

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 2026

Predictions for Entire Proteomes

RRID:SCR_002803

Type: Tool

Proper Citation

Predictions for Entire Proteomes (RRID:SCR_002803)

Resource Information

URL: <http://www.predictprotein.org/>

Proper Citation: Predictions for Entire Proteomes (RRID:SCR_002803)

Description: Web application for sequence analysis and the prediction of protein structure and function. The user interface intakes protein sequences or alignments and returned multiple sequence alignments, motifs, and nuclear localization signals., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 15,2026.

Synonyms: PredictProtein

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

Defining Citation: [PMID:24799431](#), [DOI:10.1093/nar/gkh377](#)

Keywords: sequence analysis database, protein structure prediction, protein structure, protein function, bio.tools, FASEB list

Funding: BMBF

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Predictions for Entire Proteomes

Resource ID: SCR_002803

Alternate IDs: nif-0000-00136, OMICS_07135, biotools:predictprotein

Alternate URLs: <https://bio.tools/predictprotein>,
<https://sources.debian.org/src/predictprotein/>

Old URLs: <http://cubic.bioc.columbia.edu/pep/>

License: Academic Software License Agreement

License URLs: <https://www.predictprotein.org/terms>

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260905T132955+0000

Ratings and Alerts

No rating or validation information has been found for Predictions for Entire Proteomes.

No alerts have been found for Predictions for Entire Proteomes.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 643 mentions in open access literature.

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

Wang Y, et al. (2026) Comprehensive Analysis of PAPPA2 Expression and Genetic Variants in Sheep and Their Association With Litter Size. Veterinary medicine and science, 12(1), e70793.

He Z, et al. (2026) Integrated Analysis of ATAC-Seq and RNA-Seq Reveals the Signal Transduction Regulation of the Molting Cycle in the Muscle of Chinese Mitten Crab (*Eriocheir sinensis*). Biomolecules, 16(1).

Zhou C, et al. (2026) Comparative Analysis Reveals the Adaptive Evolution of Olfactory System in the Swamp Eel (*Monopterus albus*) Based on the Chromosome-Level Genome. Ecology and evolution, 16(5), e73586.

Hendgen-Cotta UB, et al. (2026) Reverse engineering of BNIP3 identifies a mitochondrial protective peptide. Nature communications, 17(1).

Chen Q, et al. (2026) ApCtf1??-Interacting Target Proteins BDPH1 and BDEUL12 Regulate Pathogenicity in *Arthrinium phaeospermum*. Molecular plant pathology, 27(3), e70245.

Kongsomboonchoke P, et al. (2026) AAV-mediated delivery of CRISPR/Cas9 targeting conserved overlapping ORFs efficiently suppresses HBV replication in hepatocyte models. Biotechnology reports (Amsterdam, Netherlands), 51, e00961.

Samson D, et al. (2025) Expression of a multigene mushroom luciferin biosynthesis pathway as a pseudo-polycistron in plants. Scientific reports, 15(1), 25385.

Aumann RA, et al. (2025) Decoding and engineering temperature-sensitive lethality in *Ceratitis capitata* for pest control. *Proceedings of the National Academy of Sciences of the United States of America*, 122(28), e2503604122.

Naully PG, et al. (2025) Advancing therapeutic vaccines for chronic hepatitis B: Integrating reverse vaccinology and immunoinformatics. *World journal of hepatology*, 17(7), 107620.

Li J, et al. (2025) MsLHY is an active regulator of cold resistance in alfalfa (*Medicago sativa* L.). *Frontiers in plant science*, 16, 1559988.

Imran H, et al. (2025) In silico identification and functional annotation of universal stress protein (USP) gene family in *Chenopodium quinoa*. *Scientific reports*, 15(1), 18264.

Han Y, et al. (2025) Ribosome pausing in amylase producing *Bacillus subtilis* during long fermentation. *Microbial cell factories*, 24(1), 31.

Arend LB, et al. (2025) Molecular Basis for Vacuolar Iron Transport by OsVIT2, a Target for Iron Biofortification in Rice. *Proteins*, 93(10), 1717.

Wang P, et al. (2025) The StbHLH47 transcription factor negatively regulates drought tolerance in potato (*Solanum tuberosum* L.). *BMC plant biology*, 25(1), 14.

Huang J, et al. (2025) Missense Mutations in FDNC5 Associated with Morphometric Traits and Meat Quality in Hainan Black Goats. *Animals : an open access journal from MDPI*, 15(4).

Greven JA, et al. (2025) Biophysical mapping of TREM2-ligand interactions reveals shared surfaces for engagement of multiple Alzheimer's disease ligands. *Molecular neurodegeneration*, 20(1), 3.

Osinkina IA, et al. (2025) First Identification, Recombinant Production, and Structural Characterization of a Putative Structural Protein from the Haseki Tick Virus Polyprotein. *Biomolecules*, 15(12).

Chen G, et al. (2025) Polymorphism of NCAPG gene and its association with growth traits in Nanjiang Yellow goat. *Animal biotechnology*, 36(1), 2565161.

Lee L, et al. (2025) WDR75: An essential protein for ribosome assembly undergoing purifying selection. *PloS one*, 20(2), e0318395.

Cui B, et al. (2025) Harnessing magnetic cross-linked cell aggregates (CLCAs) for cost-effective preparation of Konjac mannan-oligosaccharide. *Microbial cell factories*, 24(1), 146.