

Resource Summary Report

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

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: 20260729T044329+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 [nidm-terms](#) .

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.

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

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.

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) 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.

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

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

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).