

Resource Summary Report

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BiGG Database

RRID:SCR_005809

Type: Tool

Proper Citation

BiGG Database (RRID:SCR_005809)

Resource Information

URL: <http://bigg.ucsd.edu/>

Proper Citation: BiGG Database (RRID:SCR_005809)

Description: A knowledgebase of Biochemically, Genetically and Genomically structured genome-scale metabolic network reconstructions. BiGG integrates several published genome-scale metabolic networks into one resource with standard nomenclature which allows components to be compared across different organisms. BiGG can be used to browse model content, visualize metabolic pathway maps, and export SBML files of the models for further analysis by external software packages. Users may follow links from BiGG to several external databases to obtain additional information on genes, proteins, reactions, metabolites and citations of interest.

Abbreviations: BiGG

Synonyms: BiGG: a Biochemical Genetic and Genomic knowledgebase of large scale metabolic reconstructions, BiGG - a Biochemical Genetic and Genomic knowledgebase

Resource Type: data or information resource, database

Defining Citation: [PMID:20426874](#)

Keywords: biochemical, genetics, genomics, genome, metabolic network, reconstruction, model, metabolic pathway, gene, protein, reaction, metabolite, metabolic reconstruction, compound, pathway, FASEB list

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Resource Name: BiGG Database

Resource ID: SCR_005809

Alternate IDs: nlx_149299, r3d100011567

Alternate URLs: <https://doi.org/10.17616/R3MG9M>

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260905T133132+0000

Ratings and Alerts

No rating or validation information has been found for BiGG Database.

No alerts have been found for BiGG Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 145 mentions in open access literature.

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

Zhao Y, et al. (2026) A multi-way SMILES-based hypergraph inference network for metabolic model reconstruction. Communications biology, 9(1).

Spiga L, et al. (2026) An anaerobic pathogen rewires host metabolism to fuel oxidative growth in the inflamed gut. Cell, 189(13), 3968.

Lucas M, et al. (2026) Reducibility of higher-order networks from dynamics. Nature communications, 17(1), 1551.

Jamshidi N, et al. (2026) Aryl hydrocarbon receptor in the kidney regulates metabolic cross-talk with the liver and gut microbiome. Scientific reports, 16(1).

De la Vega-Camarillo E, et al. (2026) Machine Learning-Guided Synthetic Microbial Communities Enable Functional and Sustainable Degradation of Persistent Environmental Pollutants. Environmental science & technology, 60(18), 13500.

Rose AE, et al. (2026) Rational engineering of facultative anaerobiosis enables commensal survival in the oxygenated gut. bioRxiv : the preprint server for biology.

Guo H, et al. (2026) Single-cell assembled genomes predict enhanced bacterial metabolic cross-feeding potential in carbon-enriched soils. The ISME journal, 20(1).

Richmond GR, et al. (2026) Nutrient control enables metabolic reconstruction of L. rhamnosus GG and analysis of secretions. bioRxiv : the preprint server for biology.

- Komáromyová M, et al. (2025) Insights into the role of bioactive plants for lambs infected with *Haemonchus contortus* parasite. *Frontiers in veterinary science*, 12, 1566720.
- Zhou N, et al. (2025) Quantitative Analysis of Coupled Carbon and Energy Metabolism for Lignin Carbon Utilization in *Pseudomonas putida*. *bioRxiv : the preprint server for biology*.
- Ai L, et al. (2025) Boolean matrix logic programming for active learning of gene functions in genome-scale metabolic network models. *Machine learning*, 114(11), 254.
- Guil F, et al. (2025) A fast method for extracting essential and synthetic lethality genes in GEM models. *Bioinformatics advances*, 5(1), vbaf127.
- Petri D, et al. (2025) Chicory modulates the rumen environment in lambs with endoparasites. *Scientific reports*, 15(1), 35455.
- Kumar S P, et al. (2025) Modelling reliable metabolic phenotypes by analysing the context-specific transcriptomics data. *NPJ systems biology and applications*, 11(1), 142.
- Bai C, et al. (2025) Machine Learning-Enabled Drug-Induced Toxicity Prediction. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(16), e2413405.
- Meeson KE, et al. (2025) Flux Sampling Suggests Metabolic Signatures of High Antibody-Producing CHO Cells. *Biotechnology and bioengineering*, 122(7), 1898.
- Ardalani O, et al. (2025) Rare metabolic gene essentiality is a determinant of microniche adaptation in *Escherichia coli*. *PLoS pathogens*, 21(12), e1013775.
- Zhou N, et al. (2025) Quantitative decoding of coupled carbon and energy metabolism in *Pseudomonas putida* for lignin carbon utilization. *Communications biology*, 8(1), 1310.
- Wei F, et al. (2024) Unveiling Metabolic Engineering Strategies by Quantitative Heterologous Pathway Design. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 11(45), e2404632.
- Champie A, et al. (2024) Diagnosis and mitigation of the systemic impact of genome reduction in *Escherichia coli* DGF-298. *mBio*, 15(10), e0087324.