

Resource Summary Report

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ProRule

RRID:SCR_007875

Type: Tool

Proper Citation

ProRule (RRID:SCR_007875)

Resource Information

URL: <http://www.expasy.org/tools/scanprosite>

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Description: A sister database to ProSite, is constituted of manually created rules that increase the discriminatory power of PROSITE motifs (generally profiles) by providing additional information about functionally and/or structurally critical amino acids and can automatically generate annotation based on PROSITE motifs in the UniProtKB/Swiss-Prot format. Each ProRule is defined in the UniRule format. In addition to these rules corresponding to a unique PROSITE motif, there are also rules triggered by a specific combination of PROSITE motifs called metamotifs. Metamotifs allow the definition of arrangements of domains separated by spacers of variable size, as well as the anchoring to the N- and/or C-termini and the exclusion of a PROSITE motif. ProRule uses the UniRule format that is common to all types of rules created to annotate UniProtKB/Swiss-Prot, including the HAMAP family rules. Each rule contains information used to provide template based annotation associated with the domain or family detected by the PROSITE motif. ProRule is used to create UniProtKB/Swiss-Prot lines with basic and complex annotation derived from the presence of the domain and of biologically critical amino acids: domain name and boundaries, EC number, function, keywords, associated PROSITE patterns, PTMs, active sites, disulfide bonds, etc.). ProRule contains notably the position of structurally and/or functionally critical amino acid(s), as well as the condition(s) they must fulfil to play their biological role(s). Part of these supplementary data are used by ScanProsite that not only provides the protein sequence matched by a profile, but also information about the relevance of biologically meaningful residues, like active sites, binding sites, post-translational modification sites or disulfide bonds, to help function determination

Synonyms: ProRule

Resource Type: data or information resource, database

Resource Name: ProRule

Resource ID: SCR_007875

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260804T043334+0000

Ratings and Alerts

No rating or validation information has been found for ProRule.

No alerts have been found for ProRule.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 95 mentions in open access literature.

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

Sangster AG, et al. (2025) Zero-shot segmentation using embeddings from a protein language model identifies functional regions in the human proteome. PLoS computational biology, 21(11), e1012929.

Fu D, et al. (2022) Three Heat Shock Protein Genes and Antioxidant Enzymes Protect *Pardosa pseudoannulata* (Araneae: Lycosidae) from High Temperature Stress. International journal of molecular sciences, 23(21).

M Victorio VC, et al. (2021) NanoUPLC-MSE reveals differential abundance of gluten proteins in wheat flours of different technological qualities. Journal of proteomics, 239, 104181.

Geng M, et al. (2021) Evolutionary history and functional characterization of Lj-TICAM-a and Lj-TICAM-b formed via lineage-specific tandem duplication in lamprey (*Lampetra japonica*). Genomics, 113(4), 2756.

Kim JW, et al. (2020) First report of cathepsin E in a teleost (Korean rose bitterling, *Rhodeus uyekii*): Molecular characterisation and tissue distribution. Developmental and comparative immunology, 106, 103607.

Zhao Z, et al. (2020) Structural Insights into the Binding Modes of Viral RNA-Dependent RNA Polymerases Using a Function-Site Interaction Fingerprint Method for RNA Virus Drug Discovery. Journal of proteome research, 19(11), 4698.

Hahm HS, et al. (2020) Global targeting of functional tyrosines using sulfur-triazole exchange chemistry. Nature chemical biology, 16(2), 150.

Zhang C, et al. (2019) Genome-Wide Analysis of the Zn(II)?Cys? Zinc Cluster-Encoding Gene Family in *Tolypocladium guangdongense* and Its Light-Induced Expression. *Genes*, 10(3).

Wen J, et al. (2019) The auxin response factor gene family in allopolyploid *Brassica napus*. *PloS one*, 14(4), e0214885.

Greb-Markiewicz B, et al. (2019) The subcellular localization of bHLH transcription factor TCF4 is mediated by multiple nuclear localization and nuclear export signals. *Scientific reports*, 9(1), 15629.

Li YX, et al. (2019) Construction of MC1R and ASIP Eukaryotic Expression Vector and its Regulation of Plumage Color in Japanese Quail (*Coturnix japonica*). *The journal of poultry science*, 56(2), 84.

Teng H, et al. (2019) Novel insights into the evolution of the caveolin superfamily and mechanisms of antiapoptotic effects and cell proliferation in lamprey. *Developmental and comparative immunology*, 95, 118.

Zhang XX, et al. (2019) Cloning of a new HSP70 gene from western flowerthrips, *Frankliniella occidentalis*, and expression patterns during thermal stress. *PeerJ*, 7, e7687.

Cho M, et al. (2019) Codon usage patterns of LT-Ag genes in polyomaviruses from different host species. *Virology journal*, 16(1), 137.

Bordenave CD, et al. (2019) Defining novel plant polyamine oxidase subfamilies through molecular modeling and sequence analysis. *BMC evolutionary biology*, 19(1), 28.

Babirye P, et al. (2018) Identity and validity of conserved B cell epitopes of filovirus glycoprotein: towards rapid diagnostic testing for Ebola and possibly Marburg virus disease. *BMC infectious diseases*, 18(1), 498.

Greb-Markiewicz B, et al. (2018) Multiple sequences orchestrate subcellular trafficking of neuronal PAS domain-containing protein 4 (NPAS4). *The Journal of biological chemistry*, 293(29), 11255.

Akbar N, et al. (2018) Characterization of metabolic network of oxalic acid biosynthesis through RNA seq data analysis of developing spikes of finger millet (*Eleusine coracana*): Deciphering the role of key genes involved in oxalate formation in relation to grain calcium accumulation. *Gene*, 649, 40.

Iribarren PA, et al. (2018) SUMO polymeric chains are involved in nuclear foci formation and chromatin organization in *Trypanosoma brucei* procyclic forms. *PloS one*, 13(2), e0193528.

Wang MM, et al. (2018) Global Analysis of WOX Transcription Factor Gene Family in *Brassica napus* Reveals Their Stress- and Hormone-Responsive Patterns. *International journal of molecular sciences*, 19(11).