

Functional Annotation Clustering

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Current Gene List: List\_1  
Current Background: Homo sapiens  
72 DAVID IDs

Options
































































Classification Stringency


















































Medium ▼

Rerun using options

Create Sublist

13 Cluster(s) [Download File](#)

Annotation Cluster 1		Enrichment Score: 1.88	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Cyclin, N-terminal</a>	RT		3	6.5E-3	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Cyclin</a>	RT		3	8.0E-3	2.6E-1
<input type="checkbox"/>	SMART	<a href="#">CYCLIN</a>	RT		3	1.0E-2	6.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Cyclin-like</a>	RT		3	1.1E-2	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Cell cycle</a>	RT		6	6.7E-2	8.9E-1
Annotation Cluster 2		Enrichment Score: 1.14	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">GTPase activity</a>	RT		5	1.5E-2	9.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">GDP binding</a>	RT		3	2.0E-2	9.2E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">GTP-binding</a>	RT		5	2.8E-2	6.1E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Protein transport</a>	RT		6	5.4E-2	7.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">GTP binding</a>	RT		5	6.9E-2	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein transport</a>	RT		5	7.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	RT		4	8.8E-2	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">P-loop containing nucleoside triphosphate hydrolase</a>	RT		7	9.2E-2	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Small GTP-binding protein domain</a>	RT		3	1.2E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">small GTPase mediated signal transduction</a>	RT		3	2.5E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transport</a>	RT		8	5.0E-1	1.0E0
Annotation Cluster 3		Enrichment Score: 1.02	G		Count	P_Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Cholinergic synapse</a>	RT		4	2.0E-2	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Oxytocin signaling pathway</a>	RT		4	4.3E-2	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Estrogen signaling pathway</a>	RT		3	9.4E-2	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">cAMP signaling pathway</a>	RT		3	2.8E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Pathways in cancer</a>	RT		4	3.4E-1	1.0E0
Annotation Cluster 4		Enrichment Score: 0.78	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein serine/threonine/tyrosine kinase activity</a>	RT		3	6.1E-3	5.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">FoxO signaling pathway</a>	RT		4	3.2E-2	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Nucleotide-binding</a>	RT		12	3.5E-2	6.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Serine/threonine-protein kinase, active site</a>	RT		4	1.0E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein phosphorylation</a>	RT		5	1.0E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Serine/threonine-protein kinase</a>	RT		4	1.5E-1	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase, ATP binding site</a>	RT		4	1.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein serine/threonine kinase activity</a>	RT		4	1.9E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Proton acceptor	RT		5	1.9E-1	1.0E0
<input type="checkbox"/>	SMART	<a href="#">S_TKc</a>	RT		4	2.0E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase	RT		4	2.2E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Kinase</a>	RT		5	2.3E-1	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase, catalytic domain</a>	RT		4	2.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ATP binding</a>	RT		9	2.5E-1	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase-like domain</a>	RT		4	2.9E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:ATP	RT		4	2.9E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">ATP-binding</a>	RT		7	3.2E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Cytoskeleton</a>	RT		6	3.3E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein kinase activity</a>	RT		3	4.3E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT		5	4.4E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transferase</a>	RT		7	5.1E-1	1.0E0
Annotation Cluster 5		Enrichment Score: 0.77	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Cell cycle</a>	RT		6	6.7E-2	8.9E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Cell division</a>	RT		4	1.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cell cycle</a>	RT		3	2.1E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cell division</a>	RT		3	4.0E-1	1.0E0
Annotation Cluster 6		Enrichment Score: 0.76	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of apoptotic process</a>	RT		4	5.1E-2	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Apoptosis</a>	RT		4	2.7E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">apoptotic process</a>	RT		4	3.9E-1	1.0E0
Annotation Cluster 7		Enrichment Score: 0.66	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of transcription from RNA polymerase II promoter</a>	RT		7	6.3E-2	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">transcription corepressor activity</a>	RT		3	2.0E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of transcription, DNA-templated</a>	RT		4	3.1E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Repressor</a>	RT		3	5.9E-1	1.0E0
Annotation Cluster 8		Enrichment Score: 0.62	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">mitochondrial outer membrane</a>	RT		3	1.1E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">mitochondrion</a>	RT		8	2.4E-1	1.0E0

Annotation Cluster 1		Enrichment Score: 1.88	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Mitochondrion</a>	RT		5	5.2E-1	1.0E0
Annotation Cluster 9		Enrichment Score: 0.62	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of transcription from RNA polymerase II promoter</a>	RT		7	6.3E-2	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transcription</a>	RT		12	1.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">transcription, DNA-templated</a>	RT		11	2.3E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transcription regulation</a>	RT		11	2.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">transcription factor activity, sequence-specific DNA binding</a>	RT		6	3.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of transcription, DNA-templated</a>	RT		5	8.5E-1	1.0E0
Annotation Cluster 10		Enrichment Score: 0.32	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Zinc</a>	RT		11	2.6E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Metal-binding</a>	RT		14	4.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">metal ion binding</a>	RT		9	6.0E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Zinc-finger</a>	RT		6	7.2E-1	1.0E0
Annotation Cluster 11		Enrichment Score: 0.32	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	lipid moiety-binding region:S-palmitoyl cysteine	RT		4	2.5E-2	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Palmitate</a>	RT		4	9.5E-2	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Neuroactive ligand-receptor interaction</a>	RT		3	4.3E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transducer</a>	RT		4	5.9E-1	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">G protein-coupled receptor, rhodopsin-like</a>	RT		3	7.3E-1	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">GPCR, rhodopsin-like, 7TM</a>	RT		3	7.4E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">G-protein coupled receptor</a>	RT		3	7.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">integral component of plasma membrane</a>	RT		5	7.9E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Receptor</a>	RT		4	9.2E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain:Extracellular	RT		7	9.2E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	transmembrane region	RT		13	9.5E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT		8	9.6E-1	1.0E0
Annotation Cluster 12		Enrichment Score: 0.18	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Membrane</a>	RT		29	2.7E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">plasma membrane</a>	RT		18	3.9E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Glycoprotein</a>	RT		17	4.6E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Cell membrane</a>	RT		12	5.0E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		14	7.0E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transmembrane helix</a>	RT		17	8.2E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transmembrane</a>	RT		17	8.2E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain:Extracellular	RT		7	9.2E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	transmembrane region	RT		13	9.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">integral component of membrane</a>	RT		15	9.5E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT		8	9.6E-1	1.0E0
Annotation Cluster 13		Enrichment Score: 0.15	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Glycoprotein</a>	RT		17	4.6E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Disulfide bond</a>	RT		13	4.9E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	disulfide bond	RT		10	6.7E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		14	7.0E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">extracellular space</a>	RT		5	7.6E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Secreted</a>	RT		6	8.0E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">extracellular region</a>	RT		5	8.7E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	signal peptide	RT		9	9.0E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Signal</a>	RT		9	9.8E-1	1.0E0

98 terms were not clustered.