

Resource Summary Report

Generated by [NIF](#) on Apr 22, 2025

[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 resource, software application

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

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

Funding:

Resource Name: MapMan

Resource ID: SCR_003543

Alternate IDs: nlx_157682

Record Creation Time: 20220129T080219+0000

Record Last Update: 20250421T053359+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 1174 mentions in open access literature.

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

Orlovskis Z, et al. (2025) The phytoplasma SAP54 effector acts as a molecular matchmaker for leafhopper vectors by targeting plant MADS-box factor SVP. *eLife*, 13.

Chen X, et al. (2025) PcWRKY1 Represses Transcription of Yellow Stripe-Like 3 (PcYSL3) to Negatively Regulate Radial Cadmium Transport in Poplar Stems. *Advanced science* (Weinheim, Baden-Wurtemberg, Germany), 12(1), e2405492.

Berger MMJ, et al. (2025) Grapevine cell response to carbon deficiency requires transcriptome and methylome reprogramming. *Horticulture research*, 12(1), uhae277.

Prigigallo MI, et al. (2025) Resistance-breaking strains of tomato spotted wilt virus hamper photosynthesis and protein synthesis pathways in a virus accumulation-dependent manner in Sw5-carrying tomatoes. *Scientific reports*, 15(1), 3630.

Zhong Y, et al. (2025) ZmCCD8 regulates sugar and amino acid accumulation in maize kernels via strigolactone signalling. *Plant biotechnology journal*, 23(2), 492.

Ribeyre Z, et al. (2025) De novo transcriptome assembly and discovery of drought-responsive genes in white spruce (*Picea glauca*). *PloS one*, 20(1), e0316661.

Shi J, et al. (2025) Identification of genes associated with sex expression and sex determination in hemp (*Cannabis sativa* L.). *Journal of experimental botany*, 76(1), 175.

Žnidarič MT, et al. (2025) Chloroplast Vesiculation and Induced Chloroplast Vesiculation and Senescence-Associated Gene 12 Expression During Tomato Flower Pedicel Abscission. *Plant direct*, 9(1), e70035.

Mansueto L, et al. (2024) Building a community-driven bioinformatics platform to facilitate *Cannabis sativa* multi-omics research. *GigaByte* (Hong Kong, China), 2024, gigabyte137.

Gupta S, et al. (2024) The genome of *Haberlea rhodopensis* provides insights into the

mechanisms for tolerance to multiple extreme environments. *Cellular and molecular life sciences : CMLS*, 81(1), 117.

Avidan O, et al. (2024) Direct and indirect responses of the *Arabidopsis* transcriptome to an induced increase in trehalose 6-phosphate. *Plant physiology*, 196(1), 409.

Hou LY, et al. (2024) The impact of light and thioredoxins on the plant thiol-disulfide proteome. *Plant physiology*, 195(2), 1536.

Baales J, et al. (2024) Transcriptomic changes in barley leaves induced by alcohol ethoxylates indicate potential pathways of surfactant detoxification. *Scientific reports*, 14(1), 4535.

Chen K, et al. (2024) Cuticle development and the underlying transcriptome-metabolome associations during early seedling establishment. *Journal of experimental botany*, 75(20), 6500.

Wang X, et al. (2024) A Transcriptome Analysis of *Poncirus trifoliata*, an Aurantioideae Species Tolerant to Asian Citrus Psyllid, Has Identified Potential Genes and Events Associated with Psyllid Resistance. *Insects*, 15(8).

He X, et al. (2024) Identification of crucial drought-tolerant genes of barley through comparative transcriptomic analysis and yeast-based stress assay. *Frontiers in genetics*, 15, 1524118.

Li Z, et al. (2024) Phosphoregulation in the N-terminus of NRT2.1 affects nitrate uptake by controlling the interaction of NRT2.1 with NAR2.1 and kinase HPCAL1 in *Arabidopsis*. *Journal of experimental botany*, 75(7), 2127.

Basso MF, et al. (2024) Genome-wide transcript expression analysis reveals major chickpea and lentil genes associated with plant branching. *Frontiers in plant science*, 15, 1384237.

Hohenfeld CS, et al. (2024) Comparative analysis of infected cassava root transcriptomics reveals candidate genes for root rot disease resistance. *Scientific reports*, 14(1), 10587.

Peleke FF, et al. (2024) Deep learning the cis-regulatory code for gene expression in selected model plants. *Nature communications*, 15(1), 3488.