

Gene set enrichment – DAVID and KEGG

<http://david.abcc.ncifcrf.gov/> Use microarray dataset file provided

Start analysis

DAVID Bioinformatics Resources 2008
National Institute of Allergy and Infectious Diseases (NIAID), NIH

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Shortcut to DAVID Tools

Functional Annotation
Annotation enrichment analysis, 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](#)

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

Welcome to DAVID Bioinformatics Resources 2003 - 2009

The Database for Annotation, Visualization and Integrated Discovery (DAVID) 2008 is the sixth version of our original web-accessible programs. DAVID now provides a comprehensive set of functional annotation tools for investigators to understand biological meaning behind large list of genes. For any given gene list, DAVID tools are able to:

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

What's Important in DAVID 2008?

- New requirement to 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 per year
Based on Google Scholar
Updated in Jan 2009

Year	Citations
2003	8
2004	40
2005	99
2006	149
2007	246
2008	285

Screen Shot 1 Screen Shot 2 Screen Shot 3

Analysis Wizard
DAVID Bioinformatics Resources 2008, NIAID/NIH

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Upload List Background

Upload Gene List

Demolist 1 Demolist 2
[Upload Help](#)

Step 1: Submit your gene list through left panel.

A: Paste a list
Note: Affy Exon IDs and Affy Gene IDs are supported. ["affy_id" type](#)

An example:
1446550_at
1435000_at
1455721_at

B: Choose From a File
Choose File no file selected

Step 2: Select Background Identifier
AFFY_ID

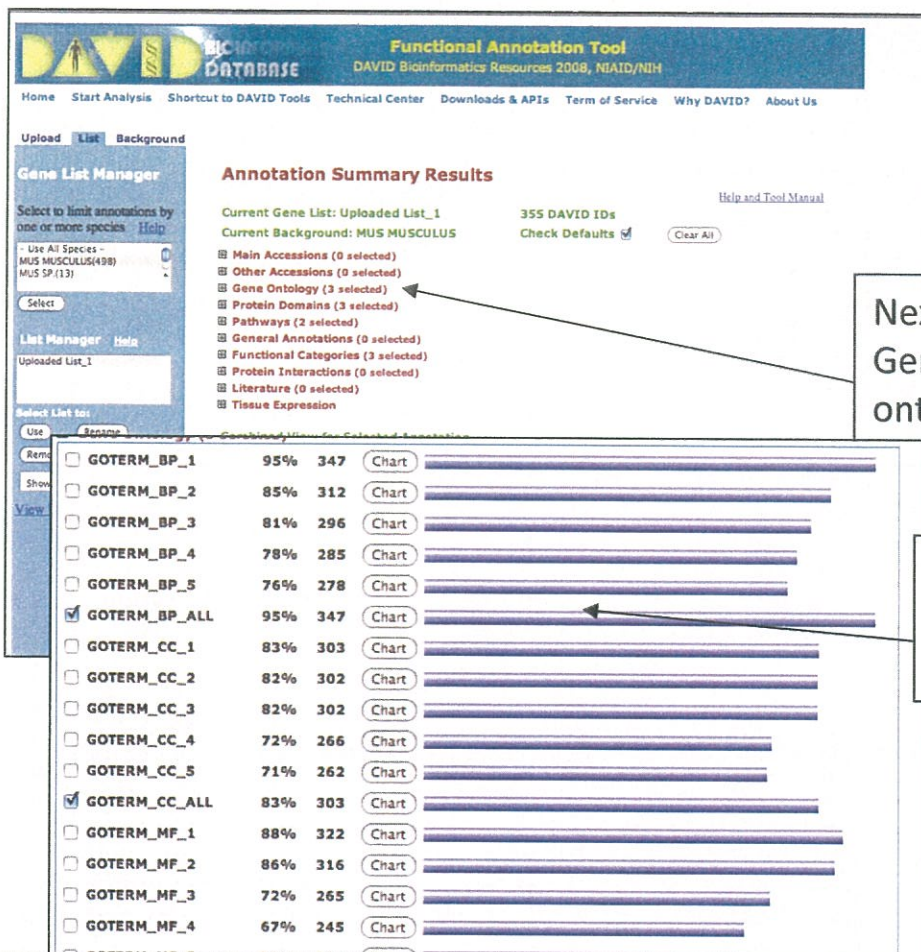
Step 3: Select Identifier
box A

Step 4: Submit List
Submit List

Upload gene list

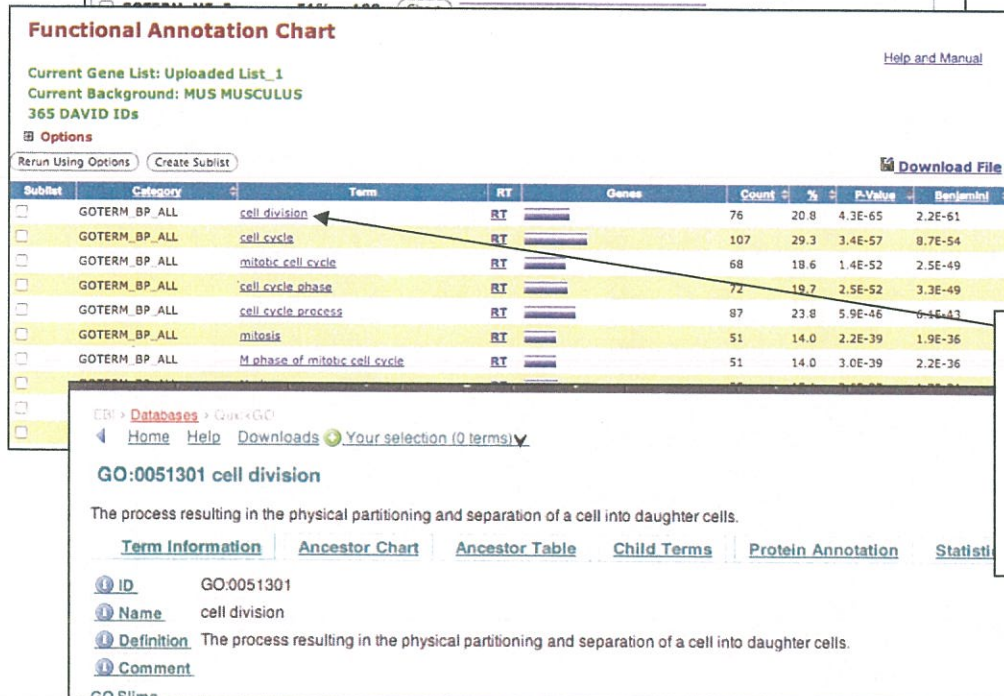
Choose Identifiers

Choose gene list or background



Next view
Gene
ontologies

View "All
Biological
processes"



Click term of
interest to
view more
details in GO
database

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Upload List Background

Gene List Manager

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

Use All Species - MUS MUSCULUS(498) MUS SP(13)

Select

List Manager [Help](#)

Uploaded List_1

Select List for:

Use Rename Remove Combine Show Gene List [new!](#) View Unmapped IDs

Annotation Summary Results

Current Gene List: Uploaded List_1 355 DAVID IDs
Current Background: MUS MUSCULUS Check Defaults [Clear All](#)

[Help and Tool Manual](#)

- Main Accessions (0 selected)
- Other Accessions (0 selected)
- Gene Ontology (3 selected)
- Protein Domains (3 selected)
- Pathways (2 selected)
- General Annotations (0 selected)
- Functional Categories (3 selected)
- Protein Interactions (0 selected)
- Literature (0 selected)
- Tissue Expression

Combined View for Selected Annotation

Functional Annotation Clustering [new!](#)

Functional Annotation Chart

Functional Annotation Table

Next view
KEGG
pathways

Functional Annotation Chart

Current Gene List: Uploaded List_1
Current Background: MUS MUSCULUS
365 DAVID IDs

[Help and Manual](#)

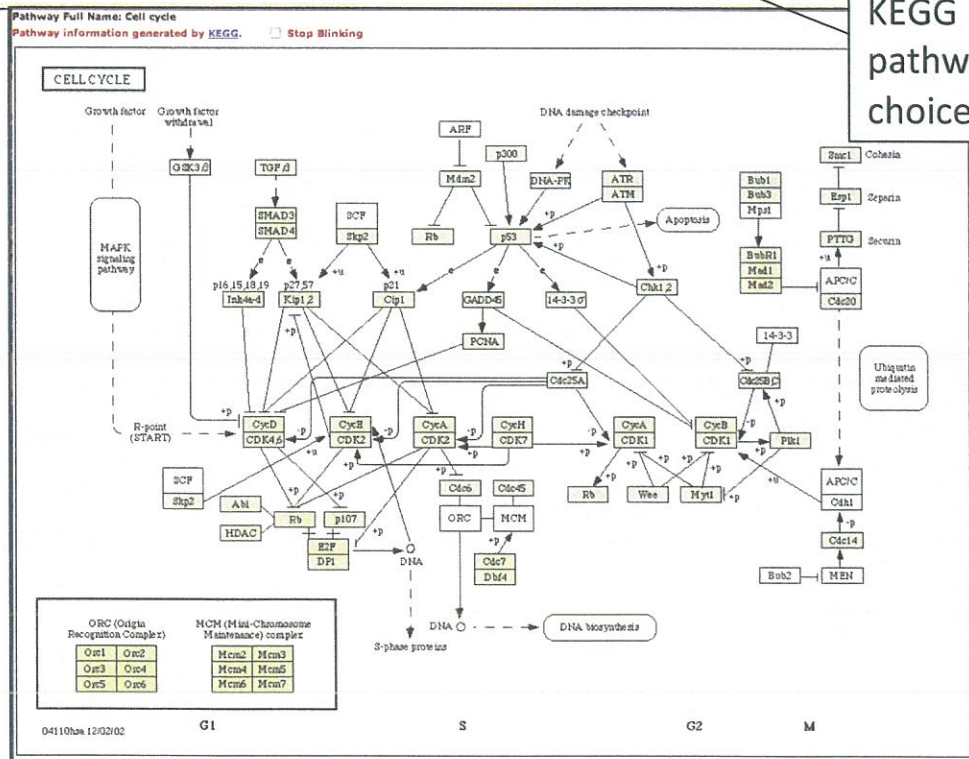
Options

Rerun Using Options Create Sublist

[Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	KEGG PATHWAY	Cell cycle	RT		21	5.8	3.6E-10	7.0E-8
<input type="checkbox"/>	KEGG PATHWAY	Nicotinate and nicotinamide metabolism	RT		8	2.2	3.8E-6	3.7E-4
<input type="checkbox"/>	KEGG PATHWAY	Pantothenate and CoA biosynthesis	RT		5	1.4	1.9E-3	1.1E-1
<input type="checkbox"/>	KEGG PATHWAY	Valine, leucine and isoleucine degradation	RT		7	1.9	2.8E-3	1.3E-1
<input type="checkbox"/>	KEGG PATHWAY	Long-term potentiation	RT		8	2.2	5.4E-3	
<input type="checkbox"/>	KEGG PATHWAY	Bisphenol A degradation	RT		4	1.1	1.6E-2	
<input type="checkbox"/>	KEGG PATHWAY	Riboflavin metabolism	RT		4	1.1	2.2E-2	

Click to view
KEGG
pathway of
choice



Coloring pathways in KEGG

http://www.genome.jp/kegg/tool/color_pathway.html

Search against: Mus musculus (mouse)

Enter objects one per line followed by bgcolor, fgcolor:

```
Ccnb1-rs1 /// Ccnb1 green
Ccnb1 green
Ccnb1 green
Cdc37l1 green
Gspt1 green
Gspt1 green
Gspt1 green
Gspt2 green
```

(Examples for Reference pathway (KO))
K01803 red,blue
C00118 pink
1.2.1.12

(Examples for Homo sapiens (Hs))
7167 red,blue
C00118 pink
1.2.1.12

Alternatively, enter the file name containing the data:
Choose File no file selected

Default bgcolor: white

Genes bgcolor: white (to change the default color of blue or green)

☐ Display objects NOT found in the search

Exec **Clear**

[Feedback | KEGG2 | KEGG1]

Choose organism

Input gene list (not probe list) from WE file and color to represent fold change (note: color is written in lower case)

Default and genes color to be white

Execute

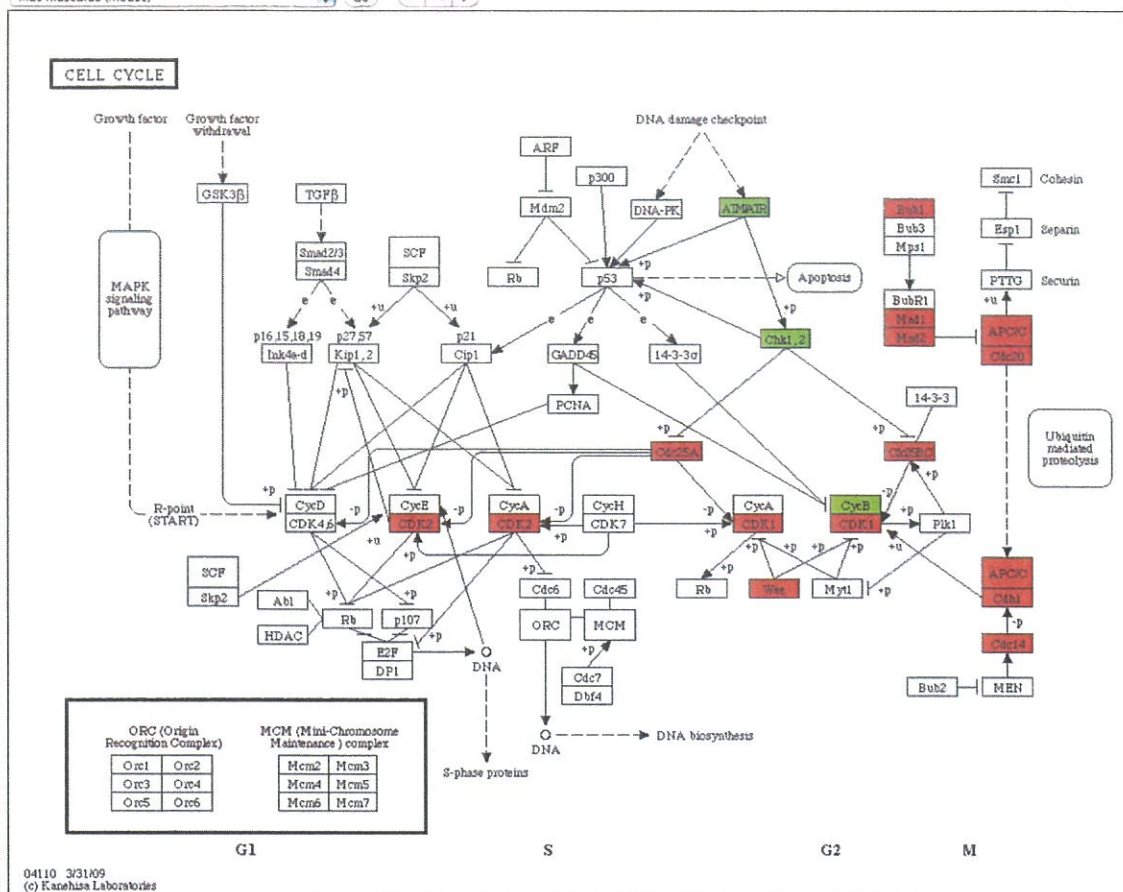
Pathway Search Result

mmu04110 Cell cycle - Mus musculus (mouse)

mmu04110 Anapc11; anaphase promoting complex subunit 11; K03358 anaphase-promoting complex component APC11
mmu04110 Anapc5; anaphase promoting complex subunit 5; K03352 anaphase-promoting complex component APC5
mmu04110 Anapc7; anaphase promoting complex subunit 7; K03354 anaphase-promoting complex component APC7
mmu04110 Atm; ataxia telangiectasia mutated homolog (human) (EC:2.7.11.1); K04728 ataxia telangiectasia mutated homolog (human) (EC:2.7.11.1)
mmu04110 Bub1; budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae) (EC:2.7.11.1)
mmu04110 Ccnb1; cyclin B1; K05868 cyclin B
mmu04110 Cdc14a; CDC14 cell division cycle 14 homolog A (S. cerevisiae) (EC:3.1.3.16 3.1.3.16)
mmu04110 Cdc20; cell division cycle 20 homolog (S. cerevisiae); K03363 cell division cycle 20 homolog (S. cerevisiae) (EC:3.1.3.16 3.1.3.16)
mmu04110 Cdc23; CDC23 (cell division cycle 23, yeast, homolog); K03355 anaphase-promoting complex component APC23
mmu04110 Cdc25a; cell division cycle 25 homolog A (S. pombe) (EC:3.1.3.48); K06645 cell division cycle 25 homolog A (S. pombe) (EC:3.1.3.48)
mmu04110 Cdc25b; cell division cycle 25 homolog B (S. pombe) (EC:3.1.3.48); K05867 cell division cycle 25 homolog B (S. pombe) (EC:3.1.3.48)
mmu04110 Cdc25c; cell division cycle 25 homolog C (S. pombe) (EC:3.1.3.48); K05867 cell division cycle 25 homolog C (S. pombe) (EC:3.1.3.48)
mmu04110 Cdc26; cell division cycle 26; K03359 anaphase-promoting complex component APC12
mmu04110 Cdc27; cell division cycle 27 homolog (S. cerevisiae); K03350 anaphase-promoting complex component APC27
mmu04110 Cdc28a; cell division cycle 28 homolog A (S. pombe) (EC:2.7.11.22); K04927 cell division cycle 28 homolog A (S. pombe) (EC:2.7.11.22)
mmu04110 Cdk2; cyclin-dependent kinase 2 (EC:2.7.11.22); K02206 cyclin-dependent kinase 2 (EC:2.7.11.22)
mmu04110 Cke1; checkpoint kinase 1 homolog (S. pombe) (EC:2.7.11.1); K02216 serine/threonine kinase 1 (EC:2.7.11.1)
mmu04110 Fzr1; fizzy/cell division cycle 20 related 1 (Drosophila); K03364 cell division cycle 20 related 1 (Drosophila) (EC:3.1.3.16 3.1.3.16)
mmu04110 Mad1l1; mitotic arrest deficient 1-like 1; K06638 mitotic spindle assembly checkpoint protein 1 (EC:3.1.3.16)
mmu04110 Mad2l2; MAD2 mitotic arrest deficient-like 2 (yeast); K02537 mitotic spindle assembly checkpoint protein 2 (EC:3.1.3.16)
mmu04110 Wee1; WEE1 homolog 1 (S. pombe) (EC:2.7.10.2); K06632 wee1-like protein kinase (EC:2.7.10.2)

Summary of pathways, similar to DAVID result. No significance calculated, just pathways that your genes of interest are in.

Click pathway to view with colors.



Remember: DAVID provides the significance, KEGG provides the pretty picture!

Tasks

Using the task example gene list

- How many DAVID IDs are there?
- What are the most significant GO terms
 - How do the different levels of GO terms affect the results
- What are the most significant KEGG pathways?
- Can you color these pathways using KEGG?

