

Resource Summary Report

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Plant Metabolic Network

RRID:SCR_003778

Type: Tool

Proper Citation

Plant Metabolic Network (RRID:SCR_003778)

Resource Information

URL: <http://www.plantcyc.org/>

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Description: Broad network of plant metabolic pathway databases with two types of databases: a reference database called PlantCyc and single species/taxon databases, such as AraCyc. Additional external metabolic pathway databases are affiliated with the PMN. These databases remain under the autonomous control of the PMN collaborators who provide them. PMN draws upon the work of many individuals with expertise in annotating genomes, generating metabolic pathway databases, curating biochemical information from the literature, and forming extensive network of collaborations with biological databases and biochemistry researchers. In addition to providing biochemical reaction diagrams, organism-specific metabolic maps, detailed descriptions of enzymes and pathways, and links to other resources, the PMN website houses tutorials to help guide teachers and students as they learn more about the valuable bioinformatic data and analysis tools that are crucial elements of modern biological research. Please help expand the content of the PMN databases, including AraCyc and PlantCyc! Any and all new data submissions related to plant biochemical pathways are welcomed. You can also correct an existing pathway. The PMN has several tools available for analyzing the data presented in PlantCyc and the other species-specific metabolic databases. You may browse the pathway ontology, compound ontology, and enzyme commission ontology. *PlantCyc: a comprehensive plant biochemical pathway database, containing curated information from the literature and computational analyses about the genes, enzymes, compounds, reactions, and pathways involved in primary and secondary metabolism. It provides access to manually curated or reviewed information about shared and unique metabolic pathways present in over 350 plant species. * AraCyc: provides access to manually curated or reviewed information about metabolic pathways for the model plant *Arabidopsis thaliana*. The pathways may be unique to *Arabidopsis* or shared with other organisms. Data from gene expression, proteomic, and metabolomic experiments in *Arabidopsis* can be overlaid on a metabolic pathway map using the OMICS Viewer. * PoplarCyc: provides access to manually curated or reviewed information about metabolic pathways for the model tree *Populus trichocarpa* and a few other related *Populus* species and hybrids. The

pathways may be unique to poplar or shared with other organisms. Data from gene expression, proteomic, and metabolomic experiments in poplar can be overlaid on a metabolic pathway map using the OMICS Viewer.

Abbreviations: PMN

Resource Type: data analysis service, data or information resource, analysis service resource, data repository, portal, topical portal, storage service resource, service resource, ontology, database, training resource, image collection, production service resource, controlled vocabulary

Defining Citation: [PMID:20522724](#)

Keywords: metabolism, plant metabolism, metabolic pathway, gene, protein, compound, pathway, enzyme, biochemical reaction, metabolic map, reaction

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Resource Name: Plant Metabolic Network

Resource ID: SCR_003778

Alternate IDs: nlx_15806

Record Creation Time: 20220129T080220+0000

Record Last Update: 20260903T235740+0000

Ratings and Alerts

No rating or validation information has been found for Plant Metabolic Network.

No alerts have been found for Plant Metabolic Network.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 126 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Singh DP, et al. (2023) Untargeted Metabolomics of Alternaria solani-Challenged Wild Tomato Species Solanum cheesmaniae Revealed Key Metabolite Biomarkers and Insight into Altered Metabolic Pathways. Metabolites, 13(5).

Perez-Matas E, et al. (2023) Exploring the Interplay between Metabolic Pathways and Taxane Production in Elicited Taxus baccata Cell Suspensions. Plants (Basel,

Switzerland), 12(14).

Naika MBN, et al. (2022) Exploring the medicinally important secondary metabolites landscape through the lens of transcriptome data in fenugreek (*Trigonella foenum graecum* L.). *Scientific reports*, 12(1), 13534.

Tan YC, et al. (2022) Bioinformatics approaches and applications in plant biotechnology. *Journal, genetic engineering & biotechnology*, 20(1), 106.

Foerster H, et al. (2021) Metabolic networks of the *Nicotiana* genus in the spotlight: content, progress and outlook. *Briefings in bioinformatics*, 22(3).

Squeri C, et al. (2021) Gas exchange, vine performance and modulation of secondary metabolism in *Vitis vinifera* L. cv Barbera following long-term nitrogen deficit. *Planta*, 253(3), 73.

Zhao K, et al. (2021) A novel bivalent chromatin associates with rapid induction of camalexin biosynthesis genes in response to a pathogen signal in *Arabidopsis*. *eLife*, 10.

Sorrentino M, et al. (2021) Seed Priming With Protein Hydrolysates Improves *Arabidopsis* Growth and Stress Tolerance to Abiotic Stresses. *Frontiers in plant science*, 12, 626301.

Fei X, et al. (2021) Transcriptome and Metabolome Dynamics Explain Aroma Differences between Green and Red Prickly Ash Fruit. *Foods (Basel, Switzerland)*, 10(2).

Allwood JW, et al. (2021) Assessing the impact of nitrogen supplementation in oats across multiple growth locations and years with targeted phenotyping and high-resolution metabolite profiling approaches. *Food chemistry*, 355, 129585.

Vo KTX, et al. (2021) Proteomics and Metabolomics Studies on the Biotic Stress Responses of Rice: an Update. *Rice (New York, N.Y.)*, 14(1), 30.

Ceccarelli AV, et al. (2021) Foliar Application of Different Vegetal-Derived Protein Hydrolysates Distinctively Modulates Tomato Root Development and Metabolism. *Plants (Basel, Switzerland)*, 10(2).

Qin G, et al. (2020) Diversity of metabolite accumulation patterns in inner and outer seed coats of pomegranate: exploring their relationship with genetic mechanisms of seed coat development. *Horticulture research*, 7, 10.

Lucini L, et al. (2020) Combining Molecular Weight Fractionation and Metabolomics to Elucidate the Bioactivity of Vegetal Protein Hydrolysates in Tomato Plants. *Frontiers in plant science*, 11, 976.

Muthuramalingam P, et al. (2020) Integrated transcriptomic and metabolomic analyses of glutamine metabolism genes unveil key players in *Oryza sativa* (L.) to ameliorate the unique and combined abiotic stress tolerance. *International journal of biological macromolecules*, 164, 222.

Maver M, et al. (2020) New insights in the allelopathic traits of different barley genotypes: Middle Eastern and Tibetan wild-relative accessions vs. cultivated modern barley. *PloS one*, 15(4), e0231976.

Azodi CB, et al. (2020) The cis-regulatory codes of response to combined heat and drought stress in *Arabidopsis thaliana*. *NAR genomics and bioinformatics*, 2(3), lqaa049.

Mareya CR, et al. (2020) Adaptive defence-related changes in the metabolome of *Sorghum bicolor* cells in response to lipopolysaccharides of the pathogen *Burkholderia andropogonis*. *Scientific reports*, 10(1), 7626.

Corrado G, et al. (2020) Metabolic Insights into the Anion-Anion Antagonism in Sweet Basil: Effects of Different Nitrate/Chloride Ratios in the Nutrient Solution. *International journal of molecular sciences*, 21(7).

Astolfi S, et al. (2020) Single and Combined Fe and S Deficiency Differentially Modulate Root Exudate Composition in Tomato: A Double Strategy for Fe Acquisition? *International journal of molecular sciences*, 21(11).