PANTHER Pathway

A Database of SBML-Based Biological Models coupled with Data Analysis Tools

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http://www.pantherdb.org/pathway/

Free access

D284-D288 Nucleic Acids Research, 2005, Vol. 33, Database issue doi:10.1093/nar/gki078

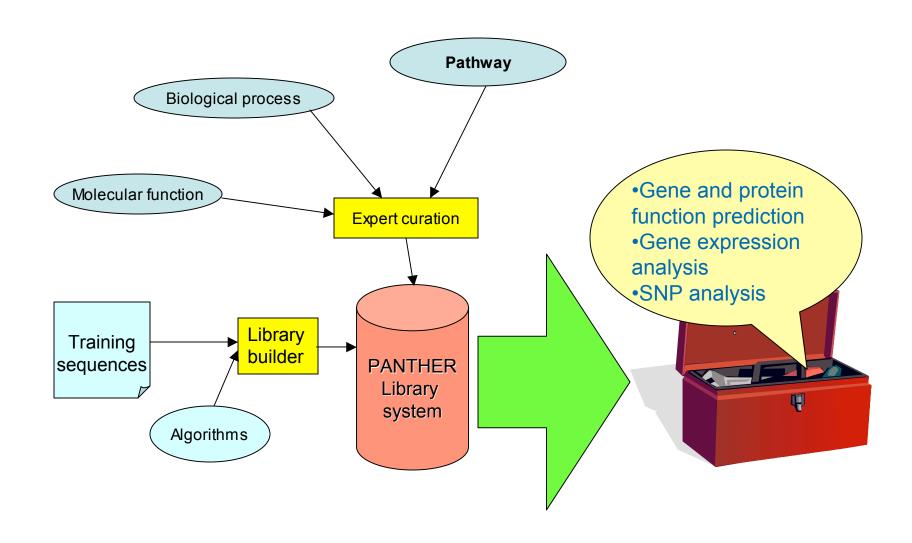
The PANTHER database of protein families, subfamilies, functions and pathways

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Goals

- To build an integrated infrastructure with expert-curated pathways.
- To help to establish a **standard** that will enable the content to be used across a large number of software applications.
- The system should allow users to:
 - Predict gene and protein functions
 - Analyze research data
 - Navigate or browse literatures
 - Design new experiments



PANTHER pathway Infrastructure

- Pathway index (or ontology).
- Pathway diagrams.
- Sequence association.
- Literature references.
- Analysis tools

PANTHER Pathway Index (Ontology)

A list of controlled vocabulary describing various components and their relationships within a pathway.

Components

- Proteins: receptor, kinase
- Genes: receptor gene, kinase gene
- Organic or inorganic molecules: Glucose, pyruvate, Calcium ion

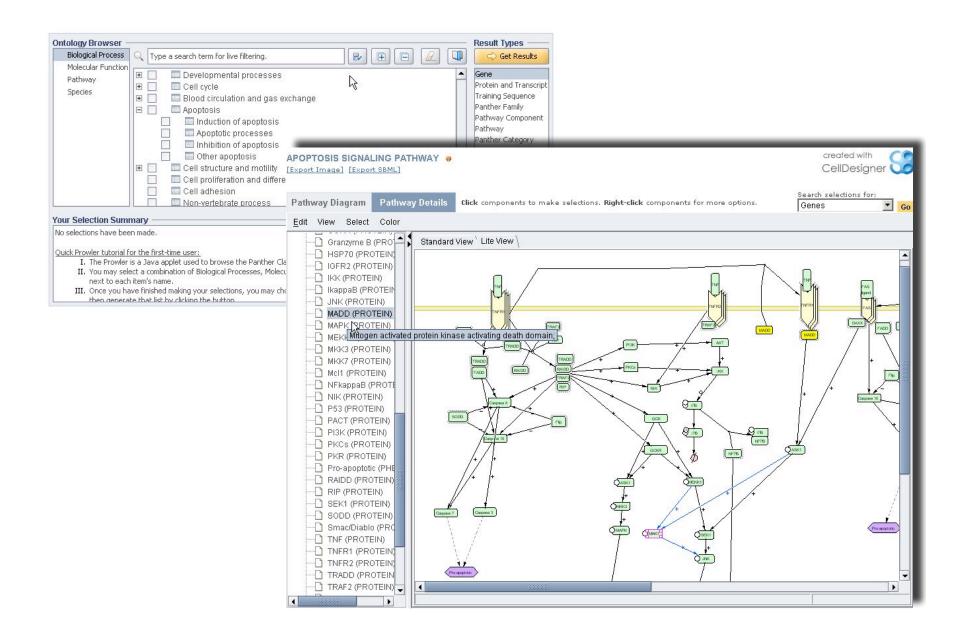
Relationships

- Upstream / downstream
- Activation / Inhibition
- Phosphorylation / dephosphorylation
- Complex formation
- Transportation
- •

Cell type and subcellular location

- Nucleus
- Mitochondria
- Cytoplasm
- Nerve terminal
- Muscle cell

Biological process ontology vs. Pathway



Pathway Diagram

- To graphically represent pathways while capturing structured data.
- To use controlled graphic notation to illustrate components (proteins, genes, simple molecules, etc), relationships (inhibition, phosphorylation, etc) in pathways.
- To capture comprehensive molecular events of the pathways
- To be able to store the diagram in a standard format so that the data can be easily parsed, or shared by different software

CellDesigner



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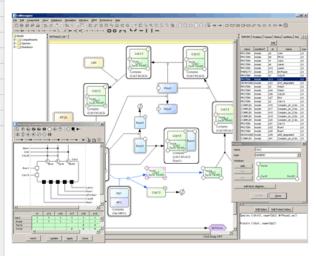
Related Link

systems-biology.org Kitano Symbiotic Systems Project PANTHER database





CellDesigner™: A modeling tool of biochemical networks

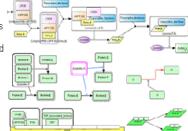


CellDesigner is a structured diagram editor for drawing gene-regulatory and biochemical networks. Networks are drawn based on the process diagram, with graphical notation system proposed by Kitano, and are stored using the Systems Biology Markup Language (SBML), a standard for representing models of biochemical and gene-regulatory networks. Networks are able to link with simulation and other analysis packages through Systems Biology Workbench (SBW).

CellDesigner 3.0.1 Released!

A New look of Graphical Notation that enhanced previous process diagram into gene and RNA, as well as protein complex structure.

Version 3.0 implements most part of notations described in Kitano, et al. ("Using process diagrams for the graphical representation of biological networks", Nature Biotechnology 23(8), 961 - 966 (2005)).



Running Simulation with Control Panel! CellDesigner3.0 supports simulation and parameter scan



Headlines

For Mac OS user (Jan 27st, 2006) There is a Mac OS X bug that affects CellDesigner on OS X systems with the QuickTime 7.0.4 upgrade. The current workaround is to revert to QuickTime 7.0.1, through a reinstaller available from Apple on the Support/Downloads page. details...

CellDesigner 3.0.1 Released! (Jan 26st, CellDesigner3.0.1 fixed bugs on complex handling. versionup info..

CellDesigner 3.0 Released! (Oct 15st, 2005) CellDesigner3.0 now supports new graphical notation as well as seamless simulation using integrated SBML ODE versionup info..

CellDesigner 2.5 Released! (Sept 1st, 2005) CellDesigner 2.5 now supports seamless simulation using integrated SBML ODE solver. versionup info...

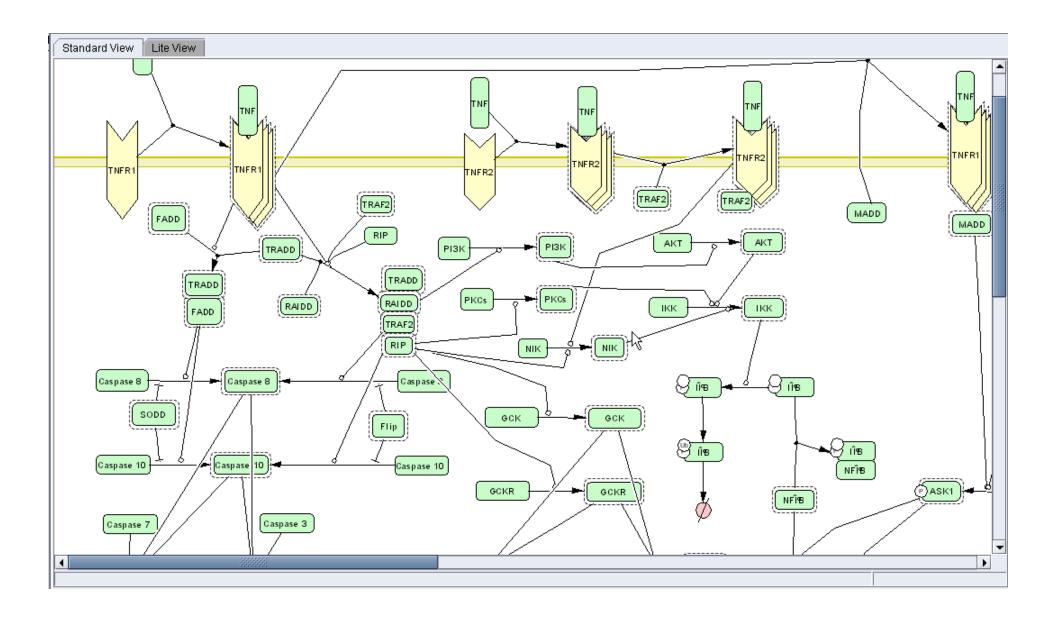
CellDesigner 3.0 alpha Notation Preview Version Released! (Aug 5,

CellDesigner 3.0 alpha version is to preview the new notation scheme. versionup info.

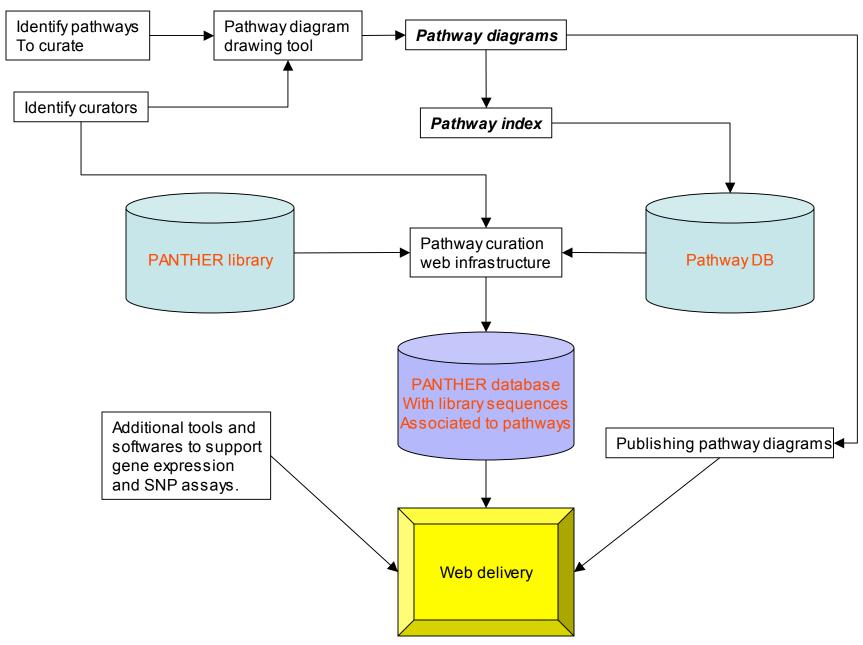
PANTHER Pathway Module released (January 3, 2005)

Applied Biosystems Inc. (ABI) today

released PANTHER™ pathway module that contains over 100 signal transduction pathways all created using CellDesigner full story...



Curation Process



Linking pathways to genomes

- Each pathway component (protein or gene) is associated with sequences in the PANTHER™ library
- This links pathway information to statistical models (Hidden Markov Models) of protein families, molecular functions, and biological processes of the proteins, and the evolutionary relationships among them
- This also allows users to browse and search for genes in pathways and analyze research results in the context of pathways
- Confidence code and evidence (e.g. PubMed articles) are assigned to all associations.

PANTHER™ Pathway Statistics Feb. 2006

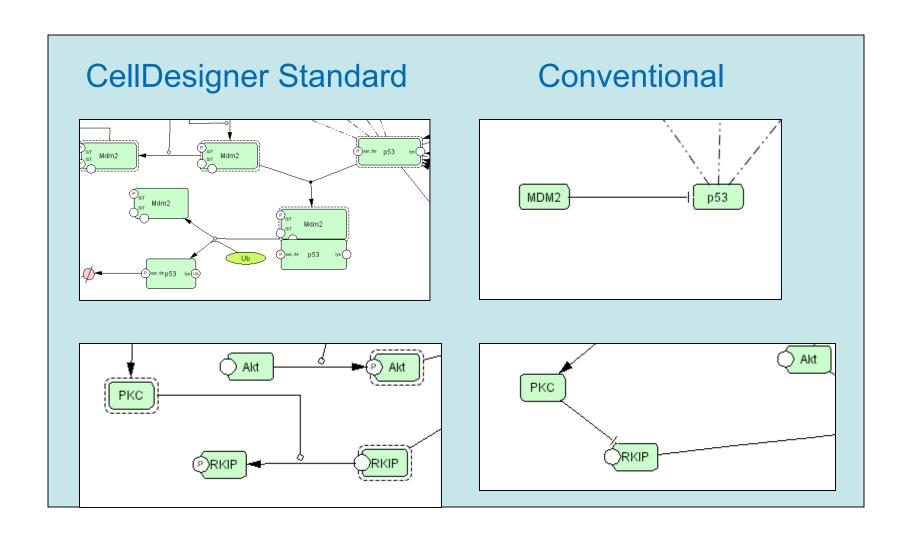
# of Pathways	107
# of Components	1798
# of Sequences directly associated with pathways	17513
# of publications used as evidence	3340

Conventional

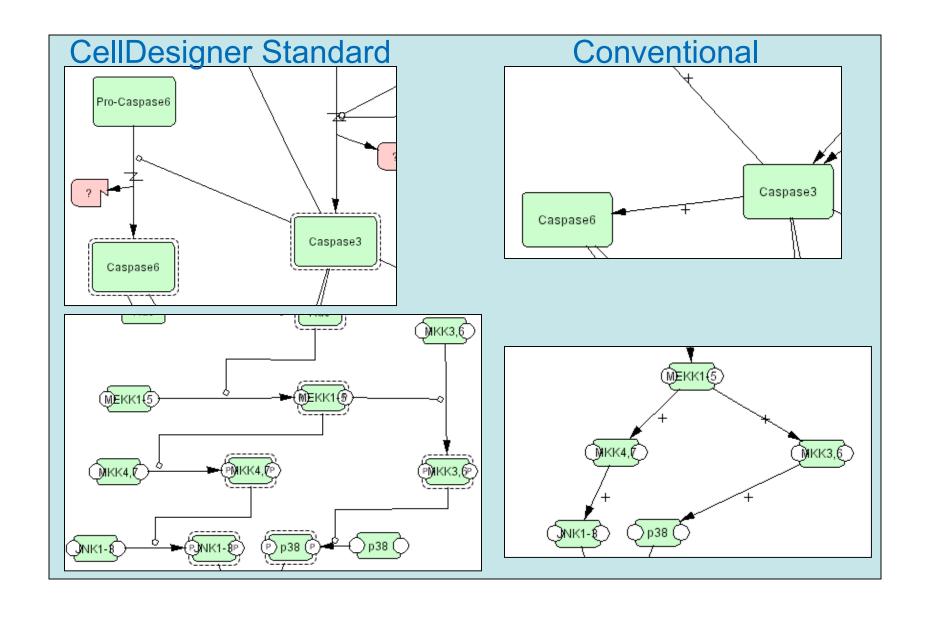
VS.

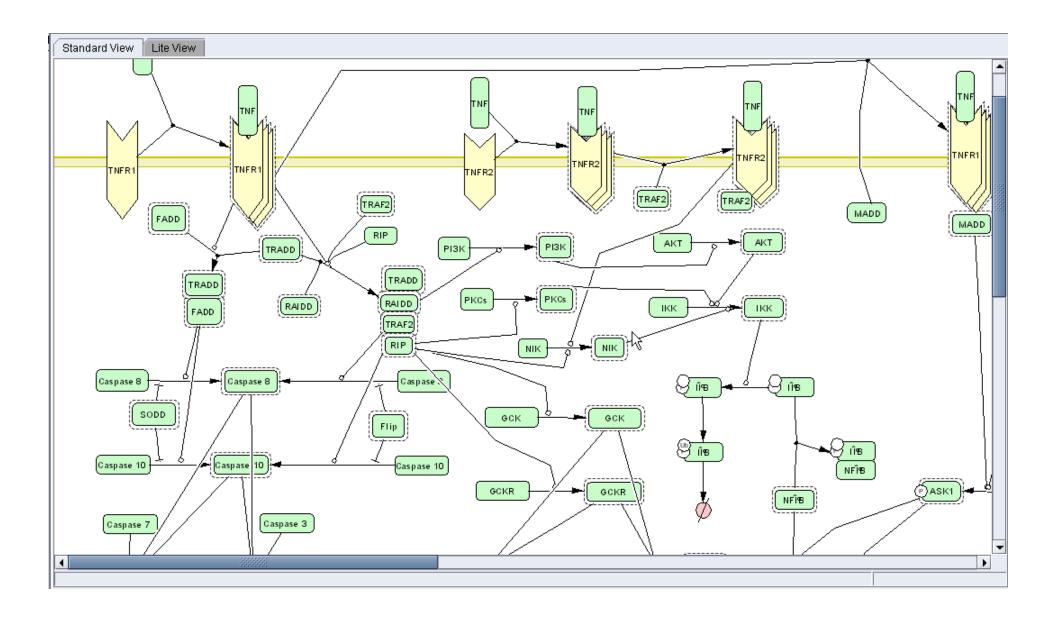
Standard

Two views of inhibition

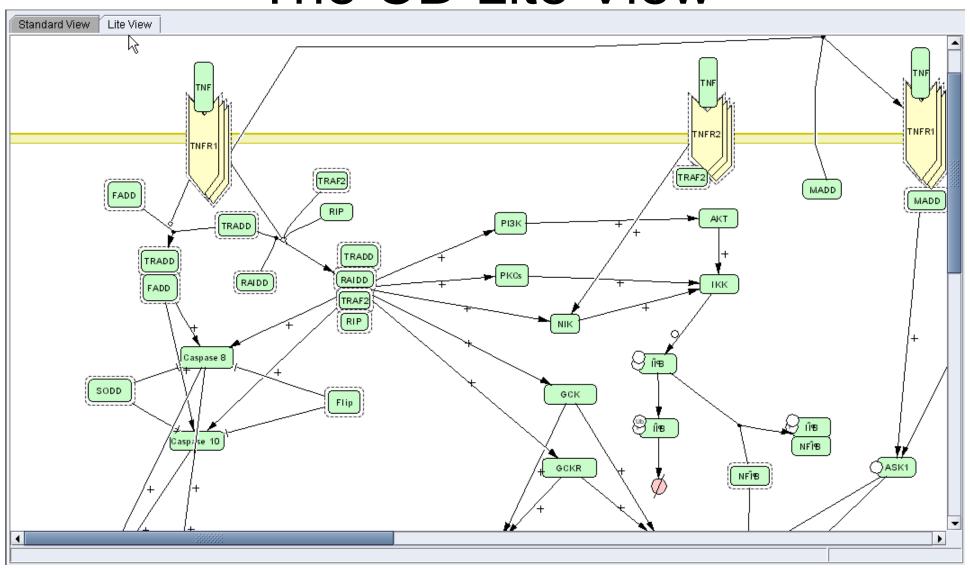


Two views of activation





The CD Lite View



Acknowledgments

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