

Resource Summary Report

Generated by T1D on Jul 30, 2026

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: analysis service resource, service resource, data analysis service, production service resource

Defining Citation: [PMID:18274516](#)

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

Resource Name: Cell-PLoc

Resource ID: SCR_011966

Alternate IDs: OMICS_01617

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260728T043401+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 203 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Jiang L, et al. (2025) Genome-Wide Characterization and Expression Analysis of the Cysteine-Rich Polycomb-like Protein Gene Family in Response to Hormone Signaling in Apple (*Malus domestica*). *International journal of molecular sciences*, 26(12).

Qian Y, et al. (2025) Identification of the ACA/ECA gene family and preliminary verification of their functional in calcium transport in lettuce. *Scientific reports*, 15(1), 20370.

Luo H, et al. (2025) Cloning and functional analysis of transcription factor AaCMB1 on carotenoid accumulation in spathe of *Anthurium andraeanum*. *Plant signaling & behavior*, 20(1), 2527961.

Hu X, et al. (2025) Genome-wide identification of VOZ gene family in ten cotton species and the function analysis of GhVOZ2 involved in heat stress response. *BMC genomics*, 26(1), 753.

Wu Y, et al. (2025) Genome-wide identification and expression analysis of the GARP superfamily in response to abiotic stresses in alfalfa (*Medicago sativa* L.). *BMC plant biology*, 25(1), 1395.

Li X, et al. (2025) Characterization of fatty acid desaturase gene family in *Glycine max* and their expression patterns in seeds after *Fusarium fujikuroi* infection. *Frontiers in plant science*, 16, 1540003.

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

Tian Y, et al. (2025) Genome-wide identification, phylogeny, and expression analysis of PEBP gene family in *Castanea mollissima*. *Frontiers in genetics*, 16, 1530910.

Yu Y, et al. (2025) The ERF transcription factor TaERF13-2B functions as a negative regulator of drought tolerance in *Arabidopsis* and wheat. *Frontiers in plant science*, 16, 1535850.

Hu ZY, et al. (2025) Genome-wide identification of invertase genes in sweetpotato and its response to nitrogen and planting densities. *BMC plant biology*, 25(1), 281.

Huang S, et al. (2025) Genome-wide identification and characterization of Ethylene-Insensitive 3 (EIN3/EIL) gene family in *Camellia oleifera*. *PloS one*, 20(5), e0324651.

Liu X, et al. (2025) Integrating single-cell sequencing and transcriptome analysis to unravel the mechanistic role of sialylation-related genes in sepsis-induced acute respiratory distress syndrome. *Frontiers in immunology*, 16, 1528769.

Wang J, et al. (2025) Characterization of DREB family genes in loquat and their co-expression network analysis in response to drought. *BMC plant biology*, 25(1), 1385.

Zhao G, et al. (2025) Genome-Wide Identification and Expression Analysis of the CaM Gene Family in Tree Peony (*Paeonia ostii*) During the Pistil Pollination Process. *Current issues in molecular biology*, 47(10).

Zhang J, et al. (2025) Genome-wide identification, transcriptional profiling, and miRNA-binding site analysis of the LBD gene family in the camphor tree. *Frontiers in plant science*, 16, 1591736.

Tian X, et al. (2025) Genome-Wide Identification of Luffa Sucrose Synthase Genes Reveals LaSUS1-Mediated Sugar Metabolism Boosting Drought Tolerance. *International journal of molecular sciences*, 26(12).

Li Z, et al. (2025) Evolutionary and functional insights into HSF gene family underpin thermal adaptation in the plateau plant *Anisodus tanguticus*. *BMC plant biology*, 25(1), 1452.

Ma X, et al. (2025) Genome-wide identification and expression pattern analysis of the CPP transcription factor family in *Medicago sativa* L. *BMC plant biology*, 25(1), 1400.

Liu C, et al. (2025) Genome-wide identification of the bZIP transcription factor family and expression analysis under abiotic stress in *Zanthoxylum bungeanum*. *PloS one*, 20(5), e0324447.

Gao Y, et al. (2025) Genome identification of the LRR-RLK gene family in maize (*Zea mays*) and expression analysis in response to *Fusarium verticillioides* infection. *BMC plant biology*, 25(1), 524.