NCIBI

National Center for Integrative Biomedical Informatics

ConceptGen
User Guide

This work is supported by the
National Center for Integrative Biomedical Informatics
through NIH Grant# 1U54DA021519-01A1

CONTENTS

OVERVIEW

About ConceptGen

ConceptGen is a tool that can help you identify, explore, and visualize relationships and significant overlaps among sets of genes (concepts), using the following types of analysis.

Gene set enrichment testing

For gene set enrichment testing, you upload a list of genes (larger lists tend to yield better results) to find other predefined concepts that are significantly enriched with the genes in your set.

You can also search or browse predefined concepts and select one to compare with other concepts, rather than uploading your own gene list.

Gene set relation mapping

With gene set relation mapping, you can create a network graph to visualize the interconnectivity among concepts.

You can also create a heatmap view that helps you visualize how genes and concepts are related, and which genes are driving the enrichment of which groups of concepts.

Gene-to-gene enrichment analysis

In gene-to-gene enrichment analysis, genes replace the concepts used in gene set enrichment testing, and concept membership replaces genes. The analysis provides a statistical measure of the closeness of any two genes by annotations, and can also be used simply to query all concepts in which any specific gene is a member.

About data sources

ConceptGen is built on a repository of conceptual data drawn from diverse areas, including:

Functional annotations

- **Gene Ontology (GO) Biological Process**
  GO Molecular Function
  GO Cellular Component
  (http://www.geneontology.org/)
- **Protein Domains (Pfam)**
  (http://pfam.sanger.ac.uk/)

- **Kyoto Encyclopedia of Genes and Genomes (KEGG) Pathways** (http://www.genome.jp/kegg/pathway.html)
- **Protein ANalysis THrough Evolutionary Relationships (Panther) Pathways** (http://www.pantherdb.org/pathway/)
- **Biocarta Pathways** (http://www.biocarta.com/Default.aspx)

Literature derived

- **Medical Subject Headings (MeSH)** (http://www.ncbi.nlm.nih.gov/mesh and http://gene2mesh.ncibi.org)
- **Online Mendelian Inheritance in Man (OMIM)** (http://www.ncbi.nlm.nih.gov/omim/)

Targets

- **Drug Bank** target sets (http://www.drugbank.ca/)
- Transcription factor binding targets
- **microRNA** predicted targets (http://www.ebi.ac.uk/enright-srv/microcosm/htdocs/targets/)

Experimental

- **Gene Expression Omnibus (GEO)** datasets (http://www.ncbi.nlm.nih.gov/geo/)

Interactions

- **MiMI Protein-interactions** (http://mimi.ncibi.org/MimiWeb/main-page.jsp)

Other

- Metabolites
- Cytoband (chromosomal locations)

Workflow overview

The basic steps in the workflow include:

1. Enter data. You can upload your own gene list or use a predefined concept. For gene-to-gene enrichment analysis, you specify a single gene.

2. Refine the concepts or genes you want to work with.

   For gene set enrichment testing:

   - Filter the list of enriched concepts.
   - Select the enriched concepts to include.
   - Compare your gene list to enriched concepts.

   For gene-to-gene enrichment analysis:

   - Filter the list of genes.
   - Select the genes to include.
   - Compare an enriched gene with your selected gene.

3. Visually explore the relationships among your data.

   For gene set enrichment testing:

   - Create a network graph.
   - Create a heatmap.

   For gene-to-gene enrichment analysis:

   - Create a network graph.

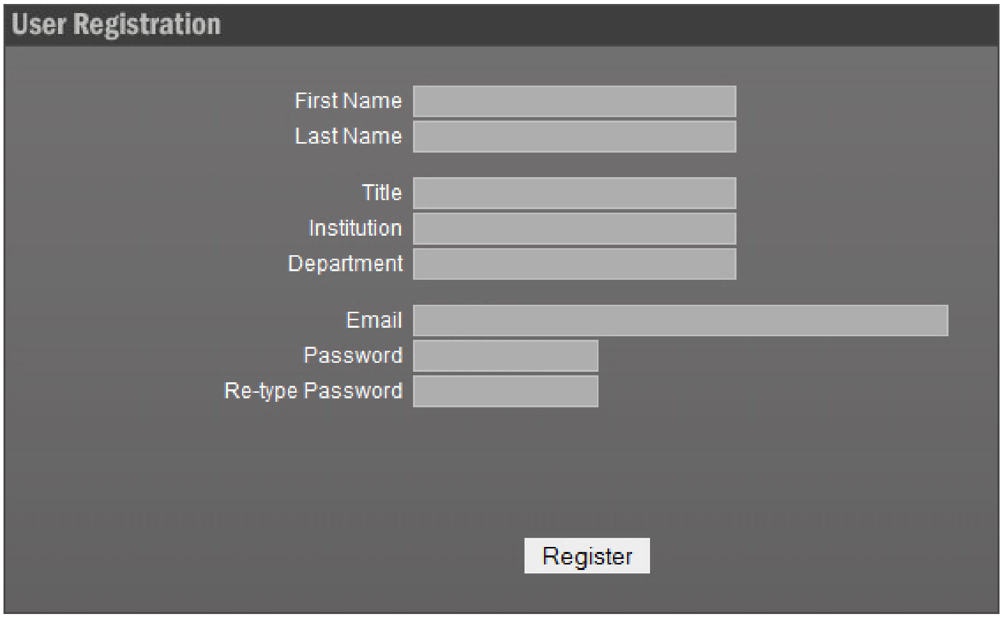
ACCESSING CONCEPTGEN

You can access and use ConceptGen without creating a user account, but to upload and save private concepts (gene lists), you must create a free account.

Registering for a ConceptGen account

1. Go to the ConceptGen website at http://conceptgen.ncibi.org.

2. Click **Register** in the upper-right corner.

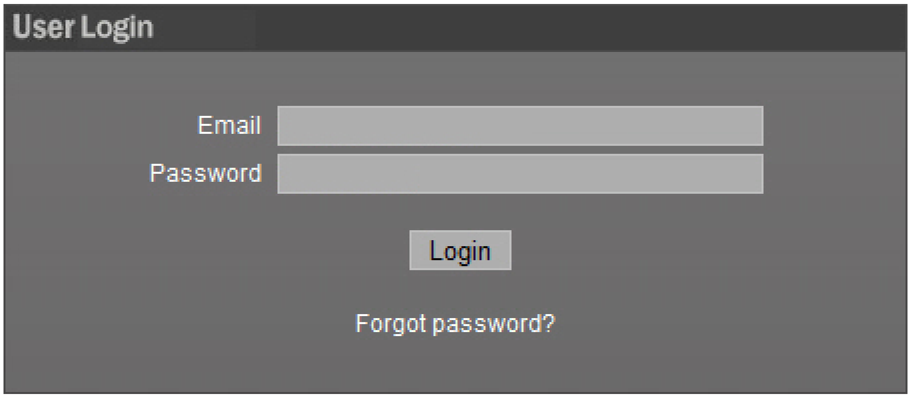


3. Enter your account information. All fields are required.
4. Click the **Register** button.

Logging in to ConceptGen

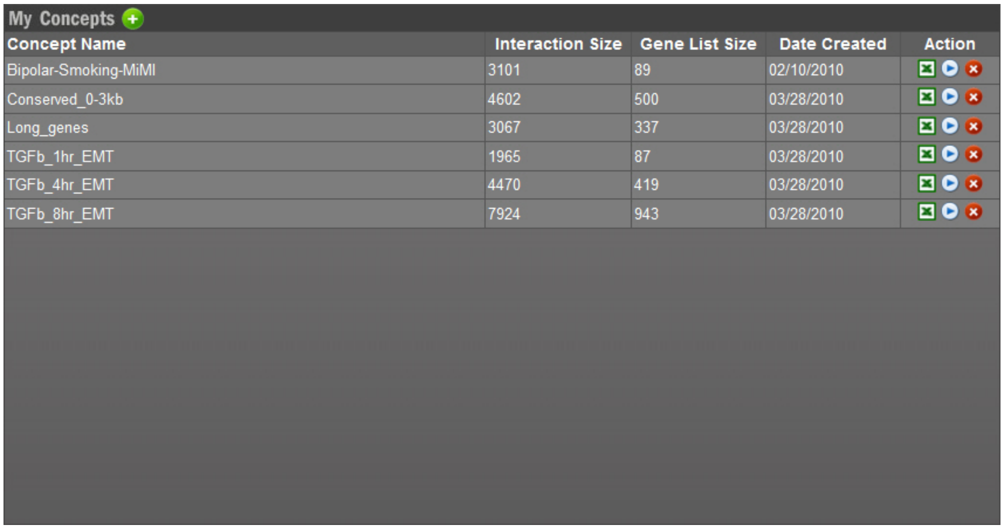
To log in to ConceptGen:

1. Go to the ConceptGen website at http://conceptgen.ncibi.org.
2. Click **Login** in the upper-right corner.



3. Enter the email address and password you used when you registered for your ConceptGen account.
4. Click the **Login** button.

If you have already uploaded private concepts, they are listed in **My Concepts**:



My Concepts

Concept Name	Interaction Size	Gene List Size	Date Created	Action
Bipolar-Smoking-MiMI	3101	89	02/10/2010	☒ ▶ ✖
Conserved_0-3kb	4602	500	03/28/2010	☒ ▶ ✖
Long_genes	3067	337	03/28/2010	☒ ▶ ✖
TGFb_1hr_EMT	1965	87	03/28/2010	☒ ▶ ✖
TGFb_4hr_EMT	4470	419	03/28/2010	☒ ▶ ✖
TGFb_8hr_EMT	7924	943	03/28/2010	☒ ▶ ✖

Accessing ConceptGen without logging in

To access ConceptGen without logging in or creating an account:

1. Go to the ConceptGen website at http://conceptgen.ncibi.org.
2. Begin using ConceptGen.

You can use all of ConceptGen's features, but you cannot upload or work with your own gene lists.

ENTERING A GENE LIST FOR GENE SET ENRICHMENT TESTING

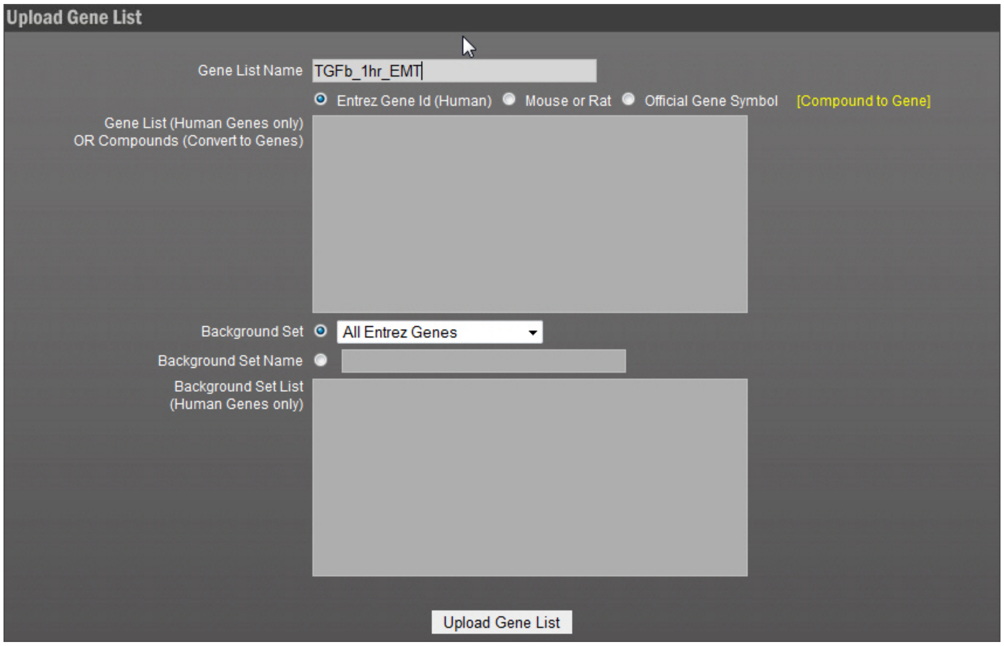
Use gene set enrichment testing to find pre-defined concepts (gene sets) that are significantly enriched with the genes in your set.

1. If you have a ConceptGen account, log in.

   If you have not already done so, create a free ConceptGen account.

2. When **My Concepts** appears, click the **Upload new gene list** icon.

3. In the **Upload Gene List** dialog, enter a name for your gene list.



Gene List Name: TGFb_1hr_EMT

● Entrez Gene Id (Human)

Background Set: ● All Entrez Genes

4. Choose one of the following methods to specify the gene list.

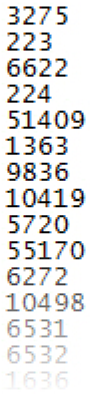
Option 1: Enter a list of Entrez human gene IDs or symbols

Use to upload a list of human gene symbols or IDs.

1. In the **Upload Gene List** dialog, select the method you will use to identify human genes by clicking **Entrez Gene Id (Human)** or **Official Gene Symbol**.
2. In the **Gene List (Human Genes only)** box, type in the list of symbols or IDs, or copy and paste them from a text or spreadsheet file. The symbols or IDs must appear one per line.

Examples:

Entrez gene IDs (text)



```
3275
223
6622
224
51409
1363
9836
10419
5720
55170
6272
10498
6531
6532
1636
```

Official gene symbols (spreadsheet)

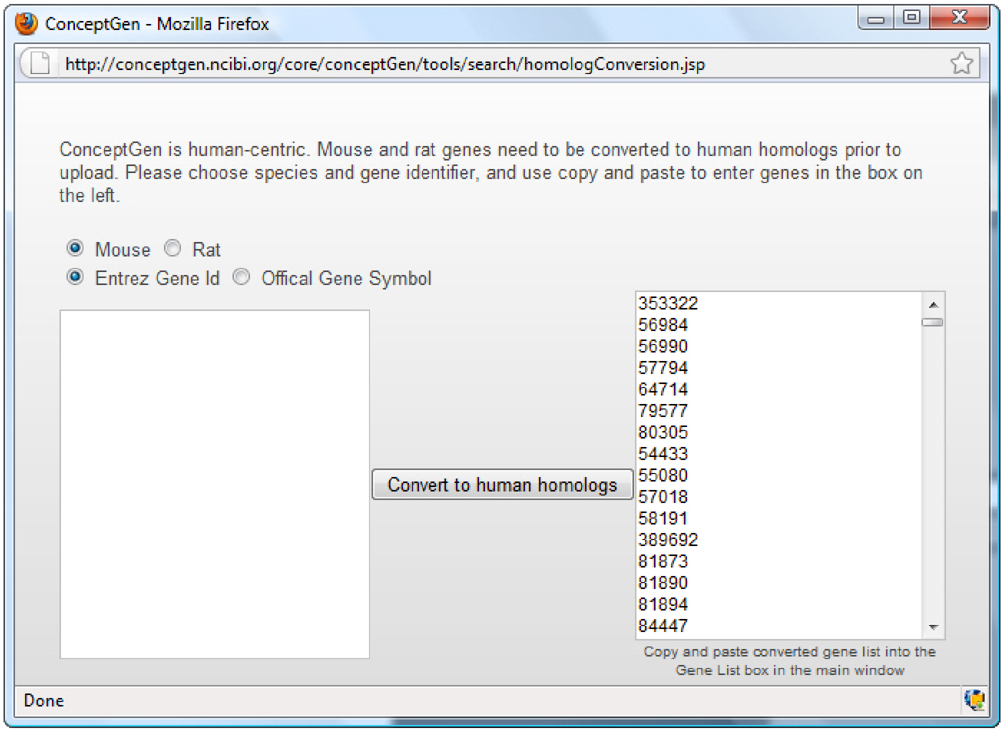
	A
1	INDOL1
2	TYR
3	PRMT3
4	GNB2L1
5	INDO
6	TAF1
7	ESR1
8	COMT
9	AHCY
10	AOC3
11	PRMT7
12	XRN2
13	BCL6
14	DBH
15	PRMT8

Option 2: Enter a list of mouse or rat gene IDs or symbols

Use to upload a list of mouse or rat gene IDs or symbols, which will be converted to human homologs for use in ConceptGen.

1. In the **Upload Gene List** dialog, select **Mouse or Rat**.
2. In the conversion dialog, select the species, **Mouse** or **Rat**.
3. Select the method you will use to identify genes by clicking **Entrez Gene Id** or **Official Gene Symbol**.
4. In the box on the left, type in the list of mouse or rat gene symbols or IDs, or copy and paste them from a text or spreadsheet file. The symbols or IDs must appear one per line. Values of “NA” will be ignored.

5. Click the **Convert to human homologs** button. The mouse or rat genes on the left are converted to human homologs on the right:



ConceptGen is human-centric. Mouse and rat genes need to be converted to human homologs prior to upload. Please choose species and gene identifier, and use copy and paste to enter genes in the box on the left.

● Mouse ○ Rat
● Entrez Gene Id ○ Offical Gene Symbol

353322
56984
56990
57794
64714
79577
80305
54433
55080
57018
58191
389692
81873
81890
81894
84447

Copy and paste converted gene list into the Gene List box in the main window

6. From the box on the right, copy the list of human gene IDs or symbols to the clipboard.
7. Close the conversion dialog window.
8. In the **Gene List (Human Genes only)** box, paste the list of converted gene IDs.

Option 3: Enter a list of compounds

Use to create a list of genes from a list of associated compounds.

1. Click the **[Compound to Gene]** link.
2. Under **Look up compound name**, type a compound name. As you type, matching compound names are displayed in a dropdown list, from which you can select the correct compound.
3. After you select a compound from the list, click the **Add compound to list below** icon ⊕ to add it to the list.
4. When you are done entering compounds, click the **Find Genes** button.
5. Copy the resulting gene IDs to the clipboard.

6. Close the compound lookup dialog window.
7. In the **Gene List (Human Genes only**) box, paste the gene IDs.

Specifying a background set of genes

After entering your list of genes, choose one of the following methods to specify the background set of genes. The background set of genes is the set of possible genes against which your list of genes will be compared.

Option 1: Select a predefined background set

1. Select **Background Set**.
2. Select one of the following predefined background sets, depending on the species whose genes are included in your gene list:
   - **All Entrez Genes**. The predefined background set for human genes.
   - **All Entrez Genes – Mouse**. The predefined background set for mouse genes converted to human homologs.
   - **All Entrez Genes - Rat**. The predefined background set for rat genes converted to human homologs.

Option 2: Upload a custom background set (human genes only)

If you're uploading a microarray dataset, or other dataset for which the complete human gene list was not assessed or measured, then upload a custom background set.

1. Select **Background Set Name**.
2. Provide a name for your background set.
3. For **Background Set List**, copy and paste the list of human genes from a text or spreadsheet file.

Uploading the gene list

1. After specifying the gene list and the background set, click the **Upload Gene List** button.
2. If ConceptGen reports any genes that were not matched, you can:
   - Click **<< Go Back** to return to the **Upload Gene List** dialog and edit your entries.
   - Click **Continue to Upload >>** to continue the upload with the matched genes only.

3. After the **My Concepts** dialog reappears, you can click the uploaded concept’s name in the **Concept Name** column to open the data in ConceptGen’s Concept Explorer.

For more information, see “Using the Concept Explorer for Gene Set Enrichment Testing.”

SEARCHING AND BROWSING PREDEFINED CONCEPTS

You can search and browse predefined concepts for gene set enrichment testing rather than upload your own concepts. You do not need to register or log in to search and browse.

Searching for predefined concepts

When you search for predefined concepts, you enter search text that you want to match against the names of predefined concepts. For example, using the search text “cyto,” you can find the following predefined concepts:

- actin cytoskeleton
- Astrocytoma
- Cycling of Ran in nucleocytoplasmic transport
- Cytochromes b5
- positive regulation of endocytosis

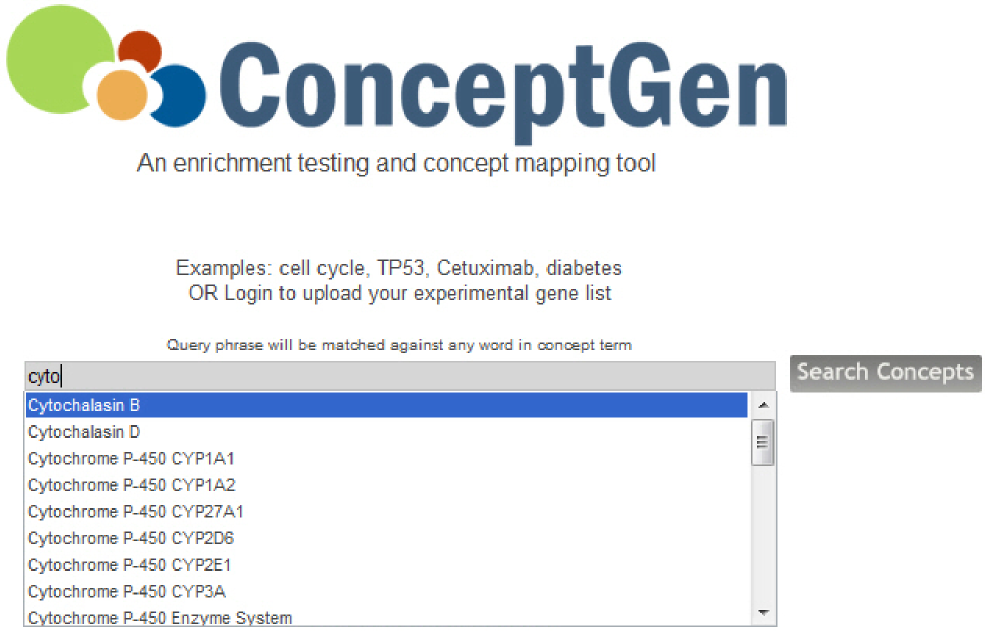
To search for predefined concepts:

1. Go to the ConceptGen home page at http://conceptgen.ncibi.org.

   If you are logged in, you can return to the home page from the **My Concepts** page by clicking the ConceptGen logo in the upper-left corner of the page.

2. In the search box on the ConceptGen home page, enter the search text.

   As you type, a list of concept names that match the beginning of your text appears below the search box. If the concept name you want appears in the list, you can click it to select it.



ConceptGen

An enrichment testing and concept mapping tool

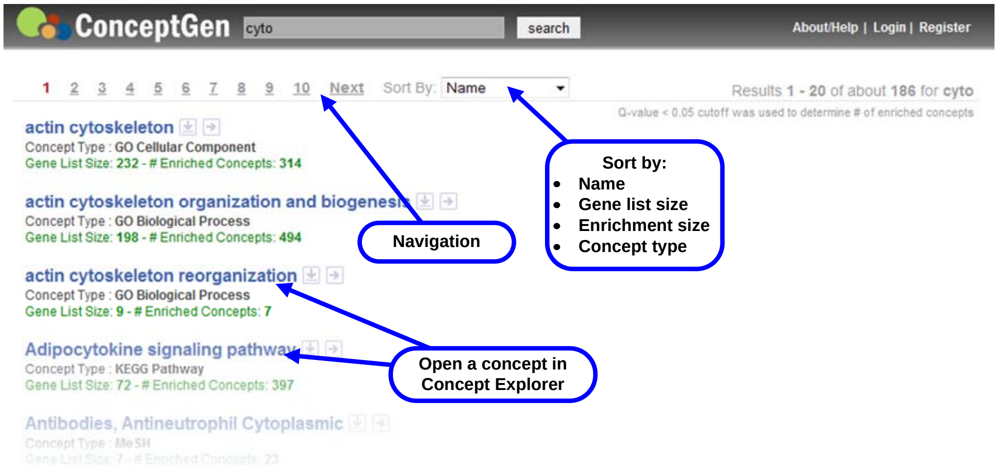
Examples: cell cycle, TP53, Cetuximab, diabetes
OR Login to upload your experimental gene list

Query phrase will be matched against any word in concept term

cyto

Cytochalasin B
Cytochalasin D
Cytochrome P-450 CYP1A1
Cytochrome P-450 CYP1A2
Cytochrome P-450 CYP27A1
Cytochrome P-450 CYP2D6
Cytochrome P-450 CYP2E1
Cytochrome P-450 CYP3A
Cytochrome P-450 Enzyme System

3. Click the **Search Concepts** button. A list of matching concepts appears on the search results page. (If you selected a concept from the drop-down list, only that concept appears.)



Results 1 - 20 of about 186 for cyto

Q-value < 0.05 cutoff was used to determine # of enriched concepts

actin cytoskeleton
Concept Type : GO Cellular Component
Gene List Size: 232 - # Enriched Concepts: 314

actin cytoskeleton organization and biogenesis
Concept Type : GO Biological Process
Gene List Size: 198 - # Enriched Concepts: 494

actin cytoskeleton reorganization
Concept Type : GO Biological Process
Gene List Size: 9 - # Enriched Concepts: 7

Adipocytokine signaling pathway
Concept Type : KEGG Pathway
Gene List Size: 72 - # Enriched Concepts: 397

Antibodies, Antineutrophil Cytoplasmic
Concept Type : MeSH
Gene List Size: 7 - # Enriched Concepts: 23

Navigation

Sort by:
- Name
- Gene list size
- Enrichment size
- Concept type

Open a concept in Concept Explorer

4. Find the concept you want among the search results. You can:
   - Navigate using the page number and **Next** links above the list.
   - Sort the concept names by:

     Name. Concept name (the default).

     Gene list size. The number of genes in the predefined concept.

     Enrichment size. The number of other concepts with a significant number of overlapping genes.

     Concept type. The basis for the concept, such as **GO Biological Process** or **MeSH**.
5. Click the concept name link to open the concept data in ConceptGen's Concept Explorer.

For more information, see "Using the Concept Explorer for Gene Set Enrichment Testing."

Browsing for predefined concepts

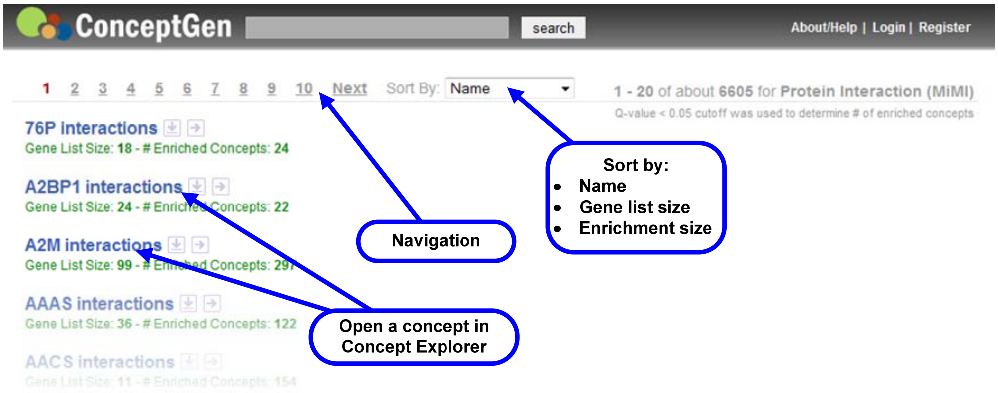
1. Go to the ConceptGen home page at http://conceptgen.ncibi.org.

   If you are logged in, you can return to the home page from the **My Concepts** page by clicking the **ConceptGen** logo in the upper-left corner of the page.
2. Click **Click here to browse all concepts**. The **Browse** dialog appears.

Browse

Concept Type	Category	Concept Size
Gene Expression	Experimental	603
Biocarta Pathway	Functional Annotations	245
GO Biological Process	Functional Annotations	2477
GO Cellular Component	Functional Annotations	446
GO Molecular Function	Functional Annotations	1075
KEGG Pathway	Functional Annotations	195
Panther Pathway	Functional Annotations	86
pFAM	Functional Annotations	770
Protein Interaction (MiMI)	Interactions	6823
MeSH	Literature derived	5214
OMIM	Literature derived	52
Cytoband	Other	1178
Metabolite	Other	960
Drug Bank	Targets	256
TransFac	Targets	119
miRBase	Targets	587

3. In the **Concept Type** column, click the name of a concept type. (The number in the **Concept Size** column is the number of predefined concepts of that type.)



1 - 20 of about 6605 for Protein Interaction (MiMI)
Q-value < 0.05 cutoff was used to determine # of enriched concepts

76P interactions
Gene List Size: 18 - # Enriched Concepts: 24

A2BP1 interactions
Gene List Size: 24 - # Enriched Concepts: 22

A2M interactions
Gene List Size: 99 - # Enriched Concepts: 297

AAAS interactions
Gene List Size: 36 - # Enriched Concepts: 122

AACS interactions
Gene List Size: 11 - # Enriched Concepts: 154

Navigation

Sort by:
- Name
- Gene list size
- Enrichment size

Open a concept in Concept Explorer

4. Find the concept you want among the search results. You can:

   - Navigate using the page number and **Next** links above the list.
   - Sort the concept names by:

     Name. Concept name (the default).

     Gene list size. The number of genes in the predefined concept.

     Enrichment size. The number of other concepts with a significant number of overlapping genes.

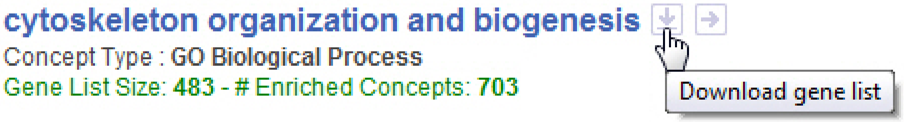
5. Click the concept name link to open the concept data in ConceptGen's Concept Explorer.

For more information, see "Using the Concept Explorer for Gene Set Enrichment Testing."

Downloading the gene list of a predefined concept

To download the list of genes in a predefined concept:

1. On a search results page, click the **Download gene list** icon to the right of the concept name.


cytoskeleton organization and biogenesis
Concept Type : GO Biological Process
Gene List Size: 483 - # Enriched Concepts: 703

2. In the dialog box, select **Save File** to download the file.
3. Click **OK**.

4. Navigate to a location for the file, and optionally rename the file.
5. Click **Save**.

The gene list file is saved with an **.xls** file extension.

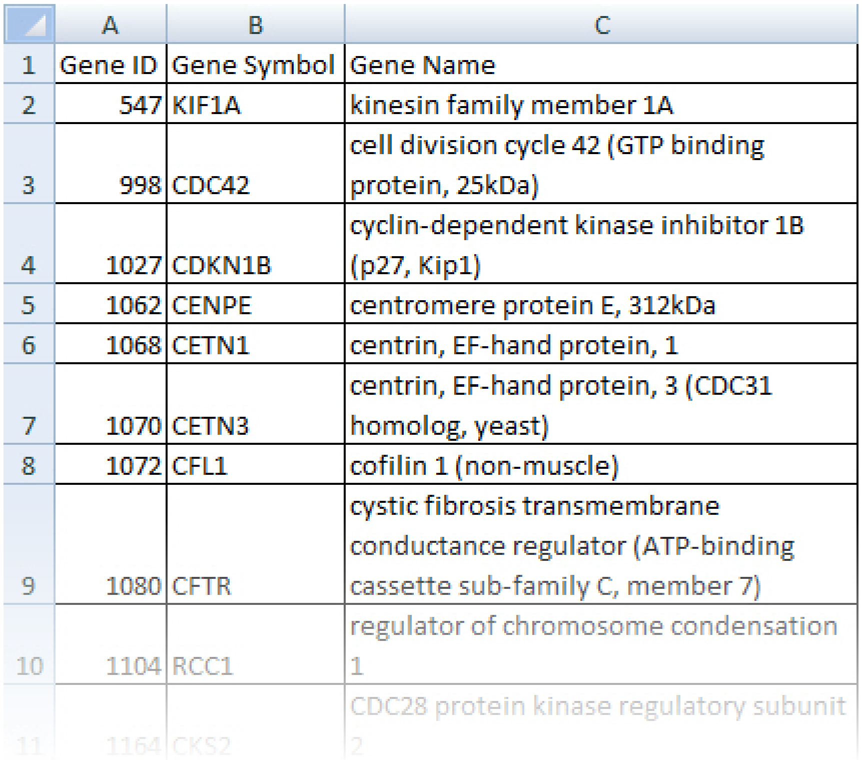
Opening a saved gene list file

You can open a downloaded gene list file for a predefined concept in Microsoft® Excel.

1. Open the file in Excel.

   You may get a message that the file is in a different format than specified by the file extension (the file contains HTML although the file extension indicates it is an Excel 97-2003 worksheet file with an **.xls** extension).

2. Click **Yes** to open the file:



	A	B	C
1	Gene ID	Gene Symbol	Gene Name
2	547	KIF1A	kinesin family member 1A
3	998	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)
4	1027	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)
5	1062	CENPE	centromere protein E, 312kDa
6	1068	CETN1	centrin, EF-hand protein, 1
7	1070	CETN3	centrin, EF-hand protein, 3 (CDC31 homolog, yeast)
8	1072	CFL1	cofilin 1 (non-muscle)
9	1080	CFTR	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)
10	1104	RCC1	regulator of chromosome condensation 1
11	1164	CKS2	CDC28 protein kinase regulatory subunit 2

Note: If you want to save the file as a true Excel worksheet file, select **File → Save As...**, select the **Excel 97-2003 Workbook (*.xls)** option from the **Save as type** dropdown, and click **Save**.

Viewing source information for a predefined concept

To view source information describing the composition of a predefined concept:

- On a search results page, click the **Source Link** icon to the right of the concept name.

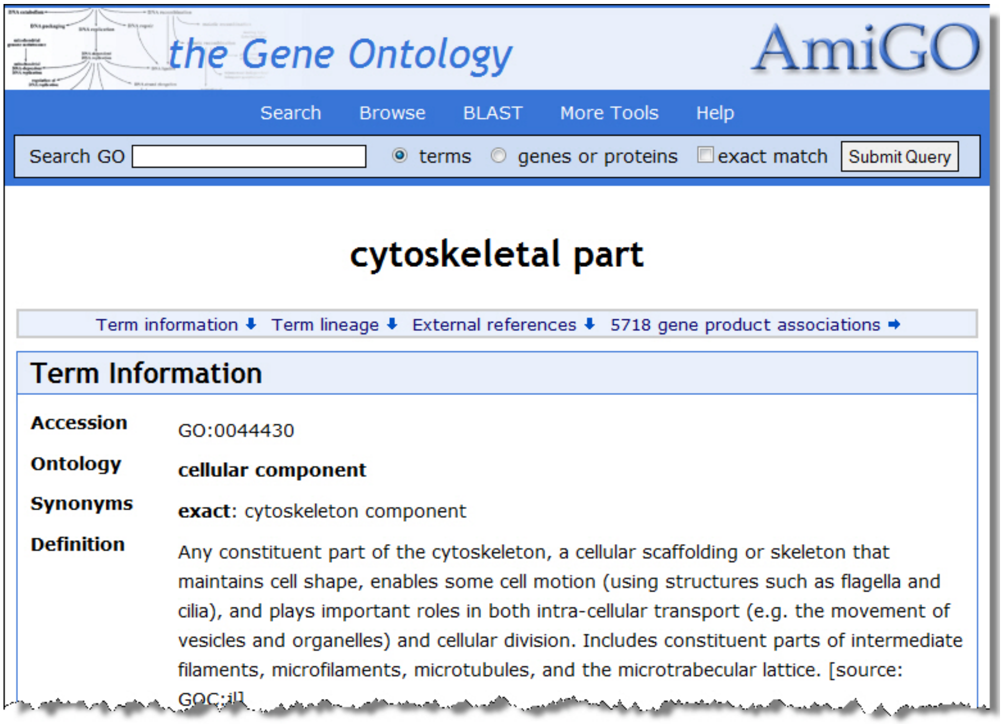
Source information appears in a new browser tab or window. The link destination depends on the source of the concept data, indicated by **Concept Type** on the search results page.

Example 1:

microtubule cytoskeleton

Concept Type : GO Cellular Component

Gene List Size: 381 - # Enriched Concepts



cytoskeletal part

Term Information

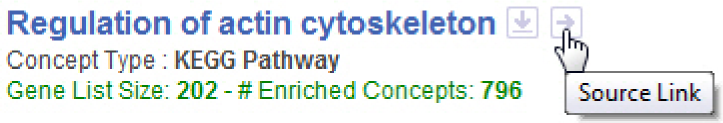
Accession GO:0044430

Ontology **cellular component**

Synonyms **exact**: cytoskeleton component

Definition Any constituent part of the cytoskeleton, a cellular scaffolding or skeleton that maintains cell shape, enables some cell motion (using structures such as flagella and cilia), and plays important roles in both intra-cellular transport (e.g. the movement of vesicles and organelles) and cellular division. Includes constituent parts of intermediate filaments, microfilaments, microtubules, and the microtrabecular lattice. [source: GOC:jl]

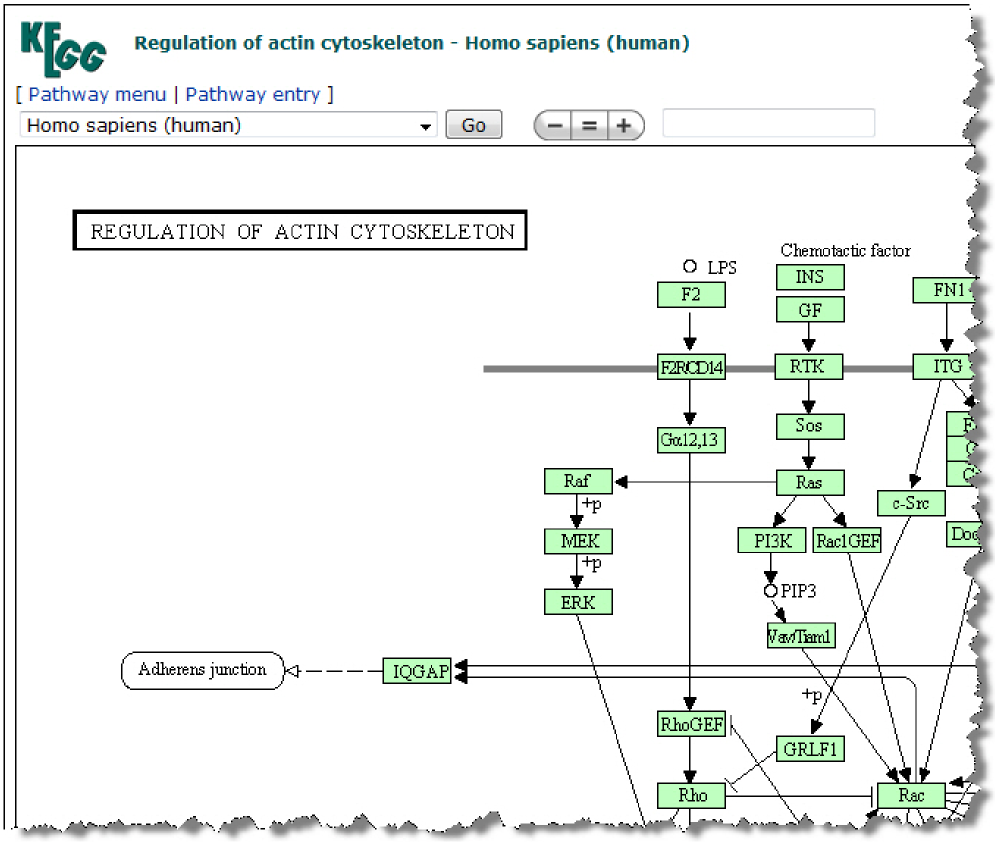
Example 2:



Regulation of actin cytoskeleton

Concept Type : **KEGG Pathway**

Gene List Size: **202** - # Enriched Concepts: **796**



Regulation of actin cytoskeleton - Homo sapiens (human)

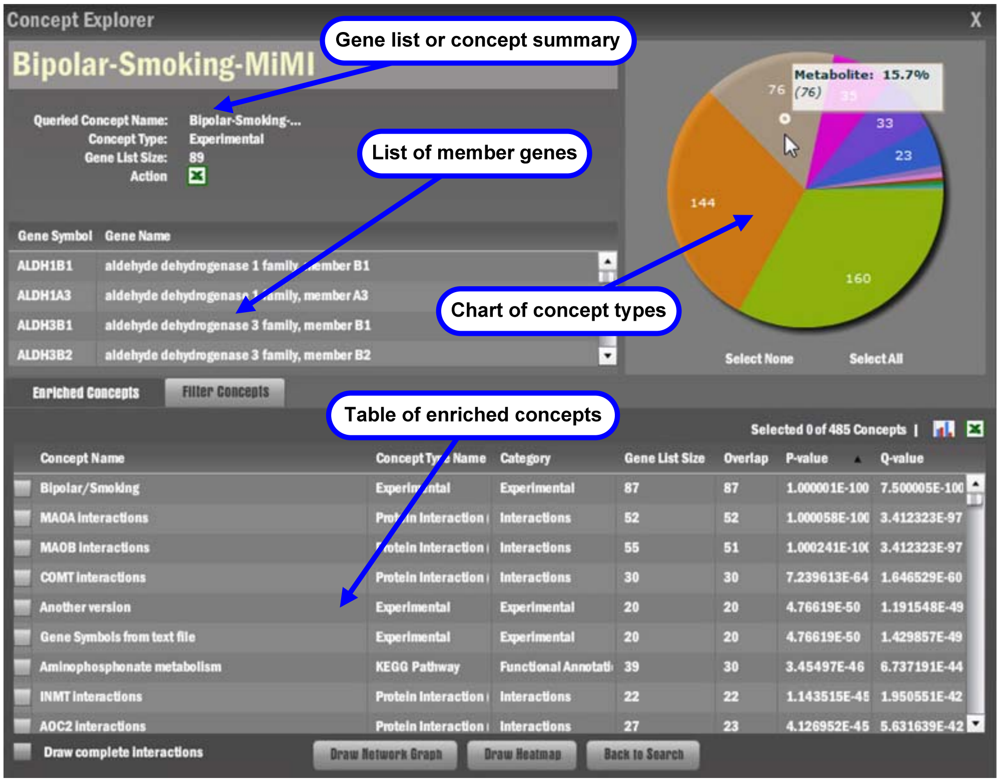
USING THE CONCEPT EXPLORER FOR GENE SET ENRICHMENT TESTING

Overview of the Concept Explorer

Whether you upload your own concept or select a predefined concept, you can explore concept relationships in the Concept Explorer.

This section describes the Concept Explorer for gene set enrichment testing. The Concept Explorer differs if you select a gene for gene-to-gene enrichment analysis. See "Using the Concept Explorer for Gene-to-Gene Enrichment Analysis."

The Concept Explorer includes the following major sections:



Bipolar-Smoking-MiMI

Queried Concept Name: Bipolar-Smoking-...
Concept Type: Experimental
Gene List Size: 89
Action ☒

Gene Symbol	Gene Name
ALDH1B1	aldehyde dehydrogenase 1 family, member B1
ALDH1A3	aldehyde dehydrogenase 1 family, member A3
ALDH3B1	aldehyde dehydrogenase 3 family, member B1
ALDH3B2	aldehyde dehydrogenase 3 family, member B2

Selected 0 of 485 Concepts |

	Concept Name	Concept Type Name	Category	Gene List Size	Overlap	P-value ▲	Q-value
☐	Bipolar/Smoking	Experimental	Experimental	87	87	1.000001E-100	7.500005E-100
☐	MAOA interactions	Protein Interaction	Interactions	52	52	1.000058E-100	3.412323E-97
☐	MAOB interactions	Protein Interaction	Interactions	55	51	1.000241E-100	3.412323E-97
☐	COMT interactions	Protein Interaction	Interactions	30	30	7.239613E-64	1.646529E-60
☐	Another version	Experimental	Experimental	20	20	4.76619E-50	1.191548E-49
☐	Gene Symbols from text file	Experimental	Experimental	20	20	4.76619E-50	1.429857E-49
☐	Aminophosphonate metabolism	KEGG Pathway	Functional Annotati	39	30	3.45497E-46	6.737191E-44
☐	INMT interactions	Protein Interaction	Interactions	22	22	1.143515E-45	1.950551E-42
☐	AOC2 interactions	Protein Interaction	Interactions	27	23	4.126952E-45	5.631639E-42

☐ Draw complete interactions

- **Gene list information**. Information about your experimental gene list, or about the selected predefined concept, including the list of genes constituting the concept. You can:
  - Sort the gene list by clicking the **Gene Symbol** or **Gene Name** column heading; click a column heading a second time to sort in the reverse order.
  - Export the gene list by clicking the Excel icon ☒. The resulting file contains HTML. To save the file as a true Excel worksheet file, open it and save it as an **Excel 97-2003 Workbook (*.xls).**
  - Display the MiMI Gene Details page for a gene by double-clicking its row in the gene list.

- **Chart of concept types**. A pie or bar chart showing the proportionate number of concepts related to the gene list, classified by type. You can:
  - Switch to bar chart view by clicking the bar chart icon 📊, and back to pie chart view by clicking ◔.
  - Hover the mouse cursor over an individual pie slice or bar to view the concept type, the percentage of the total number of enriched concepts, and the number of enriched concepts.
  - Click one or more individual pie slices or bars to select the enriched concepts of those concept types.
- **Table of enriched concepts**. Details on overrepresented concepts for the gene list (concepts with a q-value < 0.05). You can:
  - Sort the list of concepts by clicking a column heading; click a column heading a second time to sort in the reverse order.
  - Export information about one or more selected concepts by clicking the Excel icon ☒ above the right end of the table. The resulting file contains HTML. To save the file as a true Excel worksheet file, open it and save it as an **Excel 97-2003 Workbook (*.xls).**

  The exported file has several columns, including the p-value and q-value test statistics and the gene IDs of the genes overlapping between the concept and the gene list.

Filtering the list of enriched concepts

To filter the table of enriched concepts:

1. Click the **Filter Concepts** tab.
2. Filter the concepts using one or both of the following methods:
   - In the list of concept types on the left, select the concept types you want to use; deselect those concept types you want to filter out.
   - Using the **P-Value** and **Q-Value** sliders on the right, adjust one or both values.

3. Click **Execute Filter**.

Queried Concept Name: Bipolar-Smoking-...
Concept Type: Experimental
Gene List Size: 89
Action

Gene Symbol	Gene Name
ALDH1B1	aldehyde dehydrogenase 1 family, member B1
ALDH1A3	aldehyde dehydrogenase 1 family, member A3
ALDH3B1	aldehyde dehydrogenase 3 family, member
ALDH3B2	aldehyde dehydrogenase 3 family, member B2

	Concept Type	Category	Size
☑	TransFac	Targets	1
☑	Panther Pathway	Functional Annotations	2
☑	pFAM	Functional Annotations	2
☑	Gene Expression	Experimental	2
☑	Drug Bank	Targets	3
☑	Experimental	Experimental	4
☑	GO Molecular Function	Functional Annotations	23
☑	GO Biological Process	Functional Annotations	33
☑	KEGG Pathway	Functional Annotations	35

Click Filter Concepts tab

Select/deselect concept types

Adjust values using sliders

Click Execute Filter

The pie or bar chart is redrawn to include only the selected concept types, and only concepts with p-values and q-values matching the filter criteria.

4. Click the **Enriched Concepts** tab to return to the table of enriched concepts.

   The table is updated to include only the selected concept types, and only concepts with the specified p-values and q-values.

Removing a filter

To remove a filter:

1. Click the **Filter Concepts** tab.
2. Click **Remove Filter**.

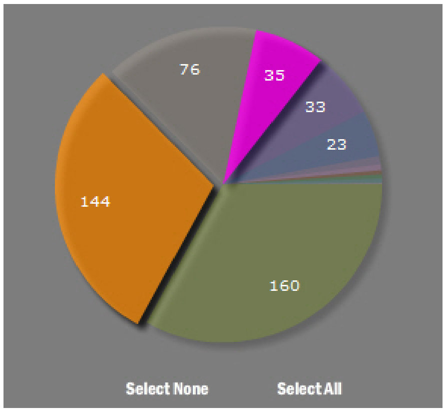
Selecting enriched concepts

You can select enriched concepts for other operations such as relation mapping by using the pie/bar chart or the table of enriched concepts.

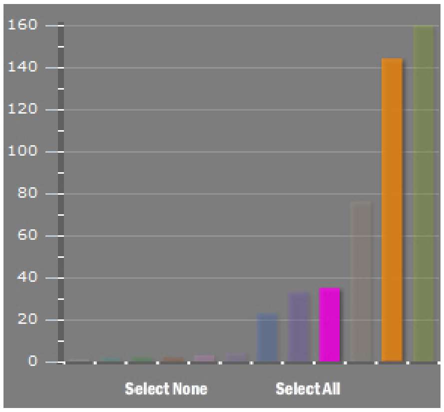
Selecting entire concept types

- To select or deselect all enriched concepts of a particular concept type, click the corresponding segment of the pie or bar chart. Selected segments are highlighted in the chart, and all concepts of the selected type(s) are selected in the table of enriched concepts.

Pie chart—two selected concept types



Bar chart—two selected concept types



- Use **Select All** to select all concept types, and **Select None** to return to the initial state of no concepts selected.

Selecting individual concepts

To select or deselect an individual concept of interest, click the checkbox column on the concept row in the table of enriched concepts.

Comparing an enriched concept with the queried concept

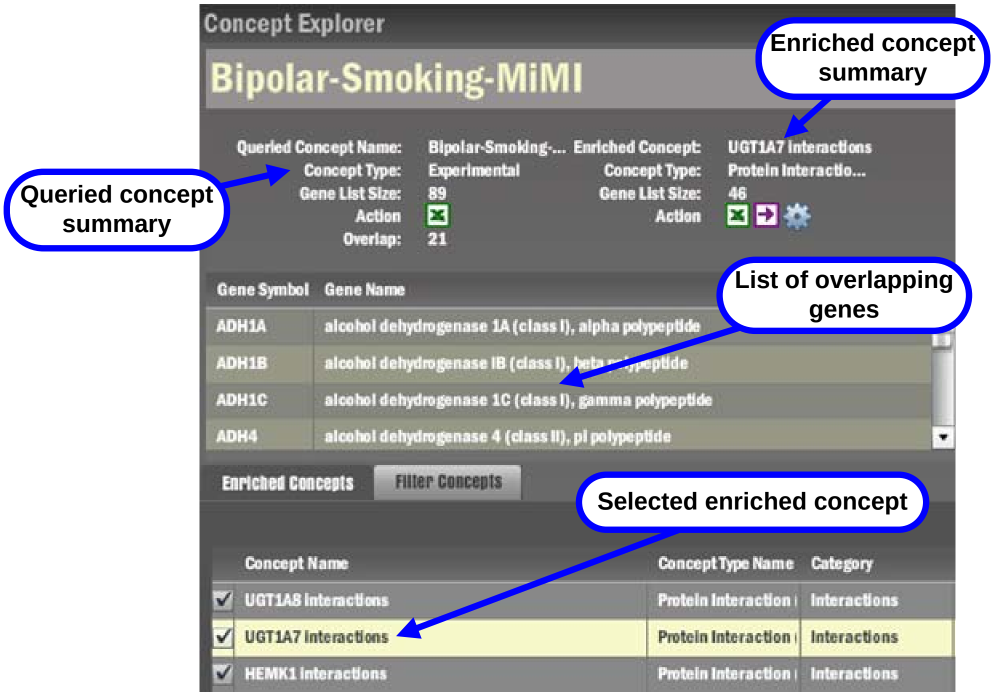
You can compare your gene list or queried predefined concept to one of the enriched concepts in the table.

Viewing summary information

Click the enriched concept's row in the table to highlight it.

Summary information for the enriched concept appears to the right of the summary information for the queried concept.

Overlap indicates the number of genes that appear in both gene sets. The gene list below the summary information is a list of the overlapping genes.



Concept Explorer

Bipolar-Smoking-MiMI

Queried Concept Name: Bipolar-Smoking-...
Concept Type: Experimental
Gene List Size: 89
Action
Overlap: 21

Enriched Concept: UGT1A7 interactions
Concept Type: Protein Interactio...
Gene List Size: 46
Action

Gene Symbol	Gene Name
ADH1A	alcohol dehydrogenase 1A (class I), alpha polypeptide
ADH1B	alcohol dehydrogenase IB (class I), beta polypeptide
ADH1C	alcohol dehydrogenase 1C (class I), gamma polypeptide
ADH4	alcohol dehydrogenase 4 (class II), pi polypeptide

Enriched Concepts | Filter Concepts

	Concept Name	Concept Type Name	Category
☑	UGT1A8 interactions	Protein Interaction	Interactions
☑	UGT1A7 interactions	Protein Interaction	Interactions
☑	HEMK1 interactions	Protein Interaction	Interactions

Enriched concept summary

Queried concept summary

List of overlapping genes

Selected enriched concept

Exporting the list of overlapping genes

Export gene ID, symbol, and name for the overlapping genes by clicking the Excel icon at the bottom of the enriched concept summary. The resulting file contains HTML. To save the file as a true Excel worksheet file, open it and save it as an **Excel 97-2003 Workbook (*.xls).**

Viewing source information

To view source information describing the composition of the enriched concept:

- Click the view source icon at the bottom of the enriched concept summary.

Source information appears in a new browser tab or window. The link destination depends on the source of the concept data. For example:

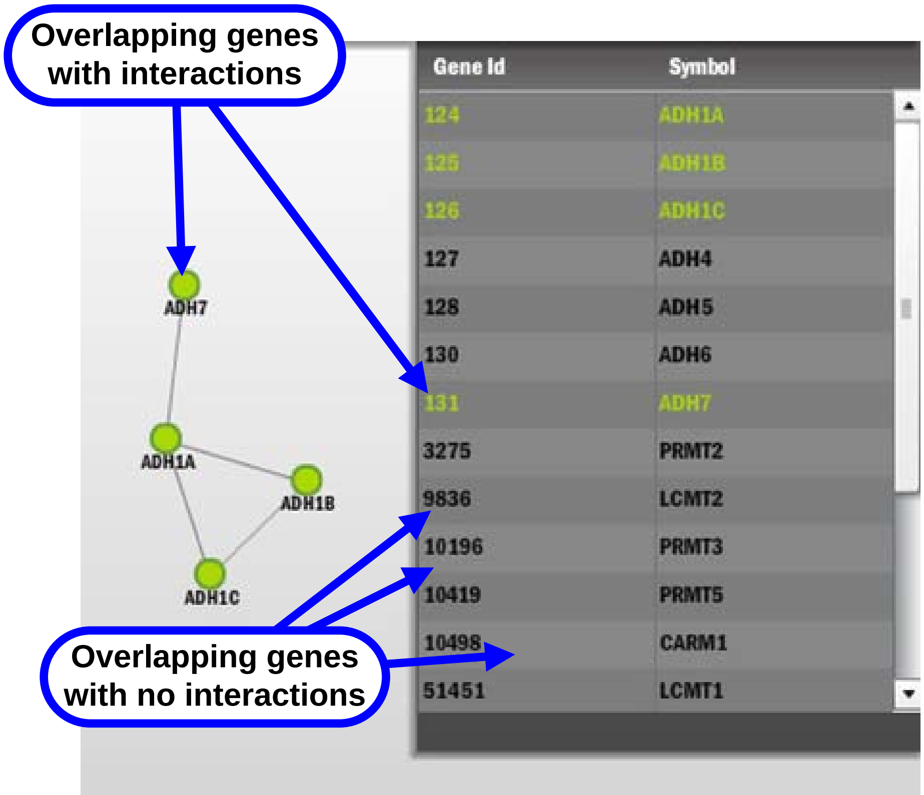
- For a **MeSH** concept type, the **Gene2MeSH** page appears.
- For a **KEGG Pathway** concept type, the **KEGG pathway diagram** appears.

Viewing interactions among overlapping genes in MiMI Netbrowser

To explore interactions among the genes that overlap between the queried and enriched concepts, click the gene list interactions icon at the bottom of the enriched concept summary.

To explore the network of overlapping genes, you can perform the following actions.

- To move the network or move to another area of a large network, click on any empty space within the network view and drag.
- To move a node, click and drag the node.
- To redraw the network, click the **Reset Graph** button.
- To view the complete list of overlapping genes, click **View Gene List** in the upper-right corner. Only genes with interactions appear in the network view, and these are highlighted in the gene list. Click **Close Gene List** to remove the list.

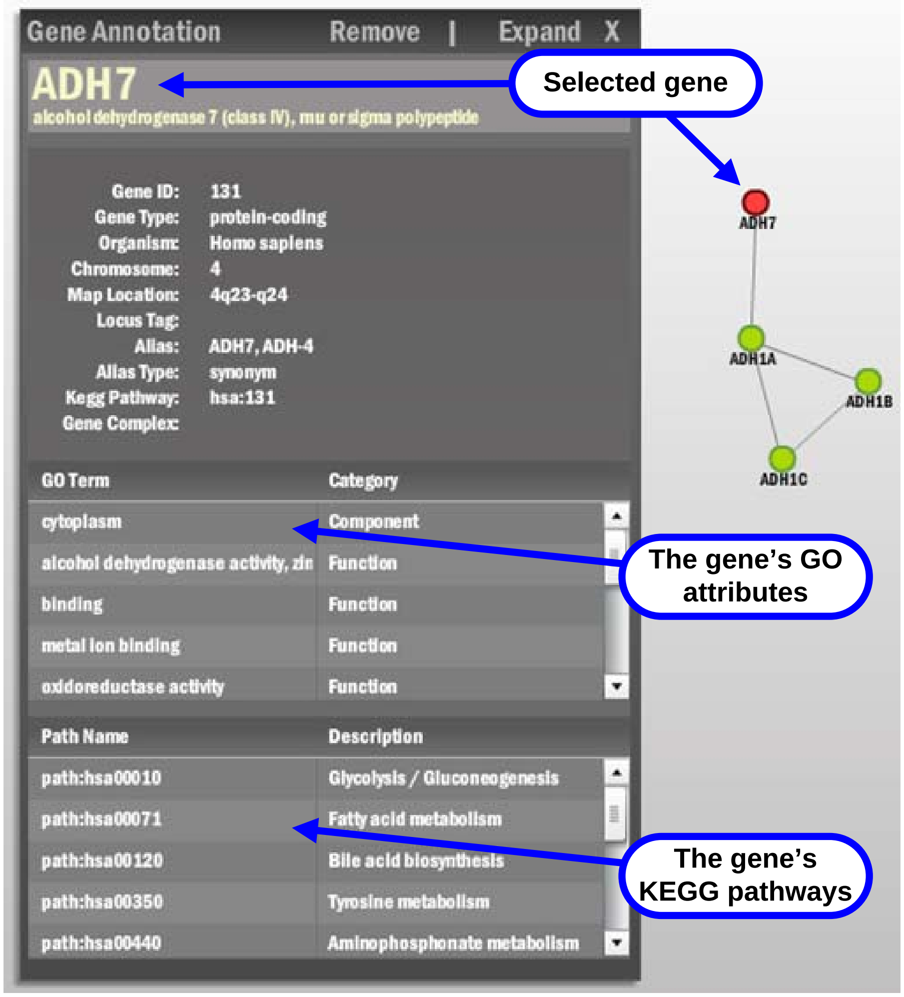


Overlapping genes with interactions

Overlapping genes with no interactions

Gene Id	Symbol
124	ADH1A
125	ADH1B
126	ADH1C
127	ADH4
128	ADH5
130	ADH6
131	ADH7
3275	PRMT2
9836	LCMT2
10196	PRMT3
10419	PRMT5
10498	CARM1
51451	LCMT1

- To view additional information about a gene appearing as a network node, double-click the node. The Gene Annotation window appears.



Selected gene

ADH7
alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide

Gene ID:	131
Gene Type:	protein-coding
Organism:	Homo sapiens
Chromosome:	4
Map Location:	4q23-q24
Locus Tag:	
Alias:	ADH7, ADH-4
Alias Type:	synonym
Kegg Pathway:	hsa:131
Gene Complex:	

GO Term	Category
cytoplasm	Component
alcohol dehydrogenase activity, zin	Function
binding	Function
metal ion binding	Function
oxidoreductase activity	Function

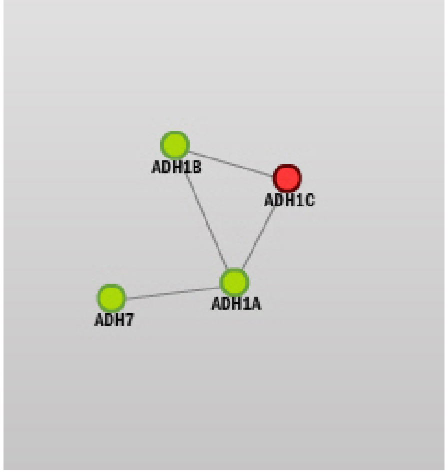
The gene's GO attributes

Path Name	Description
path:hsa00010	Glycolysis / Gluconeogenesis
path:hsa00071	Fatty acid metabolism
path:hsa00120	Bile acid biosynthesis
path:hsa00350	Tyrosine metabolism
path:hsa00440	Aminophosphonate metabolism

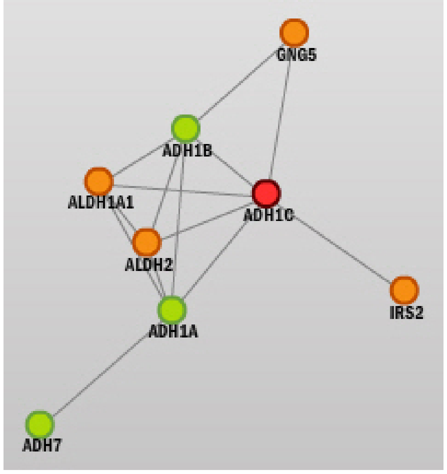
The gene's KEGG pathways

- To expand the network to additional genes interacting with any of the overlapping genes, click Expand in the Gene Annotation window. Any added gene nodes, and their entries in the gene list, appear in a different color. To collapse an expanded gene node, click Collapse in the Gene Annotation window.

Network before expansion



Network expanded and redrawn



- To remove one of the overlapping gene nodes from the network view, double-click the node and then click **Remove**.
- To export a set of gene nodes to SAGA (Substructure Index-based Approximate Graph Alignment) to compare and match them to a database of known biological pathways:
  - Click the **Select Nodes** button.
  - Select a series of multiple nodes to compare to known pathways by clicking each node.
  - Click the **Export to SAGA** button. The SAGA results appear in a new browser tab or window.
  - To end SAGA mode, click **Select Nodes** again.

CONCEPT RELATION MAPPING FOR GENE SET ENRICHMENT TESTING

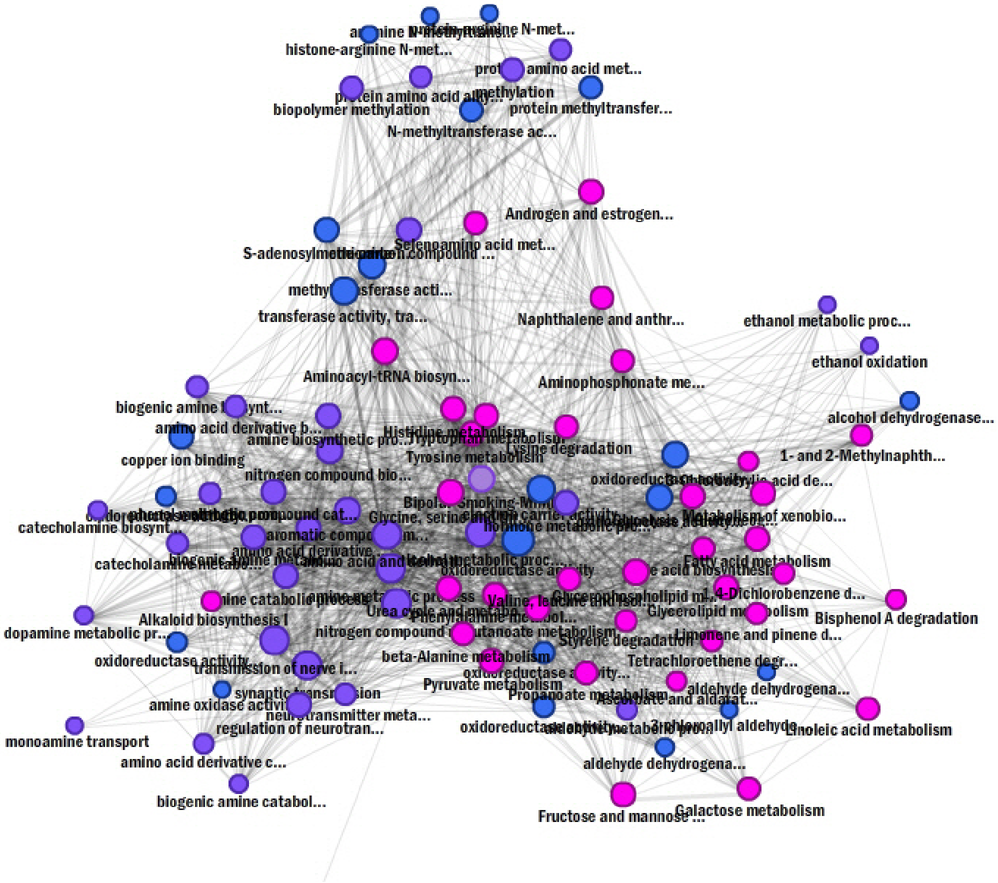
You can explore the interconnectivity of nodes that represent concepts by using relation mapping.

This section describes concept relation mapping for gene set enrichment testing. For mapping in gene-to-gene enrichment analysis, see “Relation Mapping for Gene-to-Gene Enrichment Analysis.”

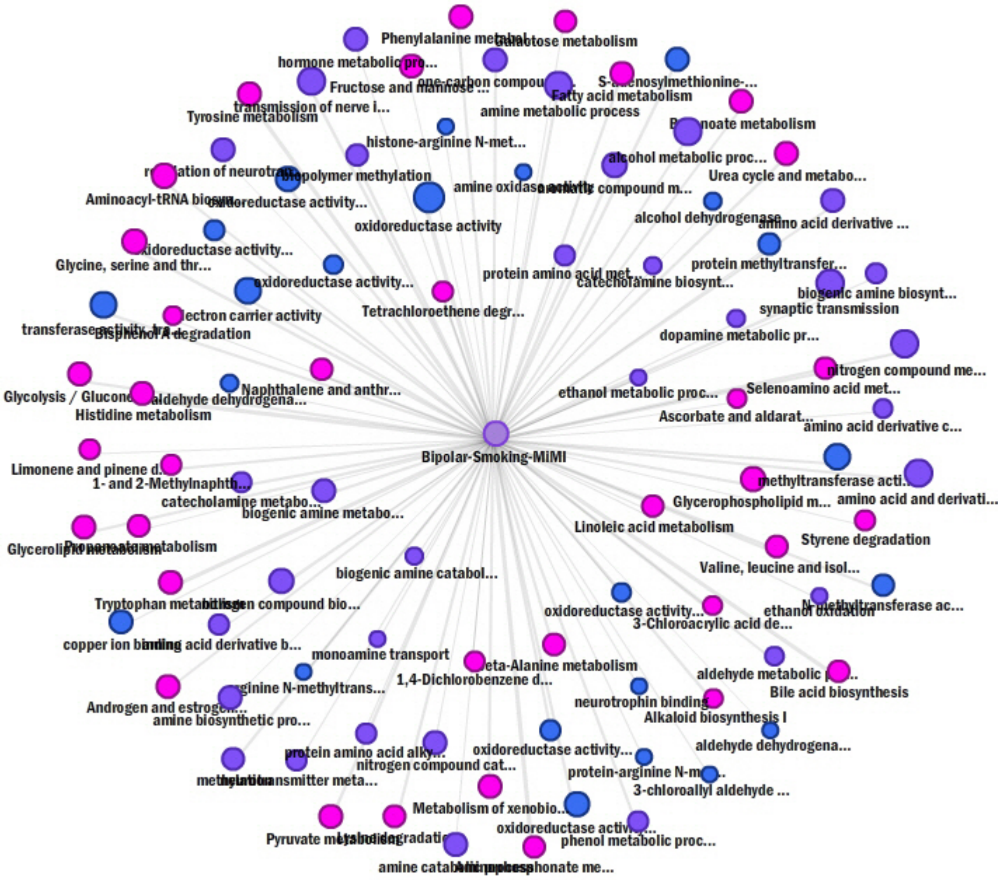
Creating a network graph

1. Select from 1 to 100 concepts.

2. Choose an option for which interactions to include:
   - Select **Draw complete interactions** to include links between *all* selected concepts. Example:

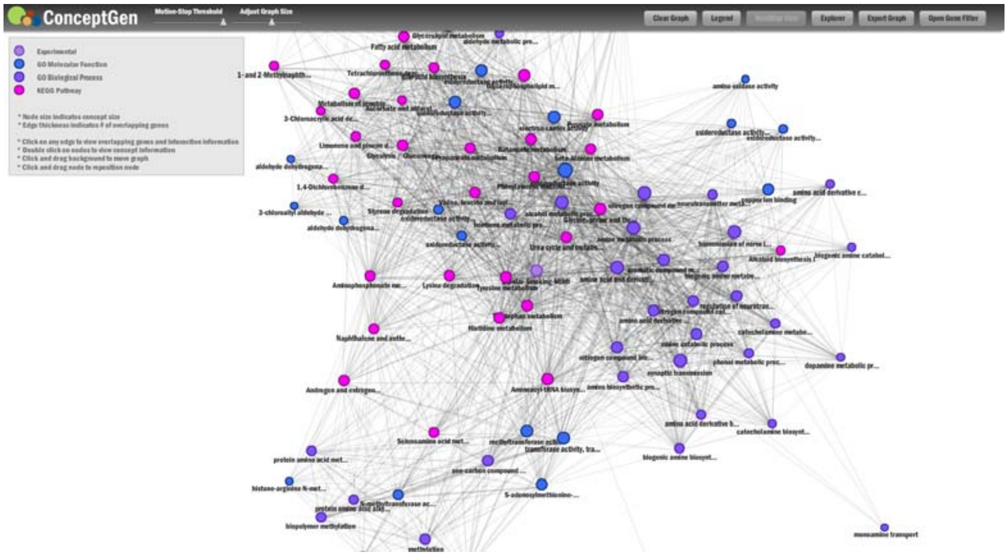


- Deselect **Draw complete interactions** to include only those links between the gene list and the enriched concepts selected. Example:



3. Click **Draw Network Graph**.

The ConceptGen network window appears, showing the specified network.



* Node size indicates concept size
* Edge thickness indicates # of overlapping genes

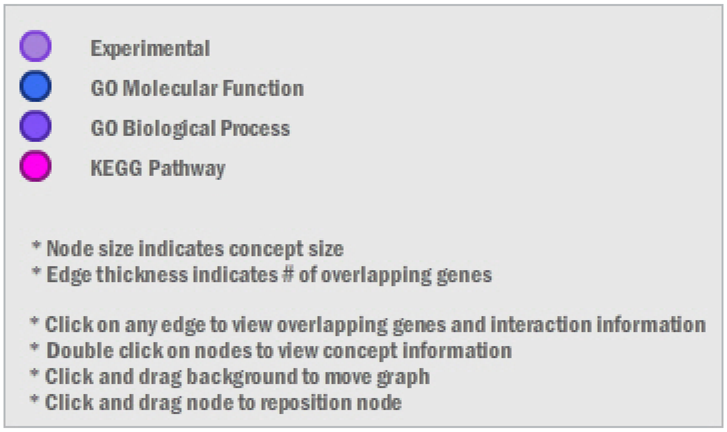
* Click on any edge to view overlapping genes and interaction information
* Double click on nodes to view concept information
* Click and drag background to move graph
* Click and drag node to reposition node

Working with the network graph

On the network graph page, you can:

Hide/show the legend

Use the legend to interpret visual styles used in the graph and to view reminders for common operations.



● Experimental
● GO Molecular Function
● GO Biological Process
● KEGG Pathway

* Node size indicates concept size
* Edge thickness indicates # of overlapping genes

* Click on any edge to view overlapping genes and interaction information
* Double click on nodes to view concept information
* Click and drag background to move graph
* Click and drag node to reposition node

- The concept type of a concept node is shown by the color indicated in the legend.
- The size of a concept node is based on the number of genes in the concept—the more genes, the larger the node.
- The thickness of an edge line between two concept nodes is based on the number of genes the concepts have in common—the more genes in common, the thicker the edge line.

To hide or show the legend, click the **Legend** button.

Adjust the graph size

To adjust the overall graph size, use the **Adjust Graph Size** slider in the top-left corner.

Move or pan the graph

To move the network or pan to another area of it, click on any empty space outside the bounds of the network and drag.

Move a node

To move a node, click and drag the node.

Save an image of the network graph

To save an image of the graph in an image file:

1. Click **Export Graph**.
2. Navigate to a location for the file, and optionally rename the file.
3. Click **Save**.

A screenshot of the network graph window is saved in **.png** format.

Add additional concepts

To add more concepts to the existing network graph:

1. Click the **Explorer** button to return to the Concept Explorer.
2. Select additional concepts.
3. Click **Draw Network Graph** again.

The newly added concepts are merged with the existing concepts in the network graph, and the graph is redrawn to reflect any additional interactions among them.

Create a new network graph

To abandon a graph and begin a new one:

1. Click **Clear Graph** to delete the existing network graph and return to the Concept Explorer with no concepts selected.
2. Select concepts for the new graph.
3. Click **Draw Network Graph** again.

A new network graph is drawn.

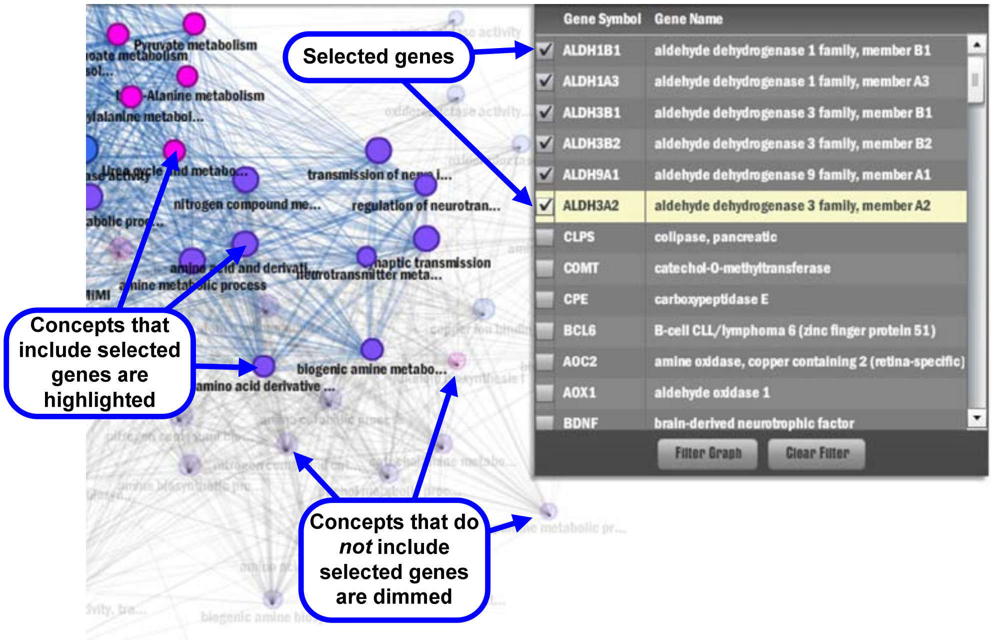
Filter concepts by gene

When you filter concepts by gene, you can highlight concepts associated with genes you select, while concepts not associated with those genes will be dimmed in the network graph. To filter concepts:

1. Click **Open Gene Filter** to display the gene filter window.
2. Select the gene(s) to include.

3. Click the **Filter Graph** button.

   The network graph is redrawn. Concept nodes and edges that are not associated with any of the genes you selected are dimmed in the network graph.



Selected genes

Concepts that include selected genes are highlighted

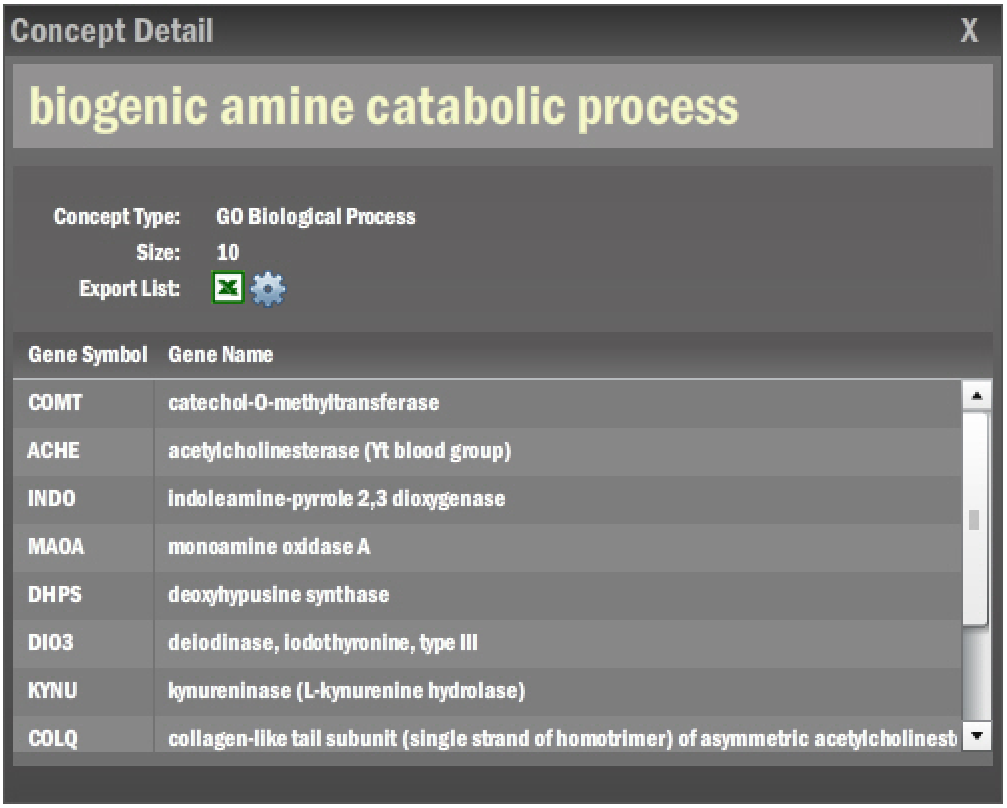
Concepts that do *not* include selected genes are dimmed

	Gene Symbol	Gene Name
☑	ALDH1B1	aldehyde dehydrogenase 1 family, member B1
☑	ALDH1A3	aldehyde dehydrogenase 1 family, member A3
☑	ALDH3B1	aldehyde dehydrogenase 3 family, member B1
☑	ALDH3B2	aldehyde dehydrogenase 3 family, member B2
☑	ALDH9A1	aldehyde dehydrogenase 9 family, member A1
☑	ALDH3A2	aldehyde dehydrogenase 3 family, member A2
☐	CLPS	colipase, pancreatic
☐	COMT	catechol-O-methyltransferase
☐	CPE	carboxypeptidase E
☐	BCL6	B-cell CLL/lymphoma 6 (zinc finger protein 51)
☐	AOC2	amine oxidase, copper containing 2 (retina-specific)
☐	AOX1	aldehyde oxidase 1
☐	BDNF	brain-derived neurotrophic factor

4. To clear the gene filter, click **Clear Filter**.

Display details for concepts (nodes)

- Double-click a concept node. The **Concept Detail** window appears with detailed information about the concept, including its list of genes.



biogenic amine catabolic process

Concept Type: GO Biological Process
Size: 10
Export List:

Gene Symbol	Gene Name
COMT	catechol-O-methyltransferase
ACHE	acetylcholinesterase (Yt blood group)
INDO	indoleamine-pyrrole 2,3 dioxygenase
MAOA	monoamine oxidase A
DHPS	deoxyhypusine synthase
DIO3	deiodinase, iodothyronine, type III
KYNU	kynureninase (L-kynurenine hydrolase)
COLQ	collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinest

You can:

- Sort the gene list by clicking the **Gene Symbol** or **Gene Name** column heading; click a column heading a second time to sort in the reverse order.
- Export the gene list by clicking the Excel icon. The resulting file contains HTML. To save the file as a true Excel worksheet file, open it and save it as an **Excel 97-2003 Workbook (*.xls).**
- Display the **MiMI Gene Details** page for a gene by double-clicking its row in the gene list.
- View a network of all gene interactions in MiMI Netbrowser by clicking the gene list interaction icon.

Display details for overlaps between concepts (edges)

- Single-click an edge between two concept nodes. The **Edge Detail** window appears with detailed information about the overlapping genes between the two concepts.

Concept Name: biogenic amine biosynthetic process
Concept Type: GO Biological Process
Size: 26

Concept Name: amino acid derivative biosynthetic process
Concept Type: GO Biological Process
Size: 30

Odds Ratio: 76407.5
P-Value: 1.618014E-71
Overlap: 26
Export List:

Gene Symbol	Gene Name
CHRNA7	cholinergic receptor, nicotinic, alpha 7
AMD1	adenosylmethionine decarboxylase 1
ASMT	acetylserotonin O-methyltransferase
PNMT	phenylethanolamine N-methyltransferase
OAZ1	ornithine decarboxylase antizyme 1
ODC1	ornithine decarboxylase 1
HDC	histidine decarboxylase
GATA3	GATA binding protein 3
DBH	dopamine beta-hydroxylase (dopamine beta-monooxygenase)
DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)
ASMTL	acetylserotonin O-methyltransferase-like

You can:

- Sort the overlapping gene list by clicking the **Gene Symbol** or **Gene Name** column heading; click a column heading a second time to sort in the reverse order.
- Export the overlapping gene list by clicking the Excel icon . The resulting file contains HTML. To save the file as a true Excel worksheet file, open it and save it as an **Excel 97-2003 Workbook (*.xls).**

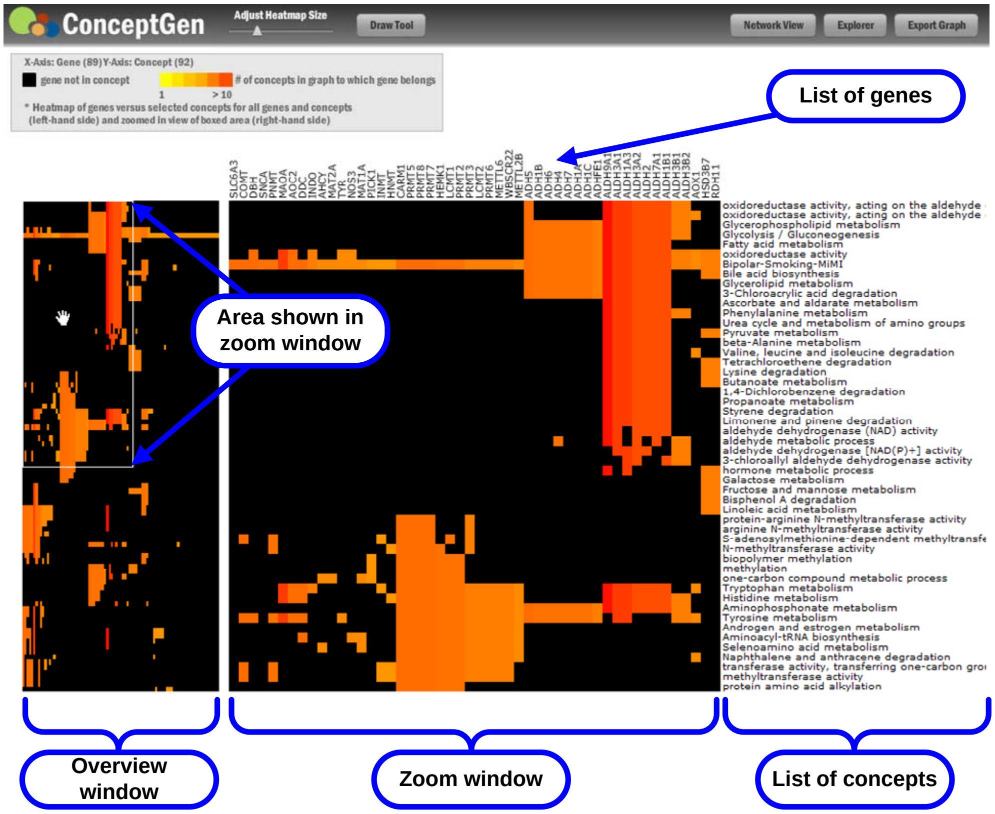
- Display the **MiMI Gene Details** page for a gene by double-clicking its row in the gene list.
- View a network of the interactions between all overlapping genes in MiMI Netbrowser by clicking the gene list interaction icon ⚙.

Creating a heatmap

You can create a heatmap view to visualize how genes and concepts are related, and which genes are driving the enrichment of which groups of concepts.

Creating a heatmap

1. Select the concepts you want to include in the heatmap. The queried or experimental concept is always included.
2. Click **Draw Heatmap** at the bottom of the Concept Explorer window. The heatmap view appears.



* Heatmap of genes versus selected concepts for all genes and concepts (left-hand side) and zoomed in view of boxed area (right-hand side)

List of genes

Area shown in zoom window

Overview window

Zoom window

List of concepts

- The leftmost rectangle is an overview window of the heatmap, the rightmost rectangle is a zoom window corresponding to the boxed area of the overview window.

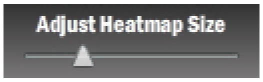
- Along the X axis are the genes in your gene list; along the Y axis are the concepts you selected and the queried or experimental concept.
- The scale in the legend describes the color coding of the gene columns, from black (the gene does not belong to the enriched concept) to bright red (the gene belongs to the most enriched concepts).

Working with the heatmap

In heatmap view, you can:

Adjust the heatmap size

Use the **Adjust Heatmap Size** slider to change the size of both the overview and zoom rectangles.



Pan the graph

- In the overview window, click and drag the area on which the cursor becomes a hand.
- In the zoom window, click and drag anywhere to move the zoom view to another location.

Add or remove concepts

1. Click the **Explorer** button to return to the Concept Explorer.
2. Select or deselect concepts as needed.
3. Click **Draw Heatmap** again.

A revised heatmap is drawn.

Save an image of the heatmap

1. Arrange the view you want of the heatmap by adjusting the heatmap size and panning as necessary.
2. Click **Export Graph**.
3. Navigate to a location for the file, and optionally rename the file.
4. Click **Save**.

A screenshot of the heatmap window is saved in **.png** format.

Create a new heatmap

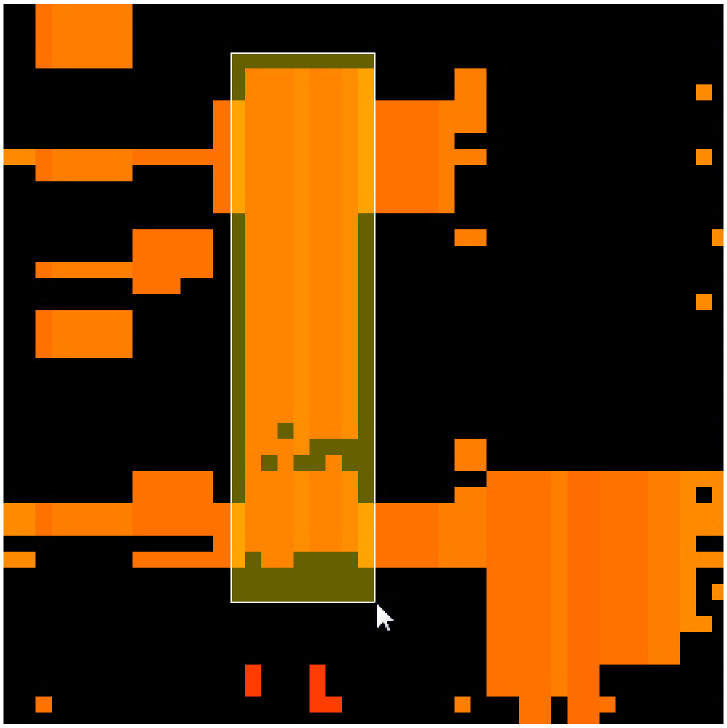
To abandon a heatmap and create a new one:

1. Click the **Explorer** button to return to the Concept Explorer.
2. If you want to start from scratch, click **Select None**.
3. Select concepts for the new heatmap.
4. Click **Draw Heatmap** again.

A new heatmap is drawn.

View selected heatmap data as a network graph

1. Navigate to an area of interest on the heatmap.
2. Adjust the heatmap size and pan as necessary to include the area in which you are interested. The data used for the network graph will be limited to what's visible in the zoom view.
3. Click the **Draw Tool** button.
4. In the zoom view, click and drag a rectangle around the area of interest to select it.



5. Click **Draw Network Graph** to create the network graph.
6. To return to the heatmap, click the **Heatmap View** button.

7. If you want to add to the network graph you created, create another selection using **Draw Tool**, and click **Draw Network Graph** again.

   The new data will be merged into the existing network graph, which will be redrawn.

View selected heatmap data in MiMI Netbrowser

1. Navigate to an area of interest on the heatmap.
2. Adjust the heatmap size and pan as necessary to include the area in which you are interested. The data used in MiMI Netbrowser will be limited to what's visible in the zoom view.
3. Click the **Draw Tool** button.
4. In the zoom view, click and drag a rectangle around the area of interest to select it.
5. Click **MiMI NetBrowser**. The selected data appears in MiMI Netbrowser in a new browser tab or window.

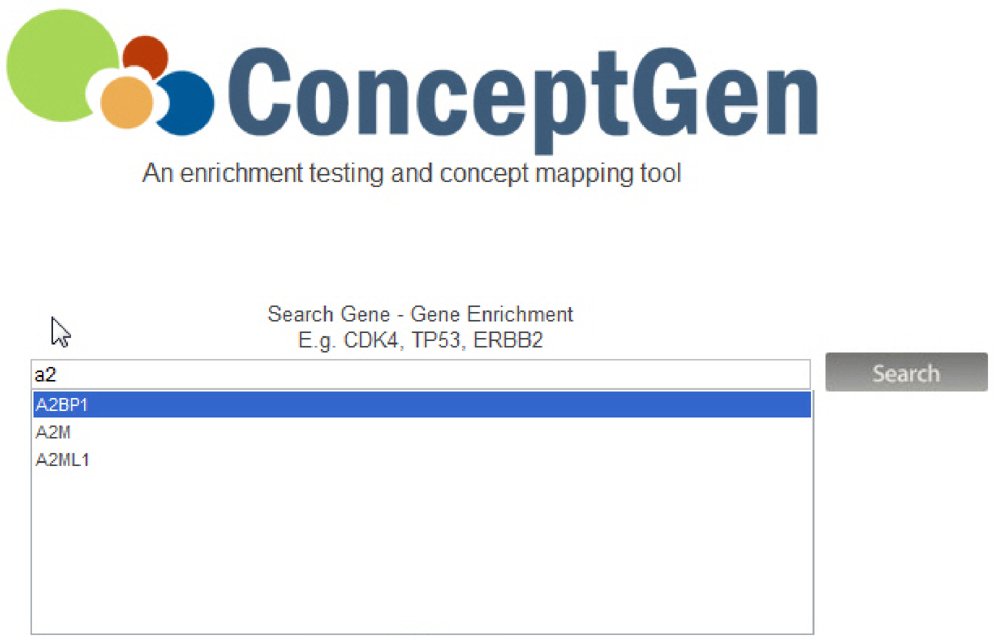
ENTERING DATA FOR GENE-TO-GENE ENRICHMENT ANALYSIS

Use gene-to-gene enrichment analysis to obtain a statistical measure of the closeness of any two genes by annotations, or to find all concepts in which a specific gene is a member. With this method, you work with a single gene rather than a gene list.

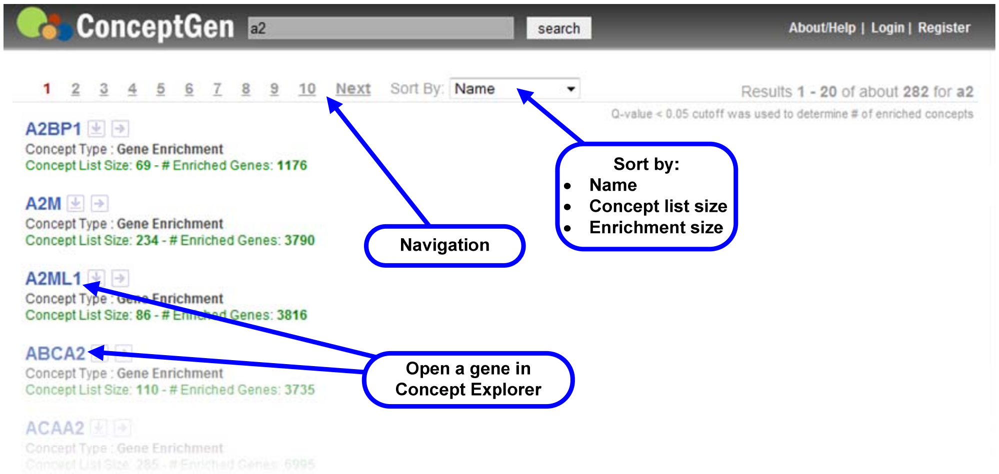
1. Go to the ConceptGen home page at http://conceptgen.ncibi.org.

   If you are logged in, you can return to the home page from the **My Concepts** page by clicking the ConceptGen logo in the upper-left corner of the page.
2. Click the link **Gene – Gene Enrichment Analysis** above the NCIBI logo near the bottom of the page.
3. On the **Search Gene - Gene Enrichment** page, enter a full or partial gene symbol.

As you type, a list of gene symbols that match the beginning of your text appears below the search box. If the gene you want appears in the list, you can click it to select it.



4. Click the **Search** button. A list of matching gene symbols appears on the search results page. (If you selected a gene from the drop-down list, only that gene appears.)



Results 1 - 20 of about 282 for a2

Q-value < 0.05 cutoff was used to determine # of enriched concepts

A2BP1
Concept Type : Gene Enrichment
Concept List Size: 69 - # Enriched Genes: 1176

A2M
Concept Type : Gene Enrichment
Concept List Size: 234 - # Enriched Genes: 3790

A2ML1
Concept Type : Gene Enrichment
Concept List Size: 86 - # Enriched Genes: 3816

ABCA2
Concept Type : Gene Enrichment
Concept List Size: 110 - # Enriched Genes: 3735

ACAA2
Concept Type : Gene Enrichment
Concept List Size: 285 - # Enriched Genes: 6995

Navigation

Sort by:
- Name
- Concept list size
- Enrichment size

Open a gene in Concept Explorer

5. Find the gene you want among the search results. You can:
   - Navigate using the page number and **Next** links above the list.
   - Sort the gene symbols by:

     Name. Gene symbol name (the default).

     Concept list size. The number of concepts that include the gene.

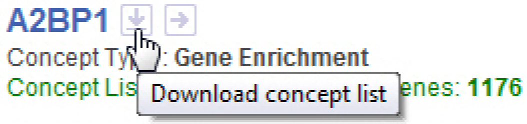
     Enrichment size. The number of enriched genes.
6. Click the gene symbol link to open the gene data in ConceptGen's Concept Explorer.

For more information, see "Using the Concept Explorer for Gene-to-Gene Enrichment Analysis."

Downloading the concept list for a gene

To download the list of concepts that includes a gene:

1. On the search results page for gene-to-gene enrichment, click the **Download concept list** icon ⤓ to the right of the gene symbol.

2. In the dialog box, select **Save File** to download the file.
3. Click **OK**.
4. Navigate to a location for the file, and optionally rename the file.
5. Click **Save**.

The concept list file is saved with an **.xls** file extension.

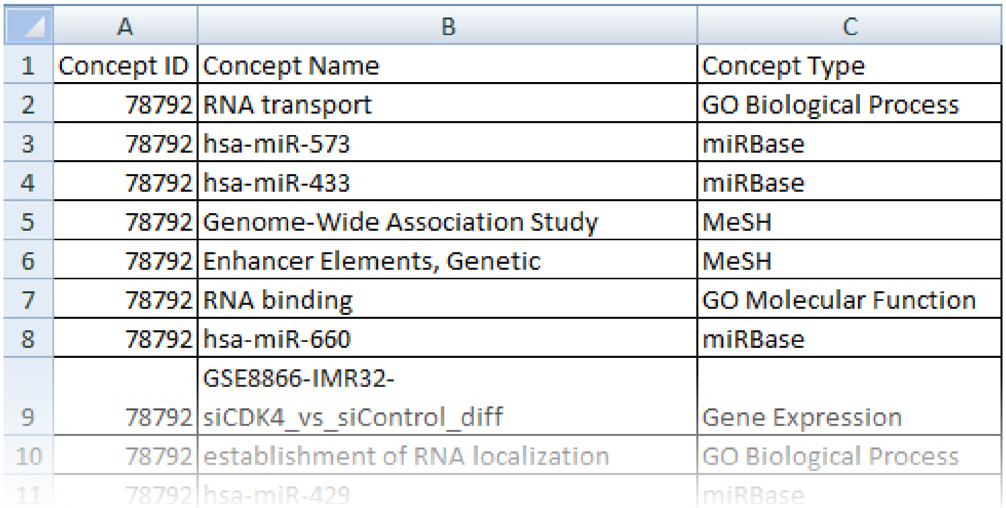
Opening a saved concept list file

You can open a downloaded concept list file for a gene in Microsoft Excel.

1. Open the file in Excel.

   You may get a message that the file is in a different format than specified by the file extension (the file contains HTML although the file extension indicates it is an Excel 97-2003 worksheet file with an **.xls** extension).

2. Click **Yes** to open the file:



	A	B	C
1	Concept ID	Concept Name	Concept Type
2	78792	RNA transport	GO Biological Process
3	78792	hsa-miR-573	miRBase
4	78792	hsa-miR-433	miRBase
5	78792	Genome-Wide Association Study	MeSH
6	78792	Enhancer Elements, Genetic	MeSH
7	78792	RNA binding	GO Molecular Function
8	78792	hsa-miR-660	miRBase
9	78792	GSE8866-IMR32-siCDK4_vs_siControl_diff	Gene Expression
10	78792	establishment of RNA localization	GO Biological Process
11	78792	hsa-miR-429	miRBase

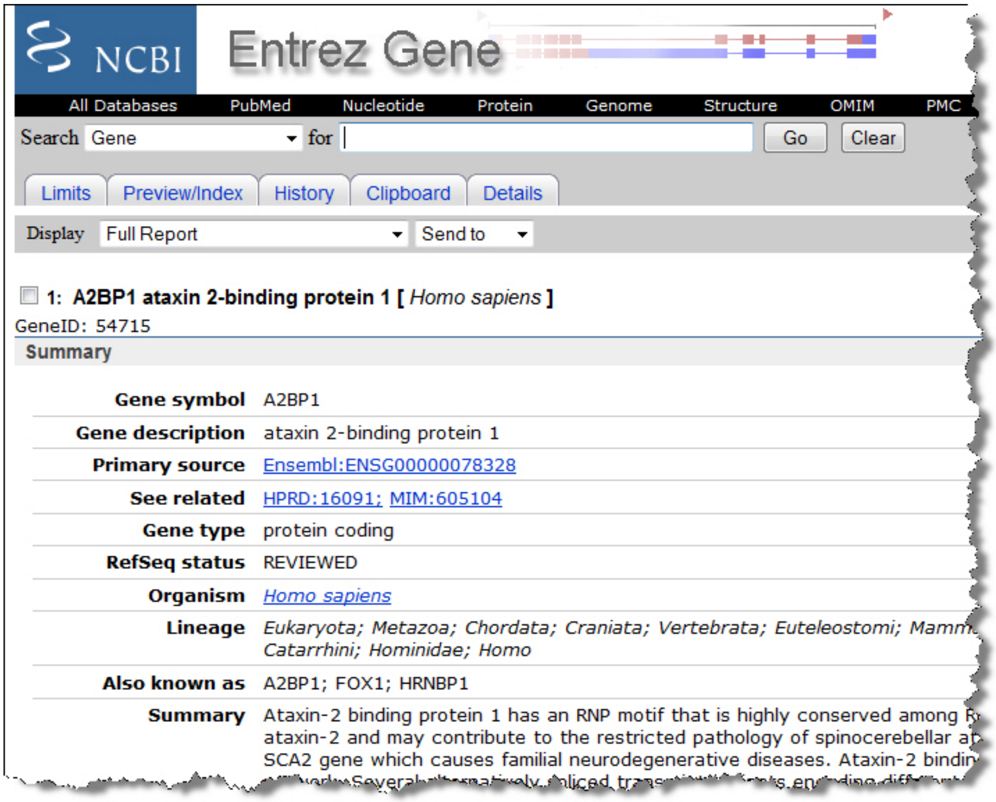
Note: If you want to save the file as a true Excel worksheet file, select **File → Save As…**, select the **Excel 97-2003 Workbook (*.xls)** option from the **Save as type** dropdown, and click **Save**.

Viewing the Entrez Gene entry for a gene

To view a gene's entry in Entrez Gene:

- On a gene-to-gene enrichment search results page, click the **Source Link** icon → to the right of the gene symbol.

The gene's entry in Entrez Gene appears in a new browser tab or window.



☐ 1: **A2BP1 ataxin 2-binding protein 1 [** *Homo sapiens* **]**

GeneID: 54715

Summary

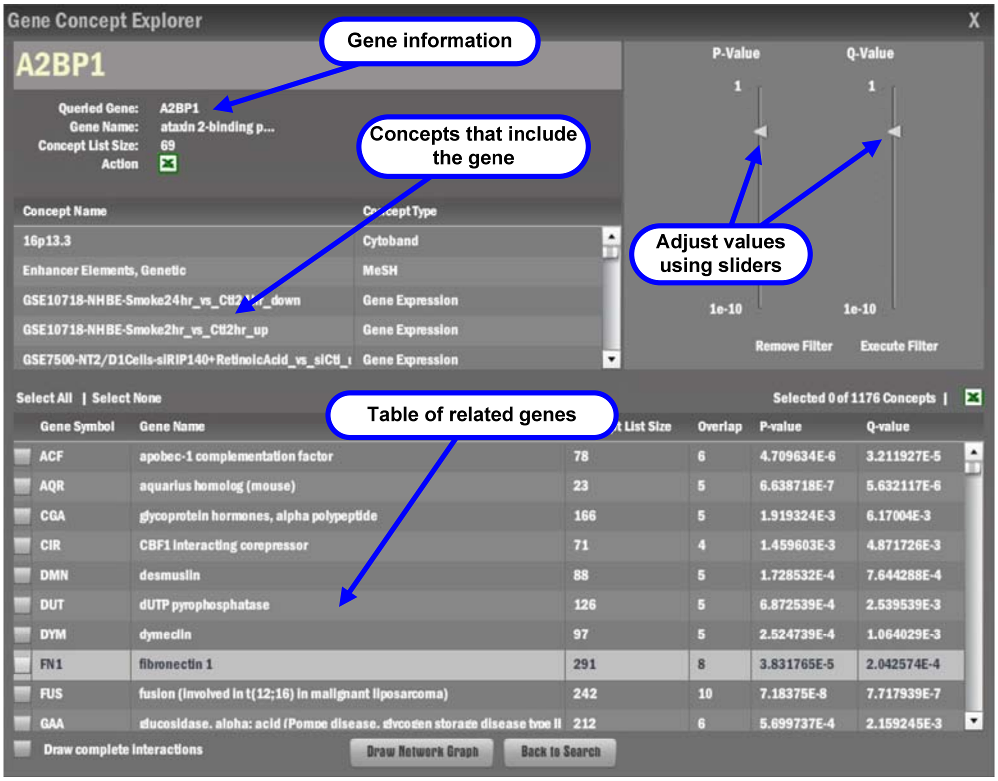
Gene symbol	A2BP1
Gene description	ataxin 2-binding protein 1
Primary source	Ensembl:ENSG00000078328
See related	HPRD:16091; MIM:605104
Gene type	protein coding
RefSeq status	REVIEWED
Organism	*Homo sapiens*
Lineage	*Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamm* *Catarrhini; Hominidae; Homo*
Also known as	A2BP1; FOX1; HRNBP1
Summary	Ataxin-2 binding protein 1 has an RNP motif that is highly conserved among R ataxin-2 and may contribute to the restricted pathology of spinocerebellar at SCA2 gene which causes familial neurodegenerative diseases. Ataxin-2 bindin

USING THE CONCEPT EXPLORER FOR GENE-TO-GENE ENRICHMENT ANALYSIS

Overview of the Concept Explorer

This section describes the Concept Explorer for gene-to-gene enrichment analysis. The Concept Explorer differs for gene set enrichment testing. See "Using the Concept Explorer for Gene Set Enrichment Testing."

The Concept Explorer includes the following major sections:



Queried Gene: A2BP1
Gene Name: ataxin 2-binding p...
Concept List Size: 69
Action

Concept Name	Concept Type
16p13.3	Cytoband
Enhancer Elements, Genetic	MeSH
GSE10718-NHBE-Smoke24hr_vs_Ctl2[illegible]r_down	Gene Expression
GSE10718-NHBE-Smoke2hr_vs_Ctl2hr_up	Gene Expression
GSE7500-NT2/D1Cells-siRIP140+RetinoicAcid_vs_siCtl_	Gene Expression

	Gene Symbol	Gene Name	t List Size	Overlap	P-value	Q-value
☐	ACF	apobec-1 complementation factor	78	6	4.709634E-6	3.211927E-5
☐	AQR	aquarius homolog (mouse)	23	5	6.638718E-7	5.632117E-6
☐	CGA	glycoprotein hormones, alpha polypeptide	166	5	1.919324E-3	6.17004E-3
☐	CIR	CBF1 interacting corepressor	71	4	1.459603E-3	4.871726E-3
☐	DMN	desmuslin	88	5	1.728532E-4	7.644288E-4
☐	DUT	dUTP pyrophosphatase	126	5	6.872539E-4	2.539539E-3
☐	DYM	dymeclin	97	5	2.524739E-4	1.064029E-3
☐	FN1	fibronectin 1	291	8	3.831765E-5	2.042574E-4
☐	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	242	10	7.18375E-8	7.717939E-7
☐	GAA	glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II	212	6	5.699737E-4	2.159245E-3

- **Gene information**. Information about the gene selected for the analysis, including the list of concepts that include it. You can:
  - Sort the concept list by clicking the **Concept Name** or **Concept Type** column heading; click a column heading a second time to sort in the reverse order.
  - Export the concept list by clicking the Excel icon ☒. The resulting file contains HTML. To save the file as a true Excel worksheet file, open it and save it as an **Excel 97-2003 Workbook (*.xls).**
- **P-Value** and **Q-Value** filters. Sliders to adjust the p-value and q-value for stringency.

- **Table of genes**. Details on related genes.

  You can:

  - Sort the list of genes by clicking a column heading; click a column heading a second time to sort in the reverse order.
  - Export information about one or more selected genes by clicking the Excel icon above the right end of the table. The resulting file contains HTML. To save the file as a true Excel worksheet file, open it and save it as an **Excel 97-2003 Workbook (*.xls).**

    The exported file includes the p-value and q-value test statistics and the concept IDs of the overlapping concepts.

Filtering the list of genes

To filter the table of related genes:

1. Use the **P-Value** and **Q-Value** sliders to adjust one or both values.
2. Click **Execute Filter**.

   The table of genes is updated to include genes matching the filter criteria.
3. Click **Remove Filter** to return the **P-Value** and **Q-Value** sliders to their default values.

Selecting genes

You can select genes for other operations such as relation mapping.

- Use **Select All** above the left end of the table of genes to select all genes, and **Select None** to return to the initial state of no genes selected.
- To select or deselect an individual gene, click the checkbox column on the gene row.

Comparing an enriched gene with the queried gene

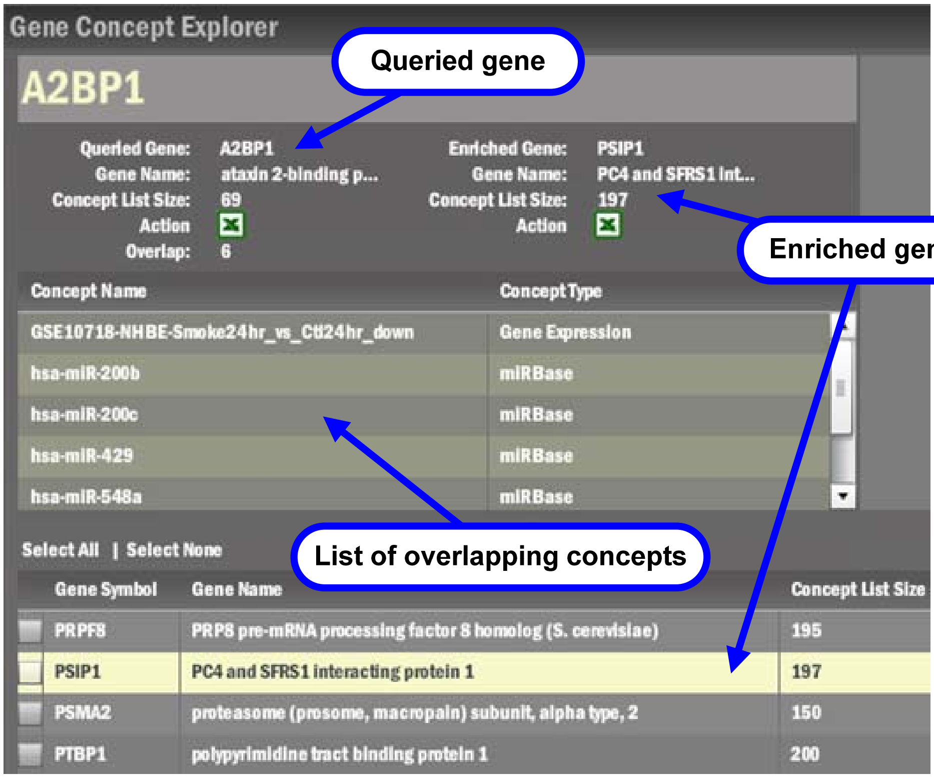
You can compare the queried gene to one of the enriched genes in the table.

Viewing summary information

Click the enriched gene's row in the table to highlight it.

Summary information for the enriched gene appears to the right of the summary information for the queried gene.

Overlap indicates the number of concepts that include both genes. The concept list below the summary information is a list of the common concepts.



A2BP1

Queried Gene: A2BP1
Gene Name: ataxin 2-binding p...
Concept List Size: 69
Action ☒
Overlap: 6

Enriched Gene: PSIP1
Gene Name: PC4 and SFRS1 int...
Concept List Size: 197
Action ☒

Concept Name	Concept Type
GSE10718-NHBE-Smoke24hr_vs_Ctl24hr_down	Gene Expression
hsa-miR-200b	miRBase
hsa-miR-200c	miRBase
hsa-miR-429	miRBase
hsa-miR-548a	miRBase

	Gene Symbol	Gene Name	Concept List Size
☐	PRPF8	PRP8 pre-mRNA processing factor 8 homolog (S. cerevisiae)	195
☐	PSIP1	PC4 and SFRS1 interacting protein 1	197
☐	PSMA2	proteasome (prosome, macropain) subunit, alpha type, 2	150
☐	PTBP1	polypyrimidine tract binding protein 1	200

Exporting the list of overlapping concepts

Export concept ID, name, and type for the overlapping concepts by clicking the Excel icon ☒ at the bottom of the enriched gene summary. The resulting file contains HTML. To save the file as a true Excel worksheet file, open it and save it as an **Excel 97-2003 Workbook (*.xls).**

RELATION MAPPING FOR GENE-TO-GENE ENRICHMENT ANALYSIS

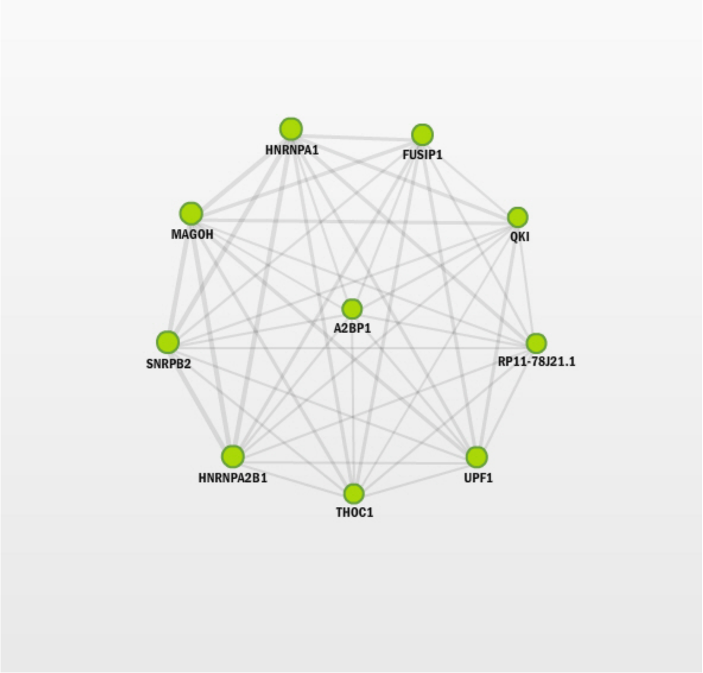
You can explore the interconnectivity of nodes that represent genes by using relation mapping.

This section describes relation mapping for gene-to-gene enrichment analysis. For mapping in gene set enrichment testing, see "Relation Mapping for Gene Set Enrichment Testing."

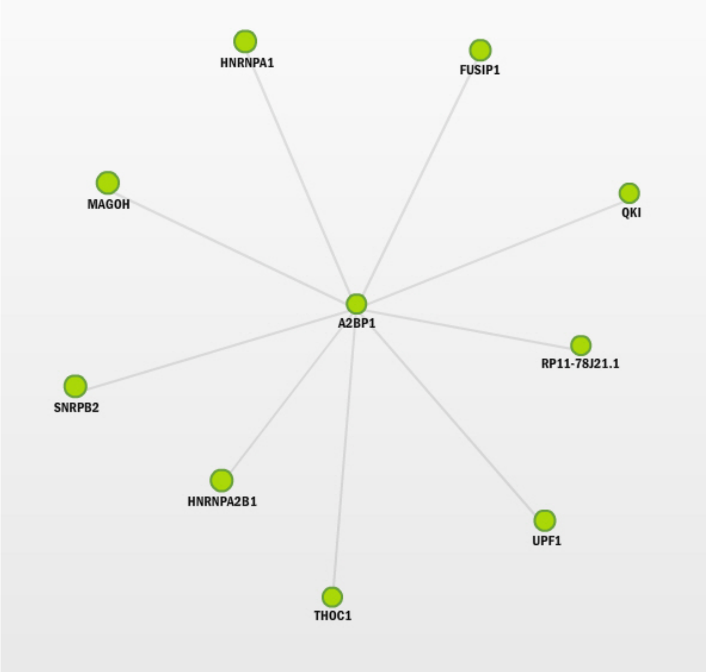
Note: A heatmap view is not available in gene-to-gene enrichment analysis.

Creating a network graph

1. Select from 1 to 100 genes.
2. Choose an option for which interactions to include:
    - Select **Draw complete interactions** to include links between *all* selected genes. Example:

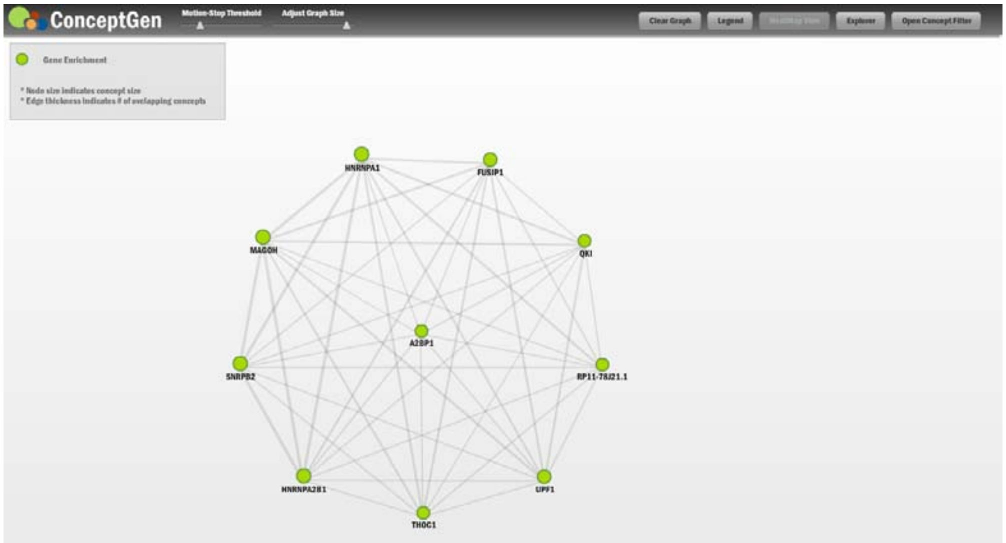


- Deselect **Draw complete interactions** to include only those links between the queried gene and the enriched genes you selected. Example:



3. Click **Draw Network Graph**.

   The ConceptGen network window appears, showing the specified network.



Working with the network graph

On the network graph page, you can:

Hide / show the legend

Use the legend to interpret visual styles used in the graph.

● Gene Enrichment

* Node size indicates concept size
* Edge thickness indicates # of ovelapping concepts

- In gene-to-gene enrichment analysis, all nodes are classified as **Gene Enrichment**.
- The size of a gene node is based on the number of concepts in which it is included—the more concepts, the larger the node.
- The thickness of an edge line between two gene nodes is based on the number of concepts that the genes have in common—the more concepts in common, the thicker the edge line.

To hide or show the legend, click the **Legend** button.

Adjust the graph size

To adjust the overall graph size, use the **Adjust Graph Size** slider in the top-left corner.

Move or pan the graph

To move the network or pan to another area of it, click on any empty space outside the bounds of the network and drag.

Move a node

To move a node, click and drag the node.

Add additional genes

To add more genes to the existing network graph:

1. Click the **Explorer** button to return to the Concept Explorer.
2. Select additional genes.
3. Click **Draw Network Graph** again.

The newly added genes are merged with the existing genes in the network graph, and the graph is redrawn to reflect any additional interactions among them.

Create a new network graph

To abandon a graph and begin a new one:

1. Click **Clear Graph** to delete the existing network graph and return to the Concept Explorer with no genes selected.
2. Select genes for the new graph.
3. Click **Draw Network Graph** again.

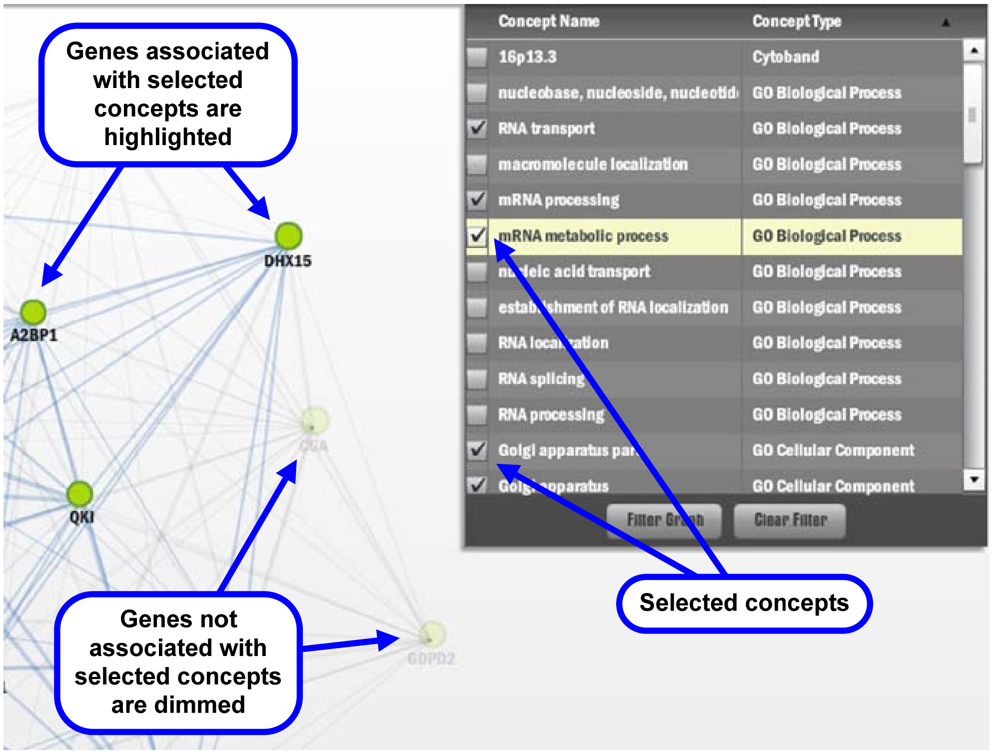
A new network graph is drawn.

Filter genes by concept

When you filter genes by concept, you can highlight genes associated with the concepts you select, while genes not associated with those concepts will be dimmed in the network graph. To filter genes:

1. Click **Open Concept Filter** to display the concept filter window.
2. Select the concepts to include.
3. Click the **Filter Graph** button.

The network graph is redrawn. Gene nodes and edges that are not associated with any of the concepts you selected are dimmed in the network graph.



Genes associated with selected concepts are highlighted

Genes not associated with selected concepts are dimmed

Selected concepts

	Concept Name	Concept Type
☐	16p13.3	Cytoband
☐	nucleobase, nucleoside, nucleotid	GO Biological Process
☑	RNA transport	GO Biological Process
☐	macromolecule localization	GO Biological Process
☑	mRNA processing	GO Biological Process
☑	mRNA metabolic process	GO Biological Process
☐	nucleic acid transport	GO Biological Process
☐	establishment of RNA localization	GO Biological Process
☐	RNA localization	GO Biological Process
☐	RNA splicing	GO Biological Process
☐	RNA processing	GO Biological Process
☑	Golgi apparatus par	GO Cellular Component
☑	Golgi apparatus	GO Cellular Component

4. To clear the concept filter, click **Clear Filter**.

Display details for genes (nodes)

- Double-click a gene node. The **Concept Detail** window appears with detailed information about the gene, including a list of the concepts in which it is included.

Gene Name: mago-nashi homolog, proliferation-associated (Drosophila)
Size: 215
Export List:

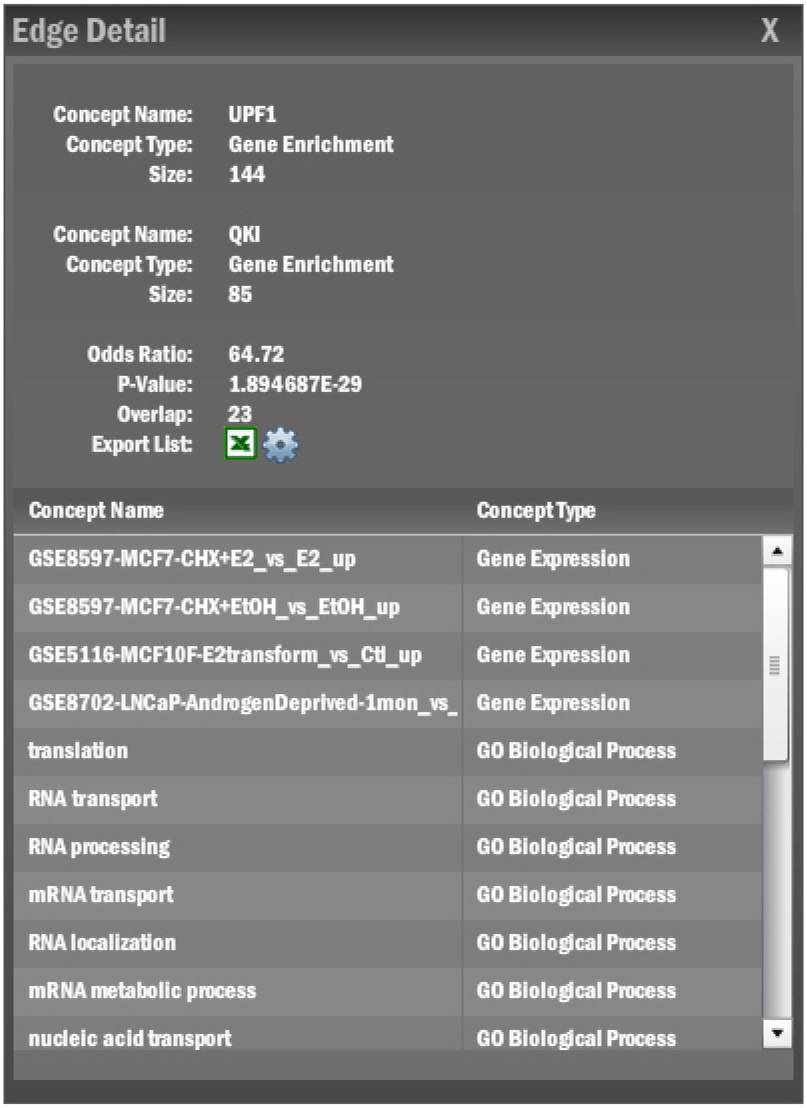
Concept Name	Concept Type
1p34-p33	Cytoband
Drosophila Proteins	MeSH
Eukaryotic Initiation Factor-4A	MeSH
Exons	MeSH
GSE10289-Hep3B-siSDBH_vs_siControl_down	Gene Expression
GSE10479-HUVEC-bgCAT_vs_Control_up	Gene Expression
GSE10879-EstrogenDepriveMCF7:5C_vs_MCF7_down	Gene Expression
GSE11550-Melanoma-Paclitaxel+Elesclomol_vs_Elesclomol_diff	Gene Expression

You can:

- Sort the concept list by clicking the **Concept Name** or **Concept Type** column heading; click a column heading a second time to sort in the reverse order.
- Export the concept list by clicking the Excel icon ☒. The resulting file contains HTML. To save the file as a true Excel worksheet file, open it and save it as an **Excel 97-2003 Workbook (*.xls).**

Display details for overlaps between genes (edges)

- Single-click an edge between two gene nodes. The **Edge Detail** window appears with detailed information about the overlapping concepts between the two genes.



Concept Name: UPF1
Concept Type: Gene Enrichment
Size: 144

Concept Name: QKI
Concept Type: Gene Enrichment
Size: 85

Odds Ratio: 64.72
P-Value: 1.894687E-29
Overlap: 23
Export List:

Concept Name	Concept Type
GSE8597-MCF7-CHX+E2_vs_E2_up	Gene Expression
GSE8597-MCF7-CHX+EtOH_vs_EtOH_up	Gene Expression
GSE5116-MCF10F-E2transform_vs_Ctl_up	Gene Expression
GSE8702-LNCaP-AndrogenDeprived-1mon_vs_	Gene Expression
translation	GO Biological Process
RNA transport	GO Biological Process
RNA processing	GO Biological Process
mRNA transport	GO Biological Process
RNA localization	GO Biological Process
mRNA metabolic process	GO Biological Process
nucleic acid transport	GO Biological Process

You can:

- Sort the overlapping concept list by clicking the **Concept Name** or **Concept Type** column heading; click a column heading a second time to sort in the reverse order.
- Export the overlapping concept list by clicking the Excel icon. The resulting file contains HTML. To save the file as a true Excel worksheet file, open it and save it as an **Excel 97-2003 Workbook (*.xls).**