

Resource Summary Report

Generated by T1D on Aug 3, 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: database, data or information resource, ontology, controlled vocabulary

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: 20260803T040446+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 [T1D](#).

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.