

Resource Summary Report

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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 processing software, data analysis software, software resource, sequence analysis software, software application, 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: 20260805T044044+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 578 mentions in open access literature.

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

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

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.

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.

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

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

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.

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

- Chen G, et al. (2025) Polymorphism of NCAPG gene and its association with growth traits in Nanjiang Yellow goat. *Animal biotechnology*, 36(1), 2565161.
- 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.
- Yu D, et al. (2025) Epidemiological investigation and genomic characterization of Gyrovirus galga1 in Guangxi, China. *Poultry science*, 104(11), 105776.
- Lee L, et al. (2025) WDR75: An essential protein for ribosome assembly undergoing purifying selection. *PloS one*, 20(2), e0318395.
- Costa AJO, et al. (2025) Expression of L-Amino Acid Oxidase (MI-LAAO) from the Venom of the Micrurus lemniscatus Snake in a Mammalian Cell System. *Toxins*, 17(10).
- Huo J, et al. (2025) Exploration and mutagenesis of the germacrene A synthase from *Solidago canadensis* to enhance germacrene A production in *E. coli*. *Synthetic and systems biotechnology*, 10(2), 620.
- Zhang M, et al. (2025) Identification and functional analysis of AvLACS genes unveils their role in lipid homeostasis and waterlogging tolerance in kiwifruit (*Actinidia valvata* Dunn). *Frontiers in plant science*, 16, 1580003.
- H??ppner S, et al. (2025) Deciphering the membrane topology of the pestiviral non-structural protein 4B (NS4B). *Journal of virology*, 99(9), e0082525.
- Hua M, et al. (2025) The basic helix-loop-helix (bHLH) transcription factor DTT1 is part of a paired key that unlocks the tapetum transition in barley anther development. *The Plant cell*, 37(10).
- Cheng G, et al. (2025) Genomic Insights into Cobweb Disease Resistance in *Agaricus bisporus*: A Comparative Analysis of Resistant and Susceptible Strains. *Journal of fungi* (Basel, Switzerland), 11(3).
- Obuobi A, et al. (2025) Unveiling the Plasmodium inositol (pyro)phosphate pathway: Highlighting inositol polyphosphate multikinase as a novel therapeutic target for malaria. *PloS one*, 20(12), e0338411.
- Waury K, et al. (2025) Data-driven evaluation of suitable immunogens for improved antibody selection. *Protein science : a publication of the Protein Society*, 34(4), e70100.