

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 28, 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 [SPARC SAWG](#) .

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.

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.

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.

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

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.

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.

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.

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.

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.

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).

Wang SW, et al. (2025) RGF Gene Family Analysis and Functional Evidence for RGF8-Mediated Salt Stress Tolerance in Brassica Species. *Biology*, 14(3).

Cheng G, et al. (2025) Genomic Insights into Cobweb Disease Resistance in *Agaricus bisporus*: A Comparative Analysis of Resistant and Susceptible Strains. *Journal of fungi* (Basel, Switzerland), 11(3).

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.

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).

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.

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.