

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 1, 2026

MapMan

RRID:SCR_003543

Type: Tool

Proper Citation

MapMan (RRID:SCR_003543)

Resource Information

URL: <http://mapman.gabipd.org/web/guest/mapman>

Proper Citation: MapMan (RRID:SCR_003543)

Description: Software tool that displays large genomics datasets (e.g. gene expression data from Arabidopsis Affymetrix arrays) onto diagrams of metabolic pathways or other biological processes.

Abbreviations: MapMan

Synonyms: MapMan Application Software

Resource Type: software application, software resource

Defining Citation: [PMID:19389052](#), [PMID:14996223](#), [PMID:16009995](#), [PMID:16649112](#)

Keywords: metabolic pathway, biological process, genomics, pathway, array, visualization, gene, transcript, protein, enzyme, metabolite

Resource Name: MapMan

Resource ID: SCR_003543

Alternate IDs: nlx_157682

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260829T183042+0000

Ratings and Alerts

No rating or validation information has been found for MapMan.

No alerts have been found for MapMan.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1251 mentions in open access literature.

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

Vivek AT, et al. (2026) Integrative multi-omics analysis widens annotation and functional insights into long non-coding RNAs of *Arabidopsis thaliana*. *Biology direct*, 21(1), 14.

Podio M, et al. (2026) Leaf transcriptome differences between diploid and tetraploid bahiagrass. *The plant genome*, 19(1), e70212.

Godec T, et al. (2026) Functional Genomics Screening in *Chlamydomonas reinhardtii* Maps the Genetic Landscape of Tolerance to Paraquat and Diuron. *Environmental science & technology*, 60(22), 15570.

Lin X, et al. (2026) An integrated fine-mapping, re-sequencing and transcriptome analysis provides further insights and candidate genes for silique number in oilseed rape (*Brassica napus* L.). *BMC plant biology*, 26(1).

Zhao Y, et al. (2026) The transcription factor ANAC017 links mitochondrial retrograde signaling with the ubiquitin-proteasome system to control mitochondrial function in *Arabidopsis*. *Plant communications*, 7(2), 101667.

Tamiru-Oli M, et al. (2026) Insights into glandular trichome biology from analysis of organ-specific gene expression programmes in cannabis, hop and tomato. *The Plant journal : for cell and molecular biology*, 125(6), e70774.

Ontoy J, et al. (2026) Characterization of resistance to bacterial panicle blight in rice revealed by transcriptome and QTL mapping analyses. *Frontiers in plant science*, 17, 1857873.

Lukan T, et al. (2026) ERF transcription factor StPti5 is a regulator of endophyte community maintenance in potato. *The New phytologist*, 251(3), 1344.

Yoo YH, et al. (2026) Unravelling mechanisms of drought tolerance in a soybean cultivar (Daewonkong roots): insights into integrative transcriptomic and metabolite analyses. *BMC plant biology*, 26(1), 274.

Moya-Cuevas J, et al. (2026) Identification of a novel link connecting indole-3-acetamide with abscisic acid biosynthesis and signaling. *The New phytologist*, 249(5), 2452.

Pal D, et al. (2026) Integrative transcriptome and genome resequencing reveals conserved flowering regulators and allelic variants in early- and late-flowering linseed (*Linum usitatissimum* L.) accessions. *Scientific reports*, 16(1).

Zhang K, et al. (2026) Multi-tissue transcriptomic profiling of foxtail millet in response to drought and rewatering. *BMC plant biology*, 26(1).

Rico A, et al. (2026) Basal Differences in the Transcriptional Profiles of Tomato Roots Associated with the Presence/Absence of the Resistance Gene Mi-1 and Time-Course Changes During the Compatible and Incompatible Interactions with the Root-Knot Nematode *Meloidogyne javanica*. *Plants (Basel, Switzerland)*, 15(10).

Sanches M, et al. (2026) Integrating natural variation through GWAS - genetics of drought and flood tolerance in grass pea reveal independent yet interconnected mechanisms. *BMC plant biology*, 26(1).

Nguyen TNG, et al. (2026) Splicing regulation and intron evolution in the short-intron ciliate model of endosymbiosis *Paramecium bursaria*. *Nucleic acids research*, 54(3).

Ha X, et al. (2026) Candidate genes and molecular mechanisms regulating tiller development in wild Kentucky bluegrass. *BMC plant biology*, 26(1), 212.

Tang X, et al. (2026) ZmbHLH30 Enhances Cold Tolerance During Maize Germination. *Plants (Basel, Switzerland)*, 15(4).

Santoro DF, et al. (2026) Traversing the effects of ploidy changes in different *Eragrostis curvula* genotypes through high-throughput RNA sequencing. *The plant genome*, 19(2), e70227.

Jordine A, et al. (2026) Insights into enhanced, divergent, and additive responses to single and combined hypoxia-salt stress. *BMC plant biology*, 26(1).

Zhang Y, et al. (2026) Mechanistic insights into adventitious root formation in *Cinnamomum kanehirae* stem cuttings based on phenotypic, physiological, and transcriptomic analyses. *BMC plant biology*, 26(1).