

BioModels Database, MIRIAM Registry, and Identifiers.org

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Waiheke, March 13th 2012

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EBI is an Outstation of the European Molecular Biology Laboratory.

Outline

- BioModels Database
- MIRIAM annotations
- MIRIAM registry
- Identifiers.org

<http://biomodels.net>



[Home](#) [Database](#) [MIRIAM](#) [SBO](#) [MIASE](#) [KisAO](#) [TEDDY](#) [Qualifiers](#) [Events](#) [Contact](#)

BioModels.net

The Next Step After Standard Formats

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

Helping to Define Community Standards

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.

Standards and Processes Developed Hand-in-Hand with a New Database

The database component of BioModels.net is especially designed for working with *annotated* computational models: each model is carefully reviewed and augmented by human annotators on the BioModels.net team to add metadata linking the model elements to other biological databases and resources. The **BioModels Database** at the **EBI** system goes far beyond other collections of models by being a

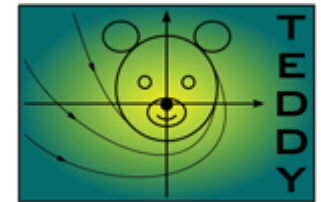
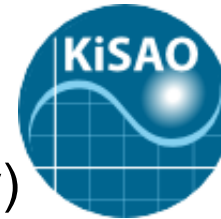
Biomodels.net

Standards and Guidelines:

- MIRIAM (Minimal Information Required In the Annotation of Models)
 - MIRIAM Registry
 - BioModels.net Qualifiers
- MIASE (Minimal Information About a Simulation Experiment)

Ontologies:

- KiSAO (Kinetic Simulation Algorithm Ontology)
- TEDDY (TERminology for the Description of DYnamics)
- SBO (Systems Biology Ontology)



BioModels Database

BioModels Database: An enhanced, curated and annotated resource for published quantitative kinetic models.

Li C. et al., BMC Systems Biology (2010), 4:92

BioModels Database: A Free, Centralized Database of Curated, Published, Quantitative Kinetic Models of Biochemical and Cellular Systems.

Le Novère N. et al., Nucleic Acids Research, (2006), 34: D689-D691

BioModels

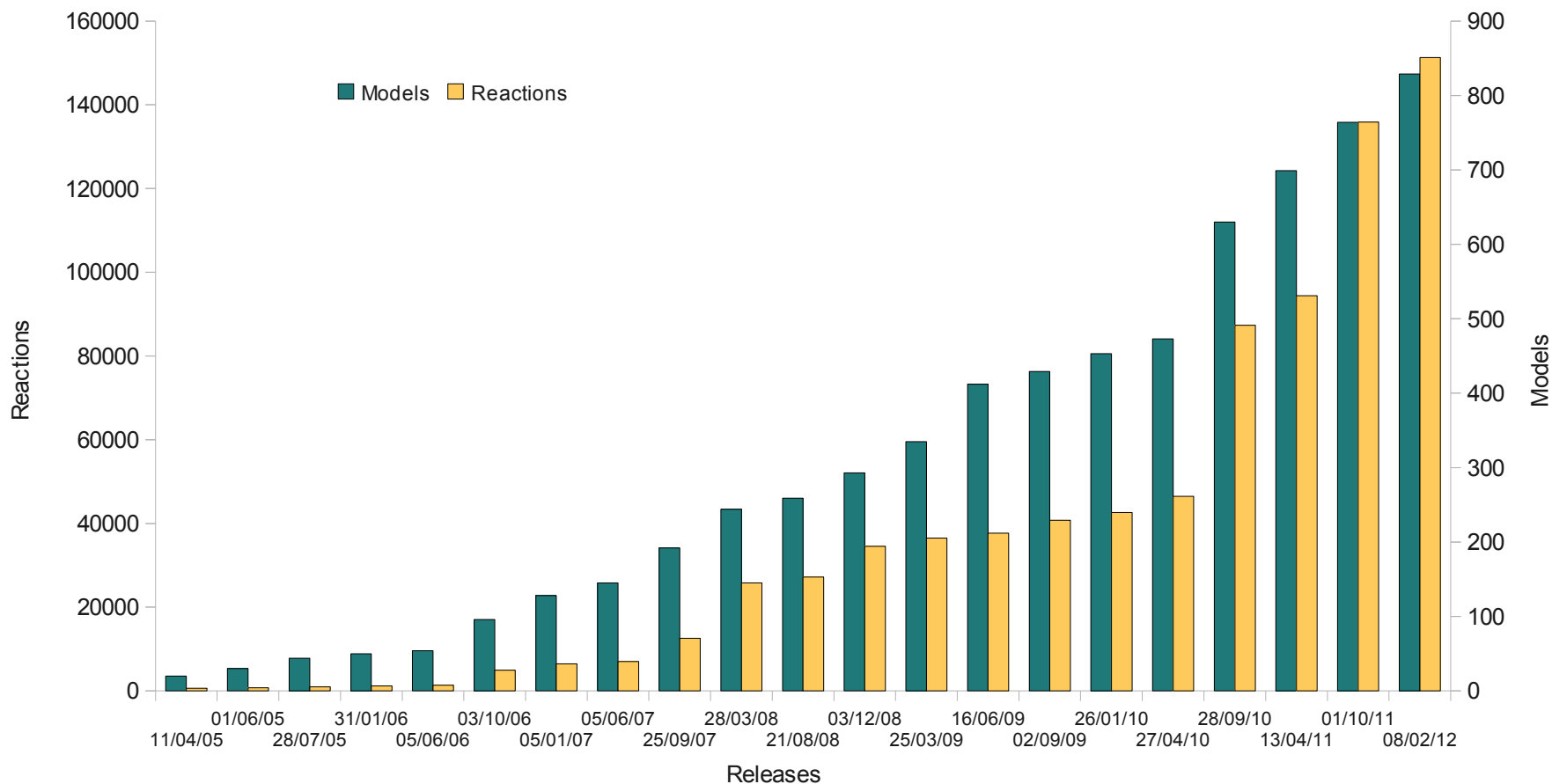
<http://www.ebi.ac.uk/biomodels/>

BioModels Database

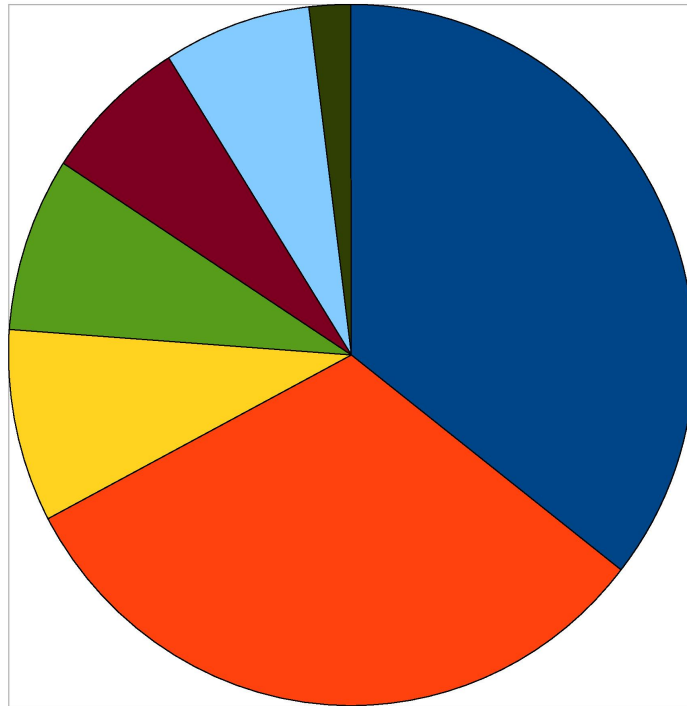
- contains only models from the peer reviewed literature
- models are manually curated and checked to ensure reliability (MIRIAM* compliance)
 - the model faithfully reflects the description in its reference publication
 - it can reproduce the results given in the reference publication
- unique identifiers for models
 - can be referenced, eg. in publications
- models freely accessible and reusable
- stored in SBML and exported in many other formats
- models and model elements cross-linked to and annotated with controlled vocabularies and databases
 - allows for complex queries and detailed searching
 - adds information and eases identification of model elements

* MIRIAM: Minimal Information Required In the Annotation of Biochemical Models
Nicolas Le Novère et al., *Nature Biotechnology*, **23**(12), 2005

Database Growth



Types of Models



- cellular metabolic process (GO:0044237, wo. translation & transcription)
- signal transduction (GO:0007165)
- cell cycle (GO:0007049)
- circadian rhythm (GO:0007623)
- cytosolic calcium ion homeostasis (GO:0051480)
- transmission of nerve impulse (GO:0019226)
- cell differentiation (GO:0030154)

Model Formats



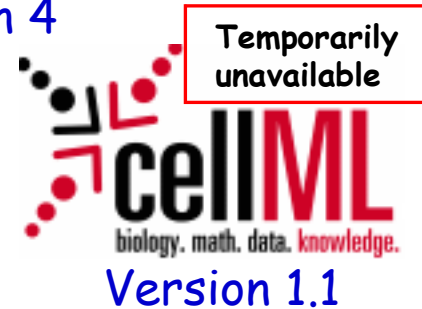
Level 1 Version 1
Level 1 Version 2
Level 2 Version 1
Level 2 Version 3
Level 2 Version 4



Version 1.0
Version 1.1



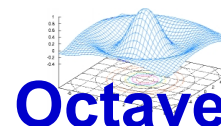
Level 2 Version 1
Level 2 Version 2
Level 2 Version 3
Level 2 Version 4



XPP-Aut



VCell
BioPAX



Model Submission

Where do models come from?

- submitted by curators
 - from other repositories (JWS online, DOQCS, VCell and CellML repositories, ...)
 - reimplemented from literature
 - from journals webpages
- from authors before publication
 - some journals advocate submission to BioModels DB:
 - Molecular Systems Biology
 - PLoS journals
 - BioMedCentral journals
- various people working on a model

model accession ID is unique and perennial
and can be used as a reference in publications
and for searching and retrieving the model

cellcycle.xml

and with name:

Tyson1991_CellCycle_6variable

has been successfully completed.

The model has been assigned the unique ID:

MODEL8232600906

[Submit Another Model](#)

Subject: BioModels Database - Notification of New Model Submission

From: biomodels-database-mailer@ebi.ac.uk

Date: 09:30

To: viji@ebi.ac.uk

PLEASE DO NOT REPLY TO THIS EMAIL

Dear submitter,

Thank you for submitting the model Tyson1991_CellCycle_6variable, published in

Proc Natl Acad Sci U S A 1991 Aug;88(16):7328-32.
Modeling the cell division cycle: cdc2 and cyclin interactions.
Tyson JJ.

The model is now in the process pipeline with the unique accession **MODEL8232600906**. This identifier is unique and can be used, for instance in scientific publications or grant applications. Our team of curators will now verify the syntax and the semantic of the model. You will be notified when this is done and the model enters the annotation phase.

We welcome any updates, comments, or other notices about this or any other models. Please feel free to contact us at:

The BioModels Database team
Computational Neurobiology
EMBL-EBI
Wellcome-Trust Genome Campus
Hinxton Cambridge
CB10 1SD
United-Kingdom

E-mail: biomodels-cura@ebi.ac.uk

Tel: +44 (0)1223 494521

Fax: +44 (0)1223 494468

Thank you,
The BioModels Database Team

BioModels Database is developed in collaboration by the teams of Nicolas Le Novère (EMBL-EBI, United-Kingdom), Michael Hucka (SBML Team, Caltech, USA), Herbert Sauro (Keck Graduate Institute, USA) and Jacky Snoep (JWS Online, Stellenbosch University, ZA), as part of the BioModels.net initiative. BioModels Database development is funded by the European Molecular Biology Laboratory and the National Institute of General Medical Sciences.

Please quote the reference publication associated with the model, when quoting a model present in the BioModels Database.

Ligand-Specific c-Fos Expression Emerges from the Spatiotemporal Control of ErbB Network Dynamics

Takashi Nakakuki,^{1,7} Marc R. Birtwistle,^{2,3,4,7} Yuko Saeki,^{1,5} Noriko Yumoto,^{1,5} Kaori Ide,¹ Takeshi Nagashima,^{1,5} Lutz Brusch,⁶ Babatunde A. Ogunnaike,³ Mariko Okada-Hatakeyama,^{1,5,*} and Boris N. Kholodenko^{2,4,*}

¹Computational Systems Biology Research Group, Advanced Computational Sciences Department, RIKEN Advanced Science Institute, 1-7-22 Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

²Systems Biology Ireland, University College Dublin, Belfield,

³University of Delaware, Department of Chemical Engineering

⁴Department of Pathology, Anatomy, and Cell Biology, Thom

⁵Laboratory for Cellular Systems Modeling, RIKEN Research Japan

⁶Dresden University of Technology, Center for Information Science

⁷These authors contributed equally to this work

BioModels Database - A Database of Annotated Published Models

BioModels Database is a data resource that allows biologists to store, search and retrieve published mathematical models linked to relevant data resources, such as publications, databases of compounds and controlled vocabularies. BioModels Database also allows users to generate sub-models, provides access to online simulation tools and f

Model Simulation

We describe the biochemical reactions and connectivity of signaling molecules using ordinary differential equations (ODEs) known as chemical kinetic equations. The ODE models were developed and simulated with MATLAB (Mathworks) and are available from the BioModels database under the IDs 1004300000 (mechanistic model) and 1003170000 (core model) (<http://www.ebi.ac.uk/biomodels/>). Detailed descriptions are in the [Extended Experimental Procedures](#).



<http://www.ebi.ac.uk/biomodels-main/MODEL1004300000>

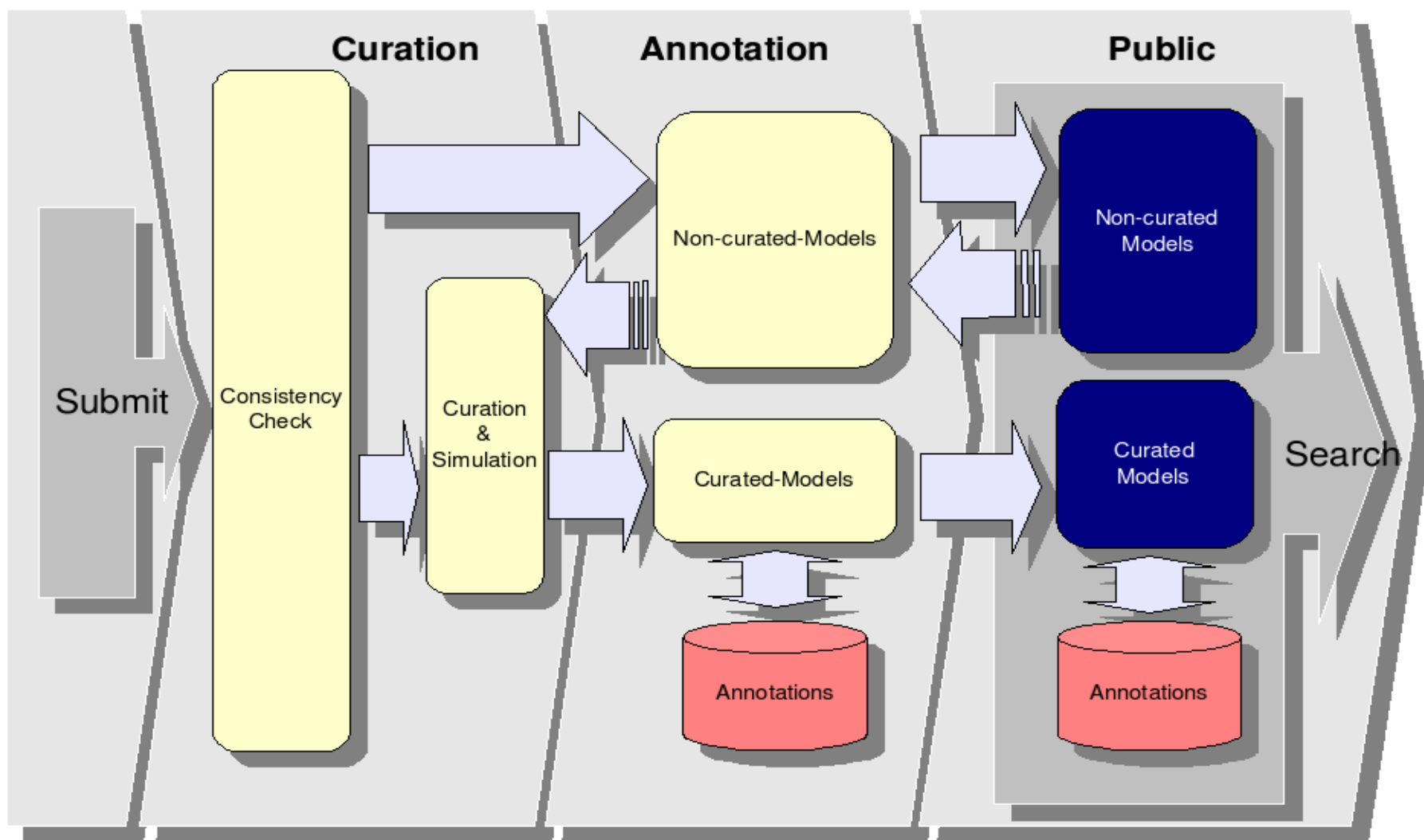
1004300000 Search Go to the model Advanced search

BIOMD0000000250 - Nakakuki2010_CellFateDecision_Mechanistic



Download SBML | Other formats (auto-generated) | Actions | Submit Model Comment/Bug

Model	Overview	Math	Physical entities	Parameters	Curation
Reference Publication					
Publication ID: 10.1016/j.cell.2010.04.010 Cell Ligand-specific c-Fos expression emerges from the spatiotemporal control of ErbB network dynamics. Takashi Nakakuki, Marc R. Birtwistle, Yuko Saeki, Noriko Yumoto, Kaori Ide, Takeshi Nagashima, Lutz Brusch, Babatunde A. Ogunnaike, Mariko Hatakeyama, and Boris N. Kholodenko RIKEN Advanced Science Institute, Computational Systems Biology Research Group, Advanced Computational Sciences Department, Japan [more]					
Model					
Original Model: BIOMD0000000250.xml.orig	set #1	bqbiol:occursin	Taxonomy Homo sapiens		
Submitter: Lutz Brusch	set #2	bqbiol:isPartOf	KEGG Pathway hsa04010		
Submission ID: MODEL 1004300000	set #3	bqbiol:isVersionOf	Gene Ontology MAPKKK cascade involved in epidermal growth factor receptor signalling		
Submission Date: 30 Apr 2010 20:00:20 UTC	set #4	bqbiol:hasVersion	Reactome REACT_634		
Last Modification Date: 24 May 2010 16:29:59 UTC	set #5	bqbiol:isVersionOf	Reactome REACT_9417		
Creation Date: 30 Apr 2010 11:41:28 UTC	set #6	bqbiol:occursin	Brenda Tissue Ontology BTO:0000093		



Curated and Non-curated Branch

Curated models

- models reproduce results, fully annotated, MIRIAM compliant

Non-Curated models

- valid SBML, not curated or annotated by the curators.
 - not MIRIAM compliant
 - can not reproduce results published in the paper.
 - non kinetic models (eg. FBA, stoichiometric maps).
 - MIRIAM compliant
 - models contain kinetics that we cannot curate up to now.
 - back lag in curation, the curators just did not have the time → these models will be moved into the curated branch as soon as possible.

MIRIAM Annotations

Each model element is linked to **external data resources**. This

- enhances model semantics
- is essential for searching.

Taxonomy, Gene Ontology, ChEBI, UniPROT, KEGG, Reactome, Enzyme Nomenclature, etc.

MIRIAM Annotations are represented as a triplet which consists of:

- data collection (eg. Enzyme Nomenclature)
- identifier (eg. EC 3.1.3.16 = phosphoprotein phosphatase)
- qualifier (eg. *is Version of*)

Data collection and identifier together, are in the form of **URI** (*Uniform Resource Identifier*):

urn:miriam:ec-code:3.1.3.16

these are resolved to a **URL** using the MIRIAM Registry
(<http://www.ebi.ac.uk/miriam/>)

cdc2k dephosphorylation [cdc2k-P] → [cdc2k];		
Math:	cell × CP × k9 (Detail)	
Annotations:	set #1 bqbiol:isVersionOf	Enzyme Nomenclature 3.1.3.16
		Gene Ontology protein amino acid dephosphorylation

BIOMD0000000005 - Tyson1991_CellCycle_6var


[SBML formats](#) | [Other formats](#) | [Actions](#) | [Submit Model Comment/Bug](#)

Model	Overview	Math	Physical entities	Parameters	Curation
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Reference Publication

Publication ID: [1831270](#)

Proc Natl Acad Sci U S A 1991 Aug;88(16):7328-32.
 Modeling the cell division cycle: cdc2 and cyclin interactions.
 Tyson JJ.
 Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg 24061. [\[more\]](#)

Model

Original Model: [BIOMD0000000005.xml.origin](#)Submitter: [Nicolas Le Novère](#)

Submission ID: MODEL6614644188

Submission Date: 13 Sep 2005 12:31:08 UTC

Last Modification Date: 10 Aug 2009 14:09:39 UTC

Creation Date: 08 Feb 2005 18:28:27 UTC

 Encoders: [Bruce Shapiro](#)
[Vijayalakshmi Chelliah](#)

set #1	bqbiol:hasVersion	Reactome REACT_152
	bqbiol:isVersionOf	KEGG Pathway sce04111 Gene Ontology mitotic cell cycle
	bqmodel:is	Taxonomy Funqi/Metazoa group

Notes

This a model from the article:

Modeling the cell division cycle: cdc2 and cyclin interactions.Tyson JJ *Proc. Natl. Acad. Sci. U.S.A.* 1991; 88(16); 7328-32 [1831270](#).**Abstract:**

The proteins cdc2 and cyclin form a heterodimer (maturation promoting factor) that controls the major events of the cell cycle. A mathematical model for the interactions of cdc2 and cyclin is constructed. Simulation and analysis of the model show that the control system can operate in three modes: as a steady state with high maturation promoting factor activity, as a spontaneous oscillator, or as an excitable switch. We associate the steady state with metaphase arrest in unfertilized eggs, the spontaneous oscillations with rapid division cycles in early embryos, and the excitable switch with growth-controlled division cycles typical of nonembryonic cells.

This model originates from BioModels Database: A Database of Annotated Published Models. It is copyright (c) 2005-2010 The BioModels Team.

For more information see the [terms of use](#).

To cite BioModels Database, please use [Le Novère N., Bornstein B., Broicher A., Courtot M., Donizelli M., Dharuri H., Li L., Sauro H., Schilstra M., Shapiro B., Snoep J.L., Hucka M. \(2006\) BioModels Database: A Free, Centralized Database of Curated, Published, Quantitative Kinetic Models of Biochemical and Cellular Systems Nucleic Acids Res. 34: D689-D691.](#)

SBML formats | Other formats | Actions | [Submit Model Comment/Bug](#)

Model | Overview | Math | Physical entities | Parameters

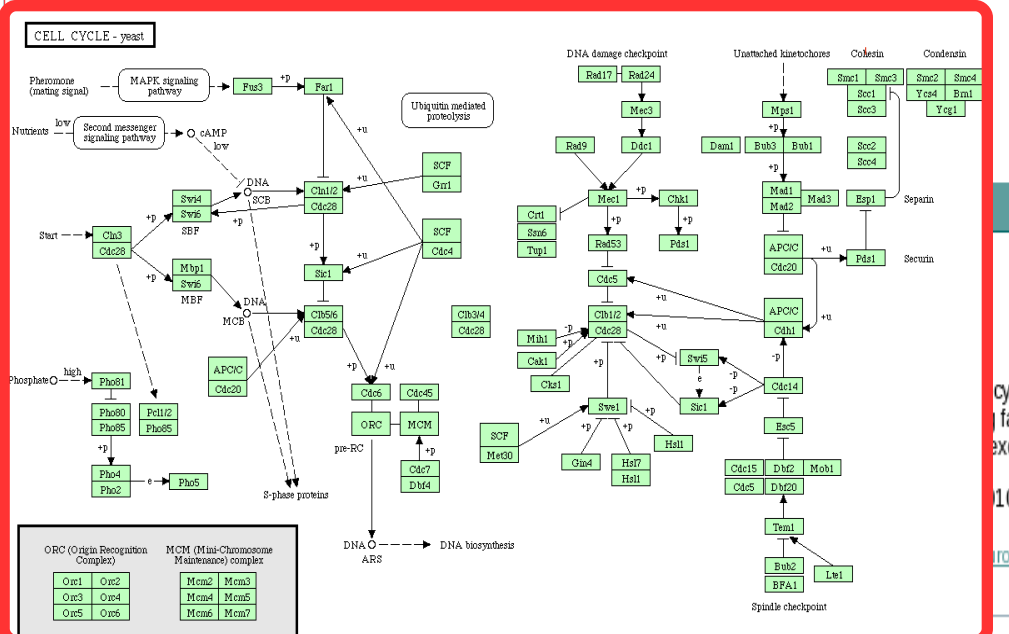
Reference Publications

Publication ID: [1831270](#)
Proc Natl Acad Sci U S A 1991 Aug;88(16):7328-32.
Modeling the cell division cycle: cdc2 and cyclin interactions.
Tyson JJ.
Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg, VA 24061-0400, USA

Model

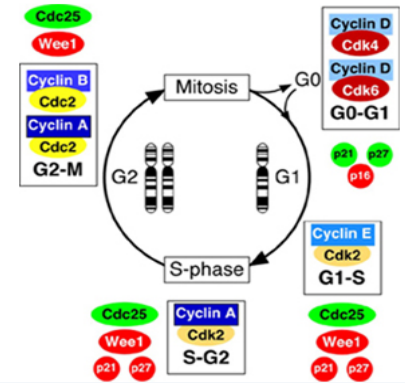
Original Model: [BIOMD0000000005.xml.orig.in](#)
Submitter: [Nicolas Le Novère](#)
Submission ID: MODEL661464418
Submission Date: 13 Sep 2005 12:31:08 UTC

bqbiol:hasVersion [Reactome REACT_152](#)
set#1 bqbiol:isVersionOf [KEGG Pathway sce04111](#)
bqmodel:is [Taxonomy Fungi/Metazoa group](#)



Stable identifier	REACT_152.2
Authoried	O'Connell, M, Walworth, N, Bosco, G, 2005-01-01
Reviewed	Manfredi, J

The replication of the genome and the subsequent segregation of chromosomes into daughter cells are controlled by DNA replication is carried out during a discrete temporal period known as the S (synthesis)-phase, and chromosome segregation occurs during the M (mitosis)-phase. Cellular architecture at mitosis. Two gap-phases separate these major cell cycle events: G1 between mitosis and S phase, and G2 between S phase and mitosis. In the development of the human body, cells can exit the cell cycle for a period and enter a quiescent state known as G0, but again, but undergo morphological development to carry out the wide variety of specialized functions of individual tissue types. A family of protein serine/threonine kinases known as the cyclin-dependent kinases (CDKs) controls progression through the cell cycle. The catalytic subunit is dependent on binding to a cyclin partner. The human genome encodes several cyclins and several CDKs, but only a few are active at the relevant time and place. Additional regulatory proteins and post-translational modifications ensure that CDK activity is restricted to a narrow window of activity.



Lineage	Taxonomy identifier	33154
	Scientific name	Fungi/Metazoa group
	Common name	-
• Eukaryota	Other NCBI synonyms	Opisthokonta opisthokonts
	Rank	no rank
	Number of UniProtKB/Swiss-Prot entries	114913
	Number of UniProtKB/TrEMBL entries	1459130

Taxonomy navigation	
Up taxonomy tree	Down taxonomy tree
Eukaryota	• Choanoflagellida
	• Fungi
	• Fungi/Metazoa incertae sedis
	• Metazoa

MIRIAM Annotation in SBML

- included as RDF
- linked via MetaID of model element
- URIs can be combined in a bag

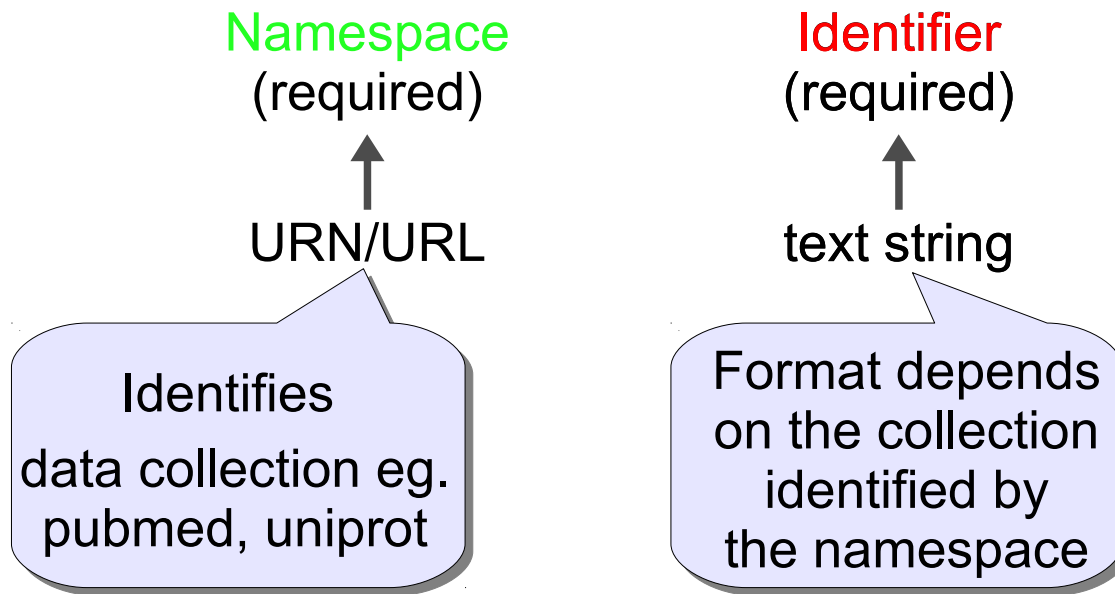
```
[...]
<species metaid="heme"
  id="heme"
  compartment="Comp01"
  initialConcentration="0">
  <annotation>
    <rdf:RDF xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#"
      xmlns:bqbiol="http://biomodels.net/biology-qualifiers/"
      <rdf:Description rdf:about="#heme">
        <bqbiol:hasPart>
          <rdf:Bag>
            <rdf:li rdf:resource="urn:miriam:uniprot:P69905" />
            <rdf:li rdf:resource="urn:miriam:uniprot:P68871" />
            <rdf:li rdf:resource="urn:miriam:obo.chebi:CHEBI%3A17627" />
          </rdf:Bag>
        </bqbiol:hasPart>
      </rdf:Description>
    </rdf:RDF>
  </annotation>
</species>
[...]
```

Hemoglobin subunit alpha

Hemoglobin subunit beta

ferroheme b

MIRIAM Annotations



the namespace and the identifier are combined into a single URN

`urn:miriam:datatype:identifier`

`urn:miriam:pubmed:16333295`

MIRIAM publication

`urn:miriam:uniprot:P69905`

Alpha-globin (human)

`urn:miriam:taxonomy:9606`

Homo sapiens

http://identifiers.org

[Home](#)[News](#)[Help](#)[Examples](#)[Registry](#)[About](#)

Welcome to Identifiers.org!

Identifiers.org is a system providing resolvable persistent URIs used to identify data for the scientific community, with a current focus on the Life Sciences domain. The provision of a resolvable identifiers (URLs) fits well with the [Semantic Web](#) vision, and the [Linked Data](#) initiative.

Links

- [About](#)
- [News](#)
- [Help](#)
- [Examples URIs](#)
- [MIRIAM Registry](#)

Board of trustees

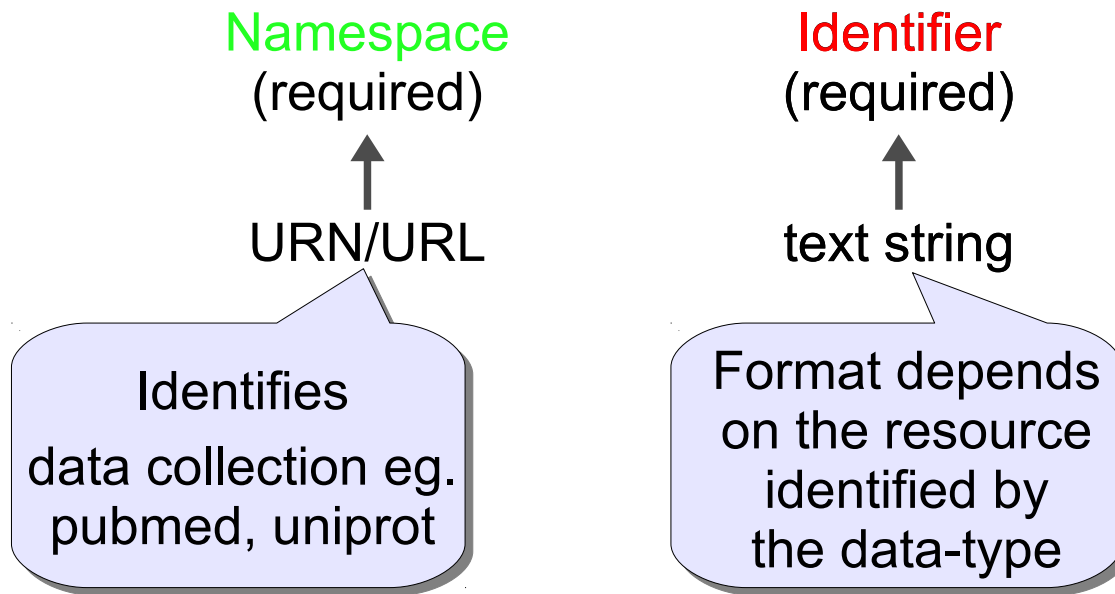
Identifiers.org is a community project which activities are overseen by the following board of trustees:

- [Michel Dumontier](#) (Carleton University, Ottawa, Canada - [Bio2RDF](#), [W3C HCLS](#))
- [Michael Galperin](#) (NCBI, USA - [NAR Database issue](#))
- [Pascale Gaudet](#) (Swiss Institute of Bioinformatics, Geneva, Switzerland - [BioDBCore](#))
- [Lee Harland](#) (Connected Discovery, UK - [Open PHACTS](#))
- [Michael Hucka](#) (California Institute of Technology, Pasadena, USA - [SBML](#))
- [Toshiaki Katayama](#) (University of Tokyo, Japan - [BioRuby](#), [KEGG](#))
- [Nicolas Le Novère](#) (EMBL-EBI, Hinxton, UK - [BioModels Database](#))
- [Philippe Rocca-Serra](#) (Oxford University, Oxford, UK - [BioSharing](#))
- [Mark Wilkinson](#) (St. Paul's Hospital/UBC Vancouver, Canada - [LSRN](#), [SADI](#))

Contact

If you have any queries or experience any issues with this service, please contact: **biomodels-net-support [AT] lists.sf.net**

MIRIAM Annotations



alternatively an equivalent, directly resolvable URL version exists:

urn:miriam:namespace:identifier	http://identifiers.org/namespace/identifier
urn:miriam:pubmed:16333295	http://identifiers.org/pubmed/16333295
urn:miriam:uniprot:P69905	http://identifiers.org/uniprot/P69905
urn:miriam:taxonomy:9606	http://identifiers.org/taxonomy/9606

MIRIAM Registry

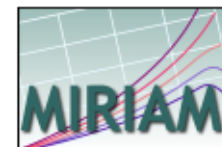
EBI > Groups > Computational Neurobiology > Research > MIRIAM Registry

MIRIAM Registry

MIRIAM Registry are a set of online services created in support of [MIRIAM](#), a set of guidelines for the annotation and curation of computational models.

The core of *MIRIAM Registry* is a catalogue of data collections (corresponding to controlled vocabularies or databases), their URIs and the corresponding physical URLs or resources. Access to this data is made available via exports (XML) and Web Services (SOAP).

MIRIAM Registry is developed and maintained under the [BioModels.net](#) initiative, and are free for use by all.



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- :: Web Services
- :: Documents

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- Support
- SourceForge project

- Curator Sign in



sourceforge

Browse

[by data collection name](#)
[by tags](#)

Web Services

[services available](#)
[usage of the services](#)
[online demonstration](#)

Search

[generic search](#)

Exports

[XML](#)

Registry

MIRIAM Registry is composed of four components: [a database](#), [some Web Services](#), [a Java library](#) and [this web application](#).

Database

<http://www.ebi.ac.uk/miriam>


EMBL-EBI The EMBL-EBI logo consists of a circular arrangement of small green and red dots.

Data Collections

EBI > Groups > Computational Neurobiology > Research > MIRIAM Registry

Browse data collections: *recently updated*

Recently updated | [A](#) | [B](#) | [C](#) | [D](#) | [E](#) | [F](#) | [G](#) | [H](#) | [I](#) | [J](#) | [K](#) | [L](#) | [M](#) | [N](#) | [O](#) | [P](#) | [Q](#) | [R](#) | [S](#) | [T](#) | [U](#) | [V](#) | [W](#) | [X](#) | [Y](#) | [Z](#)

Name	Namespace	Definition
Pathway Ontology	obo.pw	The Pathway Ontology captures information on biological networks, the relationships between networks and the alterations or malfunctioning of such networks within a hierarchical structure. The five main branches of the ontology are: classic metabolic pathways, regulatory, signaling, drug, and disease pathways for complex human conditions.
Pfam	pfam	The Pfam database contains information about protein domains and families. For each entry a protein sequence alignment and a Hidden Markov Model is stored.
Ensembl Plants	ensembl.plant	Ensembl Genomes consists of five sub-portals (for bacteria, protists, fungi, plants and invertebrate metazoa) designed to complement the availability of vertebrate genomes in Ensembl. This collection is concerned with plant genomes.
Nucleotide Sequence Database	insdc	The International Nucleotide Sequence Database Collaboration (INSDC) consists of a joint effort to collect and disseminate databases containing DNA and RNA sequences.
 CAS	cas	CAS (Chemical Abstracts Service) is a division of the American Chemical Society and is the producer of comprehensive databases of chemical information.
Japan Chemical Substance Dictionary	jcsd	The Japan Chemical Substance Dictionary is an organic compound dictionary database prepared by the Japan Science and Technology Agency (JST).
Enzyme Nomenclature	ec-code	The Enzyme Classification contains the recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology on the nomenclature and classification of enzyme-catalysed reactions.
HSSP	hssp	HSSP (homology-derived structures of proteins) is a derived database merging structural (2-D and 3-D) and sequence information (1-D). For each protein of known 3D structure from the Protein Data Bank, the database has a file with all sequence homologues, properly aligned to the PDB protein.
NARCIS	narcis	NARCIS provides access to scientific information, including (open access) publications from the repositories of all the Dutch universities, KNAW, NWO and a number of research institutes, which is not referenced in other citation databases.
3DMET	3dmet	3DMET is a database collecting three-dimensional structures of natural metabolites.
KEGG Pathway	kegg.pathway	KEGG PATHWAY is a collection of manually drawn pathway maps representing our knowledge on the molecular interaction and reaction networks.
KEGG Metagenome	kegg.metagenome	The KEGG Metagenome Database collection information on environmental samples (ecosystems) of genome sequences for multiple species.
KEGG Genome	kegg.genome	KEGG Genome is a collection of organisms whose genomes have been completely sequenced.
neXtProt	neXtProt	neXtProt is a resource on human proteins, and includes information such as proteins' function, subcellular location, expression, interactions and

Collection Entry

Data collection: *PubMed*

Overview

Categories

Miscellaneous

Name

Identifier	MIR:00000015
Name	PubMed

Information

Definition	PubMed is a service of the U.S. National Library of Medicine that includes citations from MEDLINE and other life science journals for biomedical articles back to the 1950s.
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Identifier pattern	^id+\$
--------------------	--------

URIs

Namespace	pubmed
Root URL	http://identifiers.org/pubmed/
Root URN	urn:miriam:pubmed:

Related Locations

Resource MIR:00100032	Access URL	http://www.ebi.ac.uk/citexplore/citationDetails.do?dataSource=MED&externalId=\$id [Example: 16333295]
	Website	http://www.ebi.ac.uk/citexplore/
	Description	CiteXplore
	Institution	European Bioinformatics Institute, United Kingdom
Resource MIR:00100028	Access URL	http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-view+MedlineFull+[medline-PMID:\$id] [Example: 16333295]
	Website	http://www.ebi.ac.uk/Databases/MEDLINE/medline.html
	Description	SRS@EBI
	Institution	European Bioinformatics Institute, United Kingdom
Resource MIR:00100023	Access URL	http://www.ncbi.nlm.nih.gov/pubmed/\$id [Example: 16333295]
	Website	http://www.ncbi.nlm.nih.gov/PubMed/
	Description	free digital archive of biomedical and life sciences journal literature
	Institution	National Center for Biotechnology Information, USA
Resource MIR:00100064	Access URL	http://www.hubmed.org/display.cgi?uids=\$id [Example: 16333295]
	Website	http://www.hubmed.org/
	Description	HubMed
	Institution	Alfred D. Eaton, United Kingdom

References

http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-view+MedlineFull+[medline-PMID:16381840]

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EMBL-EBI




Resource Information

Resource: MIR:00100028

General information about the resource: **SRS@EBI** (associated with the data collection: [PubMed](#)).

Health statistics

Last known state	up
Last check	2012-03-11 06:38:21
Uptime ratio	99% (1 089 checks)
Downtime ratio	0% (6 checks)
Unknown ratio	0% (0 checks)
URL used	http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-view+MedlineFull+[medline-PMID:16333295] 

Health history

Full record of the health checks performed on this resource.

2012

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
January																															
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September																															
October																															
November																															
December																															

2011

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
January																															
February																															
March																															

What resources are suitable to become data types?

- resource must be freely accessible to academic users and commercial users without restrictions
- access should not require registration
- must be actively maintained and accepted by the community
- identifiers must be stable, perennial and unique for the data type and point to a single piece of information
- atomicity of information should be on the same level (not proteins, reactions, and pathways in same data type)
eg. KEGG – split into compounds, reactions, genes, pathways

Basic Access:

Collections:

<http://identifiers.org/pubmed>

Record (location independent):

<http://identifiers.org/pubmed/16333295>

Custom queries + format:

Specific resource:

<http://identifiers.org/pubmed/16333295?resource=MIR:00100028>

Format (html/rdfxml):

<http://identifiers.org/pubmed/16333295?format=rdfxml>

Profiles (list of settings for collections, user-interface not yet implemented):

http://identifiers.org/pubmed/16333295?profile=most_reliable

<http://identifiers.org/pubmed/16333295>

<http://identifiers.org/pubmed/16333295>

4 physical locations (or resources) are available for accessing 16333295 (from [PubMed](#)):

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Entity available from 4 providers, for more information please refer to: <http://identifiers.org/pubmed/16333295>.

Powered by: [Identifiers.org](#) & [MIRIAM Registry](#)

[Related Articles by NCBI](#)

☐ 1. *Nat Biotechnol* 2005, 23 (12):1509-15

Minimum information requested in the annotation of biochemical models (MIRIAM).

[Le Novère,N.](#) , [Finney,A.](#) , [Hucka,M.](#) , [Bhalla,U.S.](#) , [Campagne,F.](#) , [Collado-Vides,J.](#) , [Crampin,E.J.](#) , [Halstead,M.](#) , [Klipp,E.](#) , [Mendes,P.](#) , [Nielsen,P.](#) , [Sauro,H.](#) , [Shapiro,B.](#) , [Snoep,J.L.](#) , [Spence,H.D.](#) , [Wanner,B.L.](#)

European Bioinformatics Institute, Hinxton, CB10 1SD, UK. lenov@ebi.ac.uk

Most of the published quantitative models in biology are lost for the community because they are either not made available or they are insufficiently characterized to allow them to be reused. The lack of a standard description format, lack of stringent reviewing and authors' carelessness are the main causes for incomplete model descriptions. With today's increased interest in detailed biochemical models, it is necessary to define a minimum quality standard for the encoding of those models. We propose a set of rules for curating quantitative models of biological systems. These rules define procedures for encoding and annotating models represented in machine-readable form. We believe their application will enable users to (i) have confidence that curated models are an accurate reflection of their associated reference descriptions, (ii) search collections of curated models with precision, (iii) quickly identify the biological phenomena that a given curated model or model constituent represents and (iv) facilitate model reuse and composition into large subcellular models.

PMID: [16333295](#)

ISSN: 1087-0156 (Print)

Publication Type:

● Journal Article



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<http://identifiers.org/pubmed/16333295>


Close 


Access to 16333295 (from [PubMed](#)) using the preferred resource of the profile [most_reliable](#).


Entity available from 4 providers, for more information please refer to: <http://identifiers.org/pubmed/16333295>.


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[Display Settings:](#)  Abstract[Send to:](#) [Nat Biotechnol.](#) 2005 Dec;23(12):1509-15.**Minimum information requested in the annotation of biochemical models (MIRIAM).**[Le Novère N](#), [Finney A](#), [Hucka M](#), [Bhalla US](#), [Campagne F](#), [Collado-Vides J](#), [Crampin EJ](#), [Halstead M](#), [Klipp E](#), [Mendes P](#), [Nielsen P](#), [Sauro H](#), [Shapiro B](#), [Snoep JL](#), [Spence HD](#), [Wanner BL](#).European Bioinformatics Institute, Hinxton, CB10 1SD, UK. lenov@ebi.ac.uk**Abstract**

Most of the published quantitative models in biology are lost for the community because they are either not made available or they are insufficiently characterized to allow them to be reused. The lack of a standard description format, lack of stringent reviewing and authors' carelessness are the main causes for incomplete model descriptions. With today's increased interest in detailed biochemical models, it is necessary to define a minimum quality standard for the encoding of those models. We propose a set of rules for curating quantitative models of biological systems. These rules define procedures for encoding and annotating models represented in machine-readable form. We believe their application will enable users to (i) have confidence that curated models are an accurate reflection of their associated reference descriptions, (ii) search collections of curated models with precision, (iii) quickly identify the biological phenomena that a given curated model or model constituent represents and (iv) facilitate model reuse and composition into large subcellular models.

PMID: 16333295 [PubMed - indexed for MEDLINE]

 **MeSH Terms** **LinkOut - more resources****Related citations** 

Model storage, exchange and integration. [BMC Neurosci. 2006]

MIRIAM Resources: tools to generate and resolve robust cross-refer [BMC Syst Biol. 2007]

DICOM structured report document type definition. [IEEE Trans Inf Technol Biomed....]

[Review](#) Evolving a lingua franca and associated software infrastru [Syst Biol (Stevenage). 2004][Review](#) Cataloging the relationships between proteins: a review of intera [Mol Biotechnol. 2006][See reviews...](#)[See all...](#)**Cited by 78 PubMed Central articles** 

Identifiers.org and MIRIAM Registry: community resources to provide pe [Nucleic Acids Res. 2012]

SABIO-RK--database for biochemical reaction kinetics. [Nucleic Acids Res. 2012]

PathCase-SB architecture and database design. [BMC Syst Biol. 2011]

Camille Laibe



Nicolas Le Novère



Michael Hucka



Vijayalakshmi
Chelliah



Nicolas Rodriguez



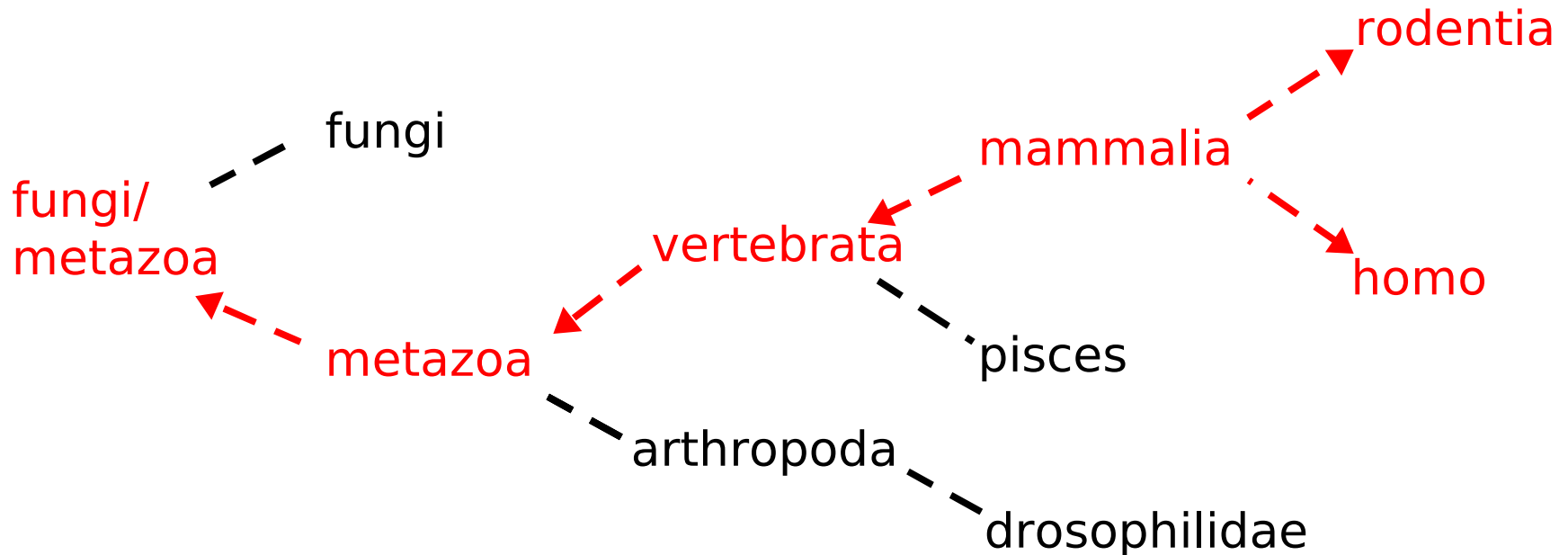
Nick Juty



Taxonomic Searches

linking to hierarchical controlled vocabularies allows for more elaborate searching:

e.g.: searching BioModels DataBase for all models fitting mammals



Resource:

Taxonomy

mammalia

Resource:

Publication

oscillations

26 Curated Models returned.

BioModels ID	Name	Publication ID	Last Modified
BIOMD0000000005	Tyson1991_CellCycle_6var	1831270	2009-02-25T14:58:48+00:00
BIOMD0000000006	Tyson1991_CellCycle_2var	1831270	2009-02-25T14:41:44+00:00
BIOMD0000000024	Scheper1999_CircClock	9870936	2008-08-21T11:46:43+00:00
BIOMD0000000043	Borghans1997_CaOscillation_model1	17029867	2009-04-21T12:52:44+00:00
BIOMD0000000044	Borghans1997_CaOscillation_model2	17029867	2008-08-21T11:53:55+00:00
BIOMD0000000045	Borghans1997_CaOscillation_model3	17029867	2008-08-21T11:54:12+00:00
BIOMD0000000047	Oxhamre2005_Ca_oscillation	15596518	2008-08-21T11:54:50+00:00
BIOMD0000000057	Sneyd2002_IP3_Receptor	11842185	2008-08-21T11:58:43+00:00
BIOMD0000000059	Fridlyand2003_Calcium_flux	12644446	2008-10-01T17:23:42+00:00
BIOMD0000000073	Leibup2003_CircClock_DD	12775757	2008-08-21T12:04:54+00:00
BIOMD0000000114	Somogyi1990_CaOscillations	1904060	2008-08-21T12:20:25+00:00
BIOMD0000000115	Somogyi1990_CaOscillations_SingleCaSpike	1904060	2008-08-21T12:20:44+00:00
BIOMD0000000124	Wu2006_K+Channel	16375866	2007-09-25T10:20:25+00:00
BIOMD0000000154	Zatorsky2006_p53_Model3	16773083	2008-01-14T21:29:55+00:00
BIOMD0000000155	Zatorsky2006_p53_Model6	16773083	2008-01-14T21:30:52+00:00
BIOMD0000000156	Zatorsky2006_p53_Model5	16773083	2008-01-14T21:33:20+00:00
BIOMD0000000157	Zatorsky2006_p53_Model4	16773083	2008-01-14T21:39:09+00:00
BIOMD0000000158	Zatorsky2006_p53_Model2	16773083	2008-01-14T21:40:04+00:00
BIOMD0000000159	Zatorsky2006_p53_Model1	16773083	2008-01-14T21:42:38+00:00
BIOMD0000000170	Weimann2004_CircadianOscillator	15347590	2008-08-20T18:28:56+00:00
BIOMD0000000181	Sriram2007_CellCycle	18203579	2009-04-22T10:19:56+00:00
BIOMD0000000184	Lavrentovich2008_Ca_Oscillations	18275973	2008-09-30T12:47:46+00:00
BIOMD0000000185	Locke2008_Circadian_Clock	18312618	2008-12-02T13:59:46+00:00
BIOMD0000000188	Proctor2003_p53_Mdm2_ATM	18706112	2008-12-02T14:44:00+00:00
BIOMD0000000189	Proctor2008_p53_Mdm2_ARF	18706112	2008-12-02T14:44:22+00:00
BIOMD0000000201	Goldbeter2008_Somite_Segmentation_Clock_Notch_Wnt_FGF	18308339	2009-03-16T14:34:11+00:00

metazoa/fungi

hamster

rattus










homo sapiens

mammalia

amniota



Ranking and retrieval

Model	BioModel	Score	p-val num	
Huang1996_MAPK_ultrasens	BIOMD0000000009	1.000	< 1/1000	
Levchenko2000_MAPK_noScaffold	BIOMD0000000011	0.925	< 1/1000	
Levchenko2000_MAPK_Scaffold	BIOMD0000000014	0.865	< 1/1000	
Kholodenko2000_MAPK_feedback	BIOMD0000000010	0.816	< 1/1000	
Markevich2004_MAPK_orderedElementary	BIOMD0000000026	0.737	< 1/1000	
Markevich2004_MAPK_phosphoRandomElementary	BIOMD0000000028	0.690	< 1/1000	
Markevich2004_MAPK_AllRandomElementary	BIOMD0000000030	0.690	< 1/1000	
Markevich2004_MAPK_orderedMM	BIOMD0000000027	0.673	< 1/1000	
Markevich2004_MAPK_orderedMM2kinases	BIOMD0000000031	0.673	< 1/1000	
Markevich2004_MAPK_phosphoRandomMM	BIOMD0000000029	0.617	< 1/1000	
Hornberg2005_ERKcascade	BIOMD0000000084	0.468	< 1/1000	
McClean2007_CrossTalk	BIOMD0000000116	0.397	< 1/1000	
Kofahl2004_pheromone	BIOMD0000000032	0.348	< 1/1000	
Kim2007_Wnt_ERK_Crosstalk	BIOMD0000000149	0.323	< 1/1000	
Brown2004_NGF_EGF_signaling	BIOMD0000000033	0.260	< 1/1000	
Goldbeter1995_CircClock	BIOMD0000000016	0.244	< 1/1000	
Sasagawa2005_MAPK	BIOMD0000000049	0.240	< 1/1000	
Ung2008_EGFR_Endocytosis	BIOMD0000000205	0.234	< 1/1000	
Leloup1999_CircClock	BIOMD0000000021	0.229	< 1/1000	
Goldbeter1991_MinMitOscil_ExplInact	BIOMD0000000004	0.222	< 1/1000	
Goldbeter1991_MinMitOscil	BIOMD0000000003	0.214	< 1/1000	
Leloup1998_CircClock_LD	BIOMD0000000171	0.201	< 1/1000	
Tyson1991_CellCycle_6var	BIOMD0000000005	0.199	< 1/1000	
Veening2008_DegU_Regulation	BIOMD0000000240	0.180	< 1/1000	
Neves2008_Cell_Shape	BIOMD0000000182	0.168	4.0e-03	
Fisher2006_Ca_Oscillation_dpdnt_NFAT_dynamics	BIOMD0000000122	0.164	5.0e-03	
Leloup2003_CircClock_DD	BIOMD0000000073	0.163	5.0e-03	

improved searching

- search query expansion
- uses ontologies
- uses resolved identifier information
- returns ranked list of models

Henkel *et al* (2010) *BMC Bioinformatics*, 11:423




















































































































































Semantic SBML

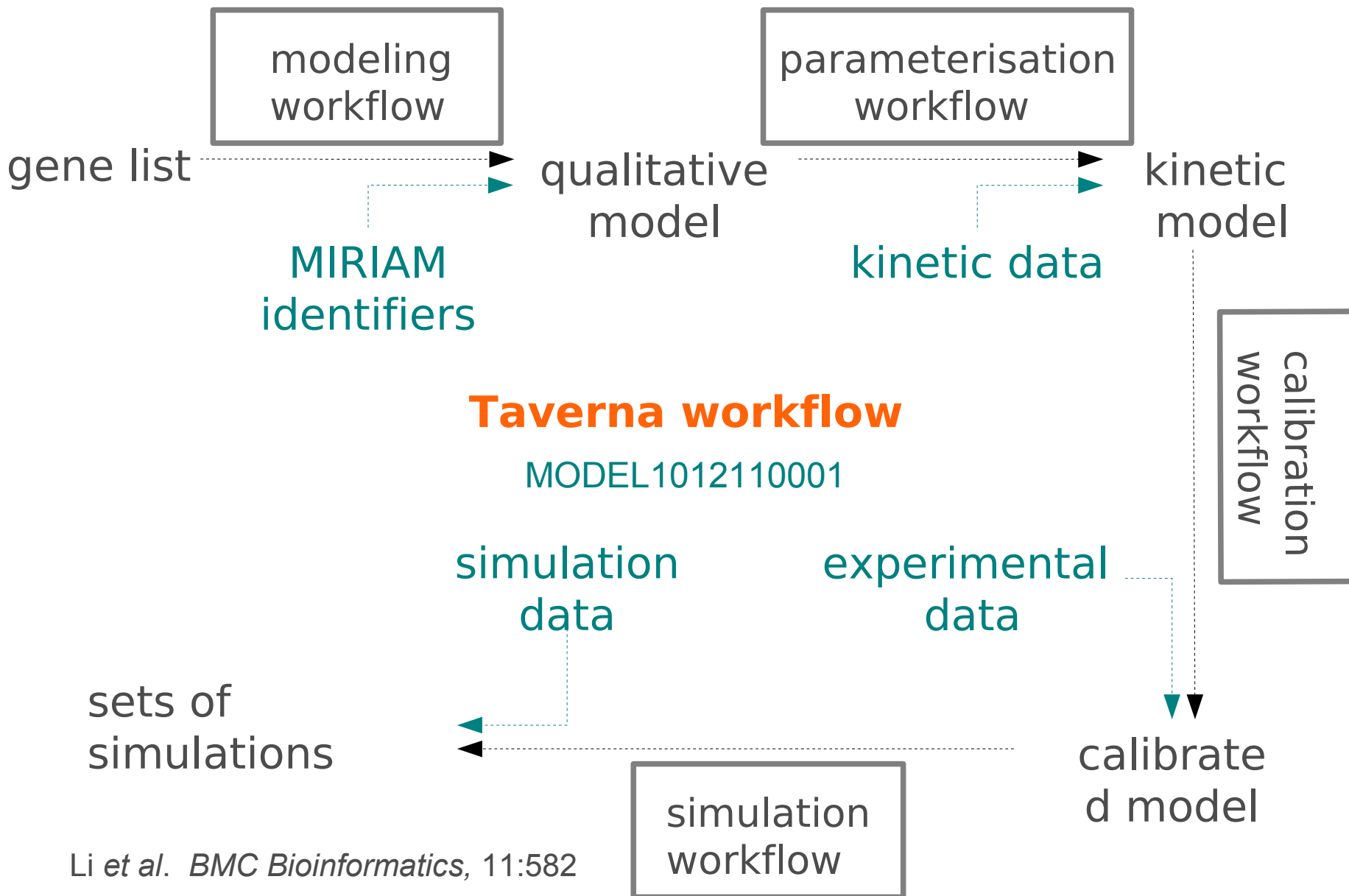
<http://www.semanticsbml.org/>

BioModels similar to BIOMD0000000042.xml

[Click for help](#)

Add to Model list

	BioModel	Element	Similarity	Overlap
		alignment	score p-value graph	score p-value graph
Nielsen1998_Glycolysis	BIOMD0000000042		1.000 <=1e-3 	67 -2.2e-16 
add Hynne2001_Glycolysis	BIOMD0000000061		0.737 <=1e-3 	48 -2.2e-16 
add Teusink2000_Glycolysis	BIOMD0000000064		0.615 <=1e-3 	41 -2.2e-16 
add Wolf2000_Glycolytic_Oscillations	BIOMD00000000206		0.808 <=1e-3 	27 -2.2e-16 
add Pritchard2002_glycolysis	BIOMD00000000172		0.585 <=1e-3 	36 -2.2e-16 
add Conant2007_WGD_glycolysis_2A3AB	BIOMD00000000176		0.579 <=1e-3 	35 -2.2e-16 
add Ralser2007_Carbohydrate_Rerouting_ROS	BIOMD00000000247		0.564 <=1e-3 	41 -2.2e-16 
add Conant2007_glycolysis_2C	BIOMD00000000177		0.551 <=1e-3 	35 -2.2e-16 
add Bakker2001_Glycolysis	BIOMD00000000071		0.538 <=1e-3 	31 -2.2e-16 
add Holzhtuter2004_Erythrocyte_Metabolism	BIOMD00000000070		0.500 <=1e-3 	42 -2.2e-16 
add Galazzo1990_pathway_kinetics	BIOMD00000000063		0.496 <=1e-3 	29 -2.2e-16 
add Teusink1998_Glycolysis_TurboDesign	BIOMD00000000253		0.450 <=1e-3 	21 6.3e-14 
add Albert2005_Glycolysis	BIOMD00000000211		0.433 <=1e-3 	29 -2.2e-16 
add Chassagnole2002_Carbon_Metabolism	BIOMD00000000051		0.393 <=1e-3 	29 -2.2e-16 
add Westermarck2003_Pancreatic_GlycOsc_extended	BIOMD00000000236		0.311 <=1e-3 	10 3.7e-04 
add Jiang2007_GSISsystem_PancreaticBetaCells	BIOMD00000000239		0.243 <=1e-3 	16 6.6e-09 
add Westermarck2003_Pancreatic_GlycOsc_basic	BIOMD00000000225		0.231 <=1e-3 	5 1.5e-01 
add Poolman2004_CalvinCycle	BIOMD00000000013		0.219 <=1e-3 	15 5.2e-08 
add Valero2006_Adenine_TernaryCycle	BIOMD00000000231		0.206 <=1e-3 	6 5.9e-02 
add Rohwer2000_Phosphotransferase_System	BIOMD00000000038		0.199 <=1e-3 	5 1.5e-01 
add Lei2001_Yeast_Aerobic_Metabolism	BIOMD00000000245		0.194 <=1e-3 	7 2.0e-02 
add Hoefnagel2002_PyruvateBranches	BIOMD00000000017		0.194 <=1e-3 	10 3.7e-04 
add Nazaret2009_TCA_RC_ATP	BIOMD00000000232		0.178 <=1e-3 	7 2.0e-02 
add Rohwer2001_Sucrose	BIOMD00000000023		0.149 2.0e-03 	5 1.5e-01 
add Bier2000_GlycolyticOscillation	BIOMD00000000254		0.137 2.0e-03 	2 7.8e-01 
add Kotte2010_Ecoli_Metabolic_Adaption	BIOMD00000000244		0.124 1.8e-02 	5 1.5e-01 
add Ataullahkhanov1996_Adenylate	BIOMD00000000054		0.120 2.0e-02 	3 5.4e-01 
add Fridlyand2003_Calcium_flux	BIOMD00000000059		0.095 1.1e-01 	4 3.1e-01 
add Wolf2001_respiratory_oscillations	BIOMD00000000090		0.089 1.6e-01 	5 1.5e-01 
add Bruggeman2005_AmmmoniumAssimilation	BIOMD00000000017		0.082 2.4e-01 	3 5.4e-01 
add Sriram2007_CellCycle	BIOMD00000000181		0.075 3.3e-01 	0 1.0e+00 
add Ferreira2003_CML_generation2	BIOMD00000000053		0.069 4.2e-01 	1 9.4e-01 
add Hsp90model_basis510	BIOMD00000000091		0.068 4.2e-01 	2 7.8e-01 
add Proctor2007_ubiquitine	BIOMD00000000105		0.066 4.6e-01 	3 5.4e-01 
add Kongas2001_creatine	BIOMD00000000041		0.064 4.9e-01 	2 7.8e-01 
add Olsen2003_peroxidase	BIOMD00000000046		0.060 5.4e-01 	2 7.8e-01 
add Bray1995_chemotaxis_receptorlinkedcomplex	BIOMD00000000200		0.059 5.5e-01 	0 1.0e+00 
add Gardner1998_CellCycle_Golbeter	BIOMD00000000008		0.058 5.8e-01 	1 9.4e-01 
add Lai2007_O2_Transport_Metabolism	BIOMD00000000248		0.057 5.9e-01 	2 7.8e-01 
add Görllich2003_RanGTP_gradient	BIOMD00000000192		0.055 6.2e-01 	1 9.4e-01 
add Neves2008_Cell_Shape	BIOMD00000000182		0.055 6.2e-01 	3 5.4e-01 
add Fernandez2006_ModelB	BIOMD00000000153		0.054 6.3e-01 	1 9.4e-01 
add Brands2002_MonosaccharideCasein	BIOMD00000000052		0.053 6.4e-01 	1 9.4e-01 
add Chen2004_CellCycle	BIOMD00000000056		0.052 6.6e-01 	0 1.0e+00 
add Tyson2001_Cell_Cycle_Regulation	BIOMD00000000195		0.051 6.7e-01 	0 1.0e+00 
add Aguda1999_CellCycle	BIOMD00000000189		0.049 7.0e-01 	0 1.0e+00 
add Chassagnole2001_Threonine_Synthesis	BIOMD00000000066		0.048 7.2e-01 	2 7.8e-01 
add Suh2004_KCNQ_Regulation	BIOMD00000000081		0.047 7.2e-01 	2 7.8e-01 
add Ibrahim2008_Cdc20_Sequestering_Template_Model	BIOMD00000000194		0.045 7.5e-01 	1 9.4e-01 



Li et al. *BMC Bioinformatics*, 11:582

Some Software supporting MIRIAM annotations

- SBMLharvester (<http://code.google.com/p/sbmlharvester/>)
Robert Hoehndorf et al., Department of Genetics, Cambridge Univ.
 - creates an OWL representation of model and annotations
 - allows reasoning on and checking of annotation
- RICORDO toolset (<http://bioonto.gen.cam.ac.uk:8080/ricordo/>)
Sarala M. Wimalaratne et. al, EBI
 - creates a smartly indexed RDF triple storage of annotated models and allows complex queries
- SemanticSBML (Krause et al., *Bioinformatics* (2010), 26: 421)
 - model merging, SBO term prediction, checking annotations, model comparison and clustering via metadata
- SAINT (Lister et al., *Bioinformatics* (2009) 25(22): 3026-3027)
- libAnnotationSBML (Swainston and Mendes, *Bioinformatics* (2009), 25: 2292)
 - access some resources over webservices, finds potential annotations, checks balancing of chemical formulas in reactions

Modelling efforts using MIRIAM annotations

- Herrgård et al (2008) A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. *Nature Biotechnology*, 26: 1155-1160
 - MODEL0072364382: 2152 species, 1857 reactions
 - stoichiometric map, no concentrations, no kinetics
- Smallbone et al (2010) Towards a genome-scale kinetic model of cellular metabolism. *BMC Systems Biology*, 4:6
 - MODEL1001200000: 1748 species, 1059 reactions
 - Concentrations and flux added from BioModels Database
 - Constraint-based model and simplified linlog kinetics
- Dobson et al (2010) Further developments towards a genome-scale metabolic model of yeast. *BMC Systems Biology*, 4:145
 - MODEL1012110000: 2657 species, 1865 reactions