

Resource Summary Report

Generated by PRECISE-TBI on Aug 1, 2026

UniProtKB Keywords

RRID:SCR_004313

Type: Tool

Proper Citation

UniProtKB Keywords (RRID:SCR_004313)

Resource Information

URL: <http://www.uniprot.org/keywords/>

Proper Citation: UniProtKB Keywords (RRID:SCR_004313)

Description: UniProtKB entries are tagged with keywords that can be used to retrieve particular subsets of entries. There are 10 categories of keywords: Biological process Cellular component Coding sequence diversity Developmental stage Disease Domain Ligand Molecular function Post-translation modification Technical term You may browse by hierarchy, search in Keywords, or list all keywords. By default, searching the keywords will look for matches in both name and definition.

Abbreviations: SP KW

Resource Type: ontology, controlled vocabulary, data or information resource, database

Resource Name: UniProtKB Keywords

Resource ID: SCR_004313

Alternate IDs: nlx_32497

Record Creation Time: 20220129T080223+0000

Record Last Update: 20260801T190235+0000

Ratings and Alerts

No rating or validation information has been found for UniProtKB Keywords.

No alerts have been found for UniProtKB Keywords.

Data and Source Information

Usage and Citation Metrics

We found 264 mentions in open access literature.

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

Chen K, et al. (2025) Exploring the role of BpPIN3 in hormonal regulation and branching morphogenesis of *Betula pendula*. *BMC plant biology*, 25(1), 1772.

Chen K, et al. (2024) BpWOX11 promotes adventitious root formation in *Betula pendula*. *BMC plant biology*, 24(1), 17.

Lussi YC, et al. (2023) Searching and Navigating UniProt Databases. *Current protocols*, 3(3), e700.

Tan J, et al. (2020) Transcriptome profiling of venom gland from wasp species: de novo assembly, functional annotation, and discovery of molecular markers. *BMC genomics*, 21(1), 427.

Nasir A, et al. (2017) Identification of Capsid/Coat Related Protein Folds and Their Utility for Virus Classification. *Frontiers in microbiology*, 8, 380.

Chandrashekar DS, et al. (2017) UALCAN: A Portal for Facilitating Tumor Subgroup Gene Expression and Survival Analyses. *Neoplasia (New York, N.Y.)*, 19(8), 649.

Li HH, et al. (2014) Membrane labeling of coral gastrodermal cells by biotinylation: the proteomic identification of surface proteins involving cnidaria-dinoflagellate endosymbiosis. *PloS one*, 9(1), e85119.

Rogler A, et al. (2014) Loss of MTUS1/ATIP expression is associated with adverse outcome in advanced bladder carcinomas: data from a retrospective study. *BMC cancer*, 14, 214.

Zhi XY, et al. (2014) The futasine pathway played an important role in menaquinone biosynthesis during early prokaryote evolution. *Genome biology and evolution*, 6(1), 149.

Zhang X, et al. (2014) Molecular diagnosis of putative Stargardt disease by capture next generation sequencing. *PloS one*, 9(4), e95528.

Kumar N, et al. (2014) The effect of silver nanoparticles on seasonal change in arctic tundra bacterial and fungal assemblages. *PloS one*, 9(6), e99953.

Peñate Medina TA, et al. (2014) Identification of Sphingomyelinase on the Surface of *Chlamydia pneumoniae*: Possible Role in the Entry into Its Host Cells. *Interdisciplinary perspectives on infectious diseases*, 2014, 412827.

Bhargava K, et al. (2014) Molecular Docking studies of D2 Dopamine receptor with Risperidone derivatives. *Bioinformation*, 10(1), 8.

Mártonfalvi Z, et al. (2014) Individual globular domains and domain unfolding visualized in overstretched titin molecules with atomic force microscopy. PloS one, 9(1), e85847.

Ma J, et al. (2014) O-GlcNAc profiling: from proteins to proteomes. Clinical proteomics, 11(1), 8.

Crump SM, et al. (2014) Arrhythmogenic KCNE gene variants: current knowledge and future challenges. Frontiers in genetics, 5, 3.

Rosenberg MI, et al. (2014) Dual mode of embryonic development is highlighted by expression and function of *Nasonia* pair-rule genes. eLife, 3, e01440.

Dekaminaviciute D, et al. (2014) Development and characterization of new monoclonal antibodies against human recombinant CA XII. BioMed research international, 2014, 309307.

Xu T, et al. (2014) Comparative functional analysis of wheat (*Triticum aestivum*) zinc finger-containing glycine-rich RNA-binding proteins in response to abiotic stresses. PloS one, 9(5), e96877.

Laehnemann D, et al. (2014) Genomics of rapid adaptation to antibiotics: convergent evolution and scalable sequence amplification. Genome biology and evolution, 6(6), 1287.