

Resource Summary Report

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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, data analysis service, production service resource, 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: 20260829T183008+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 254 mentions in open access literature.

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

Quan X, et al. (2026) Genome-wide characterization and transcriptional profiling of the glycerol-3-phosphate acyltransferase (GPAT) family in barley reveals the role of HvGPAT1 in low nitrogen tolerance. *BMC plant biology*, 26(1).

Tang Y, et al. (2026) Genome-Wide Analysis of the TIFY Gene Family in Litchi (*Litchi chinensis* Sonn.): Identification and Expression Profiling. *Biology*, 15(5).

Zhao Q, et al. (2026) Genome-wide characterization of the HSF gene family in *Setaria italica* (foxtail millet) and functional elucidation of SiHSF3 in abiotic stress tolerance. *BMC plant biology*, 26(1).

Wang D, et al. (2026) Importin Alpha Is Implicated in the Nuclear Import of Novel Duck Reovirus Protein p18. *Viruses*, 18(2).

Rojas-Pirela M, et al. (2026) Characterization of GH18 chitinase in *Leishmania braziliensis*: expression, structural insights, and implications for vaccine and therapeutic development. *Biological research*, 59(1).

Yang L, et al. (2026) Functional characterization of 2,3-oxidosqualene cyclase8 in *Taraxacum mongolicum*: overexpression enhances taraxasterol biosynthesis and antioxidant capacity. *BMC genomics*, 27(1), 221.

Sun X, et al. (2026) Genome-Wide Analysis of AGPase Identifies CsAGP4 as a Regulator of Watermelon Mosaic Virus Resistance in Cucumber. *International journal of molecular sciences*, 27(11).

Shen Q, et al. (2026) Cadmium Stress Disrupts Auxin Signaling and Growth in *Ilex verticillata*: Insights from Physiological and Transcriptomic Analyses. *Plants (Basel, Switzerland)*, 15(2).

Niu E, et al. (2026) Comprehensive Analysis of the AP2/ERF Superfamily Identifies Key Genes Related to Various Stress Responses in Olive Tree (*Olea europaea* L.). *Current issues in molecular biology*, 48(2).

Liu R, et al. (2026) Genome-wide identification of the ATL gene family and their expression analysis in sweetpotato and its two diploid relatives. *BMC plant biology*, 26(1).

Istomina EA, et al. (2026) Genome-Wide Identification and Expression Analysis of the Thaumatin-like Protein Genes in *Filipendula ulmaria* under *Bipolaris sorokiniana* Infection.

Current issues in molecular biology, 48(6).

Zhu W, et al. (2026) Genome-Wide Identification and Expression Analysis of the PEBP Gene Family in *Cymbidium sinense* Reveals CsFTL3 as a Floral Inhibitor. *Plants* (Basel, Switzerland), 15(2).

Zhang C, et al. (2026) RpnACs transcription factors coordinate leaf margin development in *Rosa persica*. *BMC genomics*, 27(1), 132.

Jin W, et al. (2026) Genome-wide identification, structural characterization, and gene expression analysis of the MYB transcription factor family in faba bean (*Vicia faba* L.). *BMC plant biology*, 26(1), 251.

Fu J, et al. (2026) Identification and validation of prognostic genes associated with integrative stress response in lung adenocarcinoma and construction of the risk models. *Scientific reports*, 16(1).

Yang M, et al. (2026) Genome-wide analysis of the SOS2 gene family in melon (*Cucumis melo* L.) and functional characterization of MELO3C010334 in response to salt stress. *BMC plant biology*, 26(1).

Zhang Y, et al. (2026) Genetic Origin of AHAS2 Genes in Brassica Allotetraploids and Association of Its Orthologs with Agronomic Traits in *B. napus*. *Plants* (Basel, Switzerland), 15(7).

Yang M, et al. (2026) Identification of the SAUR Gene Family in *Pinus massoniana* and Analysis of Its Expression Patterns Under Drought Stress. *Biology*, 15(12).

Zhang Q, et al. (2026) Identification and characterization of the DREB family in Chinese yam and functional study of DoDREB28 under drought stress. *BMC plant biology*, 26(1).

He H, et al. (2026) WRKY transcription factors govern selenium metabolism in *Broussonetia papyrifera*: genome-wide identification, expression profiling, and regulatory network analysis. *BMC plant biology*, 26(1).