Resource Summary Report

Generated by NIF on May 19, 2025

SBML

RRID:SCR_007422
Type: Tool

Proper Citation

SBML (RRID:SCR_007422)

Resource Information

URL: http://sbml.org

Proper Citation: SBML (RRID:SCR_007422)

Description: A computer-readable format for representing models of biochemical reaction networks in software. It''s applicable to models of metabolism, cell-signaling, and many others. This website is the portal for the global SBML development effort; you can find information about all aspects of SBML.

Abbreviations: SBML

Synonyms: Systems Biology Markup Language, The Systems Biology Markup Language

Resource Type: interchange format, narrative resource, markup language, data or information resource, standard specification

Keywords: metabolism, cell-signaling, computational modeling, FASEB list

Funding:

Resource Name: SBML

Resource ID: SCR_007422

Alternate IDs: nif-0000-00530

Record Creation Time: 20220129T080241+0000

Record Last Update: 20250517T055819+0000

Ratings and Alerts

No rating or validation information has been found for SBML.

No alerts have been found for SBML.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 102 mentions in open access literature.

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

Du Y, et al. (2024) Multi-omics technologies and molecular biomarkers in brain tumor-related epilepsy. CNS neuroscience & therapeutics, 30(4), e14717.

Villaverde AF, et al. (2022) A protocol for dynamic model calibration. Briefings in bioinformatics, 23(1).

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

Koblitz J, et al. (2021) The Metano Modeling Toolbox MMTB: An Intuitive, Web-Based Toolbox Introduced by Two Use Cases. Metabolites, 11(2).

Johnson ME, et al. (2021) Quantifying the roles of space and stochasticity in computer simulations for cell biology and cellular biochemistry. Molecular biology of the cell, 32(2), 186.

Keating SM, et al. (2020) SBML Level 3: an extensible format for the exchange and reuse of biological models. Molecular systems biology, 16(8), e9110.

Lee NR, et al. (2020) Genome-Scale Metabolic Network Reconstruction and In Silico Analysis of Hexanoic acid Producing Megasphaera elsdenii. Microorganisms, 8(4).

Koduru L, et al. (2020) Genome-scale metabolic reconstruction and in silico analysis of the rice leaf blight pathogen, Xanthomonas oryzae. Molecular plant pathology, 21(4), 527.

Romijn LB, et al. (2020) Modelling the effect of subcellular mutations on the migration of cells in the colorectal crypt. BMC bioinformatics, 21(1), 95.

Torres M, et al. (2019) Identifying important parameters in the inflammatory process with a mathematical model of immune cell influx and macrophage polarization. PLoS computational biology, 15(7), e1007172.

Sompairac N, et al. (2019) Metabolic and signalling network maps integration: application to cross-talk studies and omics data analysis in cancer. BMC bioinformatics, 20(Suppl 4), 140.

Hucka M, et al. (2019) The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core Release 2. Journal of integrative bioinformatics, 16(2).

Elmokadem A, et al. (2019) Quantitative Systems Pharmacology and Physiologically-Based Pharmacokinetic Modeling With mrgsolve: A Hands-On Tutorial. CPT: pharmacometrics & systems pharmacology, 8(12), 883.

Anderson R, et al. (2019) Length-independent telomere damage drives post-mitotic cardiomyocyte senescence. The EMBO journal, 38(5).

Murakami T, et al. (2019) Numerical modelling of the effects of cold atmospheric plasma on mitochondrial redox homeostasis and energy metabolism. Scientific reports, 9(1), 17138.

Zhou S, et al. (2018) Chronic platelet-derived growth factor receptor signaling exerts control over initiation of protein translation in glioma. Life science alliance, 1(3), e201800029.

de Lorenzo V, et al. (2018) Biological standards for the Knowledge-Based BioEconomy: What is at stake. New biotechnology, 40(Pt A), 170.

Smith RW, et al. (2018) DMPy: a Python package for automated mathematical model construction of large-scale metabolic systems. BMC systems biology, 12(1), 72.

Lambusch F, et al. (2018) Identifying frequent patterns in biochemical reaction networks: a workflow. Database : the journal of biological databases and curation, 2018.

Hucka M, et al. (2018) The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core. Journal of integrative bioinformatics, 15(1).