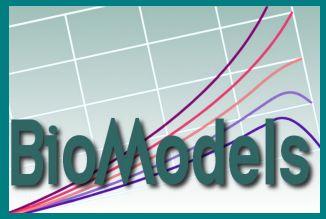
BioModels Database

a database of quantitative, kinetic models



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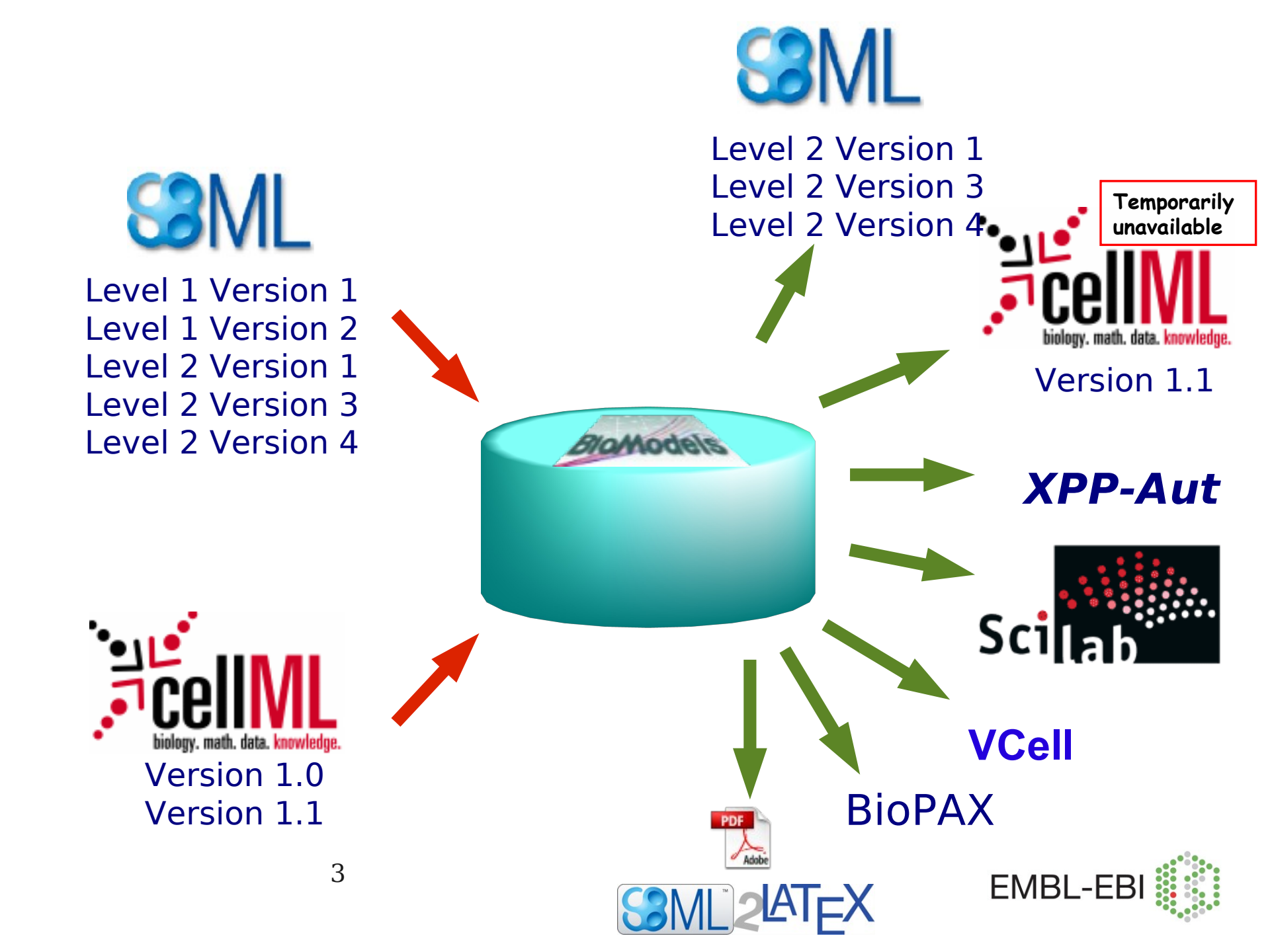
CCB 2010
Hinxton, UK

Lukas Endler
<lukas@ebi.ac.uk>

BioModels Database

- contains only models from the peer reviewed literature
- unique perennial identifiers for models
  - can be referenced, eg. in publications
- models freely accessible and reusable
- models are manually curated and checked to ensure reliability
  - curated and non curated branch
- 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


SBML
Level 1 Version 1
Level 1 Version 2
Level 2 Version 1
Level 2 Version 3
Level 2 Version 4
SBML
Level 2 Version 1
Level 2 Version 3
Level 2 Version 4
Temporarily unavailable
cellML
biology. math. data. knowledge.
Version 1.1
BioModels
XPP-Aut
Scilab
cellML
biology. math. data. knowledge.
Version 1.0
Version 1.1
VCell
BioPAX
PDF
Adobe
SBML2LATEX
EMBL-EBI

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 that deem the model to be of interest

BMC Systems Biology

IMPACT FACTOR 3.71

Methodology article

Open Access

Towards a genome-scale kinetic model of cellular metabolism

Kieran Smallbone, **Evangelos Simeonidis**, **Neil Swainston** and **Pedro Mendes**

BMC Systems Biology 2010, **4**:6 doi:10.1186/1752-0509-4-6

Published: 28 January 2010

Abstract (provisional)

Background

Advances in bioinformatic techniques and analyses have led to the availability of genome-scale metabolic reconstructions. The size and complexity of such networks often means that their potential behaviour can only be analysed with constraint-based methods. Whilst requiring minimal experimental data, such methods are unable to give insight into cellular substrate concentrations. Instead, the long-term goal of systems biology is to use kinetic modelling to characterize fully the mechanics of each enzymatic reaction, and to combine such knowledge to predict system behaviour.

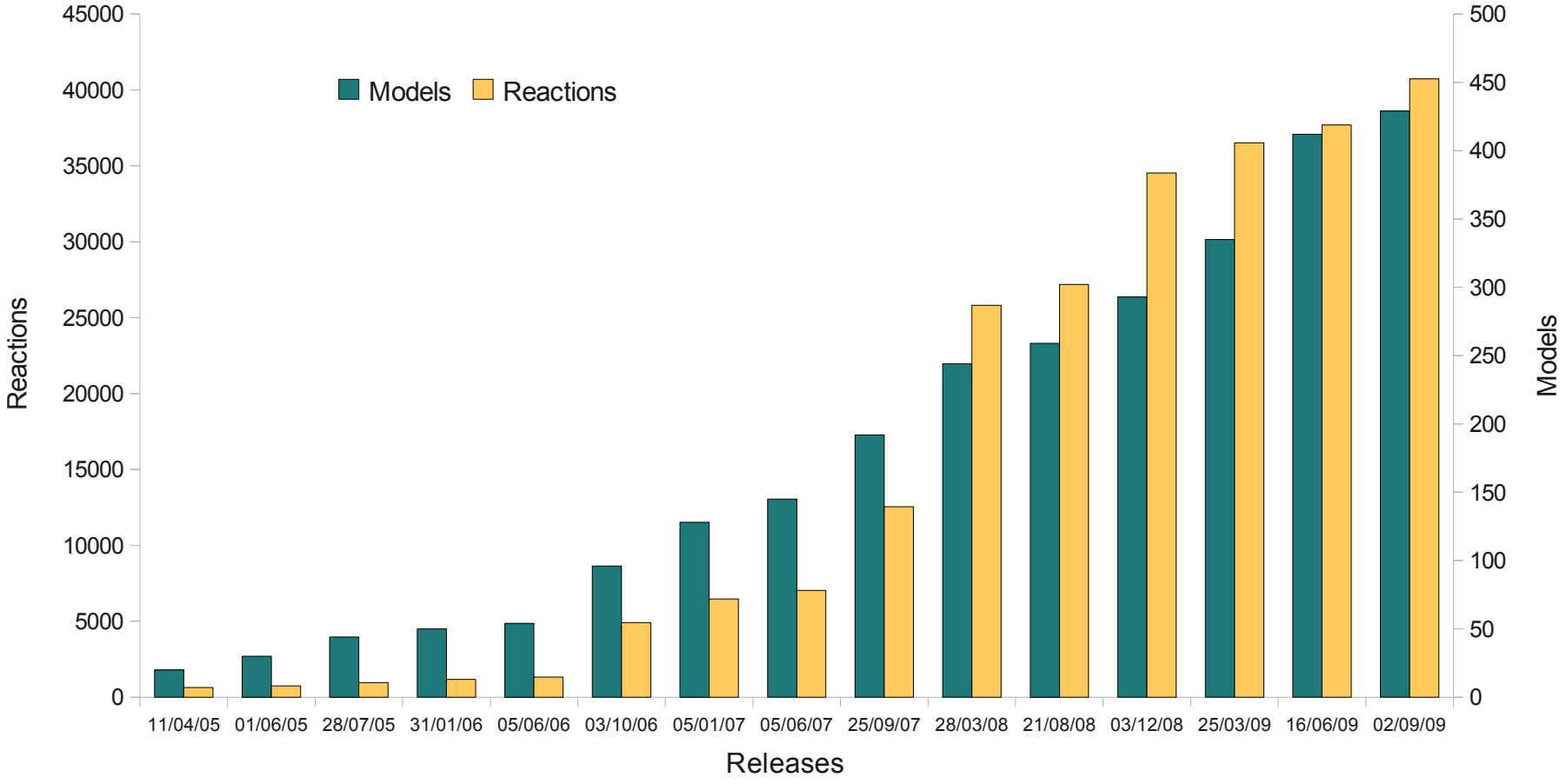
Results

We describe a method for building a parameterized genome-scale kinetic model of a metabolic network. Simplified linlog kinetics are used and the parameters are extracted from a kinetic model repository. We demonstrate our methodology by applying it to yeast metabolism. The resultant model has 956 metabolic reactions involving 820 metabolites, and, whilst approximative, has considerably broader remit than any existing models of its type. Control analysis is used to identify key steps within the system.

Conclusions

Our modelling framework may be considered a stepping-stone toward the long-term goal of a fully-parameterized model of yeast metabolism. The model (see additional file 1) is available in SBML format from the BioModels database (BioModels ID: MODEL1001200000) and at http://www.mcisb.org/resources/genomescale/.

Models in BioModels DB



curated branch : 241

non-cura. branch: 213

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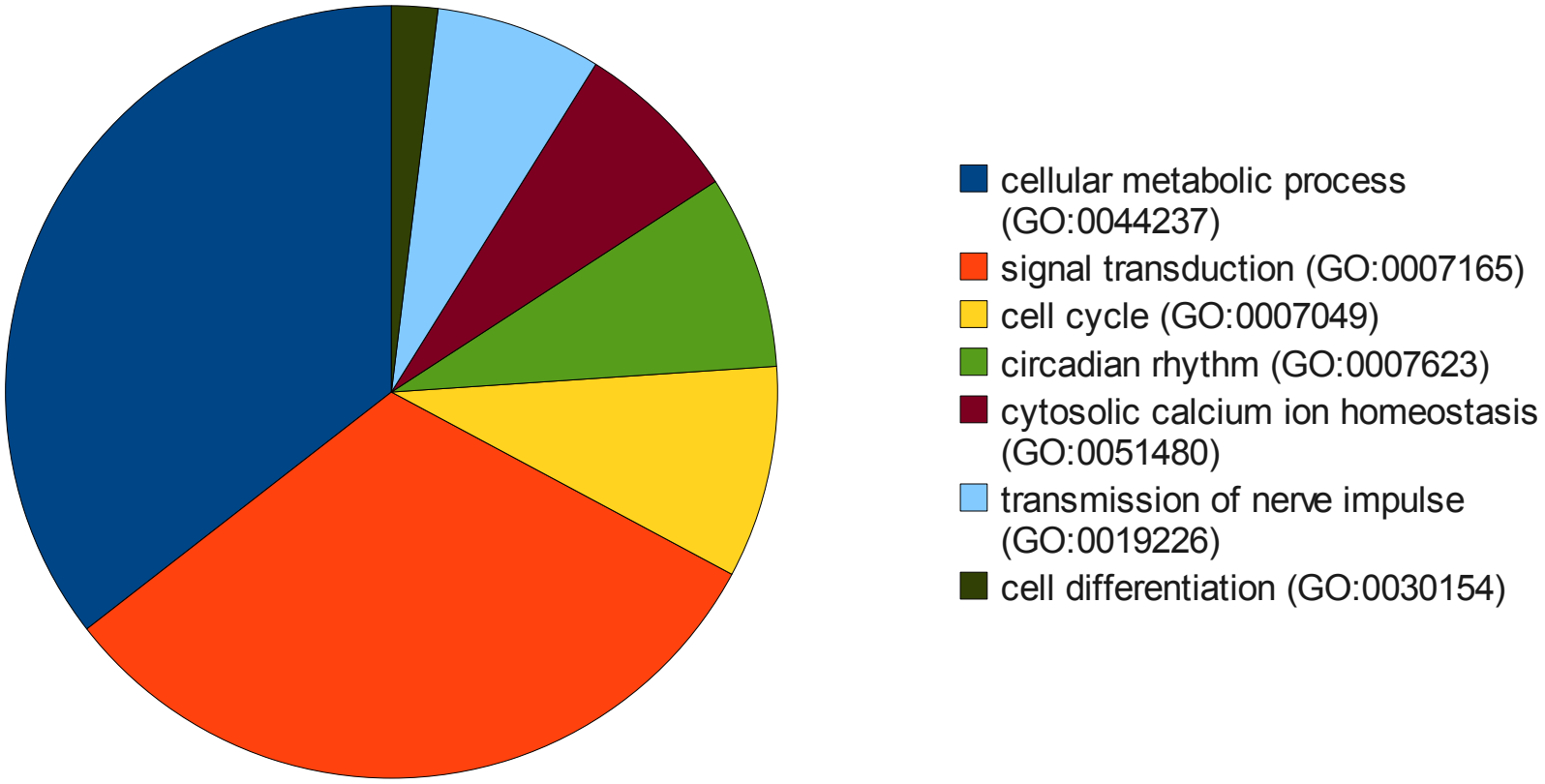
Models in BioModels DB



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Curated and Noncurated 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.

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

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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 of biological interests. Models present in BioModels Database are annotated and linked to relevant data resources, such as publications, databases of compounds and pathways, controlled vocabularies, etc.

Search | Go to the model | Advanced search

Browse models

- Curated models (241)
- Browse models using GO
- Non-curated models (212)

Simulate in JWS Online

Submit a model

Mirror at California Institute of Technology http://biomodels.caltech.edu

BioModels AT SourceForge http://sourceforge.net/projects/biomodels/

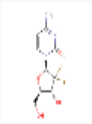
Web Services http://www.ebi.ac.uk/biomodels-main/webservices

Download archived models http://www.ebi.ac.uk/biomodels/models-main/tars/

Model of the month

January, 2010

The pharmacodynamic model deducing the potency and time course of the anticancer agent in shrinking the primary tumours can have potential role to decide dosage and treatment duration.



Read more...

News

26th January 2010 **Sixteenth release**
Download All Models Under SBML Format

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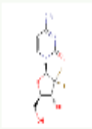
Read more...



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Browse - Curated models

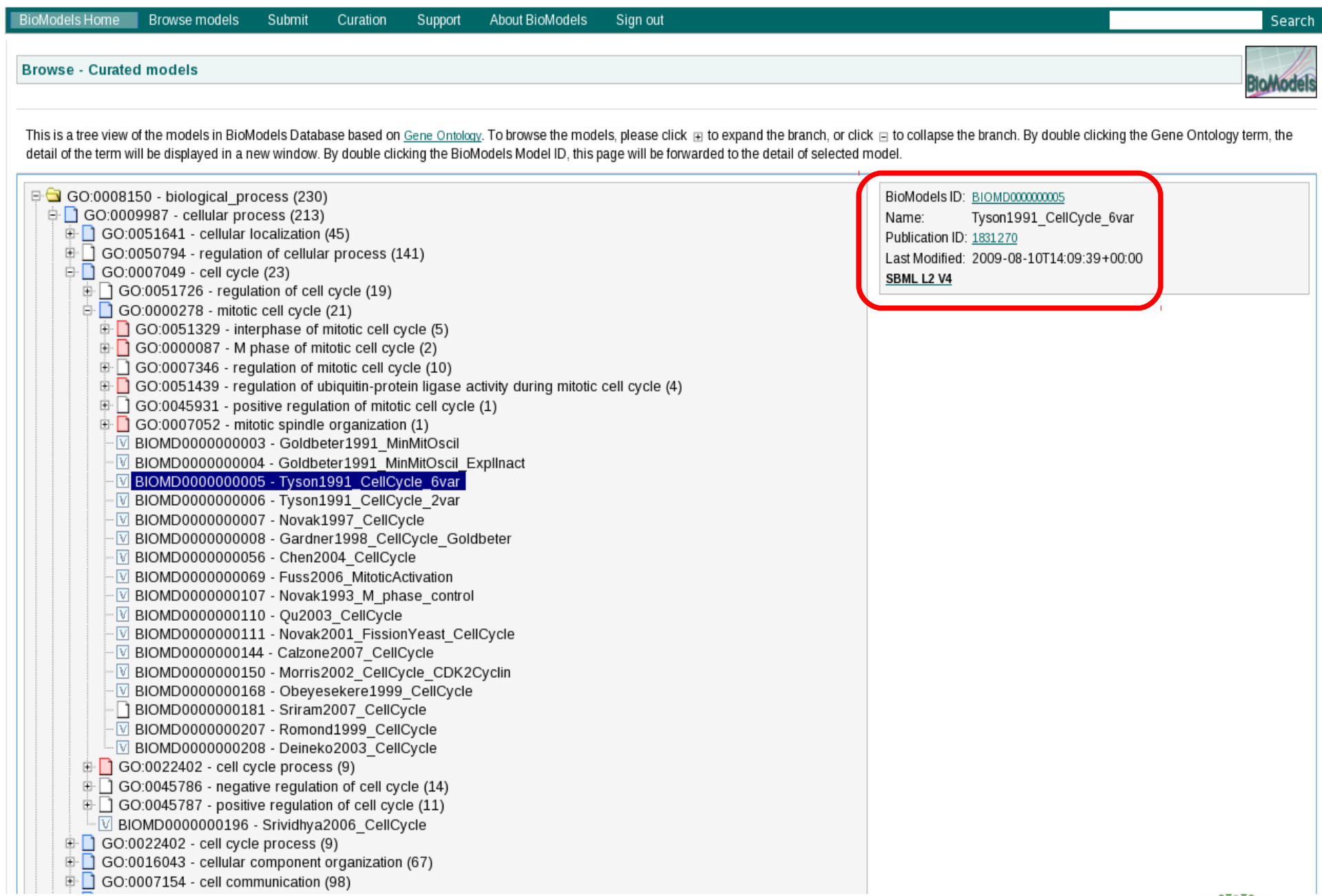
This is a tree view of the models in BioModels Database based on Gene Ontology. To browse the models, please click ⊞ to expand the branch, or click ⊟ to collapse the branch. By double clicking the Gene Ontology term, the detail of the term will be displayed in a new window. By double clicking the BioModels Model ID, this page will be forwarded to the detail of selected model.

- GO:0008150 - biological_process (230)
- GO:0005575 - cellular_component (200)
- GO:0003674 - molecular_function (154)

BioModels ID: *Unspecified*
Name: *N/A*
Publication ID: *N/A*
Last Modified: *N/A*

The relationships between terms are represented by different icons.

- BioModels qualifiers:
  - bqbiol:is
  - bqbiol:isVersionOf
  - bqbiol:hasPart
- Gene Ontology relationships:
  - is a
  - part of
  - develops from
  - other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BioModels
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GO:0008150 - biological_process (230)
GO:0009987 - cellular process (213)
GO:0051641 - cellular localization (45)
GO:0050794 - regulation of cellular process (141)
GO:0007049 - cell cycle (23)
GO:0051726 - regulation of cell cycle (19)
GO:0000278 - mitotic cell cycle (21)
GO:0051329 - interphase of mitotic cell cycle (5)
GO:0000087 - M phase of mitotic cell cycle (2)
GO:0007346 - regulation of mitotic cell cycle (10)
GO:0051439 - regulation of ubiquitin-protein ligase activity during mitotic cell cycle (4)
GO:0045931 - positive regulation of mitotic cell cycle (1)
GO:0007052 - mitotic spindle organization (1)
BIOMD0000000003 - Goldbeter1991_MinMitOscil
BIOMD0000000004 - Goldbeter1991_MinMitOscil_ExpInact
BIOMD0000000005 - Tyson1991_CellCycle_6var
BIOMD0000000006 - Tyson1991_CellCycle_2var
BIOMD0000000007 - Novak1997_CellCycle
BIOMD0000000008 - Gardner1998_CellCycle_Goldbeter
BIOMD0000000056 - Chen2004_CellCycle
BIOMD0000000069 - Fuss2006_MitoticActivation
BIOMD0000000107 - Novak1993_M_phase_control
BIOMD0000000110 - Qu2003_CellCycle
BIOMD0000000111 - Novak2001_FissionYeast_CellCycle
BIOMD0000000144 - Calzone2007_CellCycle
BIOMD0000000150 - Morris2002_CellCycle_CDK2Cyclin
BIOMD0000000168 - Obeyesekere1999_CellCycle
BIOMD0000000181 - Sriram2007_CellCycle
BIOMD0000000207 - Romond1999_CellCycle
BIOMD0000000208 - Deineko2003_CellCycle
GO:0022402 - cell cycle process (9)
GO:0045786 - negative regulation of cell cycle (14)
GO:0045787 - positive regulation of cell cycle (11)
BIOMD0000000196 - Srividhya2006_CellCycle
GO:0022402 - cell cycle process (9)
GO:0016043 - cellular component organization (67)
GO:0007154 - cell communication (98)
BioModels ID: BIOMD0000000005
Name: Tyson1991_CellCycle_6var
Publication ID: 1831270
Last Modified: 2009-08-10T14:09:39+00:00
SBML L2 V4

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Complex Searches

Search - Models

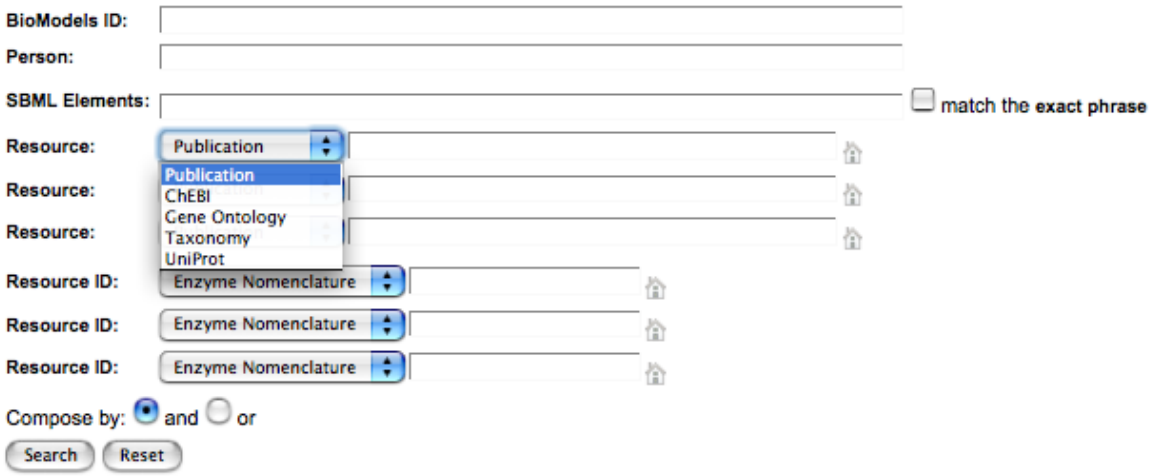
Text Search

You can search BioModels Database for models using one or more of the following criteria:

- *BioModels ID* → Search BioModels Database for *exact* BioModels identifiers (for example *BIOMD0000000001* or *BIOMD0000000022*).
- *Person* → Search BioModels Database for model submitter and/or creator(s) names, or model reference publication author(s) names (for example *Nicolas Le Novère*, *Nicolas*, *Bruce Shapiro* or *Shapiro*, *Edelstein* or *Novak*).
- *SBML Elements* → Search BioModels Database using the content of either "name" or "*notes*" SBML elements (for example *Edelstein* or *nicotinic*). Select the checkbox behind, if you want to find documents which matches the exact phrase; otherwise, all words will be searched as default.
- *Resource* → Search BioModels Database for related information found in the models reference publication or third-party resources, by either publication/resource identifier or text (for example *9256450* or *cyclin* for publication, *GO:0000278* or *cell cycle* for Gene Ontology, *P04551* or *cell division* for UniProt).
- *Resource ID* → Search BioModels Database for annotations, by third-party resource identifiers (for example *IPR002394* for InterPro, *hsa04080* for KEGG Pathway, *68910* for Reactome).

A part from the *BioModels ID* -based search, for every other criteria the search operates on a *contains the entered string basis*, case-insensitive. That is, searching *Person* for *Shapi* or *shapi* will return the same results as searching for *Shapiro* or *shapiro*. In addition, since search strings are treated as words, do not enter regular expressions.

Multiple criteria can be combined with either *and* or *or*. If *and* is selected, only those models satisfying all the criteria will be returned. If instead *or* is selected, all the models satisfying at least one of the criteria will be returned.



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BIOMD0000000005 - Tyson1991_CellCycle_6var

SBML formats | Other formats | Actions | Submit Model Comment/Bug

Model | Overview | Math | Physical entities | Parameters | Curation

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 Fungi/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.

BIOMD0000000005 - Tyson1991_CellCycle_6var

SBML formats | Other formats | Actions | Submit Model Comment/Bug

Model | Overview | Math | Physical entities | Parameters

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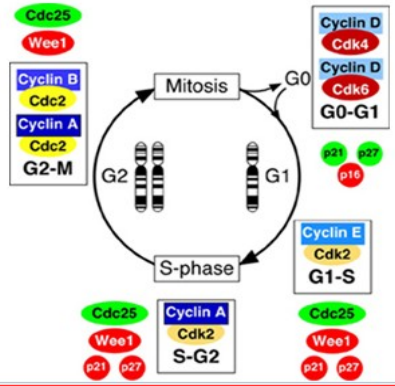
Model

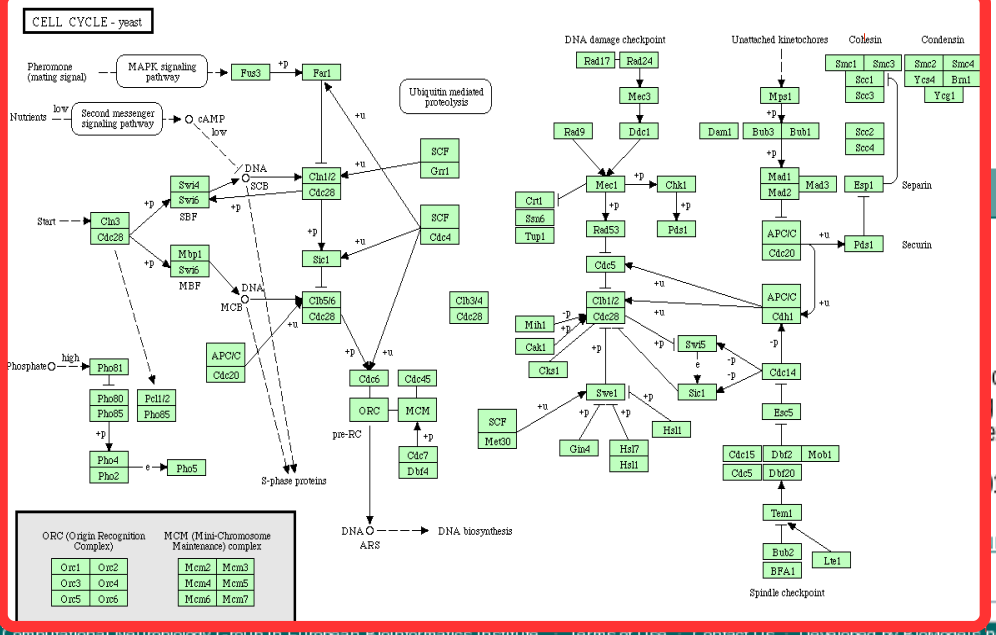
Original Model: BIOMD0000000005.xml.origin	bqbiol:hasVersion	Reactome REACT_152
Submitter: Nicolas Le Novère	set #1 bqbiol:isVersionOf	KEGG Pathway sce04111 Gene Ontology mitotic cell cycle
Submission ID: MODEL6614644188	bqmodel:is	Taxonomy Fungi/Metazoa group
Submission Date: 13 Sep 2005 12:31:08 UTC		

Cell Cycle, Mitotic

Stable identifier	REACT_152.2
Authored	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
cellular architecture at mitosis. Two gap-phases separate these major cell cycle events: G1 between mitosis and S
development of the human body, cells can exit the cell cycle for a period and enter a quiescent state known as G0,
again, but undergo morphological development to carry out the wide variety of specialized functions of individual tissue
A family of protein serine/threonine kinases known as the cyclin-dependent kinases (CDKs) controls progression throu
the catalytic subunit is dependent on binding to a cyclin partner. The human genome encodes several cyclins and se
order in which they were identified. The oscillation of cyclin abundance is one important mechanism by which these en
at the relevant time and place. Additional regulatory proteins and post-translational modifications ensure that CDK
narrow window of activity.

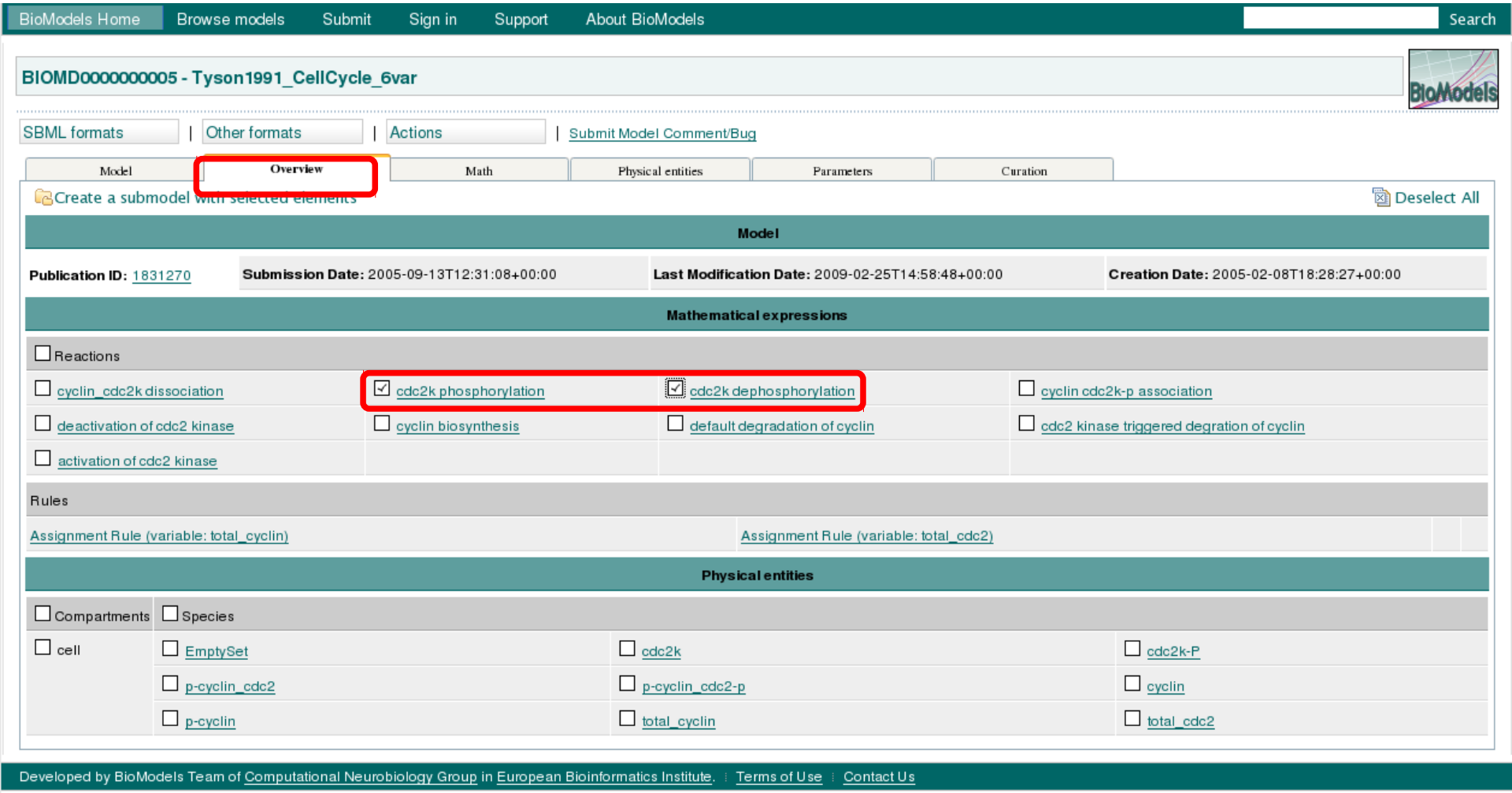




Lineage	Taxonomy identifier	33154
• Eukaryota	Scientific name	Fungi/Metazoa group
	Common name	-
	Other NCBI synonyms	Opisthokonta opisthokonts
	Rank	no rank
	Number of UniProtKB/Swiss-Prot entries	114913
	Number of UniProtKB/TrEMBL entries	1459130

Taxonomy navigation

Up taxonomy tree	Down taxonomy tree
Eukaryota	• Choanoflagellida • Fungi • Fungi/Metazoa incertae sedis • Metazoa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Other formats
Actions
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Model
Overview
Math
Physical entities
Parameters
Curation
Create a submodel with selected elements
Deselect All
Model
Publication ID: 1831270
Submission Date: 2005-09-13T12:31:08+00:00
Last Modification Date: 2009-02-25T14:58:48+00:00
Creation Date: 2005-02-08T18:28:27+00:00
Mathematical expressions
Reactions
cyclin_cdc2k dissociation
cdc2k phosphorylation
cdc2k dephosphorylation
cyclin cdc2k-p association
deactivation of cdc2 kinase
cyclin biosynthesis
default degradation of cyclin
cdc2 kinase triggered degration of cyclin
activation of cdc2 kinase
Rules
Assignment Rule (variable: total_cyclin)
Assignment Rule (variable: total_cdc2)
Physical entities
Compartments
Species
cell
EmptySet
cdc2k
cdc2k-P
p-cyclin_cdc2
p-cyclin_cdc2-p
cyclin
p-cyclin
total_cyclin
total_cdc2
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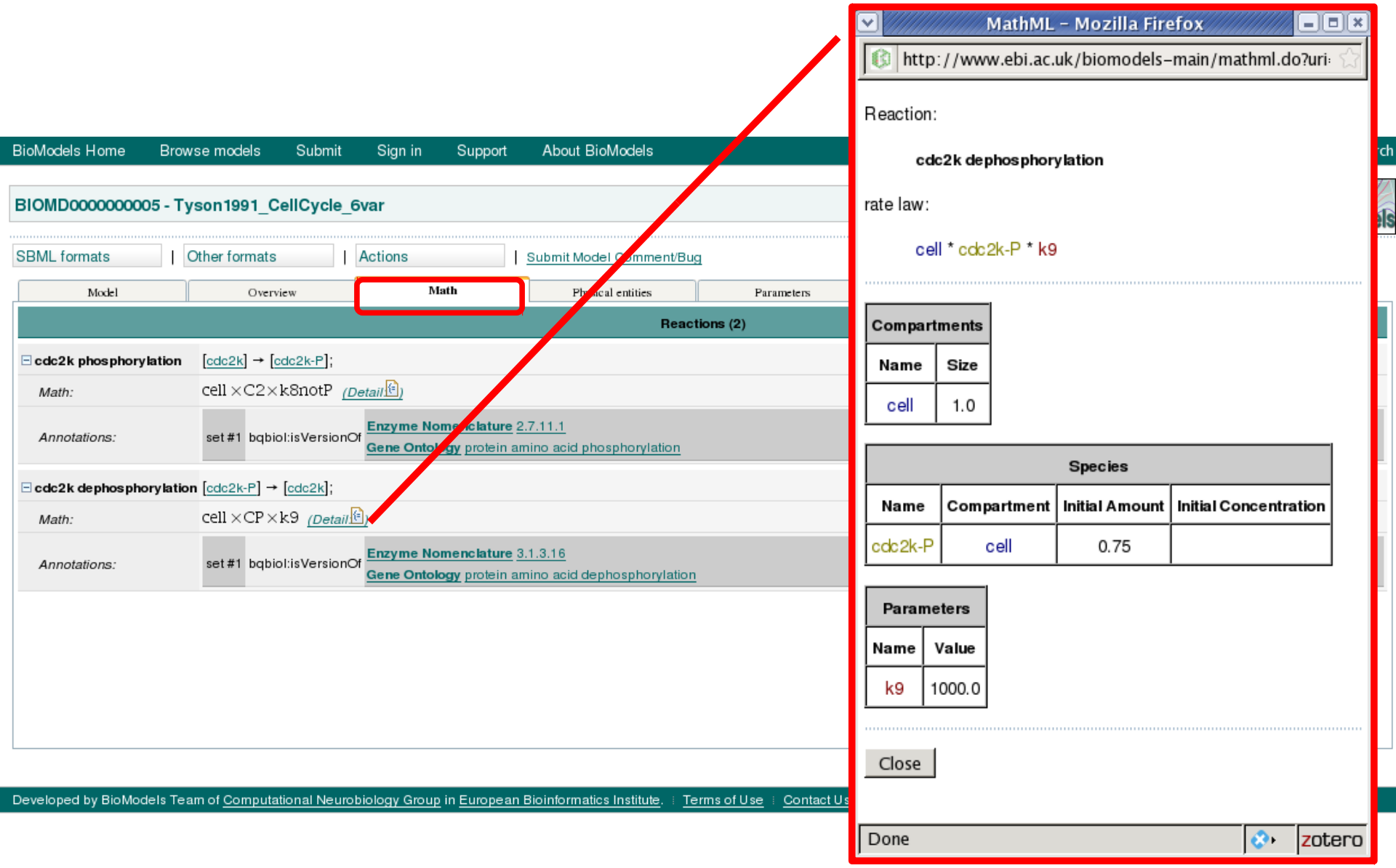
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SBML formats
Other formats
Actions
Submit Model Comment/Bug
Model
Overview
Math
Physical entities
Parameters
Reactions (2)
cdc2k phosphorylation
[cdc2k] → [cdc2k-P];
Math:
cell ×C2×k8notP (Detail)
Annotations:
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Enzyme Nomenclature 2.7.11.1
Gene Ontology protein amino acid phosphorylation
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
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http://www.ebi.ac.uk/biomodels-main/mathml.do?uri
Reaction:
cdc2k dephosphorylation
rate law:
cell * cdc2k-P * k9
Compartments
Name
Size
cell
1.0
Species
Name
Compartment
Initial Amount
Initial Concentration
cdc2k-P
cell
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Parameters
Name
Value
k9
1000.0
Close
Done
zotero

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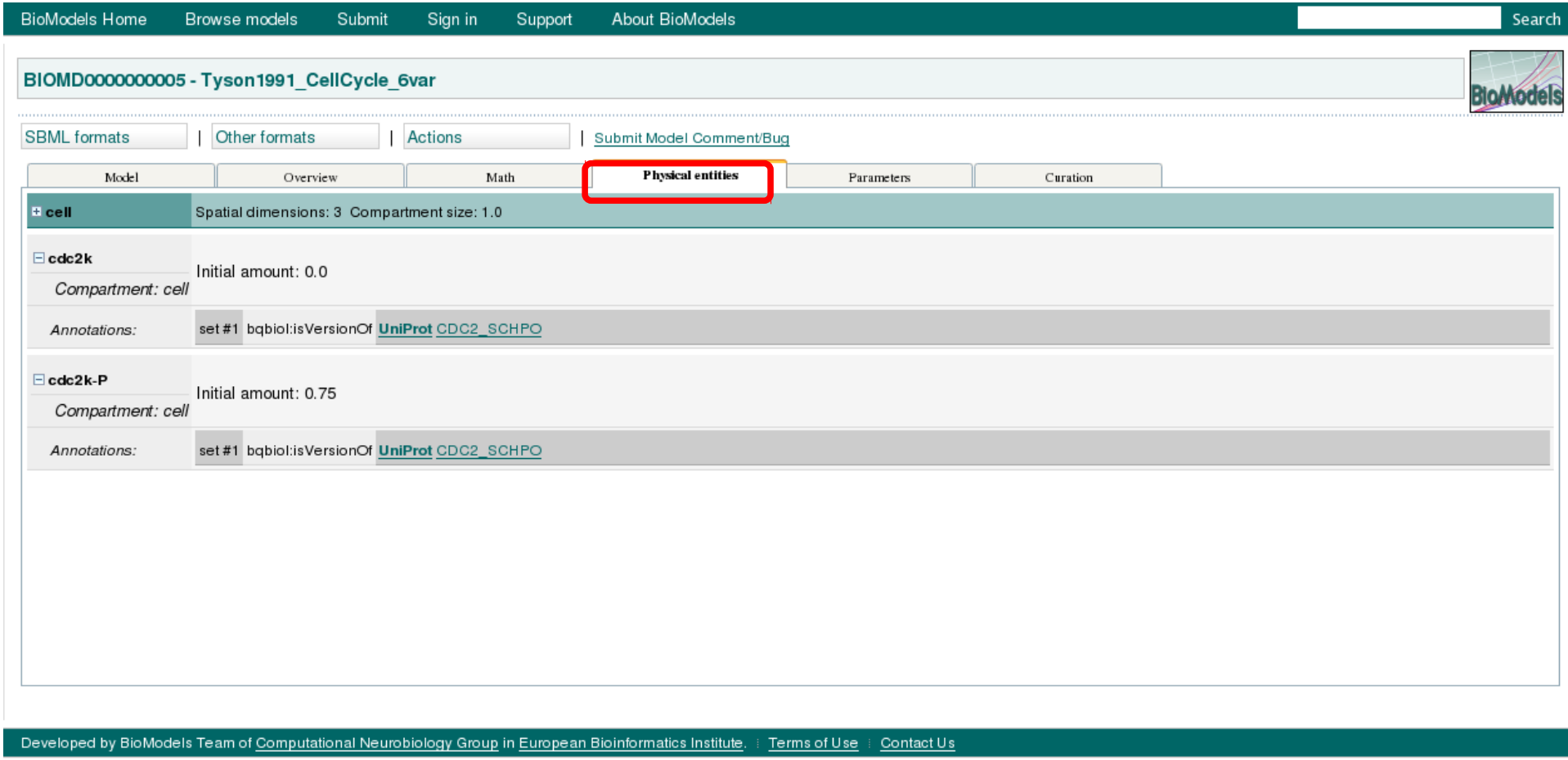
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Math
Physical entities
Parameters
Curation
cell
Spatial dimensions: 3 Compartment size: 1.0
cdc2k
Compartment: cell
Initial amount: 0.0
Annotations:
set #1 bqbiol:isVersionOf UniProt CDC2_SCHPO
cdc2k-P
Compartment: cell
Initial amount: 0.75
Annotations:
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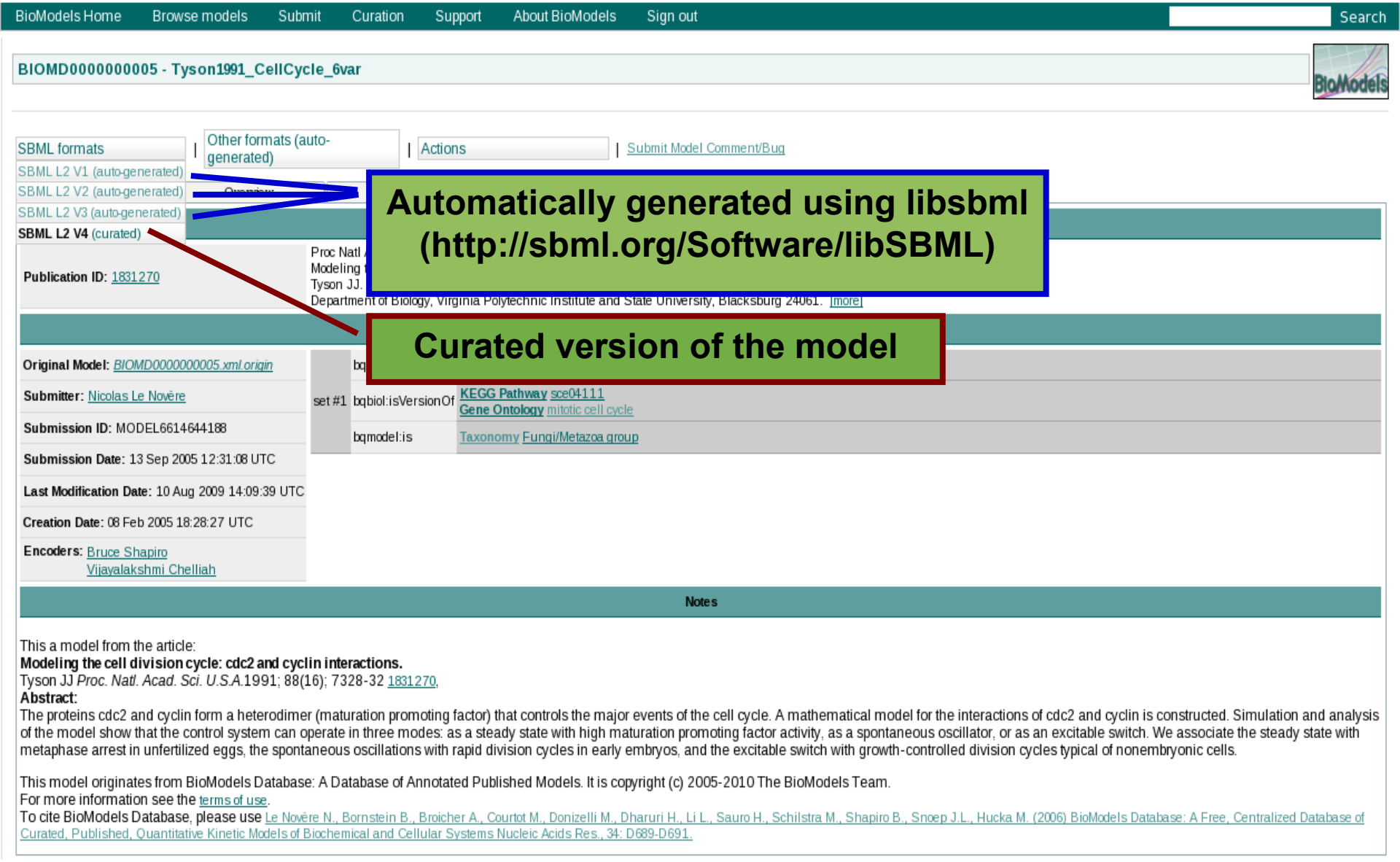
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SBML L2 V2 (auto-generated)
SBML L2 V3 (auto-generated)
SBML L2 V4 (curated)
Automatically generated using libsbml (http://sbml.org/Software/libSBML)
Curated version of the model
Publication ID: 1831270
Tyson JJ.
Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg 24061. [more]
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
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set #1
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Gene Ontology mitotic cell cycle
bqmodel:is
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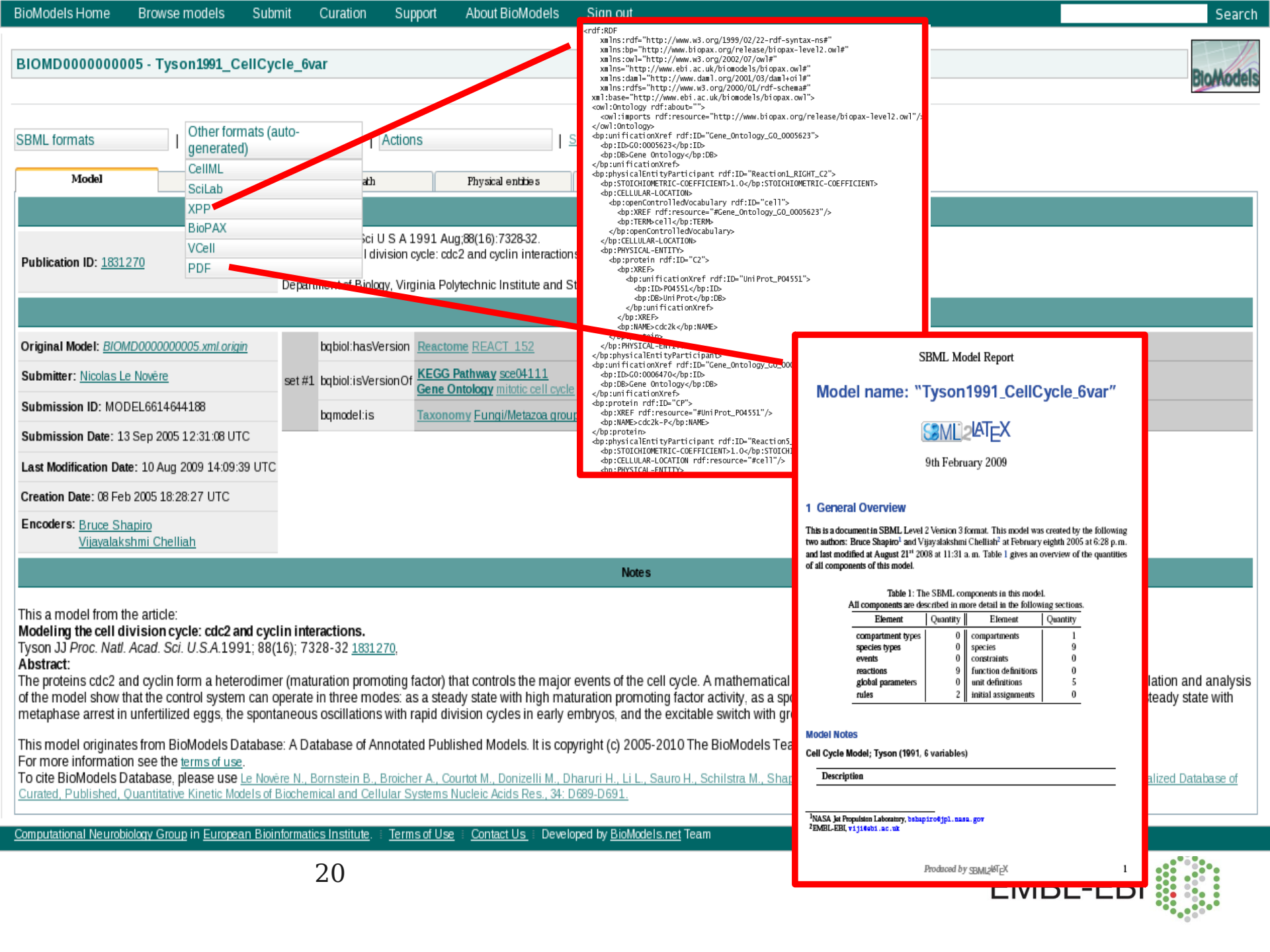
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Publication ID: 1831270
Original Model: BIOMD0000000005.xml.origin
Submitter: Nicolas Le Novère
Submission ID: MODEL6614644188
Submission Date: 13 Sep 2005 12:31:08 UTC
Last Modification Date: 10 Aug 2009 14:09:39 UTC
Creation Date: 08 Feb 2005 18:28:27 UTC
Encoders: Bruce Shapiro
Vijayalakshmi Chelliah
bqbiol:hasVersion
Reactome REACT_152
set #1
bqbiol:isVersionOf
KEGG Pathway sce04111
Gene Ontology mitotic cell cycle
bqmodel:is
Taxonomy Fungi/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:
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SBML Model Report
Model name: "Tyson1991_CellCycle_6var"
9th February 2009
1 General Overview
Model Notes
Cell Cycle Model; Tyson (1991, 6 variables)
Description
Produced by SBML2LaTeX
1

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BIOMD0000000005 - Tyson1991_CellCycle_6var

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- JWS Online Simulation
- BioModels Online Simulation

Model | Overview | Math | Parameters

Reference Publication

Publication ID: 1831270

Proc Natl Acad Sci U
Modeling the cell di ctions.
Tyson JJ.
Department of Biology, Virginia Polytechnic Institute and State University, Black

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set #1	bqbiol:hasVersion	Reactome REACT_152
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	bqmodel:is	Taxonomy Fungi/Metazoa group

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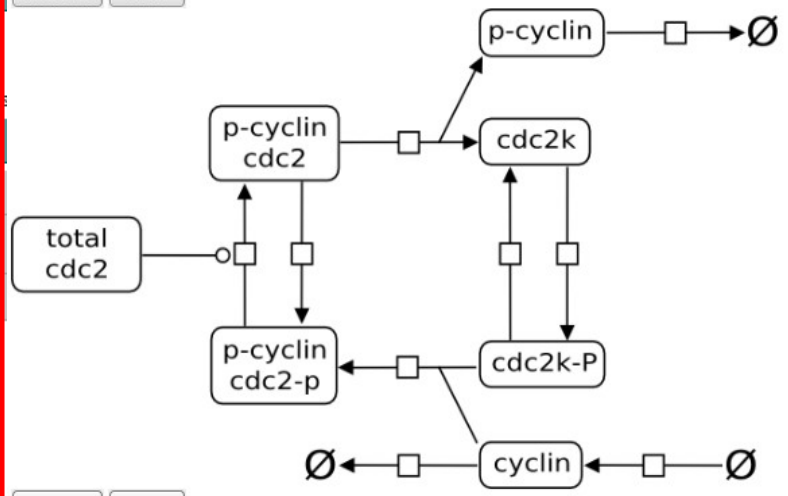
http://www.ebi.ac.uk/biomodels/models-main/publ/BIOMD0000000005.html

BIOMD0000000005

Refresh | Close



Refresh | Close

Done

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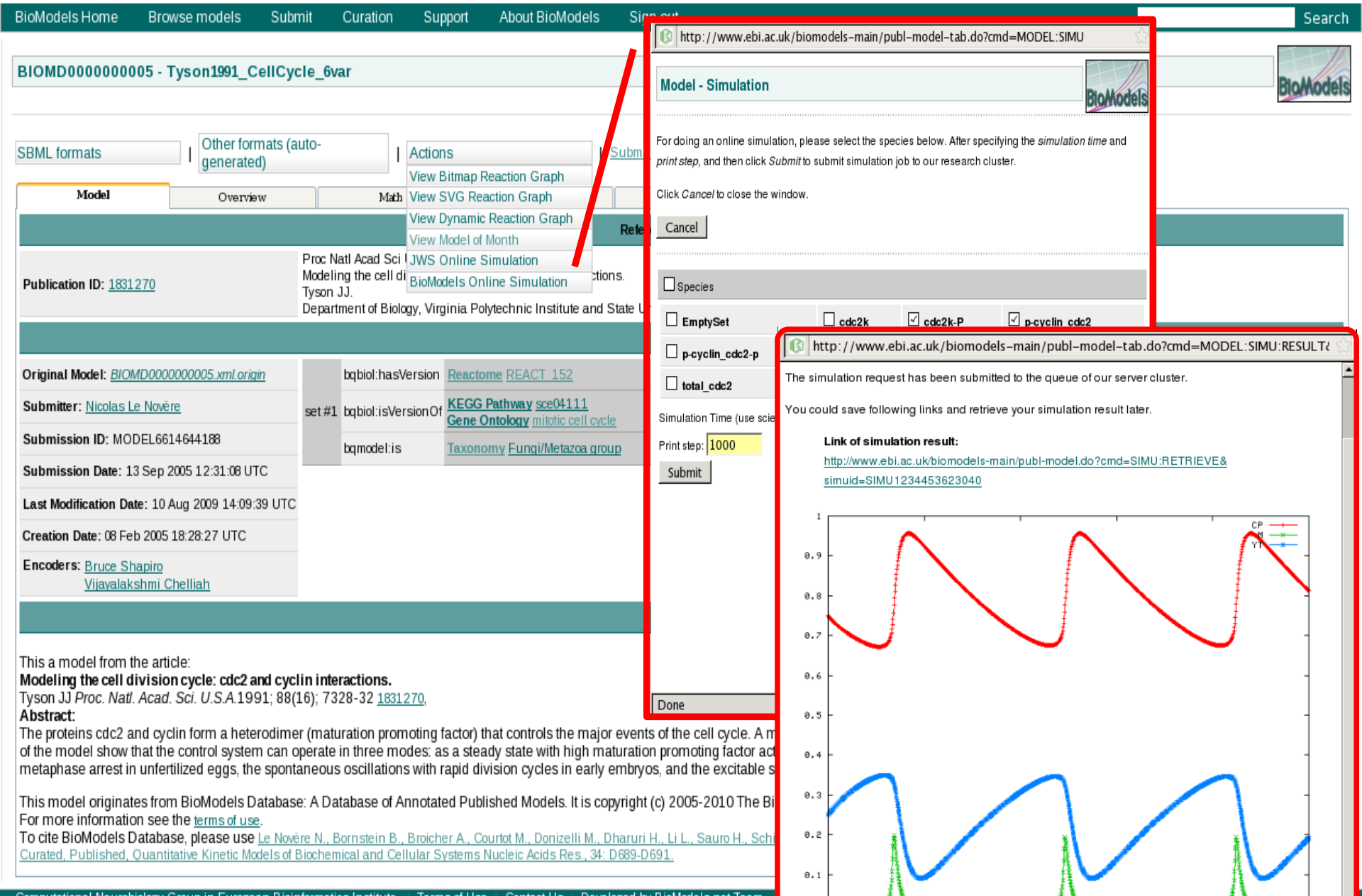
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http://www.ebi.ac.uk/biomodels-main/publ-model-tab.do?cmd=MODEL:SIMU
Model - Simulation
For doing an online simulation, please select the species below. After specifying the simulation time and print step, and then click Submit to submit simulation job to our research cluster.
Click Cancel to close the window.
Cancel
Species
EmptySet
cdc2k
cdc2k-P
p-cyclin_cdc2
p-cyclin_cdc2-p
total_cdc2
Simulation Time (use scie
Print step: 1000
Submit
Done
http://www.ebi.ac.uk/biomodels-main/publ-model-tab.do?cmd=MODEL:SIMU:RESULT
The simulation request has been submitted to the queue of our server cluster.
You could save following links and retrieve your simulation result later.
Link of simulation result:
http://www.ebi.ac.uk/biomodels-main/publ-model.do?cmd=SIMU:RETRIEVE&simuid=SIMU1234453623040
CP
M
YT
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
20
40
60
80
100
Close
http://www.ebi.ac.uk/biomodels/models-main/ode_simu/SIMU1234453623...
zotero

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Proc Natl Acad Sci U
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Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg 240

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

Encoders: Bruce Shapiro
Vijayalakshmi Chelliah

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

This a model from the article:
Modeling the cell division cycle: cd
Tyson JJ *Proc. Natl. Acad. Sci. U.S.A*
Abstract:
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metaphase arrest in unfertilized eggs

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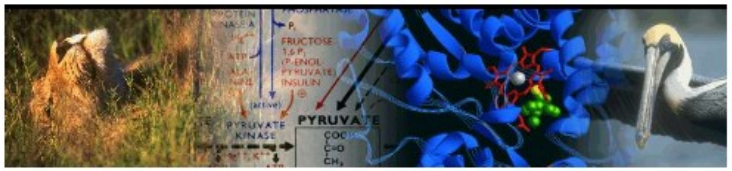
http://jjj.mib.ac.uk/biomodels/Tyson1991/index.html



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Tyson1991
Powered by JWS Online

JWSApplet – ver 5.0.3 Tyson1991

	Parameter	Value
P1_v1	cell	1
P2_v1	k6	1
P3_v1	k8notP	1.0e6
P4_v1	k9	1000
P5_v1	k3	200
P6_v1	k5notP	0.
P7_v1	k1aa	0.015
P8_v1	k2	0.
P9_v1	k7	0.6
P10_v1	k4	180
P11_v1	k4prime	0.018
E1	EmptySet	0.
I1	C2[0]	0.
I2	CP[0]	1
I3	Mvar[0]	0.
I4	Y[0]	0.
I5	YP[0]	0.
I6	pM[0]	0.3

Evaluate Model

Sim | State

StartTime 0 EndTime 100

Rates Metabolites

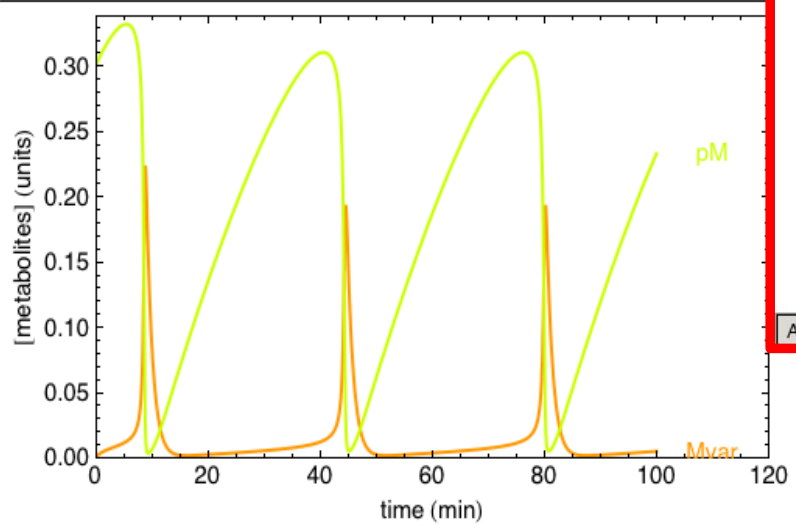
Type	Output	Plot
M1	C2	
M2	CP	
M3	Mvar	✓
M4	Y	
M5	YP	
M6	pM	✓
F1	v[Rea...	
F2	v[Rea...	
F3	v[Rea...	
F4	v[Rea...	
F5	v[Rea...	
F6	v[Rea...	
F7	v[Rea...	

POWERED BY webMATHEMATICA2

Reset

Applet jjjApplet started | zotero

http://jjj.mib.ac.uk/webMathematica/Examples/PlotScript11.jsp?fun="JWS



Download the results in text or comma separated value format (e.g. for Excel import):

Snoep J.L., Hucka M. (2006) BioModels Database: A Free, Centralized Database of

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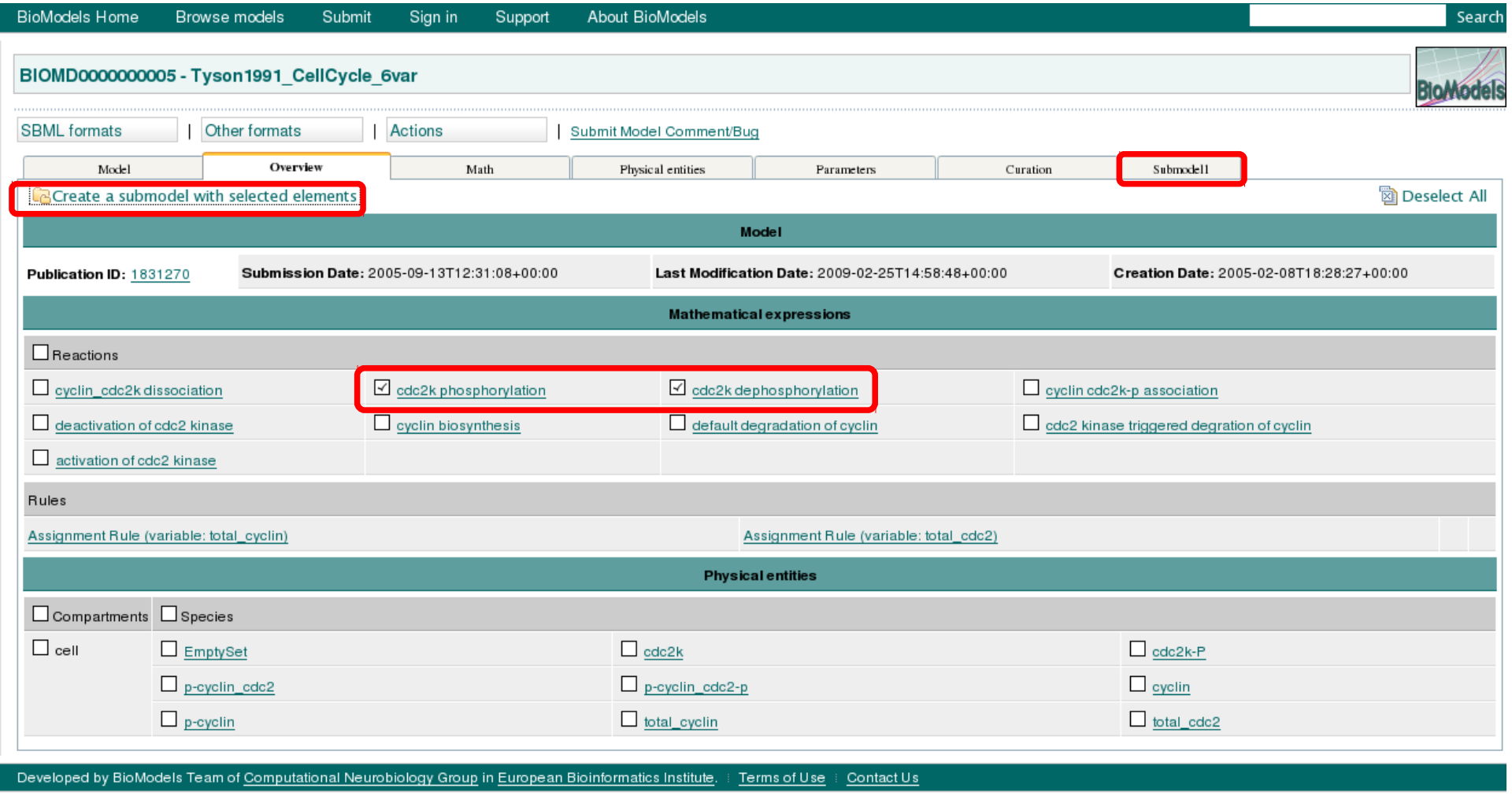
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Last Modification Date: 2009-02-25T14:58:48+00:00
Creation Date: 2005-02-08T18:28:27+00:00
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cyclin_cdc2k dissociation
cdc2k phosphorylation
cdc2k dephosphorylation
cyclin cdc2k-p association
deactivation of cdc2 kinase
cyclin biosynthesis
default degradation of cyclin
cdc2 kinase triggered degration of cyclin
activation of cdc2 kinase
Rules
Assignment Rule (variable: total_cyclin)
Assignment Rule (variable: total_cdc2)
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cell
EmptySet
cdc2k
cdc2k-P
p-cyclin_cdc2
p-cyclin_cdc2-p
cyclin
p-cyclin
total_cyclin
total_cdc2
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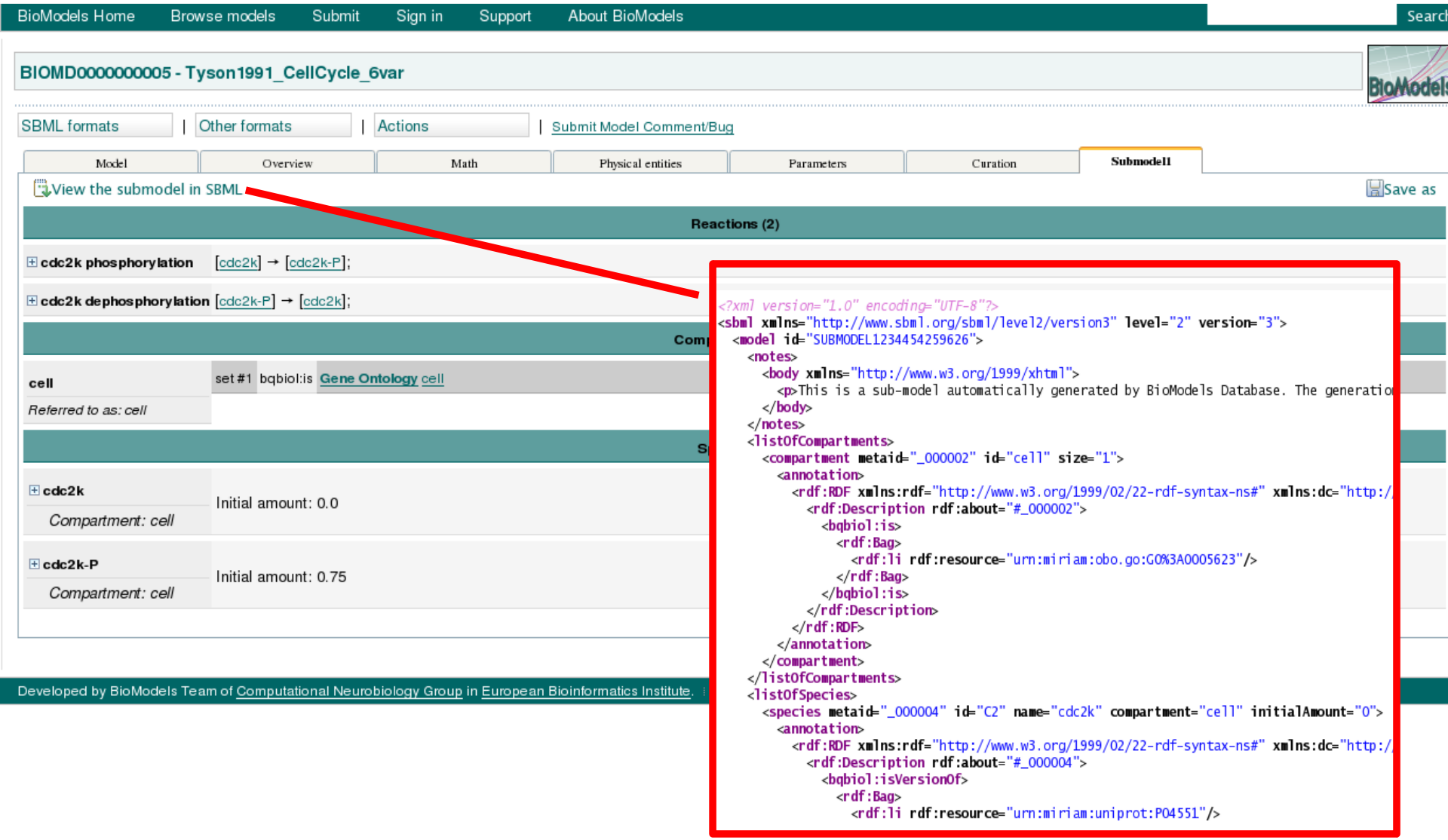
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Save as
Reactions (2)
cdc2k phosphorylation [cdc2k] → [cdc2k-P];
cdc2k dephosphorylation [cdc2k-P] → [cdc2k];
cell
set #1 bqbiol:is Gene Ontology cell
Referred to as: cell
cdc2k
Compartment: cell
Initial amount: 0.0
cdc2k-P
Compartment: cell
Initial amount: 0.75
Developed by BioModels Team of Computational Neurobiology Group in European Bioinformatics Institute.
<?xml version="1.0" encoding="UTF-8"?>
<sbml xmlns="http://www.sbml.org/sbml/level2/version3" level="2" version="3">
<model id="SUBMODEL1234454259626">
<notes>
<body xmlns="http://www.w3.org/1999/xhtml">
<p>This is a sub-model automatically generated by BioModels Database. The generatio
</body>
</notes>
<listOfCompartments>
<compartment metaid="_000002" id="cell" size="1">
<annotation>
<rdf:RDF xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#" xmlns:dc="http:/
<rdf:Description rdf:about="#_000002">
<bqbiol:is>
<rdf:Bag>
<rdf:li rdf:resource="urn:miriam:obo.go:GO%3A0005623"/>
</rdf:Bag>
</bqbiol:is>
</rdf:Description>
</rdf:RDF>
</annotation>
</compartment>
</listOfCompartments>
<listOfSpecies>
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<annotation>
<rdf:RDF xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#" xmlns:dc="http:/
<rdf:Description rdf:about="#_000004">
<bqbiol:isVersionOf>
<rdf:Bag>
<rdf:li rdf:resource="urn:miriam:uniprot:P04551"/>

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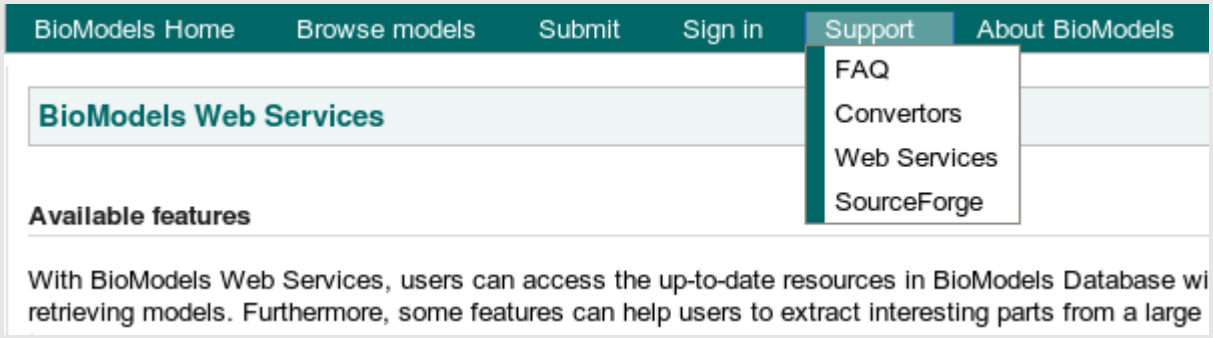
Software and Webservices



- Convertors: convertors for SBML to various formats, tools for graph generation and other related software (http://www.ebi.ac.uk/compneur-srv/sbml/convertors/SBMLConvertors.html)
- Web Services: http://www.ebi.ac.uk/biomodels-main/webservices

  Java library for accessing Biomodels DB, searching models, creating submodels, ...
- BiomodelsDB: http://sourceforge.net/projects/biomodels/

  (latest code available on demand)

Nicolas
Le Novère

Michael
Hucka

Development

Camille Laibe

Nicolas Rodriguez

Curation

Lukas Endler

Vijayalakshmi
Chelliah

Melanie Stefan

In cooperation with:
Upinder Bhalla (**DOQCS**, NCBS, Bangalore)
Ion Moraru (the **Virtual Cell**, University of Connecticut Health Center)
Jacky Snoep (**JWS Online**, Stellenbosch (ZA) University, ZA)

Major Differences to the CellML Model Repository

- models need to be described in the peer reviewed literature
  - no public access to unpublished models
- models are only publicly available after the curation process
- two branches
  - curated: manually checked and annotated models
  - non curated: valid SBML, but neither checked nor annotated
- elements of curated models are manually annotated
- models, model elements and annotations are stored in a database
- models have unique perennial IDs, that can be used for retrieval

Minimal Information Requested in the Annotation of Biochemical Models (MIRIAM)*

- encoded in a machine readable format
  - SBML (http://sbml.org)
  - CellML for submission (http://www.cellml.org)
- clearly related to a peer reviewed reference publication containing a set of results
- model's structure must reflect the biological processes in the reference description
- the model must reproduce the results given in the reference description

*Nicolas Le Novère et al., *Nature Biotechnology*, **23**(12), 2005