A Quick Tutorial/An Example to Use the DAVID Bioinformatics Resources

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Step 1: Start Analysis Wizard

Welcome to DAVID Bioinformatic Resources

The Database for Annotation, Visualization and Integrated Discovery (DAVID) 2006 is an expanded version of our original web-accessible programs of DAVID 2.1, 2.0 & 1.0. DAVID 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
- Visualize genes on BioCarta & KEGG pathway maps
- 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

What's New in DAVID 2006?
- Functional Annotation Clustering
- Pre-built Affy gene backgrounds
- User's customized gene background
- Updated annotation databases
- Enhanced calculating speed

DAVID Bioinformatic Forum

- Technical notes & help
- Ask questions & get answers
- Share experiences
- Comments and feedback
- Bug report

Statistics About DAVID
Step 2: Submit gene list or use built-in demo lists
Step 3: Select one of the DAVID Tools
For example, Gene Functional Classification Tool
Step 4. View and explore results of gene functional groups
Step 5. Get back to analysis center for other DAVID tools for the same gene list.
Step 6: Now choose another DAVID Tool
For example, Functional Annotation Tool
Step 8. View and explore results of annotation cluster
Step 9: Gene back to the analysis wizard and select next DAVID tool