DAVID Bioinformatics Resources 6.7
National Institute of Allergy and Infectious Diseases (NIAID), NIH

Functional Annotation Clustering

Help and Manual

Current Gene List: List_1
Current Background: Mus musculus
196 DAVID IDs

⊞ **Options** **Classification Stringency** Medium

Rerun using options   Create Sublist

15 Cluster(s)

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	Annotation Cluster 1	Enrichment Score: 2.96	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	transcription regulation	RT	▬	34	7.8E-5	9.1E-3
☐	SP_PIR_KEYWORDS	Transcription	RT	▬	34	9.1E-4	6.8E-2
☐	SP_PIR_KEYWORDS	nucleus	RT	▬	59	1.6E-3	8.8E-2
☐	SP_PIR_KEYWORDS	activator	RT	▬	14	2.0E-3	8.9E-2
☐	SP_PIR_KEYWORDS	dna-binding	RT	▬	26	7.2E-3	2.1E-1
	Annotation Cluster 2	Enrichment Score: 1.92	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	isopeptide bond	RT	▬	9	9.5E-3	2.4E-1
☐	SP_PIR_KEYWORDS	ubl conjugation	RT	▬	13	1.0E-2	2.3E-1
☐	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO)	RT	▬	5	1.9E-2	9.6E-1
	Annotation Cluster 3	Enrichment Score: 1.79	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	calcium-binding region:2	RT	▬	7	1.7E-3	7.6E-1
☐	UP_SEQ_FEATURE	calcium-binding region:1	RT	▬	7	2.6E-3	6.7E-1
☐	UP_SEQ_FEATURE	domain:EF-hand 2	RT	▬	7	1.0E-2	9.5E-1
☐	UP_SEQ_FEATURE	domain:EF-hand 1	RT	▬	6	3.8E-2	9.9E-1
☐	UP_SEQ_FEATURE	domain:EF-hand 3	RT	▬	4	6.8E-2	1.0E0
☐	SP_PIR_KEYWORDS	calcium	RT	▬	12	1.5E-1	6.4E-1
	Annotation Cluster 4	Enrichment Score: 1.12	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	potassium transport	RT	▬	5	2.7E-2	3.9E-1
☐	SP_PIR_KEYWORDS	potassium	RT	▬	5	3.7E-2	4.7E-1
☐	SP_PIR_KEYWORDS	potassium channel	RT	▬	4	3.8E-2	4.5E-1
☐	SP_PIR_KEYWORDS	voltage-gated channel	RT	▬	5	5.5E-2	5.0E-1
☐	SP_PIR_KEYWORDS	ion transport	RT	▬	9	2.2E-1	7.5E-1
☐	SP_PIR_KEYWORDS	ionic channel	RT	▬	5	3.9E-1	8.8E-1
	Annotation Cluster 5	Enrichment Score: 0.99	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	atp-binding	RT	▬	23	1.8E-2	3.2E-1
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT	▬	26	3.8E-2	4.4E-1
☐	SP_PIR_KEYWORDS	kinase	RT	▬	13	7.3E-2	5.5E-1
☐	SP_PIR_KEYWORDS	transferase	RT	▬	21	9.7E-2	5.9E-1
☐	UP_SEQ_FEATURE	binding site:ATP	RT	▬	11	9.8E-2	1.0E0
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT	▬	16	9.9E-2	1.0E0
☐	SP_PIR_KEYWORDS	tyrosine-protein kinase	RT	▬	4	1.3E-1	6.2E-1
☐	UP_SEQ_FEATURE	domain:Protein kinase	RT	▬	9	1.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	serine/threonine-protein kinase	RT	▬	7	2.2E-1	7.5E-1
☐	UP_SEQ_FEATURE	active site:Proton acceptor	RT	▬	9	4.9E-1	1.0E0
	Annotation Cluster 6	Enrichment Score: 0.76	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	egf-like domain	RT	▬	6	8.8E-2	5.8E-1
☐	UP_SEQ_FEATURE	domain:EGF-like 3	RT	▬	3	1.8E-1	1.0E0

☐	UP_SEQ_FEATURE	domain:EGF-like 1	RT		3	3.4E-1	1.0E0
	Annotation Cluster 7	**Enrichment Score: 0.68**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	UP_SEQ_FEATURE	repeat:ANK 9	RT		3	5.8E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 8	RT		3	7.4E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 7	RT		3	1.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	ank repeat	RT		5	2.1E-1	7.4E-1
☐	UP_SEQ_FEATURE	repeat:ANK 6	RT		3	2.3E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 3	RT		4	2.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 5	RT		3	3.5E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 1	RT		4	3.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 2	RT		4	3.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 4	RT		3	4.3E-1	1.0E0
	Annotation Cluster 8	**Enrichment Score: 0.64**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	golgi apparatus	RT		10	1.3E-1	6.3E-1
☐	SP_PIR_KEYWORDS	Signal-anchor	RT		7	2.6E-1	7.8E-1
☐	UP_SEQ_FEATURE	topological domain:Lumenal	RT		7	3.4E-1	1.0E0
	Annotation Cluster 9	**Enrichment Score: 0.44**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	zinc finger	RT		3	1.5E-1	6.3E-1
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 3	RT		5	3.3E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	RT		5	3.3E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	RT		5	3.5E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 4	RT		4	4.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc-finger	RT		14	5.1E-1	9.2E-1
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 5	RT		3	6.4E-1	1.0E0
	Annotation Cluster 10	**Enrichment Score: 0.34**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	palmitate	RT		4	3.7E-1	8.8E-1
☐	SP_PIR_KEYWORDS	lipoprotein	RT		8	4.3E-1	8.9E-1
☐	UP_SEQ_FEATURE	lipid moiety-binding region:S-palmitoyl cysteine	RT		3	6.0E-1	1.0E0
	Annotation Cluster 11	**Enrichment Score: 0.29**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	UP_SEQ_FEATURE	domain:Ig-like C2-type 1	RT		3	4.4E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Ig-like C2-type 2	RT		3	4.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	Immunoglobulin domain	RT		5	6.9E-1	9.7E-1
	Annotation Cluster 12	**Enrichment Score: 0.17**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	signal	RT		33	4.9E-1	9.1E-1
☐	SP_PIR_KEYWORDS	glycoprotein	RT		39	5.4E-1	9.3E-1
☐	SP_PIR_KEYWORDS	Secreted	RT		15	6.5E-1	9.6E-1
☐	UP_SEQ_FEATURE	signal peptide	RT		33	6.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	disulfide bond	RT		24	7.8E-1	9.9E-1
☐	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		36	8.2E-1	1.0E0
☐	UP_SEQ_FEATURE	disulfide bond	RT		24	8.4E-1	1.0E0
	Annotation Cluster 13	**Enrichment Score: 0.15**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	zinc-finger	RT		14	5.1E-1	9.2E-1
☐	SP_PIR_KEYWORDS	zinc	RT		18	7.9E-1	9.9E-1
☐	SP_PIR_KEYWORDS	metal-binding	RT		24	8.9E-1	1.0E0
	Annotation Cluster 14	**Enrichment Score: 0.13**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	glycoprotein	RT		39	5.4E-1	9.3E-1
☐	UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT		32	6.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	membrane	RT		58	6.1E-1	9.5E-1
☐	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		36	8.2E-1	1.0E0
☐	UP_SEQ_FEATURE	topological domain:Extracellular	RT		22	8.3E-1	1.0E0
☐	UP_SEQ_FEATURE	transmembrane region	RT		41	9.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	transmembrane	RT		41	1.0E0	1.0E0

	Annotation Cluster 15	Enrichment Score: 0.04	G			Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	transit peptide	**RT**	▮		4	8.7E-1	1.0E0
☐	**UP_SEQ_FEATURE**	transit peptide:Mitochondrion	**RT**	▮		4	8.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	mitochondrion	**RT**	▮		5	9.7E-1	1.0E0

83 terms were not clustered.

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