

Resource Summary Report

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Plant mPLoc

RRID:SCR_023014

Type: Tool

Proper Citation

Plant mPLoc (RRID:SCR_023014)

Resource Information

URL: <http://www.csbio.sjtu.edu.cn/bioinf/plant-multi/>

Proper Citation: Plant mPLoc (RRID:SCR_023014)

Description: Web application for predicting subcellular localization of plant proteins including those with multiple sites.Top Down Strategy to Augment Power for Predicting Plant Protein Subcellular Localization.

Synonyms: Plant-mPLoc

Resource Type: software resource, data access protocol, web service

Defining Citation: [PMID:20596258](#)

Keywords: Predicting Plant Protein Subcellular Localization, predicting subcellular localization, plant proteins,

Funding: National Natural Science Foundation of China ;
Science and Technology Commission of Shanghai Municipality ;
Shanghai Pujiang Program

Availability: Free, Freely available

Resource Name: Plant mPLoc

Resource ID: SCR_023014

Record Creation Time: 20221130T050154+0000

Record Last Update: 20260818T043715+0000

Ratings and Alerts

No rating or validation information has been found for Plant mPLOC.

No alerts have been found for Plant mPLOC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 362 mentions in open access literature.

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

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).

Luan X, et al. (2026) Identification and Expression Analysis of MADS-Box Gene Family in *Pinus koraiensis* and Overexpression of PkMADS9 Promoting Early Flowering in Transgenic Arabidopsis. *Plants (Basel, Switzerland)*, 15(4).

Wang C, et al. (2026) Identification, Characterization and Expression Profiles of Xylogen-like Gene Family in Kiwifruit in Different Developmental Tissues and Under Various Abiotic Stresses. *Biology*, 15(3).

Li B, et al. (2026) Genome-Wide Analysis of YTH Domain Proteins in *Metasequoia glyptostroboides* and Functional Validation of MgYTH5 as an m6A Reader. *Plants (Basel, Switzerland)*, 15(10).

Shi X, et al. (2026) Comprehensive Analyses of Serine Protease-like Protease (SBT) in Regulating Yield Characters in Rapeseed (*Brassica napus* L.). *Plants (Basel, Switzerland)*, 15(9).

Wang Q, et al. (2026) Genome-Wide Identification and Characterization of the Calmodulin-Binding Transcription Activators (CAMTA) Gene Family in *Brassica U-Triangle* Species and Its Potential Role in Response to Phytohormones and Abiotic Stresses. *Plants (Basel, Switzerland)*, 15(3).

Chen C, et al. (2026) Genome wide identification of serotonin N-acetyltransferase (PbSNAT) gene family and their role in pear (*Pyrus bretschneideri*) fruit development. *Frontiers in plant science*, 17, 1767313.

Hao XY, et al. (2026) Comparative genomics revealed the gene evolution and functional divergence of TaMRS2/CorA/NIPA magnesium transporter families in wheat (*Triticum aestivum* L.). *Frontiers in plant science*, 17, 1737134.

Yu R, et al. (2026) Identification, cloning and expression analysis of chloroplast TOC-TIC complex components in a C4 halophyte *Suaeda aralocaspica* without Kranz anatomy. *BMC plant biology*, 26(1).

Sun Y, et al. (2026) Genome-wide identification of WRKY gene family members in *Populus trichocarpa* and their response to biotic stresses. *PeerJ*, 14, e21132.

Huang J, et al. (2026) Genome-wide identification and expression analysis of the LBD gene family in *Jasminum sambac*. *Scientific reports*, 16(1).

Guo WL, et al. (2026) Genome-wide analysis of WRKY gene family in *Cucurbita moschata* and involvement of CmWRKY22/63/84 in powdery mildew resistance. *BMC genomics*, 27(1), 23.

Liu X, et al. (2026) Identification, evolution, and expression analysis of the PEBP gene family in tobacco (*Nicotiana tabacum*) and its role in flowering regulation via interaction with 14-3-3 proteins. *BMC plant biology*, 26(1).

Han L, et al. (2026) Genome-Wide Identification and Characterization of Stress-Responsive SNARE Genes in Quinoa (*Chenopodium quinoa* Willd.). *Biology*, 15(5).

Liu K, et al. (2026) Characterization of histone acetyltransferase and histone deacetylase genes under abiotic and hormone stresses in soybean. *Frontiers in plant science*, 17, 1753615.

Li L, et al. (2026) Genome-wide identification and expression analysis of the PnNPR-PnTGA gene family reveal its potential role in response to biotic stresses in *Panax notoginseng*. *BMC plant biology*, 26(1).

Song Y, et al. (2026) Genome-Wide Analysis of the Hsf Family and Functional Characterization of CiHsf10 Under Low-Temperature Stress in *Chrysanthemum indicum*. *Plants (Basel, Switzerland)*, 15(8).

Yang Y, et al. (2026) Systematic Analysis of the *Populus* ADF Gene Family and the Expression Patterns Under Osmotic Stress. *Life (Basel, Switzerland)*, 16(5).

Feng CH, et al. (2026) Genome-Wide Characterization and Expression Profiling of the CCR Gene Family Associated with Stem Strength in Upland Cotton (*Gossypium hirsutum* L.). *Life (Basel, Switzerland)*, 16(5).

Wang S, et al. (2026) Genome-Wide Identification of the BPC Gene Family in *Brassica juncea* and Expression Analysis of Its Regulatory Mechanisms in Response to Light and Salicylic Acid. *International journal of molecular sciences*, 27(6).