

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 COstraint-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: 20250519T203718+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 [dkNET](#).

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.

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

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.

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

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

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).

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).

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.

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.

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

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.

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

Glass EM, et al. (2024) Niche-specific metabolic phenotypes can be used to identify antimicrobial targets in pathogens. *PLoS biology*, 22(11), e3002907.

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.