Resource Summary Report

Generated by dkNET on Apr 29, 2025

Cell-PLoc

RRID:SCR_011966

Type: Tool

Proper Citation

Cell-PLoc (RRID:SCR_011966)

Resource Information

URL: http://www.csbio.sjtu.edu.cn/bioinf/Cell-PLoc/

Proper Citation: Cell-PLoc (RRID:SCR_011966)

Description: A package of web-servers for predicting subcellular localization of proteins in

different organisms.

Abbreviations: Cell-PLoc

Synonyms: Cell-PLoc: A package of web-servers for predicting subcellular localization of

proteins in different organisms

Resource Type: production service resource, data analysis service, analysis service

resource, service resource

Defining Citation: PMID:18274516

Keywords: subcellular localization, protein, gram-negative protein, gram-positive protein,

virus

Funding:

Resource Name: Cell-PLoc

Resource ID: SCR_011966

Alternate IDs: OMICS 01617

Record Creation Time: 20220129T080307+0000

Record Last Update: 20250429T055457+0000

Ratings and Alerts

No rating or validation information has been found for Cell-PLoc.

No alerts have been found for Cell-PLoc.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 167 mentions in open access literature.

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

Huang R, et al. (2025) The Identification of Auxin Response Factors and Expression Analyses of Different Floral Development Stages in Roses. Genes, 16(1).

Zhao Y, et al. (2025) Genome-Wide Identification of CONSTANS-like (COL) Gene Family and the Potential Function of ApCOL08 Under Salt Stress in Andrographis paniculata. International journal of molecular sciences, 26(2).

Euceda-Padilla EA, et al. (2024) Trichomonas vaginalis Legumain-2, TvLEGU-2, Is an Immunogenic Cysteine Peptidase Expressed during Trichomonal Infection. Pathogens (Basel, Switzerland), 13(2).

Wei H, et al. (2024) Comprehensive analysis of annexin gene family and its expression in response to branching architecture and salt stress in crape myrtle. BMC plant biology, 24(1), 78.

Cheng R, et al. (2024) Genome-wide survey of KT/HAK/KUP genes in the genus Citrullus and analysis of their involvement in K+-deficiency and drought stress responses in between C. lanatus and C. amarus. BMC genomics, 25(1), 836.

Zhang W, et al. (2024) Discovery and Characterization of an Atypical Crustin Antimicrobial Peptide from Pollicipes pollicipes. Marine drugs, 22(12).

Yang X, et al. (2024) Genome-wide identification and characterization of bZIP gene family explore the responses of PsebZIP44 and PsebZIP46 in Pseudoroegneria libanotica under drought stress. BMC plant biology, 24(1), 1085.

Pan J, et al. (2024) Genome-wide characterization of TCP family and their potential roles in abiotic stress resistance of oat (Avena sativa L.). Frontiers in plant science, 15, 1382790.

Hao X, et al. (2024) Genome-wide identification, classification and expression analysis of the heat shock transcription factor family in Garlic (Allium sativum L.). BMC plant biology, 24(1), 421.

Tian Y, et al. (2024) Genome-wide identification and expression analysis of NF-Y gene family in tobacco (Nicotiana tabacum L.). Scientific reports, 14(1), 5257.

Tan C, et al. (2024) Development of multi-epitope mRNA vaccine against Clostridioides difficile using reverse vaccinology and immunoinformatics approaches. Synthetic and systems biotechnology, 9(4), 667.

Chen B, et al. (2024) Genome-wide analysis of UDP-glycosyltransferases family and identification of UGT genes involved in drought stress of Platycodon grandiflorus. Frontiers in plant science, 15, 1363251.

He S, et al. (2024) Genome-wide identification, characterization and expression analysis of the bZIP transcription factors in garlic (Allium sativum L.). Frontiers in plant science, 15, 1391248.

Zheng L, et al. (2024) Cloning and functional characterization of the legumin A gene (EuLEGA) from Eucommia ulmoides Oliver. Scientific reports, 14(1), 14111.

Sharma GK, et al. (2024) Advancing microbial diagnostics: a universal phylogeny guided computational algorithm to find unique sequences for precise microorganism detection. Briefings in bioinformatics, 25(6).

Liao R, et al. (2024) MYB transcription factors in Peucedanum Praeruptorum Dunn: the diverse roles of the R2R3-MYB subfamily in mediating coumarin biosynthesis. BMC plant biology, 24(1), 1135.

Zhao Y, et al. (2024) Identification of potential biomarkers from amino acid transporter in the activation of hepatic stellate cells via bioinformatics. Frontiers in genetics, 15, 1499915.

Lv WB, et al. (2024) CDPK protein in cotton: genomic-wide identification, expression analysis, and conferring resistance to heat stress. BMC plant biology, 24(1), 842.

Li Y, et al. (2024) Bioinformatic Identification and Expression Analyses of the MAPK-MAP4K Gene Family Reveal a Putative Functional MAP4K10-MAP3K7/8-MAP2K1/11-MAPK3/6 Cascade in Wheat (Triticum aestivum L.). Plants (Basel, Switzerland), 13(7).

Tang H, et al. (2024) Genome-Wide Identification of Peanut B-Boxs and Functional Characterization of AhBBX6 in Salt and Drought Stresses. Plants (Basel, Switzerland), 13(7).