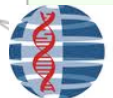


REACTOME

A curated database of reactions, pathways and biological processes

Robin Haw
5th April 2012
GMOD Community Meeting
www.reactome.org



International Cancer Genome Consortium



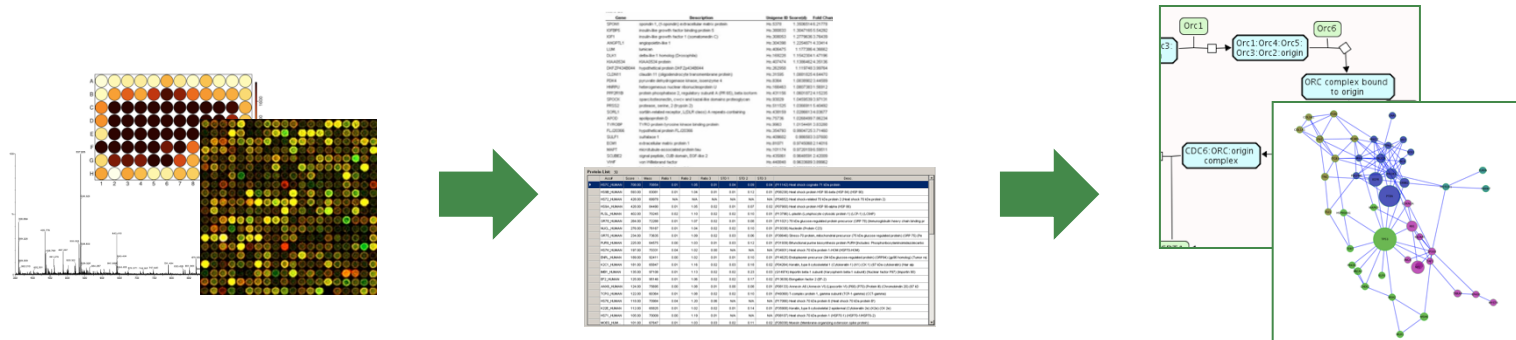
Ministry of Economic Development and Innovation



National Human Genome Research Institute

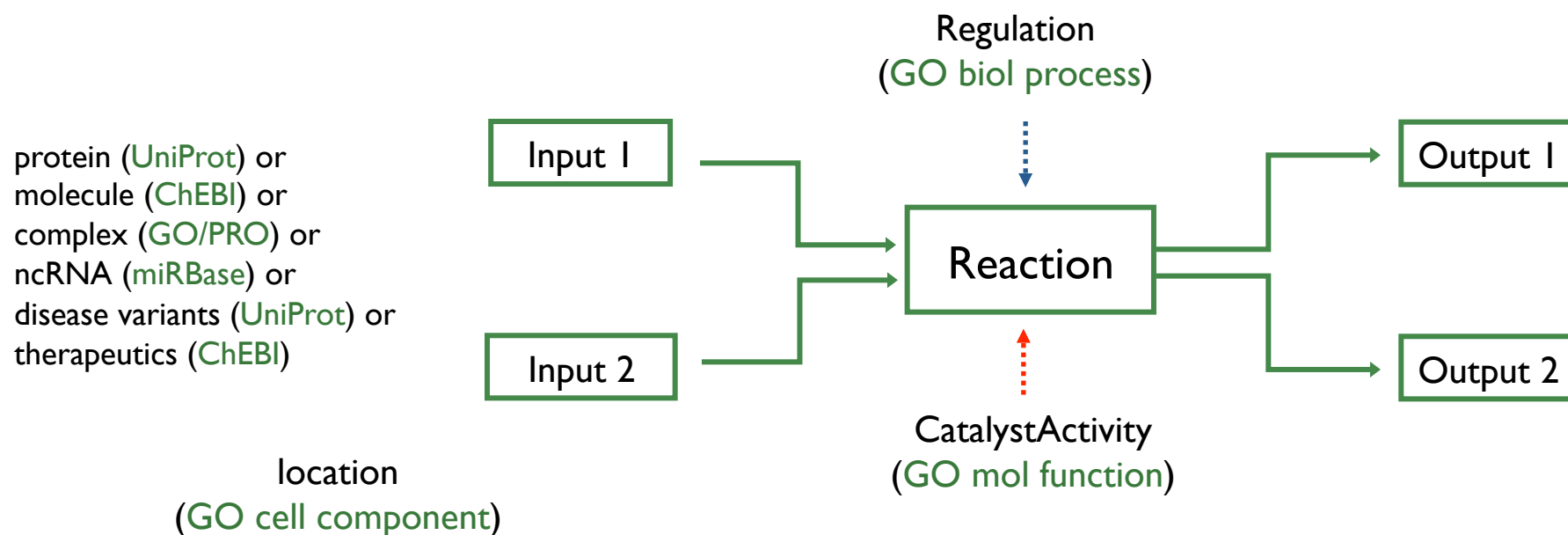
What is Reactome?

- Open source and open access pathway database
 - Metabolism, signaling, gene expression, DNA replication and repair and other biological processes in human biology
- Expert authored, manually curated and peer-reviewed
 - Rigorous curation standards – every reaction traceable to primary literature
 - Inferred and manually curated model organism pathways
- Extensively cross-referenced to external bioinformatics databases
- Provides tools and datasets for browsing, querying, analyzing and visualizing pathway data



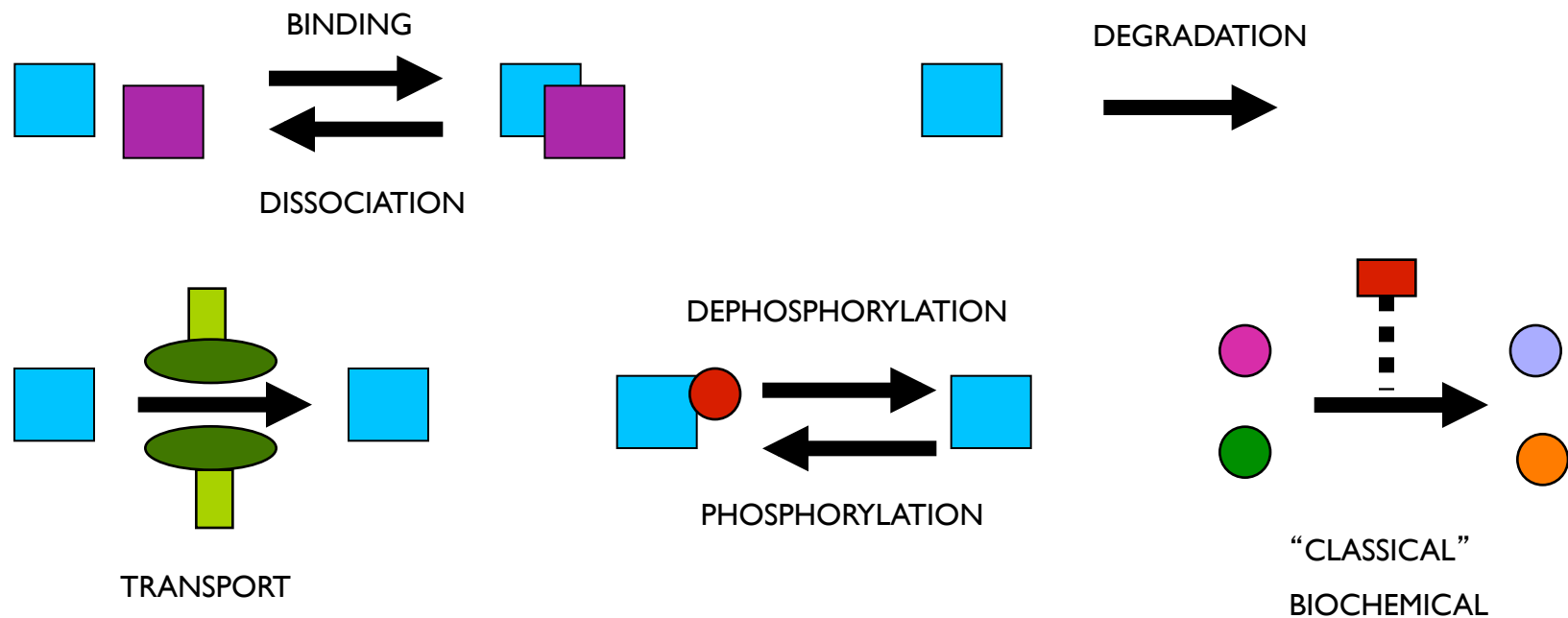
Data model in a nutshell

- Basic “unit” of Reactome

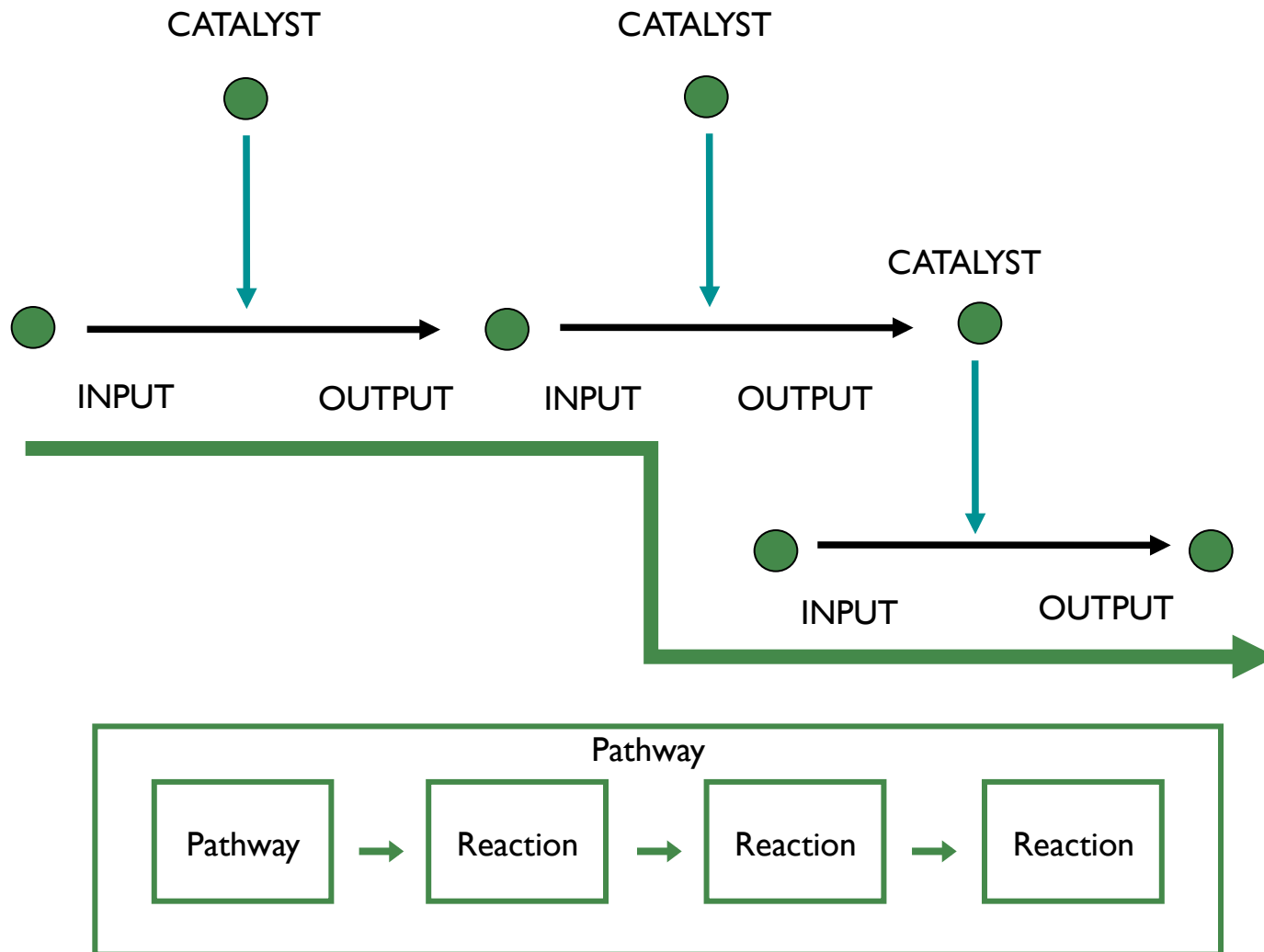


Theory - Reactions

- Represents many events and states found in biology.



Reactions Connect into Pathways



Where the Data Comes From?

- Recruit bench scientists to write modules.
 - All molecules are identified explicitly
 - All assertions backed by literature references
- Curator works with author to ensure consistency and completeness
- Module is checked by peer review and software prior to publication
- Public release of curated data every 3 months
- Regular pathway updates and rolling review

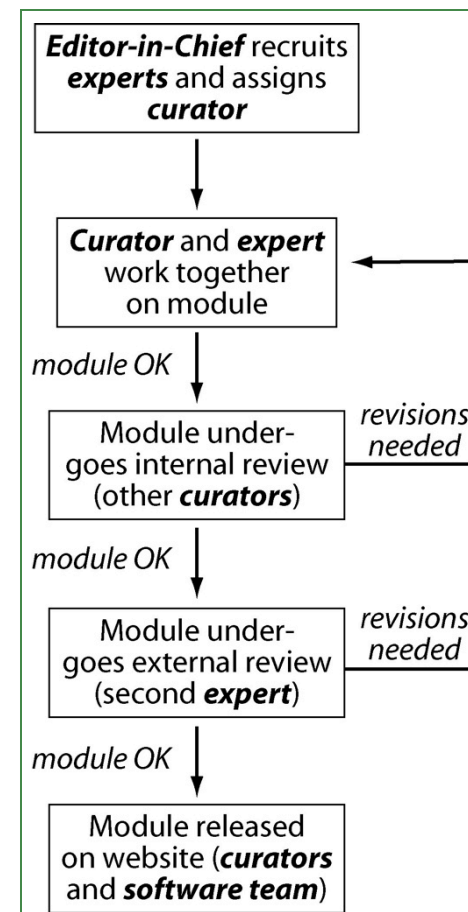


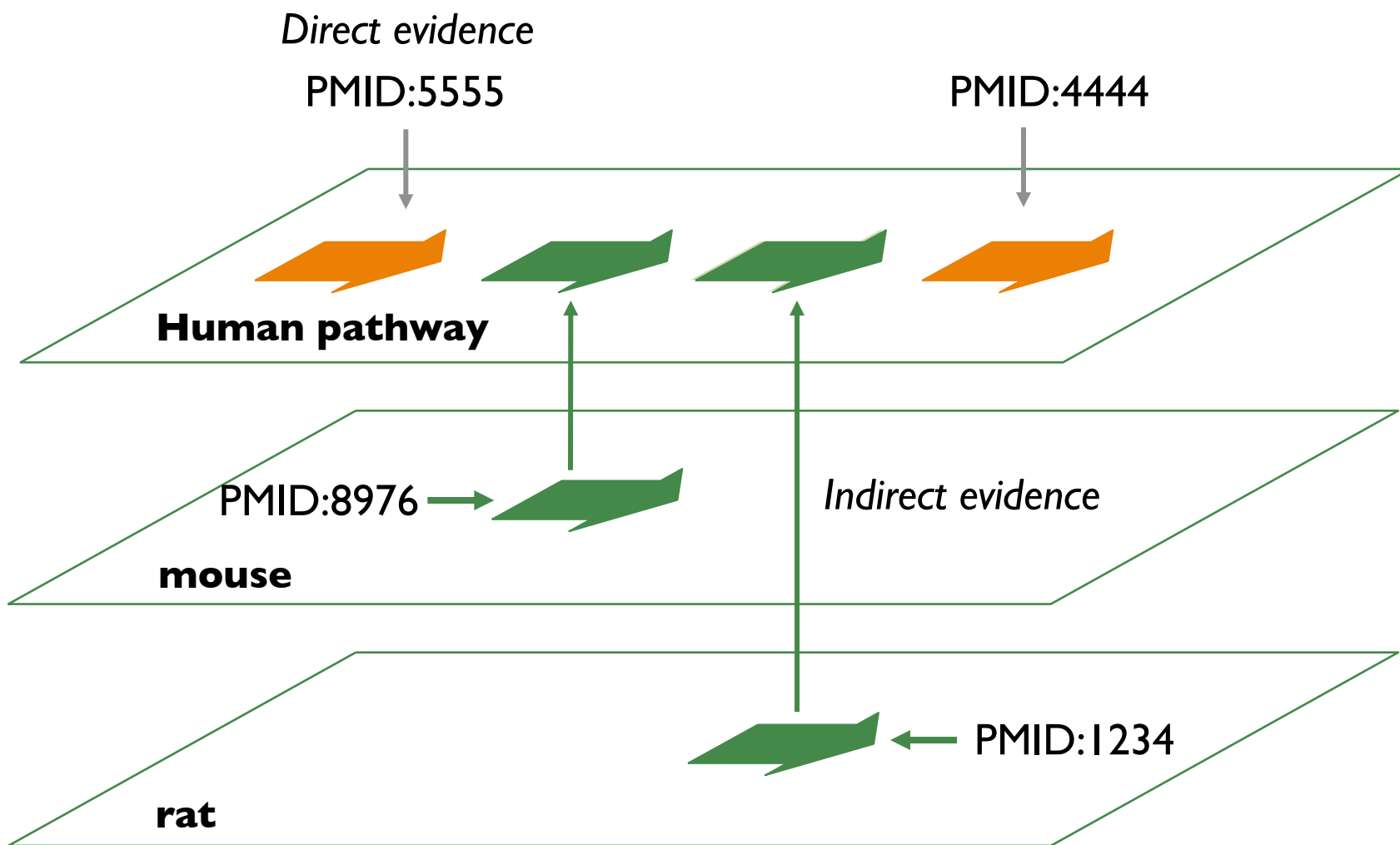
Table of Contents and Editorial Calendar

Topic	Authors	Released	Revised	Reviewers	Editors
Apoptosis [Homo sapiens] <ul style="list-style-type: none"> - Extrinsic Pathway for Apoptosis (DOI) - Intrinsic Pathway for Apoptosis (DOI) - Apoptotic execution phase - Regulation of Apoptosis 	Alnemri, E, Hengartner, M, Tschopp, J, Tsujimoto, Y, Hardwick, JM, Gillespie, ME, Matthews, L, Matthews, L, Jakobi, R, Gopinathrao, G, Schulze-Osthoff, K, Garapati, P V, Ranganathan, S, Williams, MG	2004-09-20		Hengartner, M, Ranganathan, S, Vaux, DL, Chang, E, Widlak, P, Cooper, HM, Silverman, N, Lemaire, B	Gopinathrao, G, Matthews, L, Gillespie, ME, Joshi-Tope, G, Matthews, L, Garapati, P V
Cell Cycle [Homo sapiens] <ul style="list-style-type: none"> - Cell Cycle Checkpoints - Cell Cycle, Mitotic - Chromosome Maintenance 	Hoffmann, I, Khanna, KK, O'Connell, M, Walworth, N, Yen, TJ, Bosco, G, Matthews, L, Orlic-Milacic, M, Gillespie, ME, Yen, T, Blackburn, EH, Seidel, J, D'Eustachio, P, May, B, Borowiec, JA, Pagano, M, Lorca, T, Castro, A, Matthews, L, Gopinathrao, G, Tom, S, Bambara, RA, Lee, KS, Davey, MJ, O'Donnell, M, Tye, BK, Sanchez, Y, Joshi-Tope, G, Watanabe, N, Hunter, T	2011-12-06		Sanchez, Y, Knudsen, E, Hardwick, KG, Manfredi, J, MacPherson, D, Grana, X, Price, C, Bolcun-Filas, E,	Matthews, L, Matthews, L, Gopinathrao, G, Joshi-Tope, G, May, B, D'Eustachio, P, Gillespie,
Cell-Cell communication [Homo sapiens] <ul style="list-style-type: none"> - Cell junction organization (DOI) - Signal regulatory protein (SIRP) family interactions (DOI) - DSCAM interactions - Nephrin interactions (DOI) 	Garapati, P V, de Bono, B, Matthews, L	2011-09-20			
Circadian Clock [Homo sapiens] (DOI) <ul style="list-style-type: none"> - BMAL1:CLOCK/NPAS2 Activates Circadian Expression - Circadian Repression of Expression by REV-ERBA - RORA Activates Circadian Expression 	May, B	2010-12-14 UPDATED			

Next Release - Ver 41 : June 2012 Reactome

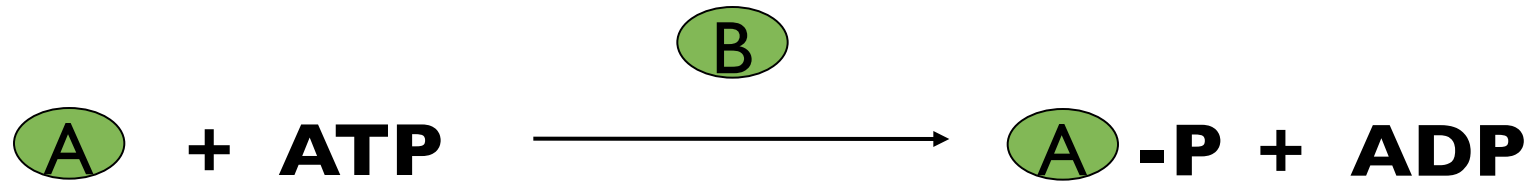
Curator	Pathway Topic	Author	Reviewer
Bijay Jassal	Activation of arylsulfatases	B Jassal	R Stephan
Steve Jupe	Chromatin modifying enzymes	TBA	TBA
Phani Garapati	DAP12 and C-type Lectins in phagocytosis	P Garapati	TBA
Phani Garapati	FCGR mediated phagocytosis	P Garapati	TBA
Marc Gillespie	Fertilization	M Gillespie	TBA
Karen Rothfels	FGFR in disease	S Ezzat	TBA
Bruce May	GLUT4 Translocation	B May	A Klip
M Williams	Glycerophospholipid Biosynthesis Pathway	M Williams	TBA
Bijay Jassal	Glycosaminoglycan metabolism	B Jassal	TBA
Bruce May	Hydration of Carbon Dioxide	B May	TBA
Bijay Jassal	Latent infection of Homo sapiens with Mycobacterium tuberculosis	R Stephan	TBA
Bruce May	Metabolism of Angiotensinogen to Angiotensin	B May	TBA
Mark Williams	Metabolism of Arachidonic acid	M Williams	TBA
Phani Garapati	Metabolism Linoleic acid and alpha-linolenic acid	P Garapati	G Burdge
Mark Williams	Metabolism of phosphatidylinositol	M Williams	TBA
Mark Williams	Metabolism of inositol phosphate	M Williams	TBA
Phani Garapati	MHC Class II mediated antigen processing & presentation	P Garapati	TBA
Bruce May	Mitochondrial biogenesis	B May	TBA
Bruce May	Mitochondrial iron-sulfur cluster biogenesis	B May	TBA
Bruce May	O2/CO2 exchange	B May	TBA
Bijay Jassal	Post translational modifications	B Jassal	TBA
Bruce May	Regulation of cholesterol by SREBP's	B May	TBA
Bruce May	Regulation of hypoxia-inducible factor by oxygen	B May	TBA
Marija Milacic	Signaling by TGF beta (update)	TBA	TBA
Mark Williams	Ubiquinol Biosynthesis	M Williams	TBA

Evidence Tracking – Inferred Reactions

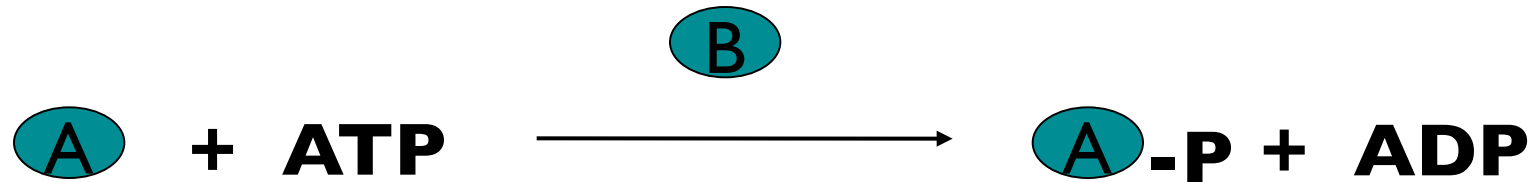


Data Expansion – Projecting to Other Species

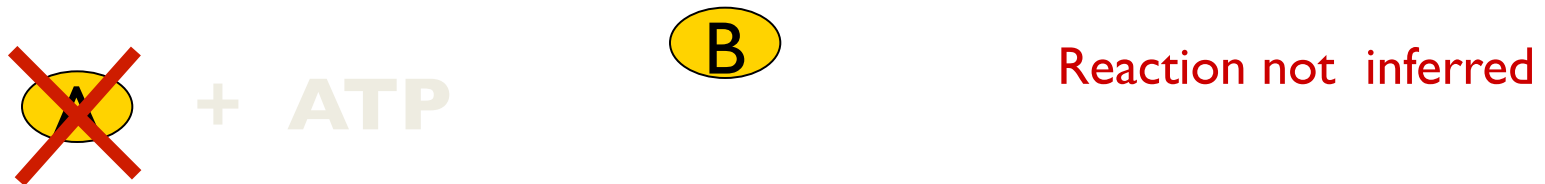
Human



Mouse

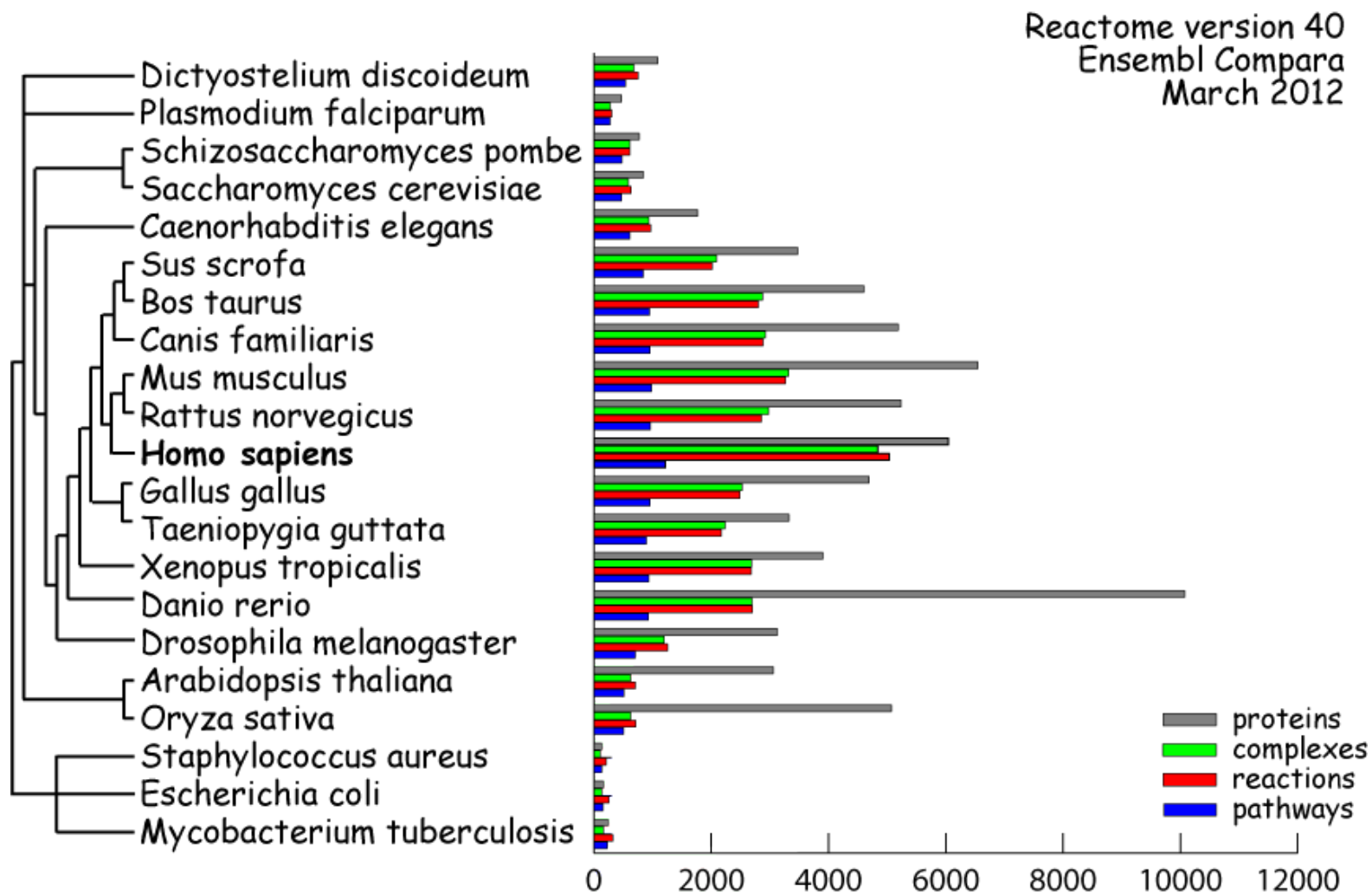


Drosophila



No ortholog –
Protein not inferred

Data Expansion – Projecting to Other Species



Focus on disease areas



- Infectious Proteins: An infection introduces new proteins into the cell
- Cancer mutants: Precisely annotate protein sequence changes
- Gain/loss of function: Show how cancer mutations affect protein function
- Anti-cancer therapeutics: Visualize mode of action of anti-cancer drugs
- Pathology: List different cancer types in which a mutant protein has been identified

Link-outs from Reactome

- Gene Ontology - Molecular Function, Cellular Component, Biological process
- Small molecules - KEGG Compound, ChEBI, PubChem Compound
- Proteins - UniProt
- Genes and Genomes - Ensembl, Entrez Gene, dbSNP , KEGG Gene, RefSeq, HapMap, UCSC
- Disease - COSMIC, Disease Ontology
- Literature evidence - PubMed
- Structural Biology - PDB, DockBlaster
- Toxicology - Comparative Toxicogenomics Database
- Other - BioGPS

Data Warehouses integration and other exports

NCBI BioSystems

Search: BioSystems for [Go] [Clear]

UID:bsid106337 Related BioSystems, Literature, Sequences, Small Molecules, Other Links

Signaling by EGFR
 Type : organism-specific biosystem
 Description : The epidermal growth factor receptor (EGFR) is one member of the ErbB family of transmembrane glycoprotein tyrosine receptor kinases (RTK). Binding of EGFR to its ligands leads to autophosphorylation of tyrosine residues on the receptor and subsequent activation of signal transduction pathways that are involved in regulating cellular proliferation, differentiation, and survival. Ligand binding with EGFR results in receptor homo- or heterodimerization at the cell surface. Trans-autophosphorylation of the EGFR tyrosine kinase domains occurs and the phosphorylated tyrosine kinase residues serve as [more...](#)
 Organism: [Homo sapiens](#)
 Source : [REACTOME \[REACT_9417\]](#)

Diagram not available

Genes Proteins Small Molecules Related BioSystems Citations Comments

Gene ID	Gene Symbol	External ID	Name
<input type="checkbox"/> 8874	ARHGEF7	144164	Rho guanine nucleotide exchange factor (GEF) 7
<input type="checkbox"/> 1173	AP2M1	49286	adaptor-related protein complex 2, mu 1 subunit
<input type="checkbox"/> 30011	SH3KBP1	101547	SH3-domain kinase binding protein 1
<input type="checkbox"/> 10254	STAM2	182922	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2
<input type="checkbox"/> 7314	UBB	104245	ubiquitin B
<input type="checkbox"/> 6233	RPS27A	104245	ribosomal protein S27a
<input type="checkbox"/> 728590	RPS27AP11	104245	ribosomal protein S27a pseudogene 11
<input type="checkbox"/> 732088		104245	
<input type="checkbox"/> 7316	UBC	104245	ubiquitin C
<input type="checkbox"/> 7311	UBA52	104245	ubiquitin A-52 residue ribosomal protein fusion product 1

Page 1 of 6

EMBL-EBI EB-eye Search All Databases egfr signaling [Go]

Databases Tools EBI Groups Training Industry About Us Help

Search for **egfr signaling** in **Reactome**

Goto other results for this search in: All the EBI - Reactions & Pathways

4 results found in Reactome

REACT_9417.3
 Signaling by EGFR
 The epidermal growth factor receptor (EGFR) is one member of the ErbB family of transmembrane glycoprotein tyrosine receptor kinases (RTK). Binding of EGFR to its ligands leads to autophosphorylation of tyrosine residues on the receptor and subsequent activation of signal transduction pathways that are involved in regulating cellular proliferation, differentiation, and survival. Ligand binding with EGFR results in receptor homo- or heterodimerization at the cell surface. Trans-autophosphorylation of the EGFR tyrosine kinase domains occurs and the phosphorylated tyrosine kinase residues serve as binding sites for the recruitment of signal transducers and activators of intracellular substrates, such as Ras, which then stimulate an intracellular signal transduction cascade.
 References: [UniProtKB](#) [GO](#) [ChEBI](#) [Taxonomy](#)

Pathway Commons Search and visualize public biological pathway information. Single point of access. [more...]

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Search Pathway Commons:
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 Search

For example, if you enter: **BRCA1**, you will get back the list of pathways containing the keyword "BRCA1", and the list of pathways that contain the BRCA1 gene.

Current filter settings: All Organisms, All Data Sources. [Set filters.](#)

Using Pathway Commons:
Biologists: Browse and search pathways across multiple valuable public pathway databases.
Computational biologists: Download an integrated set of pathways in BioPAX format for global analysis.
Software developers: Build software on top of Pathway Commons using our [web service API](#). Download and install the [cPath software](#) to create a local mirror.

Current Data Sources:
 Pathway Commons currently contains the following data sources ([batch download](#)):

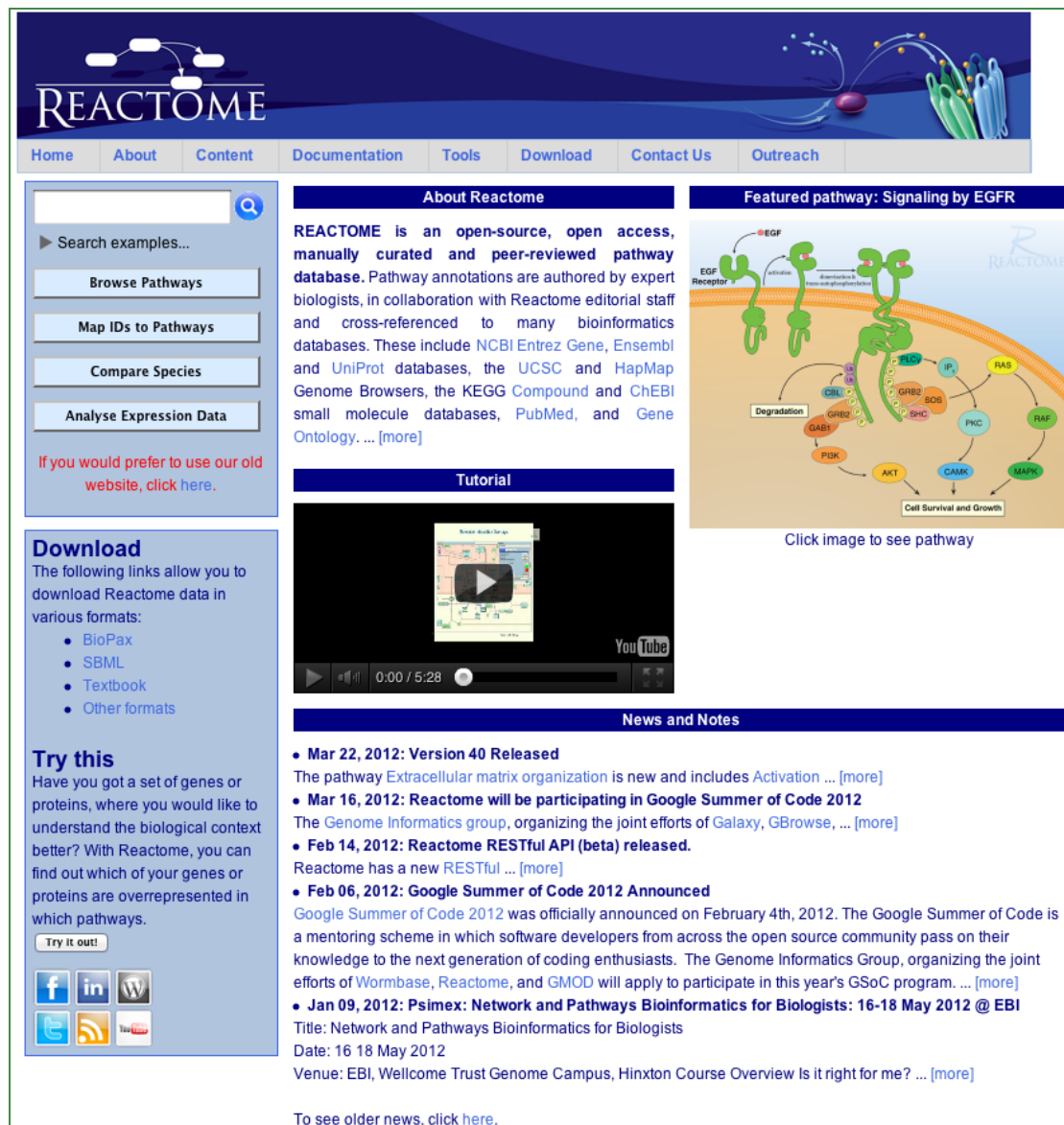
What's New:
 • **NEW!** September 7, 2010:
 ◦ BioGRID data set (July 31, 2010 Version 30.0.67).
 ◦ HPRD data set (April 13, 2010 Version 9).
 ◦ HumanCyc data set (June 16, 2010 Version 14.1).
 ◦ IntAct data set (August 8, 2010 Version 3.1, r14760).
 ◦ MINT data set (July 28, 2010).
 ◦ NCI/Nature Pathway Interaction Database (August 10, 2010).
 ◦ Reactome data set (June 18, 2010 Version 33).
 • October 15, 2009:
 ◦ Improved search functionality.

Other Data Exports

- Gene Ontology, Protein Ontology
- HapMap and UCSC Genome Browsers
- GSEA
- WikiPathways, Wormbase


Reactome Home Page

www.reactome.org



The screenshot shows the Reactome website interface. At the top is the Reactome logo and a navigation menu with links: Home, About, Content, Documentation, Tools, Download, Contact Us, and Outreach. Below the menu is a search bar with a magnifying glass icon and a search button. To the right of the search bar are several utility buttons: "Browse Pathways", "Map IDs to Pathways", "Compare Species", and "Analyse Expression Data". Below these buttons is a red text link: "If you would prefer to use our old website, click here." The main content area is divided into three columns. The left column has a "Download" section with the text "The following links allow you to download Reactome data in various formats:" followed by a bulleted list: "BioPax", "SBML", "Textbook", and "Other formats". Below this is a "Try this" section with the text "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." and a "Try it out!" button. Below the text are social media icons for Facebook, LinkedIn, and Wikipedia, and a row of icons for Twitter, RSS, and YouTube. The middle column has an "About Reactome" section with a blue header and text describing Reactome as an open-source, open access, manually curated and peer-reviewed pathway database. Below this is a "Tutorial" section with a blue header and a video player showing a thumbnail of a pathway diagram. The right column has a "Featured pathway: Signaling by EGFR" section with a blue header and a detailed diagram of the EGFR signaling pathway. Below the diagram is a caption: "Click image to see pathway". At the bottom of the page is a "News and Notes" section with a blue header and a list of news items, including "Mar 22, 2012: Version 40 Released", "Mar 16, 2012: Reactome will be participating in Google Summer of Code 2012", "Feb 14, 2012: Reactome RESTful API (beta) released.", "Feb 06, 2012: Google Summer of Code 2012 Announced", and "Jan 09, 2012: Psimex: Network and Pathways Bioinformatics for Biologists: 16-18 May 2012 @ EBI". At the very bottom of the page is a link: "To see older news, click here."

Basic Search



Search for: in

All 6 results

Pathways (2) Reactions (2) Proteins (1) Others (1)

Protein: UniProt:P60174 **TPI1** (Homo sapiens)
Last changed: 2010-04-23 01:23:29


Pathway: Gluconeogenesis (Homo sapiens)
The reactions of gluconeogenesis convert mitochondrial pyruvate to cytosolic glucose 6-phosphate which in turn can be hydrolyzed to glucose and exported from the cell. Gluconeogenesis is confined to cells of the liver and kidney and enables glucose synthesis from molecules such as lactate and alanine and other amino acids when exogenous glucose is not available. The process of gluconeogenesis as diagrammed in the following pathway.
Last changed: 2010-04-16 06:02:43

Pathway: Glycolysis (Homo sapiens)
The reactions of glycolysis convert glucose 6-phosphate to pyruvate. The entire process is cytosolic. Glucose 6-phosphate is reversibly isomerized to form fructose 6-phosphate. Phosphofructokinase 1 catalyzes the physiologically irreversible phosphorylation of fructose 6-phosphate to form fructose 1,6-bisphosphate. In six reversible reactions, fructose 1,6-bisphosphate is converted to two molecules of dihydroxyacetone phosphate.
Last changed: 2010-04-16 06:02:43


Reaction: dihydroxyacetone phosphate \rightleftharpoons D-glyceraldehyde 3-phosphate (Homo sapiens)
Cytosolic triose phosphate isomerase catalyzes the freely reversible interconversion of dihydroxyacetone phosphate and glyceraldehyde 3-phosphate (Lu et al. 1984). The active form of the enzyme is a homodimer (Kinoshita et al. 2005).
Last changed: 2010-04-16 06:02:43

Reaction: D-glyceraldehyde 3-phosphate \rightleftharpoons dihydroxyacetone phosphate (Homo sapiens)
The reversible conversion of glyceraldehyde-3-phosphate to dihydroxyacetone phosphate is catalyzed by cytosolic triose phosphate isomerase (Watanabe et al. 1996; Lu et al. 1984).
Last changed: 2010-04-16 06:02:43

Complex: triosephosphate isomerase dimer [cytosol] (Homo sapiens)
triosephosphate isomerase dimer
Last changed: 2009-12-16 23:26:50



OICR
Ontario Institute
for Cancer Research

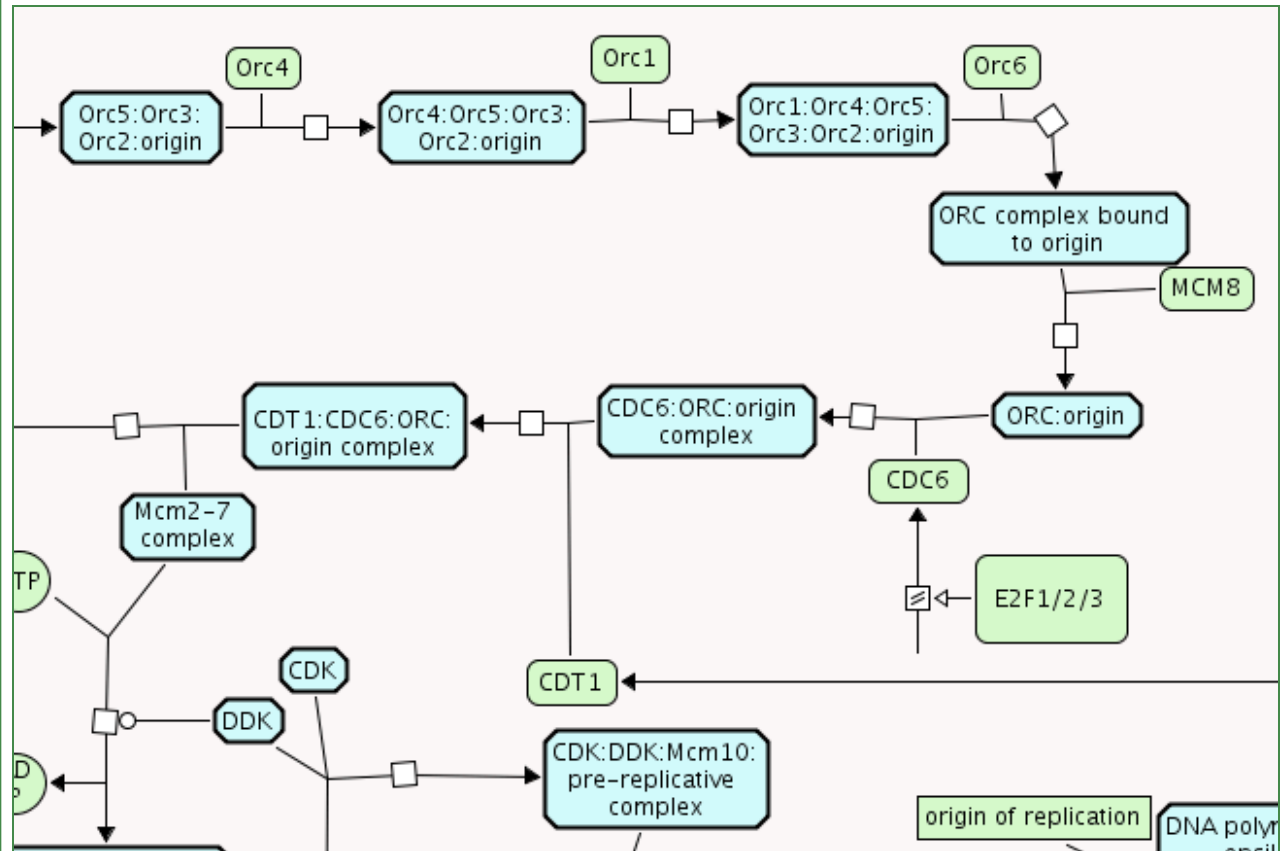


REACTOME

Divide reaction space into ~160 canonical pathways

- DNA Replication
- + Mitotic M-M/G1 phases
- + Synthesis of DNA
- + Regulation of DNA replication
- + UPDATED Gene Expression
- + Hemostasis
- + HIV Infection
- + UPDATED Immune System
- + Influenza Infection
- + Integration of energy metabolism
- + Integrin cell surface interactions
- + Interactions of the immunoglobulin su
- + Meiotic Recombination
- + Membrane Trafficking
- + UPDATED Metabolism of amino acids
- + Metabolism of carbohydrates
- + NEW Metabolism of hormones
- + Metabolism of lipids and lipoproteins
- + Metabolism of nitric oxide
- + Metabolism of nucleotides
- + Metabolism of porphyrins
- + Metabolism of proteins
- + UPDATED Metabolism of RNA

Each represented by an SBGN-like diagram



Browsing EGFR Signaling Pathway

Switch Species: Homo sapiens

Pathways Help

- Signaling by EGFR in Cancer
 - Signaling by EGFR
 - Signaling by constitutively active EGFR
 - Binding of ligand-responsive EGFR mutants to chaperoning
 - Binding of EGF to ligand-responsive EGFR mutants
 - EGF-induced dimerization of ligand-responsive EGFR mutant
 - Spontaneous dimerization of ligand-responsive EGFR mutant
 - Trans-autophosphorylation of activated ligand-responsive EGFR
 - EGFRvIII mutant binds chaperone proteins HSP90 and CDC37
 - Ligand-independent dimerization of EGFRvIII mutant
 - Trans-autophosphorylation of EGFRvIII mutant dimers
 - Binding of GRB2:SOS1 complex to phosphorylated EGFR mutants
 - SOS-mediated nucleotide exchange of RAS (mediated by GRB2)
 - Binding of SHC1 to p-EGFR mutants
 - Phosphorylation of SHC1 by p-EGFR mutants
 - Phosphorylated SHC1 in complex with p-EGFR mutants recruits RAS
 - SOS-mediated nucleotide exchange of RAS (mediated by SHC1)

Signaling by constitutively active EGFR

Stable Identifier	REACT_115852.2
Authored	Orlic-Milacic, M, 2011-11-04
Reviewed	Greulich, H, 2011-11-15 Savas, S, 2011-11-15

Signaling by EGFR is frequently activated in cancer through either genomic amplification of the EGFR locus, resulting in over-expression of the wild-type protein, or through activating mutations in the coding sequence of the EGFR gene, resulting in expression of a constitutively active mutant protein.

Epidermal growth factor receptor kinase domain mutants are present in ~16% of non-small-cell lung cancers (NSCLCs), but are also found in other cancer types, such as breast cancer, colorectal cancer, ovarian cancer and thyroid cancer. EGFR kinase domain mutants harbor activating mutations in exons 18-21 which code for the kinase domain (amino acids 712-979). Small deletions, insertions or substitutions of amino acids within the kinase domain lock EGFR in its active conformation in which the enzyme can dimerize and undergo autophosphorylation spontaneously, without ligand binding (although ligand binding ability is preserved), and activate downstream signaling pathways that promote cell survival (Greulich et al. 2005, Zhang et al. 2006, Yun et al. 2007, Red Brewer et al. 2009).

Pathway Analysis – ID Mapping & Overrepresentation

Pathway Assignment

For each of your identifiers, this table provides the pathways in which it takes part. Note that the column sort operation will be very slow if you have more than 1000 identifiers, and no "busy" cursor will appear to let you know that sorting is in progress.

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:

ID ▼▲	UniProt ID ▼▲	Species ▼▲	Pathway names ▼▲
O00139	O00139	Homo sapiens	Factors involved in megakaryocyte development and platelet production; Kinesins; Mitotic M-M/G1 phases
O00186	O00186	Homo sapiens	Response to elevated platelet cytosolic Ca2+
O00187	O00187	Homo sapiens	Complement cascade
O00204	O00204	Homo sapiens	Phase II conjugation
O00217	O00217	Homo sapiens	Respiratory electron uncoupling proteins
O00231	O00231	Homo sapiens	APC/C-mediated degradation of cyclins; Metabolism of amino acids and derivatives; Mitotic M-M/G1 phases; Wnt signaling pathway; Synthesis of DNA; Synthesis of RNA
O00232	O00232	Homo sapiens	APC/C-mediated degradation of cyclins; Metabolism of amino acids and derivatives; Mitotic M-M/G1 phases; Wnt signaling pathway; Synthesis of DNA; Synthesis of RNA

Statistically over-represented events in hierarchy

Each Event is coloured according to the **un-adjusted**, i.e. **not corrected for multiple testing**, probability (from **hypergeometric test**) of seeing given number or more genes in this Event by chance. Please note that only those "child" events are shown which have a p-value lower than the "parent" event. The top-level (root) Events are ordered according to the lowest p-value of their components.

Colour key for probabilities:

1e+00 3e-01 1e-01 3e-02 1e-02 3e-03 1e-03 3e-04 1e-04 3e-05 1e-05 3e-06 1e-06 3e-07 1e-07 3e-08 1e-08 3e-09 1e-09 3e-10 >

|

- Gene Expression** 5.1e-29, 174/413
- Cell Cycle, Mitotic** 6.8e-26, 135/299
- DNA Replication** 1.1e-19, 90/187
- Signalling by NGF** 4.9e-18, 95/212
- Transcription** 4.5e-19, 74/141
- Apoptosis** 6.1e-18, 71/137
- DNA Repair** 2.8e-16, 58/106
- Cell Cycle Checkpoints** 6.8e-17, 62/115
- Metabolism of carbohydrates** 1.2e-16, 62/116
- Integrin cell surface interactions** 6.3e-16, 50/85
- miRNA Processing** 6.7e-15, 66/136
- HIV infection** 3.4e-03, 102/414
- Hemostasis** 3.8e-05, 115/426
- Chromosome Maintenance** 5.8e-06, 25/54
- Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins** 6.7e-11, 46/94
- Metabolism of amino acids and derivatives** 3.0e-10, 76/200
- Cdc20:Phospho-APC/C mediated degradation of Cyclin A** 1.4e-09, 35/67

Species Comparison

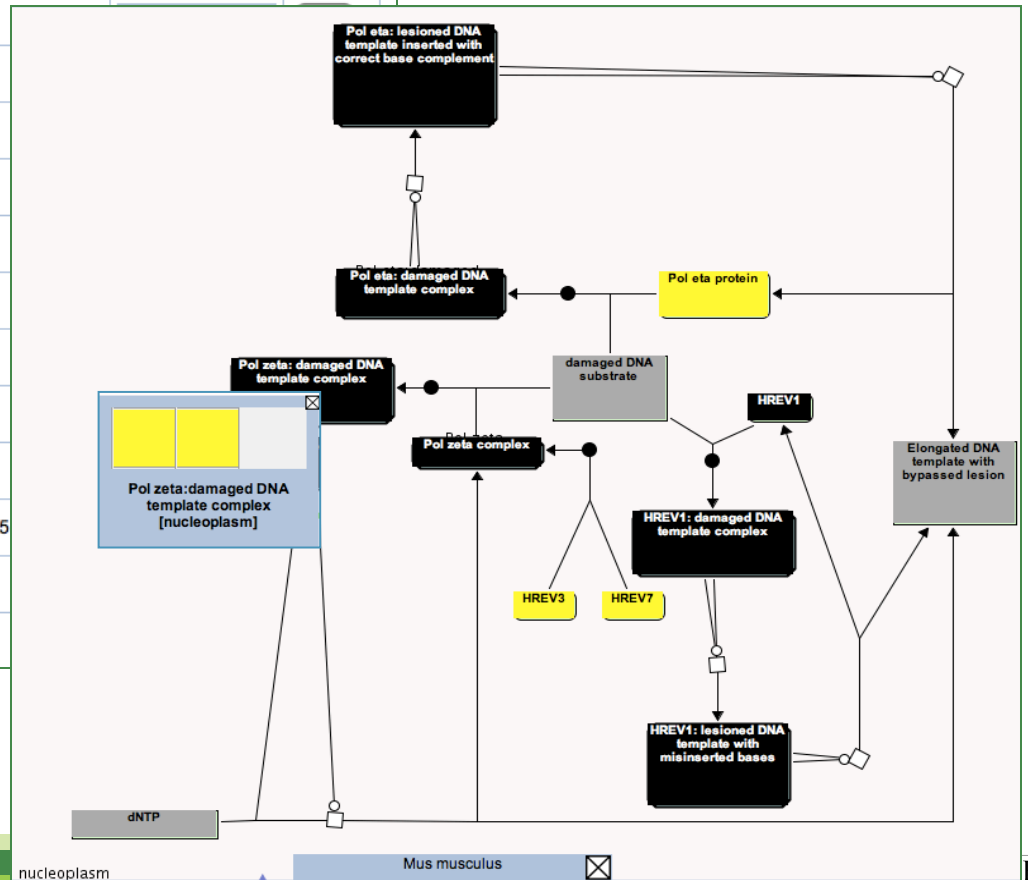
Species Comparison

This tool allows you to compare pathways between human and any of the other species inferred from Reactome by orthology. [More...](#)

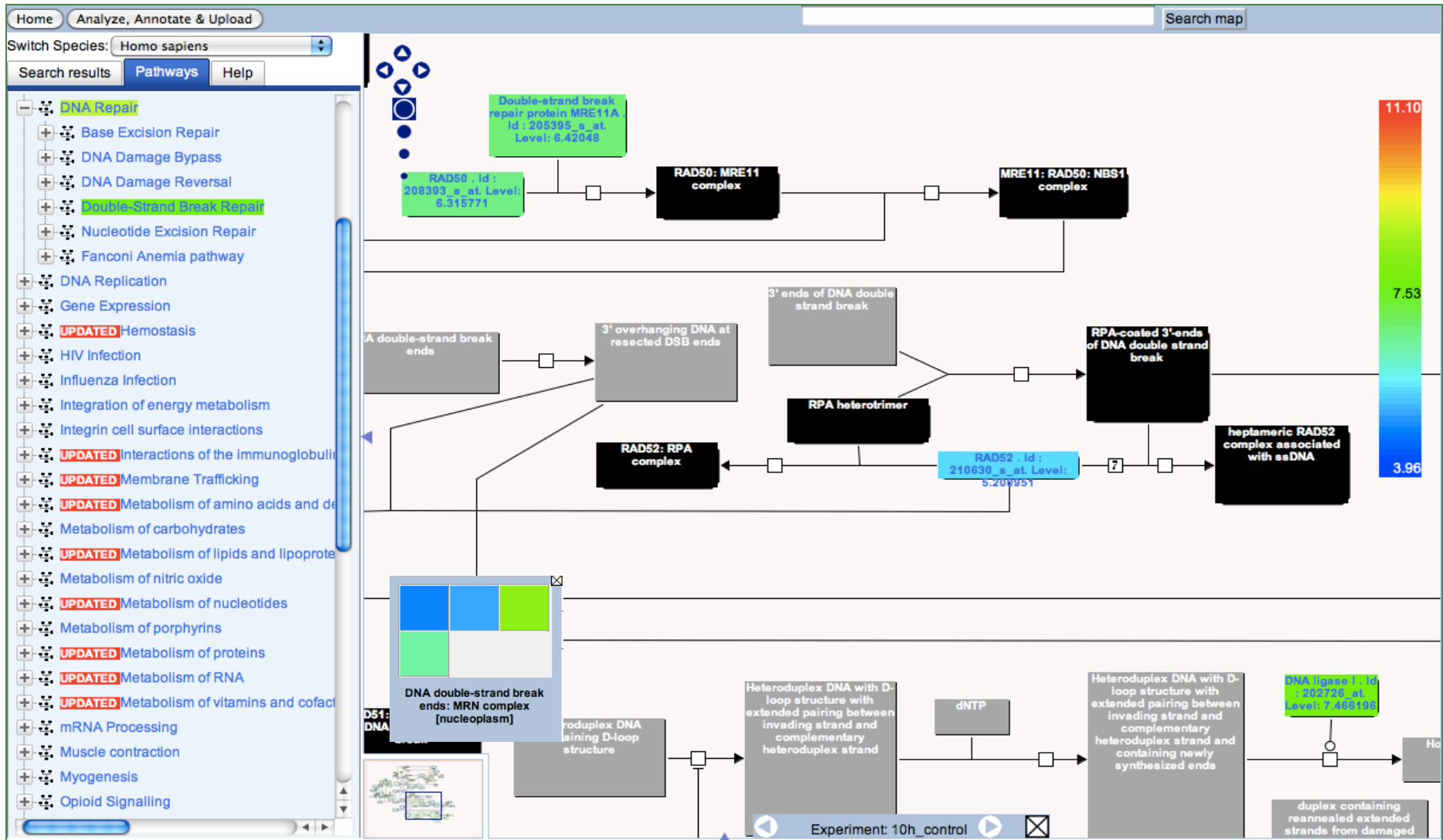
WARNING: if you navigate away from this page, you will lose the displayed data. Use the download facility to secure it.

Select format to download this table:

Pathway name ▼▲	Other species ▼▲	Proteins, human ▼▲	Proteins, other species ▼▲	% in other species ▼▲	Click button to view pathway
ABC-family proteins mediated transport	Mus musculus	15	15	100%	<input type="button" value="View"/>
Advanced glycosylation endproduct receptor signaling	Mus musculus	13	6		
APC/C-mediated degradation of cell cycle proteins	Mus musculus	79	74		
Apoptotic execution phase	Mus musculus	48	46		
Aquaporin-mediated transport	Mus musculus	30	21		
Asparagine N-linked glycosylation	Mus musculus	85	23		
Base Excision Repair	Mus musculus	19	19		
Bile acid and bile salt metabolism	Mus musculus	27	27		
Binding of RNA by Insulin-like Growth Factor-2 mRNA Binding Proteins (IGF2BPs/IMPs/VICKZs)	Mus musculus	3	3		
Botulinum neurotoxicity	Mus musculus	10	4		
Cell Cycle Checkpoints	Mus musculus	120	115		
Cell junction organization	Mus musculus	82	66		
Cell surface interactions at the vascular wall	Mus musculus	93	88		



Expression Analysis



Reactome data is open access and open source

The whole content of the Reactome can be downloaded as:

- [MySQL database dump](#) (To use skypainter you also need [this database](#))

Several narrower datasets and download formats are also available:

- [Human protein-protein interaction pairs in tab-delimited format.](#)
- [Full list of protein-protein interactions, including non-human species.](#)
- [Human protein-protein interaction pairs in PSI-MITAB format.](#)
- [Uniprot to pathways plus stable id mappings](#)
- [Uniprot to pathways mappings](#)
- [Curated and inferred Uniprot to pathways mappings](#)
- [Gene association file \(GO annotation in Reactome\)](#)
- [Human reactions in SBML \(level 2, version 3\) format.](#)
- [Events in the BioPAX level 2 format](#)
- [Events in the BioPAX level 3 format](#)
- [Reactome Pathways Gene Set](#)
- [Protégé 2.0 ontology for Reactome data model: pins file, pont file, pprj file](#)
- [Human pathway diagrams: PDF, or PNG](#)

The complete Reactome textbook of biological pathways and processes can be downloaded in:

- [PDF format \(ZIP archive\).](#)
- [RTF format \(ZIP archive, split into files on a per-chapter basis\).](#)

The Reactome website can be installed locally:

- [Instructions for local installation of Reactome database and website.](#)
- [Download Reactome website contents and perl code](#) (requires additional n...)

Two **Java tools** are available for Reactome data entry. The **Author tool** is designed for biologists to input data into Reactome, while the **Curator tool** is meant for use by curators to annotate biological pathways based on the Reactome schema. N.B. these tools will only work with a database using our internal database format, the database available from this web page will **not** work with them. Click on the help link at the top of this page to request a copy of our internal database.

- [Curator Tool \(version 3.1, build 66, January 24, 2012\)](#)
- [Author Tool Version 4.0 in Java Web Start](#)
- [Author Tool Version 4.0 in Java Applet](#)
- [Author Tool \(version 2.1, build 25, for some old projects\)](#)

A list of **functional interactions (FIs)** can be downloaded in three formats. For details about FIs, please see [Wu G, Feng X, Stein L.](#)

- [MySQL database dump](#)
- [Tab delimited text files](#)
- [PSI-MITAB format](#)

A **SOAP** based Web Services API is available to access the Reactome data. For details about this API, please follow the following links:

- [Simple Description for the Reactome Web Services API](#)
- [Training Materials for the Reactome Web Services API](#)
 - [Reactome SOAP WS User's Guide in PDF \(1M\)](#)
 - [Reactome SOAP WS Tutorial in Power Point Slides \(2M\)](#)
 - [Reactome SOAP WS Tutorial in Flash Movie \(640 x 480\) \(11M\)](#)
 - [Reactome SOAP WS Tutorial in Flash Movie \(800 x 600\) \(12M\)](#)
- [XML Schema for the data model](#)
- [WSDL file for the Reactome Web Services API](#)

A **RESTful API (beta)** is available too to access the Reactome data. For details about this API, please see this document: [Reactome RESTful API](#)

Programmatic Access

- Application programming interfaces (API) are important to connect and automate data exchange between local programs and databases.
 - BioMart API
 - MySQL/Perl API
 - MySQL/Java API
 - SOAP/WSDL
 - RESTful API (beta)

Continuing Priorities.....

- Expand curated pathway content
 - Model organism
 - Disease, e.g. cancer, cardiovascular, infectious, etc.
 - Work with the community for improved ontology/link out support
 - GO, PRO, MGI, RGD, DO, etc.
- Develop new visualization and analysis tools
 - HTML5 canvas based pathway browser
 - Bioconductor and Galaxy pipelines for Pathway analysis
 - Pathway tracks for Genome Browsers
 - Mobile-friendly Reactome
 - Reactome in the Cloud

Summary

- Pathway databases are an integral part of the scientific community.
- Reactome is a highly reliable, human-curated database of biological pathways and reactions.
- Deployed a user-friendly web site and tools that promotes integrated research on pathways and networks.
 - Data visualization
 - Data analysis
 - Data expansion
 - Data integration
 - Data standards
 - Data exports
- Develop and distribute open software and standard operating procedures for the management of pathway information.

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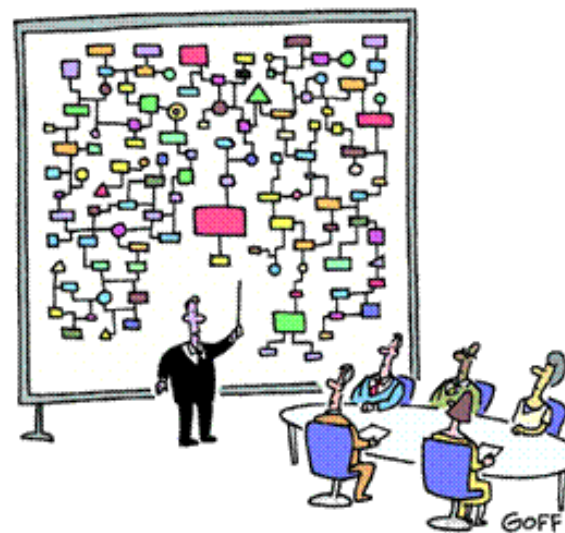


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"And that's why we need a computer."



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REACTOME