

A Quick Tutorial/An Example to Use the DAVID Bioinformatics Resources

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Step 1: Start Analysis Wizard



DAVID 2006 Functional Annotation Bioinformatics (LIB, NIAID/NIH, SAIC-Frederick) - Microsoft Internet Explorer

Address: <http://david.abcc.ncifcrf.gov/home.jsp>

DAVID Bioinformatic Resources 2006

National Institute of Allergy and Infectious Diseases (NIAID), NIH

Home **Start Analysis** Shortcut to DAVID Tools Technical Center Archives Term of Service DAVID Forum Credits About Us

Shortcut to DAVID Tools

- Functional Annotation**
Gene-annotation, enrichment analysis, functional annotation clustering, BioCarta & KEGG pathway mapping, gene-disease association, homologue match, ID translation, literature match and [more](#)
- Gene Functional Classification**
Provide a rapid means to reduce large lists of genes into functionally related groups of genes to help unravel the biological content captured by high throughput technologies. [More](#)
- Gene ID Conversion**
Convert list of gene ID/accessions to others of your choice with the most comprehensive gene ID mapping repository. The ambiguous accessions in the list can also be determined semi-automatically.
- List Gene Names in Batch**

Welcome to DAVID Bioinformatic Resources

The Database for Annotation, Visualization and Integrated Discovery (DAVID) 2006 is an expanded version of our original web-accessible programs of DAVID 2.1, 2.0 & 1.0. DAVID provides a comprehensive set of functional annotation tools for investigators to understand biological meaning behind large list of genes. For any given gene list, DAVID tools are able to:

- Identify enriched biological themes, particularly GO terms
- Discover enriched functional-related gene groups
- Visualize genes on BioCarta & KEGG pathway maps
- Search for other functionally related genes not in the list
- List interacting proteins
- Explore gene names in batch
- Link gene-disease associations
- Highlight protein functional domains and motifs
- Redirect to related literatures

What's New in DAVID 2006?

- [Functional Annotation Clustering](#)
- [Pre-built Affy gene backgrounds](#)
- [User's customized gene background](#)
- [Updated annotation databases](#)
- [Enhanced calculating speed](#)

DAVID Bioinformatic Forum

- [Technical notes & help](#)
- [Ask questions & get answers](#)
- [Share experiences](#)
- [Comments and feedback](#)
- [Bug report](#)

Statistics About DAVID

Step 2: Submit gene list or use built-in demo lists

DAVID 2006: functional annotation result summary - Microsoft Internet Explorer

File Edit View Favorites Tools Help

Address <http://david.abcc.ncifcrf.gov/tools.jsp>

Google

Analysis Wizard
DAVID Bioinformatic Resources 2006, NIAID/NIH

Home Start Analysis Shortcut to DAVID Tools Technical Center Archives Term of Service DAVID Forum Credits About Us

Upload List Background

Upload Gene List

[Demo list 1](#) [Demo list 2](#)
[Upload Help](#)

Step 1: Enter Gene List

A: Paste a list

Clear

Or

B: Choose From a File

Browse...

Step 2: Select Identifier

AFFY_ID

Step 3: List Type

Gene List
Background

Step 4: Submit List

Submit List

Analysis Wizard

[Tell us how you like the tool](#)
[Contact us for questions](#)

← Step 1. Submit your gene list through left panel.

An example:

Copy/paste IDs to "box A" -> Select Identifier as "Affy_ID" -> List Type as "Gene List" -> Click "Submit" button

1007_e_at
1053_at
117_at
121_at
1255_g_at
1294_at
1316_at
1329_at
1405_i_at
1431_at
1438_at
1487_at
1494_f_at
1598_g_at

Step 3: Select one of the DAVID Tools

For example, Gene Functional Classification Tool

The screenshot shows the DAVID 2006 web interface in Microsoft Internet Explorer. The browser title is "DAVID 2006: functional annotation result summary - Microsoft Internet Explorer". The address bar shows "http://david.abcc.ncifcrf.gov/tools.jsp". The page header includes the "Analysis Wizard" logo and "DAVID Bioinformatic Resources 2006, NIAID/NIH". The navigation menu includes "Home", "Start Analysis", "Shortcut to DAVID Tools", "Technical Center", "Archives", "Term of Service", "DAVID Forum", "Credits", and "About Us".

The main content area is titled "Analysis Wizard" and shows the following steps:

- Step 1. Successfully submitted gene list**
Current Gene List: Demo_List_2
Current Background: HOMO SAPIENS
- Step 2. Analyze above gene list with one of DAVID tools**

A blue arrow points down from Step 2 to a list of tools:

- Functional Annotation Tool
 - Functional Annotation Clustering
 - Functional Annotation Chart
 - Functional Annotation Table
- Gene Functional Classification Tool (highlighted with a red arrow)
- Gene ID Conversion Tool
- Show Gene List Tool

On the left side, there is a "Gene List Manager" section with a dropdown menu for species selection (currently set to "HOMO SAPIENS(403)"), a "Select" button, and a "List Manager" section with a dropdown menu for list selection (currently set to "Demo_List_2") and buttons for "Use", "Rename", "Remove", "Combine", and "Show Gene List ^{new!}".

Step 4. View and explore results of gene functional groups

The screenshot displays the DAVID 2006 Gene Functional Classification tool interface. The browser window title is "DAVID 2006: Gene Functional Classification - Microsoft Internet Explorer". The address bar shows the URL "http://david.abcc.ncifcrf.gov/gene2gene.jsp". The page header includes the DAVID logo and the text "Gene Functional Classification Tool" and "DAVID Bioinformatic Resources 2006, NIAID/NIH".

The main content area is titled "Gene Functional Classification" and shows the following information:

- Current Gene List: Demo_List_2
- Current Background: HOMO SAPIENS
- 394 DAVID IDs

Options include "Classification Stringency" set to "Medium". Buttons for "Rerun using options", "Create Sublist", and "Heatmap" are visible. A "Download File" link is also present.

The results are organized into 16 clusters. The first cluster, "Gene Group 1", has an enrichment score of 3.37 and contains 6 genes:

Gene ID	Gene Name
34375_at, 875_o_at	chemokine (c-c motif) ligand 2
40385_at	chemokine (c-c motif) ligand 20
36103_at	chemokine (c-c motif) ligand 3
36674_at	chemokine (c-c motif) ligand 4
408_at	chemokine (c-c motif) ligand 1 (melanoma growth stimulating activity, alpha)
1369_s_at, 35372_r_at	interleukin 8

The second cluster, "Gene Group 2", has an enrichment score of 2.89 and contains 8 genes:

Gene ID	Gene Name
1857_at	smad, mothers against dec homology 7 (drosophila)
39421_at	runx-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)
36999_at	jumoniv, at rich interactive domain 1a (rbbe2-like)
1994_at	activating transcription factor 2
1895_at, 32583_at	v-jun sarcoma virus 17 oncogene homolog (avian)
35768_at	ring finger protein 40
36226_r_at	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)
789_at	early growth response 1

Step 5. Get back to analysis center for other DAVID tools for the same gene list.

The screenshot shows the DAVID 2006 Gene Functional Classification tool interface. The browser window title is "DAVID 2006: Gene Functional Classification - Microsoft Internet Explorer". The address bar shows "http://david.abcc.ncifcrf.gov/gene2gene.jsp". The page header includes the DAVID logo and "Gene Functional Classification Tool" with "DAVID Bioinformatic Resources 2006, NIAID/NIH". The navigation menu includes "Home", "Start Analysis", "Shortcut to DAVID Tools", "Technical Center", "Archives", "Term of Service", "DAVID Forum", "Credits", and "About Us". A red arrow points to the "Start Analysis" link.

The main content area is titled "Gene Functional Classification" and shows "Current Gene List: Demo_List_2" and "Current Background: HOMO SAPIENS" with "394 DAVID IDs". There are buttons for "Options", "Classification Stringency" (set to "Medium"), "Rerun using options", "Create Sublist", and "Heatmap". A "Download File" link is also present.

The results are displayed in two clusters:

16 Cluster(s)

Gene Group 1 (Enrichment Score: 3.37)

Gene ID	Description
34375_at, 875_o_at	chemokine (c-c motif) ligand 2
40385_at	chemokine (c-c motif) ligand 20
36103_at	chemokine (c-c motif) ligand 3
36674_at	chemokine (c-c motif) ligand 4
408_at	chemokine (c-c motif) ligand 1 (melanoma growth stimulating activity, alpha)
1369_s_at, 35372_r_at	interleukin 8

Gene Group 2 (Enrichment Score: 2.89)

Gene ID	Description
1857_at	smad, mothers against dec homology 7 (drosophila)
39421_at	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)
36999_at	jumonji, at rich interactive domain 1a (rbbe2-like)
1994_at	activating transcription factor 2
1895_at, 32583_at	v-jun sarcoma virus 17 oncogene homolog (avian)
35768_at	ring finger protein 40
36226_r_at	salivary factor proline/glutamine-rich (polypyrimidine tract binding protein associated)
789_at	early growth response 1

Step 6: Now choose another DAVID Tool

For example, Functional Annotation Tool

DAVID 2006: functional annotation result summary - Microsoft Internet Explorer

Address: <http://david.abcc.ncifcrf.gov/tools.jsp>

Analysis Wizard
DAVID Bioinformatic Resources 2006, NIAID/NIH

Home | Start Analysis | **Shortcut to DAVID Tools** | Technical Center | Archives | Term of Service | DAVID Forum | Credits | About Us

Upload | **List** | Background

Gene List Manager

Select to limit annotations by one or more species [Help](#)

- Use All Species -
HOMO SAPIENS(403)
SYNTHETIC.CONSTRUCT(6)

Select

List Manager [Help](#)

Demo_List_2

Select List to:

Use Rename
Remove Combine

Show Gene List new!

Analysis Wizard

Step 1. Successfully submitted gene list
Current Gene List: Demo_List_2
Current Background: HOMO SAPIENS

Step 2. Analyze above gene list with one of DAVID tools

[Which DAVID tools to use?](#)

↪ [Functional Annotation Tool](#) ←

- [Functional Annotation Clustering](#)
- [Functional Annotation Chart](#)
- [Functional Annotation Table](#)

↪ [Gene Functional Classification Tool](#)

↪ [Gene ID Conversion Tool](#)

↪ [Show Gene List Tool](#)

[Tell us how you like the tool](#)
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Internet

Step 8. View and explore results of annotation cluster

http://david.abcc.ncifcrf.gov - DAVID: Database for Annotation, Visualization, and Integrated D - Microsoft Internet Explorer

DAVID Bioinformatic Resources 2006
National Institute of Allergy and Infectious Diseases (NIAID), NIH

Functional Annotation Clustering

Current Gene List: Demo_List_2
394 DAVID IDs

Options Classification Stringency Medium

Rerun using options Create Sublist Download File

Annotation Cluster 1		Enrichment Score: 5.38			
<input type="checkbox"/>	GOTERM_BP_ALL	negative regulation of biological process	RT	40	1.1E-6
<input type="checkbox"/>	GOTERM_BP_ALL	negative regulation of cellular process	RT	38	1.2E-6
<input type="checkbox"/>	GOTERM_BP_ALL	negative regulation of physiological process	RT	35	5.3E-6
<input type="checkbox"/>	GOTERM_BP_ALL	negative regulation of cellular physiological process	RT	32	4.2E-5
Annotation Cluster 2		Enrichment Score: 4.36			
<input type="checkbox"/>	GOTERM_BP_ALL	cell communication	RT	116	1.4E-6
<input type="checkbox"/>	GOTERM_BP_ALL	signal transduction	RT	106	8.0E-6
<input type="checkbox"/>	GOTERM_MF_ALL	signal transducer activity	RT	82	7.6E-3
Annotation Cluster 3		Enrichment Score: 3.75			
<input type="checkbox"/>	GOTERM_BP_ALL	response to stress	RT	54	6.3E-8
<input type="checkbox"/>	GOTERM_BP_ALL	inflammatory response	RT	19	1.2E-6
<input type="checkbox"/>	GOTERM_BP_ALL	response to external stimulus	RT	29	1.3E-5
<input type="checkbox"/>	GOTERM_BP_ALL	response to pest, pathogen or parasite	RT	30	2.4E-5
<input type="checkbox"/>	GOTERM_BP_ALL	response to wounding	RT	24	2.7E-5
<input type="checkbox"/>	GOTERM_BP_ALL	response to other organism	RT	30	7.2E-5
<input type="checkbox"/>	GOTERM_BP_ALL	response to stimulus	RT	81	2.5E-3
<input type="checkbox"/>	GOTERM_BP_ALL	organismal physiological process	RT	73	7.3E-3
<input type="checkbox"/>	GOTERM_BP_ALL	response to biotic stimulus	RT	43	1.0E-2

Step 9: Gene back to the analysis wizard and select next DAVID tool

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Upload List Background

Gene List Manager

Select to limit annotations by one or more species [Help](#)

- Use All Species -
HOMO SAPIENS(403)
SYNTHETIC.CONSTRUCT(6)

Select

List Manager [Help](#)

Demo_List_2

Select List to:

Use Rename
Remove Combine

Show Gene List new!

Analysis Wizard

[Tell us how you like the tool](#)
[Contact us for questions](#)

Step 1. Successfully submitted gene list
Current Gene List: Demo_List_2
Current Background: HOMO SAPIENS

Step 2. Analyze above gene list with one of DAVID tools

↓

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[Which DAVID tools to use?](#)

Internet