

Gene list analysis

Typical output from a gene expression experiment: a list with up- and down-regulated genes

- How to make sense of this list?
- Tools or PubMed search?

Case study: Duchenne Muscular Dystrophy

- Expression profiling of skeletal muscle
- Gene annotation:
 - Inflammatory response
 - Extracellular matrix (ECM) remodelling
 - Muscular regeneration
 - Energy metabolism
 - Morphogenic signaling-Wnt pathway
 - Notch pathway
 - Bone Morphogenetic Protein pathway

FASEB J. 2007 Apr;21(4):1210-26. Epub 2007 Jan 30.

Gene expression profiling in the early phases of DMD: a constant molecular signature characterizes DMD muscle from early postnatal life throughout disease progression.

Pescatori M, Broccolini A, Minetti C, Bertini E, Bruno C, D'amico A, Bernardini C, Mirabella M, Silvestri G, Giglio V, Modoni A, Pedemonte M, Tasca G, Galluzzi G, Mercuri E, Tonali PA, Ricci E.

DAVID web tool

- Database for Annotation, Visualization and Integrated Discovery
- Example analyses:
 - Gene-annotation enrichment analysis
 - Gene ID conversion



Nature Protocols **4**, 44 - 57 (2008)

Published online: 18 December 2008 | doi:10.1038/nprot.2008.211

Subject Category: [Computational and theoretical biology](#)

Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources

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Summary results

Upload **List** Background

Gene List Manager

Select to limit annotations by one or more species

[Help](#)

- Use All Species -
Homo sapiens(106)

Select Species

List Manager [Help](#)

List_1

Select List to:

Use

Rename

Remove

Combine

Show Gene List

Annotation Summary Results

Current Gene List: List_1

Current Background: Human Genome U133A Array

91 DAVID IDs
Check Defaults



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

Red annotation categories denote DAVID defined defaults

Combined View for Selected Annotation

Functional Annotation Clustering

Functional Annotation Chart

Functional Annotation Table

Annotation results

Functional Annotation Chart

[Help and Manual](#)

Current Gene List: List_1

Current Background: Human Genome U133A Array

91 DAVID IDs

Options

Thresholds: Count EASE









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

Rerun Using Options

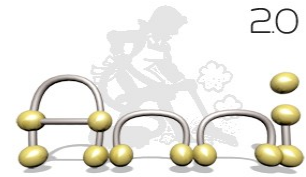
Create Sublist

 [Download File](#)

106 chart records

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_ALL	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	RT		7	7.7	1.9E-9	1.7E-6
<input type="checkbox"/>	GOTERM_BP_ALL	immunoglobulin mediated immune response	RT		8	8.8	1.9E-7	8.8E-5
<input type="checkbox"/>	GOTERM_BP_ALL	B cell mediated immunity	RT		8	8.8	2.2E-7	6.7E-5
<input type="checkbox"/>	GOTERM_BP_ALL	lymphocyte mediated immunity	RT		8	8.8	1.0E-6	2.3E-4
<input type="checkbox"/>	GOTERM_BP_ALL	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	RT		8	8.8	2.0E-6	3.7E-4
<input type="checkbox"/>	GOTERM_BP_ALL	adaptive immune response	RT		8	8.8	2.0E-6	3.7E-4
<input type="checkbox"/>	GOTERM_BP_ALL	collagen fibril organization	RT		6	6.6	2.3E-6	3.5E-4
<input type="checkbox"/>	GOTERM_BP_ALL	inflammatory response	RT		13	14.3	3.5E-6	4.7E-4

Anni Java Web Start tool



- Interface to concept profiles
- Example analysis:
 - Gene-annotation enrichment analysis
 - Gene ID conversion


Genome Biology
IMPACT FACTOR 9.04

Search for

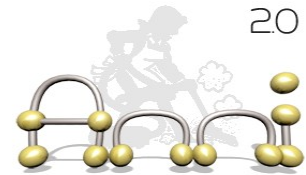
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Software Highly accessed Open Access

Anni 2.0: a multipurpose text-mining tool for the life sciences

Rob Jelier¹, Martijn J Schuemie^{1*}, Antoine Veldhoven¹, Lambert CJ Dorssers², Guido Jenster³ and Jan A Kors¹



Gene import results

Anni 2.1 - Copyright 2006-2009 Medical Informatics, Erasmus MC

File Concept sets Help

Erasmus MC

Explorer

- User concept sets
 - New concept set (95)
- Predefined concept sets

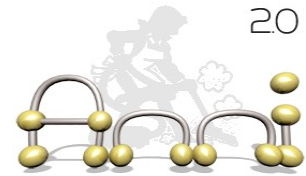
New concept set (95)

Concept set

Default view Relational view

Concept	Has profile	ID	column 1
HLA-DPB1	<input checked="" type="checkbox"/>	3000425	3115
HLA-DRB3	<input checked="" type="checkbox"/>	3000429	3125
HLA-DRB4	<input checked="" type="checkbox"/>	3000430	3126
IFI16	<input checked="" type="checkbox"/>	3000484	3428
MYL5	<input checked="" type="checkbox"/>	3000692	4636
TMSB10	<input checked="" type="checkbox"/>	3001202	9168
PRUNE2	<input checked="" type="checkbox"/>	3002863	158471
ANXA2P3	<input type="checkbox"/>	3076815	305
EEF1AL3	<input type="checkbox"/>	3077074	158078
PPIAL3	<input type="checkbox"/>	3077686	653214
HLA-DRB1	<input checked="" type="checkbox"/>	3079832	3126
EMP3	<input checked="" type="checkbox"/>	3087459	2014
HLA-DRB1	<input checked="" type="checkbox"/>	3087622	3123
ACTC1	<input checked="" type="checkbox"/>	3087834	70
LRRC17	<input type="checkbox"/>	3087859	10234
HLA-DMA	<input checked="" type="checkbox"/>	3088106	3108
CHRNA1	<input checked="" type="checkbox"/>	3088162	1134
VCAM1	<input checked="" type="checkbox"/>	3088183	7412
VAMP8	<input checked="" type="checkbox"/>	3088232	8673

Annotation results



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File Concept sets Help

Filter: None

Include Exclude

Erasmus MC

Explorer

- User concept sets
 - New concept set (95)
 - Biological Process matched against New concept set
- Predefined concept sets
 - Chemicals
 - Filters
 - Genes
 - GO
 - Biological Process (7689)
 - Cellular Component
 - Molecular Function
 - Semantic Groups
 - Toxic Effect (RTECS & IARC)

New concept set (95) Biological Process matched against New concept set

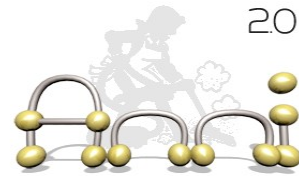
Matched concept sets

Matrix Relational view List Cluster matched concept set

Highlight co-occurrence below: 1

Concept	Sum	HLA-DPB1	HLA-DRB3	HLA-DRB4	IF16
major histocompatibility complex location	1.0299	0.0544	0.0271	0.0466	0.0039
collagen biosynthetic process	0.8675	0.0053	0.0017	0.0032	0.0022
Antigen Presentation	0.8286	0.0337	0.0166	0.0249	0.0035
Cell Adhesion	0.8123	0.0053	0.0028	0.0038	0.004
Complement Activation	0.8052	0.0044	0.0019	0.0048	0.0023
Cell Movement	0.7798	0.0057	0.0024	0.0041	0.0034
Chondrogenesis	0.7406	0.0039	0.0012	0.0025	0.0045
collagen catabolic process	0.6983	0.0033	0.0011	0.0018	0.0014
osteoblast differentiation	0.6961	0.0029	0.001	0.0021	0.0066
tissue remodeling	0.6955	0.0027	0.0011	0.0018	0.0026
Transcriptional Activation	0.6738	0.0043	0.0021	0.0036	0.0112
cell-matrix junction	0.6725	0.0042	0.002	0.0029	0.0026
epithelial to mesenchymal transition	0.6713	0.003	0.0011	0.002	0.0041
chondrocyte differentiation	0.6694	0.0022	0.0006	0.0013	0.008
classical pathway complement activation	0.6675	0.0029	0.0016	0.0049	0.0012
Osteogenesis	0.6643	0.005	0.002	0.004	0.0033
tumor suppressor activity	0.6506	0.0057	0.0024	0.004	0.0234
Angiogenesis	0.6493	0.0049	0.0018	0.0032	0.0047

Advanced: Web services



DAVID Web Service

[Comments and Suggestions!](#)

DAVID [web service](#) allows users to programmatically (Java, Perl, Python, etc) interact with the DAVID to automate user tasks. It is an enhancement and extension of current url-based [DAVID API](#) with more control and less limitations for users. To begin to use please [register](#) and download the client code. For license information, check our [license](#) page.

Service EPR : <http://david.abcc.ncifcrf.gov/webservice/services/DAVIDWebService>

The screenshot shows the BioCatalogue interface for the ConceptRecognizerService. The page includes a search bar, navigation links (Home, Services, Register a Service, Providers), and a breadcrumb trail (Home » Services » ConceptRecognizerService). The service details section shows the name 'ConceptRecognizerService' with a SOAP icon, and alternative names: 'ConceptProfileMiningWS', 'conceptprofile', and 'Anni'. The category is 'Named Entity Recognition'. There are 1452 views and 1 star rating. The provider is 'ws-biosemanatics-org'. The page also features a 'Members Responsible for this Service (1)' section.

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