

Resource Summary Report

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UniProtKB Subcellular Locations

RRID:SCR_004373

Type: Tool

Proper Citation

UniProtKB Subcellular Locations (RRID:SCR_004373)

Resource Information

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

Proper Citation: UniProtKB Subcellular Locations (RRID:SCR_004373)

Description: The subcellular locations in which a protein is found are described in UniProtKB entries with a controlled vocabulary, which includes also membrane topology and orientation terms. You may search in subcellular locations or list them all along with their definitions (490). By default, searching the subcellular locations will look for matches in both name and definition.

Abbreviations: SP SL

Synonyms: UniProt Subcellular Locations

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

Resource Name: UniProtKB Subcellular Locations

Resource ID: SCR_004373

Alternate IDs: nlx_38886

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260731T042658+0000

Ratings and Alerts

No rating or validation information has been found for UniProtKB Subcellular Locations.

No alerts have been found for UniProtKB Subcellular Locations.

Data and Source Information

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

, et al. (2023) UniProt: the Universal Protein Knowledgebase in 2023. *Nucleic acids research*, 51(D1), D523.

Kustatscher G, et al. (2016) Multiclassifier combinatorial proteomics of organelle shadows at the example of mitochondria in chromatin data. *Proteomics*, 16(3), 393.

Chen YS, et al. (2014) The Chlamydia trachomatis type III secretion chaperone Slc1 engages multiple early effectors, including TepP, a tyrosine-phosphorylated protein required for the recruitment of Crkl-II to nascent inclusions and innate immune signaling. *PLoS pathogens*, 10(2), e1003954.

Friedman Y, et al. (2014) miRror-Suite: decoding coordinated regulation by microRNAs. *Database : the journal of biological databases and curation*, 2014.

Sun J, et al. (2014) Network-assisted prediction of potential drugs for addiction. *BioMed research international*, 2014, 258784.

Wen F, et al. (2014) Genome-wide evolutionary characterization and expression analyses of WRKY family genes in *Brachypodium distachyon*. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 21(3), 327.

Ren J, et al. (2013) Identifying protein complexes based on density and modularity in protein-protein interaction network. *BMC systems biology*, 7 Suppl 4(Suppl 4), S12.

McWilliam H, et al. (2013) Analysis Tool Web Services from the EMBL-EBI. *Nucleic acids research*, 41(Web Server issue), W597.

Trivedi DK, et al. (2013) Molecular characterization of cyclophilin A-like protein from *Piriformospora indica* for its potential role to abiotic stress tolerance in *E. coli*. *BMC research notes*, 6, 555.

Trivedi DK, et al. (2013) Multiple abiotic stress responsive rice cyclophilin: (OsCYP-25) mediates a wide range of cellular responses. *Communicative & integrative biology*, 6(5), e25260.

Fan J, et al. (2012) MRmaid: The SRM Assay Design Tool for Arabidopsis and Other Species. *Frontiers in plant science*, 3, 164.

Gosu V, et al. (2012) Molecular evolution and structural features of IRAK family members. *PloS one*, 7(11), e49771.

Liu X, et al. (2012) Histone acetyltransferases in rice (*Oryza sativa* L.): phylogenetic analysis, subcellular localization and expression. *BMC plant biology*, 12, 145.

Patel A, et al. (2012) Pentamers not found in the universal proteome can enhance antigen specific immune responses and adjuvant vaccines. PloS one, 7(8), e43802.

Sharma V, et al. (2012) Identification of drought responsive proteins using gene ontology hierarchy. Bioinformation, 8(13), 595.

Hammerschmidt A, et al. (2012) Binding of regulatory subunits of cyclic AMP-dependent protein kinase to cyclic CMP agarose. PloS one, 7(7), e39848.