource Summary Report

Generated by [NIF](#) on Aug 23, 2026

ProtTest

RRID:SCR_014628

Type: Tool

Proper Citation

ProtTest (RRID:SCR_014628)

Resource Information

URL: http://darwin.uvigo.es/software/prottest_server.html

Proper Citation: ProtTest (RRID:SCR_014628)

Description: Web-based software used for the selection of best-fit models of protein evolution., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Resource Type: data analysis software, data processing software, software application, software resource, web application

Defining Citation: [PMID:15647292](#), [DOI:10.1093/bioinformatics/btr088](#)

Keywords: bioinformatics, model, best fit model, protein evolution, amino acid replacement, server, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: ProtTest

Resource ID: SCR_014628

Alternate IDs: OMICS_11547, biotools:prottest

Alternate URLs: <https://github.com/ddarriba/prottest3>, <https://bio.tools/prottest>, <https://sources.debian.org/src/prottest/>

License: GNU General Public License

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260821T194025+0000

Ratings and Alerts

No rating or validation information has been found for ProtTest.

No alerts have been found for ProtTest.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1984 mentions in open access literature.

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

Liu L, et al. (2026) Cross-stage single-cell and spatial metabolome analyses reveal periderm specialization and tanshinone biosynthesis in *Salvia miltiorrhiza* roots. *The New phytologist*, 251(3), 1267.

Baeza JA, et al. (2025) Assembly of Mitochondrial Genomes Using Nanopore Long-Read Technology in Three Sea Chubs (Teleostei: Kyphosidae). *Molecular ecology resources*, 25(1), e14034.

Cai Y, et al. (2025) Nine complete chloroplast genomes of the *Camellia* genus provide insights into evolutionary relationships and species differentiation. *Scientific reports*, 15(1), 8783.

Eckhart L, et al. (2025) Caspase Domain Duplication During the Evolution of Caspase-16. *Journal of molecular evolution*, 93(3), 395.

Yacoub E, et al. (2025) A sweeping view of avian mycoplasmas biology drawn from comparative genomic analyses. *BMC genomics*, 26(1), 24.

Zeng X, et al. (2025) The complete mitochondrial genome of *Gyrodactylus pseudorasbora* (Platyhelminthes: Monogenea) with a phylogeny of Gyrodactylidae parasites. *BMC genomics*, 26(1), 34.

De Koch MD, et al. (2025) Novel lineage of anelloviruses with large genomes identified in dolphins. *Journal of virology*, 99(1), e0137024.

De Koch MD, et al. (2025) Diverse Anelloviruses Identified in Leporids from Arizona (USA). *Viruses*, 17(2).

Costa-Silva S, et al. (2025) Novel paramyxovirus in wild pinnipeds, Brazil. *Veterinary research communications*, 49(4), 242.

Ho R, et al. (2025) Structure, function and assembly of soybean primary cell wall cellulose synthases. *eLife*, 13.

Xu W, et al. (2025) Specificities of Chemosensory Receptors in the Human Gut Microbiota. *bioRxiv : the preprint server for biology*.

Padgett K, et al. (2025) The Mitochondrial Genome of the Imperiled Goliath Grouper *Epinephelus itajara*: Selective Pressures in Protein Coding Genes, Secondary Structure of tRNA Genes, and Phylogenetic Placement. *Ecology and evolution*, 15(7), e71795.

Liu K, et al. (2025) Scaffold protein RhCASPL1D1 stabilizes RhPIP2 aquaporins and promotes flower recovery after dehydration in rose (*Rosa hybrida*). *Horticulture research*, 12(8), uhaf119.

Mu W, et al. (2025) Characterization of the complete mitochondrial genomes of two sea cucumbers, *Deima validum* and *Oneirophanta mutabilis* (Holothuroidea, Synallactida, Deimatidae): Insight into deep-sea adaptive evolution of Deimatidae. *PloS one*, 20(5), e0323612.

Wang P, et al. (2025) Transcriptomic and Metabolomic Insights into Key Genes Involved in Kinsenoside Biosynthesis in *Anoectochilus roxburghii*. *Plants* (Basel, Switzerland), 14(5).

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.

de Oliveira B, et al. (2025) Characterization of a novel *Leishmania* antigen containing a repetitive domain and its potential use as a prophylactic and therapeutic vaccine. *mSphere*, 10(5), e0009725.

Clark-Flores D, et al. (2025) Vacuolar Proteases of *Candida auris* from Clades III and IV and Their Relationship with Autophagy. *Journal of fungi* (Basel, Switzerland), 11(5).

Sakuta K, et al. (2025) Novel endornaviruses infecting *Phytophthora cactorum* that attenuate vegetative growth, promote sporangia formation and confer hypervirulence to the host oomycete. *The Journal of general virology*, 106(5).

Li ZB, et al. (2025) The complete mitochondrial genome analysis of *Haemaphysalis hystrix* Supino, 1897 (Ixodida: Ixodidae) and its phylogenetic implications. *Open life sciences*, 20(1), 20220875.