Functional Annotation Clustering

Current Gene List: List_2
Current Background: Mus musculus
91 DAVID IDs

Options   **Classification Stringency** Medium ⬍

[Rerun using options]   [Create Sublist]

37 Cluster(s)   📥 **Download File**

	Annotation Cluster 1	Enrichment Score: 9.45	**G**		Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	cytoplasmic membrane-bounded vesicle	RT	▬	20	3.6E-11	1.8E-9
☐	GOTERM_CC_FAT	membrane-bounded vesicle	RT	▬	20	4.6E-11	1.8E-9
☐	GOTERM_CC_FAT	cytoplasmic vesicle	RT	▬	21	1.6E-10	4.5E-9
☐	GOTERM_CC_FAT	vesicle	RT	▬	21	2.3E-10	5.8E-9
☐	GOTERM_CC_FAT	melanosome	RT	▬	10	6.0E-9	1.1E-7
☐	GOTERM_CC_FAT	pigment granule	RT	▬	10	6.0E-9	1.1E-7

	Annotation Cluster 2	Enrichment Score: 8.33	**G**		Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Ribosome	RT	▬	14	4.4E-12	3.6E-10
☐	SP_PIR_KEYWORDS	ribosomal protein	RT	▬	14	4.9E-12	1.3E-10
☐	SP_PIR_KEYWORDS	ribonucleoprotein	RT	▬	15	6.2E-11	1.4E-9
☐	GOTERM_MF_FAT	structural constituent of ribosome	RT	▬	13	2.2E-10	3.9E-8
☐	GOTERM_CC_FAT	ribosome	RT	▬	14	5.7E-10	1.3E-8
☐	GOTERM_CC_FAT	ribonucleoprotein complex	RT	▬	18	1.3E-8	1.8E-7
☐	GOTERM_BP_FAT	translation	RT	▬	14	3.4E-8	2.3E-5
☐	GOTERM_MF_FAT	structural molecule activity	RT	▬	16	1.7E-7	4.9E-6
☐	SP_PIR_KEYWORDS	ribosome	RT	▬	5	5.0E-6	4.8E-5
☐	GOTERM_CC_FAT	ribosomal subunit	RT	▬	6	8.8E-5	8.1E-4

	Annotation Cluster 3	Enrichment Score: 6.6	**G**		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	atp-binding	RT	▬	28	9.1E-11	1.9E-9
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT	▬	30	7.6E-10	1.2E-8
☐	GOTERM_MF_FAT	adenyl nucleotide binding	RT	▬	29	1.9E-7	4.6E-6
☐	GOTERM_MF_FAT	ATP binding	RT	▬	28	2.0E-7	4.4E-6
☐	GOTERM_MF_FAT	purine nucleoside binding	RT	▬	29	2.2E-7	4.3E-6
☐	GOTERM_MF_FAT	nucleoside binding	RT	▬	29	2.5E-7	4.4E-6
☐	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT	▬	28	2.5E-7	4.0E-6
☐	GOTERM_MF_FAT	nucleotide binding	RT	▬	33	2.6E-6	3.8E-5
☐	GOTERM_MF_FAT	purine nucleotide binding	RT	▬	30	3.2E-6	4.3E-5
☐	GOTERM_MF_FAT	purine ribonucleotide binding	RT	▬	29	4.5E-6	5.7E-5
☐	GOTERM_MF_FAT	ribonucleotide binding	RT	▬	29	4.5E-6	5.7E-5
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT	▬	18	1.0E-5	1.3E-3

	Annotation Cluster 4	Enrichment Score: 4.53	**G**		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	myosin	RT	▬	11	2.8E-14	1.5E-12
☐	UP_SEQ_FEATURE	domain:Myosin head-like	RT	▬	10	3.4E-14	1.3E-11
☐	SMART	MYSc	RT	▬	10	2.0E-13	9.7E-12
☐	INTERPRO	Myosin head, motor region	RT	▬	10	2.1E-13	5.7E-11
☐	SP_PIR_KEYWORDS	actin-binding	RT	▬	16	4.3E-13	1.7E-11
☐	GOTERM_CC_FAT	actin cytoskeleton	RT	▬	17	5.3E-13	1.1E-10
☐	GOTERM_CC_FAT	myosin complex	RT	▬	11	9.4E-12	9.5E-10
☐	SMART	IQ	RT	▬	11	3.1E-11	7.5E-10

	Category	Term		Count	P-Value	
☐	INTERPRO	IQ calmodulin-binding region	RT	11	3.4E-11	4.7E-9
☐	GOTERM_MF_FAT	actin binding	RT	16	4.2E-10	3.6E-8
☐	SP_PIR_KEYWORDS	motor protein	RT	11	6.0E-10	1.1E-8
☐	SP_PIR_KEYWORDS	calmodulin-binding	RT	10	2.4E-9	3.5E-8
☐	GOTERM_CC_FAT	stress fiber	RT	7	8.2E-9	1.4E-7
☐	GOTERM_CC_FAT	actin filament bundle	RT	7	1.1E-8	1.7E-7
☐	GOTERM_MF_FAT	motor activity	RT	11	1.9E-8	1.1E-6
☐	GOTERM_CC_FAT	actomyosin	RT	7	2.3E-8	3.1E-7
☐	GOTERM_MF_FAT	calmodulin binding	RT	10	4.8E-8	2.1E-6
☐	GOTERM_MF_FAT	cytoskeletal protein binding	RT	16	5.7E-8	2.0E-6
☐	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT	34	1.6E-7	2.0E-6
☐	GOTERM_CC_FAT	non-membrane-bounded organelle	RT	34	1.6E-7	2.0E-6
☐	UP_SEQ_FEATURE	region of interest:Actin-binding	RT	5	9.1E-6	1.8E-3
☐	UP_SEQ_FEATURE	domain:IQ	RT	6	1.2E-5	1.2E-3
☐	GOTERM_MF_FAT	actin filament binding	RT	6	1.5E-5	1.7E-4
☐	UP_SEQ_FEATURE	domain:IQ 2	RT	5	1.7E-5	1.4E-3
☐	UP_SEQ_FEATURE	domain:IQ 1	RT	5	2.0E-5	1.1E-3
☐	INTERPRO	Myosin, N-terminal, SH3-like	RT	4	2.7E-5	1.0E-3
☐	INTERPRO	Myosin tail	RT	4	4.4E-5	1.3E-3
☐	GOTERM_CC_FAT	cytoskeletal part	RT	17	6.5E-5	6.2E-4
☐	GOTERM_CC_FAT	cortical cytoskeleton	RT	5	2.1E-4	1.6E-3
☐	GOTERM_CC_FAT	cell cortex	RT	7	2.3E-4	1.7E-3
☐	GOTERM_CC_FAT	cytoskeleton	RT	19	5.2E-4	3.7E-3
☐	GOTERM_BP_FAT	actin filament-based process	RT	7	5.5E-4	4.2E-2
☐	GOTERM_MF_FAT	actin-dependent ATPase activity	RT	3	6.1E-4	5.1E-3
☐	GOTERM_MF_FAT	microfilament motor activity	RT	3	8.5E-4	6.8E-3
☐	INTERPRO	Myosin tail 2	RT	3	8.9E-4	1.9E-2
☐	GOTERM_CC_FAT	cell cortex part	RT	5	1.6E-3	8.6E-3
☐	GOTERM_BP_FAT	actin cytoskeleton organization	RT	6	2.7E-3	1.3E-1
☐	KEGG_PATHWAY	Tight junction	RT	7	2.9E-3	4.0E-2
☐	KEGG_PATHWAY	Viral myocarditis	RT	6	3.1E-3	3.6E-2
☐	UP_SEQ_FEATURE	domain:IQ 3	RT	3	3.1E-3	1.1E-1
☐	GOTERM_MF_FAT	ATPase activity, coupled	RT	7	3.2E-3	2.0E-2
☐	GOTERM_BP_FAT	actin filament-based movement	RT	3	3.3E-3	1.5E-1
☐	SP_PIR_KEYWORDS	cell shape	RT	3	7.0E-3	3.0E-2
☐	KEGG_PATHWAY	Regulation of actin cytoskeleton	RT	8	7.7E-3	6.9E-2
☐	GOTERM_MF_FAT	ATPase activity	RT	7	9.7E-3	5.2E-2
☐	GOTERM_BP_FAT	cell projection organization	RT	7	1.1E-2	3.1E-1
☐	GOTERM_BP_FAT	cytoskeleton organization	RT	7	1.2E-2	3.2E-1
☐	GOTERM_BP_FAT	cytoskeleton-dependent intracellular transport	RT	3	1.6E-2	3.9E-1
☐	GOTERM_CC_FAT	cell projection	RT	10	1.7E-2	8.1E-2
☐	GOTERM_BP_FAT	regulation of cell shape	RT	3	3.0E-2	5.5E-1
☐	GOTERM_CC_FAT	ruffle	RT	3	4.1E-2	1.7E-1
☐	GOTERM_CC_FAT	cell leading edge	RT	4	4.2E-2	1.7E-1
☐	GOTERM_CC_FAT	site of polarized growth	RT	3	4.8E-2	1.9E-1
☐	GOTERM_CC_FAT	growth cone	RT	3	4.8E-2	1.9E-1
☐	GOTERM_BP_FAT	striated muscle cell differentiation	RT	3	9.5E-2	7.8E-1
☐	GOTERM_BP_FAT	regulation of cell morphogenesis	RT	3	1.1E-1	8.1E-1
☐	GOTERM_BP_FAT	muscle cell differentiation	RT	3	1.5E-1	8.7E-1
☐	KEGG_PATHWAY	Focal adhesion	RT	5	1.6E-1	6.7E-1
☐	GOTERM_CC_FAT	axon	RT	3	1.7E-1	4.7E-1
☐	GOTERM_BP_FAT	striated muscle tissue development	RT	3	1.7E-1	8.9E-1

						Count	P_Value	Benjamini
	GOTERM_BP_FAT	muscle tissue development	RT			3	1.9E-1	8.9E-1
	KEGG_PATHWAY	Adherens junction	RT			3	1.9E-1	7.2E-1
	GOTERM_CC_FAT	neuron projection	RT			4	2.4E-1	5.8E-1
	GOTERM_BP_FAT	muscle organ development	RT			3	2.7E-1	9.5E-1
	KEGG_PATHWAY	Leukocyte transendothelial migration	RT			3	3.6E-1	8.9E-1
	GOTERM_CC_FAT	synapse	RT			4	3.8E-1	7.5E-1
	SP_PIR_KEYWORDS	coiled coil	RT			8	7.8E-1	9.9E-1
	Annotation Cluster 5	Enrichment Score: 4.21	G			Count	P_Value	Benjamini
	SP_PIR_KEYWORDS	coated pit	RT			9	1.6E-12	5.3E-11
	GOTERM_CC_FAT	coated pit	RT			9	3.3E-11	2.2E-9
	GOTERM_CC_FAT	clathrin coat	RT			9	5.6E-11	1.9E-9
	GOTERM_CC_FAT	membrane coat	RT			9	5.2E-9	1.1E-7
	GOTERM_CC_FAT	coated membrane	RT			9	5.2E-9	1.1E-7
	GOTERM_BP_FAT	vesicle-mediated transport	RT			15	4.1E-7	1.4E-4
	GOTERM_BP_FAT	endocytosis	RT			10	1.4E-6	3.2E-4
	GOTERM_BP_FAT	membrane invagination	RT			10	1.4E-6	3.2E-4
	GOTERM_BP_FAT	membrane organization	RT			11	3.7E-6	6.5E-4
	SP_PIR_KEYWORDS	Endocytosis	RT			7	7.4E-6	6.7E-5
	INTERPRO	Clathrin adaptor, alpha/beta/gamma-adaptin, appendage, Ig-like subdomain	RT			4	1.0E-5	4.7E-4
	SMART	Alpha_adaptinC2	RT			4	1.1E-5	1.8E-4
	GOTERM_BP_FAT	protein transport	RT			15	2.0E-5	2.8E-3
	GOTERM_BP_FAT	establishment of protein localization	RT			15	2.2E-5	2.5E-3
	GOTERM_CC_FAT	clathrin adaptor complex	RT			5	2.4E-5	2.4E-4
	GOTERM_CC_FAT	AP-type membrane coat adaptor complex	RT			5	2.4E-5	2.4E-4
	GOTERM_BP_FAT	protein localization	RT			16	2.4E-5	2.4E-3
	KEGG_PATHWAY	Endocytosis	RT			11	4.4E-5	1.8E-3
	INTERPRO	Clathrin/coatomer adaptor, adaptin-like, N-terminal	RT			4	4.4E-5	1.3E-3
	SP_PIR_KEYWORDS	protein transport	RT			11	1.1E-4	7.6E-4
	GOTERM_CC_FAT	internal side of plasma membrane	RT			10	1.5E-4	1.3E-3
	SP_PIR_KEYWORDS	cytoplasmic vesicle	RT			8	1.7E-4	1.1E-3
	GOTERM_BP_FAT	intracellular transport	RT			11	1.9E-4	1.6E-2
	GOTERM_CC_FAT	clathrin coat of coated pit	RT			3	6.9E-4	4.6E-3
	GOTERM_CC_FAT	endomembrane system	RT			12	1.1E-3	5.9E-3
	GOTERM_BP_FAT	intracellular protein transport	RT			8	1.1E-3	7.4E-2
	GOTERM_BP_FAT	cellular protein localization	RT			8	1.7E-3	1.0E-1
	GOTERM_BP_FAT	cellular macromolecule localization	RT			8	1.8E-3	9.9E-2
	GOTERM_MF_FAT	protein transporter activity	RT			4	8.9E-3	4.9E-2
	GOTERM_CC_FAT	plasma membrane part	RT			20	1.4E-2	6.8E-2
	KEGG_PATHWAY	Huntington's disease	RT			6	4.4E-2	3.1E-1
	SP_PIR_KEYWORDS	transport	RT			14	5.1E-2	1.7E-1
	INTERPRO	Armadillo-like helical	RT			3	1.4E-1	8.3E-1
	SP_PIR_KEYWORDS	golgi apparatus	RT			6	1.5E-1	4.1E-1
	GOTERM_CC_FAT	Golgi apparatus	RT			8	1.9E-1	5.0E-1
	GOTERM_CC_FAT	secretory granule	RT			3	1.9E-1	5.0E-1
	KEGG_PATHWAY	Lysosome	RT			3	3.6E-1	8.9E-1
	GOTERM_CC_FAT	Golgi apparatus part	RT			3	4.6E-1	8.4E-1
	Annotation Cluster 6	Enrichment Score: 3.79	G			Count	P_Value	Benjamini
	SP_PIR_KEYWORDS	rrna-binding	RT			4	5.4E-5	4.2E-4
	SP_PIR_KEYWORDS	rna-binding	RT			11	1.6E-4	1.1E-3
	GOTERM_MF_FAT	rRNA binding	RT			4	4.8E-4	4.2E-3
	Annotation Cluster 7	Enrichment Score: 3.5	G			Count	P_Value	Benjamini
	SP_PIR_KEYWORDS	endoplasmic reticulum	RT			19	6.3E-9	8.6E-8

	Category	Term			Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	microsome	RT		9	3.9E-8	4.9E-7
☐	GOTERM_CC_FAT	microsome	RT		11	3.3E-7	3.9E-6
☐	GOTERM_CC_FAT	vesicular fraction	RT		11	4.5E-7	5.1E-6
☐	SP_PIR_KEYWORDS	Monooxygenase	RT		8	1.2E-6	1.3E-5
☐	SP_PIR_KEYWORDS	chromoprotein	RT		6	1.7E-6	1.7E-5
☐	INTERPRO	Cytochrome P450, C-terminal region	RT		7	3.4E-6	3.1E-4
☐	INTERPRO	Cytochrome P450	RT		7	5.2E-6	3.5E-4
☐	INTERPRO	Cytochrome P450, conserved site	RT		7	5.9E-6	3.2E-4
☐	PIR_SUPERFAMILY	PIRSF000045:cytochrome P450 CYP2D6	RT		6	7.4E-6	5.6E-4
☐	GOTERM_MF_FAT	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	RT		6	9.0E-6	1.0E-4
☐	SP_PIR_KEYWORDS	metalloprotein	RT		6	9.1E-6	7.8E-5
☐	SP_PIR_KEYWORDS	electron transfer	RT		5	9.7E-6	7.9E-5
☐	GOTERM_CC_FAT	endoplasmic reticulum	RT		19	1.2E-5	1.3E-4
☐	COG_ONTOLOGY	Secondary metabolites biosynthesis, transport, and catabolism	RT		7	1.4E-5	1.0E-4
☐	UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	RT		7	2.0E-5	1.3E-3
☐	INTERPRO	Cytochrome P450, E-class, group I	RT		6	2.8E-5	9.5E-4
☐	GOTERM_MF_FAT	aromatase activity	RT		5	6.5E-5	6.7E-4
☐	SP_PIR_KEYWORDS	heme	RT		7	8.2E-5	6.1E-4
☐	KEGG_PATHWAY	Drug metabolism	RT		7	1.3E-4	3.5E-3
☐	GOTERM_CC_FAT	cell fraction	RT		14	2.0E-4	1.6E-3
☐	GOTERM_MF_FAT	heme binding	RT		7	3.4E-4	3.3E-3
☐	GOTERM_CC_FAT	extrinsic to membrane	RT		12	3.7E-4	2.7E-3
☐	GOTERM_MF_FAT	tetrapyrrole binding	RT		7	4.3E-4	4.0E-3
☐	SP_PIR_KEYWORDS	transmembrane protein	RT		9	5.6E-4	3.4E-3
☐	SP_PIR_KEYWORDS	oxidoreductase	RT		11	6.0E-4	3.5E-3
☐	KEGG_PATHWAY	Metabolism of xenobiotics by cytochrome P450	RT		6	6.2E-4	1.3E-2
☐	GOTERM_CC_FAT	membrane fraction	RT		12	7.2E-4	4.7E-3
☐	GOTERM_CC_FAT	insoluble fraction	RT		12	9.5E-4	5.8E-3
☐	BIOCARTA	Mechanism of Acetaminophen Activity and Toxicity	RT		3	1.3E-3	3.4E-2
☐	KEGG_PATHWAY	Linoleic acid metabolism	RT		5	1.4E-3	2.2E-2
☐	GOTERM_MF_FAT	electron carrier activity	RT		7	2.0E-3	1.3E-2
☐	BIOCARTA	Nuclear Receptors in Lipid Metabolism and Toxicity	RT		4	2.1E-3	2.7E-2
☐	GOTERM_BP_FAT	oxidation reduction	RT		11	5.4E-3	2.1E-1
☐	KEGG_PATHWAY	Retinol metabolism	RT		5	5.7E-3	5.7E-2
☐	SP_PIR_KEYWORDS	iron	RT		7	5.7E-3	2.5E-2
☐	GOTERM_MF_FAT	iron ion binding	RT		7	2.4E-2	1.2E-1
☐	KEGG_PATHWAY	Arachidonic acid metabolism	RT		3	2.2E-1	7.5E-1
☐	SP_PIR_KEYWORDS	metal-binding	RT		11	8.9E-1	1.0E0
☐	GOTERM_MF_FAT	metal ion binding	RT		18	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	transition metal ion binding	RT		11	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	cation binding	RT		18	9.8E-1	1.0E0
☐	GOTERM_MF_FAT	ion binding	RT		18	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc	RT		4	1.0E0	1.0E0
☐	GOTERM_MF_FAT	zinc ion binding	RT		4	1.0E0	1.0E0
	Annotation Cluster 8	Enrichment Score: 2.9	G		Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	melanosome	RT		10	6.0E-9	1.1E-7
☐	GOTERM_CC_FAT	pigment granule	RT		10	6.0E-9	1.1E-7
☐	GOTERM_CC_FAT	endoplasmic reticulum lumen	RT		6	1.3E-4	1.2E-3
☐	INTERPRO	Protein disulphide isomerase	RT		3	1.5E-4	4.1E-3

☐	UP_SEQ_FEATURE	short sequence motif:Prevents secretion from ER	RT	▬		5	3.3E-4	1.6E-2
☐	INTERPRO	Disulphide isomerase	RT	▬		3	3.8E-4	9.3E-3
☐	INTERPRO	Thioredoxin-like	RT	▬		4	8.0E-4	1.8E-2
☐	UP_SEQ_FEATURE	domain:Thioredoxin 1	RT	▬		3	8.5E-4	3.3E-2
☐	UP_SEQ_FEATURE	domain:Thioredoxin 2	RT	▬		3	8.5E-4	3.3E-2
☐	SP_PIR_KEYWORDS	Redox-active center	RT	▬		4	9.9E-4	5.2E-3
☐	GOTERM_CC_FAT	endoplasmic reticulum part	RT	▬▬		8	1.0E-3	6.0E-3
☐	GOTERM_MF_FAT	protein disulfide isomerase activity	RT	▬		3	1.1E-3	8.6E-3
☐	GOTERM_MF_FAT	intramolecular oxidoreductase activity, transposing S-S bonds	RT	▬		3	1.1E-3	8.6E-3
☐	INTERPRO	Thioredoxin-like subdomain	RT	▬		3	1.4E-3	2.4E-2
☐	GOTERM_MF_FAT	intramolecular oxidoreductase activity, interconverting keto- and enol-groups	RT	▬		3	1.4E-3	1.1E-2
☐	GOTERM_BP_FAT	cell redox homeostasis	RT	▬		4	5.6E-3	2.0E-1
☐	INTERPRO	Thioredoxin, conserved site	RT	▬		3	7.1E-3	1.1E-1
☐	INTERPRO	Thioredoxin domain	RT	▬		3	7.6E-3	1.1E-1
☐	INTERPRO	Thioredoxin fold	RT	▬		4	1.7E-2	2.0E-1
☐	GOTERM_MF_FAT	intramolecular oxidoreductase activity	RT	▬		3	2.5E-2	1.2E-1
☐	SP_PIR_KEYWORDS	Isomerase	RT	▬		3	1.2E-1	3.6E-1
☐	GOTERM_BP_FAT	cellular homeostasis	RT	▬		4	3.2E-1	9.7E-1
☐	GOTERM_BP_FAT	homeostatic process	RT	▬		5	4.4E-1	9.9E-1
☐	UP_SEQ_FEATURE	disulfide bond	RT	▬▬		10	9.3E-1	1.0E0
	Annotation Cluster 9	Enrichment Score: 2.54	**G**		▓	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	stress response	RT	▬		4	1.5E-3	7.4E-3
☐	SP_PIR_KEYWORDS	molecular chaperone	RT	▬		3	2.2E-3	1.0E-2
☐	SP_PIR_KEYWORDS	Chaperone	RT	▬		5	7.0E-3	2.9E-2
	Annotation Cluster 10	Enrichment Score: 2.54	**G**		▓	Count	P_Value	Benjamini
☐	INTERPRO	Heat shock protein 70	RT	▬		3	1.4E-3	2.4E-2
☐	INTERPRO	Heat shock protein Hsp70	RT	▬		3	1.4E-3	2.4E-2
☐	SP_PIR_KEYWORDS	stress response	RT	▬		4	1.5E-3	7.4E-3
☐	PIR_SUPERFAMILY	PIRSF002581:chaperone HSP70	RT	▬		3	1.6E-3	5.8E-2
☐	INTERPRO	Heat shock protein 70, conserved site	RT	▬		3	1.9E-3	3.2E-2
☐	KEGG_PATHWAY	Antigen processing and presentation	RT	▬		4	7.2E-2	4.0E-1
	Annotation Cluster 11	Enrichment Score: 1.99	**G**		▓	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	cytoplasmic vesicle	RT	▬▬		8	1.7E-4	1.1E-3
☐	GOTERM_CC_FAT	clathrin-coated vesicle	RT	▬▬		6	7.4E-4	4.6E-3
☐	GOTERM_CC_FAT	coated vesicle	RT	▬		6	1.6E-3	8.6E-3
☐	GOTERM_CC_FAT	clathrin coated vesicle membrane	RT	▬		3	2.5E-2	1.2E-1
☐	GOTERM_CC_FAT	vesicle membrane	RT	▬		4	2.9E-2	1.3E-1
☐	GOTERM_CC_FAT	coated vesicle membrane	RT	▬		3	5.1E-2	2.0E-1
☐	GOTERM_CC_FAT	cytoplasmic vesicle membrane	RT	▬		3	1.2E-1	3.8E-1
☐	GOTERM_CC_FAT	cytoplasmic vesicle part	RT	▬		3	1.4E-1	4.1E-1
	Annotation Cluster 12	Enrichment Score: 1.9	**G**		▓	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	lipid metabolism	RT	▬		6	6.2E-4	3.5E-3
☐	GOTERM_BP_FAT	lipid transport	RT	▬		4	3.2E-2	5.4E-1
☐	GOTERM_MF_FAT	lipid transporter activity	RT	▬		3	3.3E-2	1.5E-1
☐	GOTERM_BP_FAT	lipid localization	RT	▬		4	3.8E-2	5.6E-1
	Annotation Cluster 13	Enrichment Score: 1.68	**G**		▓	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	lipid metabolism	RT	▬		6	6.2E-4	3.5E-3
☐	GOTERM_MF_FAT	long-chain-fatty-acid-CoA ligase activity	RT	▬		3	3.1E-3	2.0E-2
☐	SP_PIR_KEYWORDS	fatty acid metabolism	RT	▬		4	3.6E-3	1.6E-2
☐	GOTERM_MF_FAT	fatty-acid ligase activity	RT	▬		3	4.1E-3	2.4E-2
☐	INTERPRO	AMP-dependent synthetase and ligase	RT	▬		3	1.0E-2	1.3E-1
☐	GOTERM_MF_FAT	ligase activity, forming carbon-sulfur bonds	RT	▬		3	1.4E-2	7.2E-2

					Count	P_Value	Benjamini
SP_PIR_KEYWORDS	ligase	RT			6	1.6E-2	5.9E-2
KEGG_PATHWAY	PPAR signaling pathway	RT			4	5.1E-2	3.3E-1
GOTERM_BP_FAT	fatty acid metabolic process	RT			4	9.2E-2	7.7E-1
UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT			7	1.0E0	1.0E0
UP_SEQ_FEATURE	transmembrane region	RT			8	1.0E0	1.0E0

Annotation Cluster 14 Enrichment Score: 1.42 G

					Count	P_Value	Benjamini
GOTERM_BP_FAT	negative regulation of actin filament depolymerization	RT			3	6.5E-3	2.2E-1
GOTERM_BP_FAT	regulation of actin filament depolymerization	RT			3	8.5E-3	2.7E-1
GOTERM_BP_FAT	cell projection organization	RT			7	1.1E-2	3.1E-1
GOTERM_BP_FAT	negative regulation of protein complex disassembly	RT			3	1.8E-2	4.0E-1
GOTERM_BP_FAT	regulation of protein complex disassembly	RT			3	2.6E-2	5.2E-1
SP_PIR_KEYWORDS	cytoskeleton	RT			8	2.8E-2	9.9E-2
GOTERM_BP_FAT	negative regulation of cytoskeleton organization	RT			3	3.2E-2	5.5E-1
GOTERM_BP_FAT	regulation of actin polymerization or depolymerization	RT			3	3.4E-2	5.5E-1
GOTERM_BP_FAT	regulation of actin filament length	RT			3	3.5E-2	5.5E-1
GOTERM_BP_FAT	regulation of actin cytoskeleton organization	RT			3	4.8E-2	6.1E-1
GOTERM_BP_FAT	regulation of actin filament-based process	RT			3	4.9E-2	6.1E-1
GOTERM_BP_FAT	negative regulation of organelle organization	RT			3	5.0E-2	6.1E-1
GOTERM_BP_FAT	negative regulation of cellular component organization	RT			3	1.0E-1	7.9E-1
GOTERM_BP_FAT	regulation of cytoskeleton organization	RT			3	1.1E-1	8.1E-1
GOTERM_BP_FAT	regulation of organelle organization	RT			3	2.3E-1	9.3E-1
GOTERM_BP_FAT	regulation of cellular component size	RT			3	2.4E-1	9.3E-1

Annotation Cluster 15 Enrichment Score: 1.35 G

					Count	P_Value	Benjamini
SP_PIR_KEYWORDS	Chaperone	RT			5	7.0E-3	2.9E-2
GOTERM_MF_FAT	unfolded protein binding	RT			3	7.5E-2	3.1E-1
GOTERM_BP_FAT	protein folding	RT			3	1.7E-1	8.9E-1

Annotation Cluster 16 Enrichment Score: 1.31 G

					Count	P_Value	Benjamini
GOTERM_CC_FAT	basolateral plasma membrane	RT			6	2.8E-3	1.5E-2
GOTERM_CC_FAT	adherens junction	RT			4	3.7E-2	1.6E-1
GOTERM_CC_FAT	anchoring junction	RT			4	5.3E-2	2.0E-1
GOTERM_CC_FAT	focal adhesion	RT			3	5.8E-2	2.2E-1
GOTERM_CC_FAT	cell-substrate adherens junction	RT			3	6.6E-2	2.4E-1
GOTERM_CC_FAT	cell-substrate junction	RT			3	7.6E-2	2.6E-1
GOTERM_CC_FAT	cell junction	RT			5	4.1E-1	7.8E-1

Annotation Cluster 17 Enrichment Score: 1.17 G

					Count	P_Value	Benjamini
GOTERM_BP_FAT	positive regulation of endocytosis	RT			3	1.7E-2	4.0E-1
GOTERM_BP_FAT	regulation of endocytosis	RT			3	3.7E-2	5.6E-1
GOTERM_BP_FAT	regulation of vesicle-mediated transport	RT			3	8.4E-2	7.5E-1
GOTERM_BP_FAT	positive regulation of cellular component organization	RT			3	1.6E-1	8.8E-1
GOTERM_BP_FAT	positive regulation of transport	RT			3	1.8E-1	8.9E-1

Annotation Cluster 18 Enrichment Score: 1.04 G

					Count	P_Value	Benjamini
GOTERM_CC_FAT	endoplasmic reticulum lumen	RT			6	1.3E-4	1.2E-3
UP_SEQ_FEATURE	short sequence motif:Prevents secretion from ER	RT			5	3.3E-4	1.6E-2
GOTERM_CC_FAT	endoplasmic reticulum part	RT			8	1.0E-3	6.0E-3
INTERPRO	Endoplasmic reticulum, targeting sequence	RT			4	1.3E-3	2.6E-2
GOTERM_BP_FAT	homeostatic process	RT			5	4.4E-1	9.9E-1
GOTERM_CC_FAT	intracellular organelle lumen	RT			9	5.2E-1	8.8E-1
GOTERM_CC_FAT	organelle lumen	RT			9	5.3E-1	8.8E-1
GOTERM_CC_FAT	membrane-enclosed lumen	RT			9	5.7E-1	9.0E-1

	Category	Term			Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	disulfide bond	RT		12	7.2E-1	9.7E-1
☐	UP_SEQ_FEATURE	disulfide bond	RT		10	9.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	signal	RT		9	9.9E-1	1.0E0
☐	UP_SEQ_FEATURE	signal peptide	RT		9	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	glycoprotein	RT		8	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		7	1.0E0	1.0E0

Annotation Cluster 19	Enrichment Score: 0.95	**G**		Count	P_Value	Benjamini

	Category	Term			Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	ligase	RT		6	1.6E-2	5.9E-2
☐	GOTERM_BP_FAT	nitrogen compound biosynthetic process	RT		4	2.6E-1	9.4E-1
☐	GOTERM_MF_FAT	ligase activity, forming carbon-nitrogen bonds	RT		3	3.6E-1	8.5E-1

Annotation Cluster 20	Enrichment Score: 0.95	**G**		Count	P_Value	Benjamini

	Category	Term			Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular amino acid biosynthetic process	RT		3	2.7E-2	5.2E-1
☐	GOTERM_BP_FAT	amine biosynthetic process	RT		3	6.7E-2	6.9E-1
☐	GOTERM_BP_FAT	organic acid biosynthetic process	RT		3	2.0E-1	9.0E-1
☐	GOTERM_BP_FAT	carboxylic acid biosynthetic process	RT		3	2.0E-1	9.0E-1
☐	GOTERM_BP_FAT	nitrogen compound biosynthetic process	RT		4	2.6E-1	9.4E-1

Annotation Cluster 21	Enrichment Score: 0.91	**G**		Count	P_Value	Benjamini

	Category	Term			Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	repeat:6	RT		3	6.0E-2	8.7E-1
☐	UP_SEQ_FEATURE	repeat:5	RT		3	8.1E-2	9.1E-1
☐	UP_SEQ_FEATURE	repeat:4	RT		3	1.1E-1	9.5E-1
☐	UP_SEQ_FEATURE	repeat:3	RT		3	1.4E-1	9.8E-1
☐	UP_SEQ_FEATURE	repeat:1	RT		3	2.0E-1	9.9E-1
☐	UP_SEQ_FEATURE	repeat:2	RT		3	2.1E-1	9.9E-1

Annotation Cluster 22	Enrichment Score: 0.89	**G**		Count	P_Value	Benjamini

	Category	Term			Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	contractile fiber part	RT		3	1.2E-1	3.8E-1
☐	GOTERM_CC_FAT	myofibril	RT		3	1.3E-1	3.9E-1
☐	GOTERM_CC_FAT	contractile fiber	RT		3	1.4E-1	4.1E-1

Annotation Cluster 23	Enrichment Score: 0.87	**G**		Count	P_Value	Benjamini

	Category	Term			Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cell killing	RT		3	3.8E-3	1.6E-1
☐	GOTERM_BP_FAT	positive regulation of apoptosis	RT		4	1.8E-1	8.9E-1
☐	GOTERM_BP_FAT	positive regulation of programmed cell death	RT		4	1.8E-1	8.9E-1
☐	GOTERM_BP_FAT	positive regulation of cell death	RT		4	1.8E-1	8.9E-1
☐	GOTERM_BP_FAT	regulation of apoptosis	RT		6	2.2E-1	9.2E-1
☐	GOTERM_BP_FAT	regulation of programmed cell death	RT		6	2.3E-1	9.2E-1
☐	GOTERM_BP_FAT	regulation of cell death	RT		6	2.3E-1	9.2E-1
☐	GOTERM_BP_FAT	induction of apoptosis	RT		3	2.5E-1	9.4E-1
☐	GOTERM_BP_FAT	induction of programmed cell death	RT		3	2.5E-1	9.4E-1

Annotation Cluster 24	Enrichment Score: 0.84	**G**		Count	P_Value	Benjamini

	Category	Term			Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin)	RT		4	6.9E-2	8.9E-1
☐	SP_PIR_KEYWORDS	isopeptide bond	RT		4	1.6E-1	4.4E-1
☐	SP_PIR_KEYWORDS	ubl conjugation	RT		5	2.7E-1	6.2E-1

Annotation Cluster 25	Enrichment Score: 0.72	**G**		Count	P_Value	Benjamini

	Category	Term			Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cell projection organization	RT		7	1.1E-2	3.1E-1
☐	GOTERM_BP_FAT	neuron projection development	RT		3	3.6E-1	9.8E-1
☐	GOTERM_BP_FAT	neuron development	RT		3	5.1E-1	1.0E0
☐	GOTERM_BP_FAT	neuron differentiation	RT		3	6.8E-1	1.0E0

Annotation Cluster 26	Enrichment Score: 0.67	**G**		Count	P_Value	Benjamini

	Category	Term			Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	peroxisome	RT		3	8.5E-2	2.7E-1
☐	GOTERM_CC_FAT	microbody	RT		3	1.6E-1	4.6E-1
☐	GOTERM_CC_FAT	peroxisome	RT		3	1.6E-1	4.6E-1
☐	UP_SEQ_FEATURE	transmembrane region	RT		8	1.0E0	1.0E0

Annotation Cluster 27	Enrichment Score: 0.65	**G**		Count	P_Value	Benjamini

	Category	Term			Count	P_Value	Benjamini
☐	INTERPRO	EF-HAND_1	RT		4	9.2E-2	7.0E-1

						Count	P_Value	Benjamini
☐	INTERPRO	EF hand	RT			3	1.4E-1	8.3E-1
☐	INTERPRO	Calcium-binding EF-hand	RT			3	1.5E-1	8.4E-1
☐	SMART	EFh	RT			3	1.6E-1	8.2E-1
☐	UP_SEQ_FEATURE	domain:EF-hand 2	RT			3	2.3E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:EF-hand 1	RT			3	2.3E-1	9.9E-1
☐	INTERPRO	EF-HAND 2	RT			3	2.8E-1	9.7E-1
☐	SP_PIR_KEYWORDS	calcium	RT			6	3.1E-1	6.6E-1
☐	INTERPRO	EF-Hand type	RT			3	3.2E-1	9.8E-1
☐	GOTERM_MF_FAT	calcium ion binding	RT			6	6.4E-1	9.9E-1
	Annotation Cluster 28	Enrichment Score: 0.62	G			Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular protein complex assembly	RT			3	1.3E-1	8.4E-1
☐	GOTERM_BP_FAT	cellular macromolecular complex assembly	RT			4	1.3E-1	8.4E-1
☐	GOTERM_BP_FAT	cellular macromolecular complex subunit organization	RT			4	1.7E-1	8.9E-1
☐	GOTERM_BP_FAT	macromolecular complex assembly	RT			4	3.1E-1	9.7E-1
☐	GOTERM_BP_FAT	macromolecular complex subunit organization	RT			4	3.6E-1	9.8E-1
☐	GOTERM_BP_FAT	protein complex assembly	RT			3	3.8E-1	9.8E-1
☐	GOTERM_BP_FAT	protein complex biogenesis	RT			3	3.8E-1	9.8E-1
	Annotation Cluster 29	Enrichment Score: 0.58	G			Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	cellular component morphogenesis	RT			6	5.3E-2	6.2E-1
☐	GOTERM_BP_FAT	cell morphogenesis	RT			5	1.1E-1	8.0E-1
☐	GOTERM_BP_FAT	cell morphogenesis involved in differentiation	RT			4	1.3E-1	8.4E-1
☐	GOTERM_BP_FAT	in utero embryonic development	RT			4	2.0E-1	9.1E-1
☐	GOTERM_BP_FAT	forebrain development	RT			3	2.5E-1	9.4E-1
☐	GOTERM_BP_FAT	cell migration	RT			3	4.1E-1	9.9E-1
☐	GOTERM_BP_FAT	chordate embryonic development	RT			4	4.4E-1	9.9E-1
☐	GOTERM_BP_FAT	embryonic development ending in birth or egg hatching	RT			4	4.5E-1	9.9E-1
☐	GOTERM_BP_FAT	localization of cell	RT			3	4.9E-1	1.0E0
☐	GOTERM_BP_FAT	cell motility	RT			3	4.9E-1	1.0E0
☐	GOTERM_BP_FAT	cell motion	RT			3	6.3E-1	1.0E0
	Annotation Cluster 30	Enrichment Score: 0.54	G			Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	duplication	RT			5	3.2E-3	1.5E-2
☐	GOTERM_BP_FAT	positive regulation of response to stimulus	RT			3	2.9E-1	9.6E-1
☐	GOTERM_CC_FAT	extracellular space	RT			4	6.9E-1	9.6E-1
☐	GOTERM_CC_FAT	extracellular region part	RT			4	9.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	Secreted	RT			3	1.0E0	1.0E0
☐	GOTERM_CC_FAT	extracellular region	RT			5	1.0E0	1.0E0
	Annotation Cluster 31	Enrichment Score: 0.53	G			Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	lymphocyte mediated immunity	RT			3	7.2E-2	7.1E-1
☐	GOTERM_BP_FAT	leukocyte mediated immunity	RT			3	9.5E-2	7.8E-1
☐	GOTERM_BP_FAT	immune effector process	RT			3	1.7E-1	8.9E-1
☐	GOTERM_BP_FAT	defense response	RT			3	7.4E-1	1.0E0
☐	GOTERM_BP_FAT	immune response	RT			3	7.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	glycoprotein	RT			8	1.0E0	1.0E0
	Annotation Cluster 32	Enrichment Score: 0.46	G			Count	P_Value	Benjamini
☐	GOTERM_BP_FAT	secretion	RT			4	1.4E-1	8.5E-1
☐	GOTERM_BP_FAT	secretion by cell	RT			3	2.9E-1	9.6E-1
☐	GOTERM_BP_FAT	neurological system process	RT			3	1.0E0	1.0E0
	Annotation Cluster 33	Enrichment Score: 0.29	G			Count	P_Value	Benjamini
☐	GOTERM_MF_FAT	protein homodimerization activity	RT			3	3.6E-1	8.5E-1
☐	GOTERM_MF_FAT	identical protein binding	RT			3	5.6E-1	9.7E-1
☐	GOTERM_MF_FAT	protein dimerization activity	RT			3	6.5E-1	9.9E-1
	Annotation Cluster 34	Enrichment Score: 0.12	G			Count	P_Value	Benjamini
☐	GOTERM_CC_FAT	organelle envelope	RT			4	7.3E-1	9.7E-1

					Count	P_Value	Benjamini
GOTERM_CC_FAT	organelle envelope	RT			4	7.2E-1	9.7E-1
GOTERM_CC_FAT	mitochondrial membrane	RT			3	7.2E-1	9.7E-1
GOTERM_CC_FAT	envelope	RT			4	7.3E-1	9.7E-1
GOTERM_CC_FAT	mitochondrial envelope	RT			3	7.6E-1	9.7E-1
GOTERM_CC_FAT	mitochondrial part	RT			3	8.8E-1	1.0E0

Annotation Cluster 35	Enrichment Score: 0.12	G			Count	P_Value	Benjamini
UP_SEQ_FEATURE	binding site:ATP	RT			4	6.0E-1	1.0E0
INTERPRO	Protein kinase, ATP binding site	RT			3	6.9E-1	1.0E0
SP_PIR_KEYWORDS	kinase	RT			4	7.0E-1	9.7E-1
INTERPRO	Protein kinase, core	RT			3	7.2E-1	1.0E0
GOTERM_BP_FAT	phosphate metabolic process	RT			5	7.5E-1	1.0E0
GOTERM_BP_FAT	phosphorus metabolic process	RT			5	7.5E-1	1.0E0
UP_SEQ_FEATURE	domain:Protein kinase	RT			3	7.5E-1	1.0E0
GOTERM_BP_FAT	phosphorylation	RT			4	8.0E-1	1.0E0
SP_PIR_KEYWORDS	transferase	RT			6	8.4E-1	9.9E-1
UP_SEQ_FEATURE	active site:Proton acceptor	RT			3	8.9E-1	1.0E0
GOTERM_BP_FAT	protein amino acid phosphorylation	RT			3	8.9E-1	1.0E0
GOTERM_MF_FAT	protein kinase activity	RT			3	9.0E-1	1.0E0

Annotation Cluster 36	Enrichment Score: 0.07	G			Count	P_Value	Benjamini
GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	RT			3	8.2E-1	1.0E0
GOTERM_BP_FAT	cellular protein catabolic process	RT			3	8.3E-1	1.0E0
GOTERM_BP_FAT	protein catabolic process	RT			3	8.4E-1	1.0E0
GOTERM_BP_FAT	proteolysis	RT			5	8.6E-1	1.0E0
GOTERM_BP_FAT	cellular macromolecule catabolic process	RT			3	8.7E-1	1.0E0
GOTERM_BP_FAT	macromolecule catabolic process	RT			3	9.0E-1	1.0E0

Annotation Cluster 37	Enrichment Score: 0	G			Count	P_Value	Benjamini
UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT			7	1.0E0	1.0E0
UP_SEQ_FEATURE	transmembrane region	RT			8	1.0E0	1.0E0
SP_PIR_KEYWORDS	transmembrane	RT			9	1.0E0	1.0E0
GOTERM_CC_FAT	integral to membrane	RT			10	1.0E0	1.0E0
GOTERM_CC_FAT	intrinsic to membrane	RT			10	1.0E0	1.0E0

[53 terms] were not clustered.

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