

Resource Summary Report

Generated by [RRID](#) on Aug 5, 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 processing software, data analysis software, software resource, software application, 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: 20260805T044329+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 1981 mentions in open access literature.

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

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.

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.

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

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

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

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

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

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.

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

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.

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.

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.

Seale T, et al. (2025) Diversity of Environmental *Escherichia coli* in Subtropical Freshwater Systems of South Africa. *Current microbiology*, 82(9), 414.

Fan BL, et al. (2025) Analysis of gene expansion and defense-related genes in Anacardiaceae family from an evolutionary aspect. *Frontiers in plant science*, 16, 1638044.

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).

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).

Wang G, et al. (2025) Mitochondrial genomes of *Meghimatium pictum* and *Succinea arundinetorum* provide insight into the gene order rearrangement within Stylommatophora (Gastropoda, Panpulmonata). *BMC zoology*, 10(1), 16.

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

Varsani A, et al. (2025) Bacilladnaviridae: refined taxonomy and new insights into the biology and evolution of diatom-infecting DNA viruses. *The Journal of general virology*, 106(3).