

# Resource Summary Report

Generated by [dkNET](#) on Apr 23, 2025

## SBML

RRID:SCR\_007422

Type: Tool

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### Proper Citation

SBML (RRID:SCR\_007422)

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

**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:** 20250423T060403+0000

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## Ratings and Alerts

No rating or validation information has been found for SBML.

No alerts have been found for SBML.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 102 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [dkNET](#).

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.

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.

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.

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).

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.