Resource Summary Report

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PROSITE

RRID:SCR_003457
Type: Tool

Proper Citation

PROSITE (RRID:SCR_003457)

Resource Information

URL: http://prosite.expasy.org/

Proper Citation: PROSITE (RRID:SCR_003457)

Description: Database of protein families and domains that is based on the observation that, while there is a huge number of different proteins, most of them can be grouped, on the basis of similarities in their sequences, into a limited number of families. Proteins or protein domains belonging to a particular family generally share functional attributes and are derived from a common ancestor. It is complemented by ProRule, a collection of rules based on profiles and patterns, which increases the discriminatory power of profiles and patterns by providing additional information about functionally and/or structurally critical amino acids. ScanProsite finds matches of your protein sequences to PROSITE signatures. PROSITE currently contains patterns and profiles specific for more than a thousand protein families or domains. Each of these signatures comes with documentation providing background information on the structure and function of these proteins. The database is available via FTP.

Abbreviations: PROSITE

Synonyms: PROSITE - Database of protein domains families and functional sites

Resource Type: data or information resource, service resource, analysis service resource, data analysis service, production service resource, database

Defining Citation: PMID:23161676, PMID:19858104, PMID:12230035

Keywords: protein domain, protein family, functional site, protein, structure, function, pattern, profile

Funding: Swiss Federal government through the Federal Office of Education and Science ;

European Union contract FELICS 021902RII3;
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FNS 315200-116864

Availability: Acknowledgement requested, License fee for commercial users, Free for academic use

Resource Name: PROSITE

Resource ID: SCR_003457

Alternate IDs: nif-0000-03351, OMICS_01699

Old URLs: http://www.expasy.org/prosite, http://www.expasy.ch/prosite/

Record Creation Time: 20220129T080219+0000

Record Last Update: 20250412T054835+0000

Ratings and Alerts

No rating or validation information has been found for PROSITE.

No alerts have been found for PROSITE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2065 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Lagunas-Rangel FA, et al. (2025) Giardia fibrillarin: a bioinformatics exploration of sequence and structure. Journal of applied genetics, 66(1), 241.

Ghosh Roy S, et al. (2025) Multiple mutations in polyketide synthase led to disruption of Psittacofulvin production across diverse parrot species. Communications biology, 8(1), 69.

Chang H, et al. (2025) iTRAQ proteomic analysis of the anterior insula in morphine-induced conditioned place preference rats with high-frequency deep brain stimulation intervention. Addiction biology, 30(1), e70014.

Xie L, et al. (2025) Structural Analysis of Amylin and Amyloid ? Peptide Signaling in Alzheimer's Disease. Biomolecules, 15(1).

Li H, et al. (2025) Molecular Characterization, Recombinant Expression, and Functional Analysis of Carboxypeptidase B in Litopenaeus vannamei. Genes, 16(1).

Steichele M, et al. (2025) Notch signaling mediates between two pattern-forming processes during head regeneration in Hydra. Life science alliance, 8(1).

Petroll R, et al. (2025) Enhanced sensitivity of TAPscan v4 enables comprehensive analysis of streptophyte transcription factor evolution. The Plant journal : for cell and molecular biology, 121(1), e17184.

Li Q, et al. (2025) Quantitative DIA-based proteomics unveils ribosomal biogenesis pathways associated with increased final size in three-year-old Chinese mitten crab (Eriocheir sinensis). BMC genomics, 26(1), 45.

Maldutyte J, et al. (2025) ER export via SURF4 uses diverse mechanisms of both client and coat engagement. The Journal of cell biology, 224(1).

Chen F, et al. (2025) Data-independent acquisition-based blood proteomics unveils predictive biomarkers for neonatal necrotizing enterocolitis. Analytical and bioanalytical chemistry, 417(1), 199.

Miller D, et al. (2025) Pooled PPIseq: Screening the SARS-CoV-2 and human interface with a scalable multiplexed protein-protein interaction assay platform. PloS one, 20(1), e0299440.

An L, et al. (2025) Genome-Wide Identification and Characterization of the CDPK Family of Genes and Their Response to High-Calcium Stress in Yinshania henryi. Genes, 16(1).

Zhang M, et al. (2025) Identification of Critical Phosphorylation Sites Enhancing Kinase Activity With a Bimodal Fusion Framework. Molecular & cellular proteomics : MCP, 24(1), 100889.

Zhang J, et al. (2025) Genome- and Transcriptome-Wide Characterization and Expression Analyses of bHLH Transcription Factor Family Reveal Their Relevance to Salt Stress Response in Tomato. Plants (Basel, Switzerland), 14(2).

Li W, et al. (2025) Integrating proteomics and metabolomics to elucidate the regulatory mechanisms of pimpled egg production in chickens: Multi-omics analysis of the mechanism of pimpled egg formation. Poultry science, 104(2), 104818.

De la Cruz MA, et al. (2025) The transcriptional regulator Lrp activates the expression of genes involved in the biosynthesis of tilimycin and tilivalline enterotoxins in Klebsiella oxytoca. mSphere, 10(1), e0078024.

Wan S, et al. (2024) SPARC Stabilizes ApoE to Induce Cholesterol-Dependent Invasion and Sorafenib Resistance in Hepatocellular Carcinoma. Cancer research, 84(11), 1872.

Mu F, et al. (2024) Genome-wide systematic survey and analysis of the RNA helicase gene family and their response to abiotic stress in sweetpotato. BMC plant biology, 24(1), 193.

Shams MH, et al. (2024) Designing a T-cell epitope-based vaccine using in silico approaches against the Sal k 1 allergen of Salsola kali plant. Scientific reports, 14(1), 5040.

Zhang WW, et al. (2024) Genetic mechanism of body size variation in groupers: Insights from phylotranscriptomics. Zoological research, 45(2), 314.