

PathwayExplorer Tutorial

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1. PathwayExplorer overview
2. Select and open a single pathway
3. Upload a dataset
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7. Mapped pathway
8. Change display options
9. Show experiments / time points of the mapped dataset
10. Show pathway description
11. Show gene information
12. Display OMIM gene information
13. Create a PDF document with all available pathway information
14. Search options

1. PathwayExplorer overview

Bioinformatics Graz Pathway Explorer
Microarray Data Mapping System

Tutorial Feedback Contact Links

Homo Sapiens Choose Dataset Map Dataset Filter Dataset Settings Search Return

RefSeq (loc2ref)

Pathway Explorer
Web service for visualizing high-throughput data on biological pathways

Developed by: Bernhard Mlecnik
Scientific advice: Marcel Scheideler

Change organism (points to Homo Sapiens dropdown)

Open dataset (points to Choose Dataset button)

Change gene ID library (points to RefSeq (loc2ref) dropdown)

Change display options (points to Settings button)

Search options (points to Search button)

Pathway exploring tree (points to the left sidebar tree)

Search options (points to the search input field)

514 pathways available (8947)
51 Pathways (30)
11 Pathways (30)
120 KEGG Pathways (4099)
1. Metabolism (170)
2. Genetic Information Processing (100)
3. Environmental Information Processing (100)
4. Cellular Processes (100)
5. Human Diseases (100)
311 BioCarta Pathways (100)
Main Categories (2209)
Adhesion (276)
Apoptosis (272)
Cell Activation (188)
Cell Cycle Regulation (267)
Cell Signalling (1000)
Cytokines/Chemokines (306)
Developmental Biology (307)
Expression (528)
Hematopoiesis (91)
Immunology (297)
Metabolism (312)
Neuroscience (184)
82 GenMapp (6374)
Contributed (1977)
GO Mapps (5267)

Server load: 0.72 (18.0%) © 2004 - Institute for Genomics and Bioinformatics - Graz University of Technology

Waiting for pathwayexplorer.genome.tugraz.at... Time: 00:56:00

2. Select and open a single pathway

Switch to scalable vector graphics view if plugin is installed

Create a PDF document of the current pathway

Show description of the pathway

Download a PNG or SVG image of the current pathway by clicking on the right mouse button (save link target as)

1. Choose a pathway and click on the link to load it

Gene element

Tutorial Feedback Contact Links Log in

Homo Sapiens

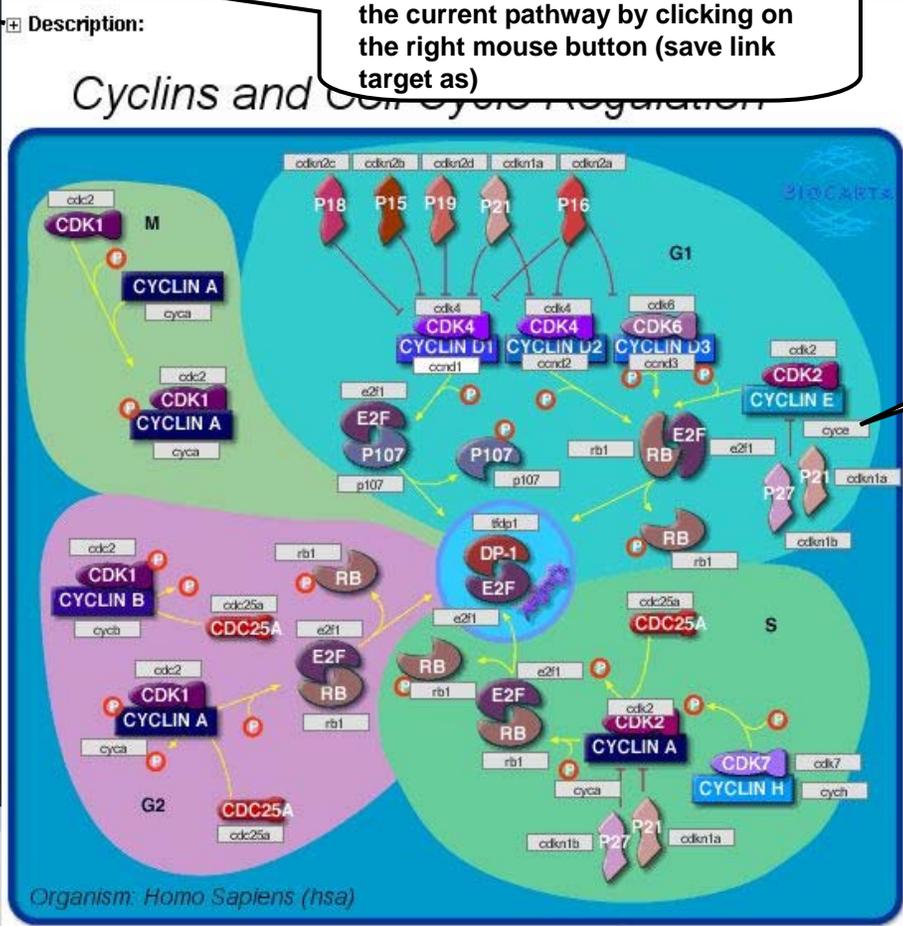
Choose Dataset

Settings Search Return

Last update: Wed, 9 Feb, 2005

[514] pathways available (8947)

- [1] Pathways (30)
- Self Annotated (30)
- [120] KEGG Pathways (4099)
- 1. Metabolism (1714)
- 2. Genetic Information Processing
- 3. Environmental Information Proc
- 4. Cellular Processes (892)
- 5. Human Diseases (221)
- [311] BioCarta Pathways (2209)
- Main Categories (2209)
- Adhesion (276)
- Apoptosis (272)
- Cell Activation (188)
- Cell Cycle Regulation (267)
- Cyclins and Cell Cycle Re
- h_cellcyclePathway (311)**
- RB Tumor Suppressor/Ch
- Activation of Src by Protei
- cdc25 and p115 Regulator
- Protein Kinase A at the Ce
- Cell Cycle: G2/M Checkpo
- Regulation of p27 Phospho
- Influence of Ras and Rho
- Stathmin and breast cance
- Cell Cycle: G1/S Check P
- Regulation of cell cycle pr
- Role of Ran in mitotic spin
- Tumor Suppressor Arf Inhi



3. Upload a dataset

Dataset Format:

	A	B	C	D	E
1	UniqueID	Name	TP1 (day-2)	TP2 (day0-0hr)	TP3 (day0-8hr)
2	NM_014232	vesicle-associated membrane protein 2 (synaptobrevin 2); vamp2	-0.18725334	0.1531857	-0.051753625
3	NM_000668	class i alcohol dehydrogenase, beta subunit; adh1b	-0.005982075	0.34848127	0.93900555
4	NM_003240	transforming growth factor, beta 4; ebaf	-0.112653494	-0.0135629885	0.16890651
5	NM_018443	zinc finger znf140-like protein; znf302	0.08047339	NaN	NaN
6	NM_004138	type i hair keratin 3a; krtha3a	-0.2854154	-0.40987158	-0.43591157

1. All fields must be tab delimited
2. 1st column must contain the UNIQID as 'RefSeq' and/or 'GenBank', 'UniGene', 'GeneOntology'.
3. 2nd column must contain the gene name
4. The other columns may contain the expression data

3. Upload a dataset

Bioinformatics Graz Pathway Explorer
Microarray Data Mapping System

Tutorial Feedback Contact Links Log in Last update: Wed, 9 Feb, 2005

Homo Sapiens Choose Dataset Map Dataset Filter Dataset Settings Search Return

RefSeq (loc2ref)

[514] pathways available (8947)

- [1] Pathways (30)
 - Self Annotated (30)
 - Adipogenesis
 - Insulin (30)
- [120] KEGG Pathways (4099)
 - 1. Metabolism (1714)
 - 2. Genetic Information Processing (300)
 - 3. Environmental Information Processing (120)
 - 4. Cellular Processes (892)
 - 5. Human Diseases (221)
- [311] BioCarta Pathways (2209)
 - Main Categories (2209)
 - Adhesion (276)
 - Apoptosis (272)
 - Cell Activation (188)
 - Cell Cycle Regulation (267)
 - Cell Signalling (1000)
 - Cytokines/Chemokines (306)
 - Developmental Biology (307)
 - Expression (528)
 - Hematopoiesis (91)
 - Immunology (297)
 - Metabolism (312)
 - Neuroscience (184)
- [82] GenMapp (6374)
 - Contributed (1977)
 - GO Mapps (5267)

Load Dataset

Upload File Browse... Select Organism Homo Sapiens Upload ?

No.	File Name	Organism	Open Dataset	Download Dataset	Remove Dataset
1	MEF_logratio(Mouse).txt				
2	3T3-L1_differentiation(Mouse).txt				
3	Fibroblasts_12TP(Human).txt	Homo Sapiens			
4	Sporulation(Yeast).txt	Saccaromyces Cerevisiae			
5	diabetes_study_new_logratio(Mouse).txt	Mus Musculus			
6	Adipogenesis_Wnt_new_logratio(Mouse).txt	Mus Musculus			
7	3T3_L1_Adipocyte_differentiation(Mouse).txt	Mus Musculus			

1. Choose a new dataset to upload

2. Choose a organism

3. Press the upload button

Open dataset

Download dataset from web server

Remove dataset from web server

Upload a dataset to web server

1

2

3

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4. Open a dataset

The screenshot shows the Pathway Explorer interface. At the top, there's a navigation bar with 'Tutorial', 'Feedback', 'Contact', 'Links', and 'Log in'. Below that, a dropdown menu shows 'Homo Sapiens' and 'RefSeq (loc2ref)'. A 'Filter Dataset' button is circled in red and labeled with a '3' in a red circle. A callout bubble points to it with the text 'Filter the dataset'. Another callout bubble points to the 'Filter Dataset' button in the table below with the text 'Filter the dataset'. A third callout bubble points to the 'Close Dataset' button in the table with the text 'Close the dataset'. A fourth callout bubble points to the 'Open Dataset' button in the table with the text 'Open the dataset'. A fifth callout bubble points to the 'RefSeq (loc2ref)' dropdown with the text '2'. A sixth callout bubble points to the 'Load your Dataset here' column in the table with the text '1'. The table below shows a list of datasets with columns for 'No.', 'File Name', 'Organism Name', 'Load your Dataset here', 'Download Dataset', and 'Remove Dataset'. The 'Fibroblasts_12TP(Human).txt' dataset is highlighted.

Create ranking list

3

Filter the dataset

Filter the dataset

Close the dataset

Open the dataset

2

1

Currently Opened Dataset	Found Genes	Found TimePoints/Experiments	Map Dataset To All Pathways	Filter Dataset	Close Dataset
Fibroblasts_12TP(Human).txt	478	12			

No.	File Name	Organism Name	Load your Dataset here	Download Dataset	Remove Dataset
1	MEF_logratio(Mouse).txt	Mus Musculus			
2	3T3-L1_differentiation(Mouse).txt	Mus Musculus			
3	Fibroblasts_12TP(Human).txt	Homo Sapiens			
4	Sporulation(Yeast).txt	Saccaromyces Cerevisiae			
5	diabetes_study_new_logratio(Mouse).txt	Mus Musculus			
6	Adipogenesis_Wnt_new_logratio(Mouse).txt	Mus Musculus			
7	3T3_L1_Adipocyte_differentiation(Mouse).txt	Mus Musculus			

1. Choose a new dataset to load and click on the icon
2. Select gene identifier library (Human, Mouse, Rat)
3. Now the dataset can be filtered

5. Filter the dataset

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Microarray Data Mapping System

Tutorial Feedback Contact Links Log in Last update: Wed, 9 Feb, 2005

Homo Sapiens Choose Dataset Map Dataset Filter Dataset Settings Search Return Current Loaded Dataset: Fibroblasts_12TP(Human).txt

RefSeq (loc2ref)

- [514] pathways available (8947)
- [1] Pathways (30)
 - Self Annotated (30)
 - Adipogenesis
 - Insulin (30)
- [120] KEGG Pathways (4099)
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 - Cell Signalling (1000)
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 - Developmental Biology (307)
 - Expression (528)
 - Hematopoiesis (91)
 - Immunology (297)
 - Metabolism (312)
 - Neuroscience (184)
- [82] GenMapp (6374)
 - Contributed (1977)
 - GO Mapps (5267)

Filter Options

Dataset Filter Options	
<input type="checkbox"/> Number of experiments present >=	12
<input type="checkbox"/> Standard deviation >=	0.0
<input checked="" type="checkbox"/> Number of experiments to pass >=	1
Upper log2 ratio threshold	1.0 within threshold
Lower log2 ratio threshold	-1.0 beyond threshold

425 genes out of 478 (88.9%) passed!

Test Apply Cancel

Number of experiments / timepoints which should be present for a gene

Standard deviation of experiments / timepoints for a gene

Number of experiments / timepoints to pass the selected thresholds

1

2

3

1. Check the requested options
2. Test the checked options → adjust options
3. Apply selected options to the dataset (the ranking list will be automatically created)

6. Ranking list of all available pathways

Bioinformatics Graz Pathway Explorer
 Microarray Data Mapping System

Tutorial Feedback Contact Links Log in Last update: Wed, 9 Feb, 2005

Homo Sapiens Choose Dataset Ranking Filter Dataset Settings Search Return Current Loaded Dataset: Fibroblasts_12TP(Human).txt

RefSeq (loc2ref) ave Ranking List Close Ranking List

STATISTICS	Passed UniqIDs	Filtered out UniqIDs	Σ
Assigned to Pathways	198	20	218
Not mapped to Pathways	227	33	260
Total	425	53	478

All gene ids found in the dataset

Id	Section	Subsection	Pathway	Pathway UniqID	Passed UniqID	% Passed UniqID	Filtered UniqID	p-value
			519	9048	198	2.19	20	0
	GenMapp			386	15	3.89	2	0.581
	GenMapp	Biological Process	cell proliferation	336	12	3.57	0	1.0
	KEGG Pathways			150	11	7.33	1	0.76
hsa04010	KEGG Pathways		signaling pathway	41	10	2.18	2	0.392
hsa04060	KEGG Pathways	3.3 Ligand-Receptor	Cytokine-cytokine receptor interaction	383	10	2.61	0	1.0
	GenMapp		inhibitor	273	10	3.66	1	0.729
	GenMapp		synthesis	202	10	4.95	1	0.729
	GenMapp	Biological Process	cytokinesis	173	10	5.78	0	1.0
go_actin_binding	GenMapp	Molecular Funktion	actin binding	329	9	2.74	0	1.0
go_chromosome	GenMapp	Cellular Component	chromosome	253	9	3.56	1	0.695
Hs_Smooth_muscle:contraction	GenMapp	Physiological Process	Myometrial Relaxation and Contraction Pathways	215	9	4.19	0	1.0
Hs_G1_to_S_cellcycle_control	GenMapp	Cellular Process	G1 to S cell cycle control	90	9	10.0	1	0.695

No. of mapped unique gene ids in the pathways

All gene ids found in the pathway

Passed genes which are mapping to the pathway

Filtered genes which would have mapped to the pathway

p-values of Fisher's Exact Test

No. of available unique gene ids in the pathways

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6. Ranking list of all available pathways

Download tab delimited ranking list

Display the pathway ranking list

Remove ranking list

Pathway Explorer
Microarray Data Mapping System

Tutorial Feedback
Homo Sapiens
RefSeq (loc2ref)

Choose Dataset Ranking Filter Data Settings Search Return
Last update: Wed, 9 Feb, 2005
Current Loaded Dataset: Fibroblasts_12TP(Human).txt

Save Ranking List Close Ranking List

STATISTICS	Passed UniqIDs	Filtered out UniqIDs	Σ
Mapped to Pathways	198	20	218
Not Mapped to Pathways	227	33	260
Σ	425	53	478

[514] pathways available (8947|198|2.21%)

- [1] Pathways (30|1|3.33%)
 - Self Annotated (30|1|3.33%)
 - Adipogenesis
 - Insulin (30|1|3.33%)
- [120] KEGG Pathways (4099|93|2.27%)
 - 1. Metabolism (1714|39|2.28%)
 - 2. Genetic Information Processing (3)
 - 3. Environmental Information Processi
 - 4. Cellular Processes (892|26|2.91%)
 - 5. Human Diseases (221|4|1.81%)
- [311] BioCarta Pathways (2209|63|2.85%)
 - Main Categories (2209|63|2.85%)
 - Adhesion (276|6|2.17%)
 - Apoptosis (272|7|2.57%)
 - Cell Activation (188|7|3.72%)
 - Cell Cycle Regulation (267|13|4.1)
 - Cell Signalling (1000|31|3.1%)**
 - Cytokines/Chemokines (306|9|2.9)
 - Developmental Biology (307|10|3.25%)
 - Expression (528|11|2.08%)
 - Hematopoiesis (91|4|4.4%)
 - Immunology (297|9|3.03%)
 - Metabolism (312|10|3.21%)
 - Neuroscience (184|5|2.72%)
- [82] GenMapp (6374|150|2.35%)
 - Contributed (1977|58|2.93%)
 - GO Mapps (5267|128|2.43%)

No.	Id	Section	Subsection	Pathway	Pathway UniqID	Passed UniqID	% Passed UniqID	Filtere UniqID
Σ				519	9048	198	2.19	20
1	go_extracellular_matrix	GenMapp	Cellular Component	extracellular matrix	386	15	3.89	20
2	go_cell_proliferation	GenMapp	Biological Process	cell proliferation	336	12	3.57	20
3	hsa04110	KEGG Pathways	4.2 Cell Growth and Death	Cell cycle	150	11	7.33	20
4	hsa04010	KEGG Pathways	3.2 Signal Transduction	MAPK signaling pathway	458	10	2.18	20
5	hsa04060	KEGG Pathways	3.3 Ligand-Receptor Interaction	Cytokine-cytokine receptor interaction	383	10	2.61	20
6	go_enzyme_inhibitor_activity	GenMapp	Molecular Function	enzyme inhibitor activity	273	10	3.66	20
7	go_lipid_biosynthesis	GenMapp	Biological Process	lipid biosynthesis	202	10	4.95	20
8	go_cytokinesis	GenMapp	Cellular Process	cytokinesis	173	10	5.78	20
9	go_actin_binding	GenMapp	Molecular Function	actin binding	329	9	2.74	20
10	go_chromosome	GenMapp	Cellular Component	chromosome	253	9	3.56	20
11	Hs_Smooth_muscle:contraction	GenMapp	Physiological Process	Myometrial Relaxation and Contraction Pathways	215	9	4.19	20
12	Hs_G1_to_S_cellcycle_control	GenMapp	Cellular Process	G1 to S cell cycle control	90	9	10.0	20

1. Click onto the icon to sort the column

2. Click to load the pathway

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Time: 01:15:02

7. Mapped pathway

Bioinformatics Graz **Pathway Explorer**
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Switch to SVG view if an appropriate plugin is available

Create a PDF document of the current mapped pathway

Show experiments

Save a tab delimited list of current mapped genes

No. of available unique gene ids in the pathway

Mapped gene with all available experiments / time points

act Links Log in Last update: Wed, 9 Feb, 2005

Choose Dataset Ranking Filter Dataset Settings Search Return Current Loaded Dataset: Fibroblasts_12TP(Human).txt

Homo Sapiens RefSeq (loc2ref)

[514] pathways available (8947|198|2.21%)

- [1] Pathways (30|1|3.33%)
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 - Insulin (30|1|3.33%)
- [120] KEGG Pathways (4099|93|2.27%)
 - 1. Metabolism (1714|39|2.28%)
 - 2. Genetic Information Processing
 - 3. Environmental Information Process
 - 4. Cellular Processes (892|26|2.91%)
 - 5. Human Diseases (221|41|8.1%)

Cyclins and Cell Cycle Regulation

Organism: Homo Sapiens (hsa)

Experiments: (Homo Sapiens|Fibroblasts_12TP(Human).txt|N)

1 2 3 4 5 6 7 8 9 10 11 12

1 2 3 4

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8. Change display options

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Microarray Data Mapping System

Tutorial Feedback Contact Links Log in Last update: Wed, 9 Feb, 2005

Homo Sapiens Choose Dataset Ranking Filter Dataset Settings Search Return Current Loaded Dataset: Fibroblasts_12TP(Human).txt

RefSeq (loc2ref)

[514] pathways available (8947|198|2.21%)
[1] Pathways (30|1|3.33%)
Self Annotated (30|1|3.33%)
Adipogenesis
Insulin (30|1|3.33%)
[120] KEGG Pathways (4099|93|2.27%)
1. Metabolism (1714|39|2.28%)
2. Genetic Information Processing (1024|21|2.14%)
3. Environmental Information Processing (1024|21|2.14%)
4. Cellular Processes (892|26|2.91%)
5. Human Diseases (221|4|1.81%)
[311] BioCarta Pathways (2209|63|2.85%)
Main Categories (2209|63|2.85%)
Adhesion (276|6|2.17%)
Apoptosis (272|7|2.57%)
Cell Activation (188|7|3.72%)
Cell Cycle Regulation (267|13|4.87%)
Cyclins and Cell Cycle Regulation (267|13|4.87%)
h_cellcyclePathway (34|1|2.91%)
RB Tumor Suppressor/Checkpoints (34|1|2.91%)
Activation of Src by Protein-Tyrosine Kinase (34|1|2.91%)
cdc25 and chk1 Regulatory Network (34|1|2.91%)
Protein Kinase A at the Centrioles (34|1|2.91%)
Cell Cycle: G2/M Checkpoint (34|1|2.91%)
Regulation of p27 Phosphorylation (34|1|2.91%)
Influence of Ras and Rho proteins on the Cell Cycle (34|1|2.91%)
Stathmin and breast cancer (34|1|2.91%)
Cell Cycle: G1/S Checkpoint (34|1|2.91%)
Regulation of cell cycle progression (34|1|2.91%)

Display Options

Possible color schemes

Select color schema			
Colorschema 1:		Colorschema 2:	
Colorschema 3:		Colorschema 4:	
Colorschema 5:		Colorschema 6:	

Possible display options

Display mapped genes names	<input type="checkbox"/>	Skip missing genes	<input checked="" type="checkbox"/>
Display all gene names	<input type="checkbox"/>	Select label color	black
Display all compound names	<input type="checkbox"/>	Max log2 ratio value:	3.0

Set Cancel

1. Check the requested color scheme
2. Check and adjust requested display options
3. Apply selected options to the pathway

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https://pathwayexplorer.genome.tugraz.at/loadSettingsAction.do?action=LoadSettings

8. Change display options (pathway with applied options)

Bioinformatics Graz Pathway Explorer
Microarray Data Mapping System

Tutorial Feedback Contact Links Log in Last update: Wed, 9 Feb, 2005

Homo Sapiens Current Loaded Dataset: Fibroblasts_12TP(Human).txt

Choose Dataset Ranking Filter Dataset Settings Search Return

RefSeq (loc2ref)

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 - RB Tumor Suppressor/Check Point
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 - Cell Cycle: G1/S Check Point
 - Regulation of cell cycle progression

Description:

Cyclins and Cell Cycle Regulation

Organism: Homo Sapiens (hsa)

Experiments: (Homo Sapiens|Fibroblasts_12TP(Human).txt|N)

1	2	3	4	5	6	7	8	9	10	11	12
1	2	3	4	5	6	7	8	9	10	11	12

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9. Show experiments / time points of the mapped dataset

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Homo Sapiens Choose Dataset Filter Dataset Settings Search Return Current Loaded Dataset: Fibroblasts_12TP(Human).txt

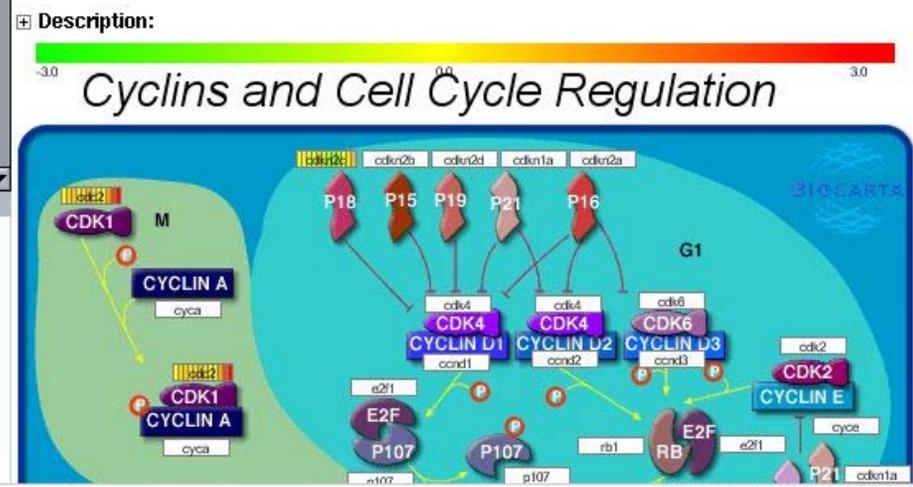
RefSeq (loc2ref)

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 - Protein Kinase A at the Centrioles
 - Cell Cycle: G2/M Checkpoint
 - Regulation of p27 Phosphorylation
 - Influence of Ras and Rho proteins on the Cell Cycle
 - Stathmin and breast cancer
 - Cell Cycle: G1/S Check Point
 - Regulation of cell cycle progression

Hide experiments

No.	Experiment	Experiment Header
1	<input checked="" type="checkbox"/>	0HR
2	<input checked="" type="checkbox"/>	15MIN
3	<input checked="" type="checkbox"/>	30MIN
4	<input checked="" type="checkbox"/>	1HR
5	<input checked="" type="checkbox"/>	2HR
6	<input checked="" type="checkbox"/>	4HR
7	<input checked="" type="checkbox"/>	6HR
8	<input checked="" type="checkbox"/>	8HR
9	<input checked="" type="checkbox"/>	12HR
10	<input checked="" type="checkbox"/>	16HR
11	<input checked="" type="checkbox"/>	20HR
12	<input checked="" type="checkbox"/>	24HR



1. Enable/disable the mapped experiments / time points on the pathway
2. Click on the icon again to hide the experiment list

10. Show pathway description

Bi informatics Graz Pathway Explorer
Microarray Data Mapping System

Hide the pathway description again

Tutorial Feedback

Homo Sapiens RefSeq (loc2ref)

Choose Dataset | Ranking | Filter Dataset | Settings | Search | Return Last update: Wed, 9 Feb, 2005

Current Loaded Dataset: Fibroblasts_12TP(Human).txt

514 pathways available (8947|198|2.21%)
[1] Pathways (30|1|3.33%)
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Cell Cycle Regulation (267|13|4.87%)
Cyclins and Cell Cycle Regulation (34|1|2.94%)
h_cellcyclePathway (34|1|2.94%)
RB Tumor Suppressor/Check
Activation of Src by Protein-
cdc25 and chk1 Regulatory
Protein Kinase A at the Cent
Cell Cycle: G2/M Checkpoir
Regulation of p27 Phosphory
Influence of Ras and Rho pro
Stathmin and breast cancer
Cell Cycle: G1/S Check Point
Regulation of cell cycle prog

Description:
The cell cycle is regulated by the interplay of many molecules. Key among these are the cyclins which are expressed and then degraded in a concerted fashion to drive the stages of the cell cycle. Cyclins combine with cyclin dependent kinases (cdks) to form activated kinases that phosphorylate targets leading to cell cycle regulation. A breakdown in the regulation of this cycle can lead to out of control growth and contribute to tumor formation. Defects in many of the molecules that regulate the cell cycle have been implicated in cancer. Key among these are p53, the cdk inhibitors (p15, p16, p18, p19, p21, p27), and Rb, all of which act to keep the cell cycle from progressing until all repairs to damaged DNA have been completed.

Cyclins and Cell Cycle Regulation

Organism: Homo Sapiens (hsa)

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Time: 01:19:04

Server load: 0.77 (19.25%)

Waiting for pathwayexplorer.genome.tugraz.at...

11. Show gene information



Homo Sapiens

Choose Dataset

Ranking

Filter Dataset

Settings

Search

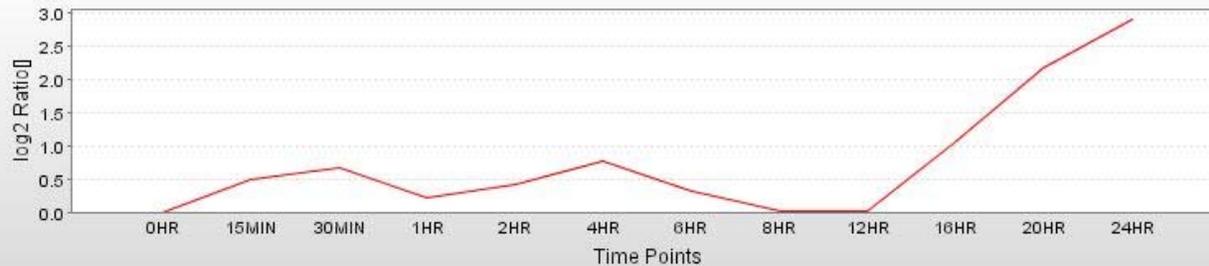
Return

Current Loaded Dataset: Fibroblasts_12TP(Human).t

RefSeq (loc2ref)

- [514] pathways available (8947|198|2.21%)
- [1] Pathways (30|1|3.33%)
 - Self Annotated (30|1|3.33%)
 - Adipogenesis
 - Insulin (30|1|3.33%)
- [120] KEGG Pathways (4099|93|2.27%)
 - 1. Metabolism (1714|39|2.28%)
 - 2. Genetic Information Processing
 - 3. Environmental Information Process
 - 4. Cellular Processes (892|26|2.91%)
 - 5. Human Diseases (221|4|1.81%)
- [311] BioCarta Pathways (2209|63|2.85%)
 - Main Categories (2209|63|2.85%)
 - Adhesion (276|6|2.17%)
 - Apoptosis (272|7|2.57%)
 - Cell Activation (188|7|3.72%)
 - Cell Cycle Regulation (267|13|4.12%)
 - Cyclins and Cell Cycle Regu**
 - h_cellcyclePathway (34|1|0.32%)
 - RB Tumor Suppressor/Check
 - Activation of Src by Protein-
 - cdc25 and chk1 Regulatory
 - Protein Kinase A at the Cent
 - Cell Cycle: G2/M Checkpoi
 - Regulation of p27 Phosphory
 - Influence of Ras and Rho pro
 - Stathmin and breast cancer
 - Cell Cycle: G1/S Check Poi
 - Regulation of cell cycle prog

Expression Profile



1. Click to get OMIM information

GENE	
Symbol Name	cdc2
Gene Name	cell division cycle 2, G1 to S and G2 to M
Accession number (RefSeq)	NM_001788

Link to OMIM to get more gene information

Link to ENTREZ

PROTEIN	
Accession Number (RefSeq)	NP_001777
Accession Number (SWISS-Prot)	

NCBI nucleotide link

NCBI protein link

FUNCTION	
Location	
Classification	
Description/Overview	

LITERATURE	
References	

LINKS	

12. Display OMIM gene information

Bioinformatics Graz Pathway Explorer
Microarray Data Mapping System

Tutorial Feedback Contact Links Log in Last update: Wed, 9 Feb, 2005

Homo Sapiens Choose Dataset Ranking Filter Dataset Settings Search Return Current Loaded Dataset: Fibroblasts_12TP(Human).txt

RefSeq (loc2ref)

[514] pathways available (8947|198|2.21%)

- [1] Pathways (30|1|3.33%)
 - Self Annotated (30|1|3.33%)
 - Adipogenesis
 - Insulin (30|1|3.33%)
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 - Cell Activation (188|7|3.72%)
 - Cell Cycle Regulation (267|13|4.87%)
 - Cyclins and Cell Cycle Regulation**
 - h_cellcyclePathway (34|1|2.87%)
 - RB Tumor Suppressor/Check Point
 - Activation of Src by Protein Tyrosine Kinase
 - cdc25 and chk1 Regulatory Network
 - Protein Kinase A at the Centrioles
 - Cell Cycle: G2/M Checkpoint
 - Regulation of p27 Phosphorylation
 - Influence of Ras and Rho proteins
 - Stathmin and breast cancer
 - Cell Cycle: G1/S Check Point
 - Regulation of cell cycle progression

Expression Profile

Time	log2 Ratio
0HR	0.0
15MIN	~0.5
30MIN	~3.0

OMIM - CELL DIVISION CYCLE 2, G1 TO S AND G2 TO M; CDC2 - Mozilla

File Edit View Go Bookmarks Tools Window Help

NCBI

OMIM

Online Mendelian Inheritance in Man

Johns Hopkins University

PubMedNucleotideProteinGenomeStructurePMCTaxonomyOMIM

Search for

LimitsPreview/IndexHistoryClipboardDetails

Display Show: Send to

All: 1

***116940** Links

CELL DIVISION CYCLE 2, G1 TO S AND G2 TO M; CDC2

Alternative titles; symbols

CELL CYCLE CONTROLLER CDC2
p34(CDC2)
CYCLIN-DEPENDENT KINASE 1; CDK1

Gene map Locus [10q21.1](#)

TEXT

DESCRIPTION

GENE	
Symbol Name	cdc2
Gene Name	cell div
Accession number (RefSeq)	NM_00
PROTEIN	
Accession Number (RefSeq)	NP_00
Accession Number (SWISS-Prot)	
FUNCTION	
Location	
Classification	
Description/Overview	
LITERATURE	
References	
LINKS	

Server load: 0.63 (15.75%) © 2004 - Institute for Genomics and Bioinformatics - Graz University of Technology

Time: 01:21:45

13. Create a PDF document with all available pathway information

Bioinformatics Graz Pathway Explorer
Microarray Data Mapping System

Tutorial Feedback Contact Links Log in Last update: Wed, 9 Feb, 2005

Homo Sapiens Choose Dataset Ranking Filter Dataset Settings Search Return Current Loaded Dataset: Fibroblasts_12TP(Human).txt

RefSeq (loc2ref)

514 pathways available (8947|198|2.21%)
[1] Pathways (30|1|3.33%)
Self Annotated (30|1|3.33%)
Adipogenesis
Insulin (30|1|3.33%)
[120] KEGG Pathways (4099|93|2.27%)
1. Metabolism (1714|39|2.28%)
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Activation of Src by Protein-
cdc25 and chk1 Regulatory
Protein Kinase A at the Cent
Cell Cycle: G2/M Checkpoi
Regulation of p27 Phosphory
Influence of Ras and Rho pro
Stathmin and breast cancer
Cell Cycle: G1/S Check Poi
Regulation of cell cycle prog

Description:

Cyclins and Cell Cycle Regulation

Organism: Homo Sapiens (hsa)

Experiments: (Homo Sapiens|Fibroblasts_12TP(Human).txt|N)

1 2 3 4 5 6 7 8 9 10 11 12

Server load: 0.63 (15.75%) © 2004 - Institute for Genomics and Bioinformatics - Graz University of Technology Time: 01:22:26

To create the PDF document click here. This could take some time and when it has finished the Acrobat Reader should popup automatically.

15. Search options

Bioinformatics Graz Pathway Explorer
Microarray Data Mapping System

Tutorial Feedback Contact Links Log in Last update: Wed, 9 Feb, 2005

Homo Sapiens Choose Dataset Ranking Filter Dataset Settings Search Return Current Loaded Dataset: Fibroblasts_12TP(Human).txt

RefSeq (loc2ref)

Search results will be displayed in the tree

Search Options

- [514] pathways a
- [1] Pathways
- [120] KEGG R
- [311] BioCarta P
- [82] Gene Ontology (6374|150|2.35%)
- Search results
- Search results for 'ppar'
 - Pathways
 - Adipogenesis Regulatory Netwo
 - Peroxisome Proliferator Active
 - Multi-step Regulation of Transcri
 - PPAR binding protein []
 - Mechanism of Gene Regulation I
 - PPAR binding protein []
 - Role of ppar in mitotic spindle reg
 - nuclear mitotic apparatus prot
 - nuclear mitotic apparatus prot
 - CARM1 and Regulation of the E:
 - PPAR binding protein []
 - HIV-1 Nef: negative effector of F:
 - nuclear mitotic apparatus prot
 - Role of PPAR-gamma Coactivat
 - PPAR binding protein []

Search String	ppar
Options	Gene Name
Case Sensitive	<input type="checkbox"/>
<input type="button" value="Search"/> <input type="button" value="Cancel"/>	

1. Choose a search option
2. Enter a search string and check the case sensitive box if requested
3. Click on the search button the result will be added to the tree on the left side
4. To select a found gene or pathway click on the appropriate tree icon

TUG
Institute for Genomics and Bioinformatics
Petersgasse 14, 8010 Graz, Austria
Graz University of Technology

Server load: 0.78 (19.5%) © 2004 - Institute for Genomics and Bioinformatics - Graz University of Technology Time: 01:34:28

javascript: trees[1].toggle(16)

14. Search option (results)

Bioinformatics Graz **Pathway Explorer**
Microarray Data Mapping System

Tutorial Feedback Contact Links Log in Last update: Wed, 9 Feb, 2005

Homo Sapiens Choose Dataset Ranking Filter Dataset Settings Search Return Current Loaded Dataset: Fibroblasts_12TP(Human).txt

RefSeq (loc2ref) PNG SVG

Description:

[514] pathways available (8947|198|2.21%)

- [1] Pathways (30|1|3.33%)
- [120] KEGG Pathways (4099|93|2.27%)
- [311] BioCarta Pathways (2209|63|2.85%)
- [82] GenMapp (6374|150|2.35%)

Search results

- Search results for 'ppar'
- Pathways
 - Adipogenesis Regulatory Netwo
 - Peroxisome Proliferator Active
 - Multi-step Regulation of Transcri
 - PPAR binding protein []**
 - Mechanism of Gene Regulation I
 - PPAR binding protein []
 - Role of Ran in mitotic spindle reg
 - nuclear mitotic apparatus prot
 - nuclear mitotic apparatus prot
 - CARM1 and Regulation of the E:
 - PPAR binding protein []
 - HIV-1 Nef: negative effector of F:
 - nuclear mitotic apparatus prot
 - Role of PPAR-gamma Coactivat
 - PPAR binding protein []

Multi-step Regulation of Transcription by Pitx2

Organism: Homo Sapiens (hsa)

Found gene displayed in turquoise. If you want to unselect the gene reload the pathway by clicking on the pathway tree icon.

Experiments: (Homo Sapiens)Fibroblasts_12TP(Human).txt(N)

Server load: 0.77 (19.25%) © 2004 - Institute for Genomics and Bioinformatics - Graz University of Technology Time: 01:35:24

https://pathwayexplorer.genome.tugraz.at/treeAction.do?action=LoadPathway&pw=1566_6