

Resource Summary Report

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BioModels

RRID:SCR_001993

Type: Tool

Proper Citation

BioModels (RRID:SCR_001993)

Resource Information

URL: <http://www.ebi.ac.uk/biomodels-main/>

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Description: Repository of mathematical models of biological and biomedical systems. Hosts selection of existing literature based physiologically and pharmaceutically relevant mechanistic models in standard formats. Features programmatic access via Web Services. Each model is curated to verify that it corresponds to reference publication and gives proper numerical results. Curators also annotate components of models with terms from controlled vocabularies and links to other relevant data resources allowing users to search accurately for models they need. Models can be retrieved in SBML format and import/export facilities are being developed to extend spectrum of formats supported by resource.

Abbreviations: BIOMD

Synonyms: BioModels Database - A Database of Annotated Published Models, BioModels Database, BioModels

Resource Type: service resource, data or information resource, data repository, database, storage service resource, topical portal, portal

Defining Citation: [PMID:20587024](#), [PMID:16381960](#)

Keywords: FAIR sharing, mathematical model, computational model, simulation, kinetic model, annotation, web service, data analysis service, systems biology, biological model, biology, molecular biology, nucleotide sequence, gene expression, protein, gene, dna, rna, genetics, gold standard

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NIGMS R01 GM070923

Availability: CC0, Public Domain Dedication, Cf. our terms of use.

Resource Name: BioModels

Resource ID: SCR_001993

Alternate IDs: nif-0000-02609, r3d100010789

Alternate URLs: <http://www.ebi.ac.uk/biomodels/>

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260729T044019+0000

Ratings and Alerts

No rating or validation information has been found for BioModels.

No alerts have been found for BioModels.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 249 mentions in open access literature.

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

Masison J, et al. (2025) Mathematical modeling reveals ferritin as the strongest cellular driver of dietary iron transfer block in enterocytes. PLoS computational biology, 21(3), e1012374.

Dubey P, et al. (2025) Predicting oxytocin binding dynamics in receptor genetic variants through computational modeling. npj women's health, 3(1).

Parera Olm I, et al. (2025) Synthetic Microbial Cocultivation for Targeted Production of Odd-Chain Carboxylates and Alcohols from Carbon Monoxide. Environmental science & technology, 59(35), 18706.

Pigozzi F, et al. (2025) Associative conditioning in gene regulatory network models increases integrative causal emergence. Communications biology, 8(1), 1027.

Raajaraam L, et al. (2025) COmmunity and Single Microbe Optimisation System (COSMOS). NPJ systems biology and applications, 11(1), 51.

Currie C, et al. (2025) Assessing the potential for in vivo modulation of FTH1 gene expression with small peptides to restore and enhance androgen receptor pathway inhibition in prostate cancer. Cancer biology & therapy, 26(1), 2503417.

Hellerstein JL, et al. (2025) Discovering subnetworks in SBML models. Bioinformatics (Oxford, England), 41(9).

Meeson KE, et al. (2025) Flux Sampling Suggests Metabolic Signatures of High Antibody-Producing CHO Cells. *Biotechnology and bioengineering*, 122(7), 1898.

Park SG, et al. (2025) A systems biology approach to understand temporal evolution of silver nanoparticle toxicity. *NPJ systems biology and applications*, 11(1), 80.

Babaev D, et al. (2025) Mathematical modeling of pharmacokinetics and pharmacodynamics of losartan in relation to CYP2C9 allele variants. *Frontiers in systems biology*, 5, 1504077.

Kumar S P, et al. (2025) Modelling reliable metabolic phenotypes by analysing the context-specific transcriptomics data. *NPJ systems biology and applications*, 11(1), 142.

van Lent P, et al. (2025) Jaxkineticmodel: Neural ordinary differential equations inspired parameterization of kinetic models. *PLoS computational biology*, 21(7), e1012733.

Etcheverry M, et al. (2025) AI-driven automated discovery tools reveal diverse behavioral competencies of biological networks. *eLife*, 13.

Linkevicius D, et al. (2025) Fitting and comparison of calcium-calmodulin kinetic schemes to a common data set using non-linear mixed effects modelling. *PloS one*, 20(2), e0318646.

Blasco-Roset A, et al. (2025) Acyl CoA-binding protein in brown adipose tissue acts as a negative regulator of adaptive thermogenesis. *Molecular metabolism*, 96, 102153.

Renz A, et al. (2025) Metabolic modeling elucidates phenformin and atpenin A5 as broad-spectrum antiviral drugs against RNA viruses. *Communications biology*, 8(1), 791.

Balaur I, et al. (2025) FAIRification of computational models in biology. *bioRxiv : the preprint server for biology*.

Kodate S, et al. (2025) Simulating metabolic pathways to enhance interpretations of metabolome genome-wide association studies. *Scientific reports*, 15(1), 17035.

Cooper HB, et al. (2024) A validated pangenome-scale metabolic model for the *Klebsiella pneumoniae* species complex. *Microbial genomics*, 10(2).

Matzko RO, et al. (2024) BioNexusSentinel: a visual tool for bioregulatory network and cytohistological RNA-seq genetic expression profiling within the context of multicellular simulation research using ChatGPT-augmented software engineering. *Bioinformatics advances*, 4(1), vbae046.