

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 analysis service, data or information resource, database, service resource, production service resource, analysis 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: 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: 20260801T042533+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 2165 mentions in open access literature.

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

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.

Mu W, et al. (2025) The haplotype-resolved T2T genome for *Bauhinia × blakeana* sheds light on the genetic basis of flower heterosis. *GigaScience*, 14.

Garg J, et al. (2025) Bromodomain proteins IBD1 and IBD2 link histone acetylation to SWR1- and INO80-mediated H2A.Z regulation in *Tetrahymena*. *Epigenetics & chromatin*, 18(1), 51.

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

Costa VA, et al. (2025) Limited similarity in microbial composition among coral reef fishes from the Great Barrier Reef, Australia. *FEMS microbiology ecology*, 101(3).

Santini S, et al. (2025) Pacmanvirus isolated from the Lost City hydrothermal field extends the concept of transpoviron beyond the family Mimiviridae. *The ISME journal*, 19(1).

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.

Tarkowski P, et al. (2025) Antimicrobial Peptides as Part of the Arsenal of Constitutive and Inducible Seed Defences in Tomato Seed Exudates Against Pathogens. *Molecular plant pathology*, 26(10), e70164.

Guío J, et al. (2025) NsrM (AlI0345) and NsrX (Alr1976), two FurC (PerR)-targeted transcriptional regulators, modulate nitrogen metabolism and heterocyst differentiation genes in the cyanobacterium *Anabaena* sp. strain PCC 7120. *Microbiology spectrum*, 13(11), e0231125.

Arantes LS, et al. (2025) Haplotype-resolved reference genomes of the sea turtle clade unveil ultra-syntenic genomes with hotspots of divergence. *GigaScience*, 14.

Lefoulon E, et al. (2025) Evolutionary Diversification and Functions of the Candidate Male Killing Gene *wmk*. *Genome biology and evolution*, 17(10).

Dimond A, et al. (2025) PBK/TOPK mediates Ikaros, Aiolos and CTCF displacement from mitotic chromosomes and alters chromatin accessibility at selected C2H2-zinc finger protein binding sites. *Nature communications*, 16(1), 8348.

Peng F, et al. (2025) An updated compendium of *Caenorhabditis elegans* RNA-binding proteins and their regulation. *G3 (Bethesda, Md.)*, 15(9).

He J, et al. (2025) Chromosome-level genome assembly of stem borer *Batocera rufomaculata* using PacBio HiFi and Hi-C sequencing. *Scientific data*, 12(1), 1099.

Lailaja VP, et al. (2025) Tapping the untapped: type II L-asparaginase from marine crustacean-derived *Chryseomicrobium amycolyticum* as a potential bio better for blood cancer therapy. *Scientific reports*, 15(1), 26759.

Liu F, et al. (2025) Role of carbohydrate-active enzymes in brown planthopper virulence and adaptability. *Frontiers in plant science*, 16, 1554498.

Jeyaraj A, et al. (2025) The regulation of auxin receptor gene *CsAFB2* by *csn-miR393a* confers resistance against *Colletotrichum gloeosporioides* in tea plants. *Molecular plant pathology*, 26(4), e13499.

Tariq TB, et al. (2025) Molecular modelling and gene expression analysis to probe the GT-? trihelix transcription factors in *Solanum tuberosum* under drought stress. *Scientific reports*, 15(1), 12471.

Xu S, et al. (2025) Multi-omics analysis of yolk and allantoic fluid in chicken embryonic development and sexual differentiation. *Poultry science*, 104(8), 105349.

Martín-Zamora FM, et al. (2025) A dynamic histone-based chromatin regulatory toolkit underpins genome and developmental evolution in an invertebrate clade. *Genome biology*, 26(1), 160.