

Resource Summary Report

Generated by [dkNET](#) on Aug 5, 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: database, data or information resource

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: 20260805T044157+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 1761 mentions in open access literature.

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

Helm ET, et al. (2026) Lawsonia intracellularis infection induces changes in microbial community function and composition associated with reduced pig growth and feed efficiency. *Animal microbiome*, 8(1), 1.

Verna G, et al. (2026) A missense mutation in Muc2 promotes gut microbiome and metabolome-dependent colitis-associated tumorigenesis. *The Journal of clinical investigation*, 136(1).

Obayashi N, et al. (2026) Prevalence and Ecological Role of Streptococcus toyakuensis in Saliva of Healthy Young Individuals. *International dental journal*, 76(1), 103987.

Zhao H, et al. (2026) Early life fecal microbiota transplantation enhances fermentation potential by changing the microbial profiles in broiler chickens. *Poultry science*, 105(1), 106189.

Dinesh D, et al. (2026) Gut Microbial Variations Associated With Proton Pump Inhibitor Use in the Boston Puerto Rican Health Study. *Pharmacology research & perspectives*, 14(1), e70205.

Yun Y, et al. (2026) Gut microbiome plasticity explains the altitudinal distribution pattern and adaptability in a small mammal species (*Apodemus draco*). *Microbiology spectrum*, 14(1), e0238825.

Zhang L, et al. (2026) Gut microbiome-mediated transformation of dietary phytonutrients is associated with health outcomes. *Nature microbiology*, 11(1), 94.

Jin S, et al. (2025) Disruption of the transsulfuration pathway by acute kidney injury causes intestinal damage. *iScience*, 28(10), 113511.

Wang S, et al. (2025) Deterministic succession patterns in the rumen and fecal microbiome associate with host metabolic shifts in peripartum dairy cattle. *GigaScience*, 14.

von Ameln Lovison O, et al. (2025) Unveiling the role of the upper respiratory tract microbiome in susceptibility and severity to COVID-19. *Frontiers in cellular and infection microbiology*, 15, 1531084.

Pu Y, et al. (2025) Gut metagenome and plasma metabolome profiles in older adults suggest pyruvate metabolism as a link between sleep quality and frailty. *Cell reports*, 44(10), 116297.

Lev?? M, et al. (2025) Metabolomics and metagenomics in mice reveal the role of the gut microbiota in tryptophan metabolism. *iScience*, 28(11), 113751.

Shi W, et al. (2025) Association of Multi-Kingdom Skin Microbiota With Radiation Dermatitis in Patients With Breast Cancer After Reconstructive Surgery: A Prospective, Longitudinal Study. *International journal of radiation oncology, biology, physics*, 123(1), 161.

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.

Wang D, et al. (2025) Effect of *Lacticaseibacillus casei* LC2W Supplementation on Glucose Metabolism and Gut Microbiota in Subjects at High Risk of Metabolic Syndrome: A Randomized, Double-blinded, Placebo-controlled Clinical Trial. *Probiotics and antimicrobial proteins*, 17(6), 3811.

Otte A, et al. (2025) High-resolution multiomics links nutrients and mixotrophy to toxicity in a harmful bloom of the haptophyte *Chrysochromulina leadbeateri*. *Science advances*, 11(26), eadv3390.

Xia Y, et al. (2025) Multi-omics analyses reveal altered gut microbial thiamine production in obesity. *Frontiers in microbiology*, 16, 1516393.

Mancabelli L, et al. (2025) Dissecting the molecular interactions between botanical extracts and the human gut microbiota. *Frontiers in microbiology*, 16, 1610170.

Shi H, et al. (2025) Multi-omics integration reveals functional signatures of gut microbiome in atherosclerosis. *Gut microbes*, 17(1), 2542384.

Altaie AM, et al. (2025) Integrated metagenomics and transcriptomics analysis reveals pathways associated with oral periapical lesions formation and progression. *Current research in microbial sciences*, 9, 100443.