

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

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: 20260912T195745+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 341 mentions in open access literature.

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

Krishnamurthy MB, et al. (2026) NAViFluX: a visualization-centric platform for interactive analysis, refinement and design of genome-scale metabolic networks. *Bioinformatics* (Oxford, England), 42(5).

Goryanin I, et al. (2026) EHMN 2026: A Thermodynamically Refined, SBML-Standardised Human Metabolic Network for Genome-Scale Analysis and QSP Integration. *Metabolites*, 16(4).

Champie A, et al. (2026) Comparative analysis of gene importance in *Escherichia coli* across growth conditions. *mSystems*, 11(5), e0142525.

Melet L, et al. (2026) The Phenylpropanoid Pathway Is a Central Roundabout in Peach Fruit Pre- and Postharvest Physiology. *Metabolites*, 16(3).

Ardalani O, et al. (2026) Annotating the pangenome reveals the diversity in the genetic basis for metabolic enzymes. *Science advances*, 12(27), eaeb3363.

Mostolizadeh R, et al. (2026) MCC: automated mass and charge curation at the genome scale applied to *C. tuberculostearicum*. *Microbiology spectrum*, 14(2), e0320024.

Tan SI, et al. (2026) High yield production of 3-hydroxypropionic acid using *Issatchenkia orientalis*. *Nature communications*.

Giovannini M, et al. (2026) Modelling *Fusobacterium* lifestyles transitions by integrating transcriptomics and growth data. *Current research in microbial sciences*, 10, 100573.

Feigis M, et al. (2026) Multicriteria evaluation of ethylene glycol assimilation pathways. *Journal of industrial microbiology & biotechnology*, 53.

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).

Reynolds RC, et al. (2026) Defining metabolic niches for marine microbial heterotrophs. *Science advances*, 12(17), eadz0537.

Corbín-Agustí P, et al. (2026) Incorporation of Cryptic Plasmid Energetics Improves Genome-Scale Metabolic Predictions in Probiotic *E. coli* Nissle 1917. *Microbial biotechnology*, 19(5), e70361.

Welland JWJ, et al. (2026) Ensemble Machine Learning Approaches Predict Survival in Lower-Grade Glioma Based on Glycosphingolipid Gene Expression and Metabolic

Modeling. Computational and structural biotechnology journal, 35(1), 0143.

Pham KN, et al. (2026) Hybrid metabolic engineering enables xylose-driven co-production of polyhydroxybutyrate and violacein in *Escherichia coli*. Journal of biological engineering, 20(1).

Lin DW, et al. (2026) Protocol for single-cell optimization objective and trade-off inference. STAR protocols, 7(1), 104373.

Bjurström EY, et al. (2026) Investigating uncharacterised genes in *Saccharomyces cerevisiae* using robot scientists. Scientific reports, 16(1).

Bras JE, et al. (2026) High-throughput generation and comparison of genome-scale metabolic models reveal strain-specific metabolic diversity in 439 *Lactococcus* strains. mSystems, 11(4), e0151725.

Luo J, et al. (2026) Reconstruction of human metabolic models with large language models. Proceedings of the National Academy of Sciences of the United States of America, 123(15), e2516511123.

Mueller J, et al. (2026) Multi-strain analysis of *Pseudomonas putida* reveals the metabolic and genetic diversity of the species. mSystems, 11(4), e0159425.

Bian X, et al. (2026) Transcriptome-constrained genome-scale metabolic modeling reveals central carbon and amino acid metabolic reprogramming underlying colistin-sulbactam synergy in *Acinetobacter baumannii*. Antimicrobial agents and chemotherapy, 70(6), e0184825.