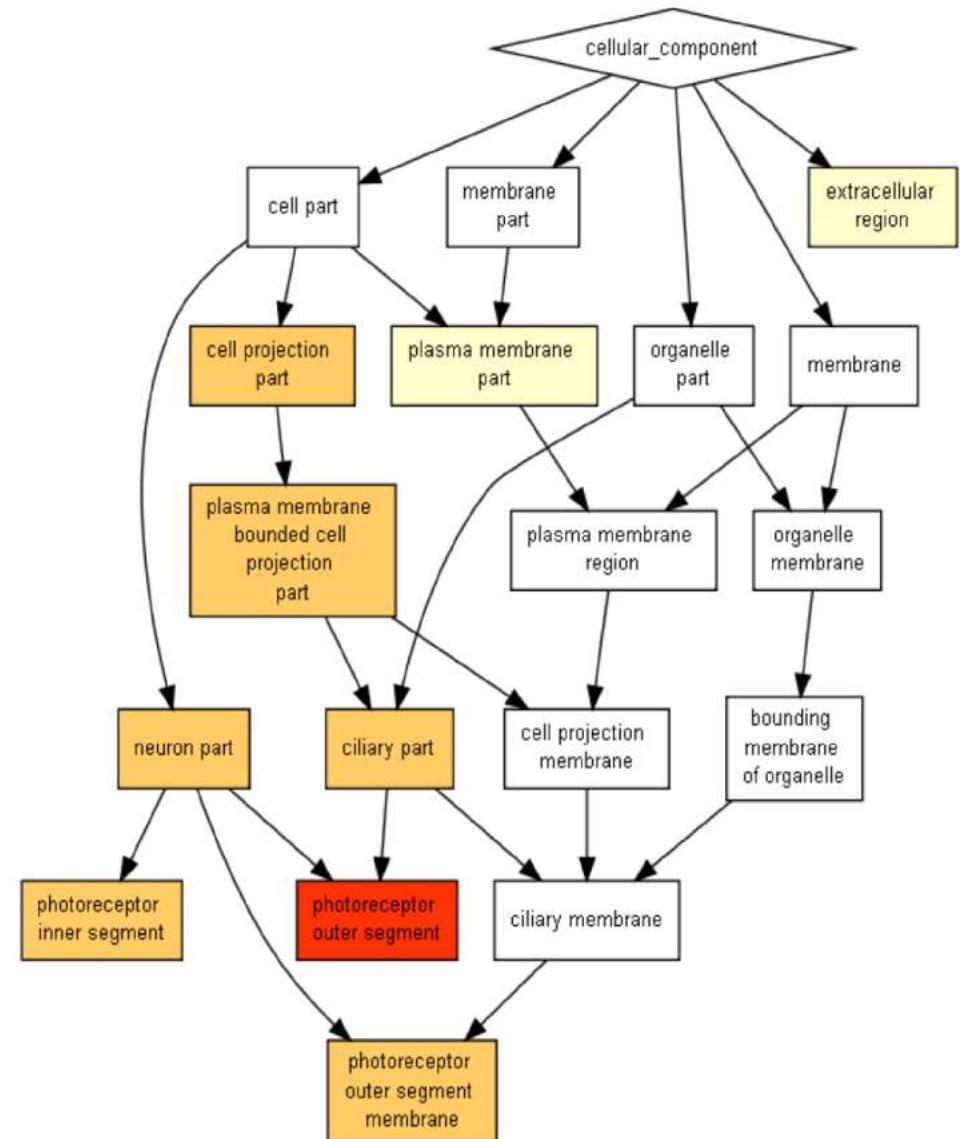


Gene Set Enrichment analysis

- It can be hard to interpret all differentially expressed genes one by one (too many DEGs);
- You often want to get bigger picture of what is changing in transcriptomes (which pathways or categories of genes are changing);
- You may want to ask specific questions about particular groups/categories of genes;
- You may want to check if the list of genes you have is completely random or reflects some biology;
- Common approach is an identification of predefined sets of genes that are over-represented among genes of interest (e.g. differentially expressed genes) – **gene set enrichment analysis (or functional enrichment analysis)**;

Gene Ontology - ontologies

- GO is a collection of controlled hierarchical vocabularies of defined terms representing gene properties;
- GO is structured as a directed acyclic graph where each term has defined relationships to one or more other domains ("parent" – "child");
- GO terms may have more than one parent term;
- GO vocabulary is designed to be species-agnostic;
- There are three separate domains of GO:
 - Biological Process (BP): "Visual perception" (GO:0007601);
 - Molecular Function (MF): "**G-protein coupled receptor activity**";
 - Cellular component (CC): "photoreceptor outer segment".
- GO can be browsed at:
 - http://amigo.geneontology.org/amigo/dd_browse





AmiGO 2

More information on quick search [?](#)

Quick search

Search

Search Templates



Use predefined **templates** to explore Gene Ontology data.

[Go »](#)

Advanced Search



Interactively **search** the Gene Ontology data for annotations, gene products, and terms using a powerful search syntax and filters.

[Search ▾](#)

Browse the Ontology



Use the drill-down **browser** to view the ontology structure with annotation counts.

[Go »](#)

GOOSE



Use **GOOSE** to query the legacy GO database with **SQL**.

[Go »](#)

Gene Set Enrichment analysis

- There are MANY databases and annotations that can be used for functional enrichment analysis:
 - Gene Ontology – major framework for functional annotation of all genes in all species using controlled vocabulary (<http://www.geneontology.org/>) ;
 - KEGG pathways – manually curated database of biological pathways (<http://www.genome.jp/kegg/>) ;
 - Molecular Signatures Database (MSigDB) – collections of annotated gene sets for GSEA tool;
- There are MANY tools, packages and online-servers for functional analysis of gene lists (DAVID, GSEA*, Gorilla, many packages in Bioconductor: `limma`, `goseq`, `gostats`, `topGO` etc);

GSEA (free): <http://www.broadinstitute.org/gsea/index.jsp> – Use GSEAPreranked for complex study designs

GOStats R package: (free) <http://www.bioconductor.org/packages/release/bioc/html/GOstats.html>

topGO R package (free): <http://www.bioconductor.org/packages/release/bioc/html/topGO.html>

Ingenuity Pathway Analysis (not free)

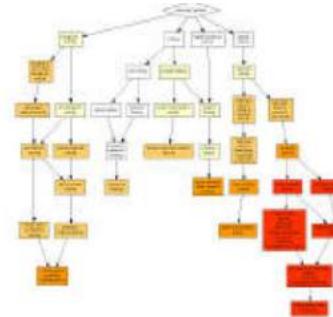
<https://biit.cs.ut.ee/gprofiler/gost> => Also available in R

Gene Ontology analysis using GOrilla

<http://cbl-gorilla.cs.technion.ac.il/>



GOrILLA



Gene Ontology enRICHment anaLysis and visuaLizAtion tool

[HTML] **GOrilla**: a tool for discovery and visualization of enriched GO terms in ranked gene lists

E Eden, R Navon, I Steinfeld... - BMC ..., 2009 - bmcbioinformatics.biomedcentral.com

Since the inception of the GO annotation project, a variety of tools have been developed that support exploring and searching the GO database. In particular, a variety of tools that perform GO enrichment analysis are currently available. Most of these tools require as input

☆ ⓘ Cited by 1341 Related articles All 22 versions Web of Science: 926 ☰

Gene Ontology visualization by GOrilla

Choosing your final gene set for GO analysis:

1. p-value
2. Logfoldchange
3. Association with your condition

- You need 3 files :
 - 1) Gene upregulated
 - 2) Gene downregulated
 - 3) Background gene
- *Comparison to proper background set of genes can be critical;*
- Upload files to the GOrilla:
 - <http://cbl-gorilla.cs.technion.ac.il/>

What is the proper **background gene list** to use when performing pathway analysis?

- The conclusion is that we should use a **list of background genes that are expressed in the samples** but not using the **entire mouse genes** in the mouse genome [a list of genes whose average expression (raw counts) is **greater than 10** in **at least one** of the two groups, that you will be comparing].

Gene Ontology analysis using GOrilla

Step 1: Choose organism
choose species →

Step 2: Choose running mode
 Single ranked list of genes Two unranked lists of genes (target and background lists)

Step 3: Paste a ranked list of gene/protein names
Names should be separated by an <ENTER>. The preferred format is gene symbol. Other supported formats are: gene and protein RefSeq, UniProt, Unigene and Ensembl. Use [WebGestalt](#) for conversion from other identifier formats.

Target set:

Or upload a file: genes.down.txt ← file with a list of DEGs

Background set:

Or upload a file: genes.all.txt ← file with a background set of genes

Step 4: Choose an ontology
choose ontology → Process Function Component All

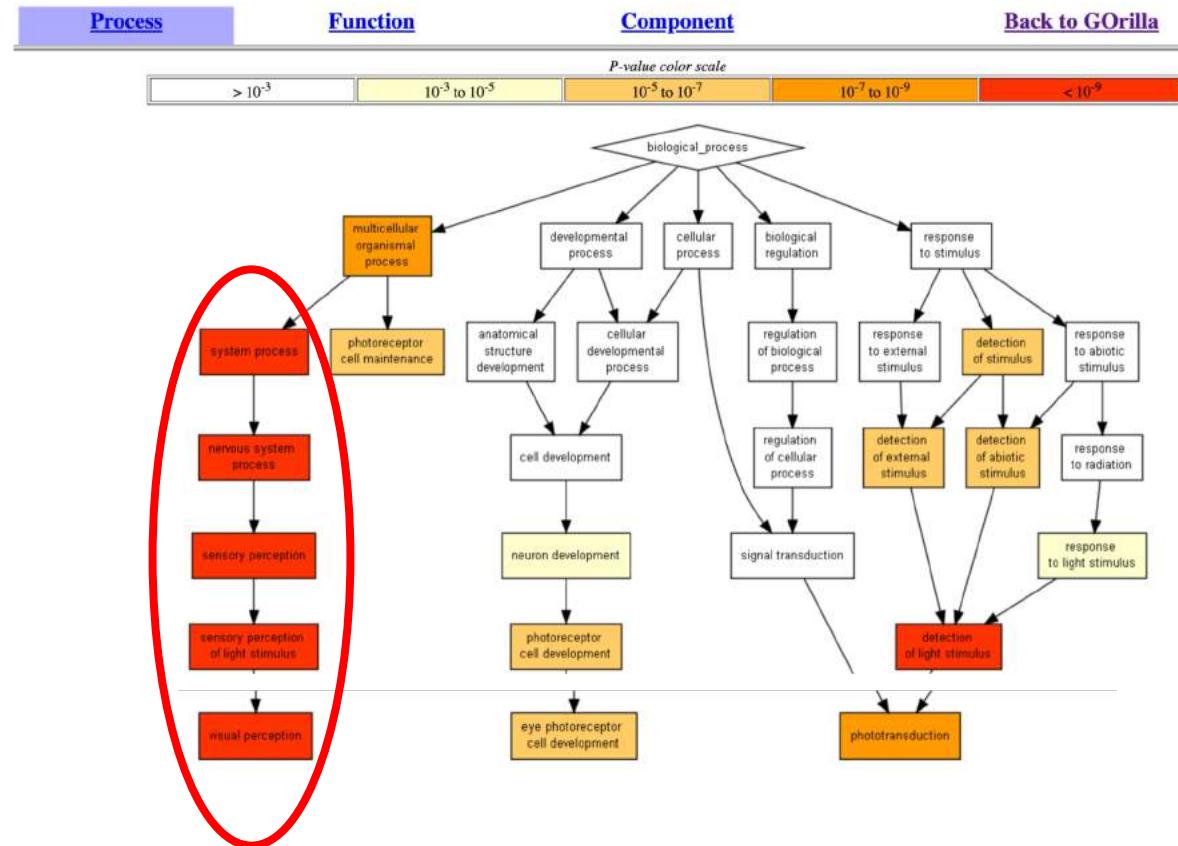
Reset form

Advanced parameters
p-value threshold: →
Analysis name: (optional)
E-mail address: (optional - enter an e-mail address if you would like to receive a link to your results)

Results for “DOWN”-regulated genes - GOrilla

Process

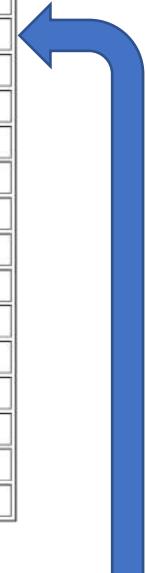
“GO” terms can be very broad, But it gives a “big picture”, but interpreting some particular can be difficult, not so easy



Results for “DOWN”-regulated genes - GOrilla

Process

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0007601	visual perception	4.94E-17	6.94E-13	8.72 (12074,112,309,25)	[+] Show genes
GO:0050953	sensory perception of light stimulus	6.19E-17	4.36E-13	8.64 (12074,113,309,25)	[+] Show genes
GO:0007600	sensory perception	1.01E-12	4.72E-9	4.61 (12074,263,309,31)	[+] Show genes
GO:0050877	nervous system process	9E-12	3.16E-8	3.11 (12074,566,309,45)	[+] Show genes
GO:0009583	detection of light stimulus	1.02E-11	2.86E-8	12.70 (12074,40,309,13)	[+] Show genes
GO:0003008	system process	1.15E-11	2.69E-8	2.72 (12074,777,309,54)	[+] Show genes
GO:0032501	multicellular organismal process	1.62E-8	3.25E-5	1.72 (12074,2187,309,96)	[+] Show genes
GO:0007602	phototransduction	2.56E-8	4.5E-5	14.89 (12074,21,309,8)	[+] Show genes
GO:0009582	detection of abiotic stimulus	1.24E-7	1.93E-4	6.27 (12074,81,309,13)	[+] Show genes
GO:0009581	detection of external stimulus	1.24E-7	1.74E-4	6.27 (12074,81,309,13)	[+] Show genes
GO:0042461	photoreceptor cell development	1.65E-7	2.11E-4	10.05 (12074,35,309,9)	[+] Show genes
GO:0051606	detection of stimulus	6.18E-7	7.24E-4	5.07 (12074,108,309,14)	[+] Show genes
GO:0042462	eye photoreceptor cell development	1.04E-6	1.12E-3	9.77 (12074,32,309,8)	[+] Show genes
GO:0045494	photoreceptor cell maintenance	3.4E-6	3.41E-3	8.45 (12074,37,309,8)	[+] Show genes



Species used: *Mus musculus*

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0007601	visual perception	4.94E-17	6.94E-13	8.72 (12074,112,309,25)	[-] Hide genes Gucy2f - guanylate cyclase 2f Abca4 - atp-binding cassette, sub-family a (abc1), member 4 Cabp4 - calcium binding protein 4 Gm11744 - predicted gene 11744 Myo7a - myosin viia Impg1 - interphotoreceptor matrix proteoglycan 1 Rom1 - rod outer segment membrane protein 1 Unc119 - unc-119 homolog (c. elegans) Rdh12 - retinol dehydrogenase 12 Rdh8 - retinol dehydrogenase 8 Prph2 - peripherin 2 Pdc - phosducin Vax2 - ventral anterior homeobox containing gene 2 Nxnl2 - nucleoredoxin-like 2 Revm - recoverin Pde6b - phosphodiesterase 6b, cggmp, rd receptor, beta polypeptide Pde6a - phosphodiesterase 6a, cgmp-specific, rod, alpha Cngal - cyclic nucleotide gated channel alpha 1 Pde6g - phosphodiesterase 6g, cgmp-specific, rod, gamma Guca1b - guanylate cyclase activator 1b Epas1 - endothelial pas domain protein 1 Gnat1 - guanine nucleotide binding protein, alpha transducing 1 Cabp2 - calcium binding protein 2 Rho - rhodopsin

Results for “DOWN”-regulated genes - GOrilla

[Process](#)

[Function](#)

[Component](#)

[Back to GOrilla](#)

No GO Enrichment Found

There are no GO terms with an enrichment p-value above the value you specified

Species used: *Mus musculus*

The system has recognized 12535 genes out of 12946 gene terms entered by the user.

12535 genes were recognized by gene symbol and 0 genes by other gene IDs .

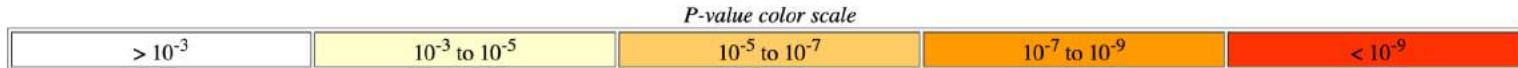
322 duplicate genes were removed (keeping the highest ranking instance of each gene) leaving a total of 12213 genes.

Only 12074 of these genes are associated with a GO term.

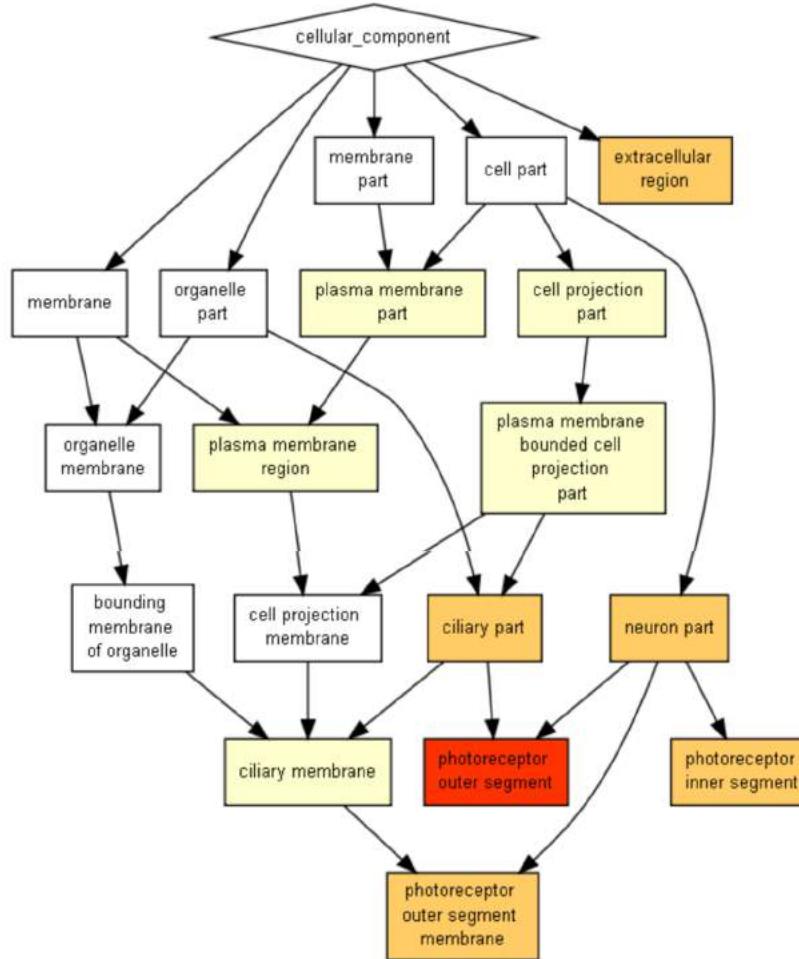
The GOrilla database is periodically updated using the [GO database](#) and other sources.

The GOrilla database was last updated on Oct 26, 2019

Results for “DOWN”-regulated genes - GOrilla



Component



Component

Results for “DOWN”-regulated genes - GOrilla

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0001750	photoreceptor outer segment	4.86E-11	9.12E-8	9.16 (12074,64,309,15)	[+] Show genes
GO:0042622	photoreceptor outer segment membrane	1.11E-7	1.04E-4	21.31 (12074,11,309,6)	[+] Show genes
GO:0001917	photoreceptor inner segment	2.33E-7	1.46E-4	8.31 (12074,47,309,10)	[+] Show genes
GO:0005576	extracellular region	8.88E-7	4.17E-4	2.37 (12074,610,309,37)	[+] Show genes
GO:0044441	ciliary part	9.28E-7	3.49E-4	2.93 (12074,347,309,26)	[+] Show genes
GO:0097458	neuron part	1.86E-6	5.84E-4	1.75 (12074,1545,309,69)	[+] Show genes

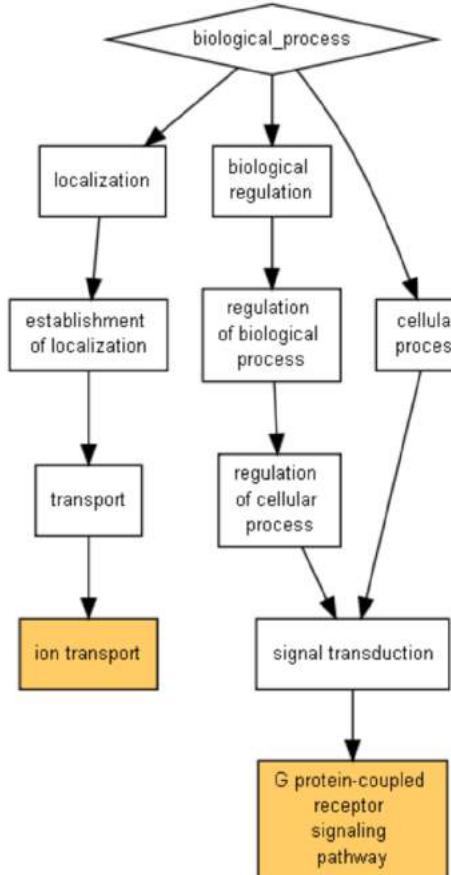
Species used: *Mus musculus*



GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0001750	photoreceptor outer segment	4.86E-11	9.12E-8	9.16 (12074,64,309,15)	[-] Hide genes Abca4 - atp-binding cassette, sub-family a (abc1), member 4 Pde6b - phosphodiesterase 6b, cgmp, rod receptor, beta polypeptide Gm11744 - predicted gene 11744 Gngt1 - guanine nucleotide binding protein (g protein), gamma transducing activity polypeptide 1 Cngb1 - cyclic nucleotide gated channel beta 1 Cnga1 - cyclic nucleotide gated channel alpha 1 Rom1 - rod outer segment membrane protein 1 Guca1b - guanylate cyclase activator 1b Prph2 - peripherin 2 Gnat1 - guanine nucleotide binding protein, alpha transducing 1 Sag - s-antigen, retina and pineal gland (arrestin) Bbs7 - bardet-biedl syndrome 7 (human) Pdc - phosducin Gnb1 - guanine nucleotide binding protein (g protein), beta 1 Rho - rhodopsin

Results for “UP”-regulated genes - GOrilla

Process	Function	Component	Back to GOrilla	
<i>P-value color scale</i>				
> 10 ⁻³	10 ⁻³ to 10 ⁻⁵	10 ⁻⁵ to 10 ⁻⁷	10 ⁻⁷ to 10 ⁻⁹	< 10 ⁻⁹



GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0007186	G protein-coupled receptor signaling pathway	1.69E-6	2.38E-2	2.83 (12074,284,390,26)	[+] Show genes
GO:0006811	ion transport	5.82E-6	4.09E-2	2.01 (12074,694,390,45)	[+] Show genes

Species used: *Mus musculus*

Results for “UP”-regulated genes - GOrilla

[Process](#)[Function](#)[Component](#)[Back to GOrilla](#)

No GO Enrichment Found

There are no GO terms with an enrichment p-value above the value you specified

Species used: *Mus musculus*

The system has recognized 12617 genes out of 13022 gene terms entered by the user.

12617 genes were recognized by gene symbol and 0 genes by other gene IDs .

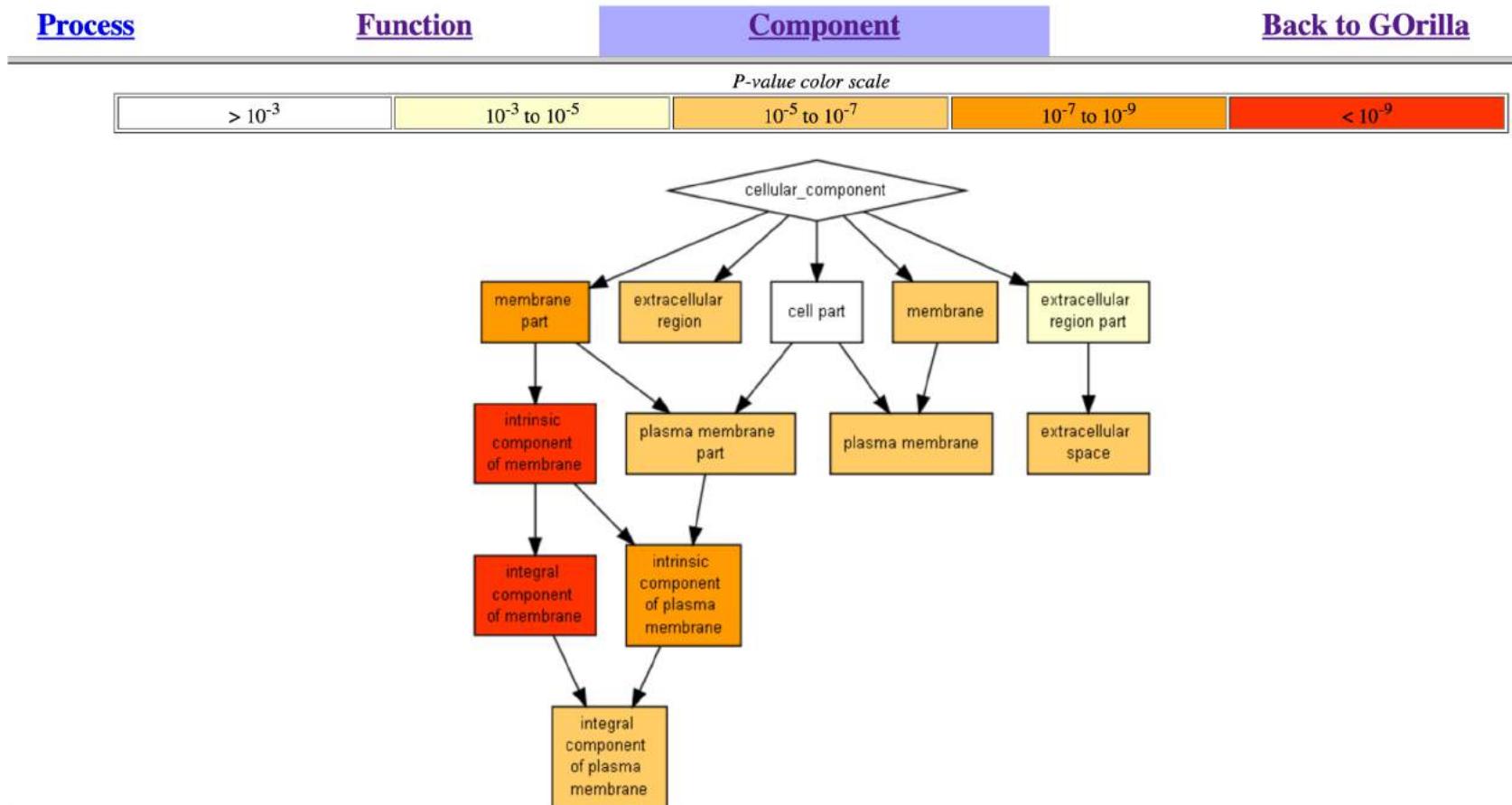
404 duplicate genes were removed (keeping the highest ranking instance of each gene) leaving a total of 12213 genes.

Only 12074 of these genes are associated with a GO term.

The GOrilla database is periodically updated using the [GO database](#) and other sources.

The GOrilla database was last updated on Oct 26, 2019

Results for “UP”-regulated genes - GOrilla



Results for “UP”-regulated genes - GOrilla

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0031224	intrinsic component of membrane	3.76E-11	7.06E-8	1.64 (12074,2715,390,144)	[+] Show genes
GO:0016021	integral component of membrane	8.32E-10	7.82E-7	1.61 (12074,2618,390,136)	[+] Show genes
GO:0044425	membrane part	2.09E-8	1.31E-5	1.43 (12074,3684,390,170)	[+] Show genes
GO:0031226	intrinsic component of plasma membrane	2.98E-8	1.4E-5	2.34 (12074,635,390,48)	[+] Show genes
GO:0005887	integral component of plasma membrane	1.37E-7	5.13E-5	2.33 (12074,585,390,44)	[+] Show genes
GO:0044459	plasma membrane part	1.87E-7	5.85E-5	1.74 (12074,1497,390,84)	[+] Show genes
GO:0005886	plasma membrane	1.95E-7	5.24E-5	1.53 (12074,2442,390,121)	[+] Show genes
GO:0005615	extracellular space	2.66E-6	6.24E-4	2.21 (12074,546,390,39)	[+] Show genes
GO:0016020	membrane	2.74E-6	5.72E-4	1.28 (12074,4944,390,204)	[+] Show genes
GO:0005576	extracellular region	2.75E-6	5.17E-4	2.13 (12074,610,390,42)	[+] Show genes

Species used: *Mus musculus*

Example 1

Functional analysis

Description of data:

1. Condition: pain versus healthy
2. Sample: saliva
3. Human genome

Functional analysis for miRNAs

www.mirbase.org/cgi-bin/mirna_entry.pl?acc=MI0016879

miRBase

MANCHESTER 1824

Home Search Browse Help Download Blog Submit hsa-mir-4513

Mature sequence hsa-miR-4513

Accession Sequence Deep sequencing Evidence Predicted targets

Find miRNA gene targets [Mirbase & TargetScan]

Ortholog of target Representative transcript 3P-seq tags Total sites 8mer sites 7mer-m8 si 7mer-A1 si 6mer sites Representative Cumulative Total conte Aggregate

		A	B	C	D	E	F	G	H	I	J	K	L	M
1	Ortholog of target	Representative transcript	3P-seq tags	Total sites	8mer sites	7mer-m8 si	7mer-A1 si	6mer sites	Representative	Cumulative	Total conte	Aggregate		
2	CDR1as	CDR1as		1	1	1	0	0	0	0	0	-1.98	-1.98 N/A	
3	FLG2	ENST00000388718	5	5	2	0	1	1	1	1	1	-1.08	-1.08 N/A	
4	FM02	ENST00000441535	1	5	3	3	0	0	0	2	2	-0.92	-0.92 N/A	
5	PROZ	ENST00000375547	2	14	1	1	0	0	0	0	0	-0.8	-0.8 N/A	
6	USE1	ENST00000596136	1	308	1	1	0	0	0	0	0	-0.75	-0.75 N/A	
7	ZNF667	ENST00000591790	1	24	2	1	1	0	0	3	3	-0.75	-0.75 N/A	
8	MDH1B	ENST00000374412	3	20	2	1	1	0	0	0	0	-0.73	-0.95 N/A	
9	MRGPRX4	ENST00000314254	3	5	1	1	0	0	0	0	0	-0.71	-0.71 N/A	
10	TSPAN8	ENST00000393330	2	127	1	1	0	0	0	0	0	-0.7	-0.7 N/A	
11	PDZD2	ENST00000438447	1	5	3	2	1	0	1	1	1	-0.69	-0.69 N/A	
12	PPP2R2A	ENST00000380737	3	236	3	0	1	2	0	0	0	-0.67	-0.7 N/A	
13	TOMM5	ENST00000377773	5	12658	1	1	0	0	0	0	0	-0.67	-0.68 N/A	
14	SPZ1	ENST00000296739	4	5	1	1	0	0	0	0	0	-0.67	-0.67 N/A	
15	GSAP	ENST00000257626	7	5	1	1	0	0	0	0	0	-0.64	-0.64 N/A	
16	AP3M2	ENST00000174653	3	792	2	1	1	0	1	1	1	-0.63	-0.64 N/A	
17	GCSAM	ENST00000308910	4	5	2	1	0	1	1	1	1	-0.63	-0.63 N/A	
18	PHYKPL	ENST00000308158	5	150	1	1	0	0	0	0	0	-0.63	-0.63 N/A	
19	RBBP5	ENST00000264515	6	166	3	1	0	2	0	0	0	-0.62	-0.65 N/A	
20	VMA21	ENST00000330374	6	2162	2	0	2	0	0	0	0	-0.62	-0.62 N/A	
21	BTLA	ENST00000334529	5	5	2	0	2	0	0	0	0	-0.6	-0.6 N/A	
22	RGS7	ENST00000348120	2	8	1	1	0	0	1	1	1	-0.59	-0.59 N/A	
23	GLRA2	ENST00000218075	4	5	2	1	0	1	0	0	0	-0.58	-0.58 N/A	
24	LGSN	ENST00000370658	5	21	2	1	1	0	0	0	0	-0.58	-0.58 N/A	
25	CLK4	ENST00000316308	4	218	2	1	0	1	0	1	1	-0.58	-0.65 N/A	
26	CA3	ENST00000285381	2	5	1	1	0	0	0	0	0	-0.57	-0.57 N/A	
27	SERP1	ENST00000239944	2	3242	2	1	0	1	2	2	2	-0.57	-0.7 N/A	
28	C12orf60	ENST00000330828	2	11	1	1	0	0	0	0	0	-0.56	-0.56 N/A	
29	CLEC4D	ENST00000299665	2	5	1	1	0	0	0	0	0	-0.56	-0.56 N/A	
30	DCAF16	ENST00000382247	1	202	2	1	0	1	1	1	1	-0.56	-0.56 N/A	
31	RAD54B	ENST00000297592	5	36	2	0	2	0	0	0	0	-0.55	-0.64 N/A	
32	DLD	ENST00000205402	5	1623	2	1	0	1	0	0	0	-0.55	-0.59 N/A	
33	AKR1C2	ENST00000380753	4	5	2	1	0	1	0	0	0	-0.55	-0.55 N/A	

MiR-4513..... more than 3000 target genes



DAVID database



KEGG database



GoMiner

David



Functional Annotation Tool

DAVID Bioinformatics Resources 6.8, NIAID/NIH

[Home](#) [Start Analysis](#) [Shortcut to DAVID Tools](#) [Technical Center](#) [Downloads & APIs](#) [Term of Service](#) [Why DAVID?](#)

Mir-4513

*** Welcome to DAVID 6.8 ***

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

[Upload](#) [List](#) [Background](#)

Gene List Manager

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

- Use All Species -
Homo sapiens(2860)
Unknown(197)

Select Species

[List Manager](#) [Help](#)

List_1

Select List to:

Annotation Summary Results

Current Gene List: List_1

Current Background: Homo sapiens

2852 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)

*** Welcome to DAVID 6.8 ***

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

Functional Annotation Chart

[Help and Manual](#)

Current Gene List: List_1

Current Background: Homo sapiens

2852 DAVID IDs

Options

Rerun Using Options

Create Sublist

8 chart records

[Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GAD_DISEASE_CLASS	CHEMDEPENDENCY	RT		684	24,0	2,2E-13	4,2E-12
<input type="checkbox"/>	GAD_DISEASE_CLASS	HEMATOLOGICAL	RT		288	10,1	1,3E-5	1,3E-4
<input type="checkbox"/>	GAD_DISEASE_CLASS	METABOLIC	RT		874	30,6	3,0E-5	1,9E-4
<input type="checkbox"/>	GAD_DISEASE_CLASS	CARDIOVASCULAR	RT		719	25,2	4,3E-5	2,1E-4
<input type="checkbox"/>	GAD_DISEASE_CLASS	PSYCH	RT		351	12,3	2,2E-4	8,5E-4
<input type="checkbox"/>	GAD_DISEASE_CLASS	NEUROLOGICAL	RT		481	16,9	4,7E-3	1,5E-2
<input type="checkbox"/>	GAD_DISEASE_CLASS	IMMUNE	RT		492	17,3	8,7E-3	2,3E-2
<input type="checkbox"/>	GAD_DISEASE_CLASS	DEVELOPMENTAL	RT		248	8,7	5,9E-2	1,4E-1

*** Welcome to DAVID 6.8 ***
*** If you are looking for DAVID 6.7, please visit our [development site](#). ***

Functional Annotation Chart

[Help and Manual](#)

Current Gene List: List_1

Current Background: Homo sapiens

2852 DAVID IDs

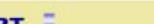
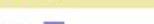
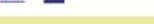
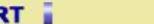
[Options](#)

[Rerun Using Options](#) [Create Sublist](#)

Mir-4513

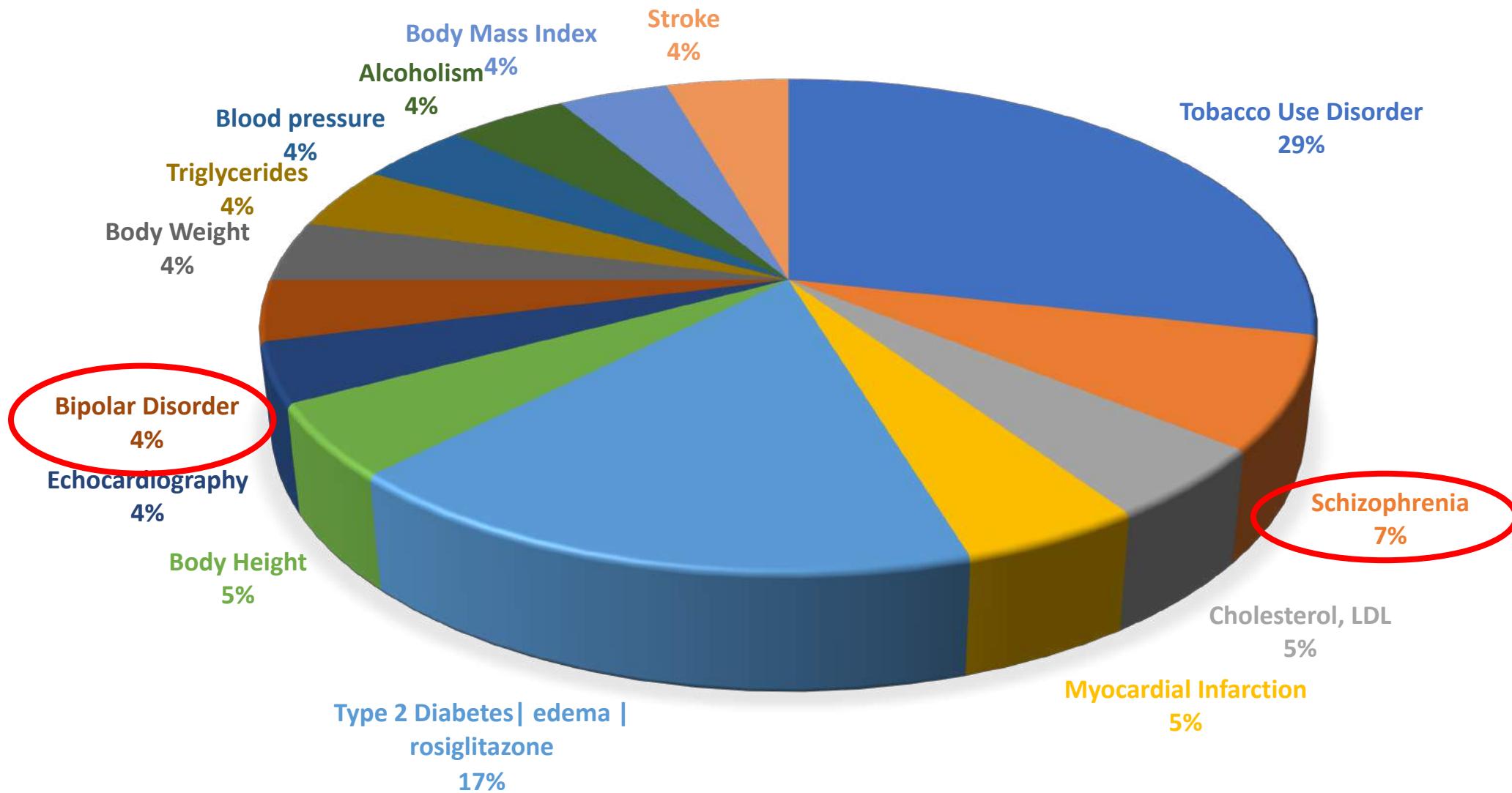
91 chart records

[Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
	GAD_DISEASE	Tobacco Use Disorder	RT		607	21,3	7,4E-18	3,6E-14
	GAD_DISEASE	Schizophrenia	RT		156	5,5	1,4E-4	2,9E-1
	GAD_DISEASE	Echocardiography	RT		83	2,9	5,9E-4	6,1E-1
	GAD_DISEASE	Cholesterol, LDL	RT		100	3,5	6,2E-4	5,3E-1
	GAD_DISEASE	Hip	RT		78	2,7	7,6E-4	5,2E-1
	GAD_DISEASE	Bipolar Disorder	RT		85	3,0	1,3E-3	6,4E-1
	GAD_DISEASE	Creatinine	RT		40	1,4	1,4E-3	6,2E-1
	GAD_DISEASE	Forced Expiratory Volume	RT		25	0,9	1,5E-3	6,0E-1
	GAD_DISEASE	Cholesterol, HDL	RT		89	3,1	1,7E-3	6,0E-1
	GAD_DISEASE	Exercise Test	RT		32	1,1	2,2E-3	6,5E-1
	GAD_DISEASE	Body Weight	RT		84	2,9	2,4E-3	6,5E-1
	GAD_DISEASE	Intercellular Adhesion Molecule-1	RT		10	0,4	3,0E-3	7,0E-1
	GAD_DISEASE	Triglycerides	RT		87	3,1	4,6E-3	8,2E-1
	GAD_DISEASE	meningioma	RT		8	0,3	5,7E-3	8,6E-1

Mir-4513

DISEASES





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Functional Annotation Chart

[Help and Manual](#)

Current Gene List: List_1

Current Background: Homo sapiens

2852 DAVID IDs

Options

Rerun Using Options Create Sublist[Download File](#)

14 chart records

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
	UP_KEYWORDS	Phosphoprotein	RT	1387	48,6	4,4E-27	2,5E-24	
	UP_KEYWORDS	Alternative splicing	RT	1667	58,5	8,9E-20	2,5E-17	
	UP_KEYWORDS	Zinc-finger	RT	343	12,0	6,2E-12	1,2E-9	
	UP_KEYWORDS	Zinc	RT	429	15,0	2,6E-11	3,7E-9	
	UP_KEYWORDS	Transcription regulation	RT	420	14,7	3,4E-10	3,9E-8	
	UP_KEYWORDS	Metal-binding	RT	617	21,6	4,5E-10	4,2E-8	
	UP_KEYWORDS	Transcription	RT	428	15,0	7,3E-10	5,9E-8	
	UP_KEYWORDS	Nucleus	RT	827	29,0	3,0E-7	2,2E-5	
	UP_KEYWORDS	Coiled coil	RT	500	17,5	1,5E-6	9,4E-5	
	UP_KEYWORDS	Transferase	RT	294	10,3	1,2E-5	7,0E-4	
	UP_KEYWORDS	Golgi apparatus	RT	154	5,4	1,7E-5	8,6E-4	
	UP_KEYWORDS	DNA-binding	RT	342	12,0	3,4E-5	1,6E-3	
	UP_KEYWORDS	Cell projection	RT	121	4,2	1,2E-2	1,6E-1	
	UP_KEYWORDS	Cell junction	RT	114	4,0	1,2E-2	1,6E-1	
	UP_KEYWORDS	Cell cycle	RT	110	3,9	1,3E-2	1,7E-1	
	UP_KEYWORDS	Signal-anchor	RT	80	2,8	1,4E-2	1,8E-1	
	UP_KEYWORDS	Potassium	RT	28	1,0	1,5E-2	1,8E-1	
	UP_KEYWORDS	Ion channel	RT	65	2,3	1,5E-2	1,8E-1	
	UP_KEYWORDS	cAMP	RT	11	0,4	1,9E-2	2,2E-1	
	UP_KEYWORDS	Wnt signaling pathway	RT	36	1,3	2,0E-2	2,2E-1	
	UP_KEYWORDS	ATP-binding	RT	217	7,6	2,1E-2	2,3E-1	
	UP_KEYWORDS	Transmembrane helix	RT	816	28,6	2,2E-2	2,3E-1	
	UP_KEYWORDS	Serine/threonine-protein kinase	RT	69	2,4	2,3E-2	2,4E-1	
	UP_KEYWORDS	Transmembrane	RT	817	28,6	2,5E-2	2,5E-1	
	UP_KEYWORDS	mRNA processing	RT	59	2,1	2,8E-2	2,7E-1	
	UP_KEYWORDS	Chromatin regulator	RT	52	1,8	2,9E-2	2,7E-1	
	UP_KEYWORDS	DNA damage	RT	62	2,2	2,9E-2	2,7E-1	
	UP_KEYWORDS	Calcium	RT	140	4,9	3,3E-2	3,0E-1	
	UP_KEYWORDS	Bromodomain	RT	11	0,4	3,3E-2	3,0E-1	
	UP_KEYWORDS	SH2 domain	RT	23	0,8	3,4E-2	3,0E-1	
	UP_KEYWORDS	Lipoprotein	RT	136	4,8	3,6E-2	3,0E-1	
	UP_KEYWORDS	Ligand-gated ion channel	RT	18	0,6	4,1E-2	3,3E-1	
	UP_KEYWORDS	Methylation	RT	157	5,5	4,3E-2	3,4E-1	
	UP_KEYWORDS	Postsynaptic cell membrane	RT	34	1,2	4,4E-2	3,4E-1	
	UP_KEYWORDS	Cytoskeleton	RT	176	6,2	4,7E-2	3,6E-1	
	UP_KEYWORDS	Methyltransferase	RT	36	1,3	4,8E-2	3,6E-1	
	UP_KEYWORDS	Sodium	RT	25	0,9	4,8E-2	3,6E-1	
	UP_KEYWORDS	Guanine-nucleotide releasing factor	RT	29	1,0	4,8E-2	3,5E-1	

<input type="checkbox"/> UP_KEYWORDS	Cytoplasm	RT	<div style="width: 100px; height: 10px; background-color: #3366CC;"></div>	742	26,0	4,8E-5	2,1E-3
<input type="checkbox"/> UP_KEYWORDS	Membrane	RT	<div style="width: 100px; height: 10px; background-color: #3366CC;"></div>	1114	39,1	1,1E-4	4,4E-3
<input type="checkbox"/> UP_KEYWORDS	Actin-binding	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	59	2,1	4,0E-4	1,5E-2
<input type="checkbox"/> UP_KEYWORDS	Ubl conjugation	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	281	9,9	4,0E-4	1,4E-2
<input type="checkbox"/> UP_KEYWORDS	Acetylation	RT	<div style="width: 100px; height: 10px; background-color: #3366CC;"></div>	530	18,6	5,6E-4	1,8E-2
<input type="checkbox"/> UP_KEYWORDS	Epilepsy	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	32	1,1	7,9E-4	2,5E-2
<input type="checkbox"/> UP_KEYWORDS	Transport	RT	<div style="width: 100px; height: 10px; background-color: #3366CC;"></div>	318	11,2	9,3E-4	2,7E-2
<input type="checkbox"/> UP_KEYWORDS	Repressor	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	108	3,8	1,4E-3	3,8E-2
<input type="checkbox"/> UP_KEYWORDS	Glycosyltransferase	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	50	1,8	1,6E-3	4,4E-2
<input type="checkbox"/> UP_KEYWORDS	Polymorphism	RT	<div style="width: 100px; height: 10px; background-color: #3366CC;"></div>	1717	60,2	2,1E-3	5,3E-2
<input type="checkbox"/> UP_KEYWORDS	Developmental protein	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	161	5,6	2,5E-3	6,0E-2
<input type="checkbox"/> UP_KEYWORDS	Chromosomal rearrangement	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	65	2,3	3,0E-3	6,8E-2
<input type="checkbox"/> UP_KEYWORDS	Ubl conjugation pathway	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	119	4,2	3,5E-3	7,6E-2
<input type="checkbox"/> UP_KEYWORDS	Disease mutation	RT	<div style="width: 100px; height: 10px; background-color: #3366CC;"></div>	393	13,8	4,5E-3	9,5E-2
<input type="checkbox"/> UP_KEYWORDS	RNA editing	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	9	0,3	4,7E-3	9,4E-2
<input type="checkbox"/> UP_KEYWORDS	Endosome	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	87	3,1	5,2E-3	9,9E-2
<input type="checkbox"/> UP_KEYWORDS	Synapse	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	67	2,3	6,1E-3	1,1E-1
<input type="checkbox"/> UP_KEYWORDS	Ion transport	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	111	3,9	6,8E-3	1,2E-1
<input type="checkbox"/> UP_KEYWORDS	Potassium transport	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	27	0,9	6,8E-3	1,2E-1
<input type="checkbox"/> UP_KEYWORDS	Nucleotide-binding	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	280	9,8	8,0E-3	1,3E-1
<input type="checkbox"/> UP_KEYWORDS	Mental retardation	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	57	2,0	8,3E-3	1,3E-1
<input type="checkbox"/> UP_KEYWORDS	Neurogenesis	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	49	1,7	8,8E-3	1,4E-1
<input type="checkbox"/> UP_KEYWORDS	Protein transport	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	105	3,7	9,6E-3	1,4E-1
<input type="checkbox"/> UP_KEYWORDS	Isopeptide bond	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	183	6,4	9,6E-3	1,4E-1
<input type="checkbox"/> UP_KEYWORDS	Biological rhythms	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	28	1,0	9,8E-3	1,4E-1
<input type="checkbox"/> UP_KEYWORDS	Endoplasmic reticulum	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	173	6,1	1,1E-2	1,5E-1
<input type="checkbox"/> UP_KEYWORDS	Prenylation	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	32	1,1	4,9E-2	3,5E-1
<input type="checkbox"/> UP_KEYWORDS	Activator	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	106	3,7	5,5E-2	3,9E-1
<input type="checkbox"/> UP_KEYWORDS	Alternative promoter usage	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	19	0,7	6,0E-2	4,1E-1
<input type="checkbox"/> UP_KEYWORDS	Deafness	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	36	1,3	6,5E-2	4,3E-1
<input type="checkbox"/> UP_KEYWORDS	Kinase	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	116	4,1	6,6E-2	4,3E-1
<input type="checkbox"/> UP_KEYWORDS	Alternative initiation	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	21	0,7	7,0E-2	4,4E-1
<input type="checkbox"/> UP_KEYWORDS	cAMP-binding	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	6	0,2	7,1E-2	4,5E-1
<input type="checkbox"/> UP_KEYWORDS	Sodium transport	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	23	0,8	7,3E-2	4,5E-1
<input type="checkbox"/> UP_KEYWORDS	Potassium channel	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	16	0,6	7,4E-2	4,5E-1
<input type="checkbox"/> UP_KEYWORDS	Myristate	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	35	1,2	7,9E-2	4,7E-1
<input type="checkbox"/> UP_KEYWORDS	Voltage-gated channel	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	28	1,0	8,0E-2	4,7E-1
<input type="checkbox"/> UP_KEYWORDS	Tyrosine-protein kinase	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	22	0,8	8,0E-2	4,6E-1
<input type="checkbox"/> UP_KEYWORDS	Charcot-Marie-Tooth disease	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	12	0,4	8,1E-2	4,6E-1
<input type="checkbox"/> UP_KEYWORDS	SH3 domain	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	38	1,3	8,1E-2	4,6E-1
<input type="checkbox"/> UP_KEYWORDS	WD repeat	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	48	1,7	8,1E-2	4,6E-1
<input type="checkbox"/> UP_KEYWORDS	Cholesterol metabolism	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	13	0,5	8,1E-2	4,5E-1
<input type="checkbox"/> UP_KEYWORDS	Synapsome	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	13	0,5	8,1E-2	4,5E-1
<input type="checkbox"/> UP_KEYWORDS	Cell division	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	64	2,2	8,3E-2	4,5E-1
<input type="checkbox"/> UP_KEYWORDS	Protein phosphatase	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	25	0,9	9,2E-2	4,9E-1
<input type="checkbox"/> UP_KEYWORDS	Cell adhesion	RT	<div style="width: 10px; height: 10px; background-color: #3366CC;"></div>	77	2,7	9,2E-2	4,8E-1

Gene_Ontology (3 selected)

<input type="checkbox"/> GOTERM_BP_1	84.9%	2421	Chart	
<input type="checkbox"/> GOTERM_BP_2	84.8%	2418	Chart	
<input type="checkbox"/> GOTERM_BP_3	84.3%	2404	Chart	
<input type="checkbox"/> GOTERM_BP_4	83.3%	2376	Chart	
<input type="checkbox"/> GOTERM_BP_5	82.4%	2349	Chart	
<input type="checkbox"/> GOTERM_BP_ALL	84.9%	2421	Chart	
<input checked="" type="checkbox"/> GOTERM_BP_DIRECT	84.9%	2421	Chart	
<input type="checkbox"/> GOTERM_BP_FAT 	84.2%	2402	Chart	
<input type="checkbox"/> GOTERM_CC_1	91.8%	2619	Chart	
<input type="checkbox"/> GOTERM_CC_2	90.9%	2592	Chart	
<input type="checkbox"/> GOTERM_CC_3	90.9%	2592	Chart	
<input type="checkbox"/> GOTERM_CC_4	89.1%	2542	Chart	
<input type="checkbox"/> GOTERM_CC_5	82.3%	2347	Chart	
<input type="checkbox"/> GOTERM_CC_ALL	91.8%	2619	Chart	
<input checked="" type="checkbox"/> GOTERM_CC_DIRECT	91.8%	2619	Chart	
<input type="checkbox"/> GOTERM_CC_FAT 	73.9%	2109	Chart	
<input type="checkbox"/> GOTERM_MF_1	85.4%	2437	Chart	
<input type="checkbox"/> GOTERM_MF_2	85.0%	2423	Chart	
<input type="checkbox"/> GOTERM_MF_3	76.8%	2190	Chart	
<input type="checkbox"/> GOTERM_MF_4	74.1%	2114	Chart	
<input type="checkbox"/> GOTERM_MF_5	61.5%	1753	Chart	
<input type="checkbox"/> GOTERM_MF_ALL	85.4%	2437	Chart	
<input checked="" type="checkbox"/> GOTERM_MF_DIRECT	85.4%	2437	Chart	
<input type="checkbox"/> GOTERM_MF_FAT 	78.1%	2227	Chart	

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Functional Annotation Chart

[Help and Manual](#)

Current Gene List: List_1

Current Background: Homo sapiens

2852 DAVID IDs

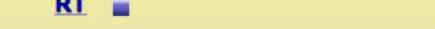
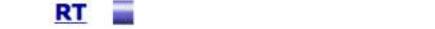
 [Options](#)

[Rerun Using Options](#)

[Create Sublist](#)

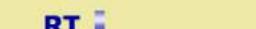
10 chart records

 [Download File](#)

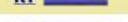
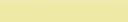
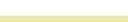
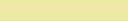
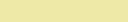
Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_1	cellular process	RT		2302	80,7	1,3E-7	3,3E-6
<input type="checkbox"/>	GOTERM_BP_1	biological regulation	RT		1773	62,2	1,3E-7	1,7E-6
<input type="checkbox"/>	GOTERM_BP_1	regulation of biological process	RT		1674	58,7	2,4E-6	2,0E-5
<input type="checkbox"/>	GOTERM_BP_1	metabolic process	RT		1678	58,8	8,7E-5	5,4E-4
<input type="checkbox"/>	GOTERM_BP_1	developmental process	RT		880	30,9	9,5E-4	4,7E-3
<input type="checkbox"/>	GOTERM_BP_1	rhythmic process	RT		60	2,1	1,6E-2	6,6E-2
<input type="checkbox"/>	GOTERM_BP_1	behavior	RT		99	3,5	1,9E-2	6,7E-2
<input type="checkbox"/>	GOTERM_BP_1	signaling	RT		948	33,2	2,1E-2	6,4E-2
<input type="checkbox"/>	GOTERM_BP_1	cellular component organization or biogenesis	RT		942	33,0	4,2E-2	1,1E-1
<input type="checkbox"/>	GOTERM_BP_1	growth	RT		154	5,4	4,3E-2	1,0E-1

50 chart records

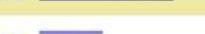
Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
	GOTERM_BP_2	regulation of cellular process	RT		1619	56,8	7,1E-7	1,5E-4
	GOTERM_BP_2	cellular metabolic process	RT		1578	55,3	8,1E-7	8,4E-5
	GOTERM_BP_2	regulation of metabolic process	RT		996	34,9	9,8E-7	6,8E-5
	GOTERM_BP_2	regulation of signaling	RT		522	18,3	6,3E-6	3,3E-4
	GOTERM_BP_2	biosynthetic process	RT		999	35,0	4,8E-5	2,0E-3
	GOTERM_BP_2	organic substance metabolic process	RT		1621	56,8	2,5E-4	8,5E-3
	GOTERM_BP_2	single-mitochondrial organism process	RT		932	32,7	3,5E-4	1,0E-2
	GOTERM_BP_2	single-organism developmental process	RT		862	30,2	4,2E-4	1,1E-2
	GOTERM_BP_2	primary metabolic process	RT		1548	54,3	7,7E-4	1,8E-2
	GOTERM_BP_2	anatomical structure development	RT		857	30,0	9,1E-4	1,9E-2
	GOTERM_BP_2	negative regulation of signaling	RT		209	7,3	1,1E-3	2,0E-2
	GOTERM_BP_2	negative regulation of cellular process	RT		682	23,9	1,2E-3	2,1E-2
	GOTERM_BP_2	negative regulation of response to stimulus	RT		233	8,2	3,4E-3	5,3E-2
	GOTERM_BP_2	negative regulation of biological process	RT		723	25,4	3,5E-3	5,0E-2
	GOTERM_BP_2	developmental growth	RT		107	3,8	6,0E-3	8,0E-2
	GOTERM_BP_2	positive regulation of cellular protein localization	RT		71	2,5	6,1E-3	7,6E-2
	GOTERM_BP_2	regulation of multicellular organismal process	RT		426	14,9	6,6E-3	7,7E-2
	GOTERM_BP_2	nitrogen compound metabolic process	RT		1058	37,1	7,5E-3	8,2E-2
	GOTERM_BP_2	regulation of localization	RT		395	13,8	1,1E-2	1,2E-1
	GOTERM_BP_2	regulation of molecular function	RT		453	15,9	1,2E-2	1,2E-1
	GOTERM_BP_2	positive regulation of developmental process	RT		184	6,5	1,3E-2	1,2E-1
	GOTERM_BP_2	response to endogenous stimulus	RT		254	8,9	1,3E-2	1,2E-1
	GOTERM_BP_2	positive regulation of multicellular organismal process	RT		236	8,3	1,4E-2	1,2E-1
	GOTERM_BP_2	regulation of developmental process	RT		342	12,0	1,4E-2	1,1E-1
	GOTERM_BP_2	anatomical structure morphogenesis	RT		417	14,6	1,5E-2	1,2E-1
	GOTERM_BP_2	macromolecule localization	RT		443	15,5	1,8E-2	1,4E-1
	GOTERM_BP_2	single-organism behavior	RT		73	2,6	2,0E-2	1,4E-1
	GOTERM_BP_2	regulation of response to stimulus	RT		565	19,8	2,1E-2	1,4E-1
	GOTERM_BP_2	anatomical structure formation involved in morphogenesis	RT		191	6,7	2,2E-2	1,5E-1
	GOTERM_BP_2	positive regulation of establishment of protein localization	RT		92	3,2	2,2E-2	1,4E-1
	GOTERM_BP_2	single organism signaling	RT		939	32,9	2,6E-2	1,6E-1
	GOTERM_BP_2	cellular localization	RT		400	14,0	2,6E-2	1,6E-1
	GOTERM_BP_2	positive regulation of cellular process	RT		725	25,4	2,8E-2	1,6E-1
	GOTERM_BP_2	response to abiotic stimulus	RT		171	6,0	2,8E-2	1,6E-1
	GOTERM_BP_2	cellular component organization	RT		923	32,4	3,0E-2	1,7E-1
	GOTERM_BP_2	cellular response to stimulus	RT		1040	36,5	3,7E-2	2,0E-1
	GOTERM_BP_2	negative regulation of metabolic process	RT		394	13,8	3,9E-2	2,0E-1
	GOTERM_BP_2	positive regulation of transport	RT		151	5,3	5,3E-2	2,6E-1
	GOTERM_BP_2	positive regulation of signaling	RT		248	8,7	5,5E-2	2,6E-1
	GOTERM_BP_2	cell growth	RT		76	2,7	5,6E-2	2,6E-1
	GOTERM_BP_2	regulation of biological quality	RT		542	19,0	5,9E-2	2,6E-1
	GOTERM_BP_2	negative regulation of homeostatic process	RT		34	1,2	6,6E-2	2,8E-1
	GOTERM_BP_2	cell proliferation	RT		291	10,2	7,1E-2	3,0E-1
	GOTERM_BP_2	ovulation cycle	RT		22	0,8	7,2E-2	3,0E-1
	GOTERM_BP_2	protein folding	RT		42	1,5	8,1E-2	3,2E-1
	GOTERM_BP_2	establishment of localization	RT		720	25,2	8,3E-2	3,2E-1
	GOTERM_BP_2	pigmentation	RT		20	0,7	8,4E-2	3,2E-1
	GOTERM_BP_2	positive regulation of biological process	RT		792	27,8	8,6E-2	3,2E-1
	GOTERM_BP_2	single-organism localization	RT		547	19,2	9,5E-2	3,4E-1
	GOTERM_BP_2	positive regulation of sequence-specific DNA binding transcription factor activity	RT		42	1,5	9,9E-2	3,5E-1

<input type="checkbox"/>	GOTERM_BP_3 cardiac septum development	RT 	20	0,7	9,1E-2	5,7E-1
<input type="checkbox"/>	GOTERM_BP_3 organic substance catabolic process	RT 	293	10,3	9,1E-2	5,7E-1
<input type="checkbox"/>	GOTERM_BP_3 developmental cell growth	RT 	35	1,2	9,4E-2	5,7E-1
<input type="checkbox"/>	GOTERM_BP_3 cardiac muscle tissue growth	RT 	15	0,5	9,5E-2	5,8E-1
<input type="checkbox"/>	GOTERM_BP_3 positive regulation of muscle tissue development	RT 	15	0,5	9,5E-2	5,8E-1
<input type="checkbox"/>	GOTERM_BP_3 regulation of female receptivity	RT 	4	0,1	9,6E-2	5,8E-1
<input type="checkbox"/>	GOTERM_BP_3 amyloid precursor protein biosynthetic process	RT 	4	0,1	9,6E-2	5,8E-1
<input type="checkbox"/>	GOTERM_BP_3 negative regulation of nervous system development	RT 	47	1,6	9,7E-2	5,8E-1
<input type="checkbox"/>	GOTERM_BP_3 regulation of membrane potential	RT 	62	2,2	9,8E-2	5,8E-1
<input type="checkbox"/>	GOTERM_BP_3 regulation of erythrocyte differentiation	RT 	10	0,4	9,9E-2	5,9E-1
<input type="checkbox"/>	GOTERM_BP_3 transport	RT 	700	24,5	9,9E-2	5,8E-1
<input type="checkbox"/>	GOTERM_BP_3 positive regulation of sequence-specific DNA binding transcription factor activity	RT 	42	1,5	1,0E-1	5,8E-1
<input type="checkbox"/>	GOTERM_BP_4 regulation of endocytic recycling	RT 	4	0,1	9,6E-2	7,3E-1
<input type="checkbox"/>	GOTERM_BP_4 cardiac muscle tissue growth	RT 	15	0,5	9,7E-2	7,3E-1
<input type="checkbox"/>	GOTERM_BP_4 positive regulation of muscle tissue development	RT 	15	0,5	9,7E-2	7,3E-1
<input type="checkbox"/>	GOTERM_BP_4 developmental cell growth	RT 	35	1,2	9,7E-2	7,3E-1
<input type="checkbox"/>	GOTERM_BP_4 positive regulation of macromolecule biosynthetic process	RT 	250	8,8	9,7E-2	7,3E-1
<input type="checkbox"/>	GOTERM_BP_4 regulation of neuron death	RT 	46	1,6	9,8E-2	7,3E-1
<input type="checkbox"/>	GOTERM_BP_4 regulation of cellular senescence	RT 	8	0,3	9,9E-2	7,3E-1

703 chart records

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini	Download File
		GOTERM_BP_ALL regulation of cellular macromolecule biosynthetic process	RT		678	23,8	1,3E-7	1,2E-3	
		GOTERM_BP_ALL cellular process	RT		2302	80,7	1,3E-7	6,0E-4	
		GOTERM_BP_ALL biological regulation	RT		1773	62,2	1,3E-7	4,1E-4	
		GOTERM_BP_ALL regulation of cellular biosynthetic process	RT		722	25,3	1,4E-7	3,2E-4	
		GOTERM_BP_ALL cellular macromolecule metabolic process	RT		1326	46,5	1,9E-7	3,4E-4	
		GOTERM_BP_ALL regulation of biosynthetic process	RT		729	25,6	2,0E-7	3,1E-4	
		GOTERM_BP_ALL regulation of RNA metabolic process	RT		640	22,4	2,9E-7	3,8E-4	
		GOTERM_BP_ALL regulation of transcription, DNA-templated	RT		614	21,5	4,4E-7	5,0E-4	
		GOTERM_BP_ALL regulation of gene expression	RT		727	25,5	4,4E-7	4,4E-4	
		GOTERM_BP_ALL regulation of nucleic acid-templated transcription	RT		617	21,6	4,9E-7	4,5E-4	
		GOTERM_BP_ALL regulation of macromolecule biosynthetic process	RT		690	24,2	5,3E-7	4,4E-4	
		GOTERM_BP_ALL regulation of cellular metabolic process	RT		950	33,3	5,7E-7	4,4E-4	
		GOTERM_BP_ALL cellular macromolecule biosynthetic process	RT		826	29,0	5,9E-7	4,2E-4	
		GOTERM_BP_ALL regulation of cellular process	RT		1619	56,8	6,8E-7	4,4E-4	
		GOTERM_BP_ALL regulation of nucleobase-containing compound metabolic process	RT		689	24,2	6,8E-7	4,1E-4	
		GOTERM_BP_ALL regulation of Notch signaling pathway	RT		16	0,6	7,1E-2	7,6E-1	
		GOTERM_BP_ALL regulation of mitochondrial membrane permeability	RT		16	0,6	7,1E-2	7,6E-1	
		GOTERM_BP_ALL protein targeting	RT		116	4,1	7,1E-2	7,6E-1	
		GOTERM_BP_ALL positive regulation of epithelial cell migration	RT		22	0,8	7,2E-2	7,6E-1	
		GOTERM_BP_ALL ovulation cycle	RT		22	0,8	7,2E-2	7,6E-1	
		GOTERM_BP_ALL positive regulation of cell communication	RT		245	8,6	7,2E-2	7,6E-1	
		GOTERM_BP_ALL muscle organ development	RT		64	2,2	7,4E-2	7,7E-1	
		GOTERM_BP_ALL regulation of protein secretion	RT		68	2,4	7,4E-2	7,7E-1	
		GOTERM_BP_ALL cellular response to oxygen-containing compound	RT		148	5,2	7,4E-2	7,7E-1	
		GOTERM_BP_ALL cranial skeletal system development	RT		14	0,5	7,4E-2	7,7E-1	
		GOTERM_BP_ALL gliogenesis	RT		44	1,5	7,4E-2	7,7E-1	
		GOTERM_BP_ALL salivary gland development	RT		10	0,4	7,5E-2	7,7E-1	
		GOTERM_BP_ALL regulation of Ras protein signal transduction	RT		38	1,3	7,6E-2	7,7E-1	
		GOTERM_BP_ALL positive regulation of pathway-restricted SMAD protein phosphorylation	RT		12	0,4	7,6E-2	7,7E-1	
		GOTERM_BP_ALL cation transmembrane transport	RT		116	4,1	7,6E-2	7,7E-1	
		GOTERM_BP_ALL positive regulation of Wnt signaling pathway	RT		30	1,1	7,7E-2	7,7E-1	
		GOTERM_BP_ALL negative regulation of mononuclear cell proliferation	RT		15	0,5	7,7E-2	7,8E-1	
		GOTERM_BP_ALL cyclic-nucleotide-mediated signaling	RT		15	0,5	7,7E-2	7,8E-1	
		GOTERM_BP_ALL regulation of smoothened signaling pathway	RT		15	0,5	7,7E-2	7,8E-1	
		GOTERM_BP_ALL post-Golgi vesicle-mediated transport	RT		15	0,5	7,7E-2	7,8E-1	
Download File									
158 5,5 3,9E-2 6,5E-1									
20 0,7 3,9E-2 6,6E-1									
20 0,7 3,9E-2 6,6E-1									
10 0,4 4,0E-2 6,6E-1									
10 0,4 4,0E-2 6,6E-1									
24 0,8 4,0E-2 6,6E-1									
14 0,5 4,0E-2 6,6E-1									
14 0,5 4,0E-2 6,6E-1									
6 0,2 4,0E-2 6,6E-1									
63 2,2 4,1E-2 6,7E-1									
13 0,5 4,2E-2 6,8E-1									
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60 2,1 4,2E-2 6,8E-1									
132 4,6 4,2E-2 6,8E-1									
942 33,0 4,2E-2 6,8E-1									

[GOTERM_BP_ALL regulation of transferase activity](#)[RT](#) 158 5,5 3,9E-2 6,5E-1[GOTERM_BP_ALL proteoglycan metabolic process](#)[RT](#) 20 0,7 3,9E-2 6,6E-1[GOTERM_BP_ALL response to heat](#)[RT](#) 20 0,7 3,9E-2 6,6E-1[GOTERM_BP_ALL neuron recognition](#)[RT](#) 10 0,4 4,0E-2 6,6E-1[GOTERM_BP_ALL salivary gland morphogenesis](#)[RT](#) 10 0,4 4,0E-2 6,6E-1[GOTERM_BP_ALL smoothened signaling pathway](#)[RT](#) 24 0,8 4,0E-2 6,6E-1[GOTERM_BP_ALL lung morphogenesis](#)[RT](#) 14 0,5 4,0E-2 6,6E-1[GOTERM_BP_ALL positive regulation of extrinsic apoptotic signaling pathway](#)[RT](#) 14 0,5 4,0E-2 6,6E-1[GOTERM_BP_ALL regulation of hematopoietic progenitor cell differentiation](#)[RT](#) 6 0,2 4,0E-2 6,6E-1[GOTERM_BP_ALL epithelial cell proliferation](#)[RT](#) 63 2,2 4,1E-2 6,7E-1[GOTERM_BP_ALL exocrine system development](#)[RT](#) 13 0,5 4,2E-2 6,8E-1[GOTERM_BP_ALL lipopolysaccharide-mediated signaling pathway](#)[RT](#) 13 0,5 4,2E-2 6,8E-1[GOTERM_BP_ALL protein import](#)[RT](#) 60 2,1 4,2E-2 6,8E-1[GOTERM_BP_ALL regulation of kinase activity](#)[RT](#) 132 4,6 4,2E-2 6,8E-1[GOTERM_BP_ALL cellular component organization or biogenesis](#)[RT](#) 942 33,0 4,2E-2 6,8E-1

<input type="checkbox"/>	GOTERM_BP_ALL neurogenesis	RT 	255	8,9	2,9E-4	5,0E-2
<input type="checkbox"/>	GOTERM_BP_ALL glycoprotein biosynthetic process	RT 	76	2,7	3,1E-4	5,2E-2
<input type="checkbox"/>	GOTERM_BP_ALL cellular nitrogen compound biosynthetic process	RT 	785	27,5	3,7E-4	6,1E-2
<input type="checkbox"/>	GOTERM_BP_ALL central nervous system neuron differentiation	RT 	43	1,5	3,7E-4	6,0E-2
<input type="checkbox"/>	GOTERM_BP_ALL single-multicellular organism process	RT 	932	32,7	3,9E-4	6,1E-2
<input type="checkbox"/>	GOTERM_BP_ALL neuron differentiation	RT 	219	7,7	3,9E-4	6,1E-2
<input type="checkbox"/>	GOTERM_BP_ALL multicellular organism development	RT 	774	27,1	4,0E-4	6,1E-2
<input type="checkbox"/>	GOTERM_BP_ALL cell development	RT 	335	11,7	4,2E-4	6,3E-2
<input type="checkbox"/>	GOTERM_BP_ALL single-organism developmental process	RT 	862	30,2	4,3E-4	6,4E-2
<input type="checkbox"/>	GOTERM_BP_ALL generation of neurons	RT 	238	8,3	6,3E-4	9,0E-2
<input type="checkbox"/>	GOTERM_BP_ALL regulation of fatty acid metabolic process	RT 	25	0,9	7,0E-4	9,8E-2
<input type="checkbox"/>	GOTERM_BP_ALL primary metabolic process	RT 	1548	54,3	7,1E-4	9,8E-2
<input type="checkbox"/>	GOTERM_BP_ALL cellular aromatic compound metabolic process	RT 	930	32,6	8,1E-4	1,1E-1
<input type="checkbox"/>	GOTERM_BP_ALL nucleobase-containing compound metabolic process	RT 	905	31,7	8,5E-4	1,1E-1
<input type="checkbox"/>	GOTERM_BP_ALL anatomical structure development	RT 	857	30,0	8,9E-4	1,2E-1

■ Pathways (3 selected)

<input checked="" type="checkbox"/> BBID	1.9%	53	Chart	
<input checked="" type="checkbox"/> BIOCARTA	9.0%	257	Chart	
<input type="checkbox"/> EC_NUMBER	22.6%	644	Chart	
<input checked="" type="checkbox"/> KEGG_PATHWAY	33.2%	946	Chart	
<input type="checkbox"/> REACTOME_PATHWAY	45.8%	1307	Chart	

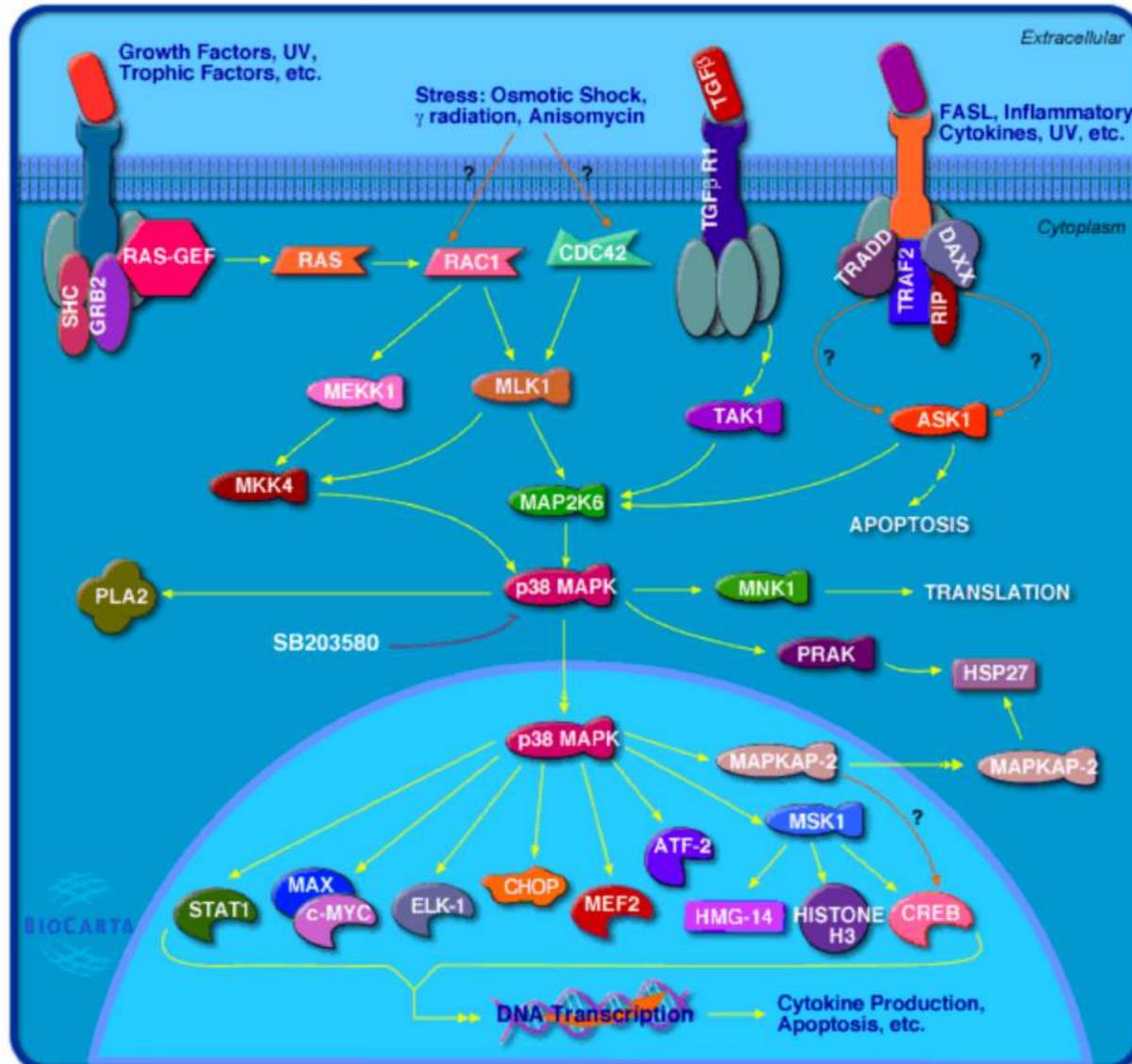
Functional Annotation Chart

[Help and Manual](#)**Current Gene List:** List_1**Current Background:** Homo sapiens**2852 DAVID IDs****Options**[Rerun Using Options](#)[Create Sublist](#)**9 chart records** [Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	BIOCARTA	PKC-catalyzed phosphorylation of inhibitory phosphoprotein of myosin phosphatase	RT	9	0,3	8,0E-4	2,0E-1	
<input type="checkbox"/>	BIOCARTA	Dicer Pathway	RT	5	0,2	2,6E-3	3,0E-1	
<input type="checkbox"/>	BIOCARTA	Thrombin signaling and protease-activated receptors	RT	10	0,4	5,6E-3	4,0E-1	
<input type="checkbox"/>	BIOCARTA	Signal transduction through IL1R	RT	11	0,4	2,5E-2	8,3E-1	
<input type="checkbox"/>	BIOCARTA	p38 MAPK Signaling Pathway	RT	12	0,4	3,9E-2	8,9E-1	
<input type="checkbox"/>	BIOCARTA	Attenuation of GPCR Signaling	RT	6	0,2	4,1E-2	8,5E-1	
<input type="checkbox"/>	BIOCARTA	CD40L Signaling Pathway	RT	6	0,2	7,3E-2	9,5E-1	
<input type="checkbox"/>	BIOCARTA	Metabolism of Anandamide, an Endogenous Cannabinoid	RT	4	0,1	8,3E-2	9,5E-1	
<input type="checkbox"/>	BIOCARTA	CTCF	RT	8	0,3	8,5E-2	9,3E-1	

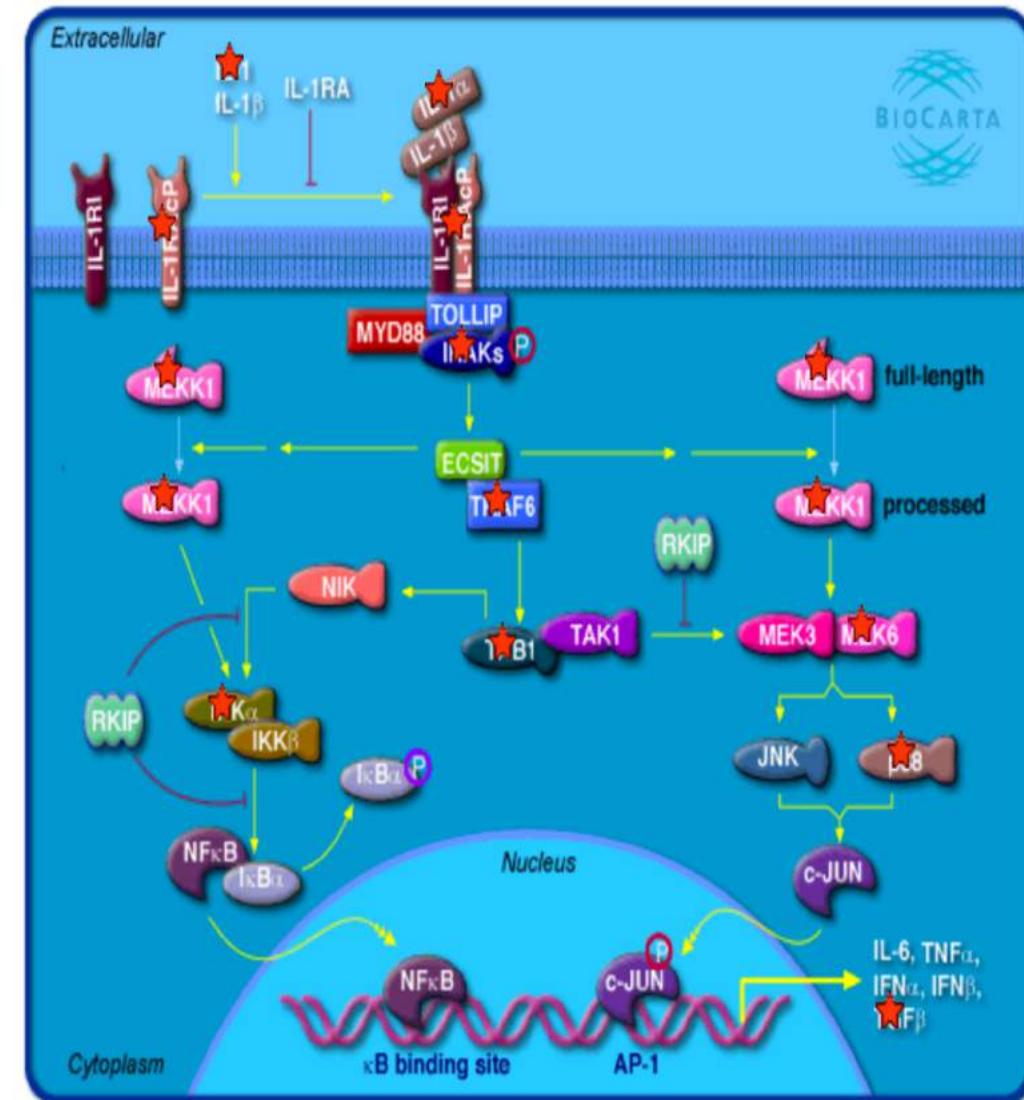
Pathway:p38 MAPK Signaling Pathway

Pathway information generated by Biocarta. Link to [Biocarta](#) CGAP Legend Stop Blinking



Pathway:Signal transduction through IL1R

Pathway information generated by Biocarta. Link to [Biocarta](#) CGAP Legend Stop Blinking



64 chart records

[Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
	KEGG_PATHWAY	Retrograde endocannabinoid signaling	RT	28	1,0	3,8E-4	1,0E-1	
	KEGG_PATHWAY	Morphine addiction	RT	26	0,9	3,9E-4	5,4E-2	
	KEGG_PATHWAY	GABAergic synapse	RT	24	0,8	8,3E-4	7,6E-2	
	KEGG_PATHWAY	Sphingolipid signaling pathway	RT	30	1,1	1,4E-3	9,3E-2	
	KEGG_PATHWAY	mTOR signaling pathway	RT	18	0,6	1,5E-3	8,2E-2	
	KEGG_PATHWAY	Cholinergic synapse	RT	28	1,0	1,8E-3	8,2E-2	
	KEGG_PATHWAY	Axon guidance	RT	30	1,1	3,4E-3	1,3E-1	
	KEGG_PATHWAY	Dopaminergic synapse	RT	30	1,1	3,9E-3	1,3E-1	
	KEGG_PATHWAY	Inflammatory mediator regulation of TRP channels	RT	24	0,8	6,1E-3	1,8E-1	
	KEGG_PATHWAY	Prolactin signaling pathway	RT	19	0,7	6,2E-3	1,6E-1	
	KEGG_PATHWAY	Non-small cell lung cancer	RT	16	0,6	7,1E-3	1,7E-1	
	KEGG_PATHWAY	Chronic myeloid leukemia	RT	19	0,7	7,3E-3	1,6E-1	
	KEGG_PATHWAY	Circadian entrainment	RT	23	0,8	8,4E-3	1,7E-1	
	KEGG_PATHWAY	Ras signaling pathway	RT	45	1,6	9,3E-3	1,7E-1	
	KEGG_PATHWAY	Glutamatergic synapse	RT	26	0,9	1,1E-2	1,8E-1	
	KEGG_PATHWAY	Neurotrophin signaling pathway	RT	27	0,9	1,1E-2	1,8E-1	
	KEGG_PATHWAY	Pathways in cancer	RT	71	2,5	1,1E-2	1,7E-1	
	KEGG_PATHWAY	Glycosaminoglycan biosynthesis - heparan sulfate / heparin	RT	9	0,3	1,2E-2	1,7E-1	
	KEGG_PATHWAY	Thyroid hormone signaling pathway	RT	26	0,9	1,2E-2	1,6E-1	
	KEGG_PATHWAY	ErbB signaling pathway	RT	21	0,7	1,3E-2	1,7E-1	
	KEGG_PATHWAY	Glioma	RT	17	0,6	1,3E-2	1,6E-1	
	KEGG_PATHWAY	T cell receptor signaling pathway	RT	23	0,8	1,5E-2	1,8E-1	
	KEGG_PATHWAY	Cell adhesion molecules (CAMs)	RT	30	1,1	1,7E-2	1,9E-1	
	KEGG_PATHWAY	MAPK signaling pathway	RT	48	1,7	1,7E-2	1,9E-1	
	KEGG_PATHWAY	Steroid hormone biosynthesis	RT	15	0,5	2,3E-2	2,3E-1	
	KEGG_PATHWAY	Neuroactive ligand-receptor interaction	RT	51	1,8	2,4E-2	2,3E-1	
	KEGG_PATHWAY	Other types of O-glycan biosynthesis	RT	8	0,3	2,4E-2	2,2E-1	
	KEGG_PATHWAY	Signaling pathways regulating pluripotency of stem cells	RT	29	1,0	2,4E-2	2,2E-1	
	KEGG_PATHWAY	FoxO signaling pathway	RT	28	1,0	2,4E-2	2,1E-1	
	KEGG_PATHWAY	Ascorbate and aldarate metabolism	RT	9	0,3	2,5E-2	2,1E-1	
	KEGG_PATHWAY	Pancreatic cancer	RT	16	0,6	2,8E-2	2,3E-1	
	KEGG_PATHWAY	cAMP signaling pathway	RT	38	1,3	2,9E-2	2,3E-1	
	KEGG_PATHWAY	Renal cell carcinoma	RT	16	0,6	3,1E-2	2,4E-1	
	KEGG_PATHWAY	Focal adhesion	RT	39	1,4	3,3E-2	2,4E-1	
	KEGG_PATHWAY	Measles	RT	27	0,9	3,7E-2	2,7E-1	
	KEGG_PATHWAY	GnRH signaling pathway	RT	20	0,7	3,8E-2	2,7E-1	
	KEGG_PATHWAY	Fc epsilon RI signaling pathway	RT	16	0,6	4,0E-2	2,7E-1	
	KEGG_PATHWAY	Nicotine addiction	RT	11	0,4	4,0E-2	2,6E-1	
	KEGG_PATHWAY	Epstein-Barr virus infection	RT	25	0,9	4,2E-2	2,7E-1	
	KEGG_PATHWAY	Endometrial cancer	RT	13	0,5	4,6E-2	2,8E-1	
	KEGG_PATHWAY	Estrogen signaling pathway	RT	21	0,7	4,7E-2	2,8E-1	
								Download File

KEGG PATHWAY analysis

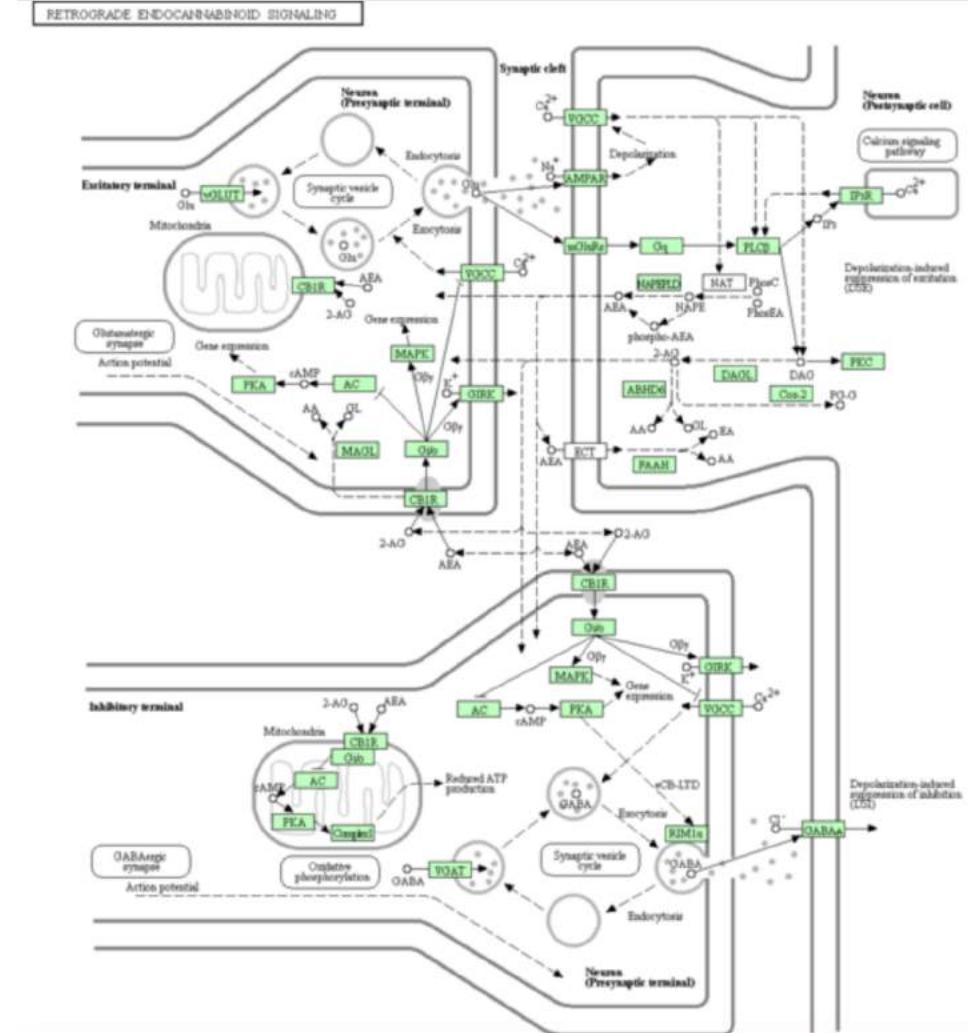
[Pathway menu | Organism menu | Pathway entry | Download KGML | Hide description | User data mapping]

Endogenous cannabinoids (endocannabinoids) serve as retrograde messengers at synapses in various regions of the brain. The family of endocannabinoids includes at least five derivatives of arachidonic acid; the two best characterized are arachidonoyl ethanolamide (anandamide, AEA) and 2-arachidonoyl glycerol (2AG). They are released from postsynaptic neurons upon postsynaptic depolarization and/or receptor activation. The released endocannabinoids then activate the CB1 receptors (CB1R) at presynaptic terminals and suppress the release of inhibitory transmitter GABA (depolarization-induced suppression of inhibition, DSI) or excitatory transmitter glutamate (depolarization-induced suppression of excitation, DSE) by inhibiting Ca^{2+} channels. Besides the well-known expression of the CB1R in the plasma membrane, this receptor is also present in mitochondrial membranes, where it reduces the mitochondrial respiration and contributes to DSI. Whereas DSI and DSE result in short-term synaptic plasticity, endocannabinoids also mediate long-term synaptic changes (eCB-LTD). Persistent activation of CB1 receptors over a period of minutes triggers eCB-LTD by a RIM1alpha-dependent mechanism.

Homo sapiens (human)

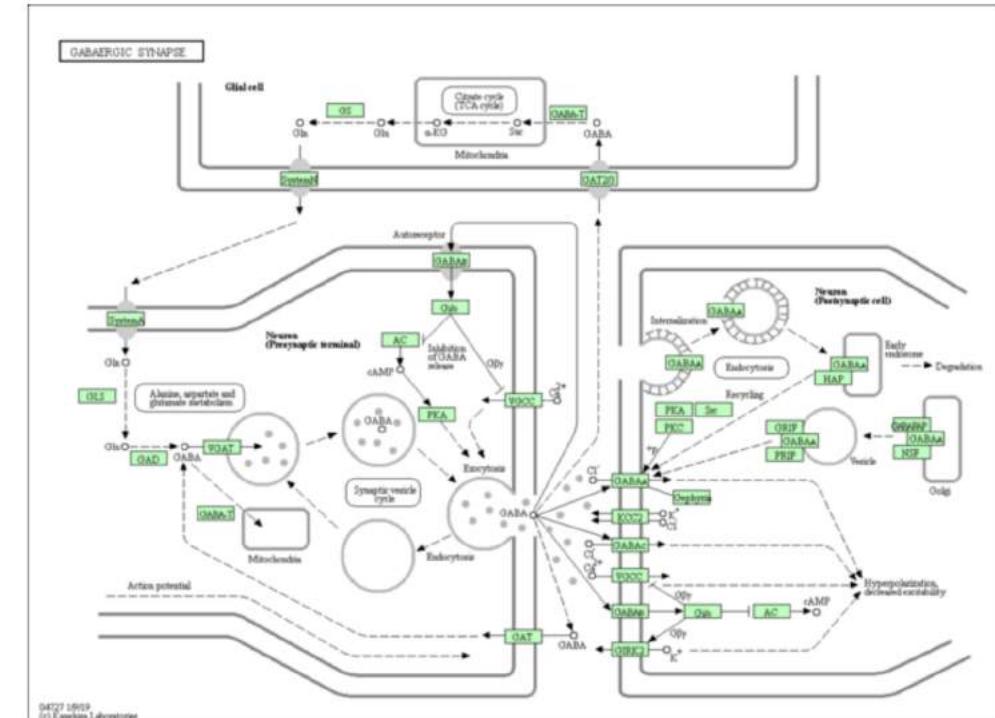
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[Pathway menu | Organism menu | Pathway entry | Download KGML | Hide description | User data mapping]

Gamma aminobutyric acid (GABA) is the most abundant inhibitory neurotransmitter in the mammalian central nervous system (CNS). When released in the synaptic cleft, GABA binds to three major classes of receptors: GABAA, GABAB, and GABAC receptors. GABAA and GABAC receptors are ionotropic and mediate fast GABA responses by triggering chloride channel openings, while GABAB receptors are metabotropic and mediate slower GABA responses by activating G-proteins and influencing second messenger systems. GABAA receptors, the major sites for fast inhibitory neurotransmission in the CNS, are regulated by phosphorylation mechanisms, affecting both their functional properties and their cell surface mobility and trafficking. GABA release by the presynaptic terminal is negatively regulated by GABAB autoreceptors, and is cleared from the extracellular space by GABA transporters (GATs) located either on the presynaptic terminal or neighboring glial cells.



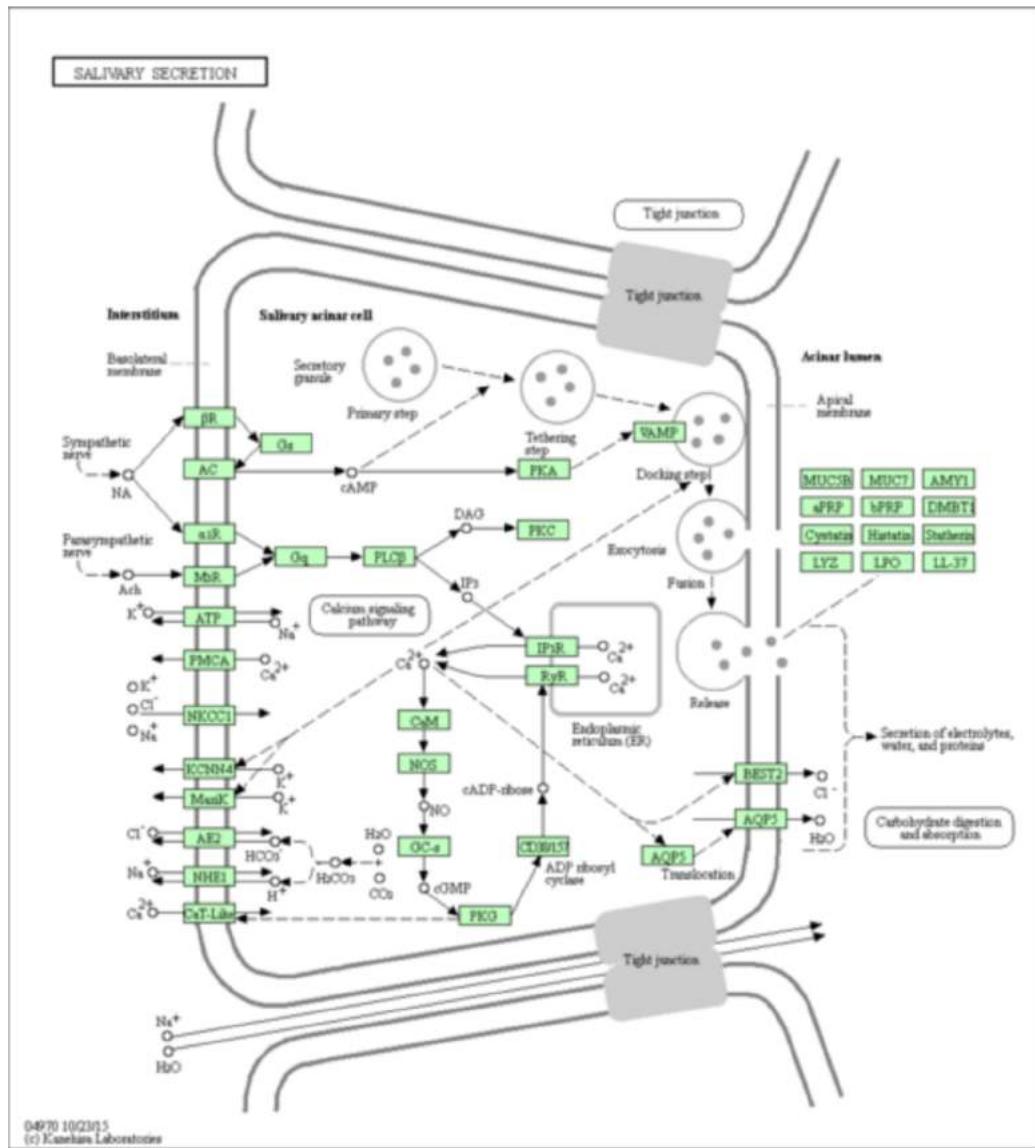
Annotation Cluster 99	Enrichment Score: 0.65	G		Count	P_Value	Benjamini
KEGG_PATHWAY	Endocrine and other factor-regulated calcium reabsorption	RT	I	11	8.1E-2	3.5E-1
KEGG_PATHWAY	Insulin secretion	RT	I	16	1.8E-1	4.9E-1
KEGG_PATHWAY	Thyroid hormone synthesis	RT	I	13	2.5E-1	5.7E-1
KEGG_PATHWAY	Salivary secretion	RT	I	15	2.9E-1	6.1E-1
KEGG_PATHWAY	Pancreatic secretion	RT	I	16	2.9E-1	6.1E-1
KEGG_PATHWAY	Gastric acid secretion	RT	I	12	4.2E-1	7.1E-1



Salivary secretion - Homo sapiens (human)

[[Pathway menu](#) | [Organism menu](#) | [Pathway entry](#) | [Download KGML](#) | [Hide description](#) | [User data mapping](#)]

Saliva has manifold functions in maintaining the integrity of the oral tissues, in protecting teeth from caries, in the tasting and ingestion of food, in speech and in the tolerance of tenures, for example. Salivary secretion occurs in response to stimulation by neurotransmitters released from autonomic nerve endings. There are two secretory pathways: protein exocytosis and fluid secretion. Sympathetic stimulation leads to the activation of adenylate cyclase and accumulation of intracellular cAMP. The elevation of cAMP causes the secretion of proteins such as amylase and mucin. In contrast, parasympathetic stimulation activates phospholipase C and causes the elevation of intracellular Ca²⁺, which leads to fluid secretion; that is, water and ion transport. Ca²⁺ also induces amylase secretion, but the amount is smaller than that induced by cAMP.



Annotation Cluster 33		Enrichment Score: 1.05		G			Count	P_Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	Non-small cell lung cancer		RT			16	7.1E-3	1.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	Chronic myeloid leukemia		RT			19	7.3E-3	1.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Glioma		RT			17	1.3E-2	1.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Pancreatic cancer		RT			16	2.8E-2	2.3E-1
<input type="checkbox"/>	KEGG_PATHWAY	Endometrial cancer		RT			13	4.6E-2	2.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	Melanoma		RT			15	1.0E-1	3.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	Colorectal cancer		RT			13	1.4E-1	4.3E-1
<input type="checkbox"/>	KEGG_PATHWAY	Hepatitis B		RT			24	2.6E-1	5.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	Central carbon metabolism in cancer		RT			11	3.8E-1	6.9E-1
<input type="checkbox"/>	KEGG_PATHWAY	Prostate cancer		RT			14	4.3E-1	7.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	B cell receptor signaling pathway		RT			10	6.2E-1	8.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	Acute myeloid leukemia		RT			7	8.0E-1	9.1E-1

35 chart records

 [Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-212436	RT		85	3,0	2,0E-6	2,2E-3
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-1989781	RT		27	0,9	9,1E-3	9,9E-1
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-2022928	RT		11	0,4	9,2E-3	9,6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-156588	RT		8	0,3	9,4E-3	9,2E-1
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-426496	RT		5	0,2	1,0E-2	8,9E-1
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-83936	RT		5	0,2	1,0E-2	8,9E-1
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-1433557	RT		12	0,4	1,2E-2	8,9E-1
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-5628897	RT		21	0,7	1,6E-2	9,2E-1
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-1912408	RT		10	0,4	1,7E-2	9,0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-1296041	RT		9	0,3	2,0E-2	9,1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-997272	RT		9	0,3	2,0E-2	9,1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-975298	RT		9	0,3	2,5E-2	9,4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-977441	RT		6	0,2	2,9E-2	9,4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-426486	RT		5	0,2	2,9E-2	9,3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-1660516	RT		6	0,2	4,0E-2	9,7E-1
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-112314	RT		6	0,2	4,0E-2	9,7E-1
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-193368	RT		8	0,3	4,7E-2	9,8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	R-HSA-193807	RT		6	0,2	5,3E-2	9,8E-1

KO (KEGG Orthology Database)



KO (KEGG ORTHOLOGY) Database

Linking genomes to pathways by ortholog annotation

Menu PATHWAY BRITE MODULE KO Annotation ENZYME RModule BlastKOALA

Search KO for

Go

KO Database of Molecular Functions

The **KO (KEGG Orthology)** database is a database of molecular functions represented in terms of functional orthologs. A functional ortholog is manually defined in the context of KEGG molecular networks, namely, KEGG pathway maps, BRITE hierarchies and KEGG modules. For example, when a pathway map is drawn, each box is given a KO identifier (called K number) and experimentally characterized genes and proteins in specific organisms are used to find orthologs in other organisms. The granularity of "function" is context-dependent, and the resulting KO grouping may correspond to a highly similar sequence group and a limited organism group or it may be a more divergent group.

The KO system is a network-based classification of KOs shown below:

KEGG Orthology (KO)

It consists of six top categories (09100 to 09160) for KEGG pathway maps and one top category (09180) for BRITE hierarchies, as well as one top category (09190) for those KOs that are not yet included in either of them. The category numbers for these top categories and the second-level categories under metabolism (09101 to 09112) are used to define color coding of functions (see [KEGG Color Codes](#)).

Major efforts have been made to associate each KO entry with experimental evidence of functionally characterized sequence data, now shown in the SEQUENCE subfield of the REFERENCE field. Similar efforts have also been made for EC numbers in [Enzyme Nomenclature](#). The addendum category of the GENES database, which allows functionally characterized individual protein sequences to be included in KEGG, have played major roles in these efforts.

KO Assignment and KEGG Mapping

KO Mappings

File Edit View Insert Format

fx

	A	B
1	Gene Symbol	KO Code
2	HMGB1	K00750
3	CREBZF	K19668
4	RFX7	K19862
5	DCAF5	K19668
6	JMJD1C	K00750
7	ANKRD13C	K01623
8	PCDH9	K19862
9	ACACA	#N/A
10	FOXP1	K01223
11	ARID4B	K01623
12	GCNT1	K01223
13	BRD4	K00694
14	RAPGEF2	K19862
15	ACSL3	#N/A
16	HNMT	K00750
17	ZEB1	K07742
18	GSE1	K20812
19	ZBTB11	K07742

Pathway Search Result

Sort by the pathway list

Show all objects

- ko00500 Starch and sucrose metabolism (7)
- ko01100 Metabolic pathways (7)
- ko04360 Axon guidance (4)
- ko05200 Pathways in cancer (4)
- ko01110 Biosynthesis of secondary metabolites (3)
- ko05145 Toxoplasmosis (3)
- ko05163 Human cytomegalovirus infection (3)
- ko05142 Chagas disease (American trypanosomiasis) (3)
- ko04380 Osteoclast differentiation (3)
- ko04659 Th17 cell differentiation (2)
- ko04658 Th1 and Th2 cell differentiation (2)
- ko04062 Chemokine signaling pathway (2)
- ko05133 Pertussis (2)
- ko04010 MAPK signaling pathway (2)
- ko05132 Salmonella infection (2)
- ko04625 C-type lectin receptor signaling pathway (2)
- ko05418 Fluid shear stress and atherosclerosis (2)
- ko05140 Leishmaniasis (2)
- ko04611 Platelet activation (2)
- ko04024 cAMP signaling pathway (2)
- ko04015 Rap1 signaling pathway (2)
- ko05206 MicroRNAs in cancer (2)
- ko05321 Inflammatory bowel disease (IBD) (2)
- ko05167 Kaposi sarcoma-associated herpesvirus infection (2)
- ko05152 Tuberculosis (2)
- ko05165 Human papillomavirus infection (2)
- ko04144 Endocytosis (2)
- ko04722 Neurotrophin signaling pathway (2)
- ko05164 Influenza A (2)
- ko05162 Measles (2)
- ko04660 T cell receptor signaling pathway (2)
- ko04218 Cellular senescence (2)
- ko01130 Biosynthesis of antibiotics (2)
- ko04066 HIF-1 signaling pathway (2)
- ko04071 Sphingolipid signaling pathway (2)
- ko05168 Herpes simplex infection (2)
- ko04151 PI3K-Akt signaling pathway (2)
- ko05170 Human immunodeficiency virus 1 infection (2)
- ko05030 Cocaine addiction (2)
- ko04926 Relaxin signaling pathway (2)
- ko05203 Viral carcinogenesis (2)
- ko00010 Glycolysis / Gluconeogenesis (2)
- ko00051 Fructose and mannose metabolism (1)
- ko04650 Natural killer cell mediated cytotoxicity (1)
- ko04727 GABAergic synapse (1)
- ko00680 Methane metabolism (1)
- ko04670 Leukocyte transendothelial migration (1)
- ko04512 ECM-receptor interaction (1)
- ko04510 Focal adhesion (1)
- ko04662 B cell receptor signaling pathway (1)
- ko04924 Renin secretion (1)
- ko04060 Cytokine-cytokine receptor interaction (1)
- ko05146 Amoebiasis (1)
- ko04920 Adipocytokine signaling pathway (1)
- ko04624 Toll and Imd signaling pathway (1)
- ko04668 TNF signaling pathway (1)
- ko05160 Hepatitis C (1)
- ko04210 Apoptosis (1)
- ko05202 Transcriptional misregulation in cancer (1)
- ko04012 ErbB signaling pathway (1)
- ko04621 NOD-like receptor signaling pathway (1)
- ko01200 Carbon metabolism (1)
- ko05220 Chronic myeloid leukemia (1)
- ko04370 VEGF signaling pathway (1)
- ko04919 Thyroid hormone signaling pathway (1)
- ko04730 Long-term depression (1)
- ko05212 Pancreatic cancer (1)
- ko04623 Cytosolic DNA-sensing pathway (1)
- ko04726 Serotonergic synapse (1)

- ko04810 Regulation of actin cytoskeleton (1)
- ko05410 Hypertrophic cardiomyopathy (HCM) (1)
- ko05412 Arrhythmogenic right ventricular cardiomyopathy (ARVC) (1)
- ko05032 Morphine addiction (1)
- ko04725 Cholinergic synapse (1)
- ko01523 Antifolate resistance (1)
- ko04923 Regulation of lipolysis in adipocytes (1)
- ko05134 Legionellosis (1)
- ko04728 Dopaminergic synapse (1)
- ko05120 Epithelial cell signaling in Helicobacter pylori infection (1)
- ko04916 Melanogenesis (1)
- ko04724 Glutamatergic synapse (1)
- ko05166 Human T-cell leukemia virus 1 infection (1)
- ko04014 Ras signaling pathway (1)
- ko04934 Cushing syndrome (1)
- ko04142 Lysosome (1)
- ko04657 IL-17 signaling pathway (1)
- ko04921 Oxytocin signaling pathway (1)
- ko05161 Hepatitis B (1)
- ko04064 NF-kappa B signaling pathway (1)
- ko04971 Gastric acid secretion (1)
- ko05222 Small cell lung cancer (1)
- ko05131 Shigellosis (1)
- ko04340 Hedgehog signaling pathway (1)
- ko02026 Biofilm formation - Escherichia coli (1)
- ko04931 Insulin resistance (1)
- ko04630 JAK-STAT signaling pathway (1)
- ko04723 Retrograde endocannabinoid signaling (1)
- ko00030 Pentose phosphate pathway (1)
- ko04933 AGE-RAGE signaling pathway in diabetic complications (1)
- ko01120 Microbial metabolism in diverse environments (1)
- ko05215 Prostate cancer (1)
- ko04928 Parathyroid hormone synthesis, secretion and action (1)
- ko01230 Biosynthesis of amino acids (1)
- ko04917 Prolactin signaling pathway (1)
- ko04713 Circadian entrainment (1)
- ko04371 Apelin signaling pathway (1)
- ko04261 Adrenergic signaling in cardiomyocytes (1)
- ko05205 Proteoglycans in cancer (1)
- ko04145 Phagosome (1)
- ko04915 Estrogen signaling pathway (1)
- ko04320 Dorso-ventral axis formation (1)
- ko04620 Toll-like receptor signaling pathway (1)
- ko04211 Longevity regulating pathway (1)
- ko00710 Carbon fixation in photosynthetic organisms (1)
- ko04622 RIG-I-like receptor signaling pathway (1)
- ko04022 cGMP-PKG signaling pathway (1)
- ko04640 Hematopoietic cell lineage (1)
- ko05034 Alcoholism (1)
- ko05221 Acute myeloid leukemia (1)
- ko05130 Pathogenic Escherichia coli infection (1)
- ko05012 Parkinson disease (1)
- ko05210 Colorectal cancer (1)
- ko05169 Epstein-Barr virus infection (1)
- ko04914 Progesterone-mediated oocyte maturation (1)
- ko04217 Necroptosis (1)
- ko02020 Two-component system (1)
- ko04540 Gap junction (1)
- ko04932 Non-alcoholic fatty liver disease (NAFLD) (1)
- ko00900 Terpenoid backbone biosynthesis (1)
- ko05414 Dilated cardiomyopathy (DCM) (1)

GOMiner

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GOMINER™
 Application Build: 469 Database Build: 2011-01
Genomics and Pharmacology Facility
DTB, CCR, National Cancer Institute

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This is the web interface for High-Throughput GoMiner™. You need to upload two files to the server, a total file with all of the genes in your experiment, and one of two types of changed files. Detailed descriptions of the [input files](#) are available. You will receive an email message with instructions on how to download your results once they are complete. Documentation for both the [output files](#) generated and possible [error codes](#) are also online.

Step 1:

Select total file

OR

Select [Auto-Generate](#) option

Step 2: Select the changed file

Przeglądaj... Nie wybrano pliku.

Input should be a text file with '.txt' extension, if no file is specified

[Auto-Generate](#) (Increases Computation Time Significantly)

Step 3: Select DataSource(s)

Data sources:

WB (*C. elegans*)
ZFIN (*D. rerio*)
GR_protein (*Oryza*)
dictyBase (*discoideum*)
PDB (*H. sapiens* et al.)

Specify semicolon separated list of data sources:

You find possible values at the [Gene Ontology web site](#); look at the abbrev. For example, UniProtKB and Mouse Consortium would be UniProtKB;MGI

Step 4: Select Organism(s)

Organisms:

All
H. sapiens
M. musculus
R. norvegicus

From list

OR

Enter list

Gene list intersection

File Edit View Insert Format Data Tools Add-ons

Enseble Gene Name

	A	B	C
1	Enseble Gene Name	List	Intersection
2	DDX11L1	CDR1as	AL627309.1
3	WASH7P	FLG2	SDF4
4	MIR6859-1	FMO2	B3GALT6
5	MIR1302-2HG	PROZ	GNB1
6	MIR1302-2	USE1	HES5
7	FAM138A	ZNF667	MEGF6
8	OR4G4P	MDH1B	TP73
9	OR4G11P	MRGPRX4	LRRC47
10	OR4F5	TSPAN8	AJAP1
11	AL627309.1	PDZD2	CHD5
12	AL627309.3	PPP2R2A	ICMT
13	CICP27	TOMM5	ESPN
14	AL627309.6	SPZ1	PER3
15	AL627309.7	GSAP	TNFRSF9
16	AL627309.2	AP3M2	GPR157
17	AL627309.5	GCSAM	H6PD
18	RNU6-1100P	PHYKPL	TMEM201

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Application Build: 469 Database Build: 2011-01

Genomics and Pharmacology Facility
DTB, CCR, National Cancer Institute

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https://discover.nci.nih.gov/gominer/GoCommandWebInterface.jsp

HTGM Job Summary

Input and Parameters

Type	File	Description
Total File	mart_export-3.txt	User-submitted list of total genes in the experiment or analysis
Changed File	mir_4513_genenames_new.txt	User-submitted list of changed genes in the experiment or analysis
Summary of options	userinputparam.txt	A summary of the parameters selected by the user for this job
Database version	GODBVersion.txt	The version of the GO database used to process this job

Results

Type	File	Description
Archive Results (Zip)	HighThruputResult1592868075.zip	An archive of all of the result files for this job
Browsable Results (HTML)	Browse Results	A browsable collection of pages to navigate the result files for this job

Results for mir_4513_genenames_new.txt

Input Files

Type	File
Total File (Text)	mart_export-3.txt
Changed File (Text)	mir_4513_genenames_new.txt

Results files

Type	Text	Excel	HTML
Gene Category Summary (Changed Genes)	mir_4513_genenames_new.txt.change	mir_4513_genenames_new.txt.change.xls	mir_4513_genenames_new.txt.change.html
Gene Category Mapping (Changed Genes)	mir_4513_genenames_new.txt.change.gce	mir_4513_genenames_new.txt.change.gce.xls	mir_4513_genenames_new.txt.change.gce.html
CIM (Changed)	mir_4513_genenames_new.txt.change.gce.CIM		mir_4513_genenames_new.txt.change.gce.CIM.html

Navigation

[Up to Parent\(Results for Total File\)](#)

Category Summary Report for mir_4513_genenames_new.txt

	<u>TOTAL GENES</u>	<u>CHANGED GENES</u>	<u>ENRICHMENT LOG10(p)</u>	<u>CUMULATIVE NUMBER OF CATEGORIES</u>	<u>CUMULATIVE RANDOMS LOWER BOUND</u>	<u>CUMULATIVE RANDOMS MEAN</u>	<u>CUMULATIVE RANDOMS UPPER BOUND</u>	<u>CUMULATIVE FALSE DISCOVERY RATE</u>
GO:0050794 regulation of cellular process	6254	1112	1.138209	-8.777806 1	0.000000	0.0	0.000000	0.000000
GO:0005622 intracellular	10943	1837	1.074602	-8.584237 2	0.000000	0.0	0.000000	0.000000
GO:0009987 cellular process	11524	1921	1.067085	-8.246395 3	0.000000	0.0	0.000000	0.000000
GO:0044260 cellular macromolecule metabolic process	5677	1008	1.136623	-7.498204 4	0.000000	0.0	0.000000	0.000000
GO:0065007 biological regulation	7166	1243	1.110374	-7.272322 5	0.000000	0.0	0.000000	0.000000
GO:0019222 regulation of metabolic process	4089	747	1.169441	-7.191222 6	0.000000	0.0	0.000000	0.000000
GO:0044464 cell part	14268	2310	1.036392	-7.109467 7	0.000000	0.0	0.000000	0.000000
GO:2000112 regulation of cellular macromolecule biosy	2862	542	1.212285	-7.100658 8	0.000000	0.0	0.000000	0.000000
GO:0005623 cell	14269	2310	1.036319	-7.087311 9	0.000000	0.0	0.000000	0.000000
GO:0031323 regulation of cellular metabolic process	3792	697	1.176629	-7.074385 10	0.000000	0.0	0.000000	0.000000
GO:0031326 regulation of cellular biosynthetic process	3066	576	1.202611	-7.061067 11	0.000000	0.0	0.000000	0.000000
GO:0031326 regulation of cellular biosynthetic process	2918	551	1.208763	-7.045161 12	0.000000	0.0	0.000000	0.000000
GO:0010556 regulation of macromolecule biosynthetic	3087	579	1.200651	-6.996209 13	0.000000	0.0	0.000000	0.000000
GO:0009889 regulation of biosynthetic process	6667	1780	1.068902	-6.949089 14	0.000000	0.0	0.000000	0.000000
GO:0044424 intracellular part	6667	1160	1.113788	-6.862420 15	0.000000	0.0	0.000000	0.000000
GO:0050789 regulation of biological process	3628	668	1.178648	-6.858753 16	0.000000	0.0	0.000000	0.000000
GO:0009059 macromolecule biosynthetic process	3050	571	1.198426	-6.774949 17	0.000000	0.0	0.000000	0.000000
GO:0009059 macromolecule biosynthetic process	2973	558	1.201474	-6.764442 18	0.000000	0.0	0.000000	0.000000
GO:0009059 macromolecule biosynthetic process	3561	656	1.179253	-6.754995 19	0.000000	0.0	0.000000	0.000000

Gene Category Report for mir_4513_genenames_new.txt

<u>HYPERLINKED GO CATEGORY</u>							<u>HYPERLINKED GENE NAME</u>				
		<u>TOTAL GENES</u>	<u>CHANGED GENES</u>	<u>ENRICHMENT</u>	<u>LOG10(p)</u>	<u>CUMULATIVE NUMBER OF CATEGORIES</u>	<u>CUMULATIVE RANDOMS MEAN</u>	<u>CUMULATIVE RANDOMS MEAN</u>	<u>FALSE DISCOVERY RATE</u>		
<u>GO:0050794 regulation of cellular process</u>	<u>USP6NL</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		
<u>GO:0050794 regulation of cellular process</u>	<u>ATF2</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		
<u>GO:0050794 regulation of cellular process</u>	<u>GMFB</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		
<u>GO:0050794 regulation of cellular process</u>	<u>TMEM97</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		
<u>GO:0050794 regulation of cellular process</u>	<u>PREX2</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		
<u>GO:0050794 regulation of cellular process</u>	<u>NDST1</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		
<u>GO:0050794 regulation of cellular process</u>	<u>HTR6</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		
<u>GO:0050794 regulation of cellular process</u>	<u>ALKBH1</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		
<u>GO:0050794 regulation of cellular process</u>	<u>AKT3</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		
<u>GO:0050794 regulation of cellular process</u>	<u>DPYSL3</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		
<u>GO:0050794 regulation of cellular process</u>	<u>LIPG</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		
<u>GO:0050794 regulation of cellular process</u>	<u>BBX</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		
<u>GO:0050794 regulation of cellular process</u>	<u>GTSE1</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		
<u>GO:0050794 regulation of cellular process</u>	<u>ZNF284</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		
<u>GO:0050794 regulation of cellular process</u>	<u>CSNK2A1</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		
<u>GO:0050794 regulation of cellular process</u>	<u>ZNF283</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		
<u>GO:0050794 regulation of cellular process</u>	<u>UNC5B</u>	6254	1112	1.138209	-8.777806	1	0.0	0.0	0.000000		

[Home](#) | [One Matrix CIM](#) | [Two Matrix CIM](#) | [Help](#) | [Results](#)**Column Names****Order:** clustered**Distance method:**

Euclidean

Cluster**algorithm:**

Average Linkage

1:HDAC2

2:EPB41L5

3:TGFB2

4:SEMA3A

5:TACR1

6:MCC

7:BMPR2

8:HIF1A

9:ADNP

10:ADRA1A

11:SLC24A2

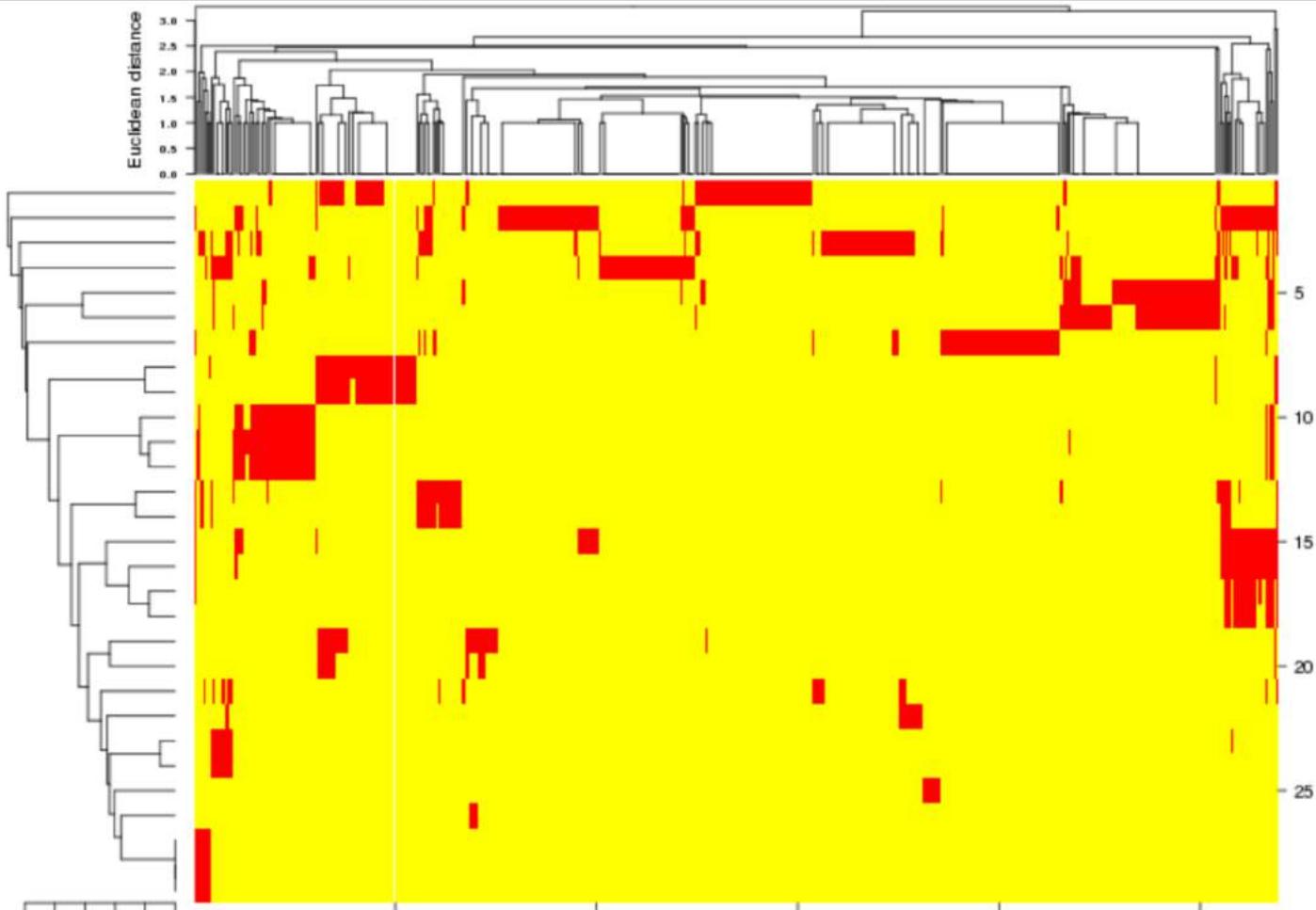
12:CD38

13:GNAI3

14:DRD5

15:STXBP1

16:GABBR1

**Row Names****Order:** clustered**Distance method:** Euclidean**Cluster algorithm:** Average Linkage

1:GO:0000139_Golgi_membrane

2:GO:0007417_central_nervous_system_devel

3:GO:0043005_neuron_projection

4:GO:0010648_negative_regulation_of_cell_co

5:GO:0007265_Ras_protein_signal_transductio

6:GO:0051056_regulation_of_small_GTPase_1

7:GO:0003779_actin_binding

8:GO:0009100_glycoprotein_metabolic_proce

9:GO:0009101_glycoprotein_biosynthetic_pro

10:GO:0051223_regulation_of_protein_transpo

11:GO:0032880_regulation_of_protein_localiz

12:GO:0070201_regulation_of_establishment_

13:GO:0031344_regulation_of_cell_projection

14:GO:0010975_regulation_of_neuron_project

15:GO:0030900_forebrain_development

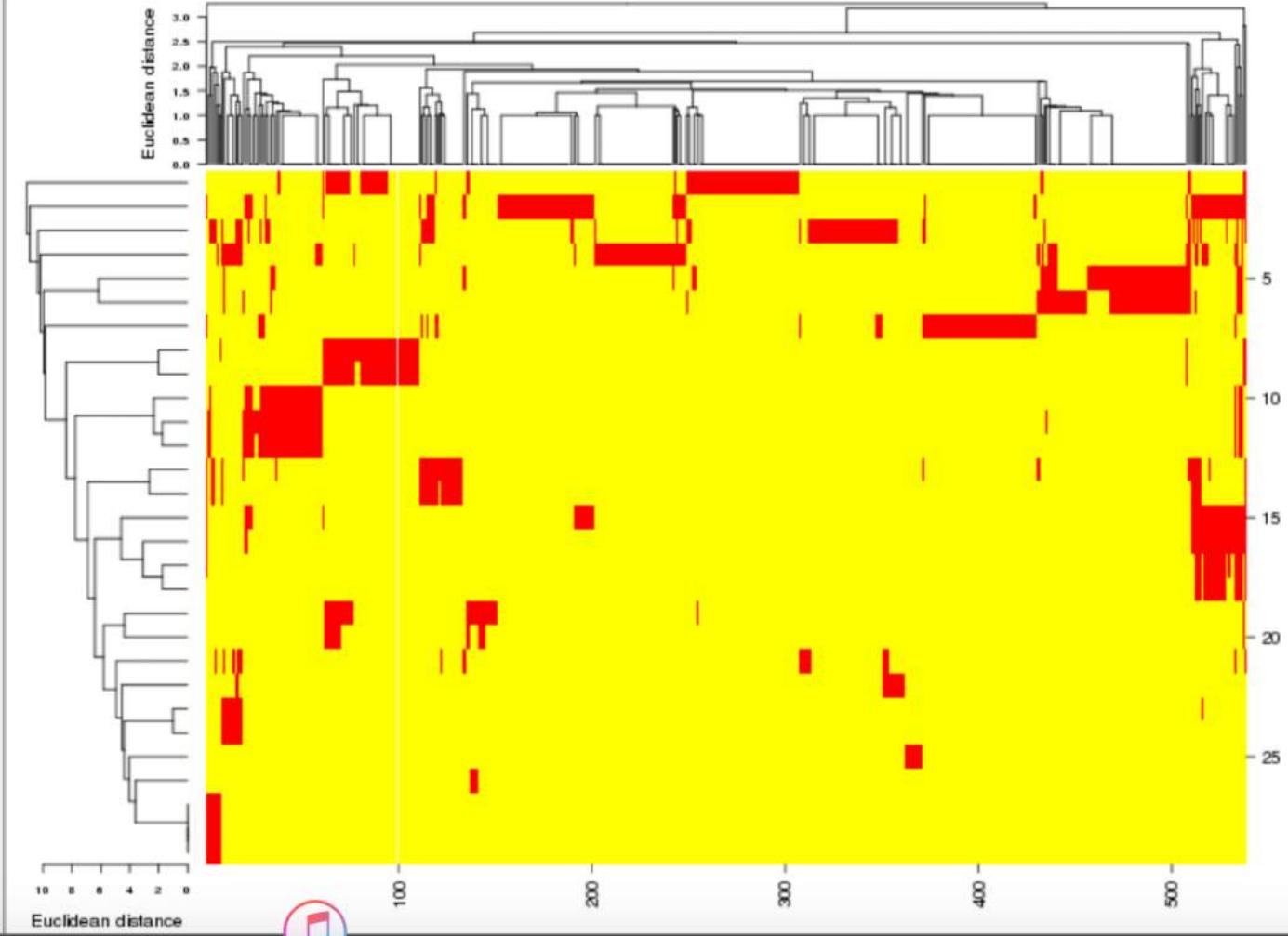
16:GO:0021537_telencephalon_development

17:GO:0021543_pallium_development

18:GO:0021987_cerebral_cortex_development



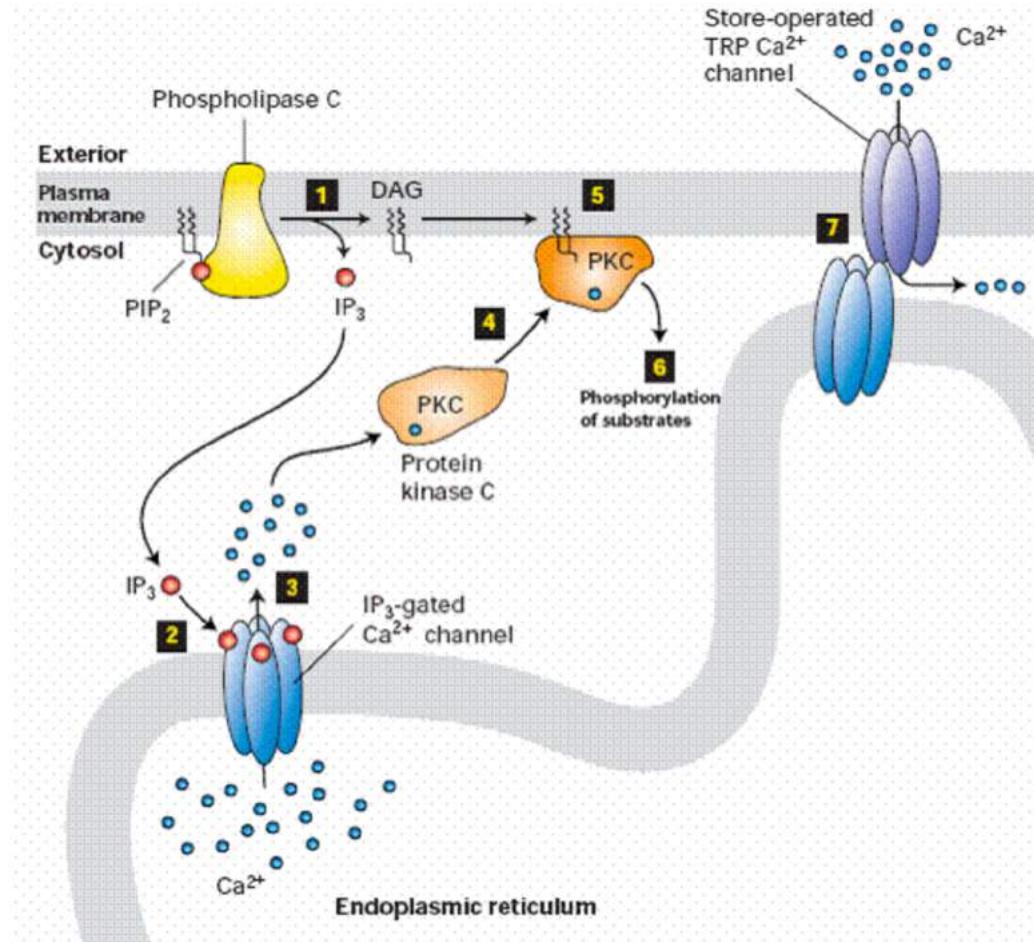
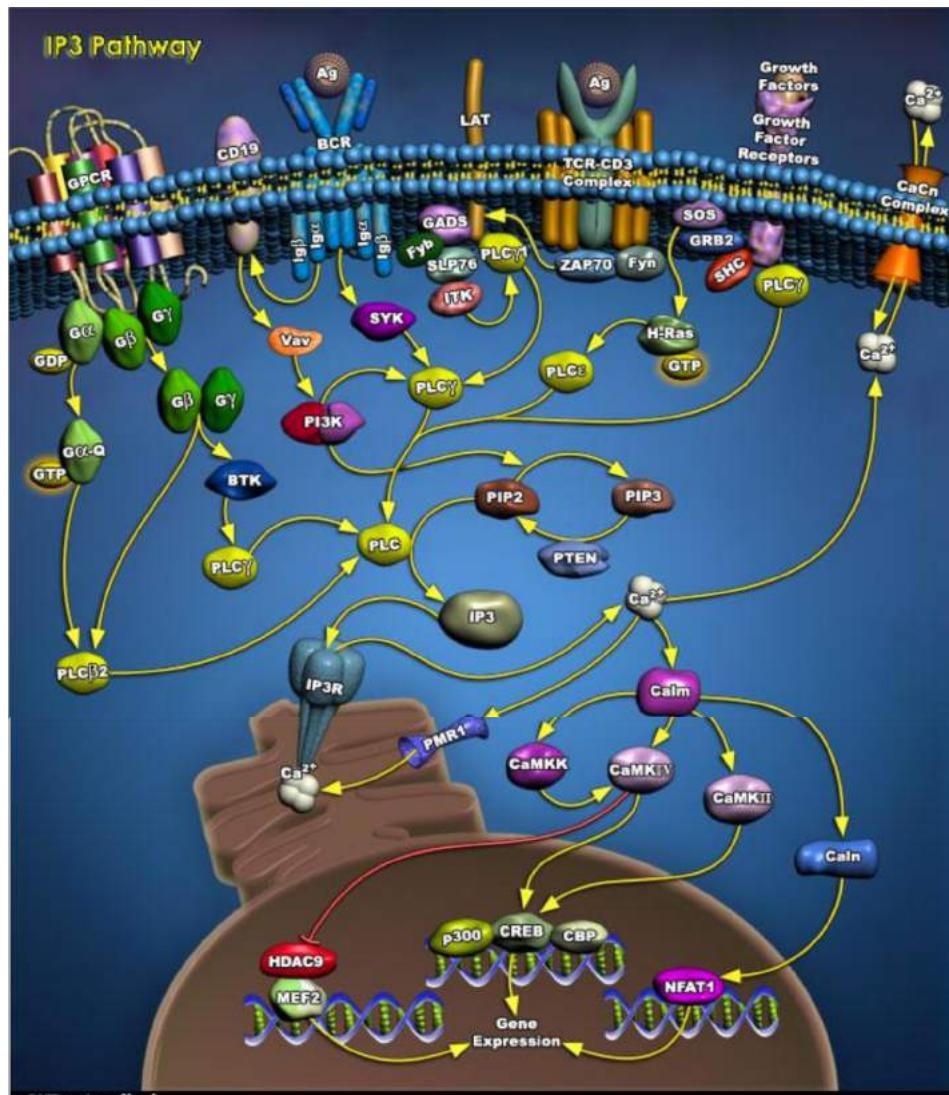
Column Names
Order: clustered
Distance method: Euclidean
Cluster algorithm:
Average
Linkage
1:HDAC2
2:EPB41L5
3:TGFB2
4:SEMA3A
5:TACR1
6:MCC
7:BMPR2
8:HIF1A
9:ADNP
10:ADRA1A
11:SLC24A2
12:CD38
13:GNAI3
14:DRD5



- 7:GO:0003779_actin_binding
- 8:GO:0009100_glycoprotein_metabolic_process
- 9:GO:0009101_glycoprotein_biosynthetic_process
- 10:GO:0051223_regulation_of_protein_transport
- 11:GO:0032880_regulation_of_protein_localization
- 12:GO:0070201_regulation_of_establishment_of_protein_loc
- 13:GO:0031344_regulation_of_cell_projection_organization
- 14:GO:0010975_regulation_of_neuron_projection_developm
- 15:GO:0030900_forebrain_development
- 16:GO:0021537_telencephalon_development
- 17:GO:0021543_pallium_development
- 18:GO:0021987_cerebral_cortex_development
- 19:GO:0008194_UDP-glycosyltransferase_activity
- 20:GO:0008375_acetylglucosaminyltransferase_activity
- 21:GO:0007270_nerve-nerve_synaptic_transmission
- 22:GO:0008066 glutamate_receptor_activity
- 23:GO:0051970_negative_regulation_of_transmission_of_nei
- 24:GO:0050805_negative_regulation_of_synaptic_transmissi
- 25:GO:0015932_nucleobase_nucleoside_nucleotide_and_n
- 26:GO:0051552_flavone_metabolic_process
- 27:GO:0010631_epithelial_cell_migration
- 28:GO:0010632_regulation_of_epithelial_cell_migration
- 29:GO:0090132_epithelium_migration

Link: CNS – Salivary content

inositol triphosphate (*IP₃*) and diacylglycerol (*DAG*)/ These nerves release acetylcholine and substance P, which activate the *IP₃* and *DAG* pathways respectively.



DAG Pathway

Example 2

Functional analysis:

Description of data:

1. Condition: chronic kidney disease versus healthy
2. Sample: plasma
3. Mouse genome

Mouse mine
(underexpressed)



Search: e.g. Parkinson, Hox*, MGI:96677

GO

Gene Ontology Enrichment

GO terms enriched for items in this list.

Number of Genes in this list not analysed in this widget: 61

Test Correction Max p-value Ontology

Holm-Bonferroni 0.05 biological_process

Background population

Default Change

View Download

GO Term	p-Value	Matches
positive regulation of signaling [GO:0023056]	3.455584e-5	83
regulation of protein metabolic process [GO:0051246]	3.861581e-5	111
cellular developmental process [GO:0048869]	3.940415e-5	152
inflammatory response [GO:0006954]	4.464164e-5	42
regulation of molecular function [GO:0065009]	5.487216e-5	128
negative regulation of cellular process [GO:0048523]	5.915760e-5	162
positive regulation of cell communication [GO:0010647]	6.560536e-5	82

inflammatory genes

GENE ONTOLOGY

function

T=65			
No.	Name	UNDExpressed	
1	Ackr1	atypical chemokine receptor	MGI:109761 Mus musculus GO:000695 inflammatory response GO:000695 inflammatory response
2	Adora2b	adenosine A2b receptor	MGI:99403 Mus musculus GO:000288 positive regulation of chronic inflammatory response GO:000695 inflammatory response
3	C3	complement component 3	MGI:88227 Mus musculus GO:000179 positive regulation of type Ila hypersensitivity GO:000695 inflammatory response
4	C3	complement component 3	MGI:88227 Mus musculus GO:000695 inflammatory response GO:000695 inflammatory response
5	C3ar1	complement component 3	MGI:109761 Mus musculus GO:000695 inflammatory response GO:000695 inflammatory response
6	Casp12	caspase 12	MGI:131297 Mus musculus GO:005072 regulation of inflammatory response GO:000695 inflammatory response
7	Ccl17	chemokine (C-C motif) ligaa	MGI:132907 Mus musculus GO:000695 inflammatory response GO:000695 inflammatory response
8	Ccl2	chemokine (C-C motif) ligaa	MGI:98259 Mus musculus GO:000252 leukocyte migration involved in inflammatory response GO:000695 inflammatory response
9	Ccl2	chemokine (C-C motif) ligaa	MGI:98259 Mus musculus GO:000695 inflammatory response GO:000695 inflammatory response
10	Ccl9	chemokine (C-C motif) ligaa	MGI:104533 Mus musculus GO:000695 inflammatory response GO:000695 inflammatory response
11	Ccn3	cellular communication nu	MGI:109187 Mus musculus GO:005072 negative regulation of inflammatory response GO:000695 inflammatory response
12	Cd300a	CD300A molecule	MGI:244347 Mus musculus GO:000255 serotonin secretion by mast cell GO:000695 inflammatory response
13	Cd44	CD44 antigen	MGI:88338 Mus musculus GO:000224 wound healing involved in inflammatory response GO:000695 inflammatory response
14	Cd44	CD44 antigen	MGI:88338 Mus musculus GO:000695 inflammatory response GO:000695 inflammatory response
15	Cd44	CD44 antigen	MGI:88338 Mus musculus GO:005072 negative regulation of inflammatory response GO:000695 inflammatory response
16	Clicf1	cardiotrophin-like cytokin	MGI:193001 Mus musculus GO:005072 regulation of inflammatory response GO:000695 inflammatory response
17	Clu	clusterin	MGI:884237 Mus musculus GO:000177 microglial cell activation GO:000695 inflammatory response
18	Cxcl1	chemokine (C-X-C motif) li	MGI:108061 Mus musculus GO:000255 acute inflammatory response GO:000695 inflammatory response
19	Cxcl1	chemokine (C-X-C motif) li	MGI:108061 Mus musculus GO:000695 inflammatory response GO:000695 inflammatory response
20	Cxcl17	chemokine (C-X-C motif) li	MGI:238761 Mus musculus GO:005072 negative regulation of inflammatory response GO:000695 inflammatory response
21	Epha2	Eph receptor A2	MGI:95278 Mus musculus GO:000695 inflammatory response GO:000695 inflammatory response
22	Fcgr1	Fc receptor, IgG, high affin	MGI:95498 Mus musculus GO:000178 antibody-dependent cellular cytotoxicity GO:000695 inflammatory response
23	Fcgr1	Fc receptor, IgG, high affin	MGI:95498 Mus musculus GO:000179 positive regulation of type Ila hypersensitivity GO:000695 inflammatory response
24	Fcgr1	Fc receptor, IgG, high affin	MGI:95498 Mus musculus GO:000180 positive regulation of type III hypersensitivity GO:000695 inflammatory response
25	Fcgr3	Fc receptor, IgG, low affin	MGI:95500 Mus musculus GO:000178 antibody-dependent cellular cytotoxicity GO:000695 inflammatory response
26	Fcgr3	Fc receptor, IgG, low affin	MGI:95500 Mus musculus GO:000179 positive regulation of type Ila hypersensitivity GO:000695 inflammatory response
27	Fcgr3	Fc receptor, IgG, low affin	MGI:95500 Mus musculus GO:000180 positive regulation of type III hypersensitivity GO:000695 inflammatory response
28	Fcgr3	Fc receptor, IgG, low affin	MGI:95500 Mus musculus GO:000181 positive regulation of type I hypersensitivity GO:000695 inflammatory response
29	Icam1	intercellular adhesion mol	MGI:963921 Mus musculus GO:000243 acute inflammatory response to antigenic stimulus GO:000695 inflammatory response
30	Ifngr2	interferon gamma recepto	MGI:107651 Mus musculus GO:000177 microglial cell activation GO:000695 inflammatory response
31			GO:000695 inflammatory response

Phenotype ontology

inflammatory genes (top 30)

function

Mammalian Phenotype Ontology Enrichment						
MP terms enriched for items in this list.						
Number of Genes in this list not analysed in this widget: 165						
Test Correction	Max p-value	Background population				
Holm-Bonferroni	0.05	Default	Change			
View	Download					
<input type="checkbox"/> MP Term	p-Value ?	Matches				
<input type="checkbox"/> abnormal myeloid leukocyte morphology	6.468516e-13	61				
[MP:0008250]						
<input type="checkbox"/> abnormal phagocyte morphology	8.973938e-12	54				
[MP:0008251]						
<input type="checkbox"/> hematopoietic system phenotype	1.003586e-10	132				
[MP:0005397]						
<input type="checkbox"/> abnormal innate immunity [MP:0002419]	3.769259e-10	42				
<input type="checkbox"/> abnormal inflammatory response [MP:0001845]	4.325748e-10	71				
<input type="checkbox"/> abnormal macrophage physiology	1.298955e-9	33				
[MP:0002451]						
<input type="checkbox"/> abnormal mononuclear phagocyte morphology	2.850317e-9	43				
[MP:0008248]						

Phenotype ontology

Mammalian Phenotype Ontology Enrichment

MP terms enriched for items in this list.

Number of Genes in this list not analysed in this widget: 165

Test Correction Max p-value Background population

Holm-Bonferroni 0.05 Default Change

[View](#) [Download](#)

<input type="checkbox"/> MP Term	p-Value	Matches
abnormal cytokine level [MP:0008713]	6.682226e-6	29
abnormal immune cell physiology [MP:0001819]	7.208789e-6	63
increased granulocyte number [MP:0000322]	7.410008e-6	26
abnormal leukocyte physiology [MP:0002442]	7.928410e-6	62
abnormal acute inflammation [MP:0002498]	8.218671e-6	25
abnormal blood cell physiology [MP:0012382]	9.287819e-6	65
cellular phenotype [MP:0005384]	9.535994e-6	126
altered susceptibility to bacterial infection [MP:0020186]	1.037339e-5	26
abnormal intercellular signalling peptide or	1.329028e-5	29

Mammalian Phenotype Ontology Enrichment

MP terms enriched for items in this list.

Number of Genes in this list not analysed in this widget: 165

Test Correction Max p-value Background population

Holm-Bonferroni 0.05 Default Change

[View](#) [Download](#)

<input type="checkbox"/> MP Term	p-Value	Matches
abnormal bone marrow cell morphology/development [MP:0002398]	4.836889e-5	33
decreased inflammatory response [MP:0001876]	6.543465e-5	21
decreased acute inflammation [MP:0005087]	7.367401e-5	17
homeostasis/metabolism phenotype [MP:0005376]	8.342624e-5	156
abnormal neutrophil morphology [MP:0005065]	8.668118e-5	25
abnormal granulocyte physiology [MP:0002462]	9.124927e-5	20
increased sensitivity to induced morbidity/mortality [MP:0009763]	9.748834e-5	24

Mammalian Phenotype Ontology Enrichment

MP terms enriched for items in this list.

Number of Genes in this list not analysed in this widget: 165

Test Correction Max p-value Background population

Holm-Bonferroni 0.05 Default Change

[View](#) [Download](#)

<input type="checkbox"/> MP Term	p-Value	Matches
abnormal cell physiology [MP:0005621]	1.767455e-7	121
increased inflammatory response [MP:0001846]	1.861698e-7	60
mortality/aging [MP:0010768]	3.640161e-7	159
abnormal macrophage morphology [MP:0002446]	5.269732e-7	33
abnormal hematopoietic cell morphology [MP:0013656]	5.570643e-7	101
abnormal hematopoietic system morphology/development [MP:0002396]	9.774276e-7	111
abnormal hematopoietic cell number [MP:0011180]	1.066767e-6	82

David
(underexpressed)

Genes underexpressed in 4 vs. 3 group and overexpressed in 3 vs. 1 group



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

KEGG PATHWAY ANALYSIS

38 chart records

[Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	Staphylococcus aureus infection	RT	■	9	2,0	1,1E-5	2,1E-3
<input type="checkbox"/>	KEGG_PATHWAY	Complement and coagulation cascades	RT	■	10	2,2	3,9E-5	3,6E-3
<input type="checkbox"/>	KEGG_PATHWAY	TNF signaling pathway	RT	■	11	2,4	1,3E-4	8,2E-3
<input type="checkbox"/>	KEGG_PATHWAY	Bladder cancer	RT	■	7	1,5	2,4E-4	1,1E-2
<input type="checkbox"/>	KEGG_PATHWAY	Hepatitis B	RT	■	12	2,6	3,5E-4	1,3E-2
<input type="checkbox"/>	KEGG_PATHWAY	Phagosome	RT	■	13	2,8	3,6E-4	1,1E-2
<input type="checkbox"/>	KEGG_PATHWAY	Osteoclast differentiation	RT	■	11	2,4	4,3E-4	1,2E-2
<input type="checkbox"/>	KEGG_PATHWAY	Leishmaniasis	RT	■	8	1,7	4,7E-4	1,1E-2
<input type="checkbox"/>	KEGG_PATHWAY	HTLV-I infection	RT	■	16	3,5	1,1E-3	2,2E-2
<input type="checkbox"/>	KEGG_PATHWAY	PI3K-Akt signaling pathway	RT	■	18	3,9	1,8E-3	3,3E-2
<input type="checkbox"/>	KEGG_PATHWAY	p53 signaling pathway	RT	■	7	1,5	3,4E-3	5,6E-2
<input type="checkbox"/>	KEGG_PATHWAY	Chronic myeloid leukemia	RT	■	7	1,5	4,9E-3	7,3E-2
<input type="checkbox"/>	KEGG_PATHWAY	Proteoglycans in cancer	RT	■	12	2,6	5,0E-3	7,0E-2
<input type="checkbox"/>	KEGG_PATHWAY	Cytokine-cytokine receptor interaction	RT	■	13	2,8	6,9E-3	8,9E-2
<input type="checkbox"/>	KEGG_PATHWAY	Epstein-Barr virus infection	RT	■	9	2,0	1,0E-2	1,2E-1
<input type="checkbox"/>	KEGG_PATHWAY	Hepatitis C	RT	■	9	2,0	1,0E-2	1,2E-1
<input type="checkbox"/>	KEGG_PATHWAY	ECM-receptor interaction	RT	■	7	1,5	1,3E-2	1,4E-1
<input type="checkbox"/>	KEGG_PATHWAY	Viral carcinogenesis	RT	■	12	2,6	1,3E-2	1,3E-1
<input type="checkbox"/>	KEGG_PATHWAY	Amoebiasis	RT	■	8	1,7	1,4E-2	1,4E-1
<input type="checkbox"/>	KEGG_PATHWAY	Tuberculosis	RT	■	10	2,2	1,5E-2	1,4E-1
<input type="checkbox"/>	KEGG_PATHWAY	Herpes simplex infection	RT	■	11	2,4	1,6E-2	1,4E-1
<input type="checkbox"/>	KEGG_PATHWAY	Malaria	RT	■	5	1,1	2,1E-2	1,7E-1
<input type="checkbox"/>	KEGG_PATHWAY	Cell adhesion molecules (CAMs)	RT	■	9	2,0	2,6E-2	2,0E-1
<input type="checkbox"/>	KEGG_PATHWAY	Measles	RT	■	8	1,7	3,0E-2	2,2E-1

Potential role of Akt signaling in chronic kidney disease FREE

Aiping Lan ✉, Jie Du

PI3K- Akt signaling pathway

Nephrology Dialysis Transplantation, Volume 30, Issue 3, March 2015, Pages

385–394, <https://doi.org/10.1093/ndt/gfu196>

Published: 02 June 2014 Article history ▾

Spp1	
Col4a1	ENSMUSG00000029304, ENSMUSG00000031502,
Tnc	ENSMUSG00000028364, ENSMUSG00000022146,
Osmr	ENSMUSG00000027995, ENSMUSG00000006728,
Tlr2	ENSMUSG00000027852, ENSMUSG00000020108,
Cdk4	ENSMUSG00000018965, ENSMUSG00000000555,
Nras	ENSMUSG00000053007, ENSMUSG00000026043,
Ddit4	ENSMUSG00000026042, ENSMUSG00000027859,
Ywhah	ENSMUSG00000059552, ENSMUSG00000023067,
Itga5	ENSMUSG00000022346, ENSMUSG00000006445
Creb5	
Col3a1	
Col5a2	
Ngf	
Trp53	
Cdkn1a	
Myc	
Epha2	

18 genes

Abstract

Renal fibrosis, particularly tubulointerstitial fibrosis, is the common final outcome of almost all chronic kidney diseases. However, the mechanisms involved in the development of renal fibrosis are poorly understood. The Akt (also known as protein kinase B, PKB) family is serine/threonine protein kinases that play critical roles in regulating growth, proliferation, survival, metabolism and other cellular activities. Cytokines, high-glucose medium, transforming growth factor- β 1 or advanced glycation end-products activate Akt in different renal cells. Increased Akt activation has been found in experimental tubulointerstitial fibrosis. In addition, Akt activation is also an important node in diverse signaling cascades involved in kidney damage. These data give evidence for a role for Akt in renal fibrosis, but no reviews are available on the role of Akt in the process. Thus, our aim is to review the role of Akt activation and signaling in renal fibrosis.



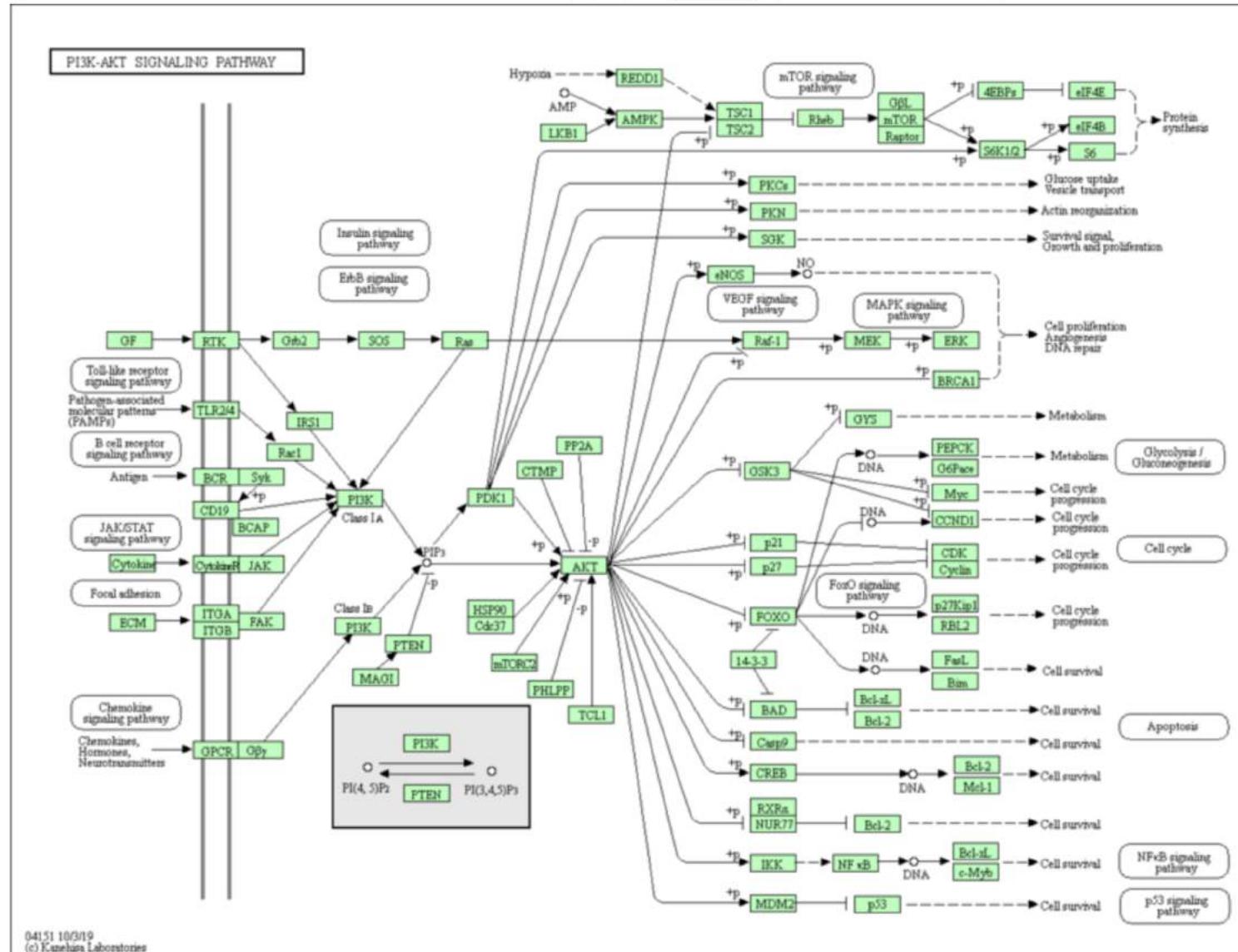
PI3K-Akt signaling pathway - Homo sapiens (human)

[Pathway menu | Organism menu | Pathway entry | Download KGML | Show description | User data mapping]

Homo sapiens (human)

Go

67%





Review

TNF receptors: signaling pathways and contribution to renal dysfunction

Rafia S. Al-Lamki ¹ , Tanya N. Mayadas ²

Show more

<https://doi.org/10.1038/ki.2014.285>

Under an Elsevier user license

TNF signaling pathway

Tumor necrosis factor (TNF), initially reported to induce tumor cell apoptosis and cachexia, is now considered a central mediator of a broad range of biological activities from cell proliferation, cell death and differentiation to induction of inflammation and immune modulation.

TNF exerts its biological responses via interaction with two cell surface receptors: TNFR1 and TNFR2. (TNFRs). These receptors trigger shared and distinct signaling pathways upon TNF binding, which in turn result in cellular outputs that may promote tissue injury on one hand but may also induce protective, beneficial responses. Yet the role of TNF and its receptors specifically in renal disease is still not well understood. This review describes the expression of the TNFRs, the signaling pathways

induced by them and the biological responses of TNF and its receptors in various animal models of renal diseases, and discusses the current outcomes from use of TNF biologics and TNF biomarkers in renal disorders.

11 genes

ENSMUSG00000052684, ENSMUSG00000029380,
ENSMUSG00000053175, ENSMUSG00000034394,
ENSMUSG00000027962, ENSMUSG00000000957,
ENSMUSG00000037405, ENSMUSG00000053113,
ENSMUSG00000035385, ENSMUSG00000021367,
ENSMUSG00000053007

Jun
Cxcl1
Bcl3
Lif
Vcam1
Mmp14
Icam1
Socs3
Ccl2
Edn1
Creb5



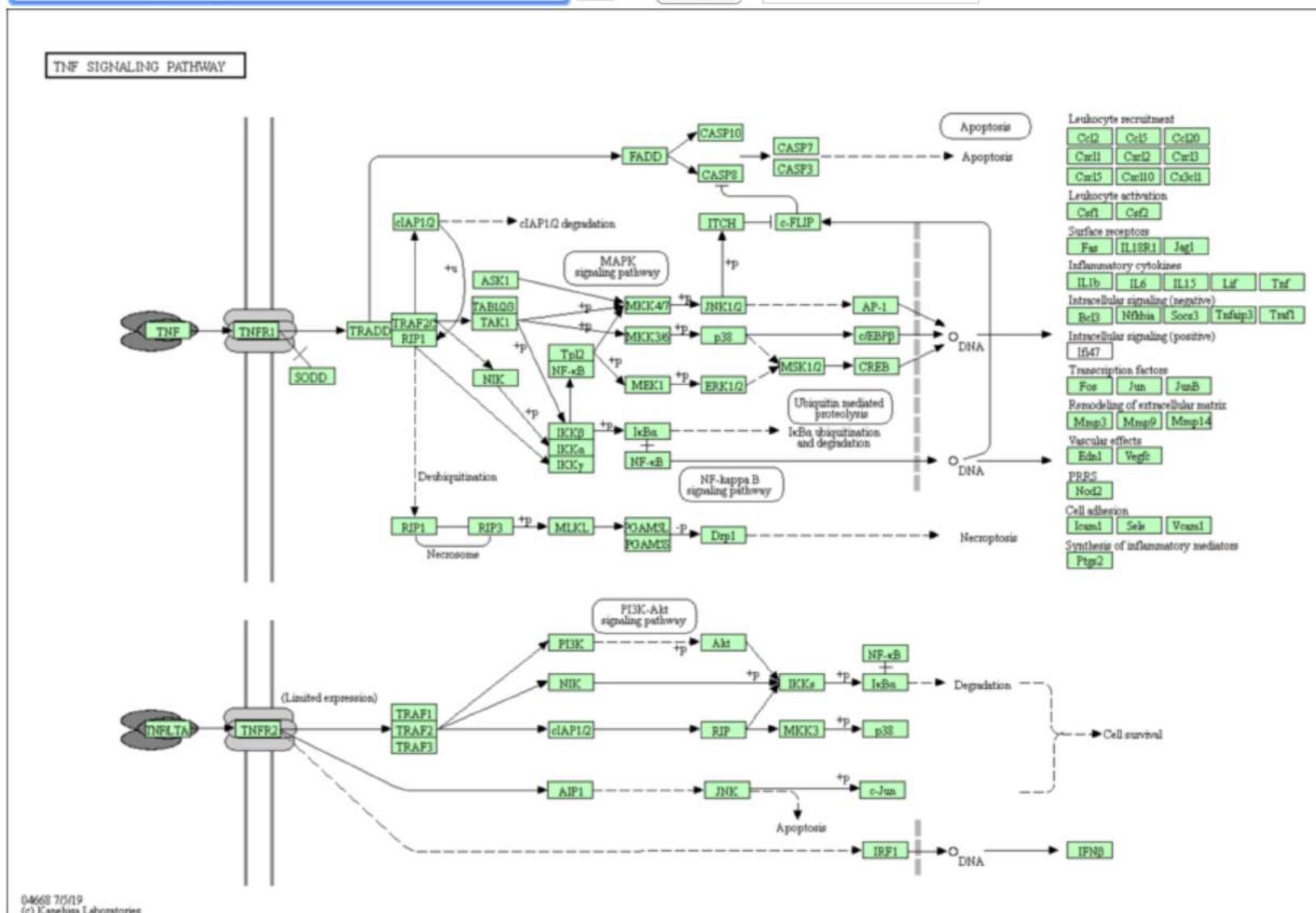
TNF signaling pathway - Homo sapiens (human)

[Pathway menu | Organism menu | Pathway entry | Download KGML | Show description | User data mapping]

Mus musculus (mouse)

Go

67%



Mouse mine
(overexpressed)



Mammalian Phenotype Ontology Enrichment

MP terms enriched for items in this list.

Number of Genes in this list not analysed in this widget: 153

Test Correction Max p-value Background population

Holm-Bonferroni

Bonferroni

[View](#) [Download](#)

MP Term

p-Value *i* Matches

Redacted content

2.527975e-8 110

Page 1 of 1

Page 1 of 1

- ☐ homeostasis/metabolism phenotype [MP:0005376]

abnormal blood homeostasis [MP:0009642]

6.338036e-7 87

abnormal urination [MP:0001756]

9 963413e-7 16

polyuria [MP:0001762]

1.739077e-6 13

abnormal lipid homeostasis [MR:0002118]

3.033614e-6 48

genes involved in kidney function

function

T=27	Name	OVERexpressed	Function
1	Agrp1	angiotensin MGI:87964	Mus muscul
2	Agrp1	angiotensin MGI:87964	Mus muscul
3	Agrp1	angiotensin MGI:87964	Mus muscul
4	Apela	apeelin recep MGI:36423	Mus muscul
5	Aqp1	aquaporin 1 MGI:10320	Mus muscul
6	Aqp1	aquaporin 1 MGI:10320	Mus muscul
7	Aqp2	aquaporin 2 MGI:10968	Mus muscul
8	Aqp2	aquaporin 2 MGI:10968	Mus muscul
9	Aqp2	aquaporin 2 MGI:10968	Mus muscul
10	Aqp2	aquaporin 2 MGI:10968	Mus muscul
11	Aqp3	aquaporin 3 MGI:13337	Mus muscul
12	Aqp4	aquaporin 4 MGI:10738	Mus muscul
13	Bcat2	branched ch MGI:12765	Mus muscul
14	Bcat2	branched ch MGI:12765	Mus muscul
15	Bcat2	branched ch MGI:12765	Mus muscul
16	Bsnl	barttin CLC1 MGI:21534	Mus muscul
17	Bsnl	barttin CLC1 MGI:21534	Mus muscul
18	Cav1	caveolin 1, c MGI:10270	Mus muscul
19	Ccni	cyclin I MGI:13410	Mus muscul
20	Clcnka	chloride ch MGI:13290	Mus muscul
21	Col4a3	collagen, ty MGI:10468	Mus muscul
22	Col4a3	collagen, ty MGI:10468	Mus muscul
23	Col4a3	collagen, ty MGI:10468	Mus muscul
24	Corin	corin, serine MGI:13494	Mus muscul
25	Dhtkd1	dehydrogen MGI:24450	Mus muscul
26	Dio1	deiodinase, MGI:94896	Mus muscul
27	Ednrb	endothelin 1 MGI:10272	Mus muscul
28	Ednrb	endothelin 1 MGI:10272	Mus muscul
29	Gal3st1	galactose-3- MGI:18582	Mus muscul
30	Gal3st1	galactose-3- MGI:18582	Mus muscul



Phenotype ontology

Mammalian Phenotype Ontology Enrichment

MP terms enriched for items in this list.

Number of Genes in this list not analysed in this widget: 153

Test Correction Max p-value Background population

Holm-Bonferroni 0.05 Default Change

[View](#)

[Download](#)

MP Term [p-Value](#) [Matches](#)

abnormal homeostasis [MP:0001764] 2.527975e-8 110

abnormal urine homeostasis [MP:0009643] 3.192282e-7 27

abnormal fatty acid level [MP:0005280] 3.265765e-7 21

homeostasis/metabolism phenotype [MP:0005376] 4.341024e-7 118

abnormal blood homeostasis [MP:0009642] 6.338036e-7 87

abnormal urination [MP:0001756] 9.963413e-7 16

polyuria [MP:0001762] 1.739077e-6 13

abnormal lipid homeostasis [MP:0002118] 3.033614e-6 48

abnormal body composition [MP:0005451] 3.271121e-6 71

genes involved in kidney function

T=16	Name	OVERExpressed	function
1	Agtr1a	angiotensin	[MGI:87964] Mus muscul MP:000362 oliguria MP:000175 abnormal urination
2	Aqp2	aquaporin 2	[MGI:10968] Mus muscul MP:000176 polyuria MP:000175 abnormal urination
3	Aqp3	aquaporin 3	[MGI:13337] Mus muscul MP:000176 polyuria MP:000175 abnormal urination
4	Bcat2	branched ch	[MGI:12765] Mus muscul MP:000176 polyuria MP:000175 abnormal urination
5	Bsnd	barttin CLCN	[MGI:21534] Mus muscul MP:000176 polyuria MP:000175 abnormal urination
6	Clcnka	chloride cha	[MGI:13290] Mus muscul MP:000176 polyuria MP:000175 abnormal urination
7	Col4a3	collagen, ty	[MGI:10468] Mus muscul MP:000176 polyuria MP:000175 abnormal urination
8	Ednrb	endothelin 1	[MGI:10272] Mus muscul MP:000362 oliguria MP:000175 abnormal urination
9	Gal3st1	galactose-3-	[MGI:18582] Mus muscul MP:000176 polyuria MP:000175 abnormal urination
10	Irs2	insulin rece	[MGI:10933] Mus muscul MP:000176 polyuria MP:000175 abnormal urination
11	Nr3c2	nuclear rece	[MGI:99459] Mus muscul MP:000176 polyuria MP:000175 abnormal urination
12	Scd1	stearoyl-Co	[MGI:98239] Mus muscul MP:000176 polyuria MP:000175 abnormal urination
13	Slc12a1	solute carrie	[MGI:10315] Mus muscul MP:000176 polyuria MP:000175 abnormal urination
14	Slc26a7	solute carrie	[MGI:23847] Mus muscul MP:000362 oliguria MP:000175 abnormal urination
15	Slc4a1	solute carrie	[MGI:10939] Mus muscul MP:000176 polyuria MP:000175 abnormal urination
16	Slc4a5	solute carrie	[MGI:24432] Mus muscul MP:000176 polyuria MP:000175 abnormal urination



Search: e.g. Parkinson, Hox*, MGI:96677

GO

Phenotype ontology

Mammalian Phenotype Ontology Enrichment

MP terms enriched for items in this list.

Number of Genes in this list not analysed in this widget: 153

Test Correction Max p-value Background population
Holm-Bonferroni ▾ 0.05 Default Change

View Download

MP Term	p-Value	Matches
abnormal body composition [MP:0003451]	3.271121e-0	11
increased fatty acid level [MP:0005281]	2.333757e-5	14
abnormal renal/urinary system physiology [MP:0005502]	3.291501e-5	31
abnormal liver morphology [MP:0000598]	4.580074e-5	39
abnormal lipid level [MP:0001547]	5.273133e-5	44
renal/urinary system phenotype [MP:0005367]	6.390027e-5	44
abnormal circulating amino acid level [MP:0005311]	6.501897e-5	18
abnormal amino acid level [MP:0005322]	6.968772e-5	20
abnormal hepatobiliary system morphology [MP:0002138]	9.450072e-5	41

genes involved in kidney function

function

No.	Name	OVERExpressed				
1	Agtr1a	angiotensin MGI:87964	Mus muscul	MP:000213	abnormal ki	MP:000550
2	Agtr1a	angiotensin MGI:87964	Mus muscul	MP:000362	oliguria	MP:000550
3	Agtr1a	angiotensin MGI:87964	Mus muscul	MP:000552	decreased re	MP:000550
4	Agtr1a	angiotensin MGI:87964	Mus muscul	MP:000561	decreased u	MP:000550
5	Agtr1a	angiotensin MGI:87964	Mus muscul	MP:000805	increased ur	MP:000550
6	Agtr1a	angiotensin MGI:87964	Mus muscul	MP:001010	abnormal re	MP:000550
7	Agtr1a	angiotensin MGI:87964	Mus muscul	MP:001147	decreased u	MP:000550
8	Apela	apelin recep MGI:36423	Mus muscul	MP:000296	increased ur	MP:000550
9	Aqp1	aquaporin 1 MGI:10320	Mus muscul	MP:000298	decreased u	MP:000550
10	Aqp1	aquaporin 1 MGI:10320	Mus muscul	MP:000631	decreased u	MP:000550
11	Aqp1	aquaporin 1 MGI:10320	Mus muscul	MP:001144	abnormal re	MP:000550
12	Aqp2	aquaporin 2 MGI:10968	Mus muscul	MP:000176	polyuria	MP:000550
13	Aqp2	aquaporin 2 MGI:10968	Mus muscul	MP:000213	abnormal ki	MP:000550
14	Aqp2	aquaporin 2 MGI:10968	Mus muscul	MP:000298	abnormal u	MP:000550
15	Aqp2	aquaporin 2 MGI:10968	Mus muscul	MP:000298	decreased u	MP:000550
16	Aqp2	aquaporin 2 MGI:10968	Mus muscul	MP:000964	abnormal u	MP:000550
17	Aqp2	aquaporin 2 MGI:10968	Mus muscul	MP:001141	colorless ur	MP:000550
18	Aqp3	aquaporin 3 MGI:13337	Mus muscul	MP:000176	polyuria	MP:000550
19	Aqp3	aquaporin 3 MGI:13337	Mus muscul	MP:000298	decreased u	MP:000550
20	Aqp3	aquaporin 3 MGI:13337	Mus muscul	MP:001144	abnormal re	MP:000550
21	Aqp4	aquaporin 4 MGI:10738	Mus muscul	MP:000298	decreased u	MP:000550
22	Aqp4	aquaporin 4 MGI:10738	Mus muscul	MP:001144	abnormal re	MP:000550
23	Bcat2	branched ch MGI:12765	Mus muscul	MP:000176	polyuria	MP:000550
24	Bcat2	branched ch MGI:12765	Mus muscul	MP:000289	ketoaciduri	MP:000550
25	Bcat2	branched ch MGI:12765	Mus muscul	MP:001146	abnormal ui	MP:000550
26	Bcat2	branched ch MGI:12765	Mus muscul	MP:001147	decreased u	MP:000550
27	Bsnd	barttin CLC1 MGI:21534	Mus muscul	MP:000176	polyuria	MP:000550
28	Bsnd	barttin CLC1 MGI:21534	Mus muscul	MP:000213	abnormal ki	MP:000550
29	Bsnd	barttin CLC1 MGI:21534	Mus muscul	MP:000298	decreased u	MP:000550
30	Bsnd	barttin CLC1 MGI:21534	Mus muscul	MP:000631	decreased u	MP:000550



Search: e.g. Parkinson, Hox*, MGI:96677

GO

Phenotype ontology

Mammalian Phenotype Ontology Enrichment

MP terms enriched for items in this list.

Number of Genes in this list not analysed in this widget: 153

Test Correction Max p-value Background population
Holm-Bonferroni 0.05 Default Change

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MP Term	p-Value	Matches
abnormal hepatobiliary system morphology [MP:0002126]	9.450072e-5	41
abnormal urine osmolality [MP:0002987]	1.084910e-4	10
abnormal body weight [MP:0001259]	1.462086e-4	63
abnormal circulating glucose level [MP:0000188]	1.790429e-4	33
abnormal circulating lipid level [MP:0003949]	2.108219e-4	38
abnormal heart size [MP:0005406]	2.735200e-4	36
abnormal triglyceride level [MP:0000187]	2.808101e-4	26
cardiovascular system phenotype [MP:0005385]	3.360537e-4	72
abnormal gas homeostasis [MP:0003948]	3.430709e-4	24
abnormal renal water transport [MP:0011442]	3.804750e-4	5

genes involved in kidney function

function

T=10	Name	OVERexpressed								
1	Agtr1a	angiotensin	MGI:87964	Mus muscul	MP:000805	increased ur	MP:000298	abnormal urine osmolality		
2	Aqp1	aquaporin 1	MGI:10320	Mus muscul	MP:000298	decreased u	MP:000298	abnormal urine osmolality		
3	Aqp2	aquaporin 2	MGI:109680	Mus muscul	MP:000298	abnormal ui	MP:000298	abnormal urine osmolality		
4	Aqp2	aquaporin 2	MGI:109680	Mus muscul	MP:000298	decreased u	MP:000298	abnormal urine osmolality		
5	Aqp3	aquaporin 3	MGI:13337	Mus muscul	MP:000298	decreased u	MP:000298	abnormal urine osmolality		
6	Aqp4	aquaporin 4	MGI:10738	Mus muscul	MP:000298	decreased u	MP:000298	abnormal urine osmolality		
7	Bsnd	barttin CLCN	MGI:215346	Mus muscul	MP:000298	decreased u	MP:000298	abnormal urine osmolality		
8	Clcnka	chloride cha	MGI:132901	Mus muscul	MP:000298	decreased u	MP:000298	abnormal urine osmolality		
9	Slc12a1	solute carrie	MGI:103150	Mus muscul	MP:000298	decreased u	MP:000298	abnormal urine osmolality		
10	Slc12a1	solute carrie	MGI:103150	Mus muscul	MP:000805	increased ur	MP:000298	abnormal urine osmolality		
11	Slc26a7	solute carrie	MGI:238479	Mus muscul	MP:000805	increased ur	MP:000298	abnormal urine osmolality		
12	Slc4a1	solute carrie	MGI:109393	Mus muscul	MP:000298	decreased u	MP:000298	abnormal urine osmolality		



Phenotype ontology

Mammalian Phenotype Ontology Enrichment

MP terms enriched for items in this list.

Number of Genes in this list not analysed in this widget: 153

Test Correction Max p-value Background population

Holm-Bonferroni 0.05 Default Change

View Download

 MP Term

p-Value

Matches

 abnormal gas homeostasis [MP:0003948] 3.430709e-4 24 abnormal renal water transport [MP:0011443] 3.904750e-4 5 decreased fatty acid level [MP:0005282] 4.533288e-4 13 liver/biliary system phenotype [MP:0005370] 5.360840e-4 42 abnormal total tissue mass [MP:0012321] 6.171862e-4 59 abnormal renal water homeostasis [MP:0011444] 7.092568e-4 5 abnormal circulating bicarbonate level [MP:0003015] 8.171308e-4 6 hepatic steatosis [MP:0002628] 9.246903e-4 16 abnormal pH regulation [MP:0004043] 9.637432e-4 8

genes involved in kidney function

T=5

Name

1 [Agtr1a](#)2 [Aqp1](#)3 [Aqp3](#)4 [Aqp4](#)5 [Slc12a1](#)

OVERExpressed

angiotensin	MGI:87964	Mus muscul	MP:001010	abnormal re	MP:001144	abnormal renal water transport
aquaporin 1	MGI:10320	Mus muscul	MP:001144	abnormal re	MP:001144	abnormal renal water transport
aquaporin 3	MGI:13337	Mus muscul	MP:001144	abnormal re	MP:001144	abnormal renal water transport
aquaporin 4	MGI:10738	Mus muscul	MP:001144	abnormal re	MP:001144	abnormal renal water transport
solute carrier	MGI:103150	Mus muscul	MP:001010	abnormal re	MP:001144	abnormal renal water transport

T=5

Name

1 [Agtr1a](#)2 [Aqp1](#)3 [Aqp3](#)4 [Aqp4](#)5 [Slc12a1](#)

OVERExpressed

angiotensin	MGI:87964	Mus muscul	MP:001010	abnormal re	MP:001144	abnormal renal water homeostasis
aquaporin 1	MGI:10320	Mus muscul	MP:001144	abnormal re	MP:001144	abnormal renal water homeostasis
aquaporin 3	MGI:13337	Mus muscul	MP:001144	abnormal re	MP:001144	abnormal renal water homeostasis
aquaporin 4	MGI:10738	Mus muscul	MP:001144	abnormal re	MP:001144	abnormal renal water homeostasis
solute carrier	MGI:103150	Mus muscul	MP:001010	abnormal re	MP:001144	abnormal renal water homeostasis



Search: e.g. Parkinson, Hox*, MGI:96677

GO

Phenotype ontology

Mammalian Phenotype Ontology Enrichment			
MP terms enriched for items in this list.			
Number of Genes in this list not analysed in this widget: 153			
Test Correction	Max p-value	Background population	
Holm-Bonferroni	0.05	Default	Change
View	Download		
MP Term	p-Value <small>i</small>	Matches	
<input type="checkbox"/> mortality/aging [MP:0010768]	0.004058	104	
<input type="checkbox"/> abnormal renal transport [MP:0011417]	0.004215	6	
<input type="checkbox"/> decreased urine osmolality [MP:0002988]	0.004470	8	
<input type="checkbox"/> abnormal survival [MP:0010769]	0.004662	99	
<input type="checkbox"/> abnormal glycogen homeostasis [MP:0005438]	0.004989	12	
<input type="checkbox"/> abnormal heart morphology [MP:0000266]	0.005661	48	
<input type="checkbox"/> abnormal free fatty acids level [MP:0010358]	0.005831	14	
<input type="checkbox"/> increased cellular glucose import [MP:0003927]	0.006443	8	
<input type="checkbox"/> abnormal liver triglyceride level [MP:0012778]	0.006764	13	

genes involved in kidney function

T=6	Name	OVERExpressed									
1	Agtr1a	angiotensin	MGI:87964	Mus muscul	MP:001010	abnormal re	MP:001141	abnormal renal transport			
2	Aqp1	aquaporin 1	MGI:10320	Mus muscul	MP:001144	abnormal re	MP:001141	abnormal renal transport			
3	Aqp3	aquaporin 3	MGI:13337	Mus muscul	MP:001144	abnormal re	MP:001141	abnormal renal transport			
4	Aqp4	aquaporin 4	MGI:10738	Mus muscul	MP:001144	abnormal re	MP:001141	abnormal renal transport			
5	Nr3c2	nuclear rece	MGI:99459	Mus muscul	MP:001010	abnormal re	MP:001141	abnormal renal transport			
6	Nr3c2	nuclear rece	MGI:99459	Mus muscul	MP:001144	abnormal re	MP:001141	abnormal renal transport			
7	Slc12a1	solute carrier	MGI:10315	Mus muscul	MP:001010	abnormal re	MP:001141	abnormal renal transport			
T=8	Name	OVERExpressed									
1	Aqp1	aquaporin 1	MGI:10320	Mus muscul	MP:000298	decreased u	MP:000298	decreased urine osmolality			
2	Aqp2	aquaporin 2	MGI:10968	Mus muscul	MP:000298	decreased u	MP:000298	decreased urine osmolality			
3	Aqp3	aquaporin 3	MGI:13337	Mus muscul	MP:000298	decreased u	MP:000298	decreased urine osmolality			
4	Aqp4	aquaporin 4	MGI:10738	Mus muscul	MP:000298	decreased u	MP:000298	decreased urine osmolality			
5	Bsnl	barttin CLCN	MGI:21534	Mus muscul	MP:000298	decreased u	MP:000298	decreased urine osmolality			
6	Clcnka	chloride cha	MGI:13290	Mus muscul	MP:000298	decreased u	MP:000298	decreased urine osmolality			
7	Slc12a1	solute carrier	MGI:10315	Mus muscul	MP:000298	decreased u	MP:000298	decreased urine osmolality			
8	Slc4a1	solute carrier	MGI:10939	Mus muscul	MP:000298	decreased u	MP:000298	decreased urine osmolality			

David
(overexpressed)



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

KEGG PATHWAY ANALYSIS

24 chart records

[Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
	KEGG_PATHWAY	Valine, leucine and isoleucine degradation	RT		11	3,3	5,2E-8	1,0E-5
	KEGG_PATHWAY	Metabolic pathways	RT		48	14,2	9,5E-7	9,4E-5
	KEGG_PATHWAY	Fatty acid metabolism	RT		9	2,7	3,8E-6	2,5E-4
	KEGG_PATHWAY	Propanoate metabolism	RT		7	2,1	8,0E-6	3,9E-4
	KEGG_PATHWAY	AMPK signaling pathway	RT		10	3,0	6,0E-4	2,3E-2
	KEGG_PATHWAY	Biosynthesis of antibiotics	RT		13	3,8	6,1E-4	2,0E-2
	KEGG_PATHWAY	Butanoate metabolism	RT		5	1,5	1,4E-3	4,0E-2
	KEGG_PATHWAY	Fatty acid degradation	RT		6	1,8	2,0E-3	4,9E-2
	KEGG_PATHWAY	beta-Alanine metabolism	RT		5	1,5	3,1E-3	6,5E-2
	KEGG_PATHWAY	Insulin resistance	RT		8	2,4	4,3E-3	8,1E-2
	KEGG_PATHWAY	Carbon metabolism	RT		8	2,4	5,7E-3	9,8E-2
	KEGG_PATHWAY	Adipocytokine signaling pathway	RT		6	1,8	1,1E-2	1,6E-1
	KEGG_PATHWAY	Malaria	RT		5	1,5	1,2E-2	1,7E-1
	KEGG_PATHWAY	Fatty acid elongation	RT		4	1,2	1,2E-2	1,6E-1
	KEGG_PATHWAY	PPAR signaling pathway	RT		6	1,8	1,6E-2	1,9E-1
	KEGG_PATHWAY	African trypanosomiasis	RT		4	1,2	2,7E-2	2,8E-1
	KEGG_PATHWAY	Bile secretion	RT		5	1,5	4,3E-2	4,0E-1
	KEGG_PATHWAY	Vasopressin-regulated water reabsorption	RT		4	1,2	4,5E-2	4,0E-1
	KEGG_PATHWAY	Biosynthesis of amino acids	RT		5	1,5	5,3E-2	4,3E-1
	KEGG_PATHWAY	Tryptophan metabolism	RT		4	1,2	5,6E-2	4,4E-1
	KEGG_PATHWAY	Histidine metabolism	RT		3	0,9	6,7E-2	4,8E-1
	KEGG_PATHWAY	Peroxisome	RT		5	1,5	6,8E-2	4,7E-1
	KEGG_PATHWAY	Biosynthesis of unsaturated fatty acids	RT		3	0,9	8,9E-2	5,5E-1
	KEGG_PATHWAY	Glycerolipid metabolism	RT		4	1,2	9,3E-2	5,5E-1

Vasopresin-regulated water re-absorption signaling pathway

Pflugers Arch. 2008 Sep;456(6):1005-24. doi: 10.1007/s00424-008-0498-1. Epub 2008 Apr 23.

Physiology and pathophysiology of the vasopressin-regulated renal water reabsorption.

Boone M¹, Deen PM.

Author information

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Abstract

To prevent dehydration, terrestrial animals and humans have developed a sensitive and versatile system to maintain their water homeostasis. In states of hypernatremia or hypovolemia, the antidiuretic hormone vasopressin (AVP) is released from the pituitary and binds its type-2 receptor in renal principal cells. This triggers an intracellular cAMP signaling cascade, which phosphorylates aquaporin-2 (AQP2) and targets the channel to the apical plasma membrane. Driven by an osmotic gradient, pro-urinary water then passes the membrane through AQP2 and leaves the cell on the basolateral side via AQP3 and AQP4 water channels. When water homeostasis is restored, AVP levels decline, and AQP2 is internalized from the plasma membrane, leaving the plasma membrane watertight again. The action of AVP is counterbalanced by several hormones like prostaglandin E2, bradykinin, dopamine, endothelin-1, acetylcholine, epidermal growth factor, and purines. Moreover, AQP2 is strongly involved in the pathophysiology of disorders characterized by renal concentrating defects, as well as conditions associated with severe water retention. This review focuses on our recent increase in understanding of the molecular mechanisms underlying AVP-regulated renal water transport in both health and disease.

PMID: 18431594 PMCID: [PMC2518081](#) DOI: [10.1007/s00424-008-0498-1](https://doi.org/10.1007/s00424-008-0498-1)

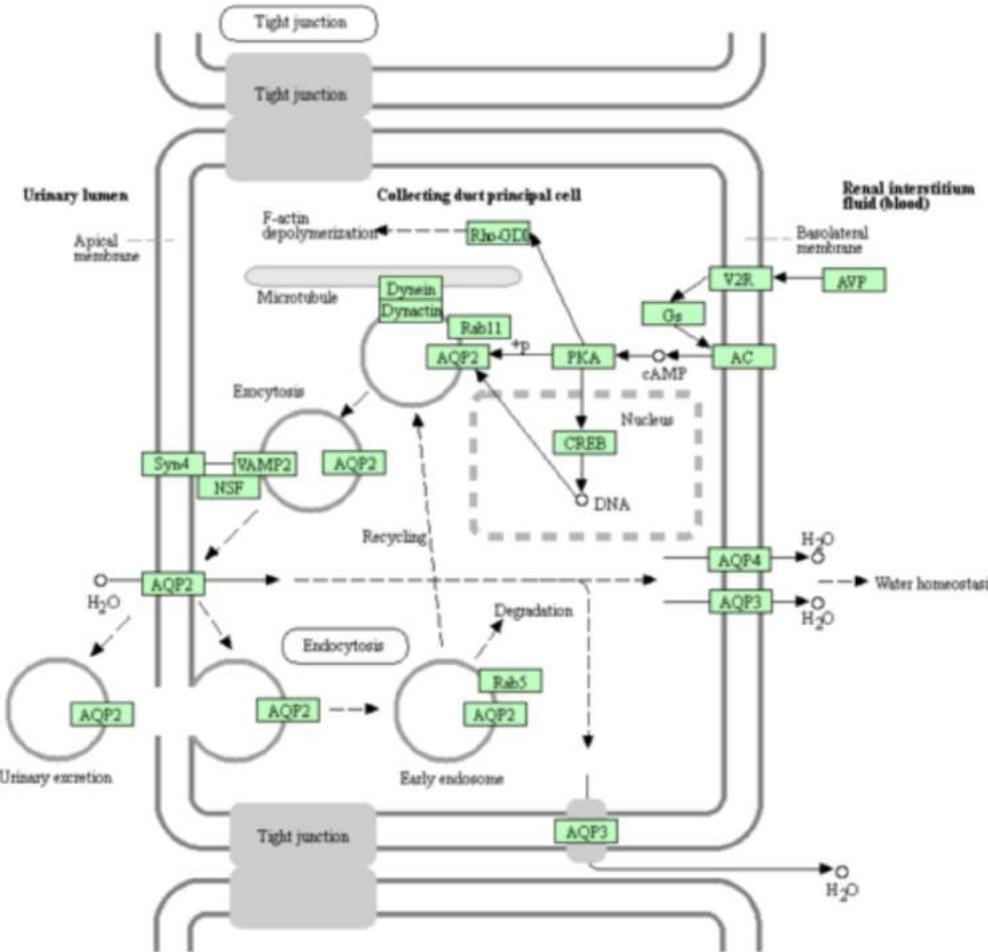
[Indexed for MEDLINE] [Free PMC Article](#)

Vasopresin-regulated water re-absorption signaling pathway 4 genes

Aqp4
Aqp3
Rab5b
Aqp2

ENSMUSG00000024411, ENSMUSG00000028435,
ENSMUSG00000000711, ENSMUSG00000023013

VASOPRESSIN-REGULATED WATER REABSORPTION



*** Welcome to DAVID 6.8 ***

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

Functional Annotation Clustering

Current Gene List: List_2

Current Background: Mus musculus

338 DAVID IDs

 Options
 Classification Stringency
Medium
 Rerun using options
 Create Sublist

57 Cluster(s)

[Help and Manual](#)

	Annotation Cluster 6	Enrichment Score: 3.43	G			Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	Major intrinsic protein, conserved site	RT			5	6.2E-6	4.2E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	glycerol channel activity	RT			5	1.3E-5	2.6E-3
<input type="checkbox"/>	INTERPRO	Major intrinsic protein	RT			5	2.4E-5	7.9E-3
<input type="checkbox"/>	INTERPRO	Aquaporin-like	RT			5	2.4E-5	7.9E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:NPA 2	RT			5	3.2E-5	1.3E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:NPA 1	RT			5	3.2E-5	1.3E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	water channel activity	RT			5	4.1E-5	5.0E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular water homeostasis	RT			5	4.5E-5	1.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	water transport	RT			5	1.1E-4	2.1E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	transporter activity	RT			12	7.9E-4	5.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	glycerol transport	RT			3	1.6E-3	1.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	renal water absorption	RT			3	3.8E-3	2.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	ion transmembrane transport	RT			5	7.2E-3	3.5E-1
<input type="checkbox"/>	UP_KEYWORDS	Porin	RT			3	1.2E-2	1.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	porin activity	RT			3	1.5E-2	3.3E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	pore complex	RT			3	2.2E-2	2.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Vasopressin-regulated water reabsorption	RT			4	4.5E-2	4.0E-1

gProfiler (online tool)

<https://biit.cs.ut.ee/gprofiler/gost>

Downregulated genes

The screenshot shows the g:Profiler web interface. At the top, there's a navigation bar with links like Apps, AWS, SDCX g, Microservices, beluca, kursy, napomoc, fit, coding interview, trading, WolowTube - Wat..., and Table Browser-USC. Below the navigation bar is the main header with the g:Profiler logo and links for News, Archives, Beta, API, FAQ, Docs, Contact, Cite g:Profiler, Services using g:P, and List of organisms.

The main content area has four tabs: g:GOst (Functional profiling), g:Convert (Gene ID conversion), g:Orth (Orthology search), and g:SNPense (SNP id to gene name). The g:GOst tab is selected and highlighted in orange.

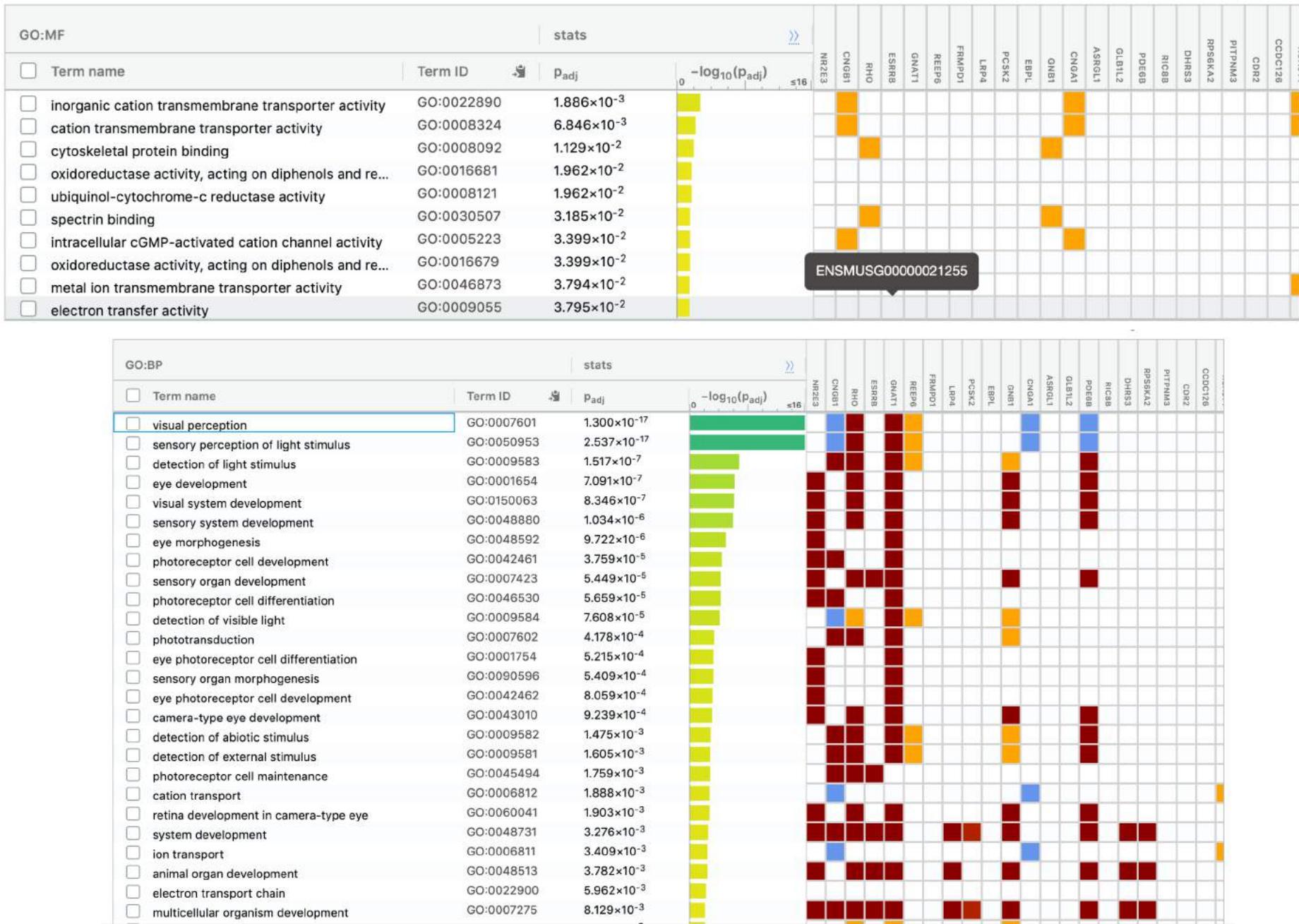
On the left, there's a sidebar with a list of genes: Rnf26, Klc3, Ccl27a, Fgd3, Gm5460, Ccdc88b, Hmx1, Rpl29, Olfm3, Col8a1, Eps8l1, Smad6, Dpm3, Grin2d. Below this list are two buttons: "Run query" (orange) and "random".

The central part of the interface is the "Options" section. It includes fields for "Organism:" (set to Mus musculus (Mouse)), "Query type:" (checkboxes for "Ordered query" and "Run as multiquery"), and "Advanced options" (checkboxes for "All results" and "Measure underrepresentation"). There are also dropdown menus for "Statistical domain scope" (set to "Only annotated genes") and "Significance threshold" (set to "g:SCS threshold"). The "User threshold" is set to "0.05".

On the right side, there's a "Data sources" section with buttons for "select all" and "clear all", and a link to "Show data versions". This section lists various databases and ontologies with checkboxes: Gene Ontology (GO molecular function, GO cellular component, GO biological process, No electronic GO annotations), biological pathways (KEGG, Reactome, WikiPathways), regulatory motifs in DNA (TRANSFAC, miRTarBase), protein databases (Human Protein Atlas, CORUM), and Human phenotype ontology (HP).

gProfiler online

<https://biit.cs.ut.ee/gprofiler/gost>



gProfiler online

<https://biit.cs.ut.ee/gprofiler/gost>

