Resource Summary Report

Generated by NIF on Apr 8, 2025

UniProtKB

RRID:SCR_004426
Type: Tool

Proper Citation

UniProtKB (RRID:SCR_004426)

Resource Information

URL: http://www.uniprot.org/help/uniprotkb

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Description: Central repository for collection of functional information on proteins, with accurate and consistent annotation. In addition to capturing core data mandatory for each UniProtKB entry (mainly, the amino acid sequence, protein name or description, taxonomic data and citation information), as much annotation information as possible is added. This includes widely accepted biological ontologies, classifications and cross-references, and experimental and computational data. The UniProt Knowledgebase consists of two sections, UniProtKB/Swiss-Prot and UniProtKB/TrEMBL. UniProtKB/Swiss-Prot (reviewed) is a high quality manually annotated and non-redundant protein sequence database which brings together experimental results, computed features, and scientific conclusions. UniProtKB/TrEMBL (unreviewed) contains protein sequences associated with computationally generated annotation and large-scale functional characterization that await full manual annotation. Users may browse by taxonomy, keyword, gene ontology, enzyme class or pathway.

Synonyms: UniProtKB, UniProtKB/Swiss-Prot, UniProtKB/TrEMBL, UniProt Knowledgebase

Resource Type: storage service resource, data repository, service resource, database, data or information resource

Defining Citation: PMID:15888679, PMID:18287689

Keywords: protein, annotation, amino acid sequence, taxonomy, proteome

Funding:

Availability: Available to the research community, The community can contribute to this resource

Resource Name: UniProtKB

Resource ID: SCR_004426

Alternate IDs: nlx_53981

Record Creation Time: 20220129T080224+0000

Record Last Update: 20250407T215427+0000

Ratings and Alerts

No rating or validation information has been found for UniProtKB.

No alerts have been found for UniProtKB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6007 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Lützkendorf J, et al. (2025) Blobby is a synaptic active zone assembly protein required for memory in Drosophila. Nature communications, 16(1), 271.

Boger RS, et al. (2025) Functional protein mining with conformal guarantees. Nature communications, 16(1), 85.

Yan Y, et al. (2025) Degenerated vision, altered lipid metabolism, and expanded chemoreceptor repertoires enable Lindaspio polybranchiata to thrive in deep-sea cold seeps. BMC biology, 23(1), 13.

Zhang Q, et al. (2025) Apoptotic breast cancer cells after chemotherapy induce pro-tumour extracellular vesicles via LAP-competent macrophages. Redox biology, 80, 103485.

Seye AO, et al. (2025) Clinical Features of Human Parvovirus B19-Associated Encephalitis Identified in the Dakar Region, Senegal, and Viral Genome Characterization. Viruses, 17(1).

Wang X, et al. (2025) A novel approach for target deconvolution from phenotype-based screening using knowledge graph. Scientific reports, 15(1), 2414.

Guinet B, et al. (2025) Dating the origin of a viral domestication event in parasitoid wasps attacking Diptera. Proceedings. Biological sciences, 292(2039), 20242135.

Myszczynski K, et al. (2025) In-Depth Analysis of miRNA Binding Sites Reveals the Complex Response of Uterine Epithelium to miR-26a-5p and miR-125b-5p During Early Pregnancy. Molecular & cellular proteomics : MCP, 24(1), 100879.

Fay CX, et al. (2025) Global proteomics and affinity mass spectrometry analysis of human Schwann cells indicates that variation in and loss of neurofibromin (NF1) alters protein expression and cellular and mitochondrial metabolism. Scientific reports, 15(1), 3883.

Jeyagaran A, et al. (2025) ECM Proteins Nidogen-1 and Decorin Restore Functionality of Human Islets of Langerhans upon Hypoxic Conditions. Advanced healthcare materials, 14(2), e2403017.

Kang YS, et al. (2025) Leveraging a new data resource to define the response of Cryptococcus neoformans to environmental signals. Genetics, 229(1), 1.

Buzzao D, et al. (2025) FunCoup 6: advancing functional association networks across species with directed links and improved user experience. Nucleic acids research, 53(D1), D658.

Herrera LPT, et al. (2025) GPCRdb in 2025: adding odorant receptors, data mapper, structure similarity search and models of physiological ligand complexes. Nucleic acids research, 53(D1), D425.

Oh S, et al. (2025) Genome-wide association studies in lettuce reveal the interplay of seed age, color, and germination under high temperatures. Scientific reports, 15(1), 733.

Gjorgjevikj D, et al. (2025) The Psu protein of phage satellite P4 inhibits transcription termination factor ? by forced hyper-oligomerization. Nature communications, 16(1), 550.

Frolov A, et al. (2025) Responsivity of Two Pea Genotypes to the Symbiosis with Rhizobia and Arbuscular Mycorrhiza Fungi-A Proteomics Aspect of the "Efficiency of Interactions with Beneficial Soil Microorganisms" Trait. International journal of molecular sciences, 26(2).

Sangkapat S, et al. (2025) Potential Interaction of Pinocembrin with Drug Transporters and Hepatic Drug-Metabolizing Enzymes. Pharmaceuticals (Basel, Switzerland), 18(1).

Subramanian V, et al. (2025) Long-Term Effects of Radiation Therapy on Cerebral Microvessel Proteome: A Six-Month Post-Exposure Analysis. bioRxiv : the preprint server for biology.

Prattico C, et al. (2025) Identification of novel fructo-oligosaccharide bacterial consumers by pulse metatranscriptomics in a human stool sample. mSphere, 10(1), e0066824.

Baltsavia I, et al. (2025) MjCyc: Rediscovering the pathway-genome landscape of the first sequenced archaeon, Methanocaldococcus (Methanococcus) jannaschii. iScience, 28(1), 111546.