

Resource Summary Report

Generated by T1D on Aug 2, 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 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

Resource Name: MapMan

Resource ID: SCR_003543

Alternate IDs: nlx_157682

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260801T191046+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 1225 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Ishihara H, et al. (2025) Growth conditions trigger genotype-specific metabolic responses that affect the nutritional quality of kale cultivars. *Journal of experimental botany*, 76(5), 1427.

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

Gliwa K, et al. (2025) Biophysical and structural insights into AAV genome ejection. *Journal of virology*, 99(3), e0089924.

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.

Yingtao L, et al. (2025) Integrated analysis of transcriptomics and metabolomics and high-throughput amplicon sequencing reveals the synergistic effects of secondary metabolites and rhizosphere microbiota on root rot resistance in *Psammosilene tunicoides*. *Frontiers in microbiology*, 16, 1554406.

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-Wurttemberg, Germany), 12(1), e2405492.

Ziegler FMR, et al. (2025) A full genome assembly reveals drought stress effects on gene expression and metabolite profiles in blackcurrant (*Ribes nigrum* L.). *Horticulture research*, 12(2), uhae313.

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.

Zhou T, et al. (2025) TCP19 regulates nitrogen-dependent sheath blight susceptibility by modulating nitrogen uptake and signalling in rice. *Plant biotechnology journal*, 23(9), 4140.

Zhou R, et al. (2025) Transcriptome analysis of peach seedlings (*Prunus davidiana*) experiencing drought stress. *Science progress*, 108(3), 368504251358640.

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.

Zhang S, et al. (2025) A *Candidatus liberibacter Asiaticus* effector, CLIBASIA_00185 controls sugar metabolism, phenylpropanoid biosynthesis, and endocytosis pathway in *Citrus sinensis*. *BMC genomics*, 26(1), 717.

Doron S, et al. (2025) Two opposing redox signals mediated by 2-cys peroxiredoxin shape the redox proteome during photosynthetic induction. *Redox biology*, 86, 103810.

Lang J, et al. (2025) Complexome profiling of the *Chlamydomonas psb28* mutant reveals TEF5 as an early PSII assembly factor. *The Plant cell*, 37(6).

Nešić S, et al. (2025) *Paraburkholderia phytofirmans* PsJN triggers local and systemic transcriptional reprogramming in *Arabidopsis thaliana* and increases resistance against *Botrytis cinerea*. *Frontiers in plant science*, 16, 1554036.

Moormann J, et al. (2025) Cysteine Signalling in Plant Pathogen Response. *Plant, cell & environment*, 48(10), 7107.

Liu K, et al. (2025) GWAS Combined with Meta-Analysis Identifies OsDREB6 as a Regulator of Coleoptile Elongation Under Anaerobic Conditions in Rice. *Rice (New York, N.Y.)*, 18(1), 51.

Tan D, et al. (2025) Transcriptome analysis reveals key immune pathways and metabolites associated with resistance to *Verticillium dahliae* in GbMBL1.1A-overexpressing cotton. *The plant genome*, 18(4), e70120.