

Tutorial for PLEXdb Gene List Suite

<http://www.plexdb.org/modules/glSuite/>

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2. **Creating gene lists**
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1. Introduction

The [Gene List Suite](#) combines all of the PLEXdb tools for creating, visualizing, annotating and analyzing gene lists into one place.

A **gene list** is simply a set of one or more probe set ids. The PLEXdb Gene List Suite provides the means for creating, annotating and analyzing groups of genes. Gene lists can be input into a number of the PLEXdb tools, for example, [Find Your Gene](#), the [Microarray Platform Translator](#).

If you wish to save your gene lists for more than a day, you will need to have an account with PLEXdb (registration is a quick [process](#)) and be logged in.

An **analysis** is a set of steps linked together to create and/or analyze a set of genes. If you are logged in, you can save your analysis for future reference.

The Gene List Suite is divided into 4 major sections. These will be described briefly below.

2. Creating gene lists

- 2.1. **Import a gene list**
- 2.2. **Translate gene lists**
- 2.3. **Translate between microarray designs**
- 2.4. **Create gene lists from existing gene lists**
- 2.5. **Additional methods**

Although several tools on the PLEXdb website will generate gene lists (e.g. [Find Your Gene](#), the [Microarray Platform Translator](#), visualization tools inside the [Experiment Browser](#)), all means of creating gene lists are presented together inside the [Gene List Suite](#).

as ecannon

Gene List Suite

- Home
- Create
- Analyze
- Annotate
- Manage

Create a New Gene List

- Select a method

 - Select a method
 - Import gene list
 - Combine gene lists
 - Blast against array sequence
 - Translate to probe sets
 - Translate between microarrays
 - Fold Change
 - Profile Neighbors
 - GO Category

Here you can create a new gene list (list of probe ids) from the drop-down list above.

Please select a method for creating a gene list

[ent Data](#)

2.1. Import a gene list

You can create a PLEXdb gene list from your own list of favorite genes. The list may be typed into an input box or uploaded from a file. Note that large lists (> 500) may cause time-out errors for some visualizations and analyses.

- Home
- Create
- Analyze
- Annotate
- Manage

Create a New Gene List : Import gene list

Import gene list

* Gene List Name

Gene list names must be unique

* Array design

Select Microarray Design

Probe set ids

* (names may be separated by commas, spaces, tabs, or new-lines)

Type or paste ids into the text box or upload a file containing probe set ids.

upload file:

Browse...

Notes:

Import

2.2. Translate gene list

If your gene list uses protein ids rather than probe set names, there may be a translator available which will return probe set names.

Gene List Suite

The screenshot shows the 'Gene List Suite' navigation bar with buttons for 'Home', 'Create', 'Analyze', 'Annotate', and 'Manage'. Below the navigation bar, the main heading is 'Create a New Gene List : Translate to probe sets'. Underneath this heading, there is a dropdown menu currently set to 'Translate to probe sets'. Below the dropdown is a text input field with the placeholder text 'Select a translation type' and a small blue arrow icon on the right side.

Create a new gene list by translating to probe set ids from other protein ids (e.g. UniProt).

Please select a type of translation from the dropdown above.

2.3. Translate between microarray designs

To translate a set of probe set ids from one microarray design to another, use either the simplified version of the MPT inside the Gene List Suite, or go to the full-feature version.

Gene List Suite

The screenshot shows the 'Gene List Suite' navigation bar with buttons for 'Home', 'Create', 'Analyze', 'Annotate', and 'Manage'. Below the navigation bar, the main heading is 'Create a New Gene List : Translate between microarrays'. Underneath this heading, there is a dropdown menu currently set to 'Translate between microarrays'. Below the dropdown, there is a text input field with the placeholder text 'Select a Gene List' and a small blue arrow icon on the right side. Below this field, there is a large empty text area for entering probe set ids. To the left of this area, there is a label 'Probe sets to translate:' and the text 'OR Enter one or more probe set ids'. Below this, there is another 'OR' followed by the text 'Upload a file containing probe set ids'. To the right of this text is a text input field for a file name and a 'Browse...' button. To the right of the 'Browse...' button is the text '(Limit: 5000)'. At the bottom left of the form, there is a 'Translate' button.

2.4. Create gene lists from existing gene lists

Gene List Suite

Home **Create** Analyze Annotate Manage

Create a New Gene List : Combine gene lists

Combine gene lists ▾

Select an array design then two existing gene lists for that array. You can then create new gene lists by comparing the two gene lists.

Select array design:

Gene List 1: [full details](#)

Gene List 2: [full details](#)

Choose merge options:

- All genes from both lists [279]
- Genes common to both lists [14]
- Genes unique to list 1 [248]
- Genes unique to list 2 [17]

New Gene List name:

Notes:

Two existing gene lists can be combined in various ways to form a new gene list, to look for overlap or exclusivity between the two, or to merge both.

2.5. Additional methods

Various additional methods for generate gene lists are available in the **create** section of the gene list suite. These will not be described in detail as they will change over time.

3. Managing Gene Lists

Gene lists can be viewed, renamed, deleted, edited and exported in the **manage** section. You must be logged in to manage your gene lists.

Gene List Suite

Home Create Analyze Annotate **Manage**

Manage Genelists and Analyses

Rename, delete, export your gene lists and analyses: Manage gene lists

Select array design: Arabidopsis ATH1 22k

Select a gene list: ecannon: FOLD CHANGE (2009-01-01 13:49:55) AT14 8-fold change; 38 genes [full details](#)

Information about selected gene list

Owner ecannon

Created with FOLD CHANGE

Created on 2009-01-01 13:49:55

Comments

Number of genes in the list: 38

Delete OR Rename as OR Edit OR Export as text OR Download as Excel

4. Annotating Gene Lists

Gene lists can be annotated in various ways.

Gene List Suite

Home Create Analyze **Annotate** Manage

Annotate Gene list

Select array design: Arabidopsis ATH1 22k

ecannon: FOLD CHANGE (2009-01-01 13:49:55) AT14 8-fold change; 38 genes [full details](#)

Information about selected gene list

Owner ecannon

Created with FOLD CHANGE

Created on 2009-01-01 13:49:55

Comments

Number of genes in the list: 38

Select a type of annotation:

- GO Annotation
- Genbank Protein Accessions
- UniProt IDs
- Arabidopsis Loci
- Rice Loci
- NCBI RefSeq
- TIGR Transcript Assemblies
- DCFI GeneIndex
- Consensus Sequence
- KEGG
- Manufacturer Annotation
- Community Annotation

Get annotation

5. Analyzing Gene Lists: work flows

Various methods for creating, visualizing, and analyzing gene lists can be link together in the **analysis** section of the Gene List Suite. If you are logged in, you can save your analysis for future use.

When you first enter the analysis section, you will see this:

Gene List Suite

Home Create **Analyze** Annotate Manage

Genelist Analysis: New Analysis

Create a [new analysis](#) or load saved analyses:

Analysis Name:

Analysis Description:

Analysis Content: [Save analysis](#)

[No steps set for this analysis. Please click "Add/Remove analysis steps" to begin.]

* All analyses will be deleted at the end of the day. Click [here](#) to retain analysis permanently.

Click “Add/Remove analysis steps to begin. This will pop up a box with the available steps.

Analysis: **Not specified**

Selected Steps

Available steps for analysis

Calculate fold-change
Hierarchical Clustering
Expression graph
Translate between Microarray Platforms
Heatmap

Select one or more steps, click “Add selected step(s)” then “Save Changes.”

The steps will appear in the analysis box like this:

Analysis
Content: [Add/Remove analysis steps](#) [Save analysis](#)

<input type="checkbox"/> Calculate fold-change	configure/view
<input type="checkbox"/> Expression graph	configure/view

Click the +/- box or the configure/view link to open the configuration for a step.

Analysis
Content: [Add/Remove analysis steps](#) [Save analysis](#)

<input type="checkbox"/> Calculate fold-change		
<div style="border: 1px solid black; padding: 5px;"><p>Step 1: Select an array design Arabidopsis ATH1 22k</p><p>Step 2: Select an experiment AT14:Genes affected by hog1 alleviation of CHS silencing</p><p>Step 3: Select treatment for X-Axis genotype=CHS-silenced type (ECG)</p><p>Step 4: Select treatment for Y-Axis genotype=anthocyanin-producing revertants (15B)</p><p>Step 5: Select an extraction normalization method <input checked="" type="radio"/> RMA <input type="radio"/> MAS 5.0</p><p>Output 1] View results for fold change No Gene list saved</p></div>		
<input type="checkbox"/> Expression graph	configure/view	

Fill in the form. Click the link next to the label “Output” to see the results of that step.

You will need to be logged in to save your analysis. Give your analysis a name and description, then click the link “Save analysis.”

Analysis
Content: [Add/Remove analysis steps](#) [Save analysis](#)

You can delete, rename or print your analysis in the manage section if you select “manage analyses” from the drop-down menu.

Gene List Suite

Home

Create

Analyze

Annotate

Manage

Manage Genelists and Analyses

Rename, delete, export your gene lists and analyses: Manage analyses

Select an analysis: Sample analysis

Delete

OR

Rename

as

OR

Print analysis