

Resource Summary Report

Generated by [RRID](#) on Aug 11, 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: data or information resource, database, controlled vocabulary, ontology

Resource Name: UniProtKB Keywords

Resource ID: SCR_004313

Alternate IDs: nlx_32497

Record Creation Time: 20220129T080223+0000

Record Last Update: 20260811T043217+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 265 mentions in open access literature.

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

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.

Schmidt S, et al. (2022) Primary cilia and SHH signaling impairments in human and mouse models of Parkinson's disease. *Nature communications*, 13(1), 4819.

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.

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

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.

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.

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

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

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

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.

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.

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

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.

Shrestha AM, et al. (2014) A bioinformatician's guide to the forefront of suffix array construction algorithms. Briefings in bioinformatics, 15(2), 138.

Jiang Y, et al. (2014) Identifying gastric cancer related genes using the shortest path algorithm and protein-protein interaction network. BioMed research international, 2014, 371397.

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