Resource Summary Report

Generated by dkNET on Apr 22, 2025

MetaCyc

RRID:SCR_007778
Type: Tool

Proper Citation

MetaCyc (RRID:SCR_007778)

Resource Information

URL: http://metacyc.org/

Proper Citation: MetaCyc (RRID:SCR_007778)

Description: MetaCyc is a database of nonredundant, experimentally elucidated metabolic pathways. MetaCyc contains more than 1,200 pathways from more than 1,600 different organisms, and is curated from the scientific experimental literature. MetaCyc contains pathways involved in both primary and secondary metabolism, as well as associated compounds, enzymes, and genes.

Abbreviations: MetaCyc

Resource Type: database, data or information resource

Keywords: bio.tools, FASEB list

Funding:

Resource Name: MetaCyc

Resource ID: SCR_007778

Alternate IDs: nif-0000-03114, biotools:metacyc

Alternate URLs: https://bio.tools/metacyc

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250420T015559+0000

Ratings and Alerts

No rating or validation information has been found for MetaCyc.

No alerts have been found for MetaCyc.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1464 mentions in open access literature.

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

Varela JL, et al. (2025) The gills and skin microbiota of five pelagic fish species from the Atlantic Ocean. International microbiology : the official journal of the Spanish Society for Microbiology, 28(1), 95.

Nazem-Bokaee H, et al. (2025) Analyzing sorbitol biosynthesis using a metabolic network flux model of a lichenized strain of the green microalga Diplosphaera chodatii. Microbiology spectrum, 13(1), e0366023.

Portlock T, et al. (2025) Interconnected pathways link faecal microbiota plasma lipids and brain activity to childhood malnutrition related cognition. Nature communications, 16(1), 473.

Mangin CC, et al. (2025) Magnetotactic bacteria affiliated with diverse Pseudomonadota families biomineralize intracellular Ca-carbonate. The ISME journal, 19(1).

Przemieniecki SW, et al. (2025) The Impact of Nanoparticles and Molecular Forms of TiO2 on the Rhizosphere of Plants in the Example of Common Wheat (Triticum aestivum L.)-Shifts in Microbiome Structure and Predicted Microbial Metabolic Functions. International journal of molecular sciences, 26(2).

Kim J, et al. (2025) Fecal Microbial Dysbiosis Is Associated with Colorectal Cancer Risk in a Korean Population. Cancer research and treatment, 57(1), 198.

Park HA, et al. (2025) Metagenomic Analysis Identifies Sex-Related Gut Microbial Functions and Bacterial Taxa Associated With Skeletal Muscle Mass. Journal of cachexia, sarcopenia and muscle, 16(1), e13636.

Wang W, et al. (2025) Distinct Gut Microbiota Profiles in Normal Weight Obesity and Their Association With Cardiometabolic Diseases: Results From Two Independent Cohort Studies. Journal of cachexia, sarcopenia and muscle, 16(1), e13644.

Liu Q, et al. (2025) Cyperus esculentus var. sativus Adapts to Multiple Heavy Metal Stresses

Through the Assembly of Endophytic Microbial Communities. Biology, 14(1).

Salas-López M, et al. (2025) Human Milk Archaea Associated with Neonatal Gut Colonization and Its Co-Occurrence with Bacteria. Microorganisms, 13(1).

Ou Z, et al. (2025) MiMeJF: Application of Coupled Matrix and Tensor Factorization (CMTF) for Enhanced Microbiome-Metabolome Multi-Omic Analysis. Metabolites, 15(1).

Wang X, et al. (2025) Diversity and Functional Insights into Endophytic Fungi in Halophytes from West Ordos Desert Ecosystems. Journal of fungi (Basel, Switzerland), 11(1).

Baltsavia I, et al. (2025) MjCyc: Rediscovering the pathway-genome landscape of the first sequenced archaeon, Methanocaldococcus (Methanococcus) jannaschii. iScience, 28(1), 111546.

Liu W, et al. (2025) RDBSB: a database for catalytic bioparts with experimental evidence. Nucleic acids research, 53(D1), D709.

Fan J, et al. (2025) Potential roles of cigarette smoking on gut microbiota profile among Chinese men. BMC medicine, 23(1), 25.

Tec-Campos D, et al. (2025) A genome-scale metabolic model for the denitrifying bacterium Thauera sp. MZ1T accurately predicts degradation of pollutants and production of polymers. PLoS computational biology, 21(1), e1012736.

Kim HN, et al. (2025) Gastric Microbiota Associated with Gastric Precancerous Lesions in Helicobacter pylori-Negative Patients. Microorganisms, 13(1).

Sun L, et al. (2025) Shallow-water mussels (Mytilus galloprovincialis) adapt to deep-sea environment through transcriptomic and metagenomic insights. Communications biology, 8(1), 46.

Peng Q, et al. (2025) Modeling bacterial interactions uncovers the importance of outliers in the coastal lignin-degrading consortium. Nature communications, 16(1), 639.

Nychas E, et al. (2025) Discovery of robust and highly specific microbiome signatures of non-alcoholic fatty liver disease. Microbiome, 13(1), 10.