



Bioinformatic Pathway and Ontology Analysis

David Crossman, Ph.D.
UAB Heflin Center for Genomic Science

Immersion Course
Friday, April 5, 2013

What to do with your list of genes

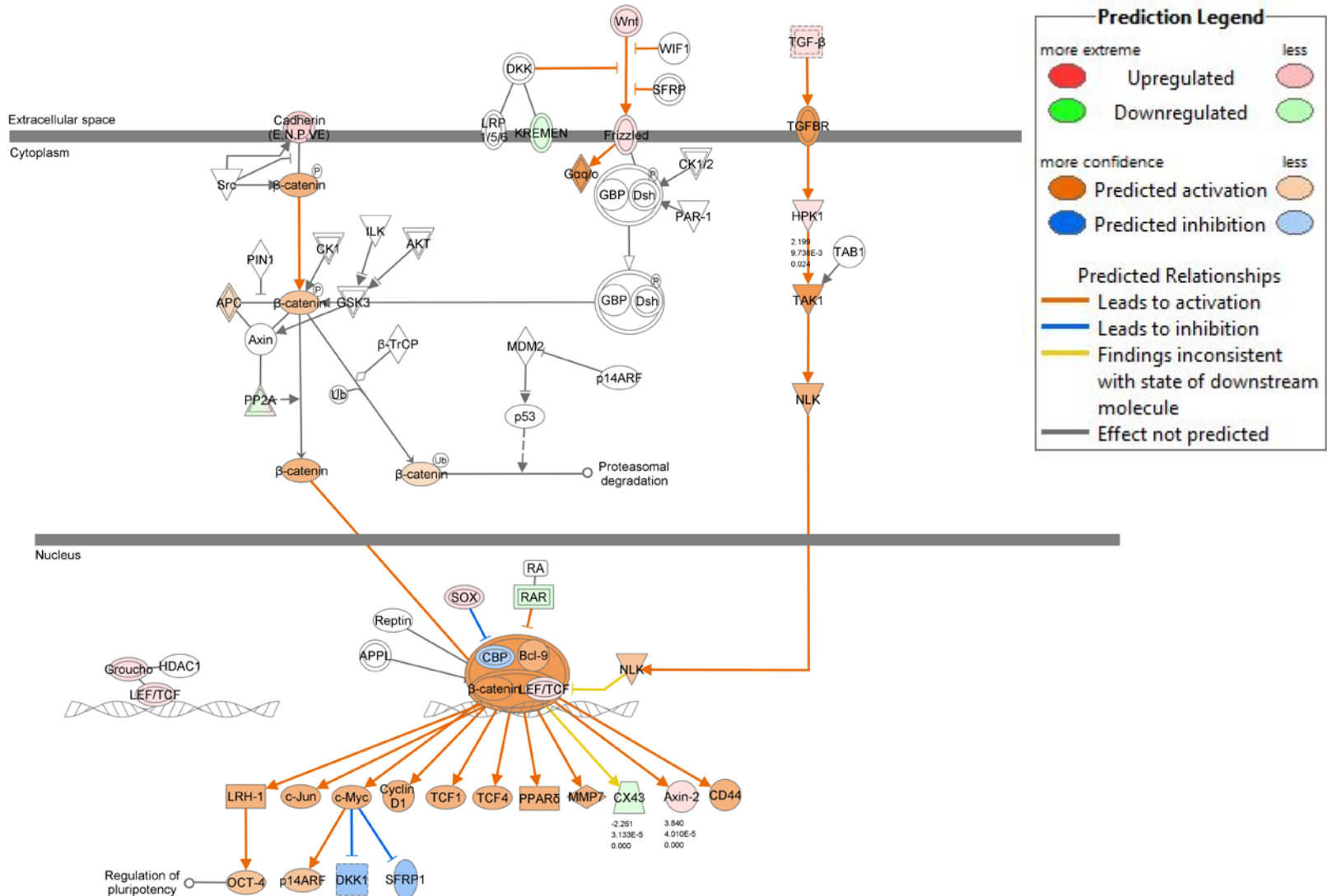
- Apply a Systems Biology approach to data mine and analyze your data
- Tools and databases available (some free, others \$\$) to define the underlying biology behind different –omics data
- These tools and databases will identify and prioritize the most relevant pathways, networks and cellular processes affected by your dataset.

Pathways & Ontology Analysis Tools

Tool	Link	Price
Reactome	http://www.reactome.org	Free
IPA	http://ingenuity.com/	\$\$\$
GeneGo Metacore	http://www.genego.com/	\$\$\$
Cytoscape	http://www.cytoscape.org/	Free
GenMAPP	http://www.genmapp.org/	Free
InterMine	http://intermine.org/	Free
KEGG	http://www.genome.jp/kegg/	Free
GO	http://www.geneontology.org/	Free
Panther	http://www.pantherdb.org/	Free
DAVID	http://david.abcc.ncifcrf.gov/	Free
And many, many more!!		

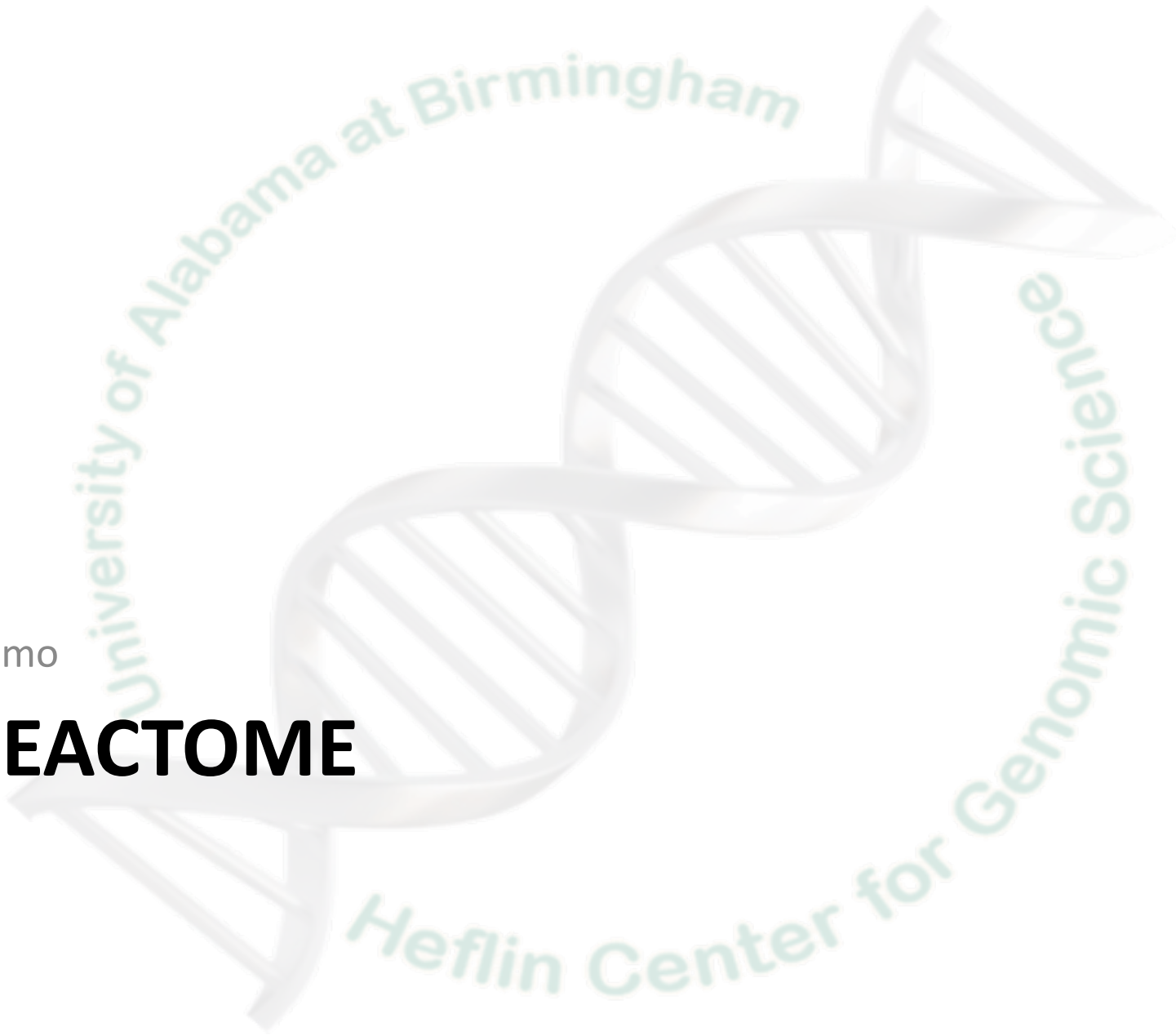
Network Example

Wnt/ β -catenin Signaling



University of Alabama at Birmingham

Heflin Center for Genomic Science



Demo

REACTOME

Reactome

- Open-source, open access.
- Manually curated.
- Peer-reviewed pathway database (pathway annotations are authored by “expert” biologists).
- Some of the tools they have:
 - Browse pathways
 - Map IDs to pathways
 - Overrepresentation analysis
 - Compare species
 - Analyze expression data

Quick links to tools most commonly used.



- Home
- About
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- Outreach

Manual & tutorials

Search examples...

Browse Pathways

Map IDs to Pathways

Compare Species

Analyze Expression Data

If you would prefer to use our old website, click here.

Download

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

- BioPax
- SBML
- Textbook
- Other formats

Try this

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

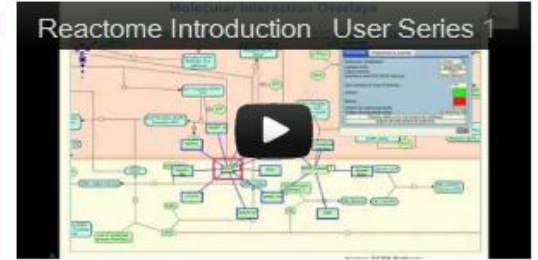
Try it out!

f in W t RSS YouTube

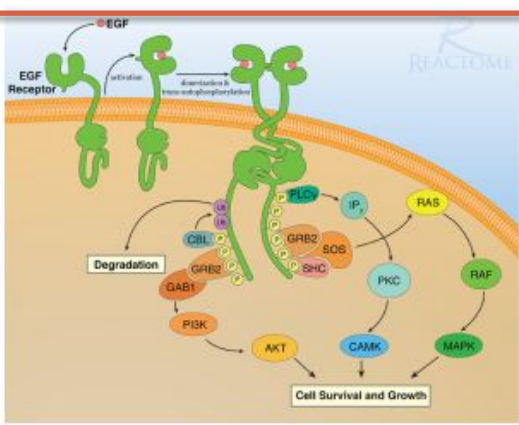
About Reactome

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

Tutorial



Featured pathway: Signaling by EGFR



Other useful tools

Click image to see pathway

News and Notes

- Jun 29, 2012: Reactome will be attending COMBINE 2012**
The Computational Modeling in Biology Network (COMBINE) is an initiative to coordinate the development of the various community standards ... [more]
- Jun 29, 2012: Reactome will be visiting Korea and Japan**
Reactome outreach coordinator, Robin Haw, will give a talk at the Current and Future in Pathway Research International Workshop at the Korea ... [more]
- Jun 26, 2012: Version 41 Released**
New in Version 41 is the topic Cellular responses to stress, including Regulation of Hypoxia-inducible ... [more]
- Mar 22, 2012: Version 40 Released**
The pathway Extracellular matrix organization is new and includes Activation ... [more]
- Mar 16, 2012: Reactome will be participating in Google Summer of Code 2012**
The Genome Informatics group, organizing the joint efforts of Galaxy, GBrowse, ... [more]

To see older news, click here.

Browse Pathways

The image shows the Reactome Pathway Browser interface. On the left, there is a sidebar with a 'Switch Species:' dropdown set to 'Homo sapiens' and a 'Pathways' list. The list includes various biological processes such as Apoptosis, Cell Cycle, Cell-Cell communication, Cellular responses to stress, Circadian Clock, Developmental Biology, Disease, DNA Repair, DNA Replication, Extracellular matrix organization, Gene Expression, Hemostasis, Immune System, Meiosis, Membrane Trafficking, Metabolism, Metabolism of proteins, Muscle contraction, Neuronal System, Signal Transduction, and Transmembrane transport of small molecule. Some items are marked with 'NEW' or 'UPDATED'. At the top right, there are filters for 'Protein', 'Small Molecule', and 'Complex', and a 'Diagram key' link.

The main content area displays a 'User Manual' window with the following text:

User Manual

Welcome to the Reactome Pathway Browser, a tool for visualizing and interacting with pathways.

To view a Pathway Diagram either:

- Click on a pathway name in the hierarchical list on the left
- Return to the Homepage (button top left) and text search using a pathway, protein or compound name, or an accession number (e.g. Q9HCN6). In the resulting list, click on pathway name to open it in the Pathway Browser.

To see a key to pathway diagrams click the Diagram Key link top right

For a detailed explanation see Section 3 of the [Reactome User Guide](#)

For help please contact us (help@reactome.org)

The Pathway Browser includes tools for several types of analysis, detailed in Section 3 of the [Reactome User Guide](#).

This beginning screen says it all on how to browse pathways

Map IDs to Pathways (ID mapping and pathway assignment)



Helpful video tutorial!

Pathway Analysis

Allows you to analyse a list of protein, gene, expression data or compound identifiers and determine how they are likely to affect pathways. [More...](#)

Video Tutorial

Paste or upload your data:

1c

Example

1a

1. Get your data to Reactome:
 - a. Paste you data, or
 - b. Choose file from your computer (tab-delimited), or
 - c. For demo purposes, click "Example"
2. Choused "ID mapping and pathway assignment"
3. Click "Analyse"

1b

Choose File No file chosen

Clear

Analyse 3

Select your desired analysis tool

Inhouse services:

- 2 **ID mapping and pathway assignment.** Takes your list of IDs and finds the corresponding pathways from Reactome, plus the corresponding UniProt IDs.
 Overrepresentation analysis. Finds the Reactome pathways in which IDs in your list are strongly enriched - can help to understand the biological context of your data.

ID mapping & pathway assignment



Pathway Assignment

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

[Video Tutorial](#)

Select format to download this table:

ID ▼▲	UniProt ID ▼▲	Species ▼▲	Pathway names ▼▲
000139	000139	Homo sapiens	Adaptive Immune System; Cell Cycle; Cell Cycle, Mitotic; DNA Replication; Factors involved in megakaryocyte development and platelet production; Hemostasis; Immune System; Kinesins; MHC class II antigen presentation; Mitotic M-M/G1 phases
000186	000186	Homo sapiens	Hemostasis; Platelet activation, signaling and aggregation; Response to elevated platelet cytosolic Ca2+
000187	000187	Homo sapiens	Complement cascade; Immune System; Innate Immune System
000204	000204	Homo sapiens	Biological oxidations; Metabolism; Phase II conjugation
000217	000217	Homo sapiens	Metabolism; Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.; The citric acid (TCA) cycle and respiratory electron transport
000231	000231	Homo sapiens	Adaptive Immune System; APC/C-mediated degradation of cell cycle proteins; Apoptosis; Cell Cycle; Cell Cycle Checkpoints; Cell Cycle, Mitotic; Class I MHC mediated antigen processing & presentation; Disease; DNA Replication; Gene Expression; HIV infection; Host Interactions of HIV factors; Immune System; Metabolism; Metabolism of amino acids and derivatives; Mitotic G1-G1/S phases; Mitotic M-M/G1 phases; Regulation of Apoptosis; Regulation of DNA replication; Regulation of mitotic cell cycle; Regulation of mRNA Stability by Proteins that Bind AU-rich Elements; S Phase; Signal Transduction; Signaling by the B Cell Receptor (BCR); Signaling by Wnt; Synthesis of DNA
000232	000232	Homo sapiens	Adaptive Immune System; APC/C-mediated degradation of cell cycle proteins; Apoptosis; Cell Cycle; Cell Cycle Checkpoints; Cell Cycle, Mitotic; Class I MHC mediated antigen processing & presentation; Disease; DNA Replication; Gene Expression; HIV infection; Host Interactions of HIV factors; Immune System; Metabolism; Metabolism of amino acids and derivatives; Mitotic G1-G1/S phases; Mitotic M-M/G1 phases; Regulation of Apoptosis; Regulation of DNA replication; Regulation of mitotic cell cycle; Regulation of mRNA Stability by Proteins that Bind AU-rich Elements; S Phase; Signal Transduction; Signaling by the B Cell Receptor (BCR); Signaling by Wnt; Synthesis of DNA
000233	000233	Homo sapiens	Adaptive Immune System; APC/C-mediated degradation of cell cycle proteins; Apoptosis; Cell Cycle; Cell Cycle Checkpoints; Cell Cycle, Mitotic; Class I MHC mediated antigen processing & presentation; Disease; DNA Replication; Gene Expression; HIV infection; Host Interactions of HIV factors; Immune System; Metabolism; Metabolism of amino acids and derivatives; Mitotic G1-G1/S phases; Mitotic M-M/G1 phases; Regulation of Apoptosis; Regulation of DNA replication; Regulation of mitotic cell cycle; Regulation of mRNA Stability by Proteins that Bind AU-rich Elements; S Phase; Signal Transduction; Signaling by the B Cell Receptor (BCR); Signaling by Wnt; Synthesis of DNA
			Gastrin-CREB signalling pathway via PKC and MAPK; GPCR downstream signaling; GPCR ligand

Table can be downloaded in various formats

Columns can be sorted

Clicking the UniProt ID # will take you to the info page about that particular molecule

Clicking on the Pathway names links will take you to the pathway map

Map IDs to Pathways (Overrepresentation analysis)



Pathway Analysis

Allows you to analyse a list of protein, gene, expression data or compound identifiers and determine how they are likely to affect pathways. [More...](#)

[Video Tutorial](#)

Paste or upload your data:

[Example](#)

Will do the same as before, but this time, choose "Overrepresentation analysis"

[Choose File](#) No file chosen

[Clear](#)

[Analyse](#)

Select your desired analysis tool

Inhouse services:

- ID mapping and pathway assignment.** Takes your list of IDs and finds the corresponding pathways from Reactome, plus the corresponding UniProt IDs.
- Overrepresentation analysis.** Finds the Reactome pathways in which IDs in your list are strongly enriched - can help to understand the biological context of your data.

Overrepresentation analysis

REACTOME

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Statistically over-represented events in hierarchy

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

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

open all | close all

- Cell Cycle 2.3e-27, 149/413
- Metabolism 3.5e-30, 343/1329
- Gene Transcription 8.3e-01, 243/1664
- Transcription 2.1e-24, 74/145
- DNA Replication 2.1e-23, 91/209
- Apoptosis 4.5e-23, 72/144
- Gene Expression 3.2e-17, 229/913
- DNA Repair 5.0e-21, 58/107
- mRNA Processing 2.5e-20, 66/136
- Disease 4.7e-08, 200/937
- Immune System 3.8e-02, 207/1219
- Hemostasis 1.7e-09, 121/477
- Cdc20-Phospho-APC/C mediated degradation of Cyclin 7.7e-13, 36/69
- Metabolism of RNA 2.1e-07, 69/249
- Proteasome mediated degradation of PAK-2p3 1.1e-10, 27/49
- Autolysis of protein 8.9e-01, 60/449
- TRIF mediated TLR3 signaling 1.5e-09, 31/67
- 5'-UTR-mediated translational regulation 2.2e-09, 42/109
- Transmembrane transport of small molecules 1.0e+00, 46/432
- Elongation arrest and recovery 3.8e-07, 17/31
- Post-Elongation Processing of the Transcript 2.4e-05, 18/43
- Developmental Biology 3.1e-01, 66/406
- Neuronal System 1.0e+00, 23/290
- Cell-Cell communication 7.2e-01, 19/137
- APC-Cdc20 mediated degradation of Nek2 1.7e-02, 8/23
- NICD traffics to nucleus 8.2e-03, 6/13
- Meiosis 6.1e-02, 18/81
- A third proteolytic cleavage releases NICD 1.1e-02, 5/10
- Steroid hormones 1.2e-02, 9/26
- Sulfate salt and organic anion SLC transporters 2.7e-01, 3/12
- Formation of the P-TEFb(Cyclin T1-Cdk9) complex 2.3e-02, 2/2
- Phosphorylated human RAF1 binds to RAS:GTP complex 2.3e-02, 2/2
- Acidic lipid and oligopeptide SLC transporters 8.9e-01, 5/49
- Receptor-ligand binding initiates the second proteolytic cleavage of Notch receptor 5.0e-02, 5/14

Total number of events assessed: 6713
Number of matching events (i.e. individual hypergeometric tests performed): 2324
Number of genes matching submitted identifiers: 965

Statistically over-represented events as an ordered list

Recreate in a tab-delimited text file

There is a wealth of info on this page, so make sure to scroll down! Categories found on this page:

1. Statistically over-represented events in hierarchy
2. Statistically over-represented events as an ordered list
3. Reactions colored according to the number of genes or compounds participating in the given reaction
4. Mapping from submitted identifiers to Reactions

Overrepresentation analysis

Cell Cycle 2.3e-27, 149/413

Matching identifiers

Cell Cycle Mitotic 1.7e-31, 137/336

Matching identifiers

- Q96CW5 TUBGCP3
- P51665 PSMD7
- P51530 DNA2
- P49792 RANBP2
- Q13409 DYNC1I2
- Q13416 ORC2
- P30291 WEE1
- P28072 PSMB6
- Q15154 PCM1
- P23258 TUBG1
- O43264 ZW10
- O96020 CCNE2
- P43686 PSMC4
- P52948 NUP98
- P49720 PSMB3
- P28065 PSMB9
- P46527 CDKN1B
- O95229 ZWINT
- P35244 RPA3
- P30305 CDC25B
- Q12769 NUP160
- P33992 MCM5
- P31323 PRKAR2B
- P28340 POLD1
- P28074 PSMB5
- Q14683 SMC1A
- P48730 CSNK1D
- P49642 PRIM1
- Q03188 CENPC1
- P30307 CDC25C
- P12004 PCNA
- Q14209 E2F2
- Q96Y1 NSL1
- P51065 UBE2E1

- Here, we are focusing in on the “Statistically over-represented events in hierarchy” category.
- Clicking on the “+” sign will expand the event (“-” will close it)
- Clicking on the colored words will open the pathway map
- Clicking on any gene name link will take you to an info page about that gene

Compare species



Species Comparison

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

Compare all **human** pathways with:

This tool will allow you to compare human pathways to any other species pathways they have in their database

Compare species



Species Comparison

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

Select format to download this table:

Pathway name ▼▲	Other species ▼▲	Proteins, human ▼▲	Proteins, other species ▼▲	% in other species ▼▲	Click button to view pathway
Abacavir transport and metabolism	Escherichia coli	10	3	30%	<input type="button" value="View"/>
ABC-family proteins mediated transport	Escherichia coli	33	13	39%	<input type="button" value="View"/>
Abnormal metabolism in phenylketonuria	Escherichia coli	4	0	0%	<input type="button" value="View"/>
Activation of Chaperone Genes by ATF6- α 1	Escherichia coli	5	1	20%	<input type="button" value="View"/>
Activation of Chaperone Genes by XBP1(S)	Escherichia coli	45	4	8%	<input type="button" value="View"/>
Activation of Genes by ATF4	Escherichia coli	7	1	14%	<input type="button" value="View"/>
Activation of Matrix Metalloproteinases	Escherichia coli	25	0	0%	<input type="button" value="View"/>
Adaptive Immune System	Escherichia coli	607	0	0%	<input type="button" value="View"/>
Advanced glycosylation endproduct recept	Escherichia coli	13	0	0%	<input type="button" value="View"/>
alpha-linolenic (omega3) and linoleic (o	Escherichia coli	11	2	18%	<input type="button" value="View"/>
Amyloids	Escherichia coli	28	1	3%	<input type="button" value="View"/>
Antiviral mechanism by IFN-stimulated ge	Escherichia coli	67	0	0%	<input type="button" value="View"/>
APC/C-mediated degradation of cell cycle	Escherichia coli	79	0	0%	<input type="button" value="View"/>
Apoptosis	Escherichia coli	138	0	0%	<input type="button" value="View"/>

Here I chose, *E. coli*, and as before, columns can be sorted, the “View” button will open the pathway map, and the table can be downloaded

Analyze expression data



Upload expression data

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

[Video Tutorial](#)

Paste or upload your data:

1c [Example](#)

1a

1. Get your expression level data to Reactome (note: can have multiple columns of data, i.e. time-course):
 - a. Paste you data, or
 - b. Choose file from your computer (tab-delimited), or
 - c. For demo purposes, click “Example”
2. Click “Analyse”

1b [Choose File](#) No file chosen

[Clear](#)

[Analyse](#) 2

Analyze expression data



Expression per pathway

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

[Video Tutorial](#)

Select format to download this table:

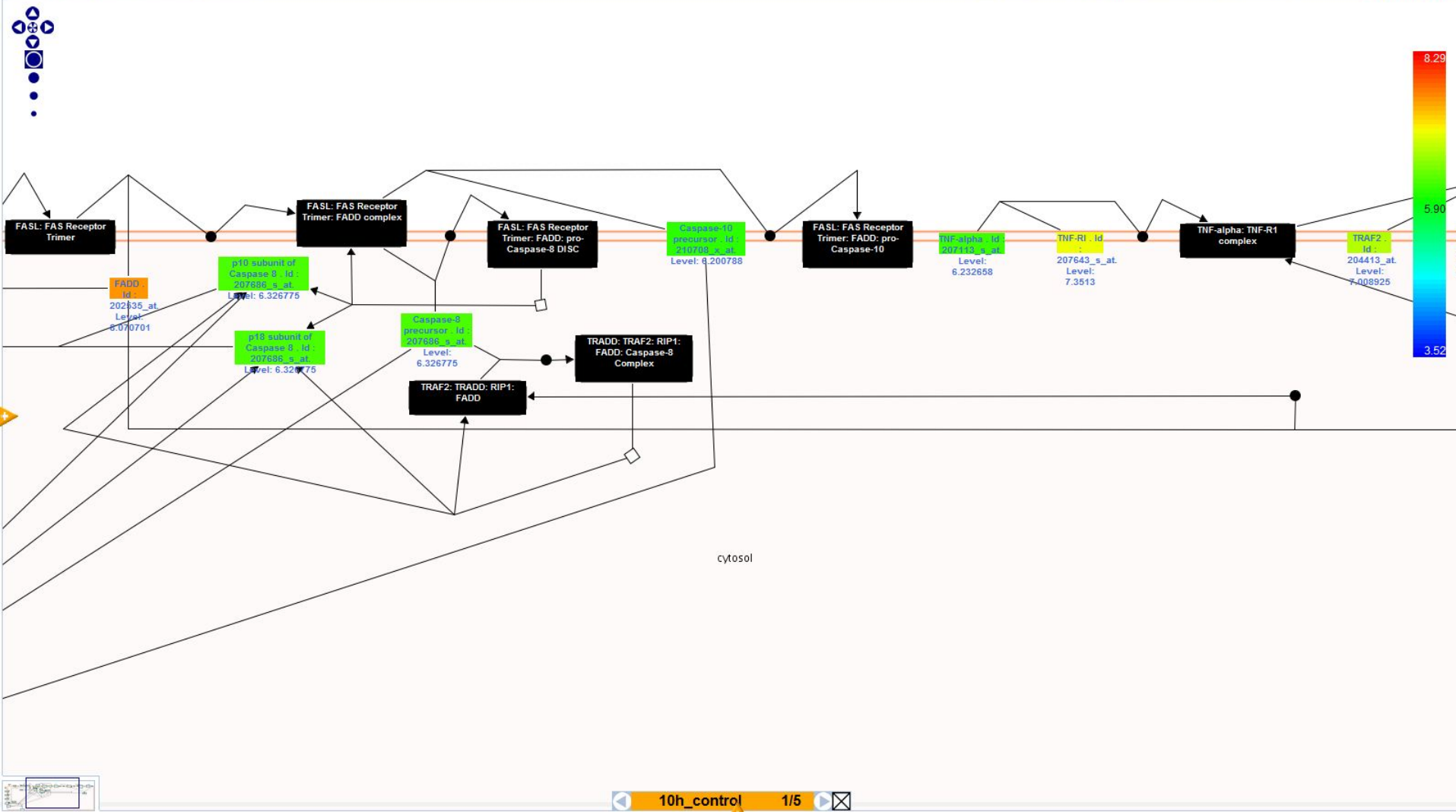
Pathway name ▼▲	Species ▼▲	Total number of proteins ▼▲	Matching proteins in data ▼▲	% in data ▲	Click button to view pathway
Extrinsic Pathway for Apoptosis	Homo sapiens	12	12	100%	<input type="button" value="View"/>
Double-Strand Break Repair	Homo sapiens	20	19	95%	<input type="button" value="View"/>
Base Excision Repair	Homo sapiens	19	18	94%	<input type="button" value="View"/>
Nucleotide Excision Repair	Homo sapiens	49	45	91%	<input type="button" value="View"/>
mRNA Capping	Homo sapiens	29	26	89%	<input type="button" value="View"/>
Intrinsic Pathway for Apoptosis	Homo sapiens	27	23	85%	<input type="button" value="View"/>
Synthesis of DNA	Homo sapiens	95	73	76%	<input type="button" value="View"/>
RNA Polymerase II Transcription	Homo sapiens	102	78	76%	<input type="button" value="View"/>
Metabolism of nucleotides	Homo sapiens	71	54	76%	<input type="button" value="View"/>
S Phase	Homo sapiens	106	80	75%	<input type="button" value="View"/>
Processing of Capped Intron-Containing Pre-mRNA	Homo sapiens	111	83	74%	<input type="button" value="View"/>
Regulation of DNA replication	Homo sapiens	71	53	74%	<input type="button" value="View"/>

Table can be downloaded in various formats

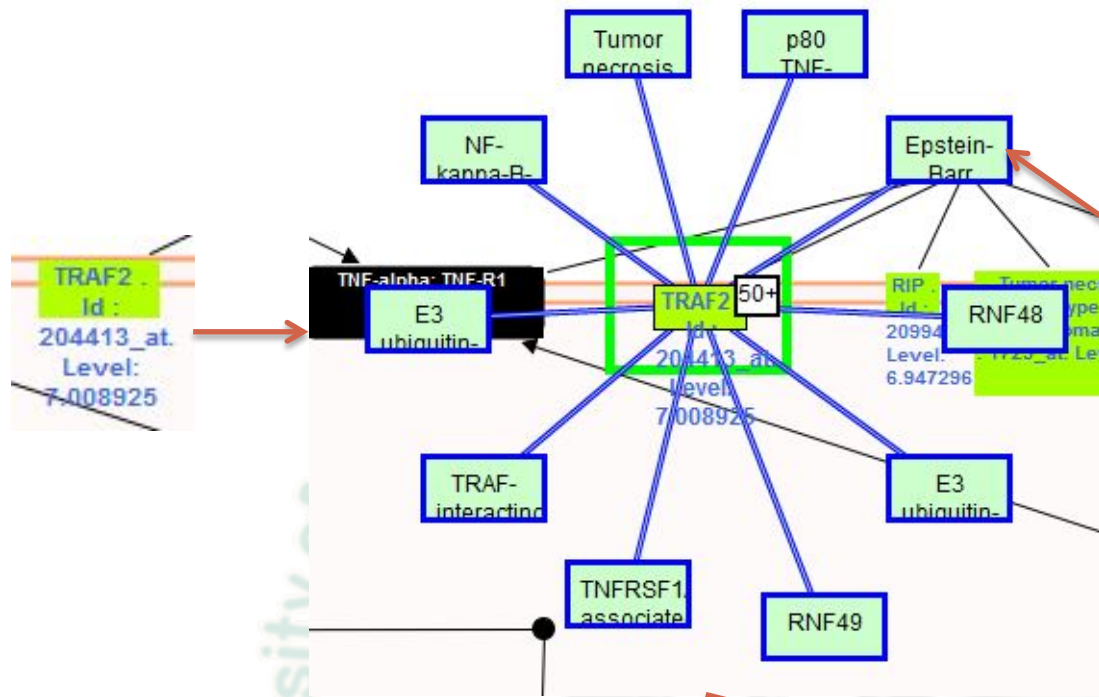
Columns can be sorted

Clicking the number link will show list of molecules involved

Clicking on the "View" button will take you to the pathway map



- Here I chose the Extrinsic Pathway for Apoptosis
- Molecules colored are those from the dataset (values are listed below the molecule name)
- Click on Diagram key (top right hand corner) to reveal the legend



- Molecules are interactive
- Click on a molecule (a green box will highlight it)
- Right-click and choose "Display interactors"
- Click on yellow triangle with a "+" sign at bottom to reveal detailed info about the molecule

Name	TRAF2 TNF receptor associated factor 2 Tumor necrosis factor type 2 receptor associated protein 3
Stable identifier	REACT_4499.2
Links to corresponding entries in other databases	BioGPS Gene:7186 CTD Gene:7186 ENSEMBL:ENSG00000127191 GeneCards:Q12933 KEGG Gene:7186 NCBI Gene:7186 OMIM:601895 Protein Data Bank:1CA4 Protein Data Bank:1CA9 Protein Data Bank:1CZY Protein Data Bank:1CZZ Protein Data Bank:1D00 Protein Data Bank:1D01 Protein Data Bank:1D0A Protein Data Bank:1D0J Protein Data Bank:1F3V Protein Data Bank:1QSC RefSeq:NP_066961 UCSC human:Q12933



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Demo

PANTHER

Panther

- Tools and data on the PANTHER site can be used to:
 - Get information about a gene of interest
 - Explore protein families, molecular functions, biological processes, cellular components and pathways
 - Generate lists of genes that belong to a given protein family or subfamily, have a given molecular function or participate in a given biological process or pathway, e.g. generate a candidate gene list for a disease
 - Analyze lists of genes, proteins or transcripts according to categories based on family, molecular function, biological process, cellular component or pathway, e.g. analyze mRNA microarray data

Other great features

Quick links

- [Whole genome function views](#)
- [Gene expression tools](#)
- [cSNP tools](#)
- [Upload multiple gene IDs](#)
- [Community Curation](#)
- [My Workspace](#)
- [HMM scoring](#)
- [Downloads](#)
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Quick links to tools most commonly used.

KEYWORD SEARCH

All

SEQUENCE SEARCH

Enter a protein sequence: ?

Sequence query limits: Protein - 50kb

Submit

The PANTHER (Protein **AN**alysis **TH**rough Evolutionary Relationships) Classification System is a unique resource that **classifies genes by their functions**, using published scientific experimental evidence and evolutionary relationships to predict function even in the absence of direct experimental evidence. Proteins are **classified by expert biologists** according to:

- ✦ [Gene families and subfamilies](#), including annotated phylogenetic trees
- ✦ [Gene Ontology classes](#): molecular function, biological process, cellular component
- ✦ [PANTHER Protein Classes](#)
- ✦ [Pathways, including diagrams](#)

PANTHER is part of the [Gene Ontology Reference Genome Project](#).

PANTHER is supported by a research grant from the National Institute of General Medical Sciences [grant [GM081084](#)] and maintained by the [Thomas lab](#) at the University of Southern California.

What can I do on the PANTHER site? 
[Guide to getting started](#)

News

(March 16, 2012)

PANTHER 7.2 is released.

[Click](#) for additional info.

Publications

[How to cite PANTHER](#)

"PANTHER version 7: [improved phylogenetic trees, orthologs and collaboration with the Gene Ontology Consortium.](#)" [Mi, et al.](#)

"[Applications for protein sequence-function evolution data: mRNA/protein expression analysis and coding SNP scoring tools.](#)" [Thomas, et al.](#)

"PANTHER: a library of protein families and subfamilies indexed by function." [Thomas, et al.](#)

Upload multiple gene IDs



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[HMM scoring](#)

[Downloads](#)

[Genome statistics](#)

[Site map](#)

Newsletter subscription

Enter your Email:

Find PANTHER-classified genes, transcripts, and proteins by uploading a list of IDs

Batch ID Search

Enter IDs: **1a**

separate IDs by a space or comma - [supported IDs](#)

Upload IDs: No file chosen
- [file format](#) **1b**

Select File Type:

- ID List
 Previously exported text search results

Select Genomes:

Homo sapiens
Mus musculus
Rattus norvegicus
Gallus gallus
Danio rerio


2

3

1. Get your data to Panther:
 - a. Paste your IDs, or
 - b. Choose a file (tab-delimited)
2. Select Genome(s)
3. Click "Search"

- Table listing all the genes in your dataset (scroll to the right to see all the columns)
- Table can be downloaded by the “Send list to:” dropdown box
- Click the pie chart icon to view the GO categories in pie charts

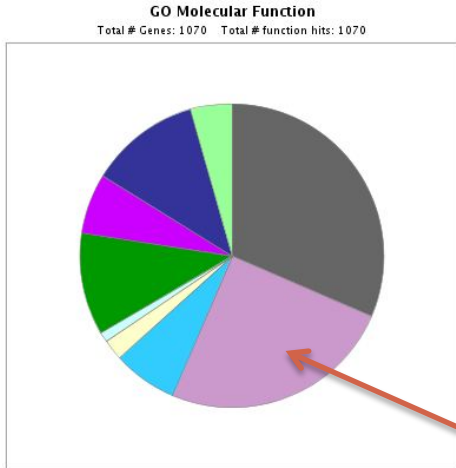
PANTHER GENE LIST [Customize Gene list](#)

Convert List to: Send list to: 

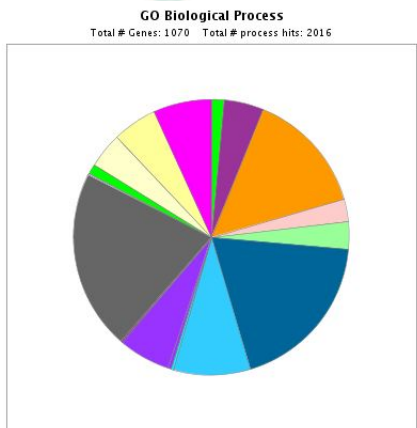
Display: items per page [Refine Search](#)

Hits 1-30 of 1070 [page: (1) [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) [9](#) [10](#) >>] Number of mapped ids found 1040 [IDs not found \(217\)](#)

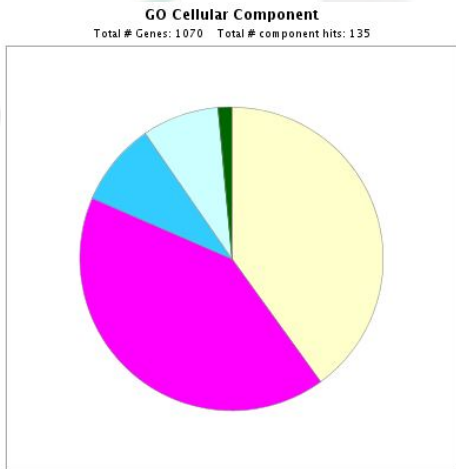
Gene ID	Mapped IDs	Gene Name Gene Symbol Ortholog	PANTHER Family/Subfamily	GO Molecular Function	GO Biological Proc
<input type="checkbox"/> 1. HUMAN ENSEMBL=ENSG00000115361 UniProtKB=P28330	ACADL	Long-chain specific acyl-CoA dehydrogenase, mitochondrial ACADL ortholog	<input checked="" type="checkbox"/> PREDICTED: SIMILAR TO ISOVALERYL COENZYME A DEHYDROGENASE, PARTIAL (PTHR10909:SF143)	<input checked="" type="checkbox"/> oxidoreductase activity	respiratory electron transport chain acyl-CoA metabolism acyl-CoA metabolic process
<input type="checkbox"/> 2. HUMAN ENSEMBL=ENSG00000005471 UniProtKB=P21439	ABCB4	Multidrug resistance protein 3 ABCB4 ortholog	SUBFAMILY NOT NAMED (PTHR24221:SF24)	ATPase activity, coupled to transmembrane movement of substances transmembrane transporter activity	extracellular transport transmembrane transport
<input type="checkbox"/> 3. HUMAN ENSEMBL=ENSG00000155893 UniProtKB=Q8TE99	ACPL2	Acid phosphatase-like protein 2 ACPL2 ortholog	HISTIDINE ACID PHOSPHATASE-RELATED (PTHR11567:SF12)	-	-
<input type="checkbox"/> 4. HUMAN ENSEMBL=ENSG00000197142 UniProtKB=Q9ULC5	ACSL5	Long-chain-fatty-acid--CoA ligase 5 ACSL5 ortholog	PUTATIVE UNCHARACTERIZED PROTEIN (PTHR24096:SF46)	ligase activity	fatty acid metabolism
<input type="checkbox"/> 5. HUMAN ENSEMBL=ENSG00000160345 UniProtKB=Q5BN46	C9orf116	UPF0691 protein C9orf116 C9orf116 ortholog	SUBFAMILY NOT NAMED (PTHR20899:SF0)	-	-
<input type="checkbox"/> 6. HUMAN ENSEMBL=ENSG00000165118 UniProtKB=Q5T6V5	C9orf64	UPF0553 protein C9orf64 C9orf64 ortholog	SUBFAMILY NOT NAMED (PTHR21314:SF0)	-	-
<input type="checkbox"/> 7. HUMAN ENSEMBL=ENSG00000182985 UniProtKB=Q9BY67	CADM1	Cell adhesion molecule 1 CADM1	NECTIN-RELATED (PTHR23277:SF8)	receptor activity	-



- Click to get gene list for a category:
- [binding \(GO:0005488\)](#)
 - [catalytic activity \(GO:0003824\)](#)
 - [enzyme regulator activity \(GO:0030234\)](#)
 - [ion channel activity \(GO:0005216\)](#)
 - [motor activity \(GO:0003774\)](#)
 - [receptor activity \(GO:0004872\)](#)
 - [structural molecule activity \(GO:0005198\)](#)
 - [transcription regulator activity \(GO:0030528\)](#)
 - [transporter activity \(GO:0005215\)](#)
- Color picker powered by Web Colors by Vizibone



- Click to get gene list for a category:
- [apoptosis \(GO:0006915\)](#)
 - [cell adhesion \(GO:0007155\)](#)
 - [cell communication \(GO:0007154\)](#)
 - [cell cycle \(GO:0007049\)](#)
 - [cellular component organization \(GO:0016043\)](#)
 - [cellular process \(GO:0009987\)](#)
 - [developmental process \(GO:0032502\)](#)
 - [generation of precursor metabolites and energy \(GO:0006091\)](#)
 - [homeostatic process \(GO:0042592\)](#)
 - [immune system process \(GO:0002376\)](#)
 - [localization \(GO:0051179\)](#)
 - [metabolic process \(GO:0008152\)](#)
 - [regulation of biological process \(GO:0050789\)](#)
 - [reproduction \(GO:0000003\)](#)
 - [response to stimulus \(GO:0050896\)](#)
 - [system process \(GO:0003026\)](#)
 - [transport \(GO:0006810\)](#)
- Color picker powered by Web Colors by Vizibone



- Click to get gene list for a category:
- [extracellular region \(GO:0005576\)](#)
 - [intracellular \(GO:0005622\)](#)
 - [plasma membrane \(GO:0005886\)](#)
 - [protein complex \(GO:0043234\)](#)
 - [ribonucleoprotein complex \(GO:0030529\)](#)
- Color picker powered by Web Colors by Vizibone

- Pie charts of the 3 GO categories:
 - Molecular Function
 - Biological Process
 - Cellular Component
- Each “wedge” can be clicked on to drill further down into the category
- Clicking on any category name link will list a table of molecules from your dataset found in that particular category