Resource Summary Report

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COBRApy

RRID:SCR_012096
Type: Tool

Proper Citation

COBRApy (RRID:SCR_012096)

Resource Information

URL: http://opencobra.sourceforge.net/openCOBRA/Welcome.html

Proper Citation: COBRApy (RRID:SCR_012096)

Description: Software Python package that provides support for basic COnstraint-Based Reconstruction and Analysis (COBRA) methods.

Synonyms: COBRA for Python

Resource Type: software resource

Defining Citation: PMID:23927696, DOI:10.1186/1752-0509-7-74

Keywords: software package, mac os x, unix/linux, windows, python, bio.tools

Funding:

Resource Name: COBRApy

Resource ID: SCR_012096

Alternate IDs: OMICS_05190, biotools:cobrapy

Alternate URLs: https://bio.tools/cobrapy

Old URLs: https://sources.debian.org/src/python3-cobra/

Record Creation Time: 20220129T080308+0000

Record Last Update: 20250410T070229+0000

Ratings and Alerts

No rating or validation information has been found for COBRApy.

No alerts have been found for COBRApy.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 257 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Kulyashov MA, et al. (2025) Modification and analysis of context-specific genome-scale metabolic models: methane-utilizing microbial chassis as a case study. mSystems, 10(1), e0110524.

Naeij HB, et al. (2025) Unraveling the metabolic landscape of Exophiala spinifera strain FM: Model reconstruction, insights into biodesulfurization and beyond. PloS one, 20(1), e0317796.

Sánchez-García S, et al. (2025) Immunometabolic Effect of Nitric Oxide on Human Macrophages Challenged With the SARS-CoV2-Induced Cytokine Storm. A Fluxomic Approach. Advanced healthcare materials, 14(1), e2401688.

Timouma S, et al. (2024) Development of a genome-scale metabolic model for the lager hybrid yeast S. pastorianus to understand the evolution of metabolic pathways in industrial settings. mSystems, 9(6), e0042924.

Agena E, et al. (2024) Evaluating the feasibility of medium-chain oleochemical synthesis using microbial chain elongation. Journal of industrial microbiology & biotechnology, 51.

Leonidou N, et al. (2024) Exploring the metabolic profile of A. baumannii for antimicrobial development using genome-scale modeling. PLoS pathogens, 20(9), e1012528.

Lambert A, et al. (2024) Community metabolic modeling of host-microbiota interactions through multi-objective optimization. iScience, 27(6), 110092.

Sprent N, et al. (2024) Metabolic modeling reveals distinct roles of sugars and carboxylic acids in stomatal opening as well as unexpected carbon fluxes. The Plant cell, 37(1).

Ginatt AA, et al. (2024) A metabolic modeling-based framework for predicting trophic dependencies in native rhizobiomes of crop plants. eLife, 13.

Ioannou A, et al. (2024) Resource sharing of an infant gut microbiota synthetic community in combinations of human milk oligosaccharides. The ISME journal, 18(1).

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.

Hasibi R, et al. (2024) Integration of graph neural networks and genome-scale metabolic models for predicting gene essentiality. NPJ systems biology and applications, 10(1), 24.

Coltman BL, et al. (2024) Characterising the metabolic rewiring of extremely slow growing Komagataella phaffii. Microbial biotechnology, 17(1), e14386.

Bae SH, et al. (2024) Intracellular Flux Prediction of Recombinant Escherichia coli Producing Gamma-Aminobutyric Acid. Journal of microbiology and biotechnology, 34(4), 978.

Gorter de Vries PJ, et al. (2024) Probing efficient microbial CO2 utilisation through metabolic and process modelling. Microbial biotechnology, 17(2), e14414.

Hedin KA, et al. (2024) Saccharomyces boulardii enhances anti-inflammatory effectors and AhR activation via metabolic interactions in probiotic communities. The ISME journal, 18(1).

Czajka JJ, et al. (2024) Genome-scale model development and genomic sequencing of the oleaginous clade Lipomyces. Frontiers in bioengineering and biotechnology, 12, 1356551.

Champie A, et al. (2024) Diagnosis and mitigation of the systemic impact of genome reduction in Escherichia coli DGF-298. mBio, 15(10), e0087324.

Neal M, et al. (2024) Pan-genome-scale metabolic modeling of Bacillus subtilis reveals functionally distinct groups. mSystems, 9(11), e0092324.

Beura S, et al. (2024) Genome-scale community modelling elucidates the metabolic interaction in Indian type-2 diabetic gut microbiota. Scientific reports, 14(1), 17259.