

An Introduction to DAVID for Functional Enrichment Analysis

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March 1, 2026

Outline

- Overview of DAVID
 - Introduction and history of DAVID
 - The importance of DAVID for scientific community
 - Introduction of DAVID tools
- Applications
 - DAVID tools
 - DAVID API
 - DAVID Webservice

DAVID Web Address: <https://davidbioinformatics.nih.gov/>

What is DAVID?

The **D**atabase for **A**nnotation, **V**isualization and **I**ntegrated **D**iscovery (**DAVID**) bioinformatics resources consist of an integrated biological knowledgebase and analytic tools aimed at systematically extracting biological meaning from large gene/protein lists thereby providing investigators with the ability to gain an in-depth understanding of the biological themes that are enriched in genome-scale studies.

DAVID Web Address: <https://davidbioinformatics.nih.gov/>



History of DAVID

<https://davidbioinformatics.nih.gov/content.jsp?file=release.html>

DAVID 1.0 June 2003
--Fisher Exact test for gene-enrichment analysis
--DAVID knowledgebase linked by LocusLink

DAVID 2.0 Beta Nov. 2004
Pathway Mapping" to allocate given genes on
static pathway pictures

DAVID 2.1 Beta Aug. 2005
Functional Classification, fuzzy heat map,
2-D heat map

DAVID 2007 Jan. 2007 4.0
The DAVID Knowledgebase available for
downloads, The DAVID API Services for linking to
DAVID from other websites

DAVID 6.7 Jan. 2010
The DAVID Knowledgebase completely rebuilt, New
annotation categories, New list identifier systems added for
list uploading and conversion

DAVID 2021 Update
The DAVID Gene system rebuilt, drug-protein and small
molecule- protein interaction added to DAVID knowledgebase.



DAVID 2.0 Alfa Sept. 2004
DAVID Gene ID centered
Knowledgebase developed

DAVID 2.1 alpha Feb. 2005
Expanded DAVID tools, optimized and
expanded databases

DAVID 2006 May. 2006 3.0
Term functional classification tool,
Added pre-built Affy gene background,
Allowed user loaded customized gene
background

DAVID 2008 April. 2008 5.0
New annotation categories added, New
gene ID added

DAVID 6.8 Oct. 2016
The DAVID Knowledgebase completely
rebuilt, New annotation categories, new
gene list ID

**11 major version updates
Quarterly Knowledgebase
updates since Jan. 2021**

DAVID Citations

TITLE	CITED BY	YEAR
DAVID Ortholog: an integrative tool to enhance functional analysis through orthologs BT Sherman, G Panzade, T Imamichi, W Chang Bioinformatics 40 (10), btae615	34	2024
DAVID: a web server for functional enrichment analysis and functional annotation of gene lists (2021 update) BT Sherman, M Hao, J Qiu, X Jiao, MW Baseler, HC Lane, T Imamichi, ... Nucleic acids research 50 (W1), W216-W221	4862	2022
DAVID-WS: a stateful web service to facilitate gene/protein list analysis X Jiao, BT Sherman, DW Huang, R Stephens, MW Baseler, HC Lane, ... Bioinformatics 28 (13), 1805-1806	1139	2012
Extracting biological meaning from large gene lists with DAVID DW Huang, BT Sherman, X Zheng, J Yang, T Imamichi, R Stephens, ... Current protocols in bioinformatics 27 (1), 13.11. 1-13.11. 13	456	2009
Bioinformatics enrichment tools: paths toward the comprehensive functional analysis of large gene lists DW Huang, BT Sherman, RA Lempicki Nucleic acids research 37 (1), 1-13	15342	2009
Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources DW Huang, BT Sherman, RA Lempicki Nature protocols 4 (1), 44-57	37630	2009
DAVID gene ID conversion tool BT Sherman, R Stephens, MW Baseler, HC Lane, RA Lempicki Bioinformatics 2 (10), 428	40	2008
DAVID gene ID conversion tool BTS Da Wei Huang, R Stephens, MW Baseler, HC Lane, RA Lempicki Bioinformatics 2 (10), 428-430	190	2008
DAVID Knowledgebase: a gene-centered database integrating heterogeneous gene annotation resources to facilitate high-throughput gene functional analysis BT Sherman, DW Huang, Q Tan, Y Guo, S Bour, D Liu, R Stephens, ... BMC bioinformatics 8 (1), 426	617	2007
The DAVID Gene Functional Classification Tool: a novel biological module-centric algorithm to functionally analyze large gene lists DW Huang, BT Sherman, Q Tan, JR Collins, WG Alvord, J Roayaei, ... Genome biology 8 (9), R183	2587	2007
DAVID Bioinformatics Resources: expanded annotation database and novel algorithms to better extract biology from large gene lists DW Huang, BT Sherman, Q Tan, J Kir, D Liu, D Bryant, Y Guo, ... Nucleic acids research 35 (suppl_2), W169-W175	2391	2007
Identifying biological themes within lists of genes with EASE DA Hosack, G Dennis Jr, BT Sherman, HC Lane, RA Lempicki Genome biology 4 (10), R70	2271	2003
DAVID: database for annotation, visualization, and integrated discovery G Dennis Jr, BT Sherman, DA Hosack, J Yang, W Gao, HC Lane, ... Genome biology 4 (9), R60	11227	2003

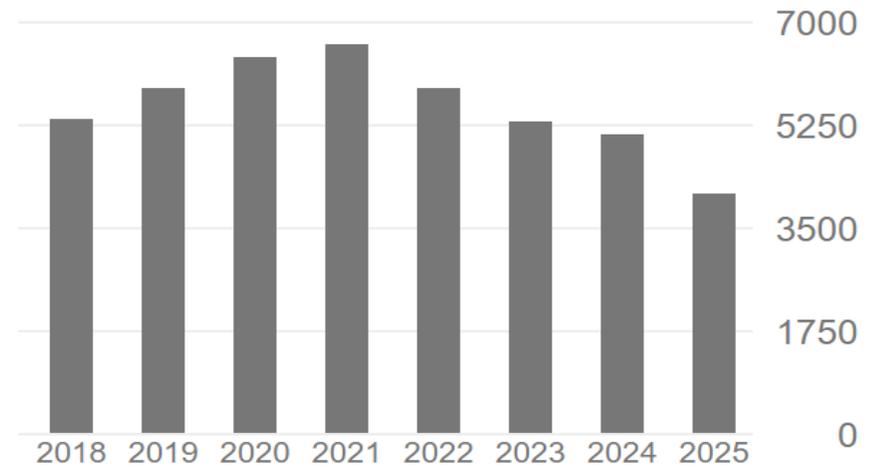
Cited by

[VIEW ALL](#)

All

Since 2020

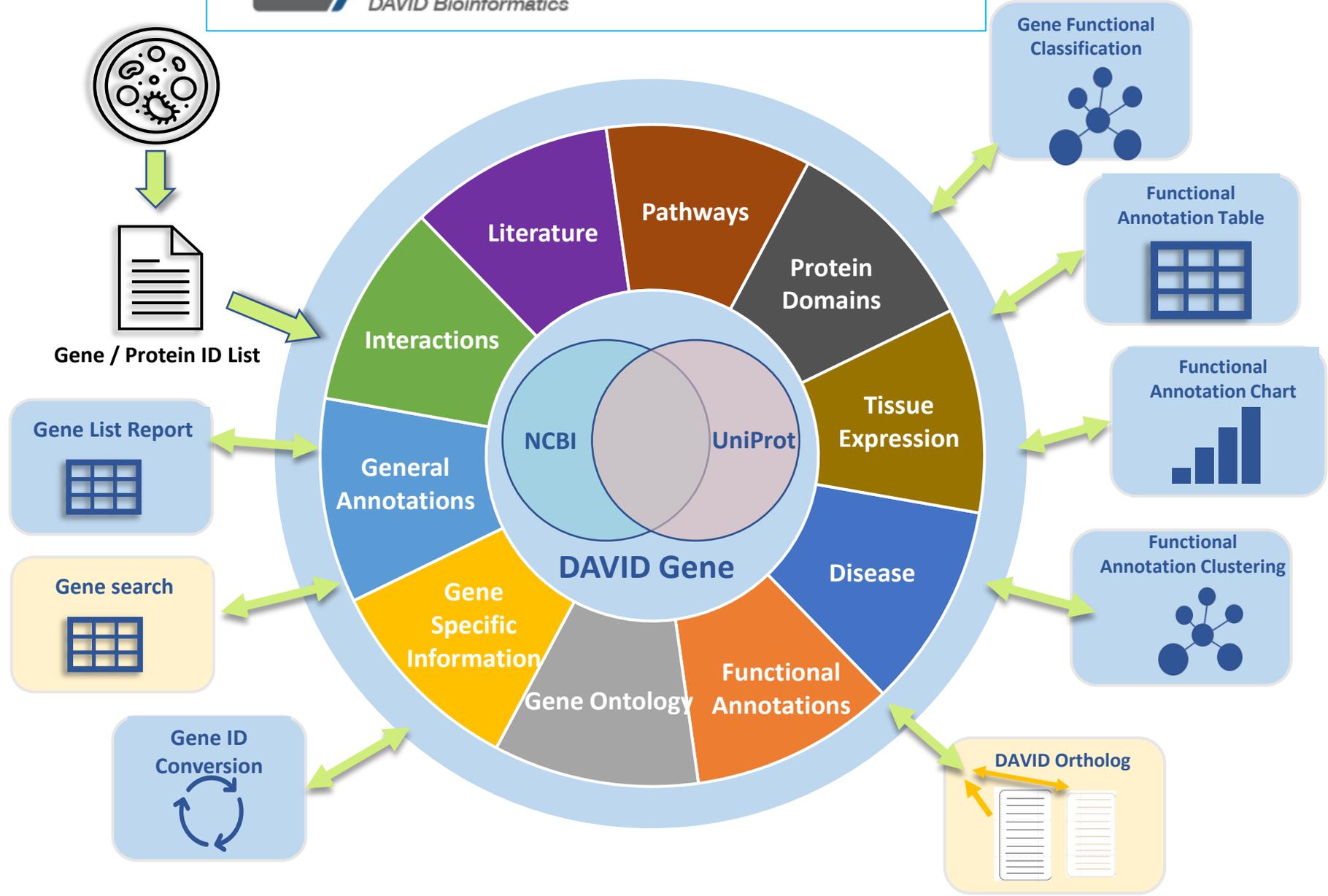
Citations	78786	33440
h-index	13	12
i10-index	13	12



DAVID Google Scholar

<https://scholar.google.com/citations?user=6mBdAXAAAAAJ&hl=en&authuser=1>

September 22, 2025



Outline

- Overview of DAVID
 - Introduction and history of DAVID
 - The importance of DAVID for scientific community and for NIH/NIH-sponsored research
 - Introduction of DAVID tools
- **Applications**
 - DAVID tools
 - DAVID Webservice
 - DAVID API

DAVID Web Address: <https://davidbioinformatics.nih.gov/>

Start DAVID Analysis

DAVID Web Address: <https://davidbioinformatics.nih.gov/>

Start DAVID Analysis

DAVID uses essential cookies to maintain your session and enable core functionality. By continuing to use DAVID, you acknowledge the use of these cookies.

Download & APIs

DAVID Knowledgebase, web services, and API.

[DAVID Knowledgebase](#)

[DAVID Web Services](#)

[DAVID API](#)

[About DAVID](#)

[Gene Search](#)

[Gene List Report](#)

[Functional Annotation](#)

[Gene Classification](#)

[Gene ID Conversion](#)

[Ortholog Tool](#)

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[DAVID Publications](#)

Welcome to DAVID

The **Database for Annotation, Visualization, and Integrated Discovery (DAVID)**

DAVID provides a comprehensive set of functional annotation tools to help understand the biological meaning behind large gene lists. Powered by the **DAVID Knowledgebase**, it integrates multiple sources of functional annotations. DAVID is free to use for all, including commercial users, without login. Please [cite DAVID](#) within any publication that makes use of any methods inspired by DAVID.

DAVID tools can:

- ✓ Identify enriched biological themes.
- ✓ Discover enriched functional-related gene groups.
- ✓ Cluster redundant annotation terms.

Spotlights

DAVID Forum: Ask questions, suggest functions, or help other users.

FAQ: Frequently Asked Questions.

LHRI Publications: Publications of the Laboratory of Human Retrovirology and Immunoinformatics.

What's New

February 28, 2026

DAVID now features modernized interfaces across all major analysis tools, including a taxonomy-based list upload workflow with support for multiple file formats. Links to legacy interfaces are available on each updated

DAVID Statistics

[78.8K Citations](#) (Updated 9/23/2025)

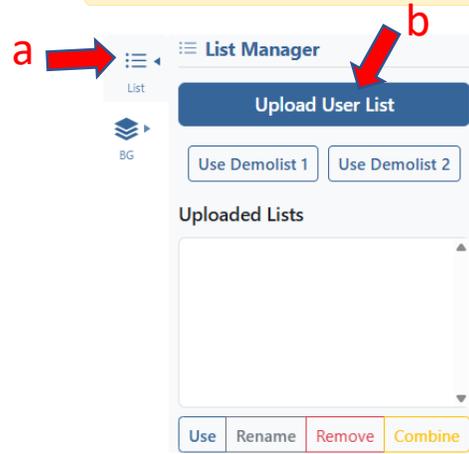
Average Daily Usage: ~2,700 gene lists/sublists from ~900 unique researchers.

Annual Usage: ~1,000,000 gene lists from over 100 countries.

DAVID Web Address: <https://davidbioinformatics.nih.gov/>

Submit Gene List

DAVID uses **essential cookies** to maintain your session and enable core functionality. By continuing to use DAVID, you acknowledge the use of these cookies. ✕



Analysis Wizard

← Step 1. Use the List Manager on the left to submit a gene/protein list to DAVID

Use the **List Manager** on the left to:

- Paste or upload a file of gene/protein identifiers
- Select your taxonomy
- Submit to DAVID for downstream analyses

Once a gene/protein list is uploaded, this page will automatically update with available analysis tools.

[You may access the legacy Analysis Wizard here.](#)

A

Copy and Paste

Upload User List

This is the new DAVID taxonomy-based upload interface. [You may access the legacy identifier type list upload interface here.](#)

Import mode: Paste identifiers Upload file

Paste your identifiers:

Provide a list name: list_1

Select your taxonomy: Provide identifiers first

Cancel Upload List

Upload file

B

Upload User List

This is the new DAVID taxonomy-based upload interface. [You may access the legacy identifier type list upload interface here.](#)

Import mode: Paste identifiers Upload file

Drag & drop a file here or click to select

Select your taxonomy: Provide identifiers first

Cancel Upload List

After the list of genes are copied and pasted (A.1) or gene list file is chosen and processed (B.1), Users will be presented available taxonomy for the genes to select (A.2, B.2). Then the gene list can be uploaded to the system (A.3, B.3).

Gene list upload side bar (b) can be expanded/collapsed by the list button (a).

Submit Background List

The screenshot shows the 'Background Manager' interface. On the left, there is a sidebar with a 'List Manager' icon (a) and an 'Upload User Background' button (b). The main area is titled 'Analysis Wizard' and contains instructions for using the List Manager. A red arrow labeled '1' points to the 'Upload User Background' button. A blue arrow labeled 'Copy and Paste' points from the 'Copy and Paste' text to the 'Upload User Background' button. A red arrow labeled '2' points to the 'Array Backgrounds' section in the sidebar. A yellow arrow points from the text box on the right to the 'Copy and Paste' text.

Background gene list can be submitted to system after gene list is submitted.
Background gene list upload side bar (b) can be expanded/collapsed by the list button (a).
Background can be uploaded (1, A, B) or chosen from the list of built-in array backgrounds (2).

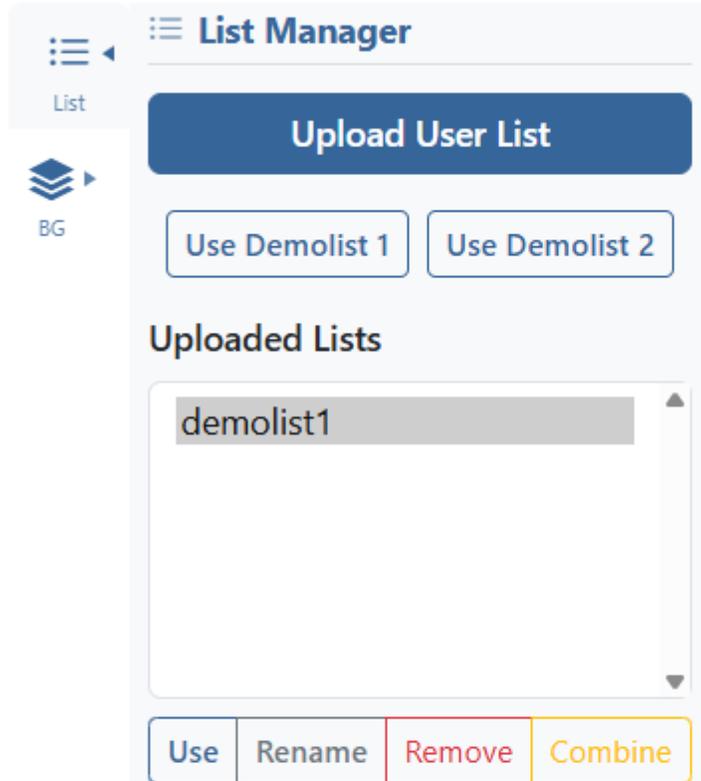
The screenshot shows the 'Upload User List' dialog box. It has a title bar with a close button. Below the title bar is a light blue banner with a warning icon and text: 'This is the new DAVID taxonomy-based upload interface. You may access the legacy identifier type list upload interface here.' Below the banner are two radio buttons for 'Import mode': 'Paste identifiers' (selected) and 'Upload file'. A large text area labeled 'Paste your identifiers:' has a red arrow labeled '1' pointing to it. Below the text area is a text input field for 'Provide a list name:' with the value 'list_1'. Below that is a dropdown menu for 'Select your taxonomy:' with the value 'Provide identifiers first'. At the bottom are 'Cancel' and 'Upload List' buttons, with a red arrow labeled '2' pointing to the 'Upload List' button.

The screenshot shows the 'Upload User List' dialog box. It has a title bar with a close button. Below the title bar is a light blue banner with a warning icon and text: 'This is the new DAVID taxonomy-based upload interface. You may access the legacy identifier type list upload interface here.' Below the banner are two radio buttons for 'Import mode': 'Paste identifiers' and 'Upload file' (selected). A large text area with the text 'Drag & drop a file here or click to select' has a red arrow labeled '1' pointing to it. Below the text area is a dropdown menu for 'Select your taxonomy:' with the value 'Provide identifiers first'. At the bottom are 'Cancel' and 'Upload List' buttons, with a red arrow labeled '2' pointing to the 'Upload List' button.

After the list of Background genes is copied and pasted (A.1) or gene list file is chosen and processed (B.1), Users will be presented available taxonomy for the genes to select (A.2, B.2). Then the gene list can be uploaded to the system (A.3, B.3).

Gene List Report

Ready for Analysis



Analysis Wizard

Step 1. Successfully submitted gene list

Current Gene List: demolist1
Current Population: Homo sapiens

Step 2. Analyze the your list with one of DAVID's tools

- Gene List Report 
- **Functional Annotation Tool**
 - Functional Annotation Table
 - Functional Annotation Chart
 - Functional Annotation Clustering
- Gene Functional Classification Tool
- Ortholog Tool
- Gene ID Conversion Tool

 [You may access the legacy Analysis Wizard here.](#)

Gene List Report

Gene List Report

Current Gene List: demolist2 1
Current Population: Homo sapiens

See the annotation in next slide

2 [Switch to Classic Versi](#)
[? He](#)

Search:

385 records (372 DAVID genes) 3

4 [Copy](#) [Excel](#) [CSV](#) [PDF](#)

User ID 5	6 Value	7 Gene Name 8 Gene Name	9 Related Genes	10 Species
1005_at		dual specificity phosphatase 1(DUSP1)	RG	Homo sapiens
1007_s_at	2	discoidin domain receptor tyrosine kinase 1(DDR1)	RG	Homo sapiens
1018_at	2	Wnt family member 10B(WNT10B)	RG	Homo sapiens
1091_at	2	protein kinase cAMP-dependent type I regulatory subunit beta(PRKAR1B)	RG	Homo sapiens
1124_at	2	lysine methyltransferase 2A(KMT2A)	RG	Homo sapiens
1139_at	2	G protein subunit alpha 13(GNA13)	RG	Homo sapiens
1148_s_at	2	neuregulin 1(NRG1)	RG	Homo sapiens
1167_s_at	2	matrix metalloproteinase 15(MMP15)	RG	Homo sapiens
1177_at	2			
1237_at	2	immediate early response 3(IER3)	RG	Homo sapiens
1242_at	2	ETS2 repressor factor(ERF)	RG	Homo sapiens
1244_at	2	signal transducer and activator of transcription 2(STAT2)	RG	Homo sapiens
1258_s_at	2	ERCC excision repair 4, endonuclease catalytic subunit(ERCC4)	RG	Homo sapiens
1263_at	2	interleukin 3(IL3)	RG	Homo sapiens
1267_at	2	protein kinase C eta(PRKCH)	RG	Homo sapiens
1270_at	2	RAP1 GTPase activating protein(RAP1GAP)	RG	Homo sapiens
1276_g_at	2	RNA binding protein, mRNA processing factor(RBPMS)	RG	Homo sapiens
131_at	2	TATA-box binding protein associated factor 11(TAF11)	RG	Homo sapiens
1332_f_at	2	growth hormone 1(GH1)	RG	Homo sapiens
136_at	2	G protein-coupled receptor 31(GPR31)	RG	Homo sapiens

Gene List Report (annotation)

1. Current Gene List & Population

Displays the active gene list and selected species or background population.

2. Help and Switch to Classic Version

Link to this help page and provides access to the legacy Gene List Report interface.

3. Search and Record Count

The search box filters table results in real time. The record count indicates total entries and the number of DAVID genes mapped.

4. Export Options

Results can be exported using Copy, Excel, CSV, or PDF. Exports reflect the current filtered and sorted view.

5. User ID

User uploaded gene ID name.

6. Sortable Columns

Click any column header to sort by User ID, Expression Value, DAVID Gene Name, Related Genes (RG), or Species.

7. Value

User uploaded expression value. (Optional)

8. Gene Name

Click the gene name link to explore the full gene report. For more information, see the [Gene Report documentation page](#).

9. Related Genes (RG)

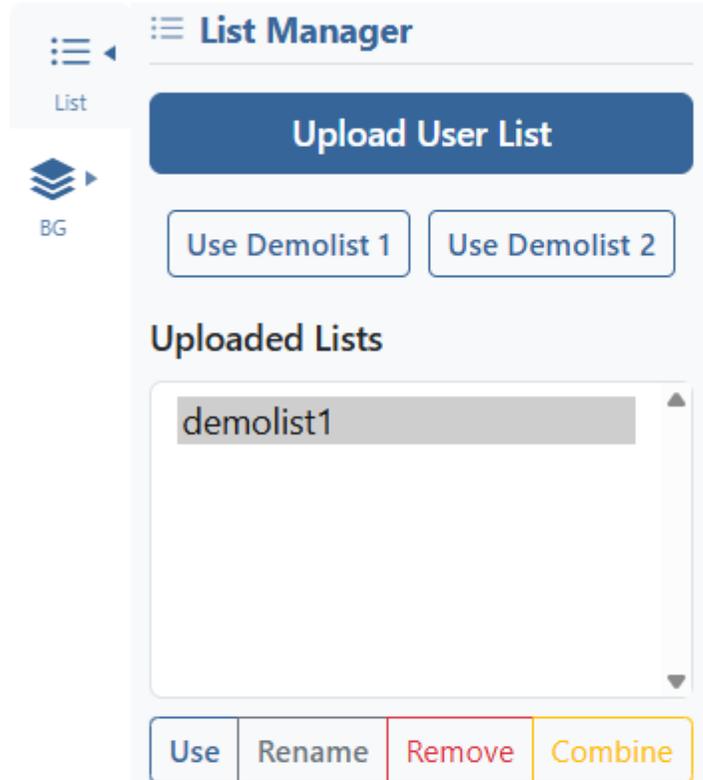
Click the **RG** link to explore functionally related genes associated with each entry. For more information, see the [Related Genes documentation page](#).

10. Species

Click the **Species** link to go to NCBI taxonomy entry.

Functional Annotation

Ready for Analysis



Analysis Wizard

Step 1. Successfully submitted gene list

Current Gene List: demolist1
Current Population: Homo sapiens

Step 2. Analyze the your list with one of DAVID's tools

- Gene List Report
- **Functional Annotation Tool**
 - [Functional Annotation Table](#)
 - [Functional Annotation Chart](#)
 - [Functional Annotation Clustering](#)
- Gene Functional Classification Tool
- Ortholog Tool
- Gene ID Conversion Tool



[You may access the legacy Analysis Wizard here.](#)

Functional Classification Annotation Summary

Annotation Summary Results

Current Gene List: demolist2 **1** See the annotation in next slide

Current Population: Homo sapiens

2 [Switch to Classic Version](#)

[? Help](#)

4 Clear All

5 Check Defaults

6 Functional Annotation Table

7 Functional Annotation Chart

8 Functional Annotation Clustering

3

Disease **2**

Functional_Annotations **6**

Gene_Ontology **3**

General_Annotations **0**

Interactions **1**

Literature **0**

Pathways **1**

Protein_Domains **4**

Tissue_Expression **0**

Transcription_Factors **0**

<input type="checkbox"/>	DISGENET	257 genes	69.09%	Chart	Cluster
<input type="checkbox"/>	GAD DISEASE	296 genes	79.57%	Chart	Cluster
<input type="checkbox"/>	GAD DISEASE CLASS	296 genes	79.57%	Chart	Cluster
<input checked="" type="checkbox"/>	OMIM DISEASE	147 genes	39.52%	Chart	Cluster
<input checked="" type="checkbox"/>	UP KW DISEASE	132 genes	35.48%	Chart	Cluster

3

9

10

11

12

Functional Classification Annotation Summary

1. **Current Gene List & Population**

Displays the active gene list and selected species or background population.

2. **Help and Switch to Classic Version**

Link to this help page and provides access to the legacy Gene List Report interface.

3. **Categories**

Click each category to expand and view additional annotation categories. Check/uncheck the items to add/remove them from your selection.

4. **Clear All**

Click this button to clear all selections.

5. **Check Default**

Click this button to undo any current selections and revert to default selections.

6. **Functional Annotation Table**

Click this button to view the **Functional Annotation Table** for all selections. This is a gene-centric view which lists the genes and their associated annotation terms. For more information, see the [Functional Annotation Table documentation page](#).

7. **Functional Annotation Chart**

Click this button to view the **Functional Annotation Chart** for all selections. Chart Report is an annotation term focused view which lists annotation terms and their associated genes under study. For more information, see the [Functional Annotation Chart documentation page](#).

8. **Functional Annotation Clustering**

Click this button to view the **Functional Annotation Clustering** for all selections. Functional Annotation Clustering integrates Kappa statistics to measure the degree of the common genes between two annotations. For more information, see the [Functional Annotation Clustering documentation page](#).

9. **Gene count**

Number of genes from the user list involved in this annotation category.

10. **Gene Percentage & Single Table**

Percentage of genes from user list involved in this category out of total genes from user list.

Click this percentage bar to be directed to a functional annotation table for user genes in this annotation category ONLY.

11. **Single Chart**

Click this button to be directed to a functional annotation chart for user genes in this annotation category ONLY.

12. **Single Cluster**

Click this button to be directed to a functional annotation cluster for user genes in this annotation category ONLY.

Function Annotation Table

Functional Classification Annotation Summary

Annotation Summary Results

Current Gene List: demolist2
Current Population: Homo sapiens

[Switch to Classic Version](#)
[Help](#)

[Clear All](#) [Check Defaults](#) [Functional Annotation Table](#) [Functional Annotation Chart](#) [Functional Annotation Clustering](#)

Disease	2
Functional_Annotations	6
Gene_Ontology	3
General_Annotations	0
Interactions	1
Literature	0
Pathways	1
Protein_Domains	4
Tissue_Expression	0
Transcription_Factors	0

<input type="checkbox"/> DISGENET	257 genes	<div style="width: 69.09%;"></div> 69.09%	Chart Cluster
<input type="checkbox"/> GAD DISEASE	296 genes	<div style="width: 79.57%;"></div> 79.57%	Chart Cluster
<input type="checkbox"/> GAD DISEASE CLASS	296 genes	<div style="width: 79.57%;"></div> 79.57%	Chart Cluster
<input checked="" type="checkbox"/> OMIM DISEASE	147 genes	<div style="width: 39.52%;"></div> 39.52%	Chart Cluster
<input checked="" type="checkbox"/> UP KW DISEASE	132 genes	<div style="width: 35.48%;"></div> 35.48%	Chart Cluster

Function Annotation Table

Functional Annotation Table

Current Gene List: demolist2 **1 See the annotation in next slide**

Current Population: Homo sapiens

2 [Switch to Classic Version](#)

[? Help](#)

Search:

3 4,184 annotation records

« < 1 2 3 **4** 5 ... 42 > »

5

Copy

Excel

CSV

PDF

Category 6	Terms 7	9 Related Genes
GOTERM_BP_DIRECT	8 2',3'-cyclic nucleotide 3' phosphodiesterase(CNP) <ul style="list-style-type: none">chemical synaptic transmissionaxonogenesisadult locomotory behaviorcyclic nucleotide catabolic processresponse to toxic substancesubstantia nigra developmentoligodendrocyte differentiation	
GOTERM_CC_DIRECT	<ul style="list-style-type: none">extracellular spacecytoplasmmicrotubulemembranemelanosomemyelin sheathsynapseextracellular exosome	
GOTERM_MF_DIRECT	<ul style="list-style-type: none">RNA binding2',3'-cyclic-nucleotide 3'-phosphodiesterase activityprotein bindinghydrolase activity	
INTERPRO	<ul style="list-style-type: none">CNPaseCyclic PdiesteraseP-loop_NTPaseCNPase_cat	

Function Annotation Table

1. Current Gene List & Population

Displays the active gene list and selected species or background population.

2. Help and Switch to Classic Version

Link to this help page and provides access to the legacy Gene List Report interface.

3. Search and Record Count

The search box filters table results in real time. The record count indicates total annotations found for all genes.

4. Pages

Click on numbers to navigate pages of results. Single arrow buttons move forward/back by one page, double arrow buttons navigate to first/last page.

5. Export Options

Results can be exported using Copy, Excel, CSV, or PDF. Exports reflect the current filtered and sorted view.

6. Categories

Categories of term results, indicating original source of information. (e.g. UP = Uniprot). Click to sort by this value.

7. Annotations

Annotations available for each item. If available, hyperlinks lead users to original resources for further details. Click to sort by this value.

8. Gene Name

Annotation results are grouped by each gene. Click the gene name link to explore the full gene report. For more information, see the [Gene Report documentation page](#).

9. Related Genes (RG)

Click the **RG** link to explore functionally related genes associated with each entry. For more information, see the [Related Genes documentation page](#).

Functional Annotation Chart

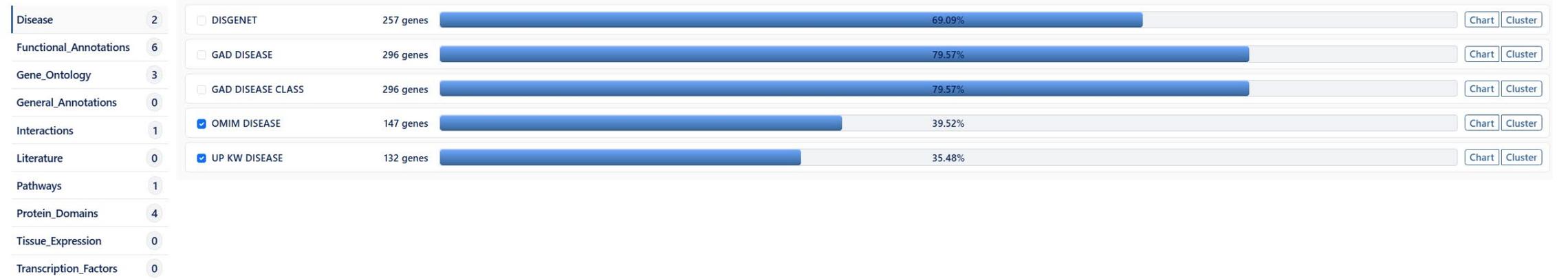
Functional Classification Annotation Summary

Annotation Summary Results

Current Gene List: demolist2
Current Population: Homo sapiens

[Switch to Classic Version](#)
[? Hel](#)

[Clear All](#) [Check Defaults](#) [Functional Annotation Table](#) [Functional Annotation Chart](#) [Functional Annotation Clustering](#)



Functional Annotation Chart

Functional Annotation Chart

Current Gene List: demolist2 ¹ See the annotation in next slide

Current Population: Homo sapiens

² [Switch to Classic Version](#)

[Help](#)

EASE Threshold: ³ Count Threshold: ⁴ [Update Table](#) ⁵

Search: 659 chart records ⁶

⁷ [Create sublist](#) [Copy](#) [Excel](#) [CSV](#) [PDF](#) [Column visibility](#) ▾

⁸

Sublist	Category ¹⁰	Term ¹¹	RT	Genes	Count	P-Value	Benjamini
<input type="checkbox"/> ⁹	GOTERM_MF_DIRECT	protein binding	¹² RT	84.95% ¹³	316	7.88e-15	¹⁴ 5.69e-12
<input type="checkbox"/>	GOTERM_MF_DIRECT	identical protein binding	RT	20.16%	75	7.03e-11	2.54e-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of transcription by RNA polymerase II	RT	12.10%	45	1.12e-7	3.00e-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	cytokine activity	RT	5.38%	20	1.22e-7	2.94e-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of inflammatory response	RT	3.76%	14	4.27e-7	4.50e-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of transcription by RNA polymerase II	RT	13.17%	49	5.02e-7	4.50e-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosol	RT	37.90%	141	7.87e-7	3.75e-4
<input type="checkbox"/>	KEGG_PATHWAY	Transcriptional misregulation in cancer	RT	5.11%	19	1.02e-6	3.03e-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	extracellular exosome	RT	18.55%	69	2.58e-6	6.14e-4
<input type="checkbox"/>	KEGG_PATHWAY	Chagas disease	RT	3.49%	13	4.65e-6	4.24e-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	glutamatergic synapse	RT	7.53%	28	5.21e-6	8.27e-4
<input type="checkbox"/>	KEGG_PATHWAY	Proteoglycans in cancer	RT	4.84%	18	5.48e-6	4.24e-4
<input type="checkbox"/>	KEGG_PATHWAY	NF-kappa B signaling pathway	RT	3.49%	13	5.69e-6	4.24e-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein domain specific binding	RT	4.57%	17	7.70e-6	1.39e-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of gene expression	RT	6.99%	26	8.10e-6	5.44e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription repressor activity, RNA polymerase II-specific	RT	5.11%	19	9.84e-6	1.42e-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	neuronal cell body	RT	5.65%	21	1.03e-5	1.23e-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of fat cell differentiation	RT	2.42%	9	1.17e-5	6.29e-3

KEGG Pathway/Wikipathway can be viewed by click here (on the 2nd slide after this slide)



Functional Annotation Chart

1. **Current Gene List & Population**

Displays the active gene list and selected species or background population.

2. **Help and Switch to Classic Version**

Link to this help page and provides access to the legacy Gene List Report interface.

3. **EASE Threshold**

Minimum P-value of results to be displayed. Click to either type a numerical value or use the up/down arrows to increment by 0.01.

4. **Count Threshold**

Minimum gene count of annotation result to be displayed. Click to either type a numerical value or use the up/down arrows to increment by 1.

5. **Update Table**

After making adjustments to filtering options, click this button to update the table using the selected parameters.

6. **Search and Record Count**

The search box filters table results in real time. The record count indicates total entries and the number of DAVID genes mapped.

7. **Create sublist, Export options & Column Visibility**

Create a sublist by clicking on checkboxes to the left of desired results, then clicking the **Create sublist** button, where you will be prompted to name the new sublist.

Sublists will then appear in the list manager as a new gene list.

Results can be exported using Copy, Excel, CSV, or PDF. Exports reflect the current filtered and sorted view.

Additional columns can be added to the current view using the **Column Visibility** drop-down button. Click on available items to add the column to the table.

8. **Sortable Columns**

Click on any table column header to sort the table by that column in ascending or descending order.

9. **Sublist**

Click on check boxes to select items for creating a sublist. [\(7\)](#)

10. **Categories**

Categories of term results, indicating original source of information. (e.g. UP = Uniprot). Click to sort by this value.

11. **Annotations**

Annotations available for each item. If available, hyperlinks lead users to original resources for further details. Click to sort by this value.

12. **Related Terms**

Click **RT** to be directed to a Functionally Related Terms search result for each term. For more information, see the [Related Terms documentation page](#).

13. **Gene Count and Percentage**

Count and percentage of genes involved in each term.

14. **P-value & Benjamini**

EASE Score where smaller means more enriched. Benjamini in DAVID requests adjusted p-values by using the linear step-up method of Benjamini and Hochberg

Functional Annotation Chart

Functional Annotation Chart

Current Gene List: demolist2
Current Population: Homo sapiens

[Switch to Classic Version](#)
[Help](#)

EASE Threshold: Count Threshold: [Update Table](#)

Search: 659 chart records

[Create sublist](#) [Copy](#) [Excel](#) [CSV](#) [PDF](#) [Column visibility](#)

Sublist	Category	Term	RT	Genes	Count [▲]	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein binding	RT	84.95%	316	7.88e-15	5.69e-12
<input type="checkbox"/>	GOTERM_MF_DIRECT	identical protein binding	RT	20.16%	75	7.03e-11	2.54e-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of transcription by RNA polymerase II	RT	12.10%	45	1.12e-7	3.00e-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	cytokine activity	RT	5.38%	20	1.22e-7	2.94e-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of inflammatory response	RT	3.75%	14	4.27e-7	4.50e-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of transcription by RNA polymerase II	RT	13.17%	49	5.02e-7	4.50e-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosol	RT	37.90%	141	7.87e-7	3.75e-4
<input type="checkbox"/>	KEGG_PATHWAY	Transcriptional misregulation in cancer	RT	5.11%	19	1.02e-6	3.03e-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	extracellular exosome	RT	18.55%	69	2.58e-6	6.14e-4
<input type="checkbox"/>	KEGG_PATHWAY	Chagas disease	RT	3.49%	13	4.65e-6	4.24e-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	glutamatergic synapse	RT	7.53%	28	5.21e-6	8.27e-4
<input type="checkbox"/>	KEGG_PATHWAY	Proteoglycans in cancer	RT	4.84%	18	5.48e-6	4.24e-4
<input type="checkbox"/>	KEGG_PATHWAY	NF-kappa B signaling pathway	RT	3.49%	13	5.69e-6	4.24e-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein domain specific binding	RT	4.57%	17	7.70e-6	1.39e-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of gene expression	RT	6.99%	26	8.10e-6	5.44e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription repressor activity, RNA polymerase II-specific	RT	5.11%	19	9.84e-6	1.42e-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	neuronal cell body	RT	5.65%	21	1.03e-5	1.23e-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of fat cell differentiation	RT	2.42%	9	1.17e-5	6.29e-3
<input type="checkbox"/>	KEGG_PATHWAY	Lipid and atherosclerosis	RT	4.84%	18	1.18e-5	6.15e-4
<input type="checkbox"/>	KEGG_PATHWAY	IL-17 signaling pathway	RT	3.23%	12	1.24e-5	6.15e-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	kinase activity	RT	8.60%	32	1.62e-5	1.94e-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell adhesion	RT	8.06%	30	1.64e-5	7.35e-3
<input type="checkbox"/>	KEGG_PATHWAY	Malaria	RT	2.42%	9	1.81e-5	7.44e-4
<input type="checkbox"/>	KEGG_PATHWAY	TNF signaling pathway	RT	3.49%	13	2.07e-5	7.44e-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleoplasm	RT	27.95%	104	2.16e-5	2.05e-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	response to xenobiotic stimulus	RT	4.57%	17	2.17e-5	8.04e-3
<input type="checkbox"/>	KEGG_PATHWAY	Human cytomegalovirus infection	RT	4.84%	18	2.25e-5	7.44e-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	angiogenesis	RT	4.84%	18	2.47e-5	8.04e-3
<input type="checkbox"/>	KEGG_PATHWAY	Amoebiasis	RT	3.23%	12	2.69e-5	8.01e-4

Gene List for a Term in Functional Annotation Chart

Filtered Gene List Report

Current Gene List: demolist2
Current Population: Homo sapiens

[Switch to Classic Version](#)

[Help](#)

Search: 316 genes

[Copy](#) [Excel](#) [CSV](#) [PDF](#)

User ID	Gene Name	Related Genes	Species
612_s_at	2',3'-cyclic nucleotide 3' phosphodiesterase(CNP)	RG	Homo sapiens
35471_g_at	5-hydroxytryptamine receptor 2A(HTR2A)	RG	Homo sapiens
37111_g_at, 39522_at	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3(PFKFB3)	RG	Homo sapiens
34184_at	APC regulator of Wnt signaling pathway 2(APC2)	RG	Homo sapiens
37270_at	ATPase Na+/K+ transporting subunit beta 2(ATP1B2)	RG	Homo sapiens
40913_at	ATPase plasma membrane Ca2+ transporting 4(ATP2B4)	RG	Homo sapiens
2043_s_at	BCR activator of RhoGEF and GTPase(BCR)	RG	Homo sapiens
37170_at	BMP2 inducible kinase(BMP2K)	RG	Homo sapiens
35500_at	BRCA1 associated protein(BRAP)	RG	Homo sapiens
37218_at	BTG anti-proliferation factor 3(BTG3)	RG	Homo sapiens
875_g_at, 34375_at	C-C motif chemokine ligand 2(CCL2)	RG	Homo sapiens
40385_at	C-C motif chemokine ligand 20(CCL20)	RG	Homo sapiens
36103_at	C-C motif chemokine ligand 3(CCL3)	RG	Homo sapiens
36674_at	C-C motif chemokine ligand 4(CCL4)	RG	Homo sapiens
408_at	C-X-C motif chemokine ligand 1(CXCL1)	RG	Homo sapiens
1369_s_at, 35372_r_at	C-X-C motif chemokine ligand 8(CXCL8)	RG	Homo sapiens
1867_at	CASP8 and FADD like apoptosis regulator(CFLAR)	RG	Homo sapiens
39587_at	CCC complex scaffolding subunit CCDC22(CCDC22)	RG	Homo sapiens
35149_at	CD40 molecule(CD40)	RG	Homo sapiens
2036_s_at, 1125_s_at, 31615_i_at	CD44 molecule (IN blood group)(CD44)	RG	Homo sapiens
37889_at	CD47 molecule(CD47)	RG	Homo sapiens

Functional Annotation Clustering

Functional Classification Annotation Summary

Annotation Summary Results

Current Gene List: demolist2
Current Population: Homo sapiens

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[Clear All](#) [Check Defaults](#) [Functional Annotation Table](#) [Functional Annotation Chart](#) [Functional Annotation Clustering](#)

Disease	2	<input type="checkbox"/> DISGENET	257 genes	69.09%	Chart Cluster
Functional_Annotations	6	<input type="checkbox"/> GAD DISEASE	296 genes	79.57%	Chart Cluster
Gene_Ontology	3	<input type="checkbox"/> GAD DISEASE CLASS	296 genes	79.57%	Chart Cluster
General_Annotations	0	<input checked="" type="checkbox"/> OMIM DISEASE	147 genes	39.52%	Chart Cluster
Interactions	1	<input checked="" type="checkbox"/> UP KW DISEASE	132 genes	35.48%	Chart Cluster
Literature	0				
Pathways	1				
Protein_Domains	4				
Tissue_Expression	0				
Transcription_Factors	0				

Functional Annotation Clustering Tool

Functional Annotation Clustering

Current Gene List: demolist2 1
Current Population: Homo sapiens

See the annotation in next two slides

2 [Switch to Classic Version](#)
[Help](#)

3 Hide options Classification Stringency: Medium 4 EASE Threshold: 1 5 6 Update Table

KAPPA SIMILARITY

Similarity Term Overlap 7 Similarity Threshold 8
3 0.50

CLASSIFICATION

Initial Group Membership 9 Final Group Membership 10 Multiple Linkage Threshold 11
3 3 0.50

Search: 12

13 Create sublist Copy Excel CSV PDF Column visibility ▼

14

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
Term Cluster 1 15		Enrichment Score: 3.18 16		17 G		18		
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of transcription by RNA polymerase II 19	20 RT	12.10% 21	45	12.10	1.12e-7	22 3.00e-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of transcription by RNA polymerase II	RT	13.17%	49	13.17	5.02e-7	4.50e-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription repressor activity, RNA polymerase II-specific	RT	5.11%	19	5.11	9.84e-6	1.42e-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	chromatin	RT	10.75%	40	10.75	5.36e-5	3.65e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase II cis-regulatory region sequence-specific DNA binding	RT	10.75%	40	10.75	7.93e-5	7.16e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription factor activity	RT	8.06%	30	8.06	1.28e-4	9.43e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription activator activity, RNA polymerase II-specific	RT	5.91%	22	5.91	1.31e-4	9.43e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	sequence-specific DNA binding	RT	5.91%	22	5.91	6.44e-4	3.32e-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	sequence-specific double-stranded DNA binding	RT	6.72%	25	6.72	8.58e-4	4.13e-2

Functional Annotation Clustering Tool

1. **Gene List**

Current gene list selected for view and background species being analyzed.

2. **Help and Switch to Classic Version**

Link to this help page and provides access to the legacy Gene List Report interface.

3. **Show/Hide Options**

Click this button to expand or hide additional filtering options.

4. **Classification Stringency**

Click to access a drop-down menu of stringency levels, then click desired level to select. A high-level single control to establish a set of detailed parameters involved in functional classification algorithms. In general, the higher stringency setting generates less functional groups with more tightly associated genes in each group, so that more genes will be unclustered.

5. **EASE Threshold**

Minimum P-value of results to be displayed. Click to either type a numerical value or use the up/down arrows to increment by 0.01.

6. **Update Table**

After making adjustments to filtering options, click this button to update the table using the selected parameters.

7. **Similarity Term Overlap**

Click to access a drop-down menu of overlap values. The minimum number of annotation terms overlapped between two genes in order to be qualified for kappa calculation. This parameter is to maintain necessary statistical power to make the kappa value more meaningful. The higher the value, the more meaningful the result is.

8. **Similarity Threshold**

Click to access a drop-down menu of threshold values. The minimum kappa value to be considered significant. A higher setting will lead to more genes going unclustered, which leads to a higher quality functional classification result with fewer groups and fewer gene members. Kappa value of 0.3 starts giving meaningful biology based on our genome-wide distribution study. Anything below 0.3 has a good chance to be noise.

9. **Initial Group Membership**

Click to access a drop-down menu of membership values. The minimum gene number in a seeding group, which affects the minimum size of each functional group in the final cluster. In general, the lower value attempts to include more genes in functional groups, and may generate a lot of small size groups.

10. **Final Group Membership**

Click to access a drop-down menu of membership values. The minimum gene number in one final group after a 'cleanup' procedure. In general, the lower value attempts to include more genes in functional groups and may generate a lot of small size groups. It cofunctions with previous parameters to control the minimum size of functional groups. If you are interested in functional groups containing only 2 or 3 genes, you need to set it to a very low value. Otherwise, the small group will not be displayed and the genes will go unclustered.

Functional Annotation Clustering Tool

11. Multiple Linkage Threshold

Click to access a drop-down menu of threshold values. This parameter controls how seeding groups merge with each other, i.e. two groups sharing the same gene members over the percentage will become one group. A higher percentage, in general, gives sharper separation (i.e. it generates more final functional groups with more tightly associated genes in each group). In addition, changing the parameter does not cause additional genes to go unclustered.

12. Search

The search box filters all table results in real time.

13. Create sublist, Export options & Column Visibility

Create a sublist by clicking on checkboxes to the left of desired results, then clicking the **Create sublist** button, where you will be prompted to name the new sublist. Sublists will then appear in the list manager as a new gene list.

Results can be exported using Copy, Excel, CSV, or PDF. Exports reflect the current filtered and sorted view.

Additional columns can be added to the current view using the **Column Visibility** drop-down button. Click on available items to add the column to the table.

14. Sortable Columns

Click on any table column header to sort the table by that column in ascending or descending order.

15. Cluster

A group of terms having similar biological meaning due to sharing similar gene members.

16. Enrichment Score

The overall enrichment score for the group based on the EASE scores of each term member. Higher value = more enriched.

17. Gene Report

Click on the red **G** to be directed to the Gene Report page for that genes in this cluster.

18. Cluster view

Click this icon to be directed to a 2D cluster view of the genes in this cluster.

19. Annotations

Annotations available for each item. If available, hyperlinks lead users to original resources for further details.

20. Related Terms

Click **RT** to be directed to a Functionally Related Terms search result for each term. For more information, see the [Related Terms documentation page](#).

21. Gene Count and Percentage

Count and percentage of genes involved in each term.

22. P-value & Benjamini

EASE Score where smaller means more enriched. Benjamini in DAVID requests adjusted p-values by using the linear step-up method of Benjamini and Hochberg

Functional Annotation Clustering Tool

Retrieve filtered gene list for the current term

Functional Annotation Clustering

Current Gene List: demolist2
Current Population: Homo sapiens

[Switch to Classic Version](#)
[Help](#)

Show options Classification Stringency: Medium EASE Threshold: 1 Update Table

Search: 102 annotation clusters Create sublist Copy Excel CSV PDF Column visibility

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
Term Cluster 1		Enrichment Score: 3.18		G				
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of transcription by RNA polymerase II	RT	12.10%	45	12.10	1.12e-7	3.00e-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of transcription by RNA polymerase II	RT	13.17%	49	13.17	5.02e-7	4.50e-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription repressor activity, RNA polymerase II-specific	RT	5.11%	19	5.11	9.84e-6	1.42e-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	chromatin	RT	10.75%	40	10.75	5.36e-5	3.65e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase II cis-regulatory region sequence-specific DNA binding	RT	10.75%	40	10.75	7.93e-5	7.16e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription factor activity	RT	8.06%	30	8.06	1.28e-4	9.43e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription activator activity, RNA polymerase II-specific	RT	5.91%	22	5.91	1.31e-4	9.43e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	sequence-specific DNA binding	RT	5.91%	22	5.91	6.44e-4	3.32e-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	sequence-specific double-stranded DNA binding	RT	6.72%	25	6.72	8.58e-4	4.13e-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of transcription by RNA polymerase II	RT	12.63%	47	12.63	1.90e-3	1.34e-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription factor activity, RNA polymerase II-specific	RT	9.95%	37	9.95	5.56e-3	1.54e-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of DNA-templated transcription	RT	10.75%	40	10.75	1.74e-2	4.78e-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA binding	RT	15.59%	58	15.59	2.34e-2	4.33e-1
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Transcription	RT	15.82%	57	15.32	2.10e-1	1.00e+0
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Transcription regulation	RT	14.78%	55	14.78	2.34e-1	1.00e+0
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	DNA-binding	RT	13.17%	49	13.17	3.10e-1	1.00e+0
Term Cluster 2		Enrichment Score: 2.96		G				
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleoplasm	RT	27.96%	104	27.96	2.16e-5	2.05e-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleus	RT	40.59%	151	40.59	1.02e-3	3.25e-2
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Nucleus	RT	33.50%	125	33.60	6.08e-2	4.98e-1
Term Cluster 3		Enrichment Score: 2.73		G				
<input type="checkbox"/>	GOTERM_CC_DIRECT	neuronal cell body	RT	5.65%	21	5.65	1.03e-5	1.23e-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	axon	RT	4.57%	17	4.57	3.87e-3	9.12e-2

Functional Annotation Clustering Tool

Filtered Gene List Report

Current Gene List: demolist2
Current Population: Homo sapiens

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[Help](#)

Search: 45 genes

[Copy](#) [Excel](#) [CSV](#) [PDF](#)

User ID	Gene Name	Related Genes	Species
38491_at	ETS variant transcription factor 6(ETV6)	RG	Homo sapiens
1242_at	ETS2 repressor factor(ERF)	RG	Homo sapiens
36669_at	FosB proto-oncogene AP-1 transcription factor subunit(FOSB)	RG	Homo sapiens
39698_at	HOP homeobox(HOPX)	RG	Homo sapiens
1895_at_32583_at	Jun proto-oncogene AP-1 transcription factor subunit(JUN)	RG	Homo sapiens
224_at_38374_at	KLF transcription factor 10(KLF10)	RG	Homo sapiens
35160_at	LIM domain binding 1(LDB1)	RG	Homo sapiens
36711_at	MAF bZIP transcription factor F(MAFF)	RG	Homo sapiens
41505_r_at	MAF bZIP transcription factor(MAF)	RG	Homo sapiens
1774_at	MAX dimerization protein 1(MXD1)	RG	Homo sapiens
1973_s_at_37724_at_1936_s_at	MYC proto-oncogene bHLH transcription factor(MYC)	RG	Homo sapiens
989_at	NCK adaptor protein 1(NCK1)	RG	Homo sapiens
1461_at	NFKB inhibitor alpha(NFKBIA)	RG	Homo sapiens
33922_at	PR/SET domain 2(PRDM2)	RG	Homo sapiens
1743_s_at_1866_g_at	SKI like proto-oncogene(SKIL)	RG	Homo sapiens
41499_at	SKI proto-oncogene(SKI)	RG	Homo sapiens
1857_at	SMAD family member 7(SMAD7)	RG	Homo sapiens
36018_at	SRY-box transcription factor 10(SOX10)	RG	Homo sapiens
1018_at	Wnt family member 10B(WNT10B)	RG	Homo sapiens
1994_at	activating transcription factor 2(ATF2)	RG	Homo sapiens
287_at	activating transcription factor 3(ATF3)	RG	Homo sapiens
40790_at	basic helix-loop-helix family member e40(BHLHE40)	RG	Homo sapiens
39304_g_at	beta-transducin repeat containing E3 ubiquitin protein ligase(BTRC)	RG	Homo sapiens
789_at	early growth response 1(EGR1)	RG	Homo sapiens
38356_at	follistatin(FST)	RG	Homo sapiens
31353_f_at	forkhead box E1(FOXE1)	RG	Homo sapiens
1911_s_at	growth arrest and DNA damage inducible alpha(GADD45A)	RG	Homo sapiens
38654_at	heterogeneous nuclear ribonucleoprotein U(HNRNPU)	RG	Homo sapiens
41216_r_at	inhibitor of DNA binding 2(ID2)	RG	Homo sapiens
36999_at	lysine demethylase 5A(KDMA5A)	RG	Homo sapiens
35992_at	musculin(MSC)	RG	Homo sapiens

Functional Annotation Clustering Tool

Functional Annotation Clustering

Current Gene List: demolist2
Current Population: Homo sapiens

[Switch to Classic Version](#)
[Help](#)

Show options Classification Stringency: Medium EASE Threshold: 1 Update Table

Search: 102 annotation clusters Create sublist Copy Excel CSV PDF Column visibility

Retrieve filtered gene list for the current cluster

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
Term Cluster 1			Enrichment Score: 3.18			G		
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of transcription by RNA polymerase II	RT	12.10%	45	12.10	1.12e-7	3.00e-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of transcription by RNA polymerase II	RT	13.17%	49	13.17	5.02e-7	4.50e-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription repressor activity, RNA polymerase II-specific	RT	5.11%	19	5.11	9.84e-6	1.42e-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	chromatin	RT	10.75%	40	10.75	5.36e-5	3.65e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase II cis-regulatory region sequence-specific DNA binding	RT	10.75%	40	10.75	7.93e-5	7.16e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription factor activity	RT	8.06%	30	8.06	1.28e-4	9.43e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription activator activity, RNA polymerase II-specific	RT	5.91%	22	5.91	1.31e-4	9.43e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	sequence-specific DNA binding	RT	5.91%	22	5.91	6.44e-4	3.32e-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	sequence-specific double-stranded DNA binding	RT	6.72%	25	6.72	8.58e-4	4.13e-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of transcription by RNA polymerase II	RT	12.63%	47	12.63	1.90e-3	1.34e-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription factor activity, RNA polymerase II-specific	RT	9.95%	37	9.95	5.56e-3	1.54e-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of DNA-templated transcription	RT	10.75%	40	10.75	1.74e-2	4.78e-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA binding	RT	15.59%	58	15.59	2.34e-2	4.33e-1
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Transcription	RT	15.82%	57	15.32	2.10e-1	1.00e+0
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Transcription regulation	RT	14.78%	55	14.78	2.34e-1	1.00e+0
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	DNA-binding	RT	13.17%	49	13.17	3.10e-1	1.00e+0
Term Cluster 2			Enrichment Score: 2.96			G		
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleoplasm	RT	27.96%	104	27.96	2.16e-5	2.05e-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleus	RT	40.59%	151	40.59	1.02e-3	3.25e-2
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Nucleus	RT	33.50%	125	33.60	6.08e-2	4.98e-1
Term Cluster 3			Enrichment Score: 2.73			G		
<input type="checkbox"/>	GOTERM_CC_DIRECT	neuronal cell body	RT	5.65%	21	5.65	1.03e-5	1.23e-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	axon	RT	4.57%	17	4.57	3.87e-3	9.12e-2

Functional Annotation Clustering Tool

Filtered Gene List Report

Current Gene List: demolist2
Current Population: Homo sapiens

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[Help](#)

Search: 107 genes

[Copy](#) [Excel](#) [CSV](#) [PDF](#)

User ID	Gene Name	Related Genes	Species
40913_at	ATPase plasma membrane Ca2+ transporting 4(ATP2B4)	RG	Homo sapiens
35149_at	CD40 molecule(CD40)	RG	Homo sapiens
35595_at	GGRP receptor component(CRCP)	RG	Homo sapiens
41099_at	DNA ligase 3(LIG3)	RG	Homo sapiens
41234_at	DnaJ heat shock protein family (Hsp40) member B6(DNAJB6)	RG	Homo sapiens
36519_at	ERCC excision repair 1_endonuclease non-catalytic subunit(ERCC1)	RG	Homo sapiens
1258_s_at	ERCC excision repair 4_endonuclease catalytic subunit(ERCC4)	RG	Homo sapiens
38491_at	ETS variant transcription factor 6(ETV6)	RG	Homo sapiens
1242_at	ETS2 repressor factor(ERF)	RG	Homo sapiens
37584_at	FA complementation group G(FANCG)	RG	Homo sapiens
36669_at	FosB proto-oncogene AP-1 transcription factor subunit(FOSB)	RG	Homo sapiens
31522_f_at	H2B clustered histone 7(H2BC7)	RG	Homo sapiens
31521_f_at	H4 clustered histone 12(H4C12)	RG	Homo sapiens
762_f_at	H4 clustered histone 9(H4C9)	RG	Homo sapiens
39698_at	HOP homeobox(HOPX)	RG	Homo sapiens
1895_at, 32583_at	Jun proto-oncogene AP-1 transcription factor subunit(JUN)	RG	Homo sapiens
224_at, 38374_at	KLF transcription factor 10(KLF10)	RG	Homo sapiens
35160_at	LIM domain binding 1(LDB1)	RG	Homo sapiens
36711_at	MAF bZIP transcription factor F(MAFF)	RG	Homo sapiens
41505_r_at	MAF bZIP transcription factor(MAF)	RG	Homo sapiens

Functional Annotation Clustering Tool

Functional Annotation Clustering

Current Gene List: demolist2
Current Population: Homo sapiens

Retrieve 2D-View for the
current cluster

[Switch to Classic Version](#)
[Help](#)

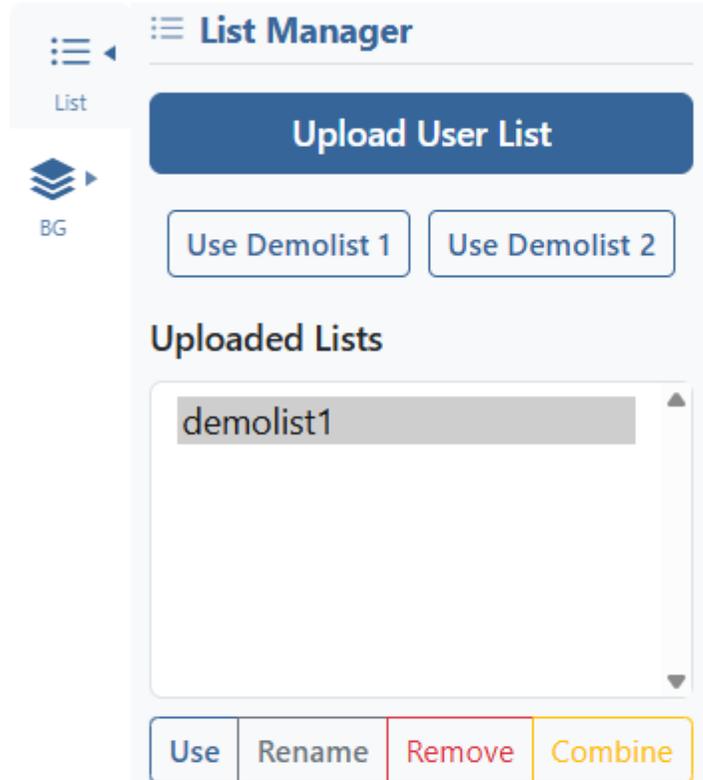
Show options Classification Stringency: Medium EASE Threshold: 1 Update Table

Search: 102 annotation clusters Create sublist Copy Excel CSV PDF Column visibility

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
Term Cluster 1			Enrichment Score: 3.18			G		
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of transcription by RNA polymerase II	RT	12.10%	45	12.10	1.12e-7	3.00e-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of transcription by RNA polymerase II	RT	13.17%	49	13.17	5.02e-7	4.50e-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription repressor activity, RNA polymerase II-specific	RT	5.11%	19	5.11	9.84e-6	1.42e-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	chromatin	RT	10.75%	40	10.75	5.36e-5	3.65e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase II cis-regulatory region sequence-specific DNA binding	RT	10.75%	40	10.75	7.93e-5	7.16e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription factor activity	RT	8.06%	30	8.06	1.28e-4	9.43e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription activator activity, RNA polymerase II-specific	RT	5.91%	22	5.91	1.31e-4	9.43e-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	sequence-specific DNA binding	RT	5.91%	22	5.91	6.44e-4	3.32e-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	sequence-specific double-stranded DNA binding	RT	6.72%	25	6.72	8.58e-4	4.13e-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of transcription by RNA polymerase II	RT	12.63%	47	12.63	1.90e-3	1.34e-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription factor activity, RNA polymerase II-specific	RT	9.95%	37	9.95	5.56e-3	1.54e-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of DNA-templated transcription	RT	10.75%	40	10.75	1.74e-2	4.78e-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA binding	RT	15.59%	58	15.59	2.34e-2	4.33e-1
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Transcription	RT	15.82%	57	15.32	2.10e-1	1.00e+0
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Transcription regulation	RT	14.78%	55	14.78	2.34e-1	1.00e+0
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	DNA-binding	RT	13.17%	49	13.17	3.10e-1	1.00e+0
Term Cluster 2			Enrichment Score: 2.96			G		
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleoplasm	RT	27.96%	104	27.96	2.16e-5	2.05e-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleus	RT	40.59%	151	40.59	1.02e-3	3.25e-2
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Nucleus	RT	33.60%	125	33.60	6.08e-2	4.98e-1
Term Cluster 3			Enrichment Score: 2.73			G		
<input type="checkbox"/>	GOTERM_CC_DIRECT	neuronal cell body	RT	5.65%	21	5.65	1.03e-5	1.23e-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	axon	RT	4.57%	17	4.57	3.87e-3	9.12e-2

Gene Functional Classification

Ready for Analysis



List Manager

Upload User List

Use Demolist 1 Use Demolist 2

Uploaded Lists

demolist1

Use Rename Remove Combine

Analysis Wizard

Step 1. Successfully submitted gene list

Current Gene List: demolist1
Current Population: Homo sapiens

Step 2. Analyze the your list with one of DAVID's tools

- Gene List Report
- **Functional Annotation Tool**
 - [Functional Annotation Table](#)
 - [Functional Annotation Chart](#)
 - [Functional Annotation Clustering](#)
- Gene Functional Classification Tool 
- Ortholog Tool
- Gene ID Conversion Tool

 [You may access the legacy Analysis Wizard here.](#)

Gene Functional Classification Tool

Gene Functional Classification

Current Gene List: demolist2
Current Population: Homo sapiens

See the annotation in next two slides

Switch to Classic Version
Help

Hide Options

Classification Stringency: Medium

Update Table

Kappa Similarity

Similarity Term Overlap

4

Similarity Threshold

0.35

Classification

Initial Group Membership

4

Final Group Membership

4

Multiple Linkage Threshold

0.50

Search:

10 gene clusters

12

Create sublist

Copy

Excel

CSV

PDF

Gene Cluster (Sublist)

Gene Name

Gene Cluster 1

Enrichment Score: 3.26

Related Genes

Terms

19

[basic helix-loop-helix family member e40\(BHLHE40\)](#)

20

[zinc finger protein 148\(ZNF148\)](#)

[PR/SET domain 2\(PRDM2\)](#)

[activating transcription factor 3\(ATF3\)](#)

[MAX dimerization protein 1\(MXD1\)](#)

[SRY-box transcription factor 10\(SOX10\)](#)

[zinc finger protein 137_pseudogene\(ZNF137P\)](#)

[polyhomeotic homolog 2\(PHC2\)](#)

[NK2 homeobox 8\(NKX2-8\)](#)

[early growth response 1\(EGR1\)](#)

Gene Functional Classification Tool

1. Gene List

Current gene list selected for view and background species being analyzed.

2. Help and Switch to Classic Version

Link to this help page and provides access to the legacy Gene List Report interface.

3. Show/Hide Options

Click this button to expand or hide additional filtering options.

4. Classification Stringency

Click to access a drop-down menu of stringency levels, then click desired level to select. A high-level single control to establish a set of detailed parameters involved in functional classification algorithms. In general, the higher stringency setting generates less functional groups with more tightly associated genes in each group, so that more genes will be unclustered.

5. Update Table

After making adjustments to filtering options, click this button to update the table using the selected parameters.

6. Similarity Term Overlap

Click to access a drop-down menu of overlap values. The minimum number of annotation terms overlapped between two genes in order to be qualified for kappa calculation. This parameter is to maintain necessary statistical power to make the kappa value more meaningful. The higher the value, the more meaningful the result is.

7. Similarity Threshold

Click to access a drop-down menu of threshold values. The minimum kappa value to be considered significant. A higher setting will lead to more genes going unclustered, which leads to a higher quality functional classification result with fewer groups and fewer gene members. Kappa value of 0.3 starts giving meaningful biology based on our genome-wide distribution study. Anything below 0.3 has a good chance to be noise.

8. Initial Group Membership

Click to access a drop-down menu of membership values. The minimum gene number in a seeding group, which affects the minimum size of each functional group in the final cluster. In general, the lower value attempts to include more genes in functional groups, and may generate a lot of small size groups.

9. Final Group Membership

Click to access a drop-down menu of membership values. The minimum gene number in one final group after a 'cleanup' procedure. In general, the lower value attempts to include more genes in functional groups and may generate a lot of small size groups. It cofunctions with previous parameters to control the minimum size of functional groups. If you are interested in functional groups containing only 2 or 3 genes, you need to set it to a very low value. Otherwise, the small group will not be displayed and the genes will go unclustered.

Gene Functional Classification Tool

10. Multiple Linkage Threshold

Click to access a drop-down menu of threshold values. This parameter controls how seeding groups merge with each other, i.e. two groups sharing the same gene members over the percentage will become one group. A higher percentage, in general, gives sharper separation (i.e. it generates more final functional groups with more tightly associated genes in each group). In addition, changing the parameter does not cause additional genes to go unclustered.

11. Search & Cluster count

The search box filters all table results in real time and shows how many clusters are present in results.

12. Create sublist, Export options & Column Visibility

Create a sublist by clicking on checkboxes to the left of desired results, then clicking the **Create sublist** button, where you will be prompted to name the new sublist. Sublists will then appear in the list manager as a new gene list.

Results can be exported using Copy, Excel, CSV, or PDF. Exports reflect the current filtered and sorted view.

Additional columns can be added to the current view using the **Column Visibility** drop-down button. Click on available items to add the column to the table.

13. Sortable Columns

Click on any table column header to sort the table by that column in ascending or descending order.

14. Cluster

A group of genes having similar biological meaning due to sharing similar terms.

15. Enrichment Score

The overall enrichment score for the group based on the EASE scores of each gene. Higher value = more enriched.

16. Related Genes (RG)

Click the **RG** link to explore functionally related genes associated with each entry. For more information, see the [Related Genes documentation page](#).

17. Terms

Click the **Terms** link to explore the Cluster Term Report for each gene. For more information, see the [Cluster Term Report documentation page](#).

18. Cluster view

Click this icon to be directed to a 2D cluster view of the genes in this cluster.

19. Sublist

Click on check boxes to select items for creating a sublist. [\(12\)](#)

20. Gene Name

Click the gene name link to explore the full gene report. For more information, see the [Gene Report documentation page](#).

Gene Functional Classification Tool



Gene Functional Classification

Current Gene List: demolist2
Current Population: Homo sapiens

[Switch to Classic Version](#)
[Help](#)

Show options

Classification Stringency: Medium

Update Table

Search: 10 gene clusters

[Create sublist](#) [Copy](#) [Excel](#) [CSV](#) [PDF](#)

Gene Cluster (<input checked="" type="checkbox"/> Sublist)	Gene Name		
Gene Cluster 1	Enrichment Score: 3.26	Related Genes	Terms
<input type="checkbox"/>	basic helix-loop-helix family member e40(BHLHE40)		
<input type="checkbox"/>	zinc finger protein 148(ZNF148)		
<input type="checkbox"/>	PR/SET domain 2(PRDM2)		
<input type="checkbox"/>	activating transcription factor 3(ATF3)		
<input type="checkbox"/>	MAX dimerization protein 1(MXD1)		
<input type="checkbox"/>	SRY-box transcription factor 10(SOX10)		
<input type="checkbox"/>	zinc finger protein 137, pseudogene(ZNF137P)		
<input type="checkbox"/>	polyhomeotic homolog 2(PHC2)		
<input type="checkbox"/>	NK2 homeobox 8(NKX2-8)		
<input type="checkbox"/>	early growth response 1(EGR1)		
<input type="checkbox"/>	homeobox C11(HOXC11)		
<input type="checkbox"/>	POU class 2 homeobox 3(POU2F3)		
<input type="checkbox"/>	musculin(MSC)		
<input type="checkbox"/>	MAF bZIP transcription factor F(MAFF)		
<input type="checkbox"/>	zinc finger protein 263(ZNF263)		
<input type="checkbox"/>	KLF transcription factor 10(KLF10)		
<input type="checkbox"/>	zinc finger protein 780A(ZNF780A)		
<input type="checkbox"/>	zinc finger protein 282(ZNF282)		

Gene Functional Classification Tool

Functionally Related Genes

Current Gene List: demolist2

Current Population: Homo sapiens

Number of genes searched: 372

[🕒 Switch to Classic Version](#)

[🔗 Help](#)

Find Related Genes in: Similarity Term Overlap: Similarity Threshold:

Similarity Score Legend: ■ Very High (0.75-1) ■ High (0.5-0.75) ■ Moderate (0.25-0.5) ■ Low (<0.25)

Search: 32 related genes

Related Gene	Species	Kappa
musculin(MSC)	Homo sapiens	0.62
MAX dimerization protein 1(MXD1)	Homo sapiens	0.61
MAF bZIP transcription factor F(MAFF)	Homo sapiens	0.61
ETS2 repressor factor(ERF)	Homo sapiens	0.58
homeobox C11(HOXC11)	Homo sapiens	0.57
KLF transcription factor 10(KLF10)	Homo sapiens	0.55
POU class 2 homeobox 3(POU2F3)	Homo sapiens	0.55
zinc finger protein 263(ZNF263)	Homo sapiens	0.51
forkhead box E1(FOXE1)	Homo sapiens	0.50
NK2 homeobox 8(NKX2-8)	Homo sapiens	0.50
activating transcription factor 3(ATF3)	Homo sapiens	0.49
POU class 2 homeobox 2(POU2F2)	Homo sapiens	0.49
FosB proto-oncogene, AP-1 transcription factor subunit(FOSB)	Homo sapiens	0.48
zinc finger and BTB domain containing 5(ZBTB6)	Homo sapiens	0.46
zinc finger protein 282(ZNF282)	Homo sapiens	0.46
SIX homeobox 6(SIX6)	Homo sapiens	0.46
zinc finger protein 148(ZNF148)	Homo sapiens	0.45
PBX homeobox 3(PBX3)	Homo sapiens	0.44
ETS variant transcription factor 6(ETV6)	Homo sapiens	0.43

Gene Functional Classification Tool



Gene Functional Classification

Current Gene List: demolist2
Current Population: Homo sapiens

[Switch to Classic Version](#)
[Help](#)

Show options

Classification Stringency: Medium

Update Table

Search: 10 gene clusters

Create sublist Copy Excel CSV PDF

Gene Cluster (<input checked="" type="checkbox"/> Sublist)	Gene Name		
Gene Cluster 1	Enrichment Score: 3.26	Related Genes	Terms
<input type="checkbox"/>	basic helix-loop-helix family member e40(BHLHE40)		
<input type="checkbox"/>	zinc finger protein 148(ZNF148)		
<input type="checkbox"/>	PR/SET domain 2(PRDM2)		
<input type="checkbox"/>	activating transcription factor 3(ATF3)		
<input type="checkbox"/>	MAX dimerization protein 1(MXD1)		
<input type="checkbox"/>	SRY-box transcription factor 10(SOX10)		
<input type="checkbox"/>	zinc finger protein 137, pseudogene(ZNF137P)		
<input type="checkbox"/>	polyhomeotic homolog 2(PHC2)		
<input type="checkbox"/>	NK2 homeobox 8(NKX2-8)		
<input type="checkbox"/>	early growth response 1(EGR1)		
<input type="checkbox"/>	homeobox C11(HOXC11)		
<input type="checkbox"/>	POU class 2 homeobox 3(POU2F3)		
<input type="checkbox"/>	musculin(MSC)		
<input type="checkbox"/>	MAF bZIP transcription factor F(MAFF)		
<input type="checkbox"/>	zinc finger protein 263(ZNF263)		
<input type="checkbox"/>	KLF transcription factor 10(KLF10)		
<input type="checkbox"/>	zinc finger protein 780A(ZNF780A)		
<input type="checkbox"/>	zinc finger protein 282(ZNF282)		

Gene Functional Classification Tool

Cluster Term Report

Current Gene List: demolist2
 Current Population: Homo sapiens
 Gene Cluster 1 (31 DAVID genes)

[Switch to Classic Version](#)
[Help](#)

Search: 539 term records

[Create sublist](#) [Copy](#) [Excel](#) [CSV](#) [PDF](#) [Column visibility](#)

Sublist	Category	Term	RT	Genes in Cluster	Count	P-Value	Genes Not in Cluster
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase II cis-regulatory region sequence-specific DNA binding	RT	87.10%	27	7.66e-29	12.90%
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA binding	RT	96.77%	30	9.12e-26	3.23%
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription factor activity, RNA polymerase II-specific	RT	80.65%	25	9.43e-24	19.35%
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	DNA-binding	RT	100.00%	31	2.62e-23	
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription factor activity	RT	67.74%	21	7.56e-22	32.26%
<input type="checkbox"/>	GOTERM_MF_DIRECT	sequence-specific double-stranded DNA binding	RT	64.52%	20	2.22e-21	35.48%
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of transcription by RNA polymerase II	RT	80.65%	25	4.88e-21	19.35%
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of DNA-templated transcription	RT	74.19%	23	1.20e-18	25.81%
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Transcription regulation	RT	87.10%	27	2.31e-18	12.90%
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Transcription	RT	87.10%	27	4.94e-18	12.90%
<input type="checkbox"/>	GOTERM_CC_DIRECT	chromatin	RT	64.52%	20	3.79e-17	35.48%
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of transcription by RNA polymerase II	RT	61.29%	19	4.29e-16	38.71%
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription activator activity, RNA polymerase II-specific	RT	48.39%	15	1.42e-15	51.61%
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Nucleus	RT	100.00%	31	2.87e-15	
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleus	RT	100.00%	31	7.73e-15	
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-binding transcription repressor activity, RNA polymerase II-specific	RT	41.94%	13	8.31e-15	58.06%
<input type="checkbox"/>	GOTERM_MF_DIRECT	sequence-specific DNA binding	RT	45.15%	14	2.35e-13	54.84%
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of transcription by RNA polymerase II	RT	54.84%	17	4.16e-12	45.16%
<input type="checkbox"/>	UP_SEQ_FEATURE	ZN_FING:C2H2-type 1	RT	35.48%	11	3.63e-9	64.52%
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Repressor	RT	41.94%	13	1.67e-8	58.06%

Gene Functional Classification Tool



Gene Functional Classification

Current Gene List: demolist2
Current Population: Homo sapiens

[Switch to Classic Version](#)
[Help](#)

Show options

Classification Stringency: Medium

Update Table

Search: 10 gene clusters

[Create sublist](#) [Copy](#) [Excel](#) [CSV](#) [PDF](#)

Gene Cluster (<input checked="" type="checkbox"/> Sublist)	Gene Name		
Gene Cluster 1	Enrichment Score: 3.26	Related Genes	Terms
<input type="checkbox"/>	basic helix-loop-helix family member e40(BHLHE40)		
<input type="checkbox"/>	zinc finger protein 148(ZNF148)		
<input type="checkbox"/>	PR/SET domain 2(PRDM2)		
<input type="checkbox"/>	activating transcription factor 3(ATF3)		
<input type="checkbox"/>	MAX dimerization protein 1(MXD1)		
<input type="checkbox"/>	SRY-box transcription factor 10(SOX10)		
<input type="checkbox"/>	zinc finger protein 137, pseudogene(ZNF137P)		
<input type="checkbox"/>	polyhomeotic homolog 2(PHC2)		
<input type="checkbox"/>	NK2 homeobox 8(NKX2-8)		
<input type="checkbox"/>	early growth response 1(EGR1)		
<input type="checkbox"/>	homeobox C11(HOXC11)		
<input type="checkbox"/>	POU class 2 homeobox 3(POU2F3)		
<input type="checkbox"/>	musculin(MSC)		
<input type="checkbox"/>	MAF bZIP transcription factor F(MAFF)		
<input type="checkbox"/>	zinc finger protein 263(ZNF263)		
<input type="checkbox"/>	KLF transcription factor 10(KLF10)		
<input type="checkbox"/>	zinc finger protein 780A(ZNF780A)		
<input type="checkbox"/>	zinc finger protein 282(ZNF282)		



Gene Functional Classification Tool

2D View

[Help](#)

■ corresponding gene-term association positively reported ■ corresponding gene-term association not reported yet

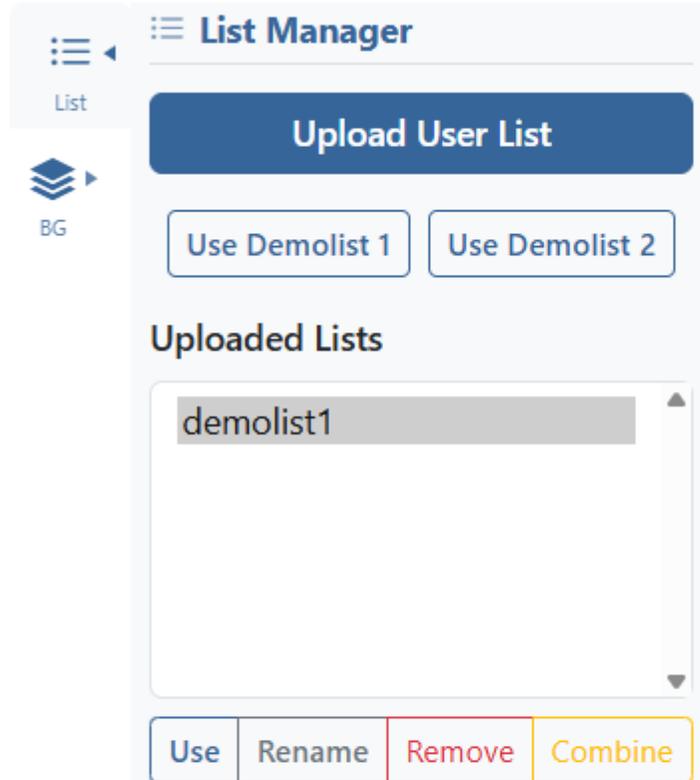
 [Download File](#)



GO:0005634-nucleus
KW-0539-nucleus
KW-0238-DNA-binding
GO:0003677-DNA binding
REGION:Disordered
KW-0904-Transcription
KW-0895-Transcription regulation
GO:0000978-RNA polymerase II cis-regulatory region sequence-specific DNA binding
GO:0006357-regulation of transcription by RNA polymerase II
GO:000981-DNA-binding transcription factor activity, RNA polymerase II-specific
GO:0005515-protein binding
GO:0006355-regulation of DNA-templated transcription
GO:0003700-DNA-binding transcription factor activity
GO:0000785-chromatin
GO:1990837-sequence-specific double-stranded DNA binding
GO:0005654-nucleoplasm
GO:0000122-negative regulation of transcription by RNA polymerase II
COMPARAS:Low complexity
GO:0005544-positive regulation of transcription by RNA polymerase II
COMPARAS:Basic and acidic residues
KW-0832-Ub1 conjugation

DAVID Ortholog Analysis

DAVID Ortholog Analysis



List Manager

Upload User List

Use Demolist 1 Use Demolist 2

Uploaded Lists

demolist1

Use Rename Remove Combine

Analysis Wizard

Step 1. Successfully submitted gene list

Current Gene List: demolist1

Current Population: Homo sapiens

Step 2. Analyze the your list with one of DAVID's tools

- Gene List Report
- **Functional Annotation Tool**
 - [Functional Annotation Table](#)
 - [Functional Annotation Chart](#)
 - [Functional Annotation Clustering](#)
- Gene Functional Classification Tool
- Ortholog Tool ←
- Gene ID Conversion Tool

[You may access the legacy Analysis Wizard here.](#)

DAVID Ortholog Analysis

DAVID Ortholog

Current Gene List: demolist2
Current Population: Homo sapiens

See the annotation on next slide

Help

Select an ortholog taxonomy: Mus musculus (house mouse)

Mus musculus (house mouse)

OMA

92.20%

Click an ortholog source to view detailed results.

Ensembl

93.01%

Load ortholog list into DAVID for analysis

Select All Multi-Orthologs

Show All Multi-Orthologs

Current Gene

Ortholog Count

ENSEMBL Mus musculus (house mouse) Orthologs

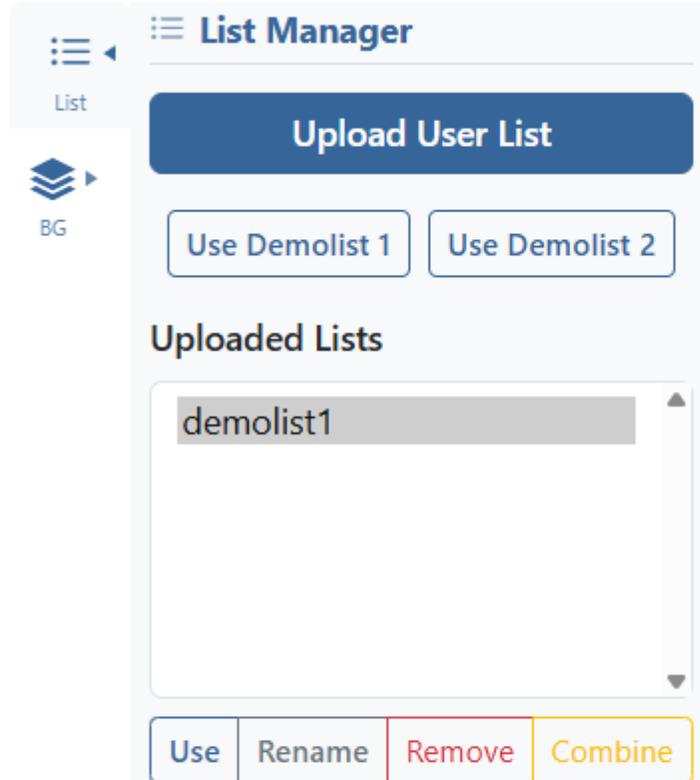
Current Gene	Ortholog Count	Ortholog Name	%Identity	Confidence
kallikrein related peptidase 3(KLK3)	14	<input checked="" type="checkbox"/> kallikrein 1-related peptidase b21(Kik1b21)	56.32	Low
serpin family A member 3(SERPINA3)	10	<input checked="" type="checkbox"/> serine (or cysteine) peptidase inhibitor, clade A, member 3N(Serpina3n)	61.23	High
serpin family B member 9(SERPINB9)	8	<input checked="" type="checkbox"/> serine (or cysteine) peptidase inhibitor, clade B, member 9c(Serpinb9c)	62.50	High
leukocyte immunoglobulin like receptor A4(LILRA4)	7	<input checked="" type="checkbox"/> paired-Ig-like receptor A12(Pira12)	49.50	Low

DAVID Ortholog Analysis

- 1. Current Gene List & Population**
Displays the active gene list and selected species or background population.
- 2. Help and Switch to Classic Version**
Link to this help page and provides access to the legacy Gene List Report interface.
- 3. Ortholog Taxonomy**
Click the dropdown box to select a target ortholog taxonomy (species). After clicking on the box, a search box is also available to type and search for taxonomies. Click on the taxonomy to select, then the ortholog sources will populate.
- 4. Species**
Click the **Species** link to go to NCBI taxonomy entry.
- 5. OMA**
Shows the percentage of genes from the list with an ortholog available for the selected taxonomy from Orthologous Matrix (OMA) Click the percentage bar to retrieve orthologs from that source.
- 6. Ensembl**
Shows the percentage of genes from the list with an ortholog available for the selected taxonomy from Ensembl Compara. Click the percentage bar to retrieve orthologs from that source.
- 7. Load to DAVID**
Load selected orthologs into a DAVID list for downstream analysis.
- 8. Select All**
Select All Multi-Orthologs will select all available orthologs. Click again to **Deselect** all. Click again to select only the first ortholog if there are multiple available (default).
- 9. Show**
Show/Hide all multi-orthologs
- 10. Sortable Columns**
Click any column header to sort by User ID, Expression Value, DAVID Gene Name, Related Genes (RG), or Species.
- 11. Gene name**
Click the gene name link to explore the full gene report. For more information, see the [Gene Report documentation page](#).
- 12. Ortholog count**
Number of ortholog genes available for the user gene in the selected taxonomy.
- 13. Expand**
Show/Hide all multi-orthologs
- 14. Select**
Selected orthologs are loaded as a new DAVID list when clicking the **Load ortholog list into DAVID for analysis** button.
- 15. Ortholog Gene name**
Click the gene name link to explore the full gene report. For more information, see the [Gene Report documentation page](#).
- 16. Identity**
Sequence identity between user gene and ortholog gene. Higher meaning more identical.
- 17. Confidence**
Confidence score. Only available for Ensembl results.

DAVID Gene ID Conversion

DAVID Gene ID Conversion



Analysis Wizard

Step 1. Successfully submitted gene list

Current Gene List: demolist1

Current Population: Homo sapiens

Step 2. Analyze the your list with one of DAVID's tools

- Gene List Report
- **Functional Annotation Tool**
 - [Functional Annotation Table](#)
 - [Functional Annotation Chart](#)
 - [Functional Annotation Clustering](#)
- Gene Functional Classification Tool
- Ortholog Tool
- Gene ID Conversion Tool 

 [You may access the legacy Analysis Wizard here.](#)

DAVID Gene ID Conversion

Gene ID Conversion Tool

Current Gene List: demolist2 **1** See the annotation on next slide

Current Population: Homo sapiens

2 [Switch to Classic Version](#)
[Help](#)

Convert To: OFFICIAL_GENE_SYMBOL (100.00%) **3**

Submit Converted List to DAVID **4**

Search: **5**

6

[Copy](#) [Excel](#) [CSV](#) [PDF](#)

OFFICIAL_GENE_SYMBOL	Original ID	Value	Gene Name	Related Genes	Species
ABHD2 7	41088_at 8	2 10	abhydrolase domain containing 2, acylglycerol lipase(ABHD2) 11	RG 12	Homo sapiens
ACADS	39408_at	2	acyl-CoA dehydrogenase short chain(ACADS)	RG	Homo sapiens
ACOT11	32405_at	2	acyl-CoA thioesterase 11(ACOT11)	RG	Homo sapiens
ACP2	36651_at	2	acid phosphatase 2, lysosomal(ACP2)	RG	Homo sapiens
ACTA1	31737_at	2	actin alpha 1, skeletal muscle(ACTA1)	RG	Homo sapiens
ADCYAP1	36754_at	2	adenylate cyclase activating polypeptide 1(ADCYAP1)	RG	Homo sapiens
ADD2	36052_at	2	adducin 2(ADD2)	RG	Homo sapiens
ADH6	37206_at	2	alcohol dehydrogenase 6 (class V)(ADH6)	RG	Homo sapiens
ADRA1D	36728_at	2	adrenoceptor alpha 1D(ADRA1D)	RG	Homo sapiens
AFDN	41105_s_at	2	afadin, adherens junction formation factor(AFDN)	RG	Homo sapiens
AGGF1	35067_at	2	angiogenic factor with G-patch and FHA domains 1(AGGF1)	RG	Homo sapiens
AHSG	36621_at	2	alpha 2-HS glycoprotein(AHSG)	RG	Homo sapiens
ALCAM	38642_at	2	activated leukocyte cell adhesion molecule(ALCAM)	RG	Homo sapiens
ALDOB	33455_at	2	aldolase, fructose-bisphosphate B(ALDOB)	RG	Homo sapiens
AMIGO2	32919_at	2	adhesion molecule with Ig like domain 2(AMIGO2)	RG	Homo sapiens
AMPD3	38463_s_at	2	adenosine monophosphate deaminase 3(AMPD3)	RG	Homo sapiens
ANGEL1	36865_at	2	angel homolog 1(ANGEL1)	RG	Homo sapiens
ANKLE2	39519_at	2	ankyrin repeat and LEM domain containing 2(ANKLE2)	RG	Homo sapiens

DAVID Gene ID Conversion

1. Current Gene List & Population

Displays the active gene list and selected species or background population.

2. Help and Switch to Classic Version

Link to this help page and provides access to the legacy Gene List Report interface.

3. Conversion Destination Selection

Save the converted list to the DAVID list manager for use in further downstream analysis.

4. Submit Converted List to DAVID

Users will first be met with this dropdown box. Click *Select Identifier type* and choose an identifier destination, then the converted gene name list will populate.

Click this dropdown box again to change identifier destination and list will automatically update.

5. Search

The search box filters table results in real time.

6. Export Options

Results can be exported using Copy, Excel, CSV, or PDF. Exports reflect the current filtered and sorted view.

7. Selected Source ID

Gene identifier from selected source.

8. User ID

User uploaded gene ID name.

9. Sortable Columns

Click any column header to sort by Destination ID, User ID, Expression Value, DAVID Gene Name, Related Genes (RG), or Species.

10. Value

User uploaded expression value. (Optional)

11. Gene Name

Click the gene name link to explore the full gene report. For more information, see the [Gene Report documentation page](#).

12. Related Genes (RG)

Click the **RG** link to explore functionally related genes associated with each entry. For more information, see the [Related Genes documentation page](#).

13. Species

Click the **Species** link to go to NCBI taxonomy entry.

DAVID Gene Search / DAVID Gene Report

DAVID Gene Search

DAVID uses essential cookies to enable core functionality. By continuing to use DAVID, you acknowledge the use of these cookies.

- Gene Search
- Gene List Report
- Functional Annotation
 - Functional Annotation Clustering
 - Functional Annotation Chart
 - Functional Annotation Table
- Gene Functional Classification
- Ortholog
- Gene ID Conversion

About DAVID

The Database for Annotation, Visualization, and Integrated Discovery (DAVID) provides a comprehensive set of functional annotation tools to help understand the biological meaning of large gene lists.



Welcome to DAVID

The Database for Annotation, Visualization, and Integrated Discovery (**DAVID**)

DAVID provides a comprehensive set of functional annotation tools to help understand the biological meaning behind large gene lists. Powered by the **DAVID Knowledgebase**, it integrates multiple sources of functional annotations. DAVID is free to use for all, including commercial users, without login. Please [cite DAVID](#) within any publication that makes use of any methods inspired by DAVID.

DAVID tools can:

- Identify enriched biological themes.
- Discover enriched functional-related gene groups.
- Cluster redundant annotation terms.
- Visualize genes on BioCarta & KEGG pathway maps.
- Display many-genes-to-many-terms relationships in 2D.
- Search for functionally related genes not in the list.
- List interacting proteins.

Spotlights

DAVID Forum: Ask questions, suggest functions, or help other users.

FAQ: Frequently Asked Questions.

LHRI Publications: Publications of the Laboratory of Human Retrovirology and Immunoinformatics.

What's New

February 28, 2026

DAVID now features modernized interfaces across all major analysis tools, including a taxonomy-based list upload workflow with support for multiple file formats. Links to legacy interfaces are available on each updated page.

December 31, 2025

DAVID Knowledgebase v2025_2 released.

September 16, 2025

New DAVID [Gene Search](#) tool released.

April 17, 2025

DAVID Knowledgebase v2025_1 released.

DAVID Statistics

[78.8K Citations](#)

Average Daily researchers.

Annual Usage:

DAVID Web Address: <https://davidbioinformatics.nih.gov/>

DAVID Gene Search

Gene Search is a lookup tool to allow users to navigate directly to a DAVID Gene Report page for a given gene.

DAVID Gene Search

1 Help

2 Identifier

3 Select Taxonomy

Results

Input ID ⁴	ID Type ⁵	DAVID Gene Name ⁶
IL27	OFFICIAL_GENE_SYMBOL	interleukin 27(IL27)

1. Help and Switch to Classic Version

Link to this help page and provides access to the legacy Gene List Report interface.

2. Identifier search box

Type full identifier (case insensitive) and click on the blue **Lookup Taxonomy** button. If any results are found, the taxonomy selection box will appear. If no results are found, a red dialogue box will appear indicating "No taxonomies found for the identifier. Please try a different identifier."

3. Select Taxonomy

Once a valid identifier is entered, all available species with the identifier are populated in the Select Taxonomy drop down menu. The list of species is displayed alphabetically and can be searched by typing in the search bar within the dropdown (case insensitive). Click on a species name to select it, then click the green **Search DAVID** button to continue.

4. Input ID

User entered identifier.

5. ID Type

6. DAVID Gene Name

Full name of gene available from DAVID. Click the gene name link to explore the full gene report. For more information, see the [Gene Report documentation page](#).

DAVID Gene Report

Gene Report

See the annotation on next slide

1 Switch to Classic Version
Help

2 interleukin 27(IL27)

3 [Related Genes](#)

4 **Species:** [Homo sapiens](#)

5 **NCBI Gene Summary:** The protein encoded by this gene is one of the subunits of a heterodimeric cytokine complex. This protein is related to interleukin 12A (IL12A). It interacts with Epstein-Barr virus induced gene 3 (EBI3), a protein similar to interleukin 12B (IL12B), and forms a complex that has been shown to drive rapid expansion of naive but not memory CD4(+) T cells. The complex is also found to synergize strongly with interleukin 12 to trigger interferon gamma (IFNG) production of naive CD4(+) T cells. The biological effects of this cytokine are mediated by the class I cytokine receptor (WSX1/TCRR). [provided by RefSeq, Jul 2008]

6 [Functional Annotations](#) [Gene Ontology](#) [General Annotations](#) [Identifiers](#) [Literature](#) [Pathways](#) [Protein Domains](#)

7 Search:

8 [Copy](#) [Excel](#) [CSV](#) [PDF](#)

Category	Terms
9 Functional Annotations	
10 UP_KW_BIOLOGICAL_PROCESS	Immunity , Inflammatory response , Innate immunity 11
UP_KW_CELLULAR_COMPONENT	Secreted
UP_KW_MOLECULAR_FUNCTION	Cytokine , Antiviral protein
UP_KW_PTM	Glycoprotein
Gene Ontology	
	<ul style="list-style-type: none">positive regulation of defense response to virus by hostimmune system processinflammatory responsesignal transductionresponse to bacteriumpositive regulation of type II interferon productionregulation of T cell proliferation
GOTERM_BP_DIRECT	

DAVID Gene Report

1. Help and Switch to Classic Version

Link to this help page and provides access to the legacy Gene List Report interface.

2. Gene name

3. Related Genes (RG)

Click the **Related Genes** link to explore functionally related genes associated with each entry. For more information, see the [Related Genes documentation page](#).

4. Species

Click the **Species** link to go to NCBI taxonomy entry.

5. Gene Summary

Summary of gene information, provided by NCBI.

6. Navigate to categories

Click the tabs to jump to desired category of annotations.

7. Search and Record Count

The search box filters table results in real time. The record count indicates total entries and the number of DAVID genes mapped.

8. Export Options

Results can be exported using Copy, Excel, CSV, or PDF. Exports reflect the current filtered and sorted view.

9. Categories

Main categories shown in blue. Navigation tabs will jump to tops of these main headers.

10. Subcategories

Subcategories available per each resource.

11. Annotations

Annotations available for each item. If available, hyperlinks lead users to original resources for further details.

DAVID API

DAVID API allows other bioinformatics web sites to directly link to DAVID tools and functions **ONLY** for light-duty jobs (i.e. a gene list with no more than 400 genes). https://davidbioinformatics.nih.gov/content.jsp?file=DAVID_API.html

- **DAVID API is not for high-throughput or large gene list jobs, such as a job for a gene list with more than 500 genes or trying to loop through multiple gene lists. These types of uses should use the DAVID Webservice.**
- The URL has a character size limitation and therefore a very large gene list may not be completely passed in the GET call.

Example API Calls:

Functional Annotation Summary Page: https://davidbioinformatics.nih.gov/api.jsp?type=ENTREZ_GENE_ID&ids=2919,6347,6348,6364&tool=summary

Functional Annotation Chart:

https://davidbioinformatics.nih.gov/api.jsp?type=ENTREZ_GENE_ID&ids=2919,6347,6348,6364&tool=chartReport&annot=GOTERM_BP_FAT,GOTERM_CC_FAT,GOTERM_MF_FAT,INTERPRO,PIR_SUPERFAMILY,SMART,BBID,BIOCARTA,KEGG_PATHWAY,COG_ONTOLOGY,SP_PIR_KEYWORDS,UP_SEQ_FEATURE,GENETIC_ASSOCIATION_DB_DISEASE,OMIM_DISEASE

Functional Annotation Table:

https://davidbioinformatics.nih.gov/api.jsp?type=ENTREZ_GENE_ID&ids=2919,6347,6348,6364&tool=annotationReport&annot=GOTERM_BP_FAT,GOTERM_CC_FAT,GOTERM_MF_FAT,INTERPRO,PIR_SUPERFAMILY,SMART,BBID,BIOCARTA,KEGG_PATHWAY,COG_ONTOLOGY,SP_PIR_KEYWORDS,UP_SEQ_FEATURE,GENETIC_ASSOCIATION_DB_DISEASE,OMIM_DISEASE

Functional Annotation Clustering:

https://davidbioinformatics.nih.gov/api.jsp?type=ENTREZ_GENE_ID&ids=2919,6347,6348,6364&tool=term2term&annot=GOTERM_BP_FAT,GOTERM_CC_FAT,GOTERM_MF_FAT,INTERPRO,PIR_SUPERFAMILY,SMART,BBID,BIOCARTA,KEGG_PATHWAY,COG_ONTOLOGY,SP_PIR_KEYWORDS,UP_SEQ_FEATURE,GENETIC_ASSOCIATION_DB_DISEASE,OMIM_DISEASE

Gene Full Report: https://davidbioinformatics.nih.gov/api.jsp?type=ENTREZ_GENE_ID&ids=2919,6347,6348,6364&tool=geneReportFull

Gene Report: https://davidbioinformatics.nih.gov/api.jsp?type=ENTREZ_GENE_ID&ids=2919,6347,6348,6364&tool=geneReport

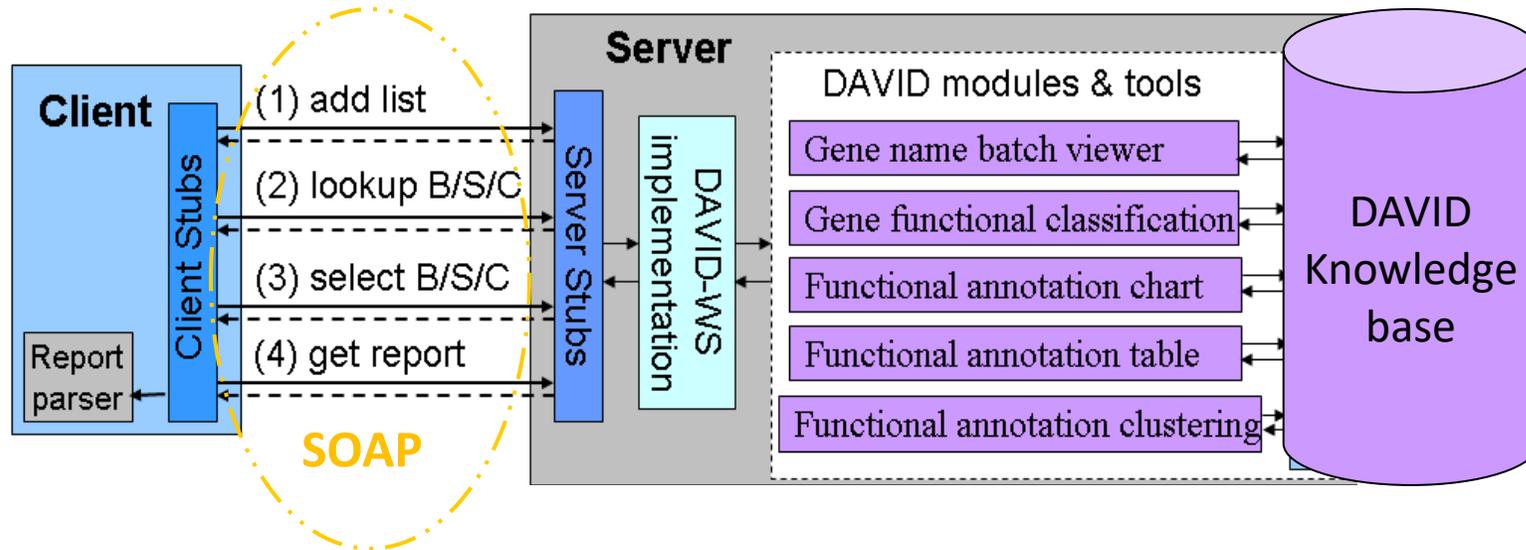
Show Gene List Names in Batch: https://davidbioinformatics.nih.gov/api.jsp?type=ENTREZ_GENE_ID&ids=2919,6347,6348,6364&tool=list

Gene Functional Classification: https://davidbioinformatics.nih.gov/api.jsp?type=ENTREZ_GENE_ID&ids=2919,6347,6348,6364,6351&tool=gene2gene

Stateful DAVID web services

Allows users to programmatically (Java, Perl, Python, R, C, etc) interact with DAVID and automate their tasks.

<https://davidbioinformatics.nih.gov/content.jsp?file=WS.html>



➤ **Simple Object Access Protocol (SOAP)**, exchanges XML messages between client and the Service provider (Java, C, Perl, Python, R, Matlab, etc...)

Example Python client for retrieving chart report

```
from suds.client import Client
import pandas as pd

url = 'https://davidbioinformatics.nih.gov/webservice/services/DAVIDWebService?wsdl'

print('url={}'.format(url))

# Create a service client using the wsdl. This only needs to be done once at the beginning of the code.
client = Client(url)
client.wsdl.services[0].setlocation('https://davidbioinformatics.nih.gov/webservice/services/DAVIDWebService.DAVIDWebServiceHttpSoap11Endpoint/')

#Authenticate user email. This only needs to be done once.
client.service.authenticate('bsherman@nih.gov')

# Define the input gene list file, identifier type, list type and a list name
inputFile = "demolist2.txt"
idType = 'AFFYMETRIX_3PRIME_IVT_ID'
listType = 0
listName = "demolist2"

# Set the annotation categories of interest and define the EASE and count thresholds for the chart report
categorySting = str(client.service.setCategories('OMIM_DISEASE,UP_KW_DISEASE,UP_KW_BIOLOGICAL_PROCESS,UP_KW_CELLULAR_COMPONENT,UP_KW_MOLECULAR_FUNCTION,UP_KW_PTM,UP_SEQ_FEATURE,GOTERM_BP_DIRECT,GOTERM_CC_DIRECT,GOTERM_MF_DIRECT,UP_KW_LIGAND,BBID,BIOCARTA,KEGG_PATHWAY,INTERPRO,PIR_SUPERFAMILY,SMART,UP_KW_DOMAIN'))
thd = 0.05
ct = 2

# Read input gene list file, convert ids to a comma-delimited string and upload the list to DAVID
df=pd.read_csv(inputFile, usecols=[0], delimiter='\t', index_col=False, names=['AFFYMETRIX_3PRIME_IVT_ID'])
inputIds = ",".join(df['AFFYMETRIX_3PRIME_IVT_ID'].astype(str).unique().tolist())
client.service.addList(inputIds, idType, listName, listType)

# Request a chart report for the input list using the previously set categories
chartReport = client.service.getChartReport(thd,ct)
numChartRecords = len(chartReport)
print('Total chart records:{}'.format(numChartRecords))

# Create a pandas dataframe from the returned chart records
dfResults = pd.DataFrame(columns = ['Category', 'Term', 'Count', 'Percent', 'PValue', 'Benjamini'])
for simpleChartRecord in chartReport:
    dfResults=dfResults.append({'Category':simpleChartRecord.categoryName, 'Term':simpleChartRecord.termName, 'Count':simpleChartRecord.listHits, 'Percent':simpleChartRecord.percent, 'PValue':simpleChartRecord.ease, 'Benjamini':simpleChartRecord.benjamini},ignore_index = True)
print(dfResults)
```

<https://davidbioinformatics.nih.gov/webservice/services/DAVIDWebService?wsdl>

getChartReport

```
▼<xs:element name="getChartReport">
  ▼<xs:complexType>
    ▼<xs:sequence>
      <xs:element name="args0" type="xs:double"/>
      <xs:element name="args1" type="xs:int"/>
    </xs:sequence>
  </xs:complexType>
</xs:element>
▼<xs:element name="getChartReportResponse">
  ▼<xs:complexType>
    ▼<xs:sequence>
      <xs:element maxOccurs="unbounded" minOccurs="0" name="result" nillable="true" type="ax22:simpleChartRecord"/>
    </xs:sequence>
  </xs:complexType>
</xs:element>
```

simpleChartRecord

```
▼<xs:complexType name="simpleChartRecord">
  ▼<xs:sequence>
    <xs:element minOccurs="0" name="EASEBonferroni" type="xs:double"/>
    <xs:element minOccurs="0" name="afdr" type="xs:double"/>
    <xs:element minOccurs="0" name="benjamini" type="xs:double"/>
    <xs:element minOccurs="0" name="bonferroni" type="xs:double"/>
    <xs:element minOccurs="0" name="categoryName" nillable="true" type="xs:string"/>
    <xs:element minOccurs="0" name="ease" type="xs:double"/>
    <xs:element minOccurs="0" name="fisher" type="xs:double"/>
    <xs:element minOccurs="0" name="foldEnrichment" type="xs:double"/>
    <xs:element minOccurs="0" name="geneIds" nillable="true" type="xs:string"/>
    <xs:element minOccurs="0" name="id" type="xs:int"/>
    <xs:element minOccurs="0" name="listHits" type="xs:int"/>
    <xs:element minOccurs="0" name="listName" nillable="true" type="xs:string"/>
    <xs:element minOccurs="0" name="listTotals" type="xs:int"/>
    <xs:element minOccurs="0" name="percent" type="xs:double"/>
    <xs:element minOccurs="0" name="popHits" type="xs:int"/>
    <xs:element minOccurs="0" name="popTotals" type="xs:int"/>
    <xs:element minOccurs="0" name="rfd" type="xs:double"/>
    <xs:element maxOccurs="unbounded" minOccurs="0" name="scores" nillable="true" type="xs:double"/>
    <xs:element minOccurs="0" name="termName" nillable="true" type="xs:string"/>
  </xs:sequence>
</xs:complexType>
```

```
url=https://davidbioinformatics.nih.gov/webservice/services/DAVIDWebService?wsdl
Total chart records:423
  Category                                     Term Count    Percent    PValue    Benjamini
0  GOTERM_MF_DIRECT                           GO:0005515~protein binding      297  79.838710  6.799082e-12  4.643773e-09
1  GOTERM_MF_DIRECT                           GO:0042802~identical protein binding      69  18.548387  4.670809e-09  1.595081e-06
2  GOTERM_BP_DIRECT                           GO:0000122~negative regulation of transcriptio...      43  11.559140  4.162287e-07  1.132975e-03
3  GOTERM_MF_DIRECT                           GO:0019904~protein domain specific binding      19   5.107527  1.538277e-06  3.502143e-04
4  GOTERM_BP_DIRECT                           GO:0043547~positive regulation of GTPase activity      16   4.301075  1.837221e-06  1.731119e-03
...
418 INTERPRO IPR004014:Cation-transporting P-type ATPase, N...      3   0.806452  4.826428e-02  1.000000e+00
419 KEGG_PATHWAY hsa04625:C-type lectin receptor signaling pathway      7   1.881720  4.916513e-02  3.054514e-01
420 GOTERM_BP_DIRECT GO:2000573~positive regulation of DNA biosynth...      3   0.806452  4.930223e-02  7.341744e-01
421 GOTERM_BP_DIRECT GO:0045747~positive regulation of Notch signal...      4   1.075269  4.932326e-02  7.341744e-01
422 GOTERM_BP_DIRECT GO:0007229~integrin-mediated signaling pathway      6   1.612903  4.974697e-02  7.341744e-01
```

Acknowledgements

NIAID, NIH

- Cliff Lane

Frederick National Laboratory

- Michael Baseler
- LHRI
 - Tomozumi Imamichi
 - Ganesh Panzade
 - Ming Hao
 - Lei Xu
 - Xuan Li
- IT Support:
 - Sharon Beck
 - Bill Wilton
 - Shawn Steward
 - James Bellande

Frederick National Laboratory

- Advanced Biomedical Computational Science (ABCS) staff:
 - Jack Collins
 - Uma Mudunuri
 - Henri Tuthill
 - Anney Che
 - David Bryant
- Previous DAVID Bioinformatics Team:
 - Richard Lempicki
 - Glynn Dennis
 - Doug Hosack
 - Da Wei Huang
 - Xiaoli Jiao
 - Ju Qiu