

Resource Summary Report

Generated by SPARC SAWG on Sep 12, 2026

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: data or information resource, database

Keywords: bio.tools, FASEB list

Resource Name: MetaCyc

Resource ID: SCR_007778

Alternate IDs: r3d100011294, nif-0000-03114, biotools:metacyc

Alternate URLs: <https://bio.tools/metacyc>, <https://doi.org/10.17616/R32K7X>

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260912T200152+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 2050 mentions in open access literature.

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

Yang J, et al. (2026) Age and sex-dependent tumor microbiome programs shape pancreatic cancer prognosis. *iScience*, 29(7), 116542.

Jastrz?b R, et al. (2026) Probiotic *Lactiplantibacillus plantarum* OL3246 supports healthy aging by enhancing quality of life, reducing inflammation, and modulating gut microbiota: a pilot study. *npj aging*, 12(1).

Chen YJ, et al. (2026) *Akkermansia Muciniphila* Ameliorates Imiquimod-Induced Skin Thickening, Colitis, and Gut Microbiota Alterations: A Metagenome Association Study. *Inflammation*, 49(1), 78.

Yoo S, et al. (2026) Functionally distinct core microbes of *Tricholoma matsutake* revealed by cross-study analysis. *Microbiome*, 14(1), 58.

Mora-Martínez C, et al. (2026) Gut microbiome signatures associated with depression and obesity. *mSystems*, 11(3), e0126325.

Corona-Cervantes K, et al. (2026) Maternal obesity alters human milk oligosaccharides content and correlates with early acquisition of late colonizers in the neonatal gut microbiome. *Gut microbes*, 18(1), 2607043.

Li Y, et al. (2026) Adjunctive probiotic therapy sustains symptom relief in gastroesophageal reflux disease through gut microbiome-metabolome remodeling. *mSystems*, 11(2), e0156825.

Phusathian B, et al. (2026) Bacterial xylanase supplementation improves nutrient utilization, gut integrity, and microbial metabolism in broilers fed energy-reduced diets. *Poultry science*, 105(4), 106515.

Peng J, et al. (2026) *Metarhizium anisopliae* Mitigates the Phytotoxicity of Lead and Nanoplastics on Rice by Modifying Physiological, Transcriptomic, Metabolomic Activities, and Soil Microbiome. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(21), e21570.

Holdaway CM, et al. (2026) Dietary Ethanolamine Increases Hepatic Lipid Accumulation in Mice Fed a High Fat Diet. *The Journal of nutrition*, 101348.

Hajjar G, et al. (2026) Metabolite names and identifiers: how far are we from interoperability? *Metabolomics : Official journal of the Metabolomic Society*, 22(2).

Sung H, et al. (2026) Unraveling the diagnostic and prognostic signatures of oral microbiota in head and neck cancer. *BMC biology*, 24(1).

Rao B, et al. (2026) Multicohort Validation of Gut Microbiome Signatures for Cholangiocarcinoma Diagnosis and Functional Characterization of *Bifidobacterium Pseudocatenulatum*. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(27), e17658.

Wang X, et al. (2026) Age-Dependent Dynamics of the Biliary Microbiome in Children with Choledochal Cysts: Functional Remodeling Underlying Taxonomic Conservation. *Pathogens* (Basel, Switzerland), 15(2).

Sajid S, et al. (2026) A Multi-Organ Atlas Links Gut Microbial Metabolites to Systemic Redox Changes in Aging Mice. *Aging cell*, 25(3), e70433.

Lin Y, et al. (2026) Gut microbiome composition and function reflect socioeconomic deprivation. *NPJ biofilms and microbiomes*, 12(1).

Liu Q, et al. (2026) Intercropping tea plants with different leguminous green manures enhances soil nutrient availability, thereby reshaping the structure and functional potential of soil microbial communities. *Frontiers in microbiology*, 17, 1700016.

Agapé L, et al. (2026) Recurrent phage treatment of *Salmonella*-infected chickens transiently reshapes gut microbiota composition and function. *Veterinary research*, 57(1).

Clucas D, et al. (2026) Host iron deficiency protects against *Plasmodium* infection and drives parasite molecular reprofiling. *Science advances*, 12(9), eaeb0828.

Tomachewski D, et al. (2026) Tree diversity shapes soil bacterial community structure under low abiotic heterogeneity in the Atlantic forest. *Archives of microbiology*, 208(5).