

Resource Summary Report

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ProFunc

RRID:SCR_004450

Type: Tool

Proper Citation

ProFunc (RRID:SCR_004450)

Resource Information

URL: <http://www.ebi.ac.uk/thornton-srv/databases/profunc/index.html>

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Description: The ProFunc server had been developed to help identify the likely biochemical function of a protein from its three-dimensional structure. It uses both sequence- and structure-based methods including fold matching, residue conservation, surface cleft analysis, and functional 3D templates, to identify both the protein's likely active site and possible homologues in the PDB. Often, where one method fails to provide any functional insight another may be more helpful. You can submit your own structure, analyze an existing PDB entry, or retrieve the results of a previously submitted run. The files are usually stored for about 6 months before being deleted. However, they are stored on a partition that is not backed up; so, in principle, they could disappear at any time.

Abbreviations: ProFunc

Synonyms: ProFunc - prediction of protein function from 3D structure, ProFunc: Analysis of a protein's 3D structure to help identify its likely biochemical function

Resource Type: service resource, production service resource, analysis service resource, data analysis service

Defining Citation: [PMID:15980588](#), [PMID:16019027](#)

Keywords: gold standard

Funding: DOE contract W-31-109-Eng-38;
NIGMS GM62414;
European Union FP6 contract LHSG-CT-2003-503265

Resource Name: ProFunc

Resource ID: SCR_004450

Alternate IDs: nlx_44430

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260731T042658+0000

Ratings and Alerts

No rating or validation information has been found for ProFunc.

No alerts have been found for ProFunc.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 63 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Saleem MZ, et al. (2025) In silico characterization, physiochemical analysis, and antifungal evaluation of the Zea mays PR-1 protein. Scientific reports, 15(1), 31523.

Maso L, et al. (2024) Molecular basis for antibody recognition of multiple drug-peptide/MHC complexes. Proceedings of the National Academy of Sciences of the United States of America, 121(22), e2319029121.

Blazie SM, et al. (2024) C. elegans LIN-66 mediates EIF-3/eIF3-dependent protein translation via a cold-shock domain. Life science alliance, 7(9).

Gorityala N, et al. (2024) Genome mining of Mycobacterium tuberculosis: targeting SufD as a novel drug candidate through in silico characterization and inhibitor screening. Frontiers in microbiology, 15, 1369645.

Panrat T, et al. (2024) Structural modelling and preventive strategy targeting of WSSV hub proteins to combat viral infection in shrimp Penaeus monodon. PloS one, 19(7), e0307976.

Sundararaj R, et al. (2024) In silico approaches for the identification of potential allergens among hypothetical proteins from Alternaria alternata and its functional annotation. Scientific reports, 14(1), 6696.

Marson NA, et al. (2024) In silico prediction of heme binding in proteins. The Journal of biological chemistry, 300(5), 107250.

Ribeiro AJM, et al. (2023) Enzyme function and evolution through the lens of bioinformatics. The Biochemical journal, 480(22), 1845.

Ishwarlall TZ, et al. (2023) Multi-epitope vaccine candidates based on mycobacterial membrane protein large (MmpL) proteins against *Mycobacterium ulcerans*. *Open biology*, 13(11), 230330.

Rajapaksha LGTG, et al. (2022) In silico detection and characterization of novel virulence proteins of the emerging poultry pathogen *Gallibacterium anatis*. *Genomics & informatics*, 20(4), e41.

Ardestani H, et al. (2022) In silico and in vivo approaches to recombinant multi-epitope immunogen of GroEL provides efficient cross protection against *S. Typhimurium*, *S. flexneri*, and *S. dysenteriae*. *Molecular immunology*, 144, 96.

Khan K, et al. (2022) Integrated bioinformatics based subtractive genomics approach to decipher the therapeutic function of hypothetical proteins from *Salmonella typhi* XDR H-58 strain. *Biotechnology letters*, 44(2), 279.

Zhang J, et al. (2022) Structural and functional characterizations and heterogenous expression of the antimicrobial peptides, Hedefensins, from black soldier fly, *Hermetia illucens* (L.). *Protein expression and purification*, 192, 106032.

Kader MA, et al. (2022) Hypothetical protein predicted to be tumor suppressor: a protein functional analysis. *Genomics & informatics*, 20(1), e6.

Delgado L, et al. (2021) Release of Soybean Isoflavones by Using a β -Glucosidase from *Alicyclobacillus herbarius*. *Chembiochem : a European journal of chemical biology*, 22(7), 1223.

Abdollahi S, et al. (2021) Physicochemical and structural characterization, epitope mapping and vaccine potential investigation of a new protein containing Tetratrico Peptide Repeats of *Acinetobacter baumannii*: An in-silico and in-vivo approach. *Molecular immunology*, 140, 22.

Fernández A, et al. (2021) Peptides Derived From the β -Core and α -Core Regions of a Putative *Silybum marianum* Flower Defensin Show Antifungal Activity Against *Fusarium graminearum*. *Frontiers in microbiology*, 12, 632008.

Al Qahtani NH, et al. (2021) Whole-Genome Sequencing Reveals Exonic Variation of ASIC5 Gene Results in Recurrent Pregnancy Loss. *Frontiers in medicine*, 8, 699672.

Chandrakanth R, et al. (2020) In silico modelling and characterization of eight blast resistance proteins in resistant and susceptible rice cultivars. *Journal, genetic engineering & biotechnology*, 18(1), 75.

Heckmann CM, et al. (2020) An (R)-Selective Transaminase From *Thermomyces stellatus*: Stabilizing the Tetrameric Form. *Frontiers in bioengineering and biotechnology*, 8, 707.