

Reactome

A database of biological pathways

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History

- Started off as *Genome Knowledgebase* (GKB) spring 2001
- Initially tried to capture and standardize the language used to describe molecular processes
- 2001/2002 realized that what we are trying to capture are reactions and pathways
- Re-branded as *Reactome* June 2004



Reactome Data Model

Events:

- Reactions
- Pathways

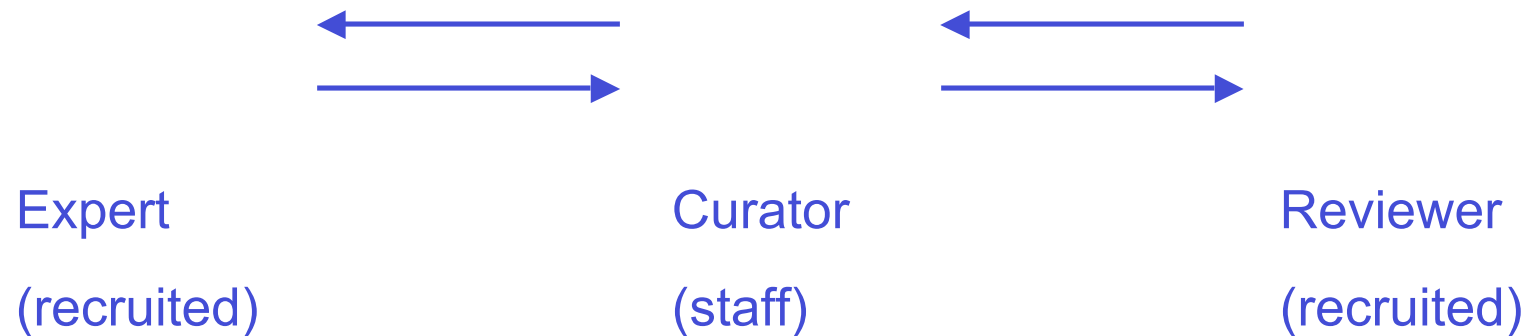
Entities:

- Proteins
- Complexes
- Small compounds

Modulation:

- Inhibition
- Activation

Where Reactome's Data Comes From



- Expert and curator create outline of new pathway
- Expert fills in details
- Curator enters information into database
- Reviewer (another expert) checks biological correctness

Coverage

- Apoptosis
- Cell cycle
- DNA repair
- Transcription, mRNA processing, translation, post-translational modification
- Signaling pathways (insulin, NOTCH, opioid, NGF, EGFR, FGFR, Rho GTPases II, Opioid, Wnt)
- Hemostasis
- Metabolism (energy, amino acid, lipid, nucleotide, xenobiotic)
- Synaptic transmission
- Lipoproteins – HDL and VLDL



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Download

The following links allow you to download Reactome data in various formats:

- BioPax
- SBML
- Textbook
- Other formats

Try this

Have you got a set of genes or proteins, where you would like to understand the biological context better? With Reactome, you can find out which of your genes or proteins are overrepresented in which pathways.

Try it out!

About Reactome

REACTOME is an open-source, open access, manually curated, peer-reviewed and highly reliable pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial, maintained by the Reactome editorial staff and cross-referenced to many bioinformatics databases. These include NCBI Entrez Gene, Ensembl and UniProt databases, the UCSC and HapMap Genome Browsers, the KEGG Compound and ChEBI small molecule databases, PubMed, and Gene Ontology. ... [more]

Pathway of the Month: Cell Cycle Checkpoints

Click image to see pathway

News and Notes

- **Jul 23, 2010: Version 3 of the FlyReactome Knowledgebase has been released**
Version 3 of the FlyReactome Knowledgebase has been released and is accessible at <http://fly.reactome.org>. FlyReactome (Mark Williams and Michael Ashburner ... [more]
- **Jul 07, 2010: Reactome@ISMB2010**
ISMB2010 is in Boston this year and Robin Haw, Christina Yung and Lincoln Stein will be attending. Robin will be talking at the 11th BioPathways – SIG Meeting on July 9th and presenting a poster entitled The Reactome Reloaded (E17). ... [more]
- **Jun 18, 2010: Version 33 Released**
Version 33 includes the new topic Chromosome maintenance regrouping existing annotations for ... [more]

Expression Analysis I



Upload expression data

Takes gene expression data (and also numerical proteomics or metabolomics data) and shows how expression levels affect reactions and pathways in living organisms. May be time-consuming, depending on the number of identifiers you are submitting; less than 5000: a few seconds, 5000 - 10000: a few minutes, 10000 or more: 10 minutes or longer. [More....](#)

Paste or upload your data: [Example](#)

```
#Probeset 10h_control 10h 14h 18h 24h
1053_at 8.040078 7.147358 6.706705 6.794622 7.475157
1729_at 6.869688 6.99104 7.129922 7.112222 7.04721
1861_at 6.437999 6.620092 6.20117 6.407735 5.717815
200000_s_at 9.381569 9.710802 9.874874 9.934639 9.495911
200002_at 12.555275 12.511045 12.564419 12.538642 12.439174
200003_s_at 12.401259 12.054083 12.275169 12.206342 12.015476
200005_at 9.609852 9.099299 9.73072 9.530097 9.194303
200012_x_at 12.486269 12.402275 12.302666 12.256543 12.282444
200014_s_at 10.371458 9.548578 9.978313 9.871472 8.753136
200016_x_at 12.110468 11.913288 11.938524 11.899243 11.458105
200022_at 12.205038 11.927471 12.064725 12.031422 11.932256
200023_s_at 10.377248 9.902753 9.990862 10.248412 9.513486
```

Expression Analysis II

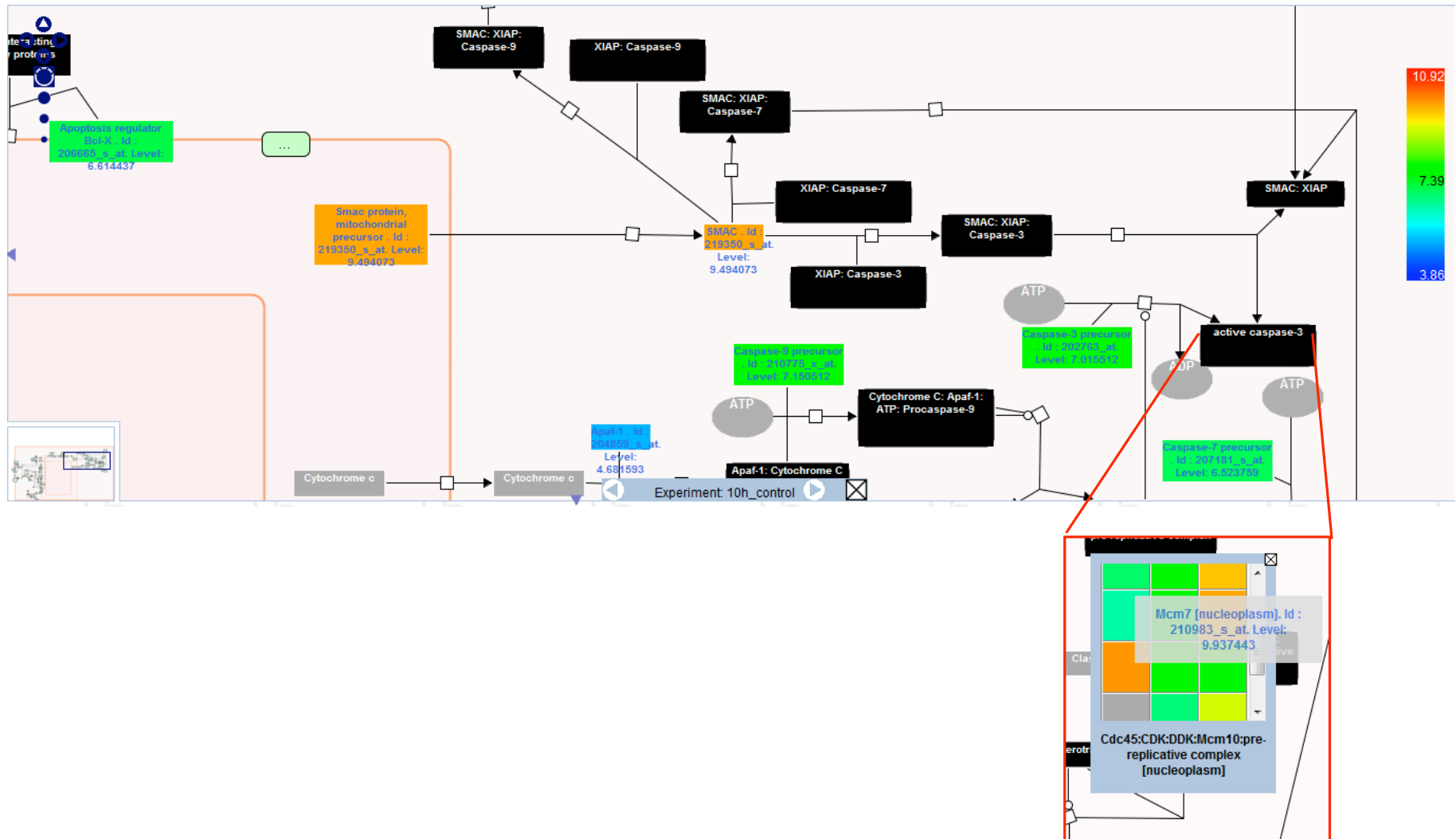
Expression per pathway

This table provides an overview of your expression data in a pathway context. [More...](#)

WARNING: if you navigate away from this page, you will lose the displayed data. Use the download facility to secure it.

Select format to download this table: <input type="text" value="Microsoft Xcel"/> <input type="button" value="Download"/>					
Pathway name ▼▲	Species ▼▲	Total number of proteins ▼▲	Matching proteins in data ▼▲	% in data ▼▲	Click button to view pathway
ABC-family proteins mediated transport	Homo sapiens	15	0	0%	<input type="button" value="View"/>
APC/C-mediated degradation of cell cycle proteins	Homo sapiens	72	39	54%	<input type="button" value="View"/>
Apoptotic execution phase	Homo sapiens	48	3	6%	<input type="button" value="View"/>
Base Excision Repair	Homo sapiens	19	18	94%	<input type="button" value="View"/>
Bile acid and bile salt metabolism	Homo sapiens	27	1	3%	<input type="button" value="View"/>
Binding of RNA by Insulin-like Growth Factor-2 mRNA Binding Proteins (IGF2BPs/IMPs/WICKZs)	Homo sapiens	3	0	0%	<input type="button" value="View"/>
Botulinum neurotoxicity	Homo sapiens	10	0	0%	<input type="button" value="View"/>
Cell Cycle Checkpoints	Homo sapiens	114	72	63%	<input type="button" value="View"/>
Cell junction organization	Homo sapiens	70	2	2%	<input type="button" value="View"/>
Cell surface interactions at the vascular wall	Homo sapiens	93	12	12%	<input type="button" value="View"/>
Cholesterol biosynthesis	Homo sapiens	22	0	0%	<input type="button" value="View"/>
Complement cascade	Homo sapiens	51	2	3%	<input type="button" value="View"/>
Costimulation by the CD28 family	Homo sapiens	62	2	3%	<input type="button" value="View"/>
Depolarization of the Presynaptic Terminal Triggers the Opening of Calcium Channels	Homo sapiens	7	1	14%	<input type="button" value="View"/>
Dissolution of Fibrin Clot	Homo sapiens	8	4	50%	<input type="button" value="View"/>

Expression Analysis III



BioPax Output

- BioPax level 2 and level 3 provided.
- Available for single pathways or for the whole database.
- OWL format dump files.
- Under level 3, the following are exported:
 - bp:Pathway (pathway name)
 - bp:pathwayComponent (reactions)
 - bp:comment (text description)
 - bp:xref (Pubmed references)
 - bp:cellularLocation
 - bp:entityReference (Protein UniProt ID)
 - bp:UnificationXref (GO terms)

SBML Output

- SBML level 2 provided.
- Available for single pathways or for the whole database.
- The following are exported:
 - listOfSpecies (proteins only, no IDs)
 - ListOfCompartments (homegrown names)
 - listOfReactions

Future Plans

- Rewrite SBML export, based on libSBML.
- Include coordinates for entities and reactions.
- Allow user to hand-pick reactions.
- Import reaction dynamics from other databases.
- Optional collapse of reactions.
- Possible inclusion of CellDesigner elements for GARUDA.

