

Resource Summary Report

Generated by [dkNET](#) on Aug 24, 2026

BioModels.net

RRID:SCR_010525

Type: Tool

Proper Citation

BioModels.net (RRID:SCR_010525)

Resource Information

URL: <http://biomodels.net/>

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Description: For computational modeling to become more widely used in biological research, researchers must be able to exchange and share their results. The development and broad acceptance of common model representation formats such as SBML is a crucial step in that direction, allowing researchers to exchange and build upon each other's work with greater ease and accuracy. The BioModels.net project is another step: an international effort to: 1. define agreed-upon standards for model curation 2. define agreed-upon vocabularies for annotating models with connections to biological data resources 3. provide a free, centralized, publicly-accessible database of annotated, computational models in SBML and other structured formats To facilitate assembling useful collections of quantitative models of biological phenomena, it is crucial to establish standards for the vocabularies used in model annotations as well as criteria for minimum quality levels of those models. The BioModels.net project aims to bring together a community of interested researchers to address these issues. We are working towards defining these standards through white papers and process definitions. All of the products of our efforts are open and freely available through this site.

Resource Type: data or information resource, international standard specification, narrative resource, portal, standard specification, topical portal

Resource Name: BioModels.net

Resource ID: SCR_010525

Alternate IDs: nlx_20867

Record Creation Time: 20220129T080259+0000

Record Last Update: 20260821T193924+0000

Ratings and Alerts

No rating or validation information has been found for BioModels.net.

No alerts have been found for BioModels.net.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Azer K, et al. (2021) History and Future Perspectives on the Discipline of Quantitative Systems Pharmacology Modeling and Its Applications. *Frontiers in physiology*, 12, 637999.

Schreiber F, et al. (2020) Specifications of standards in systems and synthetic biology: status and developments in 2020. *Journal of integrative bioinformatics*, 17(2-3).

Weis M, et al. (2019) Considerations for Adapting Pre-existing Mechanistic Quantitative Systems Pharmacology Models for New Research Contexts. *Frontiers in pharmacology*, 10, 416.

Neal ML, et al. (2019) Harmonizing semantic annotations for computational models in biology. *Briefings in bioinformatics*, 20(2), 540.

Verma M, et al. (2017) Modeling the Mechanisms by Which HIV-Associated Immunosuppression Influences HPV Persistence at the Oral Mucosa. *PloS one*, 12(1), e0168133.

Leber A, et al. (2016) Modeling the Role of Lanthionine Synthetase C-Like 2 (LANCL2) in the Modulation of Immune Responses to *Helicobacter pylori* Infection. *PloS one*, 11(12), e0167440.

Garny A, et al. (2015) OpenCOR: a modular and interoperable approach to computational biology. *Frontiers in physiology*, 6, 26.

Soliman S, et al. (2014) A constraint solving approach to model reduction by tropical equilibration. *Algorithms for molecular biology : AMB*, 9(1), 24.

Koo A, et al. (2013) In silico modeling of shear-stress-induced nitric oxide production in endothelial cells through systems biology. *Biophysical journal*, 104(10), 2295.

Wang Y, et al. (2012) Parameters in dynamic models of complex traits are containers of missing heritability. *PLoS computational biology*, 8(4), e1002459.

Waltemath D, et al. (2011) Reproducible computational biology experiments with SED-ML--the Simulation Experiment Description Markup Language. *BMC systems biology*, 5,

Manninen T, et al. (2011) Modeling signal transduction leading to synaptic plasticity: evaluation and comparison of five models. EURASIP journal on bioinformatics & systems biology, 2011(1), 797250.

Mellor N, et al. (2010) Reduction of off-flavor generation in soybean homogenates: a mathematical model. Journal of food science, 75(7), R131.

Demir E, et al. (2010) The BioPAX community standard for pathway data sharing. Nature biotechnology, 28(9), 935.

Manninen T, et al. (2010) Postsynaptic signal transduction models for long-term potentiation and depression. Frontiers in computational neuroscience, 4, 152.

Gay S, et al. (2010) A graphical method for reducing and relating models in systems biology. Bioinformatics (Oxford, England), 26(18), i575.

Materi W, et al. (2007) Computational systems biology in cancer: modeling methods and applications. Gene regulation and systems biology, 1, 91.

Le Novère N, et al. (2006) BioModels Database: a free, centralized database of curated, published, quantitative kinetic models of biochemical and cellular systems. Nucleic acids research, 34(Database issue), D689.