
Lecture 21

Pathway Analysis

MCB 416A/516A

Statistical Bioinformatics and Genomic Analysis

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Univ of Arizona

Outline

- Pathways analysis
- Public resources
- DAVID Bioinformatics

Revisit: biological process

- A biological objective to which the gene product contributes.
- Accomplished via one or more ordered assemblies of molecular functions.
- There is generally some temporal aspect to the process and it will often involve the transformation of some physical thing.
 - ◆ e.g. “cell growth and maintenance” or “signal transduction”

Biological process and pathway

- The concept of a pathway is different from that of a biological process.
- A pathway is more complex and has dependencies and dynamics that are not part of the concept of a biological process.
- After determining a list of genes involved in a given biological process, very often the next step is to map these genes to known pathways and determine which pathways are overrepresented in a given set of genes.

Pathway types

- Biochemical / Metabolic
- Signaling and Cellular Processes
 - Protein Interaction
 - ◆ Receptor + ligand
 - ◆ Phosphorylation
 - Gene Regulation
 - ◆ Transcription factor
- Gene Networks
 - Combination of the above

Major Public Pathway Resources

- KEGG first choice for scope
- Reactome project; human + model organisms pathways. Expert annotations from literature (CSHL/EBI)
- NetPath (HPRD)
- PID Pathway Interaction Database @NIH
- Biocarta
- BioCyc
- Cyclone - provides an open source Java API for easier access to BioCyc.
- RegulonDB E.coli K12 DB (operons/genes/regulatory elements)
- WikiPathways open curation of biological pathways

Related tools:

DAVID

GenMAPP

KEGG Array

GSEA

iPath

...

Bioconductor packages

SigPathway

KEGG

KEGGgraph

...

Kyoto Encyclopedia of Genes and Genomes (KEGG)

KEGG PATHWAY is a collection of manually drawn pathway maps representing our knowledge on the molecular interaction, reaction and relation networks for:

1. Metabolism
2. Genetic Information Processing
3. Environmental Information Processing
4. Cellular Processes
5. Organismal Systems
6. Human Diseases
7. Drug Development

KEGG PATHWAY is a reference database for Pathway Mapping.

Kyoto Encyclopedia of Genes and Genomes (KEGG) -2

Pathway Mapping

KEGG PATHWAY mapping is the process to map molecular datasets, especially large-scale datasets in genomics, transcriptomics, proteomics, and metabolomics, to the KEGG pathway maps for biological interpretation of higher-level systemic functions.

[Search Pathway](#) - basic pathway mapping tool

[Search&Color Pathway](#) - advanced pathway mapping tool

[Color Pathway](#) - selected pathway map coloring tool



KEGG PATHWAY Database

Wiring diagrams of molecular interactions, reactions and relations

Menu PATHWAY BRITE MODULE KO GENES LIGAND NETWORK DISEASE DRUG DBGET

Select prefix

map

Organism

Enter keywords

Go

Help

[[New pathway maps](#) | [Update history](#)]

Pathway Maps

KEGG PATHWAY is a collection of manually drawn pathway maps representing our knowledge on the molecular interaction, reaction and relation networks for:

1. Metabolism

Global/overview Carbohydrate Energy Lipid Nucleotide Amino acid Other amino Glycan
Cofactor/vitamin Terpenoid/PK Other secondary metabolite Xenobiotics Chemical structure

2. Genetic Information Processing

3. Environmental Information Processing

4. Cellular Processes

5. Organismal Systems

6. Human Diseases

7. Drug Development

KEGG PATHWAY is a reference database for **Pathway Mapping**.

Pathway Identifiers

Each pathway map is identified by the combination of 2-4 letter prefix code and 5 digit number (see KEGG Identifier). The prefix has the following meaning:

map manually drawn reference pathway

ko reference pathway highlighting KOs

- 05010 Alzheimer's disease
- 05012 Parkinson's disease
- 05014 Amyotrophic lateral sclerosis (ALS)
- 05016 Huntington's disease
- 05020 Prion diseases

Type II diabetes mellitus

6.5 Substance dependence

- 05030 Cocaine addiction
- 05031 Amphetamine addiction
- 05032 Morphine addiction
- 05033 Nicotine addiction
- 05034 Alcoholism

6.6 Cardiovascular diseases

- 05418 Fluid shear stress and atherosclerosis
- 05410 Hypertrophic cardiomyopathy (HCM)
- 05412 Arrhythmogenic right ventricular cardiomyopathy (ARVC)
- 05414 Dilated cardiomyopathy (DCM)
- 05416 Viral myocarditis

6.7 Endocrine and metabolic diseases

- 04930 Type II diabetes mellitus
- 04940 Type I diabetes mellitus
- 04950 Maturity onset diabetes of the young
- 04932 Non-alcoholic fatty liver disease (NAFLD)
- 04931 Insulin resistance
- 04933 AGE-RAGE signaling pathway in diabetic complications
- 04934 Cushing's syndrome *New!*

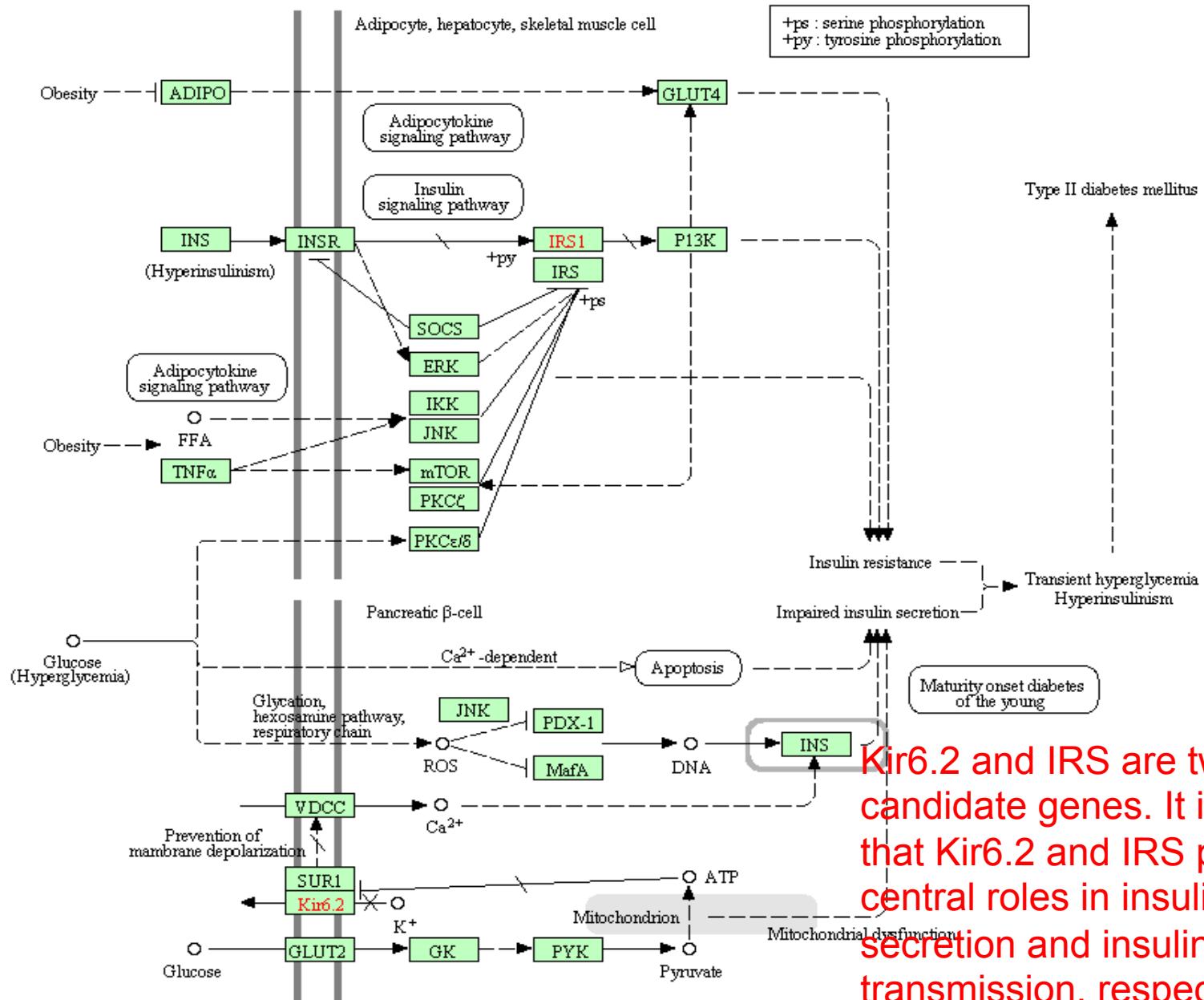
6.8 Infectious diseases: Bacterial

- 05110 Vibrio cholerae infection
- 05120 Epithelial cell signaling in Helicobacter pylori infection
- 05130 Pathogenic Escherichia coli infection
- 05132 Salmonella infection
- 05131 Shigellosis
- 05133 Pertussis
- 05134 Legionellosis
- 05150 Staphylococcus aureus infection
- 05152 Tuberculosis
- 05100 Bacterial invasion of epithelial cells

6.9 Infectious diseases: Viral

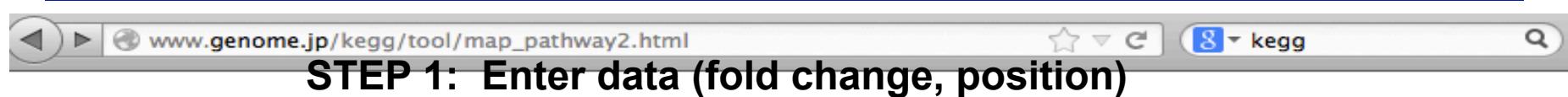
- 05166 HTLV-I infection

TYPE II DIABETES MELLITUS



Kir6.2 and IRS are two of the candidate genes. It is known that Kir6.2 and IRS play central roles in insulin secretion and insulin signal transmission, respectively.

Coloring KEGG Pathways



Coloring KEGG Pathways -2

STEP 2: Pick pathway

Pathway Search Result

Sort by the pathway list

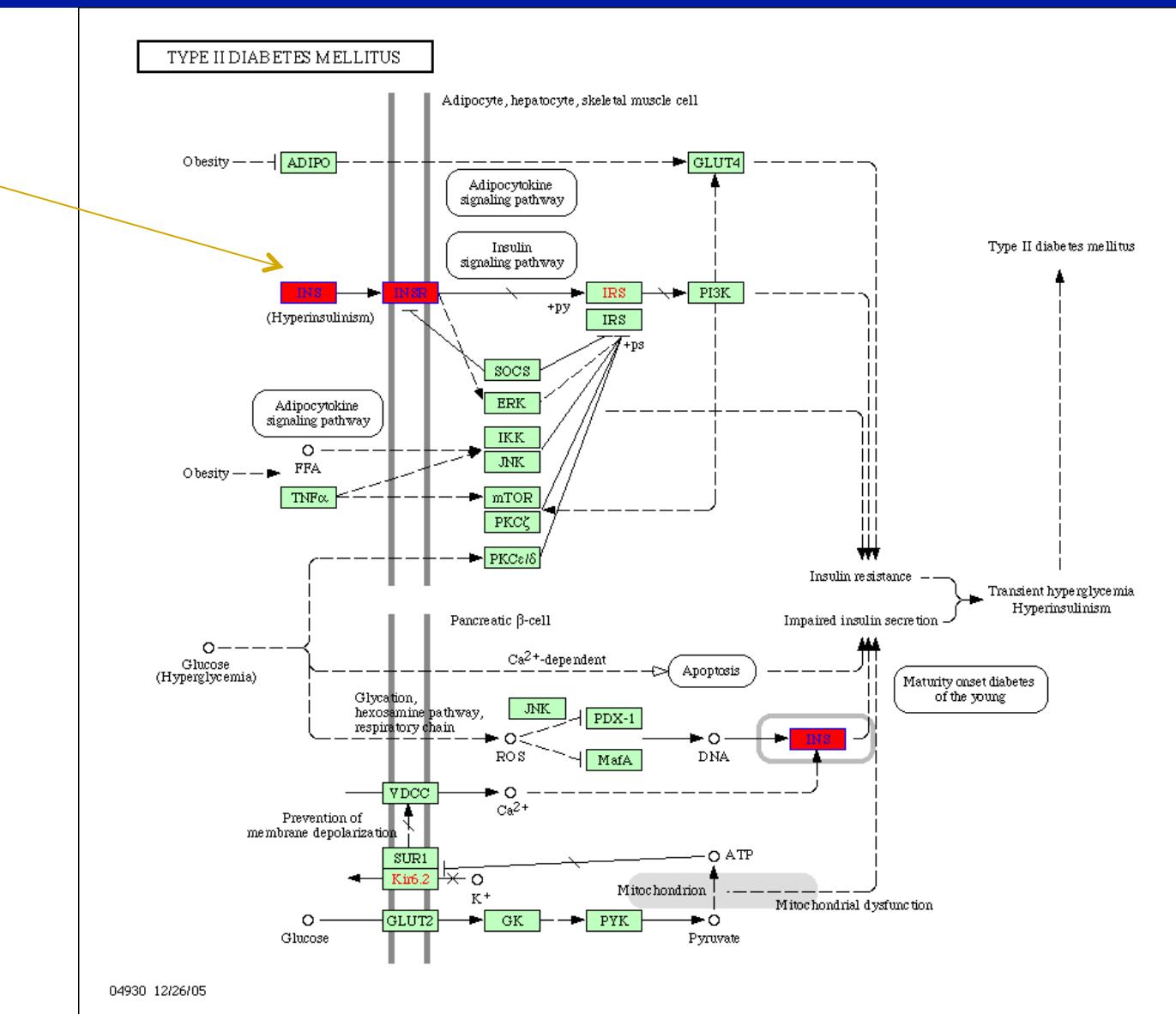
Show all objects

- ko04015 Rap1 signaling pathway (2)
- ko04014 Ras signaling pathway (2)
- ko04932 Non-alcoholic fatty liver disease (NAFLD) (2)
- ko04910 Insulin signaling pathway (2)
- ko04068 FoxO signaling pathway (2)
- ko04960 Aldosterone-regulated sodium reabsorption (2)
- ko04066 HIF-1 signaling pathway (2)
- ko04930 Type II diabetes mellitus (2)
- ko04151 PI3K-Akt signaling pathway (2)
- ko04913 Ovarian steroidogenesis (2)
- ko05215 Prostate cancer (1)
- ko04950 Maturity onset diabetes of the young (1)
- ko04810 Regulation of actin cytoskeleton (1)
- ko04911 Insulin secretion (1)
- ko04114 Oocyte meiosis (1)
- ko04150 mTOR signaling pathway (1)

Type II diabetes ...



Coloring KEGG Pathways -3



Analysis of Gene Lists

Functional Annotation

- Are particular pathways over-represented?
- Are any associated to disease?
- DAVID Bioinformatics: Tool at NIH
 - Advantage: Ease of use
 - Disadvantage: Does not consider rank of genes



Gene Set Enrichment Analysis

- Given a ranked list of genes:
 - Do genes in a particular portion of the list appear in a set of disease-associated genes?
- GSEA at Broad Institute
 - Advantages:
 - ◆ Considers rank of genes in list
 - ◆ Several unique curated data sets (MSigDB)
 - Disadvantages: Difficult to use



DAVID Bioinformatics

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

■ Functional Annotation

- Maps a gene list to:
 - ◆ KEGG
 - ◆ Gene Ontology
 - ◆ ... and over 40 other resources ...
- Enrichment analysis
 - ◆ Probability that the number of genes with a particular annotation is significant compared to background
- Functional annotation clustering
 - ◆ Sets of genes with common annotations

DAVID Bioinformatics -2

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

- Functional Classification
- Gene ID Conversion
- Gene Name Batch Viewer
- NIAID Pathogen Annotation Browser

DAVID (<http://david.abcc.ncifcrf.gov/>)

DAVID Bioinformatics Resources 6.8
Laboratory of Human Retrovirology and Immunoinformatics (LHRI)

Home Start Analysis Shortcut to DAVID Tools Technical Center Downloads & APIs Term of Service Why DAVID? About Us

*** Welcome to DAVID 6.8 ***

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

Shortcut to DAVID Tools

Functional Annotation
Gene-annotation enrichment analysis, functional annotation clustering , BioCarta & KEGG pathway mapping, gene-disease association, homologue match, ID translation, literature match and [more](#)

Gene Functional Classification
Provide a rapid means to reduce large lists of genes into functionally related groups of genes to help unravel the biological content captured by high throughput technologies. [More](#)

Gene ID Conversion
Convert list of gene ID/accessions to others of your choice with the most comprehensive gene ID mapping repository. The ambiguous accessions in the list can also be determined semi-automatically. [More](#)

Gene Name Batch Viewer
Display gene names for a given gene list; Search functionally related genes within your list or not in your list; Deep links to enriched detailed information. [More](#)

Recommending: A paper published in *Nature Protocols* describes step-by-step procedure to use DAVID!

Welcome to DAVID 6.8

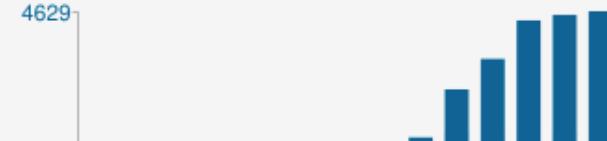
2003 - 2018

What's Important in DAVID?

- [Cite DAVID](#)
- [IDs of Affy Exon and Gene arrays supported](#)
- [Novel Classification Algorithms](#)
- [Pre-built Affymetrix and Illumina backgrounds](#)
- [User's customized gene background](#)
- [Enhanced calculating speed](#)

Statistics of DAVID

DAVID Citations (2003-2017)



- Identify enriched biological themes, particularly GO terms
- Discover enriched functional-related gene groups
- Cluster redundant annotation terms
- Visualize genes on BioCarta & KEGG pathway

Which DAVID tool to use?

- ++ 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 annotation 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 interesting 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?	+	+	+	+			++	

A Typical Analysis Flow

- Load Gene List
- View Summary Page
- Explore details through Chart Report, Table Report, Clustering Report, etc.
- Export and Save Results

DAVID: start

Analysis Wizard
DAVID Bioinformatics Resources 6.7, NIAID/NIH

Home Start Analysis Shortcut to DAVID Tools Technical Center Downloads & APIs Term of Service Why DAVID? About Us

Upload List Background

Upload Gene List

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

[Upload Help](#)

Step 1: Enter Gene List

A: Paste a list

Or

B: Choose From a File

No file selected.

Multi-List File 

Analysis Wizard

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

← Step 1. Submit your gene list through left panel.

An example:

Copy/paste IDs to "box A" -> Select Identifier as "Affy_ID" -> List Type as "Gene List" -> Click "Submit" button

```
1007_s_at
1053_at
117_at
121_at
1255_g_at
1294_at
1316_at
1320_at
1405_i_at
1431_at
1438_at
1487_at
1494_f_at
1598_g_at
```

DAVID: upload gene list

DAVID: Functional Annotation Tools - Windows Internet Explorer
http://david.abcc.ncifcrf.gov/tools.jsp

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DAVID: Functional Annotation Tools

Analysis Wizard
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*** The Gene Symbol mapping for list upload and conversion has changed. Please see the [DAVID forum announcement](#) for details.

Upload List Background

Upload Gene List

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

Step 1: Enter Gene List

A: Paste a list

31793_at
32073_at
32250_at
37166_at

Or

B: Choose From a File

Multi-List File

Analysis Wizard

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

Step 1. Submit your gene list through left panel.

An example:

Copy/paste IDs to "box A" -> Select Identifier as "Affy_ID" -> List Type as "Gene List" -> Click "Submit" button

1007_s_at
1053_at
117_at
121_at
1255_g_at
1294_at
1316_at
1320_at
1405_i_at
1431_at
1438_at
1487_at

DAVID: choose identifier

DAVID: Functional Annotation Tools - Windows Internet Explorer
http://david.abcc.ncifcrf.gov/tools.jsp

What's New Profile Mail Photos Calendar MSN Share Sign in

Google david Search Share Sidewiki Check Translate AutoFill > Sign In

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Step 1. Submit your gene list through next panel.

An example:

Copy/paste IDs to "box A" -> Select Identifier as "Affy_ID" -> List Type as "Gene List" -> Click "Submit" button

Box A content:
31793_at
32073_at
32250_at
37166_at

Or
B: Choose From a File
 Multi-List File ?

Step 2: Select Identifier

DAVID: check list type and submit

Analysis Wizard
DAVID Bioinformatics Resources 6.7, NIAID/NIH

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Upload List Background

Upload Gene List

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

[Upload Help](#)

Step 1: Enter Gene List

A: Paste a list

1431_at
1438_at
1487_at
1494_f_at
1598_g_at

Or

B: Choose From a File

No file selected.

Multi-List File 

Step 2: Select Identifier

AFFYMETRIX_3PRIME_IVT_ID

Step 3: List Type

Gene List
Background

Analysis Wizard

Tell us how you li
[Contact us for](#)

← Step 1. Submit your gene list through left panel.

An example:

Copy/paste IDs to "box A" -> Select Identifier as "Affy_ID" -> List Type as "Gene List" -> Click "Submit" button

1007_s_at
1053_at
117_at
121_at
1255_g_at
1294_at
1316_at
1320_at
1405_i_at
1431_at
1438_at
1487_at
1494_f_at
1598_g_at

24

DAVID: select species and check background

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http://david.abcc.ncifcrf.gov/tools.jsp

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DAVID: Functional Annotation Tools

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*** The Gene Symbol mapping for list upload and conversion has changed. Please see the [DAVID forum announcement](#) for details.

Upload List Background

Gene List Manager

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

- Use All Species -
Homo sapiens(90)

Select Species

List Manager Help

List_1

Select List to:
Use Rename
Remove Combine

Show Gene List

Analysis Wizard

Step 1. Successfully submitted gene list
Current Gene List: List_1
Current Background: Homo sapiens

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

↓

[Which DAVID tools to use?](#)

Functional Annotation Tool

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

Gene Functional Classification Tool

Gene ID Conversion Tool

Gene Name Batch Viewer

DAVID: Functional Annotation Result Summary - Windows Internet Explorer

http://david.abcc.ncifcrf.gov/summary.jsp

Windows Live david

Google david

DAVID: Functional Annotation Result Summary

DAVID: Functional Annotation Tool
DAVID Bioinformatics Resources 6.7, NIAID/NIH

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Upload List Background

Gene List Manager

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

- Use All Species -
Homo sapiens(90)

Select Species

List Manager [Help](#)

List_1

Select List to:

Annotation Summary Results

Current Gene List: List_1

Current Background: Homo sapiens

88 DAVID IDs

Check Defaults Clear All

Disease (1 selected)
Functional_Categories (3 selected)
Gene_Ontology (3 selected)
General Annotations (0 selected)
Literature (0 selected)
Main_Accessions (0 selected) 
Pathways (3 selected)
Protein_Domains (3 selected)
Protein_Interactions (0 selected)
Tissue_Expression (0 selected)

Combined View for Selected Annotation

Functional Annotation Clustering
Functional Annotation Chart
Functional Annotation Table

Click on symbols to expand

Individual views/reports:

Pay attention on which gene list, species and population background that the tool is being applied

The screenshot shows the DAVID Annotation Summary Results interface. On the left, the Gene List Manager panel displays a selected gene list 'demolist1' and its background species 'Homo sapiens'. The main panel shows annotation results for 171 DAVID IDs. A chart titled 'Pathways' shows the distribution of annotations across various databases. Below the chart, a section for 'Combined View for Selected Annotation' offers three options: Functional Annotation Clustering, Functional Annotation Chart, and Functional Annotation Table.

Annotation Category	Percentage	Count	Action
BBID	4%	7	Chart
BIOCARTA	11%	20	Chart
EC_NUMBER	19%	34	Chart
KEGG_COMPOUND	8%	15	Chart
KEGG_PATHWAY	33%	57	Chart
KEGG_REACTION	8%	15	Chart

1 View and select annotation categories of your interests .(7 of them is pre-selected as default)

3 Percentage, e.g. 7/171 (involved genes /total genes)

3 Genes from your list involved in this annotation category

3 Single Chart Report ONLY for this annotation categories

Combined views/reports:

4 Clustered or non-redundant chart report of annotation terms for ALL selected annotation categories above

4 Linear or redundant chart report of annotation terms for ALL selected annotation categories above

4 Table report for ALL selected annotation categories.

DAVID: Functional Annotation Result Summary - Windows Internet Explorer

http://david.abcc.ncifcrf.gov/summary.jsp

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DAVID: Functional Annotation Result Summary

DAVID: Functional Annotation Tool
DAVID Bioinformatics Resources 6.7, NIAID/NIH

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*** The Gene Symbol mapping for list upload and conversion has changed. Please see the [DAVID forum announcement](#) for details.

Upload List Background

Gene List Manager

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

- Use All Species -
Homo sapiens(90)

Select Species

List Manager Help

List_1

Select List to:
Use Rename
Remove Combine
Show Gene List

Annotation Summary Results

88 DAVID IDs [Help and Tool Manual](#)

Current Gene List: List_1
Current Background: Homo sapiens
Check Defaults Clear All

Disease (1 selected)
Functional_Categories (3 selected)
Gene_Ontology (3 selected)
General Annotations (0 selected)
Literature (0 selected)
Main_Accessions (0 selected)
Pathways (3 selected)

Click on button

<input checked="" type="checkbox"/>	BBID	4.5%	4
<input checked="" type="checkbox"/>	BIOCARTA	15.9%	14
<input type="checkbox"/>	EC_NUMBER	27.3%	24
<input checked="" type="checkbox"/>	KEGG_PATHWAY	40.9%	36
<input type="checkbox"/>	PANTHER_PATHWAY	28.4%	25
<input type="checkbox"/>	REACTOME_PATHWAY	19.3%	17

Protein_Domains (3 selected)
Protein_Interactions (0 selected)
Tissue_Expression (0 selected)

Combined View for Selected Annotation

Functional Annotation Clustering
Functional Annotation Chart
Functional Annotation Table

28

http://david.abcc.ncifcrf.gov/chartReport.jsp?annot=48



DAVID Bioinformatics Resources 6.7

National Institute of Allergy and Infectious Diseases (NIAID), NIH

*** The Gene Symbol mapping for list upload and conversion has changed. Please see the [DAVID forum announcement](#) for details.

Functional Annotation Chart

Current Gene List: List_1

Current Background: Homo sapiens

88 DAVID IDs

[Help and Manual](#)

Options

[Rerun Using Options](#)

[Create Sublist](#)

Click to see

4 chart records

[Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	Amyotrophic lateral sclerosis (ALS)	RT		4	4.5	5.5E-3	3.4E-1
<input type="checkbox"/>	KEGG_PATHWAY	Pathways in cancer	RT		7	8.0	2.3E-2	5.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	Neurotrophin signaling pathway	RT		4	4.5	5.3E-2	7.5E-1
<input type="checkbox"/>	KEGG_PATHWAY	Basal cell carcinoma	RT		3	3.4	5.4E-2	6.5E-1

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

Done

Internet | Protected Mode: On



100%

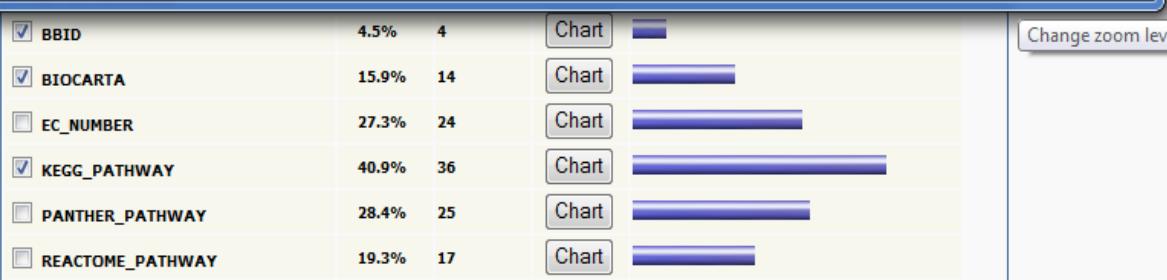
List_1

Select List to:

[Use](#) [Rename](#)

[Remove](#) [Combine](#)

[Show Gene List](#)



- Protein_Domains (3 selected)
- Protein_Interactions (0 selected)
- Tissue_Expression (0 selected)

Combined View for Selected Annotation

http://david.abcc.ncifcrf.gov/data/download/chart_9FB98EEEFA41271890552575.txt - Windows Internet Explorer

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Google Search Share Sidewiki ABC Check Translate AutoFill Sign In

Favorites Web Slice Gallery

http://david.abcc.ncifcrf.gov/data/download/ch... Page Safety Tools

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
KEGG_PATHWAY	hsa05014:Amyotrophic lateral sclerosis (ALS)	4	4.545454545454546	0.005530623231973121		1974_S_AT,38236				
KEGG_PATHWAY	hsa05200:Pathways in cancer	7	7.954545454545454	0.0227609456811958		1974_S_AT,33684_AT,1419_G_AT,20				
KEGG_PATHWAY	hsa04722:Neurotrophin signaling pathway	4	4.545454545454546	0.05259319101428395		1974_S_AT,33246_AT,1355				
KEGG_PATHWAY	hsa05217:Basal cell carcinoma	3	3.4090909090909087	0.0544506559749413		1974_S_AT,33684_AT,2090_I_AT				

Done Internet | Protected Mode: On

4 chart records

Download File

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
	KEGG_PATHWAY	Amyotrophic lateral sclerosis (ALS)	RT	■	4	4.5	5.5E-3	3.4E-1
	KEGG_PATHWAY	Pathways in cancer	RT	■	7	8.0	2.3E-2	5.8E-1
	KEGG_PATHWAY	Neurotrophin signaling pathway	RT	■	4	4.5	5.3E-2	7.5E-1
	KEGG_PATHWAY	Basal cell carcinoma	RT	■	3	3.4	5.4E-2	6.5E-1

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

Please cite [Nature Protocols 2009; 4\(1\):44](#) & [Genome Biology 2003; 4\(5\):P3](#) within any publication that makes use of any methods inspired by DAVID.

http://david.abcc.ncifcrf.gov/data/download/chart_9FB98EEEFA41271890552575.txt

Internet | Protected Mode: On



DAVID Bioinformatics Resources 6.7

National Institute of Allergy and Infectious Diseases (NIAID), NIH

** The Gene Symbol mapping for list upload and conversion has changed. Please see the [DAVID forum announcement](#) for details.

Functional Annotation Chart

[Help and Manual](#)**Current Gene List:** List_2**Current Background:** Homo sapiens**88 DAVID IDs****Options**[Rerun Using Options](#)[Create Sublist](#)

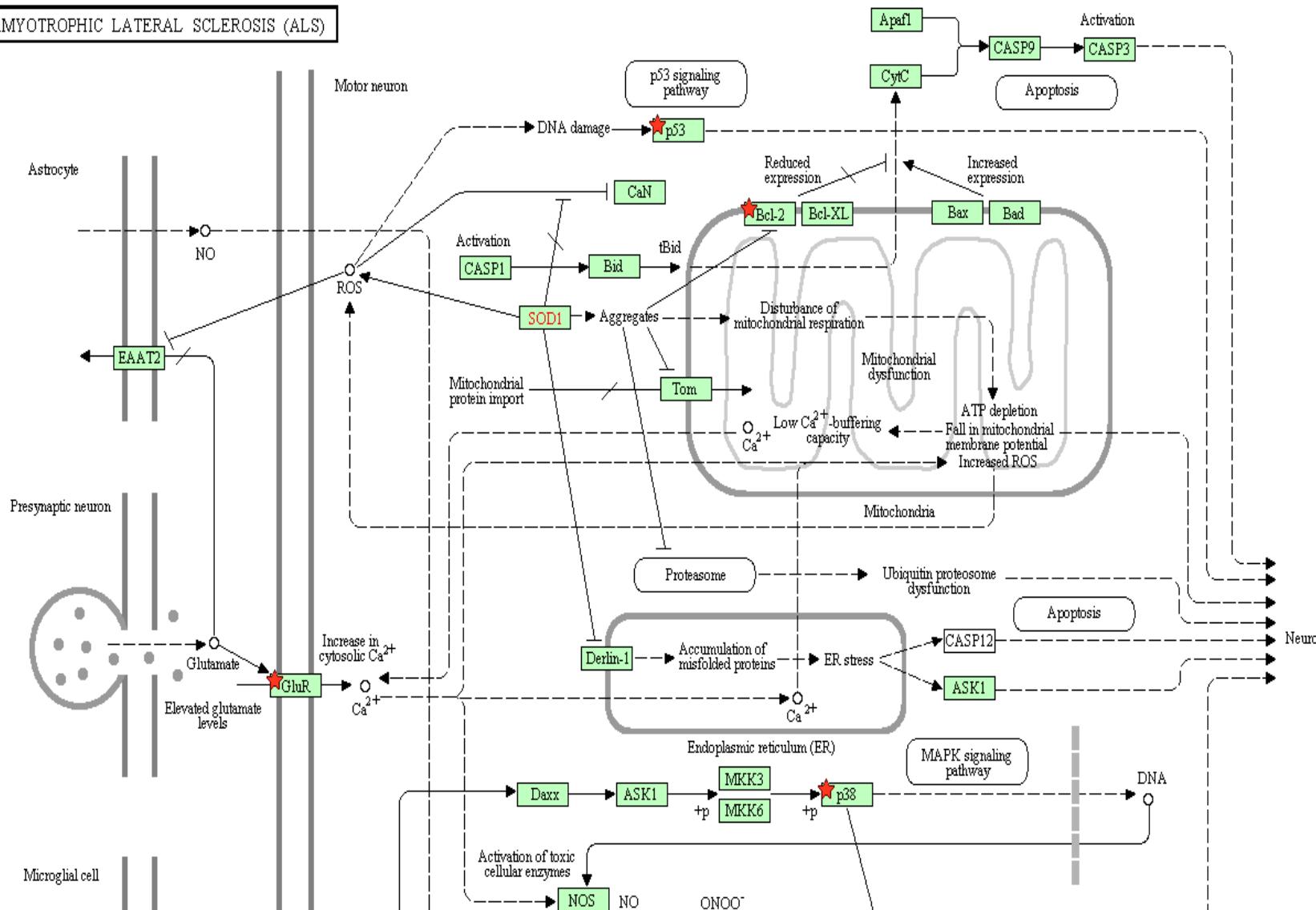
Click this
KEGG

4 chart records [Download](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	Amyotrophic lateral sclerosis (ALS)	RT		4	4.5	5.5E-3	3.4E-1
<input type="checkbox"/>	KEGG_PATHWAY	Pathways in cancer	RT		7	8.0	2.3E-2	5.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	Neurotrophin signaling pathway	RT		4	4.5	5.3E-2	7.5E-1
<input type="checkbox"/>	KEGG_PATHWAY	Basal cell carcinoma	RT		3	3.4	5.4E-2	6.5E-1



AMYOTROPHIC LATERAL SCLEROSIS (ALS)



DAVID: Functional Annotation Result Summary - Windows Internet Explorer

http://david.abcc.ncifcrf.gov/summary.jsp

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Favorites Web Slice Gallery

DAVID: Functional Annotation Result Summary

Functional Annotation Tool
DAVID Bioinformatics Resources 6.7, NIAID/NIH

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Upload List Background

Gene List Manager

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

- Use All Species -
Homo sapiens(90)

Select Species

List Manager Help

List_1

Select List to:

Annotation Summary Results

Current Gene List: List_1 88 DAVID IDs
 Current Background: Homo sapiens Check Defaults Clear All [Help and Tool Manual](#)

Click on bar

<input checked="" type="checkbox"/> BBID	4.5%	4	<input type="button" value="Chart"/>	
<input checked="" type="checkbox"/> BIOCARTA	15.9%	14	<input type="button" value="Chart"/>	
<input type="checkbox"/> EC_NUMBER	27.3%	24	<input type="button" value="Chart"/>	
<input checked="" type="checkbox"/> KEGG_PATHWAY	40.9%	36	<input type="button" value="Chart"/>	
<input type="checkbox"/> PANTHER_PATHWAY	28.4%	25	<input type="button" value="Chart"/>	
<input type="checkbox"/> REACTOME_PATHWAY	19.3%	17	<input type="button" value="Chart"/>	

Protein_Domains (3 selected)
 Protein_Interactions (0 selected)
 Tissue_Expression (0 selected)

Combined View for Selected Annotation



DAVID Bioinformatics Resources 6.7

National Institute of Allergy and Infectious Diseases (NIAID), NIH

** The Gene Symbol mapping for list upload and conversion has changed. Please see the [DAVID forum announcement](#) for details.

Functional Annotation Table

[Help and Manual](#)
Current Gene List: List_1

Current Background: Homo sapiens

88 DAVID IDs
36 record(s)
 [Download File](#)

37166_at	3-hydroxyanthranilate 3,4-dioxygenase	Related Genes	Homo sapiens
KEGG_PATHWAY	Tryptophan metabolism,		
34467_g_at	5-hydroxytryptamine (serotonin) receptor 4	Related Genes	Homo sapiens
KEGG_PATHWAY	Calcium signaling pathway, Neuroactive ligand-receptor interaction,		
40294_at	ATP-binding cassette, sub-family B (MDR/TAP), member 9	Related Genes	Homo sapiens
KEGG_PATHWAY	ABC transporters, Lysosome,		
1910_s_at	B-cell CLL/lymphoma 2	Related Genes	Homo sapiens
KEGG_PATHWAY	Apoptosis, Focal adhesion, Neurotrophin signaling pathway, Amyotrophic lateral sclerosis (ALS), Pathways in cancer, Colorectal cancer, Prostate cancer, Small cell lung cancer,		
967_g_at, 966_at	RAD54-like (S. cerevisiae)	Related Genes	Homo sapiens
KEGG_PATHWAY	Homologous recombination,		
39908_at	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	Related Genes	Homo sapiens
KEGG_PATHWAY	Basal transcription factors,		
40317_at	amiloride-sensitive cation channel 1, neuronal	Related Genes	Homo sapiens
KEGG_PATHWAY	Taste transduction,		
34636_at	arachidonate 15-lipoxygenase	Related Genes	Homo sapiens
KEGG_PATHWAY	Arachidonic acid metabolism, Linoleic acid metabolism,		
38201_at	branched chain aminotransferase 1, cytosolic	Related Genes	Homo sapiens
KEGG_PATHWAY	Valine, leucine and isoleucine degradation, Valine, leucine and isoleucine biosynthesis, Pantothenate and CoA biosynthesis,		
37172_at	carboxypeptidase B2 (plasma)	Related Genes	Homo sapiens
KEGG_PATHWAY	Complement and coagulation cascades,		
36703_at	chemokine (C-C motif) ligand 25	Related Genes	Homo sapiens
KEGG_PATHWAY	Cytokine-cytokine receptor interaction, Chemokine signaling pathway, Intestinal immune network for IgA production,		
1403_s_at	chemokine (C-C motif) ligand 5	Related Genes	Homo sapiens
KEGG_PATHWAY	Cytokine-cytokine receptor interaction, Chemokine signaling pathway, Toll-like receptor signaling pathway, NOD-like receptor signaling pathway, Cytosolic DNA-sensing pathway, Prion diseases, Epithelial cell signalling in Helicobacter pylori infection,		
37061_at	chitinase 1 (chitotriosidase)	Related Genes	Homo sapiens
KEGG_PATHWAY	Amino sugar and nucleotide sugar metabolism,		
32250_at	complement factor H	Related Genes	Homo sapiens
KEGG_PATHWAY	Complement and coagulation cascades,		
1391_s_at	cytochrome P450, family 4, subfamily A, polypeptide 11	Related Genes	Homo sapiens
KEGG_PATHWAY	Fatty acid metabolism, Arachidonic acid metabolism, Retinol metabolism, PPAR signaling pathway, Vascular smooth muscle contraction,		

Functional Annotation Table

The screenshot shows the DAVID Functional Annotation Tool running in Microsoft Internet Explorer. The title bar reads "DAVID: Functional Annotation Result Summary - Windows Internet Explorer". The address bar shows the URL "http://david.abcc.ncifcrf.gov/summary.jsp". The browser's toolbar includes links for Windows Live, Google, Favorites, and Web Slice Gallery.

The main content area features the DAVID logo and the text "Functional Annotation Tool" and "DAVID Bioinformatics Resources 6.7, NIAID/NIH". A banner at the top states: "*** The Gene Symbol mapping for list upload and conversion has changed. Please see the [DAVID forum announcement](#) for details."

The interface is divided into several sections:

- Gene List Manager:** Shows a dropdown menu set to "Homo sapiens(90)". Buttons include "Select Species", "List Manager", and "Help". A list box contains "List_1". Buttons for "Select List to:" include "Use", "Rename", "Remove", and "Combine". A "Show Gene List" button is also present.
- Annotation Summary Results:** Displays the current gene list ("List_1") and background ("Homo sapiens"). It lists 88 DAVID IDs and provides checkboxes for "Check Defaults" and "Clear All". A "Help and Tool Manual" link is available.
- Selected Annotations:** A list of selected categories: Disease (1 selected), Functional_Categories (3 selected), Gene_Ontology (3 selected), General_Annotations (0 selected), Literature (0 selected), Main_Accessions (0 selected), Pathways (3 selected), Protein_Domains (3 selected), Protein_Interactions (0 selected), and Tissue_Expression (0 selected).
- Combined View for Selected Annotation:** Buttons for "Functional Annotation Clustering", "Functional Annotation Chart", and "Functional Annotation Table". The "Functional Annotation Table" button is highlighted with a red oval.

Functional Annotation Table

Functional Annotation Table

[Help and Manual](#)

Current Gene List: [List_1](#)

Current Background: [Homo sapiens](#)

88 DAVID IDs

86 record(s)

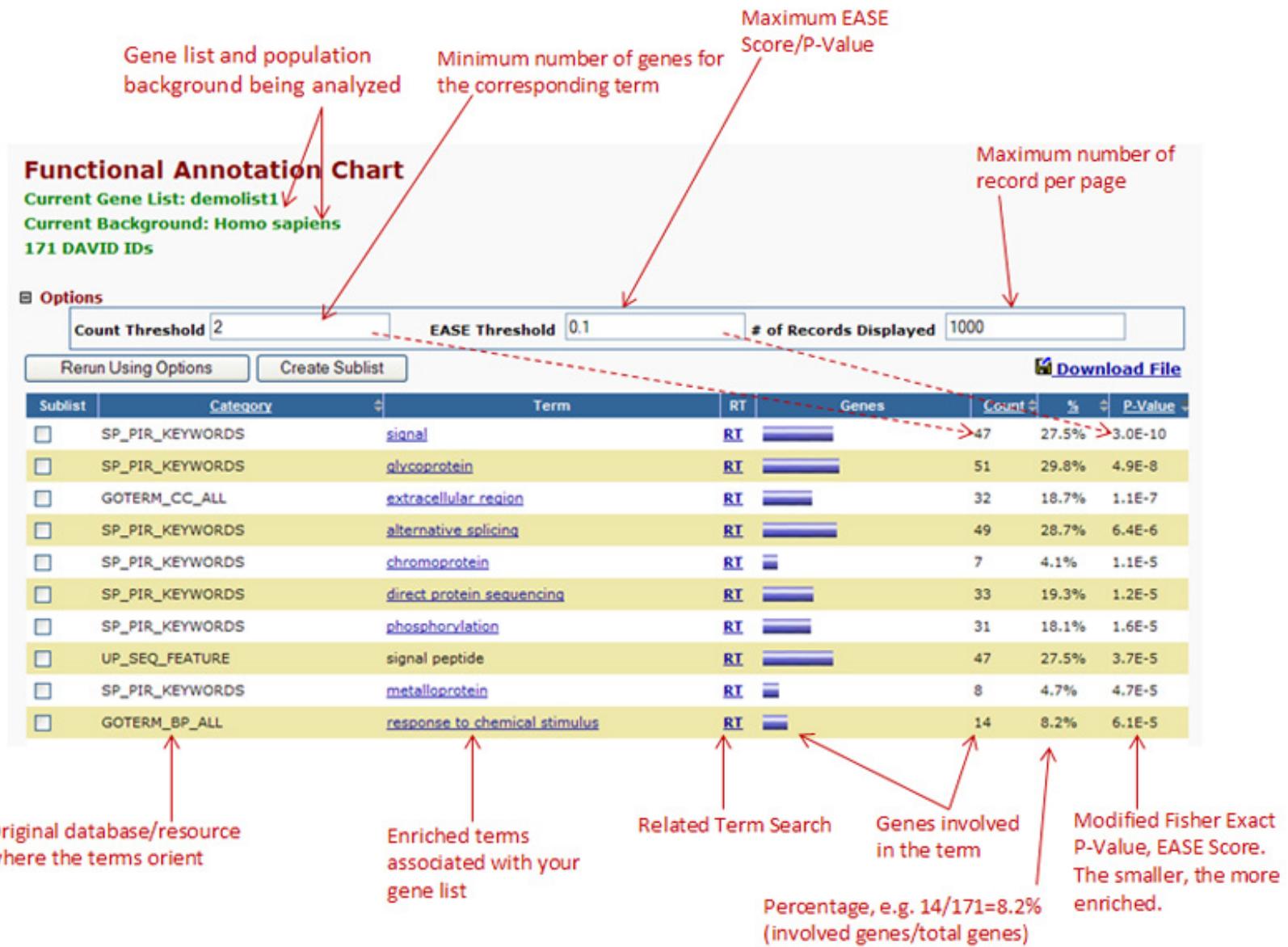
[Download File](#)

37166_at	3-hydroxyanthranilate 3,4-dioxygenase	Related Genes	Homo sapiens
GOTERM_BP_FAT	coenzyme metabolic process, oxidoreduction coenzyme metabolic process, vitamin metabolic process, water-soluble vitamin metabolic process, nicotinamide metabolic process, coenzyme biosynthetic process, vitamin biosynthetic process, nucleotide biosynthetic process, alkaloid metabolic process, response to inorganic substance, response to metal ion, response to zinc ion, organic acid biosynthetic process, pyridine nucleotide metabolic process, pyridine nucleotide biosynthetic process, NAD metabolic process, cellular homeostasis, secondary metabolic process, quinolinate biosynthetic process, nucleobase, nucleoside and nucleotide biosynthetic process, nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process, water-soluble vitamin biosynthetic process, homeostatic process, cellular amide metabolic process, dicarboxylic acid metabolic process, nitrogen compound biosynthetic process, carboxylic acid biosynthetic process, nicotinamide nucleotide metabolic process, response to cadmium ion, quinolinate metabolic process, cofactor metabolic process, cofactor biosynthetic process, oxidation reduction, anatomical structure homeostasis, neuron maintenance,		
GOTERM_CC_FAT	cell fraction, soluble fraction, mitochondrion, mitochondrial envelope, cytosol, organelle membrane, mitochondrial membrane, organelle envelope, envelope, mitochondrial part,		
GOTERM_MF_FAT	3-hydroxyanthranilate 3,4-dioxygenase activity, iron ion binding, ferrous iron binding, electron carrier activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, oxygen binding, ion binding, cation binding, metal ion binding, transition metal ion binding,		
INTERPRO	3-hydroxyanthranilic acid dioxygenase, 3-hydroxyanthranilate 3, 4-dioxygenase, metazoan,		
KEGG_PATHWAY	Tryptophan metabolism,		
PIR_SUPERFAMILY	PIRSF017681:3-hydroxyanthranilate 3,4-dioxygenase, animal type, PIRSF017681:3hydroanth_dOase_animal,		
SP_PIR_KEYWORDS	3d-structure, alternative splicing, complete proteome, cytoplasm, dioxygenase, iron, metal-binding, oxidoreductase, polymorphism, pyridine nucleotide biosynthesis,		
UP_SEQ_FEATURE	binding site:Dioxygen, binding site:Substrate, chain:3-hydroxyanthranilate 3,4-dioxygenase, helix, metal ion-binding site:Iron; catalytic, sequence variant, splice variant, strand, turn,		
34467_g_at	5-hydroxytryptamine (serotonin) receptor 4	Related Genes	Homo sapiens
GOTERM_BP_FAT	cell surface receptor linked signal transduction, G-protein coupled receptor protein signaling pathway, G-protein signaling, coupled to G-protein coupled receptor, intracellular signaling cascade, second messenger-mediated signaling, G-protein mediated,		

Table Report is a gene-centric view which lists the genes and their associated annotation terms (selected only). There is no statistics applied in this report.

Functional Annotation chart

The screenshot shows the DAVID Functional Annotation Tool interface running in Microsoft Internet Explorer. The title bar reads "DAVID: Functional Annotation Result Summary - Windows Internet Explorer". The address bar shows the URL "http://david.abcc.ncifcrf.gov/summary.jsp". The main content area displays the "Functional Annotation Tool" interface. On the left, there is a "Gene List Manager" panel with sections for "Species Selection" (set to "Homo sapiens(90)"), "List Manager" (containing "List_1"), and "Annotations" (with buttons for "Use", "Rename", "Remove", "Combine", and "Show Gene List"). On the right, the "Annotation Summary Results" section shows "88 DAVID IDs" and a list of selected categories: Disease (1 selected), Functional_Categories (3 selected), Gene_Ontology (3 selected), General Annotations (0 selected), Literature (0 selected), Main_Accessions (0 selected), Pathways (3 selected), Protein_Domains (3 selected), Protein_Interactions (0 selected), and Tissue_Expression (0 selected). Below this is a "Combined View for Selected Annotation" section with three buttons: "Functional Annotation Clustering", "Functional Annotation Chart" (which is highlighted with a red oval), and "Functional Annotation Table". A "Help and Tool Manual" link is also present in this section.



Functional Annotation Clustering

The screenshot shows a Microsoft Internet Explorer window displaying the DAVID Functional Annotation Tool. The title bar reads "DAVID: Functional Annotation Result Summary - Windows Internet Explorer". The address bar shows the URL "http://david.abcc.ncifcrf.gov/summary.jsp". The main content area displays the "Functional Annotation Tool" interface.

Functional Annotation Tool
DAVID Bioinformatics Resources 6.7, NIAID/NIH

Gene List Manager

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

- Use All Species -
Homo sapiens(90)

Select Species

List Manager Help

List_1

Select List to:
Use Rename
Remove Combine
Show Gene List

Annotation Summary Results

[Help and Tool Manual](#)

Current Gene List: List_1

Current Background: Homo sapiens

88 DAVID IDs

Check Defaults **Clear All**

Selected Annotations:

- Disease (1 selected)
- Functional_Categories (3 selected)
- Gene_Ontology (3 selected)
- General_Annotations (0 selected)
- Literature (0 selected)
- Main_Accessions (0 selected)
- Pathways (3 selected)
- Protein_Domains (3 selected)
- Protein_Interactions (0 selected)
- Tissue_Expression (0 selected)

Combined View for Selected Annotation

Functional Annotation Clustering **(circled)**

Functional Annotation Chart
Functional Annotation Table

Functional Annotation Clustering

Current Gene List: demolist1
171 DAVID IDs

Options		Classification Stringency	High	Annotation Cluster 1		Enrichment Score: 3.69	Annotation Cluster 2		Enrichment Score: 3.52	Annotation Cluster 3		Enrichment Score: 2.66	Annotation Cluster 4		Enrichment Score: 2.63
				Rerun using options	Create Sublist		RT	RT	RT	RT	RT	RT	RT	RT	RT
<input type="checkbox"/>	SP_PIR_KEYWORDS	chromoprotein													
<input type="checkbox"/>	SP_PIR_KEYWORDS	metalloprotein													
<input type="checkbox"/>	SP_PIR_KEYWORDS	iron													
<input type="checkbox"/>	GOTERM_MF_ALL	iron ion binding													
<input type="checkbox"/>	SP_PIR_KEYWORDS	heme													
<input type="checkbox"/>	GOTERM_MF_ALL	tetrapyrrole binding													
<input type="checkbox"/>	GOTERM_MF_ALL	heme binding													

The overall enrichment score for the group based on the EASE scores of each term members. The higher, the more enriched.

Related Term Search

Genes involved in individual term

ALL genes involved in this annotation cluster

EASE Score, the modified Fisher Exact P-Value. They are identical to that in the Chart Report. The smaller, the more enriched.

Gene list being analyzed

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

Summary

- Pathways analysis
 - Quickly understand the biological context for a list of genes
- Public resources
 - Growing rapidly
 - Ability to “paint” diagrams
- DAVID Bioinformatics
 - Powerful resource to map genes to many resources