

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 2026

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: 20260729T044503+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 601 mentions in open access literature.

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

Krüger T, et al. (2025) Toxin data quality: a critical examination of bacterial exotoxins and animal toxins. BMC research notes, 18(1), 418.

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. GigaScience, 14.

Bian C, et al. (2025) Telomere-to-telomere chromosome-scale genome assemblies of black and golden koi carp variants support construction of an ancient karyotype of Cypriniformes. GigaScience, 14.

Nath R, et al. (2025) Lineage-Specific Class-A GPCR Dynamics Reflect Diverse Chemosensory Adaptations in Lophotrochozoa. Molecular biology and evolution, 42(3).

Basnet N, et al. (2025) Blocking S1P4 signaling attenuates brain injury in mice with ischemic stroke. Journal of advanced research, 78, 681.

Martín-Díaz A, et al. (2025) De novo transcriptome assembly of the plant Helianthemum marifolium for the study of adaptive mechanisms. Scientific data, 12(1), 515.

de Groot R, et al. (2025) Cleavage of Cartilage Oligomeric Matrix Protein (COMP) by ADAMTS4 generates a neoepitope associated with osteoarthritis and other forms of degenerative joint disease. Matrix biology : journal of the International Society for Matrix Biology, 135, 106.

Ponz-Segrelles G, et al. (2025) Sex-specific differential gene expression during stolonization in the branching syllid Ramisyllis kingghidorahi (Annelida, Syllidae). BMC genomics, 26(1), 405.

Gu J, et al. (2025) Nascent liver proteome reveals enzymes and transcription regulators under physiological and alcohol exposure conditions. Nature communications, 16(1), 7945.

Xu N, et al. (2025) Reconstruction and application of a genome-scale metabolic model for Streptococcus suis. BMC genomics, 26(1), 997.

Krueger T, et al. (2025) Exo-Tox: Identifying Exotoxins from secreted bacterial proteins. *BioData mining*, 18(1), 52.

Blidner AG, et al. (2025) Glycosylation-driven programs coordinate immunoregulatory and pro-angiogenic functions of myeloid-derived suppressor cells. *Immunity*, 58(6), 1553.

Taggi V, et al. (2025) Targeted and Untargeted Proteomics-based Comparison of Adenoviral Infected hCMEC/D3 and hBMEC as a Human Brain Endothelial Cells to Study the OATP2B1 Transporter. *Molecular neurobiology*, 62(7), 9074.

Cao J, et al. (2025) Chromosome-level genome assembly of predatory Eocanthecona furcellata. *Scientific data*, 12(1), 1621.

Pérez-Martínez C, et al. (2025) Pronounced seasonal dynamics in transcription of vitamin B1 acquisition strategies diverge among Baltic Sea bacterioplankton. *Environmental microbiome*, 20(1), 115.

Chrysostomakis I, et al. (2025) A high-quality reference genome for the Ural Owl (*Strix uralensis*) enables investigations of cell cultures as a genomic resource for endangered species. *GigaScience*, 14.

Aruvornlop P, et al. (2025) Phosphoproteomic profiling of feline mammary carcinoma: Insights into tumor grading and potential therapeutic targets. *PloS one*, 20(8), e0330520.

Jabbari M, et al. (2025) Association between MASP2 gene polymorphisms and susceptibility to Covid-19 in Iranian patients: a case-control study. *BMC infectious diseases*, 25(1), 1405.

Flöge K, et al. (2025) OneProt: Towards multi-modal protein foundation models via latent space alignment of sequence, structure, binding sites and text encoders. *PLoS computational biology*, 21(11), e1013679.

Zarra F, et al. (2025) Novel insights into insect mediated polystyrene biodegradation through bacterial genome analyses. *Scientific reports*, 15(1), 1047.