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
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: 20240424T182919+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 213 mentions in open access literature.

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


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

Bordel S, et al. (2024) Genome-scale metabolic model of the versatile bacterium Paracoccus denitrificans Pd1222. mSystems, 9(2), e0107723.


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

Gellner G, et al. (2023) Stable diverse food webs become more common when interactions are more biologically constrained. Proceedings of the National Academy of Sciences of the United States of America, 120(31), e2212061120.

Liu L, et al. (2023) Protein engineering and iterative multimodule optimization for vitamin B6


Dhatt PS, et al. (2023) Microbial thermogenesis is dependent on ATP concentrations and the protein kinases ArcB, GlnL, and YccC. PLoS biology, 21(10), e3002180.

Bernstein DB, et al. (2023) Evaluating E. coli genome-scale metabolic model accuracy with high-throughput mutant fitness data. Molecular systems biology, 19(12), e11566.


