

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 2026

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

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: 20260731T042743+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 106 mentions in open access literature.

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

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.

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.
- 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).
- 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.