

Resource Summary Report

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

Defining Citation: [PMID:15888679](#), [PMID:18287689](#)

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

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

Resource Name: UniProtKB

Resource ID: SCR_004426

Alternate IDs: r3d100011521, nlx_53981

Alternate URLs: <https://doi.org/10.17616/R3NK9Z>

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260804T043226+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 6654 mentions in open access literature.

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

Hadarovich A, et al. (2026) PICNIC web server for predicting proteins involved in biomolecular condensates. *Bioinformatics* (Oxford, England), 42(1).

Sari E, et al. (2026) Gene duplication, horizontal gene transfer, and trait trade-offs drive evolution of postfire resource acquisition in pyrophilous fungi. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2519152123.

DiSanza BL, et al. (2026) Bi-allelic variants in BCAT1 impair mitochondrial function and are associated with a candidate neurometabolic disorder. *HGG advances*, 7(1), 100525.

Boegli A, et al. (2026) The NLRP6 inflammasome is activated by sterile or pathogen-induced endolysosomal damage. *The EMBO journal*, 45(1), 30.

Ramasamy P, et al. (2026) Assessing the relation between protein phosphorylation, AlphaFold3 models, and conformational variability. *Protein science : a publication of the Protein Society*, 35(1), e70376.

Jiang H, et al. (2026) SenSeqNet: A Deep Learning Framework for Cellular Senescence Detection From Protein Sequences. *Aging cell*, 25(1), e70344.

Qu Y, et al. (2026) Targeting NDUFS8 in basal forebrain ameliorates cognitive decline related to chronic cerebral hypoperfusion. *Theranostics*, 16(3), 1328.

Cai Z, et al. (2026) The Cullin3-Ring E3 ubiquitin ligase complex and USP14 regulate spastin-mediated microtubule severing and promotion of neurite outgrowth. *Neural*

regeneration research, 21(4), 1641.

Gooden F, et al. (2026) Pharmacogenetic hSLCO1B1*14-Guided Dosing of Methotrexate in Transgenic Arthritic Mice Normalizes Exposure and Response. *Clinical and translational science*, 19(1), e70449.

Gabrišová K, et al. (2026) Electrical pulse stimulation reflecting the episodic nature of real-life exercise modulates metabolic and secretory profile of primary human myotubes. *FEBS open bio*, 16(1), 127.

Hunker O, et al. (2026) AlphaFold-guided phylogenetic analyses suggest surprising heterogeneity in metazoan replication origin licensing mechanisms. *The EMBO journal*, 45(1), 310.

Kim JA, et al. (2026) Conserved stromal EMT program controls regenerative capacity of mesenchymal stromal cells across multiple tissues. *Science advances*, 12(1), eady9664.

Ho-Xuan H, et al. (2025) YTHDF proteins and m6A-RNA clients undergo autophagic turnover during contact inhibition. *Cell reports*, 44(9), 116188.

Morais LH, et al. (2025) The gut microbiome promotes mitochondrial respiration in the brain of a Parkinson's disease mouse model. *NPJ Parkinson's disease*, 11(1), 301.

Conn T, et al. (2025) Genome assembly and annotation of *Acropora pulchra* from Mo'orea French Polynesia. *GigaByte (Hong Kong, China)*, 2025, gigabyte153.

Villette R, et al. (2025) Integrated multi-omics highlights alterations of gut microbiome functions in prodromal and idiopathic Parkinson's disease. *Microbiome*, 13(1), 200.

Lecointre M, et al. (2025) HPV16-Expressing Tumors Release Multiple IL1 Ligands to Orchestrate Systemic Immunosuppression Whose Disruption Enables Efficacy of a Therapeutic Vaccine. *Cancer discovery*, 15(7), 1458.

Fernandez Flores LC, et al. (2025) Multiple Antibody-Coated Gold Nanoparticle-Based ExoAssay for Rapid Isolation of CNS-Specific Exosomes From Blood. *Journal of neurochemistry*, 169(10), e70263.

Han H, et al. (2025) A telomere-to-telomere phased genome of an octoploid strawberry reveals a receptor kinase conferring anthracnose resistance. *GigaScience*, 14.

Becht DC, et al. (2025) The YEATS domain is a selective reader of histone methacrylation. *Structure (London, England : 1993)*, 33(7), 1233.