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

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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-Wurttemberg, 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.

Žnidari? 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.