

Resource Summary Report

Generated by [NIF](#) on Aug 25, 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: 20260821T193825+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 [NIF](#) .

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

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.

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.

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

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).

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.

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.

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).

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

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

Dai DLY, et al. (2026) Breastfeeding may lessen socioeconomic disparities in child health through differences in the infant gut microbiome. *Cell reports. Medicine*, 7(4), 102755.

Park J, et al. (2026) Ecological network collapse and functional potential shifts in the canine oral microbiota associated with periodontal disease: a pilot study. *Scientific reports*, 16(1).

Valdez-Palomares F, et al. (2026) Human fecal transplantation from stunted children promotes metabolic dysfunction in mice fed with a high-fat and high-fructose corn syrup diet. *Gut microbes*, 18(1), 2651984.

Dixit K, et al. (2026) Multi-meta-omics reveal distinct microbial genomic profiles and metabolic dysregulation in non-celiac gluten sensitivity. *mSphere*, 11(4), e0085625.

Qin M, et al. (2026) The respiratory microbiome in pulmonary tuberculosis: a meta-analysis reveals niche-specific microbial and functional signatures. *mSystems*, 11(4), e0156325.

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

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

Toubiana D, et al. (2026) Metabolite correlation-based network analysis combined with machine learning techniques highlights LOX biosynthesis in *Vanilla planifolia* and *Vanilla pompona* source leaves. *Scientific reports*, 16(1).