Resource Summary Report

Generated by NIF on Apr 22, 2025

AraCyc

RRID:SCR_008109
Type: Tool

Proper Citation

AraCyc (RRID:SCR_008109)

Resource Information

URL: https://plantcyc.org/databases/aracyc/15.0

Proper Citation: AraCyc (RRID:SCR_008109)

Description: Curated species-specific database present at the Plant Metabolic Network. It has a large number of experimentally supported enzymes and metabolic pathways, but it also houses a substantial number of computationally predicted enzymes and pathways.

Synonyms: Arabidopsis enzymes and biochemical pathways database

Resource Type: data repository, storage service resource, data or information resource, database, service resource

Defining Citation: PMID:12805578, PMID:15888675

Keywords: enzyme, gene, arabidopsis thaliana, biochemical, pathway, reaction, metabolism, metabolic pathway, data set, data analysis service, web service, FASEB list

Funding: NSF

Availability: The community can contribute to this resource

Resource Name: AraCyc

Resource ID: SCR_008109

Alternate IDs: nif-0000-20811

Alternate URLs: http://www.arabidopsis.org/biocyc/index.jsp, http://www.plantcyc.org

Record Creation Time: 20220129T080245+0000

Record Last Update: 20250422T055434+0000

Ratings and Alerts

No rating or validation information has been found for AraCyc.

No alerts have been found for AraCyc.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 66 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Kostikova VA, et al. (2024) Chemical Composition of Methanol Extracts from Leaves and Flowers of Anemonopsis macrophylla (Ranunculaceae). International journal of molecular sciences, 25(2).

Bleker C, et al. (2024) Stress Knowledge Map: A knowledge graph resource for systems biology analysis of plant stress responses. Plant communications, 5(6), 100920.

Zhou X, et al. (2024) HNCGAT: a method for predicting plant metabolite-protein interaction using heterogeneous neighbor contrastive graph attention network. Briefings in bioinformatics, 25(5).

Raikar SV, et al. (2023) Establishment of feijoa (Acca sellowiana) callus and cell suspension cultures and identification of arctigenin - a high value bioactive compound. Frontiers in plant science, 14, 1281733.

Li Y, et al. (2023) Integrative Omic Analysis Reveals the Dynamic Change in Phenylpropanoid Metabolism in Morus alba under Different Stress. Plants (Basel, Switzerland), 12(18).

Kim JY, et al. (2021) Distinct identities of leaf phloem cells revealed by single cell transcriptomics. The Plant cell, 33(3), 511.

Dahale SK, et al. (2021) HopA1 Effector from Pseudomonas syringae pv syringae Strain 61 Affects NMD Processes and Elicits Effector-Triggered Immunity. International journal of molecular sciences, 22(14).

Zogopoulos VL, et al. (2021) Arabidopsis Coexpression Tool: a tool for gene coexpression analysis in Arabidopsis thaliana. iScience, 24(8), 102848.

Cusack SA, et al. (2021) Predictive Models of Genetic Redundancy in Arabidopsis thaliana. Molecular biology and evolution, 38(8), 3397.

Harun S, et al. (2021) Potential Arabidopsis thaliana glucosinolate genes identified from the co-expression modules using graph clustering approach. PeerJ, 9, e11876.

Doron S, et al. (2021) SPEAR: A proteomics approach for simultaneous protein expression and redox analysis. Free radical biology & medicine, 176, 366.

Garcia A, et al. (2021) Disentangling transcriptional responses in plant defense against arthropod herbivores. Scientific reports, 11(1), 12996.

Liao D, et al. (2021) Transcriptome profiles revealed molecular mechanisms of alternating temperatures in breaking the epicotyl morphophysiological dormancy of Polygonatum sibiricum seeds. BMC plant biology, 21(1), 370.

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.

Farooq M, et al. (2020) Prior Biological Knowledge Improves Genomic Prediction of Growth-Related Traits in Arabidopsis thaliana. Frontiers in genetics, 11, 609117.

Harun S, et al. (2019) SuCComBase: a manually curated repository of plant sulfur-containing compounds. Database : the journal of biological databases and curation, 2019.

Herrmann HA, et al. (2019) Flux sampling is a powerful tool to study metabolism under changing environmental conditions. NPJ systems biology and applications, 5, 32.

Chakraborty N, et al. (2019) GCR1 and GPA1 coupling regulates nitrate, cell wall, immunity and light responses in Arabidopsis. Scientific reports, 9(1), 5838.

Varela-Rodríguez L, et al. (2019) Biological and toxicological evaluation of Rhus trilobata Nutt. (Anacardiaceae) used traditionally in mexico against cancer. BMC complementary and alternative medicine, 19(1), 153.

Moore BM, et al. (2019) Robust predictions of specialized metabolism genes through machine learning. Proceedings of the National Academy of Sciences of the United States of America, 116(6), 2344.