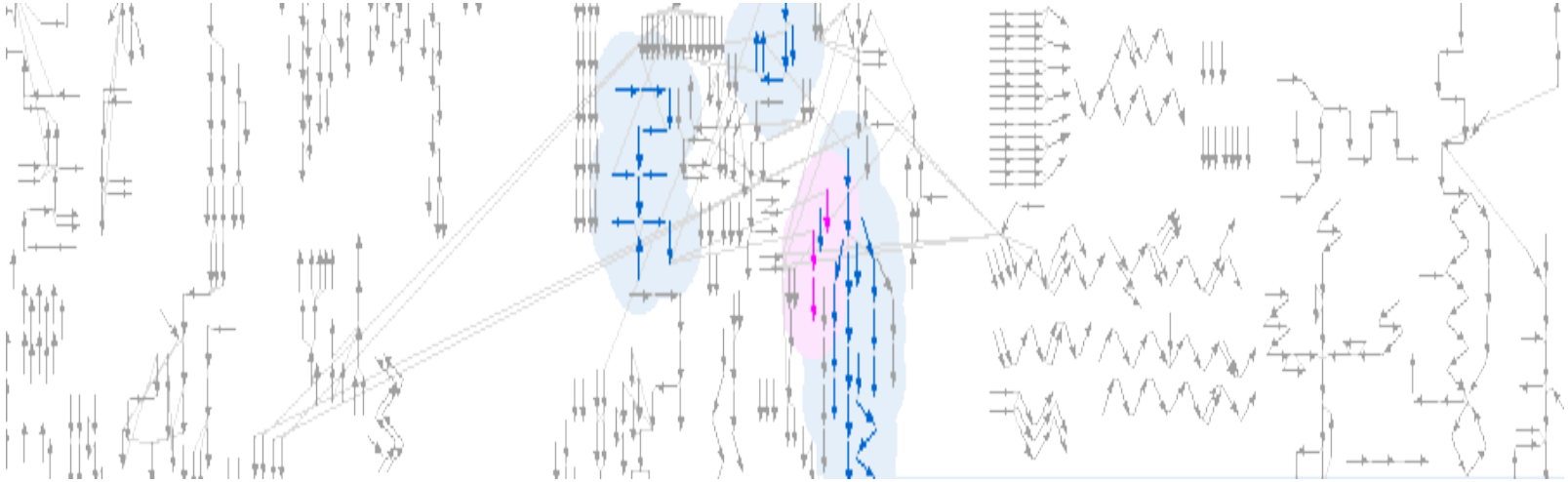
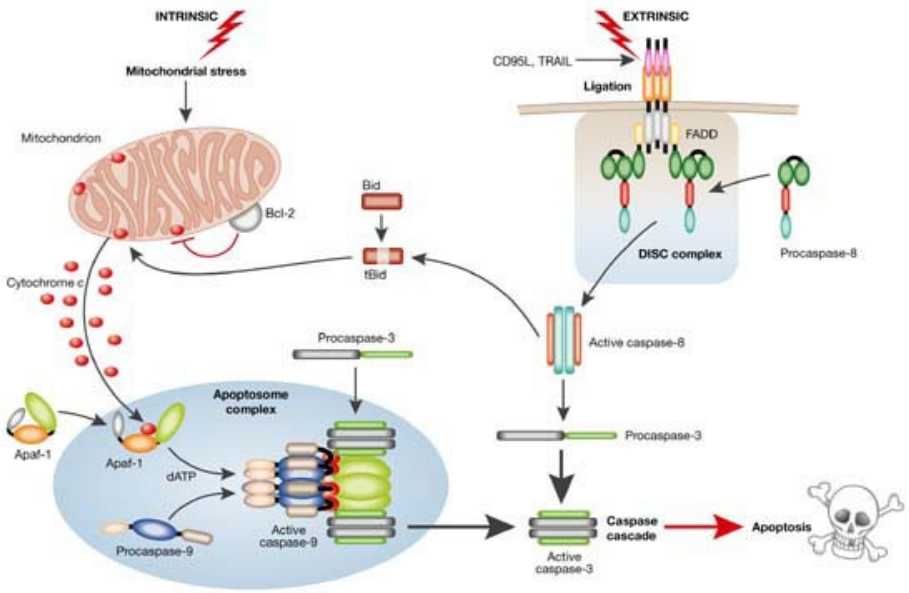
REACTOME



Nayibe L. Buitrago
Jorge Cortázar

REACTOME

www.reactome.org

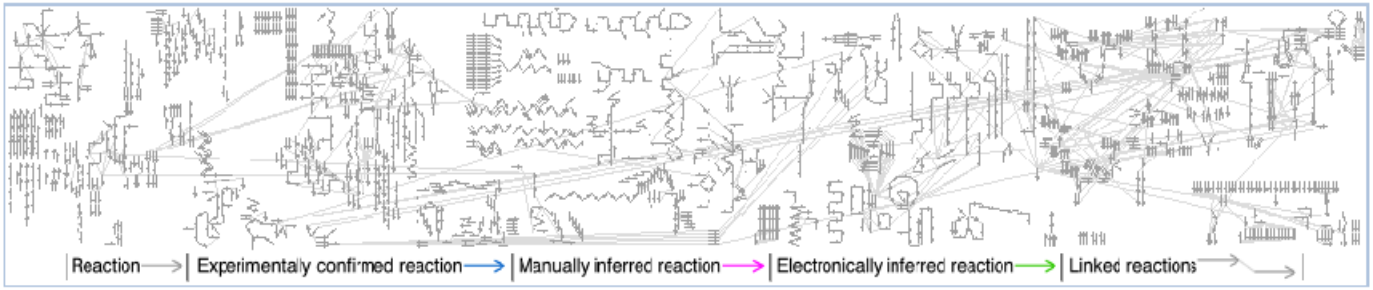


Apoptosis and disease: a life or death decision.
EMBO Rep. 2004 Jul;5(7):674-8. Epub 2004 Jun 25.

Cold Spring Harbor Laboratory
The European Bioinformatics Institute
The Gene Ontology Consortium

Reactome - a curated knowledgebase of biological pathways

The data displayed is for Homo sapiens. Use the menu to change the species. Check for cross species comparison.



Apoptosis	Cell Cycle Checkpoints	Cell Cycle, Mitotic	DNA Repair
DNA Replication	Electron Transport Chain	Epidermal Growth Factor Receptor (EGFR) signaling	Fibroblast Growth Factor Receptor (FGFR) signaling
Gap junction trafficking and regulation	Gene Expression	HIV Infection	Hemostasis
Immune System signaling	Influenza Infection	Insulin receptor mediated signaling	Integration of pathways involved in energy metabolism
Maintenance of Telomeres	Metabolism of amino acids and related nitrogen-containing molecules	Metabolism of carbohydrates	Metabolism of lipids and lipoproteins
Metabolism of nucleotides	Metabolism of porphyrins	Notch Signaling Pathway	Oxidative decarboxylation of pyruvate and TCA cycle
Post-translational modification of proteins	Transforming Growth Factor (TGF) beta signaling	Transcription	Translation
mRNA Processing	Xenobiotic metabolism		

About Reactome

The **Reactome** project is a collaboration among Cold Spring Harbor Laboratory, The European Bioinformatics Institute, and The Gene Ontology Consortium to develop a curated resource of core pathways and reactions in human biology. The information in this database is authored by biological researchers with expertise in their fields, maintained by the Reactome editorial staff, and cross-referenced with the sequence databases at NCBI, Ensembl and UniProt, the UCSC Genome Browser, HapMap, KEGG (Gene and Compound), ChEBI, PubMed and GO. In addition to curated human events inferred orthologous events in 22 non-human species including mouse, rat, chicken, zebra fish, worm, fly, yeast, two plants and E.coli are also available.

Reactome is a free on-line resource, and Reactome software is open-source. However, please take note of our disclaimer.

More...

News and Notes

- **February 28, 2007: Version 20 Released**
  New topics released in Version 20 are Fibroblast Growth Factor Receptor (FGFR) signaling, Epidermal Growth Factor Receptor (EGFR) signaling under **signaling pathways**, Gap junction trafficking under **cell biology**, and Porphyrin metabolism, Digestion of dietary carbohydrate and lipid under **metabolic pathways**. Additional events for HIV REV protein interactions, and **Influenza** virus RNP assembly have been added to corresponding infectious disease pathways. Updated release statistics and the Editorial Calendar are available. Click here to contact us.
- More...

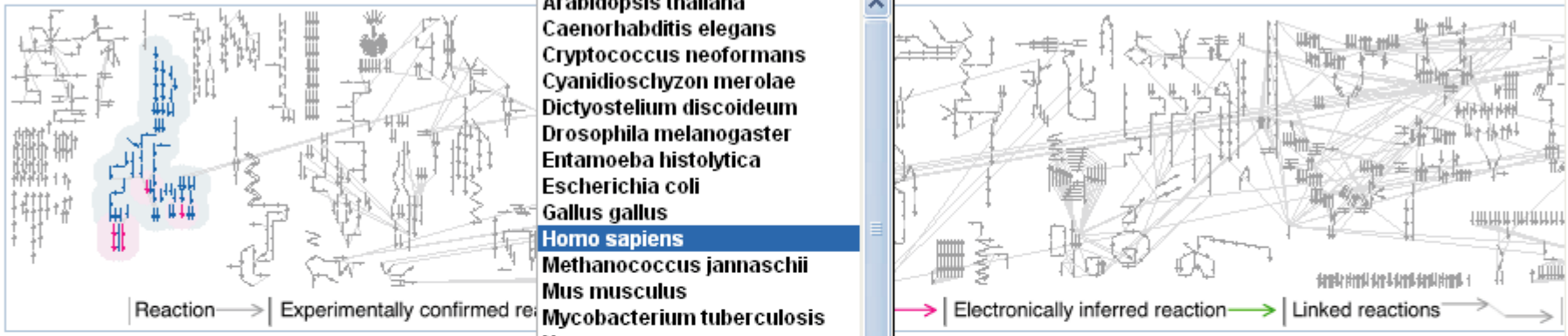
REACTOME

Reactome - a curated knowledgebase of biological pathways

The data displayed is for Homo sapiens . Use the menu to change the species.

Arabidopsis thaliana
Caenorhabditis elegans
Cryptococcus neoformans
Cyanidioschyzon merolae
Dictyostelium discoideum
Drosophila melanogaster
Entamoeba histolytica
Escherichia coli
Gallus gallus
Homo sapiens
Methanococcus jannaschii
Mus musculus
Mycobacterium tuberculosis
Neurospora crassa
Plasmodium falciparum
Rattus norvegicus
Saccharomyces cerevisiae
Schizosaccharomyces pombe
Sulfolobus solfataricus
Synechococcus sp.

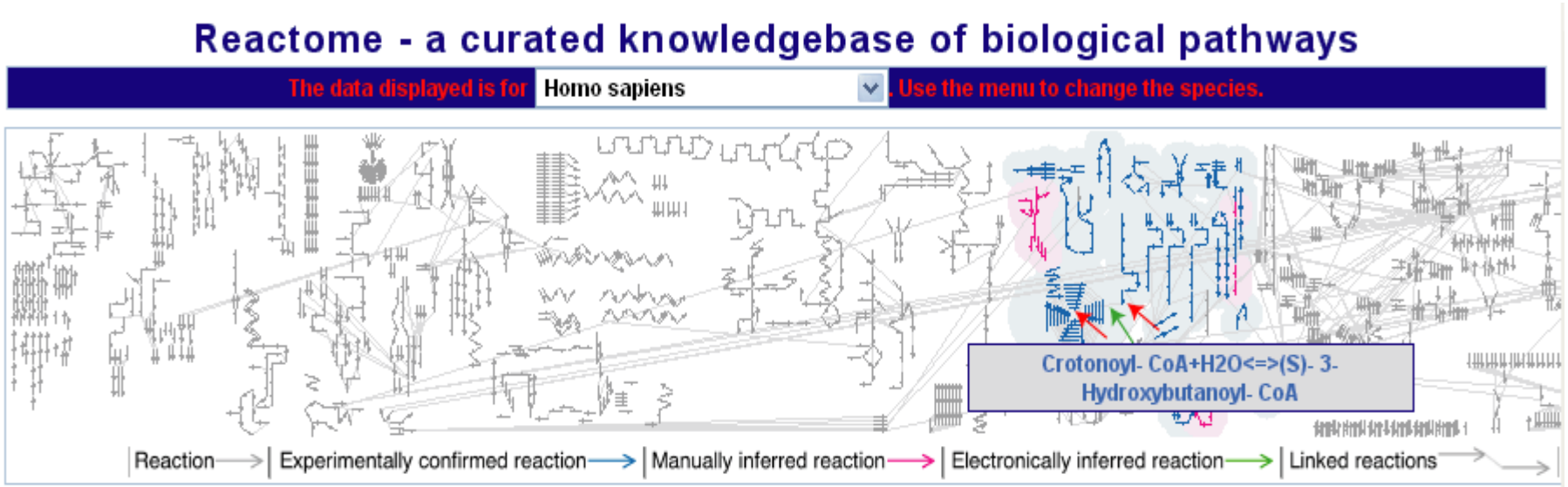
Reaction Map



Pathway Topic List

Apoptosis	Cell Cy	ell Cycle, Mitotic	DNA Repair
DNA Replication	Electror	ene Expression	Hemostasis
HIV Infection	Influ	ystem Signaling pathways	Insulin receptor mediated signaling
Integration of pathways involved in energy metabolism	Lipid metabolism	ism of amino acids and related nitrogen-containing molecules	Metabolism of glucose, other sugars, and ethanol
Notch Signaling Pathway	Nucleotide metabolism	Oxidative decarboxylation of pyruvate and TCA cycle	Post-translational modification of proteins
TGF-beta signaling pathway	Transcription	Translation	mRNA Processing
Xenobiotic metabolism			

CONVENCIONES



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BUSQUEDAS

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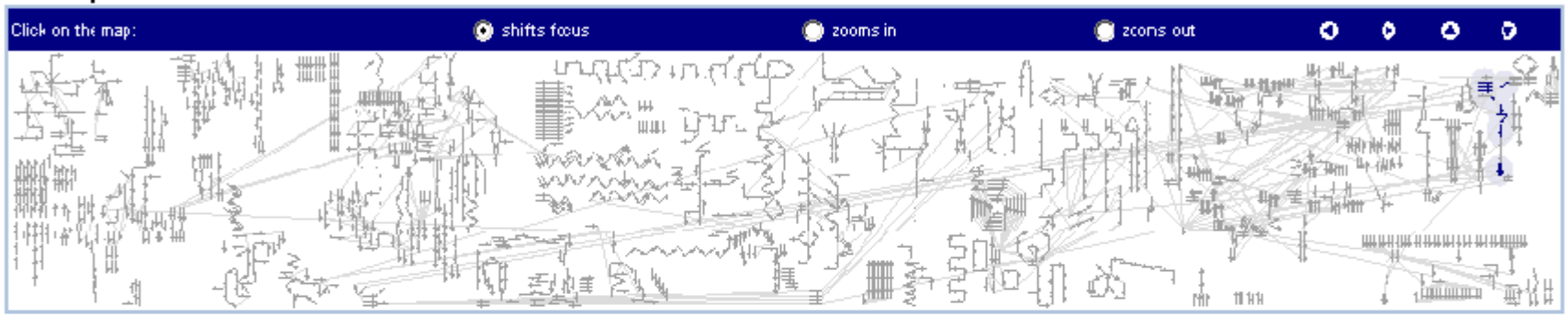
Find everything with ALL of the words In Homo sapiens Go!

glycolysis

Reactionmap



Details

Name	glycolysis
Accession	GO
Definition	The breakdown of a monosaccharide (generally glucose) into simpler components including pyruvate.
	ATP + D-fructose 6-phosphate => ADP + D-fructose 1,6-bisphosphate [Homo sapiens] ATP + D-fructose 6-phosphate => ADP + D-fructose 1,6-bisphosphate [Mus musculus] ATP + D-fructose 6-phosphate => ADP + D-fructose 1,6-bisphosphate [Rattus norvegicus] ATP + D-fructose 6-phosphate => ADP + D-fructose 1,6-bisphosphate [Gallus gallus] ATP + D-fructose 6-phosphate => ADP + D-fructose 1,6-bisphosphate [Tetraodon nigroviridis] ATP + D-fructose 6-phosphate => ADP + D-fructose 1,6-bisphosphate [Drosophila melanogaster] ATP + D-fructose 6-phosphate => ADP + D-fructose 1,6-bisphosphate [Caenorhabditis elegans] ATP + D-fructose 6-phosphate => ADP + D-fructose 1,6-bisphosphate [Cryptococcus neoformans JEC21] ATP + D-fructose 6-phosphate => ADP + D-fructose 1,6-bisphosphate [Saccharomyces cerevisiae] ATP + D-fructose 6-phosphate => ADP + D-fructose 1,6-bisphosphate [Neurospora crassa] ATP + D-fructose 6-phosphate => ADP + D-fructose 1,6-bisphosphate [Schizosaccharomyces pombe] ATP + D-fructose 6-phosphate => ADP + D-fructose 1,6-bisphosphate [Cyanidioschyzon merolae]

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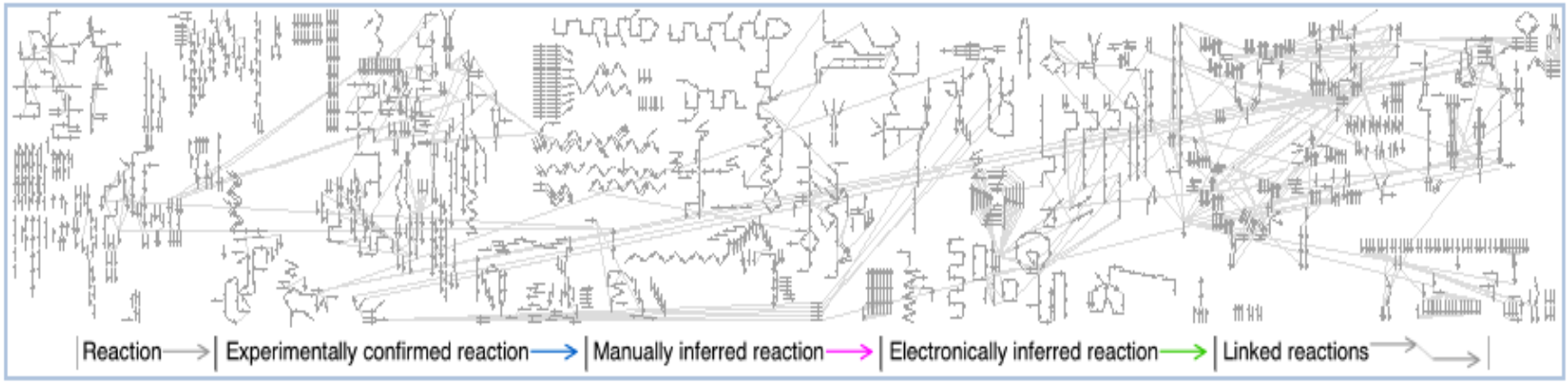

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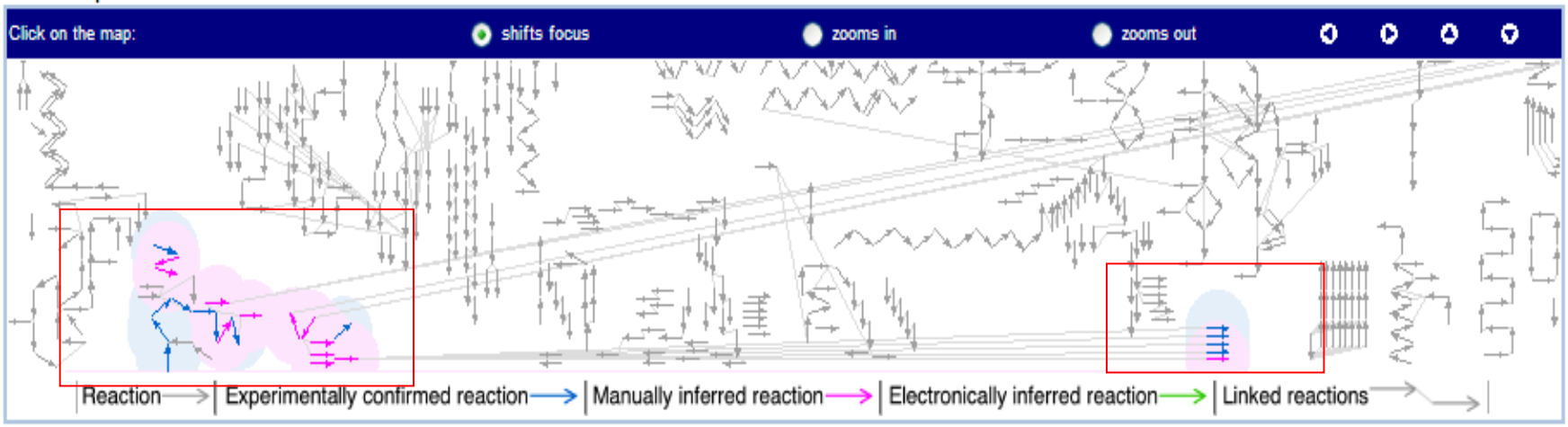
mRNA Processing	Xenobiotic metabolism		

Integration of pathways involved in energy metabolism [Homo sapiens]

Reactionmap



Details

open to selected event | open all | close all

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  - Activation of PP2A by Xylulose-5-phosphat
  - AMP inhibits the activation of fatty acid met
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Integration of pathways involved in energy metabolism	
Stable identifier	REACT_1505.1
Authored	Gopinathrao, G, D'Eustachio, P, 2005-05-11
Reviewed	Rush, MG, 2005-09-10

Many hormones that affect individual physiological processes including the regulation of appetite, absorption, transport, and oxidation of foodstuffs influence energy metabolism pathways. While **insulin** mediates the storage of excess nutrients, **glucagon** is involved in the mobilization of energy resources in response to low blood glucose levels, principally by stimulating hepatic glucose output. Small doses of glucagon are sufficient to induce significant glucose elevations. These hormone-driven regulatory pathways enable the body to sense and respond to changed amounts of nutrients in the blood and demands for energy.

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Pathway 5: Dephosphorylation of key metabolic factors by PP2A: Xy-5-P activated PP2A efficiently dephosphorylates phosphorylated PF2K-Pase resulting in the higher output of F-2,6-P2 that enhances PFK activity in the glycolytic pathway. PP2A also dephosphorylates (and thus activates) cytosolic and nuclear ChREBP.

Pathway 6: Transcriptional activation of metabolic genes by ChREBP: Dephosphorylated ChREBP activates the transcription of genes involved in glucose metabolism such as pyruvate kinase, and lipogenic genes such as acetyl-CoA carboxylase, fatty acid synthetase, acyl CoA synthase and glycerol phosphate acyl transferase.

The illustration below summarizes this network of events. Black lines are metabolic reactions, red lines are negative regulatory events, and green lines are positive regulatory events (figure reused with permission from Veech (2003) - Copyright (2003) National Academy of Sciences, U.S.A.). [Jiang & Zhang 2003, Kabashima *et al* 2003]

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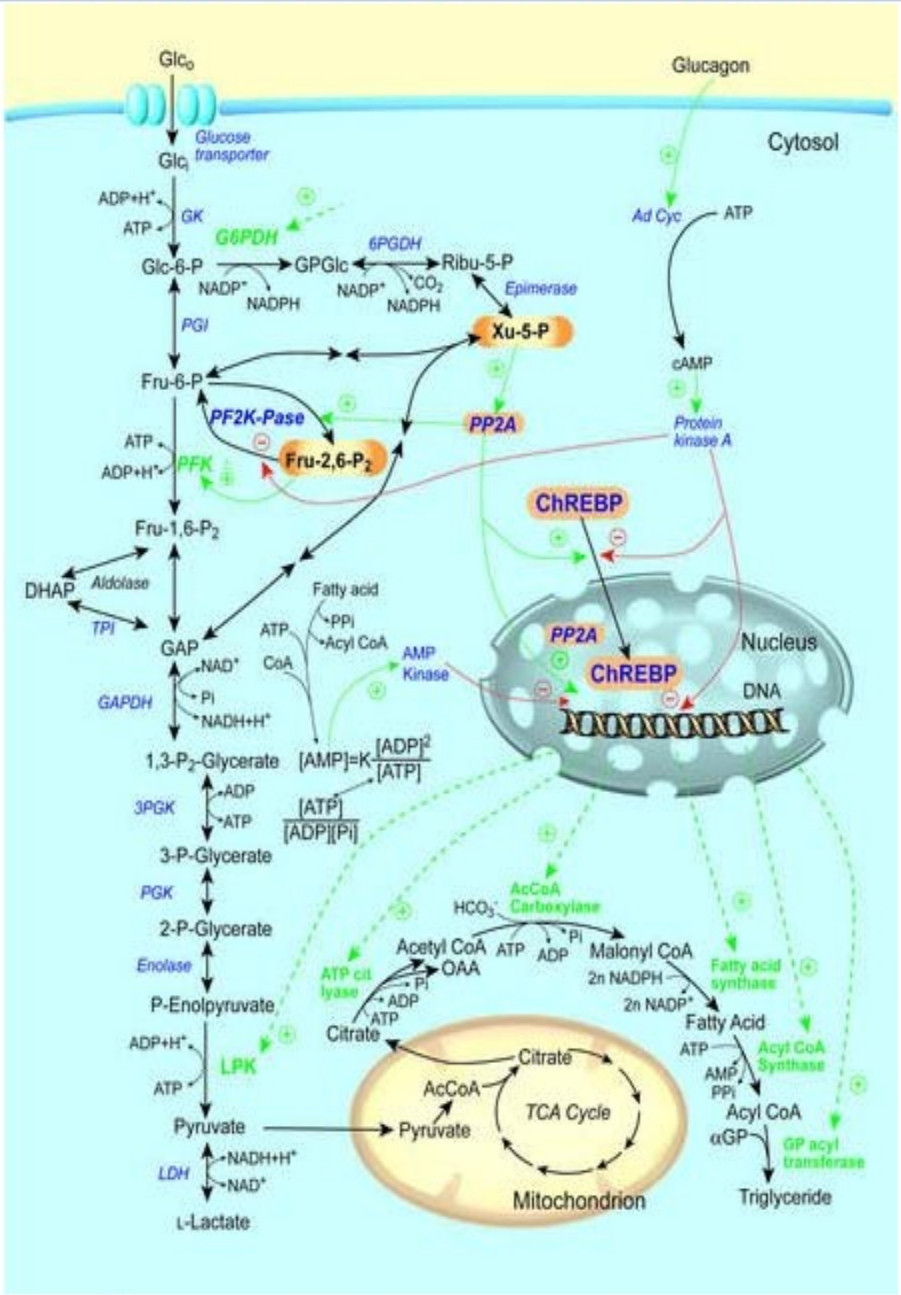

Cellular compartment	cytosol GO

References

Veech, RL *A humble hexose monophosphate pathway metabolite regulates short- and long-term control of lipogenesis* **2003** Proc Natl Acad Sci U S A PubMed

Hardie, DG *The AMP-activated protein kinase pathway--new players upstream and downstream* **2004** J Cell Sci PubMed

Jiang, G, Zhang, BB *Glucagon and regulation of glucose metabolism* **2003** Am J Physiol Endocrinol Metab PubMed

Represents GO biological process	energy reserve metabolism GO
Equivalent event(s) in other organism(s)	Integration of pathways involved in energy metabolism [Mus musculus] Integration of pathways involved in energy metabolism [Rattus norvegicus] Integration of pathways involved in energy metabolism [Gallus gallus] Integration of pathways involved in energy metabolism [Tetraodon nigroviridis] Integration of pathways involved in energy metabolism [Drosophila melanogaster] Integration of pathways involved in energy metabolism [Caenorhabditis elegans] Integration of pathways involved in energy metabolism [Cryptococcus neoformans A/D] Integration of pathways involved in energy metabolism [Saccharomyces cerevisiae] Integration of pathways involved in energy metabolism [Neurospora crassa] Integration of pathways involved in energy metabolism [Schizosaccharomyces pombe] Integration of pathways involved in energy metabolism [Cyanidioschyzon merolae] Integration of pathways involved in energy metabolism [Thalassiosira pseudonana] Integration of pathways involved in energy metabolism [Arabidopsis thaliana] Integration of pathways involved in energy metabolism [Oryza sativa] Integration of pathways involved in energy metabolism [Entamoeba histolytica] Integration of pathways involved in energy metabolism [Dictyostelium discoideum] Integration of pathways involved in energy metabolism [Plasmodium falciparum] Integration of pathways involved in energy metabolism [Sulfolobus solfataricus] Integration of pathways involved in energy metabolism [Methanococcus jannaschii] Integration of pathways involved in energy metabolism [Escherichia coli] Integration of pathways involved in energy metabolism [Synechococcus sp.] Integration of pathways involved in energy metabolism [Mycobacterium tuberculosis]

Participating molecules

- 1-acyl-sn-glycerol-3-phosphate acyltransferase alpha [cytosol] U E E E G M R R H H U R R
- 3',5'-Cyclic AMP [cytosol] C P
- 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1 [cytosol] U E G M K R H U R
- Acetyl-CoA carboxylase 2 [cytosol] U E G M K U
- Adenylate cyclase [plasma membrane]
- Adenylate cyclase, type I [plasma membrane] U E G M R H U R

Equivalent event(s) in other organism(s)	Integration of pathways involved in energy metabolism [Cryptococcus neoformans A/D] Integration of pathways involved in energy metabolism [Saccharomyces cerevisiae] Integration of pathways involved in energy metabolism [Neurospora crassa] Integration of pathways involved in energy metabolism [Schizosaccharomyces pombe] Integration of pathways involved in energy metabolism [Cyanidioschyzon merolae] Integration of pathways involved in energy metabolism [Thalassiosira pseudonana] Integration of pathways involved in energy metabolism [Arabidopsis thaliana] Integration of pathways involved in energy metabolism [Oryza sativa] Integration of pathways involved in energy metabolism [Entamoeba histolytica] Integration of pathways involved in energy metabolism [Dictyostelium discoideum] Integration of pathways involved in energy metabolism [Plasmodium falciparum] Integration of pathways involved in energy metabolism [Sulfolobus solfataricus] Integration of pathways involved in energy metabolism [Methanococcus jannaschii] Integration of pathways involved in energy metabolism [Escherichia coli] Integration of pathways involved in energy metabolism [Synechococcus sp.] Integration of pathways involved in energy metabolism [Mycobacterium tuberculosis]

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- Adenylate cyclase [plasma membrane]
- Adenylate cyclase, type I [plasma membrane]
- Adenylate cyclase, type VIII [plasma membrane]
- ADP [cytosol]
- ADP [nucleoplasm]
- AMP [nucleoplasm]
- ...

List all 82 participating molecules

[Change default viewing format] [SBML] [BioPAX] [PDF] [Cytoscape] [Protégé] [SVG] List...

Stable link for this page

Date: 2007-03-02 07:26:41

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UniProtKB Entry

PIR View

UniProtKB Entry: **P16118**

ENTRY INFORMATION	
ENTRY NAME	F261_HUMAN
ACCESSION NUMBERS	P16118; Q5JXS5; Q99951
Integrated into Swiss-Prot on	1990-04-01
Sequence was last modified on	1997-11-01 (Sequence version 3)
Annotations were last modified on	2007-02-20 (Entry version 83)

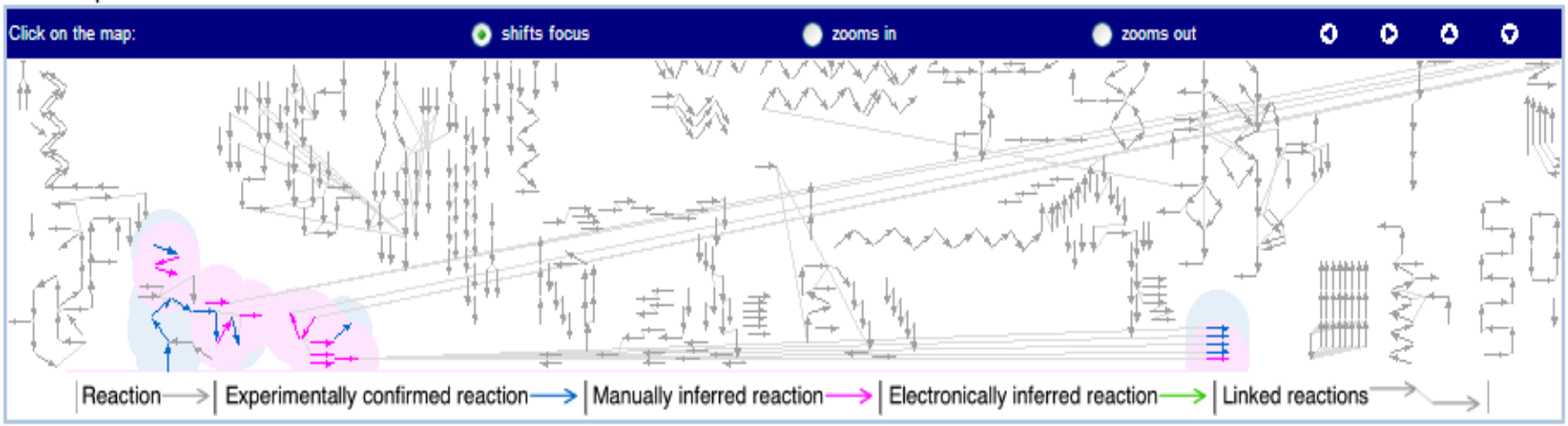
NAME AND ORIGIN OF THE PROTEIN	
PROTEIN NAME	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1
Synonyms	6PF-2-K/Fru-2,6-P2ASE liver isozyme
Includes	6-phosphofructo-2-kinase (EC 2.7.1.105) Fructose-2,6-bisphosphatase (EC 3.1.3.46)
GENE NAME	Name: PFKFB1

Link a las siguientes Bases de Datos

U UniProt
E Ensembl
G Entrez Gene
M OMIM
K KEGG (Kyoto Enciclopedia of Genes and Genomes)
R Entrez Nucleotide
H International HapMap Project
C ChEBI
P PubChem
GO Gene Ontology

Integration of pathways involved in energy metabolism [Homo sapiens]

Reactionmap



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open to selected event | open all | close all

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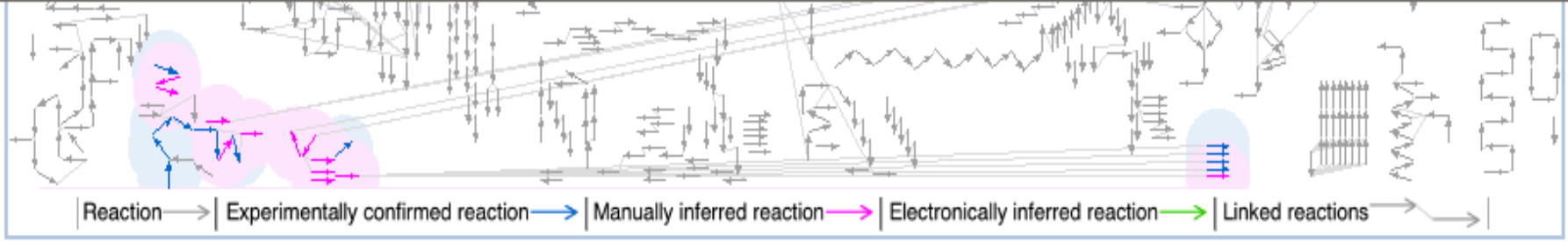

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    - Phosphorylation of ChREBP at Thr(666
    - PhosphoChREBP (Thr 666) is exporte
    - Phosphorylation of pChREBP (Thr 666
    - Nuclear transport of pChREBP (Thr 66
    - Phosphorylation of PF2K-Pase by PKA
    - D-fructose 2,6-bisphosphate + H2O =>
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    - D-glyceraldehyde 3-phosphate + D-fru
    - D-glyceraldehyde 3-phosphate + sedol
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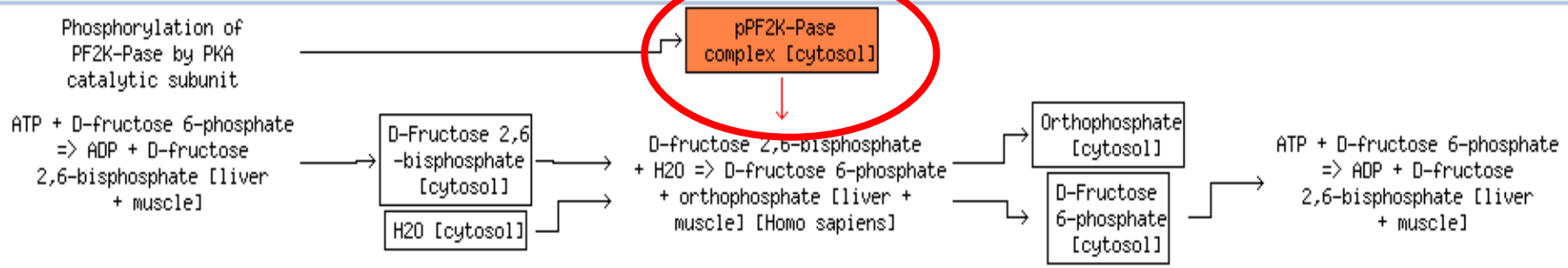
Pathway 5: Dephosphorylation of key metabolic factors by PP2A: Xy-5-P activated PP2A efficiently dephosphorylates

Diagram



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    - D-glyceraldehyde 3-phosphate + D-fru
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D-fructose 2,6-bisphosphate + H2O => D-fructose 6-phosphate + orthophosphate [liver + muscle]	
Stable identifier	REACT_1388.2
At the beginning of this reaction, 1 molecule of 'H2O', and 1 molecule of 'D-Fructose 2,6-bisphosphate' are present. At the end of this reaction, 1 molecule of 'Orthophosphate', and 1 molecule of 'D-Fructose 6-phosphate' are present. This reaction takes place in the 'cytosol' and is mediated by the 'fructose-2,6-bisphosphate 2-phosphatase activity' of 'pPF2K-Pase complex'.	
Input (present at start of reaction)	D-Fructose 2,6-bisphosphate [cytosol] C P H2O [cytosol] C P
Output (present at end of reaction)	Orthophosphate [cytosol] C P D-Fructose 6-phosphate [cytosol] C P
Catalyst	pPF2K-Pase complex [cytosol]
Essential catalyst component	Fructose-2,6-bisphosphatase
GO molecular function	fructose-2,6-bisphosphate 2-phosphatase activity GO
Preceding event(s)	ATP + D-fructose 6-phosphate => ADP + D-fructose 2,6-bisphosphate [liver + muscle] [Homo sapiens] Phosphorylation of PF2K-Pase by PKA catalytic subunit [Homo sapiens]
Following event(s)	ATP + D-fructose 6-phosphate => ADP + D-fructose 2,6-bisphosphate [liver + muscle] [Homo sapiens]
Organism	Homo sapiens
Cellular compartment	cytosol GO

Event hierarchy

open to selected event | open all | close all | show/hide hierarchy types

Event Name color indicates whether it has been:
determined experimentally
manually inferred
inferred electronically

- Notch Signaling Pathway
  - Transport of Notch receptor precursor to golgi
  - Maturation of Notch precursor via proteolytic cleavage
  - Mature Notch receptor trafficks to plasma membrane
  - Notch receptor binds with a ligand
    - **Notch 1 heterodimer binds with a Notch ligand in the extracellular space [Homo sapiens]**
    - Notch 2 heterodimer binds with a Notch ligand in the extracellular space
    - Notch 3 heterodimer binds with a Notch ligand in the extracellular space
    - Notch 4 heterodimer binds with a Notch ligand in the extracellular space
  - Receptor-ligand binding initiates the second proteolytic cleavage of Notch receptor
  - A third proteolytic cleavage releases NICD
  - NICD trafficks to nucleus
    - NICD1 trafficks to the nucleus
    - NICD2 trafficks to the nucleus
    - NICD3 trafficks to the nucleus
    - NICD4 trafficks to the nucleus

Displayed reaction

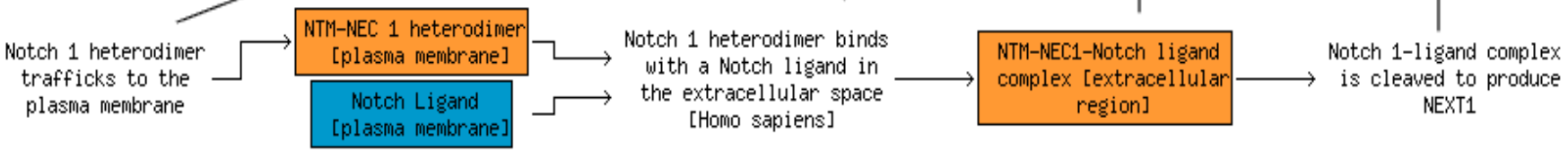
Preceding reaction

Following reaction

Inputs (starting molecules)

Outputs (molecules present at end of reaction)

Diagram



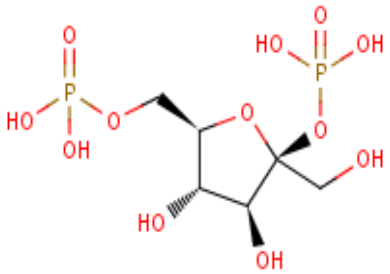
protein
non-protein genome-encoded molecule
complex
small molecule
generic entity (ie: Okazaki fragment,dNTP)
representative of a defined set of molecules that function interchangeably (ie: Notch ligand = Delta 1, Delta 4, Jagged 1, Jagged 2)
representative of an undefined (generic) set of molecules that function interchangeably (ie: Carboxylic esters , Aldehyde)

Volver inf detallada

β-D-fructofuranose 2,6-bisphosphate (CHEBI:28602)

Ir a inf detallada

Búsqueda rápida
Buscar Ayuda
- ChEBI - inicio
- Búsqueda avanzada
- Navegar
- Descargas
- Documentación
- Recursos de desarrollador
- Preferencias
- Contacte con ChEBI
- Vista para imprimir



ChEBI Name	β-D-fructofuranose 2,6-bisphosphate
ChEBI ID	CHEBI:28602
ChEBI ASCII Name	beta-D-fructofuranose 2,6-bisphosphate

☑ Image
☐ Applet

Molfile

InChI	InChI=1/C6H14O12P2/c7-2-6(18-20(13,14)15)5(9)4(8)3(17-6)1-16-19(10,11)12/h3-5,7-9H,1-2H2,(H2,10,11,12)(H2,13,14,15)/t3-,4-,5+,6+/m1/s1/f/h10-11,13-14H
SMILES	OC[C@]1(O[C@H](COP(O)(O)=O)[C@@H](O)[C@@H]1O)OP(O)(O)=O

Formula	Source
C6H14O12P2	KEGG COMPOUND

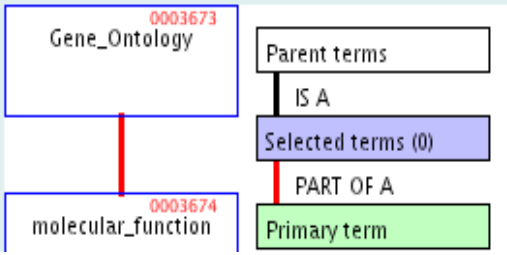
ChEBI Ontology

Tree view

Parents
β-D-fructofuranose 2,6-bisphosphate (CHEBI:28602) **is a** ketohexose bisphosphates (CHEBI:24970)
β-D-fructofuranose 2,6-bisphosphate (CHEBI:28602) **has functional parent** β-D-fructofuranose (CHEBI:28645)

GO Term GO:0004331

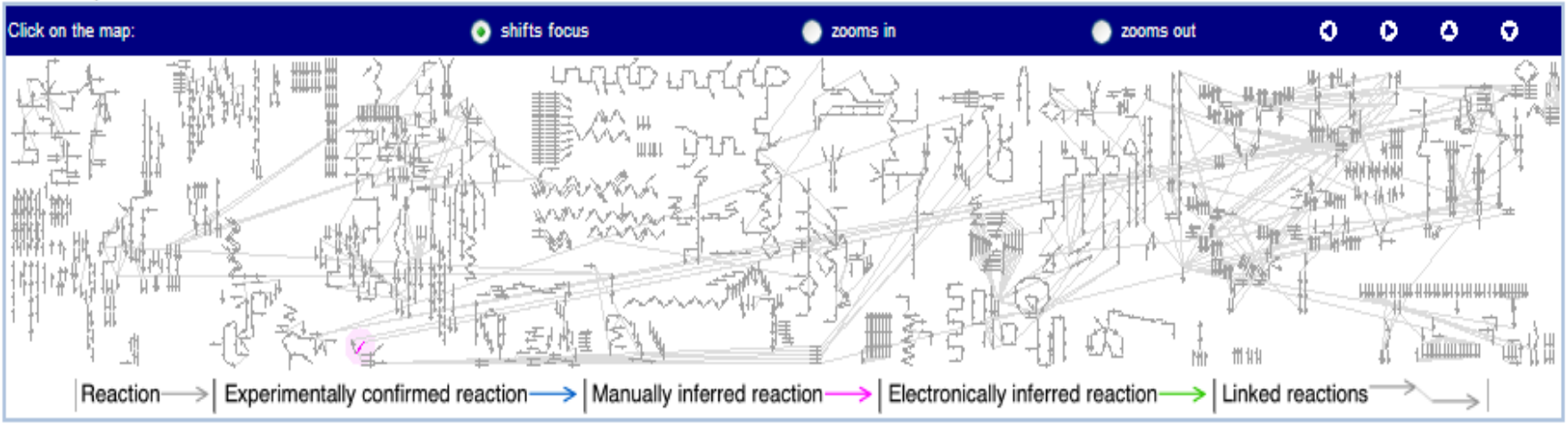
Term ID [?]	GO:0004331
Name [?]	fructose-2,6-bisphosphate 2-phosphatase activity
Last updated [?]	2001-03-30 04:29:44.0
Definition [?]	Catalysis of the reaction: D-fructose 2,6-bisphosphate + H2O = D-fructose 6-phosphate + phosphate.
Synonyms [?]	fructose-2,6-bisphosphatase
EC/TC mappings [?]	Enzyme 3.1.3.46 MetaCyc 3.1.3.46-RXN
Hierarchy [?]	• View this term's parents in a denormalised tree. • View with neither graph nor tree. • Hide all selected terms except the primary one • Add more terms to the selection with a search



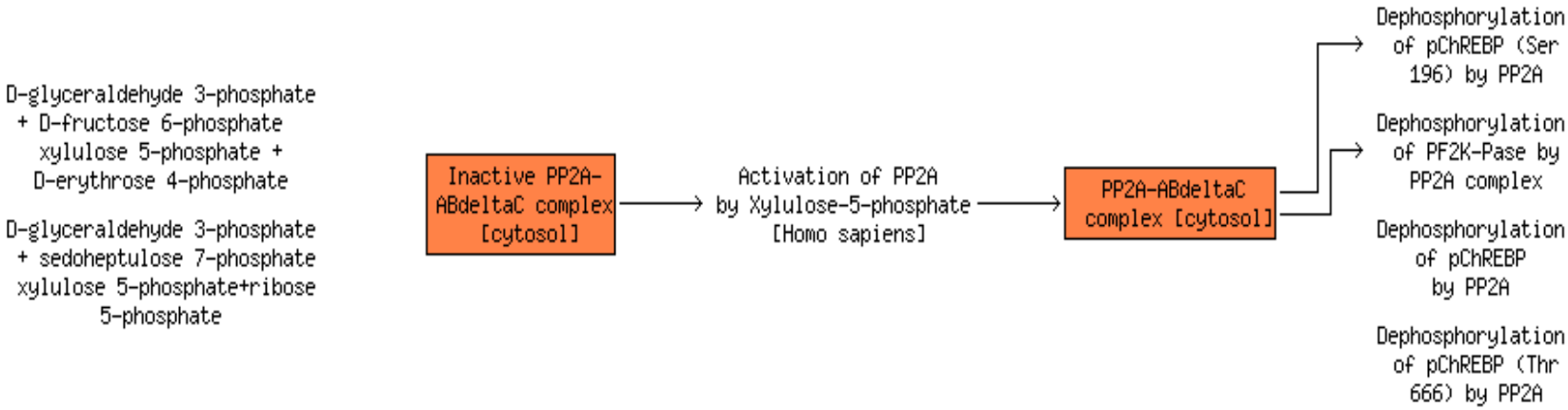
Ir a tipo de reacción

Activation of PP2A by Xylulose-5-phosphate [Homo sapiens]

Reactionmap



Diagram



Details

open to selected

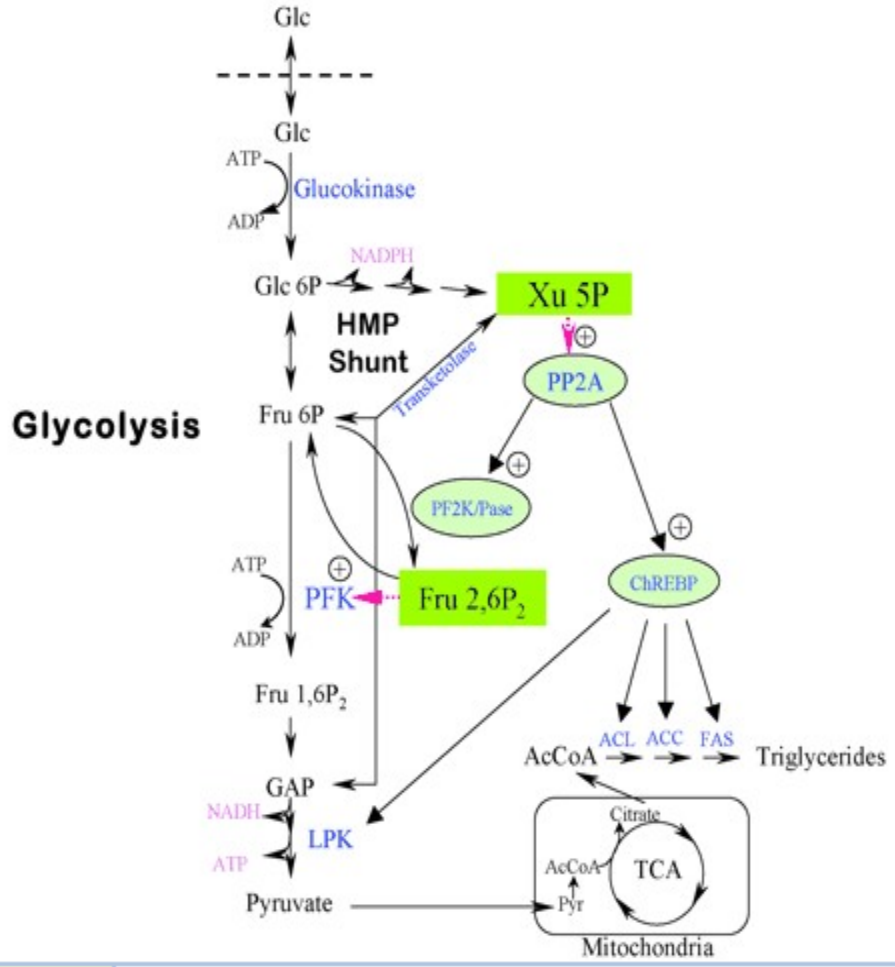
Activation of PP2A by Xylulose-5-phosphate

event | open all | close all

- Integration of pathways involved in energy me
- Glucagon signaling in metabolic regulatio
- PKA-mediated phosphorylation of key met
  - PKA catalytic subunit translocates to th
  - Phosphorylation of ChREBP at Thr(666
  - PhosphoChREBP (Thr 666) is exporte
  - Phosphorylation of pChREBP (Thr 666
  - Nuclear transport of pChREBP (Thr 66
  - Phosphorylation of PF2K-Pase by PKA
  - D-fructose 2,6-bisphosphate + H2O =>
- Insulin effects increased synthesis of Xylu
  - D-fructose 6-phosphate + D-erythrose
  - D-glyceraldehyde 3-phosphate + D-fru
  - D-glyceraldehyde 3-phosphate + sedol
- Activation of PP2A by Xylulose-5-phosph
- AMP inhibits the activation of fatty acid met
- PP2A-mediated dephosphorylation of key

Stable identifier	REACT_2177.1
Authored	Gopinathrao, G, 2005-05-14

Xylulose-5-phosphate binds to Protein phosphatase 2A (PP2A), activating it. This regulatory step may be the crucial physiological link explaining the coordinately increased rates of glycolysis and lipogenesis generally observed in individuals consuming high-carbohydrate diets. [Uyeda *et al* 2002, Kabashima *et al* 2003]



Input (present at start of reaction)	Inactive PP2A-ABdeltaC complex [cytosol]
Output (present at end of reaction)	PP2A-ABdeltaC complex [cytosol]
	D-glyceraldehyde 3-phosphate + D-fructose 6-phosphate <=> xylulose 5-phosphate + D-

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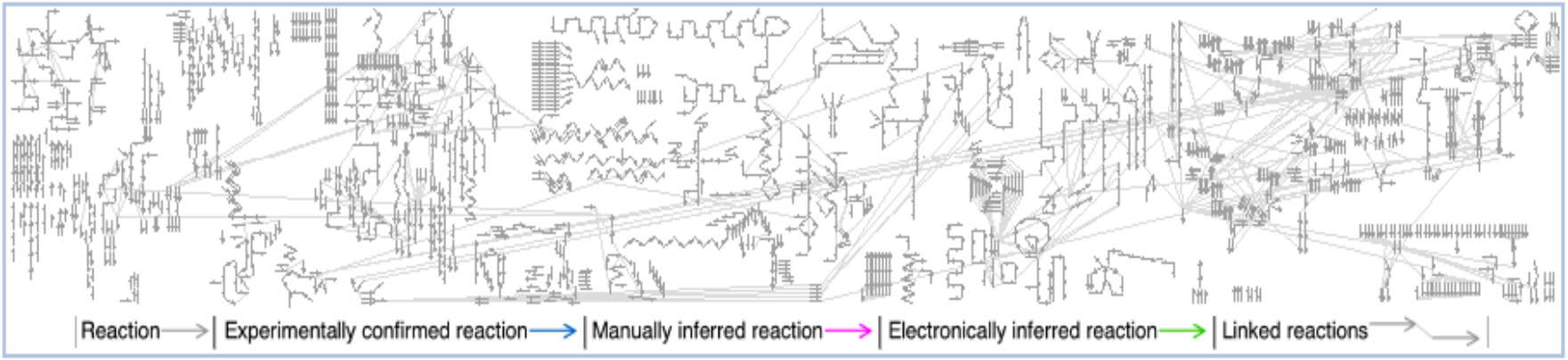

Apoptosis **Hs** Mm Rn Gg Tn Dm Ce Cn Sc Nc Sp Cm Tp At Os Dd Pf	Cell Cycle Checkpoints **Hs** Mm Rn Gg Tn Dm Ce Cn Sc Nc Sp Cm Tp At Os Eh Dd	Cell Cycle, Mitotic **Hs** Mm Rn Gg Tn Dm Ce Cn Sc Nc Sp Cm Tp At Os Eh Dd Pf Ss Mj Ec Mt	DNA Repair **Hs** Mm Rn Gg Tn Dm Ce Cn Sc Nc Sp Cm Tp At Os Eh Dd Pf Ss Mj Ec Ss Mt
DNA Replication **Hs** Mm Rn Gg Tn Dm Ce Cn Sc Nc Sp Cm Tp At Os Eh Dd Pf Ss Mj	Electron Transport Chain **Hs** Mm Rn Tn Dm Ce Cn Sc Nc Sp Cm Tp At Os Dd Ss Ec Mt	Epidermal Growth Factor Receptor (EGFR) signaling **Hs** Mm Rn Gg Tn	Fibroblast Growth Factor Receptor (FGFR) signaling **Hs** Mm Rn Gg Tn Ce
Gap junction trafficking and regulation **Hs** Mm Rn Gg Tn	Gene Expression **Hs** Mm Rn Gg Tn Dm Ce Cn Sc Nc Sp Cm Tp At Os Eh Dd Pf Ss Mj Ec Mt	HIV Infection **Hs**	Hemostasis **Hs** Mm Rn Gg Tn Dm Ce Nc Tp At Dd
Immune System signaling **Hs** Mm Rn Gg Tn Dm Nc Sp At Os	Influenza Infection **Hs**	Insulin receptor mediated signaling **Hs Dm** Mm Rn Gg Tn Dm Ce Cn Sc Nc Sp Cm Tp At Os Eh Dd Pf	Integration of pathways involved in energy metabolism **Hs** Mm Rn Gg Tn Dm Ce Cn Sc Nc Sp Cm Tp At Os Eh Dd Pf Ss Mj Ec Ss Mt
Maintenance of Telomeres **Hs** Mm Rn Gg Tn Dm Ce Cn Sc Nc Sp Cm Tp At Os Eh Dd Pf	Metabolism of amino acids and related nitrogen-containing molecules **Hs** Mm Rn Gg Tn Dm Ce Cn Sc Nc Sp Cm Tp At Os Eh Dd Pf Ss Mj Ec Ss Mt	Metabolism of carbohydrates **Hs** Mm Rn Gg Tn Dm Ce Cn Sc Nc Sp Cm Tp At Os Eh Dd Pf Ss Mj Ec Ss Mt	Metabolism of lipids and lipoproteins **Hs** Mm Rn Gg Tn Dm Ce Cn Sc Nc Sp Cm Tp At Os Eh Dd Pf Ss Mj Ec Ss Mt
			Oxidative decarboxylation of pyruvate

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Find | Reactome class attributes and relationships | in | Go!

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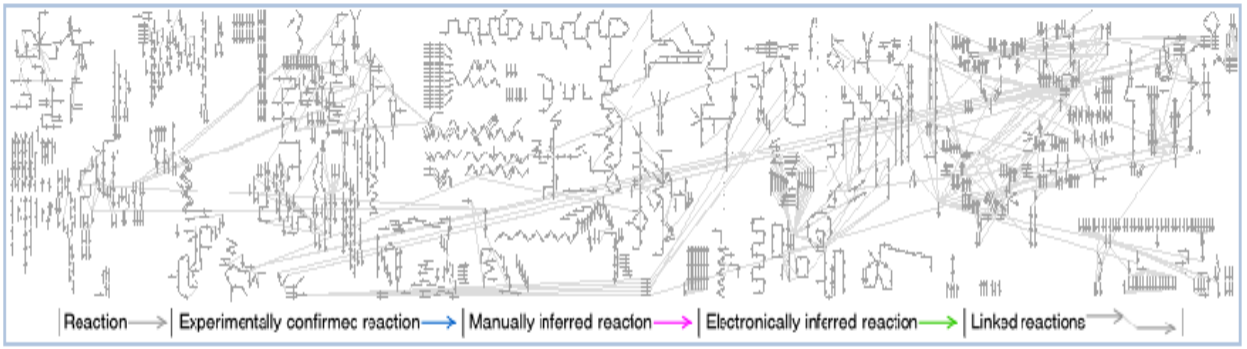

Apoptosis	Cell Cycle Checkpoints	Cell Cycle, Mitotic	DNA Repair
DNA Replication	Electron Transport Chain	Epidermal Growth Factor Receptor (EGFR) signaling	Fibroblast Growth Factor Receptor (FGFR) signaling
Gap junction trafficking and regulation	Gene Expression	HIV Infection	Hemostasis
Immune System signaling	Influenza Infection	Insulin receptor mediated signaling	Integration of pathways involved in energy metabolism
Maintenance of Telomeres	Metabolism of amino acids and related nitrogen-containing molecules	Metabolism of carbohydrates	Metabolism of lipids and lipoproteins
Metabolism of nucleotides	Metabolism of porphyrins	Notch Signaling Pathway	Oxidative decarboxylation of pyruvate and TCA cycle
Post-translational modification of proteins	Transforming Growth Factor (TGF) beta signaling	Transcription	Translation
mRNA Processing	Xenobiotic metabolism		

Topic	Authors	Released	Revised	Reviewers	Editors
Apoptosis [Homo sapiens] - Extrinsic Pathway for Apoptosis - Activation, myristolyation of BID and translocation to mitochondria - Intrinsic Pathway for Apoptosis - Activation of Effector Caspases - Apoptotic execution phase	Alnemri, E, Hengartner, M, Tschopp, J, Tsujimoto, Y, Hardwick, JM, Gillespie, ME, Gopinathrao, G, Matthews, L	2004-09-20		Vaux, D, Hengartner, M	Gopinathrao, G, Matthews, L, Gillespie, ME, Joshi-Tope, G
Cell Cycle Checkpoints [Homo sapiens] - G1/S DNA Damage Checkpoints - G2/M Checkpoints - Mitotic Spindle Checkpoint	Hoffmann, I, Khanna, K, O'Connell, M, Walworth, N, Yen, TJ, Yen, T, Borowiec, JA, Matthews, L, Matthews, L	2005-01-24		Sanchez, Y, Knudsen, E, Hardwick, KG, Peters, JM, Manfredi, J, Coqueret, O	Matthews, L, Joshi-Tope, G, D'Eustachio, P, Matthews, L
Cell Cycle, Mitotic [Homo sapiens] - G1 Phase - G1/S Transition - S Phase - G2 Phase - G2/M Transition - M Phase - M/G1 Transition - APC/C-mediated degradation of cell cycle proteins	O'Connell, M, Walworth, N, Bosco, G, Lorca, T, Castro, A, Gopinathrao, G, Pagano, M, Lee, KS, Davey, MJ, O'Donnell, M, Tye, BK, Matthews, L, Tom, S, Bambara, RA, Yen, T	2004-07-06		Manfredi, J, Lorca, T, Peters, JM, Coqueret, O	Matthews, L, Gopinathrao, G, Matthews, L, Gillespie, ME
DNA Repair [Homo sapiens] - Base Excision Repair - DNA Damage Bypass - DNA Damage Reversal - Double-Strand Break Repair - Nucleotide Excision Repair	Hoeijmakers, JH, Lees-Miller, S, Thompson, L, Gopinathrao, G, Matthews, L, Schultz, R, Pegg, A, Joshi-Tope, G	2004-07-06		Khanna, KK, Lindahl, T, West, SC, Wood, RD	Matthews, L, Gopinathrao, G, Joshi-Tope, G
DNA Replication [Homo sapiens]	Bambara, RA, Catlett, M, Davey,	2003-01-06	2005-09-	Mendez, J, Aladjem, M	D'Eustachio, P, Joshi-Tope, G,

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Reactome class attributes and relationships

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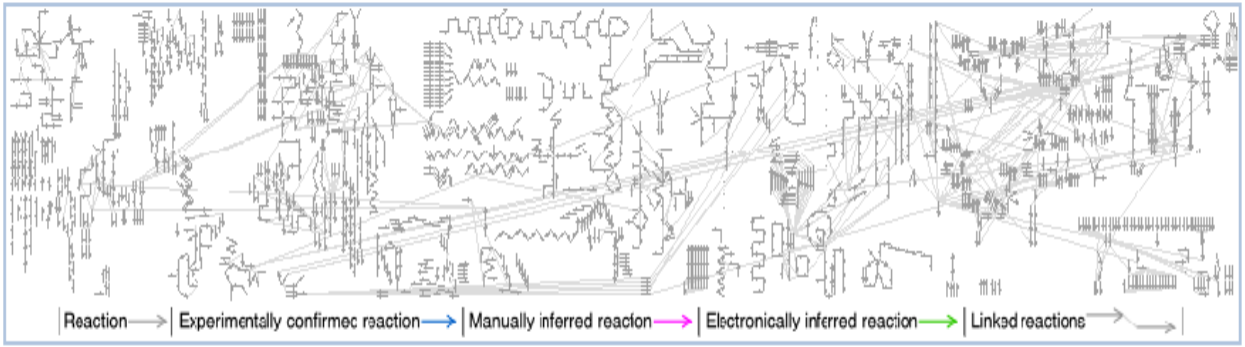

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mRNA Processing	Xenobiotic metabolism		

Data model

properties of the instances (e.g., the identities of the molecules that participate as inputs and outputs in a reaction).

Key data classes

PhysicalEntity

PhysicalEntities include individual molecules, multi-molecular complexes, and sets of molecules or complexes grouped together on the basis of shared characteristics. Molecules are further classified as genome encoded (DNA, RNA, and proteins) or not (all others). Attributes of a PhysicalEntity instance capture the chemical structure of an entity, including any covalent modifications in the case of a macromolecule, and its subcellular localization.

PhysicalEntity instances that represent, e.g., the same chemical in different compartments, or different post-translationally modified forms of a single protein, share numerous invariant features such as names, molecular structure and links to external databases like UniProt or ChEBI. To enable storage of this shared information in a single place, and to create an explicit link among all the variant forms of what can also be seen as a single chemical entity, Reactome creates instances of the separate ReferenceEntity class. A ReferenceEntity instance captures the invariant features of a molecule. A PhysicalEntity instance is then the combination of a ReferenceEntity attribute (e.g., Glycogen phosphorylase UniProt:P06737) and attributes giving specific conditional information (e.g., localization to the cytosol and phosphorylation on serine residue 14).

The PhysicalEntity class has subclasses to distinguish between different kinds of entities and to ensure data integrity while enabling different handling rules for different categories:

EntityWithAccessionedSequence - proteins and nucleic acids with known sequences.
GenomeEncodedEntity - a species-specific protein or nucleic acid whose sequence is unknown, such as an enzyme that has been characterized functionally but not yet purified and sequenced, e.g., cytosolic triokinase
SimpleEntity - other fully characterized molecules, e.g., nucleoplasmic ATP or cytosolic glutathione
Complex- a complex of two or more PhysicalEntities, e.g., FASL:FAS Receptor Trimer:FADD complex associated with the plasma membrane
EntitySet - a set of PhysicalEntities (molecules or complexes) which function interchangeably in a given situation, e.g., Notch ligand associated with the plasma membrane. This notation allows collective properties of multiple individual entities to be described explicitly.

CatalystActivity

PhysicalEntities are paired with molecular functions taken from the Gene Ontology molecular function controlled vocabulary to describe instances of biological catalysis. An optional ActiveUnit attribute indicates the specific domain of a protein or subunit of a complex that mediates the catalysis. If a PhysicalEntity has multiple catalytic activities, a separate CatalystActivity is created for each. This strategy allows the association of specific activities with specific variant forms of a protein or complex, and also enables easy retrieval of all activities of a protein, or all proteins capable of mediating a specific molecular function.

Event

Events - the conversion of input PhysicalEntities to output PhysicalEntities - are the building blocks used in Reactome to represent all biological processes. At present, only two subclasses of Event are recognized, *Reaction* and *Pathway*. A Reaction is an event that converts inputs to outputs in a single step. A pathway is any grouping of related events. An event may be a member of more than one pathway.

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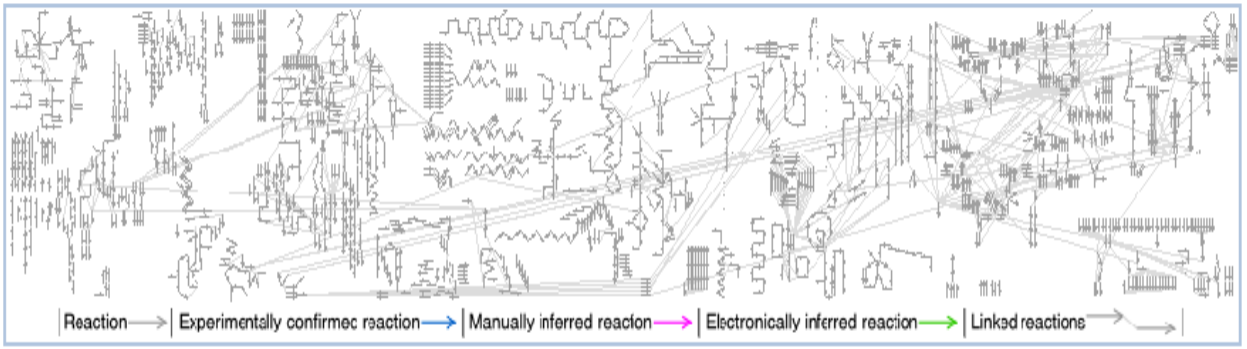

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Post-translational modification of proteins	Transforming Growth Factor (TGF) beta signaling	Transcription	Translation
mRNA Processing	Xenobiotic metabolism		

Attributes of class 'DatabaseObject'

Attribute name	Cardinality	Value type	Allowed classes	Attribute origin	Value defines instance	Db column type
DB_ID	1	INTERNAL_ID	N/A	DatabaseObject		INTEGER(10) UNSIGNED
__is_ghost	1	OTHER	N/A	DatabaseObject		ENUM('TRUE')
_displayName	1	TEXT	N/A	DatabaseObject		TEXT
_timestamp	1	OTHER	N/A	DatabaseObject		TIMESTAMP
created	1	INSTANCE	InstanceEdit	DatabaseObject		INTEGER(10) UNSIGNED
modified	+	INSTANCE	InstanceEdit	DatabaseObject		INTEGER(10) UNSIGNED
stableIdentifier	1	INSTANCE	StableIdentifier	DatabaseObject		INTEGER(10) UNSIGNED

Sidebar on the left shows the hierarchy of Reactome classes. The number of instances of this class is shown in square brackets and is hyperlinked to a page listing all instances in this class.

The main panel shows attributes of the selected class. Own attributes, i.e. the ones which are not inherited from a parent class are indicated in colour.

'+' in 'Cardinality' column indicates that this is a multi-value attribute.

'Value defines instance' column indicates the attributes the values of which determine instance identity and are used to check if an identical instance has been stored in the database already. 'ALL' indicates that that all of the values of a given attribute must be identical while 'ANY' shows that identity of any single value of a given attribute is enough. Of course, if the identity is defined by multiple attributes each of them has to match.

Attributes of class 'Pathway'

Attribute name	Cardinality	Value type	Allowed classes	Attribute origin	Value defines instance	Db column type
DB_ID	1	INTERNAL_ID	N/A	DatabaseObject		INTEGER(10) UNSIGNED
__is_ghost	1	OTHER	N/A	DatabaseObject		ENUM('TRUE')
_displayName	1	TEXT	N/A	DatabaseObject		TEXT
_doNotRelease	1	OTHER	N/A	Event		ENUM('TRUE','FALSE')
_timestamp	1	OTHER	N/A	DatabaseObject		TIMESTAMP
authored	1	INSTANCE	InstanceEdit	Event		INTEGER(10) UNSIGNED
catalystActivity	+	INSTANCE	CatalystActivity	Event		INTEGER(10) UNSIGNED
compartment	+	INSTANCE	Compartment	Event		INTEGER(10) UNSIGNED
created	1	INSTANCE	InstanceEdit	DatabaseObject		INTEGER(10) UNSIGNED
crossReference	+	INSTANCE	DatabaseIdentifier	Event		INTEGER(10) UNSIGNED
definition	1	TEXT	N/A	Event		TEXT
edited	+	INSTANCE	InstanceEdit	Event		INTEGER(10) UNSIGNED
evidenceType	1	INSTANCE	EvidenceType	Event		INTEGER(10) UNSIGNED
figure	+	INSTANCE	Figure	Event		INTEGER(10) UNSIGNED
goBiologicalProcess	1	INSTANCE	GO_BiologicalProcess	Event		INTEGER(10) UNSIGNED
hasComponent	+	INSTANCE	Event	Pathway	ALL	INTEGER(10) UNSIGNED
inferredFrom	+	INSTANCE	Event	Event		INTEGER(10) UNSIGNED
input	+	INSTANCE	PhysicalEntity	Event		INTEGER(10) UNSIGNED
literatureReference	+	INSTANCE	LiteratureReference	Event		INTEGER(10) UNSIGNED
modified	+	INSTANCE	InstanceEdit	DatabaseObject		INTEGER(10) UNSIGNED
name	+	TEXT	N/A	Event		TEXT
orthologousEvent	+	INSTANCE	Event	Event		INTEGER(10) UNSIGNED
output	+	INSTANCE	PhysicalEntity	Event		INTEGER(10) UNSIGNED
precedingEvent	+	INSTANCE	Event	Event		INTEGER(10) UNSIGNED
releaseDate	1	OTHER	N/A	Event		date
requiredInputComponent	+	INSTANCE	PhysicalEntity Domain	Event		INTEGER(10) UNSIGNED
reviewed	+	INSTANCE	InstanceEdit	Event		INTEGER(10) UNSIGNED
revised	+	INSTANCE	InstanceEdit	Event		INTEGER(10) UNSIGNED
species	+	INSTANCE	Species	Event		INTEGER(10) UNSIGNED
stableIdentifier	1	INSTANCE	StableIdentifier	DatabaseObject		INTEGER(10) UNSIGNED
summation	+	INSTANCE	Summation	Event		INTEGER(10) UNSIGNED

Referers of class 'Pathway' instances

Class name	Attribute name	Cardinality
PathwayCoordinates	locatedEvent	1
ReactionCoordinates	locatedEvent	1
ReactionCoordinates	locationContext	1
ConcurrentEventSet	concurrentEvents	+
FrontPage	frontPageItem	+
Reaction	inferredFrom	+
Event	inferredFrom	+

Attributes of class 'DatabaseObject'

Attribute name	Cardinality	Value type	Allowed classes	Attribute origin	Value defines instance	Db column type
DB_ID	1	INTERNAL_ID	N/A	DatabaseObject		INTEGER(10) UNSIGNED
__is_ghost	1	OTHER	N/A	DatabaseObject		ENUM('TRUE')
_displayName	1	TEXT	N/A	DatabaseObject		TEXT
_timestamp	1	OTHER	N/A	DatabaseObject		TIMESTAMP
created	1	INSTANCE	InstanceEdit	DatabaseObject		INTEGER(10) UNSIGNED
modified	+	INSTANCE	InstanceEdit	DatabaseObject		INTEGER(10) UNSIGNED
stableIdentifier	1	INSTANCE	StableIdentifier	DatabaseObject		INTEGER(10) UNSIGNED

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Find class: Any — instances containing: — Searc

in: Any — attribute as: Full-text in boolean mode

Found 7725 matches:

Check all | Uncheck all | View selected instances | as list of display names

- ABH2 mediated Reversal of Alkylation Damage
- ABH2 mediated Reversal of Alkylation Damage
- ABH2 mediated Reversal of Alkylation Damage
- ABH2 mediated Reversal of Alkylation Damage
- ABH2 mediated Reversal of Alkylation Damage
- ABH2 mediated Reversal of Alkylation Damage
- ABH2 mediated Reversal of Alkylation Damage
- ABH2 mediated Reversal of Alkylation Damage
- ABH3 mediated Reversal of Alkylation Damage
- ABH3 mediated Reversal of Alkylation Damage
- ABH3 mediated Reversal of Alkylation Damage
- ABH3 mediated Reversal of Alkylation Damage
- ABH3 mediated Reversal of Alkylation Damage
- ABH3 mediated Reversal of Alkylation Damage
- ABH3 mediated Reversal of Alkylation Damage
- ABH3 mediated Reversal of Alkylation Damage
- ABH3 mediated Reversal of Alkylation Damage
- Abortive elongation of HIV-1 transcript in the absence of Tat
- Acetaldehyde is oxidized by NAD+ to form acetate, NADH, and H+
- Acetaldehyde is oxidized by NAD+ to form acetate, NADH, and H+
- Acetaldehyde is oxidized by NAD+ to form acetate, NADH, and H+
- Acetaldehyde is oxidized by NAD+ to form acetate, NADH, and H+
- Acetaldehyde is oxidized by NAD+ to form acetate, NADH, and H+
- Acetaldehyde is oxidized by NAD+ to form acetate, NADH, and H+

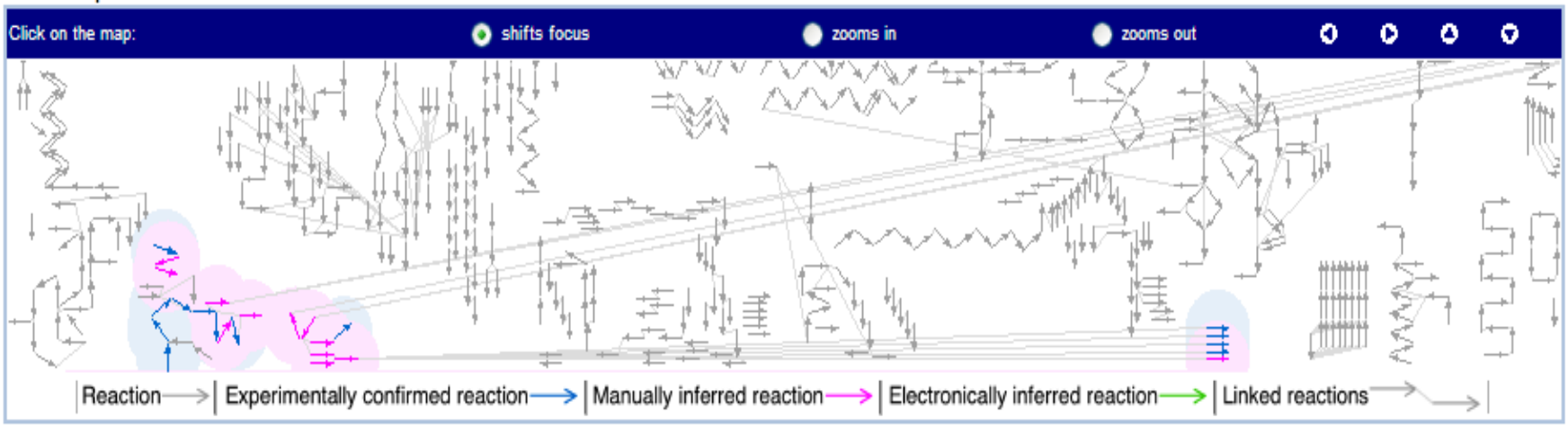
Find class [Any] instances containing [ ] Search!

in [Any] attribute as [Full-text in boolear mode]

Class:Id	Pathway:259057
_displayName	ABH3 mediated Reversal of Alkylaton Damage
_timestamp	20070222130753
compartment	[Compartment:352] nucleus
created	[InstanceEdit:255821] Schmidt, EE
evidenceType	[EvidenceType:203113] inferred byelectronic annotation
goBiologicalProcess	[GO_BiologicalProcess:17672] DNA dealkylation
hasComponent	■ [Reaction:258262] Oxidative demethylation of 1-MeA damaged DNA By ABH3 [Neurospora crassa] ■ [Reaction:258263] Oxidative demethylation of 3-MeC damaged DNA By ABH3 [Neurospora crassa] ■ [Reaction:258261] Oxidative demethylation of 1-EtA damaged DNA By ABH3 [Neurospora crassa]
inferredFrom	■ [Pathway:112126] ABH3 mediated Reversal of Alkylation Damage [Homo sapiens]
name	ABH3 mediated Reversal of Alkylaton Damage
orthologousEvent	■ [Pathway:112126] ABH3 mediated Reversal of Alkylation Damage [Homo sapiens] ■ **[Pathway:211877] ABH3 mediated Reversal of Alkylation Damage [Mus musculus]** ■ **[Pathway:221642] ABH3 mediated Reversal of Alkylation Damage [Rattus norvegicus]** ■ **[Pathway:230235] ABH3 mediated Reversal of Alkylation Damage [Gallus gallus]** ■ **[Pathway:238273] ABH3 mediated Reversal of Alkylation Damage [Tetraodon nigroviridis]** ■ *[Pathway:259057] ABH3 mediated Reversal of Alkylation Damage [Neurospora crassa]* ■ **[Pathway:268388] ABH3 mediated Reversal of Alkylation Damage [Thalassiosira pseudonana]** ■ **[Pathway:293716] ABH3 mediated Reversal of Alkylation Damage [Mycobacterium tuberculosis]**
species	[Species:176745] Neurospora crassa
summation	[Summation:203111] This event has been computationally inferred from an event t...
(hasComponent)	[Pathway:259169] Reversal of Alkylation Damage By DNA Dioxygenases [Neurospora crassa]
(orthologousEvent)	[Pathway:112126] ABH3 mediated Reversal of Alkylation Damage [Homo sapiens]

Integration of pathways involved in energy metabolism [Homo sapiens]

Reactionmap



Details

open to selected event | open all | close all

- Integration of pathways involved in energy n
  - Glucagon signaling in metabolic regulatio
  - PKA-mediated phosphorylation of key met
  - Insulin effects increased synthesis of Xylu
  - Activation of PP2A by Xylulose-5-phosphat
  - AMP inhibits the activation of fatty acid met
  - PP2A-mediated dephosphorylation of key

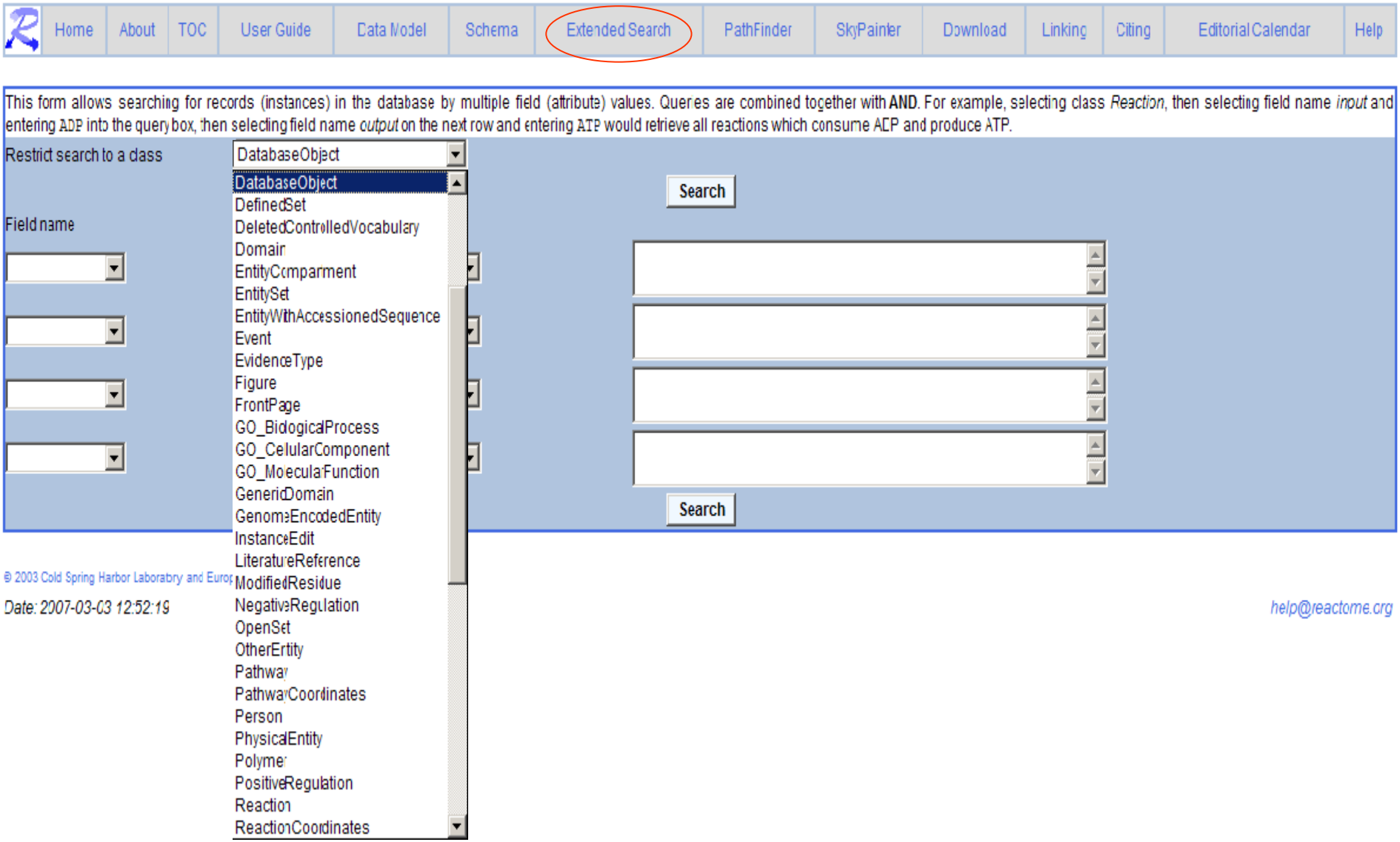
Integration of pathways involved in energy metabolism	
Stable identifier	REACT_1505.1
Authored	Gopinathrao, G, D'Eustachio, P, 2005-05-11
Reviewed	Rush, MG, 2005-09-10

Many hormones that affect individual physiological processes including the regulation of appetite, absorption, transport, and oxidation of foodstuffs influence energy metabolism pathways. While **insulin** mediates the storage of excess nutrients, **glucagon** is involved in the mobilization of energy resources in response to low blood glucose levels, principally by stimulating hepatic glucose output. Small doses of glucagon are sufficient to induce significant glucose elevations. These hormone-driven regulatory pathways enable the body to sense and respond to changed amounts of nutrients in the blood and demands for energy.

Glucagon and Insulin act through various metabolites and enzymes that target specific steps in metabolic pathways for sugar and fatty acids. The processes responsible for the long-term control of fat synthesis and short term control of glycolysis by key metabolic products and enzymes are annotated in this module as six specific pathways:

Pathway 1. Glucagon signalling in metabolic pathways: In response to low blood glucose, pancreatic alpha-cells release glucagon. The binding of glucagon to its receptor results in increased cAMP synthesis, and Protein Kinase A

BUSQUEDAS


Home
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TOC
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Data Model
Schema
Extended Search
PathFinder
SkyPainter
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Editorial Calendar
Help
This form allows searching for records (instances) in the database by multiple field (attribute) values. Queries are combined together with AND. For example, selecting class Reaction, then selecting field name input and entering ADP into the query box, then selecting field name output on the next row and entering ATP would retrieve all reactions which consume ADP and produce ATP.
Restrict search to a class
DatabaseObject
Search
Field name
DatabaseObject
DefinedSet
DeletedControlledVocabulary
Domain
EntityCompartment
EntitySet
EntityWithAccessionedSequence
Event
EvidenceType
Figure
FrontPage
GO_BiologicalProcess
GO_CelularComponent
GO_MolecularFunction
GenericDomain
GenomeEncodedEntity
InstanceEdit
LiteratureReference
ModifiedResidue
NegativeRegulation
OpenSet
OtherEntity
Pathway
PathwayCoordinates
Person
PhysicalEntity
Polymer
PositiveRegulation
Reaction
ReactionCoordinates
Search
© 2003 Cold Spring Harbor Laboratory and Europ
Date: 2007-03-03 12:52:19
help@reactome.org

This form allows searching for records (instances) in the database by multiple field (attribute) values. Queries are combined together with **AND**. For example, selecting class *Reaction*, then selecting field name *input* and entering ADP into the query box, then selecting field name *output* on the next row and entering ATP would retrieve all reactions which consume ADP and produce ATP.

Restrict search to a class: Reaction

Search

Field name

input	with the EXACT PHRASE ONLY	ADP
output	with the EXACT PHRASE ONLY	ATP
	with the EXACT PHRASE ONLY	
	with the EXACT PHRASE ONLY	

Search

Date: 2007-03-03 13:03:54

help@reactome.org

figure
goBiologicalProcess
hasMember
inferredFrom
inferredProt
input
literatureReference
maxHomologues
modified
name
orthologousEvent
output
precedingEvent
releaseDate

Home | About | TOC | User Guide | Data Model | Schema | Extended Search | PathFinder | SkyPainter | Download | Linking | Citing | Editorial Calendar | Help

Found 618 matches:

Check all | Uncheck all | View selected instances as list of display names

- ☐ ADP + Phosphoenolpyruvate => ATP + Pyruvate (pyruvate kinase R/L) [Homo sapiens]
- ☐ ADP + Orthophosphate + Succinyl-CoA <=> ATP + Succinate + CoA [Homo sapiens]
- ☐ ADP + Phosphoenolpyruvate => ATP + Pyruvate (pyruvate kinase M2) [Homo sapiens]
- ☐ ADP + 3-Phospho-D-glyceroyl phosphate <=> ATP + 3-Phospho-D-glycerate [Homo sapiens]
- ☐ uridine 5'-diphosphate (UDP) + ADP <=> uridine 5'-monophosphate (UMP) + ATP [Homo sapiens]
- ☐ adenosine 5'-diphosphate (ADP) + UTP <=> ATP + uridine 5'-diphosphate (UDP) [Homo sapiens]
- ☐ adenosine 5'-diphosphate (ADP) + CTP <=> ATP + cytidine 5'-diphosphate (CDP) [Homo sapiens]
- ☐ 2'-deoxycytidine 5'-diphosphate (dCDP) + ADP <=> deoxycytidine 5'-monophosphate (dCMP) + ATP [Homo sapiens]
- ☐ adenosine 5'-diphosphate (ADP) + dCTP <=> ATP + 2'-deoxycytidine 5'-diphosphate (dCDP) [Homo sapiens]
- ☐ cytidine 5'-diphosphate (CDP) + ADP <=> cytidine 5'-monophosphate (CMP) + ATP [Homo sapiens]
- ☐ 2'-deoxyuridine 5'-diphosphate (dUDP) + ADP <=> 2'-deoxyuridine 5'-monophosphate (dUMP) + ATP [Homo sapiens]
- ☐ 2'-deoxyuridine 5'-triphosphate (dUTP) + ADP <=> 2'-deoxyuridine 5'-diphosphate (dUDP) + ATP [Homo sapiens]
- ☐ thymidine 5'-diphosphate (TDP) + ADP <=> thymidine 5'-monophosphate (TMP) + ATP [Homo sapiens]
- ☐ adenosine 5'-diphosphate (ADP) + TTP <=> ATP + thymidine 5'-diphosphate (TDP) [Homo sapiens]
- ☐ guanosine 5'-diphosphate (GDP) + ADP <=> guanosine 5'-monophosphate (GMP) + ATP [Homo sapiens]
- ☐ 2'-deoxyguanosine 5'-diphosphate (dGDP) + ADP <=> 2'-deoxyguanosine 5'-monophosphate (dGMP) + ATP [Homo sapiens]
- ☐ 2'-deoxyadenosine 5'-diphosphate (dADP) + ADP <=> 2'-deoxyadenosine 5-monophosphate (dAMP) + ATP [Homo sapiens]
- ☐ 2'-deoxyadenosine 5'-diphosphate (dADP) + ADP <=> 2'-deoxyadenosine 5-monophosphate (dAMP) + ATP [Homo sapiens]
- ☐ 2'-deoxycytidine 5'-diphosphate (dCDP) + ADP <=> 2'-deoxycytidine 5'-monophosphate (dCMP) + ATP [Homo sapiens]
- ☐ adenosine 5'-diphosphate (ADP) + ADP <=> adenosine 5'-monophosphate (AMP) + ATP [Homo sapiens]
- ☐ adenosine 5'-diphosphate (ADP) + ADP <=> adenosine 5'-monophosphate (AMP) + ATP [Homo sapiens]
- ☐ adenosine 5'-diphosphate (ADP) + ADP <=> adenosine 5'-monophosphate (AMP) + ATP [Homo sapiens]
- ☐ cytidine 5'-diphosphate (CDP) + ADP <=> cytidine 5'-monophosphate (CMP) + ATP [Homo sapiens]
- ☐ adenosine 5'-diphosphate (ADP) + CTP <=> ATP + cytidine 5'-diphosphate (CDP) [Homo sapiens]
- ☐ adenosine 5'-diphosphate (ADP) + CTP <=> ATP + cytidine 5'-diphosphate (CDP) [Homo sapiens]
- ☐ adenosine 5'-diphosphate (ADP) + CTP <=> ATP + cytidine 5'-diphosphate (CDP) [Homo sapiens]
- ☐ adenosine 5'-diphosphate (ADP) + dATP <=> ATP + 2'-deoxyadenosine 5'-diphosphate (dADP) [Homo sapiens]
- ☐ adenosine 5'-diphosphate (ADP) + dATP <=> ATP + 2'-deoxyadenosine 5'-diphosphate (dADP) [Homo sapiens]
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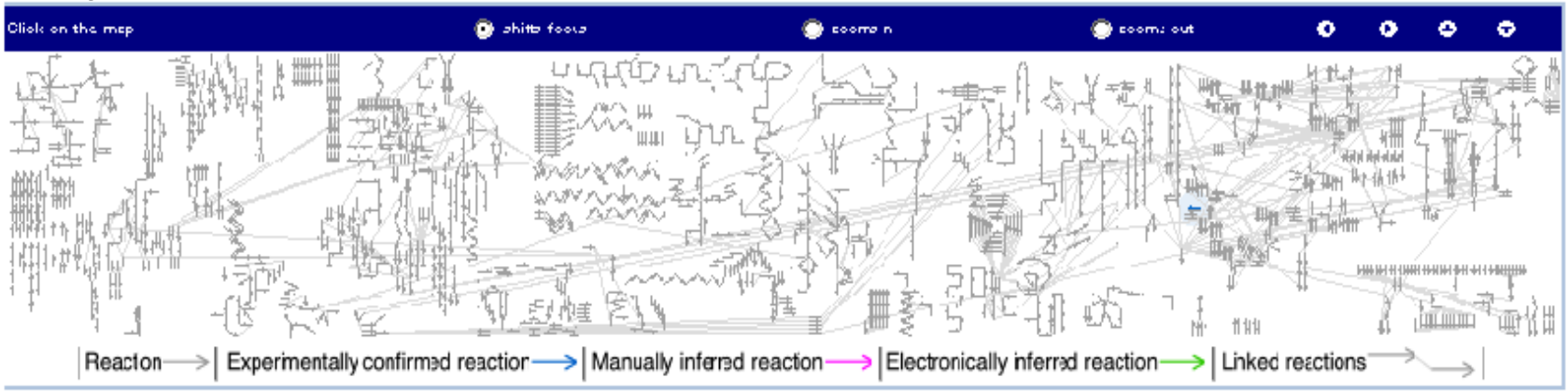
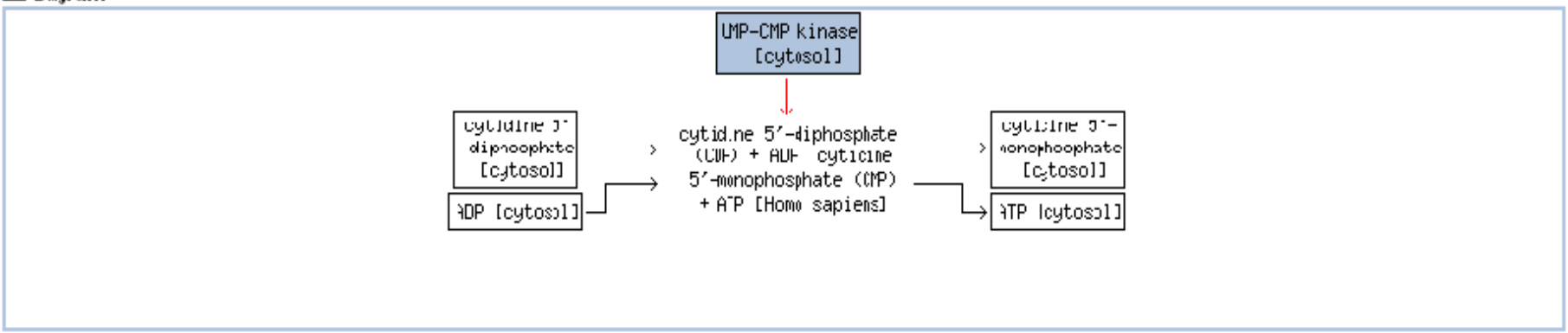
- ☐ adenosine 5'-diphosphate (ADP) + dGTP <=> ATP + 2'-deoxyguanosine 5'-diphosphate (dGDP) [Homo sapiens]
- ☐ adenosine 5'-diphosphate (ADP) + dGTP <=> ATP + 2'-deoxyguanosine 5'-diphosphate (dGDP) [Homo sapiens]
- ☐ adenosine 5'-diphosphate (ADP) + dGTP <=> ATP + 2'-deoxyguanosine 5'-diphosphate (dGDP) [Homo sapiens]

cytidine 5'-diphosphate (CDP) + ADP <=> cytidine 5'-monophosphate (CMP) + ATP [Homo sapiens]

Reactionmap



Diagram



Details

open to selected event | open all | close all

- Metabolism of nucleotides
  - Transport of nucleosides and free purine a
  - Synthesis of cytosolic 5-phospho-alpha-D-
  - Purine metabolism

cytidine 5'-diphosphate (CDP) + ADP <=> cytidine 5'-monophosphate (CMP) + ATP

Stable identifier	REACT_24712

At the beginning of this reaction, 1 molecule of 'cytidine 5-diphosphate', and 1 molecule of 'ADP' are present. At the end of this reaction, 1 molecule of 'cytidine 5'-monophosphate', and 1 molecule of 'ATP' are present

This reaction takes place in the 'cytosol' and is mediated by the 'nucleoside kinase activity' of 'UMP-CMP kinase'

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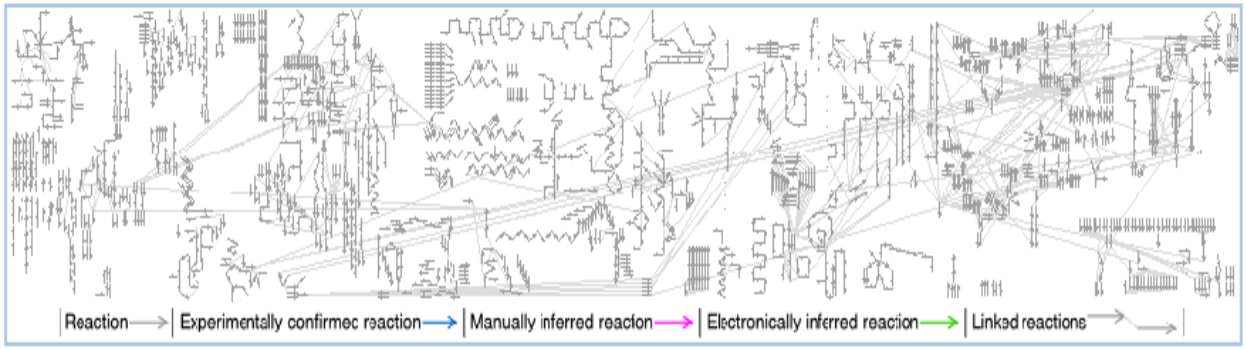
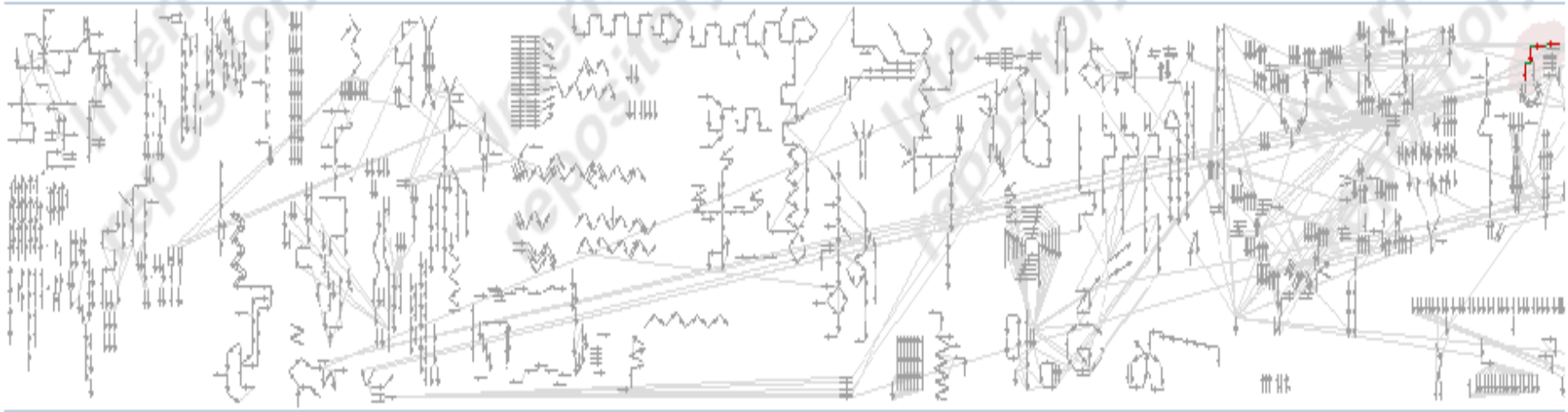
The data displayed is for Homo sapiens. Use the menu to change the species. Check for cross-species comparison.



Apoptosis	Cell Cycle Checkpoints	Cell Cycle, Mitotic	DNA Repair
DNA Replication	Electron Transport Chain	Epidermal Growth Factor Receptor (EGFR) signaling	Fibroblast Growth Factor Receptor (FGFR) signaling
Gap junction trafficking and regulation	Gene Expression	HIV Infection	Hemostasis
Immune System signaling	Influenza Infection	Insulin receptor mediated signaling	Integration of pathways involved in energy metabolism
Maintenance of Telomeres	Metabolism of amino acids and related nitrogen-containing molecules	Metabolism of carbohydrates	Metabolism of lipids and lipoproteins
Metabolism of nucleotides	Metabolism of porphyrins	Notch Signaling Pathway	Oxidative decarboxylation of pyruvate and TCA cycle
Post-translational modification of proteins	Transforming Growth Factor (TGF) beta signaling	Transcription	Translation
mRNA Processing	Xenobiotic metabolism		

Found path:
[Complex:70373] G6PD dimer [cytosol] [Homo sapiens]
[CatalystActivity:70374] glucose-6-phosphate 1-dehydrogenase activity of G6PD dimer [cytosol]
[Reaction:70377] alpha-D-glucose 6-phosphate + NADP+ => D-glucono-1,5-lactone 6-phosphate + NADPH + H+ [G6PD dimer] [Homo sapiens]
[SimpleEntity:31467] D-Glucono-1,5-lactone 6-phosphate [cytosol]
[Reaction:71296] D-glucoro-1,5-lactone 6-phosphate + H2O => 6-phospho-D-gluconate [Homo sapiens]
[SimpleEntity:29396] 6-Phospho-D-gluconate [cytosol]
[Reaction:71299] 6-phospho-D-gluconate + NADP+ => D-ribulose 5-phosphate + CO2 + NADPH + H+ [Homo sapiens]
[SimpleEntity:29732] D-Ribulose 5-phosphate [cytosol]
[Reaction:71303] D-ribulose 5-phosphate <=> xylulose 5-phosphate [Homo sapiens]
[SimpleEntity:29790] D-Xylulose 5-phosphate [cytosol]



Reactome - a curated knowledgebase of biological pathways

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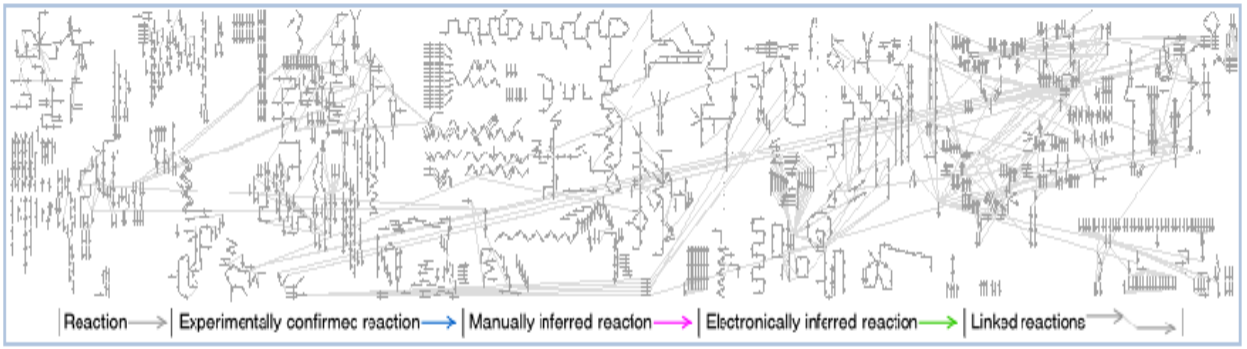

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Post-translational modification of proteins	Transforming Growth Factor (TGF) beta signaling	Transcription	Translation
mRNA Processing	Xenobiotic metabolism		

Skypainter

Paste or upload identifiers or identifiers with values

UNIPROT:P30304 ,CHEBI:7423 , COMPOUND:C0002 , GO:0030060 ,

EC:1.1.1.37, Entrez Gene:4171

Examinar...

ignore numeric values. Checking this option makes the tool to behave as if you submit identifier list only.

Focus species: (automatic)

Paint! Reset

Skypainter is a tool to determine **which events (reactions and/or pathways) are statistically overrepresented in a set of genes** as specified by submitted list of identifiers. In other words, given a list of genes, Skypainter can identify common events for these genes.

Given a set of M genes which participate in an event, the total of X genes (for the given species) that Reactome is aware of, and given the submitted list of K genes of which N genes participate in the given event, skypainter calculates (by performing the hypergeometric test) the probability of picking N or more genes involved in the given event purely by chance. Hence a low probability suggests that participation in a given event is what the genes in the submitted list have in common. Note, however, that the **probabilities as reported by Skypainter are not corrected for multiple testing** arising from evaluating the submitted list of genes against every event for the given species.

Identifiers which can be used are UniProt accession numbers and ids, GenBank/EMBL/DDBJ protein ids, RefPep, RefSeq, EntrezGene, MIM, InterPro, Affymetrix, Agilent and Ensembl protein, transcript and gene identifiers. **All purely numeric identifiers, such as from MIM and EntrezGene have to have the abbreviated database name and colon prepended** to them, i.e. MIM:602544, EntrezGene:55718.

The colour of each reaction arrow on the reaction map indicates the the number of genes in the submitted list that participates in the reaction.

Similar functionality, i.e colouring reactions according to the number of times the reaction is hit by the identifiers in the submitted list, is also available for small molecule identifiers from ChEBI and KEGG COMPOUND identifiers (e.g. ChEBI:2359, C00002), Enzyme Commission (EC) numbers (e.g. 1.1.1.1) and Gene Ontology (GO) accession numbers (e.g. GO:0004672). GO cellular component accession numbers can be used to highlight reactions involving molecules localized to that compartment or which themselves correspond to the given GO cellular component term. GO molecular function accession numbers highlight reactions which are catalysed by the activities they specify. GO biological process accession numbers highlight reactions which either correspond or are components of pathways corresponding to the given GO biological processes. **Please note that the overrepresentation analysis is not performed for those identifiers.**

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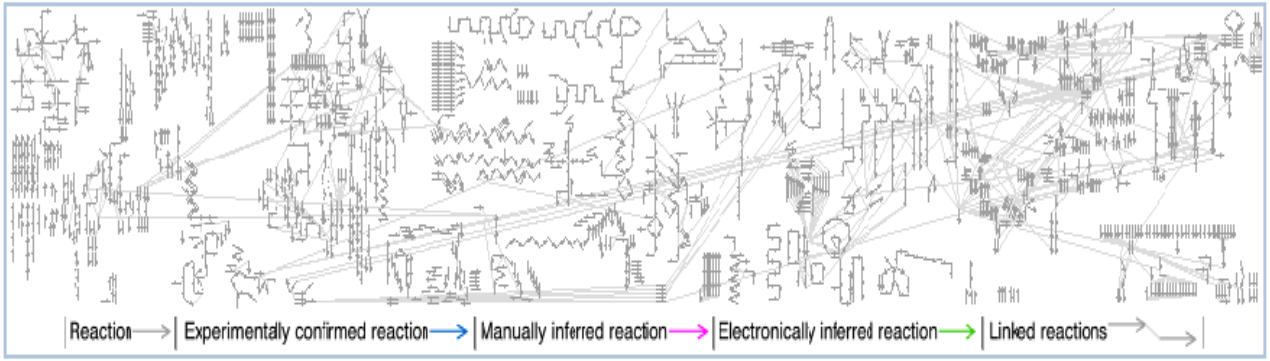
The data displayed is for Homo sapiens. Use the menu to change the species. Check for cross-species comparison.



Apoptosis	Cell Cycle Checkpoints	Cell Cycle, Mitotic	DNA Repair
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Gap junction trafficking and regulation	Gene Expression	HIV Infection	Hemostasis
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Post-translational modification of proteins	Transforming Growth Factor (TGF) beta signaling	Transcription	Translation
mRNA Processing	Xenobiotic metabolism		

Download Reactome data and code

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 reactions in SBML (level 2, version 1) format.
- Human protein-protein interaction pairs in tab-delimited format.
- Events in the BioPAX level 2 format

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

- PDF format.
- RTF format.

The Reactome website can be installed locally:

- Instructions for local installation of Reactome database and website. Please note that you need to have root privileges on the computer onto which you plan to install the copy of Reactome.
- Download Reactome website contents and perl code (requires additional non-Reactome software).

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.

- Author Tool (version 2.1, build 25, September 29, 2006)
- Curator Tool (version 2.0, build 33, December 5, 2006)

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
  - User's Guide in PDF (1M)
  - Tutorial in Power Point Slides (2M)
  - Tutorial in Flash Movie (640 x 480) (11M)
  - Tutorial in Flash Movie (800 x 600) (12M)
- XML Schema for the data model
- WSDL file for the Reactome Web Servies API

Date: 2007-03-04 22:26:29

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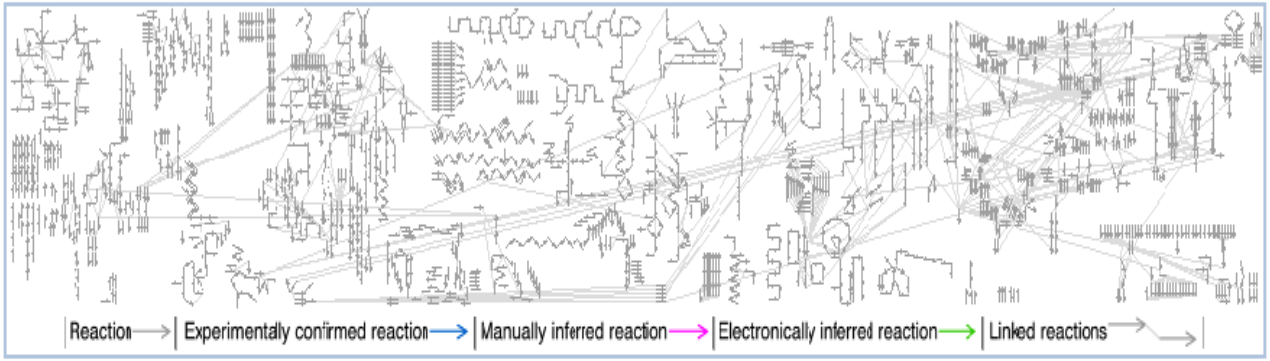
Reactome - a curated knowledgebase of biological pathways

The data displayed is for Homo sapiens. Use the menu to change the species. Check for cross-species comparison.



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Linking to Reactome

Linking to Reactome can be achieved by creating URLs containing the name of and an identifier from an "external" database in the following format:

`http://www.reactome.org/cgi-bin/link?SOURCE=Database name&ID=identifier`

Click here to see the external databases and list identifiers available in the current release of Reactome

Below are few concrete examples

- UniProt accession numbers (the 'AC' line, preferred) and identifiers (the 'ID' line), e.g. UNIPROT:P30304
  http://www.reactome.org/cgi-bin/link?SOURCE=UNIPROT&ID=P30304
- ChEBI identifiers, e.g. CHEBI:7423
  http://www.reactome.org/cgi-bin/link?SOURCE=CHEBI&ID=7423
- identifiers, e.g. COMPOUND:C00002
  http://www.reactome.org/cgi-bin/link?SOURCE=COMPOUND&ID=C00002
- Gene Ontology (GO) accession numbers, e.g. GO:0030060
  http://www.reactome.org/cgi-bin/link?SOURCE=GO&ID=0030060
- Enzyme Classification (EC) numbers, e.g. EC:1.1.1.37
  http://www.reactome.org/cgi-bin/link?SOURCE=EC&ID=1.1.1.37
- Entrez Gene, e.g. Entrez Gene:4171
  http://www.reactome.org/cgi-bin/link?SOURCE=Entrez+Gene&ID=4171

Date: 2007-03-02 07:59:30

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Please choose the database the identifiers of which you want listed. Specifying a species will restrict the identifiers to the ones found in this species only. Please be aware that some databases contain records for single species only.

Database BROAD species All species List!

List of databases:

BROAD
CME Genome Project
CO
COMPOUND
ChEBI
Dictybase
EC
EMBL
ENSEMBL
Entrez
Entrez Gene
Flybase
GO
GeneDB
HapMap
IntAct
JGI
KEGG Gene
MIM
PlasmoDB
PubChem Compound
PubChem Substance
RefSeq
SGD
TIGR
UCSC
UniProt
Wormbase

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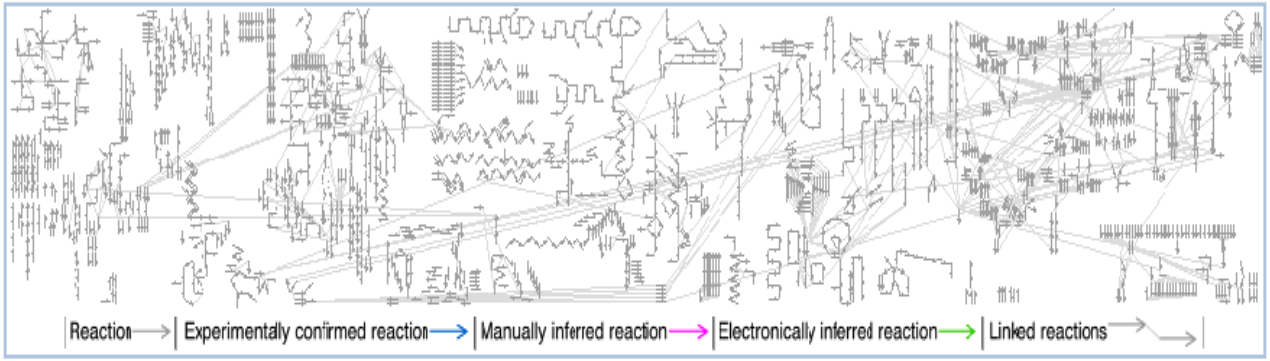
Reactome - a curated knowledgebase of biological pathways

The data displayed is for Homo sapiens. Use the menu to change the species. Check for cross-species comparison.



Apoptosis	Cell Cycle Checkpoints	Cell Cycle, Mitotic	DNA Repair
DNA Replication	Electron Transport Chain	Epidermal Growth Factor Receptor (EGFR) signaling	Fibroblast Growth Factor Receptor (FGFR) signaling
Gap junction trafficking and regulation	Gene Expression	HIV Infection	Hemostasis
Immune System signaling	Influenza Infection	Insulin receptor mediated signaling	Integration of pathways involved in energy metabolism
Maintenance of Telomeres	Metabolism of amino acids and related nitrogen-containing molecules	Metabolism of carbohydrates	Metabolism of lipids and lipoproteins
Metabolism of nucleotides	Metabolism of porphyrins	Notch Signaling Pathway	Oxidative decarboxylation of pyruvate and TCA cycle
Post-translational modification of proteins	Transforming Growth Factor (TGF) beta signaling	Transcription	Translation
mRNA Processing	Xenobiotic metabolism		

Citing Reactome

Publication to cite Reactome:

Joshi-Tope G, Gillespie M, Vastrik I, D'Eustachio P, Schmidt E, de Bono B, Jassal B, Gopinath GR, Wu GR, Matthews L, Lewis S, Birney E, Stein L. 2005. Reactome: a knowledgebase of biological pathways. Nucleic Acids Res. 2005 Jan 1;33 Database Issue:D428-32. PMID: 15608231

Joshi-Tope G., Vastrik I., Gopinathrao G., Matthews L., Schmidt E., Gillespie M., D'Eustachio P., Jassal B., Lewis S., Wu G., Birney E., and Stein L. The Genome Knowledgebase: A Resource for Biologists and Bioinformaticists. Cold Spring Harb Symp Quant Biol. 2003;68:237-43. PMID: 15338623

Citing your contribution to Reactome:

Citing a module in Reactome

[Module Author Names]. [Year of Publication]. [Module Name] in [Summation Title]. Reactome.
World Wide Web URL - http://www.reactome.org

Citing a summation in Reactome

[Summation Author names]. [Year of Publication]. Reactome.
World Wide Web URL - http://www.reactome.org

Citing Reactome (all of it)

Reactome. Cold Spring Harbor Laboratory, European Bioinformatics Institute, and GO Consortium.
World Wide Web URL - http://www.reactome.org

Date: 2007-03-02 08:00:05

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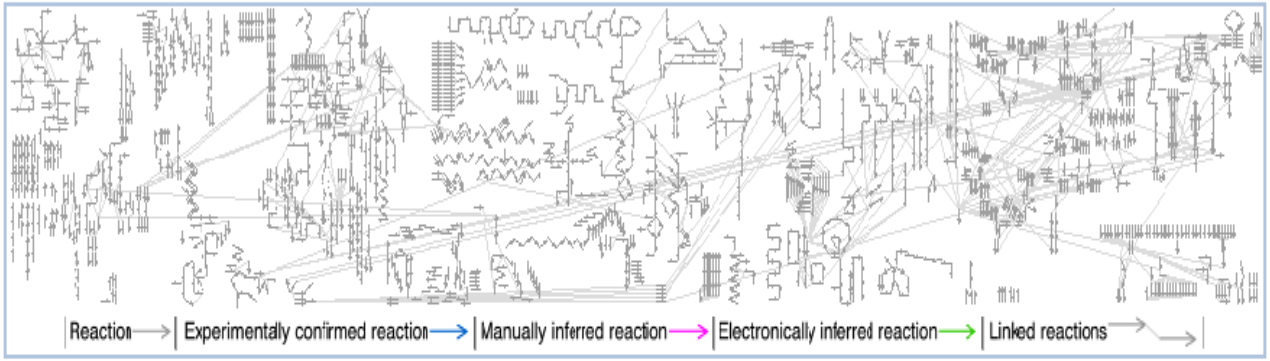

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Reactome Editorial Calendar

The Editorial Calendar shows work now under way to expand the Reactome knowledgebase, organized by planned date of public release on this web site. The Calendar also shows the Reactome curator who is managing the work on each topic. For more information, including information about how you can participate in the Reactome editorial process, e-mail the curator.

Click here for an internal version of editorial calendar with status updates from Reactome curators .

Font color key: central dogma, cell cycle metabolism signaling, transport, cell motility immune function, host-virus interaction neural function

Pathway Modules	Curator	Release Date
Porphyrin metabolism	Bijay Jassal	Current Release
Digestion of dietary lipids	Peter D'eustachio	Current Release
Digestion of carbohydrates	Peter D'eustachio	Current Release
Signaling pathways -EGFR signaling	Bijay Jassal	Current Release
Signaling pathways -FGFR signaling	Bernard de Bono	Current Release
Influenza virus life cycle- Regulation of RNPs	Marc Gillespie	Current Release
HIV life cycle - Rev protein interactions	Marc Gillespie	Current Release
Formation of gap junctions - trafficking	Lisa Matthews	Current Release
Lipoproteins - HDL and VLDL	Peter D'eustachio	mid-2007
Signaling pathways -PDGF signaling	Bijay Jassal	mid-2007
Interactions and signaling of immune synapses	Bernard de Bono	mid-2007
Neurotoxicity of Botulinum toxins	Gopal Gopinathrao	mid-2007
Influenza virus life cycle -M1 ion channel and neuraminidase	Marc Gillespie	mid-2007
Influenza virus life cycle -NS1 Pathway	Marc Gillespie	mid-2007
HIV - budding and release	Peter D'Eustachio	mid-2007
HIV life cycle - viral Assembly & Maturation	Gopal Gopinathrao	mid-2007
Signaling pathways -Rho GTPases	Gopal Gopinathrao	mid-2007
Epigenetic pathways I	Gopal Gopinathrao	mid-2007
Kinetochores	Lisa Matthews	late 2007
Obesity pathways	Peter D'Eustachio	late 2007
Cholesterol metabolism	Bijay Jassal	late 2007
HIV life cycle - Nef protein	Marc Gillespie	late 2007
Mitochondrial protein import	Marcela Tello-Ruiz	late 2007
Signaling pathways in beta cell differentiation	Marcela Tello-Ruiz	late 2007
Cell cycle, mitotic + checkpoints	Lisa Matthews	late 2007
Transcription, Pol II -revision	Marc Gillespie	future release
Cell motility: integrins, ECM attachment	Lisa Matthews	future release


GRACIAS