

# Quick Start Tutorial for the DAVID Bioinformatics Resources

Last Updated February 2022

# Start Analysis Wizard

**DAVID Bioinformatics Resources (2021 Update)**  
Laboratory of Human Retrovirology and Immunoinformatics (LHRI)

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

## Overview

The **D**atabase for **A**nnotation, **V**isualization and **I**ntegrated **D**iscovery (**DAVID**) provides a comprehensive set of functional annotation tools for investigators to understand the biological meaning behind large lists of genes. These tools are powered by the comprehensive **DAVID Knowledgebase** built upon the DAVID Gene concept which pulls together multiple sources of functional annotations. For any given gene list, DAVID tools are able to:

- Identify enriched biological themes, particularly GO terms
- Discover enriched functional-related gene groups
- Cluster redundant annotation terms
- Visualize genes on BioCarta & KEGG pathway maps
- Display related many-genes-to-many-terms on 2-D view.
- Search for other functionally related genes not in the list
- List interacting proteins
- Explore gene names in batch
- Link gene-disease associations

## Hot Links

### 🔥 Multiple positions available in LHRI 🔥

The Laboratory of Human Retrovirology and Immunoinformatics (LHRI) has collaborated with the National Institute of Allergy and Infectious Diseases (NIAID) and supported NIAID clinical trials for patients infected with HIV mutants resisting anti-retroviral therapy. LHRI has isolated the multiple-class drug-resistant (MDR) variants from patients and characterized each variant's drug sensitivity and infectivity. The study aims to define salvage therapy and develop novel therapy (chemotherapy and immunotherapy). During the investigation, LHRI has characterized the emergence of novel mutations on drug susceptibility and viral replication. LHRI is a pioneer in researching the anti-viral cytokine, Interleukin-27, DNA-repair protein (Ku70)-mediated innate immune response against HIV and other virus co-infection, and novel subsets of immune cells. LHRI maintains the Database for Annotation, Visualization and Integrated Discovery ( **DAVID** ).

# Submit gene list or use built-in demo lists

The screenshot shows the DAVID Analysis Wizard interface. At the top, there is a navigation bar with the following links: Home, Start Analysis, Shortcut to DAVID Tools, Technical Center, Downloads & APIs, Term of Service, About DAVID, and About LHRI. The main header reads "Analysis Wizard" and "DAVID Bioinformatics Resources (2021 Update), NIAID/NIH". Below the navigation bar, there are three tabs: "Upload", "List", and "Background". The "Upload" tab is selected, and the "Upload Gene List" panel is displayed. The panel contains the following sections:

- Upload Gene List**: Includes links for "Demolist 1", "Demolist 2", and "Upload Help".
- Step 1: Enter Gene List**: Contains a text input field "A: Paste a list" with the example text "IL2", "IL4", and "IL6". A "Clear" button is located to the right of the input field.
- Or**: A section separator.
- B: Choose From a File**: Contains a "Choose File" button and the text "No file chosen". There is also a checkbox for "Multi-List File" with a question mark icon.
- Step 2: Select Identifier**: Contains a dropdown menu currently set to "OFFICIAL\_GENE\_SYMBOL".
- Step 2a: Select species**: Contains a text input field with the placeholder "Type your species name or id (e.g. Homo sapiens; 9606)".
- Step 3: List Type**: Contains two radio buttons: "Gene List" (which is selected) and "Background".
- Step 4: Submit List**: Contains a "Submit List" button.

First, switch to the Upload tab

1. Click on a demo list or paste or upload your gene/protein list

2. Select the identifier type corresponding to your list.

2a. If "OFFICIAL\_GENE\_SYMBOL" is selected, a new parameter will appear allowing you to indicate your species of interest by typing the name or taxonomy id.

3. Choose your list type. Note: A gene list must be uploaded before a background.

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_s_at
1053_at
117_at
121_at
1255_g_at
1294_at
1316_at
1320_at
1405_i_at
1431_at
1438_at
1487_at
1494_f_at
1598_g_at
```

Tell us how you like the tool  
Contact us for questions

# Verify that your list has been uploaded and begin analysis

**Analysis Wizard**  
DAVID Bioinformatics Resources (2021 Update), NIAID/NIH

Home Start Analysis **Shortcut to DAVID Tools** Technical Center Downloads & APIs Term of Service About DAVID About LHRI

Upload **List** Background

### Gene List Manager

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

- Use All Species -  
Homo sapiens(390)  
Unknown(13)

Select Species

List Manager [Help](#)

demolist2

Select List to:

Use Rename  
Remove Combine  
Show Gene List

[View Unmapped Ids](#)

### Analysis Wizard

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

**Step 1. Successfully submitted gene list**  
Current Gene List: demolist2  
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
- Gene Name Batch Viewer

You can always choose a tool through the main menu shortcut

In the List tab, you will see species listed for your list and a list name.

Choose A DAVID Tool to begin exploring your gene list. Help choosing is available in DAVID and at the end of this tutorial.

# Gene Name Batch Viewer

This tool provides a view containing gene names and taxonomies for a list of identifiers as well as links to more specific annotation for a given gene (Gene Report) and methods for viewing related genes (Related Genes) from the list or background population. This tool provides a quick and informative look at the list before proceeding with more in-depth analyses. A link is provided to download a tab-delimited file for any tool output in DAVID.

**Gene List Report** [Help and Manual](#)

Current Gene List: demolist2  
Current Background: Homo sapiens  
372 DAVID IDs [Download File](#)

AFFYMETRIX_3PRIME_IVT_ID	Value1	Gene Name	Related Genes	Species
1005_at		<a href="#">dual specificity phosphatase 1(DUSP1)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1007_s_at	2	<a href="#">discoidin domain receptor tyrosine kinase 1(DDR1)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1018_at	2	<a href="#">Wnt family member 10B(WNT10B)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1091_at	2	<a href="#">protein kinase cAMP-dependent type I regulatory subunit beta(PRKAR1B)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1124_at	2	<a href="#">lysine methyltransferase 2A(KMT2A)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1125_s_at	2	<a href="#">CD44 molecule (Indian blood group)(CD44)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1139_at	2	<a href="#">G protein subunit alpha 13(GNA13)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1148_s_at	2	<a href="#">neuregulin 1(NRG1)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1167_s_at	2	<a href="#">matrix metalloproteinase 15(MMP15)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1237_at	2	<a href="#">immediate early response 3(IER3)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1242_at	2	<a href="#">ETS2 repressor factor(ERF)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1244_at	2	<a href="#">signal transducer and activator of transcription 2(STAT2)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1258_s_at	2	<a href="#">ERCC excision repair 4, endonuclease catalytic subunit(ERCC4)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1263_at	2	<a href="#">interleukin 3(IL3)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1267_at	2	<a href="#">protein kinase C eta(PRKCH)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1270_at	2	<a href="#">RAP1 GTPase activating protein(RAP1GAP)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1276_g_at	2	<a href="#">RNA binding protein, mRNA processing factor(RBPMS)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
131_at	2	<a href="#">TATA-box binding protein associated factor 11(TAF11)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1332_f_at	2	<a href="#">growth hormone 1(GH1)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1369_s_at	2	<a href="#">C-X-C motif chemokine ligand 8(CXCL8)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
136_at	2	<a href="#">G protein-coupled receptor 31(GPR31)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1372_at	2	<a href="#">TNF alpha induced protein 6(TNFAIP6)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>
1385_at	2	<a href="#">transforming growth factor beta induced(TGFBI)</a>	<a href="#">RG</a>	<a href="#">Homo sapiens</a>

# DAVID Gene Report

The DAVID Gene Report contains annotations that are more specific to a given gene. The DAVID Gene Report header will contain the user's original uploaded gene list identifier, the DAVID Gene Name, including the gene symbol, a link to find Related Genes in the user's list or background gene set, based on shared functional annotation, and the taxonomy. Links with further information for the gene specific data are also provided when available. A link is provided to download a tab-delimited file for any tool output in DAVID.

## Gene Report

[Help and Manual](#)  
[Download File](#)

List Id: 1005_at	dual specificity phosphatase 1(DUSP1)	Related Genes	Homo sapiens
CHROMOSOME	5,		
CYTOGENETIC_LOCATION	5q35.1,		
ENSEMBL_GENE_ID	<a href="#">ENSG00000120129</a> ,		
ENTREZ_GENE_ID	<a href="#">1843</a> ,		
ENTREZ_GENE_SUMMARY	The protein encoded by this gene is a phosphatase with dual specificity for tyrosine and threonine. The encoded protein can dephosphorylate MAP kinase MAPK1/ERK2, which results in its involvement in several cellular processes. This protein appears to play an important role in the human cellular response to environmental stress as well as in the negative regulation of cellular proliferation. Finally, the encoded protein can make some solid tumors resistant to both chemotherapy and radiotherapy, making it a target for cancer therapy. [provided by RefSeq, Aug 2017],		
GENERIF_SUMMARY	<a href="#">CL100 down regulation is associated with advanced stages of epithelial ovarian neoplasms, glucocorticoids synergistically enhance NTHi-induced TLR2 expression via specific up-regulation of the MAPK phosphatase-1 (MKP-1) that, in turn, leads to dephosphorylation and inactivation of p38 MAPK, Data suggest that mitogen-activated protein kinase phosphatase 1 (MKP-1) participates in a negative-feedback loop which regulates p38 function and that dexamethasone may inhibit proinflammatory gene expression in part by inducing MKP-1 expression., Expression of MKP-1 may be associated with shorter progression-free survival times, role of activation on cAMP-dependent protein kinase enhancement of CYP17 transcription, our data suggest that deletion of the hv3005 and the 3-30.3 genes may predispose individual SLE patients to the development of lupus nephritis, MKP1 is a transcriptional target of p53 involved in cell cycle regulation, Cardiopulmonary bypass reduces ERK1/2 and p38 activity in peripheral tissue, potentially by MKP-1., requirement of MAPK phosphatase-1 induction and therefore, inhibition of p38 MAPK in the ANP-mediated inhibition of TNF-alpha-induced expression of MCP-1, Jak2 is required for Ang II-induced ERK2 inactivation via induction of MKP-1 gene expression., Here we found that hypoxia induces MKP-1 expression in human hepatoma cells HepG2 in a time-dependent manner, the molecular mechanisms underlying the survival function of NGF in CESS B cell line predominantly</a>		

# Functional Annotation Summary

The Functional Annotation Summary provides annotation type specific annotation for the user's list including gene counts and percentages and organizes the annotation types into categories. From the summary, a user can use the Functional Annotation Table, Functional Annotation Chart or Functional Annotation Clustering tools with one or multiple annotation types. Default selections are made for quick usage.

**Annotation Summary Results**

Current Gene List: demolist2  
Current Background: Homo sapiens

372 DAVID IDs  
Check Defaults  [Clear All](#) [Help and Tool Manual](#)

**Disease (2 selected)**

<input type="checkbox"/> DISGENET	69.1%	257	Chart	
<input type="checkbox"/> GAD_DISEASE	79.6%	296	Chart	
<input type="checkbox"/> GAD_DISEASE_CLASS	79.6%	296	Chart	
<input checked="" type="checkbox"/> OMIM_DISEASE	36.6%	136	Chart	
<input checked="" type="checkbox"/> UP_KW_DISEASE	33.9%	126	Chart	

**Functional\_Annotations (6 selected)**

- Gene\_Ontology (3 selected)
- General\_Annotations (0 selected)
- Interactions (1 selected)
- Literature (0 selected)
- Pathways (3 selected)
- Protein\_Domains (4 selected)
- Tissue\_Expression (0 selected)

\*\*\*Red annotation categories denote DAVID defined defaults\*\*\*

**Combined View for Selected Annotation**

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

# Functional Annotation Table

The Functional Annotation Table provides annotations associated with a user's list of genes for user-selected categories in tabular format. This tool quickly links the user's list to the breadth of annotation contained in the DAVID Knowledgebase with no statistical inference and is well suited for looking at genes on an individual basis, providing links to more detailed information about the associated annotation. A link is provided to download a tab-delimited file for any tool output in DAVID.

## Functional Annotation Table

[Help and Manual](#)

Current Gene List: demolist2

Current Background: Homo sapiens

372 DAVID IDs

365 record(s)

[Download File](#)

612_s_at	2',3'-cyclic nucleotide 3' phosphodiesterase(CNP)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	<a href="#">microtubule cytoskeleton organization</a> , <a href="#">chemical synaptic transmission</a> , <a href="#">axonogenesis</a> , <a href="#">aging</a> , <a href="#">adult locomotory behavior</a> , <a href="#">cyclic nucleotide catabolic process</a> , <a href="#">response to toxic substance</a> , <a href="#">substantia nigra development</a> , <a href="#">forebrain development</a> , <a href="#">response to lipopolysaccharide</a> , <a href="#">regulation of mitochondrial membrane permeability</a> , <a href="#">oligodendrocyte differentiation</a> ,		
GOTERM_CC_DIRECT	<a href="#">extracellular space</a> , <a href="#">cytoplasm</a> , <a href="#">mitochondrial outer membrane</a> , <a href="#">mitochondrial inner membrane</a> , <a href="#">microtubule</a> , <a href="#">plasma membrane</a> , <a href="#">microvillus</a> , <a href="#">membrane</a> , <a href="#">pseudopodium</a> , <a href="#">myelin sheath abaxonal region</a> , <a href="#">myelin sheath adaxonal region</a> , <a href="#">melanosome</a> , <a href="#">synapse</a> , <a href="#">perinuclear region of cytoplasm</a> , <a href="#">extracellular exosome</a> ,		
GOTERM_MF_DIRECT	<a href="#">RNA binding</a> , <a href="#">2',3'-cyclic-nucleotide 3'-phosphodiesterase activity</a> , <a href="#">protein binding</a> , <a href="#">cyclic nucleotide binding</a> ,		
INTERPRO	<a href="#">Cyclic nucleotide phosphodiesterase</a> , <a href="#">RNA ligase/cyclic nucleotide phosphodiesterase</a> , <a href="#">P-loop containing nucleoside triphosphate hydrolase</a> ,		
OMIM_DISEASE	<a href="#">Leukodystrophy</a> , <a href="#">hypomyelinating_20</a> ,		
PIR_SUPERFAMILY	<a href="#">2',3'-cyclic-nucleotide 3'-phosphodiesterase</a> ,		
UP_KW_CELLULAR_COMPONENT	<a href="#">Membrane</a> ,		
UP_KW_DISEASE	<a href="#">Neurodegeneration</a> , <a href="#">Leukodystrophy</a> ,		
UP_KW_MOLECULAR_FUNCTION	<a href="#">Hydrolase</a> , <a href="#">RNA-binding</a> ,		
UP_KW_PTM	<a href="#">Lipoprotein</a> , <a href="#">Methylation</a> , <a href="#">Phosphoprotein</a> , <a href="#">Prenylation</a> ,		
UP_SEQ_FEATURE	<a href="#">ACT_SITE:Proton acceptor</a> , <a href="#">ACT_SITE:Proton donor</a> , <a href="#">BINDING:Substrate</a> , <a href="#">LIPID:S-farnesyl cysteine</a> , <a href="#">PROPEP:Removed in mature form</a> ,		
35345_at	3-hydroxy-3-methylglutaryl-CoA synthase 2(HMGCS2)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	<a href="#">kidney development</a> , <a href="#">liver development</a> , <a href="#">acetyl-CoA metabolic process</a> , <a href="#">cholesterol biosynthetic process</a> , <a href="#">brain development</a> , <a href="#">midgut development</a> , <a href="#">response to nutrient</a> , <a href="#">response to temperature stimulus</a> , <a href="#">response to xenobiotic stimulus</a> , <a href="#">response to metal ion</a> , <a href="#">farnesyl diphosphate biosynthetic process</a> , <a href="#">mevalonate pathway</a> , <a href="#">regulation of metabolic process</a> , <a href="#">lung development</a> , <a href="#">cellular response to insulin stimulus</a> , <a href="#">multicellular organismal response to stress</a> , <a href="#">response to testosterone</a> , <a href="#">response to glucagon</a> , <a href="#">response to triglyceride</a> , <a href="#">response to monosaccharide</a> , <a href="#">response to prostaglandin F</a> , <a href="#">response to starvation</a> , <a href="#">response to ethanol</a> , <a href="#">ketone body biosynthetic process</a> , <a href="#">response to cAMP</a> , <a href="#">response to growth hormone</a> , <a href="#">adipose tissue development</a> , <a href="#">response to linoleic acid</a> , <a href="#">cellular response to lipopolysaccharide</a> , <a href="#">cellular response to amino acid stimulus</a> , <a href="#">cellular response to glucocorticoid stimulus</a> , <a href="#">cellular response to fatty acid</a> ,		
GOTERM_CC_DIRECT	<a href="#">mitochondrion</a> , <a href="#">mitochondrial matrix</a> ,		
GOTERM_MF_DIRECT	<a href="#">hydroxymethylglutaryl-CoA synthase activity</a> , <a href="#">identical protein binding</a> ,		
INTERPRO	<a href="#">Hydroxymethylglutaryl-coenzyme A synthase</a> , <a href="#">active site</a> , <a href="#">Hydroxymethylglutaryl-CoA synthase</a> , <a href="#">eukaryotic</a> , <a href="#">Hydroxymethylglutaryl-coenzyme A synthase</a> , <a href="#">N-terminal</a> , <a href="#">Hydroxymethylglutaryl-coenzyme A synthase C-terminal</a> , <a href="#">Thiolase-like</a> ,		
KEGG_PATHWAY	<a href="#">Valine, leucine and isoleucine degradation</a> , <a href="#">Butanoate metabolism</a> , <a href="#">Terpenoid backbone biosynthesis</a> , <a href="#">PPAR signaling pathway</a> ,		



# Functional Annotation Chart

This tool provides enrichment analysis using a modified Fisher Exact Test to identify the most overrepresented annotation terms associated with a user's gene list as compared to a background gene set. Flexible options are provided to change gene count and p-value thresholds and display different aspects of the analysis. Clicking blue bars will provide details of underlying genes, related terms (RT) can be found based on shared user genes and sublists based on genes underlying one or more terms may be created for drill-down analysis.

## Functional Annotation Chart

[Help and Manual](#)














**Current Gene List: demolist2**  
**Current Background: Homo sapiens**  
**372 DAVID IDs**

**Options**

Thresholds: Count  EASE

Display:  Fold Enrichment  Bonferroni  Benjamini  FDR  Fisher Exact  LT,PH,PT # of Records

**664 chart records** [Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein binding</a>	<a href="#">RT</a>		295	79.3	1.8E-11	1.2E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cytokine-mediated signaling pathway</a>	<a href="#">RT</a>		26	7.0	1.3E-9	3.6E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">identical protein binding</a>	<a href="#">RT</a>		67	18.0	1.7E-8	5.7E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein domain specific binding</a>	<a href="#">RT</a>		20	5.4	7.9E-7	1.7E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of transcription from RNA polymerase II promoter</a>	<a href="#">RT</a>		41	11.0	8.9E-7	1.2E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of transcription from RNA polymerase II promoter</a>	<a href="#">RT</a>		47	12.6	1.3E-6	1.2E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">cytosol</a>	<a href="#">RT</a>		138	37.1	1.4E-6	6.6E-4
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Transcriptional misregulation in cancer</a>	<a href="#">RT</a>		19	5.1	2.4E-6	7.3E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of gene expression</a>	<a href="#">RT</a>		26	7.0	9.5E-6	6.4E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">extracellular exosome</a>	<a href="#">RT</a>		68	18.3	9.9E-6	2.3E-3
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Chagas disease</a>	<a href="#">RT</a>		13	3.5	1.3E-5	1.5E-3
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">NF-kappa B signaling pathway</a>	<a href="#">RT</a>		13	3.5	1.5E-5	1.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">signal transduction</a>	<a href="#">RT</a>		44	11.8	1.8E-5	7.1E-3

# Functional Annotation Clustering

This tool groups similar annotation terms together using the Kappa statistic to determine pairwise similarity scores and a novel fuzzy clustering algorithm. The fuzzy feature of the clustering algorithm allows a term to participate in multiple groups. The tool helps the user focus on biological themes associated with their gene list by reducing redundancy through the grouping of biologically similar terms. This complements the Functional Annotation Chart as some enriched terms may not be grouped if they do not have enough similarity with other terms. As with other tools, options are available for power users and defaults set for quick analyses.

## Functional Annotation Clustering

[Help and Manual](#)

**Current Gene List:** demolist2  
**Current Background:** Homo sapiens  
 372 DAVID IDs

**Options**      **Classification Stringency** Medium ▾

<b>Kappa Similarity</b>	Similarity Term Overlap 3 ▾	Similarity Threshold 0.50 ▾	
<b>Classification</b>	Initial Group Membership 3 ▾	Final Group Membership 3 ▾	Multiple Linkage Threshold 0.50 ▾
<b>Enrichment Thresholds</b>	EASE 1.0		
<b>Display</b>	<input type="checkbox"/> Fold Change	<input type="checkbox"/> Bonferroni	<input checked="" type="checkbox"/> Benjamini <input type="checkbox"/> FDR <input type="checkbox"/> LT,PH,PT

Rerun using options    Create Sublist

**96 Cluster(s)** [Download File](#)

Annotation Cluster	Enrichment Score: 3.15			Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	<a href="#">negative regulation of transcription from RNA polymerase II promoter</a>	RT		41	8.9E-7	1.2E-3
<input type="checkbox"/> GOTERM_BP_DIRECT	<a href="#">positive regulation of transcription from RNA polymerase II promoter</a>	RT		47	1.3E-6	1.2E-3
<input type="checkbox"/> GOTERM_MF_DIRECT	<a href="#">transcriptional repressor activity, RNA polymerase II transcription regulatory region sequence-specific binding</a>	RT		20	2.2E-5	3.2E-3
<input type="checkbox"/> GOTERM_MF_DIRECT	<a href="#">transcription factor activity, sequence-specific DNA binding</a>	RT		27	2.4E-5	3.2E-3
<input type="checkbox"/> GOTERM_MF_DIRECT	<a href="#">DNA binding</a>	RT		46	3.9E-5	4.3E-3
<b>Annotation Cluster 2</b> Enrichment Score: 2.99						
<input type="checkbox"/> GOTERM_CC_DIRECT	<a href="#">nucleoplasm</a>	RT		101	2.9E-5	3.3E-3
<input type="checkbox"/> GOTERM_CC_DIRECT	<a href="#">nucleus</a>	RT		134	5.5E-4	2.1E-2
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	<a href="#">Nucleus</a>	RT		121	6.5E-2	4.8E-1
<b>Annotation Cluster 3</b> Enrichment Score: 2.68						
<input type="checkbox"/> GOTERM_MF_DIRECT	<a href="#">cytokine activity</a>	RT		13	2.9E-4	1.8E-2
<input type="checkbox"/> GOTERM_MF_DIRECT	<a href="#">growth factor activity</a>	RT		11	1.3E-3	5.1E-2
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	<a href="#">Growth factor</a>	RT		8	2.4E-2	6.0E-1

# Gene Functional Classification

This tool allows a user to group genes which are functionally similar together, thereby providing a biological network view of their list. As with the Functional Annotation Clustering tool, this tool uses a Kappa statistic to measure similarity between pairs of genes based on shared association of terms and groups those genes into functionally related groups with a novel fuzzy clustering algorithm. As with other tools, options are available for power users and defaults set for quick analyses.

## Gene Functional Classification Result

[Help and Tool Manual](#)

Current Gene List: demolist2

Current Background: Homo sapiens

372 DAVID IDs

Options Classification Stringency **Medium** ▼

<b>Kappa Similarity</b>	Similarity Term Overlap	Similarity Threshold	
	4 ▼	0.35 ▼	
<b>Classification</b>	Initial Group Membership	Final Group Membership	Multiple Linkage Threshold
	4 ▼	4 ▼	0.50 ▼

Rerun using options

Create Sublist

## 10 Cluster(s)

[Download File](#)

Gene Group 1		Enrichment Score: 3.28	RG	T	
1	<input type="checkbox"/> 40790_at	<a href="#">basic helix-loop-helix family member e40(BHLHE40)</a>			
2	<input type="checkbox"/> 274_at	<a href="#">zinc finger protein 148(ZNF148)</a>			
3	<input type="checkbox"/> 33922_at	<a href="#">PR/SET domain 2(PRDM2)</a>			
4	<input type="checkbox"/> 287_at	<a href="#">activating transcription factor 3(ATF3)</a>			
5	<input type="checkbox"/> 1774_at	<a href="#">MAX dimerization protein 1(MXD1)</a>			
6	<input type="checkbox"/> 36018_at	<a href="#">SRY-box transcription factor 10(SOX10)</a>			
7	<input type="checkbox"/> 34989_at	<a href="#">zinc finger protein 137, pseudogene(ZNF137P)</a>			
Gene Group 2		Enrichment Score: 3.01	RG	T	
1	<input type="checkbox"/> 40385_at	<a href="#">C-C motif chemokine ligand 20(CCL20)</a>			
2	<input type="checkbox"/> 408_at	<a href="#">C-X-C motif chemokine ligand 1(CXCL1)</a>			
3	<input type="checkbox"/> 36674_at	<a href="#">C-C motif chemokine ligand 4(CCL4)</a>			
4	<input type="checkbox"/> 36103_at	<a href="#">C-C motif chemokine ligand 3(CCL3)</a>			
5	<input type="checkbox"/> 35372_r_at, 1369_s_at	<a href="#">C-X-C motif chemokine ligand 8(CXCL8)</a>			
6	<input type="checkbox"/> 875_g_at, 34375_at	<a href="#">C-C motif chemokine ligand 2(CCL2)</a>			

# Gene ID Conversion

This tool can efficiently convert gene/protein identifiers from one identifier type to another at the gene level. The tool can automatically suggest possible identifier types for ambiguous gene/protein identifiers and converted identifiers can be downloaded or submitted back to DAVID as a gene list or background population set.

## Gene Accession Conversion Tool

[Help](#)

### Gene Accession Conversion Statistics

 [Download File](#)

Conversion Summary			Submit Converted List to DAVID as a Gene List				Submit Converted List to DAVID as a Background			
ID Count	In DAVID DB	Conversion	From	To	Species	David Gene Name				
<a href="#">390</a>	Yes	Successful	41382_at	1755	Homo sapiens	deleted in malignant brain tumors 1(DMBT1)				
0	Yes	None	287_at	467	Homo sapiens	activating transcription factor 3(ATF3)				
0	No	None	848_at	7185	Homo sapiens	TNF receptor associated factor 1(TRAF1)				
0	Ambiguous	Pending	2030_at	7481	Homo sapiens	Wnt family member 11(WNT11)				
<b>Total Unique User IDs: 390</b>			41106_at	3783	Homo sapiens	potassium calcium-activated channel subfamily N member 4(KCNN4)				
<b>Summary of Ambiguous Gene IDs</b>			1139_at	10672	Homo sapiens	G protein subunit alpha 13(GNA13)				
ID Count	Possible Source	Convert All	1953_at	7422	Homo sapiens	vascular endothelial growth factor A(VEGFA)				
<b>All Possible Sources For Ambiguous IDs</b>			36018_at	6663	Homo sapiens	SRY-box transcription factor 10(SOX10)				
Ambiguous ID	Possibility	Convert	37206_at	130	Homo sapiens	alcohol dehydrogenase 6 (class V)(ADH6)				
			41736_g_at	22898	Homo sapiens	DENN domain containing 3(DENND3)				
			41438_at	114882	Homo sapiens	oxysterol binding protein like 8(OSBPL8)				
			35472_at	3772	Homo sapiens	potassium inwardly rectifying channel subfamily J member 15(KCNJ15)				
			1461_at	4792	Homo sapiens	NFKB inhibitor alpha(NFKBIA)				



# Which DAVID Tool and Additional Help

++ Highly Applied  
+ Relevant

	Functional Annotation Chart	Functional Annotation Clustering	Functional Annotation Table	Gene Functional Classification	Gene Name Batch Viewer	Gene ID Conversion Tool	DAVID Knowledgebase	DAVID API
Initial glance of major biological functions associated with my gene list	++	++	++	+	+			
Which biological terms/functions are specifically enriched in my gene list?	++	++						
View the genes in my list on related biological pathways	++	++						
Which diseases are associated with my gene list?	++	++						
Which protein functional domains are associated with my gene list?	++	++						
Which other genes frequently interact with the genes in my list?	++	++						
How to group the highly redundant annotations into group?		++						
What are the major gene functional groups in my gene list?				++				
View related annotations and related genes on a single graphic view		++		++				
What are other functionally similar genes in genome, but not in my list?	+	+		++	++			
What are other annotations functionally similar to my interested one?	++	++						
What are the gene names in my list?			+		++			
How to convert my gene IDs to other type of IDs?	+					++		
How to directly link to DAVID functions?								++
How can I download DAVID data for in-house study?	+	+	+	+			++	

## Additional Help

- [DAVID Documentation](#)
- [Nature Protocols Paper](#)
- [DAVID Forum](#)
- [Contact the DAVID Team](#)