Resource Summary Report

Generated by dkNET on May 21, 2025

MetaCrop

RRID:SCR_003100
Type: Tool

Proper Citation

MetaCrop (RRID:SCR_003100)

Resource Information

URL: http://metacrop.ipk-gatersleben.de

Proper Citation: MetaCrop (RRID:SCR_003100)

Description: Database that summarizes diverse information about metabolic pathways in crop plants and allows automatic export of information for the creation of detailed metabolic models. It contains manually curated, highly detailed information about metabolic pathways in crop plants, including pathway diagrams, reactions, locations, transport processes, reaction kinetics, taxonomy and literature. It contains information about seven major crop plants with high agronomical importance and two model plants.

Abbreviations: MetaCrop

Resource Type: data or information resource, database

Defining Citation: PMID:22086948, PMID:17933764, PMID:20375443

Keywords: metabolism, kinetic, enzyme, crop, pathway, substance, conversion, carbohydrate, lipid, cofactor, energy, nucleotide, amino acid, web service

Funding:

Resource Name: MetaCrop

Resource ID: SCR_003100

Alternate IDs: nif-0000-03113

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250521T060909+0000

Ratings and Alerts

No rating or validation information has been found for MetaCrop.

No alerts have been found for MetaCrop.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Gao Y, et al. (2024) Development and applications of metabolic models in plant multi-omics research. Frontiers in plant science, 15, 1361183.

Chao H, et al. (2023) Integrating omics databases for enhanced crop breeding. Journal of integrative bioinformatics, 20(4).

Kaspar-Schoenefeld S, et al. (2016) Label-free proteome profiling reveals developmental-dependent patterns in young barley grains. Journal of proteomics, 143, 106.

Beckers V, et al. (2016) In silico metabolic network analysis of Arabidopsis leaves. BMC systems biology, 10(1), 102.

Hill CB, et al. (2015) Metabolomics, Standards, and Metabolic Modeling for Synthetic Biology in Plants. Frontiers in bioengineering and biotechnology, 3, 167.

Fukushima A, et al. (2013) Recent progress in the development of metabolome databases for plant systems biology. Frontiers in plant science, 4, 73.

Junker A, et al. (2012) Visual analysis of transcriptome data in the context of anatomical structures and biological networks. Frontiers in plant science, 3, 252.