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

Functional Annotation Clustering

Help and Manual

Current Gene List: Contaminants
Current Background: Giardia intestinalis
1031 DAVID IDs

Options **Classification Stringency** Medium

Rerun using options | Create Sublist

56 Cluster(s)

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	Annotation Cluster 1	Enrichment Score: 16.12		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	translation	RT	101	1.2E-29	5.0E-27
☐	SP_PIR_KEYWORDS	ribosomal protein	RT	68	1.8E-27	1.8E-25
☐	GOTERM_MF_FAT	structural constituent of ribosome	RT	65	3.2E-24	1.2E-21
☐	GOTERM_MF_FAT	structural molecule activity	RT	72	7.1E-22	1.3E-19
☐	GOTERM_CC_FAT	ribosome	RT	70	5.2E-19	5.6E-17
☐	KEGG_PATHWAY	Ribosome	RT	65	3.1E-13	1.4E-11
☐	GOTERM_CC_FAT	ribonucleoprotein complex	RT	72	5.0E-8	2.7E-6
☐	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT	94	4.6E-4	1.2E-2
☐	GOTERM_CC_FAT	non-membrane-bounded organelle	RT	94	4.6E-4	1.2E-2
	Annotation Cluster 2	Enrichment Score: 5.33		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Aminoacyl-tRNA synthetase	RT	23	4.2E-10	2.0E-8
☐	GOTERM_MF_FAT	aminoacyl-tRNA ligase activity	RT	24	6.5E-10	7.7E-8
☐	GOTERM_MF_FAT	ligase activity, forming aminoacyl-tRNA and related compounds	RT	24	6.5E-10	7.7E-8
☐	GOTERM_MF_FAT	ligase activity, forming carbon-oxygen bonds	RT	24	6.5E-10	7.7E-8
☐	GOTERM_BP_FAT	tRNA aminoacylation	RT	23	2.8E-8	6.0E-6
☐	GOTERM_BP_FAT	amino acid activation	RT	23	2.8E-8	6.0E-6
☐	GOTERM_BP_FAT	tRNA aminoacylation for protein translation	RT	22	6.7E-8	9.6E-6
☐	KEGG_PATHWAY	Aminoacyl-tRNA biosynthesis	RT	21	1.3E-4	3.0E-3
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II, conserved region	RT	9	3.3E-4	3.7E-2
☐	SP_PIR_KEYWORDS	protein biosynthesis	RT	10	3.5E-4	5.0E-3
☐	GOTERM_BP_FAT	tRNA metabolic process	RT	27	1.4E-3	7.3E-2
☐	INTERPRO	Aminoacyl-tRNA synthetase, class I, conserved site	RT	8	3.5E-3	2.1E-1
☐	GOTERM_BP_FAT	ncRNA metabolic process	RT	30	1.8E-2	4.1E-1
☐	SP_PIR_KEYWORDS	ligase	RT	27	2.1E-2	1.2E-1
☐	INTERPRO	Rossmann-like alpha/beta/alpha sandwich fold	RT	10	7.0E-2	9.3E-1
	Annotation Cluster 3	Enrichment Score: 3.38		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	cytoplasm	RT	17	1.6E-6	5.1E-5
☐	SP_PIR_KEYWORDS	Chaperone	RT	12	4.6E-5	9.1E-4
☐	GOTERM_MF_FAT	unfolded protein binding	RT	17	1.7E-4	1.2E-2
☐	INTERPRO	Chaperonin Cpn60/TCP-1	RT	9	3.3E-4	3.7E-2
☐	GOTERM_BP_FAT	protein folding	RT	22	1.0E-3	5.9E-2
☐	INTERPRO	Chaperone, tailless complex polypeptide 1	RT	8	1.0E-3	9.8E-2
☐	INTERPRO	Chaperonin TCP-1, conserved site	RT	8	3.5E-3	2.1E-1
☐	PIR_SUPERFAMILY	PIRSF002584:molecular chaperone t-complex-type	RT	8	6.6E-2	1.0E0
	Annotation Cluster 4	Enrichment Score: 3.02		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	monosaccharide metabolic process	RT	21	5.3E-6	5.7E-4
☐	GOTERM_BP_FAT	hexose metabolic process	RT	18	5.5E-5	4.7E-3
☐	GOTERM_BP_FAT	glucose metabolic process	RT	18	5.5E-5	4.7E-3
☐	GOTERM_BP_FAT	alcohol catabolic process	RT	13	7.0E-4	4.9E-2
☐	GOTERM_BP_FAT	monosaccharide catabolic process	RT	13	7.0E-4	4.9E-2
☐	GOTERM_BP_FAT	hexose catabolic process	RT	13	7.0E-4	4.9E-2
☐	GOTERM_BP_FAT	cellular carbohydrate catabolic process	RT	13	7.0E-4	4.9E-2
☐	GOTERM_BP_FAT	glucose catabolic process	RT	13	7.0E-4	4.9E-2

☐	GOTERM_BP_FAT	carbohydrate catabolic process	RT	13	7.0E-4	4.9E-2
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT	19	2.9E-3	1.2E-1
☐	GOTERM_BP_FAT	glycolysis	RT	10	6.7E-3	2.0E-1
☐	SP_PIR_KEYWORDS	glycolysis	RT	5	1.0E-1	3.7E-1
☐	KEGG_PATHWAY	Glycolysis / Gluconeogenesis	RT	7	1.4E-1	8.1E-1
	Annotation Cluster 5	Enrichment Score: 2.71	G	Count	P_Value	Benjamini
☐	SMART	ANX	RT	11	1.2E-4	5.4E-3
☐	INTERPRO	Alpha giardin	RT	11	1.5E-4	3.3E-2
☐	INTERPRO	Annexin	RT	13	1.8E-4	2.3E-2
☐	GOTERM_MF_FAT	calcium-dependent phospholipid binding	RT	17	4.3E-4	2.5E-2
☐	SP_PIR_KEYWORDS	annexin	RT	13	7.8E-4	8.5E-3
☐	INTERPRO	Annexin repeat	RT	11	1.2E-3	1.1E-1
☐	GOTERM_MF_FAT	phospholipid binding	RT	18	3.4E-3	1.6E-1
☐	GOTERM_MF_FAT	calcium ion binding	RT	22	5.2E-2	8.0E-1
☐	GOTERM_MF_FAT	lipid binding	RT	19	5.4E-2	7.6E-1
☐	GOTERM_BP_FAT	cytoskeleton organization	RT	11	6.5E-2	7.8E-1
	Annotation Cluster 6	Enrichment Score: 2.26	G	Count	P_Value	Benjamini
☐	INTERPRO	Proteasome, subunit alpha/beta	RT	14	1.0E-6	9.2E-4
☐	SP_PIR_KEYWORDS	proteasome	RT	18	2.6E-6	6.5E-5
☐	INTERPRO	Proteasome, alpha and beta subunits	RT	13	3.3E-6	1.5E-3
☐	GOTERM_MF_FAT	threonine-type endopeptidase activity	RT	14	1.4E-5	1.2E-3
☐	GOTERM_MF_FAT	threonine-type peptidase activity	RT	14	1.4E-5	1.2E-3
☐	GOTERM_CC_FAT	proteasome complex	RT	19	3.8E-4	1.3E-2
☐	GOTERM_CC_FAT	proteasome core complex	RT	14	5.7E-4	1.2E-2
☐	KEGG_PATHWAY	Proteasome	RT	25	1.3E-3	1.9E-2
☐	GOTERM_CC_FAT	cytosol	RT	23	2.0E-3	3.5E-2
☐	INTERPRO	Proteasome, alpha-subunit, conserved site	RT	7	3.1E-3	2.3E-1
☐	SP_PIR_KEYWORDS	threonine protease	RT	6	1.8E-2	1.2E-1
☐	GOTERM_BP_FAT	protein catabolic process	RT	23	2.3E-2	4.6E-1
☐	GOTERM_MF_FAT	peptidase activity	RT	38	2.5E-2	6.0E-1
☐	SP_PIR_KEYWORDS	Protease	RT	19	2.8E-2	1.4E-1
☐	GOTERM_BP_FAT	macromolecule catabolic process	RT	23	3.3E-2	5.7E-1
☐	GOTERM_MF_FAT	peptidase activity, acting on L-amino acid peptides	RT	32	5.7E-2	7.3E-1
☐	GOTERM_MF_FAT	endopeptidase activity	RT	22	1.1E-1	8.4E-1
☐	GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	RT	18	1.4E-1	9.2E-1
☐	GOTERM_BP_FAT	cellular protein catabolic process	RT	18	1.4E-1	9.2E-1
☐	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	RT	9	1.6E-1	9.5E-1
☐	PIR_SUPERFAMILY	PIRSF001212:multicatalytic endopeptidase complex chain C9	RT	6	1.7E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule catabolic process	RT	18	1.8E-1	9.5E-1
☐	GOTERM_BP_FAT	proteolysis	RT	36	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent protein catabolic process	RT	11	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	RT	11	6.7E-1	1.0E0
	Annotation Cluster 7	Enrichment Score: 2.15	G	Count	P_Value	Benjamini
☐	INTERPRO	Thioredoxin-like	RT	12	5.0E-5	1.5E-2
☐	INTERPRO	Thioredoxin fold	RT	16	1.6E-4	2.8E-2
☐	GOTERM_BP_FAT	cellular homeostasis	RT	15	3.5E-3	1.3E-1
☐	GOTERM_BP_FAT	cell redox homeostasis	RT	14	6.6E-3	2.1E-1
☐	GOTERM_BP_FAT	homeostatic process	RT	15	7.4E-3	2.0E-1
☐	INTERPRO	Thioredoxin domain	RT	6	9.4E-3	4.1E-1
☐	INTERPRO	Thioredoxin, core	RT	6	2.5E-2	7.4E-1
☐	INTERPRO	Thioredoxin-like subdomain	RT	5	2.7E-2	7.5E-1
☐	GOTERM_MF_FAT	antioxidant activity	RT	6	6.1E-2	7.1E-1
☐	INTERPRO	Thioredoxin, conserved site	RT	5	6.3E-2	9.2E-1
☐	INTERPRO	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	RT	5	6.3E-2	9.2E-1
	Annotation Cluster 8	Enrichment Score: 2.05	G	Count	P_Value	Benjamini
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II, conserved region	RT	9	3.3E-4	3.7E-2

☐	INTERPRO	Aminoacyl-tRNA synthetase, class II (G, H, P and S), conserved region	RT		▮		5	2.7E-2	7.5E-1
☐	INTERPRO	Anticodon-binding	RT		▮		4	7.7E-2	9.4E-1
	Annotation Cluster 9	Enrichment Score: 1.96		G		🟩	Count	P_Value	Benjamini
☐	SMART	AAA	RT		▮		29	6.7E-4	2.0E-2
☐	INTERPRO	ATPase, AAA-type, conserved site	RT		▮		10	6.5E-3	3.2E-1
☐	INTERPRO	26S proteasome subunit P45	RT		▮		5	2.7E-2	7.5E-1
☐	INTERPRO	ATPase, AAA-type, core	RT		▮		13	3.4E-2	8.1E-1
☐	INTERPRO	ATPase, AAA+ type, core	RT		▮		29	3.7E-2	8.2E-1
	Annotation Cluster 10	Enrichment Score: 1.24		G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II, conserved region	RT		▮		9	3.3E-4	3.7E-2
☐	INTERPRO	Nucleic acid binding, OB-fold, tRNA/helicase-type	RT		▮		4	7.7E-2	9.4E-1
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II (D, K and N)	RT		▮		3	2.0E-1	1.0E0
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II (D, K and N)-like	RT		▮		3	2.0E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001525:lysine-tRNA ligase	RT		▮		3	5.8E-1	1.0E0
	Annotation Cluster 11	Enrichment Score: 1.2		G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	translation factor activity, nucleic acid binding	RT		▮		19	1.4E-2	4.2E-1
☐	SP_PIR_KEYWORDS	Initiation factor	RT		▮		11	6.5E-2	2.6E-1
☐	GOTERM_MF_FAT	translation initiation factor activity	RT		▮		14	7.0E-2	7.5E-1
☐	GOTERM_BP_FAT	translational initiation	RT		▮		7	2.6E-1	9.8E-1
	Annotation Cluster 12	Enrichment Score: 1.08		G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	cofactor binding	RT		▮		21	7.5E-3	2.9E-1
☐	GOTERM_MF_FAT	vitamin B6 binding	RT		▮		8	2.9E-2	6.2E-1
☐	GOTERM_MF_FAT	pyridoxal phosphate binding	RT		▮		8	2.9E-2	6.2E-1
☐	SP_PIR_KEYWORDS	Aminotransferase	RT		▮		5	4.6E-2	2.0E-1
☐	INTERPRO	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	RT		▮		6	5.1E-2	8.8E-1
☐	GOTERM_MF_FAT	vitamin binding	RT		▮		8	5.6E-2	7.5E-1
☐	GOTERM_MF_FAT	transaminase activity	RT		▮		5	5.8E-2	7.2E-1
☐	INTERPRO	Pyridoxal phosphate-dependent transferase, major region, subdomain 2	RT		▮		3	2.0E-1	1.0E0
☐	INTERPRO	Aminotransferase, class V/Cysteine desulfurase	RT		▮		3	2.0E-1	1.0E0
☐	GOTERM_MF_FAT	transferase activity, transferring nitrogenous groups	RT		▮		5	2.1E-1	9.5E-1
☐	INTERPRO	Aminotransferase, class I and II	RT		▮		3	4.5E-1	1.0E0
☐	KEGG_PATHWAY	Alanine, aspartate and glutamate metabolism	RT		▮		3	6.2E-1	9.9E-1
	Annotation Cluster 13	Enrichment Score: 1.03		G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	lyase	RT		▮		11	4.4E-2	2.0E-1
☐	GOTERM_MF_FAT	carbon-nitrogen lyase activity	RT		▮		4	1.3E-1	8.6E-1
☐	GOTERM_MF_FAT	ammonia-lyase activity	RT		▮		4	1.3E-1	8.6E-1
	Annotation Cluster 14	Enrichment Score: 1.03		G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	gtp-binding	RT		▮		21	2.1E-2	1.3E-1
☐	INTERPRO	Small GTP-binding protein	RT		▮		11	3.8E-2	8.2E-1
☐	GOTERM_MF_FAT	guanyl ribonucleotide binding	RT		▮		24	5.4E-2	7.8E-1
☐	GOTERM_MF_FAT	GTP binding	RT		▮		24	5.4E-2	7.8E-1
☐	GOTERM_MF_FAT	guanyl nucleotide binding	RT		▮		24	5.4E-2	7.8E-1
☐	GOTERM_MF_FAT	GTPase activity	RT		▮		9	2.3E-1	9.6E-1
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT		▮		9	3.1E-1	9.9E-1
☐	GOTERM_BP_FAT	intracellular signaling cascade	RT		▮		9	6.8E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 0.98		G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	threonine protease	RT		▮		6	1.8E-2	1.2E-1
☐	INTERPRO	Proteasome, beta-type subunit, conserved site	RT		▮		4	7.7E-2	9.4E-1
☐	SP_PIR_KEYWORDS	nucleus	RT		▮		10	8.6E-1	9.9E-1
	Annotation Cluster 16	Enrichment Score: 0.95		G		🟩	Count	P_Value	Benjamini
☐	COG_ONTOLOGY	Cytoskeleton	RT		▮		12	3.3E-2	2.8E-1
☐	INTERPRO	ATPase associated with various cellular activities, AAA-5	RT		▮		5	6.3E-2	9.2E-1
☐	INTERPRO	Dynein heavy chain, N-terminal region 2	RT		▮		7	6.8E-2	9.3E-1
☐	INTERPRO	Dynein heavy chain, N-terminal region 1	RT		▮		4	7.7E-2	9.4E-1
☐	SP_PIR_KEYWORDS	coiled coil	RT		▮		4	1.1E-1	3.8E-1
☐	INTERPRO	Dynein heavy chain	RT		▮		6	2.5E-1	1.0E0

☐	GOTERM_CC_FAT	dynein complex	RT		6	7.9E-1	1.0E0
	Annotation Cluster 17	Enrichment Score: 0.89	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	translational elongation	RT		6	1.0E-1	8.6E-1
☐	GOTERM_MF_FAT	translation elongation factor activity	RT		6	1.2E-1	8.5E-1
☐	SP_PIR_KEYWORDS	elongation factor	RT		5	1.8E-1	5.0E-1
	Annotation Cluster 18	Enrichment Score: 0.85	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	electron carrier activity	RT		13	7.8E-2	7.7E-1
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, conserved site	RT		5	1.1E-1	9.8E-1
☐	GOTERM_MF_FAT	4 iron, 4 sulfur cluster binding	RT		6	1.2E-1	8.5E-1
☐	GOTERM_MF_FAT	metal cluster binding	RT		11	1.4E-1	8.6E-1
☐	GOTERM_MF_FAT	iron-sulfur cluster binding	RT		11	1.4E-1	8.6E-1
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, subgroup	RT		5	2.5E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulpur binding domain	RT		5	2.5E-1	1.0E0
	Annotation Cluster 19	Enrichment Score: 0.84	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	alcohol biosynthetic process	RT		5	9.3E-2	8.5E-1
☐	GOTERM_BP_FAT	cellular carbohydrate biosynthetic process	RT		6	1.0E-1	8.6E-1
☐	GOTERM_BP_FAT	carbohydrate biosynthetic process	RT		6	1.0E-1	8.6E-1
☐	GOTERM_BP_FAT	pyruvate metabolic process	RT		4	1.9E-1	9.6E-1
☐	GOTERM_BP_FAT	monosaccharide biosynthetic process	RT		4	1.9E-1	9.6E-1
☐	GOTERM_BP_FAT	gluconeogenesis	RT		4	1.9E-1	9.6E-1
☐	GOTERM_BP_FAT	hexose biosynthetic process	RT		4	1.9E-1	9.6E-1
	Annotation Cluster 20	Enrichment Score: 0.78	G	🟩	Count	P_Value	Benjamini
☐	SMART	RAB	RT		4	3.7E-2	5.8E-1
☐	INTERPRO	Small GTP-binding protein	RT		11	3.8E-2	8.2E-1
☐	INTERPRO	Ras small GTPase, Rab type	RT		4	7.7E-2	9.4E-1
☐	INTERPRO	Ras	RT		7	1.0E-1	9.7E-1
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT		9	3.1E-1	9.9E-1
☐	INTERPRO	Ras GTPase	RT		6	3.2E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular signaling cascade	RT		9	6.8E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001710:Ras-related protein Rab	RT		4	7.5E-1	1.0E0
	Annotation Cluster 21	Enrichment Score: 0.75	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	RT		4	7.7E-2	9.4E-1
☐	INTERPRO	Pyridine nucleotide-disulphide oxidoreductase, NAD-binding region	RT		3	2.0E-1	1.0E0
☐	GOTERM_MF_FAT	FAD binding	RT		4	3.7E-1	9.9E-1
	Annotation Cluster 22	Enrichment Score: 0.7	G	🟩	Count	P_Value	Benjamini
☐	SMART	DnaJ	RT		5	8.0E-2	7.2E-1
☐	INTERPRO	Molecular chaperone, heat shock protein, Hsp40, DnaJ	RT		5	1.1E-1	9.8E-1
☐	INTERPRO	Heat shock protein DnaJ, N-terminal	RT		5	1.8E-1	1.0E0
☐	INTERPRO	Chaperone DnaJ, C-terminal	RT		3	2.0E-1	1.0E0
☐	INTERPRO	Heat shock protein DnaJ	RT		3	2.0E-1	1.0E0
☐	GOTERM_MF_FAT	heat shock protein binding	RT		5	3.1E-1	9.7E-1
☐	PIR_SUPERFAMILY	PIRSF002585:heat shock protein DnaJ	RT		3	5.8E-1	1.0E0
	Annotation Cluster 23	Enrichment Score: 0.63	G	🟩	Count	P_Value	Benjamini
☐	SMART	S_TKc	RT		28	2.8E-5	2.5E-3
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT		118	1.1E-4	1.8E-3
☐	INTERPRO	Serine/threonine protein kinase	RT		28	3.3E-3	2.2E-1
☐	SP_PIR_KEYWORDS	atp-binding	RT		102	1.7E-2	1.3E-1
☐	INTERPRO	Protein kinase, ATP binding site	RT		31	8.3E-2	9.5E-1
☐	SP_PIR_KEYWORDS	serine/threonine-protein kinase	RT		26	1.3E-1	4.2E-1
☐	INTERPRO	Serine/threonine protein kinase, active site	RT		30	2.6E-1	1.0E0
☐	GOTERM_MF_FAT	protein serine/threonine kinase activity	RT		37	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleotide binding	RT		198	8.7E-1	1.0E0
☐	GOTERM_MF_FAT	purine ribonucleotide binding	RT		194	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	ribonucleotide binding	RT		194	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	nucleotide binding	RT		209	9.1E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase-related	RT		60	9.1E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleoside binding	RT		174	9.7E-1	1.0E0

☐	GOTERM_MF_FAT	adenyl nucleotide binding	RT		174	9.7E-1	1.0E0
☐	INTERPRO	Protein kinase, core	RT		65	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	nucleoside binding	RT		175	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT		170	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	ATP binding	RT		170	9.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	kinase	RT		90	1.0E0	1.0E0
☐	GOTERM_MF_FAT	protein kinase activity	RT		66	1.0E0	1.0E0
☐	GOTERM_BP_FAT	phosphorylation	RT		74	1.0E0	1.0E0
☐	GOTERM_BP_FAT	phosphate metabolic process	RT		78	1.0E0	1.0E0
☐	GOTERM_BP_FAT	phosphorus metabolic process	RT		78	1.0E0	1.0E0
☐	GOTERM_BP_FAT	protein amino acid phosphorylation	RT		65	1.0E0	1.0E0
	Annotation Cluster 24	Enrichment Score: 0.6	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	intramolecular transferase activity, phosphotransferases	RT		4	1.3E-1	8.6E-1
☐	INTERPRO	Alpha-D-phosphohexomutase, alpha/beta/alpha domain I	RT		3	2.0E-1	1.0E0
☐	GOTERM_MF_FAT	intramolecular transferase activity	RT		5	6.0E-1	1.0E0
	Annotation Cluster 25	Enrichment Score: 0.5	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	establishment of protein localization	RT		19	7.4E-2	8.1E-1
☐	GOTERM_BP_FAT	protein transport	RT		19	7.4E-2	8.1E-1
☐	GOTERM_BP_FAT	vesicle-mediated transport	RT		17	8.1E-2	8.2E-1
☐	GOTERM_BP_FAT	protein localization	RT		19	1.0E-1	8.6E-1
☐	GOTERM_BP_FAT	cellular protein localization	RT		11	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule localization	RT		11	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular protein transport	RT		11	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular transport	RT		13	4.8E-1	1.0E0
☐	GOTERM_CC_FAT	coated membrane	RT		7	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	membrane coat	RT		7	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus	RT		5	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	endomembrane system	RT		6	9.6E-1	1.0E0
	Annotation Cluster 26	Enrichment Score: 0.48	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT		19	2.9E-3	1.2E-1
☐	GOTERM_MF_FAT	cation-transporting ATPase activity	RT		7	1.0E-1	8.5E-1
☐	GOTERM_MF_FAT	proton-transporting ATPase activity, rotational mechanism	RT		5	2.1E-1	9.5E-1
☐	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide biosynthetic process	RT		21	2.2E-1	9.8E-1
☐	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	RT		21	2.2E-1	9.8E-1
☐	GOTERM_BP_FAT	nitrogen compound biosynthetic process	RT		24	2.3E-1	9.7E-1
☐	GOTERM_BP_FAT	hydrogen transport	RT		9	2.3E-1	9.7E-1
☐	GOTERM_BP_FAT	proton transport	RT		9	2.3E-1	9.7E-1
☐	GOTERM_BP_FAT	oxidative phosphorylation	RT		8	2.5E-1	9.8E-1
☐	GOTERM_BP_FAT	ATP synthesis coupled proton transport	RT		8	2.5E-1	9.8E-1
☐	GOTERM_BP_FAT	energy coupled proton transport, down electrochemical gradient	RT		8	2.5E-1	9.8E-1
☐	GOTERM_MF_FAT	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT		14	2.5E-1	9.6E-1
☐	GOTERM_BP_FAT	purine nucleotide biosynthetic process	RT		15	2.6E-1	9.8E-1
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions	RT		10	2.6E-1	9.7E-1
☐	GOTERM_MF_FAT	monovalent inorganic cation transmembrane transporter activity	RT		8	2.7E-1	9.6E-1
☐	GOTERM_MF_FAT	hydrogen ion transmembrane transporter activity	RT		8	2.7E-1	9.6E-1
☐	GOTERM_BP_FAT	nucleoside triphosphate metabolic process	RT		14	2.8E-1	9.8E-1
☐	GOTERM_BP_FAT	nucleoside triphosphate biosynthetic process	RT		14	2.8E-1	9.8E-1
☐	GOTERM_BP_FAT	purine nucleoside triphosphate metabolic process	RT		14	2.8E-1	9.8E-1
☐	GOTERM_BP_FAT	purine nucleoside triphosphate biosynthetic process	RT		14	2.8E-1	9.8E-1
☐	GOTERM_BP_FAT	ribonucleoside triphosphate biosynthetic process	RT		14	2.8E-1	9.8E-1
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate metabolic process	RT		14	2.8E-1	9.8E-1
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate biosynthetic process	RT		14	2.8E-1	9.8E-1
☐	GOTERM_BP_FAT	ribonucleoside triphosphate metabolic process	RT		14	2.8E-1	9.8E-1

☐	GOTERM_MF_FAT	inorganic cation transmembrane transporter activity	RT	9	3.0E-1	9.7E-1
☐	GOTERM_BP_FAT	monovalent inorganic cation transport	RT	9	3.1E-1	9.9E-1
☐	GOTERM_BP_FAT	purine nucleotide metabolic process	RT	15	3.1E-1	9.9E-1
☐	INTERPRO	Haloacid dehalogenase-like hydrolase	RT	5	3.3E-1	1.0E0
☐	GOTERM_BP_FAT	ion transmembrane transport	RT	8	3.3E-1	9.9E-1
☐	GOTERM_BP_FAT	ribonucleotide metabolic process	RT	14	3.3E-1	9.9E-1
☐	GOTERM_BP_FAT	purine ribonucleotide metabolic process	RT	14	3.3E-1	9.9E-1
☐	GOTERM_BP_FAT	purine ribonucleotide biosynthetic process	RT	14	3.3E-1	9.9E-1
☐	GOTERM_BP_FAT	ribonucleotide biosynthetic process	RT	14	3.3E-1	9.9E-1
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, catalytic domain	RT	6	3.4E-1	9.9E-1
☐	GOTERM_MF_FAT	primary active transmembrane transporter activity	RT	13	3.8E-1	9.9E-1
☐	GOTERM_MF_FAT	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT	13	3.8E-1	9.9E-1
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of substances	RT	12	4.2E-1	9.9E-1
☐	GOTERM_MF_FAT	ATPase activity, coupled to movement of substances	RT	12	4.2E-1	9.9E-1
☐	GOTERM_BP_FAT	nucleotide biosynthetic process	RT	18	4.2E-1	1.0E0
☐	GOTERM_BP_FAT	ATP metabolic process	RT	12	4.5E-1	1.0E0
☐	GOTERM_BP_FAT	ATP biosynthetic process	RT	12	4.5E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex	RT	9	4.7E-1	1.0E0
☐	KEGG_PATHWAY	Oxidative phosphorylation	RT	9	5.3E-1	9.8E-1
☐	SP_PIR_KEYWORDS	ion transport	RT	3	5.4E-1	8.9E-1
☐	GOTERM_BP_FAT	cation transport	RT	11	5.4E-1	1.0E0
☐	GOTERM_BP_FAT	ion transport	RT	11	5.4E-1	1.0E0
☐	INTERPRO	ATPase, P-type, ATPase-associated region	RT	4	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	transmembrane transport	RT	9	6.8E-1	1.0E0
☐	INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT	4	7.2E-1	1.0E0
☐	INTERPRO	ATPase, P-type phosphorylation site	RT	3	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity	RT	32	7.6E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	4	8.6E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting V-type ATPase complex	RT	4	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	transmembrane	RT	8	9.2E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled	RT	19	9.8E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 0.46		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Rotamase	RT	5	2.6E-1	6.3E-1
☐	GOTERM_MF_FAT	cis-trans isomerase activity	RT	5	3.1E-1	9.7E-1
☐	GOTERM_MF_FAT	peptidyl-prolyl cis-trans isomerase activity	RT	5	3.1E-1	9.7E-1
☐	INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type	RT	3	5.6E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 0.45		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	GTPase activity	RT	9	2.3E-1	9.6E-1
☐	INTERPRO	Protein synthesis factor, GTP-binding	RT	4	4.2E-1	1.0E0
☐	INTERPRO	Translation elongation factor EFTu/EF1A, domain 2	RT	3	4.5E-1	1.0E0
	Annotation Cluster 29	Enrichment Score: 0.42		Count	P_Value	Benjamini
☐	SMART	ARF	RT	3	2.2E-1	9.2E-1
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT	9	3.1E-1	9.9E-1
☐	INTERPRO	ARF/SAR superfamily	RT	4	3.3E-1	1.0E0
☐	INTERPRO	ADP-ribosylation factor	RT	3	3.3E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001711:ADP-ribosylation factor	RT	4	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular signaling cascade	RT	9	6.8E-1	1.0E0
	Annotation Cluster 30	Enrichment Score: 0.35		Count	P_Value	Benjamini
☐	SMART	PP2Ac	RT	7	9.6E-2	7.3E-1
☐	INTERPRO	Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase	RT	7	2.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	iron	RT	8	5.3E-1	8.9E-1
☐	GOTERM_MF_FAT	iron ion binding	RT	12	5.8E-1	1.0E0
☐	INTERPRO	Metallophosphoesterase	RT	7	6.0E-1	1.0E0
☐	GOTERM_MF_FAT	phosphatase activity	RT	16	6.5E-1	1.0E0

☐	**GOTERM_MF_FAT**	phosphoprotein phosphatase activity	RT	10	7.2E-1	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF000908:serine/threonine-protein phosphatase, conventional type	RT	5	7.5E-1	1.0E0
	Annotation Cluster 31	Enrichment Score: 0.35	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	ribonucleoside metabolic process	RT	5	3.0E-1	9.9E-1
☐	**GOTERM_BP_FAT**	pyrimidine nucleoside metabolic process	RT	3	3.6E-1	9.9E-1
☐	**GOTERM_BP_FAT**	pyrimidine ribonucleoside metabolic process	RT	3	3.6E-1	9.9E-1
☐	**KEGG_PATHWAY**	Pyrimidine metabolism	RT	7	1.0E0	1.0E0
	Annotation Cluster 32	Enrichment Score: 0.34	G 🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	ABC transporter-like	RT	10	2.0E-1	1.0E0
☐	**INTERPRO**	ABC transporter, conserved site	RT	7	6.5E-1	1.0E0
☐	**COG_ONTOLOGY**	Defense mechanisms	RT	7	7.4E-1	9.3E-1
	Annotation Cluster 33	Enrichment Score: 0.28	G 🟩	Count	P_Value	Benjamini
☐	**SMART**	Kelch	RT	3	4.0E-1	9.9E-1
☐	**INTERPRO**	Kelch repeat type 1	RT	3	5.6E-1	1.0E0
☐	**INTERPRO**	Kelch-type beta propeller	RT	3	6.5E-1	1.0E0
	Annotation Cluster 34	Enrichment Score: 0.25	G 🟩	Count	P_Value	Benjamini
☐	**SMART**	TPR	RT	8	2.8E-1	9.5E-1
☐	**INTERPRO**	Tetratricopeptide-like helical	RT	10	5.7E-1	1.0E0
☐	**INTERPRO**	Tetratricopeptide repeat	RT	8	5.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	tpr repeat	RT	4	6.3E-1	9.3E-1
☐	**INTERPRO**	Tetratricopeptide TPR-1	RT	6	7.3E-1	1.0E0
☐	**INTERPRO**	Tetratricopeptide region	RT	7	7.4E-1	1.0E0
	Annotation Cluster 35	Enrichment Score: 0.22	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	nucleobase, nucleoside, nucleotide kinase activity	RT	6	2.7E-1	9.7E-1
☐	**GOTERM_MF_FAT**	phosphotransferase activity, phosphate group as acceptor	RT	4	4.9E-1	1.0E0
☐	**KEGG_PATHWAY**	Pyrimidine metabolism	RT	7	1.0E0	1.0E0
☐	**KEGG_PATHWAY**	Purine metabolism	RT	6	1.0E0	1.0E0
	Annotation Cluster 36	Enrichment Score: 0.19	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	pyridine nucleotide metabolic process	RT	4	4.7E-1	1.0E0
☐	**GOTERM_BP_FAT**	oxidoreduction coenzyme metabolic process	RT	4	4.7E-1	1.0E0
☐	**GOTERM_BP_FAT**	nicotinamide metabolic process	RT	3	6.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	secondary metabolic process	RT	3	6.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	nicotinamide nucleotide metabolic process	RT	3	6.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	alkaloid metabolic process	RT	3	6.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	cellular amide metabolic process	RT	3	6.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	cofactor metabolic process	RT	5	7.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	coenzyme metabolic process	RT	4	8.5E-1	1.0E0
	Annotation Cluster 37	Enrichment Score: 0.16	G 🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	Acyltransferase	RT	5	5.3E-1	8.9E-1
☐	**GOTERM_MF_FAT**	N-acyltransferase activity	RT	4	7.6E-1	1.0E0
☐	**INTERPRO**	Acyl-CoA N-acyltransferase	RT	3	8.4E-1	1.0E0
	Annotation Cluster 38	Enrichment Score: 0.14	G 🟩	Count	P_Value	Benjamini
☐	**SMART**	EFh	RT	4	4.6E-1	9.9E-1
☐	**INTERPRO**	Calcium-binding EF-hand	RT	4	6.6E-1	1.0E0
☐	**INTERPRO**	EF hand	RT	4	6.6E-1	1.0E0
☐	**INTERPRO**	EF-HAND 1	RT	6	7.3E-1	1.0E0
☐	**INTERPRO**	EF-Hand type	RT	5	8.1E-1	1.0E0
☐	**INTERPRO**	EF-HAND 2	RT	4	9.1E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	calcium	RT	4	9.2E-1	1.0E0
	Annotation Cluster 39	Enrichment Score: 0.12	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	GTPase activity	RT	9	2.3E-1	9.6E-1
☐	**INTERPRO**	Tubulin/FtsZ, 2-layer sandwich domain	RT	3	6.5E-1	1.0E0
☐	**INTERPRO**	Tubulin, conserved site	RT	3	7.3E-1	1.0E0
☐	**INTERPRO**	Tubulin	RT	3	7.3E-1	1.0E0
☐	**INTERPRO**	Tubulin/FtsZ, GTPase domain	RT	3	7.3E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	microtubule	RT	9	8.9E-1	9.9E-1
☐	**GOTERM_BP_FAT**	cellular protein complex assembly	RT	4	8.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	protein polymerization	RT	3	9.0E-1	1.0E0

☐	GOTERM_BP_FAT	protein complex assembly	RT	4	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex biogenesis	RT	4	9.5E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002306:tubulin	RT	3	9.7E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule	RT	9	1.0E0	1.0E0
	Annotation Cluster 40	Enrichment Score: 0.11	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide catabolic process	RT	3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid catabolic process	RT	3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	nitrogen compound catabolic process	RT	3	7.8E-1	1.0E0
	Annotation Cluster 41	Enrichment Score: 0.09	G	Count	P_Value	Benjamini
☐	INTERPRO	Dynein heavy chain	RT	6	2.5E-1	1.0E0
☐	INTERPRO	Kinesin, motor region, conserved site	RT	6	6.4E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule associated complex	RT	8	6.7E-1	1.0E0
☐	SMART	KISc	RT	6	7.9E-1	1.0E0
☐	GOTERM_CC_FAT	dynein complex	RT	6	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	microtubule motor activity	RT	14	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	motor activity	RT	14	8.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	microtubule	RT	9	8.9E-1	9.9E-1
☐	INTERPRO	Kinesin, motor region	RT	6	9.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	motor protein	RT	6	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based process	RT	17	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based movement	RT	14	9.8E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeleton	RT	19	1.0E0	1.0E0
☐	GOTERM_CC_FAT	microtubule cytoskeleton	RT	17	1.0E0	1.0E0
☐	GOTERM_CC_FAT	cytoskeletal part	RT	17	1.0E0	1.0E0
☐	GOTERM_CC_FAT	microtubule	RT	9	1.0E0	1.0E0
	Annotation Cluster 42	Enrichment Score: 0.08	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	N-acyltransferase activity	RT	4	7.6E-1	1.0E0
☐	INTERPRO	GCN5-related N-acetyltransferase	RT	3	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	N-acetyltransferase activity	RT	3	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	acetyltransferase activity	RT	3	9.2E-1	1.0E0
	Annotation Cluster 43	Enrichment Score: 0.07	G	Count	P_Value	Benjamini
☐	INTERPRO	Clathrin/coatomer adaptor, adaptin-like, N-terminal	RT	3	4.5E-1	1.0E0
☐	GOTERM_CC_FAT	coated membrane	RT	7	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	membrane coat	RT	7	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus	RT	5	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	organelle membrane	RT	5	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle membrane	RT	3	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic membrane-bounded vesicle	RT	3	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle part	RT	3	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle	RT	3	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	membrane-bounded vesicle	RT	3	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle	RT	3	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle	RT	3	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle coat	RT	3	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle membrane	RT	3	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle membrane	RT	3	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	endomembrane system	RT	6	9.6E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus part	RT	3	9.6E-1	1.0E0
	Annotation Cluster 44	Enrichment Score: 0.07	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	membrane	RT	10	5.8E-1	9.1E-1
☐	SP_PIR_KEYWORDS	transmembrane	RT	8	9.2E-1	1.0E0
☐	GOTERM_CC_FAT	intrinsic to membrane	RT	15	1.0E0	1.0E0
☐	GOTERM_CC_FAT	integral to membrane	RT	15	1.0E0	1.0E0
	Annotation Cluster 45	Enrichment Score: 0.06	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular macromolecular complex subunit organization	RT	11	6.1E-1	1.0E0
☐	INTERPRO	Histone core	RT	4	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex assembly	RT	10	7.0E-1	1.0E0

☐	GOTERM_BP_FAT	macromolecular complex subunit organization	RT		11	7.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleosome core	RT		3	7.4E-1	9.7E-1
☐	SP_PIR_KEYWORDS	chromosomal protein	RT		4	7.7E-1	9.7E-1
☐	GOTERM_BP_FAT	macromolecular complex assembly	RT		10	8.0E-1	1.0E0
☐	INTERPRO	Histone-fold	RT		4	8.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleus	RT		10	8.6E-1	9.9E-1
☐	GOTERM_BP_FAT	DNA packaging	RT		4	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome assembly	RT		4	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	protein-DNA complex assembly	RT		4	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly	RT		4	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome organization	RT		4	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly or disassembly	RT		4	9.5E-1	1.0E0
☐	GOTERM_CC_FAT	nucleosome	RT		4	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin organization	RT		4	9.8E-1	1.0E0
☐	GOTERM_CC_FAT	chromatin	RT		4	9.8E-1	1.0E0
☐	GOTERM_CC_FAT	protein-DNA complex	RT		4	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	chromosome organization	RT		4	1.0E0	1.0E0
☐	GOTERM_CC_FAT	chromosomal part	RT		4	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	dna-binding	RT		5	1.0E0	1.0E0
☐	GOTERM_CC_FAT	chromosome	RT		4	1.0E0	1.0E0
☐	GOTERM_MF_FAT	DNA binding	RT		7	1.0E0	1.0E0
	Annotation Cluster 46	Enrichment Score: 0.06	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	EGF	RT		3	6.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	egf-like domain	RT		6	7.2E-1	9.6E-1
☐	INTERPRO	EGF, extracellular	RT		6	8.4E-1	1.0E0
☐	INTERPRO	EGF-like, type 3	RT		7	9.4E-1	1.0E0
☐	INTERPRO	EGF-like region, conserved site	RT		16	1.0E0	1.0E0
☐	SMART	EGF	RT		20	1.0E0	1.0E0
☐	INTERPRO	EGF-like	RT		20	1.0E0	1.0E0
	Annotation Cluster 47	Enrichment Score: 0.06	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	tRNA modification	RT		3	5.4E-1	1.0E0
☐	GOTERM_BP_FAT	RNA modification	RT		5	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA processing	RT		4	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA processing	RT		7	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	RNA processing	RT		12	1.0E0	1.0E0
	Annotation Cluster 48	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	SMART	Pept_C1	RT		6	7.6E-1	1.0E0
☐	INTERPRO	Peptidase, cysteine peptidase active site	RT		8	8.1E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain	RT		6	9.3E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain C-terminal	RT		6	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type endopeptidase activity	RT		6	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type peptidase activity	RT		6	9.9E-1	1.0E0
	Annotation Cluster 49	Enrichment Score: 0.03	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	ribosome biogenesis	RT		7	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoprotein complex biogenesis	RT		7	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA metabolic process	RT		3	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA processing	RT		3	9.9E-1	1.0E0
	Annotation Cluster 50	Enrichment Score: 0.02	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	RNA helicase, DEAD-box type, Q motif	RT		5	7.7E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT		7	9.1E-1	1.0E0
☐	SMART	DEXDc	RT		7	9.4E-1	1.0E0
☐	SMART	HELICc	RT		7	9.5E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled	RT		19	9.8E-1	1.0E0
☐	INTERPRO	DEAD-like helicase, N-terminal	RT		7	9.9E-1	1.0E0
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT		7	9.9E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, C-terminal	RT		7	1.0E0	1.0E0
☐	GOTERM_MF_FAT	purine NTP-dependent helicase activity	RT		7	1.0E0	1.0E0
		ATP-dependent helicase activity	RT		7	1.0E0	1.0E0

☐	GOTERM_MF_FAT					
☐	SP_PIR_KEYWORDS	helicase	RT	7	1.0E0	1.0E0
☐	GOTERM_MF_FAT	helicase activity	RT	9	1.0E0	1.0E0
	Annotation Cluster 51	Enrichment Score: 0.02		Count	P_Value	Benjamini
☐	INTERPRO	WD40 repeat, conserved site	RT	7	8.9E-1	1.0E0
☐	SMART	WD40	RT	13	9.3E-1	1.0E0
☐	INTERPRO	WD40 repeat 2	RT	9	9.6E-1	1.0E0
☐	INTERPRO	WD40 repeat, region	RT	9	9.8E-1	1.0E0
☐	INTERPRO	WD40 repeat, subgroup	RT	11	9.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	wd repeat	RT	10	9.9E-1	1.0E0
☐	INTERPRO	WD40/YVTN repeat-like	RT	13	1.0E0	1.0E0
☐	INTERPRO	WD40 repeat	RT	13	1.0E0	1.0E0
	Annotation Cluster 52	Enrichment Score: 0		Count	P_Value	Benjamini
☐	SMART	ANK	RT	85	9.7E-1	1.0E0
☐	INTERPRO	Ankyrin	RT	85	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	ank repeat	RT	62	1.0E0	1.0E0
	Annotation Cluster 53	Enrichment Score: 0		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	ion binding	RT	74	1.0E0	1.0E0
☐	GOTERM_MF_FAT	cation binding	RT	74	1.0E0	1.0E0
☐	GOTERM_MF_FAT	metal ion binding	RT	71	1.0E0	1.0E0
☐	GOTERM_MF_FAT	transition metal ion binding	RT	34	1.0E0	1.0E0
	Annotation Cluster 54	Enrichment Score: 0		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular response to stress	RT	4	1.0E0	1.0E0
☐	GOTERM_BP_FAT	DNA repair	RT	3	1.0E0	1.0E0
☐	GOTERM_BP_FAT	response to DNA damage stimulus	RT	3	1.0E0	1.0E0
☐	GOTERM_BP_FAT	DNA metabolic process	RT	4	1.0E0	1.0E0
	Annotation Cluster 55	Enrichment Score: 0		Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Mismatch repair	RT	3	1.0E0	1.0E0
☐	KEGG_PATHWAY	Nucleotide excision repair	RT	3	1.0E0	1.0E0
☐	KEGG_PATHWAY	DNA replication	RT	3	1.0E0	1.0E0
	Annotation Cluster 56	Enrichment Score: 0		Count	P_Value	Benjamini
☐	SMART	EGF	RT	20	1.0E0	1.0E0
☐	SMART	FU	RT	13	1.0E0	1.0E0
☐	INTERPRO	EGF-like	RT	20	1.0E0	1.0E0
☐	INTERPRO	Furin-like repeat	RT	13	1.0E0	1.0E0
☐	INTERPRO	Giardia variant-specific surface protein	RT	11	1.0E0	1.0E0

128 terms were not clustered.

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