Resource Summary Report

Generated by NIF on May 23, 2025

libSBML

RRID:SCR_014134
Type: Tool

Proper Citation

libSBML (RRID:SCR_014134)

Resource Information

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

Proper Citation: libSBML (RRID:SCR_014134)

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: catalog, data or information resource, database

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

Funding:

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: 20250523T055018+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 38 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

Nègre 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).

diCenzo GC, et al. (2018) Robustness encoded across essential and accessory replicons of the ecologically versatile bacterium Sinorhizobium meliloti. PLoS genetics, 14(4), e1007357.

diCenzo GC, et al. (2018) Genomic and Biotechnological Characterization of the Heavy-Metal Resistant, Arsenic-Oxidizing Bacterium Ensifer sp. M14. Genes, 9(8).