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

Functional Annotation Clustering

Help and Manual

Current Gene List: BetweenBatch_FHM_InVivoTop100byFpvalue.combined
Current Background: Danio rerio
258 DAVID IDs

Options **Classification Stringency** Medium ▼

Rerun using options | Create Sublist

28 Cluster(s)

Download File

	Annotation Cluster 1	Enrichment Score: 1.99	G	🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Spliceosome	RT		7	3.8E-3	1.7E-1
☐	KEGG_PATHWAY	RNA degradation	RT		5	6.2E-3	1.4E-1
☐	INTERPRO	Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core	RT		3	1.5E-2	9.5E-1
☐	INTERPRO	Like-Sm ribonucleoprotein, core	RT		3	1.7E-2	8.9E-1
☐	SMART	Sm	RT		3	1.9E-2	5.9E-1
	Annotation Cluster 2	Enrichment Score: 1.51	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, PHD-finger	RT		5	1.2E-2	9.9E-1
☐	INTERPRO	Zinc finger, PHD-type	RT		5	1.2E-2	9.9E-1
☐	SMART	PHD	RT		5	1.8E-2	8.1E-1
☐	INTERPRO	Zinc finger, PHD-type, conserved site	RT		4	3.9E-2	9.5E-1
☐	SP_PIR_KEYWORDS	zinc	RT		13	3.0E-1	9.4E-1
	Annotation Cluster 3	Enrichment Score: 1.12	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	translation factor activity, nucleic acid binding	RT		5	2.4E-2	8.4E-1
☐	SP_PIR_KEYWORDS	Initiation factor	RT		3	1.1E-1	9.1E-1
☐	GOTERM_MF_FAT	translation initiation factor activity	RT		3	1.6E-1	9.9E-1
	Annotation Cluster 4	Enrichment Score: 1.1	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	DNA/RNA helicase, C-terminal	RT		4	6.1E-2	9.8E-1
☐	INTERPRO	DEAD-like helicase, N-terminal	RT		4	6.3E-2	9.7E-1
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT		4	6.6E-2	9.6E-1
☐	SMART	HELICc	RT		4	8.1E-2	9.3E-1
☐	SMART	DEXDc	RT		4	8.3E-2	8.7E-1
☐	GOTERM_MF_FAT	helicase activity	RT		4	1.4E-1	1.0E0
	Annotation Cluster 5	Enrichment Score: 1.02	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	translation factor activity, nucleic acid binding	RT		5	2.4E-2	8.4E-1
☐	SP_PIR_KEYWORDS	protein biosynthesis	RT		3	1.4E-1	8.9E-1
☐	GOTERM_BP_FAT	translation	RT		6	2.7E-1	1.0E0
	Annotation Cluster 6	Enrichment Score: 1	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	DNA-binding region:Homeobox	RT		6	1.7E-2	8.5E-1
☐	GOTERM_BP_FAT	regulation of transcription	RT		23	3.0E-2	1.0E0
☐	GOTERM_BP_FAT	transcription	RT		13	4.1E-2	1.0E0
☐	SP_PIR_KEYWORDS	Transcription	RT		12	4.5E-2	9.9E-1
☐	SP_PIR_KEYWORDS	transcription regulation	RT		12	4.8E-2	9.2E-1
☐	INTERPRO	Homeobox, conserved site	RT		7	7.0E-2	9.5E-1
☐	SP_PIR_KEYWORDS	developmental protein	RT		9	7.9E-2	9.4E-1
☐	GOTERM_MF_FAT	DNA binding	RT		21	1.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	Homeobox	RT		7	1.1E-1	8.7E-1
☐	INTERPRO	Homeobox	RT		7	1.2E-1	9.8E-1
☐	GOTERM_BP_FAT	regulation of transcription, DNA-	RT		16	1.3E-1	1.0E0

		dependent					
☐	INTERPRO	Homeodomain-related	RT		7	1.3E-1	9.8E-1
☐	GOTERM_BP_FAT	regulation of RNA metabolic process	RT		16	1.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-binding	RT		13	1.4E-1	8.7E-1
☐	GOTERM_MF_FAT	transcription factor activity	RT		13	1.5E-1	9.9E-1
☐	SMART	HOX	RT		7	1.8E-1	9.5E-1
☐	GOTERM_MF_FAT	transcription regulator activity	RT		15	2.5E-1	9.9E-1
☐	SP_PIR_KEYWORDS	nucleus	RT		18	3.2E-1	9.4E-1
☐	GOTERM_MF_FAT	sequence-specific DNA binding	RT		9	3.7E-1	9.8E-1
	Annotation Cluster 7	Enrichment Score: 0.96	G		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cell part morphogenesis	RT		5	3.9E-2	1.0E0
☐	GOTERM_BP_FAT	cellular component morphogenesis	RT		6	5.3E-2	9.9E-1
☐	GOTERM_BP_FAT	cell morphogenesis	RT		5	8.7E-2	1.0E0
☐	GOTERM_BP_FAT	cell projection morphogenesis	RT		4	1.3E-1	1.0E0
☐	GOTERM_BP_FAT	cell projection organization	RT		4	2.0E-1	1.0E0
☐	GOTERM_BP_FAT	cell motion	RT		4	3.9E-1	1.0E0
	Annotation Cluster 8	Enrichment Score: 0.93	G		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	determination of bilateral symmetry	RT		4	9.3E-2	1.0E0
☐	GOTERM_BP_FAT	determination of symmetry	RT		4	9.3E-2	1.0E0
☐	GOTERM_BP_FAT	pattern specification process	RT		7	1.1E-1	1.0E0
☐	GOTERM_BP_FAT	determination of left/right symmetry	RT		3	2.1E-1	1.0E0
	Annotation Cluster 9	Enrichment Score: 0.64	G		Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	integral to organelle membrane	RT		3	1.1E-1	1.0E0
☐	GOTERM_CC_FAT	intrinsic to organelle membrane	RT		3	1.5E-1	1.0E0
☐	GOTERM_CC_FAT	endomembrane system	RT		4	3.0E-1	1.0E0
☐	GOTERM_CC_FAT	organelle membrane	RT		4	5.8E-1	1.0E0
	Annotation Cluster 10	Enrichment Score: 0.6	G		Count	P_Value	Benjamini
☐	INTERPRO	Src homology-3 domain	RT		5	1.6E-1	9.9E-1
☐	SMART	SH3	RT		5	2.2E-1	9.6E-1
☐	SP_PIR_KEYWORDS	sh3 domain	RT		3	4.4E-1	9.7E-1
	Annotation Cluster 11	Enrichment Score: 0.58	G		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	pattern specification process	RT		7	1.1E-1	1.0E0
☐	GOTERM_BP_FAT	somitogenesis	RT		3	2.4E-1	1.0E0
☐	GOTERM_BP_FAT	embryonic development ending in birth or egg hatching	RT		4	2.6E-1	1.0E0
☐	GOTERM_BP_FAT	chordate embryonic development	RT		4	2.6E-1	1.0E0
☐	GOTERM_BP_FAT	segmentation	RT		3	2.7E-1	1.0E0
☐	GOTERM_BP_FAT	regionalization	RT		4	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	anterior/posterior pattern formation	RT		3	4.6E-1	1.0E0
	Annotation Cluster 12	Enrichment Score: 0.52	G		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	transit peptide	RT		3	2.0E-1	9.2E-1
☐	GOTERM_BP_FAT	translation	RT		6	2.7E-1	1.0E0
☐	UP_SEQ_FEATURE	transit peptide:Mitochondrion	RT		3	2.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	mitochondrion	RT		3	5.6E-1	9.8E-1
	Annotation Cluster 13	Enrichment Score: 0.49	G		Count	P_Value	Benjamini
☐	INTERPRO	Small GTP-binding protein	RT		5	2.1E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase activity	RT		3	2.2E-1	1.0E0
☐	INTERPRO	Ras	RT		4	2.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	gtp-binding	RT		6	2.7E-1	9.5E-1
☐	INTERPRO	Ras GTPase	RT		4	3.1E-1	1.0E0
☐	GOTERM_MF_FAT	GTP binding	RT		7	3.2E-1	9.9E-1
☐	GOTERM_MF_FAT	guanyl ribonucleotide binding	RT		7	3.3E-1	9.9E-1
☐	GOTERM_MF_FAT	guanyl nucleotide binding	RT		7	3.3E-1	9.9E-1
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT		14	4.6E-1	9.6E-1

☐	GOTERM_BP_FAT	intracellular signaling cascade	RT		7	4.7E-1	1.0E0
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT		4	5.1E-1	1.0E0
	Annotation Cluster 14	Enrichment Score: 0.42	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	embryonic organ morphogenesis	RT		3	3.0E-1	1.0E0
☐	GOTERM_BP_FAT	embryonic organ development	RT		4	3.1E-1	1.0E0
☐	GOTERM_BP_FAT	embryonic morphogenesis	RT		4	5.8E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 0.39	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	zinc	RT		13	3.0E-1	9.4E-1
☐	SP_PIR_KEYWORDS	zinc-finger	RT		7	3.7E-1	9.6E-1
☐	INTERPRO	Zinc finger, RING-type	RT		5	4.2E-1	1.0E0
☐	INTERPRO	Zinc finger, C3HC4 RING-type	RT		4	4.7E-1	1.0E0
☐	SMART	RING	RT		5	5.1E-1	1.0E0
	Annotation Cluster 16	Enrichment Score: 0.39	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	nucleoplasm part	RT		3	3.5E-1	1.0E0
☐	GOTERM_CC_FAT	intracellular organelle lumen	RT		4	3.8E-1	1.0E0
☐	GOTERM_CC_FAT	organelle lumen	RT		4	3.8E-1	1.0E0
☐	GOTERM_CC_FAT	nucleoplasm	RT		3	4.0E-1	9.9E-1
☐	GOTERM_CC_FAT	membrane-enclosed lumen	RT		4	4.1E-1	9.9E-1
☐	GOTERM_CC_FAT	nuclear lumen	RT		3	5.7E-1	1.0E0
	Annotation Cluster 17	Enrichment Score: 0.34	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	translation	RT		6	2.7E-1	1.0E0
☐	GOTERM_CC_FAT	ribonucleoprotein complex	RT		5	2.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	ribosomal protein	RT		3	4.8E-1	9.6E-1
☐	GOTERM_CC_FAT	ribosome	RT		3	5.2E-1	1.0E0
☐	GOTERM_MF_FAT	structural constituent of ribosome	RT		3	5.5E-1	9.9E-1
☐	GOTERM_MF_FAT	structural molecule activity	RT		3	9.2E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 0.32	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, C2H2-type	RT		8	3.6E-1	1.0E0
☐	INTERPRO	Zinc finger, C2H2-like	RT		7	4.9E-1	1.0E0
☐	SMART	ZnF_C2H2	RT		7	6.1E-1	1.0E0
	Annotation Cluster 19	Enrichment Score: 0.3	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Serine/threonine protein kinase	RT		5	2.6E-1	1.0E0
☐	GOTERM_MF_FAT	purine ribonucleotide binding	RT		21	3.0E-1	9.9E-1
☐	GOTERM_MF_FAT	ribonucleotide binding	RT		21	3.0E-1	9.9E-1
☐	GOTERM_MF_FAT	nucleotide binding	RT		25	3.3E-1	9.8E-1
☐	SMART	S_TKc	RT		5	3.3E-1	9.9E-1
☐	GOTERM_MF_FAT	purine nucleotide binding	RT		21	3.7E-1	9.9E-1
☐	INTERPRO	Serine/threonine protein kinase-related	RT		6	4.3E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase, active site	RT		5	4.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT		14	4.6E-1	9.6E-1
☐	GOTERM_MF_FAT	ATP binding	RT		15	4.7E-1	9.9E-1
☐	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT		15	4.7E-1	9.9E-1
☐	GOTERM_MF_FAT	adenyl nucleotide binding	RT		15	5.4E-1	9.9E-1
☐	GOTERM_MF_FAT	purine nucleoside binding	RT		15	5.5E-1	9.9E-1
☐	GOTERM_MF_FAT	protein kinase activity	RT		7	5.5E-1	9.9E-1
☐	GOTERM_MF_FAT	nucleoside binding	RT		15	5.6E-1	9.9E-1
☐	GOTERM_BP_FAT	phosphorylation	RT		8	5.7E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid phosphorylation	RT		7	5.8E-1	1.0E0
☐	GOTERM_MF_FAT	protein serine/threonine kinase activity	RT		5	5.8E-1	9.9E-1
☐	INTERPRO	Protein kinase, core	RT		6	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorus metabolic process	RT		9	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	phosphate metabolic process	RT		9	6.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	atp binding	RT		8	8.0E-1	1.0E0

☐	SP_PIR_KEYWORDS	atp-binding	RT	8	8.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	serine/threonine-protein kinase	RT	3	8.2E-1	1.0E0
☐	INTERPRO	Protein kinase, ATP binding site	RT	3	9.4E-1	1.0E0
	Annotation Cluster 20	Enrichment Score: 0.29	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	RT	3	1.9E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule catabolic process	RT	5	2.9E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecule catabolic process	RT	5	3.9E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent protein catabolic process	RT	3	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	RT	3	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	RT	3	7.1E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein catabolic process	RT	3	7.1E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis	RT	7	7.5E-1	1.0E0
☐	GOTERM_BP_FAT	protein catabolic process	RT	3	7.5E-1	1.0E0
	Annotation Cluster 21	Enrichment Score: 0.28	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	egf-like domain	RT	3	4.4E-1	9.7E-1
☐	INTERPRO	EGF-like region, conserved site	RT	4	4.5E-1	1.0E0
☐	INTERPRO	EGF-like, type 3	RT	3	4.8E-1	1.0E0
☐	INTERPRO	EGF-like	RT	3	5.2E-1	1.0E0
☐	SMART	EGF	RT	3	5.9E-1	1.0E0
☐	GOTERM_CC_FAT	extracellular region	RT	5	6.9E-1	1.0E0
	Annotation Cluster 22	Enrichment Score: 0.26	G	Count	P_Value	Benjamini
☐	INTERPRO	EF-HAND 2	RT	4	4.4E-1	1.0E0
☐	INTERPRO	EF-Hand type	RT	4	4.7E-1	1.0E0
☐	INTERPRO	Calcium-binding EF-hand	RT	3	5.4E-1	1.0E0
☐	SMART	EFh	RT	3	6.0E-1	1.0E0
☐	GOTERM_MF_FAT	calcium ion binding	RT	6	7.2E-1	1.0E0
	Annotation Cluster 23	Enrichment Score: 0.26	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	zinc	RT	13	3.0E-1	9.4E-1
☐	GOTERM_MF_FAT	zinc ion binding	RT	21	4.4E-1	9.9E-1
☐	SP_PIR_KEYWORDS	metal-binding	RT	15	4.6E-1	9.6E-1
☐	GOTERM_MF_FAT	transition metal ion binding	RT	23	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	metal ion binding	RT	30	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	cation binding	RT	30	7.6E-1	1.0E0
☐	GOTERM_MF_FAT	ion binding	RT	30	7.6E-1	1.0E0
	Annotation Cluster 24	Enrichment Score: 0.25	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	sensory organ development	RT	4	5.3E-1	1.0E0
☐	GOTERM_BP_FAT	eye development	RT	3	5.8E-1	1.0E0
☐	GOTERM_BP_FAT	embryonic morphogenesis	RT	4	5.8E-1	1.0E0
	Annotation Cluster 25	Enrichment Score: 0.22	G	Count	P_Value	Benjamini
☐	INTERPRO	WD40 repeat, conserved site	RT	4	2.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	wd repeat	RT	3	6.5E-1	9.9E-1
☐	INTERPRO	WD40 repeat	RT	3	7.1E-1	1.0E0
☐	INTERPRO	WD40/YVTN repeat-like	RT	3	7.7E-1	1.0E0
☐	SMART	WD40	RT	3	7.8E-1	1.0E0
	Annotation Cluster 26	Enrichment Score: 0.21	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	protein localization	RT	6	4.1E-1	1.0E0
☐	GOTERM_BP_FAT	establishment of protein localization	RT	4	7.6E-1	1.0E0
☐	GOTERM_BP_FAT	protein transport	RT	4	7.6E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 0.11	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	endopeptidase activity	RT	4	7.4E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis	RT	7	7.5E-1	1.0E0
☐	GOTERM_MF_FAT	peptidase activity, acting on L-amino acid peptides	RT	5	8.0E-1	1.0E0
☐	GOTERM_MF_FAT					

☐	GOTERM_MF_FAT	peptidase activity	RT	5	8.3E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 0.05	G 🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	glycoprotein	RT	5	5.8E-1	9.8E-1
☐	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT	5	7.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	membrane	RT	15	9.3E-1	1.0E0
☐	UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT	3	9.4E-1	1.0E0
☐	UP_SEQ_FEATURE	transmembrane region	RT	6	9.7E-1	1.0E0
☐	GOTERM_CC_FAT	intrinsic to membrane	RT	16	9.9E-1	1.0E0
☐	GOTERM_CC_FAT	integral to membrane	RT	15	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	transmembrane	RT	10	1.0E0	1.0E0

59 terms were not clustered.

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