

## MIRIAM

MIRIAM, the Minimum Information Required In the Annotation of Models, is a set of guidelines that helps researchers to reuse, modify and combine computer models of biochemical processes. MIRIAM has two parts: (1) a 'reference correspondence' that matches each model to its description (often a journal publication), and (2) a set of annotation schemes. The first of these documents the model's provenance and provides a stable link to its full description; the second links the components of the model to relevant bioinformatics resources. These links rely on perennial URIs generated and resolved by MIRIAM Resources ([www.ebi.ac.uk/miriam/](http://www.ebi.ac.uk/miriam/)).

## Need Help?

BioModels Database is developed and hosted by the EMBL-European Bioinformatics Institute, a part of the European Molecular Biology Laboratory. A mirror of the database is hosted by the California Institute of Technology.

[www.ebi.ac.uk/biomodels/](http://www.ebi.ac.uk/biomodels/)  
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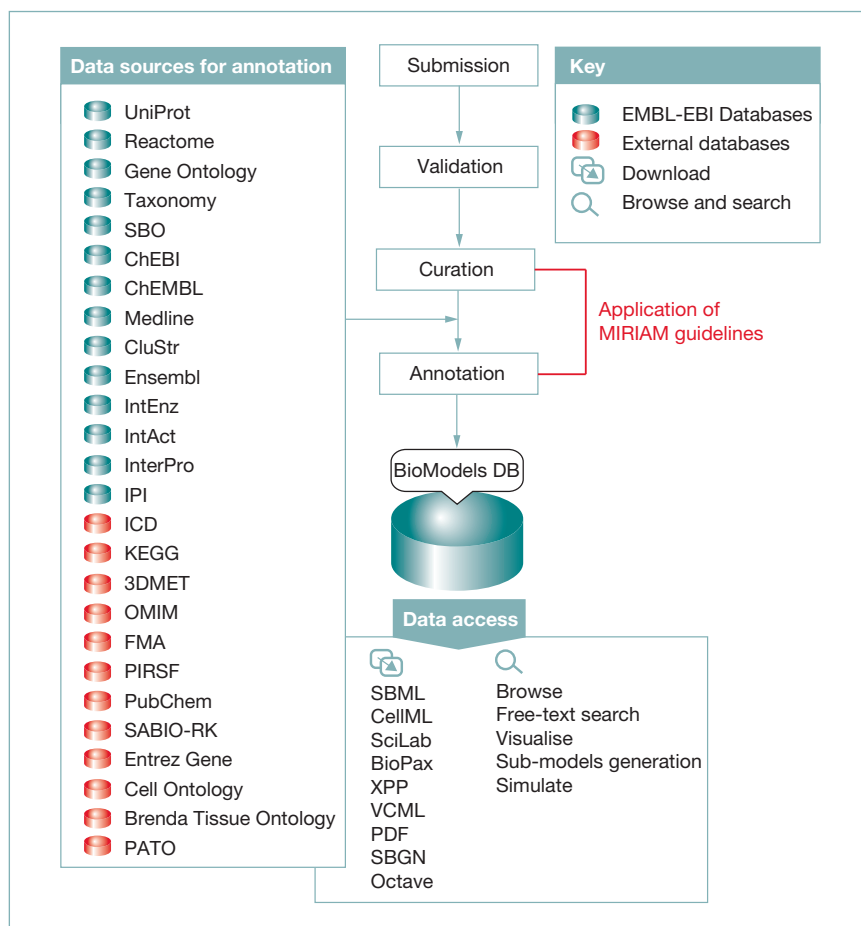
## BioModels Database

[www.ebi.ac.uk/biomodels/](http://www.ebi.ac.uk/biomodels/)

*Quantitative models are essential to understand the mechanisms of biological processes and to predict their behaviour. Until recently, most of the published quantitative models in biology were lost to the community, either because they were not made available or because they were insufficiently characterised to allow them to be reused. The rise of systems biology has increased the interest in detailed mathematical models in life science. As a consequence, academic and industrial scientists, as well as teachers of biological science, need to find, evaluate, compare and integrate models. BioModels Database not only provides a common repository for published, peer-reviewed, quantitative models of biochemical and cellular systems, but also instils confidence to users because all the models are carefully simulated and verified based on the reference publications.*

## What is BioModels Database?

BioModels Database is a data resource that allows biologists to store, search and retrieve published mathematical models of biological interest. Models present in the database are annotated and linked to relevant data resources, such as publications, databases of compounds and pathways, and controlled vocabularies. BioModels Database provides access to published, peer-reviewed, quantitative models of biochemical and cellular systems. The models are carefully checked by curators to verify that they correspond to the reference publication and that they give the proper numerical results.



A simplified version of the BioModels curation pipeline showing major sources of cross-links and ways of accessing the data.

Curators also annotate the components of the models with terms from controlled vocabularies and links to other relevant data resources. This allows you to search accurately for the models you need, and to identify the components of models precisely, an important step towards model reuse and composition. You can then retrieve the models in standard formats such as the Systems Biology Markup Language (SBML; <http://sbml.org>). BioModels Database is therefore a first step towards a Systems Biology 'shopping cart'.

BioModels Database uses a relational database (MySQL) for the storage of large volumes of annotation and a versioning system (Subversion) for the models themselves. A curation pipeline isolates models that are under curation from published models, so that publically available models can be trusted to be of a uniformly high standard.

## What can I do with BioModels Database?

- Find the kinetic models developed for a protein of interest, e.g. mitogen-activated protein kinase.
- Find the kinetic models of a biological process, for example the cell cycle.
- Visualise an SBGN graph of the process represented by the model.
- Visualise the mathematical description of the model.
- Download the models in standard formats.
- Download the models as configuration files for common simulators.
- Generate and download sub-models by selecting the components of your choice.
- Simulate the models online.
- Access all the models programmatically via Web Services.

## Submitting models to BioModels Database

We welcome submission of models to the curation pipeline of BioModels Database. To be accepted in the database, your model must comply with the rules of MIRIAM, the 'Minimum Information Required in the Annotation of Models' (see panel on page 1). Furthermore, the description of the model must be published or submitted for publication in a peer-reviewed journal. Once you have submitted your model, you will receive an accession number that you can use, for instance, in publications or grant applications. BioModels currently accepts models submitted in SBML and CellML formats.

## Retrieving models from BioModels Database

**Quick search.** Provides you with a list of models containing any of your search terms in the model components themselves, in an annotation, or in additional information related to an annotation. This option is comprehensive but can return false-positive results.

**Advanced search.** Allows you to refine your search. You can combine several elementary searches on the model components, using accession numbers of the data resources used for annotation. For some data resources you can also search associated information, such as names, synonyms or definitions.

**Model download.** Models can be retrieved in the standard SBML and CellML formats, as well as VCML, but also as configuration files for various simulators such as XPP-Aut, Octave and SciLab. The reaction graphs can be downloaded in BioPAX format and SBGN graphs. The models can also be viewed in a downloadable PDF format. ●

## Further reading

Le Novère, N. *et al.* The Systems Biology Graphical Notation, *Nature Biotechnology*, 27, 735-741 (2009)

Laibe, C. & Le Novère, N. MIRIAM Resources: tools to generate and resolve robust cross-references in Systems Biology. *BMC Systems Biology*, 1, 58 (2007)

Le Novère, N. *et al.* BioModels Database: A Free, Centralized Database of Curated, Published, Quantitative Kinetic Models of Biochemical and Cellular Systems *Nucleic Acids Res.*, 34, D689-D691 (2006)

Le Novère, N. *et al.* Minimum Information Requested In the Annotation of biochemical Models (MIRIAM) *Nature Biotechnology*, 23, 1509-1515 (2005)

## About BioModels

BioModels Database is developed in collaboration with the SBML-team (Caltech, CA, USA), DOQCS (NCBS, India), The Virtual Cell (UCHC, CO, USA), JWS Online (Stellenbosch University, South Africa) and CellML (Auckland Bioengineering Institute, New Zealand).

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