Quick Tutorial of DAVID for Functional Enrichment Analysis

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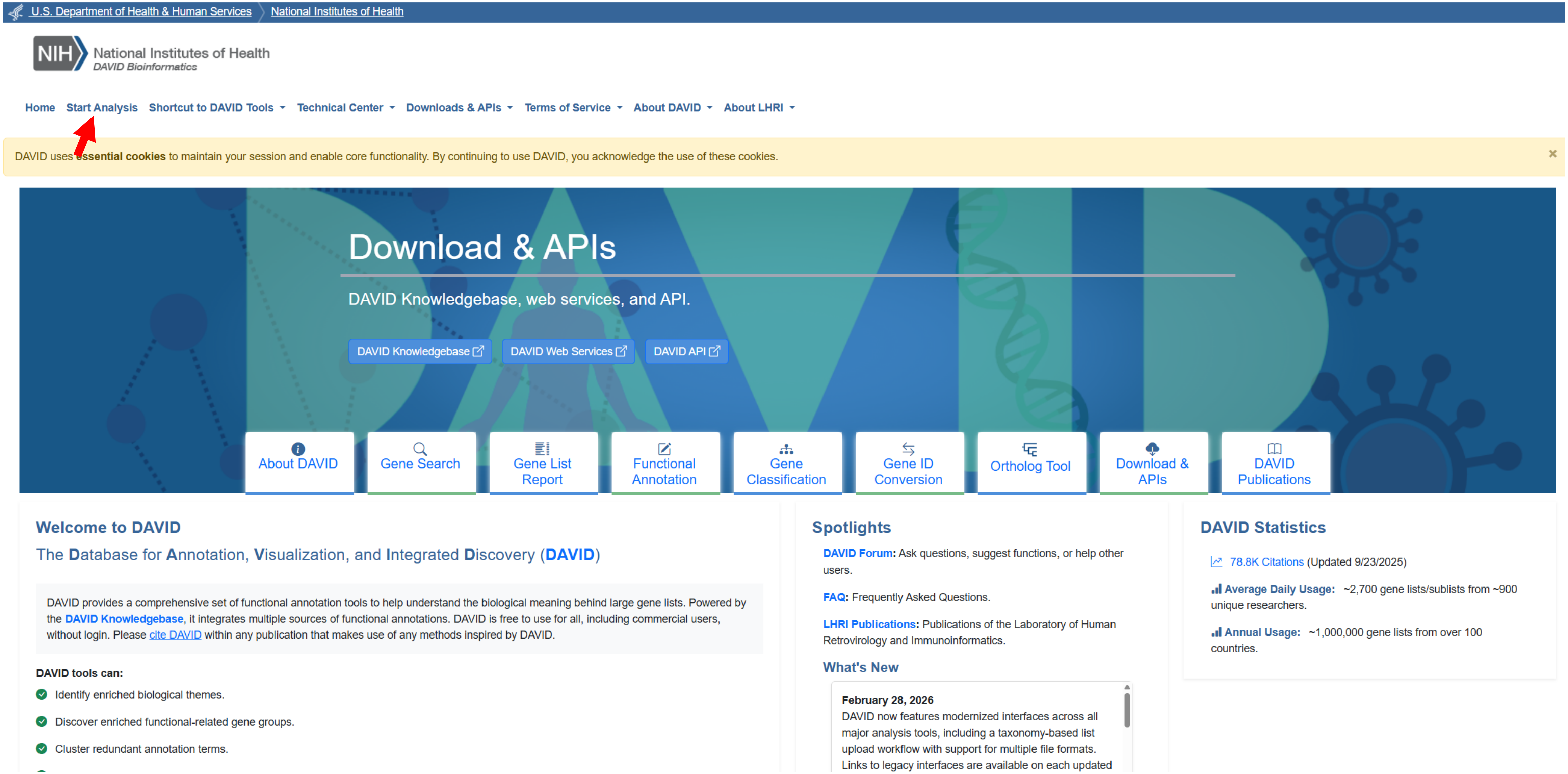
Start DAVID Analysis

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

Start DAVID Analysis



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

Download & APIs

DAVID Knowledgebase, web services, and API.

Welcome to DAVID

The **D**atabase for **A**nnotation, **V**isualization, and **I**ntegrated **D**iscovery (**DAVID**)

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

DAVID tools can:

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

Spotlights

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

FAQ: Frequently Asked Questions.

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

What's New

February 28, 2026
DAVID now features modernized interfaces across all major analysis tools, including a taxonomy-based list upload workflow with support for multiple file formats. Links to legacy interfaces are available on each updated

DAVID Statistics

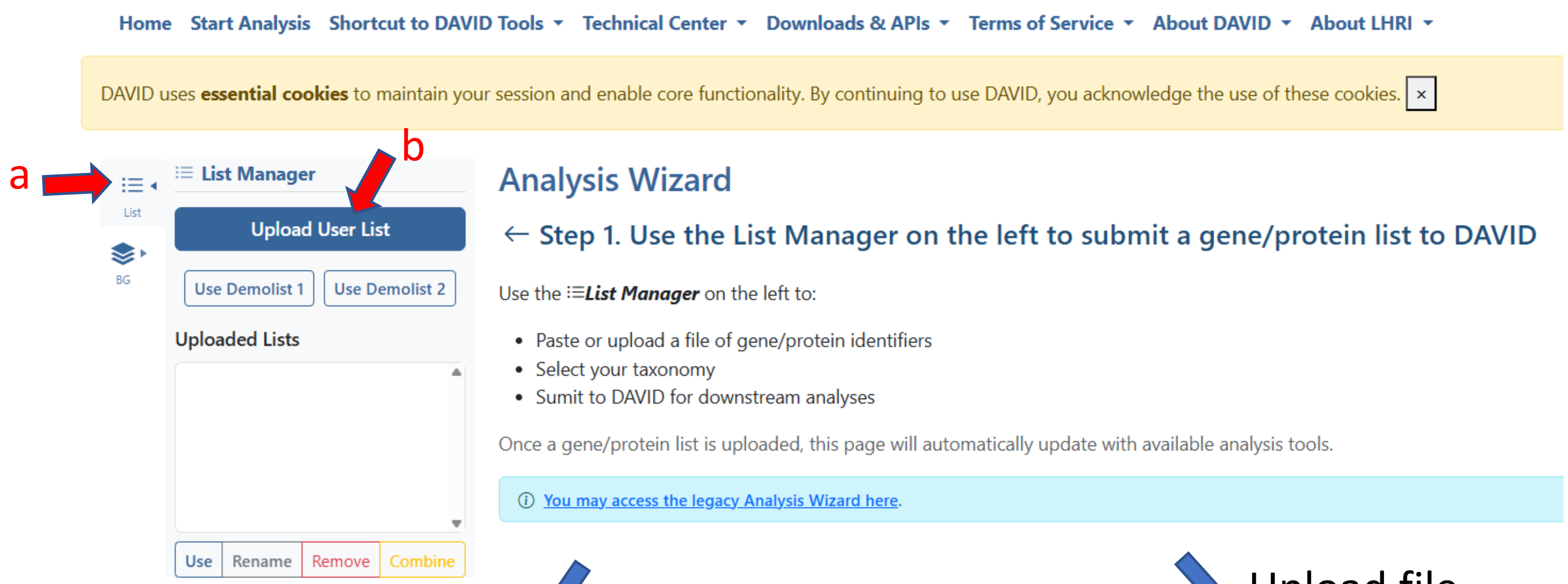
78.8K Citations (Updated 9/23/2025)

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

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

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

Submit Gene List



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Analysis Wizard

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

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

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

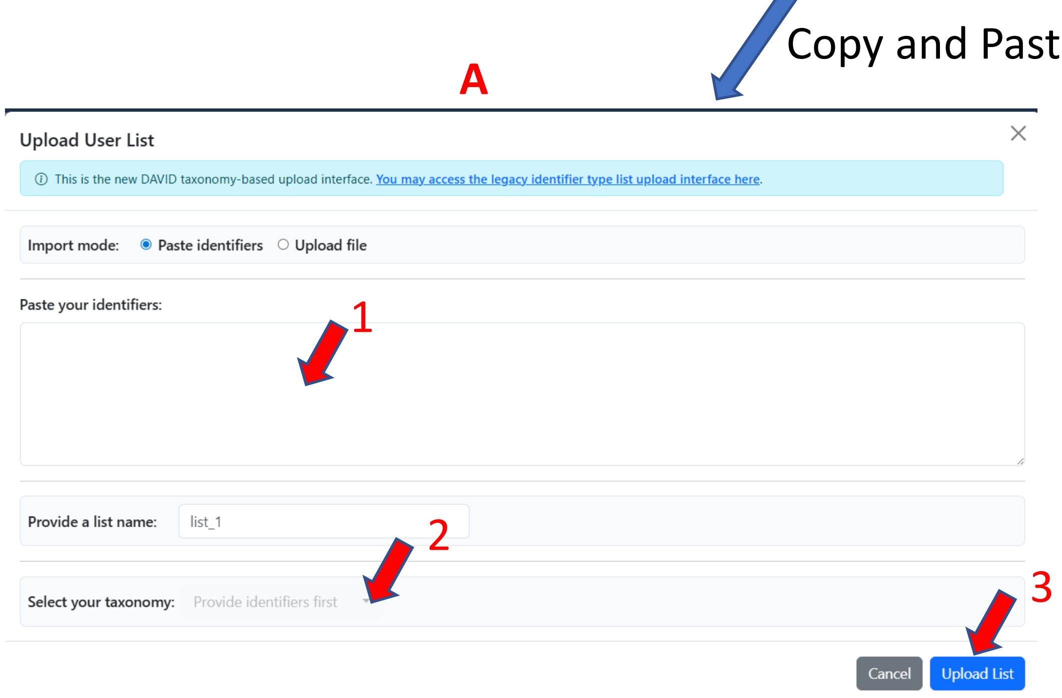
Once a gene/protein list is uploaded, this page will automatically update with available analysis tools.

ⓘ You may access the legacy Analysis Wizard here.

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

Copy and Paste

Upload file



Upload User List

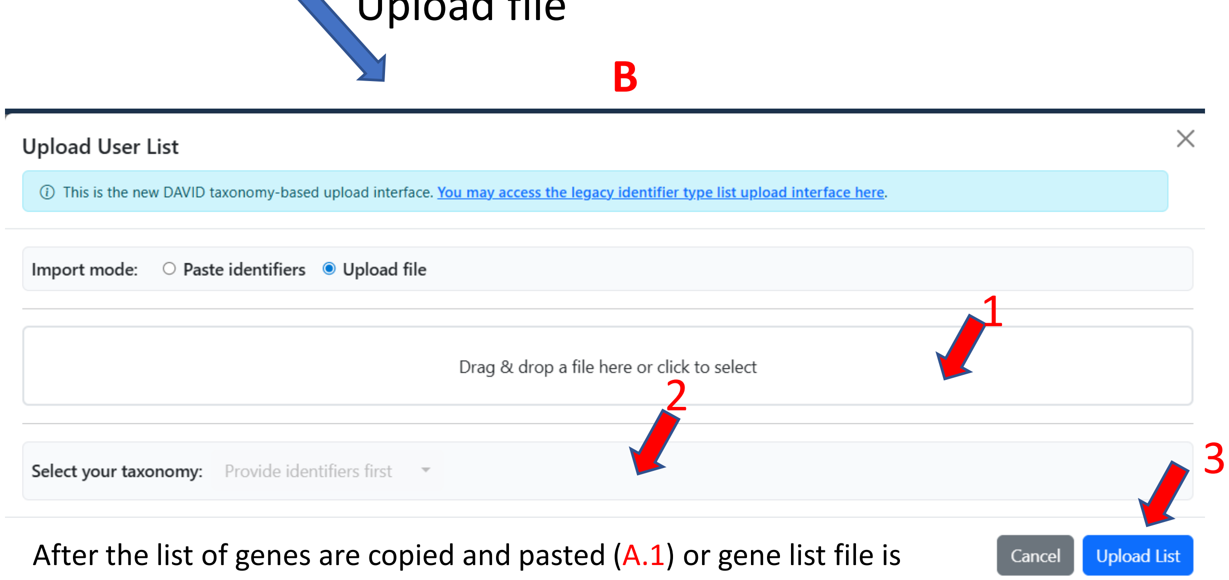
ⓘ This is the new DAVID taxonomy-based upload interface. You may access the legacy identifier type list upload interface here.

Import mode: ● Paste identifiers ○ Upload file

Paste your identifiers:

Provide a list name: list_1

Select your taxonomy: Provide identifiers first



Upload User List

ⓘ This is the new DAVID taxonomy-based upload interface. You may access the legacy identifier type list upload interface here.

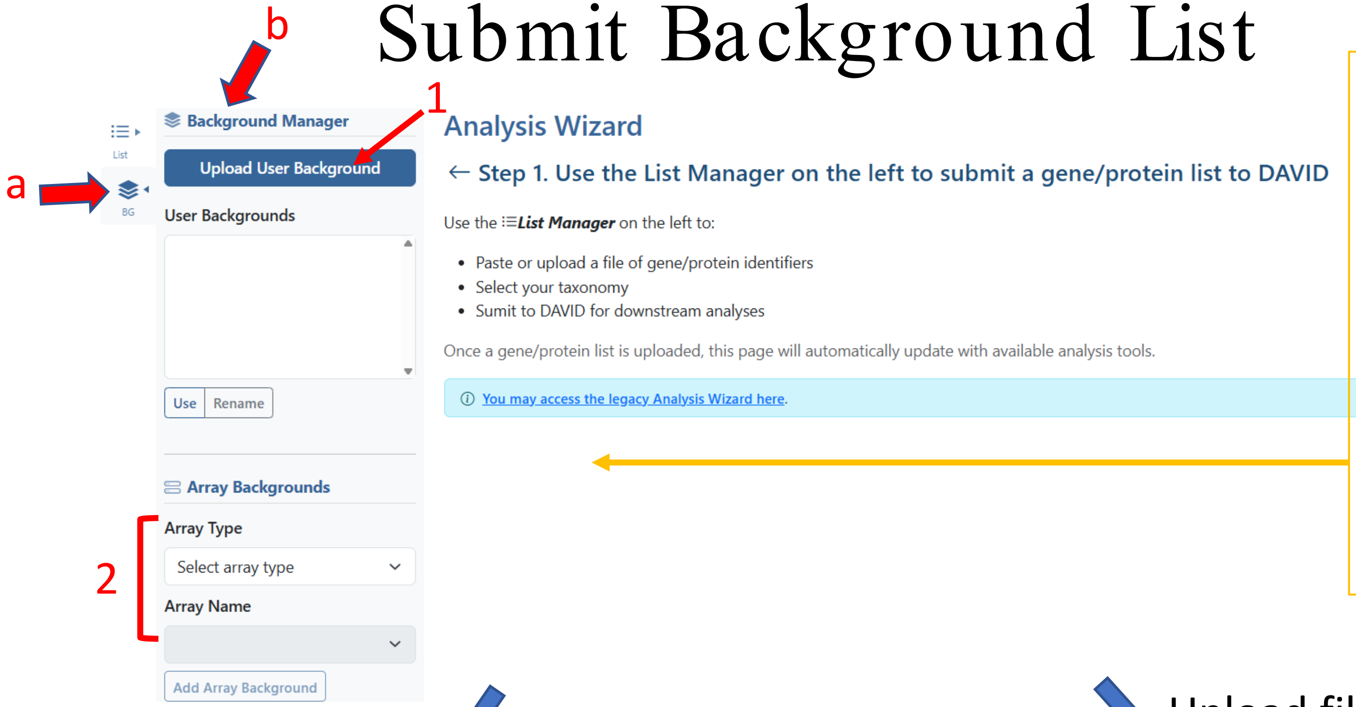
Import mode: ○ Paste identifiers ● Upload file

Drag & drop a file here or click to select

Select your taxonomy: Provide identifiers first

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

Submit Background List



Analysis Wizard

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

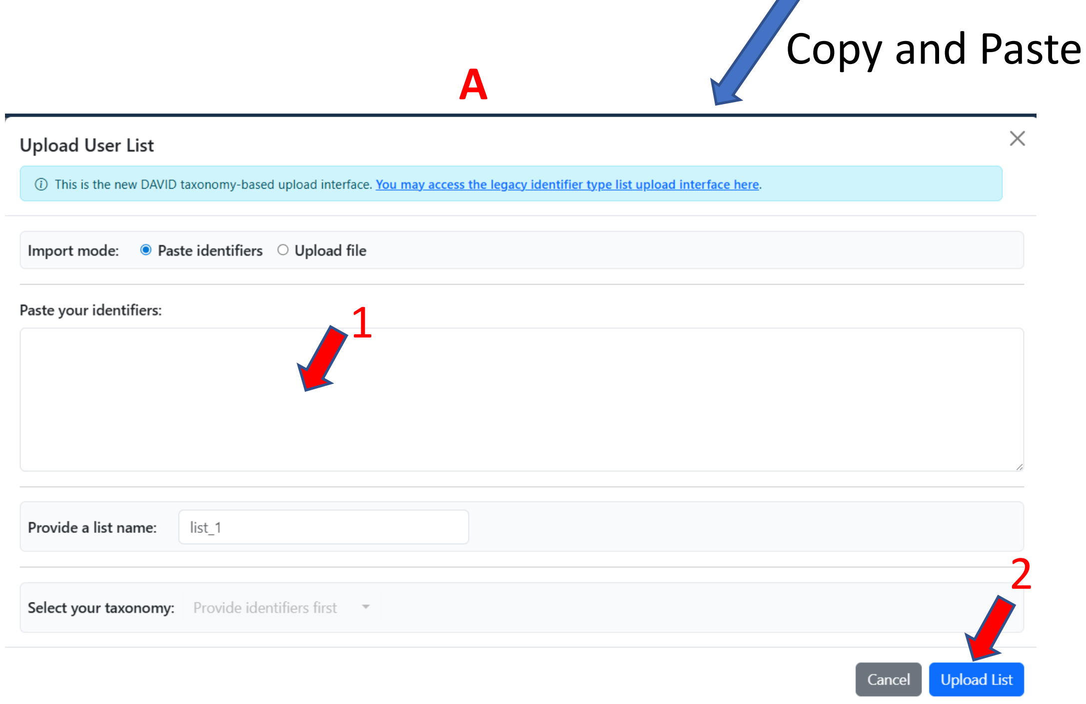
Use the ☰ ***List Manager*** on the left to:

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

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

ⓘ You may access the legacy Analysis Wizard here.

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



Upload User List

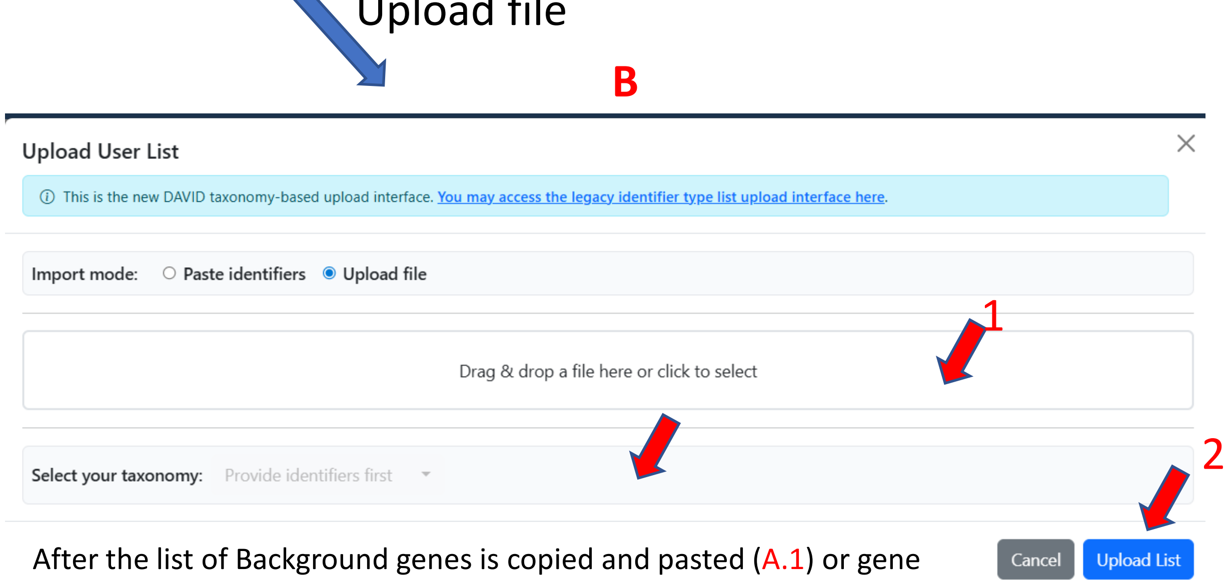
ⓘ This is the new DAVID taxonomy-based upload interface. You may access the legacy identifier type list upload interface here.

Import mode: ● Paste identifiers ○ Upload file

Paste your identifiers:

Provide a list name: list_1

Select your taxonomy: Provide identifiers first



Upload User List

ⓘ This is the new DAVID taxonomy-based upload interface. You may access the legacy identifier type list upload interface here.

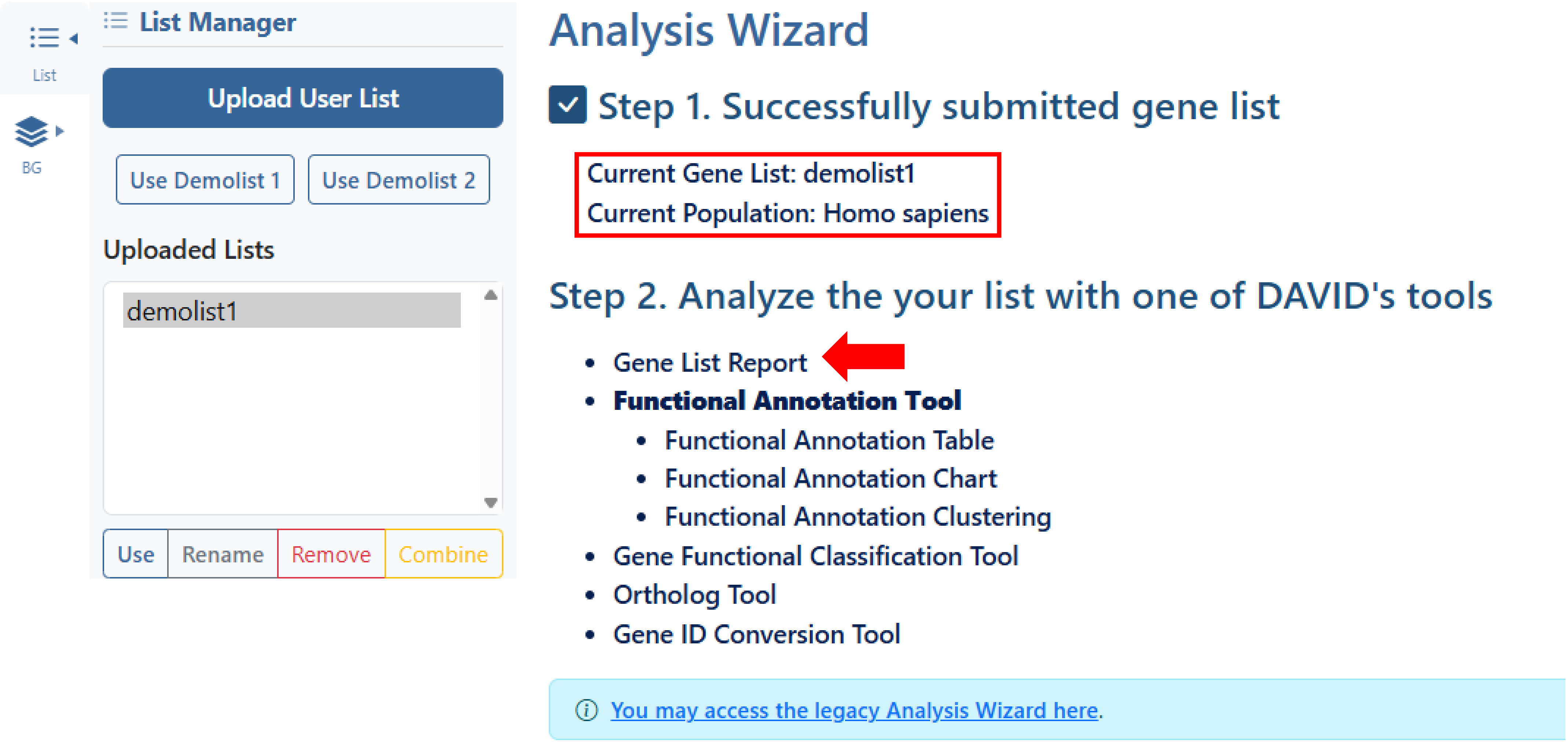
Import mode: ○ Paste identifiers ● Upload file

Select your taxonomy: Provide identifiers first

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

Gene List Report

Ready for Analysis



Uploaded Lists

demolist1

Analysis Wizard

☑ Step 1. Successfully submitted gene list

Current Gene List: demolist1
Current Population: Homo sapiens

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

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

ⓘ You may access the legacy Analysis Wizard here.

Gene List Report

Gene List Report

Current Gene List: demolist2 ①

Current Population: Homo sapiens

See the annotation in next slide

Search:

385 records (372 DAVID genes) ③

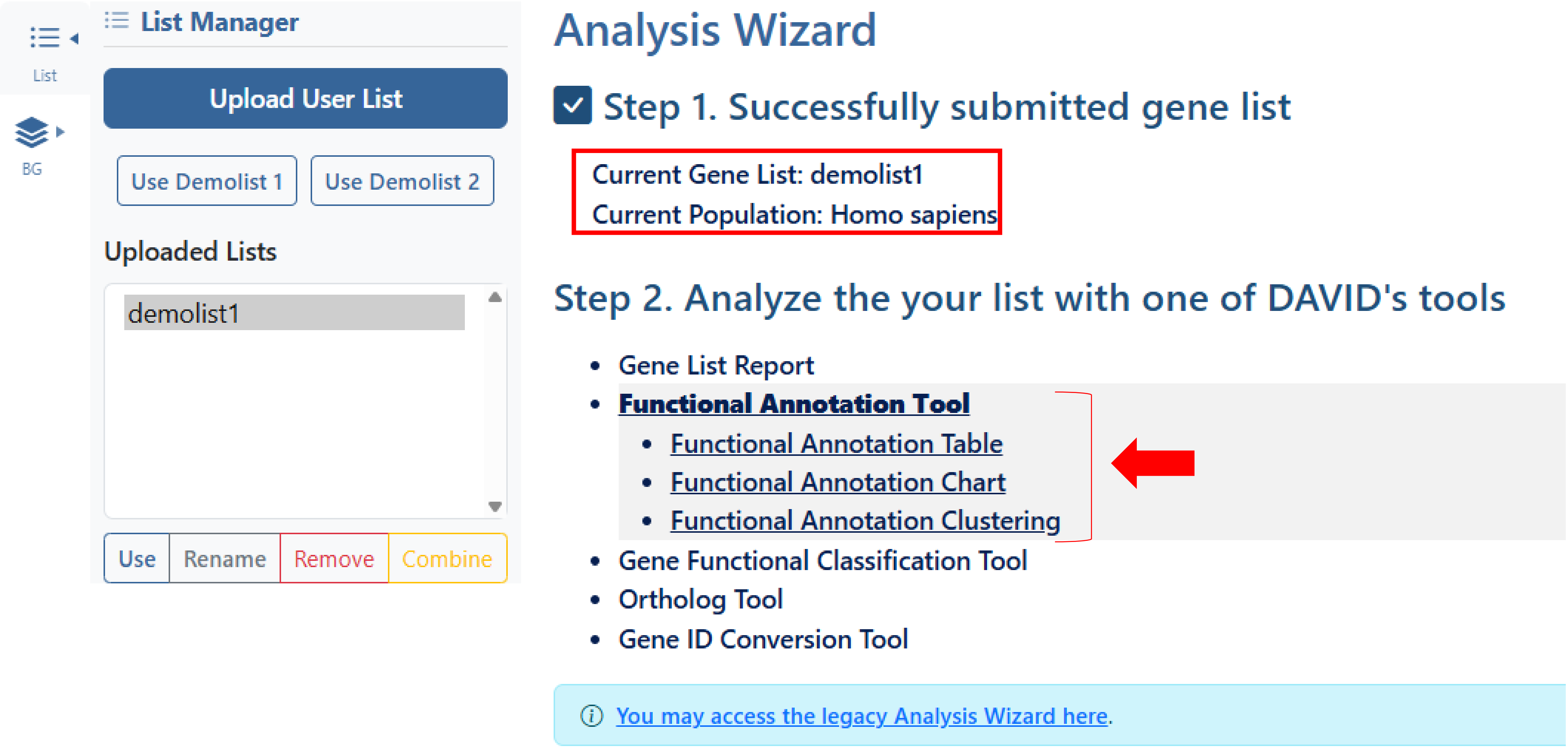
User ID ⑤	⑥ Value ⑦	Gene Name ⑧	Related Genes ⑨	Species ⑩
1005_at		dual specificity phosphatase 1(DUSP1)	RG	Homo sapiens
1007_s_at	2	discoidin domain receptor tyrosine kinase 1(DDR1)	RG	Homo sapiens
1018_at	2	Wnt family member 10B(WNT10B)	RG	Homo sapiens
1091_at	2	protein kinase cAMP-dependent type I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

Gene List Report (annotation)

1. **Current Gene List & Population**
   Displays the active gene list and selected species or background population.
2. **Help and Switch to Classic Version**
   Link to this help page and provides access to the legacy Gene List Report interface.
3. **Search and Record Count**
   The search box filters table results in real time. The record count indicates total entries and the number of DAVID genes mapped.
4. **Export Options**
   Results can be exported using Copy, Excel, CSV, or PDF. Exports reflect the current filtered and sorted view.
5. **User ID**
   User uploaded gene ID name.
6. **Sortable Columns**
   Click any column header to sort by User ID, Expression Value, DAVID Gene Name, Related Genes (RG), or Species.
7. **Value**
   User uploaded expression value. (Optional)
8. **Gene Name**
   Click the gene name link to explore the full gene report. For more information, see the Gene Report documentation page.
9. **Related Genes (RG)**
   Click the **RG** link to explore functionally related genes associated with each entry. For more information, see the Related Genes documentation page.
10. **Species**
    Click the **Species** link to go to NCBI taxonomy entry.

Functional Annotation

Ready for Analysis



Analysis Wizard

☑ Step 1. Successfully submitted gene list

Current Gene List: demolist1
Current Population: Homo sapiens

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

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

ⓘ You may access the legacy Analysis Wizard here.

Functional Classification Annotation Summary

Annotation Summary Results

Current Gene List: demolist2

Current Population: Homo sapiens

See the annotation in next slide

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

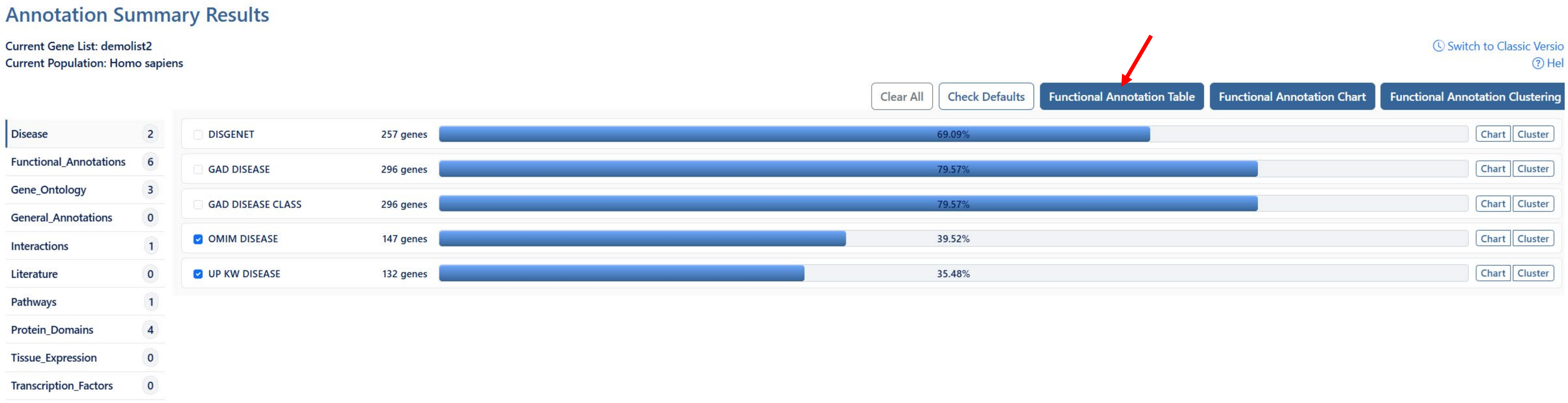
☐	DISGENET	257 genes	69.09%	Chart	Cluster
☐	GAD DISEASE	296 genes	79.57%	Chart	Cluster
☐	GAD DISEASE CLASS	296 genes	79.57%	Chart	Cluster
☑	OMIM DISEASE	147 genes	39.52%	Chart	Cluster
☑	UP KW DISEASE	132 genes	35.48%	Chart	Cluster

Functional Classification Annotation Summary

1. **Current Gene List & Population**
   Displays the active gene list and selected species or background population.
2. **Help and Switch to Classic Version**
   Link to this help page and provides access to the legacy Gene List Report interface.
3. **Categories**
   Click each category to expand and view additional annotation categories. Check/uncheck the items to add/remove them from your selection.
4. **Clear All**
   Click this button to clear all selections.
5. **Check Default**
   Click this button to undo any current selections and revert to default selections.
6. **Functional Annotation Table**
   Click this button to view the **Functional Annotation Table** for all selections. This is a gene-centric view which lists the genes and their associated annotation terms. For more information, see the Functional Annotation Table documentation page.
7. **Functional Annotation Chart**
   Click this button to view the **Functional Annotation Chart** for all selections. Chart Report is an annotation term focused view which lists annotation terms and their associated genes under study. For more information, see the Functional Annotation Chart documentation page.
8. **Functional Annotation Clustering**
   Click this button to view the **Functional Annotation Clustering** for all selections. Functional Annotation Clustering integrates Kappa statistics to measure the degree of the common genes between two annotations. For more information, see the Functional Annotation Clustering documentation page.
9. **Gene count**
   Number of genes from the user list involved in this annotation category.
10. **Gene Percentage & Single Table**
    Percentage of genes from user list involved in this category out of total genes from user list.
    Click this percentage bar to be directed to a functional annotation table for user genes in this annotation category ONLY.
11. **Single Chart**
    Click this button to be directed to a functional annotation chart for user genes in this annotation category ONLY.
12. **Single Cluster**
    Click this button to be directed to a functional annotation cluster for user genes in this annotation category ONLY.

Function Annotation Table

Functional Classification Annotation Summary



Annotation Summary Results

Current Gene List: demolist2
Current Population: Homo sapiens

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

☐	DISGENET	257 genes	69.09%	Chart Cluster
☐	GAD DISEASE	296 genes	79.57%	Chart Cluster
☐	GAD DISEASE CLASS	296 genes	79.57%	Chart Cluster
☑	OMIM DISEASE	147 genes	39.52%	Chart Cluster
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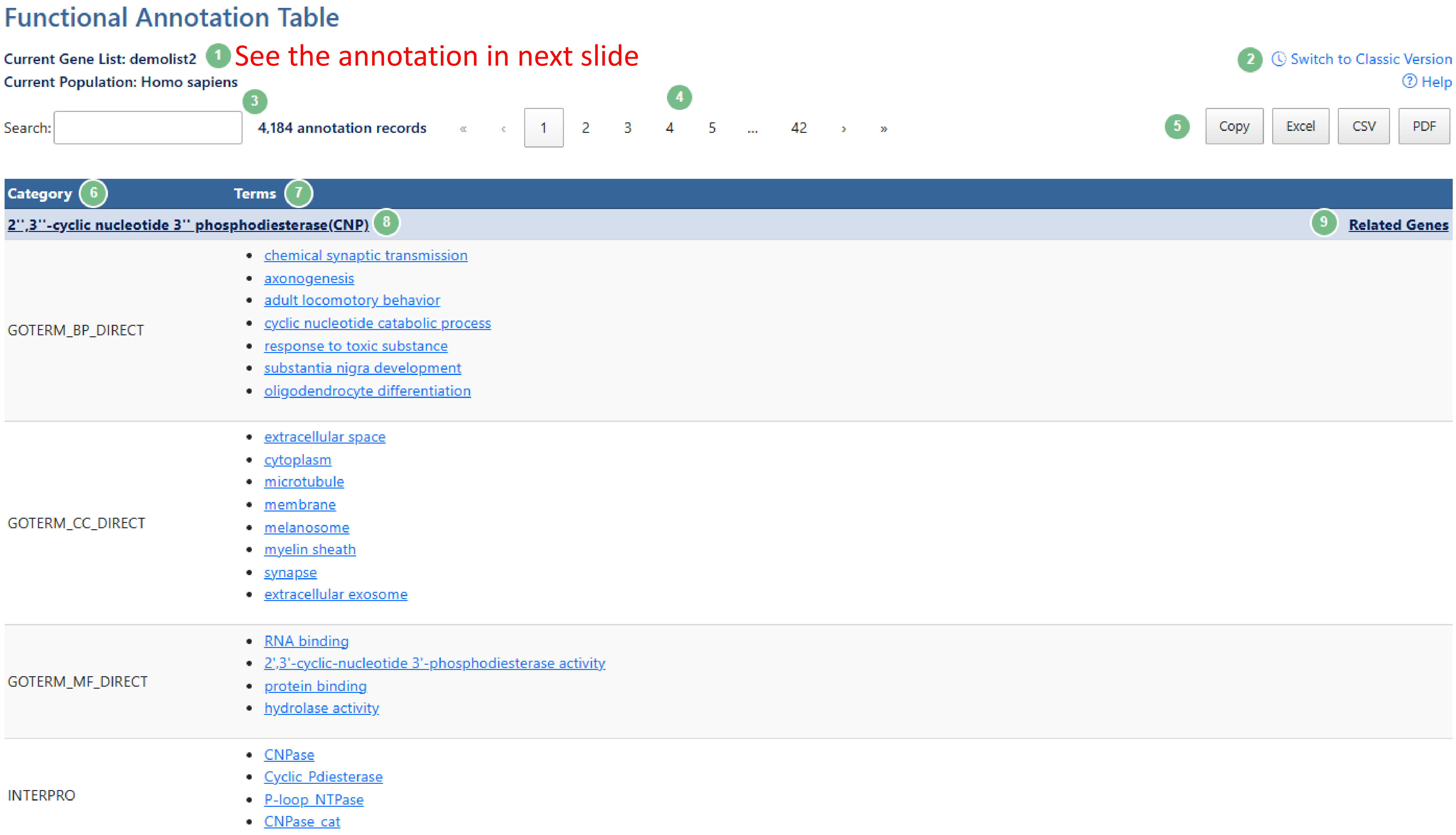
Function Annotation Table



See the annotation in next slide

Functional Annotation Table

Current Gene List: demolist2

Current Population: Homo sapiens

4,184 annotation records

2'',3''-cyclic nucleotide 3'' phosphodiesterase(CNP) — **Related Genes**

Category	Terms
GOTERM_BP_DIRECT	chemical synaptic transmission axonogenesis adult locomotory behavior cyclic nucleotide catabolic process response to toxic substance substantia nigra development oligodendrocyte differentiation
GOTERM_CC_DIRECT	extracellular space cytoplasm microtubule membrane melanosome myelin sheath synapse extracellular exosome
GOTERM_MF_DIRECT	RNA binding 2',3'-cyclic-nucleotide 3'-phosphodiesterase activity protein binding hydrolase activity
INTERPRO	CNPase Cyclic_Pdiesterase P-loop_NTPase CNPase_cat

Function Annotation Table

1. **Current Gene List & Population**

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

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

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

3. **Search and Record Count**

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

4. **Pages**

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

5. **Export Options**

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

6. **Categories**

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

7. **Annotations**

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

8. **Gene Name**

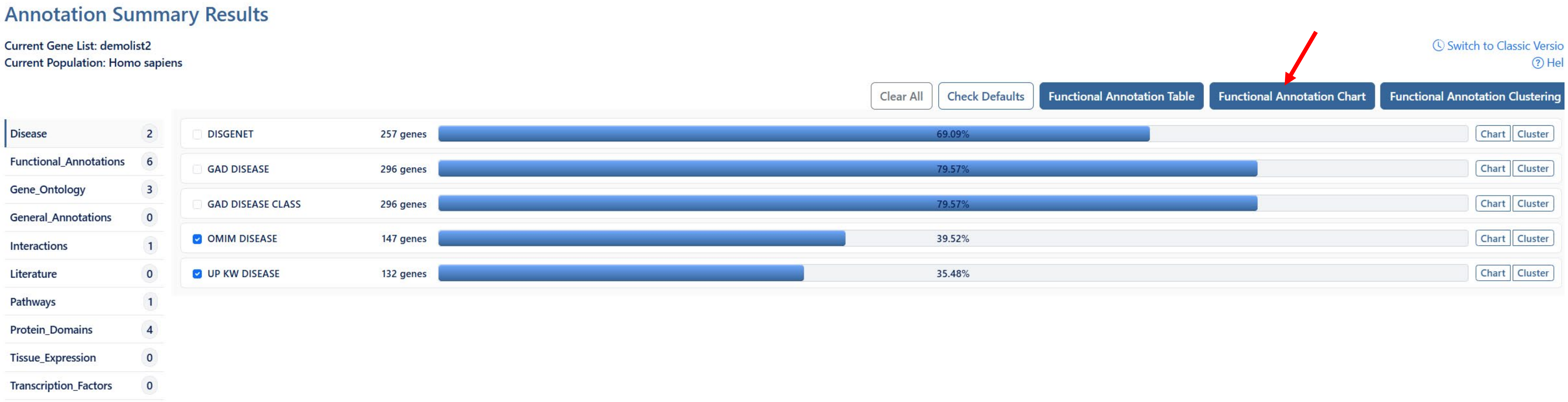
   Annotation results are grouped by each gene. Click the gene name link to explore the full gene report. For more information, see the Gene Report documentation page.

9. **Related Genes (RG)**

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

Functional Annotation Chart

Functional Classification Annotation Summary



Annotation Summary Results

Current Gene List: demolist2
Current Population: Homo sapiens

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

☐	DISGENET	257 genes	69.09%	Chart Cluster
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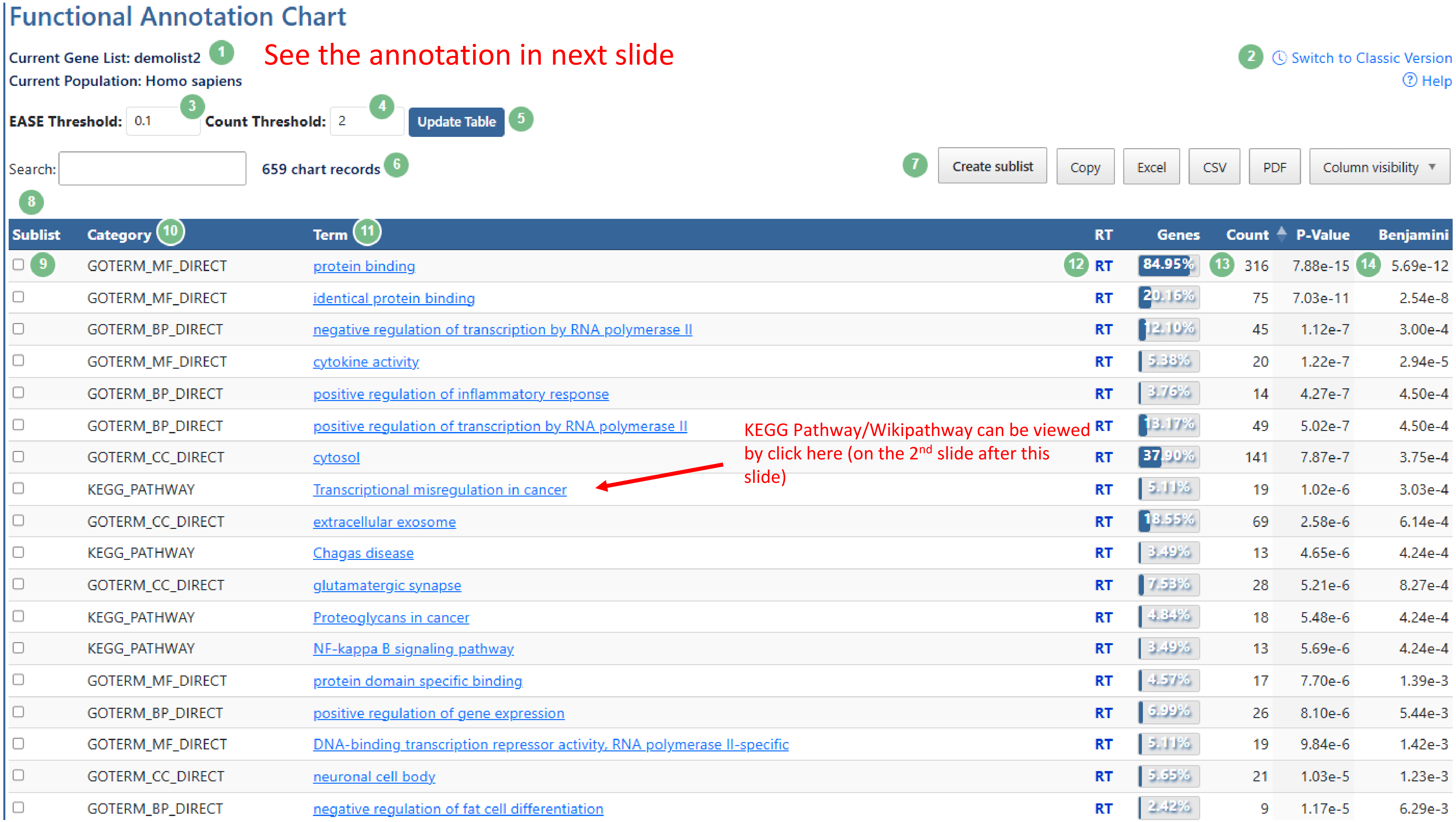
Functional Annotation Chart



Functional Annotation Chart

Current Gene List: demolist2

Current Population: Homo sapiens

See the annotation in next slide

EASE Threshold: 0.1 **Count Threshold:** 2

Search:

659 chart records

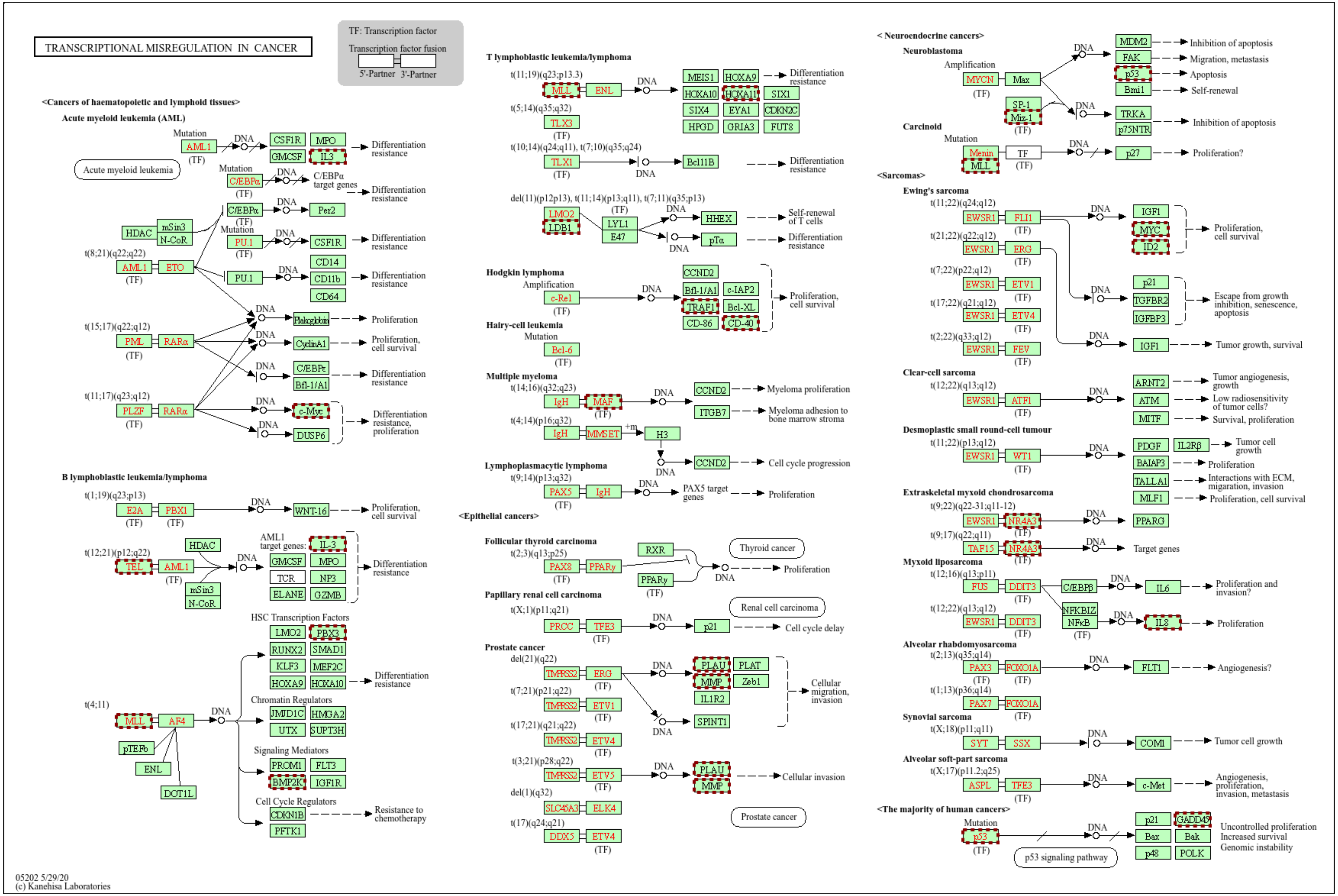
Sublist	Category	Term	RT	Genes	Count	P-Value	Benjamini
☐	GOTERM_MF_DIRECT	protein binding	RT	84.95%	316	7.88e-15	5.69e-12
☐	GOTERM_MF_DIRECT	identical protein binding	RT	20.16%	75	7.03e-11	2.54e-8
☐	GOTERM_BP_DIRECT	negative regulation of transcription by RNA polymerase II	RT	12.10%	45	1.12e-7	3.00e-4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

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

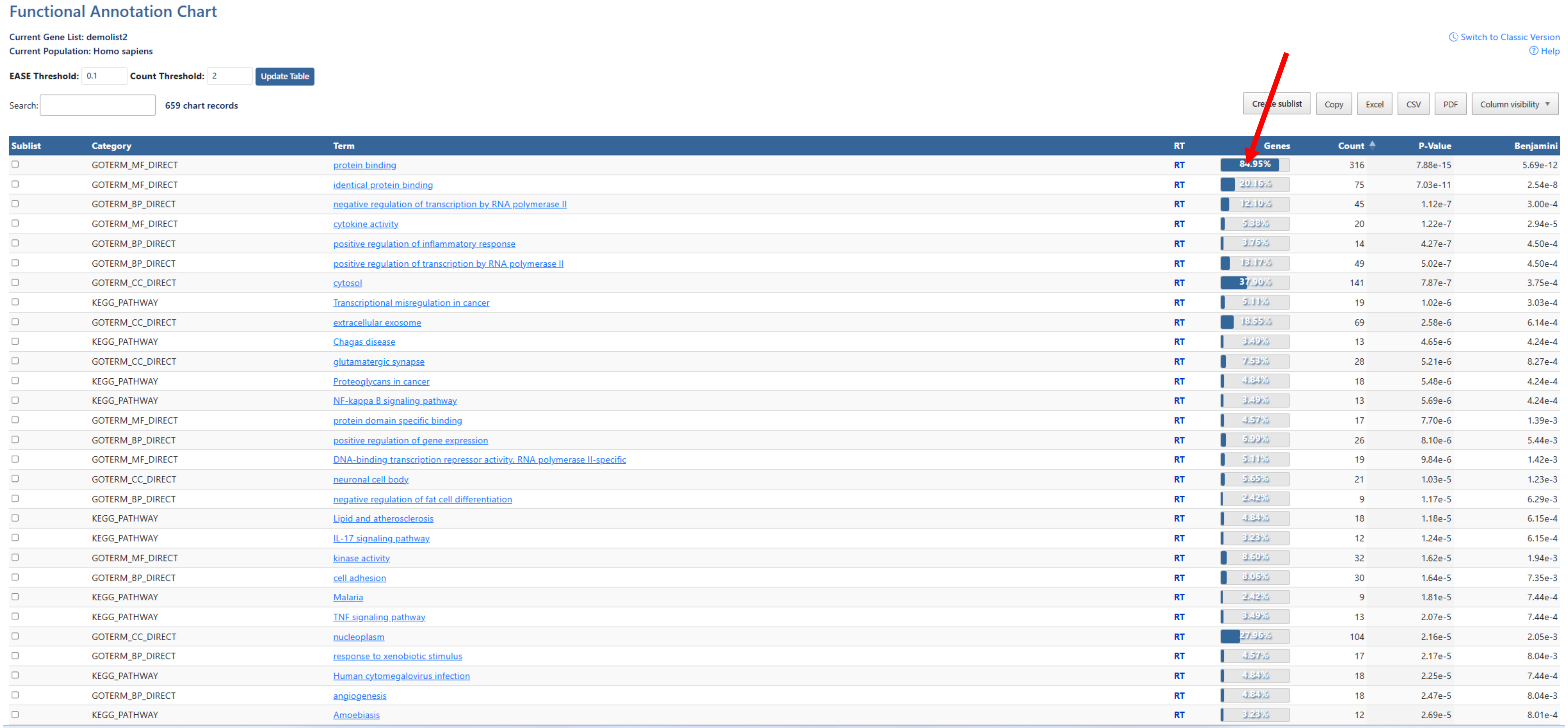
Functional Annotation Chart

1. **Current Gene List & Population**
   Displays the active gene list and selected species or background population.
2. **Help and Switch to Classic Version**
   Link to this help page and provides access to the legacy Gene List Report interface.
3. **EASE Threshold**
   Minimum P-value of results to be displayed. Click to either type a numerical value or use the up/down arrows to increment by 0.01.
4. **Count Threshold**
   Minimum gene count of annotation result to be displayed. Click to either type a numerical value or use the up/down arrows to increment by 1.
5. **Update Table**
   After making adjustments to filtering options, click this button to update the table using the selected parameters.
6. **Search and Record Count**
   The search box filters table results in real time. The record count indicates total entries and the number of DAVID genes mapped.
7. **Create sublist, Export options & Column Visibility**
   Create a sublist by clicking on checkboxes to the left of desired results, then clicking the **Create sublist** button, where you will be prompted to name the new sublist.
   Sublists will then appear in the list manager as a new gene list.
   Results can be exported using Copy, Excel, CSV, or PDF. Exports reflect the current filtered and sorted view.
   Additional columns can be added to the current view using the **Column Visibility** drop-down button. Click on available items to add the column to the table.
8. **Sortable Columns**
   Click on any table column header to sort the table by that column in ascending or descending order.
9. **Sublist**
   Click on check boxes to select items for creating a sublist. (7)
10. **Categories**
    Categories of term results, indicating original source of information. (e.g. UP = Uniprot). Click to sort by this value.
11. **Annotations**
    Annotations available for each item. If available, hyperlinks lead users to original resources for further details. Click to sort by this value.
12. **Related Terms**
    Click **RT** to be directed to a Functionally Related Terms search result for each term. For more information, see the Related Terms documentation page.
13. **Gene Count and Percentage**
    Count and percentage of genes involved in each term.
14. **P-value & Benjamini**
    EASE Score where smaller means more enriched. Benjamini in DAVID requests adjusted p-values by using the linear step-up method of Benjamini and Hochberg

Visualizing Gene in the Pathway



Functional Annotation Chart



Functional Annotation Chart

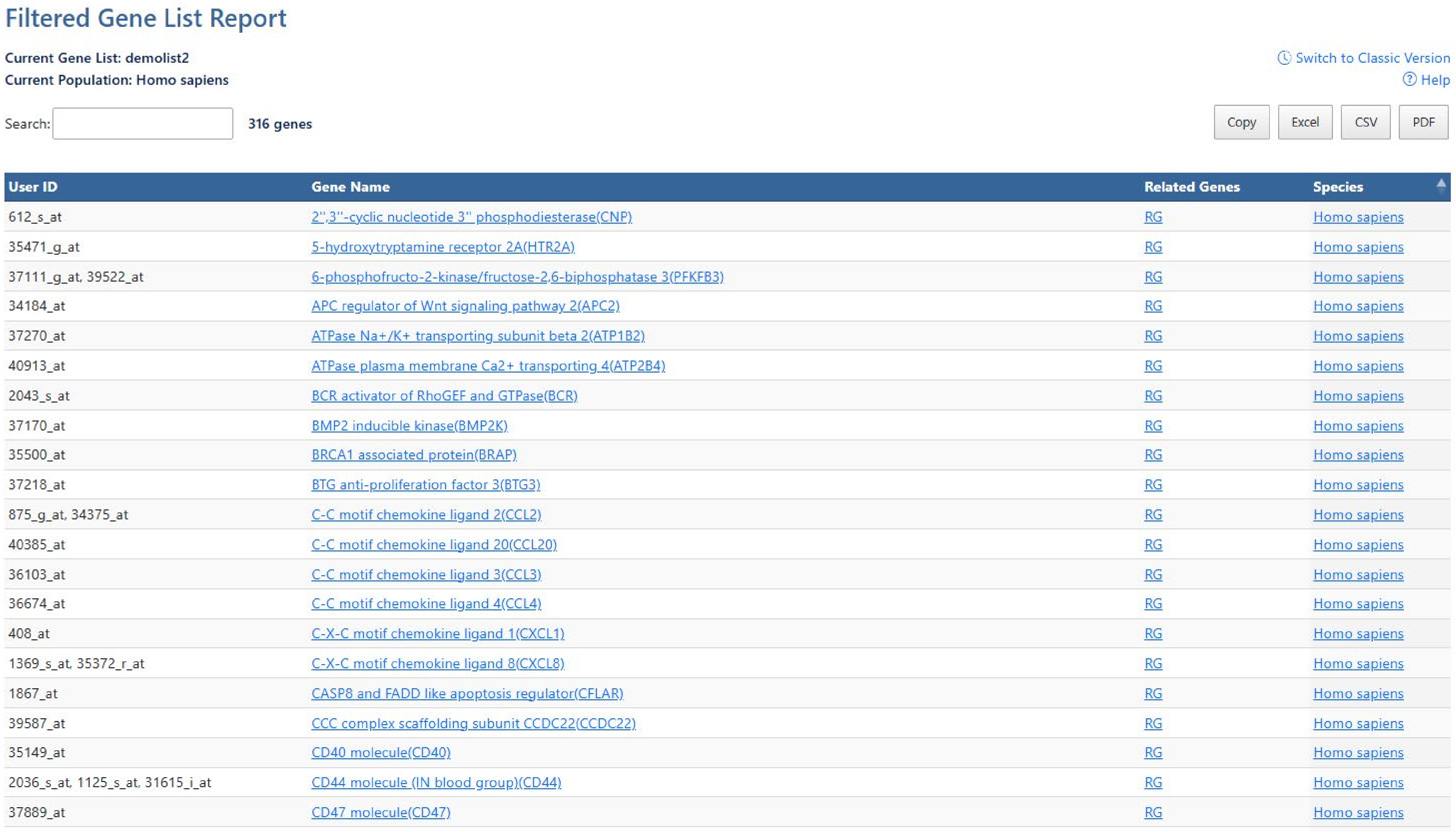
Current Gene List: demolist2
Current Population: Homo sapiens

EASE Threshold: 0.1 **Count Threshold:** 2

659 chart records

Sublist	Category	Term	RT	Genes	Count	P-Value	Benjamini
☐	GOTERM_MF_DIRECT	protein binding	RT	84.95%	316	7.88e-15	5.69e-12
☐	GOTERM_MF_DIRECT	identical protein binding	RT	20.16%	75	7.03e-11	2.54e-8
☐	GOTERM_BP_DIRECT	negative regulation of transcription by RNA polymerase II	RT	12.10%	45	1.12e-7	3.00e-4
☐	GOTERM_MF_DIRECT	cytokine activity	RT	5.38%	20	1.22e-7	2.94e-5
☐	GOTERM_BP_DIRECT	positive regulation of inflammatory response	RT	3.76%	14	4.27e-7	4.50e-4
☐	GOTERM_BP_DIRECT	positive regulation of transcription by RNA polymerase II	RT	13.17%	49	5.02e-7	4.50e-4
☐	GOTERM_CC_DIRECT	cytosol	RT	37.90%	141	7.87e-7	3.75e-4
☐	KEGG_PATHWAY	Transcriptional misregulation in cancer	RT	5.11%	19	1.02e-6	3.03e-4
☐	GOTERM_CC_DIRECT	extracellular exosome	RT	18.55%	69	2.58e-6	6.14e-4
☐	KEGG_PATHWAY	Chagas disease	RT	3.49%	13	4.65e-6	4.24e-4
☐	GOTERM_CC_DIRECT	glutamatergic synapse	RT	7.53%	28	5.21e-6	8.27e-4
☐	KEGG_PATHWAY	Proteoglycans in cancer	RT	4.84%	18	5.48e-6	4.24e-4
☐	KEGG_PATHWAY	NF-kappa B signaling pathway	RT	3.49%	13	5.69e-6	4.24e-4
☐	GOTERM_MF_DIRECT	protein domain specific binding	RT	4.57%	17	7.70e-6	1.39e-3
☐	GOTERM_BP_DIRECT	positive regulation of gene expression	RT	6.99%	26	8.10e-6	5.44e-3
☐	GOTERM_MF_DIRECT	DNA-binding transcription repressor activity, RNA polymerase II-specific	RT	5.11%	19	9.84e-6	1.42e-3
☐	GOTERM_CC_DIRECT	neuronal cell body	RT	5.65%	21	1.03e-5	1.23e-3
☐	GOTERM_BP_DIRECT	negative regulation of fat cell differentiation	RT	2.42%	9	1.17e-5	6.29e-3
☐	KEGG_PATHWAY	Lipid and atherosclerosis	RT	4.84%	18	1.18e-5	6.15e-4
☐	KEGG_PATHWAY	IL-17 signaling pathway	RT	3.23%	12	1.24e-5	6.15e-4
☐	GOTERM_MF_DIRECT	kinase activity	RT	8.60%	32	1.62e-5	1.94e-3
☐	GOTERM_BP_DIRECT	cell adhesion	RT	8.06%	30	1.64e-5	7.35e-3
☐	KEGG_PATHWAY	Malaria	RT	2.42%	9	1.81e-5	7.44e-4
☐	KEGG_PATHWAY	TNF signaling pathway	RT	3.49%	13	2.07e-5	7.44e-4
☐	GOTERM_CC_DIRECT	nucleoplasm	RT	27.96%	104	2.16e-5	2.05e-3
☐	GOTERM_BP_DIRECT	response to xenobiotic stimulus	RT	4.57%	17	2.17e-5	8.04e-3
☐	KEGG_PATHWAY	Human cytomegalovirus infection	RT	4.84%	18	2.25e-5	7.44e-4
☐	GOTERM_BP_DIRECT	angiogenesis	RT	4.84%	18	2.47e-5	8.04e-3
☐	KEGG_PATHWAY	Amoebiasis	RT	3.23%	12	2.69e-5	8.01e-4

Gene List for a Term in Functional Annotation Chart



Filtered Gene List Report

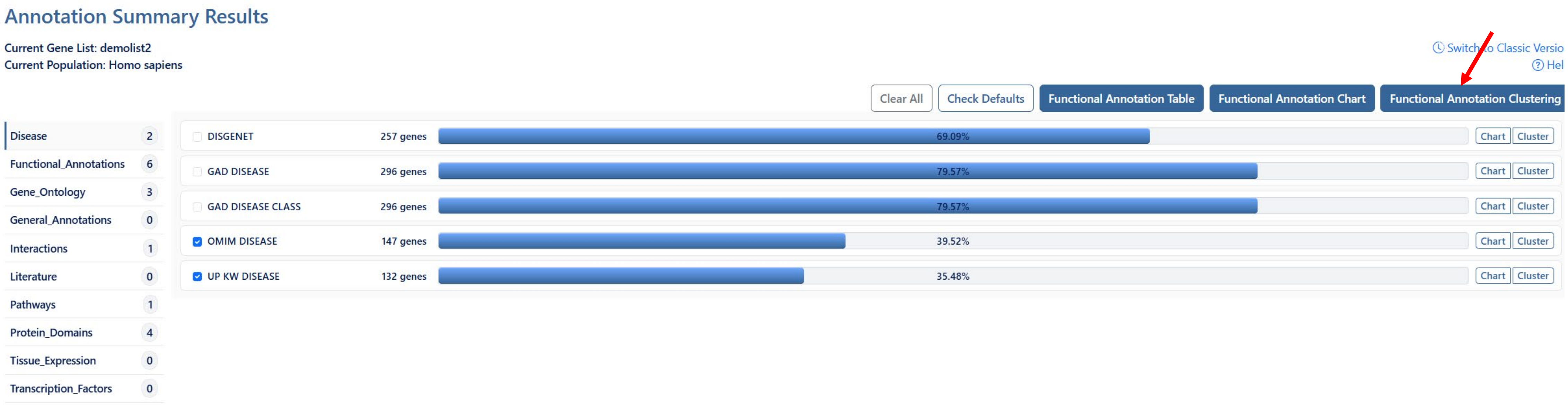
Current Gene List: demolist2
Current Population: Homo sapiens

Search: 316 genes

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

Functional Annotation Clustering

Functional Classification Annotation Summary



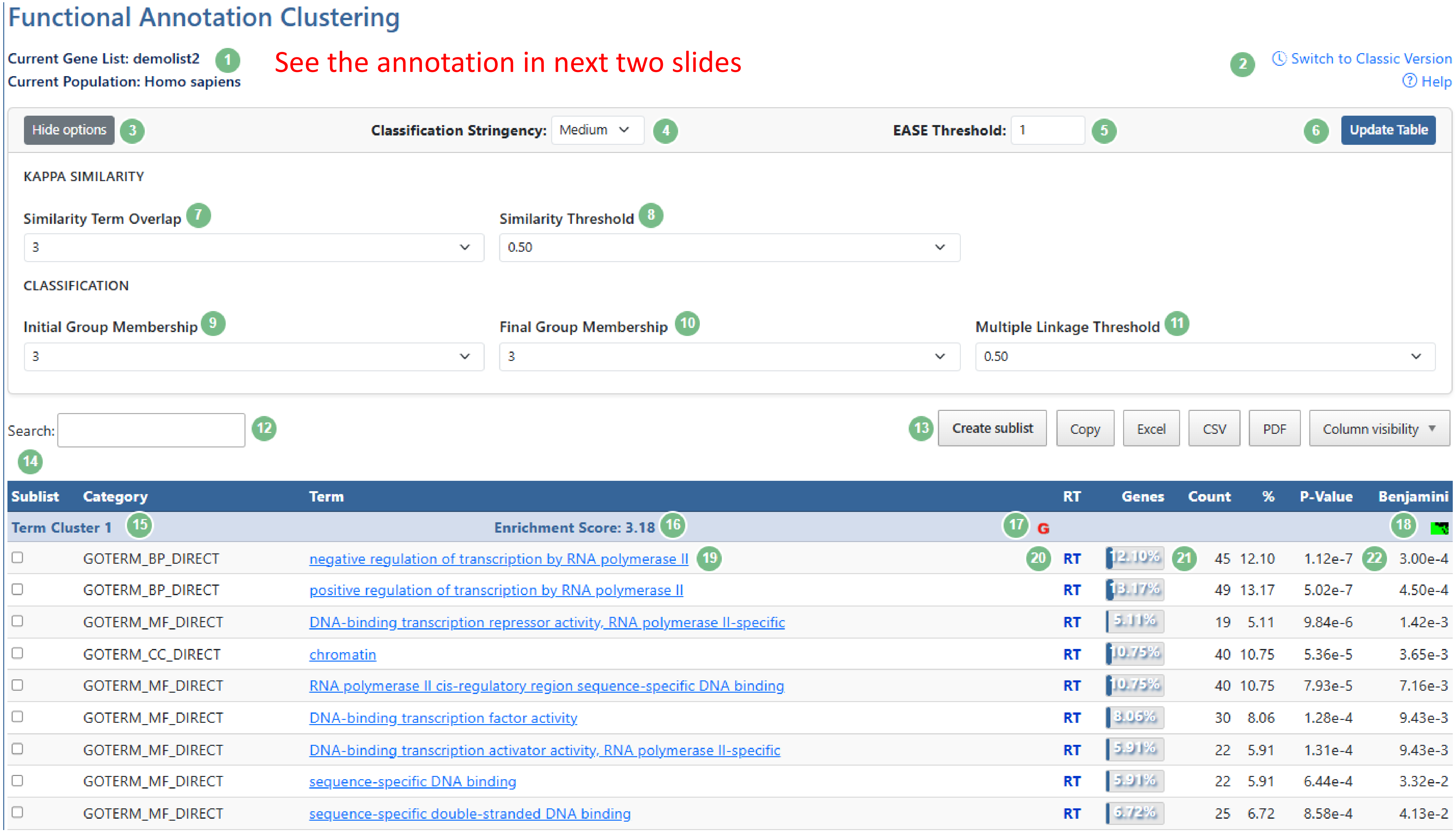
Annotation Summary Results

Current Gene List: demolist2
Current Population: Homo sapiens

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

☐	DISGENET	257 genes	69.09%	Chart Cluster
☐	GAD DISEASE	296 genes	79.57%	Chart Cluster
☐	GAD DISEASE CLASS	296 genes	79.57%	Chart Cluster
☑	OMIM DISEASE	147 genes	39.52%	Chart Cluster
☑	UP KW DISEASE	132 genes	35.48%	Chart Cluster

Functional Annotation Clustering Tool



See the annotation in next two slides

Functional Annotation Clustering

Current Gene List: demolist2 ①
Current Population: Homo sapiens

② Switch to Classic Version
Help

Classification Stringency: Medium ④
EASE Threshold: 1 ⑤

KAPPA SIMILARITY

Similarity Term Overlap ⑦: 3
Similarity Threshold ⑧: 0.50

CLASSIFICATION

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

Search: ⑫
⑭

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

Functional Annotation Clustering Tool

1. **Gene List**
   Current gene list selected for view and background species being analyzed.
2. **Help and Switch to Classic Version**
   Link to this help page and provides access to the legacy Gene List Report interface.
3. **Show/Hide Options**
   Click this button to expand or hide additional filtering options.
4. **Classification Stringency**
   Click to access a drop-down menu of stringency levels, then click desired level to select. A high-level single control to establish a set of detailed parameters involved in functional classification algorithms. In general, the higher stringency setting generates less functional groups with more tightly associated genes in each group, so that more genes will be unclustered.
5. **EASE Threshold**
   Minimum P-value of results to be displayed. Click to either type a numerical value or use the up/down arrows to increment by 0.01.
6. **Update Table**
   After making adjustments to filtering options, click this button to update the table using the selected parameters.
7. **Similarity Term Overlap**
   Click to access a drop-down menu of overlap values. The minimum number of annotation terms overlapped between two genes in order to be qualified for kappa calculation. This parameter is to maintain necessary statistical power to make the kappa value more meaningful. The higher the value, the more meaningful the result is.
8. **Similarity Threshold**
   Click to access a drop-down menu of threshold values. The minimum kappa value to be considered significant. A higher setting will lead to more genes going unclustered, which leads to a higher quality functional classification result with fewer groups and fewer gene members. Kappa value of 0.3 starts giving meaningful biology based on our genome-wide distribution study. Anything below 0.3 has a good chance to be noise.
9. **Initial Group Membership**
   Click to access a drop-down menu of membership values. The minimum gene number in a seeding group, which affects the minimum size of each functional group in the final cluster. In general, the lower value attempts to include more genes in functional groups, and may generate a lot of small size groups.
10. **Final Group Membership**
    Click to access a drop-down menu of membership values. The minimum gene number in one final group after a 'cleanup' procedure. In general, the lower value attempts to include more genes in functional groups and may generate a lot of small size groups. It cofunctions with previous parameters to control the minimum size of functional groups. If you are interested in functional groups containing only 2 or 3 genes, you need to set it to a very low value. Otherwise, the small group will not be displayed and the genes will go unclustered.

Functional Annotation Clustering Tool

11. Multiple Linkage Threshold

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

12. Search

The search box filters all table results in real time.

13. Create sublist, Export options & Column Visibility

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

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

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

14. Sortable Columns

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

15. Cluster

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

16. Enrichment Score

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

17. Gene Report

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

18. Cluster view

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

19. Annotations

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

20. Related Terms

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

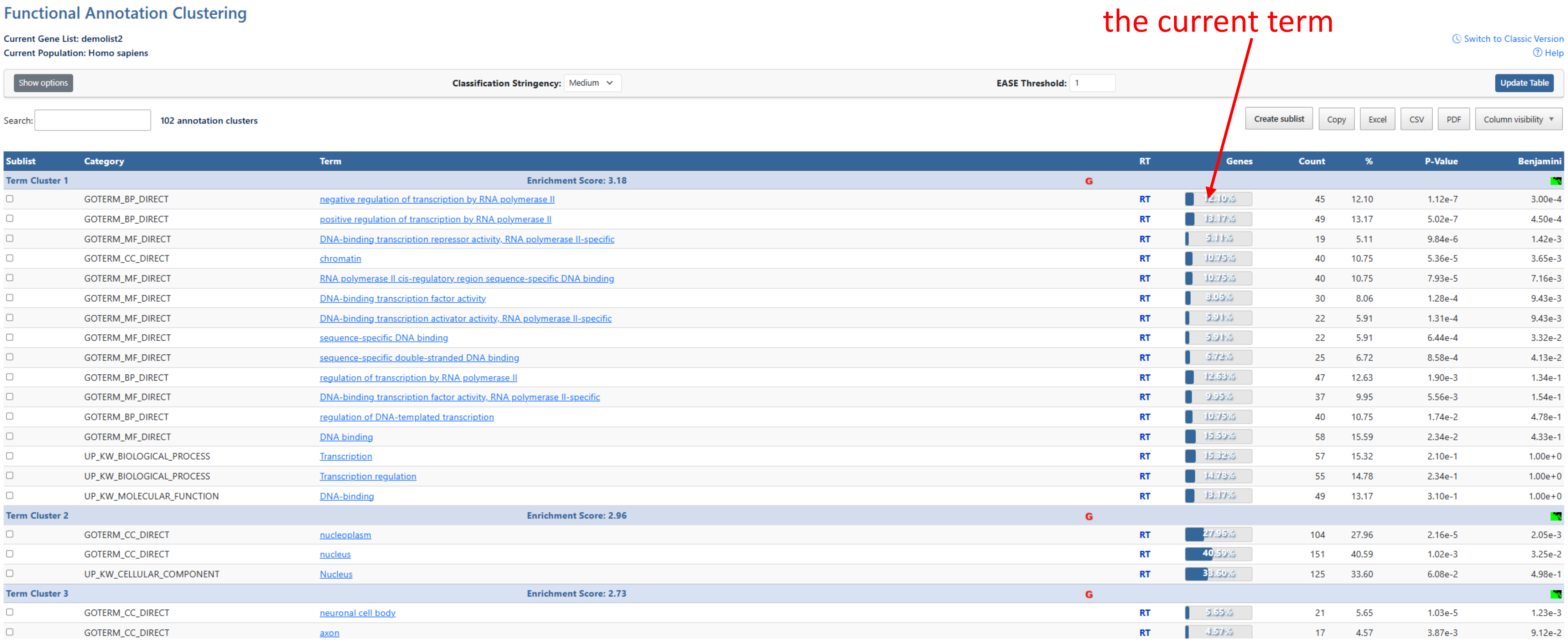
21. Gene Count and Percentage

Count and percentage of genes involved in each term.

22. *P*-value & Benjamini

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

Functional Annotation Clustering Tool



Retrieve filtered gene list for the current term

Current Gene List: demolist2
Current Population: Homo sapiens

Classification Stringency: Medium
EASE Threshold: 1

Search:

102 annotation clusters

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

Functional Annotation Clustering Tool

Filtered Gene List Report

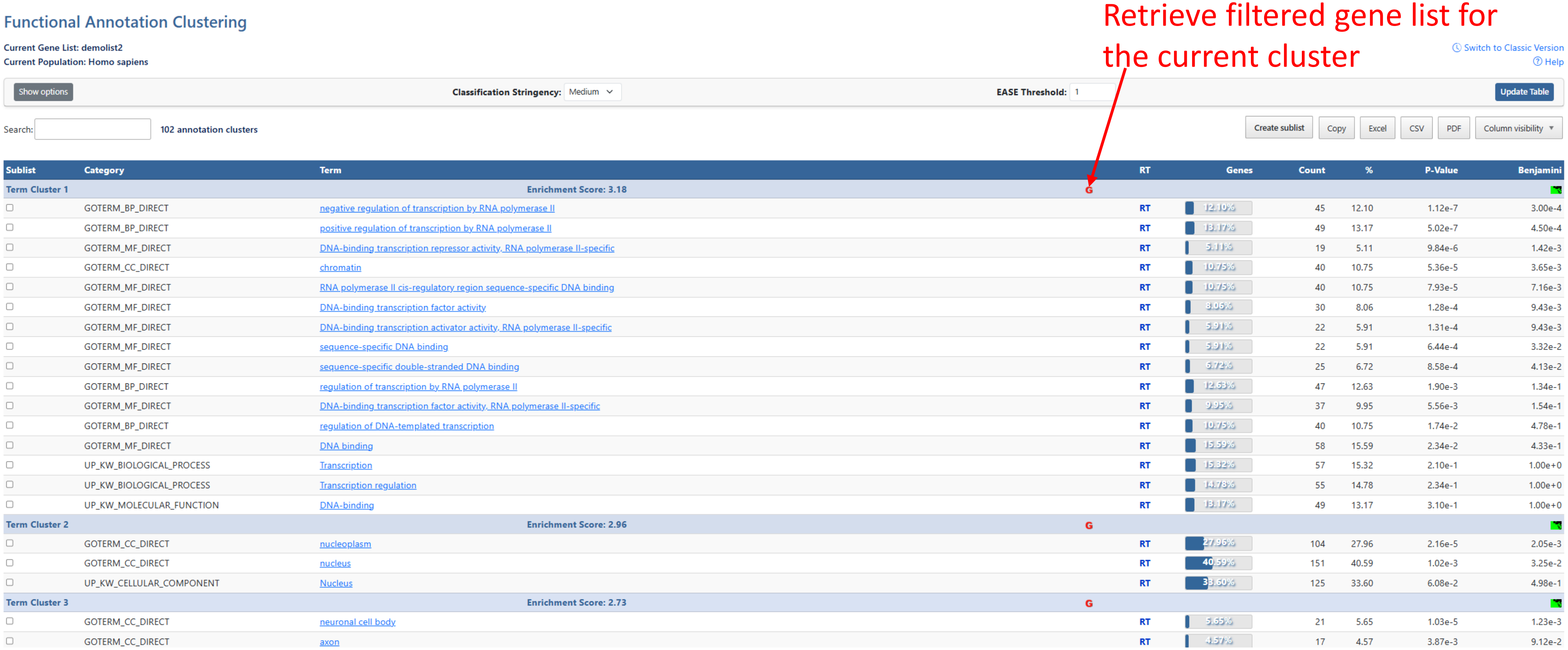
Current Gene List: demolist2
Current Population: Homo sapiens

Search:

45 genes

User ID	Gene Name	Related Genes	Species
38491_at	ETS variant transcription factor 6(ETV6)	RG	Homo sapiens
1242_at	ETS2 repressor factor(ERF)	RG	Homo sapiens
36669_at	FosB proto-oncogene, AP-1 transcription factor subunit(FOSB)	RG	Homo sapiens
39698_at	HOP homeobox(HOPX)	RG	Homo sapiens
1895_at, 32583_at	Jun proto-oncogene, AP-1 transcription factor subunit(JUN)	RG	Homo sapiens
224_at, 38374_at	KLF transcription factor 10(KLF10)	RG	Homo sapiens
35160_at	LIM domain binding 1(LDB1)	RG	Homo sapiens
36711_at	MAF bZIP transcription factor F(MAFF)	RG	Homo sapiens
41505_r_at	MAF bZIP transcription factor(MAF)	RG	Homo sapiens
1774_at	MAX dimerization protein 1(MXD1)	RG	Homo sapiens
1973_s_at, 37724_at, 1936_s_at	MYC proto-oncogene, bHLH transcription factor(MYC)	RG	Homo sapiens
989_at	NCK adaptor protein 1(NCK1)	RG	Homo sapiens
1461_at	NFKB inhibitor alpha(NFKBIA)	RG	Homo sapiens
33922_at	PR/SET domain 2(PRDM2)	RG	Homo sapiens
1743_s_at, 1866_g_at	SKI like proto-oncogene(SKIL)	RG	Homo sapiens
41499_at	SKI proto-oncogene(SKI)	RG	Homo sapiens
1857_at	SMAD family member 7(SMAD7)	RG	Homo sapiens
36018_at	SRY-box transcription factor 10(SOX10)	RG	Homo sapiens
1018_at	Wnt family member 10B(WNT10B)	RG	Homo sapiens
1994_at	activating transcription factor 2(ATF2)	RG	Homo sapiens
287_at	activating transcription factor 3(ATF3)	RG	Homo sapiens
40790_at	basic helix-loop-helix family member e40(BHLHE40)	RG	Homo sapiens
39304_g_at	beta-transducin repeat containing E3 ubiquitin protein ligase(BTRC)	RG	Homo sapiens
789_at	early growth response 1(EGR1)	RG	Homo sapiens
38356_at	follistatin(FST)	RG	Homo sapiens
31353_f_at	forkhead box E1(FOXE1)	RG	Homo sapiens
1911_s_at	growth arrest and DNA damage inducible alpha(GADD45A)	RG	Homo sapiens
38654_at	heterogeneous nuclear ribonucleoprotein U(HNRNPU)	RG	Homo sapiens
41216_r_at	inhibitor of DNA binding 2(ID2)	RG	Homo sapiens
36999_at	lysine demethylase 5A(KDM5A)	RG	Homo sapiens
35992_at	musculin(MSC)	RG	Homo sapiens

Functional Annotation Clustering Tool



Retrieve filtered gene list for the current cluster

Functional Annotation Clustering

Current Gene List: demolist2
Current Population: Homo sapiens

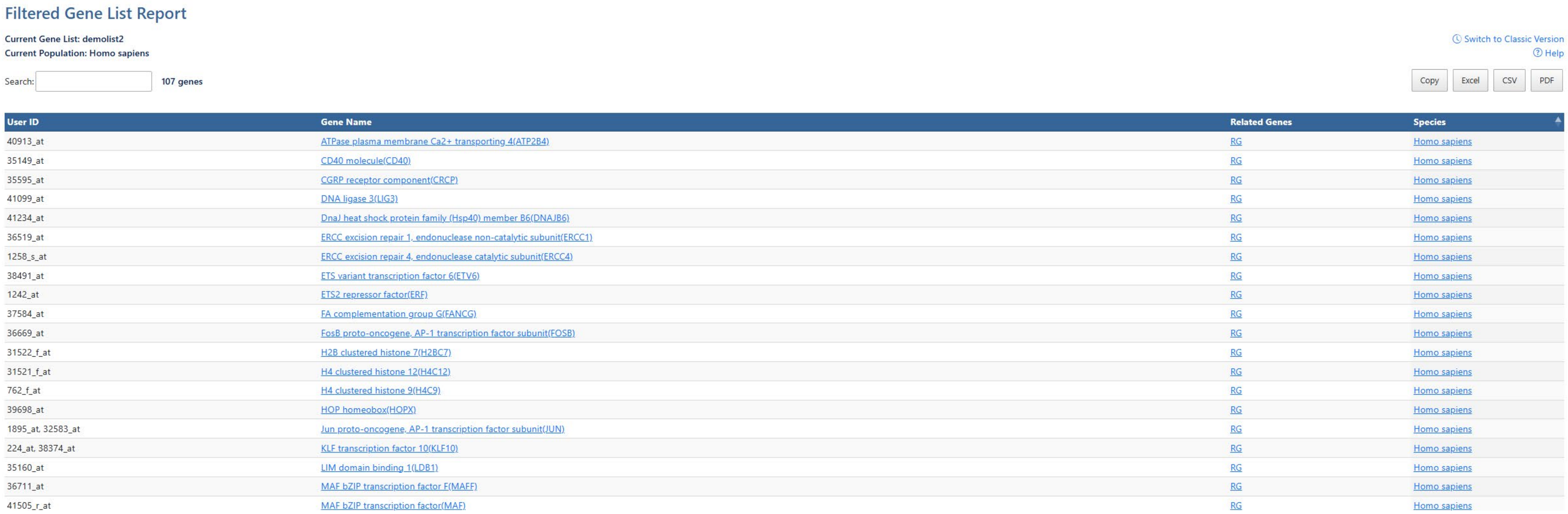
Classification Stringency: Medium

EASE Threshold: 1

102 annotation clusters

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

Functional Annotation Clustering Tool



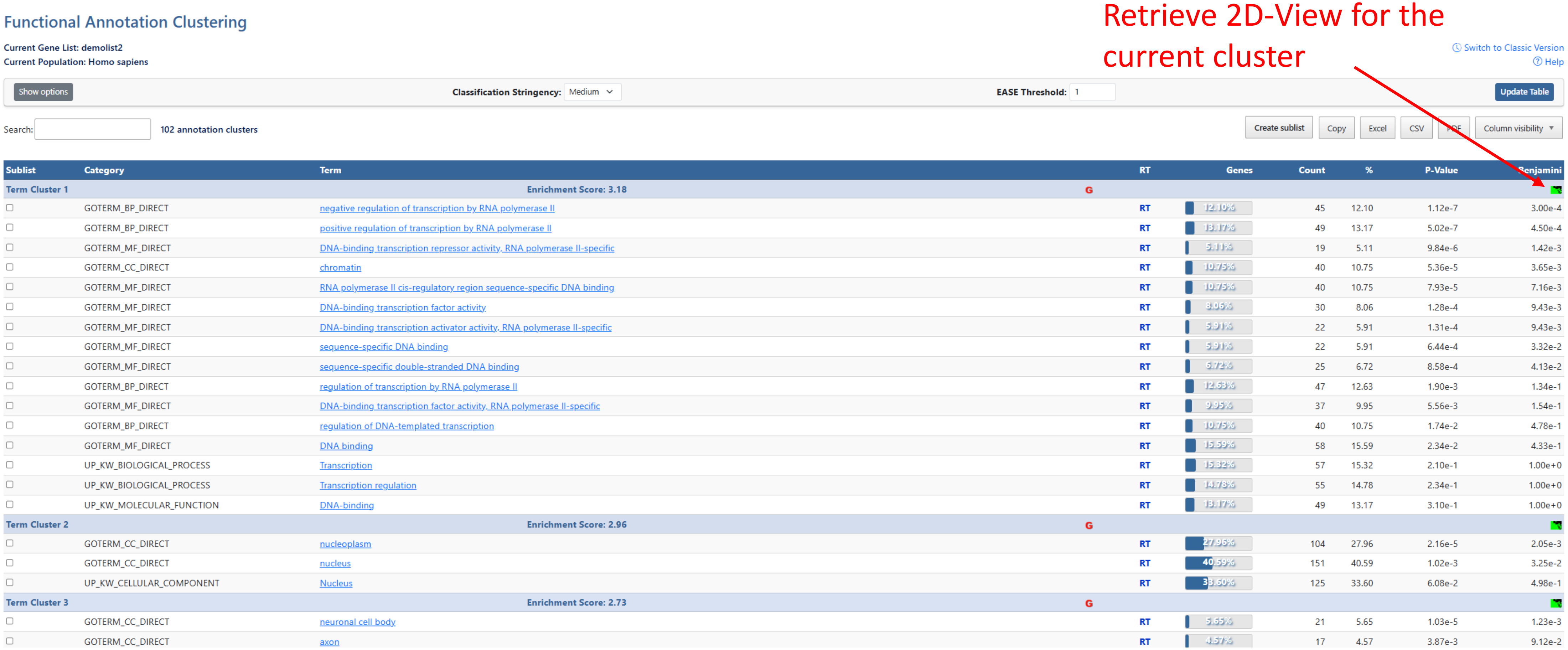
Filtered Gene List Report

Current Gene List: demolist2
Current Population: Homo sapiens

107 genes

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

Functional Annotation Clustering Tool



Retrieve 2D-View for the current cluster

Functional Annotation Clustering

Current Gene List: demolist2
Current Population: Homo sapiens

Classification Stringency: Medium

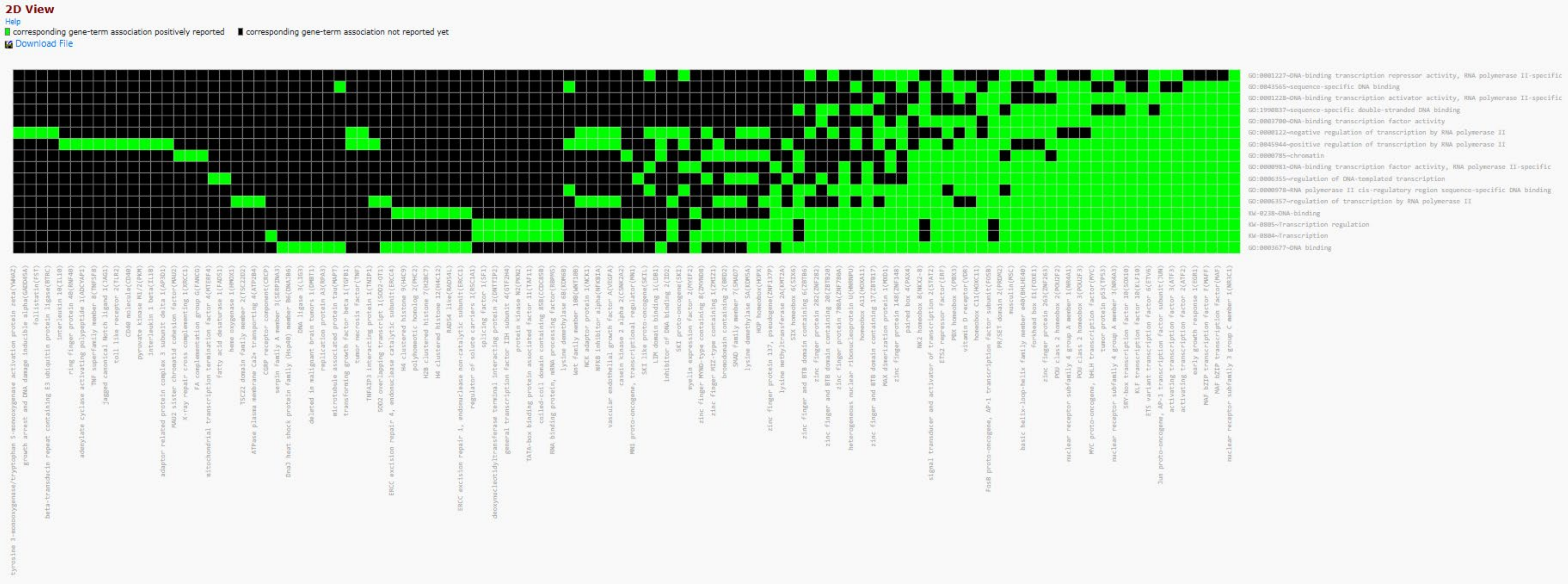
EASE Threshold: 1

Search:

102 annotation clusters

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

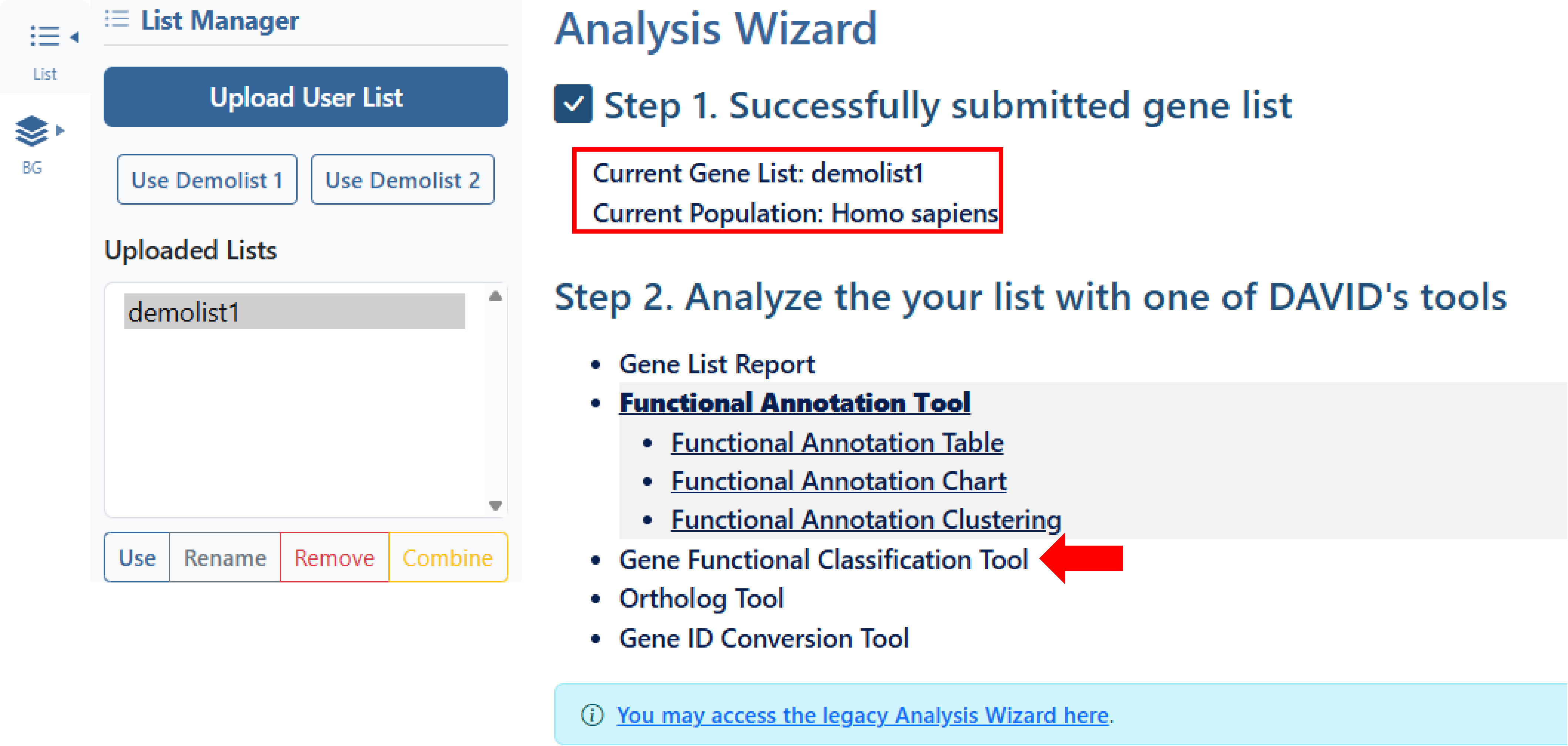
Functional Annotation Clustering Tool



2D View

Gene Functional Classification

Ready for Analysis



Analysis Wizard

☑ Step 1. Successfully submitted gene list

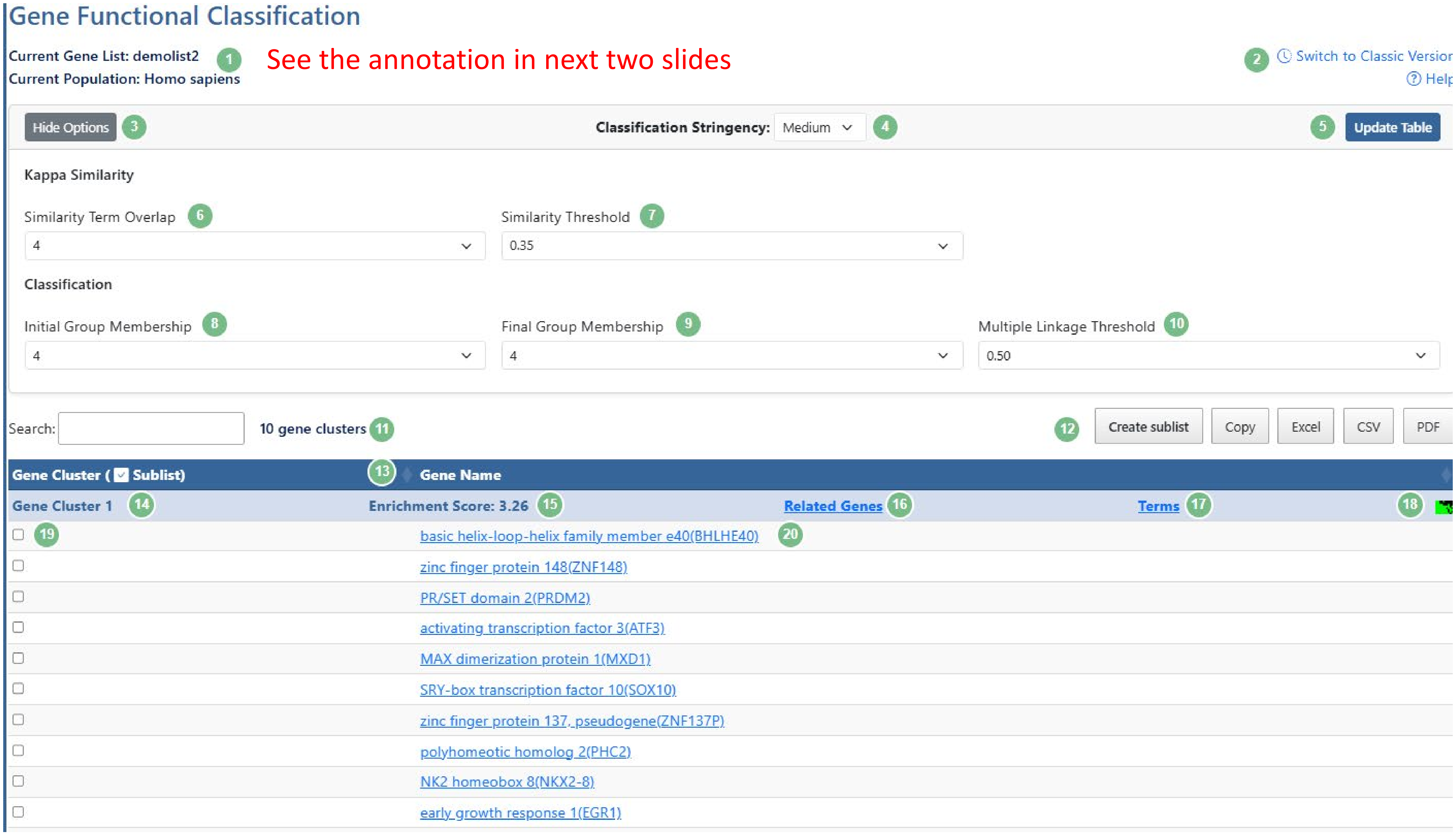
Current Gene List: demolist1
Current Population: Homo sapiens

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

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

ⓘ You may access the legacy Analysis Wizard here.

Gene Functional Classification Tool



Gene Functional Classification

Current Gene List: demolist2 ①
Current Population: Homo sapiens

See the annotation in next two slides

② Switch to Classic Versior
Help

Hide Options ③ Classification Stringency: Medium ④ ⑤ Update Table

Kappa Similarity

Similarity Term Overlap ⑥: 4
Similarity Threshold ⑦: 0.35

Classification

Initial Group Membership ⑧: 4
Final Group Membership ⑨: 4
Multiple Linkage Threshold ⑩: 0.50

Search: 10 gene clusters ⑪

⑫ Create sublist | Copy | Excel | CSV | PDF

Gene Cluster (☑ Sublist) ⑬	Gene Name
Gene Cluster 1 ⑭	Enrichment Score: 3.26 ⑮ Related Genes ⑯ Terms ⑰ ⑱
☐ ⑲	basic helix-loop-helix family member e40(BHLHE40) ⑳
☐	zinc finger protein 148(ZNF148)
☐	PR/SET domain 2(PRDM2)
☐	activating transcription factor 3(ATF3)
☐	MAX dimerization protein 1(MXD1)
☐	SRY-box transcription factor 10(SOX10)
☐	zinc finger protein 137, pseudogene(ZNF137P)
☐	polyhomeotic homolog 2(PHC2)
☐	NK2 homeobox 8(NKX2-8)
☐	early growth response 1(EGR1)

Gene Functional Classification Tool

1. **Gene List**
   Current gene list selected for view and background species being analyzed.
2. **Help and Switch to Classic Version**
   Link to this help page and provides access to the legacy Gene List Report interface.
3. **Show/Hide Options**
   Click this button to expand or hide additional filtering options.
4. **Classification Stringency**
   Click to access a drop-down menu of stringency levels, then click desired level to select. A high-level single control to establish a set of detailed parameters involved in functional classification algorithms. In general, the higher stringency setting generates less functional groups with more tightly associated genes in each group, so that more genes will be unclustered.
5. **Update Table**
   After making adjustments to filtering options, click this button to update the table using the selected parameters.
6. **Similarity Term Overlap**
   Click to access a drop-down menu of overlap values. The minimum number of annotation terms overlapped between two genes in order to be qualified for kappa calculation. This parameter is to maintain necessary statistical power to make the kappa value more meaningful. The higher the value, the more meaningful the result is.
7. **Similarity Threshold**
   Click to access a drop-down menu of theshrold values. The minimum kappa value to be considered significant. A higher setting will lead to more genes going unclustered, which leads to a higher quality functional classification result with fewer groups and fewer gene members. Kappa value of 0.3 starts giving meaningful biology based on our genome-wide distribution study. Anything below 0.3 has a good chance to be noise.
8. **Initial Group Membership**
   Click to access a drop-down menu of membership values. The minimum gene number in a seeding group, which affects the minimum size of each functional group in the final cluster. In general, the lower value attempts to include more genes in functional groups, and may generate a lot of small size groups.
9. **Final Group Membership**
   Click to access a drop-down menu of membership values. The minimum gene number in one final group after a 'cleanup' procedure. In general, the lower value attempts to include more genes in functional groups and may generate a lot of small size groups. It cofunctions with previous parameters to control the minimum size of functional groups. If you are interested in functional groups containing only 2 or 3 genes, you need to set it to a very low value. Otherwise, the small group will not be displayed and the genes will go unclustered.

Gene Functional Classification Tool

10. **Multiple Linkage Threshold**

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

11. **Search & Cluster count**

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

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

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

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

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

13. **Sortable Columns**

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

14. **Cluster**

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

15. **Enrichment Score**

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

16. **Related Genes (RG)**

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

17. **Terms**

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

18. **Cluster view**

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

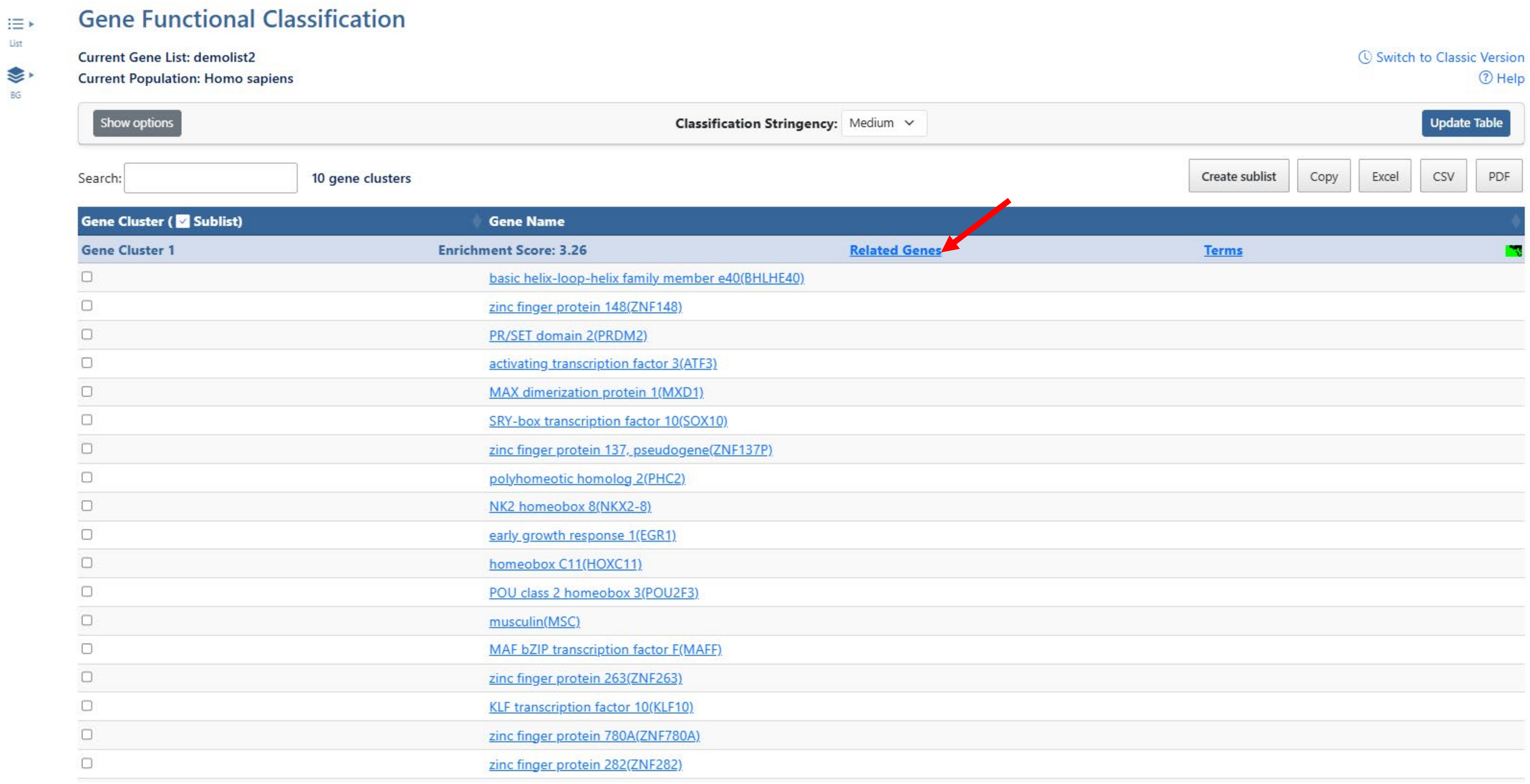
19. **Sublist**

   Click on check boxes to select items for creating a sublist. (12)

20. **Gene Name**

   Click the gene name link to explore the full gene report. For more information, see the Gene Report documentation page.

Gene Functional Classification Tool



Gene Functional Classification

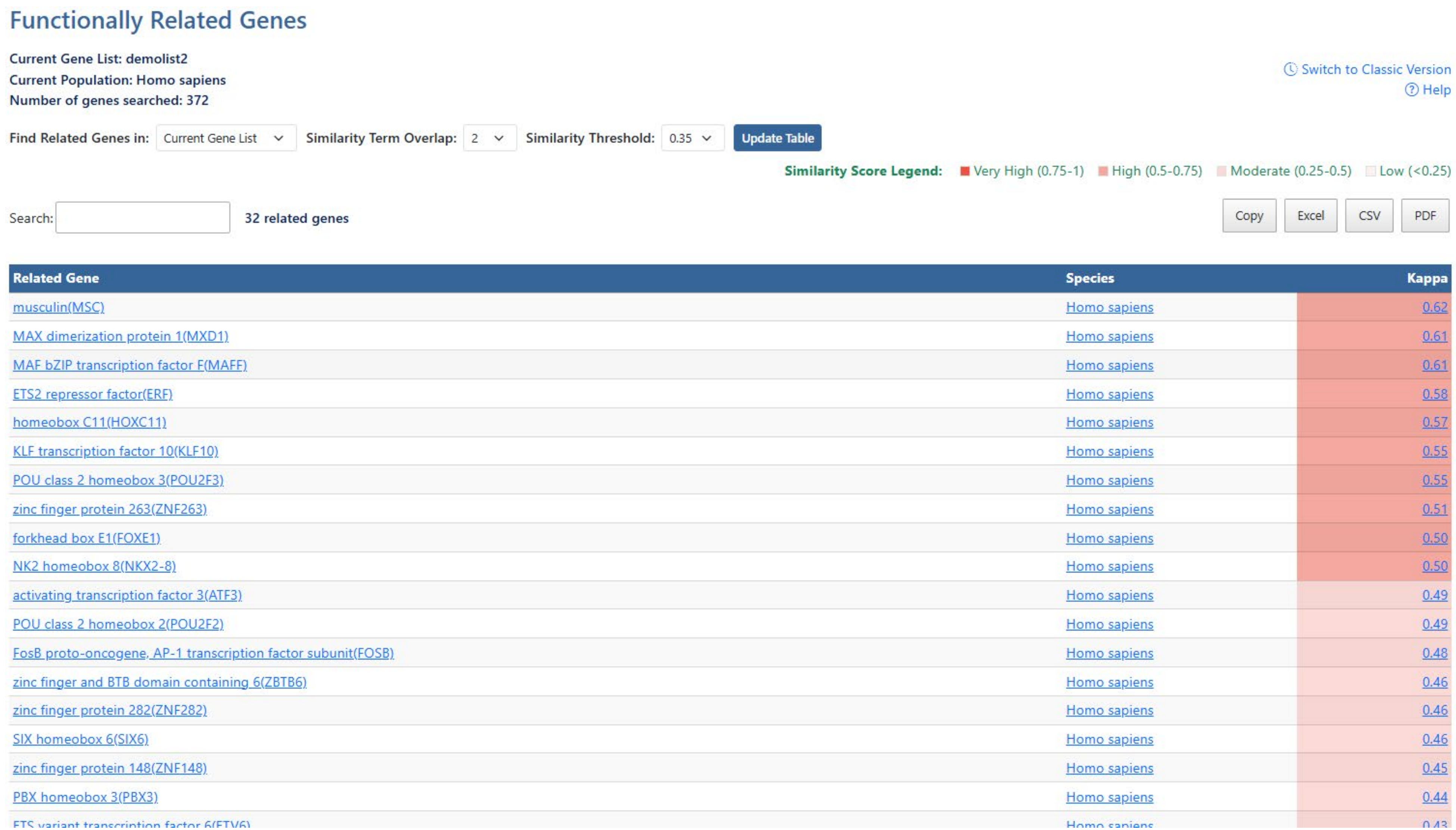
Current Gene List: demolist2
Current Population: Homo sapiens

Classification Stringency: Medium

Search: 10 gene clusters

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

Gene Functional Classification Tool



Functionally Related Genes

Current Gene List: demolist2
Current Population: Homo sapiens
Number of genes searched: 372

Find Related Genes in: Current Gene List **Similarity Term Overlap:** 2 **Similarity Threshold:** 0.35

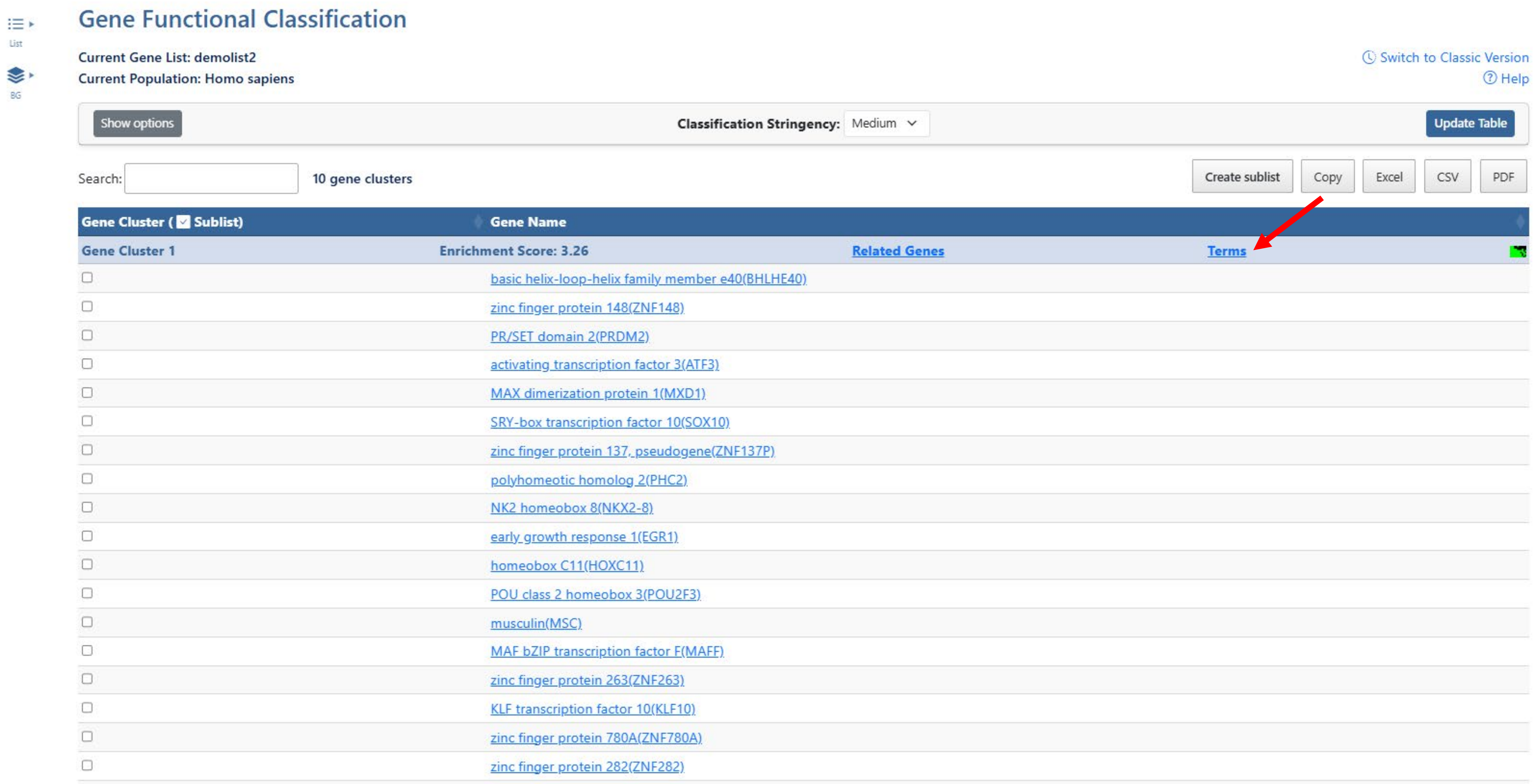
Similarity Score Legend: ■ Very High (0.75-1) ■ High (0.5-0.75) ■ Moderate (0.25-0.5) ■ Low (<0.25)

Search:

32 related genes

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

Gene Functional Classification Tool



Gene Functional Classification

Current Gene List: demolist2
Current Population: Homo sapiens

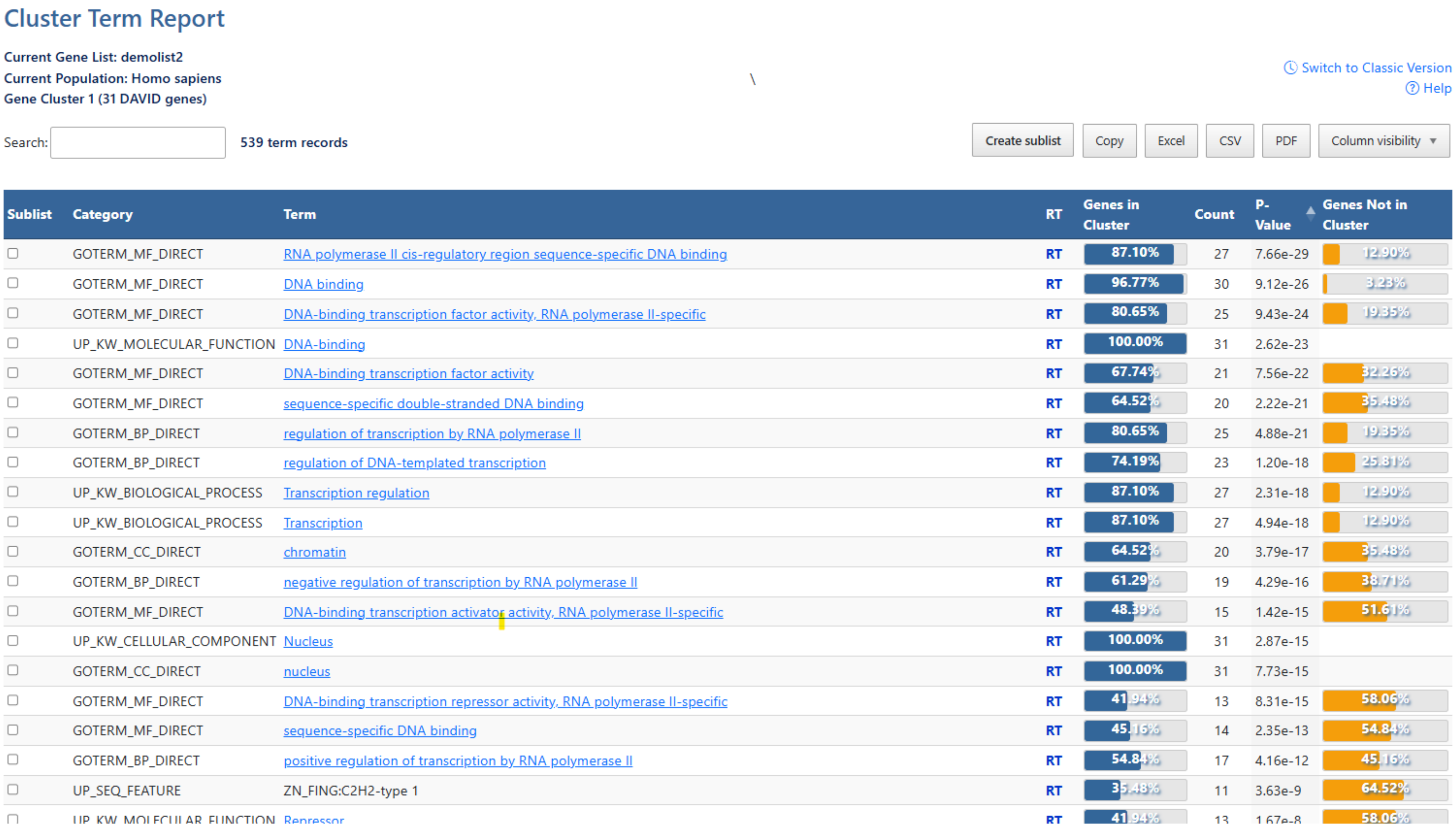
Classification Stringency: Medium

Search:

10 gene clusters

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

Gene Functional Classification Tool



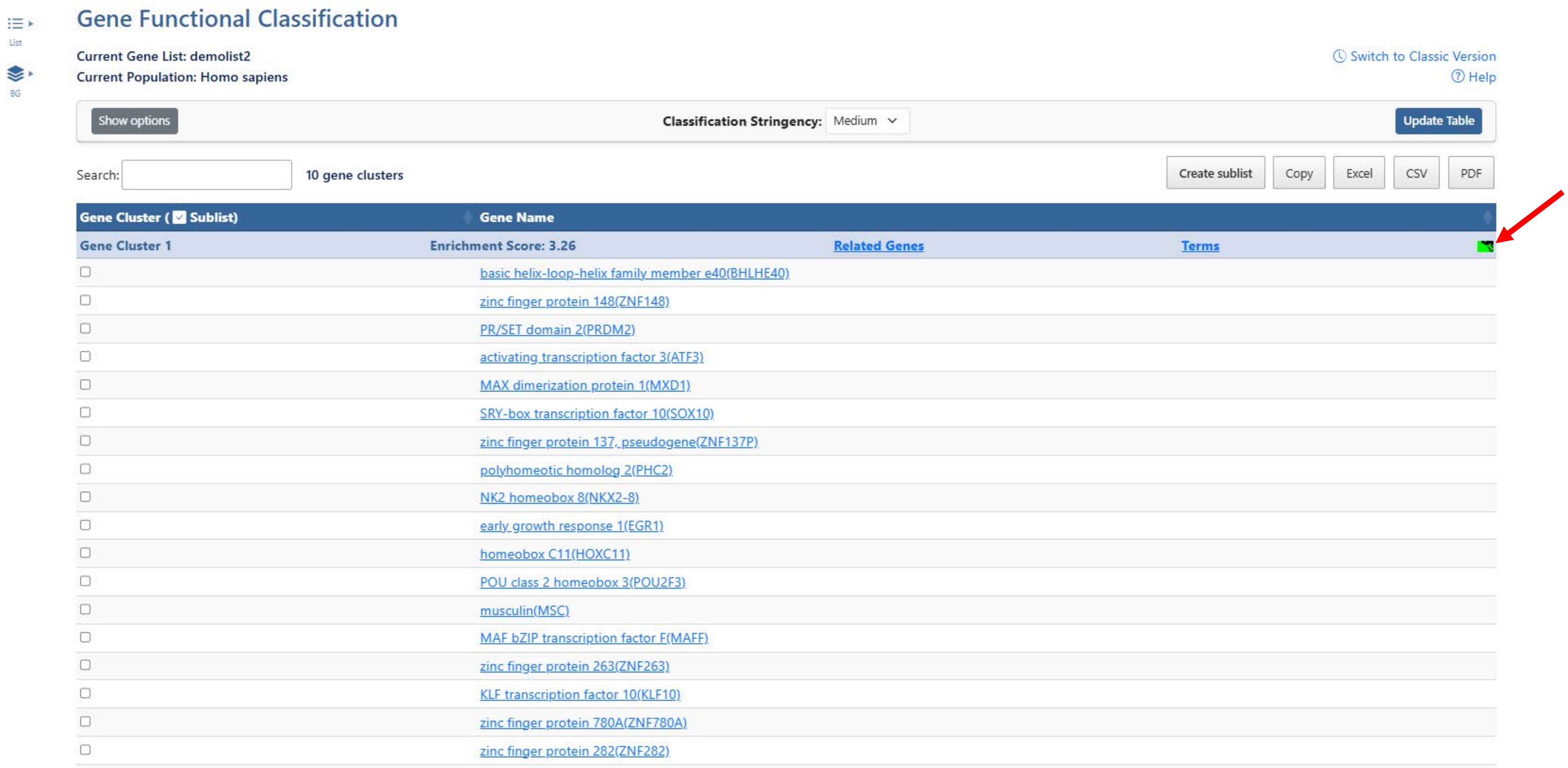
Cluster Term Report

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

Search: 539 term records

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

Gene Functional Classification Tool



Gene Functional Classification

Current Gene List: demolist2
Current Population: Homo sapiens

Switch to Classic Version
Help

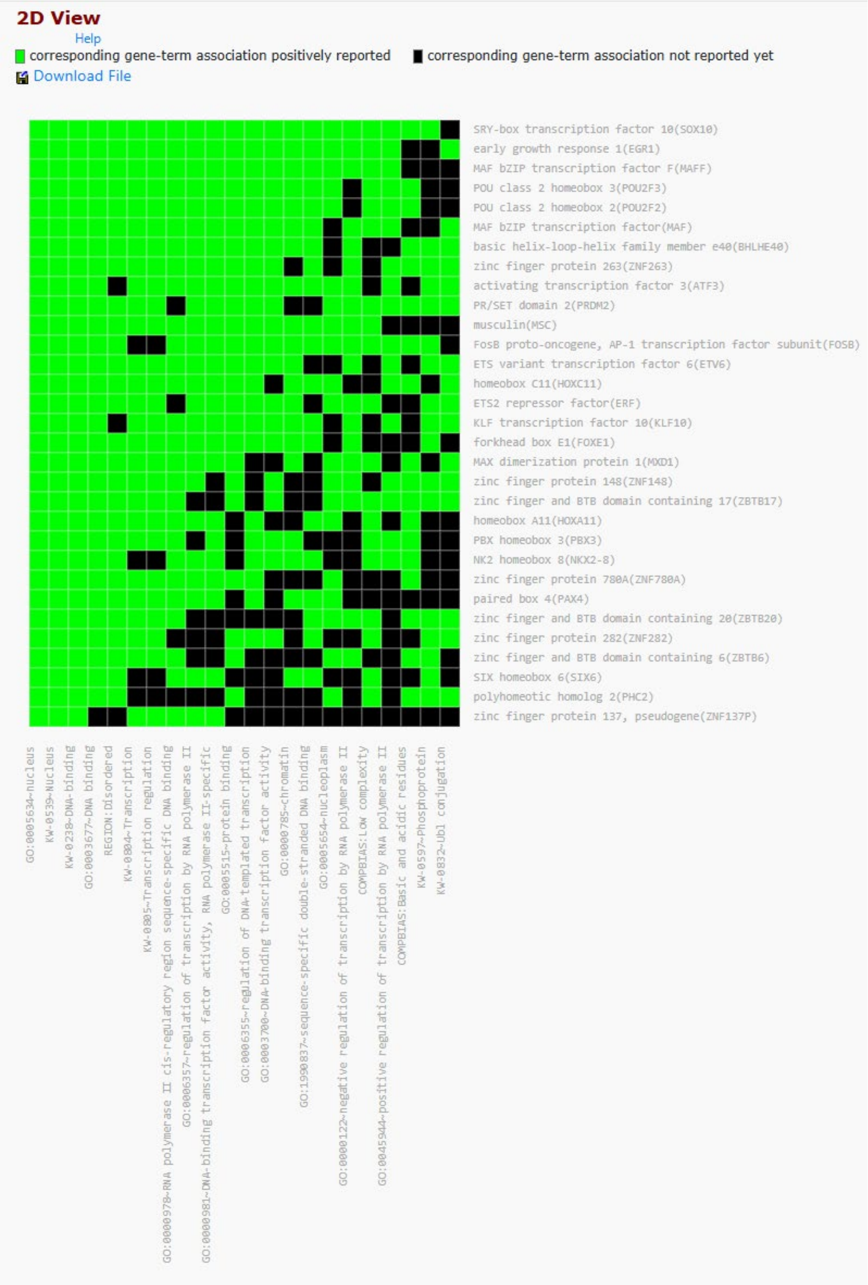
Classification Stringency: Medium

Search:

10 gene clusters

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

Gene Functional Classification Tool



2D View

Help

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

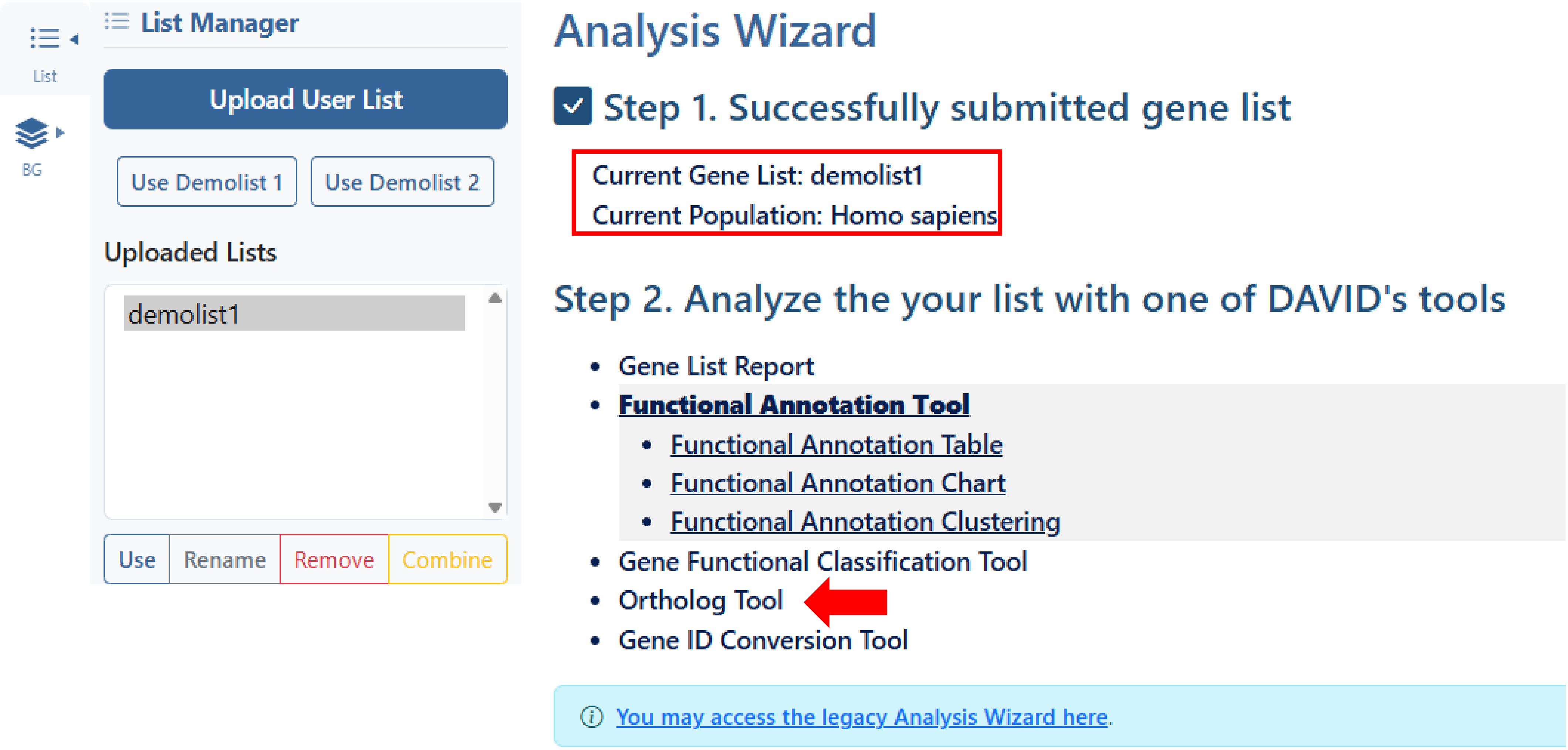
Download File

SRY-box transcription factor 10(SOX10)
early growth response 1(EGR1)
MAF bZIP transcription factor F(MAFF)
POU class 2 homeobox 3(POU2F3)
POU class 2 homeobox 2(POU2F2)
MAF bZIP transcription factor(MAF)
basic helix-loop-helix family member e40(BHLHE40)
zinc finger protein 263(ZNF263)
activating transcription factor 3(ATF3)
PR/SET domain 2(PRDM2)
musculin(MSC)
FosB proto-oncogene, AP-1 transcription factor subunit(FOSB)
ETS variant transcription factor 6(ETV6)
homeobox C11(HOXC11)
ETS2 repressor factor(ERF)
KLF transcription factor 10(KLF10)
forkhead box E1(FOXE1)
MAX dimerization protein 1(MXD1)
zinc finger protein 148(ZNF148)
zinc finger and BTB domain containing 17(ZBTB17)
homeobox A11(HOXA11)
PBX homeobox 3(PBX3)
NK2 homeobox 8(NKX2-8)
zinc finger protein 780A(ZNF780A)
paired box 4(PAX4)
zinc finger and BTB domain containing 20(ZBTB20)
zinc finger protein 282(ZNF282)
zinc finger and BTB domain containing 6(ZBTB6)
SIX homeobox 6(SIX6)
polyhomeotic homolog 2(PHC2)
zinc finger protein 137, pseudogene(ZNF137P)

GO:0005634~nucleus
KW-0539~Nucleus
KW-0238~DNA-binding
GO:0003677~DNA binding
REGION:Disordered
KW-0804~Transcription
KW-0805~Transcription regulation
GO:0000978~RNA polymerase II cis-regulatory region sequence-specific DNA binding
GO:0006357~regulation of transcription by RNA polymerase II
GO:0000981~DNA-binding transcription factor activity, RNA polymerase II-specific
GO:0005515~protein binding
GO:0006355~regulation of DNA-templated transcription
GO:0003700~DNA-binding transcription factor activity
GO:0000785~chromatin
GO:1990837~sequence-specific double-stranded DNA binding
GO:0005654~nucleoplasm
GO:0000122~negative regulation of transcription by RNA polymerase II
COMPBIAS:Low complexity
GO:0045944~positive regulation of transcription by RNA polymerase II
COMPBIAS:Basic and acidic residues
KW-0597~Phosphoprotein
KW-0832~Ubl conjugation

DAVID Ortholog Analysis

DAVID Ortholog Analysis



Analysis Wizard

☑ Step 1. Successfully submitted gene list

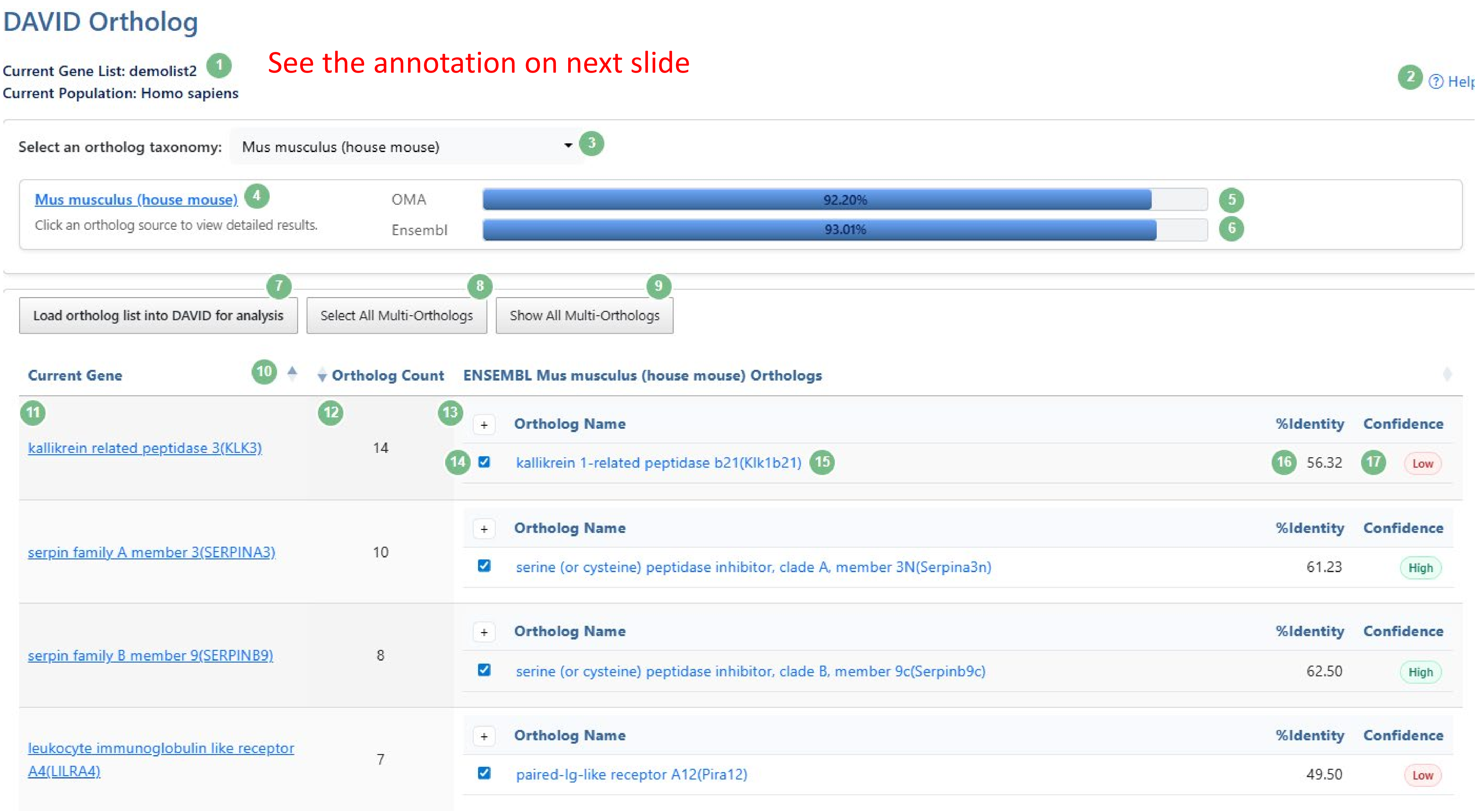
Current Gene List: demolist1
Current Population: Homo sapiens

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

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

ⓘ You may access the legacy Analysis Wizard here.

DAVID Ortholog Analysis



See the annotation on next slide

DAVID Ortholog

Current Gene List: demolist2

Current Population: Homo sapiens

Select an ortholog taxonomy: Mus musculus (house mouse)

Mus musculus (house mouse)

Click an ortholog source to view detailed results.

Source	Value
OMA	92.20%
Ensembl	93.01%

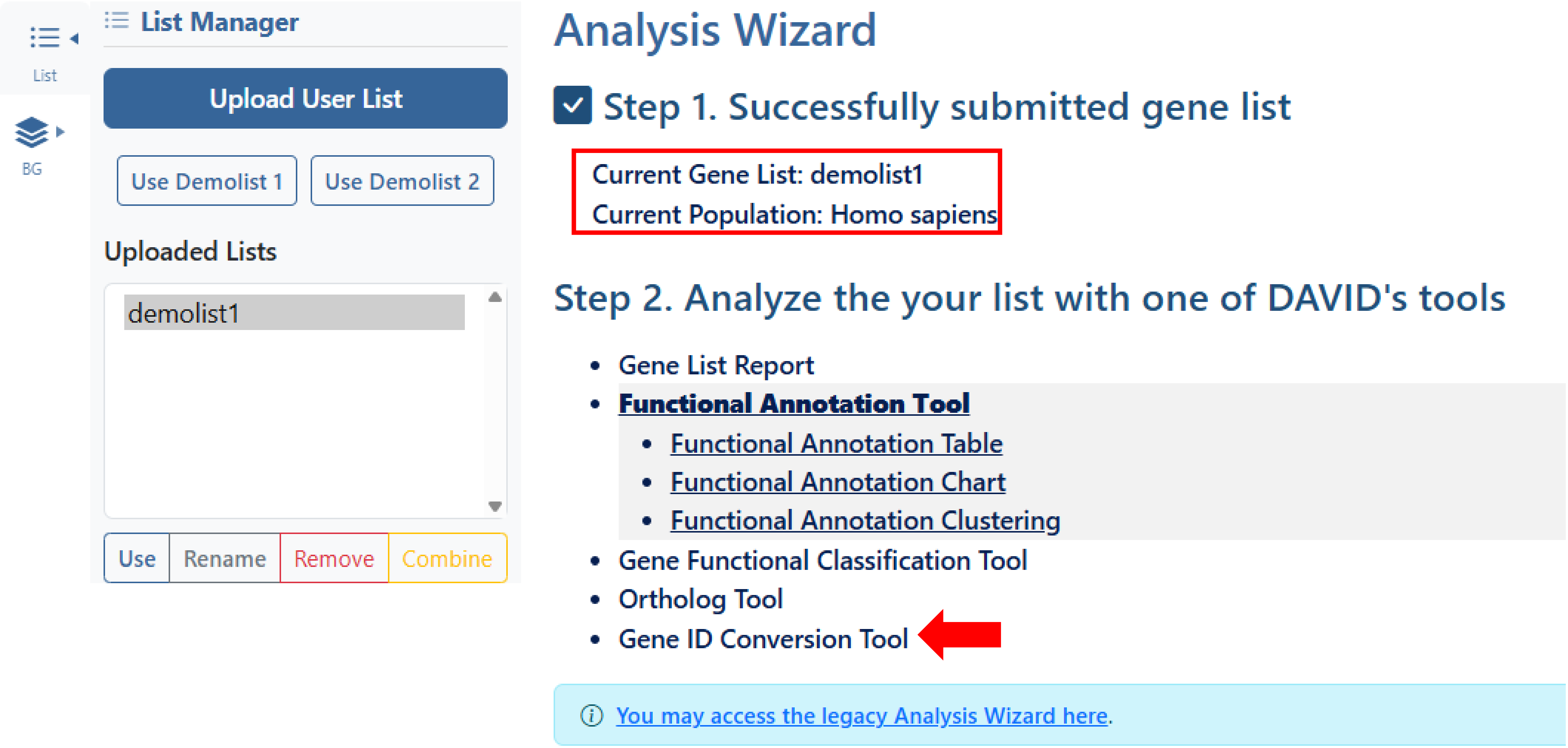
Current Gene	Ortholog Count	ENSEMBL Mus musculus (house mouse) Orthologs		
		Ortholog Name	%Identity	Confidence
kallikrein related peptidase 3(KLK3)	14	☑ kallikrein 1-related peptidase b21(Klk1b21)	56.32	Low
serpin family A member 3(SERPINA3)	10	☑ serine (or cysteine) peptidase inhibitor, clade A, member 3N(Serpina3n)	61.23	High
serpin family B member 9(SERPINB9)	8	☑ serine (or cysteine) peptidase inhibitor, clade B, member 9c(Serpinb9c)	62.50	High
leukocyte immunoglobulin like receptor A4(LILRA4)	7	☑ paired-Ig-like receptor A12(Pira12)	49.50	Low

DAVID Ortholog Analysis

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

DAVID Gene ID Conversion

DAVID Gene ID Conversion



Analysis Wizard

☑ Step 1. Successfully submitted gene list

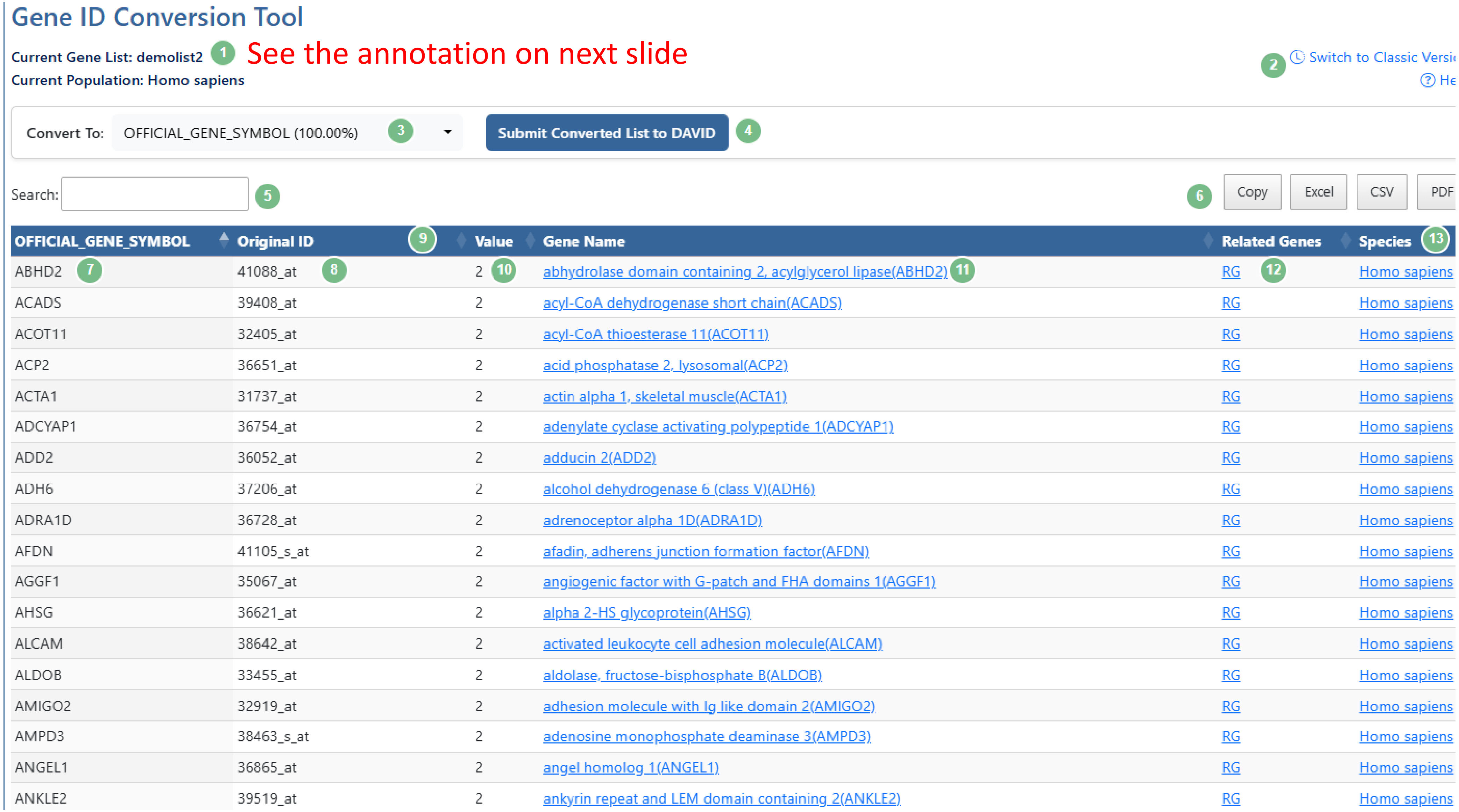
Current Gene List: demolist1
Current Population: Homo sapiens

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

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

ⓘ You may access the legacy Analysis Wizard here.

DAVID Gene ID Conversion



Gene ID Conversion Tool

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

Current Population: Homo sapiens

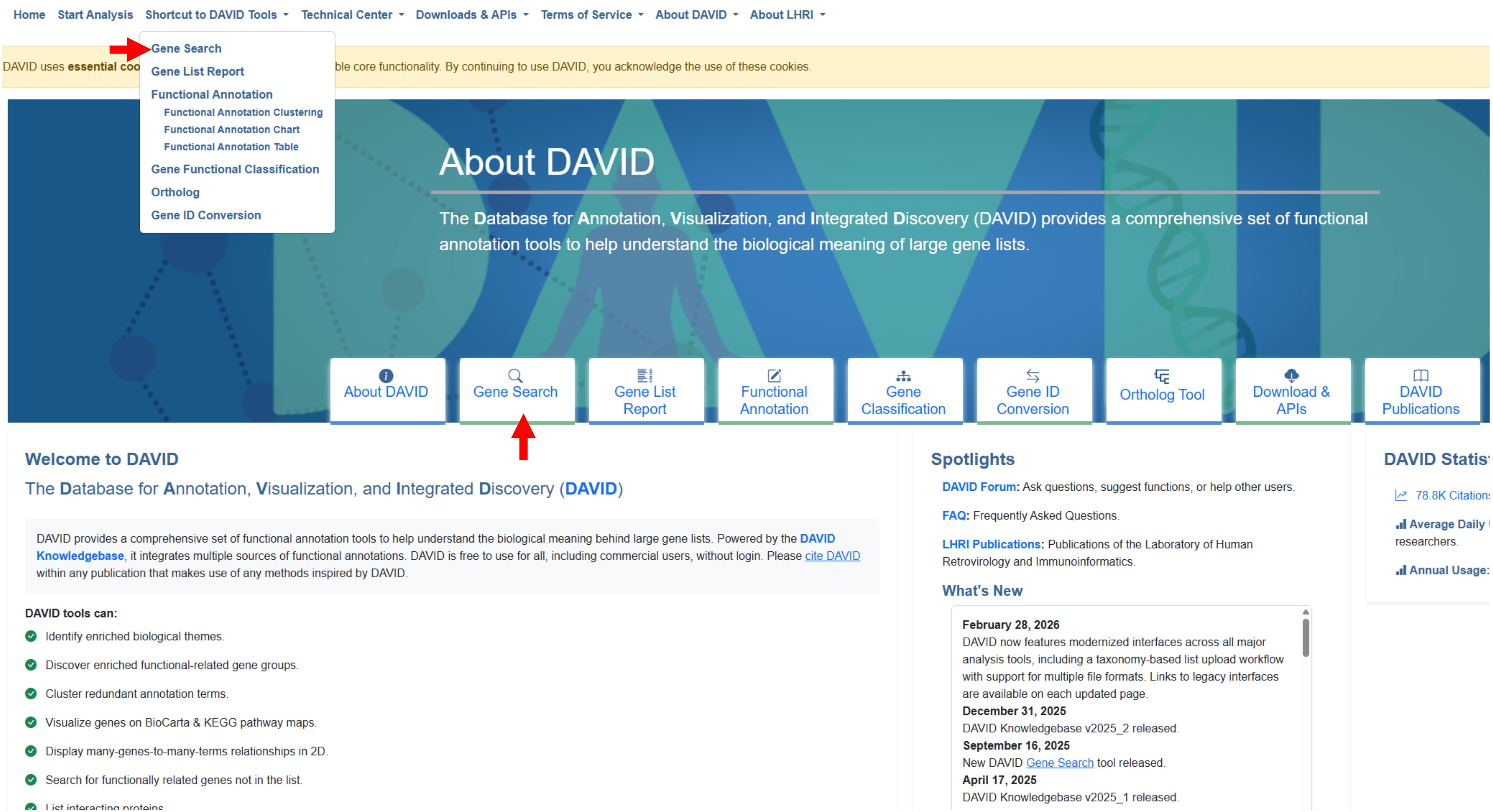
OFFICIAL_GENE_SYMBOL	Original ID ⑨	Value	Gene Name	Related Genes	Species ⑬
ABHD2 ⑦	41088_at ⑧	2 ⑩	abhydrolase domain containing 2, acylglycerol lipase(ABHD2) ⑪	RG ⑫	Homo sapiens
ACADS	39408_at	2	acyl-CoA dehydrogenase short chain(ACADS)	RG	Homo sapiens
ACOT11	32405_at	2	acyl-CoA thioesterase 11(ACOT11)	RG	Homo sapiens
ACP2	36651_at	2	acid phosphatase 2, lysosomal(ACP2)	RG	Homo sapiens
ACTA1	31737_at	2	actin alpha 1, skeletal muscle(ACTA1)	RG	Homo sapiens
ADCYAP1	36754_at	2	adenylate cyclase activating polypeptide 1(ADCYAP1)	RG	Homo sapiens
ADD2	36052_at	2	adducin 2(ADD2)	RG	Homo sapiens
ADH6	37206_at	2	alcohol dehydrogenase 6 (class V)(ADH6)	RG	Homo sapiens
ADRA1D	36728_at	2	adrenoceptor alpha 1D(ADRA1D)	RG	Homo sapiens
AFDN	41105_s_at	2	afadin, adherens junction formation factor(AFDN)	RG	Homo sapiens
AGGF1	35067_at	2	angiogenic factor with G-patch and FHA domains 1(AGGF1)	RG	Homo sapiens
AHSG	36621_at	2	alpha 2-HS glycoprotein(AHSG)	RG	Homo sapiens
ALCAM	38642_at	2	activated leukocyte cell adhesion molecule(ALCAM)	RG	Homo sapiens
ALDOB	33455_at	2	aldolase, fructose-bisphosphate B(ALDOB)	RG	Homo sapiens
AMIGO2	32919_at	2	adhesion molecule with Ig like domain 2(AMIGO2)	RG	Homo sapiens
AMPD3	38463_s_at	2	adenosine monophosphate deaminase 3(AMPD3)	RG	Homo sapiens
ANGEL1	36865_at	2	angel homolog 1(ANGEL1)	RG	Homo sapiens
ANKLE2	39519_at	2	ankyrin repeat and LEM domain containing 2(ANKLE2)	RG	Homo sapiens

DAVID Gene ID Conversion

1. **Current Gene List & Population**
   Displays the active gene list and selected species or background population.
2. **Help and Switch to Classic Version**
   Link to this help page and provides access to the legacy Gene List Report interface.
3. **Conversion Destination Selection**
   Save the converted list to the DAVID list manager for use in further downstream analysis.
4. **Submit Converted List to DAVID**
   Users will first be met with this dropdown box. Click *Select Identifier type* and choose an identifier destination, then the converted gene name list will populate. Click this dropdown box again to change identifier destination and list will automatically update.
5. **Search**
   The search box filters table results in real time.
6. **Export Options**
   Results can be exported using Copy, Excel, CSV, or PDF. Exports reflect the current filtered and sorted view.
7. **Selected Source ID**
   Gene identifier from selected source.
8. **User ID**
   User uploaded gene ID name.
9. **Sortable Columns**
   Click any column header to sort by Destination ID, User ID, Expression Value, DAVID Gene Name, Related Genes (RG), or Species.
10. **Value**
    User uploaded expression value. (Optional)
11. **Gene Name**
    Click the gene name link to explore the full gene report. For more information, see the Gene Report documentation page.
12. **Related Genes (RG)**
    Click the **RG** link to explore functionally related genes associated with each entry. For more information, see the Related Genes documentation page.
13. **Species**
    Click the **Species** link to go to NCBI taxonomy entry.

DAVID Gene Search / DAVID Gene Report

DAVID Gene Search



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

About DAVID

The **D**atabase for **A**nnotation, **V**isualization, and **I**ntegrated **D**iscovery (DAVID) provides a comprehensive set of functional annotation tools to help understand the biological meaning of large gene lists.

Welcome to DAVID

The **D**atabase for **A**nnotation, **V**isualization, and **I**ntegrated **D**iscovery (**DAVID**)

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

DAVID tools can:

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

Spotlights

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

FAQ: Frequently Asked Questions.

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

What's New

February 28, 2026
DAVID now features modernized interfaces across all major analysis tools, including a taxonomy-based list upload workflow with support for multiple file formats. Links to legacy interfaces are available on each updated page.
December 31, 2025
DAVID Knowledgebase v2025_2 released.
September 16, 2025
New DAVID Gene Search tool released.
April 17, 2025
DAVID Knowledgebase v2025_1 released.

DAVID Statis

78.8K Citation

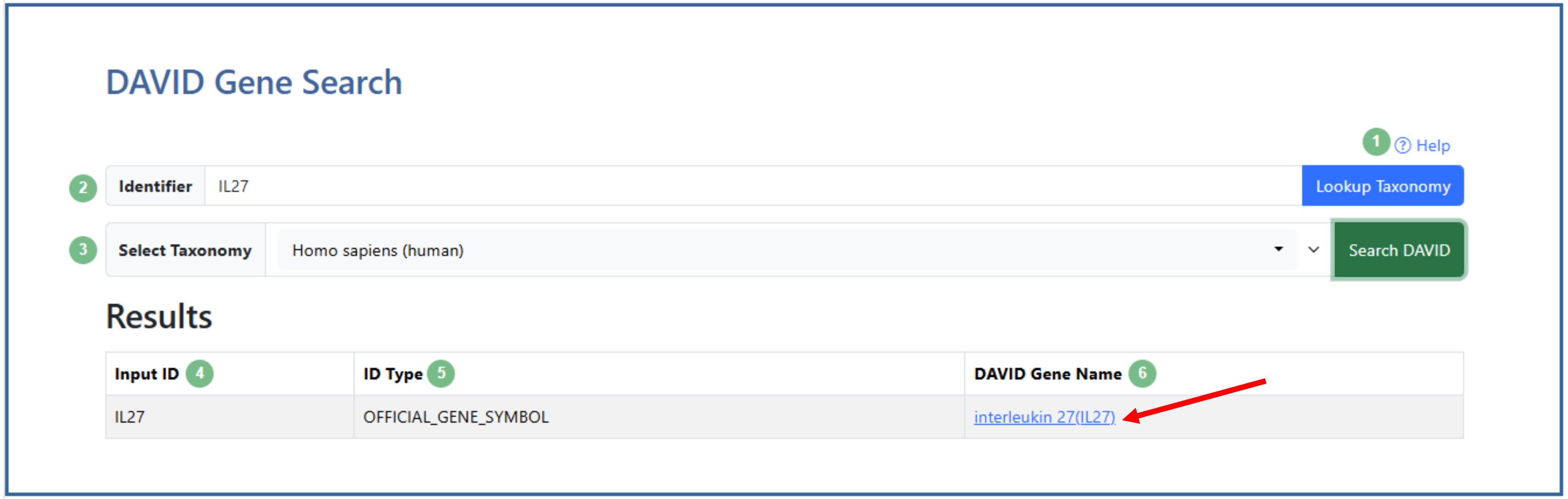
Average Daily researchers.

Annual Usage:

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

DAVID Gene Search

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



DAVID Gene Search

Identifier: IL27

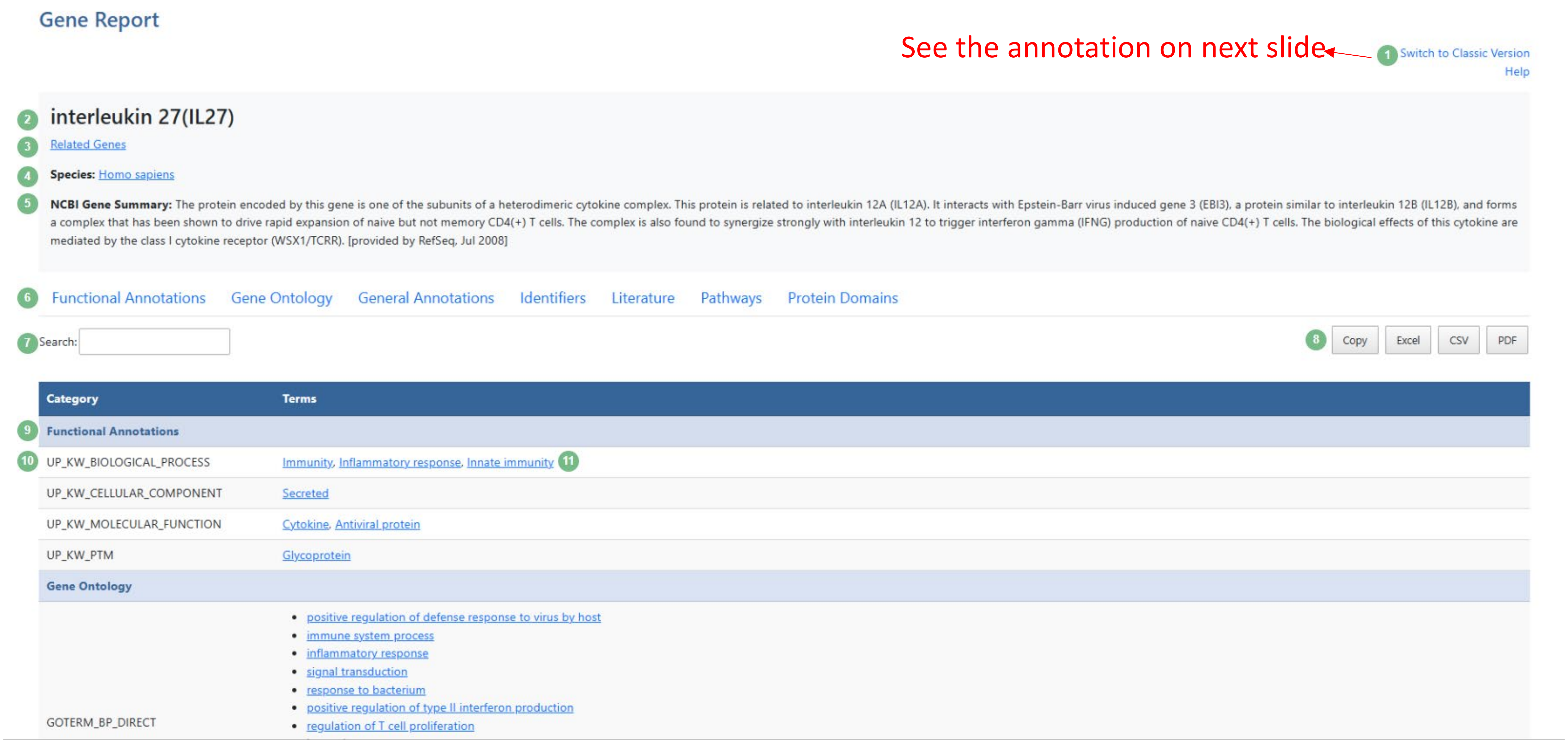
Select Taxonomy: Homo sapiens (human)

Results

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

1. **Help and Switch to Classic Version**
   Link to this help page and provides access to the legacy Gene List Report interface.
2. **Identifier search box**
   Type full identifier (case insensitive) and click on the blue **Lookup Taxonomy** button. If any results are found, the taxonomy selection box will appear. If no results are found, a red diaglogue box will appear indicating "*No taxonomies found for the identifier. Please try a different identifier.*"
3. **Select Taxonomy**
   Once a valid identifier is entered, all available species with the identifier are populated in the Select Taxonomy drop down menu. The list of species is displayed alphabetically and can be searched by typing in the search bar within the dropdown (case insensitive). Click on a species name to select it, then click the green **Search DAVID** button to continue.
4. **Input ID**
   User entered identifier.
5. **ID Type**
6. **DAVID Gene Name**
   Full name of gene available from DAVID. Click the gene name link to explore the full gene report. For more information, see the Gene Report documentation page.

DAVID Gene Report



See the annotation on next slide

② interleukin 27(IL27)

③ Related Genes

④ **Species:** Homo sapiens

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

Category	Terms
⑨ **Functional Annotations**	
⑩ UP_KW_BIOLOGICAL_PROCESS	Immunity, Inflammatory response, Innate immunity ⑪
UP_KW_CELLULAR_COMPONENT	Secreted
UP_KW_MOLECULAR_FUNCTION	Cytokine, Antiviral protein
UP_KW_PTM	Glycoprotein
Gene Ontology	
GOTERM_BP_DIRECT	• positive regulation of defense response to virus by host • immune system process • inflammatory response • signal transduction • response to bacterium • positive regulation of type II interferon production • regulation of T cell proliferation

DAVID Gene Report

1. **Help and Switch to Classic Version**
   Link to this help page and provides access to the legacy Gene List Report interface.
2. **Gene name**
3. **Related Genes (RG)**
   Click the **Related Genes** link to explore functionally related genes associated with each entry. For more information, see the Related Genes documentation page.
4. **Species**
   Click the **Species** link to go to NCBI taxonomy entry.
5. **Gene Summary**
   Summary of gene information, provided by NCBI.
6. **Navigate to categories**
   Click the tabs to jump to desired category of annotations.
7. **Search and Record Count**
   The search box filters table results in real time. The record count indicates total entries and the number of DAVID genes mapped.
8. **Export Options**
   Results can be exported using Copy, Excel, CSV, or PDF. Exports reflect the current filtered and sorted view.
9. **Categories**
   Main categories shown in blue. Navigation tabs will jump to tops of these main headers.
10. **Subcategories**
    Subcategories available per each resource.
11. **Annotations**
    Annotations available for each item. If available, hyperlinks lead users to original resources for further details.

DAVID API

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

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

Example API Calls:

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

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

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

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

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

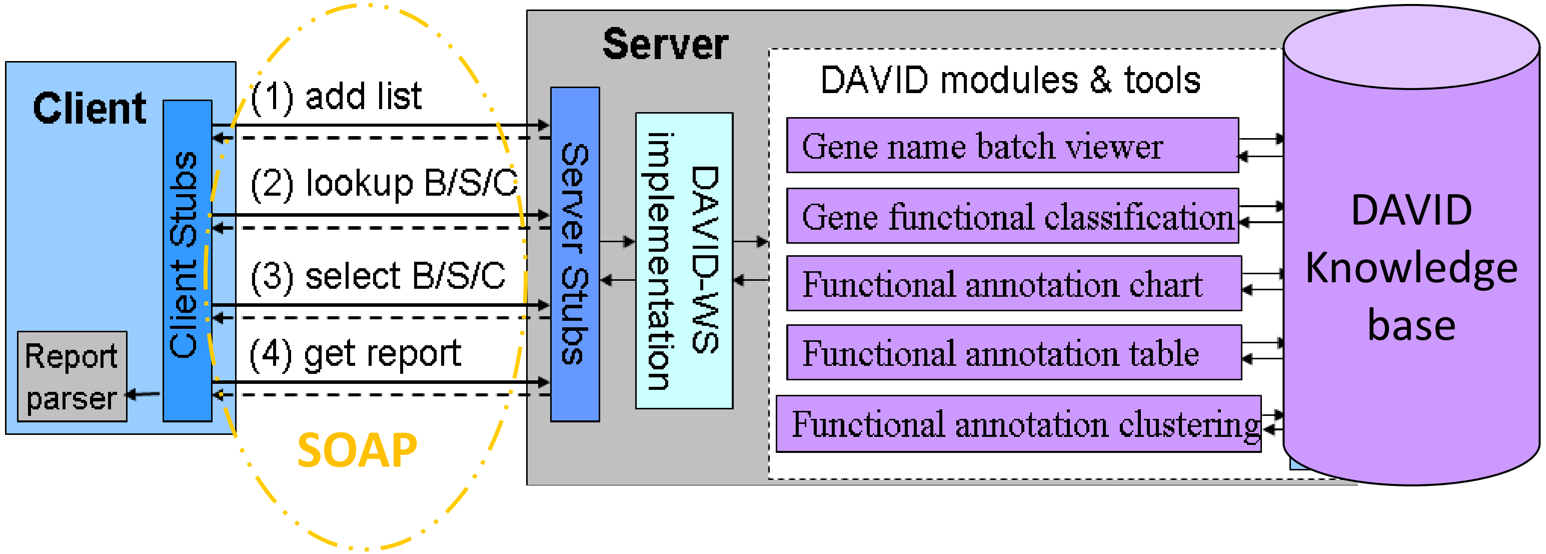
Gene Report: https://davidbioinformatics.nih.gov/api.jsp?type=ENTREZ_GENE_ID&ids=2919,6347,6348,6364&tool=geneReport

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

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

Stateful DAVID web services

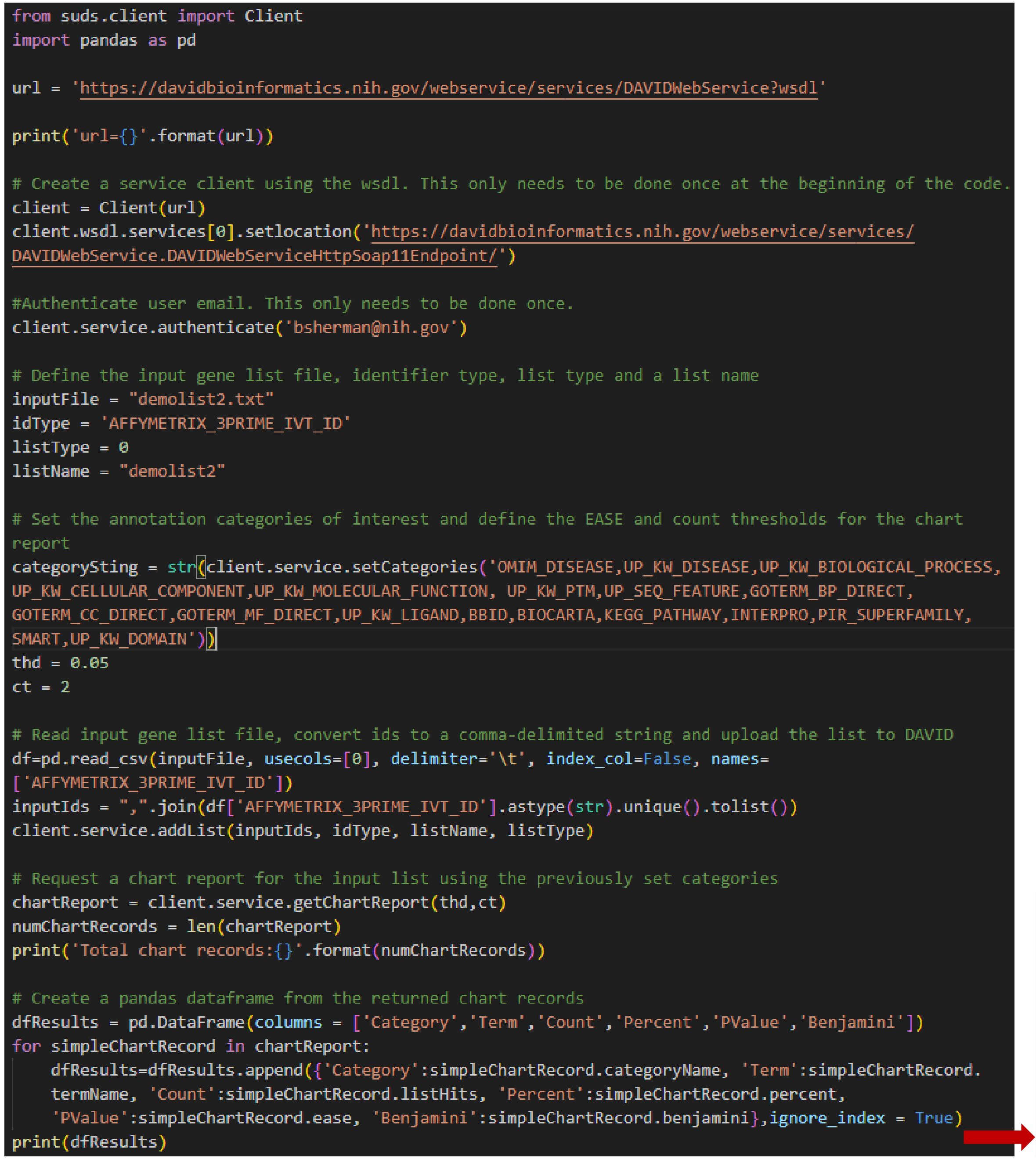
Allows users to programmatically (Java, Perl, Python, R, C, etc) interact with DAVID and automate their tasks.
https://davidbioinformatics.nih.gov/content.jsp?file=WS.html



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

Xiaoli Jiao, Brad T. Sherman, et al. DAVID-WS: A Stateful Web Service to Facilitate Gene/Protein List Analysis ***Bioinformatics*** *2012*

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

```
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  ▼<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

```
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  ▼<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"/>
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     <xs:element minOccurs="0" name="popHits" type="xs:int"/>
     <xs:element minOccurs="0" name="popTotals" type="xs:int"/>
     <xs:element minOccurs="0" name="rfdr" type="xs:double"/>
     <xs:element maxOccurs="unbounded" minOccurs="0" name="scores"
     nillable="true" type="xs:double"/>
     <xs:element minOccurs="0" name="termName" nillable="true"
     type="xs:string"/>
   </xs:sequence>
 </xs:complexType>
```

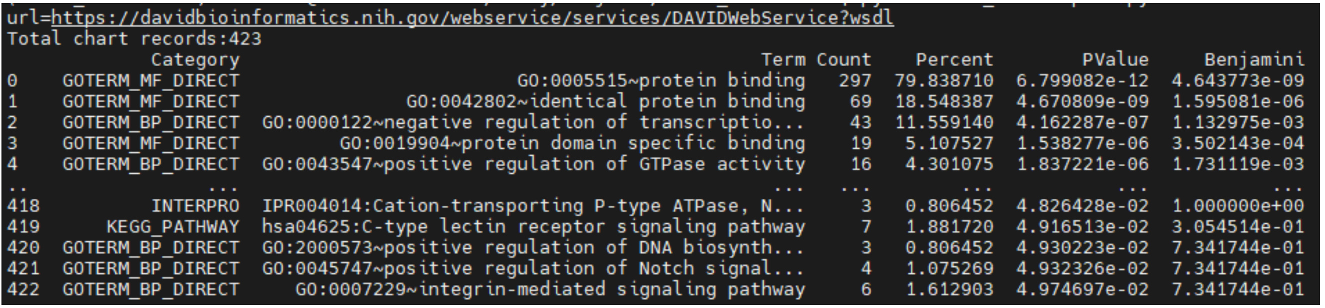

```
url=https://davidbioinformatics.nih.gov/webservice/services/DAVIDWebService?wsdl
Total chart records:423
             Category                                              Term Count    Percent        PValue     Benjamini
0    GOTERM_MF_DIRECT                         GO:0005515~protein binding  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