

An Introduction to DAVID for Functional Enrichment Analysis

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Outline

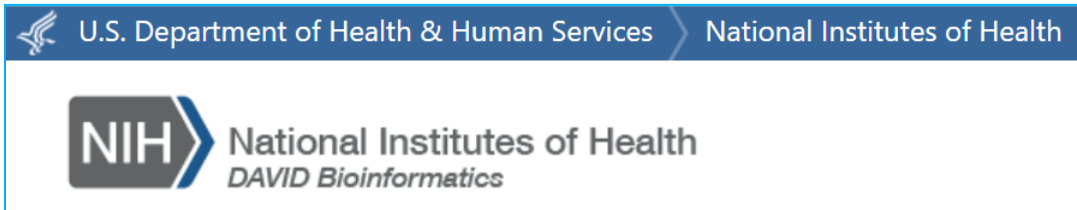
- Overview of DAVID
 - Introduction and history of DAVID
 - The importance of DAVID for scientific community
 - Introduction of DAVID tools
- Demo
 - DAVID tools
 - DAVID API
 - DAVID Webservice

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 consists 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

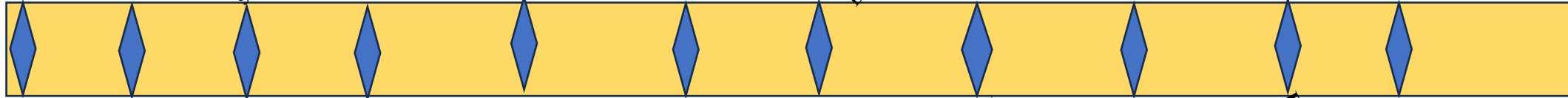
DAVID 2.0 Beta Nov. 2004
Pathway Mapping" to allocate given genes on
static pathway pictures

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 update
Quarterly knowledgebase update
since Jan. 2021**

Citation of DAVID

TITLE	CITED BY	YEAR
<input type="checkbox"/> 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	1826	2022
<input type="checkbox"/> 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	1041	2012
<input type="checkbox"/> 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	429	2009
<input type="checkbox"/> 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	12888	2009
<input type="checkbox"/> Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources DW Huang, BT Sherman, RA Lempicki Nature protocols 4 (1), 44-57	21540	2009
<input type="checkbox"/> DAVID gene ID conversion tool BTS Da Wei Huang, R Stephens, MW Baseler, HC Lane, RA Lempicki Bioinformation 2 (10), 428-430	188	2008
<input type="checkbox"/> DAVID gene ID conversion tool BT Sherman, R Stephens, MW Baseler, HC Lane, RA Lempicki Bioinformation 2 (10), 428	39	2008
<input type="checkbox"/> 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, 1-11	573	2007
<input type="checkbox"/> 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, 1-16	2374	2007
<input type="checkbox"/> 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	1871	2007
<input type="checkbox"/> Identifying biological themes within lists of genes with EASE DA Hosack, G Dennis, BT Sherman, HC Lane, RA Lempicki Genome biology 4, 1-8	2222	2003
<input type="checkbox"/> DAVID: database for annotation, visualization, and integrated discovery G Dennis, BT Sherman, DA Hosack, J Yang, W Gao, HC Lane, ... Genome biology 4, 1-11	10321	2003

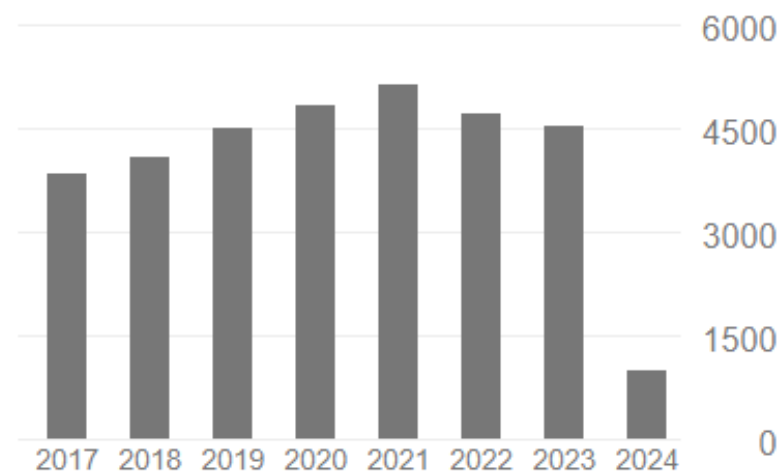
Cited by

[VIEW ALL](#)

All

Since 2019

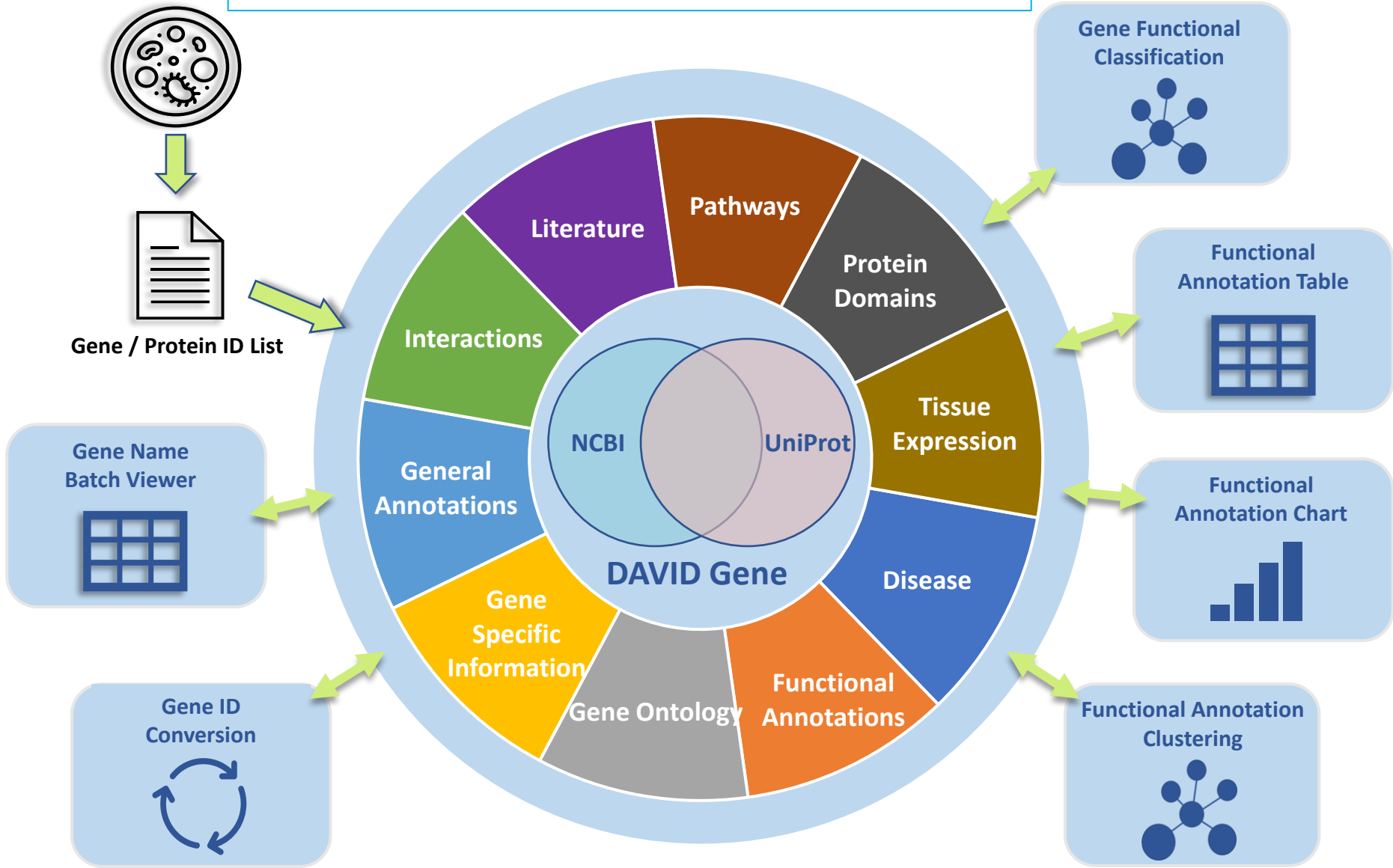
Citations	55312	24926
h-index	12	11
i10-index	12	12



DAVID Google Scholar

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

Data acquired: 03/21/2024



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
- **Demo**
 - DAVID tools
 - DAVID Webservice
 - DAVID API

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

Start DAVID Analysis

Overview

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

- Identify enriched biological themes, particularly GO terms
- Discover enriched functional-related gene groups
- Cluster redundant annotation terms
- Visualize genes on BioCarta & KEGG pathway maps
- Display related many-genes-to-many-terms on 2-D view.
- Search for other functionally related genes not in the list
- List interacting proteins
- Explore gene names in batch
- Link gene-disease associations
- Highlight protein functional domains and motifs
- Redirect to related literatures
- Convert gene identifiers from one type to another.
- And more

What's New

- **March 11, 2024**
DAVID is moving to new URL in NIH domain: <https://davidbioinformatics.nih.gov/>.
- **January 12, 2024**
New Wikipathways viewer integrated into DAVID with list gene highlighting, searchable pathway gene table, zooming, panning and download capabilities.
- **December 21, 2023**
[DAVID Knowledgebase v2023q4 released.](#)
- **October 12, 2023**

Hot Links

🇺🇸 One scientist position available in LHRI 🇺🇸

(Updated on Jan 30, 2024)

The Laboratory of Human Retrovirology and Immunoinformatics (LHRI: former LHR), Applied/ Developmental Research Directorate (<https://david.ncifcrf.gov>) has investigated drug resistance in people living with HIV/AIDS (PLWHA) in the National Institute of Allergy and Infectious Diseases (NIAID) clinical therapy since 2001 to define salvage or de novo therapies. LHRI has also studied the function of novel anti-viral cytokines (Interleukine-27 and Interferon Lambda-1) and the innate immune responses for developing novel immunotherapies.

A [Scientist I, Cellular Biologist](#) available to investigated HIV and AIDS-related virus pathogenesis in vitro and HIV translational research using molecular biology, cellular biology, virology, and bioinformatics techniques in our [Basic Research Section](#).

DAVID Forum

Forum for DAVID users to ask questions, suggest new functions and help other users by answering their questions.

FAQ

Frequently Asked Questions

LHRI Publications

Publications of the Laboratory of Human Retrovirology and Immunoinformatics, Frederick National Laboratory for Cancer Research

DAVID Publications

Publications about DAVID

DAVID Statistics

- > 69K Citations (Updated 1/12/2024)
- Average Daily Usage: ~2,700 gene lists/sublists from ~900 unique researchers.
- Average Annual Usage: ~1,000,000 gene lists/sublists from > 100 countries

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

Submit Gene List



Upload List Background

Gene ID Conversion Tool

Upload Gene List

[Demolist 1](#) [Demolist 2](#)
[Upload Help](#)

[Help and Tool Manual](#)

Step 1: Enter Gene List

A: Paste a list

Clear

Or

B: Choose From a File

Choose File [geneList1.txt](#)

Multi-List File ?

Step 2: Select Identifier

OFFICIAL_GENE_SYMBOL

Step 2a: Select species

Homo sapiens

*** You must upload a gene list before a background ***

Step 3: List Type

Gene List

Background

Step 4: Submit List

Submit List

Option 1:

Convert the gene list being selected in left panel to OFFICIAL_GENE_SYMBOL

For species: Homo sapiens

Submit to Conversion Tool

Option 2:

Go Back to Submission Form

Copy and Paste



Gene List File



Multiple List Option



Species name/Tax ID



Gene List Setting

***** Welcome to DAVID 6.8 *****
***** If you are looking for [DAVID 6.7](#), please visit our [development site](#). *****

Upload | **List** | **Background** ← 3

Gene List Manager

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

- Use All Species -

Homo sapiens(393) ← 1

Unknown(10)

Select Species ← 2

List Manager [Help](#)

demolist2

Select List to:

Use Rename

Remove Combine

Show Gene List

[View Unmapped Ids](#)

Analysis Wizard

Step 1. Successfully submitted gene list

Current Gene List: demolist2
Current Background: Affymetrix Barley Genome Array

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

↓

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

- ↷ [Gene Functional Classification Tool](#)
- ↷ [Gene ID Conversion Tool](#)
- ↷ [Gene Name Batch Viewer](#)

Background Setting



Upload **List** **Background**

Population Manager

Select a background [Help](#)

Homo sapiens

4

Select List to:

5

Affymetrix 3' IVT Backgrounds [Help](#)

- Affymetrix Barley Genome Array
- Affymetrix Bsubtilis Genome Array
- Affymetrix Mu19KsubA

Affymetrix Exon Backgrounds [Help](#)

- HuEx-1_0-st-v2
- HuGene-1_0-st-v1
- MoEx-1_0-st-v1

Analysis Wizard

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

Step 1. Successfully submitted gene list

Current Gene List: geneList1

Current Background: Homo sapiens

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



[Which DAVID tools to use?](#)

- ➔ Functional Annotation Tool
 - Functional Annotation Clustering
 - Functional Annotation Chart
 - Functional Annotation Table
- ➔ Gene Functional Classification Tool
- ➔ Gene ID Conversion Tool
- ➔ Gene Name Batch Viewer

Gene List Uploaded

U.S. Department of Health & Human Services National Institutes of Health

NIH National Institutes of Health
DAVID Bioinformatics

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Upload **List** Background

Gene List Manager

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

- Use All Species -
Homo sapiens(149)
Unknown(15)

Select Species

List Manager [Help](#)

demolist1

Select List to:
Use Rename
Remove Combine
Show Gene List

[View Unmapped Ids](#)

Annotation Summary Results

[Help and Tool Manual](#)

Current Gene List: demolist1 **145 DAVID IDs**
Current Background: Homo sapiens **Check Defaults**

- Disease** (2 selected)
- Functional_Annotations** (5 selected)
- Gene_Ontology** (3 selected)
- Gene_Report_Categories** (0 selected)
- General_Annotations** (0 selected)
- Interactions** (1 selected)
- Literature** (0 selected)
- Pathways** (3 selected)
- Protein_Domains** (4 selected)
- Tissue_Expression** (0 selected)

Red annotation categories denote DAVID defined defaults

Combined View for Selected Annotation

Ready for Analysis

Upload **List** Background

Gene List Manager

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

- Use All Species -
Homo sapiens(146)

Select Species

List Manager [Help](#)

demolist1
geneList1

Select List to:

Use Rename
Remove Combine
Show Gene List



Analysis Wizard

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

Step 1. Successfully submitted gene list

Current Gene List: geneList1
Current Background: Homo sapiens



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

[Which DAVID tools to use?](#)

Functional Annotation Tool
• Functional Annotation Clustering
• Functional Annotation Chart
• Functional Annotation Table

B

Gene Functional Classification Tool
Gene ID Conversion Tool
Gene Name Batch Viewer

A

Gene Name Batch View

Gene List Report

[Help and Manual](#)

Current Gene List: demolist1

Current Background: Homo sapiens

145 DAVID IDs

 [Download File](#)

AFFYMETRIX_3PRIME_IVT_ID	Gene Name	Related Genes	Species
1112_g_at	neural cell adhesion molecule 1(NCAM1)	RG	Homo sapiens
1331_s_at	TNF receptor superfamily member 25(TNFRSF25)	RG	Homo sapiens
1355_g_at	neurotrophic receptor tyrosine kinase 2(NTRK2)	RG	Homo sapiens
1372_at	TNF alpha induced protein 6(TNFAIP6)	RG	Homo sapiens
1391_s_at	cytochrome P450 family 4 subfamily A member 11(CYP4A11)	RG	Homo sapiens
1403_s_at	C-C motif chemokine ligand 5(CCL5)	RG	Homo sapiens
1419_g_at	nitric oxide synthase 2(NOS2)	RG	Homo sapiens
1575_at	ATP binding cassette subfamily B member 1(ABCB1)	RG	Homo sapiens
1645_at	KISS-1 metastasis suppressor(KISS1)	RG	Homo sapiens
1786_at	MER proto-oncogene, tyrosine kinase(MERTK)	RG	Homo sapiens
1855_at	fibroblast growth factor 3(FGF3)	RG	Homo sapiens
1890_at	growth differentiation factor 15(GDF15)	RG	Homo sapiens
1901_s_at	erb-b2 receptor tyrosine kinase 2(ERBB2)	RG	Homo sapiens
1910_s_at	BCL2 apoptosis regulator(BCL2)	RG	Homo sapiens
1974_s_at	tumor protein p53(TP53)	RG	Homo sapiens
1983_at	cyclin D2(CCND2)	RG	Homo sapiens
2090_i_at	Wnt family member 6(WNT6)	RG	Homo sapiens
31506_s_at	defensin alpha 1(DEFA1)	RG	Homo sapiens
31512_at	immunoglobulin kappa variable 1-13(IGKV1-13)	RG	Homo sapiens
31525_s_at	hemoglobin subunit alpha 1(HBA1)	RG	Homo sapiens
31621_s_at	elastin(ELN)	RG	Homo sapiens
31687_f_at	hemoglobin subunit beta(HBB)	RG	Homo sapiens
31715_at	TEX28 pseudogene 3(TEX28P3)	RG	Homo sapiens
31793_at	defensin alpha 1(DEFA1)	RG	Homo sapiens
32073_at	lysine demethylase 4A(KDM4A)	RG	Homo sapiens

Gene ID Conversion



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Gene List Manager

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

- Use All Species -
Homo sapiens(149)
Unknown(15)

Select Species

List Manager [Help](#)

demolist1

Select List to:

Use

Rename

Remove

Combine

Show Gene List

[View Unmapped Ids](#)

Gene ID Conversion Tool

[Help and Tool Manual](#)

Option 1:

Convert the gene list being selected in left panel to

For species:

Submit to Conversion Tool

Option 2:

Go Back to Submission Form

Gene ID Conversion

Gene Accession Conversion Tool

[Help](#)

Gene Accession Conversion Statistics

 [Download File](#)

Conversion Summary			Submit Converted List to DAVID as a Gene List		Submit Converted List to DAVID as a Background	
ID Count	In DAVID DB	Conversion	From	To	Species	David Gene Name
149	Yes	Successful	1372_at	7130	Homo sapiens	TNF alpha induced protein 6(TNFAIP6)
0	Yes	None	919_at	2768	Homo sapiens	G protein subunit alpha 12(GNA12)
0	No	None	37954_at	643650	Homo sapiens	long intergenic non-protein coding RNA 842(LINC00842)
0	Ambiguous	Pending	37983_at	185	Homo sapiens	angiotensin II receptor type 1(AGTR1)
Total Unique User IDs: 149			36766_at	6036	Homo sapiens	ribonuclease A family member 2(RNASE2)
Summary of Ambiguous Gene IDs			37953_s_at	41	Homo sapiens	acid sensing ion channel subunit 1(ASIC1)
ID Count	Possible Source	Convert All	936_s_at	27065	Homo sapiens	neuronal vesicle trafficking associated 1(NSG1)
All Possible Sources For Ambiguous IDs			34636_at	246	Homo sapiens	arachidonate 15-lipoxygenase(ALOX15)
Ambiguous ID	Possibility	Convert	40294_at	23457	Homo sapiens	ATP binding cassette subfamily B member 9(ABCB9)
			822_s_at	8738	Homo sapiens	CASP2 and RIPK1 domain containing adaptor with death domain(CRADD)
			40271_at	9688	Homo sapiens	nucleoporin 93(NUP93)
			37814_g_at	317781	Homo sapiens	DEAD-box helicase 51(DDX51)
			37061_at	1118	Homo sapiens	chitinase 1(CHIT1)
			39187_at	860	Homo sapiens	RUNX family transcription factor 2(RUNX2)
			37105_at	1511	Homo sapiens	cathepsin G(CTSG)
			966_at	8438	Homo sapiens	RAD54 like(RAD54L)
			33516_at	3045	Homo sapiens	hemoglobin subunit delta(HBD)
			35595_at	27297	Homo sapiens	CGRP receptor component(CRCP)
			38236_at	2903	Homo sapiens	glutamate ionotropic receptor NMDA type subunit 2A(GRIN2A)
			37968_at	259197	Homo sapiens	natural cytotoxicity triggering receptor 3(NCR3)
			1575_at	5243	Homo sapiens	ATP binding cassette subfamily B member 1(ABCB1)
			32148_at	10160	Homo sapiens	FERM, ARH/RhoGEF and pleckstrin domain protein 1(FARP1)
			33371_s_at	11031	Homo sapiens	RAB31, member RAS oncogene family(RAB31)
			39908_at	10629	Homo sapiens	TATA-box binding protein associated factor 6 like(TAF6L)
			34249_at	7957	Homo sapiens	EPM2A glucan phosphatase, laforin(EPM2A)
			34703_f_at	10086	Homo sapiens	HHLA1 neighbor of OC90(HHLA1)
			34436_at	10786	Homo sapiens	solute carrier family 17 member 3(SLC17A3)
			32469_at	1084	Homo sapiens	CEA cell adhesion molecule 3(CEACAM3)
			34453_at	1556	Homo sapiens	cytochrome P450 family 2 subfamily B member 7, pseudogene(CYP2B7P)
			36702_at	6270	Homo sapiens	C motif chemokine ligand 25(CCL25)

Ready for Analysis



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Upload **List** **Background**

Gene List Manager

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

- Use All Species -
Homo sapiens(146)

Select Species

List Manager [Help](#)

demolist1
geneList1

Select List to:

Use Rename
Remove Combine
Show Gene List

Analysis Wizard

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

Step 1. Successfully submitted gene list

Current Gene List: geneList1
Current Background: Homo sapiens

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

[Which DAVID tools to use?](#)

↪ Functional Annotation Tool
• Functional Annotation Clustering
• Functional Annotation Chart
• Functional Annotation Table

↪ Gene Functional Classification Tool
↪ Gene ID Conversion Tool
↪ Gene Name Batch Viewer

B

A

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Gene List Manager

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- Use All Species -
Homo sapiens(149)
Unknown(15)

Select Species

List Manager [Help](#)

demolist1

Select List to:

Use Rename
Remove Combine
Show Gene List

[View Unmapped Ids](#)

Annotation Summary Results

Current Gene List: demolist1

Current Background: Homo sapiens

- Disease (2 selected)
- Functional_Annotations (5 selected)
- Gene_Ontology (3 selected)
- Gene_Report_Categories (0 selected)
- General_Annotations (0 selected)
- Interactions (1 selected)
- Literature (0 selected)
- Pathways (3 selected)
- Protein_Domains (4 selected)
- Tissue_Expression (0 selected)

Red annotation categories denote DAVID defined defaults

145 DAVID IDs

Check Defaults

Clear All

[Help and Tool Manual](#)

Combined View for Selected Annotation

Functional Annotation Clustering

Functional Annotation Chart

Functional Annotation Table



Functional Classification Annotation Summary



Upload List Background

Gene List Manager

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

- Use All Species -
- Homo sapiens(149)
- Unknown(15)

Select Species

List Manager [Help](#)

- demolist1

Select List to:

Use Rename
Remove Combine
Show Gene List

[View Unmapped Ids](#)

Annotation Summary Results

[Help and Tool Manual](#)

Current Gene List: demolist1

145 DAVID IDs

Current Background: Homo sapiens

Check Defaults

Clear All

Disease (2 selected)

<input type="checkbox"/> DISGENET	64.8%	94	Chart	
<input type="checkbox"/> GAD_DISEASE	80.7%	117	Chart	
<input type="checkbox"/> GAD_DISEASE_CLASS	80.7%	117	Chart	
<input checked="" type="checkbox"/> OMIM_DISEASE	34.5%	50	Chart	
<input checked="" type="checkbox"/> UP_KW_DISEASE	30.3%	44	Chart	

Functional_Annotations (5 selected)

Gene_Ontology (3 selected)

Gene_Report_Categories (0 selected)

General_Annotations (0 selected)

Interactions (1 selected)

<input type="checkbox"/> BIOGRID_INTERACTION	92.4%	134	Chart	
<input type="checkbox"/> DIP	24.8%	36	Chart	
<input type="checkbox"/> DRUGBANK	31.7%	46	Chart	
<input type="checkbox"/> HIV_INTERACTION	21.4%	31	Chart	
<input type="checkbox"/> HIV_INTERACTION_CATEGORY	21.4%	31	Chart	
<input type="checkbox"/> INTACT	86.2%	125	Chart	
<input type="checkbox"/> MINT	55.9%	81	Chart	
<input type="checkbox"/> PUBCHEM	26.9%	39	Chart	
<input type="checkbox"/> UCSC_TFBS	95.2%	138	Chart	
<input checked="" type="checkbox"/> UP_KW_LIGAND	41.4%	60	Chart	

Literature (0 selected)

Pathways (3 selected)

<input checked="" type="checkbox"/> BBID	4.1%	6	Chart	
<input checked="" type="checkbox"/> BIOCARTA	17.9%	26	Chart	
<input type="checkbox"/> EC_NUMBER	25.5%	37	Chart	
<input checked="" type="checkbox"/> KEGG_PATHWAY	55.9%	81	Chart	
<input type="checkbox"/> REACTOME_PATHWAY	75.2%	109	Chart	
<input type="checkbox"/> WIKIPATHWAYS	56.6%	82	Chart	

Protein_Domains (4 selected)

Tissue_Expression (0 selected)

Functional Classification Annotation Summary

Functional Annotation Chart

[Help and Manual](#)

Current Gene List: demolist1

Current Background: Homo sapiens

145 DAVID IDs

Options

Rerun Using Options

Create Sublist

20 chart records

[Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamin
<input type="checkbox"/>	KEGG_PATHWAY	Transcriptional misregulation in cancer	RT		9	6.2	3.9E-4	5.0E-2
<input type="checkbox"/>	KEGG_PATHWAY	Gastric cancer	RT		8	5.5	4.4E-4	5.0E-2
<input type="checkbox"/>	KEGG_PATHWAY	Calcium signaling pathway	RT		8	5.5	8.7E-3	5.4E-1
<input type="checkbox"/>	KEGG_PATHWAY	Breast cancer	RT		6	4.1	1.2E-2	5.4E-1
<input type="checkbox"/>	KEGG_PATHWAY	Staphylococcus aureus infection	RT		5	3.4	1.2E-2	5.4E-1
<input type="checkbox"/>	KEGG_PATHWAY	MAPK signaling pathway	RT		8	5.5	2.1E-2	7.9E-1
<input type="checkbox"/>	KEGG_PATHWAY	Pathways in cancer	RT		11	7.6	2.4E-2	7.9E-1
<input type="checkbox"/>	KEGG_PATHWAY	Platinum drug resistance	RT		4	2.8	3.0E-2	8.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	EGFR tyrosine kinase inhibitor resistance	RT		4	2.8	3.7E-2	9.0E-1
<input type="checkbox"/>	KEGG_PATHWAY	Proteoglycans in cancer	RT		6	4.1	4.1E-2	9.0E-1
<input type="checkbox"/>	KEGG_PATHWAY	Signaling pathways regulating pluripotency of stem cells	RT		5	3.4	4.3E-2	9.0E-1
<input type="checkbox"/>	KEGG_PATHWAY	Small cell lung cancer	RT		4	2.8	5.3E-2	9.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	Prostate cancer	RT		4	2.8	6.1E-2	9.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	Endocrine resistance	RT		4	2.8	6.2E-2	9.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	Parathyroid hormone synthesis, secretion and action	RT		4	2.8	7.5E-2	9.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	Wnt signaling pathway	RT		5	3.4	7.7E-2	9.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	HIF-1 signaling pathway	RT		4	2.8	8.0E-2	9.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	NOD-like receptor signaling pathway	RT		5	3.4	9.3E-2	9.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	Hedgehog signaling pathway	RT		3	2.1	9.5E-2	9.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	Neurotrophin signaling pathway	RT		4	2.8	9.8E-2	9.8E-1

113 gene(s) from your list are not in the output.

Functional Classification Annotation Summary



Upload List Background

Gene List Manager

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

- Use All Species -
- Homo sapiens(149)
- Unknown(15)

Select Species

List Manager [Help](#)

- demolist1

Select List to:

Use Rename
Remove Combine
Show Gene List

[View Unmapped Ids](#)

Annotation Summary Results

[Help and Tool Manual](#)

Current Gene List: demolist1

145 DAVID IDs

Current Background: Homo sapiens

Check Defaults

Clear All

Disease (2 selected)

<input type="checkbox"/> DISGENET	64.8%	94	Chart	
<input type="checkbox"/> GAD_DISEASE	80.7%	117	Chart	
<input type="checkbox"/> GAD_DISEASE_CLASS	80.7%	117	Chart	
<input checked="" type="checkbox"/> OMIM_DISEASE	34.5%	50	Chart	
<input checked="" type="checkbox"/> UP_KW_DISEASE	30.3%	44	Chart	

Functional_Annotations (5 selected)

Gene_Ontology (3 selected)

Gene_Report_Categories (0 selected)

General_Annotations (0 selected)

Interactions (1 selected)

<input type="checkbox"/> BIOGRID_INTERACTION	92.4%	134	Chart	
<input type="checkbox"/> DIP	24.8%	36	Chart	
<input type="checkbox"/> DRUGBANK	31.7%	46	Chart	
<input type="checkbox"/> HIV_INTERACTION	21.4%	31	Chart	
<input type="checkbox"/> HIV_INTERACTION_CATEGORY	21.4%	31	Chart	
<input type="checkbox"/> INTACT	86.2%	125	Chart	
<input type="checkbox"/> MINT	55.9%	81	Chart	
<input type="checkbox"/> PUBCHEM	26.9%	39	Chart	
<input type="checkbox"/> UCSC_TFBS	95.2%	138	Chart	
<input checked="" type="checkbox"/> UP_KW_LIGAND	41.4%	60	Chart	

Literature (0 selected)

Pathways (3 selected)

<input checked="" type="checkbox"/> BBID	4.1%	6	Chart	
<input checked="" type="checkbox"/> BIOCARTA	17.9%	26	Chart	
<input type="checkbox"/> EC_NUMBER	25.5%	37	Chart	
<input checked="" type="checkbox"/> KEGG_PATHWAY	55.9%	81	Chart	
<input type="checkbox"/> REACTOME_PATHWAY	75.2%	109	Chart	
<input type="checkbox"/> WIKIPATHWAYS	56.6%	82	Chart	

Protein_Domains (4 selected)

Tissue_Expression (0 selected)



Functional Classification Annotation Summary

Functional Annotation Table

[Help and Manual](#)

Current Gene List: demolist1
Current Background: Homo sapiens
145 DAVID IDs

81 record(s)

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Gene ID	Gene Name	Related Genes	Species
37166_at	3-hydroxyanthranilate 3,4-dioxygenase(HAAO)		Homo sapiens
KEGG_PATHWAY	Tryptophan metabolism , Metabolic pathways , Biosynthesis of cofactors ,		
34467_g_at	5-hydroxytryptamine receptor 4(HTR4)		Homo sapiens
KEGG_PATHWAY	Calcium signaling pathway , cAMP signaling pathway , Neuroactive ligand-receptor interaction , Serotonergic synapse ,		
1575_at	ATP binding cassette subfamily B member 1(ABCB1)		Homo sapiens
KEGG_PATHWAY	ABC transporters , Bile secretion , MicroRNAs in cancer , Gastric cancer ,		
40294_at	ATP binding cassette subfamily B member 9(ABCB9)		Homo sapiens
KEGG_PATHWAY	ABC transporters , Lysosome ,		
32439_at	ATPase H⁺/K⁺ transporting subunit beta(ATP4B)		Homo sapiens
KEGG_PATHWAY	Oxidative phosphorylation , Metabolic pathways , Collecting duct acid secretion , Gastric acid secretion ,		
39469_s_at	ATPase phospholipid transporting BA2(ATPBA2)		Homo sapiens
KEGG_PATHWAY	Efferocytosis ,		
33027_at	ArfGAP with GTPase domain, ankyrin repeat and PH domain 4(AGAP4)		Homo sapiens
KEGG_PATHWAY	Endocytosis ,		
1910_s_at	BCL2 apoptosis regulator(BCL2)		Homo sapiens
KEGG_PATHWAY	EGFR tyrosine kinase inhibitor resistance , Endocrine resistance , Platinum drug resistance , NF-kappa B signaling pathway , HIF-1 signaling pathway , Sphingolipid signaling pathway , p53 signaling pathway , Autophagy - animal , Protein processing in endoplasmic reticulum , PI3K-Akt signaling pathway , Apoptosis , Apoptosis - multiple species , Necroptosis , Adrenergic signaling in cardiomyocytes , Hedgehog signaling pathway , Focal adhesion , NOD-like receptor signaling pathway , JAK-STAT signaling pathway , Neurotrophin signaling pathway , Cholinergic synapse , Estrogen signaling pathway , Parathyroid hormone synthesis, secretion and action , AGE-RAGE signaling pathway in diabetic complications , Amyotrophic lateral sclerosis , Pathways of neurodegeneration - multiple diseases , Shigellosis , Salmonella infection , Toxoplasmosis , Tuberculosis , Hepatitis B , Measles , Herpes simplex virus 1 infection , Epstein-Barr virus infection , Human immunodeficiency virus 1 infection , Pathways in cancer , MicroRNAs in cancer , Chemical carcinogenesis - receptor activation , Colorectal cancer , Prostate cancer , Small cell lung cancer , Gastric cancer , Lipid and atherosclerosis , Fluid shear stress and atherosclerosis ,		
37454_at	C-C motif chemokine ligand 13(CCL13)		Homo sapiens
KEGG_PATHWAY	Cytokine-cytokine receptor interaction , Viral protein interaction with cytokine and cytokine receptor , Chemokine signaling pathway , NF-kappa B signaling pathway ,		
36703_at	C-C motif chemokine ligand 25(CCL25)		Homo sapiens
KEGG_PATHWAY	Cytokine-cytokine receptor interaction , Viral protein interaction with cytokine and cytokine receptor , Chemokine signaling pathway , Intestinal immune network for IgA production ,		
1403_s_at	C-C motif chemokine ligand 5(CCL5)		Homo sapiens
KEGG_PATHWAY	Cytokine-cytokine receptor interaction , Viral protein interaction with cytokine and cytokine receptor , Chemokine signaling pathway , Toll-like receptor signaling pathway , NOD-like receptor signaling pathway , Cytosolic DNA-sensing pathway , TNF signaling pathway , Prion disease , Epithelial cell signaling in Helicobacter pylori infection , Shigellosis , Chagas disease , Human cytomegalovirus infection , Influenza A , Herpes simplex virus 1 infection , Rheumatoid arthritis , Lipid and atherosclerosis ,		
35595_at	CGRP receptor component(CRCP)		Homo sapiens
KEGG_PATHWAY	RNA polymerase ,		
919_at	G protein subunit alpha 12(GNA12)		Homo sapiens
KEGG_PATHWAY	MAPK signaling pathway , cGMP-PKG signaling pathway , Sphingolipid signaling pathway , Phospholipase D signaling pathway , Vascular smooth muscle contraction , Long-term depression , Regulation of actin cytoskeleton , Parathyroid hormone synthesis, secretion and action , Pathogenic Escherichia coli infection , Human cytomegalovirus infection , Pathways in cancer ,		

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Upload **List** **Background**

Gene List Manager

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

- Use All Species -
- Homo sapiens(149)
- Unknown(15)

Select Species

List Manager [Help](#)

- demolist1

Select List to:

Use Rename
Remove Combine
Show Gene List

Analysis Wizard

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[Contact us for questions](#)

Step 1. Successfully submitted gene list

Current Gene List: demolist1
Current Background: Homo sapiens

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

Which DAVID tools to use?

- Functional Annotation Tool
 - Functional Annotation Clustering
 - Functional Annotation Chart
 - Functional Annotation Table

- Gene Functional Classification Tool
- Gene ID Conversion Tool
- Gene Name Batch Viewer

B

A


Function Annotation Table Results

Functional Annotation Table

[Help and Manual](#)

Current Gene List: demolist1
 Current Background: Homo sapiens
 145 DAVID IDs

138 record(s)

 [Download File](#)

37166_at	3-hydroxyanthranilate 3,4-dioxygenase(HAAO)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	tryptophan catabolic process , NAD biosynthetic process , response to zinc ion , pyridine nucleotide biosynthetic process , quinolinate biosynthetic process , electron transport chain , 'de novo' NAD biosynthetic process from tryptophan , anthranilate metabolic process , response to cadmium ion , quinolinate metabolic process , neuron cellular homeostasis .		
GOTERM_CC_DIRECT	cytoplasm , cytosol .		
GOTERM_MF_DIRECT	3-hydroxyanthranilate 3,4-dioxygenase activity , iron ion binding , protein binding , ferrous iron binding , electron carrier activity .		
INTERPRO	3-hydroxyanthranilic acid dioxygenase , RmlC-like cupin domain , RmlC-like jelly roll fold , 3-hydroxyanthranilate 3,4-dioxygenase , metazoan .		
KEGG_PATHWAY	Tryptophan metabolism , Metabolic pathways , Biosynthesis of cofactors .		
OMIM_DISEASE	Vertebral, cardiac, renal, and limb defects syndrome 1 .		
PIR_SUPERFAMILY	3-hydroxyanthranilate 3,4-dioxygenase , animal type .		
UP_KW_BIOLOGICAL_PROCESS	Pyridine nucleotide biosynthesis .		
UP_KW_CELLULAR_COMPONENT	Cytoplasm .		
UP_KW_DISEASE	Disease variant .		
UP_KW_LIGAND	Iron , Metal-binding .		
UP_KW_MOLECULAR_FUNCTION	Dioxygenase , Oxidoreductase .		
UP_SEQ_FEATURE	REGION:Domain A (catalytic), REGION:Domain B, REGION:Linker.		
34467_g_at	5-hydroxytryptamine receptor 4(HTR4)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	G-protein coupled receptor signaling pathway , G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger , adenylate cyclase-inhibiting serotonin receptor signaling pathway , chemical synaptic transmission , maintenance of gastrointestinal epithelium , regulation of appetite , mucus secretion , G-protein coupled serotonin receptor signaling pathway .		
GOTERM_CC_DIRECT	cytoplasm , endosome , plasma membrane , integral component of plasma membrane , membrane , dendrite , synapse .		
GOTERM_MF_DIRECT	G-protein coupled serotonin receptor activity , protein binding , neurotransmitter receptor activity , serotonin binding , serotonin receptor activity .		
INTERPRO	G-protein-coupled receptor, rhodopsin-like , 5-Hydroxytryptamine 4 receptor , GPCR , rhodopsin-like , 7TM .		
KEGG_PATHWAY	Calcium signaling pathway , cAMP signaling pathway , Neuroactive ligand-receptor interaction , Serotonergic synapse .		
SMART	SM01381 .		
UP_KW_CELLULAR_COMPONENT	Membrane , Endosome , Cell membrane .		
UP_KW_DOMAIN	Transmembrane , Transmembrane helix .		
UP_KW_MOLECULAR_FUNCTION	G-protein coupled receptor , Receptor , Transducer .		
UP_KW_PTM	Glycoprotein , Lipoprotein , Palmitate , Disulfide bond .		
UP_SEQ_FEATURE	CARBOHYD:N-linked (GlcNAc...) asparagine, DOMAIN:G-protein coupled receptors family 1 profile, LIPID:S-palmitoyl cysteine, TOPO_DOM:Cytoplasmic, TOPO_DOM:Extracellular, TRANSMEM:Helical, TRANSMEM:Helical; Name=1, TRANSMEM:Helical; Name=2, TRANSMEM:Helical; Name=3, TRANSMEM:Helical; Name=4, TRANSMEM:Helical; Name=5, TRANSMEM:Helical; Name=6, TRANSMEM:Helical; Name=7.		
41703_r_at	A-kinase anchoring protein 7(AKAP7)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	action potential , ion transport , protein localization , regulation of protein kinase A signaling , intracellular signal transduction , modulation of synaptic transmission , regulation of membrane repolarization , cellular response to cAMP , positive regulation of potassium ion transmembrane transport , positive regulation of delayed rectifier potassium channel activity .		
GOTERM_CC_DIRECT	nucleus , cytosol , plasma membrane , apical plasma membrane , lateral plasma membrane , macromolecular complex , hippocampal mossy fiber to CA3 synapse .		
GOTERM_MF_DIRECT	nucleotide binding , protein binding , kinase activity , protein kinase binding , protein kinase A regulatory subunit binding , protein kinase A binding .		
INTERPRO	RNA ligase/cyclic nucleotide phosphodiesterase , Protein kinase A anchor protein , nuclear localisation signal domain , Protein kinase A anchor protein , RI-RII subunit-binding domain .		
UP_KW_CELLULAR_COMPONENT	Membrane , Nucleus , Cytoplasm , Cell membrane .		
UP_KW_LIGAND	Nucleotide-binding .		

Go Term Information



- Overview
- Synonyms
- Ancestor Chart
- Child Terms
- Annotation Guidance
- GO Discussions
- Taxon Constraints
- Blacklist
- Cross-References
- Cross-Ontology Relations
- Replaces
- Replaced By
- Co-occurring Terms
- GO Slims
- Change Log

GO:0006569 [JSON](#)

tryptophan catabolic process

Biological Process

Definition ([GO:0006569 GONUTS page](#))

The chemical reactions and pathways resulting in the breakdown of tryptophan, the chiral amino acid 2-amino-3-(1H-indol-3-yl)propanoic acid.

241,977 annotations

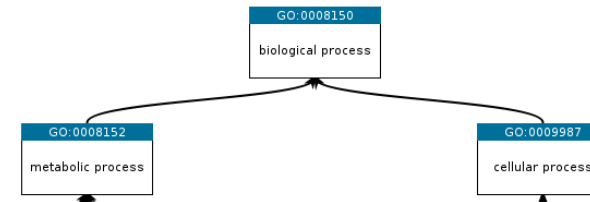
Synonyms

Synonyms are alternative words or phrases closely related in meaning to the term name, with indication of the relationship between the name and synonym given by the synonym scope.

Synonym	Type
tryptophan breakdown	exact
tryptophan catabolic process, using tryptophanase	narrow
tryptophan catabolism, using tryptophanase	narrow
tryptophan catabolism	exact
tryptophan degradation	exact

Ancestor Chart

Ancestor chart for GO:0006569 [Chart options](#)



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Gene List Manager

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

- Use All Species -
Homo sapiens(149)
Unknown(15)

Select Species

List Manager [Help](#)

demolist1

Select List to:

Use Rename

Remove Combine

Show Gene List

[View Unmapped Ids](#)

Annotation Summary Results

[Help and Tool Manual](#)

Current Gene List: demolist1

145 DAVID IDs

Current Background: Homo sapiens

Check Defaults

Clear All

- Disease (2 selected)
- Functional_Annotations (5 selected)
- Gene_Ontology (3 selected)
- Gene_Report_Categories (0 selected)
- General_Annotations (0 selected)
- Interactions (1 selected)
- Literature (0 selected)
- Pathways (3 selected)
- Protein_Domains (4 selected)
- Tissue_Expression (0 selected)

***Red annotation categories denote DAVID defined default

Combined View for Selected Annotation

Functional Annotation Clustering

Functional Annotation Chart

Functional Annotation Table



Functional Annotation Chart Results

Functional Annotation Chart

[Help and Manual](#)

Current Gene List: demolist1

Current Background: Homo sapiens

145 DAVID IDs

Options

254 chart records

[Download File](#)

Sublist	Category	Term	RT	Gene	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_DIRECT	extracellular space	RT		38	26.2	4.7E-9	1.2E-6
<input type="checkbox"/>	GOTERM_CC_DIRECT	extracellular region	RT		38	26.2	7.3E-8	9.1E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	antimicrobial humoral immune response mediated by antimicrobial peptide	RT		9	6.2	1.7E-6	2.2E-3
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Secreted	RT		35	24.1	2.5E-6	9.2E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	defense response to Gram-negative bacterium	RT		8	5.5	4.2E-6	2.3E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	innate immune response in mucosa	RT		6	4.1	5.3E-6	2.3E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	antibacterial humoral response	RT		7	4.8	1.4E-5	4.6E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	azurophil granule lumen	RT		7	4.8	3.2E-5	2.7E-3
<input type="checkbox"/>	UP_KW_DOMAIN	Signal	RT		51	35.2	7.1E-5	1.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	defense response to fungus	RT		5	3.4	1.1E-4	2.8E-2
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Chemotaxis	RT		7	4.8	1.5E-4	1.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	chemotaxis	RT		7	4.8	2.3E-4	4.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	monocyte chemotaxis	RT		5	3.4	2.6E-4	4.8E-2
<input type="checkbox"/>	KEGG_PATHWAY	Transcriptional misregulation in cancer	RT		9	6.2	3.9E-4	5.0E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	apical plasma membrane	RT		11	7.6	4.0E-4	2.5E-2
<input type="checkbox"/>	KEGG_PATHWAY	Gastric cancer	RT		8	5.5	4.4E-4	5.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	killing of cells of other organism	RT		6	4.1	4.4E-4	7.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	response to xenobiotic stimulus	RT		9	6.2	6.8E-4	9.8E-2
<input type="checkbox"/>	INTERPRO	Mammalian defensins	RT		3	2.1	7.3E-4	9.1E-2
<input type="checkbox"/>	INTERPRO	Defensin propeptide	RT		3	2.1	7.3E-4	9.1E-2
<input type="checkbox"/>	INTERPRO	Alpha-defensin	RT		3	2.1	7.3E-4	9.1E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	heme binding	RT		7	4.8	7.6E-4	1.6E-1
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Antibiotic	RT		6	4.1	8.4E-4	5.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	eosinophil chemotaxis	RT		4	2.8	9.2E-4	1.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	hydrogen peroxide catabolic process	RT		4	2.8	9.2E-4	1.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of gene expression	RT		12	8.3	9.4E-4	1.0E-1
<input type="checkbox"/>	INTERPRO	Beta defensin/Neutrophil defensin	RT		3	2.1	1.0E-3	9.5E-2
<input type="checkbox"/>	UP_KW_LIGAND	Heme	RT		7	4.8	1.2E-3	2.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell-cell signaling	RT		8	5.5	1.2E-3	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of apoptotic process	RT		12	8.3	1.3E-3	1.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein heterodimerization activity	RT		10	6.9	1.4E-3	1.6E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	alpha-defensin	RT		3	2.1	1.4E-3	2.4E-2
<input type="checkbox"/>	SMART	DEFSN	RT		3	2.1	1.5E-3	1.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	signal transduction	RT		20	13.8	1.6E-3	1.4E-1
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Antibiotic	RT		6	4.1	1.6E-3	5.6E-2

Gene List for a Term in Functional Annotation Chart

Gene Report


[Help and Manual](#)

Current Gene List: demolist1

Current Background: Homo sapiens

145 DAVID IDs

38 record(s)

 [Download File](#)

AFFYMETRIX_3PRIME_IVT_ID	GENE NAME	Related Genes	Species
37454_at	C-C motif chemokine ligand 13(CCL13)	RG	Homo sapiens
36703_at	C-C motif chemokine ligand 25(CCL25)	RG	Homo sapiens
1403_s_at	C-C motif chemokine ligand 5(CCL5)	RG	Homo sapiens
33530_at	CEA cell adhesion molecule 8(CEACAM8)	RG	Homo sapiens
37905_r_at	G protein nucleolar 1.(putative)(GNL1)	RG	Homo sapiens
34618_at	Indian hedgehog signaling molecule(IHH)	RG	Homo sapiens
1645_at	KISS-1 metastasis suppressor(KISS1)	RG	Homo sapiens
1786_at	MER proto-oncogene, tyrosine kinase(MERTK)	RG	Homo sapiens
1372_at	TNF alpha induced protein 6(TNFAIP6)	RG	Homo sapiens
33684_at	Wnt family member 2B(WNT2B)	RG	Homo sapiens
2090_i_at	Wnt family member 6(WNT6)	RG	Homo sapiens
33963_at	azurocidin 1(AZU1)	RG	Homo sapiens
37172_at	carboxypeptidase B2(CPB2)	RG	Homo sapiens
37105_at, 679_at	cathepsin G(CTSG)	RG	Homo sapiens
37061_at	chitinase 1(CHIT1)	RG	Homo sapiens
35169_at	collagen type XVI alpha 1 chain(COL16A1)	RG	Homo sapiens
32250_at	complement factor H(CFH)	RG	Homo sapiens
31506_s_at, 31793_at	defensin alpha 1(DEFA1)	RG	Homo sapiens
34546_at	defensin alpha 4(DEFA4)	RG	Homo sapiens
34623_at	defensin alpha 5(DEFA5)	RG	Homo sapiens
37096_at	elastase, neutrophil expressed(ELANE)	RG	Homo sapiens
1855_at	fibroblast growth factor 3(FGF3)	RG	Homo sapiens
35367_at	galectin 3(LGALS3)	RG	Homo sapiens
1890_at	growth differentiation factor 15(GDF15)	RG	Homo sapiens
31525_s_at	hemoglobin subunit alpha 1(HBA1)	RG	Homo sapiens
31687_f_at	hemoglobin subunit beta(HBB)	RG	Homo sapiens
31512_at	immunoglobulin kappa variable 1-13(IGKV1-13)	RG	Homo sapiens
35915_at	inhibin subunit beta C(INHBC)	RG	Homo sapiens
34012_at	keratin, type I cuticular Ha4(LOC100653049)	RG	Homo sapiens
36436_at	leukocyte cell derived chemotaxin 2(LECT2)	RG	Homo sapiens
33284_at	myeloperoxidase(MPO)	RG	Homo sapiens
35090_g_at, 35091_at	neuregulin 2(NRG2)	RG	Homo sapiens
38604_at	neuropeptide Y(NPY)	RG	Homo sapiens
38646_s_at	regenerating family member 1 alpha(REG1A)	RG	Homo sapiens
36766_at	ribonuclease A family member 2(RNASE2)	RG	Homo sapiens
33979_at	ribonuclease A family member 3(RNASE3)	RG	Homo sapiens
38691_s_at	surfactant protein C(SFTPC)	RG	Homo sapiens
37898_r_at	trefoil factor 3(TFF3)	RG	Homo sapiens

Functional Annotation Clustering



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Gene List Manager

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

- Use All Species -
Homo sapiens(149)
Unknown(15)

Select Species

List Manager [Help](#)

demolist1

Select List to:

Use Rename
Remove Combine
Show Gene List

[View Unmapped Ids](#)

Annotation Summary Results

[Help and Tool Manual](#)

Current Gene List: demolist1

145 DAVID IDs

Current Background: Homo sapiens

Check Defaults

Clear All

- Disease (2 selected)
- Functional_Annotations (5 selected)
- Gene_Ontology (3 selected)
- Gene_Report_Categories (0 selected)
- General_Annotations (0 selected)
- Interactions (1 selected)
- Literature (0 selected)
- Pathways (3 selected)
- Protein_Domains (4 selected)
- Tissue_Expression (0 selected)

Red annotation categories denote DAVID defined defaults

Combined View for Selected Annotation

Functional Annotation Clustering



Functional Annotation Chart

Functional Annotation Table

Functional Annotation Tool

Functional Annotation Clustering

Current Gene List: demolist1
 Current Background: Homo sapiens
 145 DAVID IDs

Options Classification Stringency **Medium**

Rerun using options Create Sublist

[Help and Manual](#)

37 Cluster(s)

Annotation Cluster 1	Enrichment Score: 4.54
<input type="checkbox"/> GOTERM_CC_DIRECT	extracellular space
<input type="checkbox"/> GOTERM_CC_DIRECT	extracellular region
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Secreted
<input type="checkbox"/> UP_KW_DOMAIN	Signal
<input type="checkbox"/> UP_KW_PTMs	Disulfide bond
<input type="checkbox"/> UP_SEQ_FEATURE	CARBOHYD:N-linked (GlcNAc...) asparagine
<input type="checkbox"/> UP_KW_PTMs	Glycoprotein
Annotation Cluster 2	Enrichment Score: 3
<input type="checkbox"/> GOTERM_BP_DIRECT	antimicrobial humoral immune response mediated by antimicrobial peptide
<input type="checkbox"/> GOTERM_BP_DIRECT	defense response to Gram-negative bacterium
<input type="checkbox"/> GOTERM_BP_DIRECT	innate immune response in mucosa
<input type="checkbox"/> GOTERM_BP_DIRECT	antibacterial humoral response
<input type="checkbox"/> GOTERM_BP_DIRECT	defense response to fungus
<input type="checkbox"/> GOTERM_BP_DIRECT	killing of cells of other organism
<input type="checkbox"/> INTERPRO	Defensin propeptide
<input type="checkbox"/> INTERPRO	Mammalian defensin
<input type="checkbox"/> INTERPRO	Alpha-defensin
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Antibiotic
<input type="checkbox"/> INTERPRO	Beta defensin/Neutrophil defensin
<input type="checkbox"/> PIR_SUPERFAMILY	alpha-defensin
<input type="checkbox"/> SMART	DEFNS
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Antimicrobial
<input type="checkbox"/> GOTERM_BP_DIRECT	membrane disruption in other organism
<input type="checkbox"/> GOTERM_BP_DIRECT	cellular response to lipopolysaccharide
<input type="checkbox"/> GOTERM_BP_DIRECT	defense response to Gram-positive bacterium
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Fungicide
<input type="checkbox"/> KEGG_PATHWAY	Staphylococcus aureus infection
<input type="checkbox"/> GOTERM_CC_DIRECT	Golgi lumen
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Defensin
<input type="checkbox"/> KEGG_PATHWAY	NOD-like receptor signaling pathway
<input type="checkbox"/> GOTERM_BP_DIRECT	innate immune response
Annotation Cluster 3	Enrichment Score: 2.16
<input type="checkbox"/> GOTERM_MF_DIRECT	heme binding
<input type="checkbox"/> GOTERM_BP_DIRECT	hydrogen peroxide catabolic process
<input type="checkbox"/> UP_KW_LIGAND	Heme
<input type="checkbox"/> GOTERM_MF_DIRECT	haptoglobin binding
<input type="checkbox"/> GOTERM_MF_DIRECT	peroxidase activity
<input type="checkbox"/> GOTERM_MF_DIRECT	oxygen binding

Annotation Cluster 31	Enrichment Score: 0.25	Count	P_Value	Benjamini
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Nucleus	35	9.0E-1	1.0E0
Annotation Cluster 32	Enrichment Score: 0.25	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT	zinc ion binding	9	2.8E-1	1.0E0
<input type="checkbox"/> UP_KW_LIGAND	Zinc	21	7.3E-1	1.0E0
<input type="checkbox"/> UP_KW_DOMAIN	Zinc-finger	11	8.6E-1	1.0E0
Annotation Cluster 33	Enrichment Score: 0.24	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	negative regulation of transcription, DNA-templated	6	3.9E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT	nuclear body	3	6.9E-1	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Repressor	5	7.0E-1	1.0E0
Annotation Cluster 34	Enrichment Score: 0.22	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:PH	3	5.6E-1	1.0E0
<input type="checkbox"/> INTERPRO	Pleckstrin homology domain	3	5.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	Pleckstrin homology-like domain	4	6.2E-1	1.0E0
<input type="checkbox"/> SMART	PH	3	6.8E-1	1.0E0
Annotation Cluster 35	Enrichment Score: 0.15	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT	metal ion binding	19	6.3E-1	1.0E0
<input type="checkbox"/> UP_KW_LIGAND	Zinc	21	7.3E-1	1.0E0
<input type="checkbox"/> UP_KW_LIGAND	Metal-binding	33	7.8E-1	1.0E0
Annotation Cluster 36	Enrichment Score: 0.04	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:C2H2-type	3	8.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 1	3	8.9E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 5	3	8.9E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 4	3	9.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 2	3	9.2E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 3	3	9.3E-1	1.0E0
<input type="checkbox"/> INTERPRO	Zinc finger C2H2-type/integrase DNA-binding domain	4	9.3E-1	1.0E0
<input type="checkbox"/> SMART	ZnF_C2H2	4	9.7E-1	1.0E0
Annotation Cluster 37	Enrichment Score: 0.01	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=7	4	9.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=6	4	9.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=5	4	9.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=3	4	9.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=4	4	9.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=1	4	9.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=2	4	9.7E-1	1.0E0

230 terms were not clustered.

Functional Annotation Clustering Tool

Functional Annotation Clustering

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Current Gene List: demolist1
 Current Background: Homo sapiens
 145 DAVID IDs

Options Classification Stringency: **Medium** ▼

- Custom
- Lowest
- Low
- Medium**
- High
- Highest

37 Cluster(s)

Annotation Cluster	Enrichment Score	RT	Count	P-Value	Benjamini
Annotation Cluster 1	Enrichment Score: 4	G	34		
<input type="checkbox"/> GOTERM_CC_DIRECT	extracellular region	RT	38	4.7E-9	1.2E-6
<input type="checkbox"/> GOTERM_CC_DIRECT	extracellular region	RT	38	7.3E-8	9.1E-6
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Secreted	RT	35	2.5E-6	9.2E-5
<input type="checkbox"/> UP_KW_DOMAIN	Signal	RT	51	7.1E-5	1.5E-3
<input type="checkbox"/> UP_KW_PTM	Disulfide bond	RT	47	2.3E-3	5.5E-2
<input type="checkbox"/> UP_SEQ_FEATURE	CARBOHYD:N-linked (GlcNAc...) asparagine	RT	43	5.7E-3	1.0E0
<input type="checkbox"/> UP_KW_PTM	Glycoprotein	RT	51	2.1E-2	1.8E-1
Annotation Cluster 2	Enrichment Score: 3	G	34		
<input type="checkbox"/> GOTERM_BP_DIRECT	antimicrobial humoral immune response mediated by antimicrobial peptide	RT	9	1.7E-6	2.2E-3
<input type="checkbox"/> GOTERM_BP_DIRECT	defense response to Gram-negative bacterium	RT	8	4.2E-6	2.3E-3
<input type="checkbox"/> GOTERM_BP_DIRECT	innate immune response in mucosa	RT	6	5.3E-6	2.3E-3
<input type="checkbox"/> GOTERM_BP_DIRECT	antibacterial humoral response	RT	7	1.4E-5	4.6E-3
<input type="checkbox"/> GOTERM_BP_DIRECT	defense response to fungus	RT	5	1.1E-4	2.8E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	killing of cells of other organism	RT	6	4.4E-4	7.1E-2
<input type="checkbox"/> INTERPRO	Defensin propeptide	RT	3	7.3E-4	9.1E-2
<input type="checkbox"/> INTERPRO	Mammalian defensins	RT	3	7.3E-4	9.1E-2
<input type="checkbox"/> INTERPRO	Alpha-defensin	RT	3	7.3E-4	9.1E-2
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Antibiotic	RT	6	8.4E-4	5.6E-2
<input type="checkbox"/> INTERPRO	Beta defensin/Neutrophil defensin	RT	3	1.0E-3	9.5E-2
<input type="checkbox"/> PIR_SUPERFAMILY	alpha-defensin	RT	3	1.4E-3	2.4E-2
<input type="checkbox"/> SMART	DEFSN	RT	3	1.5E-3	1.7E-1
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Antimicrobial	RT	6	1.6E-3	5.6E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	membrane disruption in other organism	RT	3	2.0E-3	1.6E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	cellular response to lipopolysaccharide	RT	7	2.5E-3	1.7E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	defense response to Gram-positive bacterium	RT	6	2.8E-3	1.8E-1
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Fungicide	RT	3	4.7E-3	1.1E-1
<input type="checkbox"/> KEGG_PATHWAY	Staphylococcus aureus infection	RT	5	1.2E-2	5.4E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	Golgi lumen	RT	4	3.4E-2	4.7E-1
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Defensin	RT	3	5.7E-2	7.8E-1
<input type="checkbox"/> KEGG_PATHWAY	NOD-like receptor signaling pathway	RT	5	9.3E-2	9.8E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	innate immune response	RT	7	2.7E-1	1.0E0
Annotation Cluster 3	Enrichment Score: 2.16	G	34		
<input type="checkbox"/> GOTERM_MF_DIRECT	heme binding	RT	7	7.6E-4	1.6E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	hydrogen peroxide catabolic process	RT	4	9.2E-4	1.0E-1
<input type="checkbox"/> UP_KW_LIGAND	Heme	RT	7	1.2E-3	2.8E-2
<input type="checkbox"/> GOTERM_MF_DIRECT	haemoglobin binding	RT	3	2.1E-3	1.6E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	peroxidase activity	RT	4	2.2E-3	1.6E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	oxygen binding	RT	4	2.2E-3	1.6E-1

Functional Annotation Clustering Tool

Gene Report

38 record(s)

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ID	GENE NAME	Related Genes	Species
C-C motif chemokine ligand 13(CCL13)	C-C motif chemokine ligand 13(CCL13)	RG	Homo sapiens
C-C motif chemokine ligand 25(CCL25)	C-C motif chemokine ligand 25(CCL25)	RG	Homo sapiens
C-C motif chemokine ligand 5(CCL5)	C-C motif chemokine ligand 5(CCL5)	RG	Homo sapiens
CEA cell adhesion molecule 8(CEACAM8)	CEA cell adhesion molecule 8(CEACAM8)	RG	Homo sapiens
G protein nucleolar 1 (putative)(GNL1)	G protein nucleolar 1 (putative)(GNL1)	RG	Homo sapiens
Indian hedgehog signaling molecule(IHH)	Indian hedgehog signaling molecule(IHH)	RG	Homo sapiens
KISS-1 metastasis suppressor(KISS1)	KISS-1 metastasis suppressor(KISS1)	RG	Homo sapiens
MER proto-oncogene, tyrosine kinase(MERTK)	MER proto-oncogene, tyrosine kinase(MERTK)	RG	Homo sapiens
TNF alpha induced protein 6(TNFAIP6)	TNF alpha induced protein 6(TNFAIP6)	RG	Homo sapiens
Wnt family member 2B(WNT2B)	Wnt family member 2B(WNT2B)	RG	Homo sapiens
Wnt family member 6(WNT6)	Wnt family member 6(WNT6)	RG	Homo sapiens
azurocidin 1(AZU1)	azurocidin 1(AZU1)	RG	Homo sapiens
carboxypeptidase B2(CPB2)	carboxypeptidase B2(CPB2)	RG	Homo sapiens
cathepsin G(CTSG)	cathepsin G(CTSG)	RG	Homo sapiens
chitinase 1(CHIT1)	chitinase 1(CHIT1)	RG	Homo sapiens
collagen type XVI alpha 1 chain(COL16A1)	collagen type XVI alpha 1 chain(COL16A1)	RG	Homo sapiens
complement factor H(CFH)	complement factor H(CFH)	RG	Homo sapiens
defensin alpha 1(DEFA1)	defensin alpha 1(DEFA1)	RG	Homo sapiens
defensin alpha 4(DEFA4)	defensin alpha 4(DEFA4)	RG	Homo sapiens
defensin alpha 5(DEFA5)	defensin alpha 5(DEFA5)	RG	Homo sapiens
elastase, neutrophil expressed(ELANE)	elastase, neutrophil expressed(ELANE)	RG	Homo sapiens
fibroblast growth factor 3(FGF3)	fibroblast growth factor 3(FGF3)	RG	Homo sapiens
galectin 3(LGALS3)	galectin 3(LGALS3)	RG	Homo sapiens
growth differentiation factor 15(GDF15)	growth differentiation factor 15(GDF15)	RG	Homo sapiens
hemoglobin subunit alpha 1(HBA1)	hemoglobin subunit alpha 1(HBA1)	RG	Homo sapiens
hemoglobin subunit beta(HBB)	hemoglobin subunit beta(HBB)	RG	Homo sapiens

Functional Annotation Clustering Tool

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37 Cluster(s)

Annotation Cluster 1	Enrichment Score: 4.54	G		Count	P Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	extracellular space	RT		38	4.7E-9	1.2E-6
<input type="checkbox"/> GOTERM_CC_DIRECT	extracellular region	RT		38	7.3E-8	9.1E-6
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Secreted	RT		35	2.5E-6	9.2E-5
<input type="checkbox"/> UP_KW_DOMAIN	Signal	RT		51	7.1E-5	1.5E-3
<input type="checkbox"/> UP_KW_PTM	Disulfide bond	RT		47	2.3E-3	5.5E-2
<input type="checkbox"/> UP_SEQ_FEATURE	CARBOHYD:N-linked (GlcNAc...) asparagine	RT		43	5.7E-3	1.0E0
<input type="checkbox"/> UP_KW_PTM	Glycoprotein	RT		51	2.1E-2	1.8E-1

Gene Report

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70 record(s)

ID	GENE NAME	Related Genes	Species
5-hydroxytryptamine receptor 4(HTR4)	5-hydroxytryptamine receptor 4(HTR4)	RG	Homo sapiens
ADAM metallopeptidase domain 23(ADAM23)	ADAM metallopeptidase domain 23(ADAM23)	RG	Homo sapiens
ATP binding cassette subfamily B member 1(ABCB1)	ATP binding cassette subfamily B member 1(ABCB1)	RG	Homo sapiens
ATPase H+/K+ transporting subunit beta(ATP4B)	ATPase H+/K+ transporting subunit beta(ATP4B)	RG	Homo sapiens
C-C motif chemokine ligand 13(CCL13)	C-C motif chemokine ligand 13(CCL13)	RG	Homo sapiens
C-C motif chemokine ligand 25(CCL25)	C-C motif chemokine ligand 25(CCL25)	RG	Homo sapiens
C-C motif chemokine ligand 5(CCL5)	C-C motif chemokine ligand 5(CCL5)	RG	Homo sapiens
CEA cell adhesion molecule 3(CEACAM3)	CEA cell adhesion molecule 3(CEACAM3)	RG	Homo sapiens
CEA cell adhesion molecule 8(CEACAM8)	CEA cell adhesion molecule 8(CEACAM8)	RG	Homo sapiens
Fas apoptotic inhibitory molecule 2(FAIM2)	Fas apoptotic inhibitory molecule 2(FAIM2)	RG	Homo sapiens
G protein nucleolar 1 (putative)(GNL1)	G protein nucleolar 1 (putative)(GNL1)	RG	Homo sapiens
HHLA1 neighbor of OC90(HHLA1)	HHLA1 neighbor of OC90(HHLA1)	RG	Homo sapiens
Indian hedgehog signaling molecule(IHH)	Indian hedgehog signaling molecule(IHH)	RG	Homo sapiens
KISS-1 metastasis suppressor(KISS1)	KISS-1 metastasis suppressor(KISS1)	RG	Homo sapiens
MER proto-oncogene, tyrosine kinase(MERTK)	MER proto-oncogene, tyrosine kinase(MERTK)	RG	Homo sapiens
TNF alpha induced protein 6(TNFAIP6)	TNF alpha induced protein 6(TNFAIP6)	RG	Homo sapiens
TNF receptor superfamily member 25(TNFRSF25)	TNF receptor superfamily member 25(TNFRSF25)	RG	Homo sapiens

Functional Annotation Clustering Tool



37 Cluster(s)

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Annotation Cluster 1	Enrichment Score: 4.54	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	extracellular space	RT		38	4.7E-9	1.2E-6
<input type="checkbox"/> GOTERM_CC_DIRECT	extracellular region	RT		38	7.3E-8	9.1E-6
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Secreted	RT		35	2.5E-6	9.2E-5
<input type="checkbox"/> UP_KW_DOMAIN	Signal	RT		51	7.1E-5	1.5E-3
<input type="checkbox"/> UP_KW_PTMs	Disulfide bond	RT		47	2.3E-3	5.5E-2
<input type="checkbox"/> UP_SEQ_FEATURE	CARBOHYD:N-linked (GlcNAc...) asparagine	RT		43	5.7E-3	1.0E0
<input type="checkbox"/> UP_KW_PTMs	Glycoprotein	RT		51	2.1E-2	1.8E-1

2D View

[Help](#)

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

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KW-0964~Secreted
 GO:0005615~extracellular space
 CARBOHYD:N-linked (GlcNAc...) as
 GO:0005576~extracellular region
 KW-1015~Disulfide bond
 KW-0325~Glycoprotein
 KW-0732~Signal

keratin, type I cuticular H44(LOC100653049)
 G protein nucleolar 1 (putative)(GNL1)
 growth arrest specific 8(GAS8)
 myosin binding protein c3(WYBPC3)
 tumor protein p53(TP53)
 cytochrome P450 family 3 subfamily A member 5(CYP3A5)
 lysine demethylase 4A(KDM4A)
 claudin 7(CLDN7)
 solute carrier family 17 member 3(SLC17A3)
 solute carrier family 17 member 1(SLC17A1)
 solute carrier family 22 member 5(SLC22A5)
 Fas apoptotic inhibitory molecule 2(FAIM2)
 ATP binding cassette subfamily B member 1(ABCB1)
 ATP hemoglobin subunit alpha 1(HBA1)
 5-hydroxytryptamine receptor 4(HTR4)
 uropod 1A(UPL1A)
 acid sensing ion channel subunit 2(ASIC2)
 acid sensing ion channel subunit 1(ASIC1)
 angiotensin II receptor type 1(AGTR1)
 ATPase H+/K+ transporting subunit beta(ATP4B)
 solute carrier family 6 member 6(SLC6A6)
 CEA cell adhesion molecule 3(CEACAM3)
 oligodendrocyte myelin glycoprotein(OMG)
 surfactant protein c(SFTPC)
 galectin 3(LGALS3)
 KISS-1 metastasis suppressor(KISS1)
 neurotrophin Y(NPY)
 immunoglobulin kappa variable 1-13(IgKV1-13)
 leukocyte cell derived chemotaxin 2(LECT2)
 elastin(ELN)
 hemoglobin subunit beta(HBB)
 erb-b2 receptor tyrosine kinase 2(ERBB2)
 mannose receptor c type 2(MRC2)
 neurotrophic receptor tyrosine kinase 2(NTRK2)
 glutamate ionotropic receptor NMDA type subunit 2A(GRI2A)
 natural cytotoxicity triggering receptor 3(NCR3)
 defensin alpha 1(DEFAL1)
 C-C motif chemokine ligand 13(CCL13)
 C-C motif chemokine ligand 25(CCL25)
 trefoil factor 3(TFF3)
 defensin alpha 4(DEFM4)
 Indian hedgehog signaling molecule(IHH)
 HHLA1 neighbor of OCS9(HHLA1)
 regenerating family member 1 alpha(REG1A)
 CEA cell adhesion molecule 8(CEACAM8)
 MER proto-oncogene, tyrosine kinase(MERTK)
 collagen type XVI alpha 1 chain(COL16A1)
 fibroblast growth factor 3(FGF3)
 defensin alpha 5(DEFM5)
 C-C motif chemokine ligand 5(CCL5)
 chitinase 1(CHIT1)
 cathepsin G(CTSG)
 TNF receptor superfamily member 25(TNFRSF25)
 pregnancy specific beta-1-glycoprotein 4(PSG4)
 ADAM metalloproteinase domain 23(ADAM23)
 sex hormone binding globulin(SHBG)
 neural cell adhesion molecule 1(NCAM1)
 ribonuclease A family member 2(RNASE2)
 azurocidin 1(AZU1)
 elastase, neutrophil expressed(ELANE)
 myeloperoxidase(MPO)
 ribonuclease A family member 3(RNASE3)
 inhibin subunit beta c(IMHBC)
 growth differentiation factor 15(GDF15)
 wnt family member 6(WNT6)
 wnt family member 2B(WNT2B)
 neuregulin 2(NRG2)
 carboxypeptidase B2(CPB2)
 TNF alpha induced protein 6(TNFAIP6)
 complement factor H(CFH)

Ready for Analysis



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Gene List Manager

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

- Use All Species -
- Homo sapiens(149)
- Unknown(15)

Select Species

List Manager [Help](#)

- demolist1

Select List to:

Use Rename
Remove Combine
Show Gene List

Analysis Wizard

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

Step 1. Successfully submitted gene list

Current Gene List: demolist1
Current Background: Homo sapiens

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

[Which DAVID tools to use?](#)

- Functional Annotation Tool
 - Functional Annotation Clustering
 - Functional Annotation Chart
 - Functional Annotation Table

B

Gene Functional Classification Tool

Gene ID Conversion Tool

Gene Name Batch Viewer

A

Gene Functional Classification Tool

Gene Functional Classification Result

[Help and Tool Manual](#)

Current Gene List: demolist1

Current Background: Homo sapiens

145 DAVID IDs



Options Classification Stringency **Medium** 

Rerun using options

Create Sublist

2 Cluster(s)

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Gene Group 1	Enrichment Score: 1.13	RG	T	
1 <input type="checkbox"/> 35090_g_at, 35091_at	neuregulin 2(NRG2)			
2 <input type="checkbox"/> 33293_at	Fas apoptotic inhibitory molecule 2(FAIM2)			
3 <input type="checkbox"/> 34629_at	tumor protein p53 inducible protein 11(TP53I11)			
4 <input type="checkbox"/> 1112_g_at	neural cell adhesion molecule 1(NCAM1)			
5 <input type="checkbox"/> 35956_s_at	pregnancy specific beta-1-glycoprotein 4(PSG4)			
6 <input type="checkbox"/> 37968_at	natural cytotoxicity triggering receptor 3(NCR3)			
7 <input type="checkbox"/> 33530_at	CEA cell adhesion molecule 8(CEACAM8)			
8 <input type="checkbox"/> 40350_at	ADAM metallopeptidase domain 23(ADAM23)			
9 <input type="checkbox"/> 36378_at	uroplakin 1A(UPK1A)			
10 <input type="checkbox"/> 31512_at	immunoglobulin kappa variable 1-13(IGKV1-13)			
11 <input type="checkbox"/> 32469_at	CEA cell adhesion molecule 3(CEACAM3)			
Gene Group 2	Enrichment Score: 0.31	RG	T	
1 <input type="checkbox"/> 38945_at	metal regulatory transcription factor 1(MTF1)			
2 <input type="checkbox"/> 34606_s_at	activating transcription factor 7(ATF7)			
3 <input type="checkbox"/> 41113_at	zinc finger protein 500(ZNF500)			
4 <input type="checkbox"/> 33922_at	PR/SET domain 2(PRDM2)			

130 gene(s) from your list are not in the output.

Gene Functional Classification Tool

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

Gene Group 1	Enrichment Score: 1.13	RG	T	Icon
1 <input type="checkbox"/> 35090_g_at, 35091_at	neuregulin 2(NRG2)			
2 <input type="checkbox"/> 33293_at	Fas apoptotic inhibitory molecule 2(FAIM2)			
3 <input type="checkbox"/> 34629_at	tumor protein p53 inducible protein 11(TP53I11)			

Functional Related Genes

[Help and Manual](#)

Search Scope: User's List

Options

Rerun Using Options

145 gene(s) were searched. 15 genes passed the filter.

[Download File](#)

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

#	Functionally Related Gene	Species	Kappa
1	natural cytotoxicity triggering receptor 3(NCR3)	Homo sapiens	0.75
2	CEA cell adhesion molecule 3(CEACAM3)	Homo sapiens	0.62
3	neuregulin 2(NRG2)	Homo sapiens	0.60
4	uroplakin 1A(UPK1A)	Homo sapiens	0.53
5	immunoglobulin kappa variable 1-13(IGKV1-13)	Homo sapiens	0.51
6	tumor protein p53 inducible protein 11(TP53I11)	Homo sapiens	0.48
7	neural cell adhesion molecule 1(NCAM1)	Homo sapiens	0.48
8	pregnancy specific beta-1-glycoprotein 4(PSG4)	Homo sapiens	0.48
9	ADAM metallopeptidase domain 23(ADAM23)	Homo sapiens	0.43
10	CEA cell adhesion molecule 8(CEACAM8)	Homo sapiens	0.41
11	MER proto-oncogene, tyrosine kinase(MERTK)	Homo sapiens	0.39
12	TNF receptor superfamily member 25(TNFRSF25)	Homo sapiens	0.38
13	Fas apoptotic inhibitory molecule 2(FAIM2)	Homo sapiens	0.37
14	acid sensing ion channel subunit 2(ASIC2)	Homo sapiens	0.36
15	ATPase H+/K+ transporting subunit beta(ATP4B)	Homo sapiens	0.35

Gene Functional Classification Tool

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Gene Group 1	Enrichment Score: 1.13	RG	T
1 <input type="checkbox"/> 35090_g_at, 35091_at	neuregulin 2(NRG2)		
2 <input type="checkbox"/> 33293_at	Fas apoptotic inhibitory molecule 2(FAIM2)		
3 <input type="checkbox"/> 34629_at	tumor protein p53 inducible protein 11(TP53I11)		

Term Report

Gene Cluster 1
 Current Gene List: demolist1
 Current Background: Homo sapiens
 11 DAVID IDs
 183 term records


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Category	Term	RT	Genes in Group	Count	LI	PH	PT	%	P-Value	Fold Enrichment	Genes not in Group
INTERPRO	Immunoglobulin subtype	RT	6	11	527	19113	54.5	1.8E-6	1.8E1		(3)
SMART	IG	RT	6	11	527	10359	54.5	1.9E-6	1.4E1		(3)
INTERPRO	Immunoglobulin-like fold	RT	7	11	1116	19113	63.6	2.8E-6	1.0E1		(5)
UP_KW_DOMAIN	Immunoglobulin domain	RT	7	11	766	14576	63.6	3.6E-6	1.0E1		(3)
UP_SEQ_FEATURE	DOMAIN:Ig-like	RT	6	11	671	20558	54.5	8.0E-6	1.4E1		(3)
INTERPRO	Immunoglobulin-like domain	RT	6	11	763	19113	54.5	1.1E-5	1.3E1		(3)
INTERPRO	Immunoglobulin V-set	RT	5	11	475	19113	45.5	4.3E-5	1.6E1		
UP_SEQ_FEATURE	CARBOHYD:N-linked (GlcNAc...) asparagine	RT	9	11	4419	20558	81.8	1.3E-4	3.4E0		(34)
GOTERM_CC_DIRECT	cell surface	RT	5	11	657	20647	45.5	1.8E-4	1.1E1		(7)
INTERPRO	Immunoglobulin subtype 2	RT	4	11	260	19113	36.4	2.0E-4	2.2E1		(2)
SMART	IGc2	RT	4	11	260	10359	36.4	3.0E-4	1.7E1		(2)
GOTERM_CC_DIRECT	plasma membrane	RT	9	11	5455	20647	81.8	6.2E-4	2.8E0		(39)
UP_SEQ_FEATURE	TOPO_DOM:Extracellular	RT	7	11	2976	20558	63.6	1.1E-3	3.8E0		(16)
UP_SEQ_FEATURE	DOMAIN:Ig-like V-type	RT	3	11	139	20558	27.3	2.0E-3	2.7E1		
UP_KW_PTM	Glycoprotein	RT	9	11	4784	14204	81.8	3.7E-3	2.2E0		(42)
UP_SEQ_FEATURE	TOPO_DOM:Cytoplasmic	RT	7	11	3879	20558	63.6	4.7E-3	2.9E0		(19)
UP_SEQ_FEATURE	DOMAIN:Ig-like C2-type 2	RT	3	11	219	20558	27.3	4.8E-3	1.7E1		(3)
UP_SEQ_FEATURE	DOMAIN:Ig-like C2-type 1	RT	3	11	219	20558	27.3	4.8E-3	1.7E1		(3)
GOTERM_CC_DIRECT	integral component of membrane	RT	8	11	5457	20647	72.7	4.9E-3	2.4E0		(29)
UP_SEQ_FEATURE	TRANSMEM:Helical	RT	8	11	5465	20558	72.7	5.1E-3	2.4E0		(28)
UP_KW_PTM	Disulfide bond	RT	8	11	3859	14204	72.7	5.8E-3	2.3E0		(39)
UP_KW_CELLULAR_COMPONENT	Membrane	RT	10	11	8293	17836	90.9	5.9E-3	1.8E0		(49)
UP_KW_DOMAIN	Signal	RT	8	11	4410	14576	72.7	1.1E-2	2.1E0		(43)
UP_KW_CELLULAR_COMPONENT	Cell membrane	RT	7	11	4000	17836	63.6	1.1E-2	2.4E0		(29)
UP_SEQ_FEATURE	DOMAIN:Immunoglobulin V-set	RT	2	11	41	20558	18.2	2.0E-2	4.6E1		
GOTERM_MF_DIRECT	protein tyrosine kinase binding	RT	2	11	51	18967	18.2	2.1E-2	4.1E1		
GOTERM_BP_DIRECT	regulation of immune system process	RT	2	11	44	19453	18.2	2.2E-2	4.0E1		
UP_KW_CELLULAR_COMPONENT	Secreted	RT	5	11	2164	17836	45.5	2.5E-2	3.0E0		(30)
UP_KW_BIOLOGICAL_PROCESS	Cell adhesion	RT	3	11	493	11371	27.3	2.5E-2	6.6E0		(6)
GOTERM_BP_DIRECT	immune response	RT	3	11	510	19453	27.3	2.7E-2	6.9E0		(7)
GOTERM_CC_DIRECT	specific granule membrane	RT	2	11	91	20647	18.2	4.3E-2	2.1E1		
GOTERM_CC_DIRECT	anchored component of membrane	RT	2	11	114	20647	18.2	5.4E-2	1.6E1		(2)
UP_KW_DOMAIN	Transmembrane helix	RT	8	11	5887	14576	72.7	5.8E-2	1.6E0		(30)
UP_KW_DOMAIN	Transmembrane	RT	8	11	5935	14576	72.7	6.0E-2	1.6E0		(30)
INTERPRO	Immunoglobulin I-set	RT	2	11	136	19113	18.2	6.2E-2	1.4E1		(2)
UP_SEQ_FEATURE	DOMAIN:Ig-like C2-type 3	RT	2	11	133	20558	18.2	6.3E-2	1.4E1		(1)
GOTERM_CC_DIRECT	extracellular region	RT	4	11	2208	20647	36.4	8.3E-2	2.6E0		(34)
UP_KW_PTM	GPI-anchor	RT	2	11	148	14204	18.2	9.9E-2	8.7E0		(1)



Gene Functional Classification Tool

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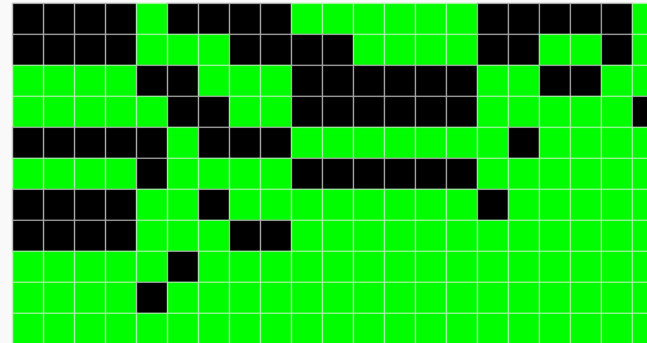
Gene Group 1	Enrichment Score: 1.13	RG	T	
1 <input type="checkbox"/> 35090_g_at, 35091_at	neuregulin 2(NRG2)			
2 <input type="checkbox"/> 33293_at	Fas apoptotic inhibitory molecule 2(FAIM2)			
3 <input type="checkbox"/> 34629_at	tumor protein p53 inducible protein 11(TP53I11)			

2D View

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

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tumor protein p53 inducible protein 11(TP53I11)
 Fas apoptotic inhibitory molecule 2(FAIM2)
 immunoglobulin kappa variable 1-13(IGKV1-13)
 pregnancy specific beta-1-glycoprotein 4(PSG4)
 uroplakin 1A(UPK1A)
 CEA cell adhesion molecule 8(CEACAM8)
 CEA cell adhesion molecule 3(CEACAM3)
 ADAM metalloproteinase domain 23(ADAM23)
 neuregulin 2(NRG2)
 natural cytotoxicity triggering receptor 3(NCR3)
 neural cell adhesion molecule 1(NCAM1)

DOMAIN: Ig-like
 IPR007110: Immunoglobulin-like domain
 IPR003599: Immunoglobulin subtype
 SM00409: IG
 REGION: Disordered
 GO: 0005515~protein binding
 KW-1003~Cell membrane
 KW-0393~Immunoglobulin domain
 IPR013783: Immunoglobulin-like fold
 TOPO_DOM: Extracellular
 TOPO_DOM: Cytoplasmic
 GO: 0016021~integral component of membrane
 TRANSMEM: Helical
 KW-1133~Transmembrane helix
 KW-0812~Transmembrane
 KW-1015~Disulfide bond
 KW-0732~Signal
 CARBOHYD: N-linked (GlcNAc...)
 KW-0325~Glycoprotein
 GO: 0005886~plasma membrane
 KW-0472~Membrane

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

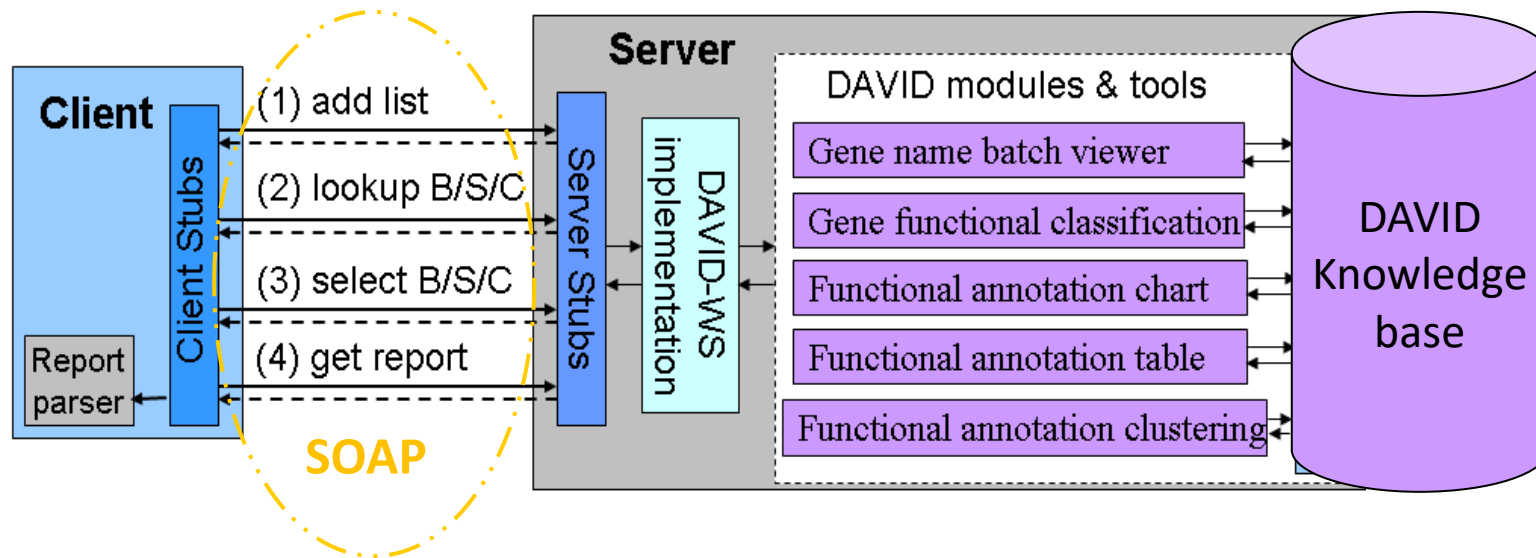
Show Gene List Names in Batch: https://davidbioinformatics.nih.gov/api.jsp?type=ENTREZ_GENE_ID&ids=2919,6347,6348,6364&tool=list

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="re" 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	G0:0005515~protein binding	297	79.838710	6.799082e-12	4.643773e-09
1	GOTERM_MF_DIRECT	G0:0042802~identical protein binding	69	18.548387	4.670809e-09	1.595081e-06
2	GOTERM_BP_DIRECT	G0:0000122~negative regulation of transcriptio...	43	11.559140	4.162287e-07	1.132975e-03
3	GOTERM_MF_DIRECT	G0:0019904~protein domain specific binding	19	5.107527	1.538277e-06	3.502143e-04
4	GOTERM_BP_DIRECT	G0:0043547~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	G0:2000573~positive regulation of DNA biosynth...	3	0.806452	4.930223e-02	7.341744e-01
421	GOTERM_BP_DIRECT	G0:0045747~positive regulation of Notch signal...	4	1.075269	4.932326e-02	7.341744e-01
422	GOTERM_BP_DIRECT	G0:0007229~integrin-mediated signaling pathway	6	1.612903	4.974697e-02	7.341744e-01

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- Cliff Lane

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 - Sharon Beck
 - Bill Wilton
 - Shawn Steward

Frederick National Laboratory

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 - Uma Mudunuri
 - Henri Tuthill
 - Anney Che
 - David Bryant
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 - Richard Lempicki
 - Glynn Dennis
 - Doug Hosack
 - Da Wei Huang
 - Xiaoli Jiao
 - Ju Qiu