

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

[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 or information resource, data repository, database, service resource, storage 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: 20260905T132618+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 69 mentions in open access literature.

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

Ducrocq F, et al. (2025) Fingerprinting and chemotyping approaches reveal a wide genetic and metabolic diversity among wild hops (*Humulus lupulus* L.). *PloS one*, 20(5), e0322330.

Kreuzer I, et al. (2025) Venus flytraps' metabolome analysis discloses the metabolic fate of prey animal foodstock. *The Plant journal : for cell and molecular biology*, 123(3), e70391.

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.

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).

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.

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).

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).

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).

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

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

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.

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

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

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.

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.

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.