

Resource Summary Report

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

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

Resource Name: SBML

Resource ID: SCR_007422

Alternate IDs: nif-0000-00530

Record Creation Time: 20220129T080241+0000

Record Last Update: 20260905T132611+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 108 mentions in open access literature.

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

Kell DB, et al. (2026) How far can you go? Extrapolating values of catalytic activity from known protein landscapes in natural and directed evolution. Chemical Society reviews, 55(11), 6417.

Stojanov R, et al. (2025) Applicability Assessment of Technologies for Predictive and Prescriptive Analytics of Nephrology Big Data. Proteomics, 25(11-12), e202400135.

Cabaj A, et al. (2025) A dynamic model of gene activation in response to hypoxia accounting for both HIF-1 and HIF-2. Briefings in functional genomics, 24.

Zhang G, et al. (2025) Synaptic and intrinsic plasticity mediated by CCK-type signaling coordinates behavioral changes during motivational state shifts. Cell reports, 44(8), 116049.

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

Malik Sheriff RS, et al. (2024) BioModels' Model of the Year 2023. Frontiers in systems biology, 4, 1363884.

Guil F, et al. (2022) Staphylococcus epidermidis RP62A's Metabolic Network: Validation and Intervention Strategies. Metabolites, 12(9).

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

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

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.

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

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.

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.

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.

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.

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.

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).

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