

Resource Summary Report

Generated by [dkNET](#) on Aug 24, 2026

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

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;
European Union contract IMPACT 213037;

FNS 315200-116864

Availability: Free, Freely available

Resource Name: PROSITE

Resource ID: SCR_003457

Alternate IDs: OMICS_01699, nif-0000-03351

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

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260821T193701+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 2341 mentions in open access literature.

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

Parnandi VA, et al. (2026) A small *Candida glabrata* protein promotes hyphal growth in *C. albicans* during mixed-species invasive candidiasis. *Current biology : CB*, 36(1), 1.

Liu T, et al. (2026) Chromosome-level genome assembly and annotation of the endangered plant *Primula kwangtungensis* (Primulaceae). *Scientific data*, 13(1), 212.

Rey F, et al. (2026) Study of POLR3A variants in a family trio suggests mutation-specific pathogenetic mechanisms: insights from integrative OMIC approaches. *Cell communication and signaling : CCS*, 24(1).

Khalid Z, et al. (2026) DPAS: disease-associated peptide anomaly score for identifying pathogenic peptides via one-class learning. *Scientific reports*, 16(1).

Pan Y, et al. (2026) Proteomic Analysis of Lotus-Derived NnAP2 Regulation of Soluble Sugar and Starch Content in Potato (*Solanum tuberosum*). *Plants (Basel, Switzerland)*, 15(4).

Guan Y, et al. (2026) Genomic survey and expression analysis of the CDPK genes in *Liriodendron Chinense* to explore their potential functions under multiple abiotic stresses.

BMC genomics, 27(1), 198.

Sharma P, et al. (2026) Structural, evolutionary and functional insights into the NAC gene family in *Stevia rebaudiana* and identification of important genes regulating steviol glycosides biosynthesis. BMC plant biology, 26(1).

Soman SP, et al. (2026) IsoProDB: an integrated map of human protein isoforms for accelerated research. Database : the journal of biological databases and curation, 2026.

Kim SH, et al. (2026) Overexpression of cytosolic NADP-malic enzyme 1 from the common ice plant enhances water-deficit and high-light stress tolerance by modulating water-use efficiency and flavonoid biosynthesis. The Plant journal : for cell and molecular biology, 126(5), e70968.

Parra-Calisto A, et al. (2026) Type VI Secretion Systems in *Salmonella* Encode New Effectors with Putative Antibacterial and Anti-Eukaryotic Activities. Microorganisms, 14(6).

Yu ZX, et al. (2026) Chromosome-level genome of *Mosla chinensis* from alpine ecotype provides insights into terpenoid biosynthesis and germplasm exploration. Frontiers in plant science, 17, 1819008.

Zou R, et al. (2026) A chromosome-level genome assembly of *Cistanche deserticola* provides insights into its evolution and molecular mechanisms of parasitism. Plant communications, 7(1), 101581.

Gao K, et al. (2026) Chromosome-level genome assembly and annotation of the schizothoracine fish *Gymnodiptychus pachycheilus*. Scientific data, 13(1).

Ha X, et al. (2026) Candidate genes and molecular mechanisms regulating tiller development in wild Kentucky bluegrass. BMC plant biology, 26(1), 212.

Arshad E, et al. (2026) Identification, Cloning and Expression of Ferritin M-like Subunit from the Indian Oyster, *Magallana bilineata* (Rafinesque, 1798). Genes, 17(3).

Joshi A, et al. (2026) CTG clade-specific proteins of the RSC chromatin-remodeling complex regulate cell cycle progression of a critical priority fungal pathogen, *Candida albicans*. mSphere, 11(4), e0008426.

Wu J, et al. (2026) Peripheral lncRNA-IL1RAP Dysregulation in Schizophrenia: A Multi-Omics Bridge Between Immunity and Diagnosis. Brain and behavior, 16(4), e71384.

Liber JA, et al. (2026) *Aimea* gen. nov. defines a novel plant-associated yeast genus in Microbotryomycetes with three novel species. bioRxiv : the preprint server for biology.

Shen L, et al. (2026) T cell receptor-engineered T cells targeting the TP53R248Q neoantigen elicit antitumor effects in human cancer models. The Journal of clinical investigation, 136(5).

Nneji LM, et al. (2026) First Chromosome-level Genome Assembly and Annotation of an Endangered Freshwater Stingray (*Fontitrygon garouaensis*) from Africa. Scientific data, 13(1).