

Resource Summary Report

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libSBML

RRID:SCR_014134

Type: Tool

Proper Citation

libSBML (RRID:SCR_014134)

Resource Information

URL: <http://www.nitrc.org/projects/libsbml>

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Description: A programming library to help users read, write, manipulate, translate, and validate SBML files and data streams. Specifically, it is a library that users may embed into their own applications.

Synonyms: Systems Biology Markup Language Library, Library for Systems Biology Markup Language

Resource Type: data or information resource, catalog, database

Keywords: markup language, systems biology, programming library, catalog

Availability: Open source

Resource Name: libSBML

Resource ID: SCR_014134

Alternate URLs: <http://sourceforge.net/p/sbml/code/HEAD/tree/>

License: GNU Lesser General Public License

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260729T044343+0000

Ratings and Alerts

No rating or validation information has been found for libSBML.

No alerts have been found for libSBML.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 39 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Hu M, et al. (2025) Parameterization of cell-free systems with time-series data using KETCHUP. PLoS computational biology, 21(11), e1013724.

Xu J, et al. (2024) Curating models from BioModels: Developing a workflow for creating OMEX files. bioRxiv : the preprint server for biology.

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

Versluis DM, et al. (2024) 2'-Fucosyllactose helps butyrate producers outgrow competitors in infant gut microbiota simulations. iScience, 27(3), 109085.

Xu J, et al. (2024) Curating models from BioModels: Developing a workflow for creating OMEX files. PloS one, 19(12), e0314875.

Leonidou N, et al. (2024) Genome-scale model of *Rothia mucilaginosa* predicts gene essentialities and reveals metabolic capabilities. Microbiology spectrum, 12(6), e0400623.

Bleker C, et al. (2024) Stress Knowledge Map: A knowledge graph resource for systems biology analysis of plant stress responses. Plant communications, 5(6), 100920.

N??gre D, et al. (2023) Reconciliation and evolution of *Penicillium rubens* genome-scale metabolic networks-What about specialised metabolism? PloS one, 18(8), e0289757.

Pinto J, et al. (2023) SBML2HYB: a Python interface for SBML compatible hybrid modeling. Bioinformatics (Oxford, England), 39(1).

Versluis DM, et al. (2022) A Multiscale Spatiotemporal Model Including a Switch from Aerobic to Anaerobic Metabolism Reproduces Succession in the Early Infant Gut Microbiota. mSystems, 7(5), e0044622.

Santos JPG, et al. (2022) A Modular Workflow for Model Building, Analysis, and Parameter Estimation in Systems Biology and Neuroscience. Neuroinformatics, 20(1), 241.

Renz A, et al. (2021) First Genome-Scale Metabolic Model of *Dolosigranulum pigrum* Confirms Multiple Auxotrophies. Metabolites, 11(4).

Payne DD, et al. (2021) An updated genome-scale metabolic network reconstruction of *Pseudomonas aeruginosa* PA14 to characterize mucin-driven shifts in bacterial metabolism. NPJ systems biology and applications, 7(1), 37.

Moretti S, et al. (2021) MetaNetX/MNXref: unified namespace for metabolites and biochemical reactions in the context of metabolic models. *Nucleic acids research*, 49(D1), D570.

Gong C, et al. (2021) A Spatial Quantitative Systems Pharmacology Platform spQSP-IO for Simulations of Tumor-Immune Interactions and Effects of Checkpoint Inhibitor Immunotherapy. *Cancers*, 13(15).

Larsson I, et al. (2020) Genome-Scale Metabolic Modeling of Glioblastoma Reveals Promising Targets for Drug Development. *Frontiers in genetics*, 11, 381.

Glont M, et al. (2020) BioModels Parameters: a treasure trove of parameter values from published systems biology models. *Bioinformatics (Oxford, England)*, 36(17), 4649.

diCenzo GC, et al. (2020) Genome-scale metabolic reconstruction of the symbiosis between a leguminous plant and a nitrogen-fixing bacterium. *Nature communications*, 11(1), 2574.

Zoledowska S, et al. (2019) Metabolic Modeling of *Pectobacterium parmentieri* SCC3193 Provides Insights into Metabolic Pathways of Plant Pathogenic Bacteria. *Microorganisms*, 7(4).

Cankorur-Cetinkaya A, et al. (2018) Process development for the continuous production of heterologous proteins by the industrial yeast, *Komagataella phaffii*. *Biotechnology and bioengineering*, 115(12), 2962.