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<h2>A Simple Mitotic Oscillator</h2>
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<p style="font-size:x-small;">This is a Systems Biology Markup Language (SBML) file, generated by MathSBML 2.4.6 (14-January-2005) 14-January-2005 18:33:39.806932. SBML is a form of XML, and most XML files will not display properly in an internet browser. To view the contents of an XML file use the "Page Source" or equivalent button on your browser.</p>
<p>This model originates from BioModels Database: A Database of Annotated Published Models. It is copyright (c) 2005-2008 The BioModels Team. <br/>For more information see the <a href="http://www.ebi.ac.uk/biomodels/legal.html" target="_blank">terms of use</a>. <br/>To cite BioModels Database, please use <a href="http://www.ncbi.nlm.nih.gov/pmc/articles/16381960/" target="_blank">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.</a></p>
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SBML Converter

Computer Science Dept.

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SBML2LATEX

SBML Converter is a tool to convert files in the System Biology Markup Language (SBML) format to various file types including PDF, TeX, DVI, PS, EPS, GIF, JPG or PNG.

Two steps to perform a conversion

1. Make sure you have a file in a valid SBML format. You can use the [online SBML validator](#).
2. Upload your file in SBML format and choose the file type it should be converted to.

Notes: To perform this job we need to temporarily store your file on our server. Your file will be used only for that purpose. Therefore it will not willingly be passed to any third party, and it will automatically be deleted after the job has been done.

Information for LaTeX users

If you wish to obtain a LaTeX file (a TeX formatted file) you will need to [download the SBML2LaTeX logo](#) of this homepage in addition to the generated file. You will probably have to adapt the path to this logo in the LaTeX file, which occurs in the author tag.

Furthermore, the generated LaTeX code is based on the KOMA script package and uses several non-standard packages, which can all be downloaded from the <http://www.ctan.org> homepage: `breqn`, `flexisym`, `fltpoint`, `mhchem`, `rccol`. Other packages you may need for a successful compilation can be downloaded from the [CTAN archive](#) as well.

SBML2LaTeX has been written by [Andreas Dräger](#), [Dieudonne Motsou Wouamba](#) (dwouamba@yahoo.fr) and [Adrian Schröder](#) in close cooperation with [Michael Hucka](#) and [Lucas Endler](#). Grid back-end and GrailsUnicorn framework provided by [Hannes Planatscher](#). © 2001-2008 University of Tübingen

<http://webservices.cs.uni-tuebingen.de/webservices/sbmlconverterGridJob/create>

SBML Model Report

Model name: "Goldbeter1991_MinMitOscil"

SBML2LATEX

December 4, 2008

1 General Overview

This is a document in SBML Level 2 Version 1 format. This model was created by Bruce Shapiro¹ at February sixth 2005 at 11:39 p.m. and last time modified at August 21st 2008 at 11:31 a.m. Table provides an overview of the quantities of all components of this model.

Table 1: Number of components in this model, which are described in the following sections.

Element	Quantity	Element	Quantity
compartment types	0	compartments	1
species types	0	species	3
events	0	constraints	0
reactions	7	function definitions	0
global parameters	5	unit definitions	0
rules	2	initial assignments	0

Model Notes

A Simple Mitotic Oscillator

This is a Systems Biology Markup Language (SBML) file, generated by MathSBML 2.4.6 (14-January-2005) 14-January-2005 18:33:39.806932. SBML is a form of XML, and most XML files will not display properly in an internet browser. To view the contents of an XML file use the "Page Source" or equivalent button on your browser.

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¹NASA Jet Propulsion Laboratory, bshapiro@jpl.nasa.gov

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