

Resource Summary Report

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UniProtKB/Swiss-Prot

RRID:SCR_021164

Type: Tool

Proper Citation

UniProtKB/Swiss-Prot (RRID:SCR_021164)

Resource Information

URL: <https://www.expasy.org/resources/uniprotkb-swiss-prot>

Proper Citation: UniProtKB/Swiss-Prot (RRID:SCR_021164)

Description: Curated component of UniProtKB (produced by the UniProt consortium). It contains hundreds of thousands of protein descriptions, including function, domain structure, subcellular location, post-translational modifications and functionally characterized variants.

Synonyms: Swiss-Prot, SwissProt

Resource Type: data or information resource, database

Defining Citation: [DOI:10.1093/nar/26.1.38](https://doi.org/10.1093/nar/26.1.38)

Keywords: protein descriptions, protein function, protein, domain structure, subcellular location, post-translational modifications, functionally characterized variants

Funding: SIB Swiss Institute of Bioinformatics

Availability: Free, Freely available

Resource Name: UniProtKB/Swiss-Prot

Resource ID: SCR_021164

Alternate IDs: r3d100010677

Alternate URLs: <https://doi.org/10.17616/R33314>

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Record Creation Time: 20220129T080354+0000

Record Last Update: 20260919T195738+0000

Ratings and Alerts

No rating or validation information has been found for UniProtKB/Swiss-Prot.

No alerts have been found for UniProtKB/Swiss-Prot.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 658 mentions in open access literature.

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

Radloff HS, et al. (2026) A single-cell derived spheroid approach to dissect intratumoural heterogeneity in colorectal cancer: cell lines show changes in proteomes and therapeutic response to 5-FU. *Journal of cancer research and clinical oncology*, 152(1), 43.

Navarro-Lérida I, et al. (2026) Loss of G?q reshapes fibroblast traits and drives tumor-stroma remodeling in oral cancer progression. *EMBO reports*, 27(10), 2639.

Saldarriaga-Córdoba M, et al. (2026) In-Depth Multi-Assembler Venom-Gland Transcriptomics of Three Medically Important Colombian Snakes Highlights Diversity of Accessory, Low-Abundance Protein Families. *Toxins*, 18(3).

Dersch L, et al. (2026) Vector venom: venomomics of *Aedes albopictus* reveals a large enzyme repertoire and novel cecropins with activity against *E. coli*. *npj drug discovery*, 3(1).

Kemunto G, et al. (2026) Advancing Extracellular Vesicle Research: A Review of Systems Biology and Multiomics Perspectives. *Proteomics*, 26(2-3), 33.

Abdulla ZI, et al. (2026) mPFC Synaptosome Proteomics Reveals Novel Pathways and Muscarinic Receptor Changes in a Learned Helplessness Mouse Model. *bioRxiv : the preprint server for biology*.

Abdulla ZI, et al. (2026) mPFC Synaptosome Proteomics Reveals Novel Pathways and Muscarinic Receptor Changes in a Learned Helplessness Mouse Model. *eNeuro*, 13(4).

Liao X, et al. (2026) Dynamic lysine acetylation and succinylation of platelet proteins regulates platelet storage lesion: mechanistic insights from multi-omics. *Annals of medicine*, 58(1), 2635200.

Guo Y, et al. (2026) BiCLUM: Bilateral contrastive learning for unpaired single-cell multi-omics integration. *PLoS computational biology*, 22(2), e1013932.

Shipova AA, et al. (2026) From Adam's rib: the Siberian moth's female W chromosome is derived from its Z counterpart. *Molecular biology and evolution*, 43(3).

Zhao T, et al. (2026) A tandem recruitment site in the pseudokinase scaffold PEAK3 is subject to phosphorylation-dependent regulation and cancer-associated mutations. *The Journal of biological chemistry*, 302(5), 111365.

Qiu K, et al. (2026) RBM15/IGF2BP2-PTPRH m6A regulatory axis in non-small cell lung cancer. *Cellular oncology (Dordrecht, Netherlands)*, 49(3).

Yin R, et al. (2026) Engineering a Fungal Non-Reducing Polyketide Synthase with an Apparently Inactive Product-Template Domain Reveals Insights into the Catalytic Reprogramming. *International journal of molecular sciences*, 27(12).

Zamperoni M, et al. (2026) EMILIN1 emerges as a TGF β /SETDB1-regulated secreted biomarker in Duchenne muscular dystrophy. *Cell death & disease*, 17(1).

Pan YC, et al. (2026) Protocol to define the in situ proteome of endogenous PRC2 bodies in the triple-negative breast cancer cell line BoM-1833 using optoproteomics. *STAR protocols*, 7(2), 104578.

Hazinia S, et al. (2026) Integrated Metabolomics, Transcriptomics, and Ultrastructural Assessment of the Myco-Heterotrophic Plant, *Monotropa uniflora*. *Plant direct*, 10(4), e70165.

Singh CM, et al. (2026) Genome-wide identification and characterization of polygalacturonase gene family in linseed (*Linum usitatissimum* L.) and comparative expression in its wild relative (*Linum bienne*) upon bud fly infestation. *BMC plant biology*, 26(1), 231.

Altayyar A, et al. (2026) FuDiCo: Gene Fusion-Initiated Path Propagation for Disease Comorbidity Prediction. *Current issues in molecular biology*, 48(6).

Zongo SV, et al. (2026) Plasma proteomic profiling reveals distinct protein signatures associated with hepatocellular carcinoma in chronic hepatitis B infection. *Clinical proteomics*, 23(1), 7.

Yan Y, et al. (2026) Genomic insights into the biosynthetic capacity of the sponge-associated fungus *Aspergillus puulaauensis* Hmp-F48. *BMC genomics*, 27(1), 213.