Resource Summary Report

Generated by RRID on May 18, 2025

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: web service, software resource, data access protocol

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: 20250517T060526+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 79 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

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.

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.

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.

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).

Farid B, et al. (2025) Expression divergence of BAG gene family in maize under heat stress. BMC plant biology, 25(1), 16.

Yang X, et al. (2025) Genome-wide characterization of the MADS-box gene family in Paeonia ostii and expression analysis of genes related to floral organ development. BMC genomics, 26(1), 49.

Tian Z, et al. (2025) Genome-wide identification and analysis of the NF-Y transcription factor family reveal its potential roles in tobacco (Nicotiana tabacum L.). Plant signaling & behavior,

20(1), 2451700.

Wang T, et al. (2024) Genome-wide identification of the B3 transcription factor family in pepper (Capsicum annuum) and expression patterns during fruit ripening. Scientific reports, 14(1), 2226.

Deng J, et al. (2024) Genome-wide analysis of the mulberry (Morus abla L.) GH9 gene family and the functional characterization of MaGH9B6 during the development of the abscission zone. Frontiers in plant science, 15, 1352635.

Pham TH, et al. (2024) Genome-wide characterization of COMT family and regulatory role of CsCOMT19 in melatonin synthesis in Camellia sinensis. BMC plant biology, 24(1), 51.

He S, et al. (2024) Genome-wide identification, characterization and expression analysis of the bZIP transcription factors in garlic (Allium sativum L.). Frontiers in plant science, 15, 1391248.

Zhang M, et al. (2024) Genome-wide identification of AP2/ERF gene family in Coptis Chinensis Franch reveals its role in tissue-specific accumulation of benzylisoquinoline alkaloids. BMC genomics, 25(1), 972.

Wang B, et al. (2024) Genome-wide analysis of R2R3-MYB transcription factors in poplar and functional validation of PagMYB147 in defense against Melampsora magnusiana. Planta, 260(2), 47.

Wang Y, et al. (2024) Identifying potential anthocyanin biosynthesis regulator in Chinese cherry by comprehensive genome-wide characterization of the R2R3-MYB transcription factor gene family. BMC genomics, 25(1), 784.

Fu C, et al. (2024) Genome-wide analysis of fatty acid desaturase genes in moso bamboo (Phyllostachys edulis) reveal their important roles in abiotic stresses responses. BMC genomics, 25(1), 1138.

Zuo Z, et al. (2024) Genome-Wide Identification and Expression Analysis of the COL Gene Family in Hemerocallis citrina Baroni. Current issues in molecular biology, 46(8), 8550.

Mao C, et al. (2024) Genome-wide analysis of the WRKY gene family and their response to low-temperature stress in elephant grass. BMC genomics, 25(1), 947.

Xu J, et al. (2024) Genome-wide identification of HSP90 gene family in Rosa chinensis and its response to salt and drought stresses. 3 Biotech, 14(9), 204.