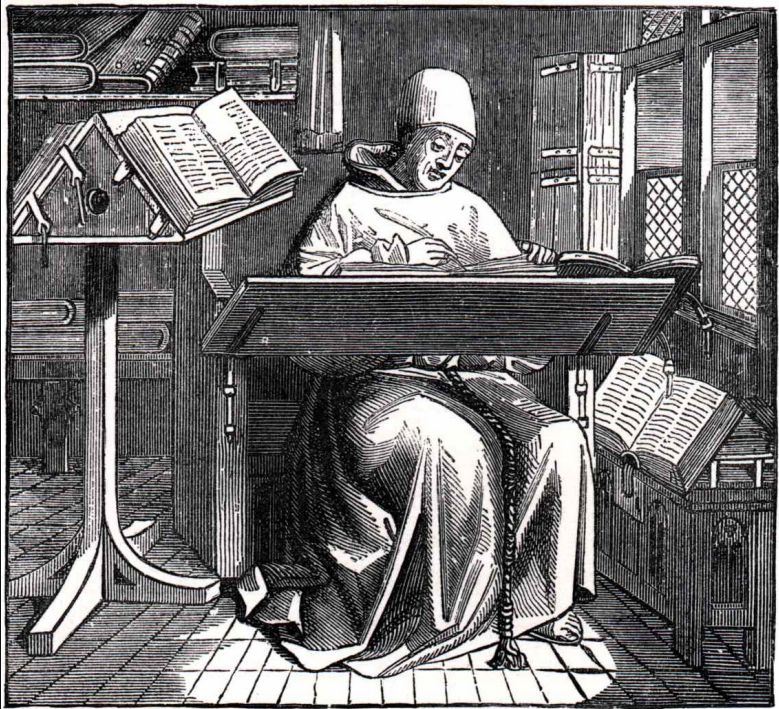


How we assist knowledge collection



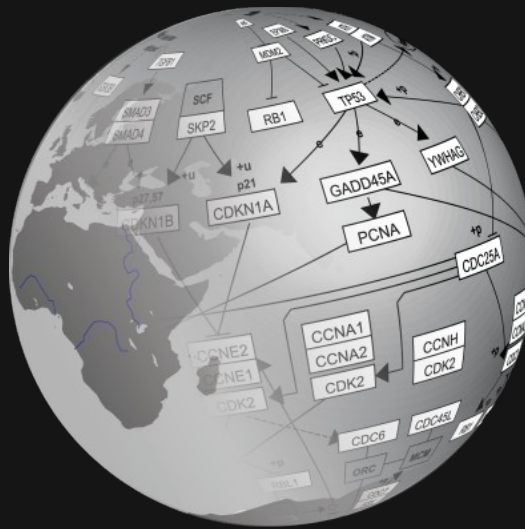
SCRIPTORIUM MONK AT WORK. (From Lacroix.)

Chris Evelo

Dept of Bioinformatics – BiGCaT
Maastricht University



Serving
the monks



WIKIPATHWAYS

Paper:

WikiPathways: Pathway Editing for the People. Alexander R. Pico, Thomas Kelder, Martijn P. van Iersel, Kristina Harbers, Bruce R. Conklin, Chris Evelo. **PLoS Biology** 2008: 6: 7. e184

Commentaries:

Big data: Wikiomics. Mitch Waldrop. **Nature** 455, 22-25 (2008)

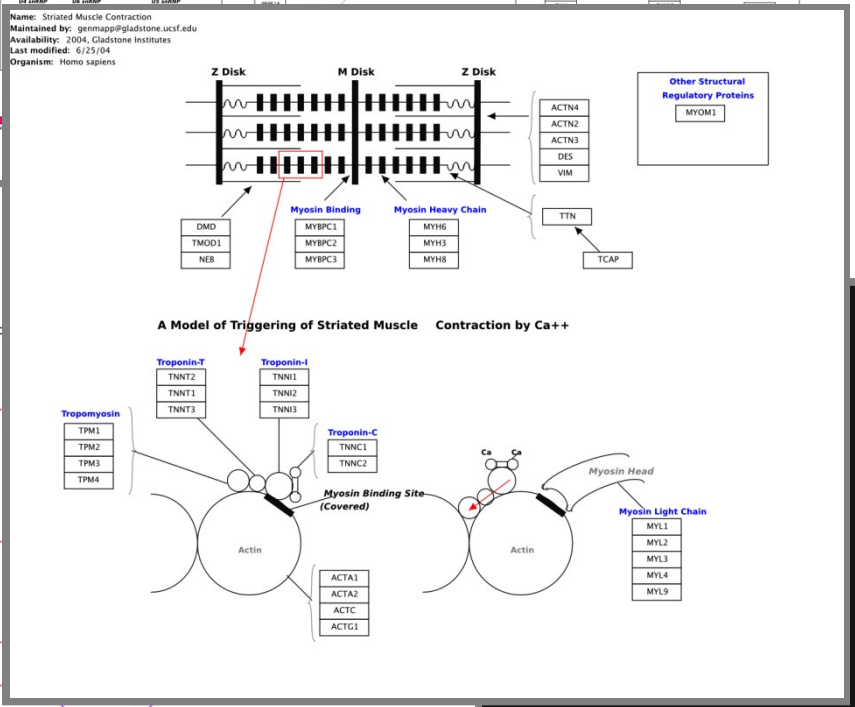
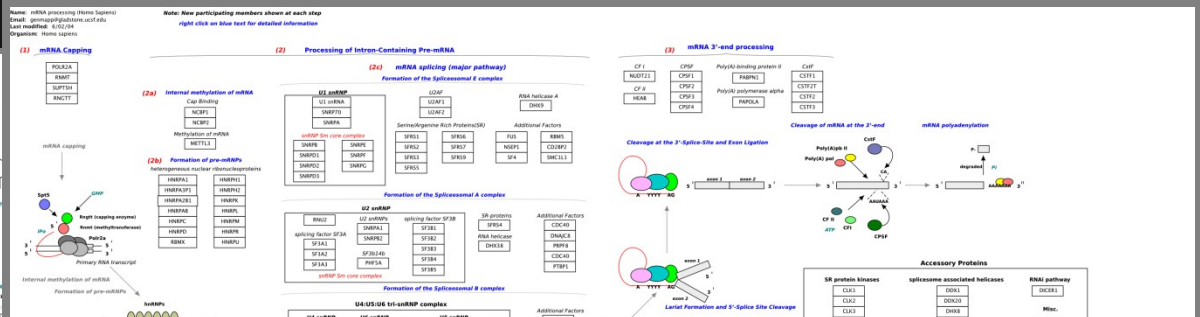
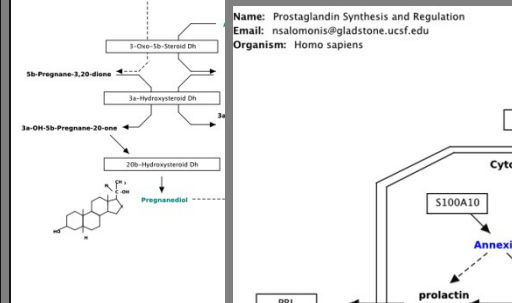
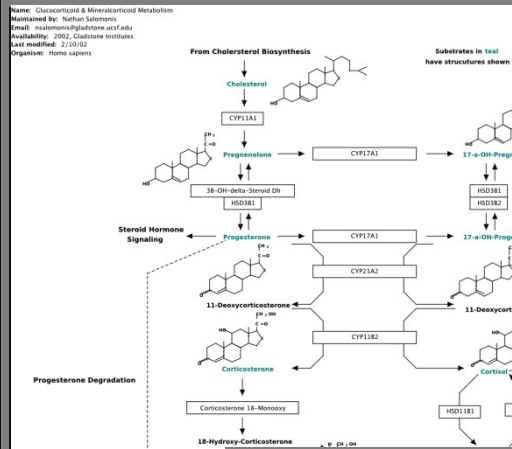
We the curators. Allison Doerr. **Nature Methods** 5, 754 - 755 (2008)



WikiPathways

- Public resource for biological pathways
- Wiki:
 - **Anyone** can contribute and curate
- More up-to-date representation of biological knowledge

What are biological pathways?

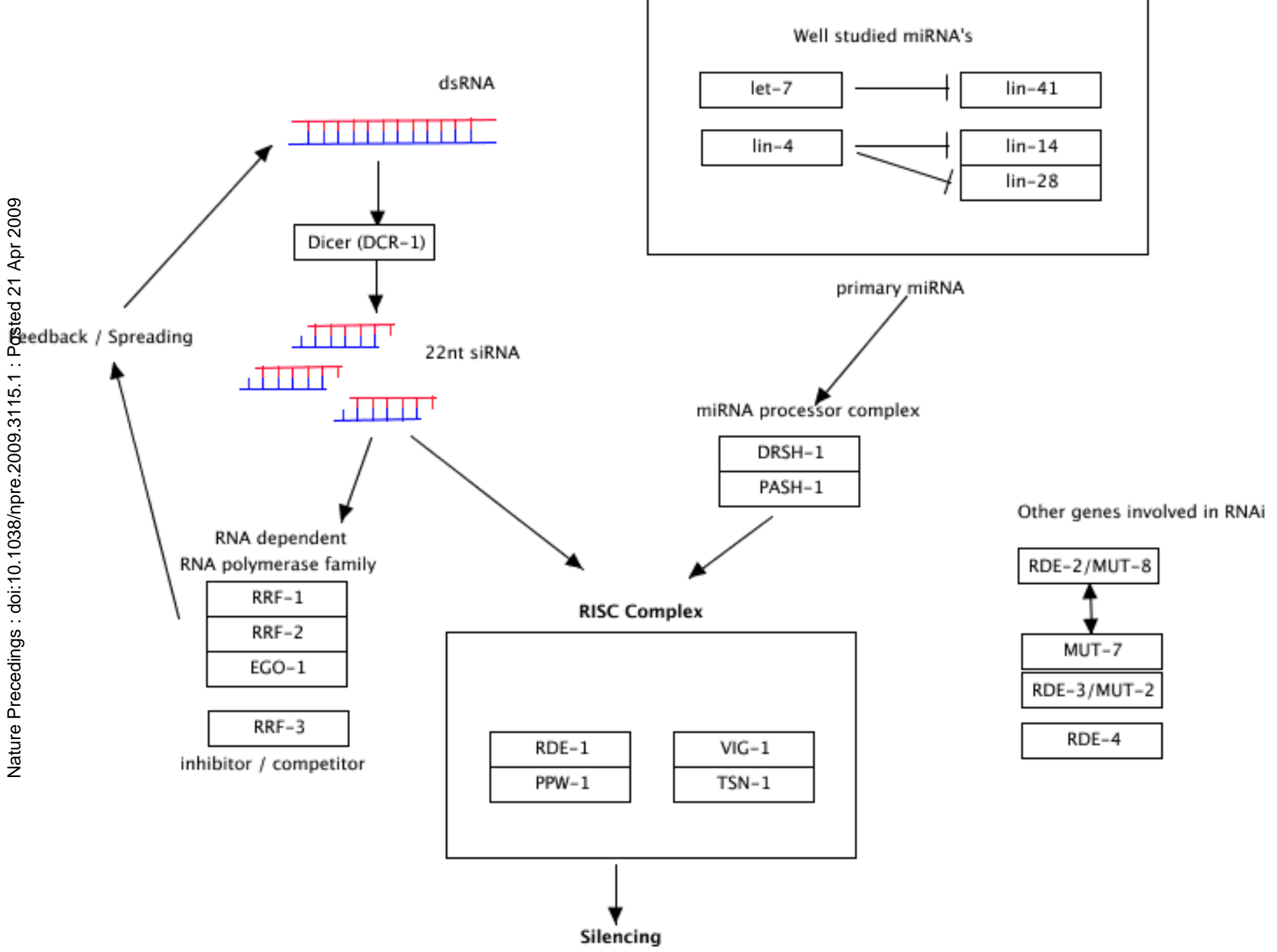


How are Pathways used?

- Example: RNA interference in *C. elegans*



The nematode *C. elegans*



Connect to Genome Databases

Ce_RNA_interference_and_miRNA - GenMAPP 2.0

File Tools Format View Data Help

End Label [Icons] More 100%

Author: Martijn van Iersel
 Maintained by: Martijn van Iersel
 E-mail: martijn.vaniersel@bigcat.unimaas.nl

RNA interference and miRNA

Some famous miRNA's

```

    graph TD
        dsRNA --> Dicer[DCR-1]
        Dicer --> siRNA[22nt siRNA]
        siRNA --> Feedback[Feedback / Spreading]
        siRNA --> RRF[RNA dependent RNA polymerase family]
        RRF --> RRF1[RRF-1]
        RRF --> RRF2[RRF-2]
        RRF --> EGO1[EGO-1]
        RRF --> RRF3[RRF-3]
        RRF --> Inhibitor[inhibitor / competitor]
    
```

No Gene Database

File Edit View History del.icio.us Bookmarks ScrapBook Tools Help

http://www.wormbase.org/db/gene/gene?name=WBGene0C

wikipathways genmapp bigcat rss pathvisio mediawiki mostused java cytoscape

Home Genome Blast / Blat WormMart Batch Sequences Markers Genetic Maps Submit Searches Site Map

Find: WBGene0006924
 Anything

WormBase The Biology and Genome of *C. elegans*.

Gene Summary for **vig-1**

Specify a gene using a gene name ([unc-26](#)), a predicted gene id ([R13A5.9](#)), or a protein ID ([CE02711](#))

[identification][location][function][expression][gene ontology][alleles][similarities][reagents][bibliography]

Identification	IDs:	Main name	Sequence name	Other name(s)	WB Gene ID
		vig-1 - (<i>VIG (Drosophila Vasa Intronic Gene) ortholog</i>) via person evidence: Ronald Plasterk	F56D12.5	2B613 (inferred automatically)	WBGene0006924

Concise Description: vig-1 encodes a predicted RNA-binding protein orthologous to Drosophila VIG (Vasa Intronic Gene); vig-1 activity is required for proper function of the let-7 miRNA in vivo and thus, for regulating the transition from late larval to adult cell fates; VIG-1 is a component of the 250 kDa RNA-induced silencing complex (RISC) complex and co-immunoprecipitates with both TSN-1, the *C. elegans* Tudor-SN ortholog, and the let-7 miRNA. [\[details\]](#)

NCBI KOGs*: Predicted RNA-binding protein [[KOG2945](#)]; [[OMpre_WH000977](#)]

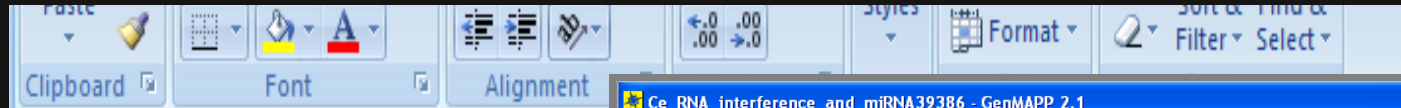
Species: *Caenorhabditis elegans*

Other sequences

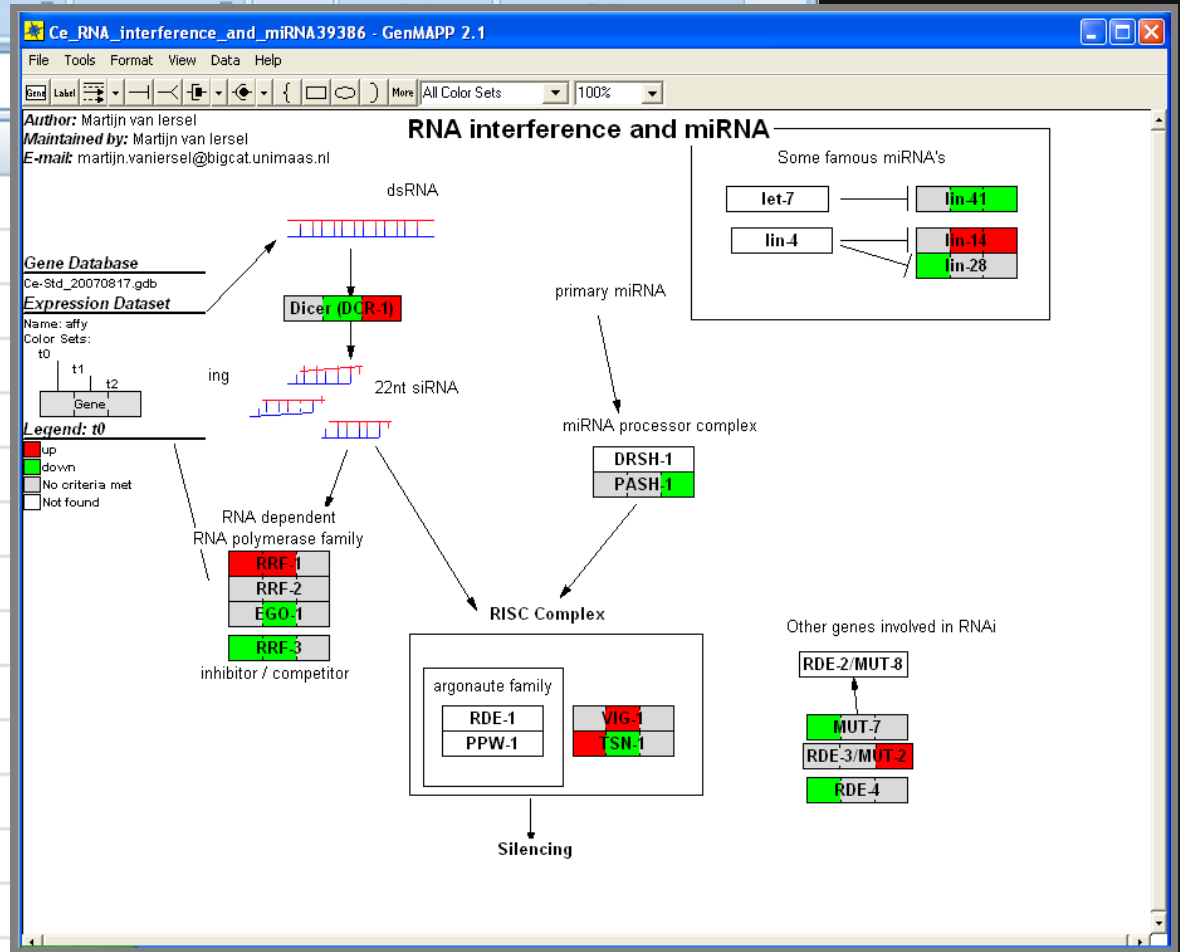
NCBI: [[AceView: 2B613](#)]

Done 4472 1087.thomaskelder@gmail.com

Data Visualization

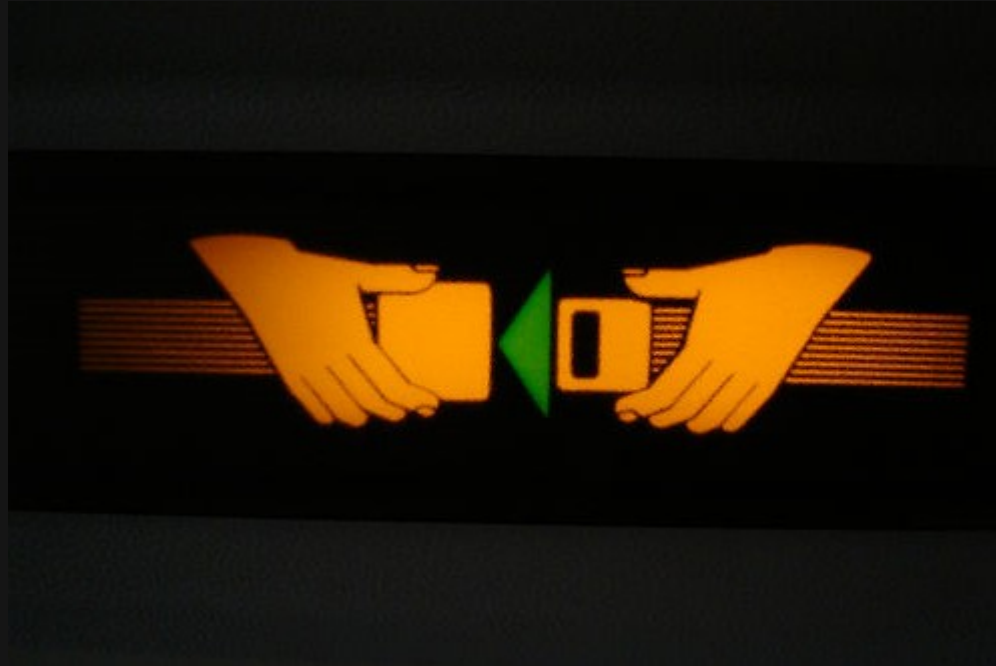


A20					
	A	B	D	E	
1	ID	System	t0	t1	t2
2	177140_s_X		0.693	-2.856	
3	186328_atX		1.327	3.497	
4	192151_atX		3.863	-3.457	
5	187703_s_X		1.16	-3.352	
6	193913_s_X		-0.435	3.356	
7	173437_atX		-2.36	-1.633	
8	173452_s_X		-2.43	0.035	
9	no affy	X	-1.878	2.211	
10	178221_atX		-1.758	-3.223	
11	173832_atX		-3.386	1.695	
12	184510_atX		0.109	-1.045	
13	192371_s_X		-3.075	-0.404	
14	172670_x_X		3.642	3.428	
15	176778_s_X		-0.112	1.072	-1.695



On to the real thing...

Fasten seat belts!



Welcome to WikiPathways BETA

In the new tradition of Wikipedia, WikiPathways is an open, public platform dedicated to the curation of biological pathways by and for the scientific community. [More about WikiPathways...](#)

Finding Pathways

Search

Google Custom Search
Search

You can search by:

- Pathway name (*Apoptosis*)
- Gene or protein name (*p53*)
- Any page content (*cancer*)

Browse

Browse pathways

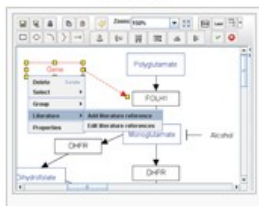
Display pathways from species: (Human) in category: Metabolic_Processes

- Autolysis/Selflysis
- Alveolar and alveolar interstitial KEGG
- Bile acid synthesis
- Cholesterol Biosynthesis
- Essential Synthesis
- Electron Transport Chain
- Fatty Acid Beta Oxidation 1 BIOCAT
- Fatty Acid Beta Oxidation 2 BIOCAT
- Fatty Acid Beta Oxidation 3 BIOCAT
- Fatty Acid Beta Oxidation Hexa BIOCAT
- Fatty Acid Omega Oxidation BIOCAT
- Fatty Acid Synthesis BIOCAT
- Glycosylated Monosaccharide Metabolism
- Glyoxylate Metabolism
- Glyoxylate and Glutamate/oxaloacetate
- Heme Biosynthesis
- Mitochondrial fatty acid betaoxidation
- Nuclear receptors in lipid metabolism and obesity
- Nucleotide Metabolism
- One-carbon metabolism

Browse by species and category

Contributing New Pathways

Create



Create a new pathway page

Suggest

Pathway wishlist

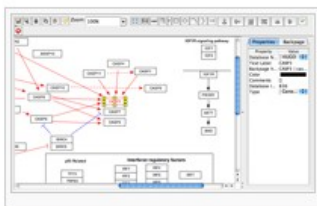
Add new entries from here

Pathway name	Requested by	Date	Comments	View	Watch	Resolve
Pathogen-mediated metabolic regulation	Enrico	07.07.08	We want to use this to include CDP data from Andrea	+	+	+
Protein Translation Regulation	Enrico	02.06.16	Should be renamed around MET, not TOR.	+	+	+
DNA Damage response	Enrico	02.06.16	According to Wilson consider this should be better DNA repair	+	+	+
Redox/oxides on transport in the kidney	Enrico	01.05.9	Can be on during discussion with professor Hans-Bernd Mueller about path. name	+	+	+

Add a pathway to the wish list

Sample Pathway Pages

Sandbox



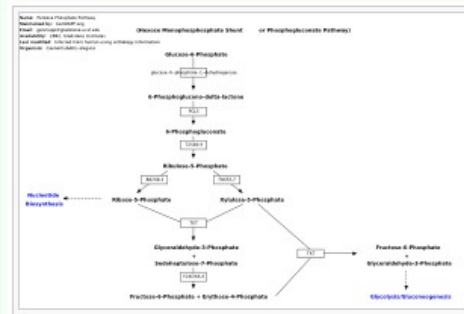
Check out the following pages:

- Show recent changes
- Show new pathways
- Show most edited pathways
- Show most viewed pathways

For more information see the [Help pages](#)

Today's featured pathway

Pentose Phosphate Pathway (Caenorhabditis elegans)



Pentose Phosphate Pathway

New!

- WikiPathways won the application showcase at the [NBIC BioRange Consortium Meeting](#)!
- Pathway [Wish List](#)
- New embedded pathway editor
- [Batch download page](#)
- Visual diff tool for comparing pathway versions

Coming Soon...

- Converted content from KEGG and Reactome
- Tagging pathways with terms from Gene Ontology and other biological ontologies

Statistics

- There are **497** pathways
- Number of **pathways (and unique genes)** per species:

Homo sapiens:	103 (3436)
Rattus norvegicus:	105 (3049)
Mus musculus:	109 (3725)
Drosophila melanogaster:	27 (553)
Caenorhabditis elegans:	23 (367)

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Pathways for the People

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Articles only

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- Permanent link

Nature Precedings: doi:10.1038/npre.2009.3151

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Finding Pathways

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Google Custom Search
Search

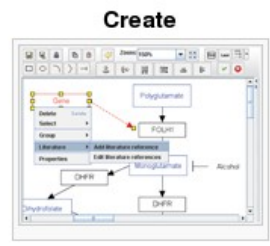
- You can search by:
- Pathway name (Apoptosis)
- Gene or protein name (p53)
- Any page content (cancer)

Browse
Browse Pathways
Display pathways from species: Human
In category: Metabolic_Process

Browse by species and category

Search: "One carbon"

Contributing New Pathways

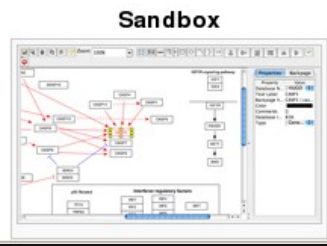


Create a new pathway page

Table with columns: Pathway name, Reported by, Date, Comments, Likes, Watch, Results. Contains a list of pathway suggestions.

Add a pathway to the wish list

Sample Pathway Pages



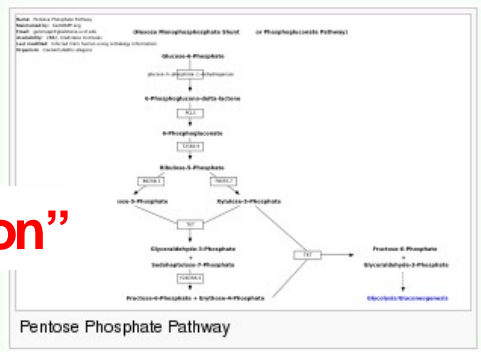
Check out the following pages:

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Navigation sidebar containing: BETA, WIKIPATHWAYS, navigation, create, browse, wish list, download, about us, overview, recent changes, most viewed, most edited, new pathways, links, GenMAPP, PathVisio, search, Google Custom Search, tool box, what links here, related changes, special pages, printable version, permanent link.

- project page
- discussion
- edit
- history
- move
- watch

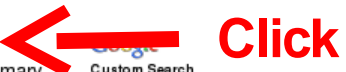
WikiPathways:GoogleSearch

Results 1 - 3 for **one carbon**. (0.04 seconds)

Refine results for **one carbon**:

- [Human](#)
- [Mouse](#)
- [Rat](#)
- [All](#)
- [Fruit Fly](#)
- [Worm](#)
- [Yeast](#)

[Pathway:Mus musculus:One-carbon metabolism - WikiPathways](#)



This **one-carbon** metabolism pathway is centered around folate. Folate is the primary methyl-group donor for processes such as DNA methylation reactions, ...
www.wikipathways.org/index.php/Pathway:Mus_musculus:One-carbon_metabolism
Labeled [Mouse](#) [All](#)

[Pathway:Saccharomyces cerevisiae:Principle Carbon Metabolism ...](#)

Pathway: Saccharomyces cerevisiae: Principle **Carbon** Metabolism ... PYK2, GeneProduct, PYK2 | Pyruvate kinase **one** of two isoforms th... YOR347C (SGD) ...
www.wikipathways.org/index.php/Pathway:Saccharomyces_cerevisiae:Principle_Carbon_Metabolism
Labeled [All](#) [Yeast](#)

[Pathway:Saccharomyces cerevisiae:Glycolysis and Gluconeogenesis ...](#)

... JR (2004) **Carbon** Metabolism in The Metabolism and Molecular Physiology of ... PYK2, GeneProduct, PYK2 | Pyruvate kinase **one** of two isoforms th. ...
www.wikipathways.org/index.php/Pathway:Saccharomyces_cerevisiae:Glycolysis_and_Gluconeogenesis
Labeled [All](#) [Yeast](#)

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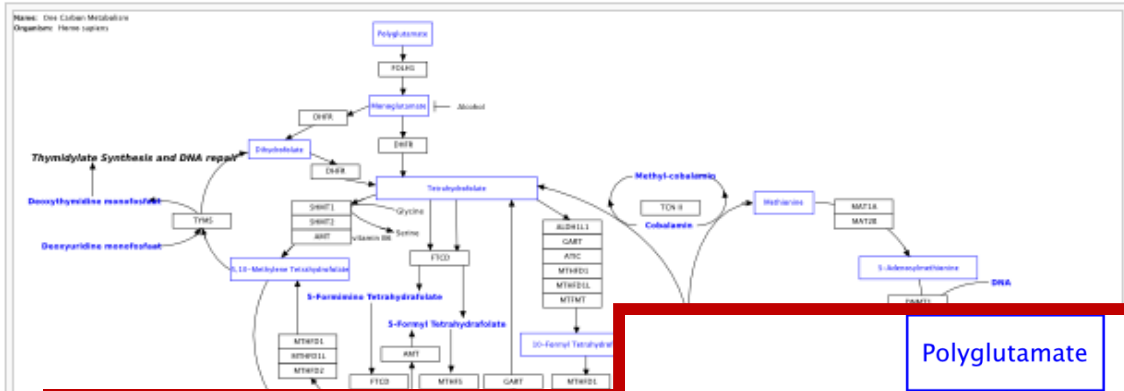
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Pathway:Homo sapiens:One-carbon metabolism



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 - 4.3 Actions

DataNodes
View all 40 DataNodes

Descriptor	Name	Type

Polyglutamate → **FOLH1** → **Monoglutamate** (Alcohol inhibition) → **DHFR** → **Tetrahydrofolate**

Tetrahydrofolate → **DHFR** → **Dihydrofolate** → **DHFR** → **Methylenetetrahydrofolate**

Methylenetetrahydrofolate → **SHMT1** / **SHMT2** → **Glycine** + **5,10-Methylene Tetrahydrofolate**

Methylenetetrahydrofolate → **AMT** → **5-Formyl Tetrahydrofolate** → **5,6-Methyltetrahydrofolate** → **5-Methyltetrahydrofolate** → **5,10-Methylenetetrahydrofolate**

Methylcobalamin → **Methylenetetrahydrofolate**

Vitamin B6 → **SHMT1** / **SHMT2** → **Glycine** + **5,10-Methylene Tetrahydrofolate**

Bibliography

- Hazra A, Wu K, Kraft P, Fuchs CS, Giovannucci EL, and Hunter DJ. Twenty-four non-synonymous polymorphisms in the one-carbon metabolic pathway and risk of colorectal adenoma in the Nurses' Health Study. *Carcinogenesis* 2007 Jul; 28(7) 1510-9. doi:10.1093/carcin/bgm062 pmid:17388610

Bibliography	GeneProduct	64/2 (Entrez Gene)
SHMT2		

1. Hazra A, Wu K, Kraft P, Fuchs CS, Giovannucci EL, and Hunter DJ. Twenty-four non-synonymous polymorphisms in the one-carbon metabolic pathway and risk of colorectal adenoma in the Nurses' Health Study. *Carcinogenesis* 2007 Jul; 28(7) 1510-9. doi:10.1093/carcin/bgm062 pmid:17388610. [PubMed Link](#) [PubMed ID](#)

Editing

21 Apr 2009
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Google Custom Search

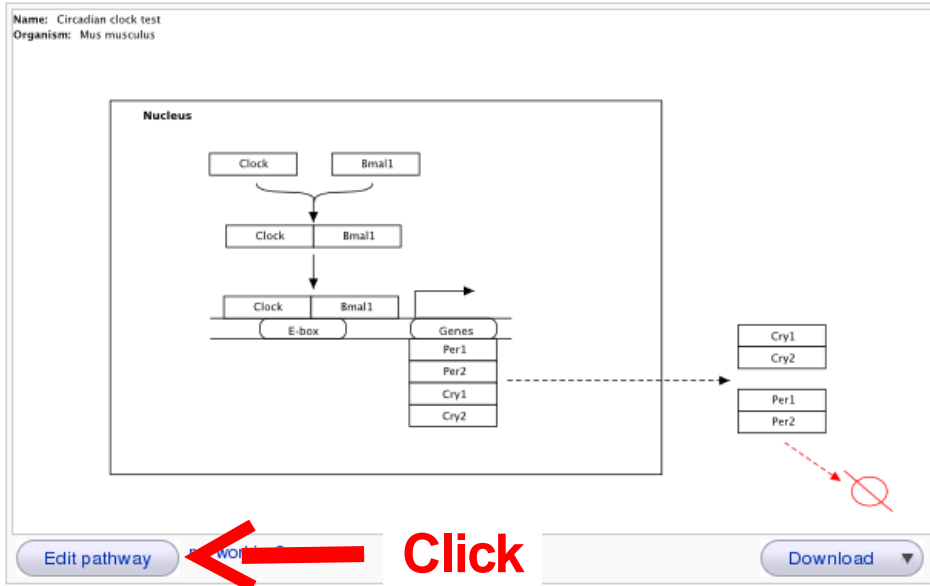
Titles only

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- history
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Pathway:Mus musculus:Circadian clock pathway



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 - 4.2 Data formats
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 - 4.4 Batch
- 5 History
- 6 Pathway Info
 - 6.1 DataNodes

Description

The circadian clock is a molecular mechanism that maintains the cell's metabolism, physiology and behaviour. This is a simplified version of t

Login needed
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All edits logged

genes, involved in [edit](#)

Draw the proteins and interactions

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Pathway:Mus musculus:Circadian clock pathway

Zoom: 100%

Name: Circadian clock test
Organism: Mus musculus

Click

Click & drag

```
graph TD
    subgraph Nucleus
        C1[Clock]
        B1[Bmal1]
        C2[Clock]
        B2[Bmal1]
        C3[Clock]
        B3[Bmal1]
        E[E-box]
        G[Genes]
        G --- P1[Per1]
        G --- P2[Per2]
        G --- C1_1[Cry1]
        G --- C1_2[Cry2]
    end
    C1 --- C2
    B1 --- B2
    C2 --- C3
    B2 --- B3
    C3 --- E
    B3 --- E
    E --- G
    G -.-> C2_1[Cry1]
    G -.-> C2_2[Per1]
    G -.-> C2_3[Per2]
```

Property	Value
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not working?

Draw the proteins and interactions

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Pathway: Mus musculus: Circadian clock pathway

Zoom: 100%

Name: Circadian clock test
Organism: Mus musculus

Click

Property	Value
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Comments	[]
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Line Style	Solid
Shape Type	Brace
Transparent	<input checked="" type="checkbox"/>

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21 Apr 2009
15:11
2009.3
10:03
doi:10.1038/nature.2009.31511

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Pathway:Mus musculus:Circadian clock pathway

Zoom: 100%

Name: Circadian clock test
Organism: Mus musculus

Properties Backpage

Property	Value
Color	

Click & drag

The diagram shows a 'Nucleus' containing 'Clock' and 'Bmal1' proteins. These form a complex that binds to an 'E-box' on DNA. This complex regulates the expression of 'Genes', which include 'Per1', 'Per2', 'Cry1', and 'Cry2'. The diagram shows the expression of these genes and their subsequent translation into proteins. A red arrow points to a yellow square handle on the diagram, with the text 'Click & drag' next to it. A red dashed circle with a slash is also visible on the diagram.

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Pathway:Mus musculus:Circadian clock pathway

Zoom: 100%

Name: Circadian clock test
Organism: Mus musculus

Nucleus

Diagram illustrating the Circadian clock pathway in *Mus musculus*. The pathway shows the interaction between Clock and Bmal1 proteins, which bind to an E-box on DNA, leading to the transcription of Genes (Per1, Per2, Cry1, Cry2). The proteins Per1, Per2, Cry1, and Cry2 then form a complex that inhibits Clock and Bmal1, completing the cycle.

Property	Value
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Database ...	Ensembl
Text Label	Different va...
Type	GenePr...

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21 Apr 2009
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doi:10.1038/nature.2009.31151

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Pathway:Mus musculus:Circadian clock pathway

Zoom: 100%

Name: Circadian clock test
Organism: Mus musculus

Nucleus

Clock Bmal1

Clock Bmal1

Clock Bmal1

E-box Genes

Per1
Per2
Cry1
Cry2

Per1
Per2
Cry1
Cry2

Per1
Per2
Cry1
Cry2

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Comments	
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Line Style	Solid
Start Line T...	Line

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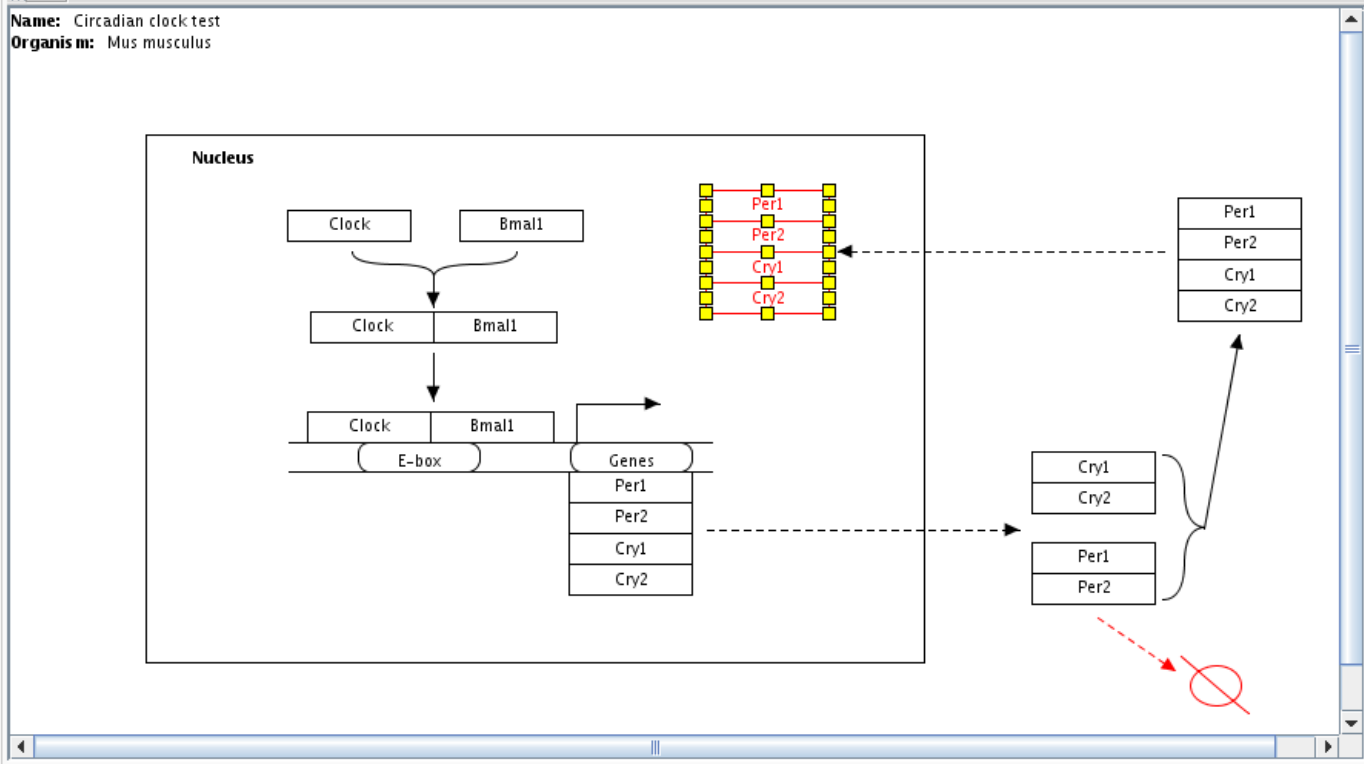
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Pathway:Mus musculus:Circadian clock pathway

Zoom: 100%



Property	Value
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Color	
Comments	[]
Database l...	Different va...
Database ...	Ensembl
Text Label	Different va...
Type	GenePr...

not working?

Draw the proteins and interactions

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Pathway: Mus musculus: Circadian clock pathway

Zoom: 100%

Name: Circadian clock test
Organism: Mus musculus

Nucleus

Clock Bmal1

Per1
Per2
Cry1
Cry2

Per1
Per2
Cry1
Cry2

Cry1
Cry2

Per1
Per2

E-box Genes

Per1
Per2
Cry1
Cry2

not working?

Property	Value
----------	-------

Annotate the proteins

21 Apr 2009 10:03 AM
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Pathways for the People

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Pathway:Mus musculus:Circadian clock pathway

Zoom: 100%

Name: Circadian clock test
Organism: Mus musculus

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Property	Value
----------	-------

not working?

Annotate the proteins

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Pathway:Mus musculus:Circadian clock pathway

Zoom: 100%

Name: Circadian clock test
Organism: Mus musculus

DataNode properties

Comments Literature **Annotation**

Search

Manual entry

Text label: Per1
Identifier: ENSMUSG000000020893
Database: Ensembl

Cancel Ok

Properties Backpage

Gene information

Gene ID:	ENSMUSG000000020
Gene Symbol:	Per1
Description:	period homolog (Drosophila) [Source:MGI.Acc:MGI:10
Chr:	11

not working?

Add reference to literature

pathway discussion edit history delete move protect unwatch

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Pathway: Mus musculus: Circadian clock pathway

Name: Circadian clock test
Organism: Mus musculus

Zoom: 100%

Literature reference properties

Pubmed ID	17430084	Query PubMed
Title	The clockwork of metabolism.	
Year	2007	
Source	Annu Rev Nutr	
Authors (separate with ;)	Ramsey KM; Marcheva B; Kohsaka A; Bass J	

Cancel Ok

Click

Delete
Select
Add anchor Ctrl-R
Order
Literature
Properties

Add literature reference
Edit literature references

Save the pathway

11 Apr 2009

BETA

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Pathway:Mus musculus:Circadian clock pathway

Zoom: 100%

Name: Circadian clock pathway
Organism: Mus musculus

Click save

not working?

Property	Value
----------	-------

Updated pathway page

21 Apr 2009
BETA
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links
■ GenMAPP
■ PathVisio

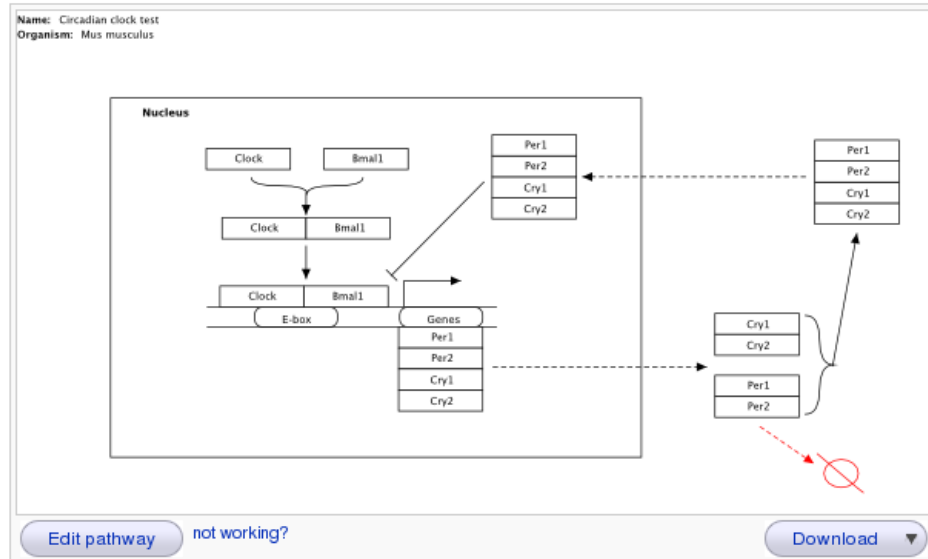
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Pathway:Mus musculus:Circadian clock pathway



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 - 4.2 Data formats
 - 4.3 Actions
 - 4.4 Batch
- 5 History
- 6 Pathway Info
 - 6.1 DataNodes

Description

The circadian clock is a molecular mechanism that maintains the cell's 24-hour molecular rhythm by driving the rhythmic expression of a wide range of genes, involved in metabolism, physiology and behaviour. This is a simplified version of the pathway, restricting to the mPer/mCry feedback loop

[edit](#)

Bibliography

1. Ramsey KM, Marcheva B, Kohsaka A, and Bass J. *The clockwork of metabolism*. Annu Rev Nutr 2007; 27 219-40. doi:10.1146/annurev.nutr.27.061406.093546 pmid:17430084. PubMed HubMed [dcb]

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Pathways for the People

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- Wish List
- Download
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- Recent Changes
- Most Viewed
- Most Edited
- New Pathways

- Links
- GenMAPP
- PathVisio

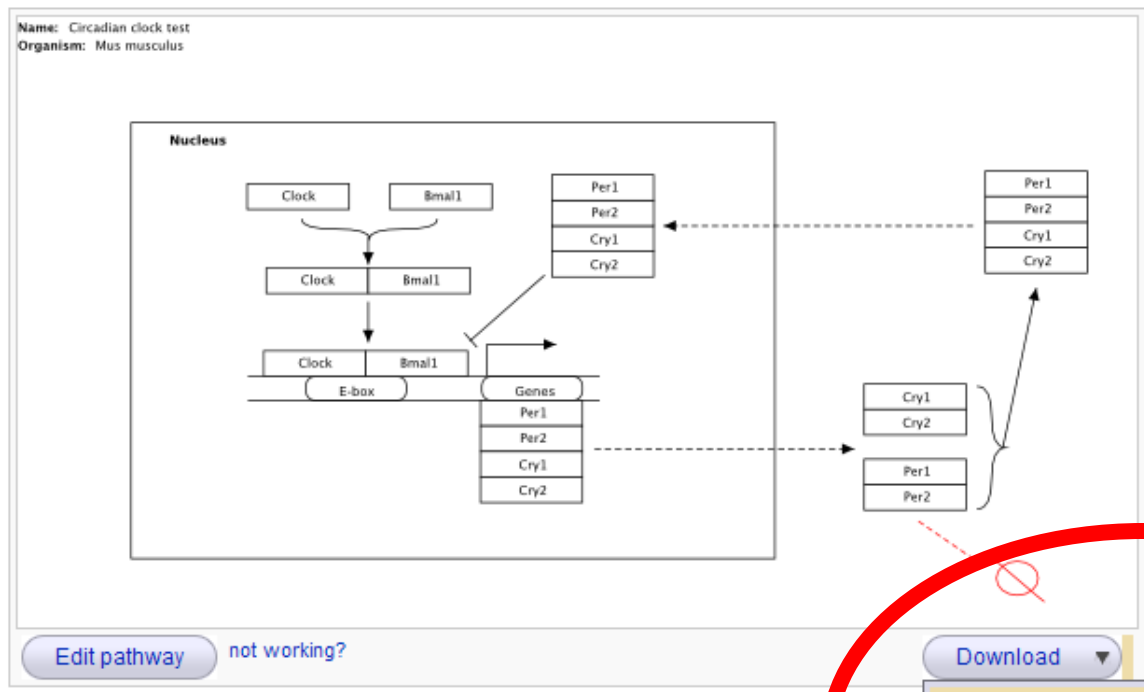
- Search
- Google Custom Search
- titles only

- toolbox
- What links here
- Related changes
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- Printable version
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- pathway
- discussion
- edit
- history
- delete
- move
- protect
- unwatch

Pathway:Mus musculus:Circadian clock pathway



- Contents [hide]
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 - 4.4 Batch
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 - 6 Pathway Info
 - 6.1 DataNodes

Download

- Download for
 - PathVisio (.gpm)
 - GenMAPP (.mapp)
 - Gene list (.txt)
 - Eu.Gene (.pwf)
 - Png image (.png)
 - Acrobat (.pdf)
- Open in Cytoscape

Description

The circadian clock is a molecular mechanism that maintains the cell's 24-hour molecular rhythm by driving the rhythmic expression of a wide range of genes, involved in metabolism, physiology and behaviour. This is a simplified version of the pathway, restricting to the mPer/mCry feedback loop

Bibliography

1. Ramsey KM, Marcheva B, Kohsaka A, and Bass J. *The clockwork of metabolism*. Annu Rev Nutr 2007; 27 219-40. doi:10.1146/annurev-nutr-061406-093546 pmid:17430084 PubMed HubMed [doi]

“ Wiki’ s work because it is easier to undo damage than to create it.

Imagine what cities would look like if it was easier to clean graffiti than to create it”

–Clay Shirkey



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article discussion edit this page history

Division by zero

From Wikipedia, the free encyclopedia
(Difference between revisions)

Revision as of 07:12, 29 January 2008 (edit)
 Adam1213 (Talk | contribs)
 (Undid revision 187649938 by *Spoofergirl* (talk))
 ← Older edit

Revision as of 12:34, 29 January 2008 (edit) (undo)
 71.235.33.246 (Talk)
 (→Historical accidents)
 Newer edit →

Line 148:

```

==Historical accidents==

* On [[September 21]], [[1997]], a divide by zero error in the
[[USS Yorktown (CG-48)]] "Remote Data Base Manager" brought
down all the machines on the network, causing the ship's
propulsion system to fail. <ref>{{cite
news|url=http://www.wired.com/news/technology/0,1282,13987,0
by Windows NT|date=[[1998-07-24]]|work=[[Wired
News]]}}</ref>

```

Line 148:

```

==Historical accidents==

* On [[September 21]], [[1997]], a divide by zero error in the
[[USS Yorktown (CG-48)]] "Remote Data Base Manager" brought
down all the machines on the network, causing the ship's
propulsion system to fail. <ref>{{cite
news|url=http://www.wired.com/news/technology/0,1282,13987,0
by Windows NT|date=[[1998-07-24]]|work=[[Wired
News]]}}</ref>

```

+ * It is a well knows fact that on [[December 20]] [[2007]], a student divided by zero on his [[TI-81]] [[Graphing calculator]] which caused a [[portal]] to open and suck in the school. it is also well known that the only way to get rid of these portals is to multiply by 1.

== Footnotes ==

== Footnotes ==

Revision as of 12:34, 29 January 2008



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Revision as of 12:34, 29 January 2008 (edit)

71.235.33.246 (Talk)
(→Historical accidents)
← Older edit

Line 148:

```

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by Windows NT|date=[[1998-07-24]]|work=[[Wired
News]]}}</ref>

```

```

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- which caused a [[portal]] to open and suck in the school. it is
also well known that the only way to get rid of these portals is to
multiply by 1.

```

== Footnotes ==

Revision as of 12:35, 29 January 2008 (edit) (undo)

Allstarecho (Talk | contribs)
m (Reverted edits by 71.235.33.246 (talk) to last version by Adam1213)
Newer edit →

Line 148:

```

==Historical accidents==
* On [[September 21]], [[1997]], a divide by zero error in the
[[USS Yorktown (CG-48)]] "Remote Data Base Manager" brought
down all the machines on the network, causing the ship's
propulsion system to fail. <ref>{{cite
news|url=http://www.wired.com/news/technology/0,1282,13987,0
by Windows NT|date=[[1998-07-24]]|work=[[Wired
News]]}}</ref>

```

== Footnotes ==

Revision history

History

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Compare selected versions

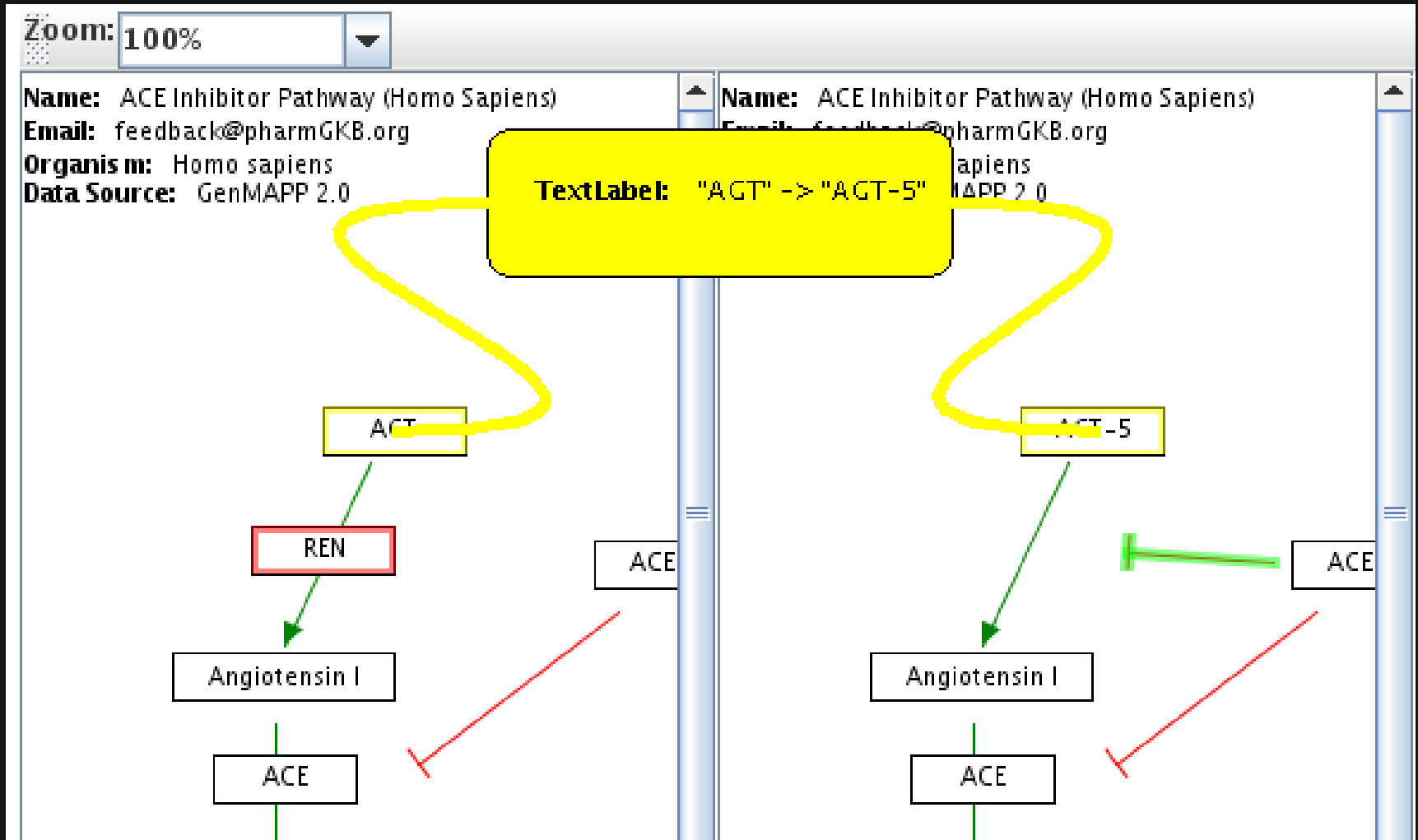
Compare	Action	Time	User	
<input checked="" type="checkbox"/>	view	11:12, 1 April 2008	Thomas	Modified categories
<input checked="" type="checkbox"/> <input type="checkbox"/>	(revert) , view	14:31, 11 March 2008	Thomas	[[Pathway:Homo sapiens:Phase I, non P450 biotransformations]]: invalid character
<input type="checkbox"/> <input type="checkbox"/>	(revert) , view	10:20, 4 March 2008	Evelo	[[Pathway:Homo sapiens:Phase I biotransformations]]: also have a P450 pathway, which belongs to P
<input type="checkbox"/> <input type="checkbox"/>	(revert) , view	10:20, 4 March 2008	Evelo	renamed
<input type="checkbox"/> <input type="checkbox"/>	(revert) , view	12:14, 3 March 2008	Thomas	added bibliography
<input type="checkbox"/> <input type="checkbox"/>	(revert) , view	12:12, 3 March 2008	Thomas	Modified description
<input type="checkbox"/> <input type="checkbox"/>	(revert) , view	12:10, 3 March 2008	Thomas	added gene annotations, translated labels
<input type="checkbox"/> <input type="checkbox"/>	(revert) , view	11:52, 3 March 2008	Thomas	[[Pathway:Homo sapiens:Phase I]] moved to [[
<input type="checkbox"/> <input type="checkbox"/>	(revert) , view	11:26, 28 February 2008	Rollie	Created Phasel pathway

Compare selected versions

Select two versions

Click

Diff tool



Growth

September 2008

More users, species,
pathways, genes

Statistics

- There are **497** pathways
- Number of **pathways** (*and unique genes*) per species:

Homo sapiens:	103 (3436)
Rattus norvegicus:	105 (3049)
Mus musculus:	109 (3725)
Drosophila melanogaster:	27 (553)
Caenorhabditis elegans:	23 (367)
Saccharomyces cerevisiae:	132 (1000)

- There are **182** registered users

February 2009

Statistics

- There are **589** pathways
- Number of **pathways** (*and unique genes*) per species:

Homo sapiens:	137
Rattus norvegicus:	116
Mus musculus:	117
Drosophila melanogaster:	28
Caenorhabditis elegans:	28
Saccharomyces cerevisiae:	132
Danio rerio:	25
Arabidopsis thaliana:	4
Oryza japonica:	2

- There are **650** registered users

Statistics

- There are **597** pathways
- Number of **pathways** (*and unique genes*) per species:

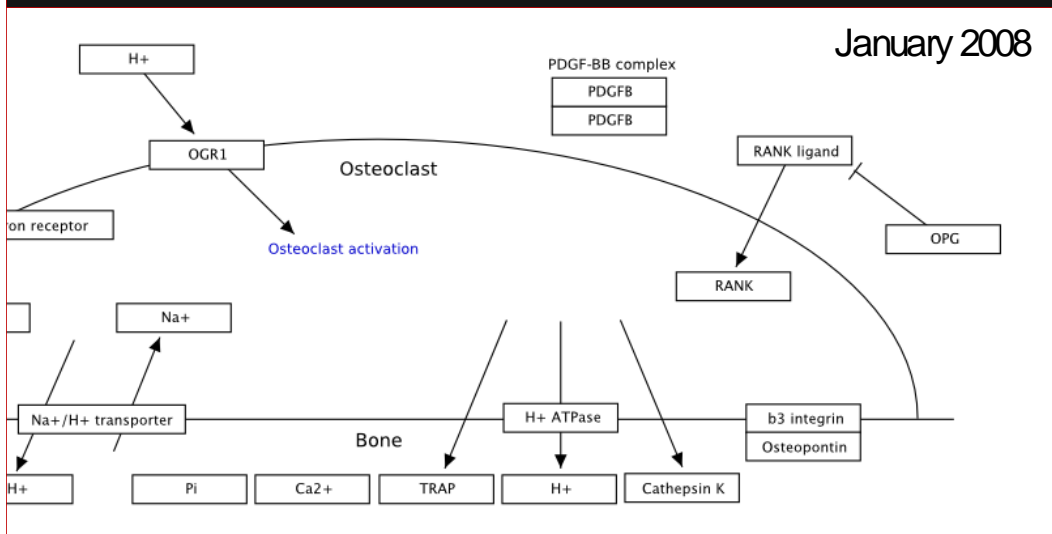
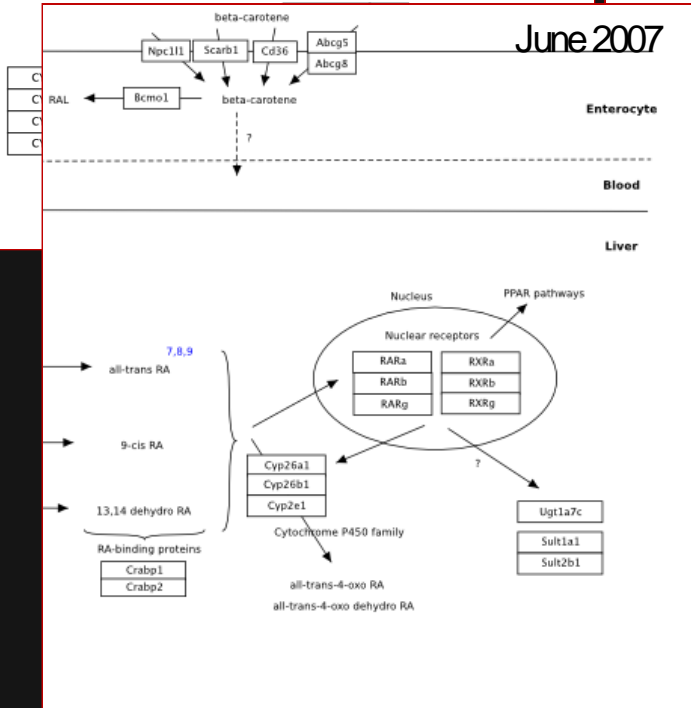
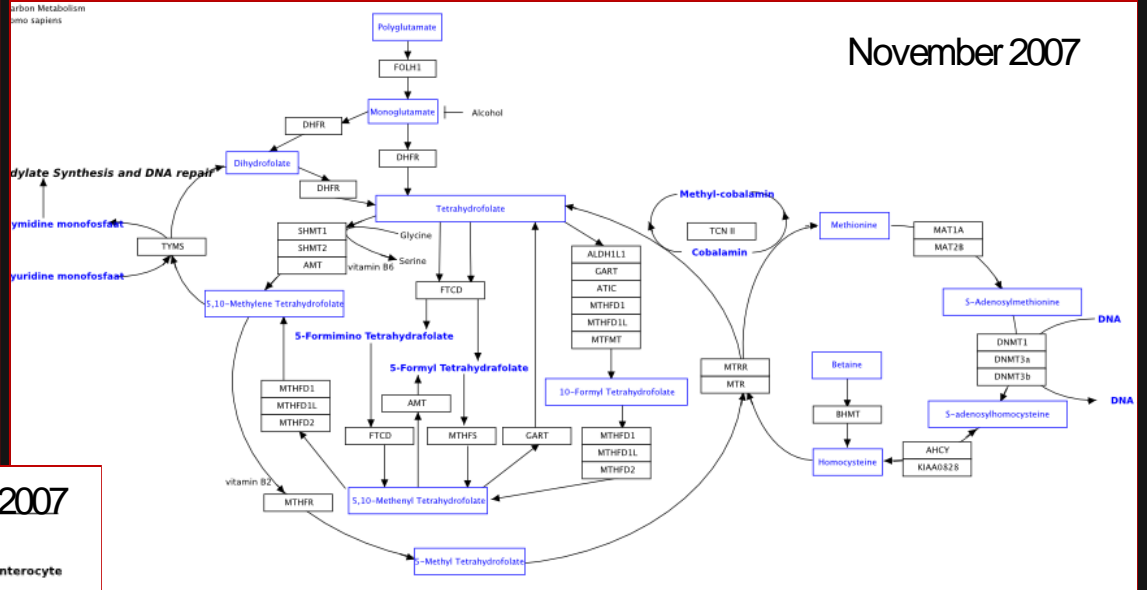
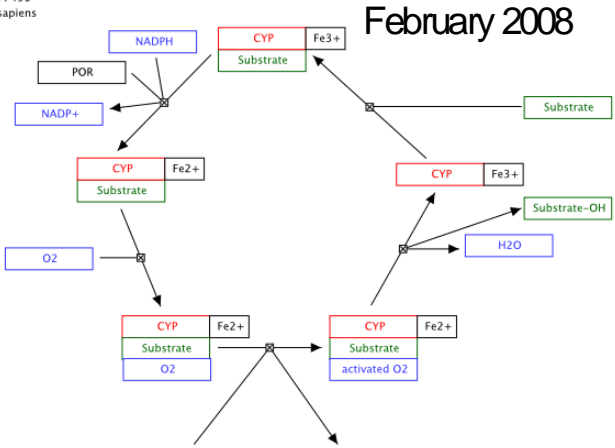
Homo sapiens:	142 (3711)
Rattus norvegicus:	115 (3147)
Mus musculus:	118 (3696)
Drosophila melanogaster:	28 (558)
Caenorhabditis elegans:	27 (490)
Saccharomyces cerevisiae:	134 (1014)
Danio rerio:	24 (925)
Arabidopsis thaliana:	6 (62)
Oryza sativa:	3 (0)

- There are **742** registered users

April 2009

Contributions – new pathways

Name: cytochrome P450
Organism: Homo sapiens



Nature Precedings : doi:10.1038/npre.2009.3115.1 : Posted 21 Apr 2009

Contributions – small edits

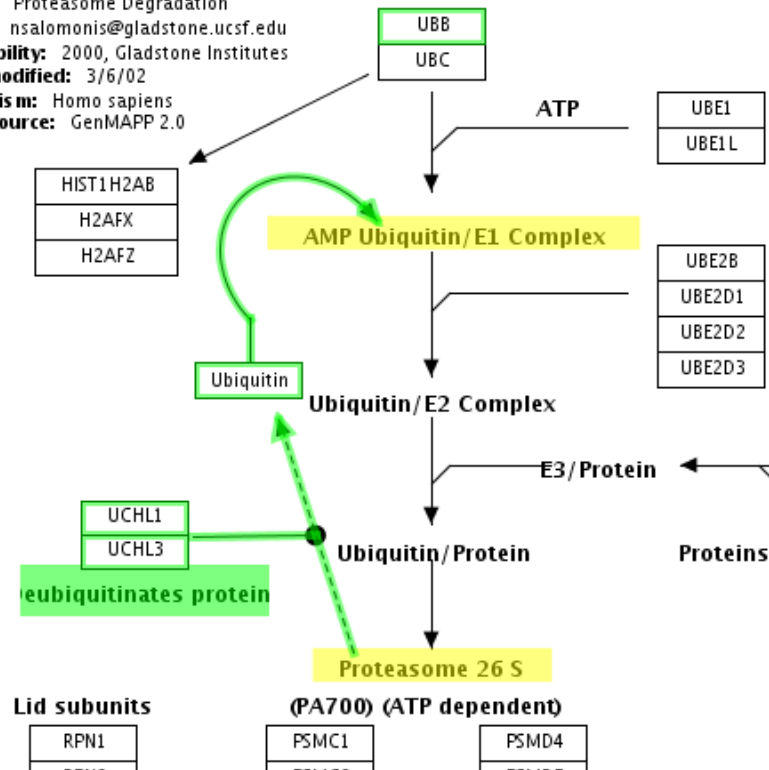
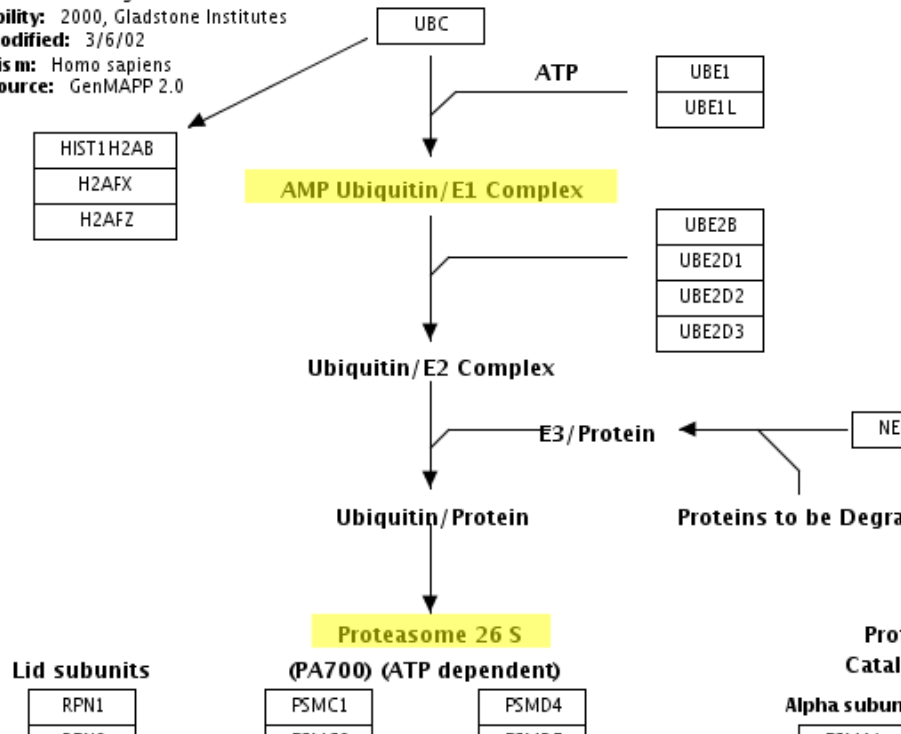
Proteasome Degradation (Homo sapiens), revision 8348

Proteasome Degradation (Homo sapiens), revision 11404

Zoom: 100%

Name: Proteasome Degradation
Email: nsalomonis@gladstone.ucsf.edu
Availability: 2000, Gladstone Institutes
Last modified: 3/6/02
Organism: Homo sapiens
Data Source: GenMAPP 2.0

Name: Proteasome Degradation
Email: nsalomonis@gladstone.ucsf.edu
Availability: 2000, Gladstone Institutes
Last modified: 3/6/02
Organism: Homo sapiens
Data Source: GenMAPP 2.0



Metabolic Pathways - GenMAPP 2.0 - Proteasome Degradation (Homo sapiens) - revision 11404

Species

- We can add any species that is in ENSEMBL
- Or anything where you create an ENSEMBL like DB
- Just ask!



Escherichia coli K12
EB1



Bacillus subtilis
EB1



Mycobacterium tuberculosis H37Rv
EB1

Ensembl Species



Aedes
Aedes aegypti



Alpaca
Vicugna pacos



Anole Lizard
Anolis carolinensis



Anopheles
Anopheles gambiae



Armadillo
Dasypus novemcinctus



Bushbaby
Otolemur gamettii



Caenorhabditis elegans



Ciona intestinalis



Ciona savignyi



Cat
Felis catus



Chicken
Gallus gallus



Chimpanzee
Pan troglodytes



Cow
Bos taurus



Dog
Canis familiaris



Dolphin
Tursiops truncatus



Elephant
Loxodonta africana



Fruitfly
Drosophila melanogaster



Gorilla
Gorilla gorilla



Guinea Pig
Cavia porcellus



Hedgehog
Erinaceus europaeus



Horse
Equus caballus



Human
Homo sapiens



Hyrax
Procavia capensis



Kangaroo rat
Dipodomys ordii



Lamprey (preview - assembly only)
Petromyzon marinus



Lesser hedgehog tenrec
Echinops telfairi



Macaque
Macaca mulatta



Medaka
Oryzias latipes



Megabat
Pteropus vampyrus



Microbat
Myotis lucifugus



Mouse
Mus musculus



Mouse Lemur
Microcebus murinus



Opossum
Monodelphis domestica



Orangutan
Pongo pygmaeus



Pig (preview - assembly only)
Sus scrofa



Pika
Ochotona princeps



Platypus
Ornithorhynchus anatinus



Rabbit
Oryctolagus cuniculus



Rat
Rattus norvegicus



Saccharomyces cerevisiae



Shrew
Sorex araneus



Sloth
Choloepus hoffmanni



Squirrel
Spermophilus tridecemlineatus



Stickleback
Gasterosteus aculeatus



Tarsier
Tarsius syrichta



Tetraodon
Tetraodon nigroviridis



Tree Shrew
Tupaia belangeri



Xenopus tropicalis



Zebra Finch
Taeniopygia guttata



Zebrafish
Danio rerio

Metabolomics

Visualization and statistics fully supported



HMDB



Chebi



NuGOwiki

Automatic content generation

GO: gene ontology visualization

- Automatic pathway (table) generator for any GO level
- Ask for tool or pathways
- Go statistics in GenMAPP, Go_Elite, R (through webservice)

Automatic content generation

KEGG

- Automatic pathway converter
- Ask for tool or pathways
- We need two versions:
 - Original
 - Community updated

Automatic content generation

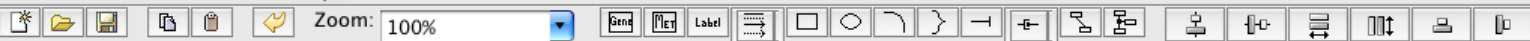
BioPAX

- Part of BioPAX already implemented
- Full converter in development using Paxtools
- Can also be used for Reactome (round trip)

Assisted content generation

Suggestions from:

- HMDB
- KEGG
- BIND
- Text mining (Phasar)



Zoom: 100%

Title: New Pathway

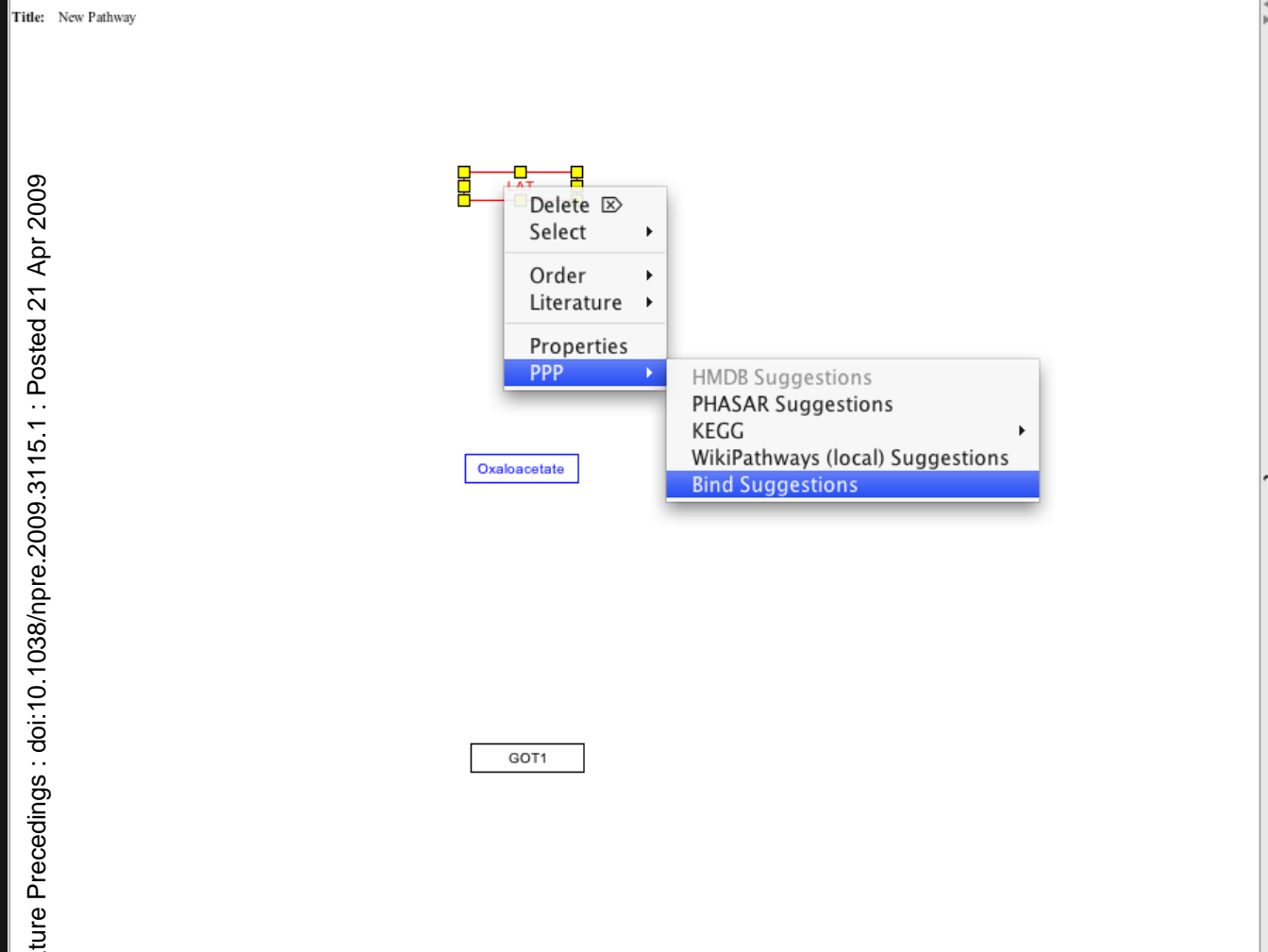


Oxaloacetate

GOT1

Properties Backpage Search PPP

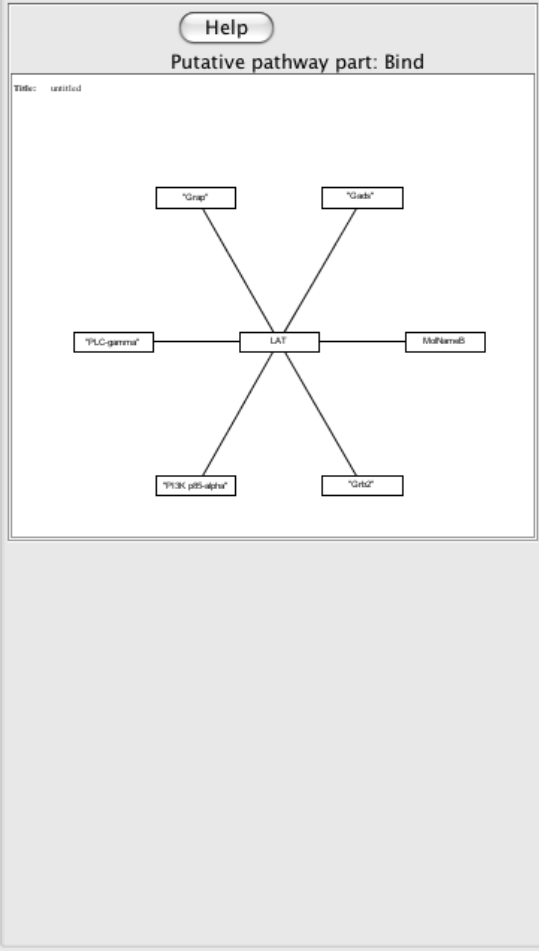
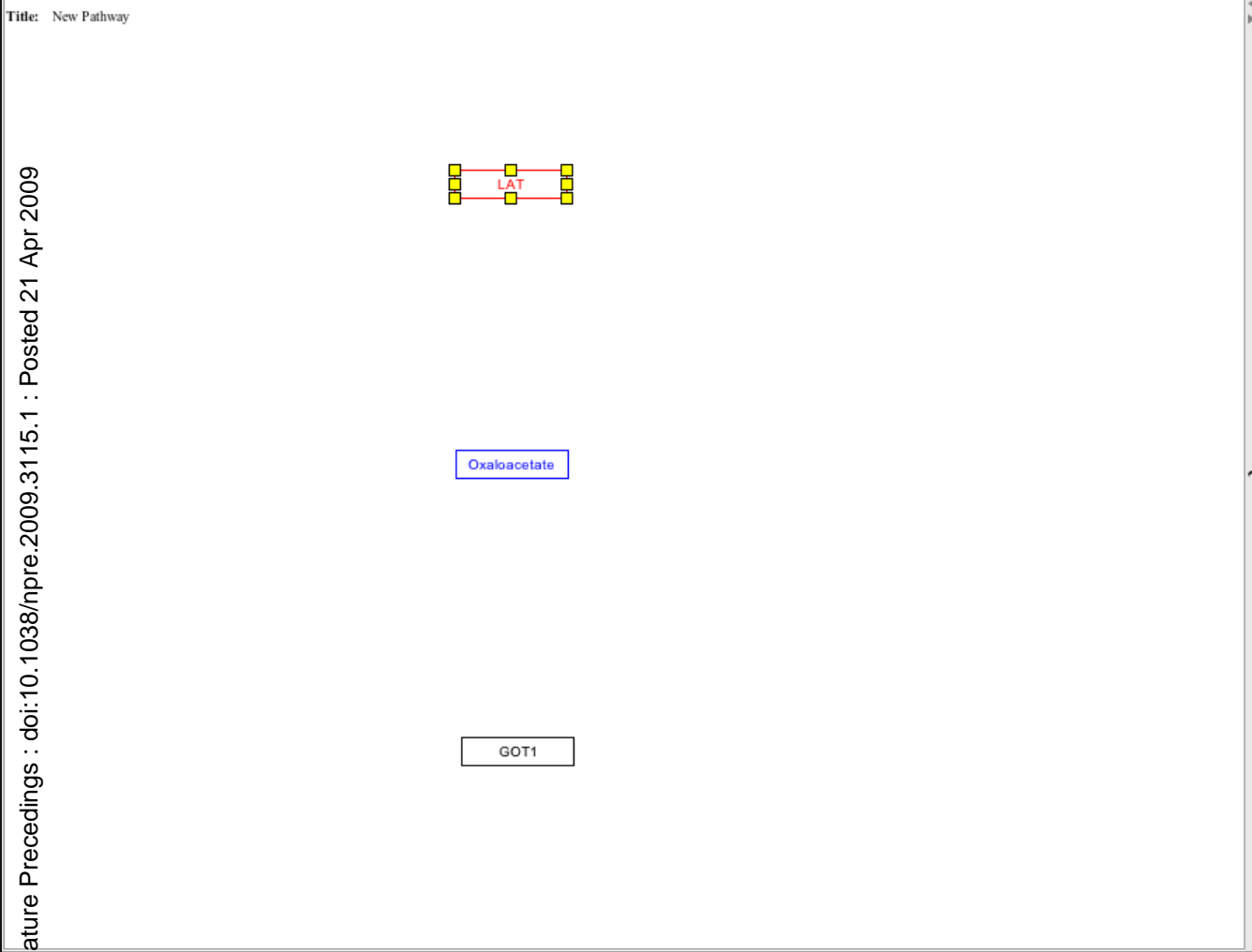
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Center Y	1980.0
Color	
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Width	1200.0



Properties Backpage Search PPP

Property	Value
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Center Y	1965.0
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Comments	
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Database Name	
Height	300.0
Text Label	LAT
Type	GeneProduct
Width	1200.0

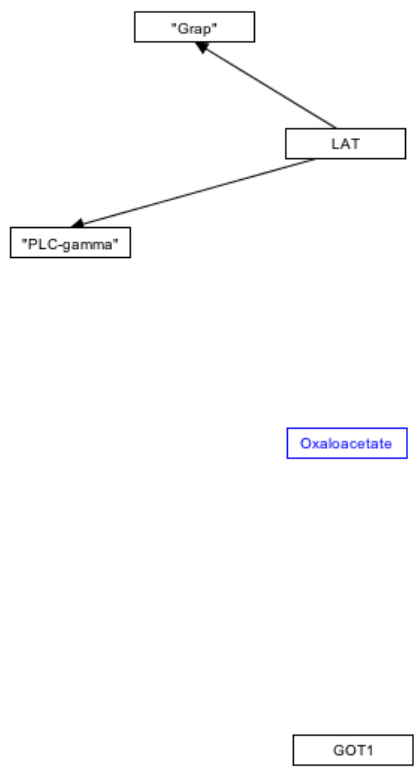
Nature Precedings : doi:10.1038/npre.2009.3115.1 : Posted 21 Apr 2009



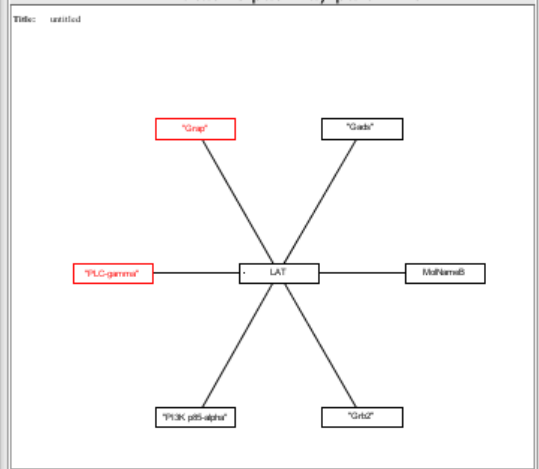
Nature Precedings : doi:10.1038/npre.2009.3115.1 : Posted 21 Apr 2009

Title: New Pathway

Nature Precedings : doi:10.1038/npre.2009.3115.1 : Posted 21 Apr 2009

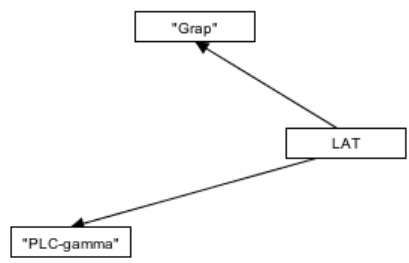


Help
Putative pathway part: Bind



Title: New Pathway

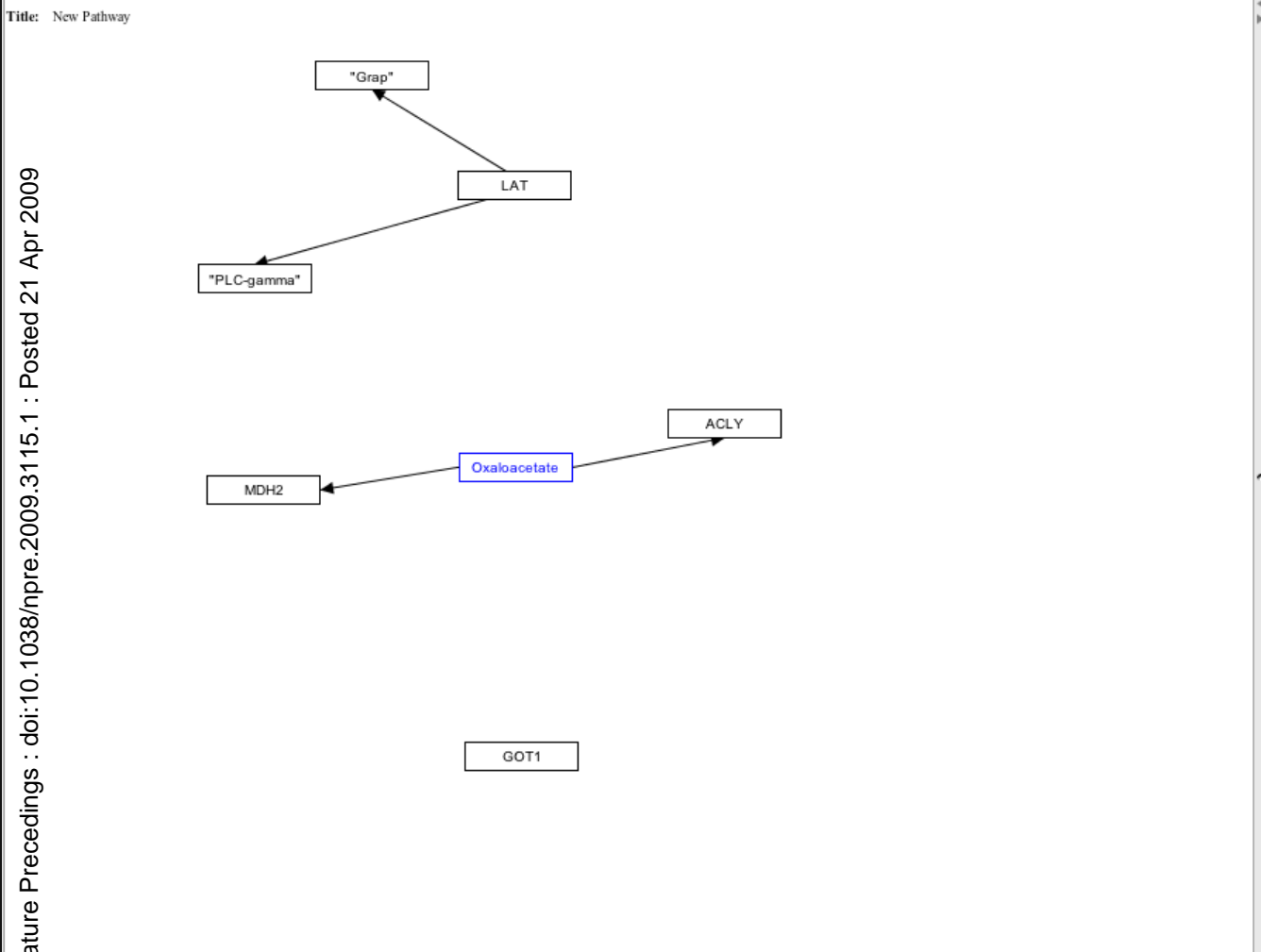
Nature Precedings : doi:10.1038/npre.2009.3115.1 : Posted 21 Apr 2009



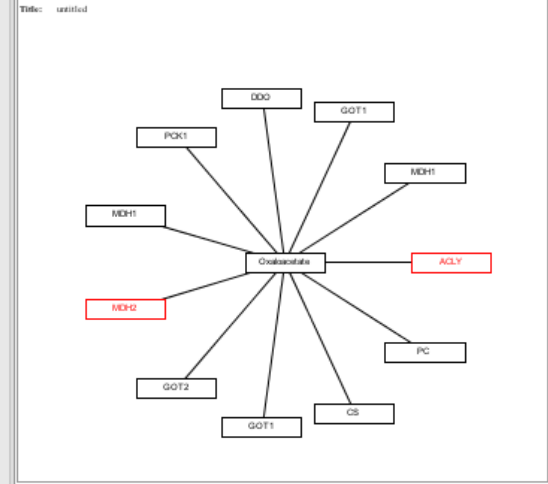
- Delete
- Select
- Order
- Literature
- Properties
- PPP
 - HMDB Suggestions
 - PHASAR Suggestions
 - KEGG
 - WikiPathways (local) Suggestions
 - Bind Suggestions

Properties Backpage Search PPP

Property	Value
Backpage head	
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Center Y	4965.0
Color	
Comments	
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Database Name	HMDB
Height	300.0
Text Label	Oxaloacetate
Type	Metabolite
Width	1200.0



Help
Putative pathway part: HMDB



Nature Precedings : doi:10.1038/npre.2009.3115.1 : Posted 21 Apr 2009



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portal discuss list view source history

Portal: Micronutrient



Welcome to the Micronutrient portal at wikipathways. From this page, you can access and collaborate in the construction of pathways and networks focused on the biological activity of micronutrients. About the micronutrient portal Essentially, the micronutrient genetics project aims at identifying all relevant genetic variations related to the biological activity on a specific micronutrient. In doing so, we provide information in a biological perspective, i.e. pathway and biological network oriented visual browsers. Controversially, for many micronutrients the biological knowledge is still fragmented. Thus, a flexible and user-friendly interface with both a wiki-editable and a permanent interface will be implemented. The genetic variation on specific genes will be derived from the basic databases embedded in the human genome project. A bioinformatics team has been established that will construct and maintain these web-based interfaces.

News

June 6 2008: The Micro-Nutrient Portal has started!
Aug 1 2008: 2 new networks have been created: the [Selenium network](#) and the [Folic acid network](#).

Pathway contributors

- Pathways**
- [Folate \(One carbon metabolism\)](#)
 - [Selenium](#)
 - [Carotenoids and retinol](#)
 - [Selenium network](#)
 - [Folic acid network](#)
- Contributors**
- [Ben van Ommen](#)
 - [Suzan Wopereis](#)
 - [Susan Coort](#)
 - [Michiel Adriaens](#)
 - [Estibaliz Goyenechea](#)
 - [Jildau Bouwman](#)



Featured Pathway

[One-carbon metabolism \(Homo sapiens\)](#)

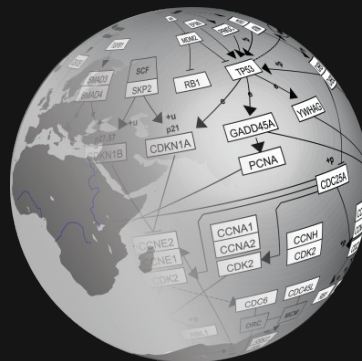
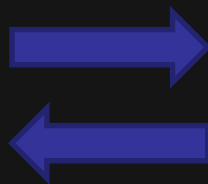
View all [Featured Pathways](#) for this Portal

Statistics

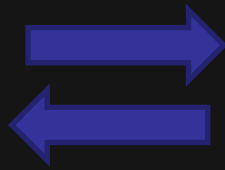
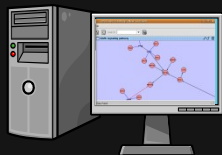
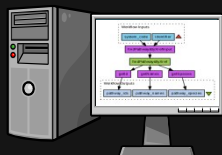
Micronutrient pathway stats coming soon!

About the Micronutrient Genomics project

Webservice



Web service



Nature Precedings : doi:10.1038/npre.2009.3115.1 : Posted 21 Apr 2009

Navigator

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 - Sample Project
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 - getRecentChanges
 - listOrganisms
 - Request 1
 - listPathways
 - login
 - removeCurationTag
 - saveCurationTag
 - updatePathway

Request 1

http://localhost/wikipathways/wpi/websevice/websevice.php

```

<soapenv:Envelope xmlns:soapenv="http://schemas.xmlsoap.org/soap/envelope/">
  <soapenv:Header/>
  <soapenv:Body>
    <xsd:listOrganisms/>
  </soapenv:Body>
</soapenv:Envelope>

```

Request

```

<soapenv:Envelope xmlns:soapenv="http://schemas.xmlsoap.org/soap/envelope/">
  <soapenv:Header/>
  <soapenv:Body>
    <ns1:listOrganismsResponse xmlns:ns1="http://www.wiki-pathways.org/wpi/websevice/websevice.xsd">
      <ns1:organisms>Homo sapiens</ns1:organisms>
      <ns1:organisms>Rattus norvegicus</ns1:organisms>
      <ns1:organisms>Mus musculus</ns1:organisms>
      <ns1:organisms>Drosophila melanogaster</ns1:organisms>
      <ns1:organisms>Caenorhabditis elegans</ns1:organisms>
      <ns1:organisms>Saccharomyces cerevisiae</ns1:organisms>
      <ns1:organisms>Danio rerio</ns1:organisms>
      <ns1:organisms>Arabidopsis thaliana</ns1:organisms>
      <ns1:organisms>Oryza japonica</ns1:organisms>
    </ns1:listOrganismsResponse>
  </soapenv:Body>
</soapenv:Envelope>

```

Response

Aut Headers (0) Attachments ... Headers (6) Attachments (0) SSL Info WSS (0)

response time: 1203ms (670 bytes)

4 : 1

What for?

- Build web applications
- Extend existing applications
- Include in workflows / analysis pipelines

Available services

- Download
 - All pathway information in various formats
 - Pathway metadata
 - Colored pathway images
 - Gene lists
- Find
 - By keyword searches
 - By gene / protein / small molecule identifier
 - Interactions by gene / protein

Available services

- Update
 - Notify community by curation tags
 - Update pathway content
 - Create new pathways
- Write access upon request

Search engine

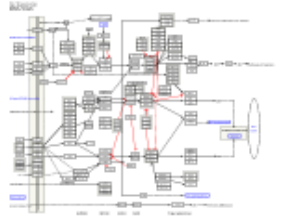
Text search Identifier search

Search by database identifier. Example: 201746_at

201746_at Affy Search


The query '201746_at' returned 8 results.

Results for organism: All




MAPK signaling pathway (Homo sapiens)
Title: MAPK signaling pathway
Organism: Homo sapiens
Pathway ID: WP382
IDs mapping to 201746_at:

- TP53 ([7157, Entrez Gene](#))



G1 to S cell cycle control (Homo sapiens)
Title: G1 to S cell cycle control
Organism: Homo sapiens
Pathway ID: WP45
IDs mapping to 201746_at:

- TP53 ([7157, Entrez Gene](#))



G1 to S cell cycle control (Homo sapiens)
Title: G1 to S cell cycle control
Organism: Homo sapiens
Pathway ID: WP45
IDs mapping to 201746_at:

- TP53 ([7157, Entrez Gene](#))

Visualizing gene expression

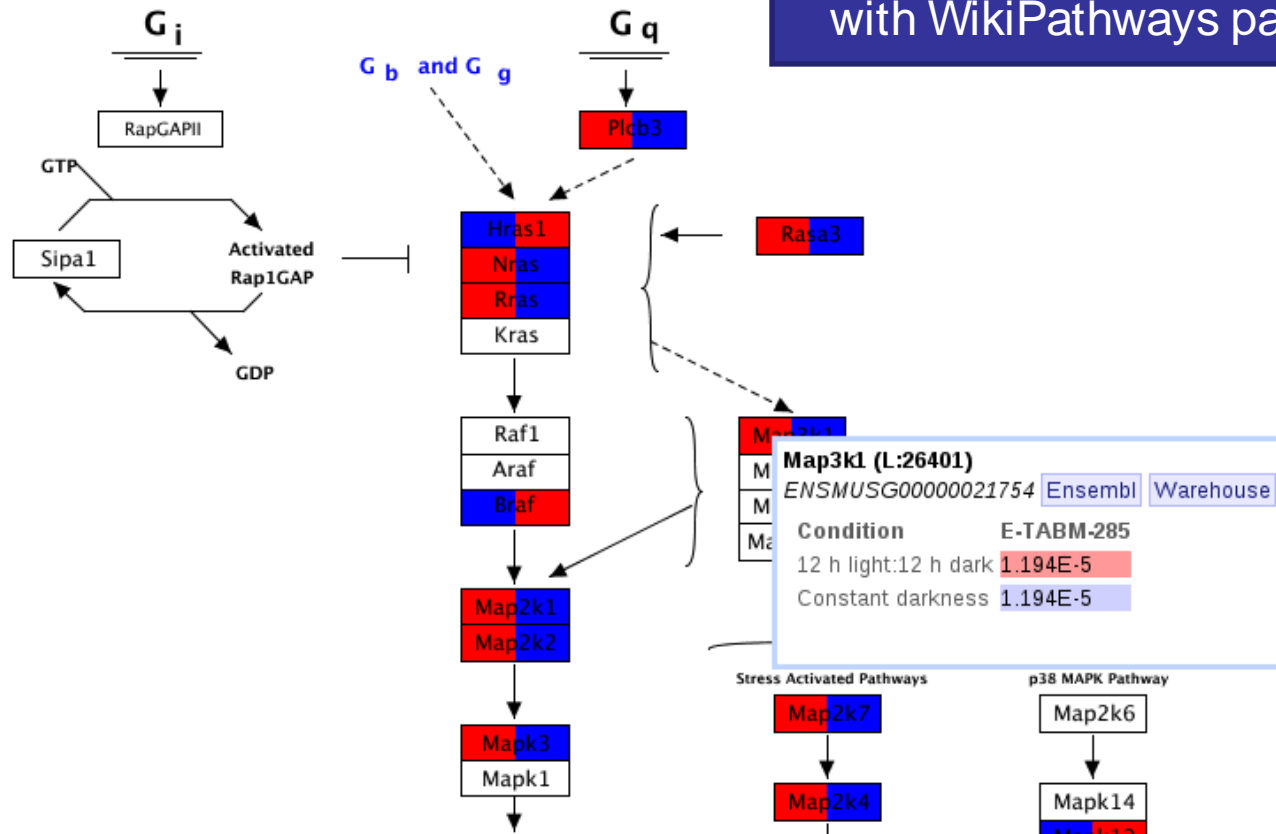
WikiPathways-Atlas Mapper

Selected pathway: WP251 (MAPK Cascade, Mus musculus) [change](#)

Selected conditions: [12 h light:12 h dark, Constant darkness] (light) [change](#)

■ = down ■ = up ■ = up/down

Click on a gene to see details.



Integrates data from
ArrayExpress Atlas
with WikiPathways pathways

Cytoscape plugin

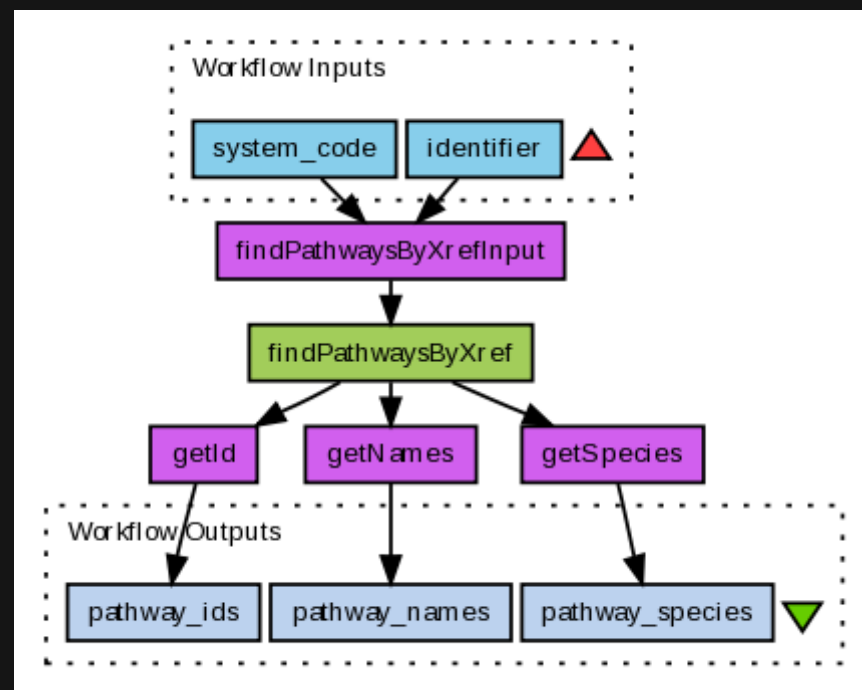
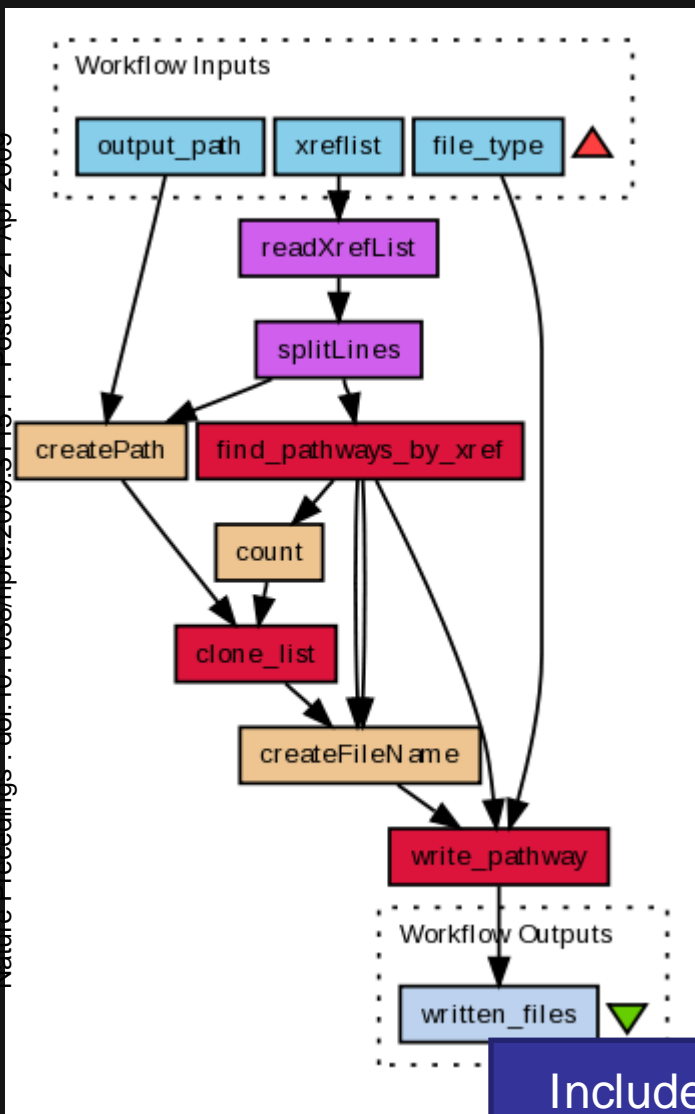
The screenshot displays the Cytoscape Desktop interface. On the left, the 'Import Network from Database' dialog is open, showing a search for 'mapk' across various organisms. The 'MAPK signaling pathway' from Homo sapiens is selected. On the right, the 'Cytoscape Desktop (New Session)' window shows a network diagram of the MAPK signaling pathway. The diagram features nodes for AKT3, AKT2, MAP2K1, MAP3K1, MAP4A1, MAP4B, RAC1, RAC2, CDC42, GSK3, and TRAF2, connected by directed edges. A 'Data Panel' at the bottom shows a table with columns for ID, GeneID, SystemCode, Type, and canonicalName. The status bar at the bottom indicates 'Welcome to Cytoscape 2.6.0' and 'Right-click + drag to ZOOM'.

Name	Organism
MAPK Cascade	Mus musculus
MAPK Cascade	Rattus norvegicus
MAPK Cascade	Homo sapiens
MAPK Signaling Pathway	Saccharomyces cerevisiae
MAPK signaling pathway	Homo sapiens
MAPK signaling pathway	Rattus norvegicus
MAPK signaling pathway	Mus musculus
zebrafish ERK1 - ERK2 MAPK casc...	Danio rerio
p38 MAPK Signaling Pathway (BioC...	Homo sapiens
p38 MAPK Signaling Pathway (BioC...	Mus musculus
p38 MAPK Signaling Pathway (BioC...	Rattus norvegicus
lungkuo	Homo sapiens
Toll Like Receptor signaling	Mus musculus
Notch Signaling Pathway	Mus musculus
Notch Signaling Pathway	Rattus norvegicus
Notch Signaling Pathway	Homo sapiens
Id Signaling Pathway	Homo sapiens
Id Signaling Pathway	Mus musculus
Id Signaling Pathway	Rattus norvegicus
Mouse Insulin Signaling	Mus musculus
Cell cycle	Drosophila melanogaster
Cell cycle	Mus musculus
Insulin Signaling	Rattus norvegicus
Cell cycle	Rattus norvegicus

ID	GeneID	SystemCode	Type	canonicalName
----	--------	------------	------	---------------

Search and open pathways from WikiPathways directly in Cytoscape.

Taverna workflows



Include pathway information in Taverna workflows.

<http://www.myexperiment.org/packs/40>



R Example

- SSOAP

<http://www.omegahat.org/SSOAP/>

```
## Install SSOAP from Bioconductor ##  
source("http://bioconductor.org/biocLite.R")  
biocLite("SSOAP")  
  
## Load the SSOAP library ##  
library(SSOAP)
```

R- example: GSEA



- Get all human pathways as gene lists
- Download a GEO dataset
(on papillary renal cell carcinoma)
- Perform Parametric Gene Set Enrichment

```
# Load the required libraries
library(SSOAP)           #To use WikiPathways web service
library(GEOquery)       #To download GEO experiments
library(GSEABase)       #Gene Set data structures
library(PGSEA)          #Parametric Gene Set Enrichment
```

Enrichment analysis

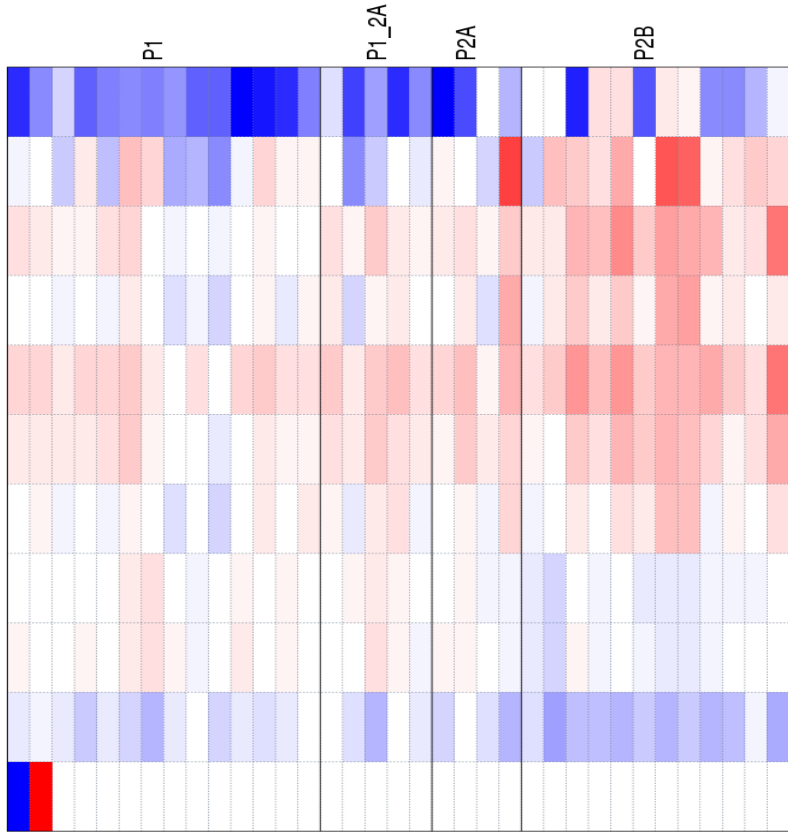
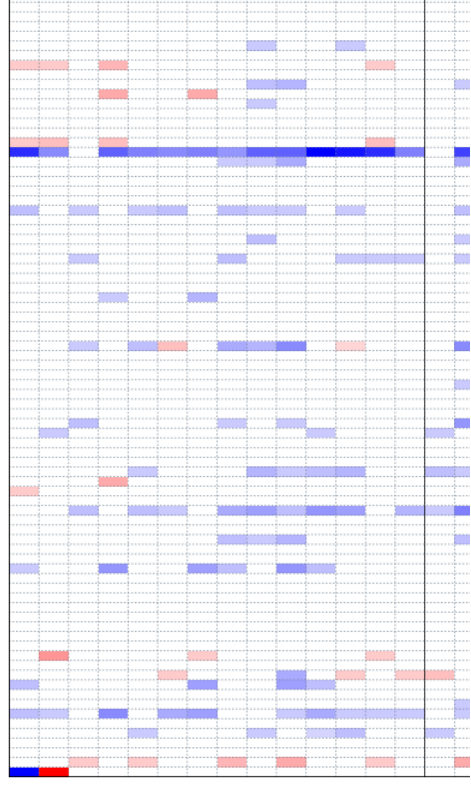
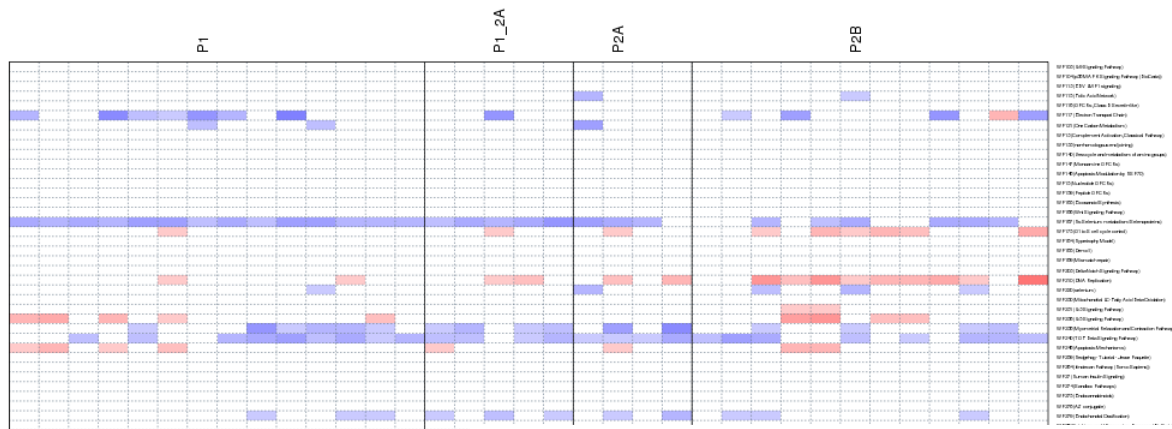


```
# Get an expression set from GEO
gse = getGEO("GSE7023", GSEMatrix = TRUE)
eset = gse[[1]]

# Reformat the phenotype labels
subtype = gsub("subtype: ", "", phenoData(eset)$characteristics_ch1)
subtype = gsub("\\.", "_", subtype)

# Run the PGSEA calculation (reference sample is 'NO')
pg = PGSEA(eset, geneSetCollection, ref = which(subtype == "NO"), p.value=0.005)

# Plot the result matrix
smcPlot(
  pg, factor(subtype), scale=c(-15,15), show.grid = TRUE, margins = c(1, 1, 4, 10),
  col = .rwb, r.cex = 0.35
)
```



WP351 (Oxidative Stress)
 WP434 (Cytoplasmic Ribosomal Protein)
 WP521 (Cell cycle)
 WP450 (Translation Factors)
 WP210 (DNA Replication)
 WP175 (G1 to S cell cycle control)
 WP359 (Eukaryotic Transcription Initiation)
 WP433 (Wnt Signaling Pathway)
 WP361 (Wnt Signaling Pathway and Cell Cycle Control)
 WP416 (Fatty Acid Beta Oxidation)
 GS

- WikiPathways web service:
 - Programmatic interface to WikiPathways data
 - Language-independent
 - Latest pathway information
- Powerful tool when combined with other web services and libraries

<http://www.wikipathways.org/webservice>

Credit system

Nature Precedings : doi:10.1038/npre.2009.3115.1 Posted 21 Apr 2009



search

Google Custom Search

titles only

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13. [S.Burel](#) ★★★★★ | 10.24
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www.wikipathways.org

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Enjoy!

