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: database, data or information resource

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

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250517T055722+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 114 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

Carter EL, et al. (2024) A temperature-induced metabolic shift in the emerging human pathogen Photorhabdus 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.

Dvo?ák P, et al. (2024) Synthetically-primed adaptation of Pseudomonas putida to a non-native substrate D-xylose. Nature communications, 15(1), 2666.

Qiu S, et al. (2024) Systematic elucidation of independently modulated genes in Lactiplantibacillus plantarum reveals a trade-off between secondary and primary metabolism. Microbial biotechnology, 17(2), e14425.

Oles RE, et al. (2024) Pathogenic Bacteroides fragilis strains can emerge from gut-resident commensals. bioRxiv : the preprint server for biology.

Heinken A, et al. (2023) Genome-scale metabolic reconstruction of 7,302 human microorganisms for personalized medicine. Nature biotechnology, 41(9), 1320.

Shin W, et al. (2023) An automated model annotation system (AMAS) for SBML models. Bioinformatics (Oxford, England), 39(11).

Tubergen PJ, et al. (2023) A computational model of Pseudomonas syringae metabolism unveils a role for branched-chain amino acids in Arabidopsis leaf colonization. PLoS computational biology, 19(12), e1011651.

Ramon C, et al. (2023) Functional comparison of metabolic networks across species. Nature communications, 14(1), 1699.

Kugler A, et al. (2023) Optimal energy and redox metabolism in the cyanobacterium Synechocystis sp. PCC 6803. NPJ systems biology and applications, 9(1), 47.

Tran TTV, et al. (2023) Artificial Intelligence in Drug Metabolism and Excretion Prediction: Recent Advances, Challenges, and Future Perspectives. Pharmaceutics, 15(4).

Potter AD, et al. (2023) Transcriptome-guided metabolic network analysis reveals rearrangements of carbon flux distribution in Neisseria gonorrhoeae during neutrophil co-culture. mSystems, 8(4), e0126522.

Paquette SE, et al. (2023) Evaluation of Neural Regulation and Microglial Responses to Brain Injury in Larval Zebrafish Exposed to Perfluorooctane Sulfonate. Environmental health perspectives, 131(11), 117008.