

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

## BioCyc

RRID:SCR\_002298

Type: Tool

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### Proper Citation

BioCyc (RRID:SCR\_002298)

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### Resource Information

**URL:** <http://biocyc.org/>

**Proper Citation:** BioCyc (RRID:SCR\_002298)

**Description:** A collection of Pathway/Genome Databases which describes the genome and metabolic pathways of a single organism. The BioCyc collection of Pathway/Genome Databases (PGDBs) provides an electronic reference source on the genomes and metabolic pathways of sequenced organisms. BioCyc PGDBs are generated by software that predicts the metabolic pathway complements of completely sequenced organisms from their genome sequences. They also include the results of a number of other computational inference procedures applied to these genomes, including predictions of which genes code for missing enzymes in metabolic pathways, and predicted operons. The BioCyc Web site provides a suite of software tools for database searching and visualization, for omics data analysis, and for comparative genomics and comparative pathway questions. The databases within the BioCyc collection are organized into tiers according to the amount of manual review and updating they have received. Tier 1 PGDBs have been created through intensive manual efforts, and receive continuous updating. Tier 2 PGDBs were computationally generated by the PathoLogic program, and have undergone moderate amounts of review and updating. Tier 3 PGDBs were computationally generated by the PathoLogic program, and have undergone no review and updating. There are 967 DBs in Tier 3. The downloadable version of BioCyc that includes the Pathway Tools software provides more speed and power than the BioCyc Web site.

**Synonyms:** BioCyc Database Collection

**Resource Type:** data or information resource, database

**Defining Citation:** [PMID:16246909](#)

**Keywords:** database, pathway/genome databases, PGDB, genome, metabolic pathway, microbiome, FASEB list

**Funding:** NIGMS GM080746

**Availability:** Restricted

**Resource Name:** BioCyc

**Resource ID:** SCR\_002298

**Alternate IDs:** nif-0000-00369, r3d100011259

**Alternate URLs:** <https://doi.org/10.17616/R36G8H>

**License URLs:** <http://www.sri.com/privacy>

**Record Creation Time:** 20220129T080212+0000

**Record Last Update:** 20260905T132446+0000

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## Ratings and Alerts

No rating or validation information has been found for BioCyc.

No alerts have been found for BioCyc.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1063 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Kahwa I, et al. (2026) Comparative Phytochemical Profiles of Medicinal Plants Used for Wound Treatment: Insights From Wild and Hydroponically Cultivated Species in Lugazi Diocese, Uganda. *Chemistry & biodiversity*, 23(1), e03018.

Kahwa I, et al. (2026) Integrative LC-HR-QTOF-MS and Computational Metabolomics Approaches for Compound Annotation, Chemometric Profiling and In Silico Antibacterial Evaluation of Ugandan Propolis. *Metabolites*, 16(2).

Profeta R, et al. (2026) Genomic diversity and host-specificity in *Corynebacterium pseudotuberculosis* using comparative population genomics. *Frontiers in microbiology*, 17, 1729846.

Kaur P, et al. (2026) A proof of concept study on the diagnostic utility of in vivo expressed mycobacterial transcripts in tuberculous pleuritis. *Scientific reports*, 16(1).

Schmitt MS, et al. (2026) Learning functional groups in complex microbiomes. *bioRxiv* : the preprint server for biology.

- Geng S, et al. (2026) Role of the *Mycoplasma bovis* deoC gene in nucleoside catabolism and host cell survival. *Applied and environmental microbiology*, 92(6), e0015626.
- Pouder E, et al. (2026) Phylogenomic and metabolic insights into iron reduction metabolism in the genus *Deferribacter* belonging to the order *Deferribacterales*. *Microbial genomics*, 12(5).
- Gonzalez Mateu M, et al. (2026) Functional and ecological drivers of bacterial interactions in glacier-fed stream biofilms. *mSystems*, 11(6), e0037026.
- Liu Q, et al. (2026) Structural basis for selective thymidine binding by the *Borrelia burgdorferi* substrate-binding protein BmpA. *The Journal of biological chemistry*, 302(7), 113206.
- Willers VP, et al. (2026) Plug-and-play - enzymatic amino acid production from methanol and carbon dioxide. *Nature communications*, 17(1).
- Rychlik KA, et al. (2026) Prenatal arsenic exposure and gene expression in fetal liver, heart, lung, and placenta. *Toxicology*, 522, 154420.
- Liu P, et al. (2026) A community screening tool for neuropsychiatric symptoms in the elderly: integrating cortisol, microbiome, and social factors with machine learning. *Translational psychiatry*, 16(1), 26.
- Ahrens AP, et al. (2026) The inflammatory path toward type 1 diabetes begins during pregnancy. *Nature communications*, 17(1), 979.
- Pontrelli S, et al. (2026) Hypersensitivity of chitin degradation to initial species densities due to monomer diffusion. *Proceedings of the National Academy of Sciences of the United States of America*, 123(2), e2512676123.
- Mostolizadeh R, et al. (2026) MCC: automated mass and charge curation at the genome scale applied to *C. tuberculostearicum*. *Microbiology spectrum*, 14(2), e0320024.
- Kleetz J, et al. (2026) The biosynthesis of N-acylated tryptazolone in *Mycobacterium tuberculosis* and related bacteria. *The Journal of biological chemistry*, 302(2), 111079.
- Kelly G, et al. (2026) Natural variation links seedling hypocotyl growth with water loss in *Arabidopsis*. *The Plant journal : for cell and molecular biology*, 126(1), e70862.
- Feigis M, et al. (2026) Multicriteria evaluation of ethylene glycol assimilation pathways. *Journal of industrial microbiology & biotechnology*, 53.
- Keller MR, et al. (2026) Global response to antibiotic exposure reveals a critical role for nucleotide metabolism in high-level  $\beta$ -lactam tolerance. *npj antimicrobials and resistance*, 4(1), 11.
- Anderson CM, et al. (2026) *Enterococcus faecalis* alters antibiotic susceptibility in *Pseudomonas aeruginosa* mixed-species biofilms. *Journal of bacteriology*, 208(5), e0054825.