Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

SBO

RRID:SCR_006753
Type: Tool

Proper Citation

SBO (RRID:SCR_006753)

Resource Information

URL: http://www.ebi.ac.uk/sbo/

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Description: A set of controlled, relational vocabularies of terms commonly used in Systems Biology, and in particular in computational modeling. The ontology consists of seven orthogonal vocabularies defining: the roles of reaction participants (eg. substrate), quantitative parameters (eg. Michaelis constant), a precise classification of mathematical expressions that describe the system (eg. mass action rate law), the modeling framework used (eg. logical framework), and a branch each to describe entity (eg. macromolecule) and interaction (eg. process) types, and a branch to define the different types of metadata that may be present within a model. SBO terms can be used to introduce a layer of semantic information into the standard description of a model, or to annotate the results of biochemical experiments in order to facilitate their efficient reuse. SBO is an Open Biomedical Ontologies (OBO) candidate ontology, and is free for use. A programmatic access to the content of the Systems Biology Ontology is provided by Web Services.

Abbreviations: SBO

Synonyms: Systems Biology Ontology

Resource Type: controlled vocabulary, data or information resource, database, ontology

Defining Citation: PMID:17118155

Keywords: systems biology, computational modeling, web service, obo, gold standard

Funding: NIGMS

Availability: Free, The community can contribute to this resource

Resource Name: SBO

Resource ID: SCR_006753

Alternate IDs: nlx_66206

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260912T200012+0000

Ratings and Alerts

No rating or validation information has been found for SBO.

No alerts have been found for SBO.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at SPARC SAWG .

Pfau T, et al. (2021) IDARE2-Simultaneous Visualisation of Multiomics Data in Cytoscape. Metabolites, 11(5).

Carey MA, et al. (2020) Community standards to facilitate development and address challenges in metabolic modeling. Molecular systems biology, 16(8), e9235.

Pfau T, et al. (2016) Towards improved genome-scale metabolic network reconstructions: unification, transcript specificity and beyond. Briefings in bioinformatics, 17(6), 1060.

McWilliam H, et al. (2009) Web services at the European Bioinformatics Institute-2009. Nucleic acids research, 37(Web Server issue), W6.