

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

Plant MPSS

RRID:SCR_007861

Type: Tool

Proper Citation

Plant MPSS (RRID:SCR_007861)

Resource Information

URL: <http://mpss.udel.edu>

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Description: It provides access to a variety of databases of plant genomics databases. These include: *Arabidopsis PARE Database *Arabidopsis SBS Database *Arabidopsis MPSS Plus Database *Rice MPSS Database *Legume SBS Database *Maize SBS Database *Gallus Gallus SBS Database *Magnaporthe MPSS Database *Grape MPSS Database These data have been generated by a series of different projects, mainly based at the University of Delaware and funded primarily by grants from the National Science Foundation and the United States Department of Agriculture. The database and the web pages that you see were produced by the Meyers lab, with data generated within our lab, by collaborating laboratories like the Green or Wang labs. Some data we've gathered from Genbank or other public sources. Much of the data was produced under contract by Illumina, Inc (Hayward, California), but some SBS libraries are now being sequenced at other sites.

Synonyms: Plant MPSS

Resource Type: data or information resource, database

Resource Name: Plant MPSS

Resource ID: SCR_007861

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260912T200154+0000

Ratings and Alerts

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

No alerts have been found for Plant MPSS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

De Quattro C, et al. (2017) Long noncoding RNAs in the model species *Brachypodium distachyon*. *Scientific reports*, 7(1), 11252.

Morea EG, et al. (2016) Functional and evolutionary analyses of the miR156 and miR529 families in land plants. *BMC plant biology*, 16, 40.

Muneer S, et al. (2016) Physiological and Proteomic Investigations to Study the Response of Tomato Graft Unions under Temperature Stress. *PloS one*, 11(6), e0157439.

Li L, et al. (2016) Genome-Wide Characterization and Expression Analysis of the Germin-Like Protein Family in Rice and Arabidopsis. *International journal of molecular sciences*, 17(10).

Singh AK, et al. (2015) Genome-wide investigation and expression analysis of Sodium/Calcium exchanger gene family in rice and Arabidopsis. *Rice (New York, N.Y.)*, 8(1), 54.

Singh A, et al. (2015) Tissue specific and abiotic stress regulated transcription of histidine kinases in plants is also influenced by diurnal rhythm. *Frontiers in plant science*, 6, 711.

Tripathi A, et al. (2015) Role of bioinformatics in establishing microRNAs as modulators of abiotic stress responses: the new revolution. *Frontiers in physiology*, 6, 286.

Ahmed F, et al. (2014) Comprehensive analysis of small RNA-seq data reveals that combination of miRNA with its isomiRs increase the accuracy of target prediction in *Arabidopsis thaliana*. *RNA biology*, 11(11), 1414.

Kakrana A, et al. (2014) sPARTA: a parallelized pipeline for integrated analysis of plant miRNA and cleaved mRNA data sets, including new miRNA target-identification software. *Nucleic acids research*, 42(18), e139.

Ma T, et al. (2014) Identification, characterization, and transcription analysis of xylogen-like arabinogalactan proteins in rice (*Oryza sativa* L.). *BMC plant biology*, 14, 299.

Neupane A, et al. (2013) Identification, nomenclature, and evolutionary relationships of mitogen-activated protein kinase (MAPK) genes in soybean. *Evolutionary bioinformatics online*, 9, 363.

Shao C, et al. (2013) Identification of novel microRNA-like-coding sites on the long-stem microRNA precursors in Arabidopsis. *Gene*, 527(2), 477.

Confraria A, et al. (2013) miRNAs mediate SnRK1-dependent energy signaling in Arabidopsis. *Frontiers in plant science*, 4, 197.

Akpan BA, et al. (2013) Genomics approaches for crop improvement against abiotic stress. *TheScientificWorldJournal*, 2013, 361921.

Zhao H, et al. (2012) Genome-wide survey and expression analysis of amino acid transporter gene family in rice (*Oryza sativa* L.). *PloS one*, 7(11), e49210.

Shao C, et al. (2012) Genome-wide identification of reverse complementary microRNA genes in plants. *PloS one*, 7(10), e46991.

Ding J, et al. (2012) Finding microRNA targets in plants: current status and perspectives. *Genomics, proteomics & bioinformatics*, 10(5), 264.

Meng Y, et al. (2012) Large-scale identification of mirtrons in Arabidopsis and rice. *PloS one*, 7(2), e31163.

Ma H, et al. (2011) The phytoeyanin gene family in rice (*Oryza sativa* L.): genome-wide identification, classification and transcriptional analysis. *PloS one*, 6(10), e25184.

Richardson CR, et al. (2010) Analysis of antisense expression by whole genome tiling microarrays and siRNAs suggests mis-annotation of Arabidopsis orphan protein-coding genes. *PloS one*, 5(5), e10710.