

# The Screen Shots of Anticipated Results

Analysis of Large Gene List Using  
DAVID Bioinformatics Resources

## Note:

- Only major steps are shown in the document
- There are many other small and fine functions provided by DAVID
- Steps and sub-step labeled in this document are consistent with that in protocol manuscript

# Step 1: Submit gene list or use built-in demo list 2

## 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  
Provides a rapid means to reduce large lists of genes into functionally related groups of genes to help unravel the biological context 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.

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

### Note

Click on "Start Analysis"

## Submit a gene list

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

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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

An example:

Copy/paste IDs to "Box A" -> Select Identifier as "Affy\_ID" -> List Type as "Gene List" -> Click "Submit" button

1007\_g\_at  
1052\_at  
121\_at  
117\_at  
1255\_g\_at  
1294\_at  
1316\_at  
1320\_at  
1403\_i\_at  
1431\_at  
1438\_at  
1487\_at  
1484\_f\_at  
1598\_g\_at

Step 1. Submit your gene list through left panel.

Tell us how you like the tool  
Contact us for questions

### Note

Follow sub steps:  
i, ii, iii, iv.

# Step 2: Tool Main Menu Page to Access DAVID Tools/Modules

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

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 <sup>new!</sup>

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](#)  
[Contact us for questions](#)

## Note

- 1) A central page to access or switch to each DAVID tool/module
- 2) Get back to this page by clicking on "start analysis" no matter where you are.

# Step 3: Gene Name Batch Viewer

## Gene Name Batch Viewer Page



### Gene Name Batch Viewer

DAVID Bioinformatics Resources 2008, NIAID/NIH

[Home](#) [Start Analysis](#) [Shortcut to DAVID Tools](#) [Technical Center](#) [Downloads & APIs](#) [Term of Service](#) [Why DAVID?](#) [About Us](#)

**Upload** **List** **Background**

#### Gene List Manager

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

- Use All Species -  
Homo sapiens(18)

Select

#### List Manager [Help](#)

demolist2  
null  
null

Select List to:

Use

Show Gene List <sup>new!</sup>

### Gene List Report

[Help and Manual](#)

**Current Gene List:** null  
**Current Background:** Homo sapiens

**18 Gene(s)** [Download File](#)

AFFY_ID	Gene Name	Related Genes	Species
875_G_AT, 34375_AT	<a href="#">chemokine (c-c motif) ligand 2</a>	RG	<a href="#">Homo sapiens</a>
39407_AT	<a href="#">bone morphogenetic protein 1</a>	RG	<a href="#">Homo sapiens</a>
36101_S_AT, 36100_AT, 1953_AT	<a href="#">vascular endothelial growth factor</a>	RG	<a href="#">Homo sapiens</a>
33012_AT	<a href="#">tumor necrosis factor (ligand) superfamily, member 8</a>	RG	<a href="#">Homo sapiens</a>
32464_AT	<a href="#">defensin, beta 4</a>	RG	<a href="#">Homo sapiens</a>
1520_S_AT, 39402_AT	<a href="#">interleukin 1, beta</a>	RG	<a href="#">Homo sapiens</a>
33092_AT	<a href="#">formyl peptide receptor-like 2</a>	RG	<a href="#">Homo sapiens</a>
36103_AT	<a href="#">chemokine (c-c motif) ligand 3</a>	RG	<a href="#">Homo sapiens</a>
1548_S_AT	<a href="#">interleukin 10</a>	RG	<a href="#">Homo sapiens</a>
40385_AT	<a href="#">chemokine (c-c motif) ligand 20</a>	RG	<a href="#">Homo sapiens</a>
41169_AT, 189_S_AT	<a href="#">plasminogen activator, urokinase receptor</a>	RG	<a href="#">Homo sapiens</a>
408_AT	<a href="#">chemokine (c-x-c motif) ligand 1 (melanoma growth stimulating activity, alpha)</a>	RG	<a href="#">Homo sapiens</a>
37310_AT	<a href="#">plasminogen activator, urokinase</a>	RG	<a href="#">Homo sapiens</a>
1369_S_AT, 35372_R_AT	<a href="#">interleukin 8</a>	RG	<a href="#">Homo sapiens</a>
1263_AT	<a href="#">interleukin 3 (colony-stimulating factor, multiple)</a>	RG	<a href="#">Homo sapiens</a>
259_S_AT, 1852_AT	<a href="#">tumor necrosis factor (tnf superfamily, member 2)</a>	RG	<a href="#">Homo sapiens</a>
887_AT	<a href="#">growth differentiation factor 1</a>	RG	<a href="#">Homo sapiens</a>
36674_AT	<a href="#">chemokine (c-c motif) ligand 4</a>	RG	<a href="#">Homo sapiens</a>

### Note

- 1) Click on gene name will lead to more detail info.
- 2) "RG" means "Related Genes" search function

# Step 4. Run and explore results of Gene Functional Classification

## Tool Menu Central Page

DAVID 2006: functional annotation result summary - Microsoft Internet Explorer

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

### Analysis Wizard

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(1)

Select

List Manager [Help](#)

Demo\_List\_2

Select List for:

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

- [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 Contact us for](#)

[Which DAVID tool](#)

## Gene Functional Classification Page

DAVID 2006: Gene Functional Classification - Microsoft Internet Explorer

Address: http://david.abcc.ncifcrf.gov/gene2gene.jsp

### Gene Functional Classification Tool

DAVID Bioinformatic Resources 2006, NIAID/NIH

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Upload **List** Background

#### Gene Functional Classification

Current Gene List: Demo\_List\_2  
Current Background: HOMO SAPIENS  
394 DAVID IDs

Options **Classification Stringency** Medium

16 Cluster(s) [Download File](#)

Gene Group 1		Enrichment Score: 3.37	BG
1	<input type="checkbox"/> 34375_at, 875_g_at	chemokine (c-c motif) ligand 2	
2	<input type="checkbox"/> 40385_at	chemokine (c-c motif) ligand 20	
3	<input type="checkbox"/> 36103_at	chemokine (c-c motif) ligand 3	
4	<input type="checkbox"/> 36674_at	chemokine (c-c motif) ligand 4	
5	<input type="checkbox"/> 408_at	chemokine (c-c motif) ligand 1 (melanoma growth stimulating activity, alpha)	
6	<input type="checkbox"/> 1369_s_at, 35372_r_at	interleukin 8	

Gene Group 2		Enrichment Score: 2.89	BG
1	<input type="checkbox"/> 1857_at	smad, mothers against dec homology 7 (drosophila)	
2	<input type="checkbox"/> 39421_at	nut-related transcription factor 1 (acute myeloid leukemia 1; sm1 oncogene)	
3	<input type="checkbox"/> 36999_at	jumonji, at rich interactive domain 1a (rbbp2-like)	
4	<input type="checkbox"/> 1994_at	activating transcription factor 2	
5	<input type="checkbox"/> 1895_at, 32583_at	v-jun sarcoma virus 17 oncogene homolog (avian)	
6	<input type="checkbox"/> 35768_at	ring finger protein 40	
7	<input type="checkbox"/> 36226_r_at	splicing factor, proline/abudamine-rich (polypyrimidine tract binding protein associated)	
8	<input type="checkbox"/> 789_at	early growth response 1	

**Note**

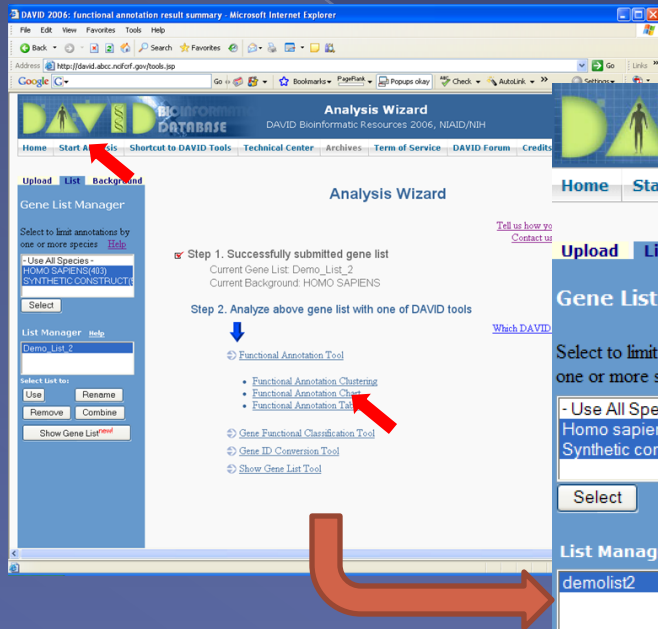
- 1) Gene functional groups are separated by the blue rows
- 2) A set of functions provided in the blue row area for each group





# Step 5: Select annotation categories and run Functional Annotation Chart

## Tool Menu Central Page



**Note**

- 1) Expand the tree structure to select annotation categories of interests
- 2) Or use default categories
- 3) Click on according button to run functions

## Select annotation categories



## Annotation Summary Results

**Current Gene List: demolist2** 394 DAVID IDs  
**Current Background: Homo sapiens** Check Defaults  Clear All

**Main Accessions (0 selected)**  
 **Other Accessions (0 selected)**  
 **Gene Ontology (3 selected)**  
 **Protein Domains (3 selected)**  
 **Pathways (3 selected)**

Category	Percentage	Count	Chart
<input checked="" type="checkbox"/> BBID	8%	34	<input type="button" value="Chart"/>
<input checked="" type="checkbox"/> BIOCARTA	19%	78	<input type="button" value="Chart"/>
<input type="checkbox"/> EC_NUMBER	23%	91	<input type="button" value="Chart"/>
<input type="checkbox"/> KEGG_COMPOUND	10%	40	<input type="button" value="Chart"/>
<input checked="" type="checkbox"/> KEGG_PATHWAY	37%	149	<input type="button" value="Chart"/>
<input type="checkbox"/> KEGG_REACTION	10%	40	<input type="button" value="Chart"/>
<input type="checkbox"/> PANTHER_PATHWAY	4%	18	<input type="button" value="Chart"/>

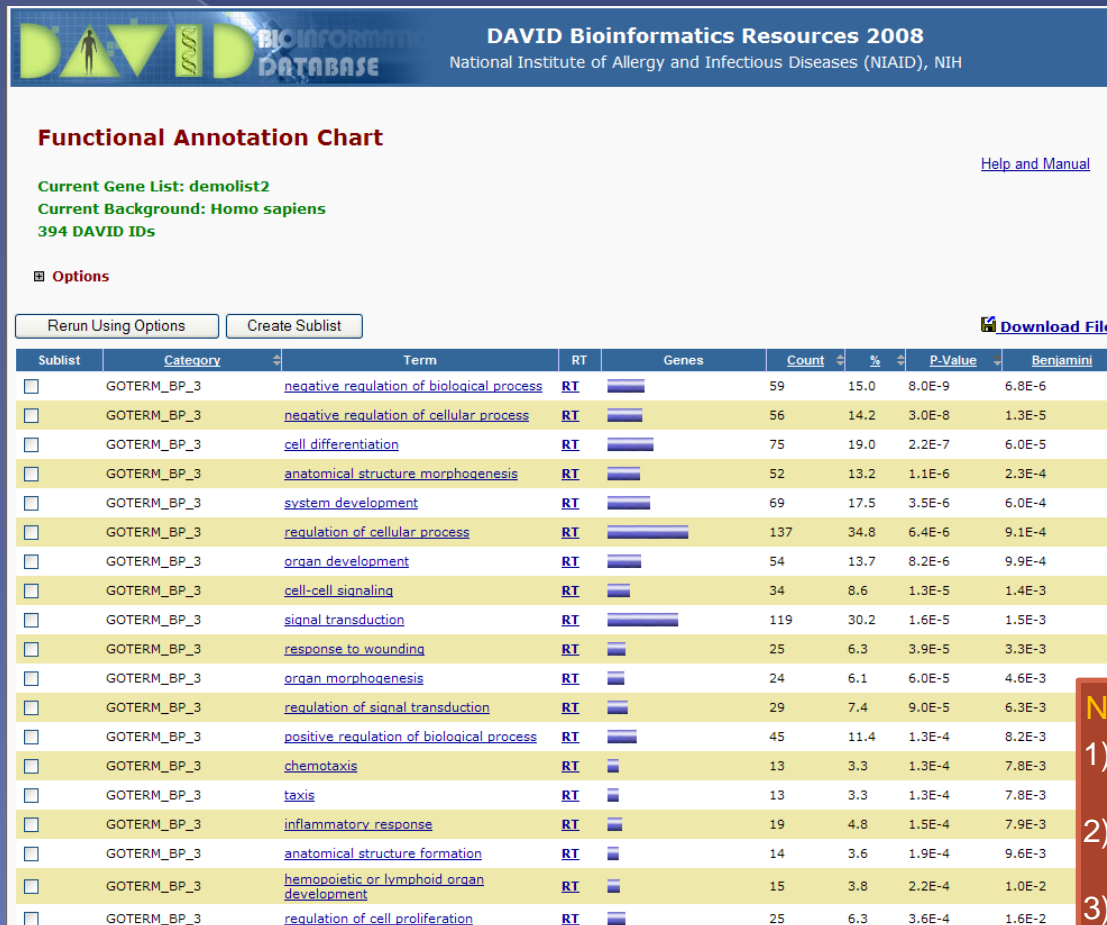
- General Annotations (0 selected)**
- Functional Categories (3 selected)**
- Protein Interactions (0 selected)**
- Literature (0 selected)**
- Disease (1 selected)**
- Tissue Expression**

### Combined View for Selected Annotation

- 
-

# Step 6: Explore results of Functional Annotation Chart

## Results of Functional Annotation Chart



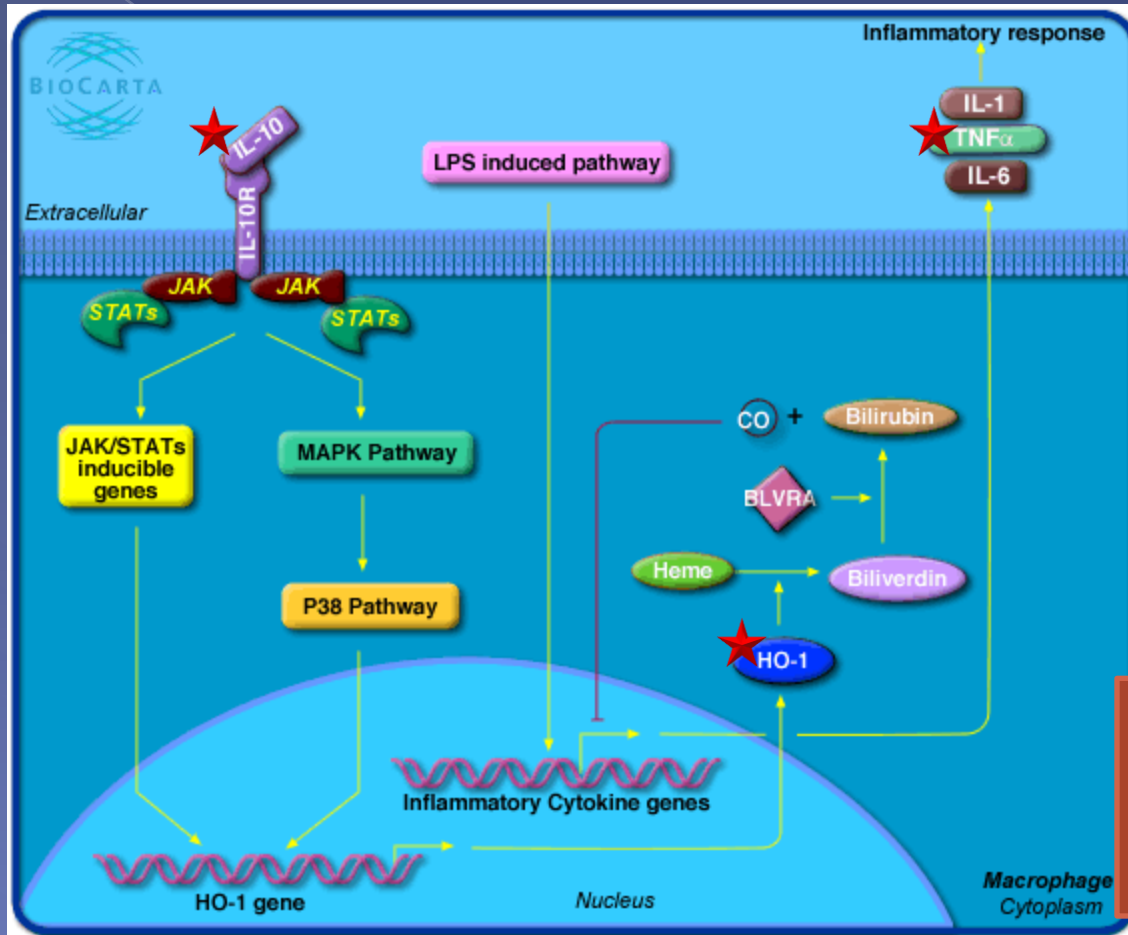
### Note

- 1) Click on term name leading to details
- 2) Click on blue bar to list all associated genes
- 3) Click on "RT" to list other related terms
- 4) Sort result by different columns



continued

Visualization of genes on the pathway of interest by clicking on pathway name in previous result page to



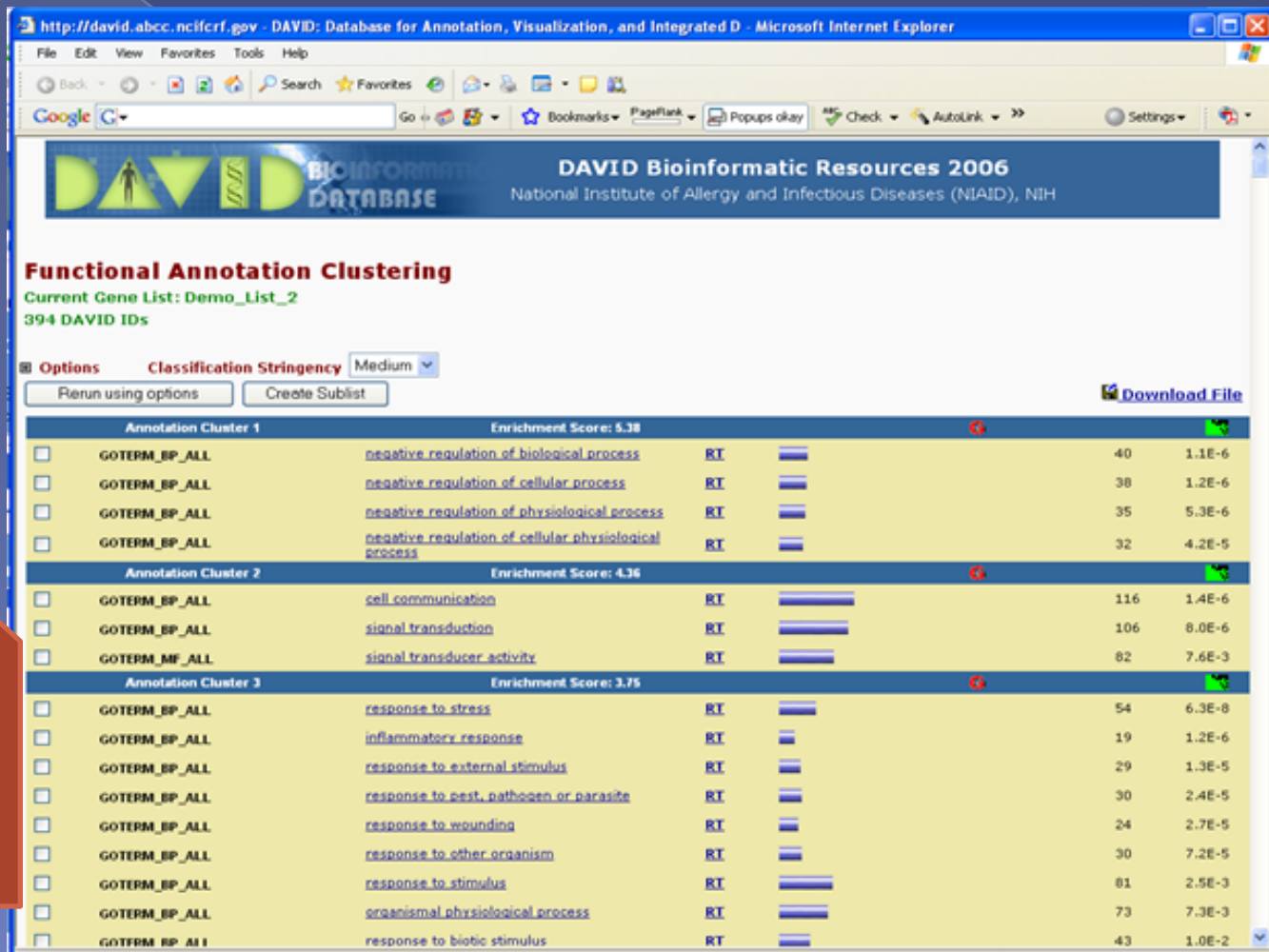
Note

Red stars indicate the association between your input genes and pathway genes

# Step 7. Select annotation categories and run Functional Annotation Cluster: See step 5 for details

## Step 8. View and explore results of annotation cluster

Results of Functional Annotation Cluster



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

### Note

- 1) Term clusters are separated by the blue rows
- 2) A set of functions provided in the blue row area for each cluster

# Step 9. Select annotation categories and run Functional Annotation Table: See step 5 for details

# Step 10. View and explore results of annotation table

## Results of Functional Annotation Table

DAVID Bioinformatics Resources 2008  
National Institute of Allergy and Infectious Diseases (NIAID), NIH

### Functional Annotation Table

Current Gene List: demolist2

394 DAVID IDs

337 records [Download File](#)

38842_AT	activated leukocyte cell adhesion molecule	Related Genes	Homo sapiens
GOTERM_BP_3		signal transduction,	
KEGG_PATHWAY		Cell adhesion molecules (CAMs),	
1244_AT	signal transducer and activator of transcription 2, 113kda	Related Genes	Homo sapiens
GOTERM_BP_3		nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, transcription, DNA-dependent, signal transduction, response to virus, regulation of gene expression, regulation of metabolic process, regulation of cellular metabolic process, biopolymer metabolic process, regulation of transcription, regulation of cellular process, response to other organism,	
BIOCARTA		IFN alpha signaling pathway,	
KEGG_PATHWAY		Jak-STAT signaling pathway,	
1461_AT	nuclear factor of kappa light polypeptide gene enhancer in b-cells inhibitor, alpha	Related Genes	Homo sapiens
GOTERM_BP_3		response to molecule of bacterial origin, transport, signal transduction, protein localization, cell death, response to bacterium, regulation of signal transduction, protein transport, cell differentiation, maintenance of cellular protein localization, regulation of cell proliferation, response to dsRNA, establishment of protein localization, maintenance of protein localization, regulation of cell differentiation, intracellular transport, organ development, negative regulation of biological process, negative regulation of cellular process, hemopoietic or lymphoid organ development, system development, regulation of developmental process, regulation of cellular process, regulation of transport, negative regulation of developmental process, regulation of binding, cytoplasmic sequestering of protein, cellular localization, establishment of cellular localization, maintenance of cellular localization, response to other organism,	
BIOCARTA		The 4-1BB-dependent immune response, HIV-1 Nef, Acetylation and Deacetylation of RelA in The Nucleus, Influence of Ras and Rho proteins on G1 to S Transition, AKT Signaling Pathway, ATM Signaling Pathway, CD40L Signaling Pathway, Cadmium induces DNA synthesis and proliferation in macrophages, Induction of apoptosis through DR3 and DR4/5 Death Receptors, Erythropoietin mediated neuroprotection through NF-kB, fMLP induced chemokine gene expression in HMC-1 cells, Signal transduction through IL1R, Keratinocyte Differentiation, MAPKinase Signaling Pathway, NF-kB Signaling Pathway, NFkB activation by Nontypeable Hemophilus influenzae, Activation of PKC through G protein coupled receptor, Mechanism of Gene Regulation by Peroxisome Proliferators via PPAR(alpha), Double Stranded RNA Induced Gene Expression, TNF/Stress Related Signaling, T Cell Receptor Signaling Pathway, Chaperones modulate interferon Signaling Pathway, TNFR2 Signaling Pathway, Toll-Like Receptor Pathway, Neuropeptides VIP and PACAP inhibit the apoptosis of activated T cells,	
KEGG_PATHWAY		Apoptosis, Toll-like receptor signaling pathway, T cell receptor signaling pathway, B cell receptor signaling pathway, Adipocytokine signaling pathway, Epithelial cell signaling in Helicobacter pylori infection, Prostate cancer, Chronic myeloid leukemia, Small cell lung cancer,	
35687_AT	mature t-cell proliferation 1	Related Genes	Homo sapiens
GOTERM_BP_3		cell cycle process, regulation of cellular process, regulation of cell cycle,	
1267_AT	protein kinase c, eta	Related Genes	Homo sapiens
GOTERM_BP_3		phosphorus metabolic process, signal transduction, protein metabolic process, biopolymer metabolic process, cellular macromolecule metabolic process,	
KEGG_PATHWAY		Tight junction,	

### Note

- 1) Each block separated by blue rows contains the contents for one gene
- 2) A set of hyperlinks lead to more detailed descriptions