

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: 20260729T044121+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 124 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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*.

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.

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.

- Ardalani O, et al. (2025) Rare metabolic gene essentiality is a determinant of microniche adaptation in *Escherichia coli*. *PLoS pathogens*, 21(12), e1013775.
- 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.
- Boer MD, et al. (2024) Improving genome-scale metabolic models of incomplete genomes with deep learning. *iScience*, 27(12), 111349.
- Kumar M, et al. (2024) Mixotrophic growth of a ubiquitous marine diatom. *Science advances*, 10(29), eado2623.
- Habibpour M, et al. (2024) Machine learning of metabolite-protein interactions from model-derived metabolic phenotypes. *NAR genomics and bioinformatics*, 6(3), lqae114.
- Baker M, et al. (2024) Convergence of resistance and evolutionary responses in *Escherichia coli* and *Salmonella enterica* co-inhabiting chicken farms in China. *Nature communications*, 15(1), 206.
- Casey J, et al. (2024) Transporter annotations are holding up progress in metabolic modeling. *Frontiers in systems biology*, 4, 1394084.
- Carter EL, et al. (2024) A temperature-induced metabolic shift in the emerging human pathogen *Photobacterium asymbiotica*. *mSystems*, 9(11), e0097023.
- Gao Y, et al. (2024) Development and applications of metabolic models in plant multi-omics research. *Frontiers in plant science*, 15, 1361183.
- Isewon I, et al. (2024) Machine learning methods for predicting essential metabolic genes from *Plasmodium falciparum* genome-scale metabolic network. *PloS one*, 19(12), e0315530.
- Oles RE, et al. (2024) Pathogenic *Bacteroides fragilis* strains can emerge from gut-resident commensals. *bioRxiv : the preprint server for biology*.