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

Functional Annotation Clustering

Help and Manual

Current Gene List: 3_Random1
Current Background: Giardia intestinalis
3000 DAVID IDs

Options **Classification Stringency** Medium

Rerun using options | Create Sublist

73 Cluster(s)

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	Annotation Cluster 1	Enrichment Score: 0.91	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	ank repeat	RT	192	8.8E-2	1.0E0
☐	INTERPRO	Ankyrin	RT	265	1.2E-1	1.0E0
☐	SMART	ANK	RT	265	1.7E-1	1.0E0
	Annotation Cluster 2	Enrichment Score: 0.62	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	protein serine/threonine kinase activity	RT	72	1.3E-2	1.0E0
☐	INTERPRO	Serine/threonine protein kinase, active site	RT	60	7.0E-2	1.0E0
☐	GOTERM_MF_FAT	purine nucleotide binding	RT	344	1.2E-1	1.0E0
☐	GOTERM_MF_FAT	ribonucleotide binding	RT	339	1.5E-1	1.0E0
☐	GOTERM_MF_FAT	purine ribonucleotide binding	RT	339	1.5E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl nucleotide binding	RT	313	2.1E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleoside binding	RT	313	2.1E-1	1.0E0
☐	GOTERM_MF_FAT	nucleotide binding	RT	361	2.3E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT	308	2.4E-1	1.0E0
☐	GOTERM_MF_FAT	ATP binding	RT	308	2.4E-1	1.0E0
☐	GOTERM_MF_FAT	nucleoside binding	RT	314	2.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	kinase	RT	200	2.7E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid phosphorylation	RT	157	2.7E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorylation	RT	167	3.2E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase	RT	37	3.2E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorus metabolic process	RT	176	3.2E-1	1.0E0
☐	GOTERM_BP_FAT	phosphate metabolic process	RT	176	3.2E-1	1.0E0
☐	INTERPRO	Protein kinase, ATP binding site	RT	51	3.4E-1	1.0E0
☐	GOTERM_MF_FAT	protein kinase activity	RT	159	3.5E-1	1.0E0
☐	SMART	S_TKc	RT	37	3.5E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase-related	RT	139	3.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	atp-binding	RT	154	4.3E-1	1.0E0
☐	INTERPRO	Protein kinase, core	RT	156	4.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	serine/threonine-protein kinase	RT	37	5.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT	158	6.2E-1	1.0E0
	Annotation Cluster 3	Enrichment Score: 0.6	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	hexose catabolic process	RT	11	2.0E-1	1.0E0
☐	GOTERM_BP_FAT	carbohydrate catabolic process	RT	11	2.0E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide catabolic process	RT	11	2.0E-1	1.0E0
☐	GOTERM_BP_FAT	alcohol catabolic process	RT	11	2.0E-1	1.0E0
☐	GOTERM_BP_FAT	cellular carbohydrate catabolic process	RT	11	2.0E-1	1.0E0
☐	GOTERM_BP_FAT	glucose catabolic process	RT	11	2.0E-1	1.0E0
☐	GOTERM_BP_FAT	glycolysis	RT	9	2.2E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide metabolic process	RT	16	2.7E-1	1.0E0
☐	GOTERM_BP_FAT	hexose metabolic process	RT	14	3.0E-1	1.0E0
☐	GOTERM_BP_FAT	glucose metabolic process	RT	14	3.0E-1	1.0E0
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT	17	3.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	glycolysis	RT	5	5.2E-1	1.0E0
	Annotation Cluster 4	Enrichment Score: 0.59	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	ion binding	RT	158	1.1E-1	1.0E0
☐	GOTERM_MF_FAT	cation binding	RT	158	1.1E-1	1.0E0

☐	**GOTERM_MF_FAT**	metal ion binding	RT		156	1.2E-1	1.0E0
☐	**GOTERM_MF_FAT**	transition metal ion binding	RT		115	1.7E-1	1.0E0
☐	**GOTERM_MF_FAT**	zinc ion binding	RT		92	2.6E-1	1.0E0
☐	**INTERPRO**	Zinc finger, RING-type	RT		43	2.7E-1	1.0E0
☐	**SMART**	RING	RT		43	3.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	zinc-finger	RT		39	3.5E-1	1.0E0
☐	**INTERPRO**	Zinc finger, C3HC4 RING-type	RT		22	4.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	zinc	RT		50	6.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	metal-binding	RT		59	6.3E-1	9.9E-1
	Annotation Cluster 5	Enrichment Score: 0.54	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	ARF/SAR superfamily	RT		7	1.4E-1	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF001711:ADP-ribosylation factor	RT		5	2.4E-1	1.0E0
☐	**INTERPRO**	ADP-ribosylation factor	RT		4	4.4E-1	1.0E0
☐	**SMART**	ARF	RT		4	4.5E-1	1.0E0
	Annotation Cluster 6	Enrichment Score: 0.49	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Zinc finger, C2H2-like	RT		13	3.2E-1	1.0E0
☐	**INTERPRO**	Zinc finger, C2H2-type	RT		13	3.2E-1	1.0E0
☐	**SMART**	ZnF_C2H2	RT		13	3.3E-1	1.0E0
	Annotation Cluster 7	Enrichment Score: 0.47	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	EGF-like	RT		118	1.8E-1	1.0E0
☐	**SMART**	EGF	RT		118	2.3E-1	1.0E0
☐	**INTERPRO**	Giardia variant-specific surface protein	RT		140	4.4E-1	1.0E0
☐	**INTERPRO**	Furin-like repeat	RT		109	4.8E-1	1.0E0
☐	**SMART**	FU	RT		109	5.5E-1	1.0E0
	Annotation Cluster 8	Enrichment Score: 0.45	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_FAT**	endomembrane system	RT		12	2.4E-1	1.0E0
☐	**GOTERM_CC_FAT**	organelle envelope	RT		5	2.8E-1	1.0E0
☐	**GOTERM_CC_FAT**	envelope	RT		5	2.8E-1	1.0E0
☐	**GOTERM_CC_FAT**	nuclear pore	RT		5	2.8E-1	1.0E0
☐	**GOTERM_CC_FAT**	nuclear envelope	RT		5	2.8E-1	1.0E0
☐	**GOTERM_CC_FAT**	pore complex	RT		5	2.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	nuclear transport	RT		3	7.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	nucleocytoplasmic transport	RT		3	7.8E-1	1.0E0
	Annotation Cluster 9	Enrichment Score: 0.42	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Small GTP-binding protein	RT		15	2.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	small GTPase mediated signal transduction	RT		12	2.4E-1	1.0E0
☐	**GOTERM_MF_FAT**	GTP binding	RT		31	2.9E-1	1.0E0
☐	**GOTERM_MF_FAT**	guanyl nucleotide binding	RT		31	2.9E-1	1.0E0
☐	**GOTERM_MF_FAT**	guanyl ribonucleotide binding	RT		31	2.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	intracellular signaling cascade	RT		14	4.0E-1	1.0E0
☐	**INTERPRO**	Ras GTPase	RT		9	5.2E-1	1.0E0
☐	**INTERPRO**	Ras	RT		8	6.2E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	gtp-binding	RT		24	6.4E-1	9.9E-1
☐	**PIR_SUPERFAMILY**	PIRSF001710:Ras-related protein Rab	RT		4	7.3E-1	1.0E0
	Annotation Cluster 10	Enrichment Score: 0.39	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	mRNA metabolic process	RT		6	1.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	mRNA processing	RT		5	2.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	mRNA capping	RT		3	6.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	RNA capping	RT		3	8.9E-1	1.0E0
	Annotation Cluster 11	Enrichment Score: 0.39	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Metallophosphoesterase	RT		16	1.6E-1	1.0E0
☐	**GOTERM_MF_FAT**	phosphatase activity	RT		28	3.6E-1	1.0E0
☐	**GOTERM_MF_FAT**	iron ion binding	RT		20	4.1E-1	1.0E0
☐	**GOTERM_MF_FAT**	phosphoprotein phosphatase activity	RT		18	4.4E-1	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF000908:serine/threonine-protein phosphatase, conventional type	RT		6	4.6E-1	1.0E0
☐	**INTERPRO**	Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase	RT		10	5.5E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	iron	RT		13	5.6E-1	1.0E0
		PP2Ac	RT		10	5.7E-1	1.0E0

☐	SMART					
	Annotation Cluster 12	Enrichment Score: 0.38		Count	P_Value	Benjamini
☐	INTERPRO	EGF, extracellular	RT	17	1.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	egf-like domain	RT	11	6.1E-1	1.0E0
☐	INTERPRO	EGF-like, type 3	RT	19	6.6E-1	1.0E0
	Annotation Cluster 13	Enrichment Score: 0.37		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	establishment of protein localization	RT	22	2.6E-1	1.0E0
☐	GOTERM_BP_FAT	protein transport	RT	22	2.6E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule localization	RT	16	2.7E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein localization	RT	16	2.7E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular protein transport	RT	16	2.7E-1	1.0E0
☐	GOTERM_BP_FAT	protein localization	RT	22	3.3E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular transport	RT	18	4.1E-1	1.0E0
☐	GOTERM_CC_FAT	membrane coat	RT	9	6.1E-1	1.0E0
☐	GOTERM_CC_FAT	coated membrane	RT	9	6.1E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus	RT	7	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	vesicle-mediated transport	RT	15	8.7E-1	1.0E0
☐	INTERPRO	Clathrin/coatomer adaptor, adaptin-like, N-terminal	RT	3	9.0E-1	1.0E0
	Annotation Cluster 14	Enrichment Score: 0.36		Count	P_Value	Benjamini
☐	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT	21	2.3E-1	1.0E0
☐	GOTERM_MF_FAT	purine NTP-dependent helicase activity	RT	25	2.9E-1	1.0E0
☐	GOTERM_MF_FAT	ATP-dependent helicase activity	RT	25	2.9E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity	RT	58	3.0E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, C-terminal	RT	28	3.9E-1	1.0E0
☐	SMART	HELICc	RT	28	4.3E-1	1.0E0
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT	27	4.4E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled	RT	42	4.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	helicase	RT	27	5.6E-1	1.0E0
☐	INTERPRO	DEAD-like helicase, N-terminal	RT	26	5.7E-1	1.0E0
☐	SMART	DEXDc	RT	26	6.0E-1	1.0E0
☐	GOTERM_MF_FAT	helicase activity	RT	31	6.7E-1	1.0E0
☐	INTERPRO	RNA helicase, DEAD-box type, Q motif	RT	10	7.6E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 0.35		Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	endoplasmic reticulum	RT	6	1.9E-1	1.0E0
☐	GOTERM_CC_FAT	organelle membrane	RT	8	4.5E-1	1.0E0
☐	GOTERM_CC_FAT	nuclear envelope-endoplasmic reticulum network	RT	3	6.0E-1	1.0E0
☐	GOTERM_CC_FAT	endoplasmic reticulum membrane	RT	3	6.0E-1	1.0E0
☐	GOTERM_CC_FAT	endoplasmic reticulum part	RT	3	6.0E-1	1.0E0
	Annotation Cluster 16	Enrichment Score: 0.33		Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	proteasome complex	RT	16	1.2E-1	1.0E0
☐	GOTERM_CC_FAT	proteasome core complex	RT	11	2.0E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type endopeptidase activity	RT	11	2.2E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type peptidase activity	RT	11	2.2E-1	1.0E0
☐	GOTERM_CC_FAT	cytosol	RT	20	2.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	proteasome	RT	15	2.2E-1	1.0E0
☐	INTERPRO	Proteasome, subunit alpha/beta	RT	11	2.3E-1	1.0E0
☐	KEGG_PATHWAY	Proteasome	RT	19	2.7E-1	1.0E0
☐	INTERPRO	Proteasome, alpha and beta subunits	RT	10	3.0E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001212:multicatalytic endopeptidase complex chain C9	RT	5	4.3E-1	1.0E0
☐	INTERPRO	Proteasome, alpha-subunit, conserved site	RT	5	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule catabolic process	RT	19	7.3E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis	RT	48	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	RT	8	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein catabolic process	RT	18	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	RT	18	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecule catabolic process	RT	21	8.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	threonine protease	RT	4	8.1E-1	9.9E-1

☐	GOTERM_BP_FAT	protein catabolic process	RT			20	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent protein catabolic process	RT			12	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	RT			12	9.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	ubl conjugation pathway	RT			4	1.0E0	1.0E0
	Annotation Cluster 17	Enrichment Score: 0.33		G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Kelch-type beta propeller	RT			6	3.8E-1	1.0E0
☐	INTERPRO	Kelch repeat type 1	RT			5	5.1E-1	1.0E0
☐	SMART	Kelch	RT			5	5.2E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 0.32		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	pyridoxal phosphate binding	RT			8	3.2E-1	1.0E0
☐	GOTERM_MF_FAT	vitamin B6 binding	RT			8	3.2E-1	1.0E0
☐	GOTERM_MF_FAT	vitamin binding	RT			8	4.6E-1	1.0E0
☐	INTERPRO	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	RT			6	5.5E-1	1.0E0
☐	INTERPRO	Aminotransferase, class I and II	RT			4	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	transferase activity, transferring nitrogenous groups	RT			5	6.6E-1	1.0E0
	Annotation Cluster 19	Enrichment Score: 0.28		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	intrinsic to membrane	RT			40	4.0E-1	1.0E0
☐	GOTERM_CC_FAT	integral to membrane	RT			40	4.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	membrane	RT			17	5.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	transmembrane	RT			17	8.0E-1	9.9E-1
	Annotation Cluster 20	Enrichment Score: 0.27		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	nitrogen compound catabolic process	RT			5	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide catabolic process	RT			5	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid catabolic process	RT			5	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	nucleotide catabolic process	RT			3	7.8E-1	1.0E0
	Annotation Cluster 21	Enrichment Score: 0.26		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	nucleoside-triphosphatase regulator activity	RT			10	2.9E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of small GTPase mediated signal transduction	RT			7	4.0E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras protein signal transduction	RT			7	4.0E-1	1.0E0
☐	GOTERM_MF_FAT	enzyme activator activity	RT			7	4.2E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase regulator activity	RT			8	4.6E-1	1.0E0
☐	GOTERM_MF_FAT	small GTPase regulator activity	RT			8	4.6E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of hydrolase activity	RT			6	5.2E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of GTPase activity	RT			6	5.2E-1	1.0E0
☐	INTERPRO	RabGAP/TBC	RT			3	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of ARF protein signal transduction	RT			4	6.2E-1	1.0E0
☐	SMART	TBC	RT			3	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras GTPase activity	RT			5	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase activator activity	RT			5	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Rab GTPase activity	RT			3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Rab protein signal transduction	RT			3	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	Ras GTPase activator activity	RT			3	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	Rab GTPase activator activity	RT			3	7.9E-1	1.0E0
	Annotation Cluster 22	Enrichment Score: 0.24		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	chromosome organization	RT			14	2.1E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex subunit organization	RT			17	3.0E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex assembly	RT			16	3.6E-1	1.0E0
☐	INTERPRO	Histone-fold	RT			10	4.3E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecular complex subunit organization	RT			17	4.7E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly or disassembly	RT			9	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin organization	RT			10	5.0E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecular complex assembly	RT			16	5.4E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002052:histone H4	RT			3	5.6E-1	1.0E0
☐	GOTERM_CC_FAT	chromatin	RT			8	5.8E-1	1.0E0
☐	INTERPRO	Histone H4	RT			3	6.2E-1	1.0E0
☐	SMART	H4	RT			3	6.3E-1	1.0E0

☐	GOTERM_CC_FAT	chromosome	RT		16	6.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-binding	RT		21	6.6E-1	9.9E-1
☐	GOTERM_BP_FAT	protein-DNA complex assembly	RT		7	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly	RT		7	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome organization	RT		7	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	DNA packaging	RT		7	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome assembly	RT		7	6.8E-1	1.0E0
☐	GOTERM_CC_FAT	nucleosome	RT		7	6.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleosome core	RT		5	6.9E-1	9.9E-1
☐	INTERPRO	Histone core	RT		7	7.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	chromosomal protein	RT		7	7.3E-1	9.9E-1
☐	SP_PIR_KEYWORDS	nucleus	RT		19	8.2E-1	9.9E-1
☐	GOTERM_CC_FAT	protein-DNA complex	RT		7	8.6E-1	1.0E0
☐	GOTERM_CC_FAT	chromosomal part	RT		9	8.6E-1	1.0E0
	Annotation Cluster 23	Enrichment Score: 0.22	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Like-Sm ribonucleoprotein, core	RT		8	4.8E-1	1.0E0
☐	INTERPRO	Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core	RT		5	6.7E-1	1.0E0
☐	SMART	Sm	RT		5	6.9E-1	1.0E0
	Annotation Cluster 24	Enrichment Score: 0.21	G	🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Purine metabolism	RT		21	3.1E-1	1.0E0
☐	KEGG_PATHWAY	RNA polymerase	RT		12	4.5E-1	1.0E0
☐	KEGG_PATHWAY	Pyrimidine metabolism	RT		20	5.4E-1	1.0E0
☐	GOTERM_MF_FAT	DNA-directed RNA polymerase activity	RT		14	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	transcription	RT		15	6.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotidyltransferase	RT		15	7.0E-1	9.9E-1
☐	GOTERM_MF_FAT	RNA polymerase activity	RT		14	7.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-directed rna polymerase	RT		8	8.3E-1	9.9E-1
☐	GOTERM_MF_FAT	nucleotidyltransferase activity	RT		37	9.2E-1	1.0E0
	Annotation Cluster 25	Enrichment Score: 0.2	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	lipoprotein biosynthetic process	RT		4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	lipoprotein metabolic process	RT		4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid lipidation	RT		4	6.2E-1	1.0E0
	Annotation Cluster 26	Enrichment Score: 0.2	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	intramolecular transferase activity, phosphotransferases	RT		4	4.3E-1	1.0E0
☐	INTERPRO	Alpha-D-phosphohexomutase, alpha/beta/alpha domain I	RT		3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	intramolecular transferase activity	RT		5	9.6E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	electron carrier activity	RT		16	3.0E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, conserved site	RT		5	6.7E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulpur binding domain	RT		6	6.9E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, subgroup	RT		6	6.9E-1	1.0E0
☐	GOTERM_MF_FAT	4 iron, 4 sulfur cluster binding	RT		5	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	iron-sulfur cluster binding	RT		11	8.2E-1	1.0E0
☐	GOTERM_MF_FAT	metal cluster binding	RT		11	8.2E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	RNA polymerase Rpb1, domain 3	RT		3	6.2E-1	1.0E0
☐	INTERPRO	RNA polymerase, alpha subunit	RT		3	6.2E-1	1.0E0
☐	INTERPRO	RNA polymerase, N-terminal	RT		3	6.2E-1	1.0E0
☐	INTERPRO	RNA polymerase Rpb1, domain 4	RT		3	6.2E-1	1.0E0
☐	INTERPRO	RNA polymerase Rpb1, domain 1	RT		3	6.2E-1	1.0E0
☐	INTERPRO	RNA polymerase Rpb1, domain 5	RT		3	6.2E-1	1.0E0
☐	SMART	RPOLA_N	RT		3	6.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	Transcription	RT		5	8.1E-1	9.9E-1
☐	SP_PIR_KEYWORDS	dna-directed rna polymerase	RT		8	8.3E-1	9.9E-1
	Annotation Cluster 29	Enrichment Score: 0.17	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	one-carbon metabolic process	RT		8	4.4E-1	1.0E0
☐	INTERPRO	Ribosomal RNA methyltransferase RrmJ/FtsJ	RT		4	4.4E-1	1.0E0

☐	GOTERM_BP_FAT	methylation	RT		7	5.5E-1	1.0E0
☐	GOTERM_BP_FAT	RNA methylation	RT		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	biopolymer methylation	RT		3	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	RNA modification	RT		5	1.0E0	1.0E0
	Annotation Cluster 30	Enrichment Score: 0.17		G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Initiation factor	RT		12	6.4E-1	9.9E-1
☐	GOTERM_MF_FAT	translation initiation factor activity	RT		15	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	translational initiation	RT		7	6.8E-1	1.0E0
☐	GOTERM_MF_FAT	translation factor activity, nucleic acid binding	RT		18	7.6E-1	1.0E0
	Annotation Cluster 31	Enrichment Score: 0.17		G	Count	P_Value	Benjamini
☐	INTERPRO	ABC transporter, conserved site	RT		15	3.9E-1	1.0E0
☐	INTERPRO	ABC transporter-like	RT		15	4.9E-1	1.0E0
☐	INTERPRO	ATPase, AAA-type, core	RT		14	8.0E-1	1.0E0
☐	INTERPRO	ATPase, AAA+ type, core	RT		39	8.2E-1	1.0E0
☐	SMART	AAA	RT		39	8.5E-1	1.0E0
☐	COG_ONTOLOGY	Defense mechanisms	RT		11	9.2E-1	1.0E0
	Annotation Cluster 32	Enrichment Score: 0.17		G	Count	P_Value	Benjamini
☐	INTERPRO	Tetratricopeptide region	RT		16	4.2E-1	1.0E0
☐	INTERPRO	Tetratricopeptide-like helical	RT		19	5.8E-1	1.0E0
☐	INTERPRO	Tetratricopeptide repeat	RT		14	7.3E-1	1.0E0
☐	SMART	TPR	RT		14	7.5E-1	1.0E0
☐	INTERPRO	Tetratricopeptide TPR-1	RT		11	8.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	tpr repeat	RT		5	8.9E-1	1.0E0
	Annotation Cluster 33	Enrichment Score: 0.16		G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	NAD or NADH binding	RT		6	5.4E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of gene expression, epigenetic	RT		4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of transcription	RT		4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin silencing	RT		4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of transcription, DNA-dependent	RT		4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of gene expression, epigenetic	RT		4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of macromolecule biosynthetic process	RT		4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of biosynthetic process	RT		4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of RNA metabolic process	RT		4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of nitrogen compound metabolic process	RT		4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of cellular biosynthetic process	RT		4	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	NAD binding	RT		4	6.4E-1	1.0E0
☐	INTERPRO	NAD-dependent histone deacetylase, silent information regulator Sir2	RT		4	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid deacetylation	RT		4	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of transcription, DNA-dependent	RT		7	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of RNA metabolic process	RT		7	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	RT		5	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	gene silencing	RT		4	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of macromolecule metabolic process	RT		4	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of gene expression	RT		4	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of transcription	RT		15	9.3E-1	1.0E0
	Annotation Cluster 34	Enrichment Score: 0.16		G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT		17	3.8E-1	1.0E0
☐	GOTERM_MF_FAT	inorganic cation transmembrane transporter activity	RT		12	4.8E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, proton-transporting domain	RT		5	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleotide metabolic process	RT		17	5.6E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleotide biosynthetic process	RT		17	5.6E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide biosynthetic process	RT		17	5.6E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide metabolic process	RT		17	5.6E-1	1.0E0

☐	GOTERM_BP_FAT	transmembrane transport	RT	▮	13	5.7E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleotide metabolic process	RT	▮	18	5.8E-1	1.0E0
☐	GOTERM_BP_FAT	nucleotide biosynthetic process	RT	▮	23	5.8E-1	1.0E0
☐	GOTERM_MF_FAT	di-, tri-valent inorganic cation transmembrane transporter activity	RT	▮	3	6.1E-1	1.0E0
☐	GOTERM_MF_FAT	primary active transmembrane transporter activity	RT	▮	18	6.1E-1	1.0E0
☐	GOTERM_MF_FAT	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT	▮	18	6.1E-1	1.0E0
☐	INTERPRO	ATPase, P-type cation-transporter, N-terminal	RT	▮	3	6.2E-1	1.0E0
☐	INTERPRO	ATPase, P-type cation-transporter, C-terminal	RT	▮	3	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside triphosphate metabolic process	RT	▮	16	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside triphosphate biosynthetic process	RT	▮	16	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside triphosphate metabolic process	RT	▮	16	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside triphosphate biosynthetic process	RT	▮	16	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate metabolic process	RT	▮	16	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate biosynthetic process	RT	▮	16	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside triphosphate metabolic process	RT	▮	16	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside triphosphate biosynthetic process	RT	▮	16	6.3E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting V-type ATPase, V0 domain	RT	▮	4	6.3E-1	1.0E0
☐	GOTERM_MF_FAT	metal ion transmembrane transporter activity	RT	▮	4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleotide biosynthetic process	RT	▮	17	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	nitrogen compound biosynthetic process	RT	▮	28	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide biosynthetic process	RT	▮	24	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	RT	▮	24	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	ion transport	RT	▮	14	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	cation transport	RT	▮	14	6.8E-1	1.0E0
☐	INTERPRO	ATPase, P-type, ATPase-associated region	RT	▮	7	7.1E-1	1.0E0
☐	GOTERM_MF_FAT	monovalent inorganic cation transmembrane transporter activity	RT	▮	9	7.2E-1	1.0E0
☐	GOTERM_MF_FAT	hydrogen ion transmembrane transporter activity	RT	▮	9	7.2E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of substances	RT	▮	16	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to movement of substances	RT	▮	16	7.3E-1	1.0E0
☐	GOTERM_BP_FAT	ATP biosynthetic process	RT	▮	14	7.5E-1	1.0E0
☐	GOTERM_BP_FAT	ATP metabolic process	RT	▮	14	7.5E-1	1.0E0
☐	GOTERM_BP_FAT	ion transmembrane transport	RT	▮	8	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	cation-transporting ATPase activity	RT	▮	6	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	▮	7	8.0E-1	1.0E0
☐	INTERPRO	Haloacid dehalogenase-like hydrolase	RT	▮	6	8.0E-1	1.0E0
☐	INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT	▮	7	8.1E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions	RT	▮	11	8.2E-1	1.0E0
☐	GOTERM_MF_FAT	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT	▮	16	8.5E-1	1.0E0
☐	GOTERM_BP_FAT	hydrogen transport	RT	▮	8	8.5E-1	1.0E0
☐	GOTERM_BP_FAT	proton transport	RT	▮	8	8.5E-1	1.0E0
☐	GOTERM_BP_FAT	oxidative phosphorylation	RT	▮	7	8.5E-1	1.0E0
☐	GOTERM_BP_FAT	ATP synthesis coupled proton transport	RT	▮	7	8.5E-1	1.0E0
☐	GOTERM_BP_FAT	energy coupled proton transport, down electrochemical gradient	RT	▮	7	8.5E-1	1.0E0
☐	KEGG_PATHWAY	Oxidative phosphorylation	RT	▮	7	8.6E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex	RT	▮	8	8.6E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting V-type ATPase complex	RT	▮	5	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	monovalent inorganic cation transport	RT	▮	8	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	ion transport	RT	▮	3	9.1E-1	9.9E-1
☐	INTERPRO	ATPase, P-type phosphorylation site	RT	▮	4	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	proton-transporting ATPase activity, rotational mechanism	RT	▮	3	9.7E-1	1.0E0

☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, catalytic domain	RT	▮		3	9.9E-1	1.0E0
	Annotation Cluster 35	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	protein kinase regulator activity	RT	▮		5	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	kinase regulator activity	RT	▮		5	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	cAMP-dependent protein kinase regulator activity	RT	▮		3	7.9E-1	1.0E0
	Annotation Cluster 36	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	endomembrane system	RT	▮		12	2.4E-1	1.0E0
☐	GOTERM_CC_FAT	organelle membrane	RT	▮		8	4.5E-1	1.0E0
☐	GOTERM_CC_FAT	coated membrane	RT	▮		9	6.1E-1	1.0E0
☐	GOTERM_CC_FAT	membrane coat	RT	▮		9	6.1E-1	1.0E0
☐	GOTERM_CC_FAT	transport vesicle membrane	RT	▮		4	6.3E-1	1.0E0
☐	GOTERM_CC_FAT	transport vesicle	RT	▮		4	6.3E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus	RT	▮		7	6.9E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle part	RT	▮		4	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle membrane	RT	▮		4	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle	RT	▮		4	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle membrane	RT	▮		4	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle coat	RT	▮		4	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle	RT	▮		4	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle	RT	▮		4	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	membrane-bounded vesicle	RT	▮		4	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic membrane-bounded vesicle	RT	▮		4	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle membrane	RT	▮		4	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	ER to Golgi transport vesicle	RT	▮		3	7.9E-1	1.0E0
☐	GOTERM_CC_FAT	COPII vesicle coat	RT	▮		3	7.9E-1	1.0E0
☐	GOTERM_CC_FAT	ER to Golgi transport vesicle membrane	RT	▮		3	7.9E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus part	RT	▮		4	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	Golgi vesicle transport	RT	▮		3	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	ER to Golgi vesicle-mediated transport	RT	▮		3	9.4E-1	1.0E0
	Annotation Cluster 37	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Protein-tyrosine phosphatase, active site	RT	▮		5	5.1E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase	RT	▮		4	6.5E-1	1.0E0
☐	INTERPRO	Dual-specific/protein-tyrosine phosphatase, conserved region	RT	▮		4	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	dephosphorylation	RT	▮		9	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid dephosphorylation	RT	▮		7	8.5E-1	1.0E0
☐	GOTERM_MF_FAT	protein tyrosine phosphatase activity	RT	▮		4	8.8E-1	1.0E0
	Annotation Cluster 38	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	calcium-dependent phospholipid binding	RT	▮		14	5.3E-1	1.0E0
☐	GOTERM_MF_FAT	lipid binding	RT	▮		22	5.3E-1	1.0E0
☐	INTERPRO	Alpha giardin	RT	▮		8	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	calcium ion binding	RT	▮		25	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	cytoskeleton organization	RT	▮		9	7.9E-1	1.0E0
☐	INTERPRO	Annexin repeat	RT	▮		8	8.2E-1	1.0E0
☐	INTERPRO	Annexin	RT	▮		9	8.2E-1	1.0E0
☐	SMART	ANX	RT	▮		8	8.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	annexin	RT	▮		9	8.4E-1	9.9E-1
☐	GOTERM_MF_FAT	phospholipid binding	RT	▮		14	8.8E-1	1.0E0
	Annotation Cluster 39	Enrichment Score: 0.13	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	endopeptidase activity	RT	▮		29	3.8E-1	1.0E0
☐	GOTERM_MF_FAT	peptidase activity, acting on L-amino acid peptides	RT	▮		40	5.6E-1	1.0E0
☐	GOTERM_MF_FAT	peptidase activity	RT	▮		46	5.9E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis	RT	▮		48	7.8E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain C-terminal	RT	▮		15	8.1E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain	RT	▮		15	8.1E-1	1.0E0
☐	SMART	Pept_C1	RT	▮		15	8.3E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type endopeptidase activity	RT	▮		13	8.3E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type peptidase activity	RT	▮		16	8.5E-1	1.0E0

☐	INTERPRO	Peptidase, cysteine peptidase active site	RT			16	8.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	Protease	RT	▮		19	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	thiol protease	RT	▮		5	9.4E-1	1.0E0
	Annotation Cluster 40	Enrichment Score: 0.13	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Mismatch repair	RT	▮		9	6.0E-1	1.0E0
☐	KEGG_PATHWAY	DNA replication	RT	▮		12	7.4E-1	1.0E0
☐	KEGG_PATHWAY	Nucleotide excision repair	RT	▮		8	9.1E-1	1.0E0
	Annotation Cluster 41	Enrichment Score: 0.13	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	coiled coil	RT	▮		4	4.6E-1	1.0E0
☐	INTERPRO	ATPase associated with various cellular activities, AAA-5	RT	▮		5	5.1E-1	1.0E0
☐	COG_ONTOLOGY	Cytoskeleton	RT	▮		11	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	dynein complex	RT	▮		6	9.2E-1	1.0E0
☐	INTERPRO	Dynein heavy chain	RT	▮		6	9.3E-1	1.0E0
☐	INTERPRO	Dynein heavy chain, N-terminal region 2	RT	▮		4	9.9E-1	1.0E0
	Annotation Cluster 42	Enrichment Score: 0.12	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	magnesium	RT	▮		9	4.1E-1	1.0E0
☐	GOTERM_BP_FAT	dephosphorylation	RT	▮		9	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	protein serine/threonine phosphatase activity	RT	▮		3	7.9E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C, N-terminal	RT	▮		4	8.0E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C-related	RT	▮		4	8.0E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C	RT	▮		4	8.0E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C, manganese/magnesium aspartate binding site	RT	▮		3	8.0E-1	1.0E0
☐	SMART	PP2C_SIG	RT	▮		4	8.0E-1	1.0E0
☐	SMART	PP2Cc	RT	▮		4	8.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	protein phosphatase	RT	▮		3	8.1E-1	9.9E-1
☐	GOTERM_BP_FAT	protein amino acid dephosphorylation	RT	▮		7	8.5E-1	1.0E0
☐	GOTERM_CC_FAT	protein serine/threonine phosphatase complex	RT	▮		4	8.7E-1	1.0E0
	Annotation Cluster 43	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular protein complex assembly	RT	▮		8	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex biogenesis	RT	▮		8	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex assembly	RT	▮		8	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	protein polymerization	RT	▮		5	7.7E-1	1.0E0
☐	INTERPRO	Tubulin	RT	▮		5	8.0E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, GTPase domain	RT	▮		5	8.0E-1	1.0E0
☐	INTERPRO	Tubulin, conserved site	RT	▮		5	8.0E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002306:tubulin	RT	▮		4	8.4E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, 2-layer sandwich domain	RT	▮		4	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase activity	RT	▮		8	9.5E-1	1.0E0
☐	INTERPRO	Beta tubulin, autoregulation binding site	RT	▮		3	9.5E-1	1.0E0
	Annotation Cluster 44	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	glycerophospholipid metabolic process	RT	▮		5	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	glycerolipid metabolic process	RT	▮		5	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	phosphoinositide metabolic process	RT	▮		5	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid metabolic process	RT	▮		7	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	organophosphate metabolic process	RT	▮		7	8.5E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid biosynthetic process	RT	▮		4	8.7E-1	1.0E0
☐	GOTERM_MF_FAT	inositol or phosphatidylinositol kinase activity	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	lipid biosynthetic process	RT	▮		7	9.1E-1	1.0E0
	Annotation Cluster 45	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cell cycle	RT	▮		5	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	M phase	RT	▮		4	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	cell cycle process	RT	▮		4	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	cell cycle phase	RT	▮		4	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	organelle fission	RT	▮		3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	mitosis	RT	▮		3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	mitotic cell cycle	RT	▮		3	7.8E-1	1.0E0
	GOTERM_BP_FAT	M phase of mitotic cell cycle	RT	▮		3	7.8E-1	1.0E0

☐								
☐	GOTERM_BP_FAT	nuclear division	RT	▮		3	7.8E-1	1.0E0
	Annotation Cluster 46	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	rRNA metabolic process	RT	▮		8	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA processing	RT	▮		8	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA processing	RT	▮		16	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	ribosome biogenesis	RT	▮		11	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoprotein complex biogenesis	RT	▮		11	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA processing	RT	▮		9	8.5E-1	1.0E0
☐	GOTERM_BP_FAT	RNA processing	RT	▮		23	9.2E-1	1.0E0
	Annotation Cluster 47	Enrichment Score: 0.1	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Chaperonin TCP-1, conserved site	RT	▮		6	6.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	cytoplasm	RT	▮		11	7.1E-1	9.9E-1
☐	PIR_SUPERFAMILY	PIRSF002584:molecular chaperone t-complex-type	RT	▮		5	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	unfolded protein binding	RT	▮		12	7.6E-1	1.0E0
☐	INTERPRO	Chaperone, tailless complex polypeptide 1	RT	▮		5	8.0E-1	1.0E0
☐	INTERPRO	Chaperonin Cpn60/TCP-1	RT	▮		5	8.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	Chaperone	RT	▮		5	9.8E-1	1.0E0
	Annotation Cluster 48	Enrichment Score: 0.1	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular response to stress	RT	▮		12	7.3E-1	1.0E0
☐	GOTERM_BP_FAT	DNA repair	RT	▮		11	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	response to DNA damage stimulus	RT	▮		11	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	DNA metabolic process	RT	▮		31	8.6E-1	1.0E0
	Annotation Cluster 49	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	transferase activity, transferring nitrogenous groups	RT	▮		5	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	transaminase activity	RT	▮		3	8.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	Aminotransferase	RT	▮		3	9.1E-1	9.9E-1
	Annotation Cluster 50	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	heme	RT	▮		4	6.7E-1	9.9E-1
☐	INTERPRO	Cytochrome b5, heme-binding site	RT	▮		3	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	heme binding	RT	▮		4	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	tetrapyrrole binding	RT	▮		4	8.8E-1	1.0E0
☐	INTERPRO	Cytochrome b5	RT	▮		3	9.0E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 0.08	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	EGF-like, type 3	RT	▮		19	6.6E-1	1.0E0
☐	INTERPRO	EGF-like, laminin	RT	▮		13	9.3E-1	1.0E0
☐	SMART	EGF_Lam	RT	▮		13	9.4E-1	1.0E0
	Annotation Cluster 52	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	EF-HAND 1	RT	▮		13	5.3E-1	1.0E0
☐	INTERPRO	EF-HAND 2	RT	▮		9	8.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	calcium	RT	▮		8	8.9E-1	1.0E0
☐	INTERPRO	EF hand	RT	▮		5	9.6E-1	1.0E0
☐	INTERPRO	Calcium-binding EF-hand	RT	▮		5	9.6E-1	1.0E0
☐	SMART	EFh	RT	▮		5	9.7E-1	1.0E0
☐	INTERPRO	EF-Hand type	RT	▮		8	9.7E-1	1.0E0
	Annotation Cluster 53	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	ncRNA metabolic process	RT	▮		28	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA aminoacylation for protein translation	RT	▮		12	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	aminoacyl-tRNA ligase activity	RT	▮		13	8.3E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-oxygen bonds	RT	▮		13	8.3E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming aminoacyl-tRNA and related compounds	RT	▮		13	8.3E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA metabolic process	RT	▮		21	8.5E-1	1.0E0
☐	GOTERM_BP_FAT	amino acid activation	RT	▮		12	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA aminoacylation	RT	▮		12	8.6E-1	1.0E0
☐	KEGG_PATHWAY	Aminoacyl-tRNA biosynthesis	RT	▮		11	8.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	Aminoacyl-tRNA synthetase	RT	▮		12	9.0E-1	1.0E0
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II, conserved region	RT	▮		4	9.7E-1	1.0E0
	SP_PIR_KEYWORDS	ligase	RT	▮		25	9.9E-1	1.0E0

☐								
	Annotation Cluster 54	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	dephosphorylation	RT	▮		9	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid dephosphorylation	RT	▮		7	8.5E-1	1.0E0
☐	GOTERM_MF_FAT	protein tyrosine/serine/threonine phosphatase activity	RT	▮		3	8.9E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase, dual specificity	RT	▮		3	9.0E-1	1.0E0
☐	INTERPRO	Dual specificity phosphatase, catalytic domain	RT	▮		3	9.0E-1	1.0E0
	Annotation Cluster 55	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Myb transcription factor	RT	▮		3	8.0E-1	1.0E0
☐	INTERPRO	Myb-type HTH DNA-binding domain	RT	▮		3	8.0E-1	1.0E0
☐	INTERPRO	Myb, DNA-binding	RT	▮		3	9.0E-1	1.0E0
☐	INTERPRO	SANT, DNA-binding	RT	▮		5	9.3E-1	1.0E0
☐	SMART	SANT	RT	▮		5	9.4E-1	1.0E0
	Annotation Cluster 56	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Na+ driven multidrug efflux pump	RT	▮		3	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	multidrug transport	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	response to drug	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	drug transport	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	drug transporter activity	RT	▮		3	8.9E-1	1.0E0
☐	INTERPRO	Multi antimicrobial extrusion protein MatE	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	antiporter activity	RT	▮		3	9.5E-1	1.0E0
	Annotation Cluster 57	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	vitamin metabolic process	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	water-soluble vitamin metabolic process	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	water-soluble vitamin biosynthetic process	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	vitamin biosynthetic process	RT	▮		3	8.9E-1	1.0E0
	Annotation Cluster 58	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Thioredoxin domain	RT	▮		4	8.0E-1	1.0E0
☐	INTERPRO	Thioredoxin fold	RT	▮		12	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	cellular homeostasis	RT	▮		10	8.6E-1	1.0E0
☐	INTERPRO	Thioredoxin-like	RT	▮		7	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	antioxidant activity	RT	▮		4	8.8E-1	1.0E0
☐	INTERPRO	Thioredoxin-like subdomain	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	homeostatic process	RT	▮		10	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	cell redox homeostasis	RT	▮		9	9.0E-1	1.0E0
☐	INTERPRO	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	RT	▮		3	9.5E-1	1.0E0
☐	INTERPRO	Thioredoxin, core	RT	▮		3	9.8E-1	1.0E0
	Annotation Cluster 59	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	membrane-enclosed lumen	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_CC_FAT	organelle lumen	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_CC_FAT	nuclear lumen	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_CC_FAT	intracellular organelle lumen	RT	▮		3	8.9E-1	1.0E0
	Annotation Cluster 60	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	carboxylic acid biosynthetic process	RT	▮		4	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	organic acid biosynthetic process	RT	▮		4	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	cellular amino acid biosynthetic process	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	amine biosynthetic process	RT	▮		3	9.4E-1	1.0E0
	Annotation Cluster 61	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	von Willebrand factor, type A	RT	▮		4	8.9E-1	1.0E0
☐	SMART	VWA	RT	▮		4	8.9E-1	1.0E0
☐	INTERPRO	Copine	RT	▮		3	9.0E-1	1.0E0
	Annotation Cluster 62	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	cytoskeleton	RT	▮		30	7.5E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule	RT	▮		18	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeletal part	RT	▮		28	8.3E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule cytoskeleton	RT	▮		28	8.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	microtubule	RT	▮		17	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based process	RT	▮		27	9.2E-1	1.0E0

☐	GOTERM_MF_FAT	motor activity	RT		21	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	microtubule motor activity	RT		21	9.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	motor protein	RT		12	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based movement	RT		23	9.4E-1	1.0E0
☐	INTERPRO	Kinesin, motor region	RT		13	9.7E-1	1.0E0
☐	INTERPRO	Kinesin, motor region, conserved site	RT		8	9.7E-1	1.0E0
☐	SMART	KISc	RT		13	9.7E-1	1.0E0
	Annotation Cluster 63	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cofactor metabolic process	RT		7	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	cofactor biosynthetic process	RT		5	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	coenzyme metabolic process	RT		5	9.2E-1	1.0E0
☐	GOTERM_BP_FAT	pyridine nucleotide metabolic process	RT		3	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	oxidoreduction coenzyme metabolic process	RT		3	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	coenzyme biosynthetic process	RT		3	9.7E-1	1.0E0
	Annotation Cluster 64	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	RNA-dependent DNA replication	RT		4	8.7E-1	1.0E0
☐	INTERPRO	RNA-directed DNA polymerase (reverse transcriptase)	RT		4	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	RNA-directed DNA polymerase activity	RT		11	9.6E-1	1.0E0
	Annotation Cluster 65	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	lipid transport	RT		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	lipid localization	RT		3	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	lipid transporter activity	RT		3	9.5E-1	1.0E0
	Annotation Cluster 66	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	ubiquitin-protein ligase activity	RT		4	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-nitrogen bonds	RT		16	9.2E-1	1.0E0
☐	GOTERM_MF_FAT	acid-amino acid ligase activity	RT		13	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	small conjugating protein ligase activity	RT		6	9.5E-1	1.0E0
☐	KEGG_PATHWAY	Ubiquitin mediated proteolysis	RT		5	9.6E-1	1.0E0
☐	INTERPRO	Ubiquitin-conjugating enzyme/RWD-like	RT		5	9.8E-1	1.0E0
☐	INTERPRO	Ubiquitin-conjugating enzyme, E2	RT		5	9.8E-1	1.0E0
☐	SMART	UBCc	RT		5	9.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	ligase	RT		25	9.9E-1	1.0E0
	Annotation Cluster 67	Enrichment Score: 0.02	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	ribonucleoprotein complex	RT		53	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	non-membrane-bounded organelle	RT		85	9.2E-1	1.0E0
☐	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT		85	9.2E-1	1.0E0
☐	GOTERM_MF_FAT	structural molecule activity	RT		42	9.5E-1	1.0E0
☐	KEGG_PATHWAY	Ribosome	RT		34	9.5E-1	1.0E0
☐	GOTERM_MF_FAT	structural constituent of ribosome	RT		34	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	translation	RT		56	9.6E-1	1.0E0
☐	GOTERM_CC_FAT	ribosome	RT		37	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	ribosomal protein	RT		36	9.7E-1	1.0E0
	Annotation Cluster 68	Enrichment Score: 0.02	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	heat shock protein binding	RT		4	9.3E-1	1.0E0
☐	INTERPRO	Heat shock protein DnaJ, N-terminal	RT		4	9.4E-1	1.0E0
☐	SMART	DnaJ	RT		4	9.4E-1	1.0E0
☐	INTERPRO	Molecular chaperone, heat shock protein, Hsp40, DnaJ	RT		3	9.8E-1	1.0E0
	Annotation Cluster 69	Enrichment Score: 0.02	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	acetyltransferase activity	RT		5	9.2E-1	1.0E0
☐	INTERPRO	Acyl-CoA N-acyltransferase	RT		5	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	N-acetyltransferase activity	RT		4	9.6E-1	1.0E0
☐	INTERPRO	GCN5-related N-acetyltransferase	RT		4	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	N-acyltransferase activity	RT		4	9.8E-1	1.0E0
	Annotation Cluster 70	Enrichment Score: 0.01	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	WD40 repeat 2	RT		21	9.6E-1	1.0E0
☐	INTERPRO	WD40 repeat, region	RT		23	9.6E-1	1.0E0
☐	INTERPRO	WD40 repeat	RT		36	9.8E-1	1.0E0
☐	SMART	WD40	RT		36	9.9E-1	1.0E0

☐	**SP_PIR_KEYWORDS**	wd repeat	**RT**	▮		23	9.9E-1	1.0E0
☐	**INTERPRO**	WD40 repeat, subgroup	**RT**	▮		26	9.9E-1	1.0E0
☐	**INTERPRO**	WD40/YVTN repeat-like	**RT**	▮		34	9.9E-1	1.0E0
☐	**INTERPRO**	WD40 repeat, conserved site	**RT**	▮		9	1.0E0	1.0E0
	Annotation Cluster 71	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	RNA-directed DNA polymerase activity	**RT**	▮		11	9.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Endonuclease	**RT**	▮		14	9.7E-1	1.0E0
☐	**GOTERM_MF_FAT**	nuclease activity	**RT**	▮		23	9.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	DNA polymerase activity	**RT**	▮		15	9.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	rna-directed dna polymerase	**RT**	▮		10	9.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	endonuclease activity	**RT**	▮		14	9.9E-1	1.0E0
	Annotation Cluster 72	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	RNA recognition motif, RNP-1	**RT**	▮		6	9.8E-1	1.0E0
☐	**SMART**	RRM	**RT**	▮		6	9.8E-1	1.0E0
☐	**INTERPRO**	Nucleotide-binding, alpha-beta plait	**RT**	▮		6	9.9E-1	1.0E0
	Annotation Cluster 73	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	cis-trans isomerase activity	**RT**	▮		3	9.9E-1	1.0E0
☐	**GOTERM_MF_FAT**	peptidyl-prolyl cis-trans isomerase activity	**RT**	▮		3	9.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Rotamase	**RT**	▮		3	9.9E-1	1.0E0

219 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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National Institute of Allergy and Infectious Diseases (NIAID), NIH

Functional Annotation Clustering

Help and Manual

Current Gene List: 3_Random2
Current Background: Giardia intestinalis
3000 DAVID IDs

Options **Classification Stringency** Medium

Rerun using options | Create Sublist

79 Cluster(s)

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	Annotation Cluster 1	Enrichment Score: 1.83		Count	P_Value	Benjamini
☐	INTERPRO	Tetratricopeptide TPR-1	RT	19	2.0E-3	8.9E-1
☐	INTERPRO	Tetratricopeptide repeat	RT	21	7.6E-3	9.9E-1
☐	SMART	TPR	RT	21	1.1E-2	8.2E-1
☐	INTERPRO	Tetratricopeptide-like helical	RT	25	1.9E-2	1.0E0
☐	SP_PIR_KEYWORDS	tpr repeat	RT	9	5.2E-2	1.0E0
☐	INTERPRO	Tetratricopeptide region	RT	19	6.4E-2	1.0E0
	Annotation Cluster 2	Enrichment Score: 1.1		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular response to stress	RT	17	4.8E-2	1.0E0
☐	GOTERM_BP_FAT	response to DNA damage stimulus	RT	16	6.7E-2	1.0E0
☐	GOTERM_BP_FAT	DNA repair	RT	16	6.7E-2	1.0E0
☐	GOTERM_BP_FAT	DNA metabolic process	RT	38	1.9E-1	1.0E0
	Annotation Cluster 3	Enrichment Score: 0.65		Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	chromosome	RT	21	3.2E-2	9.8E-1
☐	GOTERM_CC_FAT	chromosomal part	RT	14	6.0E-2	9.8E-1
☐	GOTERM_BP_FAT	cellular macromolecular complex subunit organization	RT	19	7.9E-2	1.0E0
☐	GOTERM_CC_FAT	protein-DNA complex	RT	11	9.5E-2	9.8E-1
☐	GOTERM_BP_FAT	macromolecular complex subunit organization	RT	20	9.6E-2	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex assembly	RT	18	1.1E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecular complex assembly	RT	19	1.2E-1	1.0E0
☐	GOTERM_CC_FAT	chromatin	RT	10	1.4E-1	9.9E-1
☐	GOTERM_CC_FAT	nucleosome	RT	9	2.0E-1	9.9E-1
☐	GOTERM_BP_FAT	chromatin assembly	RT	9	2.1E-1	1.0E0
☐	GOTERM_BP_FAT	protein-DNA complex assembly	RT	9	2.1E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome organization	RT	9	2.1E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome assembly	RT	9	2.1E-1	1.0E0
☐	GOTERM_BP_FAT	DNA packaging	RT	9	2.1E-1	1.0E0
☐	INTERPRO	Histone-fold	RT	11	2.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	chromosomal protein	RT	9	2.4E-1	9.9E-1
☐	SP_PIR_KEYWORDS	nucleus	RT	23	2.5E-1	9.8E-1
☐	INTERPRO	Histone core	RT	9	2.5E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly or disassembly	RT	10	2.6E-1	1.0E0
☐	INTERPRO	Histone H3	RT	4	4.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-binding	RT	22	4.5E-1	9.9E-1
☐	SMART	H3	RT	4	4.6E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin organization	RT	10	4.9E-1	1.0E0
☐	GOTERM_BP_FAT	chromosome organization	RT	12	5.4E-1	1.0E0
☐	INTERPRO	Histone H4	RT	3	6.2E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002052:histone H4	RT	3	6.2E-1	1.0E0
☐	SMART	H4	RT	3	6.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleosome core	RT	5	6.6E-1	9.8E-1
	Annotation Cluster 4	Enrichment Score: 0.61		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	egf-like domain	RT	13	2.0E-1	1.0E0
☐	INTERPRO	EGF-like, type 3	RT	22	2.4E-1	1.0E0
☐	INTERPRO	EGF, extracellular	RT	16	3.1E-1	1.0E0
	Annotation Cluster 5	Enrichment Score: 0.6		Count	P_Value	Benjamini

☐	GOTERM_MF_FAT	purine nucleotide binding	RT			338	1.3E-1	1.0E0
☐	GOTERM_MF_FAT	purine ribonucleotide binding	RT			333	1.5E-1	1.0E0
☐	GOTERM_MF_FAT	ribonucleotide binding	RT			333	1.5E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleoside binding	RT			309	1.7E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl nucleotide binding	RT			309	1.7E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid phosphorylation	RT			158	1.9E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT			304	2.0E-1	1.0E0
☐	GOTERM_MF_FAT	ATP binding	RT			304	2.0E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorylation	RT			168	2.2E-1	1.0E0
☐	GOTERM_MF_FAT	nucleoside binding	RT			309	2.4E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorus metabolic process	RT			176	2.7E-1	1.0E0
☐	GOTERM_BP_FAT	phosphate metabolic process	RT			176	2.7E-1	1.0E0
☐	GOTERM_MF_FAT	protein kinase activity	RT			158	2.7E-1	1.0E0
☐	GOTERM_MF_FAT	nucleotide binding	RT			353	2.9E-1	1.0E0
☐	INTERPRO	Protein kinase, core	RT			157	3.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	atp-binding	RT			150	4.2E-1	9.9E-1
☐	SP_PIR_KEYWORDS	kinase	RT			190	4.9E-1	9.9E-1
☐	INTERPRO	Serine/threonine protein kinase-related	RT			135	5.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT			155	5.5E-1	9.9E-1
	Annotation Cluster 6	Enrichment Score: 0.56	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	helicase	RT			31	9.4E-2	9.9E-1
☐	GOTERM_MF_FAT	ATPase activity, coupled	RT			46	1.1E-1	1.0E0
☐	GOTERM_MF_FAT	ATP-dependent helicase activity	RT			26	1.6E-1	1.0E0
☐	GOTERM_MF_FAT	purine NTP-dependent helicase activity	RT			26	1.6E-1	1.0E0
☐	GOTERM_MF_FAT	helicase activity	RT			35	2.0E-1	1.0E0
☐	INTERPRO	DEAD-like helicase, N-terminal	RT			28	3.1E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT			20	3.4E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity	RT			56	3.8E-1	1.0E0
☐	SMART	DEXDc	RT			28	3.8E-1	1.0E0
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT			27	4.3E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, C-terminal	RT			27	5.0E-1	1.0E0
☐	INTERPRO	RNA helicase, DEAD-box type, Q motif	RT			11	5.7E-1	1.0E0
☐	SMART	HELICc	RT			27	5.8E-1	1.0E0
	Annotation Cluster 7	Enrichment Score: 0.48	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	peptidyl-prolyl cis-trans isomerase activity	RT			7	2.5E-1	1.0E0
☐	GOTERM_MF_FAT	cis-trans isomerase activity	RT			7	2.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	Rotamase	RT			7	2.6E-1	9.8E-1
☐	SP_PIR_KEYWORDS	Isomerase	RT			20	4.0E-1	9.9E-1
☐	GOTERM_BP_FAT	protein folding	RT			19	4.1E-1	1.0E0
☐	INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type	RT			5	5.0E-1	1.0E0
	Annotation Cluster 8	Enrichment Score: 0.43	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	lipid binding	RT			26	7.6E-2	1.0E0
☐	GOTERM_BP_FAT	cytoskeleton organization	RT			12	2.3E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid binding	RT			18	3.1E-1	1.0E0
☐	INTERPRO	Alpha giardin	RT			9	3.8E-1	1.0E0
☐	INTERPRO	Annexin repeat	RT			10	4.2E-1	1.0E0
☐	SMART	ANX	RT			10	4.7E-1	1.0E0
☐	GOTERM_MF_FAT	calcium-dependent phospholipid binding	RT			14	4.9E-1	1.0E0
☐	GOTERM_MF_FAT	calcium ion binding	RT			25	6.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	annexin	RT			10	6.4E-1	9.9E-1
☐	INTERPRO	Annexin	RT			10	6.5E-1	1.0E0
	Annotation Cluster 9	Enrichment Score: 0.41	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	translational elongation	RT			7	1.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	elongation factor	RT			5	6.6E-1	9.8E-1
☐	GOTERM_MF_FAT	translation elongation factor activity	RT			5	7.7E-1	1.0E0
	Annotation Cluster 10	Enrichment Score: 0.41	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	tubulin-tyrosine ligase activity	RT			6	3.5E-1	1.0E0
		Tubulin-tyrosine ligase	RT			6	3.7E-1	1.0E0

☐	INTERPRO					
☐	GOTERM_MF_FAT	acid-amino acid ligase activity	RT	17	4.6E-1	1.0E0
	Annotation Cluster 11	Enrichment Score: 0.39		Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	cell projection	RT	4	4.0E-1	1.0E0
☐	GOTERM_CC_FAT	flagellum	RT	4	4.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	flagellum	RT	4	4.3E-1	9.9E-1
	Annotation Cluster 12	Enrichment Score: 0.37		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	intracellular transport	RT	19	2.5E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular protein transport	RT	16	2.6E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule localization	RT	16	2.6E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein localization	RT	16	2.6E-1	1.0E0
☐	GOTERM_BP_FAT	establishment of protein localization	RT	20	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	protein transport	RT	20	5.1E-1	1.0E0
☐	GOTERM_CC_FAT	coated membrane	RT	9	5.6E-1	1.0E0
☐	GOTERM_CC_FAT	membrane coat	RT	9	5.6E-1	1.0E0
☐	GOTERM_BP_FAT	protein localization	RT	20	5.9E-1	1.0E0
☐	GOTERM_BP_FAT	vesicle-mediated transport	RT	15	8.6E-1	1.0E0
	Annotation Cluster 13	Enrichment Score: 0.36		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	DNA helicase activity	RT	6	1.8E-1	1.0E0
☐	GOTERM_MF_FAT	DNA-dependent ATPase activity	RT	7	2.5E-1	1.0E0
☐	GOTERM_MF_FAT	ATP-dependent DNA helicase activity	RT	4	4.2E-1	1.0E0
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding, DinG/Rad3-type	RT	3	6.2E-1	1.0E0
☐	INTERPRO	DEAD2	RT	3	6.2E-1	1.0E0
☐	INTERPRO	Helicase, ATP-dependent, c2 type	RT	3	6.2E-1	1.0E0
☐	SMART	HELICc2	RT	3	6.4E-1	1.0E0
	Annotation Cluster 14	Enrichment Score: 0.33		Count	P_Value	Benjamini
☐	INTERPRO	Ankyrin	RT	257	3.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	ank repeat	RT	176	5.3E-1	9.9E-1
☐	SMART	ANK	RT	257	6.0E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 0.33		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular macromolecular complex assembly	RT	18	1.1E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein complex assembly	RT	8	4.3E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex assembly	RT	9	4.6E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex biogenesis	RT	9	4.6E-1	1.0E0
☐	GOTERM_BP_FAT	protein polymerization	RT	6	5.1E-1	1.0E0
☐	INTERPRO	Tubulin, conserved site	RT	6	5.4E-1	1.0E0
☐	INTERPRO	Tubulin	RT	6	5.4E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, GTPase domain	RT	6	5.4E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, 2-layer sandwich domain	RT	5	6.7E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002306:tubulin	RT	5	6.7E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase activity	RT	10	7.1E-1	1.0E0
	Annotation Cluster 16	Enrichment Score: 0.32		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	protein localization in organelle	RT	5	2.8E-1	1.0E0
☐	GOTERM_BP_FAT	protein targeting	RT	5	2.8E-1	1.0E0
☐	KEGG_PATHWAY	Protein export	RT	3	5.7E-1	1.0E0
☐	GOTERM_BP_FAT	protein targeting to ER	RT	3	5.9E-1	1.0E0
☐	GOTERM_BP_FAT	SRP-dependent cotranslational protein targeting to membrane	RT	3	5.9E-1	1.0E0
☐	GOTERM_BP_FAT	cotranslational protein targeting to membrane	RT	3	5.9E-1	1.0E0
☐	GOTERM_BP_FAT	protein targeting to membrane	RT	3	5.9E-1	1.0E0
	Annotation Cluster 17	Enrichment Score: 0.32		Count	P_Value	Benjamini
☐	INTERPRO	EGF-like	RT	115	3.0E-1	1.0E0
☐	INTERPRO	Giardia variant-specific surface protein	RT	141	3.4E-1	1.0E0
☐	SMART	EGF	RT	115	4.6E-1	1.0E0
☐	INTERPRO	Furin-like repeat	RT	105	6.8E-1	1.0E0
☐	SMART	FU	RT	105	8.2E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 0.31		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	nucleotide biosynthetic process	RT	26	2.0E-1	1.0E0
☐	GOTERM_BP_FAT	ATP metabolic process	RT	17	2.8E-1	1.0E0

☐	GOTERM_BP_FAT	ATP biosynthetic process	RT		17	2.8E-1	1.0E0
☐	GOTERM_BP_FAT	nitrogen compound biosynthetic process	RT	▮	31	2.9E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions	RT	▮	14	3.0E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	▮	9	3.4E-1	1.0E0
☐	GOTERM_BP_FAT	cation transport	RT	▮	16	3.4E-1	1.0E0
☐	GOTERM_BP_FAT	ion transport	RT	▮	16	3.4E-1	1.0E0
☐	INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT	▮	9	3.8E-1	1.0E0
☐	GOTERM_BP_FAT	transmembrane transport	RT	▮	14	3.8E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleotide biosynthetic process	RT	▮	18	3.9E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleotide metabolic process	RT	▮	18	3.9E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide biosynthetic process	RT	▮	18	3.9E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide metabolic process	RT	▮	18	3.9E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide biosynthetic process	RT	▮	26	3.9E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	RT	▮	26	3.9E-1	1.0E0
☐	KEGG_PATHWAY	Oxidative phosphorylation	RT	▮	9	4.2E-1	1.0E0
☐	GOTERM_MF_FAT	inorganic cation transmembrane transporter activity	RT	▮	12	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside triphosphate metabolic process	RT	▮	17	4.6E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside triphosphate metabolic process	RT	▮	17	4.6E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside triphosphate biosynthetic process	RT	▮	17	4.6E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside triphosphate biosynthetic process	RT	▮	17	4.6E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside triphosphate metabolic process	RT	▮	17	4.6E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate biosynthetic process	RT	▮	17	4.6E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate metabolic process	RT	▮	17	4.6E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside triphosphate biosynthetic process	RT	▮	17	4.6E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex	RT	▮	10	4.7E-1	1.0E0
☐	INTERPRO	ATPase, P-type, ATPase-associated region	RT	▮	8	4.7E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleotide biosynthetic process	RT	▮	18	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	hydrogen transport	RT	▮	10	4.9E-1	1.0E0
☐	GOTERM_BP_FAT	proton transport	RT	▮	10	4.9E-1	1.0E0
☐	GOTERM_MF_FAT	cation-transporting ATPase activity	RT	▮	7	5.4E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of substances	RT	▮	17	5.5E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to movement of substances	RT	▮	17	5.5E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleotide metabolic process	RT	▮	18	5.6E-1	1.0E0
☐	GOTERM_MF_FAT	primary active transmembrane transporter activity	RT	▮	18	5.7E-1	1.0E0
☐	GOTERM_MF_FAT	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT	▮	18	5.7E-1	1.0E0
☐	GOTERM_MF_FAT	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT	▮	18	5.7E-1	1.0E0
☐	GOTERM_BP_FAT	ion transmembrane transport	RT	▮	9	5.9E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting V-type ATPase, V0 domain	RT	▮	4	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	monovalent inorganic cation transport	RT	▮	10	6.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	Hydrogen ion transport	RT	▮	3	6.1E-1	9.9E-1
☐	GOTERM_CC_FAT	proton-transporting V-type ATPase complex	RT	▮	6	6.3E-1	1.0E0
☐	GOTERM_MF_FAT	proton-transporting ATPase activity, rotational mechanism	RT	▮	5	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT	▮	15	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	oxidative phosphorylation	RT	▮	8	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	ATP synthesis coupled proton transport	RT	▮	8	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	energy coupled proton transport, down electrochemical gradient	RT	▮	8	6.8E-1	1.0E0
☐	GOTERM_MF_FAT	hydrogen ion transmembrane transporter activity	RT	▮	9	7.0E-1	1.0E0
☐	GOTERM_MF_FAT	monovalent inorganic cation transmembrane transporter activity	RT	▮	9	7.0E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, catalytic domain	RT	▮	5	7.5E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, proton-transporting domain	RT	▮	4	7.5E-1	1.0E0

☐	**SP_PIR_KEYWORDS**	ion transport	RT	▮	3	8.9E-1	9.9E-1
☐	**SP_PIR_KEYWORDS**	transport	RT	▮	6	9.2E-1	9.9E-1
	Annotation Cluster 19	Enrichment Score: 0.31	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	cysteine-type endopeptidase activity	RT	▮	17	2.1E-1	1.0E0
☐	**GOTERM_MF_FAT**	cysteine-type peptidase activity	RT	▮	20	2.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	thiol protease	RT	▮	8	3.2E-1	9.9E-1
☐	**GOTERM_MF_FAT**	endopeptidase activity	RT	▮	28	4.4E-1	1.0E0
☐	**INTERPRO**	Peptidase, cysteine peptidase active site	RT	▮	19	4.8E-1	1.0E0
☐	**INTERPRO**	Peptidase C1A, papain C-terminal	RT	▮	17	5.2E-1	1.0E0
☐	**INTERPRO**	Peptidase C1A, papain	RT	▮	17	5.2E-1	1.0E0
☐	**SMART**	Pept_C1	RT	▮	17	5.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	proteolysis	RT	▮	49	6.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	peptidase activity, acting on L-amino acid peptides	RT	▮	38	6.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	peptidase activity	RT	▮	43	7.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Protease	RT	▮	19	8.6E-1	9.9E-1
	Annotation Cluster 20	Enrichment Score: 0.29	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	EGF-like, type 3	RT	▮	22	2.4E-1	1.0E0
☐	**INTERPRO**	EGF-like, laminin	RT	▮	15	7.3E-1	1.0E0
☐	**SMART**	EGF_Lam	RT	▮	15	7.8E-1	1.0E0
	Annotation Cluster 21	Enrichment Score: 0.27	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	cyclin	RT	▮	8	3.2E-1	9.9E-1
☐	**INTERPRO**	Cyclin, C-terminal	RT	▮	4	4.4E-1	1.0E0
☐	**INTERPRO**	Cyclin, N-terminal	RT	▮	5	5.0E-1	1.0E0
☐	**INTERPRO**	Cyclin	RT	▮	4	6.5E-1	1.0E0
☐	**SMART**	CYCLIN	RT	▮	4	6.7E-1	1.0E0
☐	**INTERPRO**	Cyclin-related	RT	▮	4	7.9E-1	1.0E0
	Annotation Cluster 22	Enrichment Score: 0.26	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	nuclear transport	RT	▮	4	4.1E-1	1.0E0
☐	**GOTERM_BP_FAT**	nucleocytoplasmic transport	RT	▮	4	4.1E-1	1.0E0
☐	**GOTERM_CC_FAT**	endomembrane system	RT	▮	10	5.8E-1	1.0E0
☐	**GOTERM_CC_FAT**	envelope	RT	▮	4	6.0E-1	1.0E0
☐	**GOTERM_CC_FAT**	pore complex	RT	▮	4	6.0E-1	1.0E0
☐	**GOTERM_CC_FAT**	organelle envelope	RT	▮	4	6.0E-1	1.0E0
☐	**GOTERM_CC_FAT**	nuclear envelope	RT	▮	4	6.0E-1	1.0E0
☐	**GOTERM_CC_FAT**	nuclear pore	RT	▮	4	6.0E-1	1.0E0
	Annotation Cluster 23	Enrichment Score: 0.26	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	ligase	RT	▮	36	2.1E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	protein biosynthesis	RT	▮	8	3.2E-1	9.9E-1
☐	**KEGG_PATHWAY**	Aminoacyl-tRNA biosynthesis	RT	▮	14	3.3E-1	1.0E0
☐	**GOTERM_BP_FAT**	tRNA aminoacylation for protein translation	RT	▮	14	4.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	amino acid activation	RT	▮	14	5.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	tRNA aminoacylation	RT	▮	14	5.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Aminoacyl-tRNA synthetase	RT	▮	14	6.2E-1	9.9E-1
☐	**GOTERM_MF_FAT**	ligase activity, forming aminoacyl-tRNA and related compounds	RT	▮	14	6.7E-1	1.0E0
☐	**GOTERM_MF_FAT**	ligase activity, forming carbon-oxygen bonds	RT	▮	14	6.7E-1	1.0E0
☐	**GOTERM_MF_FAT**	aminoacyl-tRNA ligase activity	RT	▮	14	6.7E-1	1.0E0
☐	**INTERPRO**	Aminoacyl-tRNA synthetase, class II, conserved region	RT	▮	6	6.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	tRNA metabolic process	RT	▮	20	9.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	ncRNA metabolic process	RT	▮	25	9.5E-1	1.0E0
	Annotation Cluster 24	Enrichment Score: 0.25	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_FAT**	non-membrane-bounded organelle	RT	▮	94	1.4E-1	9.8E-1
☐	**GOTERM_CC_FAT**	intracellular non-membrane-bounded organelle	RT	▮	94	1.4E-1	9.8E-1
☐	**GOTERM_MF_FAT**	structural molecule activity	RT	▮	46	7.1E-1	1.0E0
☐	**KEGG_PATHWAY**	Ribosome	RT	▮	36	7.7E-1	1.0E0
☐	**GOTERM_CC_FAT**	ribosome	RT	▮	40	7.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	translation	RT	▮	60	8.2E-1	1.0E0
☐	**GOTERM_CC_FAT**	ribonucleoprotein complex	RT	▮	52	8.6E-1	1.0E0

☐	GOTERM_MF_FAT	structural constituent of ribosome	RT	35	9.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	ribosomal protein	RT	37	9.2E-1	9.9E-1
	Annotation Cluster 25	Enrichment Score: 0.24	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cell cycle	RT	7	2.4E-1	1.0E0
☐	GOTERM_BP_FAT	M phase	RT	5	4.7E-1	1.0E0
☐	GOTERM_BP_FAT	cell cycle process	RT	5	4.7E-1	1.0E0
☐	GOTERM_BP_FAT	cell cycle phase	RT	5	4.7E-1	1.0E0
☐	GOTERM_BP_FAT	M phase of mitotic cell cycle	RT	3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	mitotic cell cycle	RT	3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	nuclear division	RT	3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	organelle fission	RT	3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	mitosis	RT	3	7.8E-1	1.0E0
	Annotation Cluster 26	Enrichment Score: 0.23	G 🟩	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF000908:serine/threonine-protein phosphatase, conventional type	RT	7	2.8E-1	1.0E0
☐	INTERPRO	Metallophosphoesterase	RT	14	4.4E-1	1.0E0
☐	INTERPRO	Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase	RT	10	5.4E-1	1.0E0
☐	SMART	PP2Ac	RT	10	5.9E-1	1.0E0
☐	GOTERM_MF_FAT	phosphatase activity	RT	25	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	phosphoprotein phosphatase activity	RT	16	7.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	iron	RT	11	8.2E-1	9.9E-1
☐	GOTERM_MF_FAT	iron ion binding	RT	15	9.3E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 0.23	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	9	3.4E-1	1.0E0
☐	INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT	9	3.8E-1	1.0E0
☐	GOTERM_MF_FAT	lipid transporter activity	RT	5	4.7E-1	1.0E0
☐	INTERPRO	ATPase, P-type, ATPase-associated region	RT	8	4.7E-1	1.0E0
☐	INTERPRO	Haloacid dehalogenase-like hydrolase	RT	7	5.8E-1	1.0E0
☐	GOTERM_MF_FAT	di-, tri-valent inorganic cation transmembrane transporter activity	RT	3	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	lipid transport	RT	4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	lipid localization	RT	4	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	metal ion transmembrane transporter activity	RT	4	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	aminophospholipid transporter activity	RT	4	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid transporter activity	RT	4	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid-translocating ATPase activity	RT	4	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	magnesium ion binding	RT	9	7.0E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid transport	RT	3	7.8E-1	1.0E0
☐	INTERPRO	ATPase, P-type phosphorylation site	RT	5	7.9E-1	1.0E0
☐	INTERPRO	ATPase, P-type, phospholipid-translocating, flippase	RT	3	8.0E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 0.23	G 🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	protein biosynthesis	RT	8	3.2E-1	9.9E-1
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II (D, K and N)	RT	3	6.2E-1	1.0E0
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II (D, K and N)-like	RT	3	6.2E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001525:lysine-tRNA ligase	RT	3	6.2E-1	1.0E0
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II, conserved region	RT	6	6.9E-1	1.0E0
☐	INTERPRO	Nucleic acid binding, OB-fold, tRNA/helicase-type	RT	3	8.0E-1	1.0E0
	Annotation Cluster 29	Enrichment Score: 0.22	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Haloacid dehalogenase-like hydrolase	RT	7	5.8E-1	1.0E0
☐	GOTERM_MF_FAT	phosphoglycolate phosphatase activity	RT	3	6.0E-1	1.0E0
☐	INTERPRO	HAD-superfamily hydrolase, subfamily IA, variant 1	RT	3	6.2E-1	1.0E0
	Annotation Cluster 30	Enrichment Score: 0.19	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	microtubule cytoskeleton	RT	31	4.2E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeletal part	RT	31	4.2E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeleton	RT	32	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based process	RT	32	4.9E-1	1.0E0
		microtubule	RT	19	6.2E-1	1.0E0

☐	GOTERM_CC_FAT						
☐	SP_PIR_KEYWORDS	microtubule	RT		19	6.3E-1	9.9E-1
☐	GOTERM_BP_FAT	microtubule-based movement	RT		26	7.2E-1	1.0E0
☐	GOTERM_MF_FAT	motor activity	RT		23	7.6E-1	1.0E0
☐	GOTERM_MF_FAT	microtubule motor activity	RT		23	7.6E-1	1.0E0
☐	INTERPRO	Kinesin, motor region, conserved site	RT		10	8.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	motor protein	RT		13	8.3E-1	9.9E-1
☐	INTERPRO	Kinesin, motor region	RT		15	8.5E-1	1.0E0
☐	SMART	KISc	RT		15	8.9E-1	1.0E0
	Annotation Cluster 31	Enrichment Score: 0.19	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	phosphoinositide binding	RT		4	6.2E-1	1.0E0
☐	INTERPRO	Phox-like	RT		4	6.5E-1	1.0E0
☐	SMART	PX	RT		4	6.7E-1	1.0E0
	Annotation Cluster 32	Enrichment Score: 0.19	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	zinc ion binding	RT		88	4.2E-1	1.0E0
☐	GOTERM_MF_FAT	ion binding	RT		146	5.4E-1	1.0E0
☐	GOTERM_MF_FAT	cation binding	RT		146	5.4E-1	1.0E0
☐	GOTERM_MF_FAT	transition metal ion binding	RT		106	5.7E-1	1.0E0
☐	GOTERM_MF_FAT	metal ion binding	RT		143	6.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc	RT		48	6.5E-1	9.9E-1
☐	SP_PIR_KEYWORDS	zinc-finger	RT		35	6.6E-1	9.8E-1
☐	INTERPRO	Zinc finger, RING-type	RT		38	7.2E-1	1.0E0
☐	SMART	RING	RT		38	8.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	metal-binding	RT		54	8.5E-1	9.9E-1
☐	INTERPRO	Zinc finger, C3HC4 RING-type	RT		17	9.5E-1	1.0E0
	Annotation Cluster 33	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	COG_ONTOLOGY	Nucleotide transport and metabolism	RT		6	4.3E-1	1.0E0
☐	INTERPRO	5'-Nucleotidase and apyrase	RT		3	6.2E-1	1.0E0
☐	INTERPRO	Predicted phosphoesterase, C1039.02 type	RT		3	6.2E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF017316:phosphoesterase, C1039.02 type	RT		3	6.2E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF017316:Pesterase_C1039	RT		3	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	nitrogen compound catabolic process	RT		4	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide catabolic process	RT		4	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid catabolic process	RT		4	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	nucleotide catabolic process	RT		3	7.8E-1	1.0E0
	Annotation Cluster 34	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	ligase activity, forming carbon-nitrogen bonds	RT		21	3.1E-1	1.0E0
☐	GOTERM_MF_FAT	acid-amino acid ligase activity	RT		17	4.6E-1	1.0E0
☐	GOTERM_MF_FAT	small conjugating protein ligase activity	RT		8	6.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	ubl conjugation pathway	RT		8	7.1E-1	9.9E-1
☐	INTERPRO	Ubiquitin-conjugating enzyme, E2	RT		7	8.0E-1	1.0E0
☐	INTERPRO	Ubiquitin-conjugating enzyme/RWD-like	RT		7	8.0E-1	1.0E0
☐	SMART	UBCc	RT		7	8.3E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001567:ubiquitin-protein ligase E2	RT		3	9.5E-1	1.0E0
	Annotation Cluster 35	Enrichment Score: 0.17	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	guanyl ribonucleotide binding	RT		29	4.6E-1	1.0E0
☐	GOTERM_MF_FAT	GTP binding	RT		29	4.6E-1	1.0E0
☐	GOTERM_MF_FAT	guanyl nucleotide binding	RT		29	4.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	gtp-binding	RT		24	5.6E-1	9.9E-1
☐	GOTERM_MF_FAT	GTPase activity	RT		10	7.1E-1	1.0E0
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT		9	7.8E-1	1.0E0
☐	INTERPRO	Small GTP-binding protein	RT		11	8.3E-1	1.0E0
☐	INTERPRO	Ras GTPase	RT		7	8.7E-1	1.0E0
☐	INTERPRO	Ras	RT		6	9.2E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular signaling cascade	RT		10	9.3E-1	1.0E0
	Annotation Cluster 36	Enrichment Score: 0.15	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Clathrin/coatomer adaptor, adaptin-like, N-terminal	RT		5	3.0E-1	1.0E0

☐	GOTERM_CC_FAT	organelle membrane	RT		8	4.1E-1	1.0E0
☐	GOTERM_CC_FAT	coated membrane	RT		9	5.6E-1	1.0E0
☐	GOTERM_CC_FAT	membrane coat	RT		9	5.6E-1	1.0E0
☐	GOTERM_CC_FAT	endomembrane system	RT		10	5.8E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus part	RT		5	7.5E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle membrane	RT		4	7.5E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle part	RT		4	7.5E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle	RT		4	7.5E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle	RT		4	7.5E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle membrane	RT		4	7.5E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle membrane	RT		4	7.5E-1	1.0E0
☐	GOTERM_CC_FAT	membrane-bounded vesicle	RT		4	7.5E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle	RT		4	7.5E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle coat	RT		4	7.5E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic membrane-bounded vesicle	RT		4	7.5E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus	RT		6	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	vesicle-mediated transport	RT		15	8.6E-1	1.0E0
☐	GOTERM_CC_FAT	transport vesicle membrane	RT		3	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	transport vesicle	RT		3	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	Golgi vesicle transport	RT		3	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	ER to Golgi vesicle-mediated transport	RT		3	9.4E-1	1.0E0
	Annotation Cluster 37	Enrichment Score: 0.15	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	carbohydrate biosynthetic process	RT		5	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	cellular carbohydrate biosynthetic process	RT		5	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	alcohol biosynthetic process	RT		3	8.8E-1	1.0E0
	Annotation Cluster 38	Enrichment Score: 0.14	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Pyridine nucleotide-disulphide oxidoreductase, NAD-binding region	RT		3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	FAD binding	RT		4	7.7E-1	1.0E0
☐	INTERPRO	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	RT		3	8.0E-1	1.0E0
	Annotation Cluster 39	Enrichment Score: 0.14	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	regulation of transcription	RT		18	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of RNA metabolic process	RT		7	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of transcription, DNA-dependent	RT		7	7.7E-1	1.0E0
	Annotation Cluster 40	Enrichment Score: 0.13	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	WD40 repeat	RT		43	6.3E-1	1.0E0
☐	INTERPRO	WD40 repeat, region	RT		27	7.0E-1	1.0E0
☐	INTERPRO	WD40/YVTN repeat-like	RT		41	7.0E-1	1.0E0
☐	SMART	WD40	RT		43	7.2E-1	1.0E0
☐	INTERPRO	WD40 repeat 2	RT		24	7.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	wd repeat	RT		27	7.8E-1	9.9E-1
☐	INTERPRO	WD40 repeat, subgroup	RT		31	7.9E-1	1.0E0
☐	INTERPRO	WD40 repeat, conserved site	RT		14	9.5E-1	1.0E0
	Annotation Cluster 41	Enrichment Score: 0.12	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	electron carrier activity	RT		16	2.6E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, subgroup	RT		5	8.8E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulpur binding domain	RT		5	8.8E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, conserved site	RT		4	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	4 iron, 4 sulfur cluster binding	RT		4	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	iron-sulfur cluster binding	RT		9	9.6E-1	1.0E0
☐	GOTERM_MF_FAT	metal cluster binding	RT		9	9.6E-1	1.0E0
	Annotation Cluster 42	Enrichment Score: 0.11	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Serine/threonine protein kinase-related	RT		135	5.4E-1	1.0E0
☐	INTERPRO	Protein kinase, ATP binding site	RT		48	5.9E-1	1.0E0
☐	GOTERM_MF_FAT	protein serine/threonine kinase activity	RT		57	7.5E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase, active site	RT		48	8.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	serine/threonine-protein kinase	RT		32	8.8E-1	9.9E-1
☐	INTERPRO	Serine/threonine protein kinase	RT		30	9.1E-1	1.0E0

☐	SMART	S_TKc	RT			30	9.5E-1	1.0E0
	Annotation Cluster 43	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	vitamin metabolic process	RT			4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	water-soluble vitamin metabolic process	RT			4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	vitamin biosynthetic process	RT			4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	water-soluble vitamin biosynthetic process	RT			4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	coenzyme metabolic process	RT			6	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	oxidoreduction coenzyme metabolic process	RT			4	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	pyridine nucleotide metabolic process	RT			4	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	cofactor metabolic process	RT			7	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	pyridine nucleotide biosynthetic process	RT			3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	cofactor biosynthetic process	RT			5	8.5E-1	1.0E0
☐	GOTERM_BP_FAT	coenzyme biosynthetic process	RT			4	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	secondary metabolic process	RT			3	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	nicotinamide nucleotide metabolic process	RT			3	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	nicotinamide metabolic process	RT			3	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	alkaloid metabolic process	RT			3	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	cellular amide metabolic process	RT			3	8.8E-1	1.0E0
	Annotation Cluster 44	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular amino acid biosynthetic process	RT			4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	amine biosynthetic process	RT			4	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	organic acid biosynthetic process	RT			4	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	carboxylic acid biosynthetic process	RT			4	8.6E-1	1.0E0
	Annotation Cluster 45	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Chaperonin TCP-1, conserved site	RT			6	6.9E-1	1.0E0
☐	INTERPRO	Chaperonin Cpn60/TCP-1	RT			6	6.9E-1	1.0E0
☐	INTERPRO	Chaperone, tailless complex polypeptide 1	RT			5	7.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	Chaperone	RT			7	7.9E-1	9.9E-1
☐	PIR_SUPERFAMILY	PIRSF002584:molecular chaperone t-complex-type	RT			5	8.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	cytoplasm	RT			10	8.1E-1	9.9E-1
☐	GOTERM_MF_FAT	unfolded protein binding	RT			11	8.5E-1	1.0E0
	Annotation Cluster 46	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	spindle pole	RT			3	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	spindle	RT			3	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule organizing center	RT			3	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule cytoskeleton organization	RT			3	7.8E-1	1.0E0
☐	INTERPRO	Spc97/Spc98	RT			3	8.0E-1	1.0E0
	Annotation Cluster 47	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	secretion by cell	RT			3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	exocytosis	RT			3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	vesicle docking during exocytosis	RT			3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	vesicle docking	RT			3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	secretion	RT			3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	membrane docking	RT			3	7.8E-1	1.0E0
☐	INTERPRO	Sec1-like protein	RT			3	8.0E-1	1.0E0
	Annotation Cluster 48	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Aminotransferase, class V/Cysteine desulfurase	RT			3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	vitamin B6 binding	RT			6	7.7E-1	1.0E0
☐	GOTERM_MF_FAT	pyridoxal phosphate binding	RT			6	7.7E-1	1.0E0
☐	GOTERM_MF_FAT	vitamin binding	RT			6	8.5E-1	1.0E0
☐	INTERPRO	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	RT			4	9.4E-1	1.0E0
	Annotation Cluster 49	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	RNA polymerase activity	RT			15	5.1E-1	1.0E0
☐	GOTERM_MF_FAT	DNA-directed RNA polymerase activity	RT			14	5.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-directed rna polymerase	RT			9	6.2E-1	9.9E-1
☐	KEGG_PATHWAY	RNA polymerase	RT			9	8.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotidyltransferase	RT			13	8.8E-1	9.9E-1
☐	GOTERM_BP_FAT	transcription	RT			13	8.9E-1	1.0E0

☐	KEGG_PATHWAY	Pyrimidine metabolism	RT	▮		15	9.5E-1	1.0E0
☐	GOTERM_MF_FAT	nucleotidyltransferase activity	RT	▮		35	9.6E-1	1.0E0
☐	KEGG_PATHWAY	Purine metabolism	RT	▮		14	9.7E-1	1.0E0
	Annotation Cluster 50	Enrichment Score: 0.1	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	transmembrane	RT	▮		17	7.4E-1	9.9E-1
☐	SP_PIR_KEYWORDS	membrane	RT	▮		15	7.9E-1	9.9E-1
☐	INTERPRO	Amino acid transporter, transmembrane	RT	▮		6	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	intrinsic to membrane	RT	▮		35	8.1E-1	1.0E0
☐	GOTERM_CC_FAT	integral to membrane	RT	▮		35	8.1E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 0.1	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	thiolester hydrolase activity	RT	▮		5	7.7E-1	1.0E0
☐	GOTERM_MF_FAT	ubiquitin thiolesterase activity	RT	▮		4	7.7E-1	1.0E0
☐	INTERPRO	Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2	RT	▮		4	7.9E-1	1.0E0
☐	INTERPRO	Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2, conserved site	RT	▮		3	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	RT	▮		7	9.0E-1	1.0E0
	Annotation Cluster 52	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	AMP-dependent synthetase and ligase	RT	▮		5	6.7E-1	1.0E0
☐	COG_ONTOLOGY	Lipid metabolism	RT	▮		7	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	long-chain-fatty-acid-CoA ligase activity	RT	▮		3	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	fatty-acid ligase activity	RT	▮		3	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-sulfur bonds	RT	▮		3	8.8E-1	1.0E0
	Annotation Cluster 53	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Glycolysis / Gluconeogenesis	RT	▮		5	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	hexose metabolic process	RT	▮		12	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	glucose metabolic process	RT	▮		12	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide metabolic process	RT	▮		13	7.3E-1	1.0E0
☐	GOTERM_BP_FAT	hexose catabolic process	RT	▮		7	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	carbohydrate catabolic process	RT	▮		7	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	alcohol catabolic process	RT	▮		7	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide catabolic process	RT	▮		7	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	cellular carbohydrate catabolic process	RT	▮		7	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	glucose catabolic process	RT	▮		7	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	glycolysis	RT	▮		3	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	glycolysis	RT	▮		5	9.5E-1	1.0E0
	Annotation Cluster 54	Enrichment Score: 0.08	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	microtubule associated complex	RT	▮		9	6.7E-1	1.0E0
☐	GOTERM_CC_FAT	dynein complex	RT	▮		6	9.0E-1	1.0E0
☐	INTERPRO	Dynein heavy chain	RT	▮		6	9.2E-1	1.0E0
	Annotation Cluster 55	Enrichment Score: 0.08	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Kelch repeat type 1	RT	▮		4	7.9E-1	1.0E0
☐	SMART	Kelch	RT	▮		4	8.1E-1	1.0E0
☐	INTERPRO	Kelch-type beta propeller	RT	▮		4	8.8E-1	1.0E0
	Annotation Cluster 56	Enrichment Score: 0.08	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	proteolysis	RT	▮		49	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecule catabolic process	RT	▮		22	6.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	ubl conjugation pathway	RT	▮		8	7.1E-1	9.9E-1
☐	GOTERM_BP_FAT	cellular macromolecule catabolic process	RT	▮		19	7.2E-1	1.0E0
☐	GOTERM_BP_FAT	protein catabolic process	RT	▮		21	7.4E-1	1.0E0
☐	KEGG_PATHWAY	Proteasome	RT	▮		15	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	RT	▮		18	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein catabolic process	RT	▮		18	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent protein catabolic process	RT	▮		14	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	RT	▮		14	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	proteasome complex	RT	▮		11	8.4E-1	1.0E0
☐	INTERPRO	Proteasome, alpha and beta subunits	RT	▮		7	8.7E-1	1.0E0
☐	GOTERM_CC_FAT	proteasome core complex	RT	▮		7	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	RT	▮		7	9.0E-1	1.0E0

				Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	threonine-type peptidase activity	RT	7	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type endopeptidase activity	RT	7	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	proteasome	RT	10	9.1E-1	9.9E-1
☐	INTERPRO	Proteasome, subunit alpha/beta	RT	7	9.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	threonine protease	RT	3	9.5E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001212:multicatalytic endopeptidase complex chain C9	RT	3	9.5E-1	1.0E0
☐	GOTERM_CC_FAT	cytosol	RT	13	9.6E-1	1.0E0
☐	INTERPRO	Proteasome, alpha-subunit, conserved site	RT	3	9.8E-1	1.0E0
	Annotation Cluster 57	Enrichment Score: 0.08	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT	9	7.8E-1	1.0E0
☐	INTERPRO	ADP-ribosylation factor	RT	3	8.0E-1	1.0E0
☐	SMART	ARF	RT	3	8.1E-1	1.0E0
☐	INTERPRO	ARF/SAR superfamily	RT	4	8.8E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001711:ADP-ribosylation factor	RT	3	9.0E-1	1.0E0
	Annotation Cluster 58	Enrichment Score: 0.08	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	cAMP-dependent protein kinase regulator activity	RT	3	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	protein kinase regulator activity	RT	4	8.7E-1	1.0E0
☐	GOTERM_MF_FAT	kinase regulator activity	RT	4	8.7E-1	1.0E0
	Annotation Cluster 59	Enrichment Score: 0.07	G	Count	P_Value	Benjamini
☐	INTERPRO	ATPase, AAA-type, core	RT	14	7.9E-1	1.0E0
☐	INTERPRO	ATPase, AAA+ type, core	RT	38	8.7E-1	1.0E0
☐	SMART	AAA	RT	38	9.2E-1	1.0E0
	Annotation Cluster 60	Enrichment Score: 0.06	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	translation factor activity, nucleic acid binding	RT	17	8.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	Initiation factor	RT	10	8.7E-1	9.9E-1
☐	GOTERM_MF_FAT	translation initiation factor activity	RT	12	9.3E-1	1.0E0
	Annotation Cluster 61	Enrichment Score: 0.06	G	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, C2H2-like	RT	10	8.2E-1	1.0E0
☐	SMART	ZnF_C2H2	RT	10	8.5E-1	1.0E0
☐	INTERPRO	Zinc finger, C2H2-type	RT	8	9.7E-1	1.0E0
	Annotation Cluster 62	Enrichment Score: 0.05	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	phosphoprotein phosphatase activity	RT	16	7.0E-1	1.0E0
☐	GOTERM_MF_FAT	protein tyrosine phosphatase activity	RT	4	8.7E-1	1.0E0
☐	INTERPRO	Dual-specific/protein-tyrosine phosphatase, conserved region	RT	3	9.0E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase	RT	3	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid dephosphorylation	RT	6	9.4E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase, active site	RT	3	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	dephosphorylation	RT	7	9.6E-1	1.0E0
	Annotation Cluster 63	Enrichment Score: 0.05	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	mismatch repair	RT	3	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	double-stranded DNA binding	RT	3	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	structure-specific DNA binding	RT	3	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	mismatched DNA binding	RT	3	8.8E-1	1.0E0
	Annotation Cluster 64	Enrichment Score: 0.05	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	isoprenoid metabolic process	RT	3	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	isoprenoid biosynthetic process	RT	3	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	lipid biosynthetic process	RT	7	9.0E-1	1.0E0
	Annotation Cluster 65	Enrichment Score: 0.05	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	nucleoside-triphosphatase regulator activity	RT	8	6.8E-1	1.0E0
☐	GOTERM_MF_FAT	small GTPase regulator activity	RT	6	8.5E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase regulator activity	RT	6	8.5E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of small GTPase mediated signal transduction	RT	5	8.5E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras protein signal transduction	RT	5	8.5E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of ARF protein signal transduction	RT	3	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	enzyme activator activity	RT	4	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras GTPase activity	RT	3	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase activator activity	RT	3	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of GTPase activity	RT	3	9.9E-1	1.0E0

☐	**GOTERM_BP_FAT**	regulation of hydrolase activity	RT			3	9.9E-1	1.0E0
	Annotation Cluster 66	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Thioredoxin, conserved site	RT			4	7.9E-1	1.0E0
☐	**INTERPRO**	Thioredoxin domain	RT			4	7.9E-1	1.0E0
☐	**INTERPRO**	Thioredoxin, core	RT			4	8.8E-1	1.0E0
☐	**INTERPRO**	Thioredoxin-like subdomain	RT			3	9.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	cell redox homeostasis	RT			9	9.0E-1	1.0E0
☐	**INTERPRO**	Thioredoxin fold	RT			11	9.2E-1	1.0E0
☐	**GOTERM_BP_FAT**	cellular homeostasis	RT			9	9.3E-1	1.0E0
☐	**GOTERM_BP_FAT**	homeostatic process	RT			9	9.6E-1	1.0E0
☐	**INTERPRO**	Thioredoxin-like	RT			5	9.9E-1	1.0E0
	Annotation Cluster 67	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	response to drug	RT			3	8.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	multidrug transport	RT			3	8.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	drug transport	RT			3	8.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	drug transporter activity	RT			3	8.8E-1	1.0E0
☐	**INTERPRO**	Multi antimicrobial extrusion protein MatE	RT			3	9.0E-1	1.0E0
☐	**GOTERM_MF_FAT**	antiporter activity	RT			3	9.4E-1	1.0E0
	Annotation Cluster 68	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	RNA-dependent DNA replication	RT			4	8.6E-1	1.0E0
☐	**INTERPRO**	RNA-directed DNA polymerase (reverse transcriptase)	RT			4	8.8E-1	1.0E0
☐	**INTERPRO**	RNA-directed DNA polymerase (reverse transcriptase), related	RT			3	9.0E-1	1.0E0
☐	**GOTERM_MF_FAT**	RNA-directed DNA polymerase activity	RT			11	9.5E-1	1.0E0
	Annotation Cluster 69	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	exopeptidase activity	RT			6	8.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	metalloexopeptidase activity	RT			4	8.7E-1	1.0E0
☐	**GOTERM_MF_FAT**	metallopeptidase activity	RT			5	9.8E-1	1.0E0
	Annotation Cluster 70	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	organophosphate metabolic process	RT			7	8.5E-1	1.0E0
☐	**GOTERM_BP_FAT**	phospholipid biosynthetic process	RT			4	8.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	lipid biosynthetic process	RT			7	9.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	phospholipid metabolic process	RT			6	9.1E-1	1.0E0
☐	**GOTERM_BP_FAT**	glycerophospholipid metabolic process	RT			3	9.7E-1	1.0E0
☐	**GOTERM_BP_FAT**	glycerolipid metabolic process	RT			3	9.7E-1	1.0E0
☐	**GOTERM_BP_FAT**	phosphoinositide metabolic process	RT			3	9.7E-1	1.0E0
	Annotation Cluster 71	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	EF hand	RT			6	8.7E-1	1.0E0
☐	**INTERPRO**	EF-HAND 2	RT			9	8.7E-1	1.0E0
☐	**INTERPRO**	EF-Hand type	RT			9	9.2E-1	1.0E0
☐	**INTERPRO**	EF-HAND 1	RT			10	9.2E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	calcium	RT			7	9.5E-1	1.0E0
☐	**INTERPRO**	Calcium-binding EF-hand	RT			5	9.6E-1	1.0E0
☐	**SMART**	EFh	RT			5	9.7E-1	1.0E0
	Annotation Cluster 72	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Molecular chaperone, heat shock protein, Hsp40, DnaJ	RT			4	8.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	heat shock protein binding	RT			4	9.3E-1	1.0E0
☐	**INTERPRO**	Heat shock protein DnaJ, N-terminal	RT			4	9.4E-1	1.0E0
☐	**SMART**	DnaJ	RT			4	9.5E-1	1.0E0
	Annotation Cluster 73	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Nucleotide-binding, alpha-beta plait	RT			8	9.2E-1	1.0E0
☐	**INTERPRO**	RNA recognition motif, RNP-1	RT			7	9.2E-1	1.0E0
☐	**SMART**	RRM	RT			7	9.4E-1	1.0E0
	Annotation Cluster 74	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Acyl-CoA N-acyltransferase	RT			6	8.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Acyltransferase	RT			6	8.7E-1	9.9E-1
☐	**GOTERM_MF_FAT**	N-acyltransferase activity	RT			4	9.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	acetyltransferase activity	RT			4	9.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	N-acetyltransferase activity	RT			3	9.9E-1	1.0E0

☐	**INTERPRO**	GCN5-related N-acetyltransferase	RT	3	9.9E-1	1.0E0
	Annotation Cluster 75	Enrichment Score: 0.03		Count	P_Value	Benjamini
☐	**INTERPRO**	Like-Sm ribonucleoprotein, core	RT	6	8.7E-1	1.0E0
☐	**INTERPRO**	Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core	RT	3	9.8E-1	1.0E0
☐	**SMART**	Sm	RT	3	9.8E-1	1.0E0
	Annotation Cluster 76	Enrichment Score: 0.01		Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	RNA-directed DNA polymerase activity	RT	11	9.5E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Endonuclease	RT	14	9.6E-1	1.0E0
☐	**GOTERM_MF_FAT**	nuclease activity	RT	23	9.7E-1	1.0E0
☐	**GOTERM_MF_FAT**	endonuclease activity	RT	15	9.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	DNA polymerase activity	RT	15	9.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	rna-directed dna polymerase	RT	10	9.8E-1	1.0E0
	Annotation Cluster 77	Enrichment Score: 0.01		Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	ribosome biogenesis	RT	9	9.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	ribonucleoprotein complex biogenesis	RT	9	9.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	rRNA processing	RT	5	9.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	rRNA metabolic process	RT	5	9.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	ncRNA processing	RT	11	1.0E0	1.0E0
	Annotation Cluster 78	Enrichment Score: 0.01		Count	P_Value	Benjamini
☐	**INTERPRO**	Ubiquitin	RT	3	9.8E-1	1.0E0
☐	**INTERPRO**	Ubiquitin supergroup	RT	5	9.8E-1	1.0E0
☐	**SMART**	UBQ	RT	3	9.8E-1	1.0E0
	Annotation Cluster 79	Enrichment Score: 0.01		Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	ncRNA metabolic process	RT	25	9.5E-1	1.0E0
☐	**GOTERM_BP_FAT**	tRNA processing	RT	6	9.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	ncRNA processing	RT	11	1.0E0	1.0E0
☐	**GOTERM_BP_FAT**	RNA processing	RT	16	1.0E0	1.0E0

[209 terms] were not clustered.

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Functional Annotation Clustering

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Current Gene List: 3_Random3
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3000 DAVID IDs

Options **Classification Stringency** Medium

Rerun using options | Create Sublist

75 Cluster(s)

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	Annotation Cluster 1	Enrichment Score: 0.85	G	Count	P_Value	Benjamini
☐	INTERPRO	EGF-like, laminin	RT	20	8.3E-2	1.0E0
☐	SMART	EGF_Lam	RT	20	9.0E-2	1.0E0
☐	INTERPRO	EGF-like, type 3	RT	21	3.7E-1	1.0E0

	Annotation Cluster 2	Enrichment Score: 0.85	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	ATPase activity, coupled	RT	50	2.5E-2	1.0E0
☐	SP_PIR_KEYWORDS	helicase	RT	32	6.0E-2	1.0E0
☐	GOTERM_MF_FAT	helicase activity	RT	38	7.5E-2	1.0E0
☐	GOTERM_MF_FAT	ATPase activity	RT	62	1.0E-1	1.0E0
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT	30	1.3E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, C-terminal	RT	30	1.8E-1	1.0E0
☐	SMART	HELICc	RT	30	1.9E-1	1.0E0
☐	INTERPRO	RNA helicase, DEAD-box type, Q motif	RT	13	2.1E-1	1.0E0
☐	INTERPRO	DEAD-like helicase, N-terminal	RT	29	2.1E-1	1.0E0
☐	GOTERM_MF_FAT	purine NTP-dependent helicase activity	RT	26	2.1E-1	1.0E0
☐	GOTERM_MF_FAT	ATP-dependent helicase activity	RT	26	2.1E-1	1.0E0
☐	SMART	DEXDc	RT	29	2.3E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT	20	3.4E-1	1.0E0

	Annotation Cluster 3	Enrichment Score: 0.67	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	monosaccharide metabolic process	RT	17	1.2E-1	1.0E0
☐	GOTERM_BP_FAT	hexose metabolic process	RT	15	1.4E-1	1.0E0
☐	GOTERM_BP_FAT	glucose metabolic process	RT	15	1.4E-1	1.0E0
☐	GOTERM_BP_FAT	hexose catabolic process	RT	11	1.8E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide catabolic process	RT	11	1.8E-1	1.0E0
☐	GOTERM_BP_FAT	glucose catabolic process	RT	11	1.8E-1	1.0E0
☐	GOTERM_BP_FAT	cellular carbohydrate catabolic process	RT	11	1.8E-1	1.0E0
☐	GOTERM_BP_FAT	alcohol catabolic process	RT	11	1.8E-1	1.0E0
☐	GOTERM_BP_FAT	carbohydrate catabolic process	RT	11	1.8E-1	1.0E0
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT	17	3.4E-1	1.0E0
☐	GOTERM_BP_FAT	glycolysis	RT	8	4.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	glycolysis	RT	4	7.9E-1	1.0E0

	Annotation Cluster 4	Enrichment Score: 0.66	G	Count	P_Value	Benjamini
☐	INTERPRO	EF-HAND 1	RT	16	9.1E-2	1.0E0
☐	INTERPRO	EF-HAND 2	RT	14	9.3E-2	1.0E0
☐	INTERPRO	EF-Hand type	RT	14	1.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	calcium	RT	12	1.7E-1	1.0E0
☐	GOTERM_MF_FAT	calcium ion binding	RT	29	2.2E-1	1.0E0
☐	INTERPRO	Calcium-binding EF-hand	RT	8	4.8E-1	1.0E0
☐	INTERPRO	EF hand	RT	8	4.8E-1	1.0E0
☐	SMART	EFh	RT	8	4.9E-1	1.0E0

	Annotation Cluster 5	Enrichment Score: 0.6	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	DNA polymerase activity	RT	26	4.6E-2	1.0E0
☐	GOTERM_MF_FAT	nucleotidyltransferase activity	RT	47	1.9E-1	1.0E0
☐	GOTERM_MF_FAT	RNA-directed DNA polymerase activity	RT	17	2.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	rna-directed dna polymerase	RT	16	3.2E-1	1.0E0
☐	GOTERM_MF_FAT	endonuclease activity	RT	22	4.0E-1	1.0E0

☐	GOTERM_MF_FAT	nuclease activity	RT	▮	31	4.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	Endonuclease	RT	▮	19	4.9E-1	9.9E-1
	Annotation Cluster 6	Enrichment Score: 0.57	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	WD40 repeat, subgroup	RT	▮	38	1.3E-1	1.0E0
☐	INTERPRO	WD40 repeat 2	RT	▮	29	2.1E-1	1.0E0
☐	INTERPRO	WD40 repeat, region	RT	▮	31	2.5E-1	1.0E0
☐	INTERPRO	WD40/YVTN repeat-like	RT	▮	46	2.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	wd repeat	RT	▮	32	2.7E-1	1.0E0
☐	INTERPRO	WD40 repeat	RT	▮	46	3.5E-1	1.0E0
☐	SMART	WD40	RT	▮	46	3.8E-1	1.0E0
☐	INTERPRO	WD40 repeat, conserved site	RT	▮	19	4.0E-1	1.0E0
	Annotation Cluster 7	Enrichment Score: 0.5	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide biosynthetic process	RT	▮	30	5.0E-2	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	RT	▮	30	5.0E-2	1.0E0
☐	GOTERM_BP_FAT	nucleotide biosynthetic process	RT	▮	27	1.0E-1	1.0E0
☐	GOTERM_BP_FAT	nitrogen compound biosynthetic process	RT	▮	33	1.0E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside triphosphate biosynthetic process	RT	▮	19	1.6E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside triphosphate metabolic process	RT	▮	19	1.6E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside triphosphate biosynthetic process	RT	▮	19	1.6E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate metabolic process	RT	▮	19	1.6E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside triphosphate metabolic process	RT	▮	19	1.6E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside triphosphate metabolic process	RT	▮	19	1.6E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside triphosphate biosynthetic process	RT	▮	19	1.6E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate biosynthetic process	RT	▮	19	1.6E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleotide biosynthetic process	RT	▮	20	1.8E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of substances	RT	▮	20	2.0E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to movement of substances	RT	▮	20	2.0E-1	1.0E0
☐	GOTERM_MF_FAT	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT	▮	21	2.2E-1	1.0E0
☐	GOTERM_MF_FAT	primary active transmembrane transporter activity	RT	▮	21	2.2E-1	1.0E0
☐	GOTERM_MF_FAT	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT	▮	21	2.2E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleotide metabolic process	RT	▮	19	2.3E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleotide biosynthetic process	RT	▮	19	2.3E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide biosynthetic process	RT	▮	19	2.3E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide metabolic process	RT	▮	19	2.3E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleotide metabolic process	RT	▮	20	2.5E-1	1.0E0
☐	GOTERM_BP_FAT	ATP metabolic process	RT	▮	17	2.6E-1	1.0E0
☐	GOTERM_BP_FAT	ATP biosynthetic process	RT	▮	17	2.6E-1	1.0E0
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT	▮	17	3.4E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions	RT	▮	14	3.5E-1	1.0E0
☐	GOTERM_BP_FAT	transmembrane transport	RT	▮	14	3.6E-1	1.0E0
☐	INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT	▮	9	3.8E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	▮	9	3.9E-1	1.0E0
☐	GOTERM_BP_FAT	hydrogen transport	RT	▮	10	4.7E-1	1.0E0
☐	GOTERM_BP_FAT	proton transport	RT	▮	10	4.7E-1	1.0E0
☐	INTERPRO	ATPase, P-type, ATPase-associated region	RT	▮	8	4.8E-1	1.0E0
☐	GOTERM_MF_FAT	inorganic cation transmembrane transporter activity	RT	▮	12	5.0E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex	RT	▮	10	5.5E-1	1.0E0
☐	GOTERM_MF_FAT	hydrogen ion transmembrane transporter activity	RT	▮	10	5.5E-1	1.0E0
☐	GOTERM_MF_FAT	monovalent inorganic cation transmembrane transporter activity	RT	▮	10	5.5E-1	1.0E0
☐	GOTERM_BP_FAT	ion transmembrane transport	RT	▮	9	5.6E-1	1.0E0
☐	GOTERM_BP_FAT	monovalent inorganic cation transport	RT	▮	10	5.8E-1	1.0E0
				▮			

☐	GOTERM_BP_FAT	oxidative phosphorylation	RT	8	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	ATP synthesis coupled proton transport	RT	8	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	energy coupled proton transport, down electrochemical gradient	RT	8	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	proton-transporting ATPase activity, rotational mechanism	RT	5	6.7E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting V-type ATPase complex	RT	6	7.0E-1	1.0E0
☐	KEGG_PATHWAY	Oxidative phosphorylation	RT	8	7.2E-1	1.0E0
☐	GOTERM_BP_FAT	ion transport	RT	13	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	cation transport	RT	13	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, proton-transporting domain	RT	4	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, catalytic domain	RT	5	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	cation-transporting ATPase activity	RT	6	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting V-type ATPase, V0 domain	RT	3	9.0E-1	1.0E0
	Annotation Cluster 8	Enrichment Score: 0.46	G	Count	P_Value	Benjamini
☐	INTERPRO	Pumilio RNA-binding region	RT	5	3.0E-1	1.0E0
☐	SMART	Pumilio	RT	5	3.1E-1	1.0E0
☐	INTERPRO	Armadillo-like helical	RT	14	4.5E-1	1.0E0
	Annotation Cluster 9	Enrichment Score: 0.43	G	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	intrinsic to membrane	RT	43	1.9E-1	1.0E0
☐	GOTERM_CC_FAT	integral to membrane	RT	43	1.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	membrane	RT	18	3.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	transmembrane	RT	18	6.4E-1	1.0E0
☐	INTERPRO	Amino acid transporter, transmembrane	RT	6	8.0E-1	1.0E0
	Annotation Cluster 10	Enrichment Score: 0.39	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	endopeptidase activity	RT	31	2.0E-1	1.0E0
☐	GOTERM_MF_FAT	peptidase activity	RT	51	2.0E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis	RT	54	2.1E-1	1.0E0
☐	GOTERM_MF_FAT	peptidase activity, acting on L-amino acid peptides	RT	44	2.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	Protease	RT	24	2.9E-1	1.0E0
☐	INTERPRO	Peptidase, cysteine peptidase active site	RT	19	4.9E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain C-terminal	RT	16	6.8E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain	RT	16	6.8E-1	1.0E0
☐	SMART	Pept_C1	RT	16	7.0E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type endopeptidase activity	RT	14	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type peptidase activity	RT	17	7.7E-1	1.0E0
	Annotation Cluster 11	Enrichment Score: 0.38	G	Count	P_Value	Benjamini
☐	INTERPRO	Small GTP-binding protein	RT	15	1.9E-1	1.0E0
☐	GOTERM_MF_FAT	guanyl nucleotide binding	RT	31	3.2E-1	1.0E0
☐	GOTERM_MF_FAT	GTP binding	RT	31	3.2E-1	1.0E0
☐	GOTERM_MF_FAT	guanyl ribonucleotide binding	RT	31	3.2E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular signaling cascade	RT	14	3.6E-1	1.0E0
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT	11	3.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	gtp-binding	RT	25	4.7E-1	9.9E-1
☐	INTERPRO	Ras	RT	8	6.1E-1	1.0E0
☐	INTERPRO	Ras GTPase	RT	8	7.2E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001710:Ras-related protein Rab	RT	4	7.7E-1	1.0E0
	Annotation Cluster 12	Enrichment Score: 0.38	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	pyridine nucleotide metabolic process	RT	6	1.7E-1	1.0E0
☐	GOTERM_BP_FAT	oxidoreduction coenzyme metabolic process	RT	6	1.7E-1	1.0E0
☐	GOTERM_BP_FAT	secondary metabolic process	RT	5	2.6E-1	1.0E0
☐	GOTERM_BP_FAT	cellular amide metabolic process	RT	5	2.6E-1	1.0E0
☐	GOTERM_BP_FAT	nicotinamide metabolic process	RT	5	2.6E-1	1.0E0
☐	GOTERM_BP_FAT	alkaloid metabolic process	RT	5	2.6E-1	1.0E0
☐	GOTERM_BP_FAT	nicotinamide nucleotide metabolic process	RT	5	2.6E-1	1.0E0
☐	GOTERM_BP_FAT	coenzyme metabolic process	RT	8	2.8E-1	1.0E0
☐	GOTERM_BP_FAT	pyridine nucleotide biosynthetic process	RT	4	4.0E-1	1.0E0
☐	GOTERM_BP_FAT	cofactor metabolic process	RT	8	5.4E-1	1.0E0
☐	GOTERM_BP_FAT	nicotinamide nucleotide biosynthetic process	RT	3	5.8E-1	1.0E0

☐	GOTERM_BP_FAT	NAD biosynthetic process	RT	3	5.8E-1	1.0E0
☐	GOTERM_BP_FAT	NAD metabolic process	RT	3	5.8E-1	1.0E0
☐	GOTERM_BP_FAT	vitamin metabolic process	RT	4	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	water-soluble vitamin metabolic process	RT	4	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	water-soluble vitamin biosynthetic process	RT	4	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	vitamin biosynthetic process	RT	4	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	coenzyme biosynthetic process	RT	5	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	cofactor biosynthetic process	RT	5	8.4E-1	1.0E0
☐	INTERPRO	Rossmann-like alpha/beta/alpha sandwich fold	RT	9	9.5E-1	1.0E0
	Annotation Cluster 13	Enrichment Score: 0.35		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	flagellum	RT	4	4.4E-1	1.0E0
☐	GOTERM_CC_FAT	cell projection	RT	4	4.4E-1	1.0E0
☐	GOTERM_CC_FAT	flagellum	RT	4	4.4E-1	1.0E0
	Annotation Cluster 14	Enrichment Score: 0.32		Count	P_Value	Benjamini
☐	INTERPRO	EGF, extracellular	RT	16	3.1E-1	1.0E0
☐	INTERPRO	EGF-like, type 3	RT	21	3.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	egf-like domain	RT	8	9.5E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 0.31		Count	P_Value	Benjamini
☐	INTERPRO	Ankyrin	RT	254	4.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	ank repeat	RT	179	4.8E-1	9.9E-1
☐	SMART	ANK	RT	254	5.6E-1	1.0E0
	Annotation Cluster 16	Enrichment Score: 0.28		Count	P_Value	Benjamini
☐	INTERPRO	EGF-like	RT	114	3.6E-1	1.0E0
☐	SMART	EGF	RT	114	4.1E-1	1.0E0
☐	INTERPRO	Giardia variant-specific surface protein	RT	136	6.2E-1	1.0E0
☐	INTERPRO	Furin-like repeat	RT	106	6.3E-1	1.0E0
☐	SMART	FU	RT	106	6.9E-1	1.0E0
	Annotation Cluster 17	Enrichment Score: 0.28		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	calcium ion binding	RT	29	2.2E-1	1.0E0
☐	INTERPRO	Alpha giardin	RT	9	3.8E-1	1.0E0
☐	INTERPRO	Annexin repeat	RT	10	4.2E-1	1.0E0
☐	SMART	ANX	RT	10	4.4E-1	1.0E0
☐	INTERPRO	Annexin	RT	11	4.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	annexin	RT	11	4.6E-1	1.0E0
☐	GOTERM_BP_FAT	cytoskeleton organization	RT	9	7.6E-1	1.0E0
☐	GOTERM_MF_FAT	calcium-dependent phospholipid binding	RT	12	8.4E-1	1.0E0
☐	GOTERM_MF_FAT	lipid binding	RT	19	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid binding	RT	13	9.5E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 0.27		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	microtubule-based movement	RT	30	2.4E-1	1.0E0
☐	GOTERM_MF_FAT	motor activity	RT	27	3.7E-1	1.0E0
☐	GOTERM_MF_FAT	microtubule motor activity	RT	27	3.7E-1	1.0E0
☐	INTERPRO	Dynein heavy chain	RT	9	3.8E-1	1.0E0
☐	GOTERM_CC_FAT	dynein complex	RT	9	3.8E-1	1.0E0
☐	COG_ONTOLOGY	Cytoskeleton	RT	14	5.2E-1	9.9E-1
☐	GOTERM_CC_FAT	microtubule associated complex	RT	10	5.5E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based process	RT	31	5.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	motor protein	RT	15	5.8E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule	RT	20	6.0E-1	1.0E0
☐	INTERPRO	Kinesin, motor region	RT	17	6.1E-1	1.0E0
☐	SMART	KISc	RT	17	6.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	microtubule	RT	19	6.5E-1	1.0E0
☐	INTERPRO	Kinesin, motor region, conserved site	RT	11	6.7E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeletal part	RT	30	7.0E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule cytoskeleton	RT	30	7.0E-1	1.0E0
☐	INTERPRO	Dynein heavy chain, N-terminal region 2	RT	7	7.1E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeleton	RT	30	8.1E-1	1.0E0
	Annotation Cluster 19	Enrichment Score: 0.26		Count	P_Value	Benjamini

☐	**GOTERM_BP_FAT**	intracellular transport	RT		18	3.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	cellular protein localization	RT		15	3.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	cellular macromolecule localization	RT		15	3.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	intracellular protein transport	RT		15	3.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	vesicle-mediated transport	RT		17	6.0E-1	1.0E0
☐	**GOTERM_CC_FAT**	coated membrane	RT		9	6.4E-1	1.0E0
☐	**GOTERM_CC_FAT**	membrane coat	RT		9	6.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	protein localization	RT		19	6.9E-1	1.0E0
☐	**GOTERM_CC_FAT**	Golgi apparatus	RT		7	7.1E-1	1.0E0
☐	**GOTERM_BP_FAT**	protein transport	RT		18	7.5E-1	1.0E0
☐	**GOTERM_BP_FAT**	establishment of protein localization	RT		18	7.5E-1	1.0E0
	Annotation Cluster 20	Enrichment Score: 0.26	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Aldolase-type TIM barrel	RT		7	4.3E-1	1.0E0
☐	**GOTERM_MF_FAT**	FAD binding	RT		5	5.1E-1	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF006621:Dus	RT		3	6.0E-1	1.0E0
☐	**INTERPRO**	tRNA-dihydrouridine synthase	RT		3	6.2E-1	1.0E0
☐	**GOTERM_MF_FAT**	tRNA dihydrouridine synthase activity	RT		3	6.2E-1	1.0E0
	Annotation Cluster 21	Enrichment Score: 0.25	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Protein phosphatase 2C, manganese/magnesium aspartate binding site	RT		4	4.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	protein phosphatase	RT		4	4.4E-1	1.0E0
☐	**GOTERM_MF_FAT**	protein serine/threonine phosphatase activity	RT		4	4.4E-1	1.0E0
☐	**INTERPRO**	Protein phosphatase 2C, N-terminal	RT		5	5.0E-1	1.0E0
☐	**INTERPRO**	Protein phosphatase 2C	RT		5	5.0E-1	1.0E0
☐	**INTERPRO**	Protein phosphatase 2C-related	RT		5	5.0E-1	1.0E0
☐	**SMART**	PP2C_SIG	RT		5	5.1E-1	1.0E0
☐	**SMART**	PP2Cc	RT		5	5.1E-1	1.0E0
☐	**GOTERM_MF_FAT**	magnesium ion binding	RT		10	5.5E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	magnesium	RT		8	6.1E-1	1.0E0
☐	**GOTERM_BP_FAT**	dephosphorylation	RT		9	7.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	protein amino acid dephosphorylation	RT		7	8.3E-1	1.0E0
☐	**GOTERM_CC_FAT**	protein serine/threonine phosphatase complex	RT		4	8.9E-1	1.0E0
	Annotation Cluster 22	Enrichment Score: 0.25	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	DNA-dependent ATPase activity	RT		7	2.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	DNA helicase activity	RT		4	8.0E-1	1.0E0
☐	**GOTERM_MF_FAT**	ATP-dependent DNA helicase activity	RT		3	8.0E-1	1.0E0
	Annotation Cluster 23	Enrichment Score: 0.25	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	regulation of transcription, DNA-dependent	RT		8	5.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of RNA metabolic process	RT		8	5.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of transcription	RT		18	6.1E-1	1.0E0
	Annotation Cluster 24	Enrichment Score: 0.25	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	tRNA processing	RT		13	1.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	ncRNA processing	RT		17	6.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	tRNA metabolic process	RT		21	8.1E-1	1.0E0
☐	**GOTERM_BP_FAT**	RNA processing	RT		24	8.2E-1	1.0E0
☐	**GOTERM_BP_FAT**	ncRNA metabolic process	RT		25	9.4E-1	1.0E0
	Annotation Cluster 25	Enrichment Score: 0.24	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	DNA-directed DNA polymerase activity	RT		9	1.4E-1	1.0E0
☐	**INTERPRO**	DNA-directed DNA polymerase, family B	RT		4	6.5E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	dna-directed dna polymerase	RT		4	6.5E-1	1.0E0
☐	**SMART**	POLBc	RT		4	6.6E-1	1.0E0
☐	**INTERPRO**	DNA-directed DNA polymerase, family B, conserved region2	RT		3	8.0E-1	1.0E0
☐	**INTERPRO**	DNA-directed DNA polymerase, family B, conserved site	RT		3	8.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	dna replication	RT		6	8.0E-1	9.9E-1
	Annotation Cluster 26	Enrichment Score: 0.24	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Nucleotide-binding, alpha-beta plait	RT		11	4.6E-1	1.0E0
☐	**INTERPRO**	RNA recognition motif, RNP-1	RT		9	6.3E-1	1.0E0
☐	**SMART**	RRM	RT		9	6.5E-1	1.0E0

	Annotation Cluster 27	Enrichment Score: 0.23	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	phospholipid metabolic process	RT		9	3.2E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid biosynthetic process	RT		6	3.3E-1	1.0E0
☐	GOTERM_BP_FAT	lipid biosynthetic process	RT		10	3.5E-1	1.0E0
☐	GOTERM_BP_FAT	organophosphate metabolic process	RT		9	4.4E-1	1.0E0
☐	INTERPRO	CDP-alcohol phosphatidyltransferase	RT		3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	phosphotransferase activity, for other substituted phosphate groups	RT		3	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	glycerolipid metabolic process	RT		4	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	phosphoinositide metabolic process	RT		4	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	glycerophospholipid metabolic process	RT		4	8.6E-1	1.0E0
☐	GOTERM_MF_FAT	inositol or phosphatidylinositol kinase activity	RT		3	9.0E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 0.22	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	dna-binding	RT		24	2.3E-1	1.0E0
☐	GOTERM_CC_FAT	chromosomal part	RT		12	3.8E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly or disassembly	RT		9	4.4E-1	1.0E0
☐	GOTERM_CC_FAT	protein-DNA complex	RT		9	5.2E-1	1.0E0
☐	GOTERM_CC_FAT	chromosome	RT		17	5.4E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex subunit organization	RT		15	5.7E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecular complex subunit organization	RT		16	5.8E-1	1.0E0
☐	GOTERM_CC_FAT	chromatin	RT		8	6.2E-1	1.0E0
☐	INTERPRO	Histone-fold	RT		9	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex assembly	RT		14	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	protein-DNA complex assembly	RT		7	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	DNA packaging	RT		7	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome assembly	RT		7	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome organization	RT		7	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly	RT		7	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecular complex assembly	RT		15	6.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleosome core	RT		5	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin organization	RT		9	6.7E-1	1.0E0
☐	INTERPRO	Histone core	RT		7	7.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	chromosomal protein	RT		7	7.1E-1	1.0E0
☐	GOTERM_CC_FAT	nucleosome	RT		7	7.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleus	RT		19	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	chromosome organization	RT		10	8.3E-1	1.0E0
	Annotation Cluster 29	Enrichment Score: 0.22	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	ATPase, AAA+ type, core	RT		42	5.6E-1	1.0E0
☐	SMART	AAA	RT		42	6.0E-1	1.0E0
☐	INTERPRO	ATPase, AAA-type, core	RT		15	6.6E-1	1.0E0
	Annotation Cluster 30	Enrichment Score: 0.21	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	intramolecular transferase activity	RT		8	4.8E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001430:tRNA_psdUrid_synth	RT		3	6.0E-1	1.0E0
☐	INTERPRO	Pseudouridine synthase I, TruA	RT		3	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	pseudouridine synthesis	RT		5	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	pseudouridine synthase activity	RT		5	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	RNA modification	RT		9	7.6E-1	1.0E0
	Annotation Cluster 31	Enrichment Score: 0.21	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	ARF/SAR superfamily	RT		6	3.8E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001711:ADP-ribosylation factor	RT		4	6.3E-1	1.0E0
☐	INTERPRO	ADP-ribosylation factor	RT		3	8.0E-1	1.0E0
☐	SMART	ARF	RT		3	8.0E-1	1.0E0
	Annotation Cluster 32	Enrichment Score: 0.2	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	nucleoside metabolic process	RT		9	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside metabolic process	RT		5	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside metabolic process	RT		3	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside metabolic process	RT		3	7.7E-1	1.0E0
	Annotation Cluster 33	Enrichment Score: 0.2	G	🟩	Count	P_Value	Benjamini
	GOTERM_BP_FAT	cellular response to stress	RT		13	5.3E-1	1.0E0

☐							
☐	GOTERM_BP_FAT	mismatch repair	RT		4	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	DNA repair	RT		12	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	response to DNA damage stimulus	RT		12	6.1E-1	1.0E0
☐	GOTERM_MF_FAT	double-stranded DNA binding	RT		4	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	structure-specific DNA binding	RT		4	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	mismatched DNA binding	RT		4	6.5E-1	1.0E0
☐	KEGG_PATHWAY	Mismatch repair	RT		8	8.1E-1	9.9E-1
	Annotation Cluster 34	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT		9	3.8E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT		9	3.9E-1	1.0E0
☐	INTERPRO	ATPase, P-type, ATPase-associated region	RT		8	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	lipid transport	RT		4	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	lipid localization	RT		4	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid transport	RT		3	7.7E-1	1.0E0
☐	INTERPRO	ATPase, P-type phosphorylation site	RT		5	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	lipid transporter activity	RT		4	8.0E-1	1.0E0
☐	INTERPRO	ATPase, P-type, phospholipid-translocating, flippase	RT		3	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid-translocating ATPase activity	RT		3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid transporter activity	RT		3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	aminophospholipid transporter activity	RT		3	9.0E-1	1.0E0
	Annotation Cluster 35	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	proteolysis	RT		54	2.1E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule catabolic process	RT		20	5.6E-1	1.0E0
☐	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	RT		9	5.6E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	RT		19	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein catabolic process	RT		19	6.2E-1	1.0E0
☐	INTERPRO	Proteasome, subunit alpha/beta	RT		9	6.3E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type peptidase activity	RT		9	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type endopeptidase activity	RT		9	6.4E-1	1.0E0
☐	GOTERM_CC_FAT	proteasome core complex	RT		9	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent protein catabolic process	RT		15	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	RT		15	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecule catabolic process	RT		22	6.5E-1	1.0E0
☐	INTERPRO	Proteasome, alpha-subunit, conserved site	RT		5	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	protein catabolic process	RT		21	7.1E-1	1.0E0
☐	INTERPRO	Proteasome, alpha and beta subunits	RT		8	7.2E-1	1.0E0
☐	GOTERM_CC_FAT	proteasome complex	RT		12	7.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	threonine protease	RT		4	7.9E-1	1.0E0
☐	GOTERM_CC_FAT	cytosol	RT		16	8.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	proteasome	RT		11	8.3E-1	9.9E-1
☐	KEGG_PATHWAY	Proteasome	RT		15	8.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	ubl conjugation pathway	RT		7	8.8E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001212:multicatalytic endopeptidase complex chain C9	RT		3	9.4E-1	1.0E0
	Annotation Cluster 36	Enrichment Score: 0.17	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Tetratricopeptide-like helical	RT		20	4.3E-1	1.0E0
☐	INTERPRO	Tetratricopeptide region	RT		15	5.7E-1	1.0E0
☐	INTERPRO	Tetratricopeptide repeat	RT		14	7.2E-1	1.0E0
☐	SMART	TPR	RT		14	7.4E-1	1.0E0
☐	INTERPRO	Tetratricopeptide TPR-1	RT		11	8.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	tpr repeat	RT		5	8.8E-1	9.9E-1
	Annotation Cluster 37	Enrichment Score: 0.16	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	metallopeptidase activity	RT		10	3.0E-1	1.0E0
☐	GOTERM_MF_FAT	metalloexopeptidase activity	RT		5	6.7E-1	1.0E0
☐	GOTERM_MF_FAT	exopeptidase activity	RT		7	7.1E-1	1.0E0

☐	GOTERM_MF_FAT	metallocarboxypeptidase activity	RT	3	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	carboxypeptidase activity	RT	3	8.0E-1	1.0E0
☐	INTERPRO	Peptidase M14, carboxypeptidase A	RT	3	9.0E-1	1.0E0
☐	SMART	Zn_pept	RT	3	9.0E-1	1.0E0
	Annotation Cluster 38	Enrichment Score: 0.16	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	translation factor activity, nucleic acid binding	RT	19	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	translation initiation factor activity	RT	15	6.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	Initiation factor	RT	11	7.6E-1	1.0E0
	Annotation Cluster 39	Enrichment Score: 0.16	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	alcohol biosynthetic process	RT	4	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	cellular carbohydrate biosynthetic process	RT	5	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	carbohydrate biosynthetic process	RT	5	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide biosynthetic process	RT	3	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	pyruvate metabolic process	RT	3	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	hexose biosynthetic process	RT	3	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	gluconeogenesis	RT	3	7.7E-1	1.0E0
	Annotation Cluster 40	Enrichment Score: 0.14	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	phosphorus metabolic process	RT	168	5.8E-1	1.0E0
☐	GOTERM_BP_FAT	phosphate metabolic process	RT	168	5.8E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorylation	RT	159	5.8E-1	1.0E0
☐	GOTERM_MF_FAT	nucleotide binding	RT	356	5.9E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid phosphorylation	RT	148	6.1E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleotide binding	RT	334	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	purine ribonucleotide binding	RT	328	7.1E-1	1.0E0
☐	GOTERM_MF_FAT	ribonucleotide binding	RT	328	7.1E-1	1.0E0
☐	GOTERM_MF_FAT	nucleoside binding	RT	306	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl nucleotide binding	RT	303	7.6E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleoside binding	RT	303	7.6E-1	1.0E0
☐	GOTERM_MF_FAT	ATP binding	RT	297	8.2E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT	297	8.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	atp-binding	RT	143	8.4E-1	9.9E-1
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT	150	8.5E-1	9.9E-1
☐	INTERPRO	Protein kinase, core	RT	147	8.5E-1	1.0E0
☐	GOTERM_MF_FAT	protein kinase activity	RT	150	8.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	kinase	RT	183	8.7E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase-related	RT	126	9.2E-1	1.0E0
	Annotation Cluster 41	Enrichment Score: 0.13	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	carboxylic acid biosynthetic process	RT	5	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	organic acid biosynthetic process	RT	5	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	cellular amino acid biosynthetic process	RT	3	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	amine biosynthetic process	RT	3	9.4E-1	1.0E0
	Annotation Cluster 42	Enrichment Score: 0.11	G	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	organelle membrane	RT	8	4.8E-1	1.0E0
☐	GOTERM_CC_FAT	membrane coat	RT	9	6.4E-1	1.0E0
☐	GOTERM_CC_FAT	coated membrane	RT	9	6.4E-1	1.0E0
☐	INTERPRO	Clathrin/coatomer adaptor, adaptin-like, N-terminal	RT	4	6.5E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus	RT	7	7.1E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle	RT	4	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle membrane	RT	4	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle membrane	RT	4	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle	RT	4	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle coat	RT	4	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic membrane-bounded vesicle	RT	4	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle part	RT	4	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle membrane	RT	4	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle	RT	4	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	membrane-bounded vesicle	RT	4	8.0E-1	1.0E0
		Golgi apparatus part	RT	5	8.0E-1	1.0E0

☐	GOTERM_CC_FAT					
☐	GOTERM_CC_FAT	transport vesicle membrane	RT	3	9.0E-1	1.0E0
☐	GOTERM_CC_FAT	transport vesicle	RT	3	9.0E-1	1.0E0
☐	GOTERM_CC_FAT	endomembrane system	RT	8	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	ER to Golgi vesicle-mediated transport	RT	3	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	Golgi vesicle transport	RT	3	9.4E-1	1.0E0
	Annotation Cluster 43	Enrichment Score: 0.11	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, C3HC4 RING-type	RT	22	4.7E-1	1.0E0
☐	INTERPRO	Zinc finger, RING-type	RT	39	6.3E-1	1.0E0
☐	SMART	RING	RT	39	6.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc-finger	RT	34	7.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	metal-binding	RT	55	8.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc	RT	46	8.3E-1	9.9E-1
☐	GOTERM_MF_FAT	metal ion binding	RT	142	8.5E-1	1.0E0
☐	GOTERM_MF_FAT	cation binding	RT	143	8.7E-1	1.0E0
☐	GOTERM_MF_FAT	ion binding	RT	143	8.7E-1	1.0E0
☐	GOTERM_MF_FAT	zinc ion binding	RT	80	9.5E-1	1.0E0
☐	GOTERM_MF_FAT	transition metal ion binding	RT	97	9.8E-1	1.0E0
	Annotation Cluster 44	Enrichment Score: 0.11	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core	RT	5	6.7E-1	1.0E0
☐	SMART	Sm	RT	5	6.8E-1	1.0E0
☐	INTERPRO	Like-Sm ribonucleoprotein, core	RT	6	8.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	viral nucleoprotein	RT	7	9.5E-1	1.0E0
	Annotation Cluster 45	Enrichment Score: 0.1	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	phosphatase activity	RT	25	7.4E-1	1.0E0
☐	GOTERM_BP_FAT	dephosphorylation	RT	9	7.6E-1	1.0E0
☐	GOTERM_MF_FAT	phosphoprotein phosphatase activity	RT	15	8.6E-1	1.0E0
	Annotation Cluster 46	Enrichment Score: 0.1	G 🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Ubiquitin mediated proteolysis	RT	9	2.4E-1	1.0E0
☐	INTERPRO	Ubiquitin-conjugating enzyme/RWD-like	RT	7	8.0E-1	1.0E0
☐	INTERPRO	Ubiquitin-conjugating enzyme, E2	RT	7	8.0E-1	1.0E0
☐	SMART	UBCc	RT	7	8.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	ubl conjugation pathway	RT	7	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	small conjugating protein ligase activity	RT	7	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	ubiquitin-protein ligase activity	RT	3	9.0E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001567:ubiquitin-protein ligase E2	RT	3	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-nitrogen bonds	RT	15	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	acid-amino acid ligase activity	RT	12	9.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	ligase	RT	26	9.8E-1	1.0E0
	Annotation Cluster 47	Enrichment Score: 0.1	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	M phase	RT	4	7.6E-1	1.0E0
☐	GOTERM_BP_FAT	cell cycle process	RT	4	7.6E-1	1.0E0
☐	GOTERM_BP_FAT	cell cycle phase	RT	4	7.6E-1	1.0E0
☐	GOTERM_BP_FAT	cell cycle	RT	4	9.2E-1	1.0E0
	Annotation Cluster 48	Enrichment Score: 0.1	G 🟩	Count	P_Value	Benjamini
☐	COG_ONTOLOGY	Defense mechanisms	RT	14	6.2E-1	9.9E-1
☐	INTERPRO	ABC transporter-like	RT	12	8.8E-1	1.0E0
☐	INTERPRO	ABC transporter, conserved site	RT	11	9.2E-1	1.0E0
	Annotation Cluster 49	Enrichment Score: 0.09	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Myb transcription factor	RT	3	8.0E-1	1.0E0
☐	INTERPRO	Myb-type HTH DNA-binding domain	RT	3	8.0E-1	1.0E0
☐	INTERPRO	SANT, DNA-binding	RT	6	8.0E-1	1.0E0
☐	SMART	SANT	RT	6	8.1E-1	1.0E0
☐	INTERPRO	Myb, DNA-binding	RT	3	9.0E-1	1.0E0
	Annotation Cluster 50	Enrichment Score: 0.09	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	AMP-dependent synthetase and ligase	RT	5	6.7E-1	1.0E0
☐	COG_ONTOLOGY	Lipid metabolism	RT	8	7.7E-1	9.9E-1
☐	GOTERM_MF_FAT	long-chain-fatty-acid-CoA ligase activity	RT	3	9.0E-1	1.0E0

☐	GOTERM_MF_FAT	fatty-acid ligase activity	RT			3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-sulfur bonds	RT			3	9.0E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 0.08		G	🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	DNA replication	RT			12	7.7E-1	1.0E0
☐	KEGG_PATHWAY	Mismatch repair	RT			8	8.1E-1	9.9E-1
☐	KEGG_PATHWAY	Nucleotide excision repair	RT			8	9.2E-1	1.0E0
	Annotation Cluster 52	Enrichment Score: 0.08		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	RT			9	5.6E-1	1.0E0
☐	INTERPRO	Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2, conserved site	RT			3	8.0E-1	1.0E0
☐	INTERPRO	Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2	RT			3	9.5E-1	1.0E0
☐	GOTERM_MF_FAT	ubiquitin thiolesterase activity	RT			3	9.5E-1	1.0E0
☐	GOTERM_MF_FAT	thiolester hydrolase activity	RT			3	9.9E-1	1.0E0
	Annotation Cluster 53	Enrichment Score: 0.07		G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	nucleotidyltransferase	RT			15	6.6E-1	1.0E0
☐	KEGG_PATHWAY	Pyrimidine metabolism	RT			19	7.2E-1	1.0E0
☐	KEGG_PATHWAY	Purine metabolism	RT			18	7.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	Transcription	RT			5	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	ribonucleoside binding	RT			3	8.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-directed rna polymerase	RT			7	9.2E-1	1.0E0
☐	GOTERM_BP_FAT	transcription	RT			12	9.4E-1	1.0E0
☐	KEGG_PATHWAY	RNA polymerase	RT			8	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	DNA-directed RNA polymerase activity	RT			10	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	RNA polymerase activity	RT			10	9.9E-1	1.0E0
	Annotation Cluster 54	Enrichment Score: 0.07		G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Ubiquitin supergroup	RT			7	8.0E-1	1.0E0
☐	INTERPRO	Ubiquitin	RT			4	8.8E-1	1.0E0
☐	SMART	UBQ	RT			4	8.9E-1	1.0E0
	Annotation Cluster 55	Enrichment Score: 0.06		G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	N-6 adenine-specific DNA methylase, conserved site	RT			4	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	one-carbon metabolic process	RT			6	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	methylation	RT			5	9.1E-1	1.0E0
☐	GOTERM_BP_FAT	biopolymer methylation	RT			3	9.4E-1	1.0E0
	Annotation Cluster 56	Enrichment Score: 0.06		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	protein serine/threonine kinase activity	RT			59	7.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	serine/threonine-protein kinase	RT			34	7.8E-1	1.0E0
☐	INTERPRO	Protein kinase, ATP binding site	RT			43	9.1E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase-related	RT			126	9.2E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase, active site	RT			46	9.4E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase	RT			29	9.5E-1	1.0E0
☐	SMART	S_TKc	RT			29	9.6E-1	1.0E0
	Annotation Cluster 57	Enrichment Score: 0.05		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	antioxidant activity	RT			5	6.7E-1	1.0E0
☐	INTERPRO	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	RT			4	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	cell redox homeostasis	RT			9	8.8E-1	1.0E0
☐	INTERPRO	Thioredoxin fold	RT			11	9.2E-1	1.0E0
☐	GOTERM_BP_FAT	cellular homeostasis	RT			9	9.2E-1	1.0E0
☐	INTERPRO	Thioredoxin, conserved site	RT			3	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	homeostatic process	RT			9	9.5E-1	1.0E0
☐	INTERPRO	Thioredoxin-like	RT			6	9.6E-1	1.0E0
☐	INTERPRO	Thioredoxin, core	RT			3	9.8E-1	1.0E0
	Annotation Cluster 58	Enrichment Score: 0.05		G	🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Ribosome	RT			37	8.5E-1	1.0E0
☐	GOTERM_CC_FAT	ribosome	RT			41	8.6E-1	1.0E0
☐	GOTERM_MF_FAT	structural constituent of ribosome	RT			37	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	translation	RT			58	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT			88	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	non-membrane-bounded organelle	RT			88	8.8E-1	1.0E0

☐	SP_PIR_KEYWORDS	ribosomal protein	RT		38	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	structural molecule activity	RT		44	9.1E-1	1.0E0
☐	GOTERM_CC_FAT	ribonucleoprotein complex	RT		50	9.9E-1	1.0E0
	Annotation Cluster 59	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	acetyltransferase activity	RT		6	8.0E-1	1.0E0
☐	INTERPRO	GCN5-related N-acetyltransferase	RT		5	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	N-acetyltransferase activity	RT		5	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	N-acyltransferase activity	RT		5	9.3E-1	1.0E0
☐	INTERPRO	Acyl-CoA N-acyltransferase	RT		4	9.8E-1	1.0E0
	Annotation Cluster 60	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	drug transport	RT		3	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	multidrug transport	RT		3	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	response to drug	RT		3	8.8E-1	1.0E0
☐	INTERPRO	Multi antimicrobial extrusion protein MatE	RT		3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	drug transporter activity	RT		3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	antiporter activity	RT		3	9.5E-1	1.0E0
	Annotation Cluster 61	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF000908:serine/threonine-protein phosphatase, conventional type	RT		5	7.7E-1	1.0E0
☐	GOTERM_MF_FAT	phosphoprotein phosphatase activity	RT		15	8.6E-1	1.0E0
☐	INTERPRO	Metallophosphoesterase	RT		11	8.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	iron	RT		10	9.2E-1	1.0E0
☐	INTERPRO	Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase	RT		7	9.5E-1	1.0E0
☐	SMART	PP2Ac	RT		7	9.6E-1	1.0E0
☐	GOTERM_MF_FAT	iron ion binding	RT		13	9.9E-1	1.0E0
	Annotation Cluster 62	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	GTPase activity	RT		9	8.8E-1	1.0E0
☐	INTERPRO	Translation elongation factor EFTu/EF1A, domain 2	RT		3	9.0E-1	1.0E0
☐	INTERPRO	Protein synthesis factor, GTP-binding	RT		4	9.4E-1	1.0E0
	Annotation Cluster 63	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	protein complex biogenesis	RT		7	8.3E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex assembly	RT		7	8.3E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein complex assembly	RT		6	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	protein polymerization	RT		4	9.2E-1	1.0E0
☐	INTERPRO	Tubulin	RT		4	9.4E-1	1.0E0
☐	INTERPRO	Tubulin, conserved site	RT		4	9.4E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, GTPase domain	RT		4	9.4E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002306:tubulin	RT		3	9.7E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, 2-layer sandwich domain	RT		3	9.8E-1	1.0E0
	Annotation Cluster 64	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	electron carrier activity	RT		13	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	metal cluster binding	RT		10	9.2E-1	1.0E0
☐	GOTERM_MF_FAT	iron-sulfur cluster binding	RT		10	9.2E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, subgroup	RT		4	9.7E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulpur binding domain	RT		4	9.7E-1	1.0E0
	Annotation Cluster 65	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Tyrosine protein kinase	RT		4	8.8E-1	1.0E0
☐	SMART	TyrKc	RT		4	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	protein tyrosine kinase activity	RT		11	9.9E-1	1.0E0
	Annotation Cluster 66	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	vitamin binding	RT		6	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	vitamin B6 binding	RT		5	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	pyridoxal phosphate binding	RT		5	9.3E-1	1.0E0
☐	INTERPRO	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	RT		4	9.4E-1	1.0E0
	Annotation Cluster 67	Enrichment Score: 0.03	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, C2H2-like	RT		9	9.2E-1	1.0E0
☐	SMART	ZnF_C2H2	RT		9	9.3E-1	1.0E0
☐	INTERPRO	Zinc finger, C2H2-type	RT		8	9.7E-1	1.0E0

	Annotation Cluster 68	Enrichment Score: 0.02	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	nucleoside-triphosphatase regulator activity RT	7	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	enzyme activator activity RT	5	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras protein signal transduction RT	4	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of small GTPase mediated signal transduction RT	4	9.5E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase regulator activity RT	5	9.6E-1	1.0E0
☐	GOTERM_MF_FAT	small GTPase regulator activity RT	5	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras GTPase activity RT	3	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase activator activity RT	3	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of GTPase activity RT	3	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of hydrolase activity RT	3	9.8E-1	1.0E0
	Annotation Cluster 69	Enrichment Score: 0.02	Count	P_Value	Benjamini
☐	INTERPRO	Anticodon-binding RT	3	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA metabolic process RT	21	8.1E-1	1.0E0
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II (G, H, P and S), conserved region RT	3	9.0E-1	1.0E0
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II, conserved region RT	4	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	Aminoacyl-tRNA synthetase RT	9	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA aminoacylation for protein translation RT	8	9.9E-1	1.0E0
☐	KEGG_PATHWAY	Aminoacyl-tRNA biosynthesis RT	8	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA aminoacylation RT	8	1.0E0	1.0E0
☐	GOTERM_BP_FAT	amino acid activation RT	8	1.0E0	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-oxygen bonds RT	9	1.0E0	1.0E0
☐	GOTERM_MF_FAT	aminoacyl-tRNA ligase activity RT	9	1.0E0	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming aminoacyl-tRNA and related compounds RT	9	1.0E0	1.0E0
	Annotation Cluster 70	Enrichment Score: 0.02	Count	P_Value	Benjamini
☐	INTERPRO	DNA-dependent ATPase MCM RT	3	9.5E-1	1.0E0
☐	SMART	MCM RT	3	9.5E-1	1.0E0
☐	INTERPRO	Nucleic acid-binding, OB-fold RT	9	9.7E-1	1.0E0
	Annotation Cluster 71	Enrichment Score: 0.02	Count	P_Value	Benjamini
☐	INTERPRO	Kelch repeat type 1 RT	3	9.5E-1	1.0E0
☐	SMART	Kelch RT	3	9.5E-1	1.0E0
☐	INTERPRO	Kelch-type beta propeller RT	3	9.8E-1	1.0E0
	Annotation Cluster 72	Enrichment Score: 0.01	Count	P_Value	Benjamini
☐	INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type RT	3	9.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	Rotamase RT	3	9.9E-1	1.0E0
☐	GOTERM_MF_FAT	cis-trans isomerase activity RT	3	9.9E-1	1.0E0
☐	GOTERM_MF_FAT	peptidyl-prolyl cis-trans isomerase activity RT	3	9.9E-1	1.0E0
	Annotation Cluster 73	Enrichment Score: 0.01	Count	P_Value	Benjamini
☐	INTERPRO	Chaperonin TCP-1, conserved site RT	4	9.7E-1	1.0E0
☐	INTERPRO	Chaperonin Cpn60/TCP-1 RT	4	9.7E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002584:molecular chaperone t-complex-type RT	3	9.9E-1	1.0E0
☐	INTERPRO	Chaperone, tailless complex polypeptide 1 RT	3	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	cytoplasm RT	7	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	Chaperone RT	4	1.0E0	1.0E0
☐	GOTERM_MF_FAT	unfolded protein binding RT	7	1.0E0	1.0E0
	Annotation Cluster 74	Enrichment Score: 0.01	Count	P_Value	Benjamini
☐	INTERPRO	Molecular chaperone, heat shock protein, Hsp40, DnaJ RT	3	9.8E-1	1.0E0
☐	INTERPRO	Heat shock protein DnaJ, N-terminal RT	3	9.9E-1	1.0E0
☐	GOTERM_MF_FAT	heat shock protein binding RT	3	9.9E-1	1.0E0
☐	SMART	DnaJ RT	3	9.9E-1	1.0E0
	Annotation Cluster 75	Enrichment Score: 0	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	ribonucleoprotein complex biogenesis RT	8	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	ribosome biogenesis RT	8	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA metabolic process RT	4	1.0E0	1.0E0
☐	GOTERM_BP_FAT	rRNA processing RT	4	1.0E0	1.0E0

212 terms were not clustered.

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

Functional Annotation Clustering

Help and Manual

Current Gene List: 3_Random4
Current Background: Giardia intestinalis
3000 DAVID IDs

Options **Classification Stringency** Medium

Rerun using options | Create Sublist

79 Cluster(s)

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	Annotation Cluster 1	Enrichment Score: 0.77		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	calcium ion binding	RT	32	2.7E-2	1.0E0
☐	GOTERM_MF_FAT	calcium-dependent phospholipid binding	RT	18	3.8E-2	1.0E0
☐	GOTERM_BP_FAT	cytoskeleton organization	RT	14	3.9E-2	1.0E0
☐	INTERPRO	Alpha giardin	RT	10	1.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	annexin	RT	12	2.4E-1	1.0E0
☐	INTERPRO	Annexin	RT	12	2.8E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid binding	RT	18	3.3E-1	1.0E0
☐	INTERPRO	Annexin repeat	RT	10	4.3E-1	1.0E0
☐	SMART	ANX	RT	10	4.3E-1	1.0E0
☐	GOTERM_MF_FAT	lipid binding	RT	21	6.3E-1	1.0E0
	Annotation Cluster 2	Enrichment Score: 0.74		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	protein kinase regulator activity	RT	7	1.2E-1	1.0E0
☐	GOTERM_MF_FAT	kinase regulator activity	RT	7	1.2E-1	1.0E0
☐	GOTERM_MF_FAT	cAMP-dependent protein kinase regulator activity	RT	4	4.2E-1	1.0E0
	Annotation Cluster 3	Enrichment Score: 0.57		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	cyclin	RT	9	1.2E-1	1.0E0
☐	INTERPRO	Cyclin, N-terminal	RT	6	2.1E-1	1.0E0
☐	INTERPRO	Cyclin-related	RT	6	2.1E-1	1.0E0
☐	INTERPRO	Cyclin	RT	5	3.1E-1	1.0E0
☐	SMART	CYCLIN	RT	5	3.1E-1	1.0E0
☐	INTERPRO	Cyclin, C-terminal	RT	3	8.0E-1	1.0E0
	Annotation Cluster 4	Enrichment Score: 0.54		Count	P_Value	Benjamini
☐	INTERPRO	Like-Sm ribonucleoprotein, core	RT	10	9.7E-2	1.0E0
☐	INTERPRO	Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core	RT	6	3.8E-1	1.0E0
☐	SMART	Sm	RT	6	3.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	viral nucleoprotein	RT	10	5.1E-1	1.0E0
	Annotation Cluster 5	Enrichment Score: 0.53		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	ank repeat	RT	181	2.1E-1	1.0E0
☐	SMART	ANK	RT	258	3.5E-1	1.0E0
☐	INTERPRO	Ankyrin	RT	258	3.5E-1	1.0E0
	Annotation Cluster 6	Enrichment Score: 0.48		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	RNA modification	RT	14	3.9E-2	1.0E0
☐	GOTERM_MF_FAT	pseudouridine synthase activity	RT	6	3.5E-1	1.0E0
☐	GOTERM_BP_FAT	pseudouridine synthesis	RT	6	3.6E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001430:tRNA_psdUrid_synth	RT	3	6.1E-1	1.0E0
☐	INTERPRO	Pseudouridine synthase I, TruA	RT	3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	intramolecular transferase activity	RT	7	6.8E-1	1.0E0
	Annotation Cluster 7	Enrichment Score: 0.47		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	protein serine/threonine kinase activity	RT	68	6.3E-2	1.0E0
☐	SP_PIR_KEYWORDS	kinase	RT	200	6.4E-2	1.0E0
☐	INTERPRO	Serine/threonine protein kinase, active site	RT	60	7.2E-2	1.0E0
☐	GOTERM_MF_FAT	protein kinase activity	RT	163	1.2E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid phosphorylation	RT	162	1.2E-1	1.0E0
☐	INTERPRO	Protein kinase, core	RT	162	2.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	serine/threonine-protein kinase	RT	39	2.3E-1	1.0E0

☐	GOTERM_BP_FAT	phosphorylation	RT		170	2.3E-1	1.0E0
☐	GOTERM_BP_FAT	phosphate metabolic process	RT		179	2.4E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorus metabolic process	RT		179	2.4E-1	1.0E0
☐	INTERPRO	Protein kinase, ATP binding site	RT		52	2.7E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase-related	RT		140	3.2E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase	RT		36	4.3E-1	1.0E0
☐	SMART	S_TKc	RT		36	4.3E-1	1.0E0
☐	GOTERM_MF_FAT	nucleoside binding	RT		301	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleoside binding	RT		298	6.7E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl nucleotide binding	RT		298	6.7E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT		294	6.7E-1	1.0E0
☐	GOTERM_MF_FAT	ATP binding	RT		294	6.7E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleotide binding	RT		320	8.4E-1	1.0E0
☐	GOTERM_MF_FAT	ribonucleotide binding	RT		316	8.5E-1	1.0E0
☐	GOTERM_MF_FAT	purine ribonucleotide binding	RT		316	8.5E-1	1.0E0
☐	GOTERM_MF_FAT	nucleotide binding	RT		340	8.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	atp-binding	RT		139	8.6E-1	9.9E-1
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT		142	9.5E-1	1.0E0
	Annotation Cluster 8	Enrichment Score: 0.39	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	nucleotide kinase activity	RT		5	2.8E-1	1.0E0
☐	GOTERM_MF_FAT	nucleobase, nucleoside, nucleotide kinase activity	RT		8	3.1E-1	1.0E0
☐	GOTERM_MF_FAT	phosphotransferase activity, phosphate group as acceptor	RT		6	3.5E-1	1.0E0
☐	GOTERM_MF_FAT	adenylate kinase activity	RT		3	6.0E-1	1.0E0
☐	INTERPRO	Adenylate kinase	RT		3	6.2E-1	1.0E0
	Annotation Cluster 9	Enrichment Score: 0.38	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT		29	2.2E-1	1.0E0
☐	INTERPRO	DEAD-like helicase, N-terminal	RT		29	2.2E-1	1.0E0
☐	SMART	DEXDc	RT		29	2.2E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, C-terminal	RT		29	2.9E-1	1.0E0
☐	SMART	HELICc	RT		29	2.9E-1	1.0E0
☐	GOTERM_MF_FAT	helicase activity	RT		34	3.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	helicase	RT		28	3.2E-1	1.0E0
☐	GOTERM_MF_FAT	purine NTP-dependent helicase activity	RT		23	5.2E-1	1.0E0
☐	GOTERM_MF_FAT	ATP-dependent helicase activity	RT		23	5.2E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT		18	6.5E-1	1.0E0
☐	INTERPRO	RNA helicase, DEAD-box type, Q motif	RT		10	7.6E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled	RT		34	9.6E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity	RT		45	9.8E-1	1.0E0
	Annotation Cluster 10	Enrichment Score: 0.37	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	microtubule organizing center	RT		4	4.2E-1	1.0E0
☐	GOTERM_CC_FAT	spindle	RT		4	4.2E-1	1.0E0
☐	GOTERM_CC_FAT	spindle pole	RT		4	4.2E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule cytoskeleton organization	RT		4	4.2E-1	1.0E0
☐	INTERPRO	Spc97/Spc98	RT		4	4.5E-1	1.0E0
	Annotation Cluster 11	Enrichment Score: 0.36	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	translational initiation	RT		9	2.3E-1	1.0E0
☐	GOTERM_MF_FAT	translation initiation factor activity	RT		16	4.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	Initiation factor	RT		12	5.6E-1	1.0E0
☐	GOTERM_MF_FAT	translation factor activity, nucleic acid binding	RT		19	6.0E-1	1.0E0
	Annotation Cluster 12	Enrichment Score: 0.33	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	RNA methylation	RT		5	2.9E-1	1.0E0
☐	INTERPRO	Ribosomal RNA methyltransferase RrmJ/FtsJ	RT		4	4.5E-1	1.0E0
☐	GOTERM_BP_FAT	biopolymer methylation	RT		5	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	methylation	RT		7	5.6E-1	1.0E0
☐	GOTERM_BP_FAT	one-carbon metabolic process	RT		7	6.9E-1	1.0E0
	Annotation Cluster 13	Enrichment Score: 0.32	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	EGF	RT		6	3.8E-1	1.0E0

☐	INTERPRO	EGF, extracellular	RT		15	4.9E-1	1.0E0
☐	INTERPRO	EGF-like, type 3	RT		20	5.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	egf-like domain	RT		11	5.4E-1	1.0E0
	Annotation Cluster 14	Enrichment Score: 0.32	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	RNA capping	RT		5	2.9E-1	1.0E0
☐	GOTERM_BP_FAT	mRNA metabolic process	RT		5	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	mRNA capping	RT		3	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	mRNA processing	RT		4	6.3E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 0.32	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	protein amino acid dephosphorylation	RT		10	2.7E-1	1.0E0
☐	GOTERM_MF_FAT	protein tyrosine/serine/threonine phosphatase activity	RT		5	2.8E-1	1.0E0
☐	INTERPRO	Dual specificity phosphatase, catalytic domain	RT		5	3.1E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase, dual specificity	RT		5	3.1E-1	1.0E0
☐	GOTERM_BP_FAT	dephosphorylation	RT		10	6.3E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase	RT		4	6.5E-1	1.0E0
☐	INTERPRO	Dual-specific/protein-tyrosine phosphatase, conserved region	RT		4	6.5E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase, active site	RT		4	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	protein tyrosine phosphatase activity	RT		4	8.7E-1	1.0E0
	Annotation Cluster 16	Enrichment Score: 0.3	G	🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Pyrimidine metabolism	RT		21	3.4E-1	1.0E0
☐	GOTERM_BP_FAT	transcription	RT		17	4.0E-1	1.0E0
☐	KEGG_PATHWAY	RNA polymerase	RT		12	4.1E-1	1.0E0
☐	GOTERM_MF_FAT	DNA-directed RNA polymerase activity	RT		15	4.3E-1	1.0E0
☐	GOTERM_MF_FAT	RNA polymerase activity	RT		15	5.3E-1	1.0E0
☐	KEGG_PATHWAY	Purine metabolism	RT		19	5.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-directed rna polymerase	RT		9	6.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotidyltransferase	RT		11	9.7E-1	1.0E0
	Annotation Cluster 17	Enrichment Score: 0.3	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	protein amino acid dephosphorylation	RT		10	2.7E-1	1.0E0
☐	GOTERM_MF_FAT	iron ion binding	RT		20	3.8E-1	1.0E0
☐	GOTERM_MF_FAT	phosphoprotein phosphatase activity	RT		18	4.1E-1	1.0E0
☐	GOTERM_MF_FAT	phosphatase activity	RT		27	4.4E-1	1.0E0
☐	INTERPRO	Metallophosphoesterase	RT		14	4.6E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF000908:serine/threonine-protein phosphatase, conventional type	RT		6	5.3E-1	1.0E0
☐	GOTERM_BP_FAT	dephosphorylation	RT		10	6.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	iron	RT		12	6.5E-1	9.9E-1
☐	INTERPRO	Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase	RT		9	7.4E-1	1.0E0
☐	SMART	PP2Ac	RT		9	7.5E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 0.29	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	tpr repeat	RT		7	4.0E-1	1.0E0
☐	INTERPRO	Tetratricopeptide region	RT		16	4.2E-1	1.0E0
☐	INTERPRO	Tetratricopeptide TPR-1	RT		13	5.3E-1	1.0E0
☐	INTERPRO	Tetratricopeptide repeat	RT		15	5.8E-1	1.0E0
☐	INTERPRO	Tetratricopeptide-like helical	RT		19	5.9E-1	1.0E0
☐	SMART	TPR	RT		15	5.9E-1	1.0E0
	Annotation Cluster 19	Enrichment Score: 0.28	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Furin-like repeat	RT		110	4.2E-1	1.0E0
☐	SMART	FU	RT		110	4.3E-1	1.0E0
☐	INTERPRO	Giardia variant-specific surface protein	RT		138	5.6E-1	1.0E0
☐	INTERPRO	EGF-like	RT		110	6.3E-1	1.0E0
☐	SMART	EGF	RT		110	6.4E-1	1.0E0
	Annotation Cluster 20	Enrichment Score: 0.27	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	purine nucleoside metabolic process	RT		4	4.2E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside metabolic process	RT		4	4.2E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside metabolic process	RT		5	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside metabolic process	RT		8	7.0E-1	1.0E0
	Annotation Cluster 21	Enrichment Score: 0.26	G	🟩	Count	P_Value	Benjamini

☐	INTERPRO	SANT, DNA-binding	RT	▮		8	3.4E-1	1.0E0
☐	SMART	SANT	RT	▮		8	3.4E-1	1.0E0
☐	INTERPRO	Myb, DNA-binding	RT	▮		4	6.5E-1	1.0E0
☐	INTERPRO	Myb transcription factor	RT	▮		3	8.0E-1	1.0E0
☐	INTERPRO	Myb-type HTH DNA-binding domain	RT	▮		3	8.0E-1	1.0E0
	Annotation Cluster 22	Enrichment Score: 0.26	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular response to stress	RT	▮		14	4.1E-1	1.0E0
☐	GOTERM_BP_FAT	DNA repair	RT	▮		13	4.9E-1	1.0E0
☐	GOTERM_BP_FAT	response to DNA damage stimulus	RT	▮		13	4.9E-1	1.0E0
☐	GOTERM_BP_FAT	DNA metabolic process	RT	▮		30	9.2E-1	1.0E0
	Annotation Cluster 23	Enrichment Score: 0.26	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Protein of unknown function DUF6, transmembrane	RT	▮		4	4.5E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF036436:UCP036436	RT	▮		3	6.1E-1	1.0E0
☐	INTERPRO	Uncharacterised conserved protein UCP036436, nucleotide-sugar transporter-related	RT	▮		3	6.2E-1	1.0E0
	Annotation Cluster 24	Enrichment Score: 0.25	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Radical SAM	RT	▮		4	4.5E-1	1.0E0
☐	INTERPRO	Elongator protein 3/MiaB/NifB	RT	▮		3	6.2E-1	1.0E0
☐	SMART	Elp3	RT	▮		3	6.2E-1	1.0E0
	Annotation Cluster 25	Enrichment Score: 0.25	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	nucleotide catabolic process	RT	▮		4	4.2E-1	1.0E0
☐	GOTERM_BP_FAT	nitrogen compound catabolic process	RT	▮		5	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide catabolic process	RT	▮		5	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid catabolic process	RT	▮		5	4.8E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF017316:phosphoesterase, C1039.02 type	RT	▮		3	6.1E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF017316:Pesterase_C1039	RT	▮		3	6.1E-1	1.0E0
☐	INTERPRO	5'-Nucleotidase and apyrase	RT	▮		3	6.2E-1	1.0E0
☐	INTERPRO	Predicted phosphoesterase, C1039.02 type	RT	▮		3	6.2E-1	1.0E0
☐	COG_ONTOLOGY	Nucleotide transport and metabolism	RT	▮		5	8.2E-1	1.0E0
	Annotation Cluster 26	Enrichment Score: 0.24	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	ribosome biogenesis	RT	▮		13	4.9E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoprotein complex biogenesis	RT	▮		13	4.9E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA processing	RT	▮		18	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA modification	RT	▮		3	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA metabolic process	RT	▮		8	7.0E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA processing	RT	▮		8	7.0E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 0.24	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	EGF-like, type 3	RT	▮		20	5.2E-1	1.0E0
☐	INTERPRO	EGF-like, laminin	RT	▮		16	6.1E-1	1.0E0
☐	SMART	EGF_Lam	RT	▮		16	6.1E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 0.23	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	pyridine nucleotide biosynthetic process	RT	▮		4	4.2E-1	1.0E0
☐	GOTERM_BP_FAT	pyridine nucleotide metabolic process	RT	▮		5	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	oxidoreduction coenzyme metabolic process	RT	▮		5	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	coenzyme metabolic process	RT	▮		7	5.6E-1	1.0E0
☐	GOTERM_BP_FAT	cofactor metabolic process	RT	▮		8	5.9E-1	1.0E0
☐	GOTERM_BP_FAT	NAD metabolic process	RT	▮		3	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	NAD biosynthetic process	RT	▮		3	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	nicotinamide nucleotide biosynthetic process	RT	▮		3	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	water-soluble vitamin biosynthetic process	RT	▮		4	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	vitamin metabolic process	RT	▮		4	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	secondary metabolic process	RT	▮		4	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	water-soluble vitamin metabolic process	RT	▮		4	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	nicotinamide metabolic process	RT	▮		4	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	nicotinamide nucleotide metabolic process	RT	▮		4	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	alkaloid metabolic process	RT	▮		4	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	cellular amide metabolic process	RT	▮		4	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	vitamin biosynthetic process	RT	▮		4	6.3E-1	1.0E0

☐	GOTERM_BP_FAT	coenzyme biosynthetic process	RT		5	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	cofactor biosynthetic process	RT		6	6.7E-1	1.0E0
	Annotation Cluster 29	Enrichment Score: 0.22	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	transmembrane	RT		18	5.8E-1	1.0E0
☐	INTERPRO	Amino acid transporter, transmembrane	RT		7	5.9E-1	1.0E0
☐	GOTERM_CC_FAT	integral to membrane	RT		38	6.0E-1	1.0E0
☐	GOTERM_CC_FAT	intrinsic to membrane	RT		38	6.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	membrane	RT		16	6.3E-1	9.9E-1
	Annotation Cluster 30	Enrichment Score: 0.21	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Protein phosphatase 2C, N-terminal	RT		5	5.1E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C-related	RT		5	5.1E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C	RT		5	5.1E-1	1.0E0
☐	SMART	PP2C_SIG	RT		5	5.1E-1	1.0E0
☐	SMART	PP2Cc	RT		5	5.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	magnesium	RT		8	5.8E-1	1.0E0
☐	GOTERM_CC_FAT	protein serine/threonine phosphatase complex	RT		5	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	magnesium ion binding	RT		9	7.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	protein phosphatase	RT		3	7.8E-1	9.9E-1
☐	GOTERM_MF_FAT	protein serine/threonine phosphatase activity	RT		3	7.8E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C, manganese/magnesium aspartate binding site	RT		3	8.0E-1	1.0E0
	Annotation Cluster 31	Enrichment Score: 0.21	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	lipase activity	RT		3	6.0E-1	1.0E0
☐	GOTERM_MF_FAT	triacylglycerol lipase activity	RT		3	6.0E-1	1.0E0
☐	INTERPRO	Lipase, class 3	RT		3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	carboxylesterase activity	RT		4	6.3E-1	1.0E0
	Annotation Cluster 32	Enrichment Score: 0.21	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Transcription	RT		6	5.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-directed rna polymerase	RT		9	6.0E-1	1.0E0
☐	INTERPRO	DNA-directed RNA polymerase, subunit 2	RT		3	6.2E-1	1.0E0
☐	INTERPRO	RNA polymerase, beta subunit, conserved site	RT		3	6.2E-1	1.0E0
☐	INTERPRO	DNA-directed RNA polymerase, subunit 2, domain 6	RT		3	6.2E-1	1.0E0
☐	INTERPRO	RNA polymerase Rpb2, domain 3	RT		3	6.2E-1	1.0E0
☐	INTERPRO	RNA polymerase, beta subunit, protrusion	RT		3	6.2E-1	1.0E0
☐	INTERPRO	RNA polymerase Rpb2, domain 7	RT		3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	ribonucleoside binding	RT		3	7.8E-1	1.0E0
	Annotation Cluster 33	Enrichment Score: 0.2	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	enzyme activator activity	RT		7	4.0E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of small GTPase mediated signal transduction	RT		7	4.1E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras protein signal transduction	RT		7	4.1E-1	1.0E0
☐	GOTERM_MF_FAT	nucleoside-triphosphatase regulator activity	RT		9	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of ARF protein signal transduction	RT		4	6.3E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase activator activity	RT		5	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras GTPase activity	RT		5	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase regulator activity	RT		7	6.8E-1	1.0E0
☐	GOTERM_MF_FAT	small GTPase regulator activity	RT		7	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of GTPase activity	RT		5	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of hydrolase activity	RT		5	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	Rab GTPase activator activity	RT		3	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	Ras GTPase activator activity	RT		3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Rab protein signal transduction	RT		3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Rab GTPase activity	RT		3	7.9E-1	1.0E0
	Annotation Cluster 34	Enrichment Score: 0.19	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	RNA processing	RT		28	4.7E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA processing	RT		18	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA processing	RT		10	7.3E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA metabolic process	RT		29	7.3E-1	1.0E0

☐	GOTERM_BP_FAT	tRNA metabolic process	RT		21	8.6E-1	1.0E0
	Annotation Cluster 35	Enrichment Score: 0.19	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	RNA recognition motif, RNP-1	RT		9	6.4E-1	1.0E0
☐	SMART	RRM	RT		9	6.5E-1	1.0E0
☐	INTERPRO	Nucleotide-binding, alpha-beta plait	RT		10	6.7E-1	1.0E0
	Annotation Cluster 36	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	antiporter activity	RT		5	4.8E-1	1.0E0
☐	GOTERM_MF_FAT	drug transporter activity	RT		4	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	drug transport	RT		4	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	response to drug	RT		4	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	multidrug transport	RT		4	6.3E-1	1.0E0
☐	INTERPRO	Multi antimicrobial extrusion protein MatE	RT		4	6.5E-1	1.0E0
☐	INTERPRO	Na+ driven multidrug efflux pump	RT		3	8.0E-1	1.0E0
☐	COG_ONTOLOGY	Defense mechanisms	RT		12	8.7E-1	1.0E0
	Annotation Cluster 37	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	hexose catabolic process	RT		9	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	alcohol catabolic process	RT		9	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide catabolic process	RT		9	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	cellular carbohydrate catabolic process	RT		9	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	glucose catabolic process	RT		9	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	carbohydrate catabolic process	RT		9	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	hexose metabolic process	RT		12	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	glucose metabolic process	RT		12	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	glycolysis	RT		7	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT		15	7.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	glycolysis	RT		4	7.7E-1	9.9E-1
☐	GOTERM_BP_FAT	monosaccharide metabolic process	RT		12	8.7E-1	1.0E0
	Annotation Cluster 38	Enrichment Score: 0.17	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	chromatin organization	RT		11	3.1E-1	1.0E0
☐	GOTERM_BP_FAT	chromosome organization	RT		13	3.8E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly or disassembly	RT		9	4.9E-1	1.0E0
☐	GOTERM_CC_FAT	chromatin	RT		8	5.8E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002052:histone H4	RT		3	6.1E-1	1.0E0
☐	INTERPRO	Histone H4	RT		3	6.2E-1	1.0E0
☐	SMART	H4	RT		3	6.2E-1	1.0E0
☐	INTERPRO	Histone-fold	RT		9	6.4E-1	1.0E0
☐	GOTERM_CC_FAT	nucleosome	RT		7	6.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	chromosomal protein	RT		7	6.8E-1	9.9E-1
☐	GOTERM_BP_FAT	protein-DNA complex assembly	RT		7	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly	RT		7	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	DNA packaging	RT		7	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome organization	RT		7	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome assembly	RT		7	6.9E-1	1.0E0
☐	GOTERM_CC_FAT	protein-DNA complex	RT		8	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex assembly	RT		14	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecular complex assembly	RT		15	7.1E-1	1.0E0
☐	INTERPRO	Histone core	RT		7	7.1E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex subunit organization	RT		14	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	chromosome	RT		15	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecular complex subunit organization	RT		15	7.7E-1	1.0E0
☐	INTERPRO	Histone H3	RT		3	8.0E-1	1.0E0
☐	SMART	H3	RT		3	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	chromosomal part	RT		9	8.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleosome core	RT		4	8.7E-1	9.9E-1
☐	SP_PIR_KEYWORDS	dna-binding	RT		18	8.8E-1	9.9E-1
☐	SP_PIR_KEYWORDS	nucleus	RT		17	9.1E-1	9.9E-1
	Annotation Cluster 39	Enrichment Score: 0.17	G	🟩	Count	P_Value	Benjamini

☐	INTERPRO	EF-Hand type	RT		12	5.0E-1	1.0E0
☐	INTERPRO	EF-HAND 2	RT		11	5.8E-1	1.0E0
☐	COG_ONTOLOGY	Signal transduction mechanisms / Cytoskeleton / Cell division and chromosome partitioning / General function prediction only	RT		5	7.0E-1	1.0E0
☐	INTERPRO	EF-HAND 1	RT		12	7.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	calcium	RT		9	7.1E-1	9.9E-1
☐	INTERPRO	Calcium-binding EF-hand	RT		7	7.1E-1	1.0E0
☐	SMART	EFh	RT		7	7.2E-1	1.0E0
☐	INTERPRO	EF hand	RT		6	8.8E-1	1.0E0
	Annotation Cluster 40	Enrichment Score: 0.17	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	protein biosynthesis	RT		7	5.5E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001525:lysine-tRNA ligase	RT		3	6.1E-1	1.0E0
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II (D, K and N)	RT		3	6.2E-1	1.0E0
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II (D, K and N)-like	RT		3	6.2E-1	1.0E0
☐	INTERPRO	Nucleic acid binding, OB-fold, tRNA/helicase-type	RT		3	8.0E-1	1.0E0
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II, conserved region	RT		4	9.7E-1	1.0E0
	Annotation Cluster 41	Enrichment Score: 0.17	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	dipeptidase	RT		3	6.0E-1	9.9E-1
☐	GOTERM_MF_FAT	dipeptidase activity	RT		3	6.0E-1	1.0E0
☐	GOTERM_MF_FAT	exopeptidase activity	RT		7	6.8E-1	1.0E0
☐	GOTERM_MF_FAT	metallopeptidase activity	RT		8	6.9E-1	1.0E0
☐	GOTERM_MF_FAT	metalloexopeptidase activity	RT		4	8.7E-1	1.0E0
	Annotation Cluster 42	Enrichment Score: 0.16	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	cation binding	RT		149	4.2E-1	1.0E0
☐	GOTERM_MF_FAT	ion binding	RT		149	4.2E-1	1.0E0
☐	GOTERM_MF_FAT	metal ion binding	RT		146	4.9E-1	1.0E0
☐	INTERPRO	Zinc finger, C3HC4 RING-type	RT		21	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	transition metal ion binding	RT		103	7.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc-finger	RT		33	8.0E-1	9.9E-1
☐	INTERPRO	Zinc finger, RING-type	RT		37	8.1E-1	1.0E0
☐	SMART	RING	RT		37	8.2E-1	1.0E0
☐	GOTERM_MF_FAT	zinc ion binding	RT		80	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc	RT		42	9.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	metal-binding	RT		50	9.6E-1	1.0E0
	Annotation Cluster 43	Enrichment Score: 0.16	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	fatty-acid ligase activity	RT		4	6.3E-1	1.0E0
☐	GOTERM_MF_FAT	long-chain-fatty-acid-CoA ligase activity	RT		4	6.3E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-sulfur bonds	RT		4	6.3E-1	1.0E0
☐	COG_ONTOLOGY	Lipid metabolism	RT		8	7.5E-1	1.0E0
☐	INTERPRO	AMP-dependent synthetase and ligase	RT		4	8.9E-1	1.0E0
	Annotation Cluster 44	Enrichment Score: 0.14	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	heme	RT		4	6.3E-1	9.9E-1
☐	GOTERM_MF_FAT	heme binding	RT		5	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	tetrapyrrole binding	RT		5	6.5E-1	1.0E0
☐	INTERPRO	Cytochrome b5, heme-binding site	RT		3	8.0E-1	1.0E0
☐	INTERPRO	Cytochrome b5	RT		3	9.0E-1	1.0E0
	Annotation Cluster 45	Enrichment Score: 0.14	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, C2H2-like	RT		11	6.9E-1	1.0E0
☐	SMART	ZnF_C2H2	RT		11	6.9E-1	1.0E0
☐	INTERPRO	Zinc finger, C2H2-type	RT		10	8.3E-1	1.0E0
	Annotation Cluster 46	Enrichment Score: 0.13	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	acetyltransferase activity	RT		7	5.5E-1	1.0E0
☐	GOTERM_MF_FAT	N-acetyltransferase activity	RT		6	6.6E-1	1.0E0
☐	INTERPRO	GCN5-related N-acetyltransferase	RT		6	7.0E-1	1.0E0
☐	GOTERM_MF_FAT	N-acyltransferase activity	RT		6	7.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	Acyltransferase	RT		6	8.6E-1	1.0E0
☐	INTERPRO	Acyl-CoA N-acyltransferase	RT		5	9.3E-1	1.0E0

	Annotation Cluster 47	Enrichment Score: 0.13	G	Count	P_Value	Benjamini
☐	INTERPRO	Ubiquitin-conjugating enzyme, E2	RT	9	3.9E-1	1.0E0
☐	INTERPRO	Ubiquitin-conjugating enzyme/RWD-like	RT	9	3.9E-1	1.0E0
☐	SMART	UBCc	RT	9	3.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	ligase	RT	33	4.7E-1	1.0E0
☐	GOTERM_MF_FAT	acid-amino acid ligase activity	RT	17	4.8E-1	1.0E0
☐	GOTERM_MF_FAT	small conjugating protein ligase activity	RT	9	4.8E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-nitrogen bonds	RT	19	6.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	ubl conjugation pathway	RT	8	6.9E-1	9.9E-1
☐	GOTERM_CC_FAT	proteasome complex	RT	12	7.4E-1	1.0E0
☐	GOTERM_CC_FAT	cytosol	RT	16	7.8E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001567:ubiquitin-protein ligase E2	RT	4	7.8E-1	1.0E0
☐	KEGG_PATHWAY	Proteasome	RT	15	8.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	proteasome	RT	11	8.0E-1	9.9E-1
☐	GOTERM_BP_FAT	macromolecule catabolic process	RT	21	8.2E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent protein catabolic process	RT	14	8.3E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	RT	14	8.3E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule catabolic process	RT	18	8.5E-1	1.0E0
☐	GOTERM_BP_FAT	protein catabolic process	RT	20	8.6E-1	1.0E0
☐	INTERPRO	Proteasome, alpha and beta subunits	RT	7	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	RT	17	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein catabolic process	RT	17	8.8E-1	1.0E0
☐	INTERPRO	Proteasome, alpha-subunit, conserved site	RT	4	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	ubiquitin-protein ligase activity	RT	3	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type peptidase activity	RT	7	9.1E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type endopeptidase activity	RT	7	9.1E-1	1.0E0
☐	GOTERM_CC_FAT	proteasome core complex	RT	7	9.1E-1	1.0E0
☐	INTERPRO	Proteasome, subunit alpha/beta	RT	7	9.2E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis	RT	45	9.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	threonine protease	RT	3	9.4E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001212:multicatalytic endopeptidase complex chain C9	RT	3	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	RT	6	9.7E-1	1.0E0
	Annotation Cluster 48	Enrichment Score: 0.13	G	Count	P_Value	Benjamini
☐	INTERPRO	von Willebrand factor, type A	RT	5	6.8E-1	1.0E0
☐	SMART	VWA	RT	5	6.8E-1	1.0E0
☐	INTERPRO	Copine	RT	3	9.0E-1	1.0E0
	Annotation Cluster 49	Enrichment Score: 0.13	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cell redox homeostasis	RT	11	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	homeostatic process	RT	12	6.6E-1	1.0E0
☐	INTERPRO	Thioredoxin fold	RT	13	7.2E-1	1.0E0
☐	GOTERM_BP_FAT	cellular homeostasis	RT	11	7.4E-1	1.0E0
☐	INTERPRO	Thioredoxin-like	RT	7	8.8E-1	1.0E0
☐	INTERPRO	Thioredoxin, core	RT	4	8.9E-1	1.0E0
	Annotation Cluster 50	Enrichment Score: 0.12	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	electron carrier activity	RT	14	6.0E-1	1.0E0
☐	GOTERM_MF_FAT	iron-sulfur cluster binding	RT	12	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	metal cluster binding	RT	12	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	4 iron, 4 sulfur cluster binding	RT	5	7.7E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulpur binding domain	RT	5	8.8E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, subgroup	RT	5	8.8E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, conserved site	RT	4	8.9E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 0.12	G	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	coated membrane	RT	10	3.8E-1	1.0E0
☐	GOTERM_CC_FAT	membrane coat	RT	10	3.8E-1	1.0E0
☐	GOTERM_CC_FAT	transport vesicle membrane	RT	4	6.2E-1	1.0E0
☐	GOTERM_CC_FAT	transport vesicle	RT	4	6.2E-1	1.0E0

☐	GOTERM_BP_FAT	vesicle-mediated transport	RT			17	6.6E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus part	RT			5	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	membrane-bounded vesicle	RT			4	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle	RT			4	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle part	RT			4	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic membrane-bounded vesicle	RT			4	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle membrane	RT			4	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle	RT			4	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle membrane	RT			4	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle membrane	RT			4	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle	RT			4	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle coat	RT			4	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	Golgi vesicle transport	RT			4	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	ER to Golgi vesicle-mediated transport	RT			4	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	ER to Golgi transport vesicle membrane	RT			3	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	ER to Golgi transport vesicle	RT			3	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	COPII vesicle coat	RT			3	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	endomembrane system	RT			9	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular transport	RT			15	8.3E-1	1.0E0
☐	GOTERM_BP_FAT	protein localization	RT			18	8.5E-1	1.0E0
☐	GOTERM_CC_FAT	organelle membrane	RT			6	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular protein transport	RT			12	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule localization	RT			12	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein localization	RT			12	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	establishment of protein localization	RT			17	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	protein transport	RT			17	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus	RT			5	9.5E-1	1.0E0
	Annotation Cluster 52	Enrichment Score: 0.12	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	endoribonuclease activity	RT			4	6.3E-1	1.0E0
☐	GOTERM_MF_FAT	ribonuclease activity	RT			6	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	endoribonuclease activity, producing 5'-phosphomonoesters	RT			3	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	RT			4	8.7E-1	1.0E0
	Annotation Cluster 53	Enrichment Score: 0.12	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	CDP-alcohol phosphatidyltransferase	RT			3	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid biosynthetic process	RT			5	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	phosphotransferase activity, for other substituted phosphate groups	RT			3	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid metabolic process	RT			7	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	organophosphate metabolic process	RT			7	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	lipid biosynthetic process	RT			7	9.1E-1	1.0E0
	Annotation Cluster 54	Enrichment Score: 0.12	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	RT			6	5.5E-1	1.0E0
☐	INTERPRO	Aminotransferase, class V/Cysteine desulfurase	RT			3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	vitamin binding	RT			7	6.8E-1	1.0E0
☐	GOTERM_MF_FAT	pyridoxal phosphate binding	RT			6	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	vitamin B6 binding	RT			6	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	transferase activity, transferring nitrogenous groups	RT			4	8.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	Aminotransferase	RT			3	8.9E-1	9.9E-1
☐	GOTERM_MF_FAT	transaminase activity	RT			3	8.9E-1	1.0E0
☐	INTERPRO	Aminotransferase, class I and II	RT			3	9.0E-1	1.0E0
	Annotation Cluster 55	Enrichment Score: 0.1	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	secretion by cell	RT			3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	vesicle docking	RT			3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	membrane docking	RT			3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	vesicle docking during exocytosis	RT			3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	secretion	RT			3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	exocytosis	RT			3	7.9E-1	1.0E0

☐	**INTERPRO**	Sec1-like protein	RT			3	8.0E-1	1.0E0
	Annotation Cluster 56	Enrichment Score: 0.09		G	🟩	Count	P_Value	Benjamini
☐	**KEGG_PATHWAY**	Ribosome	RT			38	6.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	translation	RT			62	7.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	ribosomal protein	RT			39	8.0E-1	9.9E-1
☐	**GOTERM_CC_FAT**	ribonucleoprotein complex	RT			54	8.1E-1	1.0E0
☐	**GOTERM_MF_FAT**	structural constituent of ribosome	RT			37	8.2E-1	1.0E0
☐	**GOTERM_CC_FAT**	ribosome	RT			40	8.6E-1	1.0E0
☐	**GOTERM_MF_FAT**	structural molecule activity	RT			44	8.6E-1	1.0E0
☐	**GOTERM_CC_FAT**	intracellular non-membrane-bounded organelle	RT			85	9.1E-1	1.0E0
☐	**GOTERM_CC_FAT**	non-membrane-bounded organelle	RT			85	9.1E-1	1.0E0
	Annotation Cluster 57	Enrichment Score: 0.08		G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	Endonuclease	RT			17	7.2E-1	9.9E-1
☐	**GOTERM_MF_FAT**	endonuclease activity	RT			19	7.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	rna-directed dna polymerase	RT			13	7.5E-1	9.9E-1
☐	**GOTERM_MF_FAT**	RNA-directed DNA polymerase activity	RT			13	8.1E-1	1.0E0
☐	**GOTERM_MF_FAT**	nuclease activity	RT			25	9.2E-1	1.0E0
☐	**GOTERM_MF_FAT**	nucleotidyltransferase activity	RT			36	9.4E-1	1.0E0
☐	**GOTERM_MF_FAT**	DNA polymerase activity	RT			15	9.8E-1	1.0E0
	Annotation Cluster 58	Enrichment Score: 0.07		G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	transmembrane transport	RT			14	4.1E-1	1.0E0
☐	**GOTERM_CC_FAT**	proton-transporting two-sector ATPase complex, proton-transporting domain	RT			5	4.8E-1	1.0E0
☐	**GOTERM_CC_FAT**	proton-transporting V-type ATPase, V0 domain	RT			4	6.2E-1	1.0E0
☐	**GOTERM_BP_FAT**	monovalent inorganic cation transport	RT			10	6.3E-1	1.0E0
☐	**GOTERM_CC_FAT**	proton-transporting V-type ATPase complex	RT			6	6.6E-1	1.0E0
☐	**KEGG_PATHWAY**	Oxidative phosphorylation	RT			8	6.6E-1	9.9E-1
☐	**GOTERM_BP_FAT**	ion transport	RT			14	6.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	cation transport	RT			14	6.9E-1	1.0E0
☐	**GOTERM_CC_FAT**	proton-transporting two-sector ATPase complex	RT			9	7.1E-1	1.0E0
☐	**GOTERM_BP_FAT**	generation of precursor metabolites and energy	RT			15	7.1E-1	1.0E0
☐	**GOTERM_MF_FAT**	magnesium ion binding	RT			9	7.1E-1	1.0E0
☐	**GOTERM_BP_FAT**	hydrogen transport	RT			9	7.1E-1	1.0E0
☐	**GOTERM_BP_FAT**	proton transport	RT			9	7.1E-1	1.0E0
☐	**GOTERM_BP_FAT**	nucleobase, nucleoside and nucleotide biosynthetic process	RT			23	7.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	RT			23	7.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	phospholipid transport	RT			3	7.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	ion transmembrane transport	RT			8	7.9E-1	1.0E0
☐	**INTERPRO**	ATPase, P-type, phospholipid-translocating, flippase	RT			3	8.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	nucleotide biosynthetic process	RT			21	8.2E-1	1.0E0
☐	**GOTERM_BP_FAT**	purine nucleotide metabolic process	RT			16	8.4E-1	1.0E0
☐	**GOTERM_MF_FAT**	hydrogen ion transmembrane transporter activity	RT			8	8.6E-1	1.0E0
☐	**GOTERM_MF_FAT**	monovalent inorganic cation transmembrane transporter activity	RT			8	8.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	oxidative phosphorylation	RT			7	8.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	ATP synthesis coupled proton transport	RT			7	8.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	energy coupled proton transport, down electrochemical gradient	RT			7	8.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	purine nucleotide biosynthetic process	RT			15	8.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	ion transport	RT			3	8.9E-1	9.9E-1
☐	**GOTERM_MF_FAT**	phospholipid-translocating ATPase activity	RT			3	8.9E-1	1.0E0
☐	**GOTERM_MF_FAT**	aminophospholipid transporter activity	RT			3	8.9E-1	1.0E0
☐	**GOTERM_MF_FAT**	phospholipid transporter activity	RT			3	8.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	lipid transport	RT			3	8.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	lipid localization	RT			3	8.9E-1	1.0E0
☐	**GOTERM_MF_FAT**	inorganic cation transmembrane transporter activity	RT			9	9.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	nitrogen compound biosynthetic process	RT			25	9.1E-1	1.0E0
☐	**GOTERM_BP_FAT**	purine ribonucleotide metabolic process	RT			14	9.1E-1	1.0E0

☐	GOTERM_BP_FAT	purine ribonucleotide biosynthetic process	RT	14	9.1E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide metabolic process	RT	14	9.1E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide biosynthetic process	RT	14	9.1E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside triphosphate metabolic process	RT	13	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside triphosphate biosynthetic process	RT	13	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside triphosphate metabolic process	RT	13	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside triphosphate biosynthetic process	RT	13	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate metabolic process	RT	13	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate biosynthetic process	RT	13	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside triphosphate metabolic process	RT	13	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside triphosphate biosynthetic process	RT	13	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	ATP metabolic process	RT	12	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	ATP biosynthetic process	RT	12	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	lipid transporter activity	RT	3	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	5	9.7E-1	1.0E0
☐	INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT	5	9.8E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, catalytic domain	RT	3	9.9E-1	1.0E0
☐	INTERPRO	ATPase, P-type phosphorylation site	RT	3	9.9E-1	1.0E0
☐	INTERPRO	ATPase, P-type, ATPase-associated region	RT	4	9.9E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions	RT	7	1.0E0	1.0E0
☐	GOTERM_MF_FAT	cation-transporting ATPase activity	RT	3	1.0E0	1.0E0
☐	GOTERM_MF_FAT	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT	11	1.0E0	1.0E0
☐	GOTERM_MF_FAT	primary active transmembrane transporter activity	RT	10	1.0E0	1.0E0
☐	GOTERM_MF_FAT	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT	10	1.0E0	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to movement of substances	RT	9	1.0E0	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of substances	RT	9	1.0E0	1.0E0
	Annotation Cluster 59	Enrichment Score: 0.07	G	Count	P_Value	Benjamini
☐	COG_ONTOLOGY	Lipid metabolism	RT	8	7.5E-1	1.0E0
☐	INTERPRO	Phospholipid/glycerol acyltransferase	RT	3	9.0E-1	1.0E0
☐	SMART	PlsC	RT	3	9.0E-1	1.0E0
	Annotation Cluster 60	Enrichment Score: 0.06	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	protein biosynthesis	RT	7	5.5E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA metabolic process	RT	29	7.3E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA metabolic process	RT	21	8.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	Aminoacyl-tRNA synthetase	RT	12	8.6E-1	9.9E-1
☐	INTERPRO	Aminoacyl-tRNA synthetase, class I, conserved site	RT	5	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-oxygen bonds	RT	12	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	aminoacyl-tRNA ligase activity	RT	12	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming aminoacyl-tRNA and related compounds	RT	12	9.0E-1	1.0E0
☐	KEGG_PATHWAY	Aminoacyl-tRNA biosynthesis	RT	10	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA aminoacylation	RT	11	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	amino acid activation	RT	11	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA aminoacylation for protein translation	RT	10	9.6E-1	1.0E0
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II, conserved region	RT	4	9.7E-1	1.0E0
	Annotation Cluster 61	Enrichment Score: 0.06	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Protease	RT	20	7.5E-1	9.9E-1
☐	SP_PIR_KEYWORDS	thiol protease	RT	6	7.8E-1	9.9E-1
☐	GOTERM_MF_FAT	peptidase activity	RT	42	8.5E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain C-terminal	RT	14	9.0E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain	RT	14	9.0E-1	1.0E0
☐	SMART	Pept_C1	RT	14	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	peptidase activity, acting on L-amino acid peptides	RT	35	9.0E-1	1.0E0

☐	GOTERM_MF_FAT	cysteine-type endopeptidase activity	RT			12	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type peptidase activity	RT			15	9.1E-1	1.0E0
☐	GOTERM_MF_FAT	endopeptidase activity	RT			23	9.2E-1	1.0E0
☐	INTERPRO	Peptidase, cysteine peptidase active site	RT			15	9.3E-1	1.0E0
	Annotation Cluster 62	Enrichment Score: 0.06		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	negative regulation of gene expression	RT			4	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of macromolecule metabolic process	RT			4	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	gene silencing	RT			4	8.7E-1	1.0E0
	Annotation Cluster 63	Enrichment Score: 0.06		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular carbohydrate biosynthetic process	RT			4	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	carbohydrate biosynthetic process	RT			4	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	alcohol biosynthetic process	RT			3	8.9E-1	1.0E0
	Annotation Cluster 64	Enrichment Score: 0.06		G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Thioredoxin, conserved site	RT			4	8.0E-1	1.0E0
☐	INTERPRO	Thioredoxin-like	RT			7	8.8E-1	1.0E0
☐	INTERPRO	Thioredoxin-like subdomain	RT			3	9.0E-1	1.0E0
☐	INTERPRO	Thioredoxin domain	RT			3	9.5E-1	1.0E0
	Annotation Cluster 65	Enrichment Score: 0.06		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	cytoskeleton	RT			29	8.2E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based process	RT			29	8.3E-1	1.0E0
☐	INTERPRO	Kinesin, motor region, conserved site	RT			10	8.3E-1	1.0E0
☐	INTERPRO	Kinesin, motor region	RT			15	8.6E-1	1.0E0
☐	SMART	KISc	RT			15	8.6E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule	RT			17	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule cytoskeleton	RT			27	8.9E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeletal part	RT			27	8.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	motor protein	RT			12	9.0E-1	9.9E-1
☐	SP_PIR_KEYWORDS	microtubule	RT			16	9.1E-1	9.9E-1
☐	GOTERM_MF_FAT	motor activity	RT			21	9.2E-1	1.0E0
☐	GOTERM_MF_FAT	microtubule motor activity	RT			21	9.2E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based movement	RT			23	9.5E-1	1.0E0
	Annotation Cluster 66	Enrichment Score: 0.05		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	intracellular organelle lumen	RT			3	8.9E-1	1.0E0
☐	GOTERM_CC_FAT	membrane-enclosed lumen	RT			3	8.9E-1	1.0E0
☐	GOTERM_CC_FAT	nuclear lumen	RT			3	8.9E-1	1.0E0
☐	GOTERM_CC_FAT	organelle lumen	RT			3	8.9E-1	1.0E0
	Annotation Cluster 67	Enrichment Score: 0.05		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	structure-specific DNA binding	RT			3	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	double-stranded DNA binding	RT			3	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	mismatched DNA binding	RT			3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	mismatch repair	RT			3	8.9E-1	1.0E0
	Annotation Cluster 68	Enrichment Score: 0.05		G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	WD40 repeat	RT			41	8.1E-1	1.0E0
☐	SMART	WD40	RT			41	8.1E-1	1.0E0
☐	INTERPRO	WD40/YVTN repeat-like	RT			39	8.6E-1	1.0E0
☐	INTERPRO	WD40 repeat, conserved site	RT			15	9.0E-1	1.0E0
☐	INTERPRO	WD40 repeat, subgroup	RT			29	9.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	wd repeat	RT			24	9.4E-1	1.0E0
☐	INTERPRO	WD40 repeat 2	RT			21	9.6E-1	1.0E0
☐	INTERPRO	WD40 repeat, region	RT			23	9.6E-1	1.0E0
	Annotation Cluster 69	Enrichment Score: 0.05		G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	ABC transporter, conserved site	RT			12	8.4E-1	1.0E0
☐	COG_ONTOLOGY	Defense mechanisms	RT			12	8.7E-1	1.0E0
☐	INTERPRO	ABC transporter-like	RT			10	9.8E-1	1.0E0
	Annotation Cluster 70	Enrichment Score: 0.05		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	antioxidant activity	RT			4	8.7E-1	1.0E0
☐	INTERPRO	Thioredoxin-like	RT			7	8.8E-1	1.0E0
☐	INTERPRO	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	RT			3	9.5E-1	1.0E0
	Annotation Cluster 71	Enrichment Score: 0.05		G	🟩	Count	P_Value	Benjamini

☐	GOTERM_BP_FAT	cell cycle	RT	5	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	M phase	RT	3	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	cell cycle phase	RT	3	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	cell cycle process	RT	3	9.4E-1	1.0E0
	Annotation Cluster 72	Enrichment Score: 0.04	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	phospholipid metabolic process	RT	7	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	organophosphate metabolic process	RT	7	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	glycerophospholipid metabolic process	RT	3	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	phosphoinositide metabolic process	RT	3	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	glycerolipid metabolic process	RT	3	9.7E-1	1.0E0
	Annotation Cluster 73	Enrichment Score: 0.04	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT	9	8.0E-1	1.0E0
☐	INTERPRO	ADP-ribosylation factor	RT	3	8.0E-1	1.0E0
☐	SMART	ARF	RT	3	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular signaling cascade	RT	11	8.7E-1	1.0E0
☐	INTERPRO	ARF/SAR superfamily	RT	4	8.9E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001711:ADP-ribosylation factor	RT	3	8.9E-1	1.0E0
☐	INTERPRO	Ras GTPase	RT	6	9.6E-1	1.0E0
☐	GOTERM_MF_FAT	guanyl ribonucleotide binding	RT	22	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	GTP binding	RT	22	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	guanyl nucleotide binding	RT	22	9.8E-1	1.0E0
☐	INTERPRO	Ras	RT	5	9.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	gtp-binding	RT	17	9.9E-1	1.0E0
☐	INTERPRO	Small GTP-binding protein	RT	8	9.9E-1	1.0E0
	Annotation Cluster 74	Enrichment Score: 0.03	G 🟩	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF002306:tubulin	RT	4	8.8E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, 2-layer sandwich domain	RT	4	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	protein polymerization	RT	4	9.3E-1	1.0E0
☐	INTERPRO	Tubulin	RT	4	9.4E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, GTPase domain	RT	4	9.4E-1	1.0E0
☐	INTERPRO	Tubulin, conserved site	RT	4	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex assembly	RT	6	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex biogenesis	RT	6	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein complex assembly	RT	5	9.6E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase activity	RT	7	9.8E-1	1.0E0
	Annotation Cluster 75	Enrichment Score: 0.02	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	26S proteasome subunit P45	RT	3	9.0E-1	1.0E0
☐	INTERPRO	ATPase, AAA-type, conserved site	RT	6	9.8E-1	1.0E0
☐	INTERPRO	ATPase, AAA-type, core	RT	9	1.0E0	1.0E0
	Annotation Cluster 76	Enrichment Score: 0.01	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Chaperonin TCP-1, conserved site	RT	4	9.7E-1	1.0E0
☐	INTERPRO	Chaperonin Cpn60/TCP-1	RT	4	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	Chaperone	RT	5	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	unfolded protein binding	RT	9	9.8E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002584:molecular chaperone t-complex-type	RT	3	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	cytoplasm	RT	7	9.9E-1	1.0E0
☐	INTERPRO	Chaperone, tailless complex polypeptide 1	RT	3	9.9E-1	1.0E0
	Annotation Cluster 77	Enrichment Score: 0.01	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	dynein complex	RT	5	9.7E-1	1.0E0
☐	INTERPRO	Dynein heavy chain	RT	5	9.8E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule associated complex	RT	6	9.8E-1	1.0E0
	Annotation Cluster 78	Enrichment Score: 0.01	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Molecular chaperone, heat shock protein, Hsp40, DnaJ	RT	3	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	heat shock protein binding	RT	3	9.9E-1	1.0E0
☐	INTERPRO	Heat shock protein DnaJ, N-terminal	RT	3	9.9E-1	1.0E0
☐	SMART	DnaJ	RT	3	9.9E-1	1.0E0
	Annotation Cluster 79	Enrichment Score: 0.01	G 🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Rotamase	RT	3	9.9E-1	1.0E0

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

Functional Annotation Clustering

Help and Manual

Current Gene List: 3_Random5
Current Background: Giardia intestinalis
3000 DAVID IDs

Options **Classification Stringency** Medium

Rerun using options | Create Sublist

84 Cluster(s)

Download File

	Annotation Cluster 1	Enrichment Score: 0.8	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	ATPase, AAA+ type, core	RT		48	1.0E-1	1.0E0
☐	**SMART**	AAA	RT		48	1.1E-1	1.0E0
☐	**INTERPRO**	ATPase, AAA-type, core	RT		17	3.5E-1	1.0E0
	Annotation Cluster 2	Enrichment Score: 0.67	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	endonuclease activity	RT		26	5.1E-2	1.0E0
☐	**GOTERM_MF_FAT**	nuclease activity	RT		34	1.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	nucleotidyltransferase activity	RT		47	2.1E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Endonuclease	RT		21	2.6E-1	1.0E0
☐	**GOTERM_MF_FAT**	RNA-directed DNA polymerase activity	RT		17	2.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	rna-directed dna polymerase	RT		16	3.6E-1	1.0E0
☐	**GOTERM_MF_FAT**	DNA polymerase activity	RT		22	4.2E-1	1.0E0
	Annotation Cluster 3	Enrichment Score: 0.62	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Annexin	RT		13	1.3E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	annexin	RT		13	1.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	calcium ion binding	RT		30	1.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	lipid binding	RT		25	2.1E-1	1.0E0
☐	**INTERPRO**	Annexin repeat	RT		11	2.3E-1	1.0E0
☐	**SMART**	ANX	RT		11	2.4E-1	1.0E0
☐	**GOTERM_MF_FAT**	phospholipid binding	RT		19	2.6E-1	1.0E0
☐	**INTERPRO**	Alpha giardin	RT		9	3.9E-1	1.0E0
☐	**GOTERM_MF_FAT**	calcium-dependent phospholipid binding	RT		15	4.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	cytoskeleton organization	RT		11	4.6E-1	1.0E0
	Annotation Cluster 4	Enrichment Score: 0.57	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Chaperonin TCP-1, conserved site	RT		8	2.0E-1	1.0E0
☐	**INTERPRO**	Chaperonin Cpn60/TCP-1	RT		8	2.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Chaperone	RT		10	2.1E-1	1.0E0
☐	**INTERPRO**	Chaperone, tailless complex polypeptide 1	RT		7	2.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	unfolded protein binding	RT		15	3.0E-1	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF002584:molecular chaperone t-complex-type	RT		7	3.2E-1	1.0E0
☐	**GOTERM_BP_FAT**	protein folding	RT		20	3.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	cytoplasm	RT		13	3.5E-1	1.0E0
	Annotation Cluster 5	Enrichment Score: 0.55	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	WD40 repeat, conserved site	RT		21	1.6E-1	1.0E0
☐	**INTERPRO**	WD40 repeat, subgroup	RT		37	2.1E-1	1.0E0
☐	**INTERPRO**	WD40 repeat 2	RT		29	2.2E-1	1.0E0
☐	**INTERPRO**	WD40 repeat	RT		47	2.8E-1	1.0E0
☐	**SMART**	WD40	RT		47	3.1E-1	1.0E0
☐	**INTERPRO**	WD40/YVTN repeat-like	RT		45	3.5E-1	1.0E0
☐	**INTERPRO**	WD40 repeat, region	RT		30	3.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	wd repeat	RT		31	4.4E-1	1.0E0
	Annotation Cluster 6	Enrichment Score: 0.51	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	protein serine/threonine kinase activity	RT		69	8.7E-2	1.0E0
☐	**INTERPRO**	Serine/threonine protein kinase, active site	RT		58	1.5E-1	1.0E0
☐	**INTERPRO**	Serine/threonine protein kinase	RT		36	4.2E-1	1.0E0
☐	**SMART**	S_TKc	RT		36	4.5E-1	1.0E0

☐	**SP_PIR_KEYWORDS**	serine/threonine-protein kinase	RT	38	4.6E-1	1.0E0
☐	**INTERPRO**	Protein kinase, ATP binding site	RT	46	7.7E-1	1.0E0
	Annotation Cluster 7	Enrichment Score: 0.5		Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	negative regulation of macromolecule metabolic process	RT	7	1.3E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of gene expression	RT	7	1.3E-1	1.0E0
☐	**GOTERM_BP_FAT**	gene silencing	RT	7	1.3E-1	1.0E0
☐	**GOTERM_BP_FAT**	protein amino acid deacetylation	RT	6	2.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of RNA metabolic process	RT	5	3.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	chromatin silencing	RT	5	3.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of cellular biosynthetic process	RT	5	3.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of nitrogen compound metabolic process	RT	5	3.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of biosynthetic process	RT	5	3.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of gene expression, epigenetic	RT	5	3.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of macromolecule biosynthetic process	RT	5	3.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	5	3.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of transcription	RT	5	3.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of gene expression, epigenetic	RT	5	3.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of transcription, DNA-dependent	RT	5	3.0E-1	1.0E0
☐	**INTERPRO**	NAD-dependent histone deacetylase, silent information regulator Sir2	RT	5	3.1E-1	1.0E0
☐	**GOTERM_MF_FAT**	NAD binding	RT	5	3.1E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of transcription	RT	20	4.2E-1	1.0E0
☐	**GOTERM_MF_FAT**	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	RT	6	5.6E-1	1.0E0
☐	**GOTERM_MF_FAT**	NAD or NADH binding	RT	6	5.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of transcription, DNA-dependent	RT	8	6.1E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of RNA metabolic process	RT	8	6.1E-1	1.0E0
☐	**GOTERM_MF_FAT**	coenzyme binding	RT	13	9.0E-1	1.0E0
	Annotation Cluster 8	Enrichment Score: 0.45		Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	cellular response to stress	RT	15	2.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	response to DNA damage stimulus	RT	14	3.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	DNA repair	RT	14	3.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	DNA metabolic process	RT	36	4.7E-1	1.0E0
	Annotation Cluster 9	Enrichment Score: 0.44		Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	ubl conjugation pathway	RT	11	1.5E-1	1.0E0
☐	**GOTERM_BP_FAT**	modification-dependent macromolecule catabolic process	RT	19	1.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	modification-dependent protein catabolic process	RT	19	1.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	proteolysis involved in cellular protein catabolic process	RT	23	2.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	cellular protein catabolic process	RT	23	2.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	protein catabolic process	RT	26	2.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	cellular macromolecule catabolic process	RT	23	2.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	macromolecule catabolic process	RT	26	2.7E-1	1.0E0
☐	**GOTERM_BP_FAT**	proteolysis	RT	55	2.9E-1	1.0E0
☐	**KEGG_PATHWAY**	Ubiquitin mediated proteolysis	RT	8	5.0E-1	9.8E-1
☐	**PIR_SUPERFAMILY**	PIRSF001567:ubiquitin-protein ligase E2	RT	5	5.5E-1	1.0E0
☐	**INTERPRO**	Ubiquitin-conjugating enzyme, E2	RT	8	6.2E-1	1.0E0
☐	**INTERPRO**	Ubiquitin-conjugating enzyme/RWD-like	RT	8	6.2E-1	1.0E0
☐	**SMART**	UBCc	RT	8	6.3E-1	1.0E0
☐	**GOTERM_BP_FAT**	ubiquitin-dependent protein catabolic process	RT	9	6.3E-1	1.0E0
☐	**GOTERM_MF_FAT**	acid-amino acid ligase activity	RT	16	7.0E-1	1.0E0
☐	**GOTERM_MF_FAT**	small conjugating protein ligase activity	RT	8	7.4E-1	1.0E0
☐	**GOTERM_MF_FAT**	ligase activity, forming carbon-nitrogen bonds	RT	17	8.8E-1	1.0E0
	Annotation Cluster 10	Enrichment Score: 0.43		Count	P_Value	Benjamini
☐	**INTERPRO**	Ankyrin	RT	260	2.6E-1	1.0E0
☐	**SMART**	ANK	RT	260	3.3E-1	1.0E0

☐	**SP_PIR_KEYWORDS**	ank repeat	RT			180	6.0E-1	1.0E0
	Annotation Cluster 11	Enrichment Score: 0.4	G		🟩	Count	P_Value	Benjamini
☐	**KEGG_PATHWAY**	Nucleotide excision repair	RT	▮		12	2.9E-1	1.0E0
☐	**KEGG_PATHWAY**	Mismatch repair	RT	▮		10	4.5E-1	1.0E0
☐	**KEGG_PATHWAY**	DNA replication	RT	▮		14	4.8E-1	9.9E-1
	Annotation Cluster 12	Enrichment Score: 0.39	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	small GTPase regulator activity	RT	▮		9	2.6E-1	1.0E0
☐	**GOTERM_MF_FAT**	GTPase regulator activity	RT	▮		9	2.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of GTPase activity	RT	▮		7	2.7E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of hydrolase activity	RT	▮		7	2.7E-1	1.0E0
☐	**GOTERM_MF_FAT**	nucleoside-triphosphatase regulator activity	RT	▮		10	3.1E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of Ras GTPase activity	RT	▮		6	3.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	GTPase activator activity	RT	▮		6	3.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of Ras protein signal transduction	RT	▮		7	4.3E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of small GTPase mediated signal transduction	RT	▮		7	4.3E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of Rab GTPase activity	RT	▮		4	4.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of Rab protein signal transduction	RT	▮		4	4.4E-1	1.0E0
☐	**GOTERM_MF_FAT**	enzyme activator activity	RT	▮		7	4.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	Rab GTPase activator activity	RT	▮		4	4.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	Ras GTPase activator activity	RT	▮		4	4.5E-1	1.0E0
☐	**INTERPRO**	RabGAP/TBC	RT	▮		3	6.2E-1	1.0E0
☐	**SMART**	TBC	RT	▮		3	6.3E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of ARF protein signal transduction	RT	▮		3	9.0E-1	1.0E0
	Annotation Cluster 13	Enrichment Score: 0.37	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	RT	▮		7	1.4E-1	1.0E0
☐	**GOTERM_MF_FAT**	endoribonuclease activity, producing 5'-phosphomonoesters	RT	▮		4	4.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	endoribonuclease activity	RT	▮		4	6.6E-1	1.0E0
☐	**GOTERM_MF_FAT**	ribonuclease activity	RT	▮		6	8.1E-1	1.0E0
	Annotation Cluster 14	Enrichment Score: 0.35	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Alcohol dehydrogenase, iron-type	RT	▮		5	3.1E-1	1.0E0
☐	**COG_ONTOLOGY**	Energy production and conversion	RT	▮		7	4.6E-1	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF000113:iron-containing alcohol dehydrogenase	RT	▮		3	6.5E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 0.32	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	vitamin binding	RT	▮		9	2.6E-1	1.0E0
☐	**GOTERM_MF_FAT**	vitamin B6 binding	RT	▮		8	3.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	pyridoxal phosphate binding	RT	▮		8	3.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	transferase activity, transferring nitrogenous groups	RT	▮		6	3.9E-1	1.0E0
☐	**INTERPRO**	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	RT	▮		6	5.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	cofactor binding	RT	▮		21	6.4E-1	1.0E0
☐	**INTERPRO**	Aminotransferase, class I and II	RT	▮		4	6.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	transaminase activity	RT	▮		4	6.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Aminotransferase	RT	▮		4	6.7E-1	1.0E0
	Annotation Cluster 16	Enrichment Score: 0.31	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	RNA polymerase activity	RT	▮		17	2.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	DNA-directed RNA polymerase activity	RT	▮		16	3.4E-1	1.0E0
☐	**KEGG_PATHWAY**	RNA polymerase	RT	▮		13	3.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	transcription	RT	▮		17	4.3E-1	1.0E0
☐	**KEGG_PATHWAY**	Purine metabolism	RT	▮		20	5.6E-1	9.8E-1
☐	**SP_PIR_KEYWORDS**	nucleotidyltransferase	RT	▮		15	7.0E-1	9.9E-1
☐	**KEGG_PATHWAY**	Pyrimidine metabolism	RT	▮		19	7.7E-1	9.9E-1
☐	**SP_PIR_KEYWORDS**	dna-directed rna polymerase	RT	▮		8	8.3E-1	9.9E-1
	Annotation Cluster 17	Enrichment Score: 0.29	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Small GTP-binding protein	RT	▮		15	2.0E-1	1.0E0
☐	**INTERPRO**	Ras	RT	▮		9	3.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	intracellular signaling cascade	RT	▮		14	4.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	guanyl nucleotide binding	RT	▮		30	4.6E-1	1.0E0
	GOTERM_MF_FAT	GTP binding	RT	▮		30	4.6E-1	1.0E0

☐						
☐	GOTERM_MF_FAT	guanyl ribonucleotide binding	RT	30	4.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	gtp-binding	RT	25	5.2E-1	1.0E0
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT	10	6.6E-1	1.0E0
☐	INTERPRO	Ras GTPase	RT	8	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase activity	RT	10	7.7E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001710:Ras-related protein Rab	RT	3	9.6E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 0.28	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	thiolester hydrolase activity	RT	7	2.9E-1	1.0E0
☐	INTERPRO	Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2	RT	5	5.1E-1	1.0E0
☐	GOTERM_MF_FAT	ubiquitin thiolesterase activity	RT	5	5.2E-1	1.0E0
☐	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	RT	9	6.3E-1	1.0E0
☐	INTERPRO	Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2, conserved site	RT	3	8.0E-1	1.0E0
	Annotation Cluster 19	Enrichment Score: 0.28	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	RT	7	1.4E-1	1.0E0
☐	INTERPRO	Deoxyribonuclease, TatD Mg-dependent	RT	3	6.2E-1	1.0E0
☐	INTERPRO	Deoxyribonuclease, TatD-related	RT	3	6.2E-1	1.0E0
☐	INTERPRO	Deoxyribonuclease, TatD	RT	3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	deoxyribonuclease activity	RT	3	6.3E-1	1.0E0
☐	GOTERM_MF_FAT	endodeoxyribonuclease activity, producing 5'-phosphomonoesters	RT	3	6.3E-1	1.0E0
☐	GOTERM_MF_FAT	endodeoxyribonuclease activity	RT	3	6.3E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF005902:DNase_TatD	RT	3	6.5E-1	1.0E0
	Annotation Cluster 20	Enrichment Score: 0.27	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	protein serine/threonine kinase activity	RT	69	8.7E-2	1.0E0
☐	INTERPRO	Serine/threonine protein kinase, active site	RT	58	1.5E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase-related	RT	137	4.7E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorus metabolic process	RT	177	4.7E-1	1.0E0
☐	GOTERM_BP_FAT	phosphate metabolic process	RT	177	4.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT	161	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorylation	RT	167	5.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	atp-binding	RT	152	5.5E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid phosphorylation	RT	155	5.7E-1	1.0E0
☐	INTERPRO	Protein kinase, core	RT	153	6.3E-1	1.0E0
☐	GOTERM_MF_FAT	purine ribonucleotide binding	RT	332	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	ribonucleotide binding	RT	332	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	protein kinase activity	RT	156	6.7E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleotide binding	RT	335	7.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	kinase	RT	191	7.2E-1	9.9E-1
☐	GOTERM_MF_FAT	ATP binding	RT	302	7.2E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT	302	7.2E-1	1.0E0
☐	GOTERM_MF_FAT	nucleotide binding	RT	354	7.6E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleoside binding	RT	305	7.6E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl nucleotide binding	RT	305	7.6E-1	1.0E0
☐	GOTERM_MF_FAT	nucleoside binding	RT	306	8.1E-1	1.0E0
	Annotation Cluster 21	Enrichment Score: 0.26	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Ribosomal protein L7A/RS6 family	RT	4	4.4E-1	1.0E0
☐	INTERPRO	Ribosomal protein L7Ae/L30e/S12e/Gadd45	RT	5	5.1E-1	1.0E0
☐	INTERPRO	High mobility group-like nuclear protein	RT	3	6.2E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002165:ribosomal protein, L7Ab/L7Aa/L7Ae/L8e types/H/ACA ribonucleoprotein complex, NHP2 subunit	RT	3	6.5E-1	1.0E0
	Annotation Cluster 22	Enrichment Score: 0.24	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Dual specificity phosphatase, catalytic domain	RT	5	3.1E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase, dual specificity	RT	5	3.1E-1	1.0E0
☐	GOTERM_MF_FAT	protein tyrosine/serine/threonine phosphatase activity	RT	5	3.1E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid dephosphorylation	RT	9	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	dephosphorylation	RT	10	6.6E-1	1.0E0

☐	GOTERM_MF_FAT	protein tyrosine phosphatase activity	RT	▮		4	8.9E-1	1.0E0
☐	INTERPRO	Dual-specific/protein-tyrosine phosphatase, conserved region	RT	▮		3	9.0E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase	RT	▮		3	9.0E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase, active site	RT	▮		3	9.5E-1	1.0E0
	Annotation Cluster 23	Enrichment Score: 0.24	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	transcription regulator activity	RT	▮		8	4.9E-1	1.0E0
☐	INTERPRO	Zinc finger, TFIIS-type	RT	▮		3	6.2E-1	1.0E0
☐	SMART	ZnF_C2C2	RT	▮		3	6.3E-1	1.0E0
	Annotation Cluster 24	Enrichment Score: 0.24	G		🟩	Count	P_Value	Benjamini
☐	COG_ONTOLOGY	Defense mechanisms	RT	▮		15	4.2E-1	1.0E0
☐	INTERPRO	ABC transporter-like	RT	▮		14	6.5E-1	1.0E0
☐	INTERPRO	ABC transporter, conserved site	RT	▮		13	7.2E-1	1.0E0
	Annotation Cluster 25	Enrichment Score: 0.24	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Acyltransferase	RT	▮		9	2.8E-1	1.0E0
☐	GOTERM_MF_FAT	acetyltransferase activity	RT	▮		7	6.0E-1	1.0E0
☐	GOTERM_MF_FAT	N-acyltransferase activity	RT	▮		7	6.0E-1	1.0E0
☐	INTERPRO	GCN5-related N-acetyltransferase	RT	▮		6	6.9E-1	1.0E0
☐	GOTERM_MF_FAT	N-acetyltransferase activity	RT	▮		6	7.0E-1	1.0E0
☐	INTERPRO	Acyl-CoA N-acyltransferase	RT	▮		6	8.0E-1	1.0E0
	Annotation Cluster 26	Enrichment Score: 0.23	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	pore complex	RT	▮		4	5.7E-1	1.0E0
☐	GOTERM_CC_FAT	nuclear pore	RT	▮		4	5.7E-1	1.0E0
☐	GOTERM_CC_FAT	nuclear envelope	RT	▮		4	5.7E-1	1.0E0
☐	GOTERM_CC_FAT	envelope	RT	▮		4	5.7E-1	1.0E0
☐	GOTERM_CC_FAT	organelle envelope	RT	▮		4	5.7E-1	1.0E0
☐	GOTERM_CC_FAT	endomembrane system	RT	▮		9	7.1E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 0.23	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	ribosome	RT	▮		44	2.8E-1	1.0E0
☐	GOTERM_CC_FAT	ribonucleoprotein complex	RT	▮		55	4.7E-1	1.0E0
☐	GOTERM_BP_FAT	translation	RT	▮		66	5.3E-1	1.0E0
☐	KEGG_PATHWAY	Ribosome	RT	▮		40	6.7E-1	9.8E-1
☐	GOTERM_MF_FAT	structural constituent of ribosome	RT	▮		40	6.9E-1	1.0E0
☐	GOTERM_CC_FAT	non-membrane-bounded organelle	RT	▮		84	7.0E-1	1.0E0
☐	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT	▮		84	7.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	ribosomal protein	RT	▮		42	7.0E-1	9.9E-1
☐	GOTERM_MF_FAT	structural molecule activity	RT	▮		46	8.3E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 0.22	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	coenzyme metabolic process	RT	▮		8	3.3E-1	1.0E0
☐	GOTERM_BP_FAT	coenzyme biosynthetic process	RT	▮		6	3.8E-1	1.0E0
☐	GOTERM_BP_FAT	cofactor metabolic process	RT	▮		9	3.8E-1	1.0E0
☐	GOTERM_BP_FAT	cofactor biosynthetic process	RT	▮		7	4.3E-1	1.0E0
☐	GOTERM_BP_FAT	pyridine nucleotide metabolic process	RT	▮		5	5.0E-1	1.0E0
☐	GOTERM_BP_FAT	oxidoreduction coenzyme metabolic process	RT	▮		5	5.0E-1	1.0E0
☐	GOTERM_BP_FAT	cellular amide metabolic process	RT	▮		4	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	nicotinamide metabolic process	RT	▮		4	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	alkaloid metabolic process	RT	▮		4	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	secondary metabolic process	RT	▮		4	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	nicotinamide nucleotide metabolic process	RT	▮		4	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	pyridine nucleotide biosynthetic process	RT	▮		3	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	water-soluble vitamin metabolic process	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	water-soluble vitamin biosynthetic process	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	vitamin metabolic process	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	vitamin biosynthetic process	RT	▮		3	9.0E-1	1.0E0
	Annotation Cluster 29	Enrichment Score: 0.22	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Translation elongation factor EFTu/EF1A, domain 2	RT	▮		5	3.1E-1	1.0E0
☐	INTERPRO	Protein synthesis factor, GTP-binding	RT	▮		6	5.5E-1	1.0E0
☐	GOTERM_BP_FAT	translational elongation	RT	▮		5	6.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	elongation factor	RT	▮		5	6.9E-1	1.0E0

☐	GOTERM_MF_FAT	GTPase activity	RT		10	7.7E-1	1.0E0
☐	GOTERM_MF_FAT	translation elongation factor activity	RT		5	8.0E-1	1.0E0
	Annotation Cluster 30	Enrichment Score: 0.2	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	translation factor activity, nucleic acid binding	RT		21	4.0E-1	1.0E0
☐	GOTERM_MF_FAT	translation initiation factor activity	RT		15	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	translational initiation	RT		7	7.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	Initiation factor	RT		11	7.9E-1	9.9E-1
	Annotation Cluster 31	Enrichment Score: 0.2	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Lecithin	RT		3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	phosphatidylcholine-sterol O-acyltransferase activity	RT		3	6.3E-1	1.0E0
☐	GOTERM_MF_FAT	O-acyltransferase activity	RT		3	6.3E-1	1.0E0
	Annotation Cluster 32	Enrichment Score: 0.2	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Cyclin-related	RT		5	5.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	cyclin	RT		7	6.1E-1	9.9E-1
☐	INTERPRO	Cyclin, N-terminal	RT		4	7.9E-1	1.0E0
	Annotation Cluster 33	Enrichment Score: 0.2	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	phosphotransferase activity, for other substituted phosphate groups	RT		4	4.5E-1	1.0E0
☐	GOTERM_BP_FAT	organophosphate metabolic process	RT		9	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid metabolic process	RT		8	6.1E-1	1.0E0
☐	INTERPRO	CDP-alcohol phosphatidyltransferase	RT		3	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	lipid biosynthetic process	RT		8	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid biosynthetic process	RT		4	8.8E-1	1.0E0
	Annotation Cluster 34	Enrichment Score: 0.19	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Thioredoxin, conserved site	RT		6	2.1E-1	1.0E0
☐	INTERPRO	Thioredoxin-like	RT		9	5.2E-1	1.0E0
☐	INTERPRO	Thioredoxin-like subdomain	RT		4	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	antioxidant activity	RT		5	6.8E-1	1.0E0
☐	INTERPRO	Thioredoxin fold	RT		13	7.2E-1	1.0E0
☐	INTERPRO	Thioredoxin domain	RT		4	7.9E-1	1.0E0
☐	INTERPRO	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	RT		4	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	cell redox homeostasis	RT		10	8.2E-1	1.0E0
☐	GOTERM_BP_FAT	homeostatic process	RT		11	8.3E-1	1.0E0
☐	GOTERM_BP_FAT	cellular homeostasis	RT		10	8.8E-1	1.0E0
	Annotation Cluster 35	Enrichment Score: 0.19	G	🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Terpenoid backbone biosynthesis	RT		5	5.2E-1	9.8E-1
☐	GOTERM_BP_FAT	isoprenoid biosynthetic process	RT		4	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	isoprenoid metabolic process	RT		4	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	lipid biosynthetic process	RT		8	8.1E-1	1.0E0
	Annotation Cluster 36	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Phox-like	RT		4	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	phosphoinositide binding	RT		4	6.6E-1	1.0E0
☐	SMART	PX	RT		4	6.6E-1	1.0E0
	Annotation Cluster 37	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	intracellular transport	RT		18	4.6E-1	1.0E0
☐	INTERPRO	Clathrin adaptor, sigma subunit/coatomer, zeta subunit	RT		3	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein localization	RT		14	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular protein transport	RT		14	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule localization	RT		14	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	protein localization	RT		20	6.7E-1	1.0E0
☐	GOTERM_CC_FAT	membrane coat	RT		8	7.1E-1	1.0E0
☐	GOTERM_CC_FAT	coated membrane	RT		8	7.1E-1	1.0E0
☐	GOTERM_BP_FAT	protein transport	RT		19	7.2E-1	1.0E0
☐	GOTERM_BP_FAT	establishment of protein localization	RT		19	7.2E-1	1.0E0
☐	GOTERM_BP_FAT	vesicle-mediated transport	RT		16	8.1E-1	1.0E0
	Annotation Cluster 38	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	EGF-like, laminin	RT		16	6.0E-1	1.0E0
☐	SMART	EGF_Lam	RT		16	6.2E-1	1.0E0
☐	INTERPRO	EGF-like, type 3	RT		18	7.8E-1	1.0E0

	Annotation Cluster 39	Enrichment Score: 0.18		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	metal ion binding	RT	154	3.0E-1	1.0E0
☐	GOTERM_MF_FAT	ion binding	RT	154	4.0E-1	1.0E0
☐	GOTERM_MF_FAT	cation binding	RT	154	4.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc	RT	49	6.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	metal-binding	RT	57	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	transition metal ion binding	RT	106	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	zinc ion binding	RT	85	8.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc-finger	RT	34	8.3E-1	9.9E-1
☐	INTERPRO	Zinc finger, RING-type	RT	35	9.1E-1	1.0E0
☐	SMART	RING	RT	35	9.3E-1	1.0E0
☐	INTERPRO	Zinc finger, C3HC4 RING-type	RT	15	9.9E-1	1.0E0

	Annotation Cluster 40	Enrichment Score: 0.17		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	lipid transport	RT	5	3.0E-1	1.0E0
☐	GOTERM_BP_FAT	lipid localization	RT	5	3.0E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, proton-transporting domain	RT	5	4.1E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid transport	RT	4	4.4E-1	1.0E0
☐	INTERPRO	ATPase, P-type, phospholipid-translocating, flippase	RT	4	4.4E-1	1.0E0
☐	GOTERM_MF_FAT	lipid transporter activity	RT	5	5.2E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside triphosphate metabolic process	RT	17	5.3E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside triphosphate metabolic process	RT	17	5.3E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside triphosphate biosynthetic process	RT	17	5.3E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate metabolic process	RT	17	5.3E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate biosynthetic process	RT	17	5.3E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside triphosphate metabolic process	RT	17	5.3E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside triphosphate biosynthetic process	RT	17	5.3E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside triphosphate biosynthetic process	RT	17	5.3E-1	1.0E0
☐	GOTERM_MF_FAT	magnesium ion binding	RT	10	5.7E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting V-type ATPase, V0 domain	RT	4	5.7E-1	1.0E0
☐	GOTERM_BP_FAT	ion transport	RT	15	5.7E-1	1.0E0
☐	GOTERM_BP_FAT	cation transport	RT	15	5.7E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide biosynthetic process	RT	25	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	RT	25	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleotide biosynthetic process	RT	17	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleotide metabolic process	RT	17	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide metabolic process	RT	17	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide biosynthetic process	RT	17	6.1E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex	RT	9	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	transmembrane transport	RT	13	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	ion transmembrane transport	RT	9	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	nucleotide biosynthetic process	RT	23	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	monovalent inorganic cation transport	RT	10	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid-translocating ATPase activity	RT	4	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid transporter activity	RT	4	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	aminophospholipid transporter activity	RT	4	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	ATP metabolic process	RT	15	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	ATP biosynthetic process	RT	15	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleotide biosynthetic process	RT	17	6.9E-1	1.0E0
☐	INTERPRO	ATPase, P-type, ATPase-associated region	RT	7	7.1E-1	1.0E0
☐	GOTERM_BP_FAT	oxidative phosphorylation	RT	8	7.2E-1	1.0E0
☐	GOTERM_BP_FAT	ATP synthesis coupled proton transport	RT	8	7.2E-1	1.0E0
☐	GOTERM_BP_FAT	energy coupled proton transport, down electrochemical gradient	RT	8	7.2E-1	1.0E0
☐	GOTERM_BP_FAT	hydrogen transport	RT	9	7.4E-1	1.0E0
☐	GOTERM_BP_FAT	proton transport	RT	9	7.4E-1	1.0E0

☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT	15	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	hydrogen ion transmembrane transporter activity	RT	9	7.5E-1	1.0E0
☐	GOTERM_MF_FAT	monovalent inorganic cation transmembrane transporter activity	RT	9	7.5E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleotide metabolic process	RT	17	7.6E-1	1.0E0
☐	INTERPRO	ATPase, P-type phosphorylation site	RT	5	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	nitrogen compound biosynthetic process	RT	27	8.0E-1	1.0E0
☐	INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT	7	8.1E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting V-type ATPase complex	RT	5	8.2E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	7	8.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	magnesium	RT	7	8.3E-1	9.9E-1
☐	GOTERM_MF_FAT	inorganic cation transmembrane transporter activity	RT	10	8.4E-1	1.0E0
☐	KEGG_PATHWAY	Oxidative phosphorylation	RT	7	8.9E-1	9.9E-1
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, catalytic domain	RT	4	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	ion transport	RT	3	9.1E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions	RT	10	9.3E-1	1.0E0
☐	INTERPRO	Haloacid dehalogenase-like hydrolase	RT	5	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of substances	RT	13	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to movement of substances	RT	13	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT	14	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	primary active transmembrane transporter activity	RT	14	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT	14	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	proton-transporting ATPase activity, rotational mechanism	RT	3	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	cation-transporting ATPase activity	RT	3	1.0E0	1.0E0
	Annotation Cluster 41	Enrichment Score: 0.17		Count	P_Value	Benjamini
☐	INTERPRO	Giardia variant-specific surface protein	RT	140	4.3E-1	1.0E0
☐	INTERPRO	EGF-like	RT	109	6.8E-1	1.0E0
☐	SMART	EGF	RT	109	7.4E-1	1.0E0
☐	INTERPRO	Furin-like repeat	RT	103	8.0E-1	1.0E0
☐	SMART	FU	RT	103	8.5E-1	1.0E0
	Annotation Cluster 42	Enrichment Score: 0.16		Count	P_Value	Benjamini
☐	INTERPRO	Uncharacterised conserved protein UCP036436, nucleotide-sugar transporter-related	RT	3	6.2E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF036436:UCP036436	RT	3	6.5E-1	1.0E0
☐	INTERPRO	Protein of unknown function DUF6, transmembrane	RT	3	8.0E-1	1.0E0
	Annotation Cluster 43	Enrichment Score: 0.16		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	phosphoprotein phosphatase activity	RT	18	4.9E-1	1.0E0
☐	INTERPRO	Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase	RT	10	5.5E-1	1.0E0
☐	SMART	PP2Ac	RT	10	5.7E-1	1.0E0
☐	INTERPRO	Metallophosphoesterase	RT	13	6.3E-1	1.0E0
☐	GOTERM_MF_FAT	phosphatase activity	RT	25	7.6E-1	1.0E0
☐	GOTERM_MF_FAT	iron ion binding	RT	17	8.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	iron	RT	11	8.6E-1	9.9E-1
☐	PIR_SUPERFAMILY	PIRSF000908:serine/threonine-protein phosphatase, conventional type	RT	4	9.5E-1	1.0E0
	Annotation Cluster 44	Enrichment Score: 0.16		Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	proteasome complex	RT	14	2.9E-1	1.0E0
☐	GOTERM_CC_FAT	cytosol	RT	18	3.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	proteasome	RT	13	5.7E-1	1.0E0
☐	KEGG_PATHWAY	Proteasome	RT	17	6.6E-1	9.9E-1
☐	GOTERM_CC_FAT	proteasome core complex	RT	8	7.1E-1	1.0E0
☐	INTERPRO	Proteasome, beta-type subunit, conserved site	RT	3	8.0E-1	1.0E0
☐	INTERPRO	Proteasome, subunit alpha/beta	RT	8	8.1E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type endopeptidase activity	RT	8	8.2E-1	1.0E0

☐	GOTERM_MF_FAT	threonine-type peptidase activity	RT	8	8.2E-1	1.0E0
☐	INTERPRO	Proteasome, alpha and beta subunits	RT	7	8.8E-1	1.0E0
☐	INTERPRO	Proteasome, alpha-subunit, conserved site	RT	4	8.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	threonine protease	RT	3	9.6E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001212:multicatalytic endopeptidase complex chain C9	RT	3	9.6E-1	1.0E0
	Annotation Cluster 45	Enrichment Score: 0.16		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	proteolysis	RT	55	2.9E-1	1.0E0
☐	GOTERM_MF_FAT	peptidase activity, acting on L-amino acid peptides	RT	41	5.4E-1	1.0E0
☐	GOTERM_MF_FAT	peptidase activity	RT	47	5.8E-1	1.0E0
☐	GOTERM_MF_FAT	endopeptidase activity	RT	27	6.7E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type endopeptidase activity	RT	14	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type peptidase activity	RT	17	7.8E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain	RT	15	8.1E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain C-terminal	RT	15	8.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	thiol protease	RT	6	8.2E-1	9.9E-1
☐	SMART	Pept_C1	RT	15	8.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	Protease	RT	19	9.0E-1	1.0E0
☐	INTERPRO	Peptidase, cysteine peptidase active site	RT	15	9.3E-1	1.0E0
	Annotation Cluster 46	Enrichment Score: 0.16		Count	P_Value	Benjamini
☐	INTERPRO	EF-Hand type	RT	12	5.0E-1	1.0E0
☐	INTERPRO	EF-HAND 2	RT	11	5.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	calcium	RT	10	5.8E-1	1.0E0
☐	INTERPRO	EF-HAND 1	RT	12	7.0E-1	1.0E0
☐	INTERPRO	Calcium-binding EF-hand	RT	6	8.8E-1	1.0E0
☐	INTERPRO	EF hand	RT	6	8.8E-1	1.0E0
☐	SMART	EFh	RT	6	8.8E-1	1.0E0
	Annotation Cluster 47	Enrichment Score: 0.15		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	hexose catabolic process	RT	9	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	alcohol catabolic process	RT	9	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	glucose catabolic process	RT	9	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide catabolic process	RT	9	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	cellular carbohydrate catabolic process	RT	9	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	carbohydrate catabolic process	RT	9	6.3E-1	1.0E0
☐	KEGG_PATHWAY	Glycolysis / Gluconeogenesis	RT	5	6.9E-1	9.7E-1
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT	15	7.4E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide metabolic process	RT	13	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	hexose metabolic process	RT	11	8.3E-1	1.0E0
☐	GOTERM_BP_FAT	glucose metabolic process	RT	11	8.3E-1	1.0E0
☐	GOTERM_BP_FAT	glycolysis	RT	6	8.7E-1	1.0E0
	Annotation Cluster 48	Enrichment Score: 0.14		Count	P_Value	Benjamini
☐	INTERPRO	Prefoldin alpha-like	RT	3	6.2E-1	1.0E0
☐	GOTERM_CC_FAT	prefoldin complex	RT	4	7.2E-1	1.0E0
☐	GOTERM_CC_FAT	cytosolic part	RT	5	8.2E-1	1.0E0
	Annotation Cluster 49	Enrichment Score: 0.14		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	dipeptidase activity	RT	3	6.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	dipeptidase	RT	3	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	exopeptidase activity	RT	7	7.2E-1	1.0E0
☐	GOTERM_MF_FAT	metallopeptidase activity	RT	8	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	metalloexopeptidase activity	RT	4	8.9E-1	1.0E0
	Annotation Cluster 50	Enrichment Score: 0.14		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular amino acid derivative biosynthetic process	RT	3	6.2E-1	1.0E0
☐	KEGG_PATHWAY	Glutathione metabolism	RT	4	6.7E-1	9.8E-1
☐	GOTERM_BP_FAT	cellular amino acid derivative metabolic process	RT	3	9.0E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 0.14		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	organophosphate metabolic process	RT	9	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid metabolic process	RT	8	6.1E-1	1.0E0
☐	GOTERM_MF_FAT	inositol or phosphatidylinositol kinase activity	RT	4	6.6E-1	1.0E0

☐	GOTERM_BP_FAT	glycerolipid metabolic process	RT	4	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	phosphoinositide metabolic process	RT	4	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	glycerophospholipid metabolic process	RT	4	8.8E-1	1.0E0
	Annotation Cluster 52	Enrichment Score: 0.13	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Cyclin-related	RT	5	5.1E-1	1.0E0
☐	INTERPRO	Cyclin	RT	3	9.0E-1	1.0E0
☐	SMART	CYCLIN	RT	3	9.0E-1	1.0E0
	Annotation Cluster 53	Enrichment Score: 0.12	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Kelch-type beta propeller	RT	5	6.7E-1	1.0E0
☐	INTERPRO	Kelch repeat type 1	RT	4	7.9E-1	1.0E0
☐	SMART	Kelch	RT	4	8.0E-1	1.0E0
	Annotation Cluster 54	Enrichment Score: 0.12	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	flagellum	RT	3	7.4E-1	1.0E0
☐	GOTERM_CC_FAT	cell projection	RT	3	7.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	flagellum	RT	3	8.1E-1	1.0E0
	Annotation Cluster 55	Enrichment Score: 0.11	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Molecular chaperone, heat shock protein, Hsp40, DnaJ	RT	5	6.7E-1	1.0E0
☐	INTERPRO	Heat shock protein DnaJ, N-terminal	RT	5	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	heat shock protein binding	RT	5	8.0E-1	1.0E0
☐	SMART	DnaJ	RT	5	8.1E-1	1.0E0
	Annotation Cluster 56	Enrichment Score: 0.11	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	ATP-dependent helicase activity	RT	23	6.0E-1	1.0E0
☐	GOTERM_MF_FAT	purine NTP-dependent helicase activity	RT	23	6.0E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT	18	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity	RT	54	7.1E-1	1.0E0
☐	INTERPRO	RNA helicase, DEAD-box type, Q motif	RT	10	7.5E-1	1.0E0
☐	INTERPRO	DEAD-like helicase, N-terminal	RT	24	7.8E-1	1.0E0
☐	SMART	DEXDc	RT	24	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled	RT	39	8.1E-1	1.0E0
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT	23	8.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	helicase	RT	24	8.6E-1	9.9E-1
☐	INTERPRO	DNA/RNA helicase, C-terminal	RT	23	9.0E-1	1.0E0
☐	SMART	HELICc	RT	23	9.1E-1	1.0E0
☐	GOTERM_MF_FAT	helicase activity	RT	28	9.3E-1	1.0E0
	Annotation Cluster 57	Enrichment Score: 0.11	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	ribonucleoside metabolic process	RT	5	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside metabolic process	RT	3	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside metabolic process	RT	3	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside metabolic process	RT	7	8.7E-1	1.0E0
	Annotation Cluster 58	Enrichment Score: 0.11	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	EGF-like, type 3	RT	18	7.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	egf-like domain	RT	10	7.8E-1	9.9E-1
☐	INTERPRO	EGF, extracellular	RT	13	7.9E-1	1.0E0
	Annotation Cluster 59	Enrichment Score: 0.1	G 🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	membrane	RT	16	7.2E-1	9.9E-1
☐	GOTERM_CC_FAT	integral to membrane	RT	34	7.9E-1	1.0E0
☐	GOTERM_CC_FAT	intrinsic to membrane	RT	34	7.9E-1	1.0E0
☐	INTERPRO	Amino acid transporter, transmembrane	RT	6	8.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	transmembrane	RT	16	8.9E-1	1.0E0
	Annotation Cluster 60	Enrichment Score: 0.1	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Protein phosphatase 2C	RT	4	7.9E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C, N-terminal	RT	4	7.9E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C-related	RT	4	7.9E-1	1.0E0
☐	SMART	PP2Cc	RT	4	8.0E-1	1.0E0
☐	SMART	PP2C_SIG	RT	4	8.0E-1	1.0E0
	Annotation Cluster 61	Enrichment Score: 0.09	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type	RT	4	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	cis-trans isomerase activity	RT	5	8.0E-1	1.0E0

☐	GOTERM_MF_FAT	peptidyl-prolyl cis-trans isomerase activity	RT		5	8.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	Rotamase	RT		5	8.1E-1	9.9E-1
	Annotation Cluster 62	Enrichment Score: 0.08	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Dynein heavy chain, N-terminal region 2	RT		7	7.1E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule associated complex	RT		8	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	dynein complex	RT		6	8.7E-1	1.0E0
☐	INTERPRO	Dynein heavy chain	RT		6	9.3E-1	1.0E0
	Annotation Cluster 63	Enrichment Score: 0.08	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	ligase	RT		32	7.2E-1	9.9E-1
☐	GOTERM_MF_FAT	aminoacyl-tRNA ligase activity	RT		14	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-oxygen bonds	RT		14	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming aminoacyl-tRNA and related compounds	RT		14	7.4E-1	1.0E0
☐	INTERPRO	Rossmann-like alpha/beta/alpha sandwich fold	RT		11	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA aminoacylation	RT		13	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	amino acid activation	RT		13	7.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	Aminoacyl-tRNA synthetase	RT		13	8.2E-1	9.9E-1
☐	GOTERM_BP_FAT	tRNA aminoacylation for protein translation	RT		12	8.4E-1	1.0E0
☐	INTERPRO	Aminoacyl-tRNA synthetase, class I, conserved site	RT		5	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA metabolic process	RT		21	8.8E-1	1.0E0
☐	KEGG_PATHWAY	Aminoacyl-tRNA biosynthesis	RT		11	9.1E-1	9.9E-1
☐	GOTERM_BP_FAT	ncRNA metabolic process	RT		27	9.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	protein biosynthesis	RT		5	9.4E-1	1.0E0
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II, conserved region	RT		4	9.7E-1	1.0E0
	Annotation Cluster 64	Enrichment Score: 0.07	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Ubiquitin supergroup	RT		7	8.1E-1	1.0E0
☐	INTERPRO	Ubiquitin	RT		4	8.9E-1	1.0E0
☐	SMART	UBQ	RT		4	8.9E-1	1.0E0
	Annotation Cluster 65	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	antiporter activity	RT		4	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	multidrug transport	RT		3	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	drug transport	RT		3	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	response to drug	RT		3	9.0E-1	1.0E0
☐	INTERPRO	Multi antimicrobial extrusion protein MatE	RT		3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	drug transporter activity	RT		3	9.0E-1	1.0E0
	Annotation Cluster 66	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Like-Sm ribonucleoprotein, core	RT		6	8.8E-1	1.0E0
☐	INTERPRO	Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core	RT		4	8.9E-1	1.0E0
☐	SMART	Sm	RT		4	8.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	viral nucleoprotein	RT		8	8.9E-1	1.0E0
	Annotation Cluster 67	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	tRNA modification	RT		3	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	RNA modification	RT		8	9.2E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA processing	RT		8	9.5E-1	1.0E0
	Annotation Cluster 68	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular carbohydrate biosynthetic process	RT		4	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	carbohydrate biosynthetic process	RT		4	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	alcohol biosynthetic process	RT		3	9.0E-1	1.0E0
	Annotation Cluster 69	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	ribonucleoprotein complex biogenesis	RT		11	8.3E-1	1.0E0
☐	GOTERM_BP_FAT	ribosome biogenesis	RT		11	8.3E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA processing	RT		6	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA metabolic process	RT		6	9.6E-1	1.0E0
	Annotation Cluster 70	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	AMP-dependent synthetase and ligase	RT		4	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	fatty-acid ligase activity	RT		3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	long-chain-fatty-acid-CoA ligase activity	RT		3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-sulfur bonds	RT		3	9.0E-1	1.0E0
	Annotation Cluster 71	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini

☐	GOTERM_BP_FAT	mismatch repair	RT		3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	double-stranded DNA binding	RT		3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	mismatched DNA binding	RT		3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	structure-specific DNA binding	RT		3	9.0E-1	1.0E0
	Annotation Cluster 72	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cell cycle	RT		5	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	cell cycle phase	RT		3	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	cell cycle process	RT		3	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	M phase	RT		3	9.5E-1	1.0E0
	Annotation Cluster 73	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Tetratricopeptide TPR-1	RT		11	8.3E-1	1.0E0
☐	INTERPRO	Tetratricopeptide-like helical	RT		16	9.0E-1	1.0E0
☐	INTERPRO	Tetratricopeptide repeat	RT		12	9.2E-1	1.0E0
☐	INTERPRO	Tetratricopeptide region	RT		12	9.2E-1	1.0E0
☐	SMART	TPR	RT		12	9.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	tpr repeat	RT		4	9.7E-1	1.0E0
	Annotation Cluster 74	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	Golgi apparatus	RT		6	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	ER to Golgi vesicle-mediated transport	RT		3	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	Golgi vesicle transport	RT		3	9.5E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus part	RT		3	9.8E-1	1.0E0
	Annotation Cluster 75	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Myb, DNA-binding	RT		3	9.0E-1	1.0E0
☐	INTERPRO	SANT, DNA-binding	RT		5	9.3E-1	1.0E0
☐	SMART	SANT	RT		5	9.4E-1	1.0E0
	Annotation Cluster 76	Enrichment Score: 0.03	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	microtubule cytoskeleton	RT		26	8.5E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeletal part	RT		26	8.5E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeleton	RT		27	8.5E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule	RT		16	8.8E-1	1.0E0
☐	INTERPRO	Kinesin, motor region, conserved site	RT		9	9.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	motor protein	RT		12	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	motor activity	RT		21	9.5E-1	1.0E0
☐	GOTERM_MF_FAT	microtubule motor activity	RT		21	9.5E-1	1.0E0
☐	INTERPRO	Kinesin, motor region	RT		13	9.7E-1	1.0E0
☐	SMART	KISc	RT		13	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based process	RT		26	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	microtubule	RT		15	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based movement	RT		22	9.8E-1	1.0E0
	Annotation Cluster 77	Enrichment Score: 0.03	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	one-carbon metabolic process	RT		6	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	methylation	RT		5	9.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	methyltransferase	RT		9	9.9E-1	1.0E0
	Annotation Cluster 78	Enrichment Score: 0.03	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	RNA recognition motif, RNP-1	RT		7	9.2E-1	1.0E0
☐	SMART	RRM	RT		7	9.3E-1	1.0E0
☐	INTERPRO	Nucleotide-binding, alpha-beta plait	RT		7	9.7E-1	1.0E0
	Annotation Cluster 79	Enrichment Score: 0.02	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	ncRNA metabolic process	RT		27	9.1E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA processing	RT		14	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA processing	RT		8	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	RNA processing	RT		21	9.9E-1	1.0E0
	Annotation Cluster 80	Enrichment Score: 0.02	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	chromosome	RT		13	8.9E-1	1.0E0
☐	GOTERM_CC_FAT	chromosomal part	RT		8	9.1E-1	1.0E0
☐	GOTERM_CC_FAT	protein-DNA complex	RT		6	9.2E-1	1.0E0
☐	INTERPRO	Histone-fold	RT		7	9.2E-1	1.0E0
☐	GOTERM_CC_FAT	nucleosome	RT		5	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex subunit organization	RT		12	9.5E-1	1.0E0

☐	**GOTERM_BP_FAT**	macromolecular complex subunit organization	RT		13	9.5E-1	1.0E0
☐	**GOTERM_CC_FAT**	chromatin	RT		5	9.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	nucleosome assembly	RT		5	9.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	DNA packaging	RT		5	9.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	nucleosome organization	RT		5	9.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	chromatin assembly	RT		5	9.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	protein-DNA complex assembly	RT		5	9.6E-1	1.0E0
☐	**INTERPRO**	Histone core	RT		5	9.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	macromolecular complex assembly	RT		12	9.7E-1	1.0E0
☐	**GOTERM_BP_FAT**	cellular macromolecular complex assembly	RT		11	9.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	chromosomal protein	RT		5	9.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	nucleosome core	RT		3	9.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	chromosome organization	RT		8	9.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	chromatin organization	RT		6	9.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	chromatin assembly or disassembly	RT		5	9.9E-1	1.0E0
	Annotation Cluster 81	**Enrichment Score: 0.02**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	**INTERPRO**	Zinc finger, C2H2-type	RT		9	9.2E-1	1.0E0
☐	**INTERPRO**	Zinc finger, C2H2-like	RT		8	9.7E-1	1.0E0
☐	**SMART**	ZnF_C2H2	RT		8	9.7E-1	1.0E0
	Annotation Cluster 82	**Enrichment Score: 0.02**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	**GOTERM_BP_FAT**	RNA modification	RT		8	9.2E-1	1.0E0
☐	**GOTERM_MF_FAT**	intramolecular transferase activity	RT		5	9.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	pseudouridine synthesis	RT		3	9.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	pseudouridine synthase activity	RT		3	9.8E-1	1.0E0
	Annotation Cluster 83	**Enrichment Score: 0.02**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	**GOTERM_MF_FAT**	electron carrier activity	RT		12	9.0E-1	1.0E0
☐	**INTERPRO**	4Fe-4S ferredoxin, iron-sulpur binding domain	RT		4	9.7E-1	1.0E0
☐	**INTERPRO**	4Fe-4S ferredoxin, iron-sulphur binding, subgroup	RT		4	9.7E-1	1.0E0
☐	**INTERPRO**	4Fe-4S ferredoxin, iron-sulphur binding, conserved site	RT		3	9.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	metal cluster binding	RT		8	9.9E-1	1.0E0
☐	**GOTERM_MF_FAT**	iron-sulfur cluster binding	RT		8	9.9E-1	1.0E0
	Annotation Cluster 84	**Enrichment Score: 0.01**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	**GOTERM_BP_FAT**	protein complex assembly	RT		6	9.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	protein complex biogenesis	RT		6	9.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	cellular protein complex assembly	RT		5	9.6E-1	1.0E0
☐	**INTERPRO**	Tubulin/FtsZ, 2-layer sandwich domain	RT		3	9.8E-1	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF002306:tubulin	RT		3	9.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	protein polymerization	RT		3	9.9E-1	1.0E0
☐	**INTERPRO**	Tubulin, conserved site	RT		3	9.9E-1	1.0E0
☐	**INTERPRO**	Tubulin	RT		3	9.9E-1	1.0E0
☐	**INTERPRO**	Tubulin/FtsZ, GTPase domain	RT		3	9.9E-1	1.0E0

[186 terms] were not clustered.

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☐	**GOTERM_MF_FAT**	cis-trans isomerase activity	**RT**	3	9.9E-1	1.0E0
☐	**GOTERM_MF_FAT**	peptidyl-prolyl cis-trans isomerase activity	**RT**	3	9.9E-1	1.0E0

194 terms were not clustered.

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

Functional Annotation Clustering

Help and Manual

Current Gene List: 3_Random6
Current Background: Giardia intestinalis
3000 DAVID IDs

Options **Classification Stringency** Medium

Rerun using options | Create Sublist

83 Cluster(s)

Download File

	Annotation Cluster 1	Enrichment Score: 1.37	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	membrane	RT		23	1.2E-2	7.3E-1
☐	GOTERM_CC_FAT	intrinsic to membrane	RT		45	3.2E-2	9.8E-1
☐	GOTERM_CC_FAT	integral to membrane	RT		45	3.2E-2	9.8E-1
☐	SP_PIR_KEYWORDS	transmembrane	RT		24	3.4E-2	8.5E-1
☐	INTERPRO	Amino acid transporter, transmembrane	RT		8	3.5E-1	1.0E0
	Annotation Cluster 2	Enrichment Score: 0.97	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	guanyl ribonucleotide binding	RT		36	2.6E-2	1.0E0
☐	GOTERM_MF_FAT	GTP binding	RT		36	2.6E-2	1.0E0
☐	GOTERM_MF_FAT	guanyl nucleotide binding	RT		36	2.6E-2	1.0E0
☐	INTERPRO	Small GTP-binding protein	RT		16	1.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	gtp-binding	RT		29	1.0E-1	9.8E-1
☐	GOTERM_MF_FAT	GTPase activity	RT		12	4.0E-1	1.0E0
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT		11	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular signaling cascade	RT		13	6.0E-1	1.0E0
	Annotation Cluster 3	Enrichment Score: 0.78	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular homeostasis	RT		16	4.2E-2	1.0E0
☐	GOTERM_BP_FAT	cell redox homeostasis	RT		15	6.0E-2	1.0E0
☐	GOTERM_BP_FAT	homeostatic process	RT		16	8.1E-2	1.0E0
☐	INTERPRO	Thioredoxin-like	RT		11	1.5E-1	1.0E0
☐	INTERPRO	Thioredoxin fold	RT		16	2.5E-1	1.0E0
☐	GOTERM_MF_FAT	antioxidant activity	RT		6	3.9E-1	1.0E0
☐	INTERPRO	Thioredoxin, core	RT		6	3.9E-1	1.0E0
☐	INTERPRO	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	RT		5	5.2E-1	1.0E0
	Annotation Cluster 4	Enrichment Score: 0.77	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Ankyrin	RT		268	1.1E-1	1.0E0
☐	SMART	ANK	RT		268	2.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	ank repeat	RT		188	2.2E-1	9.9E-1
	Annotation Cluster 5	Enrichment Score: 0.76	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	vesicle-mediated transport	RT		24	1.1E-2	9.9E-1
☐	GOTERM_BP_FAT	intracellular transport	RT		21	9.0E-2	1.0E0
☐	GOTERM_BP_FAT	protein transport	RT		23	1.8E-1	1.0E0
☐	GOTERM_BP_FAT	establishment of protein localization	RT		23	1.8E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus	RT		9	2.0E-1	1.0E0
☐	GOTERM_BP_FAT	protein localization	RT		23	2.4E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein localization	RT		16	2.9E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule localization	RT		16	2.9E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular protein transport	RT		16	2.9E-1	1.0E0
☐	GOTERM_CC_FAT	coated membrane	RT		10	3.6E-1	1.0E0
☐	GOTERM_CC_FAT	membrane coat	RT		10	3.6E-1	1.0E0
	Annotation Cluster 6	Enrichment Score: 0.67	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	ATPase, AAA-type, core	RT		19	1.2E-1	1.0E0
☐	INTERPRO	ATPase, AAA+ type, core	RT		46	2.5E-1	1.0E0
☐	SMART	AAA	RT		46	3.1E-1	1.0E0
	Annotation Cluster 7	Enrichment Score: 0.63	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Furin-like repeat	RT		118	9.5E-2	1.0E0

☐	SMART	FU	RT	118	1.5E-1	1.0E0
☐	INTERPRO	EGF-like	RT	116	3.3E-1	1.0E0
☐	INTERPRO	Giardia variant-specific surface protein	RT	143	3.5E-1	1.0E0
☐	SMART	EGF	RT	116	4.4E-1	1.0E0
	Annotation Cluster 8	Enrichment Score: 0.53	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	electron carrier activity	RT	19	3.9E-2	1.0E0
☐	GOTERM_MF_FAT	4 iron, 4 sulfur cluster binding	RT	7	2.8E-1	1.0E0
☐	GOTERM_MF_FAT	iron-sulfur cluster binding	RT	14	3.6E-1	1.0E0
☐	GOTERM_MF_FAT	metal cluster binding	RT	14	3.6E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, subgroup	RT	7	4.5E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulpur binding domain	RT	7	4.5E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, conserved site	RT	5	6.9E-1	1.0E0
	Annotation Cluster 9	Enrichment Score: 0.51	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	translational elongation	RT	7	1.3E-1	1.0E0
☐	INTERPRO	Translation elongation factor EFTu/EF1A, domain 2	RT	5	3.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	elongation factor	RT	6	4.0E-1	9.9E-1
☐	GOTERM_MF_FAT	translation elongation factor activity	RT	6	5.6E-1	1.0E0
	Annotation Cluster 10	Enrichment Score: 0.47	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	transition metal ion binding	RT	116	2.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc-finger	RT	40	2.6E-1	9.8E-1
☐	GOTERM_MF_FAT	zinc ion binding	RT	93	2.9E-1	1.0E0
☐	INTERPRO	Zinc finger, RING-type	RT	43	3.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc	RT	53	3.4E-1	9.9E-1
☐	SMART	RING	RT	43	3.6E-1	1.0E0
☐	INTERPRO	Zinc finger, C3HC4 RING-type	RT	23	3.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	metal-binding	RT	62	3.9E-1	9.9E-1
☐	GOTERM_MF_FAT	ion binding	RT	153	4.3E-1	1.0E0
☐	GOTERM_MF_FAT	cation binding	RT	153	4.3E-1	1.0E0
☐	GOTERM_MF_FAT	metal ion binding	RT	151	4.4E-1	1.0E0
	Annotation Cluster 11	Enrichment Score: 0.43	G	Count	P_Value	Benjamini
☐	INTERPRO	ATPase, P-type, ATPase-associated region	RT	10	1.0E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleotide metabolic process	RT	22	1.1E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleotide biosynthetic process	RT	21	1.4E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide biosynthetic process	RT	29	1.4E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	RT	29	1.4E-1	1.0E0
☐	GOTERM_BP_FAT	nucleotide biosynthetic process	RT	27	1.5E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleotide metabolic process	RT	20	1.7E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide metabolic process	RT	20	1.7E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide biosynthetic process	RT	20	1.7E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleotide biosynthetic process	RT	20	1.7E-1	1.0E0
☐	GOTERM_BP_FAT	ATP metabolic process	RT	18	1.9E-1	1.0E0
☐	GOTERM_BP_FAT	ATP biosynthetic process	RT	18	1.9E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	10	1.9E-1	1.0E0
☐	INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT	10	2.0E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside triphosphate biosynthetic process	RT	19	2.1E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside triphosphate biosynthetic process	RT	19	2.1E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside triphosphate metabolic process	RT	19	2.1E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside triphosphate metabolic process	RT	19	2.1E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate metabolic process	RT	19	2.1E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate biosynthetic process	RT	19	2.1E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside triphosphate metabolic process	RT	19	2.1E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside triphosphate biosynthetic process	RT	19	2.1E-1	1.0E0
☐	GOTERM_BP_FAT	nitrogen compound biosynthetic process	RT	32	2.4E-1	1.0E0
☐	INTERPRO	ATPase, P-type phosphorylation site	RT	7	2.9E-1	1.0E0

☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions	RT	▮		14	3.6E-1	1.0E0
☐	KEGG_PATHWAY	Oxidative phosphorylation	RT	▮		9	4.3E-1	9.9E-1
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, proton-transporting domain	RT	▮		5	4.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	phosphoprotein	RT	▮		4	4.6E-1	9.8E-1
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of substances	RT	▮		18	4.8E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to movement of substances	RT	▮		18	4.8E-1	1.0E0
☐	GOTERM_MF_FAT	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT	▮		19	5.1E-1	1.0E0
☐	GOTERM_MF_FAT	primary active transmembrane transporter activity	RT	▮		19	5.1E-1	1.0E0
☐	GOTERM_MF_FAT	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT	▮		19	5.1E-1	1.0E0
☐	GOTERM_MF_FAT	inorganic cation transmembrane transporter activity	RT	▮		12	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	transmembrane transport	RT	▮		13	6.0E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting V-type ATPase, V0 domain	RT	▮		4	6.1E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001292:vacuolar H(+)-transporting ATPase 16K chain	RT	▮		3	6.2E-1	1.0E0
☐	INTERPRO	ATPase, F0/V0 complex, subunit C	RT	▮		3	6.3E-1	1.0E0
☐	INTERPRO	ATPase, V0 complex, proteolipid subunit C	RT	▮		3	6.3E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex	RT	▮		9	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	oxidative phosphorylation	RT	▮		8	7.1E-1	1.0E0
☐	GOTERM_BP_FAT	ATP synthesis coupled proton transport	RT	▮		8	7.1E-1	1.0E0
☐	GOTERM_BP_FAT	energy coupled proton transport, down electrochemical gradient	RT	▮		8	7.1E-1	1.0E0
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT	▮		15	7.2E-1	1.0E0
☐	GOTERM_BP_FAT	hydrogen transport	RT	▮		9	7.2E-1	1.0E0
☐	GOTERM_BP_FAT	proton transport	RT	▮		9	7.2E-1	1.0E0
☐	GOTERM_MF_FAT	hydrogen ion transmembrane transporter activity	RT	▮		9	7.5E-1	1.0E0
☐	GOTERM_MF_FAT	monovalent inorganic cation transmembrane transporter activity	RT	▮		9	7.5E-1	1.0E0
☐	GOTERM_BP_FAT	ion transmembrane transport	RT	▮		8	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	monovalent inorganic cation transport	RT	▮		9	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	ion transport	RT	▮		13	8.3E-1	1.0E0
☐	GOTERM_BP_FAT	cation transport	RT	▮		13	8.3E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting V-type ATPase complex	RT	▮		5	8.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	ion transport	RT	▮		3	9.1E-1	1.0E0
☐	GOTERM_MF_FAT	proton-transporting ATPase activity, rotational mechanism	RT	▮		3	9.8E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, catalytic domain	RT	▮		3	9.8E-1	1.0E0
	Annotation Cluster 12	Enrichment Score: 0.4	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	translation factor activity, nucleic acid binding	RT	▮		22	2.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	Initiation factor	RT	▮		13	4.6E-1	9.8E-1
☐	GOTERM_MF_FAT	translation initiation factor activity	RT	▮		16	5.2E-1	1.0E0
	Annotation Cluster 13	Enrichment Score: 0.4	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Small GTP-binding protein	RT	▮		16	1.0E-1	1.0E0
☐	INTERPRO	Ras	RT	▮		9	4.0E-1	1.0E0
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT	▮		11	4.4E-1	1.0E0
☐	INTERPRO	Ras small GTPase, Rab type	RT	▮		4	4.5E-1	1.0E0
☐	SMART	RAB	RT	▮		4	4.7E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001710:Ras-related protein Rab	RT	▮		5	5.0E-1	1.0E0
☐	INTERPRO	Ras GTPase	RT	▮		9	5.4E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular signaling cascade	RT	▮		13	6.0E-1	1.0E0
	Annotation Cluster 14	Enrichment Score: 0.4	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Thioredoxin-like	RT	▮		11	1.5E-1	1.0E0
☐	INTERPRO	Thioredoxin domain	RT	▮		5	5.2E-1	1.0E0
☐	INTERPRO	Thioredoxin, conserved site	RT	▮		5	5.2E-1	1.0E0
☐	INTERPRO	Thioredoxin-like subdomain	RT	▮		4	6.6E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 0.36	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	endomembrane system	RT	▮		13	9.0E-2	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus	RT	▮		9	2.0E-1	1.0E0

☐	GOTERM_CC_FAT	Golgi apparatus part	RT			7	2.3E-1	1.0E0
☐	GOTERM_CC_FAT	coated membrane	RT	▮		10	3.6E-1	1.0E0
☐	GOTERM_CC_FAT	membrane coat	RT	▮		10	3.6E-1	1.0E0
☐	GOTERM_CC_FAT	organelle membrane	RT	▮		8	4.2E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle part	RT	▮		5	4.6E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic membrane-bounded vesicle	RT	▮		5	4.6E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle membrane	RT	▮		5	4.6E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle	RT	▮		5	4.6E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle membrane	RT	▮		5	4.6E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle membrane	RT	▮		5	4.6E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle	RT	▮		5	4.6E-1	1.0E0
☐	GOTERM_CC_FAT	membrane-bounded vesicle	RT	▮		5	4.6E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle	RT	▮		5	4.6E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle coat	RT	▮		5	4.6E-1	1.0E0
☐	GOTERM_BP_FAT	ER to Golgi vesicle-mediated transport	RT	▮		5	4.9E-1	1.0E0
☐	GOTERM_BP_FAT	Golgi vesicle transport	RT	▮		5	4.9E-1	1.0E0
☐	GOTERM_CC_FAT	transport vesicle membrane	RT	▮		4	6.1E-1	1.0E0
☐	GOTERM_CC_FAT	transport vesicle	RT	▮		4	6.1E-1	1.0E0
☐	INTERPRO	Clathrin/coatomer adaptor, adaptin-like, N-terminal	RT	▮		4	6.6E-1	1.0E0
☐	GOTERM_CC_FAT	ER to Golgi transport vesicle membrane	RT	▮		3	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	ER to Golgi transport vesicle	RT	▮		3	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	COPII vesicle coat	RT	▮		3	7.7E-1	1.0E0
	Annotation Cluster 16	Enrichment Score: 0.32	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	ATPase, P-type, ATPase-associated region	RT	▮		10	1.0E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	▮		10	1.9E-1	1.0E0
☐	INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT	▮		10	2.0E-1	1.0E0
☐	INTERPRO	ATPase, P-type phosphorylation site	RT	▮		7	2.9E-1	1.0E0
☐	GOTERM_MF_FAT	lipid transporter activity	RT	▮		5	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	lipid transport	RT	▮		4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	lipid localization	RT	▮		4	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	aminophospholipid transporter activity	RT	▮		4	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid transporter activity	RT	▮		4	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid-translocating ATPase activity	RT	▮		4	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid transport	RT	▮		3	7.9E-1	1.0E0
☐	INTERPRO	ATPase, P-type, phospholipid-translocating, flippase	RT	▮		3	8.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	magnesium	RT	▮		7	8.3E-1	9.9E-1
☐	GOTERM_MF_FAT	magnesium ion binding	RT	▮		8	8.8E-1	1.0E0
	Annotation Cluster 17	Enrichment Score: 0.32	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Protein synthesis factor, GTP-binding	RT	▮		7	2.9E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF003007:translation elongation factor Tu	RT	▮		3	6.2E-1	1.0E0
☐	INTERPRO	Translation elongation factor EFTu/EF1A, C-terminal	RT	▮		3	6.3E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 0.3	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	peptidase activity	RT	▮		51	2.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	Protease	RT	▮		25	2.3E-1	9.8E-1
☐	GOTERM_BP_FAT	proteolysis	RT	▮		54	3.2E-1	1.0E0
☐	INTERPRO	Peptidase, cysteine peptidase active site	RT	▮		20	3.8E-1	1.0E0
☐	GOTERM_MF_FAT	peptidase activity, acting on L-amino acid peptides	RT	▮		42	4.3E-1	1.0E0
☐	GOTERM_MF_FAT	endopeptidase activity	RT	▮		29	4.3E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type endopeptidase activity	RT	▮		15	5.9E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type peptidase activity	RT	▮		17	7.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	thiol protease	RT	▮		6	8.2E-1	9.9E-1
☐	INTERPRO	Peptidase C1A, papain	RT	▮		15	8.2E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain C-terminal	RT	▮		15	8.2E-1	1.0E0
☐	SMART	Pept_C1	RT	▮		15	8.5E-1	1.0E0
	Annotation Cluster 19	Enrichment Score: 0.3	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	vitamin binding	RT	▮		9	2.6E-1	1.0E0

☐	INTERPRO	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	RT	▮		7	2.9E-1	1.0E0
☐	GOTERM_MF_FAT	pyridoxal phosphate binding	RT	▮		8	3.4E-1	1.0E0
☐	GOTERM_MF_FAT	vitamin B6 binding	RT	▮		8	3.4E-1	1.0E0
☐	INTERPRO	Aminotransferase, class V/Cysteine desulfurase	RT	▮		3	6.3E-1	1.0E0
☐	INTERPRO	Aminotransferase, class I and II	RT	▮		4	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	transferase activity, transferring nitrogenous groups	RT	▮		5	6.8E-1	1.0E0
☐	GOTERM_MF_FAT	transaminase activity	RT	▮		3	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	Aminotransferase	RT	▮		3	9.1E-1	1.0E0
	Annotation Cluster 20	Enrichment Score: 0.29	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Purine metabolism	RT	▮		20	3.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotidyltransferase	RT	▮		17	3.9E-1	9.9E-1
☐	KEGG_PATHWAY	RNA polymerase	RT	▮		12	4.0E-1	9.9E-1
☐	GOTERM_BP_FAT	transcription	RT	▮		17	4.1E-1	1.0E0
☐	KEGG_PATHWAY	Pyrimidine metabolism	RT	▮		20	4.7E-1	9.9E-1
☐	SP_PIR_KEYWORDS	dna-directed rna polymerase	RT	▮		9	6.7E-1	9.9E-1
☐	GOTERM_MF_FAT	DNA-directed RNA polymerase activity	RT	▮		13	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	RNA polymerase activity	RT	▮		13	8.5E-1	1.0E0
	Annotation Cluster 21	Enrichment Score: 0.28	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	ABC transporter, conserved site	RT	▮		15	4.1E-1	1.0E0
☐	INTERPRO	ABC transporter-like	RT	▮		15	5.1E-1	1.0E0
☐	COG_ONTOLOGY	Defense mechanisms	RT	▮		14	6.9E-1	1.0E0
	Annotation Cluster 22	Enrichment Score: 0.27	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	AMP-dependent synthetase and ligase	RT	▮		6	3.9E-1	1.0E0
☐	COG_ONTOLOGY	Lipid metabolism	RT	▮		10	4.0E-1	9.9E-1
☐	GOTERM_MF_FAT	long-chain-fatty-acid-CoA ligase activity	RT	▮		4	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	fatty-acid ligase activity	RT	▮		4	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-sulfur bonds	RT	▮		4	6.6E-1	1.0E0
	Annotation Cluster 23	Enrichment Score: 0.26	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Mismatch repair	RT	▮		10	3.4E-1	1.0E0
☐	KEGG_PATHWAY	Nucleotide excision repair	RT	▮		10	5.7E-1	9.9E-1
☐	KEGG_PATHWAY	DNA replication	RT	▮		11	8.3E-1	1.0E0
	Annotation Cluster 24	Enrichment Score: 0.25	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Protein of unknown function DUF6, transmembrane	RT	▮		4	4.5E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF036436:UCP036436	RT	▮		3	6.2E-1	1.0E0
☐	INTERPRO	Uncharacterised conserved protein UCP036436, nucleotide-sugar transporter-related	RT	▮		3	6.3E-1	1.0E0
	Annotation Cluster 25	Enrichment Score: 0.24	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	exopeptidase activity	RT	▮		8	4.9E-1	1.0E0
☐	GOTERM_MF_FAT	dipeptidase activity	RT	▮		3	6.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	dipeptidase	RT	▮		3	6.4E-1	9.9E-1
	Annotation Cluster 26	Enrichment Score: 0.23	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	metallopeptidase activity	RT	▮		10	3.1E-1	1.0E0
☐	GOTERM_MF_FAT	metalloexopeptidase activity	RT	▮		6	3.9E-1	1.0E0
☐	INTERPRO	Peptidase M24, structural domain	RT	▮		4	4.5E-1	1.0E0
☐	GOTERM_MF_FAT	exopeptidase activity	RT	▮		8	4.9E-1	1.0E0
☐	GOTERM_MF_FAT	carboxypeptidase activity	RT	▮		3	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	metallocarboxypeptidase activity	RT	▮		3	8.0E-1	1.0E0
☐	INTERPRO	Peptidase M14, carboxypeptidase A	RT	▮		3	9.0E-1	1.0E0
☐	SMART	Zn_pept	RT	▮		3	9.1E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 0.22	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	egf-like domain	RT	▮		12	4.2E-1	9.9E-1
☐	INTERPRO	EGF, extracellular	RT	▮		14	6.7E-1	1.0E0
☐	INTERPRO	EGF-like, type 3	RT	▮		19	6.8E-1	1.0E0
☐	INTERPRO	EGF	RT	▮		5	6.9E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 0.22	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Nucleic acid binding, OB-fold, tRNA/helicase-type	RT	▮		4	4.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	protein biosynthesis	RT	▮		7	6.1E-1	9.9E-1
☐	PIR_SUPERFAMILY	PIRSF001525:lysine-tRNA ligase	RT	▮		3	6.2E-1	1.0E0

☐	**INTERPRO**	Aminoacyl-tRNA synthetase, class II (D, K and N)-like	RT			3	6.3E-1	1.0E0
☐	**INTERPRO**	Aminoacyl-tRNA synthetase, class II (D, K and N)	RT			3	6.3E-1	1.0E0
☐	**INTERPRO**	Aminoacyl-tRNA synthetase, class II, conserved region	RT			6	7.1E-1	1.0E0
	Annotation Cluster 29	Enrichment Score: 0.22		G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_FAT**	nuclear pore	RT			4	6.1E-1	1.0E0
☐	**GOTERM_CC_FAT**	envelope	RT			4	6.1E-1	1.0E0
☐	**GOTERM_CC_FAT**	organelle envelope	RT			4	6.1E-1	1.0E0
☐	**GOTERM_CC_FAT**	pore complex	RT			4	6.1E-1	1.0E0
☐	**GOTERM_CC_FAT**	nuclear envelope	RT			4	6.1E-1	1.0E0
	Annotation Cluster 30	Enrichment Score: 0.21		G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	carbohydrate biosynthetic process	RT			6	3.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	cellular carbohydrate biosynthetic process	RT			6	3.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	alcohol biosynthetic process	RT			4	6.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	hexose biosynthetic process	RT			3	7.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	pyruvate metabolic process	RT			3	7.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	monosaccharide biosynthetic process	RT			3	7.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	gluconeogenesis	RT			3	7.9E-1	1.0E0
	Annotation Cluster 31	Enrichment Score: 0.21		G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	regulation of RNA metabolic process	RT			9	3.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of transcription, DNA-dependent	RT			9	3.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of transcription	RT			19	5.4E-1	1.0E0
☐	**GOTERM_MF_FAT**	NAD or NADH binding	RT			6	5.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of RNA metabolic process	RT			4	6.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	chromatin silencing	RT			4	6.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of nitrogen compound metabolic process	RT			4	6.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	regulation of gene expression, epigenetic	RT			4	6.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of transcription	RT			4	6.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT			4	6.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of gene expression, epigenetic	RT			4	6.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of transcription, DNA-dependent	RT			4	6.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of macromolecule biosynthetic process	RT			4	6.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of biosynthetic process	RT			4	6.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of cellular biosynthetic process	RT			4	6.4E-1	1.0E0
☐	**GOTERM_MF_FAT**	NAD binding	RT			4	6.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	gene silencing	RT			5	6.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of gene expression	RT			5	6.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	negative regulation of macromolecule metabolic process	RT			5	6.6E-1	1.0E0
☐	**INTERPRO**	NAD-dependent histone deacetylase, silent information regulator Sir2	RT			4	6.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	protein amino acid deacetylation	RT			4	7.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	RT			5	8.0E-1	1.0E0
	Annotation Cluster 32	Enrichment Score: 0.2		G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	lipid biosynthetic process	RT			11	2.1E-1	1.0E0
☐	**GOTERM_BP_FAT**	phospholipid biosynthetic process	RT			6	3.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	organophosphate metabolic process	RT			9	5.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	phospholipid metabolic process	RT			8	5.9E-1	1.0E0
☐	**INTERPRO**	CDP-alcohol phosphatidyltransferase	RT			3	6.3E-1	1.0E0
☐	**GOTERM_MF_FAT**	phosphotransferase activity, for other substituted phosphate groups	RT			3	8.0E-1	1.0E0
☐	**KEGG_PATHWAY**	Inositol phosphate metabolism	RT			3	8.7E-1	1.0E0
☐	**GOTERM_BP_FAT**	glycerophospholipid metabolic process	RT			3	9.7E-1	1.0E0
☐	**GOTERM_BP_FAT**	phosphoinositide metabolic process	RT			3	9.7E-1	1.0E0
☐	**GOTERM_BP_FAT**	glycerolipid metabolic process	RT			3	9.7E-1	1.0E0
	Annotation Cluster 33	Enrichment Score: 0.2		G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	SET	RT			5	5.2E-1	1.0E0
☐	**SMART**	SET	RT			5	5.4E-1	1.0E0

☐	INTERPRO	Post-SET zinc-binding region	RT			3	6.3E-1	1.0E0
☐	SMART	PostSET	RT			3	6.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	methyltransferase	RT			11	9.0E-1	1.0E0
	Annotation Cluster 34	Enrichment Score: 0.2	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	protein amino acid lipidation	RT			4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	lipoprotein biosynthetic process	RT			4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	lipoprotein metabolic process	RT			4	6.4E-1	1.0E0
	Annotation Cluster 35	Enrichment Score: 0.2	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	acetyltransferase activity	RT			7	5.9E-1	1.0E0
☐	GOTERM_MF_FAT	N-acyltransferase activity	RT			7	5.9E-1	1.0E0
☐	INTERPRO	Acyl-CoA N-acyltransferase	RT			7	6.0E-1	1.0E0
☐	GOTERM_MF_FAT	N-acetyltransferase activity	RT			6	7.0E-1	1.0E0
☐	INTERPRO	GCN5-related N-acetyltransferase	RT			6	7.1E-1	1.0E0
	Annotation Cluster 36	Enrichment Score: 0.19	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	FAD binding	RT			5	5.1E-1	1.0E0
☐	INTERPRO	Pyridine nucleotide-disulphide oxidoreductase, NAD-binding region	RT			3	6.3E-1	1.0E0
☐	INTERPRO	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	RT			3	8.1E-1	1.0E0
	Annotation Cluster 37	Enrichment Score: 0.19	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	ARF/SAR superfamily	RT			6	3.9E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001711:ADP-ribosylation factor	RT			4	6.5E-1	1.0E0
☐	INTERPRO	ADP-ribosylation factor	RT			3	8.1E-1	1.0E0
☐	SMART	ARF	RT			3	8.2E-1	1.0E0
	Annotation Cluster 38	Enrichment Score: 0.19	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Transcription	RT			6	5.7E-1	9.9E-1
☐	INTERPRO	RNA polymerase Rpb1, domain 3	RT			3	6.3E-1	1.0E0
☐	INTERPRO	RNA polymerase, N-terminal	RT			3	6.3E-1	1.0E0
☐	INTERPRO	RNA polymerase Rpb1, domain 1	RT			3	6.3E-1	1.0E0
☐	INTERPRO	RNA polymerase Rpb1, domain 5	RT			3	6.3E-1	1.0E0
☐	INTERPRO	RNA polymerase Rpb1, domain 4	RT			3	6.3E-1	1.0E0
☐	INTERPRO	RNA polymerase, alpha subunit	RT			3	6.3E-1	1.0E0
☐	SMART	RPOLA_N	RT			3	6.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-directed rna polymerase	RT			9	6.7E-1	9.9E-1
☐	GOTERM_MF_FAT	ribonucleoside binding	RT			3	8.0E-1	1.0E0
	Annotation Cluster 39	Enrichment Score: 0.16	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	response to drug	RT			4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	multidrug transport	RT			4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	drug transport	RT			4	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	drug transporter activity	RT			4	6.6E-1	1.0E0
☐	INTERPRO	Multi antimicrobial extrusion protein MatE	RT			4	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	antiporter activity	RT			4	8.0E-1	1.0E0
☐	INTERPRO	Na+ driven multidrug efflux pump	RT			3	8.1E-1	1.0E0
	Annotation Cluster 40	Enrichment Score: 0.16	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular response to stress	RT			13	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	DNA repair	RT			12	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	response to DNA damage stimulus	RT			12	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	DNA metabolic process	RT			32	8.2E-1	1.0E0
	Annotation Cluster 41	Enrichment Score: 0.16	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	rRNA metabolic process	RT			9	5.0E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA processing	RT			9	5.0E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoprotein complex biogenesis	RT			12	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	ribosome biogenesis	RT			12	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA processing	RT			16	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA processing	RT			8	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	RNA processing	RT			22	9.6E-1	1.0E0
	Annotation Cluster 42	Enrichment Score: 0.16	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Nucleotide-binding, alpha-beta plait	RT			11	4.9E-1	1.0E0
☐	INTERPRO	RNA recognition motif, RNP-1	RT			8	8.3E-1	1.0E0
☐	SMART	RRM	RT			8	8.5E-1	1.0E0
	Annotation Cluster 43	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini

☐	GOTERM_MF_FAT	protein kinase regulator activity	RT		5	6.8E-1	1.0E0
☐	GOTERM_MF_FAT	kinase regulator activity	RT		5	6.8E-1	1.0E0
☐	GOTERM_MF_FAT	cAMP-dependent protein kinase regulator activity	RT		3	8.0E-1	1.0E0
	Annotation Cluster 44	Enrichment Score: 0.14	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	translation	RT		67	4.0E-1	1.0E0
☐	GOTERM_MF_FAT	structural molecule activity	RT		50	5.0E-1	1.0E0
☐	KEGG_PATHWAY	Ribosome	RT		38	6.2E-1	9.9E-1
☐	GOTERM_CC_FAT	ribonucleoprotein complex	RT		54	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	structural constituent of ribosome	RT		39	7.6E-1	1.0E0
☐	GOTERM_CC_FAT	ribosome	RT		40	8.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	ribosomal protein	RT		37	9.6E-1	1.0E0
☐	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT		80	9.8E-1	1.0E0
☐	GOTERM_CC_FAT	non-membrane-bounded organelle	RT		80	9.8E-1	1.0E0
	Annotation Cluster 45	Enrichment Score: 0.14	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	tubulin-tyrosine ligase activity	RT		5	6.8E-1	1.0E0
☐	INTERPRO	Tubulin-tyrosine ligase	RT		5	6.9E-1	1.0E0
☐	GOTERM_MF_FAT	acid-amino acid ligase activity	RT		15	8.2E-1	1.0E0
	Annotation Cluster 46	Enrichment Score: 0.14	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	lipid binding	RT		23	4.4E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid binding	RT		17	5.5E-1	1.0E0
☐	GOTERM_MF_FAT	calcium-dependent phospholipid binding	RT		14	5.7E-1	1.0E0
☐	INTERPRO	Annexin repeat	RT		9	6.6E-1	1.0E0
☐	SMART	ANX	RT		9	6.9E-1	1.0E0
☐	INTERPRO	Annexin	RT		9	8.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	annexin	RT		9	8.4E-1	9.9E-1
☐	GOTERM_MF_FAT	calcium ion binding	RT		20	9.8E-1	1.0E0
☐	INTERPRO	Alpha giardin	RT		5	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	cytoskeleton organization	RT		6	9.9E-1	1.0E0
	Annotation Cluster 47	Enrichment Score: 0.13	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	SANT, DNA-binding	RT		7	6.0E-1	1.0E0
☐	SMART	SANT	RT		7	6.3E-1	1.0E0
☐	INTERPRO	Myb-type HTH DNA-binding domain	RT		3	8.1E-1	1.0E0
☐	INTERPRO	Myb transcription factor	RT		3	8.1E-1	1.0E0
☐	INTERPRO	Myb, DNA-binding	RT		3	9.0E-1	1.0E0
	Annotation Cluster 48	Enrichment Score: 0.13	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	glucose metabolic process	RT		13	5.0E-1	1.0E0
☐	GOTERM_BP_FAT	hexose metabolic process	RT		13	5.0E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide metabolic process	RT		13	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	hexose catabolic process	RT		8	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	glucose catabolic process	RT		8	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide catabolic process	RT		8	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	alcohol catabolic process	RT		8	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	carbohydrate catabolic process	RT		8	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	cellular carbohydrate catabolic process	RT		8	8.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	glycolysis	RT		4	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	glycolysis	RT		5	9.6E-1	1.0E0
	Annotation Cluster 49	Enrichment Score: 0.13	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	RT		16	5.7E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent protein catabolic process	RT		16	5.7E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecule catabolic process	RT		23	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule catabolic process	RT		20	6.4E-1	1.0E0
☐	KEGG_PATHWAY	Proteasome	RT		16	6.5E-1	9.9E-1
☐	GOTERM_BP_FAT	protein catabolic process	RT		22	6.7E-1	1.0E0
☐	INTERPRO	Proteasome, alpha-subunit, conserved site	RT		5	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein catabolic process	RT		19	7.0E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	RT		19	7.0E-1	1.0E0
☐	INTERPRO	Proteasome, alpha and beta subunits	RT		8	7.4E-1	1.0E0

☐	SP_PIR_KEYWORDS	ubl conjugation pathway	RT		8	7.5E-1	9.9E-1
☐	GOTERM_CC_FAT	proteasome core complex	RT		8	7.7E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001212:multicatalytic endopeptidase complex chain C9	RT		4	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	RT		8	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type endopeptidase activity	RT		8	8.2E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type peptidase activity	RT		8	8.2E-1	1.0E0
☐	INTERPRO	Proteasome, subunit alpha/beta	RT		8	8.3E-1	1.0E0
☐	GOTERM_CC_FAT	proteasome complex	RT		10	9.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	proteasome	RT		10	9.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	threonine protease	RT		3	9.6E-1	1.0E0
☐	GOTERM_CC_FAT	cytosol	RT		13	9.7E-1	1.0E0
	Annotation Cluster 50	Enrichment Score: 0.12	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	secondary metabolic process	RT		4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	alkaloid metabolic process	RT		4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	cellular amide metabolic process	RT		4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	nicotinamide metabolic process	RT		4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	nicotinamide nucleotide metabolic process	RT		4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	pyridine nucleotide metabolic process	RT		4	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	oxidoreduction coenzyme metabolic process	RT		4	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	coenzyme metabolic process	RT		6	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	cofactor metabolic process	RT		6	9.2E-1	1.0E0
☐	GOTERM_BP_FAT	coenzyme biosynthetic process	RT		3	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	cofactor biosynthetic process	RT		3	9.9E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 0.12	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	serine/threonine-protein kinase	RT		38	4.6E-1	9.8E-1
☐	GOTERM_MF_FAT	protein serine/threonine kinase activity	RT		60	6.8E-1	1.0E0
☐	INTERPRO	Protein kinase, ATP binding site	RT		47	7.3E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase, active site	RT		51	7.3E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase-related	RT		127	9.3E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase	RT		29	9.6E-1	1.0E0
☐	SMART	S_TKc	RT		29	9.7E-1	1.0E0
	Annotation Cluster 52	Enrichment Score: 0.12	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	protein biosynthesis	RT		7	6.1E-1	9.9E-1
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II, conserved region	RT		6	7.1E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-oxygen bonds	RT		14	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	aminoacyl-tRNA ligase activity	RT		14	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming aminoacyl-tRNA and related compounds	RT		14	7.4E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA metabolic process	RT		29	7.5E-1	1.0E0
☐	GOTERM_BP_FAT	amino acid activation	RT		13	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA aminoacylation	RT		13	7.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	Aminoacyl-tRNA synthetase	RT		13	8.2E-1	9.9E-1
☐	GOTERM_BP_FAT	tRNA aminoacylation for protein translation	RT		12	8.2E-1	1.0E0
☐	KEGG_PATHWAY	Aminoacyl-tRNA biosynthesis	RT		11	8.3E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA metabolic process	RT		21	8.7E-1	1.0E0
	Annotation Cluster 53	Enrichment Score: 0.12	G	🟩	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF002585:heat shock protein DnaJ	RT		3	6.2E-1	1.0E0
☐	INTERPRO	Heat shock protein DnaJ	RT		3	6.3E-1	1.0E0
☐	INTERPRO	Chaperone DnaJ, C-terminal	RT		3	6.3E-1	1.0E0
☐	INTERPRO	Molecular chaperone, heat shock protein, Hsp40, DnaJ	RT		5	6.9E-1	1.0E0
☐	GOTERM_MF_FAT	heat shock protein binding	RT		5	8.0E-1	1.0E0
☐	INTERPRO	Heat shock protein DnaJ, N-terminal	RT		5	8.1E-1	1.0E0
☐	SMART	DnaJ	RT		5	8.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	Chaperone	RT		5	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	unfolded protein binding	RT		9	9.8E-1	1.0E0
	Annotation Cluster 54	Enrichment Score: 0.12	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Kelch-type beta propeller	RT		5	6.9E-1	1.0E0
☐	INTERPRO	Kelch repeat type 1	RT		4	8.0E-1	1.0E0

☐	SMART	Kelch	RT	4	8.2E-1	1.0E0
	Annotation Cluster 55	Enrichment Score: 0.11		Count	P_Value	Benjamini
☐	INTERPRO	Tyrosine protein kinase	RT	5	6.9E-1	1.0E0
☐	SMART	TyrKc	RT	5	7.1E-1	1.0E0
☐	GOTERM_MF_FAT	protein tyrosine kinase activity	RT	12	9.7E-1	1.0E0
	Annotation Cluster 56	Enrichment Score: 0.11		Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	cell projection	RT	3	7.7E-1	1.0E0
☐	GOTERM_CC_FAT	flagellum	RT	3	7.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	flagellum	RT	3	8.1E-1	9.9E-1
	Annotation Cluster 57	Enrichment Score: 0.1		Count	P_Value	Benjamini
☐	INTERPRO	Dynein heavy chain, N-terminal region 2	RT	8	5.0E-1	1.0E0
☐	COG_ONTOLOGY	Cytoskeleton	RT	13	7.5E-1	1.0E0
☐	GOTERM_CC_FAT	dynein complex	RT	7	7.6E-1	1.0E0
☐	INTERPRO	Dynein heavy chain	RT	7	8.2E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule associated complex	RT	8	8.4E-1	1.0E0
☐	GOTERM_MF_FAT	motor activity	RT	20	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	microtubule motor activity	RT	20	9.7E-1	1.0E0
	Annotation Cluster 58	Enrichment Score: 0.1		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	membrane docking	RT	3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	exocytosis	RT	3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	secretion	RT	3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	vesicle docking during exocytosis	RT	3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	vesicle docking	RT	3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	secretion by cell	RT	3	7.9E-1	1.0E0
☐	INTERPRO	Sec1-like protein	RT	3	8.1E-1	1.0E0
	Annotation Cluster 59	Enrichment Score: 0.1		Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, C2H2-type	RT	11	7.0E-1	1.0E0
☐	INTERPRO	Zinc finger, C2H2-like	RT	10	8.4E-1	1.0E0
☐	SMART	ZnF_C2H2	RT	10	8.6E-1	1.0E0
	Annotation Cluster 60	Enrichment Score: 0.1		Count	P_Value	Benjamini
☐	INTERPRO	Beta tubulin	RT	3	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex assembly	RT	8	7.1E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex biogenesis	RT	8	7.1E-1	1.0E0
☐	GOTERM_BP_FAT	protein polymerization	RT	5	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecular complex subunit organization	RT	15	7.8E-1	1.0E0
☐	INTERPRO	Beta tubulin, autoregulation binding site	RT	4	8.0E-1	1.0E0
☐	INTERPRO	Tubulin, conserved site	RT	5	8.1E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, GTPase domain	RT	5	8.1E-1	1.0E0
☐	INTERPRO	Tubulin	RT	5	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecular complex assembly	RT	14	8.3E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein complex assembly	RT	6	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex subunit organization	RT	13	8.8E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002306:tubulin	RT	4	8.8E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, 2-layer sandwich domain	RT	4	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex assembly	RT	12	9.1E-1	1.0E0
	Annotation Cluster 61	Enrichment Score: 0.09		Count	P_Value	Benjamini
☐	INTERPRO	Copine	RT	4	6.6E-1	1.0E0
☐	INTERPRO	von Willebrand factor, type A	RT	4	8.9E-1	1.0E0
☐	SMART	VWA	RT	4	9.0E-1	1.0E0
	Annotation Cluster 62	Enrichment Score: 0.09		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT	162	4.3E-1	9.8E-1
☐	GOTERM_BP_FAT	protein amino acid phosphorylation	RT	152	6.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	atp-binding	RT	150	6.6E-1	9.9E-1
☐	GOTERM_BP_FAT	phosphorylation	RT	162	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorus metabolic process	RT	170	7.4E-1	1.0E0
☐	GOTERM_BP_FAT	phosphate metabolic process	RT	170	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	protein kinase activity	RT	154	7.4E-1	1.0E0
☐	INTERPRO	Protein kinase, core	RT	151	7.9E-1	1.0E0

☐	GOTERM_MF_FAT	nucleotide binding	RT		352	8.1E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleotide binding	RT	▬	328	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	purine ribonucleotide binding	RT	▬	322	9.2E-1	1.0E0
☐	GOTERM_MF_FAT	ribonucleotide binding	RT	▬	322	9.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	kinase	RT	▬	184	9.3E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase-related	RT	▬	127	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	nucleoside binding	RT	▬	295	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl nucleotide binding	RT	▬	292	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleoside binding	RT	▬	292	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT	▬	286	9.9E-1	1.0E0
☐	GOTERM_MF_FAT	ATP binding	RT	▬	286	9.9E-1	1.0E0
	Annotation Cluster 63	Enrichment Score: 0.09	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	DNA-directed DNA polymerase activity	RT	▬	7	5.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna replication	RT	▬	6	8.2E-1	9.9E-1
☐	INTERPRO	DNA-directed DNA polymerase, family B	RT	▬	3	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-directed dna polymerase	RT	▬	3	9.1E-1	1.0E0
☐	SMART	POLBc	RT	▬	3	9.1E-1	1.0E0
	Annotation Cluster 64	Enrichment Score: 0.08	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	ATPase activity	RT	▬	55	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled	RT	▬	41	6.4E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT	▬	18	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	purine NTP-dependent helicase activity	RT	▬	21	8.2E-1	1.0E0
☐	GOTERM_MF_FAT	ATP-dependent helicase activity	RT	▬	21	8.2E-1	1.0E0
☐	INTERPRO	DEAD-like helicase, N-terminal	RT	▬	23	8.8E-1	1.0E0
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT	▬	23	8.8E-1	1.0E0
☐	INTERPRO	RNA helicase, DEAD-box type, Q motif	RT	▬	9	8.9E-1	1.0E0
☐	SMART	DEXDc	RT	▬	23	9.1E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, C-terminal	RT	▬	23	9.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	helicase	RT	▬	23	9.2E-1	1.0E0
☐	GOTERM_MF_FAT	helicase activity	RT	▬	28	9.2E-1	1.0E0
☐	SMART	HELICc	RT	▬	23	9.3E-1	1.0E0
	Annotation Cluster 65	Enrichment Score: 0.08	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	cis-trans isomerase activity	RT	▬	5	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	peptidyl-prolyl cis-trans isomerase activity	RT	▬	5	8.0E-1	1.0E0
☐	INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type	RT	▬	4	8.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	Rotamase	RT	▬	5	8.1E-1	9.9E-1
☐	GOTERM_BP_FAT	protein folding	RT	▬	15	9.2E-1	1.0E0
	Annotation Cluster 66	Enrichment Score: 0.08	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	adenylyltransferase activity	RT	▬	4	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	water-soluble vitamin biosynthetic process	RT	▬	3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	vitamin metabolic process	RT	▬	3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	water-soluble vitamin metabolic process	RT	▬	3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	vitamin biosynthetic process	RT	▬	3	8.9E-1	1.0E0
	Annotation Cluster 67	Enrichment Score: 0.08	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	ligase	RT	▬	33	6.2E-1	9.9E-1
☐	SP_PIR_KEYWORDS	ubl conjugation pathway	RT	▬	8	7.5E-1	9.9E-1
☐	PIR_SUPERFAMILY	PIRSF001567:ubiquitin-protein ligase E2	RT	▬	4	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	acid-amino acid ligase activity	RT	▬	15	8.2E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-nitrogen bonds	RT	▬	17	8.8E-1	1.0E0
☐	INTERPRO	Ubiquitin-conjugating enzyme/RWD-like	RT	▬	6	9.3E-1	1.0E0
☐	INTERPRO	Ubiquitin-conjugating enzyme, E2	RT	▬	6	9.3E-1	1.0E0
☐	SMART	UBCc	RT	▬	6	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	small conjugating protein ligase activity	RT	▬	6	9.6E-1	1.0E0
	Annotation Cluster 68	Enrichment Score: 0.07	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	DNA polymerase activity	RT	▬	20	6.9E-1	1.0E0
☐	GOTERM_MF_FAT	RNA-directed DNA polymerase activity	RT	▬	13	8.5E-1	1.0E0
☐	GOTERM_MF_FAT	nuclease activity	RT	▬	27	8.6E-1	1.0E0
		rna-directed dna polymerase	RT	▬	12	9.1E-1	1.0E0

☐	SP_PIR_KEYWORDS							
☐	GOTERM_MF_FAT	endonuclease activity	RT	▮		17	9.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	Endonuclease	RT	▮		15	9.4E-1	1.0E0
	Annotation Cluster 69	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	nucleobase, nucleoside, nucleotide kinase activity	RT	▮		6	8.1E-1	1.0E0
☐	GOTERM_MF_FAT	phosphotransferase activity, phosphate group as acceptor	RT	▮		4	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	nucleotide kinase activity	RT	▮		3	9.0E-1	1.0E0
	Annotation Cluster 70	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	iron ion binding	RT	▮		19	5.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	iron	RT	▮		11	8.6E-1	9.9E-1
☐	INTERPRO	Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase	RT	▮		8	8.9E-1	1.0E0
☐	SMART	PP2Ac	RT	▮		8	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	phosphoprotein phosphatase activity	RT	▮		14	9.3E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF000908:serine/threonine-protein phosphatase, conventional type	RT	▮		4	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	phosphatase activity	RT	▮		22	9.5E-1	1.0E0
☐	INTERPRO	Metallophosphoesterase	RT	▮		9	9.8E-1	1.0E0
	Annotation Cluster 71	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	nuclear lumen	RT	▮		3	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	membrane-enclosed lumen	RT	▮		3	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	intracellular organelle lumen	RT	▮		3	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	organelle lumen	RT	▮		3	8.8E-1	1.0E0
	Annotation Cluster 72	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	heme binding	RT	▮		4	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	tetrapyrrole binding	RT	▮		4	8.9E-1	1.0E0
☐	INTERPRO	Cytochrome b5	RT	▮		3	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	heme	RT	▮		3	9.1E-1	1.0E0
	Annotation Cluster 73	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	phosphoinositide binding	RT	▮		3	9.0E-1	1.0E0
☐	INTERPRO	Phox-like	RT	▮		3	9.0E-1	1.0E0
☐	SMART	PX	RT	▮		3	9.1E-1	1.0E0
	Annotation Cluster 74	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Kinesin, motor region, conserved site	RT	▮		11	7.0E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule	RT	▮		17	8.6E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeleton	RT	▮		28	8.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	microtubule	RT	▮		17	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based movement	RT	▮		24	9.1E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeletal part	RT	▮		26	9.1E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule cytoskeleton	RT	▮		26	9.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	motor protein	RT	▮		12	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based process	RT	▮		26	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	motor activity	RT	▮		20	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	microtubule motor activity	RT	▮		20	9.7E-1	1.0E0
☐	INTERPRO	Kinesin, motor region	RT	▮		12	9.9E-1	1.0E0
☐	SMART	KISc	RT	▮		12	9.9E-1	1.0E0
	Annotation Cluster 75	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Tetratricopeptide-like helical	RT	▮		17	8.4E-1	1.0E0
☐	INTERPRO	Tetratricopeptide region	RT	▮		13	8.6E-1	1.0E0
☐	INTERPRO	Tetratricopeptide TPR-1	RT	▮		10	9.3E-1	1.0E0
☐	INTERPRO	Tetratricopeptide repeat	RT	▮		11	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	tpr repeat	RT	▮		4	9.7E-1	1.0E0
☐	SMART	TPR	RT	▮		11	9.8E-1	1.0E0
	Annotation Cluster 76	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	WD40 repeat, subgroup	RT	▮		30	8.9E-1	1.0E0
☐	INTERPRO	WD40 repeat, conserved site	RT	▮		15	9.1E-1	1.0E0
☐	INTERPRO	WD40/YVTN repeat-like	RT	▮		38	9.2E-1	1.0E0
☐	INTERPRO	WD40 repeat	RT	▮		39	9.2E-1	1.0E0
☐	INTERPRO	WD40 repeat 2	RT	▮		22	9.3E-1	1.0E0
				▮				

☐	SP_PIR_KEYWORDS	wd repeat	RT		25	9.5E-1	1.0E0
☐	SMART	WD40	RT		39	9.5E-1	1.0E0
☐	INTERPRO	WD40 repeat, region	RT		23	9.7E-1	1.0E0
	Annotation Cluster 77	Enrichment Score: 0.03	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	protein tyrosine phosphatase activity	RT		4	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	phosphoprotein phosphatase activity	RT		14	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid dephosphorylation	RT		6	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	dephosphorylation	RT		7	9.7E-1	1.0E0
	Annotation Cluster 78	Enrichment Score: 0.03	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	macromolecular complex subunit organization	RT		15	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecular complex assembly	RT		14	8.3E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex subunit organization	RT		13	8.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleosome core	RT		4	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex assembly	RT		12	9.1E-1	1.0E0
☐	INTERPRO	Histone-fold	RT		7	9.3E-1	1.0E0
☐	GOTERM_CC_FAT	nucleosome	RT		5	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	DNA packaging	RT		5	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome assembly	RT		5	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome organization	RT		5	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	protein-DNA complex assembly	RT		5	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly	RT		5	9.6E-1	1.0E0
☐	INTERPRO	Histone core	RT		5	9.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	chromosomal protein	RT		5	9.7E-1	1.0E0
☐	GOTERM_CC_FAT	chromatin	RT		5	9.7E-1	1.0E0
☐	GOTERM_CC_FAT	chromosomal part	RT		7	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	chromosome organization	RT		8	9.8E-1	1.0E0
☐	GOTERM_CC_FAT	protein-DNA complex	RT		5	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin organization	RT		6	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly or disassembly	RT		5	9.9E-1	1.0E0
☐	GOTERM_CC_FAT	chromosome	RT		11	9.9E-1	1.0E0
	Annotation Cluster 79	Enrichment Score: 0.02	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Protein phosphatase 2C-related	RT		3	9.5E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C	RT		3	9.5E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C, N-terminal	RT		3	9.5E-1	1.0E0
☐	SMART	PP2Cc	RT		3	9.6E-1	1.0E0
☐	SMART	PP2C_SIG	RT		3	9.6E-1	1.0E0
	Annotation Cluster 80	Enrichment Score: 0.01	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	prefoldin complex	RT		3	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	unfolded protein binding	RT		9	9.8E-1	1.0E0
☐	GOTERM_CC_FAT	cytosolic part	RT		3	9.9E-1	1.0E0
	Annotation Cluster 81	Enrichment Score: 0.01	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core	RT		3	9.8E-1	1.0E0
☐	SMART	Sm	RT		3	9.8E-1	1.0E0
☐	INTERPRO	Like-Sm ribonucleoprotein, core	RT		4	9.9E-1	1.0E0
	Annotation Cluster 82	Enrichment Score: 0.01	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	nucleoside-triphosphatase regulator activity	RT		6	9.6E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase regulator activity	RT		4	9.9E-1	1.0E0
☐	GOTERM_MF_FAT	small GTPase regulator activity	RT		4	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of small GTPase mediated signal transduction	RT		3	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras protein signal transduction	RT		3	9.9E-1	1.0E0
	Annotation Cluster 83	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	calcium	RT		5	1.0E0	1.0E0
☐	INTERPRO	EF-HAND 1	RT		7	1.0E0	1.0E0
☐	INTERPRO	EF-HAND 2	RT		5	1.0E0	1.0E0
☐	INTERPRO	EF-Hand type	RT		4	1.0E0	1.0E0

225 terms were not clustered.

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

Functional Annotation Clustering

Help and Manual

Current Gene List: 3_Random7
Current Background: Giardia intestinalis
3000 DAVID IDs

Options **Classification Stringency** Medium

Rerun using options | Create Sublist

79 Cluster(s)

Download File

	Annotation Cluster 1	Enrichment Score: 0.98	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	phospholipid binding	RT	22	3.4E-2	9.7E-1
☐	GOTERM_MF_FAT	lipid binding	RT	28	3.5E-2	9.4E-1
☐	GOTERM_MF_FAT	calcium-dependent phospholipid binding	RT	18	6.1E-2	9.9E-1
☐	INTERPRO	Annexin repeat	RT	12	9.8E-2	1.0E0
☐	GOTERM_MF_FAT	calcium ion binding	RT	31	1.0E-1	9.9E-1
☐	SMART	ANX	RT	12	1.0E-1	1.0E0
☐	INTERPRO	Annexin	RT	13	1.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	annexin	RT	13	1.3E-1	1.0E0
☐	GOTERM_BP_FAT	cytoskeleton organization	RT	12	3.0E-1	1.0E0
☐	INTERPRO	Alpha giardin	RT	9	3.9E-1	1.0E0
	Annotation Cluster 2	Enrichment Score: 0.92	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	ncRNA processing	RT	23	4.4E-2	1.0E0
☐	GOTERM_BP_FAT	ncRNA metabolic process	RT	37	8.0E-2	1.0E0
☐	GOTERM_BP_FAT	RNA processing	RT	33	8.9E-2	1.0E0
☐	GOTERM_BP_FAT	ribonucleoprotein complex biogenesis	RT	16	1.1E-1	1.0E0
☐	GOTERM_BP_FAT	ribosome biogenesis	RT	16	1.1E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA metabolic process	RT	11	1.5E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA processing	RT	11	1.5E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA processing	RT	13	2.4E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA metabolic process	RT	27	2.7E-1	1.0E0
	Annotation Cluster 3	Enrichment Score: 0.9	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	metal ion binding	RT	167	1.6E-2	1.0E0
☐	GOTERM_MF_FAT	cation binding	RT	168	2.2E-2	9.9E-1
☐	GOTERM_MF_FAT	ion binding	RT	168	2.2E-2	9.9E-1
☐	GOTERM_MF_FAT	zinc ion binding	RT	99	7.8E-2	9.9E-1
☐	GOTERM_MF_FAT	transition metal ion binding	RT	121	8.0E-2	9.9E-1
☐	INTERPRO	Zinc finger, RING-type	RT	43	2.6E-1	1.0E0
☐	SMART	RING	RT	43	2.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc	RT	53	2.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	metal-binding	RT	61	4.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc-finger	RT	38	4.1E-1	1.0E0
☐	INTERPRO	Zinc finger, C3HC4 RING-type	RT	21	6.2E-1	1.0E0
	Annotation Cluster 4	Enrichment Score: 0.78	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	helicase activity	RT	40	3.1E-2	9.9E-1
☐	INTERPRO	DNA/RNA helicase, C-terminal	RT	32	6.3E-2	1.0E0
☐	SP_PIR_KEYWORDS	helicase	RT	32	6.6E-2	1.0E0
☐	SMART	HELICc	RT	32	6.9E-2	1.0E0
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT	31	7.9E-2	1.0E0
☐	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT	22	1.3E-1	1.0E0
☐	INTERPRO	DEAD-like helicase, N-terminal	RT	30	1.4E-1	1.0E0
☐	SMART	DEXDc	RT	30	1.5E-1	1.0E0
☐	GOTERM_MF_FAT	ATP-dependent helicase activity	RT	26	2.5E-1	1.0E0
☐	GOTERM_MF_FAT	purine NTP-dependent helicase activity	RT	26	2.5E-1	1.0E0
☐	INTERPRO	RNA helicase, DEAD-box type, Q motif	RT	10	7.5E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled	RT	39	8.4E-1	1.0E0

☐	GOTERM_MF_FAT	ATPase activity	RT	▮		50	9.4E-1	1.0E0
	Annotation Cluster 5	Enrichment Score: 0.58	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Serine/threonine protein kinase	RT	▮		40	9.9E-2	1.0E0
☐	SMART	S_TKc	RT	▮		40	1.1E-1	9.9E-1
☐	GOTERM_MF_FAT	protein serine/threonine kinase activity	RT	▮		68	1.5E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase, active site	RT	▮		56	2.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	serine/threonine-protein kinase	RT	▮		34	7.9E-1	9.9E-1
☐	INTERPRO	Protein kinase, ATP binding site	RT	▮		42	9.5E-1	1.0E0
	Annotation Cluster 6	Enrichment Score: 0.53	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Thioredoxin fold	RT	▮		17	1.2E-1	1.0E0
☐	INTERPRO	Thioredoxin-like	RT	▮		11	1.4E-1	1.0E0
☐	GOTERM_BP_FAT	cell redox homeostasis	RT	▮		14	1.8E-1	1.0E0
☐	INTERPRO	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	RT	▮		6	2.1E-1	1.0E0
☐	GOTERM_BP_FAT	cellular homeostasis	RT	▮		14	2.8E-1	1.0E0
☐	GOTERM_BP_FAT	homeostatic process	RT	▮		14	3.8E-1	1.0E0
☐	INTERPRO	Thioredoxin, core	RT	▮		6	3.8E-1	1.0E0
☐	GOTERM_MF_FAT	antioxidant activity	RT	▮		6	4.0E-1	1.0E0
☐	INTERPRO	Thioredoxin domain	RT	▮		5	5.1E-1	1.0E0
☐	INTERPRO	Thioredoxin, conserved site	RT	▮		5	5.1E-1	1.0E0
☐	INTERPRO	Thioredoxin-like subdomain	RT	▮		4	6.5E-1	1.0E0
	Annotation Cluster 7	Enrichment Score: 0.49	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	EGF-like, type 3	RT	▮		23	1.5E-1	1.0E0
☐	INTERPRO	EGF, extracellular	RT	▮		16	3.2E-1	1.0E0
☐	INTERPRO	EGF	RT	▮		6	3.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	egf-like domain	RT	▮		11	5.9E-1	9.9E-1
	Annotation Cluster 8	Enrichment Score: 0.45	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	vesicle-mediated transport	RT	▮		21	1.8E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular transport	RT	▮		20	2.2E-1	1.0E0
☐	GOTERM_CC_FAT	coated membrane	RT	▮		11	2.4E-1	1.0E0
☐	GOTERM_CC_FAT	membrane coat	RT	▮		11	2.4E-1	1.0E0
☐	GOTERM_CC_FAT	endomembrane system	RT	▮		12	2.9E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein localization	RT	▮		16	3.5E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular protein transport	RT	▮		16	3.5E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule localization	RT	▮		16	3.5E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus	RT	▮		8	5.0E-1	1.0E0
☐	GOTERM_BP_FAT	establishment of protein localization	RT	▮		20	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	protein transport	RT	▮		20	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	protein localization	RT	▮		20	7.1E-1	1.0E0
	Annotation Cluster 9	Enrichment Score: 0.44	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	SET	RT	▮		6	2.1E-1	1.0E0
☐	SMART	SET	RT	▮		6	2.1E-1	1.0E0
☐	INTERPRO	Post-SET zinc-binding region	RT	▮		3	6.2E-1	1.0E0
☐	SMART	PostSET	RT	▮		3	6.3E-1	1.0E0
	Annotation Cluster 10	Enrichment Score: 0.42	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	EGF-like, type 3	RT	▮		23	1.5E-1	1.0E0
☐	INTERPRO	EGF-like, laminin	RT	▮		16	6.0E-1	1.0E0
☐	SMART	EGF_Lam	RT	▮		16	6.2E-1	1.0E0
	Annotation Cluster 11	Enrichment Score: 0.37	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	chromosome organization	RT	▮		15	1.4E-1	1.0E0
☐	GOTERM_CC_FAT	chromosome	RT	▮		20	1.4E-1	1.0E0
☐	GOTERM_CC_FAT	chromosomal part	RT	▮		13	2.2E-1	1.0E0
☐	INTERPRO	Histone-fold	RT	▮		11	2.3E-1	1.0E0
☐	GOTERM_CC_FAT	protein-DNA complex	RT	▮		10	3.2E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly or disassembly	RT	▮		10	3.2E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin organization	RT	▮		11	3.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleosome core	RT	▮		6	3.8E-1	1.0E0
☐	GOTERM_CC_FAT	chromatin	RT	▮		9	4.0E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex assembly	RT	▮		16	4.5E-1	1.0E0
				▮				

☐	INTERPRO	Histone core	RT		8	4.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	chromosomal protein	RT		8	4.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-binding	RT		22	4.9E-1	1.0E0
☐	GOTERM_CC_FAT	nucleosome	RT		8	5.0E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly	RT		8	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	protein-DNA complex assembly	RT		8	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome organization	RT		8	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome assembly	RT		8	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	DNA packaging	RT		8	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex subunit organization	RT		16	5.5E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002052:histone H4	RT		3	5.9E-1	1.0E0
☐	INTERPRO	Histone H4	RT		3	6.2E-1	1.0E0
☐	SMART	H4	RT		3	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecular complex assembly	RT		16	6.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleus	RT		20	6.8E-1	9.9E-1
☐	GOTERM_BP_FAT	macromolecular complex subunit organization	RT		16	7.2E-1	1.0E0
	Annotation Cluster 12	Enrichment Score: 0.35	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Ubiquitin supergroup	RT		10	1.9E-1	1.0E0
☐	INTERPRO	Ubiquitin	RT		5	6.7E-1	1.0E0
☐	SMART	UBQ	RT		5	6.8E-1	1.0E0
	Annotation Cluster 13	Enrichment Score: 0.35	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	cytosolic part	RT		8	2.1E-1	1.0E0
☐	GOTERM_CC_FAT	prefoldin complex	RT		6	2.1E-1	1.0E0
☐	INTERPRO	Prefoldin alpha-like	RT		3	6.2E-1	1.0E0
☐	INTERPRO	Prefoldin beta-like	RT		3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	unfolded protein binding	RT		13	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	protein folding	RT		18	6.8E-1	1.0E0
	Annotation Cluster 14	Enrichment Score: 0.34	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	protein serine/threonine kinase activity	RT		68	1.5E-1	1.0E0
☐	INTERPRO	Protein kinase, core	RT		162	2.0E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid phosphorylation	RT		164	2.4E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase, active site	RT		56	2.8E-1	1.0E0
☐	GOTERM_MF_FAT	protein kinase activity	RT		165	2.8E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorylation	RT		174	3.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	kinase	RT		197	3.0E-1	1.0E0
☐	GOTERM_BP_FAT	phosphate metabolic process	RT		183	3.2E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorus metabolic process	RT		183	3.2E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase-related	RT		139	3.6E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl nucleotide binding	RT		311	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleoside binding	RT		311	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	ATP binding	RT		306	6.9E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT		306	6.9E-1	1.0E0
☐	GOTERM_MF_FAT	nucleoside binding	RT		312	7.1E-1	1.0E0
☐	GOTERM_MF_FAT	nucleotide binding	RT		359	7.2E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleotide binding	RT		337	7.5E-1	1.0E0
☐	GOTERM_MF_FAT	purine ribonucleotide binding	RT		332	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	ribonucleotide binding	RT		332	7.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	atp-binding	RT		141	9.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT		141	9.9E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 0.32	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Peptidase M14, carboxypeptidase A	RT		5	3.1E-1	1.0E0
☐	SMART	Zn_pept	RT		5	3.1E-1	1.0E0
☐	GOTERM_MF_FAT	metalloexopeptidase activity	RT		6	4.0E-1	1.0E0
☐	GOTERM_MF_FAT	metallocarboxypeptidase activity	RT		4	4.6E-1	1.0E0
☐	GOTERM_MF_FAT	carboxypeptidase activity	RT		4	4.6E-1	1.0E0
☐	GOTERM_MF_FAT	exopeptidase activity	RT		7	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	metallopeptidase activity	RT		7	8.9E-1	1.0E0

	Annotation Cluster 16	Enrichment Score: 0.31	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	RT	▮	6	2.1E-1	1.0E0
☐	GOTERM_MF_FAT	antioxidant activity	RT	▮	6	4.0E-1	1.0E0
☐	INTERPRO	Peroxiredoxin, C-terminal	RT	▮	3	6.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	peroxidase	RT	▮	3	6.2E-1	9.9E-1
☐	GOTERM_MF_FAT	peroxidase activity	RT	▮	3	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	oxidoreductase activity, acting on peroxide as acceptor	RT	▮	3	6.4E-1	1.0E0
	Annotation Cluster 17	Enrichment Score: 0.3	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	RNA recognition motif, RNP-1	RT	▮	10	4.3E-1	1.0E0
☐	SMART	RRM	RT	▮	10	4.4E-1	1.0E0
☐	INTERPRO	Nucleotide-binding, alpha-beta plait	RT	▮	10	6.6E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 0.3	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	coated membrane	RT	▮	11	2.4E-1	1.0E0
☐	GOTERM_CC_FAT	membrane coat	RT	▮	11	2.4E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus part	RT	▮	7	2.9E-1	1.0E0
☐	GOTERM_CC_FAT	endomembrane system	RT	▮	12	2.9E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus	RT	▮	8	5.0E-1	1.0E0
☐	GOTERM_CC_FAT	organelle membrane	RT	▮	8	5.0E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic membrane-bounded vesicle	RT	▮	5	5.2E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle part	RT	▮	5	5.2E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle membrane	RT	▮	5	5.2E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle membrane	RT	▮	5	5.2E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle membrane	RT	▮	5	5.2E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle	RT	▮	5	5.2E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle coat	RT	▮	5	5.2E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle	RT	▮	5	5.2E-1	1.0E0
☐	GOTERM_CC_FAT	membrane-bounded vesicle	RT	▮	5	5.2E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle	RT	▮	5	5.2E-1	1.0E0
☐	GOTERM_BP_FAT	ER to Golgi vesicle-mediated transport	RT	▮	5	5.2E-1	1.0E0
☐	GOTERM_BP_FAT	Golgi vesicle transport	RT	▮	5	5.2E-1	1.0E0
☐	INTERPRO	Clathrin/coatomer adaptor, adaptin-like, N-terminal	RT	▮	4	6.5E-1	1.0E0
☐	GOTERM_CC_FAT	transport vesicle membrane	RT	▮	4	6.6E-1	1.0E0
☐	GOTERM_CC_FAT	transport vesicle	RT	▮	4	6.6E-1	1.0E0
☐	GOTERM_CC_FAT	ER to Golgi transport vesicle membrane	RT	▮	3	8.1E-1	1.0E0
☐	GOTERM_CC_FAT	ER to Golgi transport vesicle	RT	▮	3	8.1E-1	1.0E0
☐	GOTERM_CC_FAT	COPII vesicle coat	RT	▮	3	8.1E-1	1.0E0
	Annotation Cluster 19	Enrichment Score: 0.3	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	EGF-like	RT	▮	116	2.7E-1	1.0E0
☐	SMART	EGF	RT	▮	116	3.1E-1	1.0E0
☐	INTERPRO	Giardia variant-specific surface protein	RT	▮	139	4.9E-1	1.0E0
☐	INTERPRO	Furin-like repeat	RT	▮	101	8.8E-1	1.0E0
☐	SMART	FU	RT	▮	101	9.1E-1	1.0E0
	Annotation Cluster 20	Enrichment Score: 0.28	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	translation factor activity, nucleic acid binding	RT	▮	21	4.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	Initiation factor	RT	▮	13	4.3E-1	1.0E0
☐	GOTERM_MF_FAT	translation initiation factor activity	RT	▮	16	5.5E-1	1.0E0
☐	GOTERM_BP_FAT	translational initiation	RT	▮	7	7.3E-1	1.0E0
	Annotation Cluster 21	Enrichment Score: 0.28	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	phosphatase activity	RT	▮	29	3.3E-1	1.0E0
☐	GOTERM_MF_FAT	iron ion binding	RT	▮	21	3.4E-1	1.0E0
☐	GOTERM_MF_FAT	phosphoprotein phosphatase activity	RT	▮	18	5.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	iron	RT	▮	13	5.4E-1	1.0E0
☐	INTERPRO	Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase	RT	▮	10	5.5E-1	1.0E0
☐	SMART	PP2Ac	RT	▮	10	5.7E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF000908:serine/threonine-protein phosphatase, conventional type	RT	▮	5	7.5E-1	1.0E0
☐	INTERPRO	Metallophosphoesterase	RT	▮	12	7.8E-1	1.0E0
	Annotation Cluster 22	Enrichment Score: 0.28			Count	P_Value	Benjamini

			G		🟩			
☐	KEGG_PATHWAY	Ribosome	RT	▮		41	2.1E-1	1.0E0
☐	GOTERM_CC_FAT	ribonucleoprotein complex	RT	▮		61	3.7E-1	1.0E0
☐	GOTERM_CC_FAT	non-membrane-bounded organelle	RT	▮		94	5.3E-1	1.0E0
☐	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT	▮		94	5.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	ribosomal protein	RT	▮		43	5.5E-1	1.0E0
☐	GOTERM_MF_FAT	structural molecule activity	RT	▮		49	6.5E-1	1.0E0
☐	GOTERM_CC_FAT	ribosome	RT	▮		44	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	translation	RT	▮		65	7.0E-1	1.0E0
☐	GOTERM_MF_FAT	structural constituent of ribosome	RT	▮		39	8.0E-1	1.0E0
	Annotation Cluster 23	Enrichment Score: 0.27	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Terpenoid backbone biosynthesis	RT	▮		5	4.2E-1	1.0E0
☐	GOTERM_BP_FAT	lipid biosynthetic process	RT	▮		10	4.5E-1	1.0E0
☐	GOTERM_BP_FAT	isoprenoid metabolic process	RT	▮		4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	isoprenoid biosynthetic process	RT	▮		4	6.7E-1	1.0E0
	Annotation Cluster 24	Enrichment Score: 0.26	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Calcium-binding EF-hand	RT	▮		8	4.8E-1	1.0E0
☐	INTERPRO	EF hand	RT	▮		8	4.8E-1	1.0E0
☐	SMART	EFh	RT	▮		8	4.9E-1	1.0E0
☐	INTERPRO	EF-HAND 1	RT	▮		13	5.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	calcium	RT	▮		10	5.6E-1	9.9E-1
☐	INTERPRO	EF-HAND 2	RT	▮		11	5.8E-1	1.0E0
☐	INTERPRO	EF-Hand type	RT	▮		10	8.3E-1	1.0E0
	Annotation Cluster 25	Enrichment Score: 0.25	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	ncRNA metabolic process	RT	▮		37	8.0E-2	1.0E0
☐	GOTERM_BP_FAT	tRNA metabolic process	RT	▮		27	2.7E-1	1.0E0
☐	INTERPRO	Anticodon-binding	RT	▮		4	4.4E-1	1.0E0
☐	KEGG_PATHWAY	Aminoacyl-tRNA biosynthesis	RT	▮		12	6.4E-1	1.0E0
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II (G, H, P and S), conserved region	RT	▮		4	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	amino acid activation	RT	▮		14	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA aminoacylation	RT	▮		14	6.8E-1	1.0E0
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II, conserved region	RT	▮		6	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA aminoacylation for protein translation	RT	▮		13	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-oxygen bonds	RT	▮		14	7.6E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming aminoacyl-tRNA and related compounds	RT	▮		14	7.6E-1	1.0E0
☐	GOTERM_MF_FAT	aminoacyl-tRNA ligase activity	RT	▮		14	7.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	Aminoacyl-tRNA synthetase	RT	▮		13	7.9E-1	9.9E-1
☐	SP_PIR_KEYWORDS	ligase	RT	▮		30	8.4E-1	9.9E-1
	Annotation Cluster 26	Enrichment Score: 0.24	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Protein phosphatase 2C, manganese/magnesium aspartate binding site	RT	▮		4	4.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	protein phosphatase	RT	▮		4	4.5E-1	1.0E0
☐	GOTERM_MF_FAT	protein serine/threonine phosphatase activity	RT	▮		4	4.6E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C, N-terminal	RT	▮		5	5.1E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C-related	RT	▮		5	5.1E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C	RT	▮		5	5.1E-1	1.0E0
☐	SMART	PP2Cc	RT	▮		5	5.2E-1	1.0E0
☐	SMART	PP2C_SIG	RT	▮		5	5.2E-1	1.0E0
☐	GOTERM_CC_FAT	protein serine/threonine phosphatase complex	RT	▮		5	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	dephosphorylation	RT	▮		10	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid dephosphorylation	RT	▮		8	7.5E-1	1.0E0
☐	GOTERM_MF_FAT	magnesium ion binding	RT	▮		9	7.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	magnesium	RT	▮		7	8.1E-1	9.9E-1
	Annotation Cluster 27	Enrichment Score: 0.23	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	methylation	RT	▮		8	3.6E-1	1.0E0
☐	INTERPRO	Ribosomal RNA methyltransferase RrmJ/FtsJ	RT	▮		4	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	one-carbon metabolic process	RT	▮		8	5.1E-1	1.0E0

☐	GOTERM_BP_FAT	RNA methylation	RT			4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	biopolymer methylation	RT			4	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	RNA modification	RT			8	9.3E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 0.23		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	translational elongation	RT			6	4.0E-1	1.0E0
☐	GOTERM_MF_FAT	translation elongation factor activity	RT			6	5.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	elongation factor	RT			5	6.8E-1	9.9E-1
☐	INTERPRO	Protein synthesis factor, GTP-binding	RT			5	8.0E-1	1.0E0
	Annotation Cluster 29	Enrichment Score: 0.22		G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, C2H2-like	RT			12	5.0E-1	1.0E0
☐	SMART	ZnF_C2H2	RT			12	5.1E-1	1.0E0
☐	INTERPRO	Zinc finger, C2H2-type	RT			10	8.3E-1	1.0E0
	Annotation Cluster 30	Enrichment Score: 0.21		G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	ATPase, AAA-type, core	RT			16	5.1E-1	1.0E0
☐	INTERPRO	ATPase, AAA+ type, core	RT			41	6.7E-1	1.0E0
☐	SMART	AAA	RT			41	7.0E-1	1.0E0
	Annotation Cluster 31	Enrichment Score: 0.2		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	enzyme activator activity	RT			7	4.6E-1	1.0E0
☐	GOTERM_MF_FAT	nucleoside-triphosphatase regulator activity	RT			9	5.5E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of GTPase activity	RT			6	5.7E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of hydrolase activity	RT			6	5.7E-1	1.0E0
☐	INTERPRO	Arf GTPase activating protein	RT			3	6.2E-1	1.0E0
☐	SMART	ArfGap	RT			3	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of ARF GTPase activity	RT			3	6.3E-1	1.0E0
☐	GOTERM_MF_FAT	ARF GTPase activator activity	RT			3	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of ARF protein signal transduction	RT			4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras GTPase activity	RT			5	6.9E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase activator activity	RT			5	7.0E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras protein signal transduction	RT			6	7.1E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of small GTPase mediated signal transduction	RT			6	7.1E-1	1.0E0
☐	GOTERM_MF_FAT	small GTPase regulator activity	RT			7	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase regulator activity	RT			7	7.4E-1	1.0E0
	Annotation Cluster 32	Enrichment Score: 0.19		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	RNA polymerase activity	RT			16	4.6E-1	1.0E0
☐	GOTERM_MF_FAT	nucleotidyltransferase activity	RT			44	5.2E-1	1.0E0
☐	GOTERM_MF_FAT	DNA-directed RNA polymerase activity	RT			15	5.3E-1	1.0E0
☐	KEGG_PATHWAY	Pyrimidine metabolism	RT			19	5.4E-1	1.0E0
☐	KEGG_PATHWAY	RNA polymerase	RT			10	7.2E-1	1.0E0
☐	KEGG_PATHWAY	Purine metabolism	RT			17	7.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotidyltransferase	RT			14	8.0E-1	9.9E-1
☐	SP_PIR_KEYWORDS	dna-directed rna polymerase	RT			8	8.2E-1	9.9E-1
☐	GOTERM_BP_FAT	transcription	RT			14	8.7E-1	1.0E0
	Annotation Cluster 33	Enrichment Score: 0.18		G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Phox-like	RT			4	6.5E-1	1.0E0
☐	SMART	PX	RT			4	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	phosphoinositide binding	RT			4	6.7E-1	1.0E0
	Annotation Cluster 34	Enrichment Score: 0.18		G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Cyclin, C-terminal	RT			4	4.4E-1	1.0E0
☐	INTERPRO	Cyclin, N-terminal	RT			5	5.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	cyclin	RT			7	5.9E-1	9.9E-1
☐	INTERPRO	Cyclin-related	RT			4	7.9E-1	1.0E0
☐	INTERPRO	Cyclin	RT			3	9.0E-1	1.0E0
☐	SMART	CYCLIN	RT			3	9.0E-1	1.0E0
	Annotation Cluster 35	Enrichment Score: 0.18		G	🟩	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF006621:Dus	RT			3	5.9E-1	1.0E0
☐	INTERPRO	tRNA-dihydrouridine synthase	RT			3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	tRNA dihydrouridine synthase activity	RT			3	6.4E-1	1.0E0
☐	INTERPRO	Aldolase-type TIM barrel	RT			6	6.9E-1	1.0E0

☐	GOTERM_MF_FAT	FAD binding	RT	4	8.1E-1	1.0E0
	Annotation Cluster 36	Enrichment Score: 0.17	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Copine	RT	4	6.5E-1	1.0E0
☐	INTERPRO	von Willebrand factor, type A	RT	5	6.7E-1	1.0E0
☐	SMART	VWA	RT	5	6.8E-1	1.0E0
	Annotation Cluster 37	Enrichment Score: 0.16	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core	RT	5	6.7E-1	1.0E0
☐	SMART	Sm	RT	5	6.8E-1	1.0E0
☐	INTERPRO	Like-Sm ribonucleoprotein, core	RT	7	7.1E-1	1.0E0
	Annotation Cluster 38	Enrichment Score: 0.16	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	RT	7	3.0E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid deacetylation	RT	5	5.2E-1	1.0E0
☐	INTERPRO	NAD-dependent histone deacetylase, silent information regulator Sir2	RT	4	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of macromolecule biosynthetic process	RT	4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of biosynthetic process	RT	4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of transcription, DNA-dependent	RT	4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin silencing	RT	4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of cellular biosynthetic process	RT	4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of gene expression, epigenetic	RT	4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of RNA metabolic process	RT	4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of gene expression, epigenetic	RT	4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of nitrogen compound metabolic process	RT	4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of transcription	RT	4	6.7E-1	1.0E0
☐	GOTERM_MF_FAT	NAD binding	RT	4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of macromolecule metabolic process	RT	4	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of gene expression	RT	4	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	gene silencing	RT	4	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of transcription, DNA-dependent	RT	6	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of RNA metabolic process	RT	6	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	NAD or NADH binding	RT	4	9.5E-1	1.0E0
	Annotation Cluster 39	Enrichment Score: 0.16	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Ankyrin	RT	251	6.2E-1	1.0E0
☐	SMART	ANK	RT	251	7.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	ank repeat	RT	174	7.6E-1	9.9E-1
	Annotation Cluster 40	Enrichment Score: 0.16	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	lipid biosynthetic process	RT	10	4.5E-1	1.0E0
☐	GOTERM_MF_FAT	phosphotransferase activity, for other substituted phosphate groups	RT	4	4.6E-1	1.0E0
☐	INTERPRO	CDP-alcohol phosphatidyltransferase	RT	3	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid metabolic process	RT	8	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid biosynthetic process	RT	5	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	organophosphate metabolic process	RT	8	7.5E-1	1.0E0
☐	GOTERM_BP_FAT	phosphoinositide metabolic process	RT	4	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	glycerophospholipid metabolic process	RT	4	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	glycerolipid metabolic process	RT	4	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	inositol or phosphatidylinositol kinase activity	RT	3	9.1E-1	1.0E0
	Annotation Cluster 41	Enrichment Score: 0.15	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular amino acid biosynthetic process	RT	4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	organic acid biosynthetic process	RT	5	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	carboxylic acid biosynthetic process	RT	5	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	amine biosynthetic process	RT	4	8.1E-1	1.0E0
	Annotation Cluster 42	Enrichment Score: 0.15	G 🟩	Count	P_Value	Benjamini
☐	COG_ONTOLOGY	Defense mechanisms	RT	14	5.8E-1	1.0E0
☐	INTERPRO	ABC transporter, conserved site	RT	13	7.2E-1	1.0E0
		ABC transporter-like	RT	12	8.9E-1	1.0E0

☐	INTERPRO					
	Annotation Cluster 43	Enrichment Score: 0.14		Count	P_Value	Benjamini
☐	INTERPRO	ADP-ribosylation factor	RT	4	4.4E-1	1.0E0
☐	SMART	ARF	RT	4	4.5E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001711:ADP-ribosylation factor	RT	4	6.1E-1	1.0E0
☐	INTERPRO	ARF/SAR superfamily	RT	5	6.7E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001710:Ras-related protein Rab	RT	4	7.6E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular signaling cascade	RT	12	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT	9	8.4E-1	1.0E0
☐	INTERPRO	Ras GTPase	RT	6	9.6E-1	1.0E0
☐	INTERPRO	Small GTP-binding protein	RT	9	9.7E-1	1.0E0
☐	INTERPRO	Ras	RT	5	9.8E-1	1.0E0
	Annotation Cluster 44	Enrichment Score: 0.14		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	DNA metabolic process	RT	35	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	response to DNA damage stimulus	RT	12	7.3E-1	1.0E0
☐	GOTERM_BP_FAT	DNA repair	RT	12	7.3E-1	1.0E0
☐	GOTERM_BP_FAT	cellular response to stress	RT	12	8.0E-1	1.0E0
	Annotation Cluster 45	Enrichment Score: 0.14		Count	P_Value	Benjamini
☐	INTERPRO	Multi antimicrobial extrusion protein MatE	RT	4	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	multidrug transport	RT	4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	drug transport	RT	4	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	response to drug	RT	4	6.7E-1	1.0E0
☐	GOTERM_MF_FAT	drug transporter activity	RT	4	6.7E-1	1.0E0
☐	INTERPRO	Na+ driven multidrug efflux pump	RT	3	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	antiporter activity	RT	4	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	transmembrane transport	RT	11	9.0E-1	1.0E0
	Annotation Cluster 46	Enrichment Score: 0.14		Count	P_Value	Benjamini
☐	INTERPRO	Kinesin, motor region, conserved site	RT	12	5.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	microtubule	RT	20	5.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	motor protein	RT	15	5.9E-1	9.9E-1
☐	INTERPRO	Kinesin, motor region	RT	17	6.2E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule	RT	20	6.3E-1	1.0E0
☐	SMART	KISc	RT	17	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based movement	RT	27	7.5E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based process	RT	30	8.3E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule cytoskeleton	RT	28	8.9E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeletal part	RT	28	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	microtubule motor activity	RT	22	9.2E-1	1.0E0
☐	GOTERM_MF_FAT	motor activity	RT	22	9.2E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeleton	RT	28	9.4E-1	1.0E0
	Annotation Cluster 47	Enrichment Score: 0.13		Count	P_Value	Benjamini
☐	INTERPRO	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	RT	6	5.5E-1	1.0E0
☐	INTERPRO	Aminotransferase, class I and II	RT	4	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	vitamin binding	RT	7	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	pyridoxal phosphate binding	RT	6	8.2E-1	1.0E0
☐	GOTERM_MF_FAT	vitamin B6 binding	RT	6	8.2E-1	1.0E0
☐	GOTERM_MF_FAT	transferase activity, transferring nitrogenous groups	RT	4	9.0E-1	1.0E0
	Annotation Cluster 48	Enrichment Score: 0.12		Count	P_Value	Benjamini
☐	INTERPRO	Amino acid transporter, transmembrane	RT	8	3.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	membrane	RT	14	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	transmembrane	RT	15	9.3E-1	1.0E0
☐	GOTERM_CC_FAT	integral to membrane	RT	34	9.6E-1	1.0E0
☐	GOTERM_CC_FAT	intrinsic to membrane	RT	34	9.6E-1	1.0E0
	Annotation Cluster 49	Enrichment Score: 0.11		Count	P_Value	Benjamini
☐	INTERPRO	Myb, DNA-binding	RT	4	6.5E-1	1.0E0
☐	INTERPRO	Myb transcription factor	RT	3	8.0E-1	1.0E0
☐	INTERPRO	Myb-type HTH DNA-binding domain	RT	3	8.0E-1	1.0E0
☐	INTERPRO	SANT, DNA-binding	RT	6	8.0E-1	1.0E0

☐	SMART	SANT	RT	6	8.1E-1	1.0E0
	Annotation Cluster 50	Enrichment Score: 0.1		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	tetrapyrrole binding	RT	5	7.0E-1	1.0E0
☐	GOTERM_MF_FAT	heme binding	RT	5	7.0E-1	1.0E0
☐	INTERPRO	Cytochrome b5	RT	3	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	heme	RT	3	9.0E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 0.1		Count	P_Value	Benjamini
☐	INTERPRO	RNA-directed DNA polymerase (reverse transcriptase), related	RT	4	6.5E-1	1.0E0
☐	INTERPRO	RNA-directed DNA polymerase (reverse transcriptase)	RT	5	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	RNA-dependent DNA replication	RT	5	6.9E-1	1.0E0
☐	GOTERM_MF_FAT	nuclease activity	RT	29	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	DNA polymerase activity	RT	19	8.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	rna-directed dna polymerase	RT	12	8.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	Endonuclease	RT	15	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	RNA-directed DNA polymerase activity	RT	12	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	endonuclease activity	RT	16	9.8E-1	1.0E0
	Annotation Cluster 52	Enrichment Score: 0.09		Count	P_Value	Benjamini
☐	INTERPRO	Spc97/Spc98	RT	3	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule organizing center	RT	3	8.1E-1	1.0E0
☐	GOTERM_CC_FAT	spindle pole	RT	3	8.1E-1	1.0E0
☐	GOTERM_CC_FAT	spindle	RT	3	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule cytoskeleton organization	RT	3	8.1E-1	1.0E0
	Annotation Cluster 53	Enrichment Score: 0.09		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	nucleoside metabolic process	RT	8	7.5E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside metabolic process	RT	3	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside metabolic process	RT	3	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside metabolic process	RT	4	8.9E-1	1.0E0
	Annotation Cluster 54	Enrichment Score: 0.09		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	GTPase activity	RT	11	6.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	gtp-binding	RT	23	7.3E-1	9.9E-1
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT	9	8.4E-1	1.0E0
☐	GOTERM_MF_FAT	guanyl nucleotide binding	RT	26	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	GTP binding	RT	26	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	guanyl ribonucleotide binding	RT	26	8.8E-1	1.0E0
☐	INTERPRO	Small GTP-binding protein	RT	9	9.7E-1	1.0E0
	Annotation Cluster 55	Enrichment Score: 0.09		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	ubl conjugation pathway	RT	8	7.3E-1	9.9E-1
☐	GOTERM_MF_FAT	small conjugating protein ligase activity	RT	8	7.5E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001567:ubiquitin-protein ligase E2	RT	4	7.6E-1	1.0E0
☐	INTERPRO	Ubiquitin-conjugating enzyme/RWD-like	RT	7	8.1E-1	1.0E0
☐	INTERPRO	Ubiquitin-conjugating enzyme, E2	RT	7	8.1E-1	1.0E0
☐	SMART	UBCc	RT	7	8.2E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-nitrogen bonds	RT	17	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	acid-amino acid ligase activity	RT	14	9.1E-1	1.0E0
☐	KEGG_PATHWAY	Ubiquitin mediated proteolysis	RT	5	9.3E-1	1.0E0
	Annotation Cluster 56	Enrichment Score: 0.08		Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	cytosol	RT	18	5.9E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecule catabolic process	RT	23	6.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	ubl conjugation pathway	RT	8	7.3E-1	9.9E-1
☐	KEGG_PATHWAY	Proteasome	RT	15	7.3E-1	1.0E0
☐	GOTERM_BP_FAT	protein catabolic process	RT	22	7.4E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001212:multicatalytic endopeptidase complex chain C9	RT	4	7.6E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	RT	15	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent protein catabolic process	RT	15	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule catabolic process	RT	19	8.2E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis	RT	49	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein catabolic process	RT	18	8.6E-1	1.0E0

☐	GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	RT		18	8.6E-1	1.0E0
☐	INTERPRO	Proteasome, alpha and beta subunits	RT		7	8.8E-1	1.0E0
☐	INTERPRO	Proteasome, alpha-subunit, conserved site	RT		4	8.9E-1	1.0E0
☐	GOTERM_CC_FAT	proteasome complex	RT		11	9.0E-1	1.0E0
☐	INTERPRO	Proteasome, subunit alpha/beta	RT		7	9.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	proteasome	RT		10	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	RT		7	9.3E-1	1.0E0
☐	GOTERM_CC_FAT	proteasome core complex	RT		7	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type endopeptidase activity	RT		7	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type peptidase activity	RT		7	9.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	threonine protease	RT		3	9.5E-1	1.0E0
	Annotation Cluster 57	Enrichment Score: 0.07	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	GTPase activity	RT		11	6.2E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, GTPase domain	RT		5	8.0E-1	1.0E0
☐	INTERPRO	Tubulin	RT		5	8.0E-1	1.0E0
☐	INTERPRO	Tubulin, conserved site	RT		5	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	protein polymerization	RT		5	8.1E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002306:tubulin	RT		4	8.6E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, 2-layer sandwich domain	RT		4	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein complex assembly	RT		6	8.9E-1	1.0E0
☐	INTERPRO	Beta tubulin, autoregulation binding site	RT		3	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex assembly	RT		6	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex biogenesis	RT		6	9.6E-1	1.0E0
	Annotation Cluster 58	Enrichment Score: 0.07	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Protease	RT		21	7.0E-1	9.9E-1
☐	INTERPRO	Peptidase, cysteine peptidase active site	RT		17	7.7E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain	RT		15	8.1E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain C-terminal	RT		15	8.1E-1	1.0E0
☐	SMART	Pept_C1	RT		15	8.2E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type endopeptidase activity	RT		13	8.7E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type peptidase activity	RT		16	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	peptidase activity	RT		43	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	peptidase activity, acting on L-amino acid peptides	RT		35	9.6E-1	1.0E0
☐	GOTERM_MF_FAT	endopeptidase activity	RT		23	9.6E-1	1.0E0
	Annotation Cluster 59	Enrichment Score: 0.07	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	pyruvate metabolic process	RT		3	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	gluconeogenesis	RT		3	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide biosynthetic process	RT		3	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	hexose biosynthetic process	RT		3	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	cellular carbohydrate biosynthetic process	RT		4	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	carbohydrate biosynthetic process	RT		4	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	alcohol biosynthetic process	RT		3	9.1E-1	1.0E0
	Annotation Cluster 60	Enrichment Score: 0.07	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	carbon-nitrogen lyase activity	RT		3	8.1E-1	1.0E0
☐	GOTERM_MF_FAT	ammonia-lyase activity	RT		3	8.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	lyase	RT		9	9.2E-1	1.0E0
	Annotation Cluster 61	Enrichment Score: 0.07	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	DNA-directed DNA polymerase activity	RT		7	6.1E-1	1.0E0
☐	INTERPRO	DNA-directed DNA polymerase, family B	RT		3	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-directed dna polymerase	RT		3	9.0E-1	1.0E0
☐	SMART	POLBc	RT		3	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna replication	RT		4	9.8E-1	1.0E0
	Annotation Cluster 62	Enrichment Score: 0.07	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	metal cluster binding	RT		12	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	iron-sulfur cluster binding	RT		12	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	4 iron, 4 sulfur cluster binding	RT		5	8.1E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, subgroup	RT		4	9.7E-1	1.0E0

☐	INTERPRO	4Fe-4S ferredoxin, iron-sulpur binding domain	RT			4	9.7E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, conserved site	RT	▮		3	9.8E-1	1.0E0
	Annotation Cluster 63	Enrichment Score: 0.07	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	protein amino acid dephosphorylation	RT	▮		8	7.5E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase, active site	RT	▮		4	7.9E-1	1.0E0
☐	INTERPRO	Dual-specific/protein-tyrosine phosphatase, conserved region	RT	▮		3	9.0E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	protein tyrosine phosphatase activity	RT	▮		3	9.8E-1	1.0E0
	Annotation Cluster 64	Enrichment Score: 0.07	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	protein amino acid dephosphorylation	RT	▮		8	7.5E-1	1.0E0
☐	INTERPRO	Dual specificity phosphatase, catalytic domain	RT	▮		3	9.0E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase, dual specificity	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	protein tyrosine/serine/threonine phosphatase activity	RT	▮		3	9.1E-1	1.0E0
	Annotation Cluster 65	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	WD40 repeat, conserved site	RT	▮		19	4.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	wd repeat	RT	▮		25	9.3E-1	1.0E0
☐	INTERPRO	WD40 repeat 2	RT	▮		21	9.6E-1	1.0E0
☐	INTERPRO	WD40 repeat, region	RT	▮		23	9.6E-1	1.0E0
☐	INTERPRO	WD40 repeat, subgroup	RT	▮		27	9.7E-1	1.0E0
☐	INTERPRO	WD40 repeat	RT	▮		36	9.8E-1	1.0E0
☐	SMART	WD40	RT	▮		36	9.8E-1	1.0E0
☐	INTERPRO	WD40/YVTN repeat-like	RT	▮		34	9.9E-1	1.0E0
	Annotation Cluster 66	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	AMP-dependent synthetase and ligase	RT	▮		4	8.9E-1	1.0E0
☐	COG_ONTOLOGY	Lipid metabolism	RT	▮		7	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	fatty-acid ligase activity	RT	▮		3	9.1E-1	1.0E0
☐	GOTERM_MF_FAT	long-chain-fatty-acid-CoA ligase activity	RT	▮		3	9.1E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-sulfur bonds	RT	▮		3	9.1E-1	1.0E0
	Annotation Cluster 67	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	nuclear envelope	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_CC_FAT	pore complex	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_CC_FAT	nuclear pore	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_CC_FAT	envelope	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_CC_FAT	organelle envelope	RT	▮		3	9.0E-1	1.0E0
	Annotation Cluster 68	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	organelle lumen	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_CC_FAT	intracellular organelle lumen	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_CC_FAT	nuclear lumen	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_CC_FAT	membrane-enclosed lumen	RT	▮		3	9.0E-1	1.0E0
	Annotation Cluster 69	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Nucleotide excision repair	RT	▮		8	8.6E-1	1.0E0
☐	KEGG_PATHWAY	Mismatch repair	RT	▮		6	9.5E-1	1.0E0
☐	KEGG_PATHWAY	DNA replication	RT	▮		9	9.6E-1	1.0E0
	Annotation Cluster 70	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Kelch-type beta propeller	RT	▮		4	8.9E-1	1.0E0
☐	INTERPRO	Kelch repeat type 1	RT	▮		3	9.5E-1	1.0E0
☐	SMART	Kelch	RT	▮		3	9.5E-1	1.0E0
	Annotation Cluster 71	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Heat shock protein DnaJ, N-terminal	RT	▮		4	9.4E-1	1.0E0
☐	SMART	DnaJ	RT	▮		4	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	heat shock protein binding	RT	▮		4	9.5E-1	1.0E0
☐	INTERPRO	Molecular chaperone, heat shock protein, Hsp40, DnaJ	RT	▮		3	9.8E-1	1.0E0
	Annotation Cluster 72	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	DNA-dependent ATPase MCM	RT	▮		3	9.5E-1	1.0E0
☐	SMART	MCM	RT	▮		3	9.5E-1	1.0E0
☐	KEGG_PATHWAY	DNA replication	RT	▮		9	9.6E-1	1.0E0
	Annotation Cluster 73	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	N-acyltransferase activity	RT	▮		5	9.4E-1	1.0E0

☐	GOTERM_MF_FAT	acetyltransferase activity	RT	5	9.4E-1	1.0E0
☐	INTERPRO	GCN5-related N-acetyltransferase	RT	4	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	N-acetyltransferase activity	RT	4	9.7E-1	1.0E0
	Annotation Cluster 74	Enrichment Score: 0.02	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	monosaccharide metabolic process	RT	12	9.1E-1	1.0E0
☐	GOTERM_BP_FAT	glucose metabolic process	RT	10	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	hexose metabolic process	RT	10	9.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	glycolysis	RT	3	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	glycolysis	RT	5	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT	12	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide catabolic process	RT	6	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	alcohol catabolic process	RT	6	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	cellular carbohydrate catabolic process	RT	6	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	glucose catabolic process	RT	6	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	carbohydrate catabolic process	RT	6	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	hexose catabolic process	RT	6	9.8E-1	1.0E0
	Annotation Cluster 75	Enrichment Score: 0.01	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, proton-transporting domain	RT	4	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	transmembrane transport	RT	11	9.0E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting V-type ATPase, V0 domain	RT	3	9.0E-1	1.0E0
☐	KEGG_PATHWAY	Oxidative phosphorylation	RT	6	9.2E-1	1.0E0
☐	GOTERM_BP_FAT	ion transmembrane transport	RT	7	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	inorganic cation transmembrane transporter activity	RT	9	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	hydrogen transport	RT	7	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	proton transport	RT	7	9.6E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex	RT	7	9.6E-1	1.0E0
☐	INTERPRO	ATPase, P-type, ATPase-associated region	RT	5	9.6E-1	1.0E0
☐	GOTERM_MF_FAT	hydrogen ion transmembrane transporter activity	RT	7	9.6E-1	1.0E0
☐	GOTERM_MF_FAT	monovalent inorganic cation transmembrane transporter activity	RT	7	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	oxidative phosphorylation	RT	6	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	energy coupled proton transport, down electrochemical gradient	RT	6	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	ATP synthesis coupled proton transport	RT	6	9.6E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting V-type ATPase complex	RT	4	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT	12	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	ion transport	RT	11	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	cation transport	RT	11	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	monovalent inorganic cation transport	RT	7	9.8E-1	1.0E0
☐	INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT	5	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	proton-transporting ATPase activity, rotational mechanism	RT	3	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	5	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	ATP metabolic process	RT	11	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	ATP biosynthetic process	RT	11	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	nitrogen compound biosynthetic process	RT	23	9.9E-1	1.0E0
☐	GOTERM_MF_FAT	cation-transporting ATPase activity	RT	4	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide biosynthetic process	RT	19	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	RT	19	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleotide biosynthetic process	RT	12	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleotide metabolic process	RT	12	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide biosynthetic process	RT	12	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide metabolic process	RT	12	9.9E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, catalytic domain	RT	3	9.9E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions	RT	8	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleotide biosynthetic process	RT	12	9.9E-1	1.0E0

☐	GOTERM_BP_FAT	nucleoside triphosphate biosynthetic process	RT			11	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside triphosphate metabolic process	RT	▮		11	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside triphosphate metabolic process	RT	▮		11	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate metabolic process	RT	▮		11	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside triphosphate biosynthetic process	RT	▮		11	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside triphosphate biosynthetic process	RT	▮		11	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside triphosphate metabolic process	RT	▮		11	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate biosynthetic process	RT	▮		11	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleotide metabolic process	RT	▮		12	1.0E0	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of substances	RT	▮		11	1.0E0	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to movement of substances	RT	▮		11	1.0E0	1.0E0
☐	GOTERM_BP_FAT	nucleotide biosynthetic process	RT	▮		16	1.0E0	1.0E0
☐	GOTERM_MF_FAT	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT	▮		11	1.0E0	1.0E0
☐	GOTERM_MF_FAT	primary active transmembrane transporter activity	RT	▮		11	1.0E0	1.0E0
☐	GOTERM_MF_FAT	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT	▮		11	1.0E0	1.0E0
	Annotation Cluster 76	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Tetratricopeptide region	RT	▮		11	9.7E-1	1.0E0
☐	INTERPRO	Tetratricopeptide repeat	RT	▮		11	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	tpr repeat	RT	▮		4	9.7E-1	1.0E0
☐	SMART	TPR	RT	▮		11	9.7E-1	1.0E0
☐	INTERPRO	Tetratricopeptide-like helical	RT	▮		14	9.8E-1	1.0E0
☐	INTERPRO	Tetratricopeptide TPR-1	RT	▮		8	9.9E-1	1.0E0
	Annotation Cluster 77	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Dynein heavy chain, N-terminal region 2	RT	▮		5	9.6E-1	1.0E0
☐	INTERPRO	Dynein heavy chain	RT	▮		5	9.8E-1	1.0E0
☐	GOTERM_CC_FAT	dynein complex	RT	▮		5	9.8E-1	1.0E0
☐	COG_ONTOLOGY	Cytoskeleton	RT	▮		8	1.0E0	1.0E0
☐	GOTERM_CC_FAT	microtubule associated complex	RT	▮		5	1.0E0	1.0E0
	Annotation Cluster 78	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Chaperonin TCP-1, conserved site	RT	▮		4	9.7E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002584:molecular chaperone t-complex-type	RT	▮		3	9.8E-1	1.0E0
☐	INTERPRO	Chaperone, tailless complex polypeptide 1	RT	▮		3	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	cytoplasm	RT	▮		7	9.9E-1	1.0E0
☐	INTERPRO	Chaperonin Cpn60/TCP-1	RT	▮		3	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	Chaperone	RT	▮		4	1.0E0	1.0E0
	Annotation Cluster 79	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Rotamase	RT	▮		3	9.9E-1	1.0E0
☐	GOTERM_MF_FAT	cis-trans isomerase activity	RT	▮		3	9.9E-1	1.0E0
☐	GOTERM_MF_FAT	peptidyl-prolyl cis-trans isomerase activity	RT	▮		3	9.9E-1	1.0E0

192 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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Functional Annotation Clustering

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Current Gene List: 3_Random8
Current Background: Giardia intestinalis
3000 DAVID IDs

Options **Classification Stringency** Medium

Rerun using options | Create Sublist

75 Cluster(s)

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				Count	P_Value	Benjamini
	Annotation Cluster 1	Enrichment Score: 0.74		Count	P_Value	Benjamini
☐	INTERPRO	EF-HAND 1	RT	17	3.6E-2	1.0E0
☐	SP_PIR_KEYWORDS	calcium	RT	13	6.5E-2	1.0E0
☐	INTERPRO	EF-HAND 2	RT	13	2.2E-1	1.0E0
☐	SMART	EFh	RT	9	2.4E-1	1.0E0
☐	INTERPRO	EF hand	RT	9	2.6E-1	1.0E0
☐	INTERPRO	Calcium-binding EF-hand	RT	9	2.6E-1	1.0E0
☐	INTERPRO	EF-Hand type	RT	13	3.2E-1	1.0E0
☐	GOTERM_MF_FAT	calcium ion binding	RT	27	4.5E-1	1.0E0
	Annotation Cluster 2	Enrichment Score: 0.67		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	microtubule-based process	RT	38	7.9E-2	1.0E0
☐	GOTERM_CC_FAT	cytoskeletal part	RT	35	1.0E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule cytoskeleton	RT	35	1.0E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeleton	RT	36	1.1E-1	1.0E0
☐	GOTERM_MF_FAT	motor activity	RT	29	1.7E-1	1.0E0
☐	GOTERM_MF_FAT	microtubule motor activity	RT	29	1.7E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based movement	RT	31	2.7E-1	1.0E0
☐	SMART	KISc	RT	19	3.0E-1	1.0E0
☐	INTERPRO	Kinesin, motor region	RT	19	3.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	microtubule	RT	21	3.6E-1	9.7E-1
☐	GOTERM_CC_FAT	microtubule	RT	21	3.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	motor protein	RT	16	4.0E-1	9.6E-1
☐	INTERPRO	Kinesin, motor region, conserved site	RT	12	5.0E-1	1.0E0
	Annotation Cluster 3	Enrichment Score: 0.51		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	lipoprotein biosynthetic process	RT	5	3.1E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid lipidation	RT	5	3.1E-1	1.0E0
☐	GOTERM_BP_FAT	lipoprotein metabolic process	RT	5	3.1E-1	1.0E0
	Annotation Cluster 4	Enrichment Score: 0.51		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	pseudouridine synthase activity	RT	7	1.4E-1	1.0E0
☐	GOTERM_BP_FAT	pseudouridine synthesis	RT	7	1.4E-1	1.0E0
☐	GOTERM_MF_FAT	intramolecular transferase activity	RT	9	2.6E-1	1.0E0
☐	GOTERM_BP_FAT	RNA modification	RT	11	4.7E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001430:tRNA_psdUrid_synth	RT	3	6.1E-1	1.0E0
☐	INTERPRO	Pseudouridine synthase I, TruA	RT	3	6.2E-1	1.0E0
	Annotation Cluster 5	Enrichment Score: 0.45		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	enzyme activator activity	RT	8	2.0E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras protein signal transduction	RT	8	2.0E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of small GTPase mediated signal transduction	RT	8	2.0E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase regulator activity	RT	9	2.6E-1	1.0E0
☐	GOTERM_MF_FAT	small GTPase regulator activity	RT	9	2.6E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of GTPase activity	RT	7	2.8E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of hydrolase activity	RT	7	2.8E-1	1.0E0
☐	GOTERM_MF_FAT	nucleoside-triphosphatase regulator activity	RT	10	3.1E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase activator activity	RT	6	3.8E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras GTPase activity	RT	6	3.9E-1	1.0E0
☐	GOTERM_MF_FAT	Rab GTPase activator activity	RT	4	4.5E-1	1.0E0

☐	GOTERM_MF_FAT	Ras GTPase activator activity	RT	4	4.5E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Rab protein signal transduction	RT	4	4.5E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Rab GTPase activity	RT	4	4.5E-1	1.0E0
☐	SMART	TBC	RT	3	6.1E-1	1.0E0
☐	INTERPRO	RabGAP/TBC	RT	3	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of ARF protein signal transduction	RT	4	6.6E-1	1.0E0
	Annotation Cluster 6	Enrichment Score: 0.39	G	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	translational initiation	RT	9	2.6E-1	1.0E0
☐	GOTERM_MF_FAT	translation initiation factor activity	RT	17	3.6E-1	1.0E0
☐	GOTERM_MF_FAT	translation factor activity, nucleic acid binding	RT	21	3.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	Initiation factor	RT	11	7.6E-1	9.9E-1
	Annotation Cluster 7	Enrichment Score: 0.38	G	Count	P_Value	Benjamini
☐	SMART	CYCLIN	RT	5	3.0E-1	1.0E0
☐	INTERPRO	Cyclin	RT	5	3.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	cyclin	RT	8	3.3E-1	9.8E-1
☐	INTERPRO	Cyclin-related	RT	5	5.1E-1	1.0E0
☐	INTERPRO	Cyclin, N-terminal	RT	4	8.0E-1	1.0E0
	Annotation Cluster 8	Enrichment Score: 0.38	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	atp-binding	RT	158	1.2E-1	1.0E0
☐	INTERPRO	Protein kinase, ATP binding site	RT	54	1.4E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase, active site	RT	58	1.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	kinase	RT	199	1.7E-1	1.0E0
☐	GOTERM_MF_FAT	protein serine/threonine kinase activity	RT	66	2.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT	162	2.6E-1	9.9E-1
☐	SMART	S_TKc	RT	37	2.9E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase-related	RT	140	3.2E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase	RT	37	3.2E-1	1.0E0
☐	GOTERM_MF_FAT	protein kinase activity	RT	161	3.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	serine/threonine-protein kinase	RT	38	3.8E-1	9.5E-1
☐	INTERPRO	Protein kinase, core	RT	158	3.9E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid phosphorylation	RT	159	4.1E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorylation	RT	170	4.2E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorus metabolic process	RT	175	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	phosphate metabolic process	RT	175	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT	301	7.2E-1	1.0E0
☐	GOTERM_MF_FAT	ATP binding	RT	301	7.2E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleoside binding	RT	304	7.6E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl nucleotide binding	RT	304	7.6E-1	1.0E0
☐	GOTERM_MF_FAT	nucleoside binding	RT	305	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	purine ribonucleotide binding	RT	325	8.5E-1	1.0E0
☐	GOTERM_MF_FAT	ribonucleotide binding	RT	325	8.5E-1	1.0E0
☐	GOTERM_MF_FAT	nucleotide binding	RT	349	8.7E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleotide binding	RT	328	8.7E-1	1.0E0
	Annotation Cluster 9	Enrichment Score: 0.37	G	Count	P_Value	Benjamini
☐	SMART	SET	RT	6	2.0E-1	1.0E0
☐	INTERPRO	SET	RT	6	2.1E-1	1.0E0
☐	SMART	PostSET	RT	3	6.1E-1	1.0E0
☐	INTERPRO	Post-SET zinc-binding region	RT	3	6.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	methyltransferase	RT	10	9.5E-1	1.0E0
	Annotation Cluster 10	Enrichment Score: 0.36	G	Count	P_Value	Benjamini
☐	SMART	FU	RT	111	3.0E-1	1.0E0
☐	INTERPRO	Giardia variant-specific surface protein	RT	142	3.4E-1	1.0E0
☐	INTERPRO	Furin-like repeat	RT	111	3.6E-1	1.0E0
☐	SMART	EGF	RT	109	6.3E-1	1.0E0
☐	INTERPRO	EGF-like	RT	109	6.8E-1	1.0E0
	Annotation Cluster 11	Enrichment Score: 0.36	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	egf-like domain	RT	13	2.1E-1	9.9E-1
☐	INTERPRO	EGF-like, type 3	RT	20	5.2E-1	1.0E0

☐	**INTERPRO**	EGF, extracellular	RT			13	7.9E-1	1.0E0
	Annotation Cluster 12	Enrichment Score: 0.36	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Alcohol dehydrogenase, iron-type	RT	▮		5	3.1E-1	1.0E0
☐	**COG_ONTOLOGY**	Energy production and conversion	RT	▮		7	4.6E-1	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF000113:iron-containing alcohol dehydrogenase	RT	▮		3	6.1E-1	1.0E0
	Annotation Cluster 13	Enrichment Score: 0.33	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	cofactor binding	RT	▮		24	2.4E-1	1.0E0
☐	**GOTERM_MF_FAT**	vitamin binding	RT	▮		9	2.6E-1	1.0E0
☐	**INTERPRO**	Aminotransferase, class I and II	RT	▮		5	3.1E-1	1.0E0
☐	**GOTERM_MF_FAT**	vitamin B6 binding	RT	▮		8	3.4E-1	1.0E0
☐	**GOTERM_MF_FAT**	pyridoxal phosphate binding	RT	▮		8	3.4E-1	1.0E0
☐	**INTERPRO**	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	RT	▮		6	5.5E-1	1.0E0
☐	**KEGG_PATHWAY**	Alanine, aspartate and glutamate metabolism	RT	▮		3	6.1E-1	1.0E0
☐	**INTERPRO**	Pyridoxal phosphate-dependent transferase, major region, subdomain 2	RT	▮		3	6.2E-1	1.0E0
☐	**GOTERM_MF_FAT**	transferase activity, transferring nitrogenous groups	RT	▮		5	6.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Aminotransferase	RT	▮		3	9.0E-1	9.9E-1
☐	**GOTERM_MF_FAT**	transaminase activity	RT	▮		3	9.0E-1	1.0E0
	Annotation Cluster 14	Enrichment Score: 0.32	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_FAT**	spindle	RT	▮		4	4.1E-1	1.0E0
☐	**GOTERM_CC_FAT**	microtubule organizing center	RT	▮		4	4.1E-1	1.0E0
☐	**GOTERM_CC_FAT**	spindle pole	RT	▮		4	4.1E-1	1.0E0
☐	**INTERPRO**	Spc97/Spc98	RT	▮		4	4.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	microtubule cytoskeleton organization	RT	▮		4	4.5E-1	1.0E0
☐	**GOTERM_BP_FAT**	cytoskeleton organization	RT	▮		9	8.3E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 0.31	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_FAT**	proton-transporting V-type ATPase complex	RT	▮		8	1.7E-1	1.0E0
☐	**GOTERM_BP_FAT**	nitrogen compound biosynthetic process	RT	▮		33	2.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	purine nucleotide metabolic process	RT	▮		21	2.3E-1	1.0E0
☐	**INTERPRO**	ATPase, P-type, ATPase-associated region	RT	▮		9	2.6E-1	1.0E0
☐	**GOTERM_CC_FAT**	proton-transporting V-type ATPase, V0 domain	RT	▮		5	2.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	purine nucleotide biosynthetic process	RT	▮		20	2.8E-1	1.0E0
☐	**INTERPRO**	ATPase, P-type phosphorylation site	RT	▮		7	2.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	purine ribonucleotide metabolic process	RT	▮		19	3.3E-1	1.0E0
☐	**GOTERM_BP_FAT**	ribonucleotide metabolic process	RT	▮		19	3.3E-1	1.0E0
☐	**GOTERM_BP_FAT**	ribonucleotide biosynthetic process	RT	▮		19	3.3E-1	1.0E0
☐	**GOTERM_BP_FAT**	purine ribonucleotide biosynthetic process	RT	▮		19	3.3E-1	1.0E0
☐	**GOTERM_BP_FAT**	ATP metabolic process	RT	▮		17	3.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	ATP biosynthetic process	RT	▮		17	3.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	nucleobase, nucleoside and nucleotide biosynthetic process	RT	▮		27	3.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	RT	▮		27	3.8E-1	1.0E0
☐	**INTERPRO**	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT	▮		9	3.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	purine nucleoside triphosphate metabolic process	RT	▮		18	3.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	nucleoside triphosphate biosynthetic process	RT	▮		18	3.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	purine nucleoside triphosphate biosynthetic process	RT	▮		18	3.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	nucleoside triphosphate metabolic process	RT	▮		18	3.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	purine ribonucleoside triphosphate metabolic process	RT	▮		18	3.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	purine ribonucleoside triphosphate biosynthetic process	RT	▮		18	3.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	ribonucleoside triphosphate metabolic process	RT	▮		18	3.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	ribonucleoside triphosphate biosynthetic process	RT	▮		18	3.9E-1	1.0E0
☐	**GOTERM_MF_FAT**	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	▮		9	3.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	nucleotide biosynthetic process	RT	▮		25	4.1E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	phosphoprotein	RT	▮		4	4.4E-1	9.6E-1
☐	**GOTERM_BP_FAT**	generation of precursor metabolites and energy	RT	▮		17	4.5E-1	1.0E0

☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, proton-transporting domain	RT			5	4.7E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex	RT	▮		10	5.0E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions	RT	▮		13	5.4E-1	1.0E0
☐	GOTERM_BP_FAT	hydrogen transport	RT	▮		10	5.6E-1	1.0E0
☐	GOTERM_BP_FAT	proton transport	RT	▮		10	5.6E-1	1.0E0
☐	GOTERM_BP_FAT	cation transport	RT	▮		15	5.9E-1	1.0E0
☐	GOTERM_BP_FAT	ion transport	RT	▮		15	5.9E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001292:vacuolar H(+)-transporting ATPase 16K chain	RT	▮		3	6.1E-1	1.0E0
☐	INTERPRO	ATPase, P-type cation-transporter, C-terminal	RT	▮		3	6.2E-1	1.0E0
☐	INTERPRO	ATPase, V0 complex, proteolipid subunit C	RT	▮		3	6.2E-1	1.0E0
☐	INTERPRO	ATPase, P-type cation-transporter, N-terminal	RT	▮		3	6.2E-1	1.0E0
☐	INTERPRO	ATPase, F0/V0 complex, subunit C	RT	▮		3	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	transmembrane transport	RT	▮		13	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	ion transmembrane transport	RT	▮		9	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	monovalent inorganic cation transport	RT	▮		10	6.7E-1	1.0E0
☐	GOTERM_MF_FAT	inorganic cation transmembrane transporter activity	RT	▮		11	6.9E-1	1.0E0
☐	KEGG_PATHWAY	Oxidative phosphorylation	RT	▮		8	7.0E-1	1.0E0
☐	GOTERM_BP_FAT	oxidative phosphorylation	RT	▮		8	7.3E-1	1.0E0
☐	GOTERM_BP_FAT	energy coupled proton transport, down electrochemical gradient	RT	▮		8	7.3E-1	1.0E0
☐	GOTERM_BP_FAT	ATP synthesis coupled proton transport	RT	▮		8	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	hydrogen ion transmembrane transporter activity	RT	▮		9	7.5E-1	1.0E0
☐	GOTERM_MF_FAT	monovalent inorganic cation transmembrane transporter activity	RT	▮		9	7.5E-1	1.0E0
☐	GOTERM_MF_FAT	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT	▮		17	7.8E-1	1.0E0
☐	INTERPRO	Haloacid dehalogenase-like hydrolase	RT	▮		6	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	cation-transporting ATPase activity	RT	▮		6	8.1E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to movement of substances	RT	▮		15	8.6E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of substances	RT	▮		15	8.6E-1	1.0E0
☐	GOTERM_MF_FAT	primary active transmembrane transporter activity	RT	▮		16	8.7E-1	1.0E0
☐	GOTERM_MF_FAT	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT	▮		16	8.7E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, catalytic domain	RT	▮		4	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	proton-transporting ATPase activity, rotational mechanism	RT	▮		3	9.8E-1	1.0E0
	Annotation Cluster 16	Enrichment Score: 0.29	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	alcohol catabolic process	RT	▮		10	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	glucose catabolic process	RT	▮		10	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	carbohydrate catabolic process	RT	▮		10	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide catabolic process	RT	▮		10	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	hexose catabolic process	RT	▮		10	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	cellular carbohydrate catabolic process	RT	▮		10	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT	▮		17	4.5E-1	1.0E0
☐	GOTERM_BP_FAT	glycolysis	RT	▮		8	4.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	glycolysis	RT	▮		5	5.0E-1	9.6E-1
☐	GOTERM_BP_FAT	monosaccharide metabolic process	RT	▮		14	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	glucose metabolic process	RT	▮		11	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	hexose metabolic process	RT	▮		11	8.4E-1	1.0E0
	Annotation Cluster 17	Enrichment Score: 0.29	G		🟩	Count	P_Value	Benjamini
☐	SMART	Pept_C1	RT	▮		18	3.6E-1	1.0E0
☐	GOTERM_MF_FAT	peptidase activity	RT	▮		49	3.8E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain C-terminal	RT	▮		18	3.8E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain	RT	▮		18	3.8E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type peptidase activity	RT	▮		19	5.1E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type endopeptidase activity	RT	▮		15	5.9E-1	1.0E0
☐	GOTERM_MF_FAT	peptidase activity, acting on L-amino acid peptides	RT	▮		40	6.2E-1	1.0E0
		Peptidase, cysteine peptidase active site	RT	▮		18	6.4E-1	1.0E0

☐	INTERPRO							
☐	SP_PIR_KEYWORDS	Protease	RT	▮		21	6.8E-1	9.8E-1
☐	GOTERM_MF_FAT	endopeptidase activity	RT	▮		25	8.5E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 0.28	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	cytosolic part	RT	▮		7	3.9E-1	1.0E0
☐	GOTERM_CC_FAT	prefoldin complex	RT	▮		5	4.7E-1	1.0E0
☐	INTERPRO	Prefoldin beta-like	RT	▮		3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	unfolded protein binding	RT	▮		13	6.4E-1	1.0E0
	Annotation Cluster 19	Enrichment Score: 0.28	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Cytochrome b5	RT	▮		5	3.1E-1	1.0E0
☐	INTERPRO	Cytochrome b5, heme-binding site	RT	▮		4	4.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	heme	RT	▮		4	6.5E-1	9.8E-1
☐	GOTERM_MF_FAT	heme binding	RT	▮		5	6.8E-1	1.0E0
☐	GOTERM_MF_FAT	tetrapyrrole binding	RT	▮		5	6.8E-1	1.0E0
	Annotation Cluster 20	Enrichment Score: 0.27	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	membrane	RT	▮		18	3.7E-1	9.7E-1
☐	SP_PIR_KEYWORDS	transmembrane	RT	▮		19	4.8E-1	9.6E-1
☐	GOTERM_CC_FAT	integral to membrane	RT	▮		37	6.8E-1	1.0E0
☐	GOTERM_CC_FAT	intrinsic to membrane	RT	▮		37	6.8E-1	1.0E0
	Annotation Cluster 21	Enrichment Score: 0.26	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	ATPase, P-type, ATPase-associated region	RT	▮		9	2.6E-1	1.0E0
☐	INTERPRO	ATPase, P-type phosphorylation site	RT	▮		7	2.8E-1	1.0E0
☐	INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT	▮		9	3.9E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	▮		9	3.9E-1	1.0E0
☐	GOTERM_MF_FAT	lipid transporter activity	RT	▮		5	5.1E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid-translocating ATPase activity	RT	▮		4	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid transporter activity	RT	▮		4	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	aminophospholipid transporter activity	RT	▮		4	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	lipid transport	RT	▮		4	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	lipid localization	RT	▮		4	6.6E-1	1.0E0
☐	INTERPRO	ATPase, P-type, phospholipid-translocating, flippase	RT	▮		3	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid transport	RT	▮		3	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	magnesium ion binding	RT	▮		8	8.8E-1	1.0E0
	Annotation Cluster 22	Enrichment Score: 0.26	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT	▮		20	3.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	helicase	RT	▮		28	3.8E-1	9.6E-1
☐	GOTERM_MF_FAT	purine NTP-dependent helicase activity	RT	▮		24	4.6E-1	1.0E0
☐	GOTERM_MF_FAT	ATP-dependent helicase activity	RT	▮		24	4.6E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity	RT	▮		56	5.4E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled	RT	▮		42	5.4E-1	1.0E0
☐	INTERPRO	RNA helicase, DEAD-box type, Q motif	RT	▮		11	5.8E-1	1.0E0
☐	SMART	HELICc	RT	▮		26	6.1E-1	1.0E0
☐	GOTERM_MF_FAT	helicase activity	RT	▮		32	6.2E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, C-terminal	RT	▮		26	6.4E-1	1.0E0
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT	▮		25	6.9E-1	1.0E0
☐	SMART	DEXDc	RT	▮		24	7.7E-1	1.0E0
☐	INTERPRO	DEAD-like helicase, N-terminal	RT	▮		24	7.9E-1	1.0E0
	Annotation Cluster 23	Enrichment Score: 0.25	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Thioredoxin-like	RT	▮		10	3.1E-1	1.0E0
☐	GOTERM_BP_FAT	cellular homeostasis	RT	▮		13	4.3E-1	1.0E0
☐	INTERPRO	Thioredoxin domain	RT	▮		5	5.1E-1	1.0E0
☐	INTERPRO	Thioredoxin, conserved site	RT	▮		5	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	cell redox homeostasis	RT	▮		12	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	homeostatic process	RT	▮		13	5.4E-1	1.0E0
☐	INTERPRO	Thioredoxin fold	RT	▮		14	5.6E-1	1.0E0
☐	INTERPRO	Thioredoxin-like subdomain	RT	▮		4	6.5E-1	1.0E0
☐	INTERPRO	Thioredoxin, core	RT	▮		5	6.8E-1	1.0E0

☐	INTERPRO	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	RT	4	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	antioxidant activity	RT	4	8.9E-1	1.0E0
	Annotation Cluster 24	Enrichment Score: 0.25		Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	microtubule associated complex	RT	10	5.0E-1	1.0E0
☐	GOTERM_CC_FAT	dynein complex	RT	8	5.7E-1	1.0E0
☐	INTERPRO	Dynein heavy chain	RT	8	6.2E-1	1.0E0
	Annotation Cluster 25	Enrichment Score: 0.24		Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	endomembrane system	RT	11	4.1E-1	1.0E0
☐	GOTERM_CC_FAT	pore complex	RT	4	6.2E-1	1.0E0
☐	GOTERM_CC_FAT	envelope	RT	4	6.2E-1	1.0E0
☐	GOTERM_CC_FAT	organelle envelope	RT	4	6.2E-1	1.0E0
☐	GOTERM_CC_FAT	nuclear pore	RT	4	6.2E-1	1.0E0
☐	GOTERM_CC_FAT	nuclear envelope	RT	4	6.2E-1	1.0E0
	Annotation Cluster 26	Enrichment Score: 0.24		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	acid-amino acid ligase activity	RT	19	2.5E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-nitrogen bonds	RT	22	2.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	ubl conjugation pathway	RT	10	3.0E-1	9.9E-1
☐	GOTERM_MF_FAT	small conjugating protein ligase activity	RT	10	3.1E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis	RT	55	3.2E-1	1.0E0
☐	SMART	UBCc	RT	9	3.7E-1	1.0E0
☐	INTERPRO	Ubiquitin-conjugating enzyme, E2	RT	9	3.9E-1	1.0E0
☐	INTERPRO	Ubiquitin-conjugating enzyme/RWD-like	RT	9	3.9E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	RT	17	4.5E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent protein catabolic process	RT	17	4.5E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecule catabolic process	RT	24	5.4E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule catabolic process	RT	21	5.5E-1	1.0E0
☐	GOTERM_BP_FAT	protein catabolic process	RT	23	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein catabolic process	RT	20	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	RT	20	6.1E-1	1.0E0
☐	GOTERM_CC_FAT	cytosol	RT	17	6.3E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001567:ubiquitin-protein ligase E2	RT	4	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	RT	8	8.2E-1	1.0E0
☐	INTERPRO	Proteasome, alpha and beta subunits	RT	7	8.8E-1	1.0E0
☐	INTERPRO	Proteasome, alpha-subunit, conserved site	RT	4	8.9E-1	1.0E0
☐	GOTERM_CC_FAT	proteasome core complex	RT	7	9.1E-1	1.0E0
☐	KEGG_PATHWAY	Proteasome	RT	14	9.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	proteasome	RT	10	9.2E-1	1.0E0
☐	INTERPRO	Proteasome, subunit alpha/beta	RT	7	9.2E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type peptidase activity	RT	7	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type endopeptidase activity	RT	7	9.3E-1	1.0E0
☐	GOTERM_CC_FAT	proteasome complex	RT	10	9.3E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001212:multicatalytic endopeptidase complex chain C9	RT	3	9.5E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 0.23		Count	P_Value	Benjamini
☐	INTERPRO	DNA-directed DNA polymerase, family B, conserved site	RT	4	4.4E-1	1.0E0
☐	INTERPRO	DNA-directed DNA polymerase, family B, conserved region2	RT	4	4.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna replication	RT	7	5.8E-1	9.8E-1
☐	SMART	POLBc	RT	4	6.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-directed dna polymerase	RT	4	6.5E-1	9.8E-1
☐	INTERPRO	DNA-directed DNA polymerase, family B	RT	4	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	DNA-directed DNA polymerase activity	RT	6	8.1E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 0.22		Count	P_Value	Benjamini
☐	SMART	ARF	RT	4	4.4E-1	1.0E0
☐	INTERPRO	ADP-ribosylation factor	RT	4	4.4E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001711:ADP-ribosylation factor	RT	4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT	10	6.7E-1	1.0E0
☐	INTERPRO	ARF/SAR superfamily	RT	5	6.8E-1	1.0E0

☐	INTERPRO	Small GTP-binding protein	RT		11	8.4E-1	1.0E0
	Annotation Cluster 29	Enrichment Score: 0.22	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	regulation of transcription	RT		21	3.1E-1	1.0E0
☐	GOTERM_CC_FAT	nucleoplasm part	RT		3	6.0E-1	1.0E0
☐	GOTERM_CC_FAT	nucleoplasm	RT		3	6.0E-1	1.0E0
☐	GOTERM_CC_FAT	transcription factor complex	RT		3	6.0E-1	1.0E0
☐	GOTERM_CC_FAT	intracellular organelle lumen	RT		4	6.2E-1	1.0E0
☐	GOTERM_CC_FAT	nuclear lumen	RT		4	6.2E-1	1.0E0
☐	GOTERM_CC_FAT	membrane-enclosed lumen	RT		4	6.2E-1	1.0E0
☐	GOTERM_CC_FAT	organelle lumen	RT		4	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of transcription, DNA-dependent	RT		7	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of RNA metabolic process	RT		7	8.1E-1	1.0E0
	Annotation Cluster 30	Enrichment Score: 0.21	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	organelle membrane	RT		8	4.3E-1	1.0E0
☐	GOTERM_CC_FAT	endoplasmic reticulum membrane	RT		3	6.0E-1	1.0E0
☐	GOTERM_CC_FAT	endoplasmic reticulum part	RT		3	6.0E-1	1.0E0
☐	GOTERM_CC_FAT	nuclear envelope-endoplasmic reticulum network	RT		3	6.0E-1	1.0E0
☐	GOTERM_CC_FAT	endoplasmic reticulum	RT		3	9.4E-1	1.0E0
	Annotation Cluster 31	Enrichment Score: 0.21	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	ribonucleoprotein complex	RT		58	4.4E-1	1.0E0
☐	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT		90	5.5E-1	1.0E0
☐	GOTERM_CC_FAT	non-membrane-bounded organelle	RT		90	5.5E-1	1.0E0
☐	GOTERM_CC_FAT	ribosome	RT		43	5.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	ribosomal protein	RT		42	6.1E-1	9.8E-1
☐	KEGG_PATHWAY	Ribosome	RT		39	6.5E-1	1.0E0
☐	GOTERM_BP_FAT	translation	RT		64	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	structural molecule activity	RT		47	7.5E-1	1.0E0
☐	GOTERM_MF_FAT	structural constituent of ribosome	RT		38	8.3E-1	1.0E0
	Annotation Cluster 32	Enrichment Score: 0.19	G	🟩	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF005902:DNase_TatD	RT		3	6.1E-1	1.0E0
☐	INTERPRO	Deoxyribonuclease, TatD Mg-dependent	RT		3	6.2E-1	1.0E0
☐	INTERPRO	Deoxyribonuclease, TatD-related	RT		3	6.2E-1	1.0E0
☐	INTERPRO	Deoxyribonuclease, TatD	RT		3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	endodeoxyribonuclease activity, producing 5'-phosphomonoesters	RT		3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	deoxyribonuclease activity	RT		3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	endodeoxyribonuclease activity	RT		3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	RT		4	8.9E-1	1.0E0
	Annotation Cluster 33	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulpur binding domain	RT		7	4.4E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, subgroup	RT		7	4.4E-1	1.0E0
☐	GOTERM_MF_FAT	electron carrier activity	RT		14	6.6E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, conserved site	RT		5	6.8E-1	1.0E0
☐	GOTERM_MF_FAT	metal cluster binding	RT		11	8.4E-1	1.0E0
☐	GOTERM_MF_FAT	iron-sulfur cluster binding	RT		11	8.4E-1	1.0E0
☐	GOTERM_MF_FAT	4 iron, 4 sulfur cluster binding	RT		4	9.4E-1	1.0E0
	Annotation Cluster 34	Enrichment Score: 0.16	G	🟩	Count	P_Value	Benjamini
☐	SMART	Sm	RT		5	6.6E-1	1.0E0
☐	INTERPRO	Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core	RT		5	6.8E-1	1.0E0
☐	INTERPRO	Like-Sm ribonucleoprotein, core	RT		7	7.1E-1	1.0E0
	Annotation Cluster 35	Enrichment Score: 0.16	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	phospholipid biosynthetic process	RT		6	3.9E-1	1.0E0
☐	GOTERM_BP_FAT	organophosphate metabolic process	RT		9	5.3E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid metabolic process	RT		8	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	lipid biosynthetic process	RT		8	8.2E-1	1.0E0
☐	GOTERM_BP_FAT	glycerolipid metabolic process	RT		4	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	glycerophospholipid metabolic process	RT		4	8.9E-1	1.0E0

☐	**GOTERM_BP_FAT**	phosphoinositide metabolic process	RT			4	8.9E-1	1.0E0
	Annotation Cluster 36	Enrichment Score: 0.16		G	🟩	Count	P_Value	Benjamini
☐	**SMART**	ANK	RT			250	5.9E-1	1.0E0
☐	**INTERPRO**	Ankyrin	RT			250	6.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	ank repeat	RT			170	8.5E-1	9.9E-1
	Annotation Cluster 37	Enrichment Score: 0.16		G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Adenylate kinase	RT			3	6.2E-1	1.0E0
☐	**GOTERM_MF_FAT**	adenylate kinase activity	RT			3	6.2E-1	1.0E0
☐	**GOTERM_MF_FAT**	nucleotide kinase activity	RT			4	6.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	phosphotransferase activity, phosphate group as acceptor	RT			5	6.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	nucleobase, nucleoside, nucleotide kinase activity	RT			5	9.3E-1	1.0E0
	Annotation Cluster 38	Enrichment Score: 0.15		G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	WD40 repeat, conserved site	RT			18	5.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	wd repeat	RT			29	6.0E-1	9.8E-1
☐	**INTERPRO**	WD40 repeat, subgroup	RT			33	6.2E-1	1.0E0
☐	**INTERPRO**	WD40 repeat 2	RT			25	6.9E-1	1.0E0
☐	**INTERPRO**	WD40 repeat, region	RT			27	7.1E-1	1.0E0
☐	**SMART**	WD40	RT			40	8.4E-1	1.0E0
☐	**INTERPRO**	WD40 repeat	RT			40	8.6E-1	1.0E0
☐	**INTERPRO**	WD40/YVTN repeat-like	RT			38	9.0E-1	1.0E0
	Annotation Cluster 39	Enrichment Score: 0.14		G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	amine biosynthetic process	RT			5	5.1E-1	1.0E0
☐	**GOTERM_BP_FAT**	cellular amino acid biosynthetic process	RT			4	6.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	organic acid biosynthetic process	RT			4	8.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	carboxylic acid biosynthetic process	RT			4	8.9E-1	1.0E0
	Annotation Cluster 40	Enrichment Score: 0.13		G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	thiolester hydrolase activity	RT			6	5.6E-1	1.0E0
☐	**INTERPRO**	Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2	RT			4	8.0E-1	1.0E0
☐	**GOTERM_MF_FAT**	ubiquitin thiolesterase activity	RT			4	8.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	ubiquitin-dependent protein catabolic process	RT			8	8.2E-1	1.0E0
	Annotation Cluster 41	Enrichment Score: 0.13		G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	unfolded protein binding	RT			13	6.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	protein folding	RT			17	7.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Chaperone	RT			7	8.0E-1	9.9E-1
	Annotation Cluster 42	Enrichment Score: 0.13		G	🟩	Count	P_Value	Benjamini
☐	**SMART**	VWA	RT			5	6.6E-1	1.0E0
☐	**INTERPRO**	von Willebrand factor, type A	RT			5	6.8E-1	1.0E0
☐	**INTERPRO**	Copine	RT			3	9.0E-1	1.0E0
	Annotation Cluster 43	Enrichment Score: 0.12		G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	Acyltransferase	RT			8	4.7E-1	9.6E-1
☐	**INTERPRO**	Acyl-CoA N-acyltransferase	RT			6	8.0E-1	1.0E0
☐	**GOTERM_MF_FAT**	N-acyltransferase activity	RT			6	8.1E-1	1.0E0
☐	**GOTERM_MF_FAT**	acetyltransferase activity	RT			6	8.1E-1	1.0E0
☐	**INTERPRO**	GCN5-related N-acetyltransferase	RT			5	8.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	N-acetyltransferase activity	RT			5	8.8E-1	1.0E0
	Annotation Cluster 44	Enrichment Score: 0.12		G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	EGF-like, type 3	RT			20	5.2E-1	1.0E0
☐	**SMART**	EGF_Lam	RT			13	9.2E-1	1.0E0
☐	**INTERPRO**	EGF-like, laminin	RT			13	9.3E-1	1.0E0
	Annotation Cluster 45	Enrichment Score: 0.12		G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Molecular chaperone, heat shock protein, Hsp40, DnaJ	RT			5	6.8E-1	1.0E0
☐	**SMART**	DnaJ	RT			5	7.9E-1	1.0E0
☐	**INTERPRO**	Heat shock protein DnaJ, N-terminal	RT			5	8.0E-1	1.0E0
☐	**GOTERM_MF_FAT**	heat shock protein binding	RT			5	8.0E-1	1.0E0
	Annotation Cluster 46	Enrichment Score: 0.11		G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	translational elongation	RT			5	6.8E-1	1.0E0
☐	**GOTERM_MF_FAT**	translation elongation factor activity	RT			5	8.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	elongation factor	RT			4	8.8E-1	9.9E-1

	Annotation Cluster 47	Enrichment Score: 0.1	G		🟩	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF002306:tubulin	RT	▮		5	6.6E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, 2-layer sandwich domain	RT	▮		5	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex assembly	RT	▮		8	7.3E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex biogenesis	RT	▮		8	7.3E-1	1.0E0
☐	INTERPRO	Beta tubulin, autoregulation binding site	RT	▮		4	8.0E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, GTPase domain	RT	▮		5	8.0E-1	1.0E0
☐	INTERPRO	Tubulin, conserved site	RT	▮		5	8.0E-1	1.0E0
☐	INTERPRO	Tubulin	RT	▮		5	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	protein polymerization	RT	▮		5	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecular complex subunit organization	RT	▮		15	8.2E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecular complex assembly	RT	▮		14	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein complex assembly	RT	▮		6	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase activity	RT	▮		9	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex subunit organization	RT	▮		13	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex assembly	RT	▮		12	9.3E-1	1.0E0
	Annotation Cluster 48	Enrichment Score: 0.08	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	exopeptidase activity	RT	▮		7	7.2E-1	1.0E0
☐	GOTERM_MF_FAT	metallopeptidase activity	RT	▮		7	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	metalloexopeptidase activity	RT	▮		4	8.9E-1	1.0E0
	Annotation Cluster 49	Enrichment Score: 0.08	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	RNA-directed DNA polymerase (reverse transcriptase)	RT	▮		5	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	RNA-dependent DNA replication	RT	▮		5	6.8E-1	1.0E0
☐	INTERPRO	RNA-directed DNA polymerase (reverse transcriptase), related	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	RNA-directed DNA polymerase activity	RT	▮		11	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	rna-directed dna polymerase	RT	▮		10	9.8E-1	1.0E0
	Annotation Cluster 50	Enrichment Score: 0.07	G		🟩	Count	P_Value	Benjamini
☐	SMART	RRM	RT	▮		8	8.0E-1	1.0E0
☐	INTERPRO	RNA recognition motif, RNP-1	RT	▮		8	8.2E-1	1.0E0
☐	INTERPRO	Nucleotide-binding, alpha-beta plait	RT	▮		8	9.2E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 0.07	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	intracellular signaling cascade	RT	▮		13	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT	▮		10	6.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	gtp-binding	RT	▮		22	8.0E-1	9.9E-1
☐	INTERPRO	Small GTP-binding protein	RT	▮		11	8.4E-1	1.0E0
☐	INTERPRO	Ras GTPase	RT	▮		7	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase activity	RT	▮		9	8.8E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001710:Ras-related protein Rab	RT	▮		3	9.5E-1	1.0E0
☐	GOTERM_MF_FAT	GTP binding	RT	▮		24	9.5E-1	1.0E0
☐	GOTERM_MF_FAT	guanyl ribonucleotide binding	RT	▮		24	9.5E-1	1.0E0
☐	GOTERM_MF_FAT	guanyl nucleotide binding	RT	▮		24	9.5E-1	1.0E0
☐	INTERPRO	Ras	RT	▮		5	9.8E-1	1.0E0
	Annotation Cluster 52	Enrichment Score: 0.07	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	DNA replication	RT	▮		12	7.5E-1	1.0E0
☐	KEGG_PATHWAY	Nucleotide excision repair	RT	▮		8	9.1E-1	1.0E0
☐	KEGG_PATHWAY	Mismatch repair	RT	▮		7	9.2E-1	1.0E0
	Annotation Cluster 53	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	iron	RT	▮		12	6.9E-1	9.8E-1
☐	GOTERM_MF_FAT	iron ion binding	RT	▮		18	7.2E-1	1.0E0
☐	SMART	PP2Ac	RT	▮		8	8.7E-1	1.0E0
☐	INTERPRO	Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase	RT	▮		8	8.8E-1	1.0E0
☐	INTERPRO	Metallophosphoesterase	RT	▮		11	8.9E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF000908:serine/threonine-protein phosphatase, conventional type	RT	▮		4	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	phosphoprotein phosphatase activity	RT	▮		11	1.0E0	1.0E0
☐	GOTERM_MF_FAT	phosphatase activity	RT	▮		18	1.0E0	1.0E0
	Annotation Cluster 54	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	organelle membrane	RT	▮		8	4.3E-1	1.0E0

☐	GOTERM_CC_FAT	membrane coat	RT	8	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	coated membrane	RT	8	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	transport vesicle membrane	RT	3	8.8E-1	1.0E0
☐	GOTERM_CC_FAT	transport vesicle	RT	3	8.8E-1	1.0E0
☐	INTERPRO	Clathrin/coatomer adaptor, adaptin-like, N-terminal	RT	3	9.0E-1	1.0E0
☐	GOTERM_CC_FAT	membrane-bounded vesicle	RT	3	9.4E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle	RT	3	9.4E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle	RT	3	9.4E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle membrane	RT	3	9.4E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle membrane	RT	3	9.4E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle coat	RT	3	9.4E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle part	RT	3	9.4E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle	RT	3	9.4E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic membrane-bounded vesicle	RT	3	9.4E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle membrane	RT	3	9.4E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus part	RT	3	9.9E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus	RT	3	1.0E0	1.0E0
	Annotation Cluster 55	Enrichment Score: 0.05	G	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	membrane coat	RT	8	7.8E-1	1.0E0
☐	GOTERM_CC_FAT	coated membrane	RT	8	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	establishment of protein localization	RT	18	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	protein transport	RT	18	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	protein localization	RT	18	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular transport	RT	14	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular protein transport	RT	11	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule localization	RT	11	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein localization	RT	11	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	vesicle-mediated transport	RT	14	9.5E-1	1.0E0
	Annotation Cluster 56	Enrichment Score: 0.05	G	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	cation binding	RT	146	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	ion binding	RT	146	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	metal ion binding	RT	144	7.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	metal-binding	RT	54	8.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc	RT	45	8.8E-1	9.9E-1
☐	GOTERM_MF_FAT	transition metal ion binding	RT	101	9.4E-1	1.0E0
☐	INTERPRO	Zinc finger, C3HC4 RING-type	RT	17	9.5E-1	1.0E0
☐	GOTERM_MF_FAT	zinc ion binding	RT	80	9.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc-finger	RT	30	9.6E-1	1.0E0
☐	SMART	RING	RT	33	9.6E-1	1.0E0
☐	INTERPRO	Zinc finger, RING-type	RT	33	9.7E-1	1.0E0
	Annotation Cluster 57	Enrichment Score: 0.05	G	Count	P_Value	Benjamini
☐	INTERPRO	ATPase, AAA-type, core	RT	14	8.0E-1	1.0E0
☐	SMART	AAA	RT	36	9.4E-1	1.0E0
☐	INTERPRO	ATPase, AAA+ type, core	RT	36	9.5E-1	1.0E0
	Annotation Cluster 58	Enrichment Score: 0.05	G	Count	P_Value	Benjamini
☐	INTERPRO	Aminoacyl-tRNA synthetase, class I, conserved site	RT	6	7.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	ligase	RT	31	7.4E-1	9.9E-1
☐	SP_PIR_KEYWORDS	protein biosynthesis	RT	6	8.0E-1	9.9E-1
☐	GOTERM_BP_FAT	tRNA aminoacylation for protein translation	RT	11	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	aminoacyl-tRNA ligase activity	RT	12	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-oxygen bonds	RT	12	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming aminoacyl-tRNA and related compounds	RT	12	9.3E-1	1.0E0
☐	KEGG_PATHWAY	Aminoacyl-tRNA biosynthesis	RT	10	9.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	Aminoacyl-tRNA synthetase	RT	11	9.5E-1	1.0E0
☐	INTERPRO	Rossmann-like alpha/beta/alpha sandwich fold	RT	9	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	amino acid activation	RT	11	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA aminoacylation	RT	11	9.5E-1	1.0E0

☐	GOTERM_BP_FAT	tRNA metabolic process	RT			19	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA metabolic process	RT			24	9.9E-1	1.0E0
	Annotation Cluster 59	Enrichment Score: 0.05		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	water-soluble vitamin biosynthetic process	RT			3	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	vitamin biosynthetic process	RT			3	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	water-soluble vitamin metabolic process	RT			3	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	vitamin metabolic process	RT			3	9.0E-1	1.0E0
	Annotation Cluster 60	Enrichment Score: 0.04		G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Chaperone	RT			7	8.0E-1	9.9E-1
☐	INTERPRO	Chaperonin Cpn60/TCP-1	RT			5	8.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	cytoplasm	RT			9	9.2E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002584:molecular chaperone t-complex-type	RT			4	9.4E-1	1.0E0
☐	INTERPRO	Chaperone, tailless complex polypeptide 1	RT			4	9.4E-1	1.0E0
☐	INTERPRO	Chaperonin TCP-1, conserved site	RT			4	9.7E-1	1.0E0
	Annotation Cluster 61	Enrichment Score: 0.04		G	🟩	Count	P_Value	Benjamini
☐	SMART	UBQ	RT			4	8.8E-1	1.0E0
☐	INTERPRO	Ubiquitin	RT			4	8.9E-1	1.0E0
☐	INTERPRO	Ubiquitin supergroup	RT			5	9.8E-1	1.0E0
	Annotation Cluster 62	Enrichment Score: 0.04		G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	ABC transporter-like	RT			12	8.9E-1	1.0E0
☐	INTERPRO	ABC transporter, conserved site	RT			11	9.2E-1	1.0E0
☐	COG_ONTOLOGY	Defense mechanisms	RT			11	9.4E-1	1.0E0
	Annotation Cluster 63	Enrichment Score: 0.03		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cytoskeleton organization	RT			9	8.3E-1	1.0E0
☐	GOTERM_MF_FAT	lipid binding	RT			19	8.9E-1	1.0E0
☐	SMART	ANX	RT			7	9.2E-1	1.0E0
☐	INTERPRO	Annexin repeat	RT			7	9.2E-1	1.0E0
☐	GOTERM_MF_FAT	calcium-dependent phospholipid binding	RT			11	9.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	annexin	RT			7	9.7E-1	1.0E0
☐	INTERPRO	Annexin	RT			7	9.7E-1	1.0E0
☐	INTERPRO	Alpha giardin	RT			5	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid binding	RT			12	9.8E-1	1.0E0
	Annotation Cluster 64	Enrichment Score: 0.03		G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	tpr repeat	RT			5	8.8E-1	1.0E0
☐	INTERPRO	Tetratricopeptide TPR-1	RT			10	9.2E-1	1.0E0
☐	INTERPRO	Tetratricopeptide region	RT			12	9.2E-1	1.0E0
☐	INTERPRO	Tetratricopeptide-like helical	RT			15	9.5E-1	1.0E0
☐	SMART	TPR	RT			11	9.6E-1	1.0E0
☐	INTERPRO	Tetratricopeptide repeat	RT			11	9.7E-1	1.0E0
	Annotation Cluster 65	Enrichment Score: 0.03		G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Rotamase	RT			4	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	peptidyl-prolyl cis-trans isomerase activity	RT			4	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	cis-trans isomerase activity	RT			4	9.4E-1	1.0E0
	Annotation Cluster 66	Enrichment Score: 0.02		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	ribosome biogenesis	RT			10	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoprotein complex biogenesis	RT			10	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA metabolic process	RT			6	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA processing	RT			6	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA processing	RT			13	9.8E-1	1.0E0
	Annotation Cluster 67	Enrichment Score: 0.02		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid catabolic process	RT			3	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide catabolic process	RT			3	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	nitrogen compound catabolic process	RT			3	9.5E-1	1.0E0
	Annotation Cluster 68	Enrichment Score: 0.02		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cofactor metabolic process	RT			6	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	coenzyme metabolic process	RT			5	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	pyridine nucleotide metabolic process	RT			3	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	oxidoreduction coenzyme metabolic process	RT			3	9.5E-1	1.0E0

☐	GOTERM_BP_FAT	cofactor biosynthetic process	RT			4	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	coenzyme biosynthetic process	RT	▮		3	9.8E-1	1.0E0
	Annotation Cluster 69	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	RNA processing	RT	▮		23	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA processing	RT	▮		8	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA metabolic process	RT	▮		19	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA processing	RT	▮		13	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA metabolic process	RT	▮		24	9.9E-1	1.0E0
	Annotation Cluster 70	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	transcription	RT	▮		14	8.6E-1	1.0E0
☐	KEGG_PATHWAY	Purine metabolism	RT	▮		15	9.6E-1	1.0E0
☐	GOTERM_MF_FAT	RNA polymerase activity	RT	▮		10	9.9E-1	1.0E0
☐	KEGG_PATHWAY	RNA polymerase	RT	▮		7	9.9E-1	1.0E0
☐	GOTERM_MF_FAT	DNA-directed RNA polymerase activity	RT	▮		9	9.9E-1	1.0E0
☐	KEGG_PATHWAY	Pyrimidine metabolism	RT	▮		13	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	dna-directed rna polymerase	RT	▮		4	1.0E0	1.0E0
	Annotation Cluster 71	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	DNA polymerase activity	RT	▮		17	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	RNA-directed DNA polymerase activity	RT	▮		11	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	rna-directed dna polymerase	RT	▮		10	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	endonuclease activity	RT	▮		15	9.9E-1	1.0E0
☐	GOTERM_MF_FAT	nuclease activity	RT	▮		23	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	Endonuclease	RT	▮		12	9.9E-1	1.0E0
	Annotation Cluster 72	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular macromolecular complex assembly	RT	▮		12	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	chromosome organization	RT	▮		8	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin organization	RT	▮		6	9.9E-1	1.0E0
☐	GOTERM_CC_FAT	nucleosome	RT	▮		4	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly or disassembly	RT	▮		5	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	chromosomal protein	RT	▮		4	9.9E-1	1.0E0
☐	INTERPRO	Histone core	RT	▮		4	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome assembly	RT	▮		4	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	DNA packaging	RT	▮		4	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly	RT	▮		4	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	protein-DNA complex assembly	RT	▮		4	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome organization	RT	▮		4	9.9E-1	1.0E0
☐	INTERPRO	Histone-fold	RT	▮		5	9.9E-1	1.0E0
☐	GOTERM_CC_FAT	chromatin	RT	▮		4	9.9E-1	1.0E0
☐	GOTERM_CC_FAT	chromosomal part	RT	▮		6	9.9E-1	1.0E0
☐	GOTERM_CC_FAT	chromosome	RT	▮		10	1.0E0	1.0E0
☐	GOTERM_CC_FAT	protein-DNA complex	RT	▮		4	1.0E0	1.0E0
	Annotation Cluster 73	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, C2H2-type	RT	▮		7	9.9E-1	1.0E0
☐	SMART	ZnF_C2H2	RT	▮		6	1.0E0	1.0E0
☐	INTERPRO	Zinc finger, C2H2-like	RT	▮		6	1.0E0	1.0E0
	Annotation Cluster 74	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	phosphoprotein phosphatase activity	RT	▮		11	1.0E0	1.0E0
☐	GOTERM_BP_FAT	protein amino acid dephosphorylation	RT	▮		4	1.0E0	1.0E0
☐	GOTERM_BP_FAT	dephosphorylation	RT	▮		4	1.0E0	1.0E0
	Annotation Cluster 75	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	response to DNA damage stimulus	RT	▮		7	1.0E0	1.0E0
☐	GOTERM_BP_FAT	DNA repair	RT	▮		7	1.0E0	1.0E0
☐	GOTERM_BP_FAT	cellular response to stress	RT	▮		7	1.0E0	1.0E0

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

Functional Annotation Clustering

Help and Manual

Current Gene List: 3_Random9
Current Background: Giardia intestinalis
3000 DAVID IDs

Options **Classification Stringency** Medium

[Rerun using options] [Create Sublist]

79 Cluster(s)

Download File

	Annotation Cluster 1	Enrichment Score: 0.85		Count	P_Value	Benjamini
☐	INTERPRO	EGF-like, type 3	RT	24	8.2E-2	1.0E0
☐	INTERPRO	EGF-like, laminin	RT	19	1.8E-1	1.0E0
☐	SMART	EGF_Lam	RT	19	1.9E-1	1.0E0
	Annotation Cluster 2	Enrichment Score: 0.81		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	nucleotidyltransferase	RT	20	7.8E-2	1.0E0
☐	KEGG_PATHWAY	Purine metabolism	RT	25	1.0E-1	9.2E-1
☐	KEGG_PATHWAY	RNA polymerase	RT	15	1.4E-1	9.1E-1
☐	GOTERM_MF_FAT	RNA polymerase activity	RT	18	1.4E-1	1.0E0
☐	GOTERM_BP_FAT	transcription	RT	19	1.5E-1	1.0E0
☐	KEGG_PATHWAY	Pyrimidine metabolism	RT	25	1.6E-1	8.7E-1
☐	GOTERM_MF_FAT	DNA-directed RNA polymerase activity	RT	17	1.8E-1	1.0E0
☐	GOTERM_MF_FAT	nucleotidyltransferase activity	RT	46	2.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-directed rna polymerase	RT	11	2.9E-1	1.0E0
	Annotation Cluster 3	Enrichment Score: 0.78		Count	P_Value	Benjamini
☐	INTERPRO	Giardia variant-specific surface protein	RT	151	5.1E-2	1.0E0
☐	INTERPRO	EGF-like	RT	119	1.5E-1	1.0E0
☐	SMART	EGF	RT	119	1.9E-1	1.0E0
☐	INTERPRO	Furin-like repeat	RT	113	2.6E-1	1.0E0
☐	SMART	FU	RT	113	3.1E-1	1.0E0
	Annotation Cluster 4	Enrichment Score: 0.75		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular response to stress	RT	16	1.4E-1	1.0E0
☐	GOTERM_BP_FAT	response to DNA damage stimulus	RT	15	1.8E-1	1.0E0
☐	GOTERM_BP_FAT	DNA repair	RT	15	1.8E-1	1.0E0
☐	GOTERM_BP_FAT	DNA metabolic process	RT	38	2.4E-1	1.0E0
	Annotation Cluster 5	Enrichment Score: 0.69		Count	P_Value	Benjamini
☐	INTERPRO	EGF-like, type 3	RT	24	8.2E-2	1.0E0
☐	INTERPRO	EGF	RT	7	1.4E-1	1.0E0
☐	INTERPRO	EGF, extracellular	RT	16	3.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	egf-like domain	RT	12	4.6E-1	9.9E-1
	Annotation Cluster 6	Enrichment Score: 0.67		Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	ribosome	RT	49	2.5E-2	9.6E-1
☐	GOTERM_CC_FAT	ribonucleoprotein complex	RT	60	8.9E-2	9.8E-1
☐	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT	90	1.8E-1	1.0E0
☐	GOTERM_CC_FAT	non-membrane-bounded organelle	RT	90	1.8E-1	1.0E0
☐	GOTERM_MF_FAT	structural constituent of ribosome	RT	45	2.0E-1	1.0E0
☐	GOTERM_MF_FAT	structural molecule activity	RT	52	3.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	ribosomal protein	RT	46	4.0E-1	1.0E0
☐	KEGG_PATHWAY	Ribosome	RT	43	6.7E-1	9.8E-1
☐	GOTERM_BP_FAT	translation	RT	63	7.1E-1	1.0E0
	Annotation Cluster 7	Enrichment Score: 0.62		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	nucleoside binding	RT	326	5.2E-2	1.0E0
☐	GOTERM_MF_FAT	adenyl nucleotide binding	RT	322	7.5E-2	1.0E0
☐	GOTERM_MF_FAT	purine nucleoside binding	RT	322	7.5E-2	1.0E0
☐	GOTERM_MF_FAT	ATP binding	RT	317	9.0E-2	1.0E0
☐	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT	317	9.0E-2	1.0E0

☐	GOTERM_MF_FAT	nucleotide binding	RT	369	1.1E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleotide binding	RT	347	1.4E-1	1.0E0
☐	GOTERM_MF_FAT	purine ribonucleotide binding	RT	342	1.6E-1	1.0E0
☐	GOTERM_MF_FAT	ribonucleotide binding	RT	342	1.6E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid phosphorylation	RT	157	3.7E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorylation	RT	167	4.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	kinase	RT	200	4.8E-1	9.9E-1
☐	GOTERM_BP_FAT	phosphate metabolic process	RT	175	4.8E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorus metabolic process	RT	175	4.8E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase-related	RT	137	4.9E-1	1.0E0
☐	GOTERM_MF_FAT	protein kinase activity	RT	157	5.5E-1	1.0E0
☐	INTERPRO	Protein kinase, core	RT	155	5.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	atp-binding	RT	155	5.6E-1	9.9E-1
☐	GOTERM_MF_FAT	protein serine/threonine kinase activity	RT	61	5.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT	162	6.1E-1	9.9E-1
	Annotation Cluster 8	Enrichment Score: 0.56		Count	P_Value	Benjamini
☐	INTERPRO	Tetratricopeptide region	RT	19	7.0E-2	1.0E0
☐	INTERPRO	Tetratricopeptide repeat	RT	17	2.7E-1	1.0E0
☐	SMART	TPR	RT	17	2.9E-1	1.0E0
☐	INTERPRO	Tetratricopeptide-like helical	RT	21	3.0E-1	1.0E0
☐	INTERPRO	Tetratricopeptide TPR-1	RT	14	3.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	tpr repeat	RT	6	7.4E-1	9.9E-1
	Annotation Cluster 9	Enrichment Score: 0.49		Count	P_Value	Benjamini
☐	INTERPRO	WD40 repeat, subgroup	RT	37	2.2E-1	1.0E0
☐	INTERPRO	WD40 repeat 2	RT	29	2.3E-1	1.0E0
☐	INTERPRO	WD40 repeat, region	RT	31	2.7E-1	1.0E0
☐	INTERPRO	WD40 repeat	RT	47	2.9E-1	1.0E0
☐	SMART	WD40	RT	47	3.3E-1	1.0E0
☐	INTERPRO	WD40/YVTN repeat-like	RT	45	3.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	wd repeat	RT	32	4.0E-1	1.0E0
☐	INTERPRO	WD40 repeat, conserved site	RT	17	7.1E-1	1.0E0
	Annotation Cluster 10	Enrichment Score: 0.47		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	peptidyl-prolyl cis-trans isomerase activity	RT	7	2.8E-1	1.0E0
☐	GOTERM_MF_FAT	cis-trans isomerase activity	RT	7	2.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	Rotamase	RT	7	3.2E-1	1.0E0
☐	INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type	RT	5	5.1E-1	1.0E0
	Annotation Cluster 11	Enrichment Score: 0.46		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	homeostatic process	RT	15	1.8E-1	1.0E0
☐	GOTERM_BP_FAT	cellular homeostasis	RT	14	2.3E-1	1.0E0
☐	GOTERM_BP_FAT	cell redox homeostasis	RT	13	2.9E-1	1.0E0
☐	INTERPRO	Thioredoxin fold	RT	15	3.9E-1	1.0E0
☐	INTERPRO	Thioredoxin-like	RT	9	5.3E-1	1.0E0
☐	INTERPRO	Thioredoxin, core	RT	5	6.8E-1	1.0E0
	Annotation Cluster 12	Enrichment Score: 0.45		Count	P_Value	Benjamini
☐	INTERPRO	Ankyrin	RT	262	2.2E-1	1.0E0
☐	SMART	ANK	RT	262	2.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	ank repeat	RT	182	6.9E-1	9.9E-1
	Annotation Cluster 13	Enrichment Score: 0.4		Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Nucleotide excision repair	RT	13	2.3E-1	9.2E-1
☐	KEGG_PATHWAY	DNA replication	RT	15	4.7E-1	9.9E-1
☐	KEGG_PATHWAY	Mismatch repair	RT	10	5.9E-1	9.8E-1
	Annotation Cluster 14	Enrichment Score: 0.36		Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	cytosolic part	RT	7	3.2E-1	1.0E0
☐	GOTERM_CC_FAT	prefoldin complex	RT	5	4.1E-1	1.0E0
☐	INTERPRO	Prefoldin alpha-like	RT	3	6.2E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 0.35		Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	cytosol	RT	21	5.8E-2	9.8E-1
☐	GOTERM_CC_FAT	proteasome complex	RT	14	2.8E-1	1.0E0

☐	GOTERM_CC_FAT	proteasome core complex	RT		10	2.9E-1	1.0E0
☐	INTERPRO	Proteasome, alpha-subunit, conserved site	RT		6	3.8E-1	1.0E0
☐	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	RT		10	4.0E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type peptidase activity	RT		10	4.3E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type endopeptidase activity	RT		10	4.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	proteasome	RT		14	4.3E-1	1.0E0
☐	INTERPRO	Proteasome, subunit alpha/beta	RT		10	4.3E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule catabolic process	RT		21	5.0E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001212:multicatalytic endopeptidase complex chain C9	RT		5	5.1E-1	1.0E0
☐	INTERPRO	Proteasome, alpha and beta subunits	RT		9	5.3E-1	1.0E0
☐	KEGG_PATHWAY	Proteasome	RT		19	5.4E-1	9.7E-1
☐	GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	RT		20	5.6E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein catabolic process	RT		20	5.6E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent protein catabolic process	RT		16	5.7E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	RT		16	5.7E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecule catabolic process	RT		22	7.3E-1	1.0E0
☐	GOTERM_BP_FAT	protein catabolic process	RT		21	7.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	threonine protease	RT		4	8.3E-1	9.9E-1
	Annotation Cluster 16	Enrichment Score: 0.34	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	endopeptidase activity	RT		30	3.0E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type peptidase activity	RT		20	3.5E-1	1.0E0
☐	INTERPRO	Peptidase, cysteine peptidase active site	RT		20	3.6E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain	RT		18	3.9E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain C-terminal	RT		18	3.9E-1	1.0E0
☐	SMART	Pept_C1	RT		18	4.1E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type endopeptidase activity	RT		16	4.1E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis	RT		51	5.9E-1	1.0E0
☐	GOTERM_MF_FAT	peptidase activity, acting on L-amino acid peptides	RT		40	6.0E-1	1.0E0
☐	GOTERM_MF_FAT	peptidase activity	RT		46	6.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	thiol protease	RT		7	6.4E-1	9.9E-1
☐	SP_PIR_KEYWORDS	Protease	RT		22	6.7E-1	9.8E-1
	Annotation Cluster 17	Enrichment Score: 0.31	G	🟩	Count	P_Value	Benjamini
☐	COG_ONTOLOGY	Lipid metabolism	RT		11	1.5E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-sulfur bonds	RT		4	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	fatty-acid ligase activity	RT		4	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	long-chain-fatty-acid-CoA ligase activity	RT		4	6.5E-1	1.0E0
☐	INTERPRO	AMP-dependent synthetase and ligase	RT		5	6.8E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 0.31	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Amino acid transporter, transmembrane	RT		8	3.4E-1	1.0E0
☐	GOTERM_CC_FAT	intrinsic to membrane	RT		37	4.7E-1	1.0E0
☐	GOTERM_CC_FAT	integral to membrane	RT		37	4.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	transmembrane	RT		19	6.0E-1	9.9E-1
☐	SP_PIR_KEYWORDS	membrane	RT		17	6.3E-1	9.9E-1
	Annotation Cluster 19	Enrichment Score: 0.3	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	cytoplasm	RT		14	2.2E-1	1.0E0
☐	GOTERM_MF_FAT	unfolded protein binding	RT		15	2.9E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002584:molecular chaperone t-complex-type	RT		6	5.5E-1	1.0E0
☐	INTERPRO	Chaperone, tailless complex polypeptide 1	RT		6	5.6E-1	1.0E0
☐	INTERPRO	Chaperonin TCP-1, conserved site	RT		6	7.0E-1	1.0E0
☐	INTERPRO	Chaperonin Cpn60/TCP-1	RT		6	7.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	Chaperone	RT		7	8.5E-1	9.9E-1
	Annotation Cluster 20	Enrichment Score: 0.3	G	🟩	Count	P_Value	Benjamini
☐	COG_ONTOLOGY	Nucleotide transport and metabolism	RT		7	2.9E-1	9.8E-1
☐	GOTERM_BP_FAT	nucleotide catabolic process	RT		4	4.3E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide catabolic process	RT		5	4.9E-1	1.0E0
☐	GOTERM_BP_FAT	nitrogen compound catabolic process	RT		5	4.9E-1	1.0E0

☐	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid catabolic process	RT	5	4.9E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF017316:Pesterase_C1039	RT	3	6.2E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF017316:phosphoesterase, C1039.02 type	RT	3	6.2E-1	1.0E0
☐	INTERPRO	5'-Nucleotidase and apyrase	RT	3	6.2E-1	1.0E0
☐	INTERPRO	Predicted phosphoesterase, C1039.02 type	RT	3	6.2E-1	1.0E0
	Annotation Cluster 21	Enrichment Score: 0.29		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	zinc-finger	RT	41	2.4E-1	1.0E0
☐	INTERPRO	Zinc finger, RING-type	RT	43	2.7E-1	1.0E0
☐	SMART	RING	RT	43	3.1E-1	1.0E0
☐	INTERPRO	Zinc finger, C3HC4 RING-type	RT	23	3.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc	RT	51	6.1E-1	9.9E-1
☐	GOTERM_MF_FAT	cation binding	RT	148	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	ion binding	RT	148	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	metal ion binding	RT	146	6.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	metal-binding	RT	59	7.3E-1	9.9E-1
☐	GOTERM_MF_FAT	zinc ion binding	RT	85	7.7E-1	1.0E0
☐	GOTERM_MF_FAT	transition metal ion binding	RT	105	7.9E-1	1.0E0
	Annotation Cluster 22	Enrichment Score: 0.29		Count	P_Value	Benjamini
☐	INTERPRO	DEAD-like helicase, N-terminal	RT	28	3.3E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity	RT	58	3.4E-1	1.0E0
☐	SMART	DEXDc	RT	28	3.6E-1	1.0E0
☐	GOTERM_MF_FAT	helicase activity	RT	34	3.8E-1	1.0E0
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT	27	4.5E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled	RT	42	5.2E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, C-terminal	RT	27	5.2E-1	1.0E0
☐	SMART	HELICc	RT	27	5.6E-1	1.0E0
☐	GOTERM_MF_FAT	purine NTP-dependent helicase activity	RT	23	5.8E-1	1.0E0
☐	GOTERM_MF_FAT	ATP-dependent helicase activity	RT	23	5.8E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT	18	6.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	helicase	RT	26	7.4E-1	9.9E-1
☐	INTERPRO	RNA helicase, DEAD-box type, Q motif	RT	8	9.5E-1	1.0E0
	Annotation Cluster 23	Enrichment Score: 0.27		Count	P_Value	Benjamini
☐	INTERPRO	Metallophosphoesterase	RT	16	1.6E-1	1.0E0
☐	GOTERM_MF_FAT	phosphatase activity	RT	28	3.9E-1	1.0E0
☐	INTERPRO	Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase	RT	10	5.6E-1	1.0E0
☐	SMART	PP2Ac	RT	10	5.8E-1	1.0E0
☐	GOTERM_MF_FAT	iron ion binding	RT	19	5.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	iron	RT	12	7.7E-1	9.8E-1
☐	GOTERM_MF_FAT	phosphoprotein phosphatase activity	RT	15	8.6E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF000908:serine/threonine-protein phosphatase, conventional type	RT	4	9.4E-1	1.0E0
	Annotation Cluster 24	Enrichment Score: 0.27		Count	P_Value	Benjamini
☐	INTERPRO	Aminotransferase, class I and II	RT	5	3.1E-1	1.0E0
☐	GOTERM_MF_FAT	vitamin B6 binding	RT	8	3.4E-1	1.0E0
☐	GOTERM_MF_FAT	pyridoxal phosphate binding	RT	8	3.4E-1	1.0E0
☐	GOTERM_MF_FAT	vitamin binding	RT	8	4.8E-1	1.0E0
☐	INTERPRO	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	RT	6	5.6E-1	1.0E0
☐	INTERPRO	Pyridoxal phosphate-dependent transferase, major region, subdomain 2	RT	3	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	transferase activity, transferring nitrogenous groups	RT	5	6.7E-1	1.0E0
☐	KEGG_PATHWAY	Alanine, aspartate and glutamate metabolism	RT	3	6.9E-1	9.8E-1
☐	GOTERM_MF_FAT	transaminase activity	RT	3	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	Aminotransferase	RT	3	9.2E-1	1.0E0
	Annotation Cluster 25	Enrichment Score: 0.26		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	monosaccharide metabolic process	RT	16	2.9E-1	1.0E0
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT	17	4.1E-1	1.0E0
☐	GOTERM_BP_FAT	glycolysis	RT	8	4.6E-1	1.0E0

☐	GOTERM_BP_FAT	glucose metabolic process	RT		13	5.0E-1	1.0E0
☐	GOTERM_BP_FAT	hexose metabolic process	RT		13	5.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	glycolysis	RT		5	5.5E-1	9.9E-1
☐	GOTERM_BP_FAT	cellular carbohydrate catabolic process	RT		9	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	carbohydrate catabolic process	RT		9	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	glucose catabolic process	RT		9	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	hexose catabolic process	RT		9	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide catabolic process	RT		9	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	alcohol catabolic process	RT		9	6.2E-1	1.0E0
☐	KEGG_PATHWAY	Glycolysis / Gluconeogenesis	RT		3	9.9E-1	1.0E0
	Annotation Cluster 26	Enrichment Score: 0.26	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Transcription	RT		7	3.2E-1	1.0E0
☐	GOTERM_MF_FAT	ribonucleoside binding	RT		4	4.4E-1	1.0E0
☐	INTERPRO	RNA polymerase Rpb2, domain 3	RT		3	6.2E-1	1.0E0
☐	INTERPRO	RNA polymerase, beta subunit, protrusion	RT		3	6.2E-1	1.0E0
☐	INTERPRO	RNA polymerase, beta subunit, conserved site	RT		3	6.2E-1	1.0E0
☐	INTERPRO	DNA-directed RNA polymerase, subunit 2, domain 6	RT		3	6.2E-1	1.0E0
☐	INTERPRO	RNA polymerase Rpb2, domain 7	RT		3	6.2E-1	1.0E0
☐	INTERPRO	DNA-directed RNA polymerase, subunit 2	RT		3	6.2E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 0.24	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Kinesin, motor region, conserved site	RT		14	1.7E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule	RT		19	5.2E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule cytoskeleton	RT		29	5.3E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeletal part	RT		29	5.3E-1	1.0E0
☐	GOTERM_MF_FAT	microtubule motor activity	RT		25	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	motor activity	RT		25	6.2E-1	1.0E0
☐	INTERPRO	Kinesin, motor region	RT		17	6.3E-1	1.0E0
☐	SMART	KISc	RT		17	6.5E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeleton	RT		29	6.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	motor protein	RT		15	6.7E-1	9.9E-1
☐	GOTERM_BP_FAT	microtubule-based movement	RT		27	6.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	microtubule	RT		19	7.5E-1	9.8E-1
☐	GOTERM_BP_FAT	microtubule-based process	RT		30	7.6E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 0.24	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	DNA-directed DNA polymerase, family B, conserved region2	RT		4	4.5E-1	1.0E0
☐	INTERPRO	DNA-directed DNA polymerase, family B, conserved site	RT		4	4.5E-1	1.0E0
☐	GOTERM_MF_FAT	DNA-directed DNA polymerase activity	RT		7	5.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna replication	RT		7	6.4E-1	9.9E-1
☐	INTERPRO	DNA-directed DNA polymerase, family B	RT		4	6.5E-1	1.0E0
☐	SMART	POLBc	RT		4	6.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-directed dna polymerase	RT		4	6.9E-1	9.8E-1
	Annotation Cluster 29	Enrichment Score: 0.22	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	cyclin	RT		9	1.7E-1	1.0E0
☐	INTERPRO	Cyclin, N-terminal	RT		5	5.1E-1	1.0E0
☐	INTERPRO	Cyclin-related	RT		4	8.0E-1	1.0E0
☐	INTERPRO	Cyclin, C-terminal	RT		3	8.0E-1	1.0E0
☐	INTERPRO	Cyclin	RT		3	9.0E-1	1.0E0
☐	SMART	CYCLIN	RT		3	9.1E-1	1.0E0
	Annotation Cluster 30	Enrichment Score: 0.22	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	organelle membrane	RT		8	3.5E-1	1.0E0
☐	GOTERM_CC_FAT	endoplasmic reticulum part	RT		3	5.5E-1	1.0E0
☐	GOTERM_CC_FAT	nuclear envelope-endoplasmic reticulum network	RT		3	5.5E-1	1.0E0
☐	GOTERM_CC_FAT	endoplasmic reticulum membrane	RT		3	5.5E-1	1.0E0
☐	GOTERM_CC_FAT	endomembrane system	RT		8	8.5E-1	1.0E0
☐	GOTERM_CC_FAT	endoplasmic reticulum	RT		3	9.2E-1	1.0E0
	Annotation Cluster 31	Enrichment Score: 0.22	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	magnesium ion binding	RT		11	3.5E-1	1.0E0

☐	**GOTERM_BP_FAT**	phospholipid transport	RT			4	4.3E-1	1.0E0
☐	**INTERPRO**	ATPase, P-type, phospholipid-translocating, flippase	RT	ℹ		4	4.5E-1	1.0E0
☐	**INTERPRO**	ATPase, P-type phosphorylation site	RT	ℹ		6	5.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	lipid transport	RT	ℹ		4	6.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	lipid localization	RT	ℹ		4	6.4E-1	1.0E0
☐	**GOTERM_MF_FAT**	phospholipid transporter activity	RT	ℹ		4	6.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	phospholipid-translocating ATPase activity	RT	ℹ		4	6.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	aminophospholipid transporter activity	RT	ℹ		4	6.5E-1	1.0E0
☐	**INTERPRO**	ATPase, P-type, ATPase-associated region	RT	ℹ		7	7.2E-1	1.0E0
☐	**GOTERM_MF_FAT**	lipid transporter activity	RT	ℹ		4	7.9E-1	1.0E0
☐	**GOTERM_MF_FAT**	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	ℹ		7	8.1E-1	1.0E0
☐	**INTERPRO**	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT	ℹ		7	8.1E-1	1.0E0
	Annotation Cluster 32	Enrichment Score: 0.21	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Haloacid dehalogenase-like hydrolase	RT	ℹ		7	5.9E-1	1.0E0
☐	**GOTERM_MF_FAT**	phosphoglycolate phosphatase activity	RT	ℹ		3	6.2E-1	1.0E0
☐	**INTERPRO**	HAD-superfamily hydrolase, subfamily IA, variant 1	RT	ℹ		3	6.2E-1	1.0E0
	Annotation Cluster 33	Enrichment Score: 0.2	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	lipid biosynthetic process	RT	ℹ		10	4.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	isoprenoid biosynthetic process	RT	ℹ		4	6.4E-1	1.0E0
☐	**GOTERM_BP_FAT**	isoprenoid metabolic process	RT	ℹ		4	6.4E-1	1.0E0
☐	**KEGG_PATHWAY**	Terpenoid backbone biosynthesis	RT	ℹ		3	9.7E-1	1.0E0
	Annotation Cluster 34	Enrichment Score: 0.2	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	nucleobase, nucleoside, nucleotide kinase activity	RT	ℹ		7	5.9E-1	1.0E0
☐	**GOTERM_MF_FAT**	nucleotide kinase activity	RT	ℹ		4	6.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	phosphotransferase activity, phosphate group as acceptor	RT	ℹ		5	6.7E-1	1.0E0
	Annotation Cluster 35	Enrichment Score: 0.2	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	phospholipid biosynthetic process	RT	ℹ		6	3.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	lipid biosynthetic process	RT	ℹ		10	4.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	organophosphate metabolic process	RT	ℹ		9	5.0E-1	1.0E0
☐	**GOTERM_BP_FAT**	phospholipid metabolic process	RT	ℹ		8	5.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	phosphoinositide metabolic process	RT	ℹ		4	8.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	glycerolipid metabolic process	RT	ℹ		4	8.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	glycerophospholipid metabolic process	RT	ℹ		4	8.8E-1	1.0E0
☐	**KEGG_PATHWAY**	Inositol phosphate metabolism	RT	ℹ		3	9.4E-1	1.0E0
	Annotation Cluster 36	Enrichment Score: 0.18	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Thioredoxin-like	RT	ℹ		9	5.3E-1	1.0E0
☐	**GOTERM_MF_FAT**	antioxidant activity	RT	ℹ		5	6.7E-1	1.0E0
☐	**INTERPRO**	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	RT	ℹ		4	8.0E-1	1.0E0
	Annotation Cluster 37	Enrichment Score: 0.17	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	ATPase associated with various cellular activities, AAA-5	RT	ℹ		5	5.1E-1	1.0E0
☐	**INTERPRO**	Dynein heavy chain, N-terminal region 2	RT	ℹ		7	7.2E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	coiled coil	RT	ℹ		3	8.3E-1	9.9E-1
	Annotation Cluster 38	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	DNA-dependent ATPase activity	RT	ℹ		6	5.5E-1	1.0E0
☐	**GOTERM_MF_FAT**	DNA helicase activity	RT	ℹ		4	7.9E-1	1.0E0
☐	**GOTERM_MF_FAT**	ATP-dependent DNA helicase activity	RT	ℹ		3	8.0E-1	1.0E0
	Annotation Cluster 39	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_FAT**	microtubule associated complex	RT	ℹ		9	6.1E-1	1.0E0
☐	**GOTERM_CC_FAT**	dynein complex	RT	ℹ		7	7.0E-1	1.0E0
☐	**INTERPRO**	Dynein heavy chain, N-terminal region 2	RT	ℹ		7	7.2E-1	1.0E0
☐	**INTERPRO**	Dynein heavy chain	RT	ℹ		7	8.1E-1	1.0E0
	Annotation Cluster 40	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	cell cycle	RT	ℹ		6	5.3E-1	1.0E0
☐	**GOTERM_BP_FAT**	cell cycle phase	RT	ℹ		4	7.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	cell cycle process	RT	ℹ		4	7.8E-1	1.0E0
☐	**GOTERM_BP_FAT**	M phase	RT	ℹ		4	7.8E-1	1.0E0
	Annotation Cluster 41	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini

☐	GOTERM_MF_FAT	electron carrier activity	RT		16	3.2E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulpur binding domain	RT		6	7.0E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, subgroup	RT		6	7.0E-1	1.0E0
☐	GOTERM_MF_FAT	4 iron, 4 sulfur cluster binding	RT		5	8.0E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, conserved site	RT		4	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	iron-sulfur cluster binding	RT		10	9.2E-1	1.0E0
☐	GOTERM_MF_FAT	metal cluster binding	RT		10	9.2E-1	1.0E0
	Annotation Cluster 42	Enrichment Score: 0.15	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	protein kinase regulator activity	RT		5	6.7E-1	1.0E0
☐	GOTERM_MF_FAT	kinase regulator activity	RT		5	6.7E-1	1.0E0
☐	GOTERM_MF_FAT	cAMP-dependent protein kinase regulator activity	RT		3	8.0E-1	1.0E0
	Annotation Cluster 43	Enrichment Score: 0.14	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	carbohydrate biosynthetic process	RT		5	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	cellular carbohydrate biosynthetic process	RT		5	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	alcohol biosynthetic process	RT		3	8.9E-1	1.0E0
	Annotation Cluster 44	Enrichment Score: 0.13	G	🟩	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF002165:ribosomal protein, L7Ab/L7Aa/L7Ae/L8e types/H/ACA ribonucleoprotein complex, NHP2 subunit	RT		3	6.2E-1	1.0E0
☐	INTERPRO	High mobility group-like nuclear protein	RT		3	6.2E-1	1.0E0
☐	INTERPRO	Ribosomal protein L7A/RS6 family	RT		3	8.0E-1	1.0E0
☐	INTERPRO	Ribosomal protein L7Ae/L30e/S12e/Gadd45	RT		3	9.5E-1	1.0E0
	Annotation Cluster 45	Enrichment Score: 0.13	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	EF hand	RT		8	4.9E-1	1.0E0
☐	INTERPRO	EF-HAND 1	RT		13	5.4E-1	1.0E0
☐	INTERPRO	EF-Hand type	RT		11	6.9E-1	1.0E0
☐	GOTERM_MF_FAT	calcium ion binding	RT		24	7.8E-1	1.0E0
☐	INTERPRO	Calcium-binding EF-hand	RT		6	8.8E-1	1.0E0
☐	INTERPRO	EF-HAND 2	RT		9	8.8E-1	1.0E0
☐	SMART	EFh	RT		6	8.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	calcium	RT		8	9.1E-1	1.0E0
	Annotation Cluster 46	Enrichment Score: 0.13	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Thioredoxin-like	RT		9	5.3E-1	1.0E0
☐	INTERPRO	Thioredoxin, conserved site	RT		4	8.0E-1	1.0E0
☐	INTERPRO	Thioredoxin domain	RT		4	8.0E-1	1.0E0
☐	INTERPRO	Thioredoxin-like subdomain	RT		3	9.0E-1	1.0E0
	Annotation Cluster 47	Enrichment Score: 0.13	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	protein serine/threonine kinase activity	RT		61	5.8E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase, active site	RT		52	6.2E-1	1.0E0
☐	INTERPRO	Protein kinase, ATP binding site	RT		46	7.8E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase	RT		32	8.2E-1	1.0E0
☐	SMART	S_TKc	RT		32	8.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	serine/threonine-protein kinase	RT		34	8.8E-1	9.9E-1
	Annotation Cluster 48	Enrichment Score: 0.13	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Pumilio RNA-binding region	RT		4	6.5E-1	1.0E0
☐	SMART	Pumilio	RT		4	6.6E-1	1.0E0
☐	INTERPRO	Armadillo-like helical	RT		10	9.5E-1	1.0E0
	Annotation Cluster 49	Enrichment Score: 0.13	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	von Willebrand factor, type A	RT		5	6.8E-1	1.0E0
☐	SMART	VWA	RT		5	6.9E-1	1.0E0
☐	INTERPRO	Copine	RT		3	9.0E-1	1.0E0
	Annotation Cluster 50	Enrichment Score: 0.1	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular amino acid biosynthetic process	RT		4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	amine biosynthetic process	RT		4	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	organic acid biosynthetic process	RT		4	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	carboxylic acid biosynthetic process	RT		4	8.8E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 0.1	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT		17	4.1E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions	RT		13	5.3E-1	1.0E0

☐	INTERPRO	ATPase, P-type phosphorylation site	RT			6	5.6E-1	1.0E0
☐	GOTERM_MF_FAT	proton-transporting ATPase activity, rotational mechanism	RT	▮		5	6.7E-1	1.0E0
☐	GOTERM_BP_FAT	ion transport	RT	▮		14	7.0E-1	1.0E0
☐	GOTERM_BP_FAT	cation transport	RT	▮		14	7.0E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, catalytic domain	RT	▮		5	7.1E-1	1.0E0
☐	INTERPRO	ATPase, P-type, ATPase-associated region	RT	▮		7	7.2E-1	1.0E0
☐	GOTERM_MF_FAT	monovalent inorganic cation transmembrane transporter activity	RT	▮		9	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	hydrogen ion transmembrane transporter activity	RT	▮		9	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of substances	RT	▮		16	7.5E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to movement of substances	RT	▮		16	7.5E-1	1.0E0
☐	GOTERM_MF_FAT	primary active transmembrane transporter activity	RT	▮		17	7.7E-1	1.0E0
☐	GOTERM_MF_FAT	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT	▮		17	7.7E-1	1.0E0
☐	GOTERM_BP_FAT	ATP metabolic process	RT	▮		14	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	ATP biosynthetic process	RT	▮		14	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside triphosphate biosynthetic process	RT	▮		15	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside triphosphate metabolic process	RT	▮		15	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside triphosphate biosynthetic process	RT	▮		15	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleoside triphosphate metabolic process	RT	▮		15	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate metabolic process	RT	▮		15	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleoside triphosphate biosynthetic process	RT	▮		15	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside triphosphate metabolic process	RT	▮		15	7.8E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoside triphosphate biosynthetic process	RT	▮		15	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	cation-transporting ATPase activity	RT	▮		6	8.0E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	▮		7	8.1E-1	1.0E0
☐	INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT	▮		7	8.1E-1	1.0E0
☐	GOTERM_MF_FAT	inorganic cation transmembrane transporter activity	RT	▮		10	8.3E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleotide biosynthetic process	RT	▮		15	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleotide metabolic process	RT	▮		15	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide metabolic process	RT	▮		15	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide biosynthetic process	RT	▮		15	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleotide metabolic process	RT	▮		16	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	nitrogen compound biosynthetic process	RT	▮		26	8.6E-1	1.0E0
☐	GOTERM_MF_FAT	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT	▮		16	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	oxidative phosphorylation	RT	▮		7	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	ATP synthesis coupled proton transport	RT	▮		7	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	energy coupled proton transport, down electrochemical gradient	RT	▮		7	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	purine nucleotide biosynthetic process	RT	▮		15	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	nucleotide biosynthetic process	RT	▮		20	9.0E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex	RT	▮		7	9.1E-1	1.0E0
☐	GOTERM_BP_FAT	monovalent inorganic cation transport	RT	▮		8	9.1E-1	1.0E0
☐	GOTERM_BP_FAT	ion transmembrane transport	RT	▮		7	9.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	ion transport	RT	▮		3	9.2E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide biosynthetic process	RT	▮		21	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	RT	▮		21	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	transmembrane transport	RT	▮		10	9.4E-1	1.0E0
☐	GOTERM_BP_FAT	hydrogen transport	RT	▮		7	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	proton transport	RT	▮		7	9.5E-1	1.0E0
☐	KEGG_PATHWAY	Oxidative phosphorylation	RT	▮		6	9.8E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting V-type ATPase complex	RT	▮		3	9.9E-1	1.0E0
	Annotation Cluster 52	**Enrichment Score: 0.1**	G		🟩	**Count**	**P_Value**	**Benjamini**
☐	GOTERM_CC_FAT	organelle membrane	RT	▮		8	3.5E-1	1.0E0

☐	GOTERM_CC_FAT	transport vesicle membrane	RT			4	5.6E-1	1.0E0
☐	GOTERM_CC_FAT	transport vesicle	RT			4	5.6E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle part	RT			4	7.2E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle membrane	RT			4	7.2E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle membrane	RT			4	7.2E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle membrane	RT			4	7.2E-1	1.0E0
☐	GOTERM_CC_FAT	coated vesicle	RT			4	7.2E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle coat	RT			4	7.2E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic membrane-bounded vesicle	RT			4	7.2E-1	1.0E0
☐	GOTERM_CC_FAT	vesicle	RT			4	7.2E-1	1.0E0
☐	GOTERM_CC_FAT	membrane-bounded vesicle	RT			4	7.2E-1	1.0E0
☐	GOTERM_CC_FAT	cytoplasmic vesicle	RT			4	7.2E-1	1.0E0
☐	GOTERM_CC_FAT	ER to Golgi transport vesicle membrane	RT			3	7.4E-1	1.0E0
☐	GOTERM_CC_FAT	ER to Golgi transport vesicle	RT			3	7.4E-1	1.0E0
☐	GOTERM_CC_FAT	COPII vesicle coat	RT			3	7.4E-1	1.0E0
☐	GOTERM_CC_FAT	endomembrane system	RT			8	8.5E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus part	RT			4	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	ER to Golgi vesicle-mediated transport	RT			3	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	Golgi vesicle transport	RT			3	9.5E-1	1.0E0
☐	GOTERM_CC_FAT	coated membrane	RT			6	9.5E-1	1.0E0
☐	GOTERM_CC_FAT	membrane coat	RT			6	9.5E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus	RT			4	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	establishment of protein localization	RT			14	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	protein transport	RT			14	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular protein transport	RT			9	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule localization	RT			9	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein localization	RT			9	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	protein localization	RT			14	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular transport	RT			10	1.0E0	1.0E0
☐	GOTERM_BP_FAT	vesicle-mediated transport	RT			10	1.0E0	1.0E0
	Annotation Cluster 53	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Annexin	RT			10	6.7E-1	1.0E0
☐	GOTERM_MF_FAT	calcium-dependent phospholipid binding	RT			13	7.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	annexin	RT			10	7.3E-1	9.9E-1
☐	GOTERM_MF_FAT	calcium ion binding	RT			24	7.8E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid binding	RT			15	8.1E-1	1.0E0
☐	INTERPRO	Annexin repeat	RT			8	8.2E-1	1.0E0
☐	SMART	ANX	RT			8	8.3E-1	1.0E0
☐	GOTERM_MF_FAT	lipid binding	RT			19	8.8E-1	1.0E0
☐	INTERPRO	Alpha giardin	RT			6	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	cytoskeleton organization	RT			7	9.7E-1	1.0E0
	Annotation Cluster 54	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cofactor biosynthetic process	RT			6	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	cofactor metabolic process	RT			7	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	coenzyme biosynthetic process	RT			4	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	coenzyme metabolic process	RT			5	9.2E-1	1.0E0
	Annotation Cluster 55	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	DNA-dependent ATPase MCM	RT			4	8.0E-1	1.0E0
☐	SMART	MCM	RT			4	8.1E-1	1.0E0
☐	INTERPRO	Nucleic acid-binding, OB-fold	RT			11	8.4E-1	1.0E0
	Annotation Cluster 56	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Ras	RT			8	6.2E-1	1.0E0
☐	INTERPRO	Ras GTPase	RT			8	7.3E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001710:Ras-related protein Rab	RT			4	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT			9	8.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	gtp-binding	RT			23	8.1E-1	9.9E-1
☐	INTERPRO	Small GTP-binding protein	RT			11	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular signaling cascade	RT			11	8.7E-1	1.0E0

☐	GOTERM_MF_FAT	GTPase activity	RT	▮	9	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	GTP binding	RT	▮	25	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	guanyl ribonucleotide binding	RT	▮	25	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	guanyl nucleotide binding	RT	▮	25	9.0E-1	1.0E0
	Annotation Cluster 57	Enrichment Score: 0.09	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Aminoacyl-tRNA synthetase, class I, conserved site	RT	▮	7	4.4E-1	1.0E0
☐	INTERPRO	Rossmann-like alpha/beta/alpha sandwich fold	RT	▮	12	6.1E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-oxygen bonds	RT	▮	13	8.5E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming aminoacyl-tRNA and related compounds	RT	▮	13	8.5E-1	1.0E0
☐	GOTERM_MF_FAT	aminoacyl-tRNA ligase activity	RT	▮	13	8.5E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA metabolic process	RT	▮	21	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA aminoacylation	RT	▮	12	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	amino acid activation	RT	▮	12	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA metabolic process	RT	▮	27	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA aminoacylation for protein translation	RT	▮	11	9.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	Aminoacyl-tRNA synthetase	RT	▮	12	9.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	protein biosynthesis	RT	▮	5	9.5E-1	1.0E0
☐	KEGG_PATHWAY	Aminoacyl-tRNA biosynthesis	RT	▮	10	9.9E-1	1.0E0
	Annotation Cluster 58	Enrichment Score: 0.07	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	organelle lumen	RT	▮	3	8.5E-1	1.0E0
☐	GOTERM_CC_FAT	intracellular organelle lumen	RT	▮	3	8.5E-1	1.0E0
☐	GOTERM_CC_FAT	membrane-enclosed lumen	RT	▮	3	8.5E-1	1.0E0
☐	GOTERM_CC_FAT	nuclear lumen	RT	▮	3	8.5E-1	1.0E0
	Annotation Cluster 59	Enrichment Score: 0.07	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	NAD or NADH binding	RT	▮	6	5.5E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of transcription, DNA-dependent	RT	▮	7	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of RNA metabolic process	RT	▮	7	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	RT	▮	5	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of transcription	RT	▮	17	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of gene expression	RT	▮	4	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of macromolecule metabolic process	RT	▮	4	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	gene silencing	RT	▮	4	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin silencing	RT	▮	3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of cellular biosynthetic process	RT	▮	3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of macromolecule biosynthetic process	RT	▮	3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of RNA metabolic process	RT	▮	3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of biosynthetic process	RT	▮	3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of gene expression, epigenetic	RT	▮	3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of nitrogen compound metabolic process	RT	▮	3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	▮	3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of transcription	RT	▮	3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of gene expression, epigenetic	RT	▮	3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of transcription, DNA-dependent	RT	▮	3	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	NAD binding	RT	▮	3	9.0E-1	1.0E0
☐	INTERPRO	NAD-dependent histone deacetylase, silent information regulator Sir2	RT	▮	3	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid deacetylation	RT	▮	3	9.5E-1	1.0E0
	Annotation Cluster 60	Enrichment Score: 0.06	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Acyltransferase	RT	▮	7	7.6E-1	9.9E-1
☐	INTERPRO	Acyl-CoA N-acyltransferase	RT	▮	6	8.1E-1	1.0E0
☐	GOTERM_MF_FAT	N-acetyltransferase activity	RT	▮	5	8.8E-1	1.0E0
☐	INTERPRO	GCN5-related N-acetyltransferase	RT	▮	5	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	N-acyltransferase activity	RT	▮	5	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	acetyltransferase activity	RT	▮	5	9.3E-1	1.0E0
	Annotation Cluster 61	Enrichment Score: 0.06	G	🟩	Count	P_Value	Benjamini

☐	GOTERM_BP_FAT	tRNA processing	RT	▮		9	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA metabolic process	RT	▮		21	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	RNA processing	RT	▮		24	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA processing	RT	▮		15	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA metabolic process	RT	▮		27	8.9E-1	1.0E0
	Annotation Cluster 62	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	rRNA processing	RT	▮		7	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA metabolic process	RT	▮		7	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA processing	RT	▮		15	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	ribosome biogenesis	RT	▮		10	9.1E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoprotein complex biogenesis	RT	▮		10	9.1E-1	1.0E0
	Annotation Cluster 63	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	protein amino acid lipidation	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	lipoprotein metabolic process	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	lipoprotein biosynthetic process	RT	▮		3	8.9E-1	1.0E0
	Annotation Cluster 64	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	mismatch repair	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	structure-specific DNA binding	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	mismatched DNA binding	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	double-stranded DNA binding	RT	▮		3	9.0E-1	1.0E0
	Annotation Cluster 65	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	intramolecular transferase activity	RT	▮		6	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	pseudouridine synthesis	RT	▮		4	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	pseudouridine synthase activity	RT	▮		4	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	RNA modification	RT	▮		7	9.7E-1	1.0E0
	Annotation Cluster 66	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	GTPase activity	RT	▮		9	8.8E-1	1.0E0
☐	INTERPRO	Translation elongation factor EFTu/EF1A, domain 2	RT	▮		3	9.0E-1	1.0E0
☐	INTERPRO	Protein synthesis factor, GTP-binding	RT	▮		4	9.4E-1	1.0E0
	Annotation Cluster 67	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF001567:ubiquitin-protein ligase E2	RT	▮		4	8.0E-1	1.0E0
☐	KEGG_PATHWAY	Ubiquitin mediated proteolysis	RT	▮		7	8.2E-1	9.9E-1
☐	GOTERM_MF_FAT	small conjugating protein ligase activity	RT	▮		7	8.8E-1	1.0E0
☐	INTERPRO	Ubiquitin-conjugating enzyme, E2	RT	▮		6	9.3E-1	1.0E0
☐	INTERPRO	Ubiquitin-conjugating enzyme/RWD-like	RT	▮		6	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-nitrogen bonds	RT	▮		16	9.3E-1	1.0E0
☐	SMART	UBCc	RT	▮		6	9.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	ligase	RT	▮		29	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	acid-amino acid ligase activity	RT	▮		13	9.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	ubl conjugation pathway	RT	▮		6	9.7E-1	1.0E0
	Annotation Cluster 68	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	phosphoprotein phosphatase activity	RT	▮		15	8.6E-1	1.0E0
☐	GOTERM_BP_FAT	dephosphorylation	RT	▮		8	9.1E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid dephosphorylation	RT	▮		6	9.5E-1	1.0E0
	Annotation Cluster 69	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	one-carbon metabolic process	RT	▮		6	8.7E-1	1.0E0
☐	GOTERM_BP_FAT	methylation	RT	▮		5	9.2E-1	1.0E0
☐	GOTERM_BP_FAT	biopolymer methylation	RT	▮		3	9.5E-1	1.0E0
	Annotation Cluster 70	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	RecF/RecN/SMC protein, N-terminal	RT	▮		4	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	chromosome	RT	▮		11	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	chromosome organization	RT	▮		8	9.8E-1	1.0E0
	Annotation Cluster 71	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	nucleoside-triphosphatase regulator activity	RT	▮		8	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	small GTPase regulator activity	RT	▮		6	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase regulator activity	RT	▮		6	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of hydrolase activity	RT	▮		4	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of GTPase activity	RT	▮		4	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras protein signal transduction	RT	▮		4	9.6E-1	1.0E0

☐	GOTERM_BP_FAT	regulation of small GTPase mediated signal transduction	RT	▮		4	9.6E-1	1.0E0
☐	GOTERM_MF_FAT	enzyme activator activity	RT	▮		4	9.7E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras GTPase activity	RT	▮		3	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase activator activity	RT	▮		3	9.8E-1	1.0E0
	Annotation Cluster 72	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	RNA recognition motif, RNP-1	RT	▮		7	9.3E-1	1.0E0
☐	SMART	RRM	RT	▮		7	9.3E-1	1.0E0
☐	INTERPRO	Nucleotide-binding, alpha-beta plait	RT	▮		7	9.7E-1	1.0E0
	Annotation Cluster 73	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	thiolester hydrolase activity	RT	▮		4	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	ubiquitin thiolesterase activity	RT	▮		3	9.5E-1	1.0E0
☐	INTERPRO	Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2	RT	▮		3	9.5E-1	1.0E0
	Annotation Cluster 74	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	nuclease activity	RT	▮		27	8.5E-1	1.0E0
☐	GOTERM_MF_FAT	DNA polymerase activity	RT	▮		17	9.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	Endonuclease	RT	▮		15	9.6E-1	1.0E0
☐	GOTERM_MF_FAT	endonuclease activity	RT	▮		15	9.9E-1	1.0E0
☐	GOTERM_MF_FAT	RNA-directed DNA polymerase activity	RT	▮		10	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	rna-directed dna polymerase	RT	▮		10	9.9E-1	1.0E0
	Annotation Cluster 75	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Protein phosphatase 2C	RT	▮		3	9.5E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C, N-terminal	RT	▮		3	9.5E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C-related	RT	▮		3	9.5E-1	1.0E0
☐	SMART	PP2C_SIG	RT	▮		3	9.5E-1	1.0E0
☐	SMART	PP2Cc	RT	▮		3	9.5E-1	1.0E0
	Annotation Cluster 76	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Like-Sm ribonucleoprotein, core	RT	▮		5	9.6E-1	1.0E0
☐	INTERPRO	Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core	RT	▮		3	9.8E-1	1.0E0
☐	SMART	Sm	RT	▮		3	9.8E-1	1.0E0
	Annotation Cluster 77	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Initiation factor	RT	▮		9	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	translation initiation factor activity	RT	▮		11	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	translational initiation	RT	▮		4	9.9E-1	1.0E0
☐	GOTERM_MF_FAT	translation factor activity, nucleic acid binding	RT	▮		12	1.0E0	1.0E0
	Annotation Cluster 78	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	protein polymerization	RT	▮		4	9.3E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, GTPase domain	RT	▮		4	9.4E-1	1.0E0
☐	INTERPRO	Tubulin	RT	▮		4	9.4E-1	1.0E0
☐	INTERPRO	Tubulin, conserved site	RT	▮		4	9.4E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002306:tubulin	RT	▮		3	9.8E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, 2-layer sandwich domain	RT	▮		3	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	chromosome organization	RT	▮		8	9.8E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex biogenesis	RT	▮		5	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex assembly	RT	▮		5	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein complex assembly	RT	▮		4	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin organization	RT	▮		5	1.0E0	1.0E0
☐	GOTERM_CC_FAT	nucleosome	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly or disassembly	RT	▮		4	1.0E0	1.0E0
☐	GOTERM_CC_FAT	chromosomal part	RT	▮		5	1.0E0	1.0E0
☐	GOTERM_BP_FAT	macromolecular complex assembly	RT	▮		9	1.0E0	1.0E0
☐	GOTERM_CC_FAT	chromatin	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_BP_FAT	protein-DNA complex assembly	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_BP_FAT	nucleosome organization	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_BP_FAT	DNA packaging	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_BP_FAT	nucleosome assembly	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex assembly	RT	▮		8	1.0E0	1.0E0
	INTERPRO	Histone core	RT	▮		3	1.0E0	1.0E0

☐								
☐	**GOTERM_BP_FAT**	macromolecular complex subunit organization	**RT**	▮		9	1.0E0	1.0E0
☐	**GOTERM_BP_FAT**	cellular macromolecular complex subunit organization	**RT**	▮		8	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	chromosomal protein	**RT**	▮		3	1.0E0	1.0E0
☐	**GOTERM_CC_FAT**	protein-DNA complex	**RT**	▮		3	1.0E0	1.0E0
☐	**INTERPRO**	Histone-fold	**RT**	▮		3	1.0E0	1.0E0
	Annotation Cluster 79	**Enrichment Score: 0**	G		🟩	**Count**	**P_Value**	**Benjamini**
☐	**INTERPRO**	Zinc finger, C2H2-like	**RT**	▮		7	9.9E-1	1.0E0
☐	**INTERPRO**	Zinc finger, C2H2-type	**RT**	▮		7	9.9E-1	1.0E0
☐	**SMART**	ZnF_C2H2	**RT**	▮		7	9.9E-1	1.0E0

[201 terms] were not clustered.

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

Functional Annotation Clustering

Help and Manual

Current Gene List: 3_Random10
Current Background: Giardia intestinalis
3000 DAVID IDs

Options **Classification Stringency** Medium

Rerun using options | Create Sublist

83 Cluster(s)

Download File

	Annotation Cluster 1	Enrichment Score: 1.03		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cytoskeleton organization	RT	14	4.3E-2	1.0E0
☐	SP_PIR_KEYWORDS	annexin	RT	14	4.3E-2	9.9E-1
☐	GOTERM_MF_FAT	calcium-dependent phospholipid binding	RT	18	4.6E-2	1.0E0
☐	INTERPRO	Annexin	RT	14	5.0E-2	1.0E0
☐	INTERPRO	Alpha giardin	RT	11	6.8E-2	1.0E0
☐	SMART	ANX	RT	12	9.9E-2	1.0E0
☐	INTERPRO	Annexin repeat	RT	12	1.0E-1	1.0E0
☐	GOTERM_MF_FAT	calcium ion binding	RT	30	1.2E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid binding	RT	18	3.6E-1	1.0E0
☐	GOTERM_MF_FAT	lipid binding	RT	23	4.1E-1	1.0E0
	Annotation Cluster 2	Enrichment Score: 0.66		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	protein localization	RT	25	8.1E-2	1.0E0
☐	GOTERM_BP_FAT	intracellular transport	RT	21	9.3E-2	1.0E0
☐	GOTERM_BP_FAT	protein transport	RT	24	1.0E-1	1.0E0
☐	GOTERM_BP_FAT	establishment of protein localization	RT	24	1.0E-1	1.0E0
☐	GOTERM_BP_FAT	intracellular protein transport	RT	17	1.7E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein localization	RT	17	1.7E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule localization	RT	17	1.7E-1	1.0E0
☐	GOTERM_CC_FAT	Golgi apparatus	RT	9	2.7E-1	1.0E0
☐	GOTERM_BP_FAT	vesicle-mediated transport	RT	19	3.8E-1	1.0E0
☐	INTERPRO	Clathrin/coatomer adaptor, adaptin-like, N-terminal	RT	4	6.6E-1	1.0E0
☐	GOTERM_CC_FAT	coated membrane	RT	9	6.7E-1	1.0E0
☐	GOTERM_CC_FAT	membrane coat	RT	9	6.7E-1	1.0E0
	Annotation Cluster 3	Enrichment Score: 0.63		Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	integral to membrane	RT	44	1.6E-1	1.0E0
☐	GOTERM_CC_FAT	intrinsic to membrane	RT	44	1.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	transmembrane	RT	20	3.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	membrane	RT	18	3.6E-1	1.0E0
	Annotation Cluster 4	Enrichment Score: 0.62		Count	P_Value	Benjamini
☐	SMART	AAA	RT	47	1.6E-1	1.0E0
☐	INTERPRO	ATPase, AAA+ type, core	RT	47	1.6E-1	1.0E0
☐	INTERPRO	ATPase, AAA-type, core	RT	16	5.2E-1	1.0E0
	Annotation Cluster 5	Enrichment Score: 0.51		Count	P_Value	Benjamini
☐	INTERPRO	AMP-dependent synthetase and ligase	RT	7	1.4E-1	1.0E0
☐	GOTERM_MF_FAT	fatty-acid ligase activity	RT	5	3.0E-1	1.0E0
☐	GOTERM_MF_FAT	long-chain-fatty-acid-CoA ligase activity	RT	5	3.0E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-sulfur bonds	RT	5	3.0E-1	1.0E0
☐	COG_ONTOLOGY	Lipid metabolism	RT	8	7.3E-1	9.9E-1
	Annotation Cluster 6	Enrichment Score: 0.43		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	chromatin assembly	RT	9	2.4E-1	1.0E0
☐	GOTERM_BP_FAT	protein-DNA complex assembly	RT	9	2.4E-1	1.0E0
☐	GOTERM_BP_FAT	DNA packaging	RT	9	2.4E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome assembly	RT	9	2.4E-1	1.0E0
☐	GOTERM_BP_FAT	nucleosome organization	RT	9	2.4E-1	1.0E0
☐	INTERPRO	Histone-fold	RT	11	2.4E-1	1.0E0

☐	SP_PIR_KEYWORDS	chromosomal protein	RT	9	2.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleus	RT	23	2.5E-1	1.0E0
☐	INTERPRO	Histone core	RT	9	2.6E-1	1.0E0
☐	GOTERM_CC_FAT	nucleosome	RT	9	2.7E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin assembly or disassembly	RT	10	2.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-binding	RT	23	3.2E-1	1.0E0
☐	GOTERM_CC_FAT	protein-DNA complex	RT	10	3.2E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex subunit organization	RT	17	3.3E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin organization	RT	11	3.3E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecular complex subunit organization	RT	18	3.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleosome core	RT	6	3.7E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecular complex assembly	RT	16	3.9E-1	1.0E0
☐	GOTERM_CC_FAT	chromatin	RT	9	4.1E-1	1.0E0
☐	GOTERM_CC_FAT	chromosomal part	RT	12	4.1E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecular complex assembly	RT	17	4.2E-1	1.0E0
☐	GOTERM_BP_FAT	chromosome organization	RT	12	5.8E-1	1.0E0
☐	SMART	H4	RT	3	6.2E-1	1.0E0
☐	INTERPRO	Histone H4	RT	3	6.3E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002052:histone H4	RT	3	6.3E-1	1.0E0
☐	SMART	H3	RT	3	8.0E-1	1.0E0
☐	INTERPRO	Histone H3	RT	3	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	chromosome	RT	14	9.2E-1	1.0E0
	Annotation Cluster 7	Enrichment Score: 0.43		Count	P_Value	Benjamini
☐	SMART	ANK	RT	259	3.0E-1	1.0E0
☐	INTERPRO	Ankyrin	RT	259	3.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	ank repeat	RT	177	5.0E-1	1.0E0
	Annotation Cluster 8	Enrichment Score: 0.41		Count	P_Value	Benjamini
☐	SMART	UBQ	RT	6	3.8E-1	1.0E0
☐	INTERPRO	Ubiquitin	RT	6	3.9E-1	1.0E0
☐	INTERPRO	Ubiquitin supergroup	RT	9	3.9E-1	1.0E0
	Annotation Cluster 9	Enrichment Score: 0.41		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	protein kinase regulator activity	RT	6	3.7E-1	1.0E0
☐	GOTERM_MF_FAT	kinase regulator activity	RT	6	3.7E-1	1.0E0
☐	GOTERM_MF_FAT	cAMP-dependent protein kinase regulator activity	RT	4	4.4E-1	1.0E0
	Annotation Cluster 10	Enrichment Score: 0.4		Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF001711:ADP-ribosylation factor	RT	5	3.2E-1	1.0E0
☐	INTERPRO	ARF/SAR superfamily	RT	6	3.9E-1	1.0E0
☐	SMART	ARF	RT	4	4.5E-1	1.0E0
☐	INTERPRO	ADP-ribosylation factor	RT	4	4.5E-1	1.0E0
	Annotation Cluster 11	Enrichment Score: 0.39		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	intracellular signaling cascade	RT	16	1.4E-1	1.0E0
☐	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT	12	2.6E-1	1.0E0
☐	GOTERM_MF_FAT	guanyl ribonucleotide binding	RT	31	3.0E-1	1.0E0
☐	GOTERM_MF_FAT	GTP binding	RT	31	3.0E-1	1.0E0
☐	GOTERM_MF_FAT	guanyl nucleotide binding	RT	31	3.0E-1	1.0E0
☐	INTERPRO	Small GTP-binding protein	RT	14	3.6E-1	1.0E0
☐	INTERPRO	Ras	RT	9	3.9E-1	1.0E0
☐	INTERPRO	Ras GTPase	RT	9	5.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	gtp-binding	RT	24	5.7E-1	9.9E-1
☐	SMART	RAB	RT	3	8.0E-1	1.0E0
☐	INTERPRO	Ras small GTPase, Rab type	RT	3	8.0E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001710:Ras-related protein Rab	RT	4	8.1E-1	1.0E0
	Annotation Cluster 12	Enrichment Score: 0.35		Count	P_Value	Benjamini
☐	COG_ONTOLOGY	Nucleotide transport and metabolism	RT	8	8.7E-2	9.5E-1
☐	GOTERM_BP_FAT	nucleotide catabolic process	RT	4	4.3E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid catabolic process	RT	5	4.9E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide catabolic process	RT	5	4.9E-1	1.0E0

☐	**GOTERM_BP_FAT**	nitrogen compound catabolic process	RT			5	4.9E-1	1.0E0
☐	**INTERPRO**	5'-Nucleotidase and apyrase	RT			3	6.3E-1	1.0E0
☐	**INTERPRO**	Predicted phosphoesterase, C1039.02 type	RT			3	6.3E-1	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF017316:phosphoesterase, C1039.02 type	RT			3	6.3E-1	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF017316:Pesterase_C1039	RT			3	6.3E-1	1.0E0
	Annotation Cluster 13	Enrichment Score: 0.35		G	🟩	Count	P_Value	Benjamini
☐	**SMART**	RRM	RT			10	4.3E-1	1.0E0
☐	**INTERPRO**	RNA recognition motif, RNP-1	RT			10	4.4E-1	1.0E0
☐	**INTERPRO**	Nucleotide-binding, alpha-beta plait	RT			11	4.8E-1	1.0E0
	Annotation Cluster 14	Enrichment Score: 0.34		G	🟩	Count	P_Value	Benjamini
☐	**SMART**	VWA	RT			6	3.8E-1	1.0E0
☐	**INTERPRO**	von Willebrand factor, type A	RT			6	3.9E-1	1.0E0
☐	**INTERPRO**	Copine	RT			4	6.6E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 0.31		G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_FAT**	organelle membrane	RT			9	2.7E-1	1.0E0
☐	**GOTERM_CC_FAT**	Golgi apparatus	RT			9	2.7E-1	1.0E0
☐	**GOTERM_CC_FAT**	endomembrane system	RT			12	3.0E-1	1.0E0
☐	**GOTERM_CC_FAT**	ER to Golgi transport vesicle membrane	RT			4	4.6E-1	1.0E0
☐	**GOTERM_CC_FAT**	ER to Golgi transport vesicle	RT			4	4.6E-1	1.0E0
☐	**GOTERM_CC_FAT**	COPII vesicle coat	RT			4	4.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	ER to Golgi vesicle-mediated transport	RT			5	4.9E-1	1.0E0
☐	**GOTERM_BP_FAT**	Golgi vesicle transport	RT			5	4.9E-1	1.0E0
☐	**GOTERM_CC_FAT**	cytoplasmic membrane-bounded vesicle	RT			5	5.2E-1	1.0E0
☐	**GOTERM_CC_FAT**	vesicle membrane	RT			5	5.2E-1	1.0E0
☐	**GOTERM_CC_FAT**	membrane-bounded vesicle	RT			5	5.2E-1	1.0E0
☐	**GOTERM_CC_FAT**	cytoplasmic vesicle	RT			5	5.2E-1	1.0E0
☐	**GOTERM_CC_FAT**	vesicle	RT			5	5.2E-1	1.0E0
☐	**GOTERM_CC_FAT**	cytoplasmic vesicle membrane	RT			5	5.2E-1	1.0E0
☐	**GOTERM_CC_FAT**	coated vesicle membrane	RT			5	5.2E-1	1.0E0
☐	**GOTERM_CC_FAT**	coated vesicle	RT			5	5.2E-1	1.0E0
☐	**GOTERM_CC_FAT**	cytoplasmic vesicle part	RT			5	5.2E-1	1.0E0
☐	**GOTERM_CC_FAT**	vesicle coat	RT			5	5.2E-1	1.0E0
☐	**GOTERM_CC_FAT**	Golgi apparatus part	RT			6	5.7E-1	1.0E0
☐	**GOTERM_CC_FAT**	transport vesicle membrane	RT			4	6.7E-1	1.0E0
☐	**GOTERM_CC_FAT**	transport vesicle	RT			4	6.7E-1	1.0E0
☐	**GOTERM_CC_FAT**	coated membrane	RT			9	6.7E-1	1.0E0
☐	**GOTERM_CC_FAT**	membrane coat	RT			9	6.7E-1	1.0E0
	Annotation Cluster 16	Enrichment Score: 0.29		G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_FAT**	nucleobase, nucleoside, nucleotide kinase activity	RT			8	3.3E-1	1.0E0
☐	**GOTERM_MF_FAT**	nucleotide kinase activity	RT			4	6.4E-1	1.0E0
☐	**GOTERM_MF_FAT**	phosphotransferase activity, phosphate group as acceptor	RT			5	6.6E-1	1.0E0
	Annotation Cluster 17	Enrichment Score: 0.27		G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_FAT**	purine nucleotide metabolic process	RT			20	3.2E-1	1.0E0
☐	**GOTERM_BP_FAT**	ATP metabolic process	RT			17	3.3E-1	1.0E0
☐	**GOTERM_BP_FAT**	ATP biosynthetic process	RT			17	3.3E-1	1.0E0
☐	**GOTERM_BP_FAT**	nucleoside triphosphate biosynthetic process	RT			18	3.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	nucleoside triphosphate metabolic process	RT			18	3.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	purine nucleoside triphosphate biosynthetic process	RT			18	3.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	purine nucleoside triphosphate metabolic process	RT			18	3.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	ribonucleoside triphosphate metabolic process	RT			18	3.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	ribonucleoside triphosphate biosynthetic process	RT			18	3.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	purine ribonucleoside triphosphate metabolic process	RT			18	3.6E-1	1.0E0
☐	**GOTERM_BP_FAT**	purine ribonucleoside triphosphate biosynthetic process	RT			18	3.6E-1	1.0E0
☐	**GOTERM_MF_FAT**	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT			9	3.7E-1	1.0E0
☐	**GOTERM_BP_FAT**	purine nucleotide biosynthetic process	RT			19	3.8E-1	1.0E0

☐	GOTERM_BP_FAT	ion transport	RT	▮	16	3.9E-1	1.0E0
☐	GOTERM_BP_FAT	cation transport	RT	▮	16	3.9E-1	1.0E0
☐	INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT	▮	9	3.9E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleotide metabolic process	RT	▮	18	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	purine ribonucleotide biosynthetic process	RT	▮	18	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide metabolic process	RT	▮	18	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleotide biosynthetic process	RT	▮	18	4.4E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting V-type ATPase complex	RT	▮	7	4.6E-1	1.0E0
☐	GOTERM_MF_FAT	inorganic cation transmembrane transporter activity	RT	▮	12	4.8E-1	1.0E0
☐	INTERPRO	ATPase, P-type, ATPase-associated region	RT	▮	8	4.9E-1	1.0E0
☐	GOTERM_BP_FAT	nucleotide biosynthetic process	RT	▮	24	5.0E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, proton-transporting domain	RT	▮	5	5.2E-1	1.0E0
☐	GOTERM_BP_FAT	hydrogen transport	RT	▮	10	5.3E-1	1.0E0
☐	GOTERM_BP_FAT	proton transport	RT	▮	10	5.3E-1	1.0E0
☐	KEGG_PATHWAY	Oxidative phosphorylation	RT	▮	9	5.3E-1	1.0E0
☐	INTERPRO	ATPase, P-type phosphorylation site	RT	▮	6	5.6E-1	1.0E0
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT	▮	16	5.8E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex	RT	▮	10	5.8E-1	1.0E0
☐	GOTERM_BP_FAT	nitrogen compound biosynthetic process	RT	▮	29	5.8E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	RT	▮	25	5.9E-1	1.0E0
☐	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide biosynthetic process	RT	▮	25	5.9E-1	1.0E0
☐	GOTERM_MF_FAT	di-, tri-valent inorganic cation transmembrane transporter activity	RT	▮	3	6.1E-1	1.0E0
☐	GOTERM_MF_FAT	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT	▮	18	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	ion transmembrane transport	RT	▮	9	6.2E-1	1.0E0
☐	INTERPRO	ATPase, P-type cation-transporter, C-terminal	RT	▮	3	6.3E-1	1.0E0
☐	INTERPRO	ATPase, P-type cation-transporter, N-terminal	RT	▮	3	6.3E-1	1.0E0
☐	GOTERM_MF_FAT	metal ion transmembrane transporter activity	RT	▮	4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	monovalent inorganic cation transport	RT	▮	10	6.4E-1	1.0E0
☐	GOTERM_CC_FAT	proton-transporting V-type ATPase, V0 domain	RT	▮	4	6.7E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions	RT	▮	12	6.9E-1	1.0E0
☐	GOTERM_BP_FAT	oxidative phosphorylation	RT	▮	8	7.1E-1	1.0E0
☐	GOTERM_BP_FAT	ATP synthesis coupled proton transport	RT	▮	8	7.1E-1	1.0E0
☐	GOTERM_BP_FAT	energy coupled proton transport, down electrochemical gradient	RT	▮	8	7.1E-1	1.0E0
☐	GOTERM_MF_FAT	hydrogen ion transmembrane transporter activity	RT	▮	9	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	monovalent inorganic cation transmembrane transporter activity	RT	▮	9	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of substances	RT	▮	16	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled to movement of substances	RT	▮	16	7.4E-1	1.0E0
☐	GOTERM_MF_FAT	primary active transmembrane transporter activity	RT	▮	17	7.5E-1	1.0E0
☐	GOTERM_MF_FAT	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT	▮	17	7.5E-1	1.0E0
☐	GOTERM_BP_FAT	transmembrane transport	RT	▮	12	7.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	phosphoprotein	RT	▮	3	7.9E-1	9.9E-1
☐	SP_PIR_KEYWORDS	ion transport	RT	▮	3	8.9E-1	9.9E-1
☐	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, catalytic domain	RT	▮	4	9.5E-1	1.0E0
☐	GOTERM_MF_FAT	proton-transporting ATPase activity, rotational mechanism	RT	▮	3	9.7E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 0.27	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular response to stress	RT	▮	14	4.3E-1	1.0E0
☐	GOTERM_BP_FAT	DNA repair	RT	▮	13	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	response to DNA damage stimulus	RT	▮	13	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	DNA metabolic process	RT	▮	33	7.5E-1	1.0E0
	Annotation Cluster 19	Enrichment Score: 0.27	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	endomembrane system	RT	▮	12	3.0E-1	1.0E0
	GOTERM_BP_FAT	nuclear transport	RT	▮	4	4.3E-1	1.0E0

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☐	GOTERM_BP_FAT	nucleocytoplasmic transport	RT		4	4.3E-1	1.0E0
☐	GOTERM_CC_FAT	organelle envelope	RT		4	6.7E-1	1.0E0
☐	GOTERM_CC_FAT	envelope	RT		4	6.7E-1	1.0E0
☐	GOTERM_CC_FAT	pore complex	RT		4	6.7E-1	1.0E0
☐	GOTERM_CC_FAT	nuclear envelope	RT		4	6.7E-1	1.0E0
☐	GOTERM_CC_FAT	nuclear pore	RT		4	6.7E-1	1.0E0
	Annotation Cluster 20	Enrichment Score: 0.26	G	🟩	Count	P_Value	Benjamini
☐	SMART	t_SNARE	RT		4	4.5E-1	1.0E0
☐	INTERPRO	Target SNARE coiled-coil region	RT		4	4.5E-1	1.0E0
☐	KEGG_PATHWAY	SNARE interactions in vesicular transport	RT		3	8.1E-1	1.0E0
	Annotation Cluster 21	Enrichment Score: 0.26	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	ion binding	RT		155	2.4E-1	1.0E0
☐	GOTERM_MF_FAT	cation binding	RT		155	2.4E-1	1.0E0
☐	GOTERM_MF_FAT	metal ion binding	RT		152	2.9E-1	1.0E0
☐	GOTERM_MF_FAT	zinc ion binding	RT		90	4.1E-1	1.0E0
☐	GOTERM_MF_FAT	transition metal ion binding	RT		107	6.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	metal-binding	RT		57	6.7E-1	9.9E-1
☐	SP_PIR_KEYWORDS	zinc	RT		46	8.1E-1	9.9E-1
☐	SP_PIR_KEYWORDS	zinc-finger	RT		33	8.3E-1	9.9E-1
☐	SMART	RING	RT		36	8.8E-1	1.0E0
☐	INTERPRO	Zinc finger, RING-type	RT		36	8.8E-1	1.0E0
☐	INTERPRO	Zinc finger, C3HC4 RING-type	RT		18	9.1E-1	1.0E0
	Annotation Cluster 22	Enrichment Score: 0.26	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	rRNA processing	RT		9	5.0E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA metabolic process	RT		9	5.0E-1	1.0E0
☐	GOTERM_BP_FAT	ribonucleoprotein complex biogenesis	RT		13	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	ribosome biogenesis	RT		13	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA processing	RT		18	5.3E-1	1.0E0
☐	GOTERM_BP_FAT	rRNA modification	RT		3	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	RNA processing	RT		26	7.3E-1	1.0E0
	Annotation Cluster 23	Enrichment Score: 0.26	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	protein phosphatase regulator activity	RT		4	4.4E-1	1.0E0
☐	GOTERM_MF_FAT	phosphatase regulator activity	RT		4	4.4E-1	1.0E0
☐	GOTERM_MF_FAT	protein phosphatase type 2A regulator activity	RT		3	6.1E-1	1.0E0
☐	GOTERM_CC_FAT	protein phosphatase type 2A complex	RT		3	6.3E-1	1.0E0
☐	GOTERM_CC_FAT	protein serine/threonine phosphatase complex	RT		5	6.9E-1	1.0E0
	Annotation Cluster 24	Enrichment Score: 0.26	G	🟩	Count	P_Value	Benjamini
☐	SMART	HATPase_c	RT		6	3.8E-1	1.0E0
☐	INTERPRO	ATP-binding region, ATPase-like	RT		6	3.9E-1	1.0E0
☐	INTERPRO	DNA mismatch repair protein	RT		3	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	mismatch repair	RT		4	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	double-stranded DNA binding	RT		4	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	structure-specific DNA binding	RT		4	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	mismatched DNA binding	RT		4	6.4E-1	1.0E0
	Annotation Cluster 25	Enrichment Score: 0.25	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	transcription regulator activity	RT		8	4.7E-1	1.0E0
☐	SMART	ZnF_C2C2	RT		3	6.2E-1	1.0E0
☐	INTERPRO	Zinc finger, TFIIS-type	RT		3	6.3E-1	1.0E0
	Annotation Cluster 26	Enrichment Score: 0.24	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	heat shock protein binding	RT		6	5.4E-1	1.0E0
☐	SMART	DnaJ	RT		6	5.5E-1	1.0E0
☐	INTERPRO	Heat shock protein DnaJ, N-terminal	RT		6	5.6E-1	1.0E0
☐	INTERPRO	Molecular chaperone, heat shock protein, Hsp40, DnaJ	RT		5	6.8E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 0.23	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	structural constituent of ribosome	RT		42	4.3E-1	1.0E0
☐	KEGG_PATHWAY	Ribosome	RT		42	4.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	ribosomal protein	RT		43	5.0E-1	1.0E0

☐	GOTERM_BP_FAT	translation	RT			66	5.0E-1	1.0E0
☐	GOTERM_MF_FAT	structural molecule activity	RT	▮		49	5.4E-1	1.0E0
☐	GOTERM_CC_FAT	ribonucleoprotein complex	RT	▮		59	5.9E-1	1.0E0
☐	GOTERM_CC_FAT	ribosome	RT	▮		44	6.8E-1	1.0E0
☐	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT	▮		87	9.6E-1	1.0E0
☐	GOTERM_CC_FAT	non-membrane-bounded organelle	RT	▮		87	9.6E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 0.21	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	ligase	RT	▮		34	4.1E-1	1.0E0
☐	GOTERM_MF_FAT	small conjugating protein ligase activity	RT	▮		9	5.1E-1	1.0E0
☐	SMART	UBCc	RT	▮		8	6.2E-1	1.0E0
☐	INTERPRO	Ubiquitin-conjugating enzyme/RWD-like	RT	▮		8	6.2E-1	1.0E0
☐	INTERPRO	Ubiquitin-conjugating enzyme, E2	RT	▮		8	6.2E-1	1.0E0
☐	GOTERM_MF_FAT	ubiquitin-protein ligase activity	RT	▮		4	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	acid-amino acid ligase activity	RT	▮		16	6.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	ubl conjugation pathway	RT	▮		8	7.1E-1	9.9E-1
☐	GOTERM_MF_FAT	ligase activity, forming carbon-nitrogen bonds	RT	▮		18	7.6E-1	1.0E0
	Annotation Cluster 29	Enrichment Score: 0.2	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	exopeptidase activity	RT	▮		8	4.7E-1	1.0E0
☐	GOTERM_MF_FAT	metallopeptidase activity	RT	▮		9	5.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	dipeptidase	RT	▮		3	6.1E-1	9.9E-1
☐	GOTERM_MF_FAT	dipeptidase activity	RT	▮		3	6.1E-1	1.0E0
☐	SMART	Zn_pept	RT	▮		4	6.5E-1	1.0E0
☐	INTERPRO	Peptidase M14, carboxypeptidase A	RT	▮		4	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	metalloexopeptidase activity	RT	▮		5	6.6E-1	1.0E0
☐	GOTERM_MF_FAT	carboxypeptidase activity	RT	▮		3	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	metallocarboxypeptidase activity	RT	▮		3	7.9E-1	1.0E0
	Annotation Cluster 30	Enrichment Score: 0.2	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	WD40/YVTN repeat-like	RT	▮		45	3.7E-1	1.0E0
☐	SMART	WD40	RT	▮		45	4.7E-1	1.0E0
☐	INTERPRO	WD40 repeat	RT	▮		45	4.8E-1	1.0E0
☐	INTERPRO	WD40 repeat, conserved site	RT	▮		17	7.1E-1	1.0E0
☐	INTERPRO	WD40 repeat, subgroup	RT	▮		32	7.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	wd repeat	RT	▮		27	7.9E-1	9.9E-1
☐	INTERPRO	WD40 repeat 2	RT	▮		23	8.7E-1	1.0E0
☐	INTERPRO	WD40 repeat, region	RT	▮		25	8.8E-1	1.0E0
	Annotation Cluster 31	Enrichment Score: 0.2	G		🟩	Count	P_Value	Benjamini
☐	SMART	FU	RT	▮		110	4.3E-1	1.0E0
☐	INTERPRO	Furin-like repeat	RT	▮		110	4.4E-1	1.0E0
☐	INTERPRO	Giardia variant-specific surface protein	RT	▮		135	7.3E-1	1.0E0
☐	INTERPRO	EGF-like	RT	▮		105	8.7E-1	1.0E0
☐	SMART	EGF	RT	▮		105	8.8E-1	1.0E0
	Annotation Cluster 32	Enrichment Score: 0.19	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	protein amino acid lipidation	RT	▮		4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	lipoprotein metabolic process	RT	▮		4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	lipoprotein biosynthetic process	RT	▮		4	6.4E-1	1.0E0
	Annotation Cluster 33	Enrichment Score: 0.18	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	▮		9	3.7E-1	1.0E0
☐	INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT	▮		9	3.9E-1	1.0E0
☐	INTERPRO	ATPase, P-type, ATPase-associated region	RT	▮		8	4.9E-1	1.0E0
☐	INTERPRO	ATPase, P-type phosphorylation site	RT	▮		6	5.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	magnesium	RT	▮		8	6.0E-1	9.9E-1
☐	GOTERM_BP_FAT	lipid transport	RT	▮		4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	lipid localization	RT	▮		4	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	magnesium ion binding	RT	▮		9	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	lipid transporter activity	RT	▮		4	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid transport	RT	▮		3	7.9E-1	1.0E0
☐	INTERPRO	ATPase, P-type, phospholipid-translocating,	RT	▮		3	8.0E-1	1.0E0

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☐	GOTERM_MF_FAT	aminophospholipid transporter activity	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid-translocating ATPase activity	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	phospholipid transporter activity	RT	▮		3	8.9E-1	1.0E0
	Annotation Cluster 34	Enrichment Score: 0.18	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	GTPase regulator activity	RT	▮		8	4.7E-1	1.0E0
☐	GOTERM_MF_FAT	small GTPase regulator activity	RT	▮		8	4.7E-1	1.0E0
☐	GOTERM_MF_FAT	nucleoside-triphosphatase regulator activity	RT	▮		9	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of ARF protein signal transduction	RT	▮		4	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras protein signal transduction	RT	▮		6	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of small GTPase mediated signal transduction	RT	▮		6	6.8E-1	1.0E0
☐	GOTERM_MF_FAT	enzyme activator activity	RT	▮		6	6.8E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of hydrolase activity	RT	▮		5	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of GTPase activity	RT	▮		5	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of Ras GTPase activity	RT	▮		4	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	GTPase activator activity	RT	▮		4	8.8E-1	1.0E0
	Annotation Cluster 35	Enrichment Score: 0.17	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cyclic nucleotide metabolic process	RT	▮		3	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	cyclic nucleotide biosynthetic process	RT	▮		3	6.1E-1	1.0E0
☐	GOTERM_MF_FAT	phosphorus-oxygen lyase activity	RT	▮		3	6.1E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside monophosphate biosynthetic process	RT	▮		3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	nucleoside monophosphate metabolic process	RT	▮		3	7.9E-1	1.0E0
	Annotation Cluster 36	Enrichment Score: 0.16	G		🟩	Count	P_Value	Benjamini
☐	SMART	ZnF_C2H2	RT	▮		11	6.9E-1	1.0E0
☐	INTERPRO	Zinc finger, C2H2-type	RT	▮		11	6.9E-1	1.0E0
☐	INTERPRO	Zinc finger, C2H2-like	RT	▮		11	6.9E-1	1.0E0
	Annotation Cluster 37	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	hexose metabolic process	RT	▮		13	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	glucose metabolic process	RT	▮		13	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT	▮		16	5.8E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide metabolic process	RT	▮		14	6.3E-1	1.0E0
☐	GOTERM_BP_FAT	hexose catabolic process	RT	▮		8	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	alcohol catabolic process	RT	▮		8	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	glucose catabolic process	RT	▮		8	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	monosaccharide catabolic process	RT	▮		8	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	cellular carbohydrate catabolic process	RT	▮		8	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	carbohydrate catabolic process	RT	▮		8	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	glycolysis	RT	▮		6	8.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	glycolysis	RT	▮		3	9.5E-1	1.0E0
	Annotation Cluster 38	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	organophosphate metabolic process	RT	▮		9	5.0E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid metabolic process	RT	▮		8	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	lipid biosynthetic process	RT	▮		9	6.2E-1	1.0E0
☐	GOTERM_BP_FAT	phospholipid biosynthetic process	RT	▮		5	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	glycerolipid metabolic process	RT	▮		4	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	phosphoinositide metabolic process	RT	▮		4	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	glycerophospholipid metabolic process	RT	▮		4	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	inositol or phosphatidylinositol kinase activity	RT	▮		3	8.9E-1	1.0E0
	Annotation Cluster 39	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	dephosphorylation	RT	▮		10	6.4E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid dephosphorylation	RT	▮		8	7.1E-1	1.0E0
☐	GOTERM_MF_FAT	phosphatase activity	RT	▮		25	7.2E-1	1.0E0
☐	GOTERM_MF_FAT	phosphoprotein phosphatase activity	RT	▮		15	8.5E-1	1.0E0
	Annotation Cluster 40	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular carbohydrate biosynthetic process	RT	▮		5	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	carbohydrate biosynthetic process	RT	▮		5	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	alcohol biosynthetic process	RT	▮		3	8.9E-1	1.0E0
	Annotation Cluster 41	Enrichment Score: 0.13	G		🟩	Count	P_Value	Benjamini

☐	INTERPRO	ABC transporter-like	RT	▮		14	6.6E-1	1.0E0
☐	INTERPRO	ABC transporter, conserved site	RT	▮		13	7.2E-1	1.0E0
☐	COG_ONTOLOGY	Defense mechanisms	RT	▮		12	8.5E-1	1.0E0
	Annotation Cluster 42	Enrichment Score: 0.13	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	viral nucleoprotein	RT	▮		10	5.3E-1	1.0E0
☐	INTERPRO	Like-Sm ribonucleoprotein, core	RT	▮		7	7.2E-1	1.0E0
☐	SMART	Sm	RT	▮		4	8.9E-1	1.0E0
☐	INTERPRO	Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core	RT	▮		4	8.9E-1	1.0E0
	Annotation Cluster 43	Enrichment Score: 0.13	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Cyclin-related	RT	▮		5	5.1E-1	1.0E0
☐	SMART	CYCLIN	RT	▮		3	9.0E-1	1.0E0
☐	INTERPRO	Cyclin	RT	▮		3	9.0E-1	1.0E0
	Annotation Cluster 44	Enrichment Score: 0.13	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Pseudouridine synthase I, TruA	RT	▮		3	6.3E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001430:tRNA_psdUrid_synth	RT	▮		3	6.3E-1	1.0E0
☐	GOTERM_MF_FAT	intramolecular transferase activity	RT	▮		7	7.0E-1	1.0E0
☐	GOTERM_BP_FAT	RNA modification	RT	▮		9	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	pseudouridine synthesis	RT	▮		4	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	pseudouridine synthase activity	RT	▮		4	8.8E-1	1.0E0
	Annotation Cluster 45	Enrichment Score: 0.13	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	thiolester hydrolase activity	RT	▮		6	5.4E-1	1.0E0
☐	GOTERM_MF_FAT	ubiquitin thiolesterase activity	RT	▮		4	7.9E-1	1.0E0
☐	INTERPRO	Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2	RT	▮		4	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	RT	▮		7	9.2E-1	1.0E0
	Annotation Cluster 46	Enrichment Score: 0.12	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Kelch-type beta propeller	RT	▮		5	6.8E-1	1.0E0
☐	SMART	Kelch	RT	▮		4	8.0E-1	1.0E0
☐	INTERPRO	Kelch repeat type 1	RT	▮		4	8.0E-1	1.0E0
	Annotation Cluster 47	Enrichment Score: 0.12	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Cyclin-related	RT	▮		5	5.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	cyclin	RT	▮		5	9.3E-1	1.0E0
☐	INTERPRO	Cyclin, N-terminal	RT	▮		3	9.5E-1	1.0E0
	Annotation Cluster 48	Enrichment Score: 0.12	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Valine, leucine and isoleucine biosynthesis	RT	▮		5	3.1E-1	1.0E0
☐	INTERPRO	Aminoacyl-tRNA synthetase, class I, conserved site	RT	▮		7	4.4E-1	1.0E0
☐	GOTERM_BP_FAT	ncRNA metabolic process	RT	▮		30	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA aminoacylation for protein translation	RT	▮		12	8.3E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming carbon-oxygen bonds	RT	▮		13	8.4E-1	1.0E0
☐	GOTERM_MF_FAT	aminoacyl-tRNA ligase activity	RT	▮		13	8.4E-1	1.0E0
☐	GOTERM_MF_FAT	ligase activity, forming aminoacyl-tRNA and related compounds	RT	▮		13	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	tRNA metabolic process	RT	▮		21	8.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	Aminoacyl-tRNA synthetase	RT	▮		12	8.8E-1	9.9E-1
☐	GOTERM_BP_FAT	tRNA aminoacylation	RT	▮		12	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	amino acid activation	RT	▮		12	8.8E-1	1.0E0
☐	INTERPRO	Rossmann-like alpha/beta/alpha sandwich fold	RT	▮		10	8.9E-1	1.0E0
☐	KEGG_PATHWAY	Aminoacyl-tRNA biosynthesis	RT	▮		11	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	protein biosynthesis	RT	▮		5	9.3E-1	1.0E0
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II, conserved region	RT	▮		4	9.7E-1	1.0E0
	Annotation Cluster 49	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	endoribonuclease activity	RT	▮		4	6.4E-1	1.0E0
☐	GOTERM_MF_FAT	ribonuclease activity	RT	▮		6	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	endoribonuclease activity, producing 5'-phosphomonoesters	RT	▮		3	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	RT	▮		4	8.8E-1	1.0E0
	Annotation Cluster 50	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	peptidase activity, acting on L-amino acid peptides	RT	▮		40	5.8E-1	1.0E0
☐	GOTERM_MF_FAT	peptidase activity	RT	▮		46	6.0E-1	1.0E0

☐	GOTERM_BP_FAT	proteolysis	RT		51	6.0E-1	1.0E0
☐	GOTERM_MF_FAT	endopeptidase activity	RT		26	7.3E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type peptidase activity	RT		17	7.5E-1	1.0E0
☐	SMART	Pept_C1	RT		14	9.0E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain	RT		14	9.0E-1	1.0E0
☐	INTERPRO	Peptidase C1A, papain C-terminal	RT		14	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	cysteine-type endopeptidase activity	RT		12	9.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	Protease	RT		18	9.2E-1	1.0E0
☐	INTERPRO	Peptidase, cysteine peptidase active site	RT		14	9.7E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 0.11	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT		158	4.1E-1	9.9E-1
☐	SP_PIR_KEYWORDS	atp-binding	RT		148	5.5E-1	9.9E-1
☐	GOTERM_BP_FAT	phosphorus metabolic process	RT		171	7.2E-1	1.0E0
☐	GOTERM_BP_FAT	phosphate metabolic process	RT		171	7.2E-1	1.0E0
☐	GOTERM_MF_FAT	nucleotide binding	RT		349	7.5E-1	1.0E0
☐	GOTERM_BP_FAT	phosphorylation	RT		161	7.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	kinase	RT		184	7.8E-1	9.9E-1
☐	GOTERM_BP_FAT	protein amino acid phosphorylation	RT		149	8.1E-1	1.0E0
☐	GOTERM_MF_FAT	ribonucleotide binding	RT		322	8.2E-1	1.0E0
☐	GOTERM_MF_FAT	purine ribonucleotide binding	RT		322	8.2E-1	1.0E0
☐	GOTERM_MF_FAT	protein kinase activity	RT		150	8.2E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleotide binding	RT		325	8.5E-1	1.0E0
☐	INTERPRO	Protein kinase, core	RT		148	8.6E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT		291	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	ATP binding	RT		291	9.0E-1	1.0E0
☐	GOTERM_MF_FAT	nucleoside binding	RT		297	9.1E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase-related	RT		127	9.2E-1	1.0E0
☐	GOTERM_MF_FAT	purine nucleoside binding	RT		294	9.2E-1	1.0E0
☐	GOTERM_MF_FAT	adenyl nucleotide binding	RT		294	9.2E-1	1.0E0
	Annotation Cluster 52	Enrichment Score: 0.1	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	regulation of transcription	RT		20	4.1E-1	1.0E0
☐	GOTERM_MF_FAT	NAD or NADH binding	RT		6	5.4E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of RNA metabolic process	RT		8	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of transcription, DNA-dependent	RT		8	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	gene silencing	RT		5	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of gene expression	RT		5	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of macromolecule metabolic process	RT		5	6.6E-1	1.0E0
☐	GOTERM_BP_FAT	chromatin silencing	RT		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of cellular biosynthetic process	RT		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of RNA metabolic process	RT		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of biosynthetic process	RT		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of macromolecule biosynthetic process	RT		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	regulation of gene expression, epigenetic	RT		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of transcription	RT		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of nitrogen compound metabolic process	RT		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of gene expression, epigenetic	RT		3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	negative regulation of transcription, DNA-dependent	RT		3	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	NAD binding	RT		3	8.9E-1	1.0E0
☐	INTERPRO	NAD-dependent histone deacetylase, silent information regulator Sir2	RT		3	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	protein amino acid deacetylation	RT		3	9.5E-1	1.0E0
☐	GOTERM_MF_FAT	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	RT		3	9.9E-1	1.0E0
	Annotation Cluster 53	Enrichment Score: 0.1	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	lipid biosynthetic process	RT		9	6.2E-1	1.0E0

☐	GOTERM_BP_FAT	isoprenoid biosynthetic process	RT			3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	isoprenoid metabolic process	RT	▮		3	8.9E-1	1.0E0
	Annotation Cluster 54	Enrichment Score: 0.1	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	membrane docking	RT	▮		3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	exocytosis	RT	▮		3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	secretion by cell	RT	▮		3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	secretion	RT	▮		3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	vesicle docking during exocytosis	RT	▮		3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	vesicle docking	RT	▮		3	7.9E-1	1.0E0
☐	INTERPRO	Sec1-like protein	RT	▮		3	8.0E-1	1.0E0
	Annotation Cluster 55	Enrichment Score: 0.1	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	motor protein	RT	▮		15	5.6E-1	9.9E-1
☐	INTERPRO	Kinesin, motor region, conserved site	RT	▮		11	6.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	microtubule	RT	▮		18	7.6E-1	1.0E0
☐	SMART	KISc	RT	▮		16	7.6E-1	1.0E0
☐	INTERPRO	Kinesin, motor region	RT	▮		16	7.7E-1	1.0E0
☐	GOTERM_MF_FAT	motor activity	RT	▮		23	8.1E-1	1.0E0
☐	GOTERM_MF_FAT	microtubule motor activity	RT	▮		23	8.1E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based process	RT	▮		29	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	microtubule-based movement	RT	▮		25	8.6E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule	RT	▮		18	8.7E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule cytoskeleton	RT	▮		28	9.0E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeletal part	RT	▮		28	9.0E-1	1.0E0
☐	GOTERM_CC_FAT	cytoskeleton	RT	▮		29	9.1E-1	1.0E0
	Annotation Cluster 56	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	microtubule cytoskeleton organization	RT	▮		3	7.9E-1	1.0E0
☐	INTERPRO	Spc97/Spc98	RT	▮		3	8.0E-1	1.0E0
☐	GOTERM_CC_FAT	spindle pole	RT	▮		3	8.1E-1	1.0E0
☐	GOTERM_CC_FAT	spindle	RT	▮		3	8.1E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule organizing center	RT	▮		3	8.1E-1	1.0E0
	Annotation Cluster 57	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	RNA helicase, DEAD-box type, Q motif	RT	▮		12	4.0E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity	RT	▮		54	6.5E-1	1.0E0
☐	GOTERM_MF_FAT	ATPase activity, coupled	RT	▮		40	6.8E-1	1.0E0
☐	GOTERM_MF_FAT	helicase activity	RT	▮		29	8.5E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT	▮		16	8.7E-1	1.0E0
☐	GOTERM_MF_FAT	purine NTP-dependent helicase activity	RT	▮		20	8.7E-1	1.0E0
☐	GOTERM_MF_FAT	ATP-dependent helicase activity	RT	▮		20	8.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	helicase	RT	▮		23	8.8E-1	9.9E-1
☐	SMART	HELICc	RT	▮		22	9.4E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, C-terminal	RT	▮		22	9.5E-1	1.0E0
☐	SMART	DEXDc	RT	▮		21	9.6E-1	1.0E0
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT	▮		21	9.6E-1	1.0E0
☐	INTERPRO	DEAD-like helicase, N-terminal	RT	▮		21	9.6E-1	1.0E0
	Annotation Cluster 58	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Rotamase	RT	▮		5	7.9E-1	9.9E-1
☐	GOTERM_MF_FAT	cis-trans isomerase activity	RT	▮		5	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	peptidyl-prolyl cis-trans isomerase activity	RT	▮		5	7.9E-1	1.0E0
☐	INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type	RT	▮		4	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	protein folding	RT	▮		15	9.2E-1	1.0E0
	Annotation Cluster 59	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Endonuclease	RT	▮		17	7.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	rna-directed dna polymerase	RT	▮		13	7.7E-1	9.9E-1
☐	GOTERM_MF_FAT	endonuclease activity	RT	▮		19	7.7E-1	1.0E0
☐	GOTERM_MF_FAT	nuclease activity	RT	▮		27	8.4E-1	1.0E0
☐	GOTERM_MF_FAT	RNA-directed DNA polymerase activity	RT	▮		13	8.4E-1	1.0E0
☐	GOTERM_MF_FAT	nucleotidyltransferase activity	RT	▮		39	8.4E-1	1.0E0
☐	GOTERM_MF_FAT	DNA polymerase activity	RT	▮		16	9.6E-1	1.0E0

	Annotation Cluster 60	Enrichment Score: 0.08		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	proteolysis	RT	51	6.0E-1	1.0E0
☐	GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	RT	19	7.0E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein catabolic process	RT	19	7.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	ubl conjugation pathway	RT	8	7.1E-1	9.9E-1
☐	INTERPRO	Proteasome, alpha and beta subunits	RT	8	7.3E-1	1.0E0
☐	GOTERM_BP_FAT	cellular macromolecule catabolic process	RT	19	7.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	threonine protease	RT	4	7.9E-1	9.9E-1
☐	GOTERM_BP_FAT	protein catabolic process	RT	21	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type peptidase activity	RT	8	8.1E-1	1.0E0
☐	GOTERM_MF_FAT	threonine-type endopeptidase activity	RT	8	8.1E-1	1.0E0
☐	INTERPRO	Proteasome, subunit alpha/beta	RT	8	8.2E-1	1.0E0
☐	GOTERM_BP_FAT	macromolecule catabolic process	RT	21	8.3E-1	1.0E0
☐	GOTERM_CC_FAT	proteasome core complex	RT	8	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent protein catabolic process	RT	14	8.4E-1	1.0E0
☐	GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	RT	14	8.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	proteasome	RT	10	9.1E-1	1.0E0
☐	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	RT	7	9.2E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001212:multicatalytic endopeptidase complex chain C9	RT	3	9.6E-1	1.0E0
☐	GOTERM_CC_FAT	proteasome complex	RT	10	9.6E-1	1.0E0
☐	INTERPRO	Proteasome, alpha-subunit, conserved site	RT	3	9.8E-1	1.0E0
☐	GOTERM_CC_FAT	cytosol	RT	13	9.9E-1	1.0E0
☐	KEGG_PATHWAY	Proteasome	RT	12	9.9E-1	1.0E0
	Annotation Cluster 61	Enrichment Score: 0.08		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	tpr repeat	RT	6	6.8E-1	9.9E-1
☐	INTERPRO	Tetratricopeptide region	RT	14	7.4E-1	1.0E0
☐	INTERPRO	Tetratricopeptide-like helical	RT	17	8.3E-1	1.0E0
☐	INTERPRO	Tetratricopeptide TPR-1	RT	10	9.3E-1	1.0E0
☐	SMART	TPR	RT	12	9.3E-1	1.0E0
☐	INTERPRO	Tetratricopeptide repeat	RT	12	9.3E-1	1.0E0
	Annotation Cluster 62	Enrichment Score: 0.08		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	translational initiation	RT	7	7.0E-1	1.0E0
☐	GOTERM_MF_FAT	translation factor activity, nucleic acid binding	RT	17	8.6E-1	1.0E0
☐	GOTERM_MF_FAT	translation initiation factor activity	RT	13	8.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	Initiation factor	RT	9	9.4E-1	1.0E0
	Annotation Cluster 63	Enrichment Score: 0.07		Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	protein amino acid dephosphorylation	RT	8	7.1E-1	1.0E0
☐	GOTERM_MF_FAT	protein tyrosine/serine/threonine phosphatase activity	RT	3	8.9E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase, dual specificity	RT	3	9.0E-1	1.0E0
☐	INTERPRO	Dual specificity phosphatase, catalytic domain	RT	3	9.0E-1	1.0E0
	Annotation Cluster 64	Enrichment Score: 0.07		Count	P_Value	Benjamini
☐	INTERPRO	Metallophosphoesterase	RT	13	6.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	iron	RT	11	8.2E-1	9.9E-1
☐	GOTERM_MF_FAT	phosphoprotein phosphatase activity	RT	15	8.5E-1	1.0E0
☐	SMART	PP2Ac	RT	8	8.8E-1	1.0E0
☐	INTERPRO	Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase	RT	8	8.8E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF000908:serine/threonine-protein phosphatase, conventional type	RT	4	9.5E-1	1.0E0
☐	GOTERM_MF_FAT	iron ion binding	RT	14	9.8E-1	1.0E0
	Annotation Cluster 65	Enrichment Score: 0.07		Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	acetyltransferase activity	RT	6	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	N-acyltransferase activity	RT	6	7.9E-1	1.0E0
☐	GOTERM_MF_FAT	N-acetyltransferase activity	RT	5	8.7E-1	1.0E0
☐	INTERPRO	GCN5-related N-acetyltransferase	RT	5	8.8E-1	1.0E0
☐	INTERPRO	Acyl-CoA N-acyltransferase	RT	5	9.3E-1	1.0E0
	Annotation Cluster 66	Enrichment Score: 0.07		Count	P_Value	Benjamini

☐	SP_PIR_KEYWORDS	dna replication	RT			6	7.9E-1	9.9E-1
☐	GOTERM_BP_FAT	DNA replication	RT			17	8.9E-1	1.0E0
☐	KEGG_PATHWAY	DNA replication	RT			11	9.0E-1	1.0E0
	Annotation Cluster 67	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	SMART	MCM	RT			4	8.0E-1	1.0E0
☐	INTERPRO	DNA-dependent ATPase MCM	RT			4	8.0E-1	1.0E0
☐	KEGG_PATHWAY	DNA replication	RT			11	9.0E-1	1.0E0
☐	INTERPRO	Nucleic acid-binding, OB-fold	RT			8	9.9E-1	1.0E0
	Annotation Cluster 68	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Pyrimidine metabolism	RT			19	7.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	Transcription	RT			5	7.9E-1	9.9E-1
☐	GOTERM_MF_FAT	ribonucleoside binding	RT			3	7.9E-1	1.0E0
☐	GOTERM_BP_FAT	transcription	RT			14	8.4E-1	1.0E0
☐	GOTERM_MF_FAT	DNA-directed RNA polymerase activity	RT			12	8.8E-1	1.0E0
☐	GOTERM_MF_FAT	RNA polymerase activity	RT			12	9.2E-1	1.0E0
☐	KEGG_PATHWAY	RNA polymerase	RT			9	9.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotidyltransferase	RT			12	9.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-directed rna polymerase	RT			6	9.7E-1	1.0E0
☐	KEGG_PATHWAY	Purine metabolism	RT			15	9.8E-1	1.0E0
	Annotation Cluster 69	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	carboxylic acid biosynthetic process	RT			4	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	organic acid biosynthetic process	RT			4	8.8E-1	1.0E0
☐	GOTERM_BP_FAT	cellular amino acid biosynthetic process	RT			3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	amine biosynthetic process	RT			3	9.5E-1	1.0E0
	Annotation Cluster 70	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Mismatch repair	RT			8	8.3E-1	1.0E0
☐	KEGG_PATHWAY	DNA replication	RT			11	9.0E-1	1.0E0
☐	KEGG_PATHWAY	Nucleotide excision repair	RT			7	9.8E-1	1.0E0
	Annotation Cluster 71	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	EF-Hand type	RT			10	8.3E-1	1.0E0
☐	INTERPRO	EF-HAND 1	RT			11	8.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	calcium	RT			8	8.7E-1	9.9E-1
☐	INTERPRO	EF-HAND 2	RT			9	8.8E-1	1.0E0
☐	SMART	EFh	RT			5	9.6E-1	1.0E0
☐	INTERPRO	Calcium-binding EF-hand	RT			5	9.6E-1	1.0E0
☐	INTERPRO	EF hand	RT			5	9.6E-1	1.0E0
	Annotation Cluster 72	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Chaperone	RT			7	8.0E-1	9.9E-1
☐	SP_PIR_KEYWORDS	cytoplasm	RT			10	8.1E-1	9.9E-1
☐	INTERPRO	Chaperonin Cpn60/TCP-1	RT			5	8.8E-1	1.0E0
☐	INTERPRO	Chaperone, tailless complex polypeptide 1	RT			4	9.4E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002584:molecular chaperone t-complex-type	RT			4	9.5E-1	1.0E0
☐	INTERPRO	Chaperonin TCP-1, conserved site	RT			4	9.7E-1	1.0E0
☐	GOTERM_MF_FAT	unfolded protein binding	RT			9	9.8E-1	1.0E0
	Annotation Cluster 73	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Ribosomal RNA methyltransferase RrmJ/FtsJ	RT			3	8.0E-1	1.0E0
☐	GOTERM_BP_FAT	RNA methylation	RT			3	8.9E-1	1.0E0
☐	GOTERM_BP_FAT	methylation	RT			5	9.3E-1	1.0E0
☐	GOTERM_BP_FAT	biopolymer methylation	RT			3	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	one-carbon metabolic process	RT			5	9.6E-1	1.0E0
	Annotation Cluster 74	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	SMART	EGF_Lam	RT			14	8.6E-1	1.0E0
☐	INTERPRO	EGF-like, laminin	RT			14	8.6E-1	1.0E0
☐	INTERPRO	EGF	RT			4	8.9E-1	1.0E0
☐	INTERPRO	EGF, extracellular	RT			12	8.9E-1	1.0E0
☐	INTERPRO	EGF-like, type 3	RT			14	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	egf-like domain	RT			6	1.0E0	1.0E0
	Annotation Cluster 75	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Aminotransferase	RT			3	8.9E-1	9.9E-1

☐	GOTERM_MF_FAT	transaminase activity	RT	▮		3	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	transferase activity, transferring nitrogenous groups	RT	▮		3	9.7E-1	1.0E0
	Annotation Cluster 76	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Myb, DNA-binding	RT	▮		3	9.0E-1	1.0E0
☐	SMART	SANT	RT	▮		5	9.3E-1	1.0E0
☐	INTERPRO	SANT, DNA-binding	RT	▮		5	9.3E-1	1.0E0
	Annotation Cluster 77	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Serine/threonine protein kinase, active site	RT	▮		48	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	protein serine/threonine kinase activity	RT	▮		55	9.1E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase-related	RT	▮		127	9.2E-1	1.0E0
☐	INTERPRO	Protein kinase, ATP binding site	RT	▮		42	9.5E-1	1.0E0
☐	SMART	S_TKc	RT	▮		29	9.6E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase	RT	▮		29	9.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	serine/threonine-protein kinase	RT	▮		29	9.8E-1	1.0E0
	Annotation Cluster 78	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	pyridoxal phosphate binding	RT	▮		5	9.3E-1	1.0E0
☐	GOTERM_MF_FAT	vitamin B6 binding	RT	▮		5	9.3E-1	1.0E0
☐	INTERPRO	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	RT	▮		4	9.4E-1	1.0E0
☐	GOTERM_MF_FAT	vitamin binding	RT	▮		5	9.6E-1	1.0E0
	Annotation Cluster 79	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Dynein heavy chain	RT	▮		6	9.3E-1	1.0E0
☐	GOTERM_CC_FAT	dynein complex	RT	▮		6	9.4E-1	1.0E0
☐	GOTERM_CC_FAT	microtubule associated complex	RT	▮		7	9.6E-1	1.0E0
	Annotation Cluster 80	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	RNA-directed DNA polymerase (reverse transcriptase), related	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_BP_FAT	RNA-dependent DNA replication	RT	▮		3	9.7E-1	1.0E0
☐	INTERPRO	RNA-directed DNA polymerase (reverse transcriptase)	RT	▮		3	9.8E-1	1.0E0
	Annotation Cluster 81	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Thioredoxin, conserved site	RT	▮		4	8.0E-1	1.0E0
☐	INTERPRO	Thioredoxin-like subdomain	RT	▮		3	9.0E-1	1.0E0
☐	INTERPRO	Thioredoxin domain	RT	▮		3	9.5E-1	1.0E0
☐	INTERPRO	Thioredoxin, core	RT	▮		3	9.8E-1	1.0E0
☐	INTERPRO	Thioredoxin-like	RT	▮		5	9.9E-1	1.0E0
☐	INTERPRO	Thioredoxin fold	RT	▮		9	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	cell redox homeostasis	RT	▮		7	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	cellular homeostasis	RT	▮		7	9.9E-1	1.0E0
☐	GOTERM_BP_FAT	homeostatic process	RT	▮		7	1.0E0	1.0E0
	Annotation Cluster 82	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	protein complex assembly	RT	▮		6	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	protein complex biogenesis	RT	▮		6	9.5E-1	1.0E0
☐	GOTERM_BP_FAT	cellular protein complex assembly	RT	▮		5	9.6E-1	1.0E0
☐	GOTERM_BP_FAT	protein polymerization	RT	▮		3	9.9E-1	1.0E0
☐	INTERPRO	Tubulin	RT	▮		3	9.9E-1	1.0E0
☐	INTERPRO	Tubulin/FtsZ, GTPase domain	RT	▮		3	9.9E-1	1.0E0
☐	INTERPRO	Tubulin, conserved site	RT	▮		3	9.9E-1	1.0E0
	Annotation Cluster 83	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	4 iron, 4 sulfur cluster binding	RT	▮		4	9.3E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulpur binding domain	RT	▮		4	9.7E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, subgroup	RT	▮		4	9.7E-1	1.0E0
☐	INTERPRO	4Fe-4S ferredoxin, iron-sulphur binding, conserved site	RT	▮		3	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	iron-sulfur cluster binding	RT	▮		8	9.9E-1	1.0E0
☐	GOTERM_MF_FAT	metal cluster binding	RT	▮		8	9.9E-1	1.0E0
☐	GOTERM_MF_FAT	electron carrier activity	RT	▮		9	9.9E-1	1.0E0

[201 terms] were not clustered.

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