

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: 20260729T044545+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 105 mentions in open access literature.

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

Ye S, et al. (2025) TaZFP 23, a new Cys2/His2-type zinc-finger protein, is a regulator of wheat (*Triticum aestivum* L.) growth and abiotic stresses. *PeerJ*, 13, e18956.

Liu Z, et al. (2025) Genome-wide identification of the nuclear redox protein gene family revealed its potential role in drought stress tolerance in rice. *Frontiers in plant science*, 16, 1562718.

De Coninck T, et al. (2025) OsAPSE modulates non-covalent interactions between arabinogalactan protein O-glycans and pectin in rice cell walls. *Frontiers in plant science*, 16, 1588802.

Gu L, et al. (2025) Comprehensive identification and expression analysis of the CPP gene family in maize (*Zea mays* L.). *BMC plant biology*, 25(1), 731.

Zhu L, et al. (2025) Genome-wide identification and characterization of NBS-LRR gene family in tobacco (*Nicotiana benthamiana*). *Scientific reports*, 15(1), 19015.

Yu S, et al. (2025) Global identification and characterization of soybean TPR genes with expression analysis under photoperiod variations. *Scientific reports*, 15(1), 24644.

Lu S, et al. (2025) Genome-Wide identification and expression analysis of CsABF/AREB gene family in cucumber (*Cucumis sativus* L.) and in response to phytohormonal and abiotic stresses. *Scientific reports*, 15(1), 15757.

Zhao J, et al. (2025) Genome-wide identification and comparative evolution of 14-3-3 gene family members in five Brassicaceae species. *BMC genomics*, 26(1), 309.

Zhou W, et al. (2025) Genome-wide identification of CAMTA gene family in teak (*Tectona grandis*) and functional characterization of TgCAMTA1 and TgCAMTA3 in cold tolerance. *BMC plant biology*, 25(1), 35.

Chen Y, et al. (2025) Genome-Wide Identification, Phylogeny and Expression Analysis of the Magnesium Release Gene Family in Wheat (*Triticum aestivum* L.). *Current issues in molecular biology*, 47(11).

Hao Y, et al. (2025) Genome-Wide Identification and Expression Pattern Analysis of the DNA Methyltransferase Gene Family Revealed the DNA Methylation Response to Tapping in Rubber Tree. *Plants (Basel, Switzerland)*, 14(21).

Cui J, et al. (2025) Genome-wide identification and expression analysis of CBF/DREB1 gene family in *Medicago sativa* L. and functional verification of MsCBF9 affecting flowering time. *BMC plant biology*, 25(1), 87.

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

Qian X, et al. (2025) The Potassium Utilization Gene Network in *Brassica napus* and Functional Validation of BnaZSHAK5.2 Gene in Response to Potassium Deficiency. *International journal of molecular sciences*, 26(2).

Sun J, et al. (2025) Characterization analyses of MADS-box genes highlighting their functions with seed development in *Ricinus communis*. *Frontiers in plant science*, 16, 1589915.

Li Y, et al. (2025) Based on two coconut (*Cocos nucifera* L.) genome-wide investigation of NODULE-INCEPTION-like protein family: evolution and expression profiles during development and stress. *Frontiers in plant science*, 16, 1565559.

Balamurugan B, et al. (2025) Genome-wide investigation of cytokinin oxidase/dehydrogenase (CKX) family genes in *Brassica juncea* with an emphasis on yield-influencing CKX. *Scientific reports*, 15(1), 18825.

Kaur A, et al. (2025) Genome-wide characterization of PAL, C4H, and 4CL genes regulating the phenylpropanoid pathway in *Vanilla planifolia*. *Scientific reports*, 15(1), 10714.

Zhang J, et al. (2025) Genome- and Transcriptome-Wide Characterization and Expression Analyses of bHLH Transcription Factor Family Reveal Their Relevance to Salt Stress Response in Tomato. *Plants (Basel, Switzerland)*, 14(2).

Zhang J, et al. (2025) Genome-wide identification of the Sec14 gene family and the response to salt and drought stress in soybean (*Glycine max*). *BMC genomics*, 26(1), 73.