Resource Summary Report

Generated by kravitz2 on Aug 2, 2026

Rice Metabolic Pathway Database

RRID:SCR_002128
Type: Tool

Proper Citation

Rice Metabolic Pathway Database (RRID:SCR_002128)

Resource Information

URL: http://pathway.gramene.org/gramene/ricecyc.shtml

Proper Citation: Rice Metabolic Pathway Database (RRID:SCR_002128)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on August 26, 2016. RiceCyc is a catalog of known and/or predicted biochemical pathways from rice (Oryza sativa). Pathways and genes presented in this catalog are primarily based on the annotations carried out by Gramene database project on the release 5 of the TIGR-assembly of Oryza sativa japonica cv. Nipponbare genome sequenced by IRGSP.

Synonyms: Rice Metabolic Pathways, RiceCyc

Resource Type: data or information resource, database

Keywords: gene, biochemical pathway, rice

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Rice Metabolic Pathway Database

Resource ID: SCR_002128

Alternate IDs: nif-0000-20922

Old URLs: http://www.gramene.org/pathway/ricecyc.html

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260801T190908+0000

Ratings and Alerts

No rating or validation information has been found for Rice Metabolic Pathway Database.

No alerts have been found for Rice Metabolic Pathway Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Iqbal Z, et al. (2021) Toward Integrated Multi-Omics Intervention: Rice Trait Improvement and Stress Management. Frontiers in plant science, 12, 741419.

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.

Brazier-Hicks M, et al. (2020) Chemically induced herbicide tolerance in rice by the safener metcamifen is associated with a phased stress response. Journal of experimental botany, 71(1), 411.

Cen W, et al. (2020) The Wild Rice Locus CTS-12 Mediates ABA-Dependent Stomatal Opening Modulation to Limit Water Loss Under Severe Chilling Stress. Frontiers in plant science, 11, 575699.

Hong WJ, et al. (2019) Infrastructures of systems biology that facilitate functional genomic study in rice. Rice (New York, N.Y.), 12(1), 15.

Kim SW, et al. (2017) Crosstalk between diurnal rhythm and water stress reveals an altered primary carbon flux into soluble sugars in drought-treated rice leaves. Scientific reports, 7(1), 8214.

Poolman MG, et al. (2014) Metabolic trade-offs between biomass synthesis and photosynthate export at different light intensities in a genome-scale metabolic model of rice. Frontiers in plant science, 5, 656.

Cal AJ, et al. (2013) Transcriptome profiling of leaf elongation zone under drought in contrasting rice cultivars. PloS one, 8(1), e54537.

Yamakawa H, et al. (2010) Atlas of rice grain filling-related metabolism under high temperature: joint analysis of metabolome and transcriptome demonstrated inhibition of starch accumulation and induction of amino acid accumulation. Plant & cell physiology, 51(5), 795.