

Resource Summary Report

Generated by [nidm-terms](#) on Sep 3, 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: 20260829T182133+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 [nidm-terms](#) .

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).