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

Functional Annotation Clustering

Help and Manual

Current Gene List: BetweenBatch_DREtop100byFpvalueCombined.uniq_015064_D_AA_20131128.NCBIids
Current Background: Danio rerio
102 DAVID IDs

Options **Classification Stringency** Medium ▼

Rerun using options | Create Sublist

7 Cluster(s)

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				Count	P_Value	Benjamini
	Annotation Cluster 1	Enrichment Score: 2.52		Count	P_Value	Benjamini
☐	INTERPRO	Nucleotide-binding, alpha-beta plait	RT	7	7.6E-4	1.5E-1
☐	SMART	RRM	RT	6	2.1E-3	8.4E-2
☐	INTERPRO	RNA recognition motif, RNP-1	RT	6	4.9E-3	4.0E-1
☐	KEGG_PATHWAY	Spliceosome	RT	5	1.1E-2	3.0E-1
	Annotation Cluster 2	Enrichment Score: 1.25		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	ribonucleoprotein	RT	6	1.2E-3	8.6E-2
☐	GOTERM_CC_FAT	ribonucleoprotein complex	RT	7	1.4E-2	7.1E-1
☐	SP_PIR_KEYWORDS	viral nucleoprotein	RT	3	2.2E-2	4.2E-1
☐	GOTERM_BP_FAT	translation	RT	5	4.5E-2	9.9E-1
☐	SP_PIR_KEYWORDS	ribosomal protein	RT	4	5.6E-2	6.6E-1
☐	GOTERM_MF_FAT	structural molecule activity	RT	6	7.2E-2	9.9E-1
☐	GOTERM_MF_FAT	structural constituent of ribosome	RT	4	7.7E-2	9.6E-1
☐	GOTERM_CC_FAT	non-membrane-bounded organelle	RT	9	1.3E-1	1.0E0
☐	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT	9	1.3E-1	1.0E0
☐	KEGG_PATHWAY	Ribosome	RT	3	1.3E-1	7.8E-1
☐	GOTERM_CC_FAT	ribosome	RT	4	1.4E-1	9.9E-1

☐	GOTERM_MF_FAT	RNA binding	RT			3	5.6E-1	1.0E0
	Annotation Cluster 3	Enrichment Score: 0.45		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	nucleotide binding	RT			19	3.6E-2	9.9E-1
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT			9	3.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	atp-binding	RT			7	3.5E-1	9.9E-1
☐	GOTERM_MF_FAT	ATP binding	RT			9	4.3E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT			9	4.4E-1	1.0E0
☐	GOTERM_MF_FAT	purine ribonucleotide binding	RT			11	4.9E-1	1.0E0
☐	GOTERM_MF_FAT	ribonucleotide binding	RT			11	4.9E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl nucleotide binding	RT			9	4.9E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleoside binding	RT			9	5.0E-1	1.0E0
☐	GOTERM_MF_FAT	nucleoside binding	RT			9	5.0E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleotide binding	RT			11	5.4E-1	1.0E0
	Annotation Cluster 4	Enrichment Score: 0.18		G	🟩	Count	P_Value	Benjamini
☐	SMART	RING	RT			3	3.6E-1	1.0E0
☐	INTERPRO	Zinc finger, RING-type	RT			3	4.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc	RT			7	4.6E-1	9.9E-1
☐	SP_PIR_KEYWORDS	metal-binding	RT			7	7.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc-finger	RT			3	7.5E-1	1.0E0
☐	GOTERM_MF_FAT	cation binding	RT			16	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	ion binding	RT			16	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	transition metal ion binding	RT			11	8.3E-1	1.0E0
☐	GOTERM_MF_FAT	zinc ion binding	RT			9	8.3E-1	1.0E0
☐	GOTERM_MF_FAT	metal ion binding	RT			15	8.4E-1	1.0E0
	Annotation Cluster 5	Enrichment Score: 0.17		G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	gtp-binding	RT			3	5.6E-1	1.0E0
☐	GOTERM_MF_FAT	GTP binding	RT			3	7.2E-1	1.0E0
☐	GOTERM_MF_FAT	guanyl ribonucleotide binding	RT			3	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	guanyl nucleotide binding	RT			3	7.3E-1	1.0E0
	Annotation Cluster 6	Enrichment Score: 0.13		G	🟩	Count	P Value	Beniamini

☐	**UP_SEQ_FEATURE**	transmembrane region	RT	▬		7	3.3E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	membrane	RT	▬		10	7.3E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	transmembrane	RT	▬		9	9.2E-1	1.0E0
☐	**GOTERM_CC_FAT**	intrinsic to membrane	RT	▬		11	1.0E0	1.0E0
☐	**GOTERM_CC_FAT**	integral to membrane	RT	▬		10	1.0E0	1.0E0
	Annotation Cluster 7	Enrichment Score: 0.08	G		🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	nucleus	RT	▬		8	7.1E-1	1.0E0
☐	**GOTERM_BP_FAT**	transcription	RT	▬		3	7.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of transcription, DNA-dependent	RT	▬		4	8.2E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of RNA metabolic process	RT	▬		4	8.2E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of transcription	RT	▬		5	8.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	dna-binding	RT	▬		4	8.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	transcription regulator activity	RT	▬		5	8.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	DNA binding	RT	▬		6	9.3E-1	1.0E0
☐	**GOTERM_MF_FAT**	transcription factor activity	RT	▬		3	9.5E-1	1.0E0

24 terms were not clustered.

Please cite *Nature Protocols 2009; 4(1):44 & Genome Biology 2003; 4(5):P3* within any publication that makes use of any methods inspired by **DAVID**.

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