

## 2012 Mouse Liver Database Help

### Page Navigation (Quick Links):

#### Function

- 1) Project Description and Acknowledgements
- 2) Filter Options
  - a) Data type
  - b) Characteristic
  - c) Characteristic Value
- 3) List of Comparisons
- 4) Gene List
- 5) Example Section
  - a) Example: Filtered Results for Strain SJL
- 6) Additional Instructions/Information

#### Function

The 2012 Mouse Liver workflow is a gene expression database that was assembled from a number of sources including Gene Expression Omnibus (GEO), ArrayExpress and unpublished experiments. As most of the microarray studies in these repositories were carried out on Affymetrix chips, only raw data files from Affymetrix experiments were used to construct the database.

Users can obtain microarray/gene data for many comparisons. Comparisons can be searched and filtered using a variety of characteristics and options. A gene list for selected comparison(s) will be displayed and can be downloaded or copied to your clipboard. Users can use this workflow to obtain information about the comparisons run for a given criteria (e.g. Test Article, Route of Exposure). Gene lists obtained from this workflow contain the following information:

- Gene Name
- Gene Symbol
- Probeset ID
- Value

From the CEBS Homepage (<http://tools.niehs.nih.gov/cebs3/ui/>), click the '2012 Mouse Liver DB' icon under Workflows.

## 1) Project Description and Acknowledgements

All of the Affymetrix .cel files were first analyzed by Bioconductor SimpleAffy (Wilson and Miller, 2005) to assess data quality. Cel files from individual studies were normalized using Rosetta Resolver® version 7.1 Affymetrix Rosetta-Intensity Profile Builder software (Rosetta Inpharmatics, Kirkland, WA). Tables of normalized probe set expression were built using the common probe sets shared by 430A or 430\_2 chip types. For each study a number of contrasts were created using appropriate study controls. Statistically significant genes were identified by one-way ANOVA with a false discovery rate (Benjamini-Hochberg test) of  $\leq 0.01$ . No filter was applied to the fold-change.

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## 2) Filter Options

Filter Options allows users to decide which Comparisons are displayed for further selection.

Filter Options has the following options:

### a) Data type

Data type may be Unfiltered or Filtered.

### b) Characteristic

From the Characteristic dropdown box, the options in the table below are available. Selecting a Characteristic in this field will allow you to select a value for the Characteristic in the next field. A description of the selected Characteristic will appear below the dropdown box. This description can also be found in the table below.

#### *Characteristics and Definitions:*

Field	Description
<b>Age</b>	Animals of different ages were used in the comparisons
<b>Biological state</b>	Comparison was between animals in different biological states, e.g. estrous
<b>CAS Number</b>	CAS Number for chemical used as stressor
<b>Chemical</b>	Chemical used as stressor
<b>Diet</b>	Name of the diet used in comparison
<b>Dose regimen</b>	Dose administration frequency of the chemical used as stressor
<b>Environmental</b>	Name of the environmental agent used as stressor
<b>Exposure</b>	Exposure/dose amount for chemical stressor
<b>Exposure duration</b>	Duration of exposure of chemical
<b>Gene perturbed</b>	Name of gene and genotype/variation, e.g. WT, KO
<b>How gene was altered in experiment</b>	Type of genetic change made to gene
<b>Infectious agent</b>	Name of infectious agent used in the response comparison
<b>Injury</b>	Injury or surgery used in comparison
<b>Intersex comparison</b>	Comparison was between animals of different sexes
<b>Nanomaterial</b>	Nanoparticle used as stressor
<b>Route</b>	Route of chemical used as stressor
<b>Sex</b>	Sex of animals used in comparison
<b>Strain</b>	Strain of mice used in comparison
<b>Tumor type</b>	Material from a tumor was used in comparison

### c) Characteristic Value

Once you have clicked on one Characteristic in the above dropdown box, values will appear in the Characteristic Value relating to that Characteristic. For example, if you select 'BIOLOGICAL STAGE', a list of the following Characteristic Values will appear: CASTRATION, DEDIFFERENTIATION, PREGNANCY, PROESTRUS, Pregnancy, Metestrus, and Proestrus. One or multiple characteristic values may be selected.

### i) Multiple Selections

For Characteristic Value, multiple selections may be made. To select multiple values, press and hold the Ctrl key (for PC) or Command key (for Mac) while clicking your choices; your selections will be highlighted

**Note:** The background around the 'multi selection icon' has changed colors indicating that multiple selections have been chosen.

Once you have made all your desired selections under Filter, click the Get Comparisons button.

## 3) List of Comparisons

This section will allow selection of a comparison. A gene list can be generated for a selected comparison. The List of Comparisons table has the following columns:

*List of Comparisons Columns:*

Column	Description
<b>Comparison</b>	Microarray comparison unique name
<b>Age</b>	Animals of different ages were used in the comparisons
<b>Bio Stage</b>	Comparison was between animals in different biological stages, e.g. estrous
<b>CAS Number</b>	CAS Number for chemical used as stressor
<b>Chemical</b>	Chemical used as stressor
<b>Diet</b>	Dose administration frequency of the chemical used as stressor
<b>Environmental</b>	Name of the environmental agent used as stressor
<b>Exposure</b>	Exposure/dose amount for chemical stressor
<b>Exp duration</b>	Duration of exposure of chemical
<b>Gene perturbed</b>	Name of gene and genotype/variation, e.g. WT, KO
<b>Infectious agent</b>	Name of infectious agent used in the response comparison
<b>Injury</b>	Injury or surgery used in comparison
<b>Route</b>	Route of chemical used as stressor
<b>Sex</b>	Sex of animals used in comparison
<b>Strain</b>	Strain of mice used in comparison

**Note:** For many comparisons, some or many of these columns will not contain values. Often a value is only present in a column if it varied for that comparison.

Click on a Comparison row to select that comparison. Once a comparison is selected, click the Gene List button to populate the table below with results.

## 4) Gene List

The Gene List table contains all of the genes and respective values resulting from the selected microarray comparison. The list will contain over 20,000 genes and results. The list can be scrolled through using the bar on the right.

Results in the Gene List may be stored on your computer in one of two ways:

- Copy to Clipboard: Click this button to copy the entire gene list to your clipboard. You may then paste into your favorite program.  
*Note: This will add a large amount of data to your clipboard.*
- Download: Click this button to download the gene list as a tab-delimited file. For full download instructions see [Additional Instructions](#) at the end of this tutorial.

## 5) Example Section

This example should provide insight into how the 2012 Mouse Liver Database workflow can be used to get data and answer questions. Follow along with the instructions below to obtain the data for this specific example.

### a) Example: Filtered Results for Strain SJL

For this example we are interested in filtered microarray data for the SJL mouse strain.

- 1) Filter Options: Because we are interested in filtered data, select Filtered under A. Data type. To search for the strain of SJL, use the dropdown box for B. Characteristic to select 'STRAIN'. Finally, now that we have values to choose from for C. Characteristic Value, scroll down to select SJL. Once SJL is highlighted click the Get Comparisons button.
- 2) List of Comparisons: You will see two different comparisons for this strain. Use the scroll bar at the bottom of the table to scroll across to find what differs between these comparisons; the comparisons had different exposure durations. If we are interested in data for both comparisons we will need to get the gene list for each separately. Click to select the first comparison, then click the Gene List button.
- 3) Gene List: Once we have displayed results for the first comparison save the data for the first comparison using either the Copy to Clipboard or Download button (For full download instructions see [Additional Instructions](#) at the end of this tutorial). Then select the second comparison in the List of Comparisons, and click the Gene List button again to get the results for the second comparison. Save the data for the second comparison using the same method as the first. The order of the rows for each gene should be the same for both files. You may then copy and

paste the data from one excel file into the other for further analysis/viewing. Be sure to change your headings, or add a column to indicate the different comparisons.

## 6) Additional Instructions/Information

- 1) 'CEBS Home' icon returns the user back to the CEBS Home page
- 2) Downloading and displaying data in Excel
  - o Select the Download Data Icon
  - o The next screen displays available locations to save data
  - o Once a location has been determined, select Save
  - o To access the data, go to the location where the data was saved
  - o You will notice that the data is saved in text format
  - o Open in Notepad or your favorite text editor
  - o Select all by choosing Ctrl + A (PC) or Command + A (Mac). This function will highlight the entire document.
  - o Right click your mouse and select copy
  - o Open Excel
  - o Right click your mouse and select paste
  - o Save as an Excel document
  - o To add filtering options, navigate to the Data Tab in Excel and select Filter
- 3) Flash movie running flex code for CEBS indicates a software platform is being used to create graphics or texts for CEBS
- 4) CEBS data may be cited by navigating to the CEBS Support page, and selecting the [Citing CEBS](#) document under FAQs. Here, instructions can be found on citing NTP Data as well as non-NTP data in CEBS.