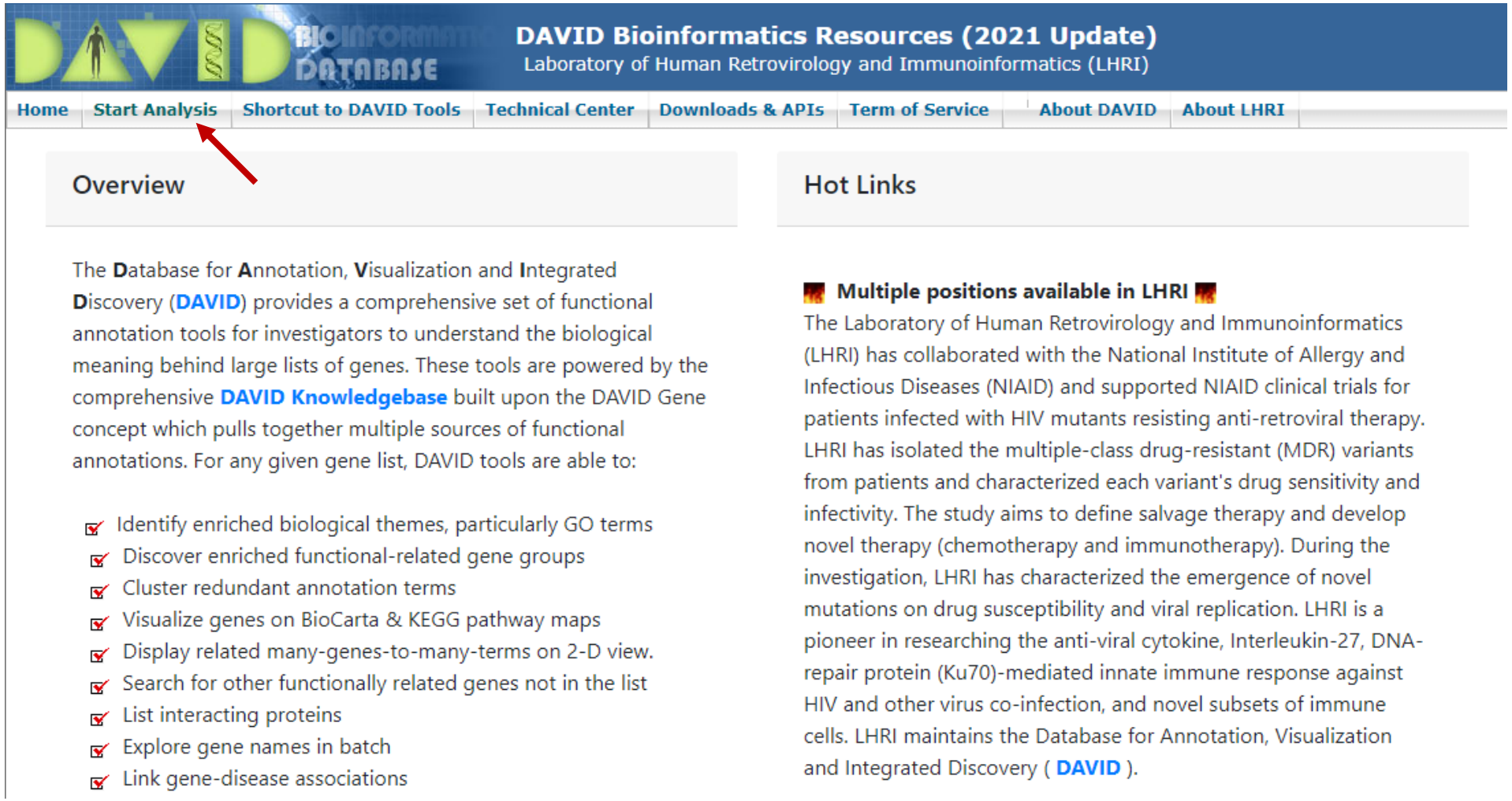
Quick Start Tutorial for the DAVID Bioinformatics Resources

Last Updated February 2022

Start Analysis Wizard



Submit gene list or use built-in demo lists

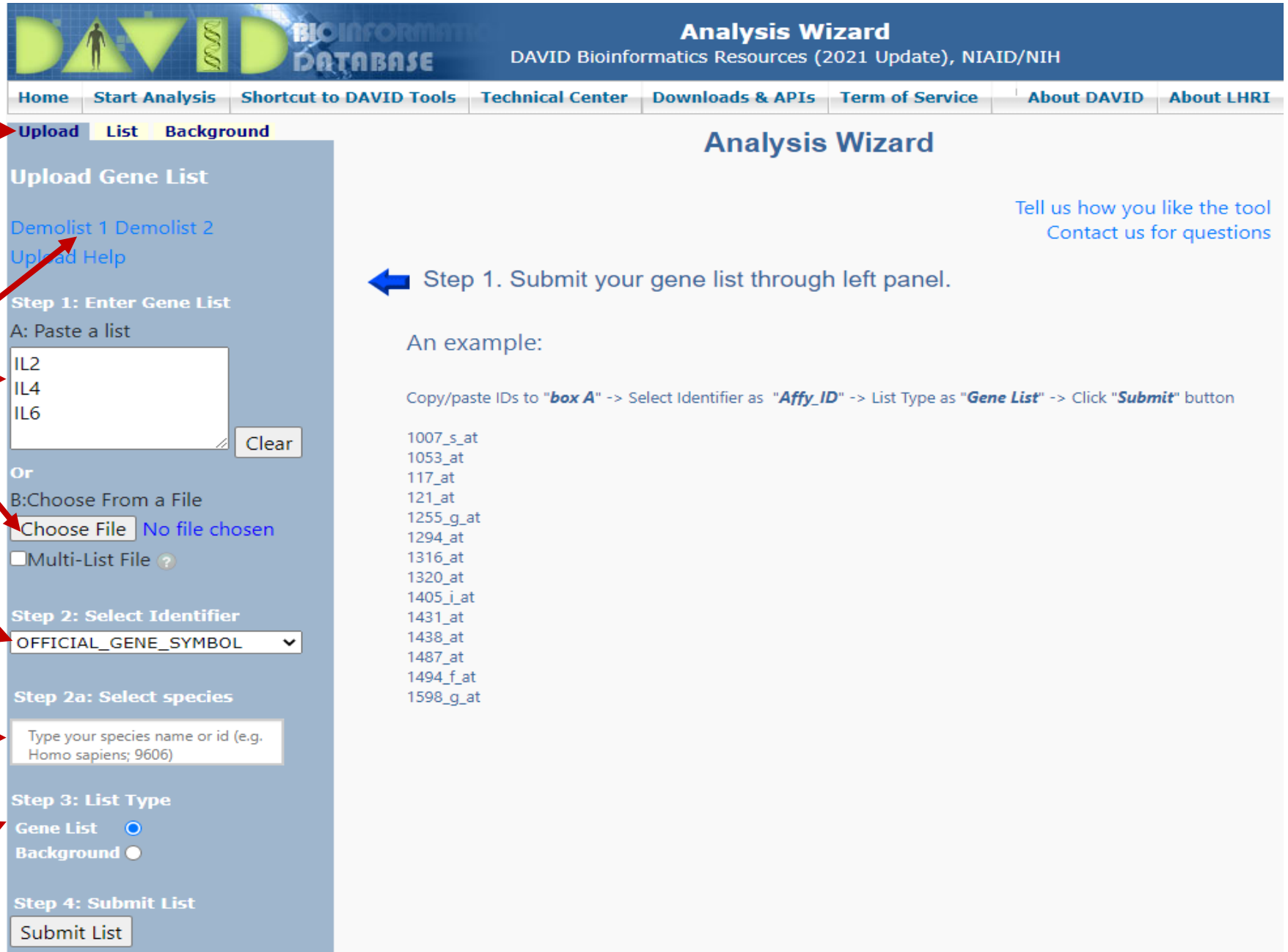
First, switch to the Upload tab

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

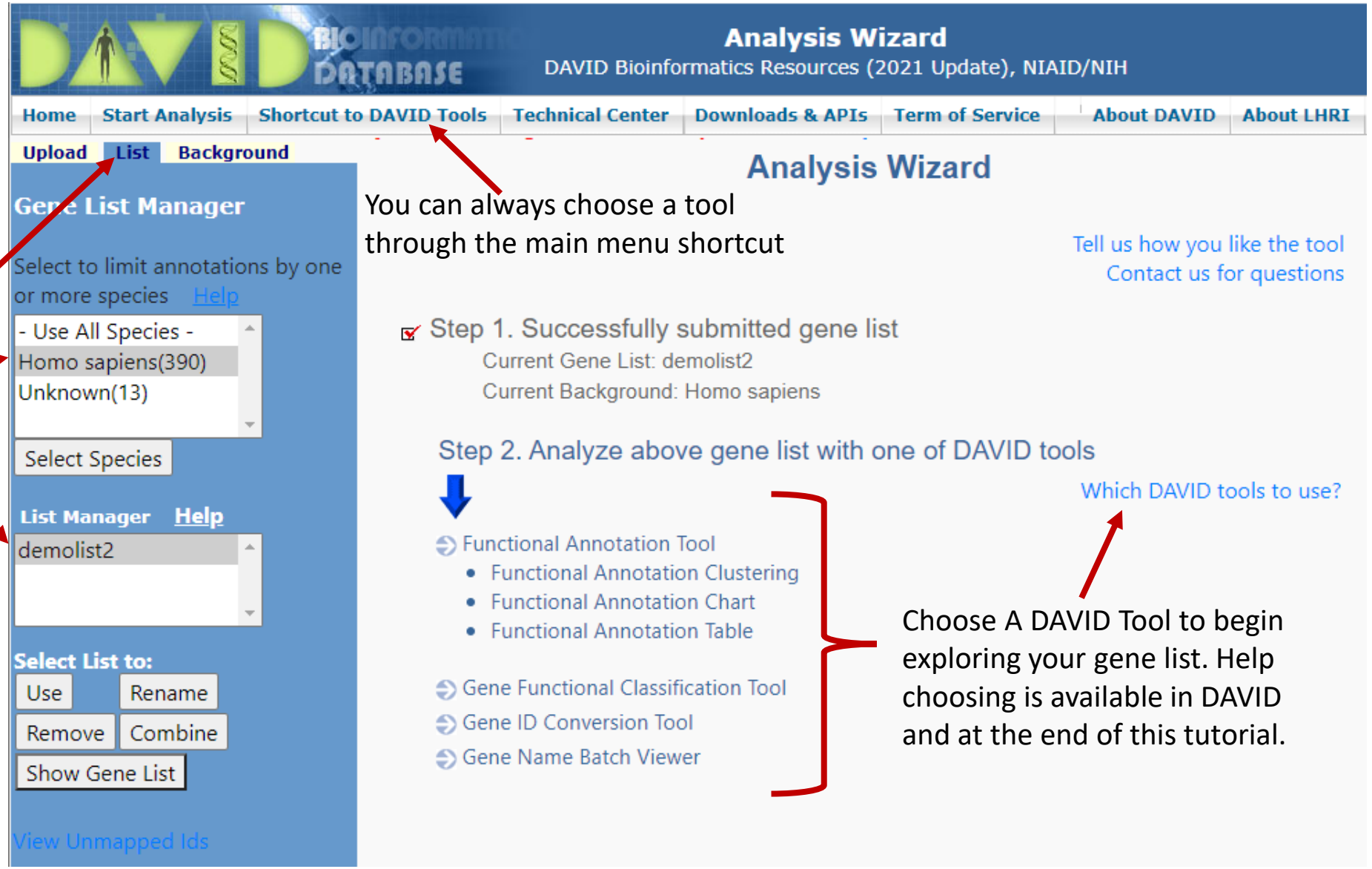
2. Select the identifier type corresponding to your list.

2a. If “OFFICIAL_GENE_SYMBOL” is selected, a new parameter will appear allowing you to indicate your species of interest by typing the name or taxonomy id.

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



Verify that your list has been uploaded and begin analysis



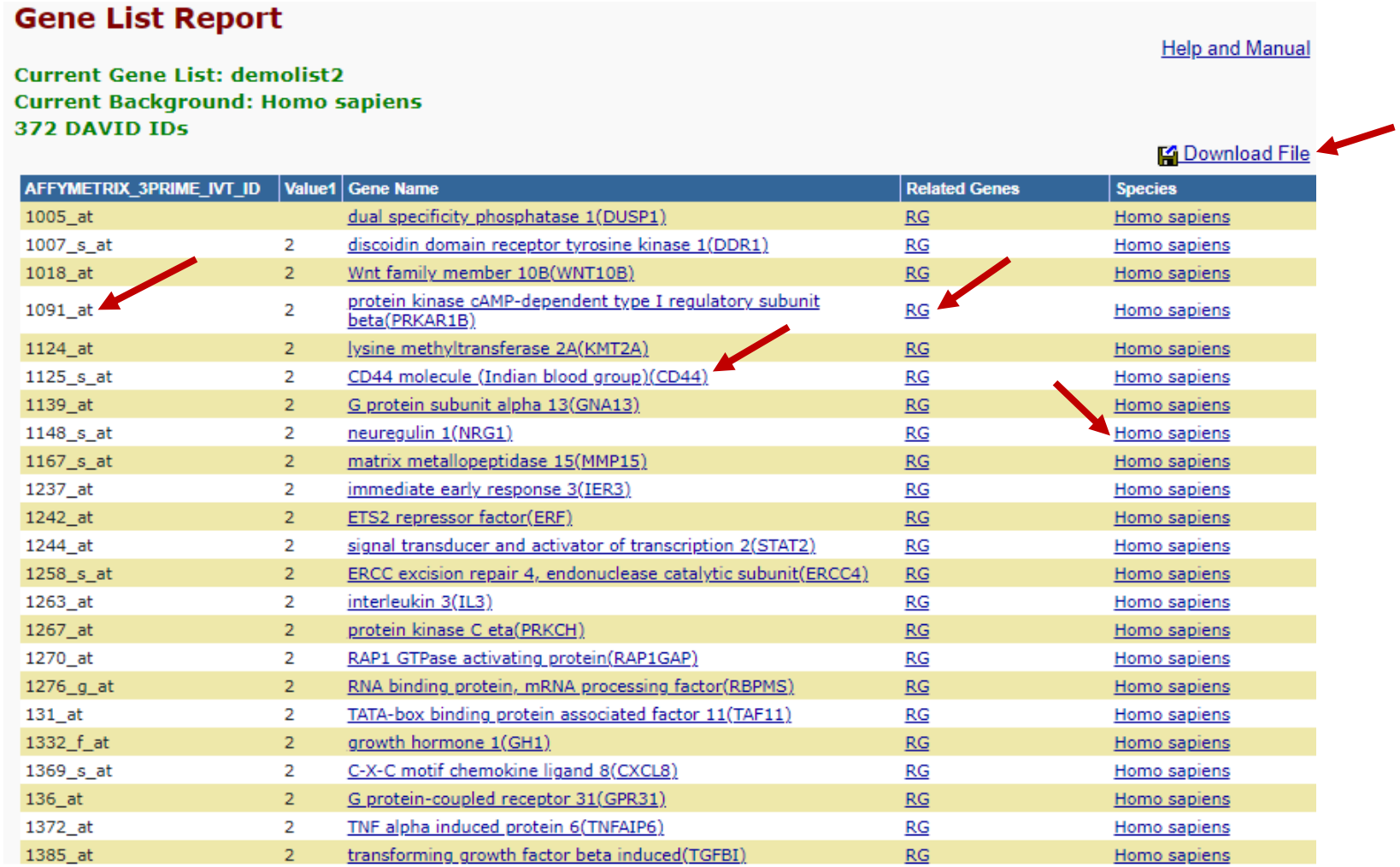
You can always choose a tool through the main menu shortcut

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

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

Gene Name Batch Viewer

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



Gene List Report

Help and Manual

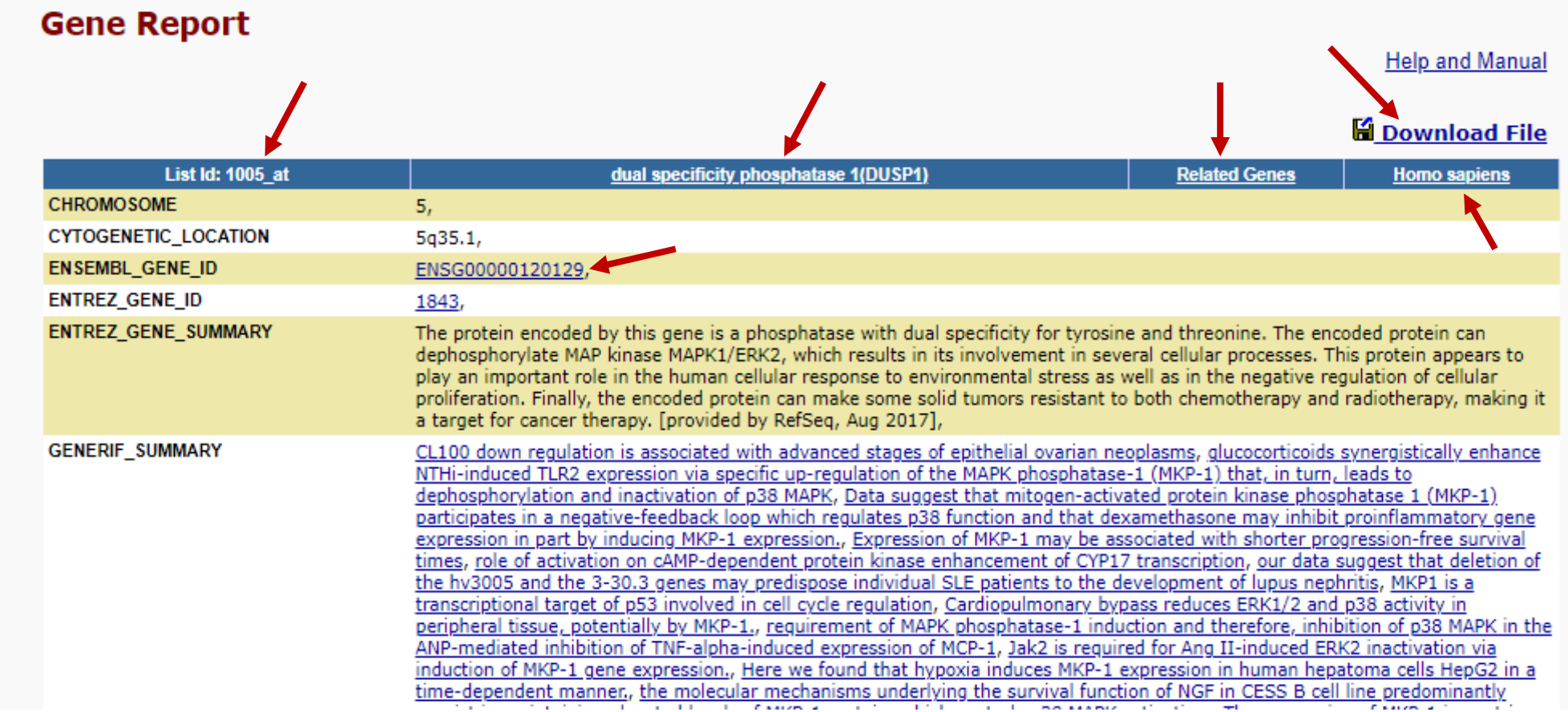
Current Gene List: demolist2
Current Background: Homo sapiens
372 DAVID IDs

Download File

AFFYMETRIX_3PRIME_IVT_ID	Value1	Gene Name	Related Genes	Species
1005_at		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
1125_s_at	2	CD44 molecule (Indian blood group)(CD44)	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 metallopeptidase 15(MMP15)	RG	Homo sapiens
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
1369_s_at	2	C-X-C motif chemokine ligand 8(CXCL8)	RG	Homo sapiens
136_at	2	G protein-coupled receptor 31(GPR31)	RG	Homo sapiens
1372_at	2	TNF alpha induced protein 6(TNFAIP6)	RG	Homo sapiens
1385_at	2	transforming growth factor beta induced(TGFBI)	RG	Homo sapiens

DAVID Gene Report

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



Gene Report

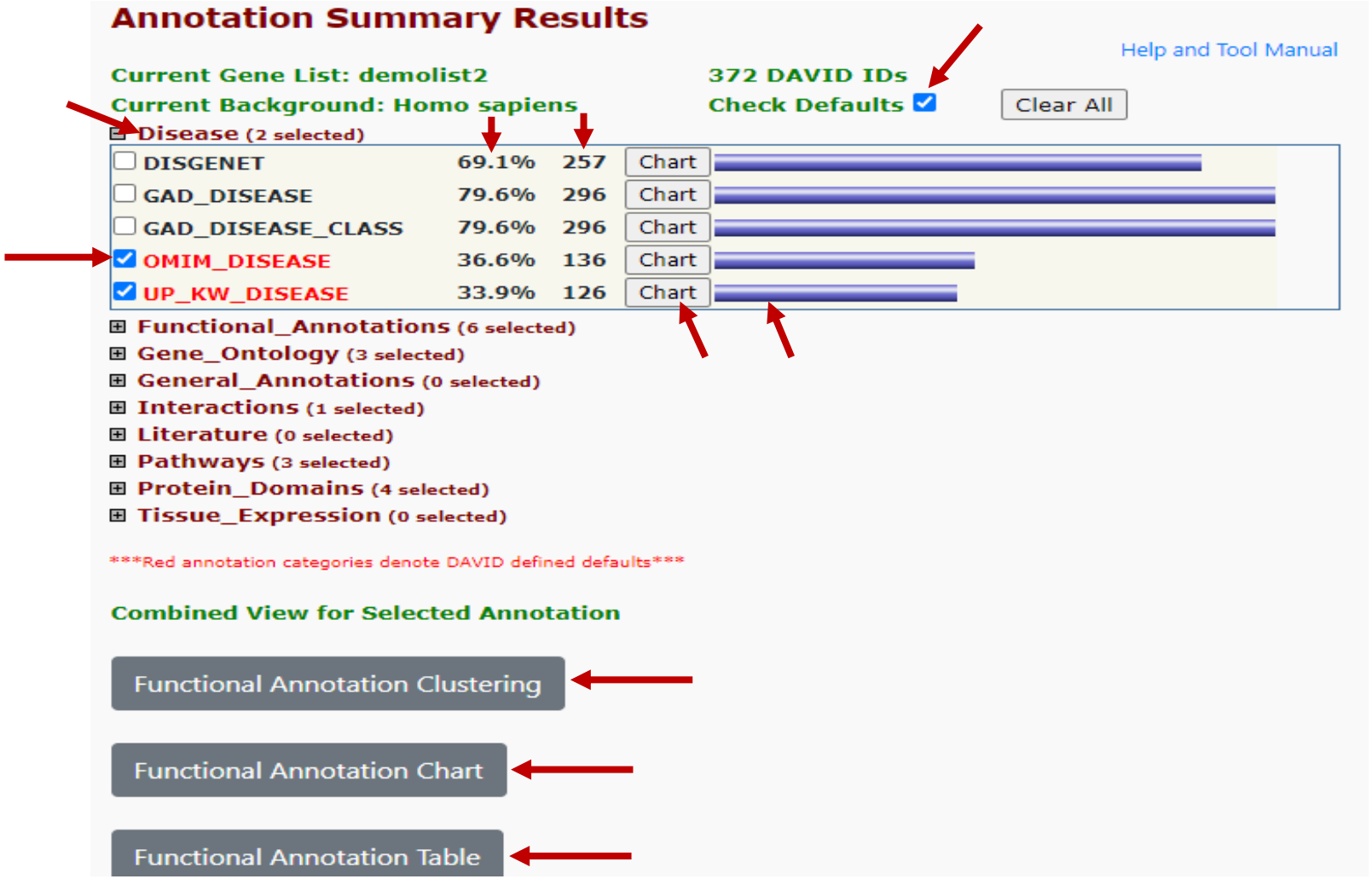
Help and Manual

Download File

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

Functional Annotation Summary

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



Functional Annotation Table

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

Functional Annotation Table

Help and Manual

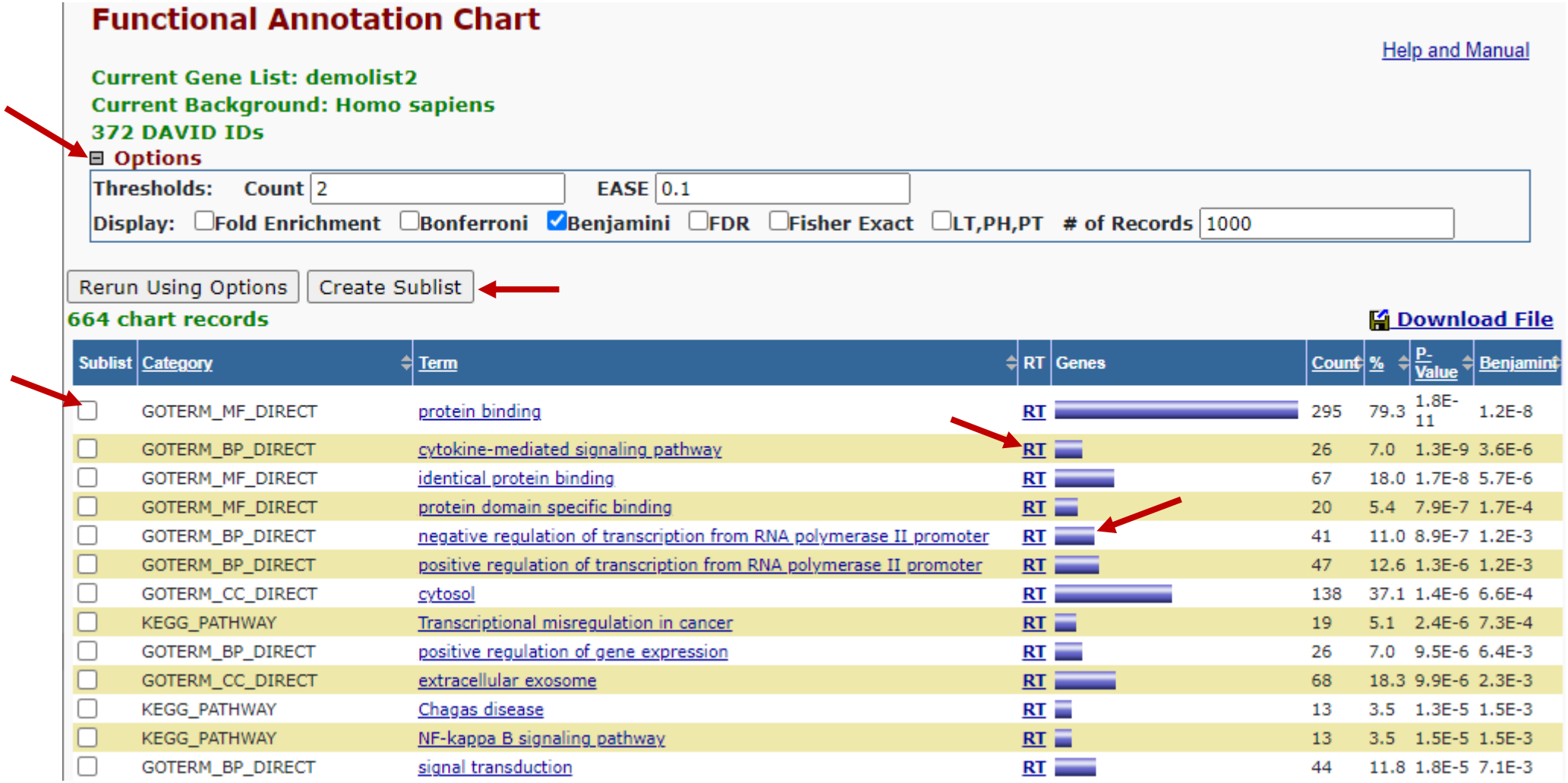
Current Gene List: demolist2
Current Background: Homo sapiens
372 DAVID IDs

365 record(s) Download File

612_s_at	2',3'-cyclic nucleotide 3' phosphodiesterase(CNP)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	microtubule cytoskeleton organization, chemical synaptic transmission, axonogenesis, aging, adult locomotory behavior, cyclic nucleotide catabolic process, response to toxic substance, substantia nigra development, forebrain development, response to lipopolysaccharide, regulation of mitochondrial membrane permeability, oligodendrocyte differentiation,		
GOTERM_CC_DIRECT	extracellular space, cytoplasm, mitochondrial outer membrane, mitochondrial inner membrane, microtubule, plasma membrane, microvillus, membrane, pseudopodium, myelin sheath abaxonal region, myelin sheath adaxonal region, melanosome, synapse, perinuclear region of cytoplasm, extracellular exosome,		
GOTERM_MF_DIRECT	RNA binding, 2',3'-cyclic-nucleotide 3'-phosphodiesterase activity, protein binding, cyclic nucleotide binding,		
INTERPRO	Cyclic nucleotide phosphodiesterase, RNA ligase/cyclic nucleotide phosphodiesterase, P-loop containing nucleoside triphosphate hydrolase,		
OMIM_DISEASE	Leukodystrophy, hypomyelinating, 20,		
PIR_SUPERFAMILY	2',3'-cyclic-nucleotide 3'-phosphodiesterase,		
UP_KW_CELLULAR_COMPONENT	Membrane,		
UP_KW_DISEASE	Neurodegeneration, Leukodystrophy,		
UP_KW_MOLECULAR_FUNCTION	Hydrolase, RNA-binding,		
UP_KW_PTM	Lipoprotein, Methylation, Phosphoprotein, Prenylation,		
UP_SEQ_FEATURE	ACT_SITE:Proton acceptor, ACT_SITE:Proton donor, BINDING:Substrate, LIPID:S-farnesyl cysteine, PROPEP:Removed in mature form,		
35345_at	**3-hydroxy-3-methylglutaryl-CoA synthase 2(HMGCS2)**	**Related Genes**	**Homo sapiens**
GOTERM_BP_DIRECT	kidney development, liver development, acetyl-CoA metabolic process, cholesterol biosynthetic process, brain development, midgut development, response to nutrient, response to temperature stimulus, response to xenobiotic stimulus, response to metal ion, farnesyl diphosphate biosynthetic process, mevalonate pathway, regulation of metabolic process, lung development, cellular response to insulin stimulus, multicellular organismal response to stress, response to testosterone, response to glucagon, response to triglyceride, response to monosaccharide, response to prostaglandin F, response to starvation, response to ethanol, ketone body biosynthetic process, response to cAMP, response to growth hormone, adipose tissue development, response to linoleic acid, cellular response to lipopolysaccharide, cellular response to amino acid stimulus, cellular response to glucocorticoid stimulus, cellular response to fatty acid,		
GOTERM_CC_DIRECT	mitochondrion, mitochondrial matrix,		
GOTERM_MF_DIRECT	hydroxymethylglutaryl-CoA synthase activity, identical protein binding,		
INTERPRO	Hydroxymethylglutaryl-coenzyme A synthase, active site, Hydroxymethylglutaryl-CoA synthase, eukaryotic, Hydroxymethylglutaryl-coenzyme A synthase, N-terminal, Hydroxymethylglutaryl-coenzyme A synthase C-terminal, Thiolase-like,		
KEGG_PATHWAY	Valine, leucine and isoleucine degradation, Butanoate metabolism, Terpenoid backbone biosynthesis, PPAR signaling pathway,		

Functional Annotation Chart

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



Functional Annotation Chart

Help and Manual

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

Options

Thresholds: Count 2 EASE 0.1

Display: ☐ Fold Enrichment ☐ Bonferroni ☑ Benjamini ☐ FDR ☐ Fisher Exact ☐ LT,PH,PT # of Records 1000

Rerun Using Options | Create Sublist

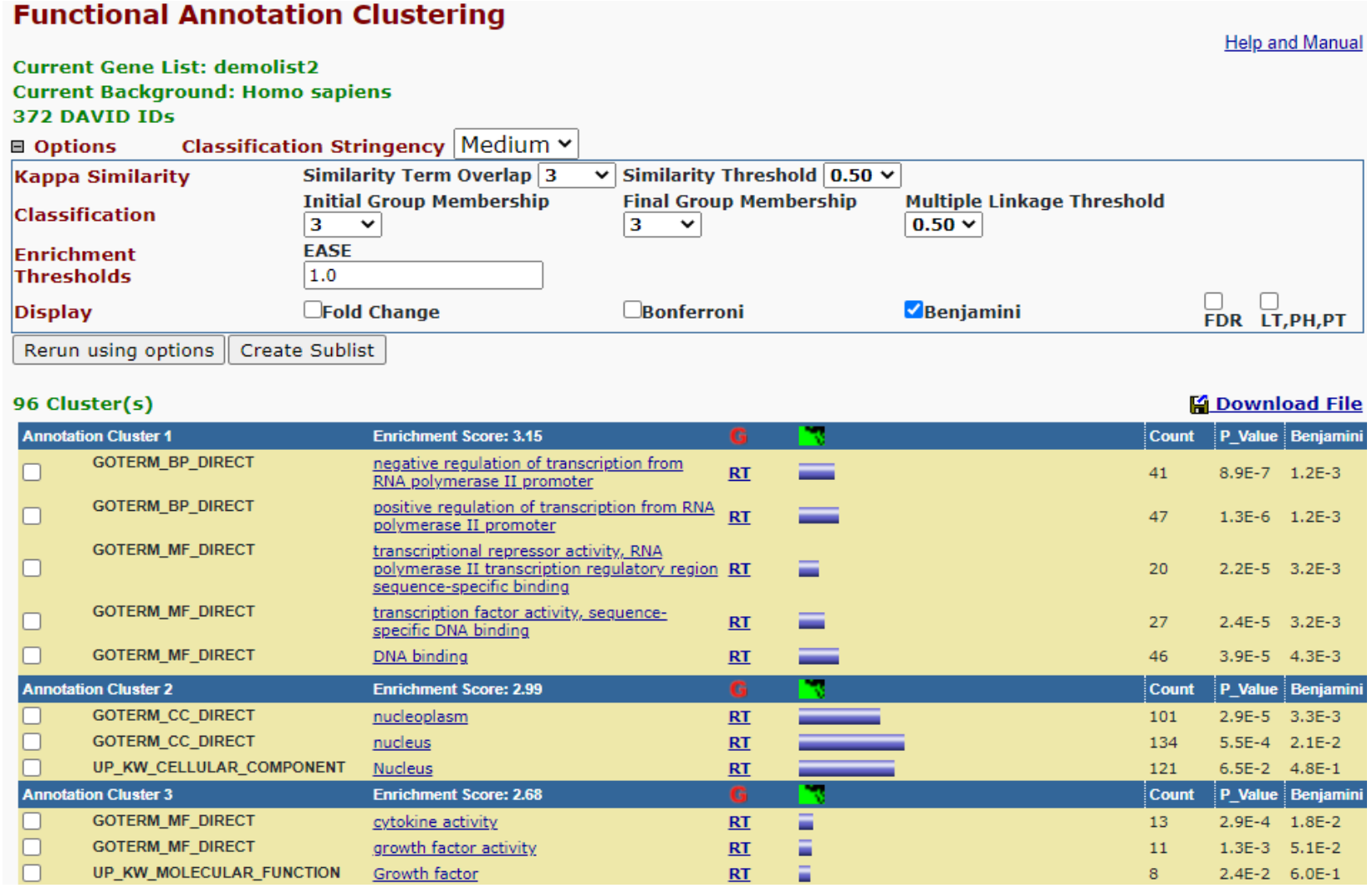
664 chart records

Download File

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

Functional Annotation Clustering

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



Functional Annotation Clustering

Help and Manual

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

Options Classification Stringency: Medium

Kappa Similarity — Similarity Term Overlap: 3 — Similarity Threshold: 0.50
Classification — Initial Group Membership: 3 — Final Group Membership: 3 — Multiple Linkage Threshold: 0.50
Enrichment Thresholds — EASE: 1.0
Display — Fold Change — Bonferroni — Benjamini — FDR — LT,PH,PT

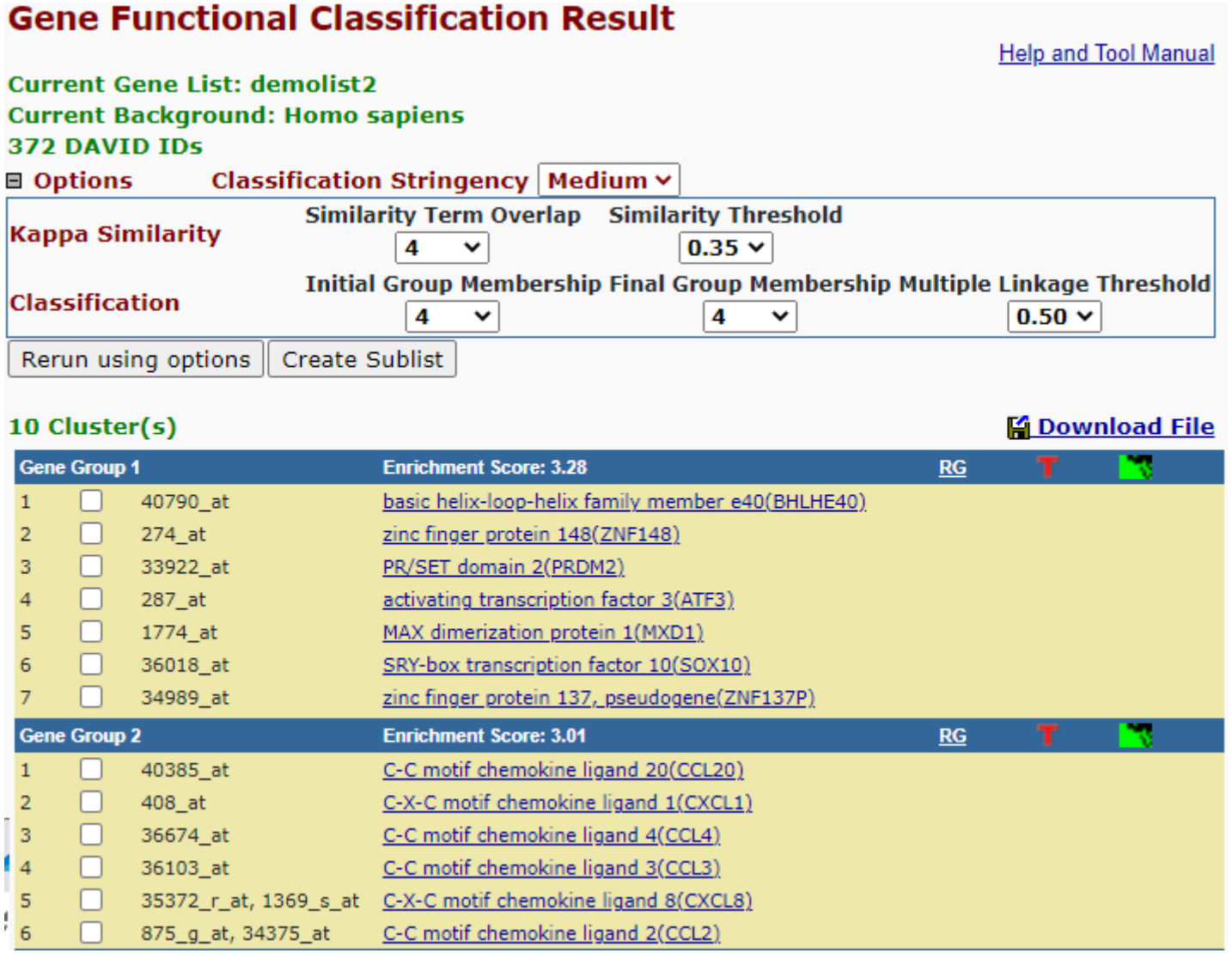
Rerun using options | Create Sublist

96 Cluster(s) Download File

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

Gene Functional Classification

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



Gene Functional Classification Result

Help and Tool Manual

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

Options Classification Stringency: Medium

	Similarity Term Overlap	Similarity Threshold	
Kappa Similarity	4	0.35	
	Initial Group Membership	Final Group Membership	Multiple Linkage Threshold
Classification	4	4	0.50

Rerun using options | Create Sublist

10 Cluster(s) Download File

Gene Group 1			Enrichment Score: 3.28	RG
1		40790_at	basic helix-loop-helix family member e40(BHLHE40)	
2		274_at	zinc finger protein 148(ZNF148)	
3		33922_at	PR/SET domain 2(PRDM2)	
4		287_at	activating transcription factor 3(ATF3)	
5		1774_at	MAX dimerization protein 1(MXD1)	
6		36018_at	SRY-box transcription factor 10(SOX10)	
7		34989_at	zinc finger protein 137, pseudogene(ZNF137P)	

Gene Group 2			Enrichment Score: 3.01	RG
1		40385_at	C-C motif chemokine ligand 20(CCL20)	
2		408_at	C-X-C motif chemokine ligand 1(CXCL1)	
3		36674_at	C-C motif chemokine ligand 4(CCL4)	
4		36103_at	C-C motif chemokine ligand 3(CCL3)	
5		35372_r_at, 1369_s_at	C-X-C motif chemokine ligand 8(CXCL8)	
6		875_g_at, 34375_at	C-C motif chemokine ligand 2(CCL2)	

Gene ID Conversion

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

Gene Accession Conversion Tool

Help

Download File

Gene Accession Conversion Statistics

Conversion Summary		
ID Count	**In DAVID DB**	**Conversion**
390	Yes	Successful
0	Yes	None
0	No	None
0	Ambiguous	Pending
Total Unique User IDs: 390		

Summary of Ambiguous Gene IDs		
ID Count	**Possible Source**	**Convert All**

All Possible Sources For Ambiguous IDs		
Ambiguous ID	**Possiblity**	**Convert**

Submit Converted List to DAVID as a Gene List **Submit Converted List to DAVID as a Background**

From	To	Species	David Gene Name
41382_at	1755	Homo sapiens	deleted in malignant brain tumors 1(DMBT1)
287_at	467	Homo sapiens	activating transcription factor 3(ATF3)
848_at	7185	Homo sapiens	TNF receptor associated factor 1(TRAF1)
2030_at	7481	Homo sapiens	Wnt family member 11(WNT11)
41106_at	3783	Homo sapiens	potassium calcium-activated channel subfamily N member 4(KCNN4)
1139_at	10672	Homo sapiens	G protein subunit alpha 13(GNA13)
1953_at	7422	Homo sapiens	vascular endothelial growth factor A(VEGFA)
36018_at	6663	Homo sapiens	SRY-box transcription factor 10(SOX10)
37206_at	130	Homo sapiens	alcohol dehydrogenase 6 (class V)(ADH6)
41736_g_at	22898	Homo sapiens	DENN domain containing 3(DENND3)
41438_at	114882	Homo sapiens	oxysterol binding protein like 8(OSBPL8)
35472_at	3772	Homo sapiens	potassium inwardly rectifying channel subfamily J member 15(KCNJ15)
1461_at	4792	Homo sapiens	NFKB inhibitor alpha(NFKBIA)

Which DAVID Tool and Additional Help

++ Highly Applied
+ Relevant

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

Additional Help

- DAVID Documentation
- Nature Protocols Paper
- DAVID Forum
- Contact the DAVID Team