



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

**Functional Annotation Clustering**

[Help and Manual](#)

Current Gene List: **liste MP**

Current Background: **Homo sapiens**

370 DAVID IDs

Options Classification Stringency **Medium**

Rerun using options

Create Sublist

172 Cluster(s)

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		Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	Annotation Cluster 1						
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">pigment granule</a>	<a href="#">RT</a>		38	3.1E-35	1.1E-32
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">melanosome</a>	<a href="#">RT</a>		38	3.1E-35	1.1E-32
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">membrane-bounded vesicle</a>	<a href="#">RT</a>		56	3.0E-17	1.8E-15
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytoplasmic membrane-bounded vesicle</a>	<a href="#">RT</a>		54	1.5E-16	5.9E-15
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">vesicle</a>	<a href="#">RT</a>		60	1.5E-16	5.1E-15
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytoplasmic vesicle</a>	<a href="#">RT</a>		58	4.8E-16	1.8E-14
<input type="checkbox"/>	Annotation Cluster 2	Enrichment Score: 14.17	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">translational elongation</a>	<a href="#">RT</a>		33	3.6E-27	7.6E-24
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">structural molecule activity</a>	<a href="#">RT</a>		69	1.8E-24	1.0E-21
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">protein biosynthesis</a>	<a href="#">RT</a>		34	2.1E-22	2.5E-20
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ribosome</a>	<a href="#">RT</a>		23	9.1E-21	8.5E-19
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytosolic ribosome</a>	<a href="#">RT</a>		26	2.2E-20	2.8E-18
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytosolic part</a>	<a href="#">RT</a>		33	3.6E-20	3.3E-18
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ribosomal protein</a>	<a href="#">RT</a>		28	3.0E-16	2.2E-14
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ribonucleoprotein</a>	<a href="#">RT</a>		32	3.2E-15	1.5E-13
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">ribosomal subunit</a>	<a href="#">RT</a>		26	3.6E-15	1.4E-13
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">translation</a>	<a href="#">RT</a>		38	1.1E-14	4.8E-12
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Ribosome</a>	<a href="#">RT</a>		25	3.6E-14	4.6E-12
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">structural constituent of ribosome</a>	<a href="#">RT</a>		27	1.7E-13	2.5E-11
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">ribosome</a>	<a href="#">RT</a>		29	3.1E-12	8.2E-11
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytosolic small ribosomal subunit</a>	<a href="#">RT</a>		14	1.7E-11	4.1E-10
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">small ribosomal subunit</a>	<a href="#">RT</a>		14	8.4E-9	1.9E-7
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">ribonucleoprotein complex</a>	<a href="#">RT</a>		38	3.6E-8	7.4E-7
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytosolic large ribosomal subunit</a>	<a href="#">RT</a>		11	3.8E-8	7.4E-7
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">large ribosomal subunit</a>	<a href="#">RT</a>		12	1.4E-6	1.9E-5
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">RNA binding</a>	<a href="#">RT</a>		32	3.6E-3	5.3E-2
<input type="checkbox"/>	Annotation Cluster 3	Enrichment Score: 13.68	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">actin-binding</a>	<a href="#">RT</a>		35	1.4E-19	1.1E-17
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">actin cytoskeleton</a>	<a href="#">RT</a>		40	2.5E-18	1.8E-16
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">actin binding</a>	<a href="#">RT</a>		16	3.3E-16	2.0E-14
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">actin binding</a>	<a href="#">RT</a>		40	8.8E-16	2.5E-13
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">cytoskeletal protein binding</a>	<a href="#">RT</a>		48	1.5E-14	2.8E-12
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytoskeleton</a>	<a href="#">RT</a>		83	1.1E-12	3.2E-11
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">cytoskeleton</a>	<a href="#">RT</a>		41	4.5E-11	1.2E-9
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytoskeletal part</a>	<a href="#">RT</a>		53	4.7E-7	6.7E-6
<input type="checkbox"/>	Annotation Cluster 4	Enrichment Score: 13.21	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">actin binding</a>	<a href="#">RT</a>		40	8.8E-16	2.5E-13
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">actin filament-based process</a>	<a href="#">RT</a>		33	6.0E-15	6.4E-12
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cytoskeleton organization</a>	<a href="#">RT</a>		44	6.1E-15	4.4E-12
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">actin cytoskeleton organization</a>	<a href="#">RT</a>		32	6.5E-15	3.4E-12

	Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
<b>Annotation Cluster 1</b>						
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">cytoskeletal protein binding</a>	<a href="#">RT</a>		48	1.5E-14	2.8E-12
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">actin filament organization</a>	<a href="#">RT</a>		14	1.9E-8	2.4E-6
<b>Annotation Cluster 5</b>	Enrichment Score: 12.53	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">non-membrane-bounded organelle</a>	<a href="#">RT</a>		128	1.5E-13	5.1E-12
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">intracellular non-membrane-bounded organelle</a>	<a href="#">RT</a>		128	1.5E-13	5.1E-12
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">cytoskeleton</a>	<a href="#">RT</a>		83	1.1E-12	3.2E-11
<b>Annotation Cluster 6</b>	Enrichment Score: 9.65	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein folding</a>	<a href="#">RT</a>		24	7.0E-11	1.3E-8
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">unfolded protein binding</a>	<a href="#">RT</a>		20	1.1E-10	6.9E-9
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">Chaperone</a>	<a href="#">RT</a>		19	1.5E-9	3.3E-8
<b>Annotation Cluster 7</b>	Enrichment Score: 9.18	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	short sequence motif:Prevents secretion from ER	<a href="#">RT</a>		19	2.8E-17	3.8E-14
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">endoplasmic reticulum lumen</a>	<a href="#">RT</a>		20	1.9E-13	5.9E-12
<input type="checkbox"/> INTERPRO	<a href="#">Endoplasmic reticulum, targeting sequence</a>	<a href="#">RT</a>		14	7.3E-12	5.5E-9
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">endoplasmic reticulum</a>	<a href="#">RT</a>		38	4.3E-8	8.1E-7
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">endoplasmic reticulum part</a>	<a href="#">RT</a>		24	5.5E-5	5.1E-4
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">endoplasmic reticulum</a>	<a href="#">RT</a>		43	9.4E-4	5.3E-3
<b>Annotation Cluster 8</b>	Enrichment Score: 8.62	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">P-loop</a>	<a href="#">RT</a>		21	7.2E-14	3.1E-12
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">GTP binding</a>	<a href="#">RT</a>		17	1.1E-13	4.4E-12
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">nucleotide binding</a>	<a href="#">RT</a>		20	1.8E-13	6.3E-12
<input type="checkbox"/> UP_SEQ_FEATURE	short sequence motif:Effector region	<a href="#">RT</a>		19	2.6E-13	1.8E-10
<input type="checkbox"/> UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	<a href="#">RT</a>		30	7.1E-13	3.2E-10
<input type="checkbox"/> UP_SEQ_FEATURE	lipid moiety-binding region:S-geranylgeranyl cysteine	<a href="#">RT</a>		19	9.5E-13	3.2E-10
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">gtp-binding</a>	<a href="#">RT</a>		31	1.7E-12	5.6E-11
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">small GTPase mediated signal transduction</a>	<a href="#">RT</a>		33	4.3E-12	1.2E-9
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">GTPase activity</a>	<a href="#">RT</a>		28	6.2E-12	7.1E-10
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">GTP binding</a>	<a href="#">RT</a>		36	3.5E-11	3.3E-9
<input type="checkbox"/> SMART	<a href="#">RAB</a>	<a href="#">RT</a>		14	4.9E-11	5.3E-9
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">guanyl ribonucleotide binding</a>	<a href="#">RT</a>		36	7.2E-11	5.2E-9
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">guanyl nucleotide binding</a>	<a href="#">RT</a>		36	7.2E-11	5.2E-9
<input type="checkbox"/> INTERPRO	<a href="#">Small GTP-binding protein</a>	<a href="#">RT</a>		22	8.9E-11	3.4E-8
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">prenylation</a>	<a href="#">RT</a>		20	1.7E-10	3.9E-9
<input type="checkbox"/> INTERPRO	<a href="#">Ras</a>	<a href="#">RT</a>		19	2.1E-10	5.3E-8
<input type="checkbox"/> INTERPRO	<a href="#">Ras small GTPase, Rab type</a>	<a href="#">RT</a>		14	4.8E-10	9.1E-8
<input type="checkbox"/> INTERPRO	<a href="#">Ras GTPase</a>	<a href="#">RT</a>		19	7.7E-10	1.2E-7
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">methylation</a>	<a href="#">RT</a>		22	9.6E-9	1.9E-7
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">prenylated cysteine</a>	<a href="#">RT</a>		8	1.7E-7	2.7E-6
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">lipoprotein</a>	<a href="#">RT</a>		34	3.0E-7	4.4E-6
<input type="checkbox"/> INTERPRO	<a href="#">RNA polymerase sigma factor 54, interaction</a>	<a href="#">RT</a>		6	1.9E-6	8.6E-5
<input type="checkbox"/> UP_SEQ_FEATURE	propeptide:Removed in mature form	<a href="#">RT</a>		18	2.4E-6	1.7E-4
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">internal side of plasma membrane</a>	<a href="#">RT</a>		24	1.3E-5	1.3E-4
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">membrane trafficking</a>	<a href="#">RT</a>		5	2.0E-4	1.5E-3
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">protein transport</a>	<a href="#">RT</a>		21	1.2E-3	7.9E-3
<input type="checkbox"/> BIOCARTA	<a href="#">Rab GTPases Mark Targets In The Endocytotic Machinery</a>	<a href="#">RT</a>		5	1.6E-3	1.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">intracellular signaling cascade</a>	<a href="#">RT</a>		46	7.0E-3	9.0E-2
<input type="checkbox"/> PIR_SUPERFAMILY	PIRSF001710:Ras-related protein Rab	<a href="#">RT</a>		5	1.0E-2	2.2E-1
<b>Annotation Cluster 9</b>	Enrichment Score: 6.13	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">contractile fiber</a>	<a href="#">RT</a>		18	2.0E-8	4.4E-7
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">contractile fiber part</a>	<a href="#">RT</a>		17	4.7E-8	8.8E-7
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">myofibril</a>	<a href="#">RT</a>		16	2.3E-7	3.8E-6

	Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> Annotation Cluster 1						
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">sarcomere</a>	<a href="#">RT</a>		15	2.9E-7	4.6E-6
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">I band</a>	<a href="#">RT</a>		10	1.3E-5	1.3E-4
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">Z disc</a>	<a href="#">RT</a>		8	1.9E-4	1.5E-3
<input type="checkbox"/> Annotation Cluster 10						
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">nucleotide-binding</a>	<a href="#">RT</a>		84	6.4E-16	3.5E-14
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">nucleotide binding</a>	<a href="#">RT</a>		102	3.9E-9	2.2E-7
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">ribonucleotide binding</a>	<a href="#">RT</a>		87	1.4E-8	7.3E-7
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">purine ribonucleotide binding</a>	<a href="#">RT</a>		87	1.4E-8	7.3E-7
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">purine nucleotide binding</a>	<a href="#">RT</a>		88	5.1E-8	2.4E-6
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">atp-binding</a>	<a href="#">RT</a>		51	3.5E-6	4.0E-5
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">adenyl ribonucleotide binding</a>	<a href="#">RT</a>		57	2.8E-3	4.7E-2
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">ATP binding</a>	<a href="#">RT</a>		56	3.4E-3	5.3E-2
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">adenyl nucleotide binding</a>	<a href="#">RT</a>		58	5.4E-3	7.4E-2
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">nucleoside binding</a>	<a href="#">RT</a>		59	5.5E-3	7.2E-2
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">purine nucleoside binding</a>	<a href="#">RT</a>		58	7.3E-3	8.3E-2
<input type="checkbox"/> Annotation Cluster 11						
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">stress response</a>	<a href="#">RT</a>		12	4.7E-8	8.1E-7
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">response to unfolded protein</a>	<a href="#">RT</a>		11	8.9E-6	4.4E-4
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">response to protein stimulus</a>	<a href="#">RT</a>		12	6.6E-5	2.4E-3
<input type="checkbox"/> Annotation Cluster 12						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">glucose catabolic process</a>	<a href="#">RT</a>		17	4.2E-13	1.5E-10
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">glycolysis</a>	<a href="#">RT</a>		15	3.9E-12	1.2E-9
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">hexose catabolic process</a>	<a href="#">RT</a>		17	7.8E-12	1.9E-9
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">monosaccharide catabolic process</a>	<a href="#">RT</a>		17	1.2E-11	2.7E-9
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">generation of precursor metabolites and energy</a>	<a href="#">RT</a>		32	4.2E-11	8.3E-9
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">alcohol catabolic process</a>	<a href="#">RT</a>		17	1.0E-10	1.7E-8
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular carbohydrate catabolic process</a>	<a href="#">RT</a>		17	2.2E-10	3.2E-8
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">glycolysis</a>	<a href="#">RT</a>		11	8.3E-9	1.7E-7
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">carbohydrate catabolic process</a>	<a href="#">RT</a>		17	9.9E-9	1.3E-6
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">glucose metabolic process</a>	<a href="#">RT</a>		19	4.2E-8	5.0E-6
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">hexose metabolic process</a>	<a href="#">RT</a>		20	2.8E-7	2.5E-5
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">gluconeogenesis</a>	<a href="#">RT</a>		7	1.1E-6	1.4E-5
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">monosaccharide metabolic process</a>	<a href="#">RT</a>		20	2.6E-6	1.5E-4
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">pentose phosphate pathway</a>	<a href="#">RT</a>		5	4.5E-6	5.0E-5
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Glycolysis / Gluconeogenesis</a>	<a href="#">RT</a>		13	4.8E-6	1.6E-4
<input type="checkbox"/> UP_SEQ_FEATURE	binding site:Substrate	<a href="#">RT</a>		19	2.1E-5	1.2E-3
<input type="checkbox"/> BIOCARTA	<a href="#">Glycolysis Pathway</a>	<a href="#">RT</a>		6	7.1E-5	9.5E-3
<input type="checkbox"/> INTERPRO	<a href="#">Lactate/malate dehydrogenase</a>	<a href="#">RT</a>		4	5.2E-4	1.2E-2
<input type="checkbox"/> INTERPRO	<a href="#">L-lactate/malate dehydrogenase</a>	<a href="#">RT</a>		4	5.2E-4	1.2E-2
<input type="checkbox"/> INTERPRO	<a href="#">Lactate dehydrogenase/glycoside hydrolase, family 4, C-terminal</a>	<a href="#">RT</a>		4	7.7E-4	1.6E-2
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">pentose shunt</a>	<a href="#">RT</a>		3	1.1E-3	7.4E-3
<input type="checkbox"/> PIR_SUPERFAMILY	PIRSF000102:Lac_mal_DH	<a href="#">RT</a>		4	2.3E-3	6.7E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">nicotinamide metabolic process</a>	<a href="#">RT</a>		6	2.9E-3	4.4E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">nicotinamide nucleotide metabolic process</a>	<a href="#">RT</a>		6	2.9E-3	4.4E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">alkaloid metabolic process</a>	<a href="#">RT</a>		6	3.2E-3	4.8E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">pyridine nucleotide metabolic process</a>	<a href="#">RT</a>		6	3.6E-3	5.3E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">oxidoreduction coenzyme metabolic process</a>	<a href="#">RT</a>		6	9.0E-3	1.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular amide metabolic process</a>	<a href="#">RT</a>		6	1.2E-2	1.4E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">pentose-phosphate shunt</a>	<a href="#">RT</a>		3	2.0E-2	1.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">secondary metabolic process</a>	<a href="#">RT</a>		6	4.6E-2	3.4E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">NADP metabolic process</a>	<a href="#">RT</a>		3	5.8E-2	4.0E-1
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Pyruvate metabolism</a>	<a href="#">RT</a>		5	8.3E-2	4.1E-1

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<input type="checkbox"/> Annotation Cluster 1						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">NAD metabolic process</a>	<a href="#">RT</a>		3	1.3E-1	6.1E-1
<input type="checkbox"/> UP_SEQ_FEATURE	active site:Proton acceptor	<a href="#">RT</a>		15	3.9E-1	1.0E0
<input type="checkbox"/> Annotation Cluster 13	Enrichment Score: 5.02	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">structural constituent of cytoskeleton</a>	<a href="#">RT</a>		17	4.9E-11	4.0E-9
<input type="checkbox"/> UP_SEQ_FEATURE	region of interest:Coil 2	<a href="#">RT</a>		12	3.6E-8	9.7E-6
<input type="checkbox"/> UP_SEQ_FEATURE	region of interest:Linker 1	<a href="#">RT</a>		12	9.3E-8	2.1E-5
<input type="checkbox"/> UP_SEQ_FEATURE	region of interest:Coil 1A	<a href="#">RT</a>		12	9.3E-8	2.1E-5
<input type="checkbox"/> UP_SEQ_FEATURE	region of interest:Coil 1B	<a href="#">RT</a>		12	9.3E-8	2.1E-5
<input type="checkbox"/> UP_SEQ_FEATURE	region of interest:Rod	<a href="#">RT</a>		12	1.1E-7	1.8E-5
<input type="checkbox"/> UP_SEQ_FEATURE	region of interest:Head	<a href="#">RT</a>		12	1.5E-7	2.2E-5
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">Intermediate filament</a>	<a href="#">RT</a>		12	2.8E-7	4.2E-6
<input type="checkbox"/> UP_SEQ_FEATURE	region of interest:Linker 12	<a href="#">RT</a>		11	3.8E-7	4.7E-5
<input type="checkbox"/> INTERPRO	<a href="#">Filament</a>	<a href="#">RT</a>		12	3.9E-7	2.3E-5
<input type="checkbox"/> INTERPRO	<a href="#">Intermediate filament protein, conserved site</a>	<a href="#">RT</a>		12	3.9E-7	2.3E-5
<input type="checkbox"/> INTERPRO	<a href="#">Intermediate filament protein</a>	<a href="#">RT</a>		12	4.5E-7	2.5E-5
<input type="checkbox"/> UP_SEQ_FEATURE	region of interest:Tail	<a href="#">RT</a>		11	1.7E-6	1.4E-4
<input type="checkbox"/> PIR_SUPERFAMILY	PIRSF002282:cytoskeletal keratin	<a href="#">RT</a>		12	9.3E-6	2.3E-3
<input type="checkbox"/> UP_SEQ_FEATURE	site:Stutter	<a href="#">RT</a>		7	3.5E-5	1.9E-3
<input type="checkbox"/> INTERPRO	<a href="#">Keratin, type I</a>	<a href="#">RT</a>		7	6.7E-5	1.8E-3
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">keratin</a>	<a href="#">RT</a>		10	1.9E-3	1.2E-2
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">intermediate filament</a>	<a href="#">RT</a>		13	3.6E-3	1.7E-2
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">intermediate filament cytoskeleton</a>	<a href="#">RT</a>		13	4.3E-3	2.0E-2
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">palmoplantar keratoderma</a>	<a href="#">RT</a>		4	5.4E-3	2.9E-2
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">keratin filament</a>	<a href="#">RT</a>		8	8.9E-3	3.8E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">intermediate filament-based process</a>	<a href="#">RT</a>		4	1.6E-2	1.7E-1
<input type="checkbox"/> INTERPRO	<a href="#">Type II keratin</a>	<a href="#">RT</a>		4	2.2E-2	2.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">intermediate filament cytoskeleton organization</a>	<a href="#">RT</a>		3	8.6E-2	5.0E-1
<input type="checkbox"/> Annotation Cluster 14	Enrichment Score: 4.63	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">cell cortex</a>	<a href="#">RT</a>		19	6.1E-8	1.1E-6
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">cortical cytoskeleton</a>	<a href="#">RT</a>		10	4.8E-6	6.0E-5
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">cell cortex part</a>	<a href="#">RT</a>		12	1.2E-5	1.3E-4
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of actin filament depolymerization</a>	<a href="#">RT</a>		7	4.1E-5	1.8E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">cortical actin cytoskeleton</a>	<a href="#">RT</a>		6	7.7E-4	4.5E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of protein complex disassembly</a>	<a href="#">RT</a>		7	1.5E-3	2.8E-2
<input type="checkbox"/> Annotation Cluster 15	Enrichment Score: 4.54	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	<a href="#">Thioredoxin-like subdomain</a>	<a href="#">RT</a>		7	1.9E-8	2.1E-6
<input type="checkbox"/> INTERPRO	<a href="#">Thioredoxin-like</a>	<a href="#">RT</a>		10	5.4E-8	4.5E-6
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">Redox-active center</a>	<a href="#">RT</a>		10	8.1E-8	1.4E-6
<input type="checkbox"/> INTERPRO	<a href="#">Thioredoxin fold</a>	<a href="#">RT</a>		14	2.7E-7	2.1E-5
<input type="checkbox"/> UP_SEQ_FEATURE	domain:Thioredoxin 2	<a href="#">RT</a>		6	3.1E-7	4.2E-5
<input type="checkbox"/> UP_SEQ_FEATURE	domain:Thioredoxin 1	<a href="#">RT</a>		6	3.1E-7	4.2E-5
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">Isomerase</a>	<a href="#">RT</a>		14	5.3E-7	7.3E-6
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">intramolecular oxidoreductase</a>	<a href="#">RT</a>		6	1.8E-6	2.2E-5
<input type="checkbox"/> INTERPRO	<a href="#">Disulphide isomerase</a>	<a href="#">RT</a>		5	3.1E-6	1.3E-4
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">redox-active disulfide</a>	<a href="#">RT</a>		5	8.8E-6	9.6E-5
<input type="checkbox"/> INTERPRO	<a href="#">Thioredoxin, conserved site</a>	<a href="#">RT</a>		7	1.6E-5	5.5E-4
<input type="checkbox"/> INTERPRO	<a href="#">Thioredoxin domain</a>	<a href="#">RT</a>		7	2.0E-5	6.1E-4
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell redox homeostasis</a>	<a href="#">RT</a>		10	2.2E-5	1.0E-3
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">intramolecular oxidoreductase activity</a>	<a href="#">RT</a>		8	4.6E-5	1.6E-3
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">protein disulfide isomerase activity</a>	<a href="#">RT</a>		5	5.0E-5	1.6E-3
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">intramolecular oxidoreductase activity, transposing S-S bonds</a>	<a href="#">RT</a>		5	5.0E-5	1.6E-3

	Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
<b>Annotation Cluster 1</b>						
<input type="checkbox"/> PIR_SUPERFAMILY	PIRSF001487:protein disulfide-isomerase	<a href="#">RT</a>		5	5.3E-5	4.3E-3
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">intramolecular oxidoreductase activity, interconverting keto- and enol-groups</a>	<a href="#">RT</a>		5	8.2E-5	2.3E-3
<input type="checkbox"/> UP_SEQ_FEATURE	site:Contributes to redox potential value	<a href="#">RT</a>		4	2.4E-4	1.1E-2
<input type="checkbox"/> UP_SEQ_FEATURE	domain:Thioredoxin 3	<a href="#">RT</a>		3	2.2E-3	7.3E-2
<input type="checkbox"/> UP_SEQ_FEATURE	site:Lowers pKa of C-terminal Cys of first active site	<a href="#">RT</a>		3	2.2E-3	7.3E-2
<input type="checkbox"/> UP_SEQ_FEATURE	site:Lowers pKa of C-terminal Cys of second active site	<a href="#">RT</a>		3	2.2E-3	7.3E-2
<input type="checkbox"/> INTERPRO	<a href="#">Protein disulphide isomerase</a>	<a href="#">RT</a>		3	2.7E-3	5.3E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular homeostasis</a>	<a href="#">RT</a>		20	2.3E-2	2.1E-1
<input type="checkbox"/> UP_SEQ_FEATURE	active site:Nucleophile	<a href="#">RT</a>		9	3.1E-2	5.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">homeostatic process</a>	<a href="#">RT</a>		25	1.2E-1	6.0E-1
<b>Annotation Cluster 16</b>	<b>Enrichment Score: 4.49</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> INTERPRO	<a href="#">EF-HAND 1</a>	<a href="#">RT</a>		22	1.1E-8	1.4E-6
<input type="checkbox"/> INTERPRO	<a href="#">EF-HAND 2</a>	<a href="#">RT</a>		21	4.9E-8	4.6E-6
<input type="checkbox"/> UP_SEQ_FEATURE	domain:EF-hand 2	<a href="#">RT</a>		18	9.5E-8	1.8E-5
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">calcium</a>	<a href="#">RT</a>		40	1.1E-7	1.7E-6
<input type="checkbox"/> UP_SEQ_FEATURE	domain:EF-hand 1	<a href="#">RT</a>		17	5.2E-7	5.4E-5
<input type="checkbox"/> INTERPRO	<a href="#">EF-Hand type</a>	<a href="#">RT</a>		20	9.9E-7	4.7E-5
<input type="checkbox"/> SMART	<a href="#">EFh</a>	<a href="#">RT</a>		14	1.9E-6	7.1E-5
<input type="checkbox"/> UP_SEQ_FEATURE	calcium-binding region:1	<a href="#">RT</a>		13	6.1E-6	3.9E-4
<input type="checkbox"/> UP_SEQ_FEATURE	calcium-binding region:2	<a href="#">RT</a>		12	1.4E-5	8.4E-4
<input type="checkbox"/> INTERPRO	<a href="#">Calcium-binding EF-hand</a>	<a href="#">RT</a>		14	1.4E-5	5.1E-4
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">EF hand</a>	<a href="#">RT</a>		9	1.8E-5	1.8E-4
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">calcium ion binding</a>	<a href="#">RT</a>		46	2.5E-5	9.4E-4
<input type="checkbox"/> UP_SEQ_FEATURE	domain:EF-hand 5	<a href="#">RT</a>		5	1.2E-4	5.7E-3
<input type="checkbox"/> INTERPRO	<a href="#">EF hand</a>	<a href="#">RT</a>		12	1.2E-4	3.0E-3
<input type="checkbox"/> UP_SEQ_FEATURE	domain:EF-hand 3	<a href="#">RT</a>		9	4.7E-4	2.0E-2
<input type="checkbox"/> UP_SEQ_FEATURE	calcium-binding region:4	<a href="#">RT</a>		4	4.0E-3	1.2E-1
<input type="checkbox"/> UP_SEQ_FEATURE	domain:EF-hand 4	<a href="#">RT</a>		6	5.6E-3	1.5E-1
<input type="checkbox"/> UP_SEQ_FEATURE	calcium-binding region:5	<a href="#">RT</a>		3	7.3E-3	1.9E-1
<input type="checkbox"/> PIR_SUPERFAMILY	PIRSF036326:reticulocalbin	<a href="#">RT</a>		3	7.4E-3	1.8E-1
<input type="checkbox"/> UP_SEQ_FEATURE	domain:EF-hand 6	<a href="#">RT</a>		3	1.2E-2	2.7E-1
<input type="checkbox"/> UP_SEQ_FEATURE	calcium-binding region:3	<a href="#">RT</a>		3	1.5E-1	9.5E-1
<b>Annotation Cluster 17</b>	<b>Enrichment Score: 4.36</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> INTERPRO	<a href="#">Chaperone, tailless complex polypeptide 1</a>	<a href="#">RT</a>		6	1.9E-6	8.6E-5
<input type="checkbox"/> INTERPRO	<a href="#">Chaperonin Cpn60/TCP-1</a>	<a href="#">RT</a>		6	1.2E-5	4.4E-4
<input type="checkbox"/> INTERPRO	<a href="#">Chaperonin TCP-1, conserved site</a>	<a href="#">RT</a>		5	4.1E-5	1.2E-3
<input type="checkbox"/> PIR_SUPERFAMILY	PIRSF002584:molecular chaperone t-complex-type	<a href="#">RT</a>		5	2.9E-4	1.8E-2
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">chaperonin-containing T-complex</a>	<a href="#">RT</a>		4	6.0E-4	3.7E-3
<b>Annotation Cluster 18</b>	<b>Enrichment Score: 4.34</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> SMART	<a href="#">ACTIN</a>	<a href="#">RT</a>		8	5.7E-6	1.2E-4
<input type="checkbox"/> INTERPRO	<a href="#">Actin, conserved site</a>	<a href="#">RT</a>		6	1.7E-5	5.5E-4
<input type="checkbox"/> INTERPRO	<a href="#">Actin/actin-like</a>	<a href="#">RT</a>		8	1.8E-5	5.6E-4
<input type="checkbox"/> PIR_SUPERFAMILY	PIRSF002337:Actin	<a href="#">RT</a>		7	1.9E-5	2.3E-3
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">methylated amino acid</a>	<a href="#">RT</a>		4	6.3E-3	3.4E-2
<b>Annotation Cluster 19</b>	<b>Enrichment Score: 4.26</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell motion</a>	<a href="#">RT</a>		39	1.5E-10	2.3E-8
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell migration</a>	<a href="#">RT</a>		16	3.6E-3	5.3E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">localization of cell</a>	<a href="#">RT</a>		17	4.1E-3	5.7E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell motility</a>	<a href="#">RT</a>		17	4.1E-3	5.7E-2
<b>Annotation Cluster 20</b>	<b>Enrichment Score: 4.23</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein localization</a>	<a href="#">RT</a>		48	4.6E-7	3.8E-5

	Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> Annotation Cluster 1						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">establishment of protein localization</a>	<a href="#">RT</a>		43	1.0E-6	7.2E-5
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein transport</a>	<a href="#">RT</a>		42	2.1E-6	1.3E-4
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">intracellular transport</a>	<a href="#">RT</a>		38	2.4E-6	1.5E-4
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular protein localization</a>	<a href="#">RT</a>		20	6.7E-3	8.7E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular macromolecule localization</a>	<a href="#">RT</a>		20	7.1E-3	9.1E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">intracellular protein transport</a>	<a href="#">RT</a>		17	2.4E-2	2.1E-1
<input type="checkbox"/> Annotation Cluster 21						
	Enrichment Score: 4.03	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of programmed cell death</a>	<a href="#">RT</a>		47	1.0E-7	1.2E-5
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of cell death</a>	<a href="#">RT</a>		47	1.2E-7	1.2E-5
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of apoptosis</a>	<a href="#">RT</a>		46	2.1E-7	2.0E-5
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">anti-apoptosis</a>	<a href="#">RT</a>		20	8.4E-7	6.4E-5
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">negative regulation of programmed cell death</a>	<a href="#">RT</a>		27	9.4E-7	7.0E-5
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">negative regulation of cell death</a>	<a href="#">RT</a>		27	1.0E-6	7.1E-5
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">negative regulation of apoptosis</a>	<a href="#">RT</a>		26	2.4E-6	1.4E-4
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">positive regulation of apoptosis</a>	<a href="#">RT</a>		19	2.1E-2	2.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">positive regulation of programmed cell death</a>	<a href="#">RT</a>		19	2.2E-2	2.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">positive regulation of cell death</a>	<a href="#">RT</a>		19	2.3E-2	2.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">induction of apoptosis</a>	<a href="#">RT</a>		14	5.5E-2	3.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">induction of programmed cell death</a>	<a href="#">RT</a>		14	5.6E-2	3.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">induction of apoptosis by extracellular signals</a>	<a href="#">RT</a>		5	3.0E-1	8.7E-1
<input type="checkbox"/> Annotation Cluster 22						
	Enrichment Score: 3.86	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	binding site:NAD	<a href="#">RT</a>		10	4.2E-7	4.8E-5
<input type="checkbox"/> INTERPRO	<a href="#">NAD(P)-binding domain</a>	<a href="#">RT</a>		16	9.4E-7	4.7E-5
<input type="checkbox"/> UP_SEQ_FEATURE	nucleotide phosphate-binding region:NAD	<a href="#">RT</a>		11	2.0E-6	1.5E-4
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">oxidoreductase</a>	<a href="#">RT</a>		28	1.3E-5	1.4E-4
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">NAD or NADH binding</a>	<a href="#">RT</a>		8	1.9E-4	4.9E-3
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">nad</a>	<a href="#">RT</a>		13	3.0E-4	2.2E-3
<input type="checkbox"/> INTERPRO	<a href="#">L-lactate/malate dehydrogenase</a>	<a href="#">RT</a>		4	5.2E-4	1.2E-2
<input type="checkbox"/> INTERPRO	<a href="#">Lactate/malate dehydrogenase</a>	<a href="#">RT</a>		4	5.2E-4	1.2E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">oxidation reduction</a>	<a href="#">RT</a>		31	5.6E-4	1.2E-2
<input type="checkbox"/> INTERPRO	<a href="#">Lactate dehydrogenase/glycoside hydrolase, family 4, C-terminal</a>	<a href="#">RT</a>		4	7.7E-4	1.6E-2
<input type="checkbox"/> PIR_SUPERFAMILY	PIRSF000102:Lac_mal_DH	<a href="#">RT</a>		4	2.3E-3	6.7E-2
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">cofactor binding</a>	<a href="#">RT</a>		15	5.4E-3	7.4E-2
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">coenzyme binding</a>	<a href="#">RT</a>		12	7.5E-3	8.1E-2
<input type="checkbox"/> Annotation Cluster 23						
	Enrichment Score: 3.82	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	<a href="#">Actinin-type, actin-binding, conserved site</a>	<a href="#">RT</a>		8	3.8E-7	2.4E-5
<input type="checkbox"/> UP_SEQ_FEATURE	domain:CH 2	<a href="#">RT</a>		8	6.0E-7	5.8E-5
<input type="checkbox"/> UP_SEQ_FEATURE	domain:CH 1	<a href="#">RT</a>		8	6.0E-7	5.8E-5
<input type="checkbox"/> UP_SEQ_FEATURE	domain:Actin-binding	<a href="#">RT</a>		7	1.5E-6	1.3E-4
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:Spectrin 4	<a href="#">RT</a>		5	6.3E-4	2.6E-2
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:Spectrin 3	<a href="#">RT</a>		5	7.6E-4	3.0E-2
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:Spectrin 2	<a href="#">RT</a>		5	1.5E-3	5.2E-2
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:Spectrin 1	<a href="#">RT</a>		5	1.5E-3	5.2E-2
<input type="checkbox"/> SMART	<a href="#">SPEC</a>	<a href="#">RT</a>		5	2.3E-3	3.1E-2
<input type="checkbox"/> INTERPRO	<a href="#">Spectrin/alpha-actinin</a>	<a href="#">RT</a>		5	4.3E-3	8.0E-2
<input type="checkbox"/> INTERPRO	<a href="#">EF-hand, Ca insensitive</a>	<a href="#">RT</a>		3	6.6E-3	1.2E-1
<input type="checkbox"/> INTERPRO	<a href="#">Spectrin repeat</a>	<a href="#">RT</a>		4	1.0E-2	1.6E-1
<input type="checkbox"/> Annotation Cluster 24						
	Enrichment Score: 3.34	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> SMART	<a href="#">CH</a>	<a href="#">RT</a>		12	4.7E-8	2.5E-6
<input type="checkbox"/> INTERPRO	<a href="#">Calponin-like actin-binding</a>	<a href="#">RT</a>		12	2.9E-7	2.0E-5
<input type="checkbox"/> INTERPRO	<a href="#">Actinin-type, actin-binding, conserved site</a>	<a href="#">RT</a>		8	3.8E-7	2.4E-5

Annotation Cluster 1		Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CH 2	<a href="#">RT</a>		8	6.0E-7	5.8E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CH 1	<a href="#">RT</a>		8	6.0E-7	5.8E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Actin-binding	<a href="#">RT</a>		7	1.5E-6	1.3E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 22	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 21	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 20	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 2	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 4	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 3	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 24	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 23	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 8	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 7	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 6	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 5	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 9	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Hinge 1	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Hinge 2	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Self-association site, tail	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 1	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 10	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 11	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 12	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 13	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 14	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 15	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 16	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 17	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 18	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Filamin 19	<a href="#">RT</a>		3	1.1E-3	4.1E-2
<input type="checkbox"/>	SMART	<a href="#">IG_FLMN</a>	<a href="#">RT</a>		3	1.4E-2	1.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Filamin/ABP280 repeat</a>	<a href="#">RT</a>		3	1.9E-2	2.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Filamin/ABP280 repeat-like</a>	<a href="#">RT</a>		3	2.3E-2	2.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Immunoglobulin-like fold</a>	<a href="#">RT</a>		6	9.9E-1	1.0E0
Annotation Cluster 25		Enrichment Score: 3.32	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">extracellular matrix</a>	<a href="#">RT</a>		21	4.6E-8	8.3E-7
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">extracellular matrix organization</a>	<a href="#">RT</a>		15	2.6E-7	2.4E-5
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">trimer</a>	<a href="#">RT</a>		8	4.3E-7	6.2E-6
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">extracellular matrix part</a>	<a href="#">RT</a>		16	4.7E-7	7.0E-6
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">Ehlers-Danlos syndrome</a>	<a href="#">RT</a>		6	1.1E-6	1.3E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">collagen fibril organization</a>	<a href="#">RT</a>		8	5.1E-6	2.7E-4
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">fibrillar collagen</a>	<a href="#">RT</a>		6	8.8E-6	1.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	propeptide:C-terminal propeptide	<a href="#">RT</a>		5	9.0E-6	5.5E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">extracellular structure organization</a>	<a href="#">RT</a>		16	1.2E-5	6.1E-4
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">hydroxylysine</a>	<a href="#">RT</a>		7	2.3E-5	2.2E-4
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">triple helix</a>	<a href="#">RT</a>		7	2.3E-5	2.2E-4
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">pyroglutamic acid</a>	<a href="#">RT</a>		8	2.5E-5	2.4E-4
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">collagen</a>	<a href="#">RT</a>		8	3.1E-5	3.0E-4
<input type="checkbox"/>	SMART	<a href="#">COLFI</a>	<a href="#">RT</a>		5	3.2E-5	5.8E-4
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">ECM-receptor interaction</a>	<a href="#">RT</a>		14	3.6E-5	9.3E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Fibrillar collagen NC1	<a href="#">RT</a>		5	4.1E-5	2.1E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Fibrillar collagen, C-terminal</a>	<a href="#">RT</a>		5	6.3E-5	1.8E-3

	Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
<b>Annotation Cluster 1</b>						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">skin development</a>	<a href="#">RT</a>		7	6.4E-5	2.3E-3
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">hydroxyproline</a>	<a href="#">RT</a>		7	6.7E-5	5.7E-4
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">platelet-derived growth factor binding</a>	<a href="#">RT</a>		5	1.3E-4	3.4E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">extracellular matrix</a>	<a href="#">RT</a>		23	1.4E-4	1.1E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">collagen biosynthetic process</a>	<a href="#">RT</a>		4	1.4E-4	4.3E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">proteinaceous extracellular matrix</a>	<a href="#">RT</a>		21	3.7E-4	2.6E-3
<input type="checkbox"/> PIR_SUPERFAMILY	PIRSF002255:collagen alpha 1(I) chain	<a href="#">RT</a>		4	4.4E-4	2.1E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">collagen metabolic process</a>	<a href="#">RT</a>		6	5.5E-4	1.2E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">multicellular organismal macromolecule metabolic process</a>	<a href="#">RT</a>		6	8.9E-4	1.8E-2
<input type="checkbox"/> OMIM_DISEASE	<a href="#">Ehlers-Danlos syndrome, type I</a>	<a href="#">RT</a>		3	1.8E-3	3.3E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">multicellular organismal metabolic process</a>	<a href="#">RT</a>		6	2.0E-3	3.4E-2
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">hydroxylation</a>	<a href="#">RT</a>		7	2.4E-3	1.4E-2
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">skin</a>	<a href="#">RT</a>		3	3.5E-3	2.0E-2
<input type="checkbox"/> UP_SEQ_FEATURE	domain:VWFC	<a href="#">RT</a>		4	4.7E-3	1.4E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">extracellular region part</a>	<a href="#">RT</a>		40	5.2E-3	2.3E-2
<input type="checkbox"/> UP_SEQ_FEATURE	propeptide:N-terminal propeptide	<a href="#">RT</a>		3	5.3E-3	1.5E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">extracellular matrix structural constituent</a>	<a href="#">RT</a>		8	6.8E-3	8.4E-2
<input type="checkbox"/> UP_SEQ_FEATURE	region of interest:Triple-helical region	<a href="#">RT</a>		4	9.5E-3	2.4E-1
<input type="checkbox"/> INTERPRO	<a href="#">Collagen triple helix repeat</a>	<a href="#">RT</a>		7	9.8E-3	1.6E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">collagen</a>	<a href="#">RT</a>		7	1.0E-2	4.9E-2
<input type="checkbox"/> SMART	<a href="#">VVC</a>	<a href="#">RT</a>		4	3.6E-2	2.7E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">growth factor binding</a>	<a href="#">RT</a>		7	5.5E-2	3.6E-1
<input type="checkbox"/> INTERPRO	<a href="#">von Willebrand factor, type C</a>	<a href="#">RT</a>		4	5.5E-2	5.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">skeletal system development</a>	<a href="#">RT</a>		13	9.8E-2	5.4E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">SMAD binding</a>	<a href="#">RT</a>		4	1.2E-1	5.9E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">extracellular space</a>	<a href="#">RT</a>		23	2.1E-1	5.1E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">signal</a>	<a href="#">RT</a>		69	2.3E-1	6.0E-1
<input type="checkbox"/> UP_SEQ_FEATURE	signal peptide	<a href="#">RT</a>		69	2.5E-1	9.9E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">Secreted</a>	<a href="#">RT</a>		37	2.8E-1	6.7E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">extracellular region</a>	<a href="#">RT</a>		53	6.1E-1	9.0E-1
<b>Annotation Cluster 26</b>	<b>Enrichment Score: 3.29</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> INTERPRO	<a href="#">Heat shock protein Hsp70</a>	<a href="#">RT</a>		5	9.4E-5	2.4E-3
<input type="checkbox"/> INTERPRO	<a href="#">Heat shock protein 70</a>	<a href="#">RT</a>		5	9.4E-5	2.4E-3
<input type="checkbox"/> INTERPRO	<a href="#">Heat shock protein 70, conserved site</a>	<a href="#">RT</a>		5	2.4E-4	5.6E-3
<input type="checkbox"/> PIR_SUPERFAMILY	PIRSF002581:chaperone HSP70	<a href="#">RT</a>		3	3.1E-2	4.8E-1
<b>Annotation Cluster 27</b>	<b>Enrichment Score: 3.22</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">calcium binding</a>	<a href="#">RT</a>		18	1.1E-11	3.6E-10
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">calcium</a>	<a href="#">RT</a>		40	1.1E-7	1.7E-6
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">calcium ion binding</a>	<a href="#">RT</a>		46	2.5E-5	9.4E-4
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">metal-binding</a>	<a href="#">RT</a>		40	1.0E0	1.0E0
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">ion binding</a>	<a href="#">RT</a>		86	1.0E0	1.0E0
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">cation binding</a>	<a href="#">RT</a>		84	1.0E0	1.0E0
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">metal ion binding</a>	<a href="#">RT</a>		83	1.0E0	1.0E0
<b>Annotation Cluster 28</b>	<b>Enrichment Score: 3.18</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> UP_SEQ_FEATURE	glycosylation site:N-linked (Glc) (glycation)	<a href="#">RT</a>		5	9.0E-6	5.5E-4
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">glycation</a>	<a href="#">RT</a>		5	4.0E-5	3.6E-4
<input type="checkbox"/> UP_SEQ_FEATURE	site:Not glycosylated	<a href="#">RT</a>		3	5.3E-3	1.5E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">oxygen binding</a>	<a href="#">RT</a>		4	9.9E-2	5.4E-1
<b>Annotation Cluster 29</b>	<b>Enrichment Score: 3.18</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">skin development</a>	<a href="#">RT</a>		7	6.4E-5	2.3E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">ectoderm development</a>	<a href="#">RT</a>		16	1.3E-4	4.0E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">epidermis development</a>	<a href="#">RT</a>		15	1.9E-4	5.1E-3

	Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> Annotation Cluster 1						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">epithelial cell differentiation</a>	<a href="#">RT</a>		7	1.2E-1	6.1E-1
<input type="checkbox"/> Annotation Cluster 30	Enrichment Score: 3	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">gluconeogenesis</a>	<a href="#">RT</a>		7	1.1E-6	1.4E-5
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">pentose phosphate pathway</a>	<a href="#">RT</a>		5	4.5E-6	5.0E-5
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Pentose phosphate pathway</a>	<a href="#">RT</a>		6	3.2E-3	3.7E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">fructose metabolic process</a>	<a href="#">RT</a>		4	7.8E-3	9.8E-2
<input type="checkbox"/> INTERPRO	<a href="#">Aldolase-type TIM barrel</a>	<a href="#">RT</a>		4	4.9E-2	4.7E-1
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Fructose and mannose metabolism</a>	<a href="#">RT</a>		4	1.7E-1	5.7E-1
<input type="checkbox"/> Annotation Cluster 31	Enrichment Score: 2.95	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">cell-substrate junction</a>	<a href="#">RT</a>		12	1.9E-4	1.5E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">adherens junction</a>	<a href="#">RT</a>		14	2.5E-4	1.8E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">focal adhesion</a>	<a href="#">RT</a>		11	3.8E-4	2.7E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">cell-substrate adherens junction</a>	<a href="#">RT</a>		11	5.2E-4	3.5E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">anchoring junction</a>	<a href="#">RT</a>		14	6.9E-4	4.2E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">basolateral plasma membrane</a>	<a href="#">RT</a>		15	1.1E-3	5.8E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">cell junction</a>	<a href="#">RT</a>		17	3.0E-1	6.5E-1
<input type="checkbox"/> Annotation Cluster 32	Enrichment Score: 2.95	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> SMART	<a href="#">14_3_3</a>	<a href="#">RT</a>		5	3.6E-6	9.9E-5
<input type="checkbox"/> UP_SEQ_FEATURE	site:Interaction with phosphoserine on interacting protein	<a href="#">RT</a>		5	4.6E-6	3.1E-4
<input type="checkbox"/> INTERPRO	<a href="#">14-3-3 protein</a>	<a href="#">RT</a>		5	7.2E-6	2.9E-4
<input type="checkbox"/> PIR_SUPERFAMILY	PIRSF000868:14-3-3 protein	<a href="#">RT</a>		5	5.3E-5	4.3E-3
<input type="checkbox"/> PIR_SUPERFAMILY	PIRSF000868:14-3-3	<a href="#">RT</a>		5	5.3E-5	4.3E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein targeting</a>	<a href="#">RT</a>		12	1.8E-2	1.8E-1
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Neurotrophin signaling pathway</a>	<a href="#">RT</a>		11	3.3E-2	2.4E-1
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Oocyte meiosis</a>	<a href="#">RT</a>		9	8.7E-2	4.1E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">protein domain specific binding</a>	<a href="#">RT</a>		12	2.4E-1	8.2E-1
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Cell cycle</a>	<a href="#">RT</a>		5	7.7E-1	9.7E-1
<input type="checkbox"/> Annotation Cluster 33	Enrichment Score: 2.91	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">tricarboxylic acid cycle</a>	<a href="#">RT</a>		6	4.0E-5	3.5E-4
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">aerobic respiration</a>	<a href="#">RT</a>		7	1.9E-4	5.0E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">tricarboxylic acid cycle</a>	<a href="#">RT</a>		6	2.1E-4	5.3E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">acetyl-CoA catabolic process</a>	<a href="#">RT</a>		6	2.1E-4	5.3E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">coenzyme catabolic process</a>	<a href="#">RT</a>		6	3.8E-4	8.8E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cofactor catabolic process</a>	<a href="#">RT</a>		6	8.9E-4	1.8E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">acetyl-CoA metabolic process</a>	<a href="#">RT</a>		6	8.9E-4	1.8E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cofactor metabolic process</a>	<a href="#">RT</a>		14	1.1E-3	2.2E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">dicarboxylic acid metabolic process</a>	<a href="#">RT</a>		6	1.4E-3	2.6E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">coenzyme metabolic process</a>	<a href="#">RT</a>		12	1.5E-3	2.7E-2
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Citrate cycle (TCA cycle)</a>	<a href="#">RT</a>		7	1.5E-3	2.1E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">oxaloacetate metabolic process</a>	<a href="#">RT</a>		4	1.6E-3	2.8E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular respiration</a>	<a href="#">RT</a>		9	2.7E-3	4.3E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">energy derivation by oxidation of organic compounds</a>	<a href="#">RT</a>		10	9.5E-3	1.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">malate metabolic process</a>	<a href="#">RT</a>		3	1.5E-2	1.6E-1
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Glyoxylate and dicarboxylate metabolism</a>	<a href="#">RT</a>		3	1.3E-1	5.2E-1
<input type="checkbox"/> Annotation Cluster 34	Enrichment Score: 2.9	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">endonexin fold</a>	<a href="#">RT</a>		5	4.0E-5	3.6E-4
<input type="checkbox"/> SMART	<a href="#">ANX</a>	<a href="#">RT</a>		5	9.4E-5	1.5E-3
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">annexin</a>	<a href="#">RT</a>		5	1.1E-4	9.2E-4
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:Annexin 2	<a href="#">RT</a>		5	1.2E-4	5.7E-3
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:Annexin 1	<a href="#">RT</a>		5	1.2E-4	5.7E-3
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:Annexin 3	<a href="#">RT</a>		5	1.2E-4	5.7E-3
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:Annexin 4	<a href="#">RT</a>		5	1.2E-4	5.7E-3

Annotation Cluster 1		Enrichment Score: 22.09	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">calcium/phospholipid-binding</a>	RT		5	1.5E-4	1.2E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Annexin</a>	RT		5	1.8E-4	4.3E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Annexin repeat</a>	RT		5	1.8E-4	4.3E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Annexin repeat, conserved site</a>	RT		5	1.8E-4	4.3E-3
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">calcium-dependent phospholipid binding</a>	RT		6	4.7E-4	1.0E-2
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF002359:annexin I	RT		5	6.5E-4	2.6E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">phospholipid binding</a>	RT		5	7.4E-4	5.1E-3
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">phospholipase inhibitor activity</a>	RT		4	3.2E-3	5.1E-2
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">lipase inhibitor activity</a>	RT		4	6.2E-3	8.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of coagulation</a>	RT		5	1.8E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of coagulation</a>	RT		4	2.5E-2	2.2E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">phospholipid binding</a>	RT		10	4.1E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of blood coagulation</a>	RT		3	2.2E-1	7.8E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">lipid binding</a>	RT		15	2.8E-1	8.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of multicellular organismal process</a>	RT		6	3.8E-1	9.3E-1
Annotation Cluster 35		Enrichment Score: 2.83	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of actin polymerization or depolymerization</a>	RT		11	2.2E-6	1.4E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of actin filament length</a>	RT		11	2.9E-6	1.7E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of actin filament depolymerization</a>	RT		7	4.1E-5	1.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of actin filament polymerization</a>	RT		9	4.9E-5	2.0E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of actin cytoskeleton organization</a>	RT		11	6.6E-5	2.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of actin filament-based process</a>	RT		11	8.8E-5	2.9E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cellular component size</a>	RT		19	1.4E-4	4.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cellular component biogenesis</a>	RT		13	2.1E-4	5.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of protein polymerization</a>	RT		9	2.6E-4	6.2E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of protein complex assembly</a>	RT		10	3.7E-4	8.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of protein complex assembly</a>	RT		6	1.4E-3	2.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of protein complex disassembly</a>	RT		7	1.5E-3	2.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">actin filament capping</a>	RT		5	1.9E-3	3.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cytoskeleton organization</a>	RT		11	2.0E-3	3.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of actin filament depolymerization</a>	RT		5	2.6E-3	4.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of cellular component organization</a>	RT		11	2.8E-3	4.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of actin filament polymerization</a>	RT		5	4.7E-3	6.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of protein polymerization</a>	RT		5	5.3E-3	7.2E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">actin capping</a>	RT		4	5.4E-3	2.9E-2
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">lamellipodium</a>	RT		7	1.1E-2	4.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of protein complex disassembly</a>	RT		5	1.8E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of organelle organization</a>	RT		12	1.9E-2	1.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cytoskeleton organization</a>	RT		5	2.5E-2	2.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of cytoskeleton organization</a>	RT		5	4.7E-2	3.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of organelle organization</a>	RT		5	1.4E-1	6.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of organelle organization</a>	RT		5	1.5E-1	6.7E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Synaptic Proteins at the Synaptic Junction</a>	RT		3	2.0E-1	9.1E-1
Annotation Cluster 36		Enrichment Score: 2.77	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">rrna-binding</a>	RT		6	1.3E-5	1.3E-4
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">rRNA binding</a>	RT		6	8.0E-4	1.6E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">rna-binding</a>	RT		12	4.6E-1	8.5E-1
Annotation Cluster 37		Enrichment Score: 2.73	G		Count	P_Value	Benjamini

Annotation Cluster 1		Enrichment Score: 22.09	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of protein metabolic process</a>	RT		20	1.9E-7	1.9E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of cellular protein metabolic process</a>	RT		19	5.0E-7	4.0E-5
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">proteasome</a>	RT		10	1.1E-6	1.3E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">proteasomal ubiquitin-dependent protein catabolic process</a>	RT		14	1.3E-6	8.7E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">proteasomal protein catabolic process</a>	RT		14	1.3E-6	8.7E-5
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">proteasome complex</a>	RT		11	4.2E-6	5.4E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of protein modification process</a>	RT		14	7.4E-6	3.9E-4
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">proteinase</a>	RT		6	1.3E-5	1.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process</a>	RT		10	2.9E-5	1.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle</a>	RT		10	2.9E-5	1.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of ubiquitin-protein ligase activity</a>	RT		10	3.7E-5	1.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of ligase activity</a>	RT		10	3.7E-5	1.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle</a>	RT		10	4.2E-5	1.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of ubiquitin-protein ligase activity</a>	RT		10	5.3E-5	2.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of ubiquitin-protein ligase activity during mitotic cell cycle</a>	RT		10	5.9E-5	2.2E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of ligase activity</a>	RT		10	7.4E-5	2.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of protein ubiquitination</a>	RT		10	8.2E-5	2.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of ubiquitin-protein ligase activity</a>	RT		10	1.2E-4	4.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of ligase activity</a>	RT		10	1.7E-4	4.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of protein ubiquitination</a>	RT		10	2.2E-4	5.4E-3
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">threonine protease</a>	RT		5	5.1E-4	3.6E-3
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Proteasome</a>	RT		9	6.2E-4	1.1E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Proteasome, subunit alpha/beta</a>	RT		5	6.5E-4	1.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of protein ubiquitination</a>	RT		10	8.1E-4	1.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ubiquitin-dependent protein catabolic process</a>	RT		16	1.0E-3	2.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of catalytic activity</a>	RT		17	1.5E-3	2.7E-2
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">threonine-type peptidase activity</a>	RT		5	1.5E-3	2.8E-2
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">threonine-type endopeptidase activity</a>	RT		5	1.5E-3	2.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cellular protein metabolic process</a>	RT		24	1.6E-3	2.9E-2
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">proteasome core complex</a>	RT		5	1.7E-3	8.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of molecular function</a>	RT		27	2.9E-3	4.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of molecular function</a>	RT		18	4.0E-3	5.7E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">protein degradation</a>	RT		4	5.4E-3	2.9E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of catalytic activity</a>	RT		23	1.0E-2	1.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cell cycle process</a>	RT		24	1.3E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cellular protein metabolic process</a>	RT		13	1.3E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of macromolecule metabolic process</a>	RT		29	1.5E-2	1.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of protein metabolic process</a>	RT		13	1.8E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of protein modification process</a>	RT		11	1.8E-2	1.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Proteasome, beta-type subunit, conserved site</a>	RT		3	2.7E-2	3.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cell cycle</a>	RT		29	2.9E-2	2.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of protein modification process</a>	RT		14	3.2E-2	2.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Proteasome, alpha and beta subunits</a>	RT		3	3.6E-2	3.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">mitotic cell cycle</a>	RT		16	4.2E-2	3.1E-1

Annotation Cluster 1		Enrichment Score: 22.09	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">hydrolase</a>	RT		36	1.8E-1	5.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">proteolysis involved in cellular protein catabolic process</a>	RT		19	2.2E-1	7.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular protein catabolic process</a>	RT		19	2.3E-1	8.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">modification-dependent macromolecule catabolic process</a>	RT		18	2.5E-1	8.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">modification-dependent protein catabolic process</a>	RT		18	2.5E-1	8.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">protein catabolic process</a>	RT		19	2.8E-1	8.4E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">Protease</a>	RT		12	3.3E-1	7.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular macromolecule catabolic process</a>	RT		21	3.5E-1	9.0E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">endopeptidase activity</a>	RT		12	3.8E-1	9.2E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">peptidase activity, acting on L-amino acid peptides</a>	RT		16	4.6E-1	9.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">macromolecule catabolic process</a>	RT		21	4.7E-1	9.6E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">peptidase activity</a>	RT		16	5.2E-1	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">proteolysis</a>	RT		27	5.3E-1	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of macromolecule metabolic process</a>	RT		16	9.4E-1	1.0E0
Annotation Cluster 38		Enrichment Score: 2.73	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribonucleotide metabolic process</a>	RT		16	3.5E-6	1.9E-4
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">proton-transporting ATP synthase complex, catalytic core F(1)</a>	RT		5	7.1E-6	8.5E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine ribonucleotide metabolic process</a>	RT		15	7.9E-6	4.0E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine ribonucleotide catabolic process</a>	RT		7	1.5E-5	7.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribonucleotide catabolic process</a>	RT		7	2.6E-5	1.2E-3
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">hydrogen ion transporting ATP synthase activity, rotational mechanism</a>	RT		6	3.9E-5	1.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	transit peptide:Mitochondrion	RT		24	4.2E-5	2.1E-3
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">transit peptide</a>	RT		24	5.2E-5	4.5E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribonucleotide biosynthetic process</a>	RT		13	5.6E-5	2.2E-3
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">cf(1)</a>	RT		4	6.8E-5	5.7E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribonucleoside triphosphate catabolic process</a>	RT		6	7.8E-5	2.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine ribonucleoside triphosphate catabolic process</a>	RT		6	7.8E-5	2.7E-3
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">atp synthesis</a>	RT		5	8.3E-5	6.8E-4
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">mitochondrial proton-transporting ATP synthase complex</a>	RT		6	1.1E-4	9.6E-4
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">mitochondrial matrix</a>	RT		18	1.2E-4	1.0E-3
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">mitochondrial lumen</a>	RT		18	1.2E-4	1.0E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine nucleoside triphosphate catabolic process</a>	RT		6	1.3E-4	4.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine nucleotide catabolic process</a>	RT		7	1.4E-4	4.2E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine ribonucleoside triphosphate metabolic process</a>	RT		12	1.5E-4	4.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine ribonucleotide biosynthetic process</a>	RT		12	1.5E-4	4.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribonucleoside triphosphate metabolic process</a>	RT		12	1.6E-4	4.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nitrogen compound biosynthetic process</a>	RT		21	1.7E-4	4.6E-3
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">mitochondrial proton-transporting ATP synthase complex, catalytic core F(1)</a>	RT		4	1.8E-4	1.4E-3
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">proton-transporting ATP synthase complex</a>	RT		6	1.9E-4	1.5E-3
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">mitochondrial inner membrane</a>	RT		21	2.0E-4	1.5E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine nucleotide metabolic process</a>	RT		15	2.1E-4	5.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine nucleoside triphosphate metabolic process</a>	RT		12	2.2E-4	5.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleoside triphosphate catabolic process</a>	RT		6	2.6E-4	6.2E-3
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">proton-transporting ATPase activity, rotational mechanism</a>	RT		6	2.6E-4	6.4E-3
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">cation-transporting ATPase activity</a>	RT		7	2.9E-4	6.9E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine nucleotide biosynthetic process</a>	RT		13	3.0E-4	7.2E-3

Annotation Cluster 1	Enrichment Score: 22.09	G	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process</a>	RT	15	3.1E-4	7.4E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">nucleobase, nucleoside and nucleotide biosynthetic process</a>	RT	15	3.1E-4	7.4E-3
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">mitochondrion inner membrane</a>	RT	13	3.7E-4	2.7E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">nucleoside triphosphate metabolic process</a>	RT	12	4.0E-4	9.1E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">organelle inner membrane</a>	RT	21	5.2E-4	3.5E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">ATP catabolic process</a>	RT	5	5.3E-4	1.2E-2
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">ATP biosynthesis</a>	RT	4	5.4E-4	3.8E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">organelle envelope</a>	RT	32	5.5E-4	3.5E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">envelope</a>	RT	32	5.8E-4	3.7E-3
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">ATPase activity, coupled to transmembrane movement of ions</a>	RT	9	6.3E-4	1.3E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">purine ribonucleoside triphosphate biosynthetic process</a>	RT	10	7.0E-4	1.5E-2
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">mitochondrion</a>	RT	31	7.2E-4	5.0E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">nucleotide biosynthetic process</a>	RT	14	7.2E-4	1.5E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">ribonucleoside triphosphate biosynthetic process</a>	RT	10	7.5E-4	1.6E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">purine nucleoside triphosphate biosynthetic process</a>	RT	10	7.5E-4	1.6E-2
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">mitochondrial membrane</a>	RT	23	8.8E-4	5.0E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">nucleoside triphosphate biosynthetic process</a>	RT	10	9.3E-4	1.9E-2
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">proton-transporting two-sector ATPase complex, catalytic domain</a>	RT	5	1.1E-3	5.9E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">ATP metabolic process</a>	RT	10	1.1E-3	2.2E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">nucleotide catabolic process</a>	RT	7	1.5E-3	2.8E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">ATP biosynthetic process</a>	RT	9	1.6E-3	2.8E-2
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">mitochondrial envelope</a>	RT	23	1.9E-3	9.5E-3
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">Hydrogen ion transport</a>	RT	6	2.2E-3	1.3E-2
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Parkinson's disease</a>	RT	14	2.4E-3	3.1E-2
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">ATPase activity</a>	RT	19	2.7E-3	4.6E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">heterocycle catabolic process</a>	RT	8	2.9E-3	4.4E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">ATP synthesis coupled proton transport</a>	RT	6	2.9E-3	4.4E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">energy coupled proton transport, down electrochemical gradient</a>	RT	6	2.9E-3	4.4E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">nucleobase, nucleoside, nucleotide and nucleic acid catabolic process</a>	RT	7	3.0E-3	4.5E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">nucleobase, nucleoside and nucleotide catabolic process</a>	RT	7	3.0E-3	4.5E-2
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">mitochondrion</a>	RT	45	3.3E-3	1.6E-2
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">mitochondrial part</a>	RT	28	4.8E-3	2.2E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">ribonucleoside diphosphate biosynthetic process</a>	RT	3	5.8E-3	7.8E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">purine ribonucleoside diphosphate biosynthetic process</a>	RT	3	5.8E-3	7.8E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">ADP biosynthetic process</a>	RT	3	5.8E-3	7.8E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">purine nucleoside diphosphate biosynthetic process</a>	RT	3	5.8E-3	7.8E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">nitrogen compound catabolic process</a>	RT	7	6.1E-3	8.1E-2
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">mitochondrial membrane part</a>	RT	10	6.2E-3	2.7E-2
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">proton-transporting two-sector ATPase complex</a>	RT	6	6.6E-3	2.9E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">ion transmembrane transport</a>	RT	6	7.0E-3	9.1E-2
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">ATPase activity, coupled to transmembrane movement of substances</a>	RT	9	7.3E-3	8.4E-2
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Huntington's disease</a>	RT	16	7.7E-3	7.4E-2
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">ATPase activity, coupled to movement of substances</a>	RT	9	7.7E-3	8.2E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">nucleoside diphosphate metabolic process</a>	RT	4	7.8E-3	9.8E-2

Annotation Cluster 1		Enrichment Score: 22.09	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances</a>	RT		9	8.1E-3	8.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ADP metabolic process</a>	RT		3	8.5E-3	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">oxidative phosphorylation</a>	RT		8	1.1E-2	1.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">ATPase activity, coupled</a>	RT		15	1.1E-2	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleoside diphosphate biosynthetic process</a>	RT		3	1.2E-2	1.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">primary active transmembrane transporter activity</a>	RT		9	1.4E-2	1.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">P-P-bond-hydrolysis-driven transmembrane transporter activity</a>	RT		9	1.4E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine ribonucleoside diphosphate metabolic process</a>	RT		3	1.5E-2	1.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine nucleoside diphosphate metabolic process</a>	RT		3	1.5E-2	1.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">proton transport</a>	RT		6	1.7E-2	1.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Alzheimer's disease</a>	RT		14	1.8E-2	1.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">monovalent inorganic cation transmembrane transporter activity</a>	RT		8	1.8E-2	1.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">hydrogen transport</a>	RT		6	1.9E-2	1.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribonucleoside diphosphate metabolic process</a>	RT		3	2.4E-2	2.2E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">hydrogen ion transmembrane transporter activity</a>	RT		7	2.9E-2	2.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">inorganic cation transmembrane transporter activity</a>	RT		9	4.3E-2	2.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">organelle membrane</a>	RT		39	5.5E-2	1.9E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Oxidative phosphorylation</a>	RT		10	9.2E-2	4.2E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">membrane-associated complex</a>	RT		3	1.3E-1	4.0E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism</a>	RT		4	1.6E-1	6.9E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">ion transport</a>	RT		13	4.3E-1	8.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">monovalent inorganic cation transport</a>	RT		8	6.7E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ion transport</a>	RT		17	7.9E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">phosphorylation</a>	RT		17	8.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cation transport</a>	RT		11	8.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">transmembrane transport</a>	RT		10	9.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">phosphorus metabolic process</a>	RT		18	9.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">phosphate metabolic process</a>	RT		18	9.5E-1	1.0E0
Annotation Cluster 39		Enrichment Score: 2.66	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">blood vessel development</a>	RT		18	1.3E-4	4.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">vasculature development</a>	RT		18	1.7E-4	4.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">angiogenesis</a>	RT		9	3.0E-2	2.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">blood vessel morphogenesis</a>	RT		11	3.7E-2	2.9E-1
Annotation Cluster 40		Enrichment Score: 2.62	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">elongation factor</a>	RT		6	4.0E-5	3.5E-4
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">eukaryotic translation elongation factor 1 complex</a>	RT		4	1.8E-4	1.4E-3
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">translation elongation factor activity</a>	RT		6	3.2E-4	7.3E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Translation elongation factor EFTu/EF1A, domain 2</a>	RT		3	4.1E-2	4.1E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">translation factor activity, nucleic acid binding</a>	RT		7	4.2E-2	2.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Protein synthesis factor, GTP-binding</a>	RT		3	5.1E-2	4.8E-1
Annotation Cluster 41		Enrichment Score: 2.58	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of cell motion</a>	RT		9	1.5E-4	4.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell motion</a>	RT		14	1.0E-3	2.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of cell migration</a>	RT		7	2.7E-3	4.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of locomotion</a>	RT		7	3.8E-3	5.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell migration</a>	RT		11	9.3E-3	1.1E-1

	Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
Annotation Cluster 1						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of locomotion</a>	<b>RT</b>		11	2.1E-2	2.0E-1
Annotation Cluster 42	Enrichment Score: 2.57	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">biological adhesion</a>	<b>RT</b>		31	2.4E-3	3.9E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell adhesion</a>	<b>RT</b>		31	2.4E-3	3.9E-2
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">cell adhesion</a>	<b>RT</b>		18	3.4E-3	2.0E-2
Annotation Cluster 43	Enrichment Score: 2.5	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">maintenance of location</a>	<b>RT</b>		9	1.7E-4	4.6E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">maintenance of location in cell</a>	<b>RT</b>		7	1.1E-3	2.2E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">maintenance of protein location in cell</a>	<b>RT</b>		5	1.8E-2	1.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">maintenance of protein location</a>	<b>RT</b>		5	3.0E-2	2.5E-1
Annotation Cluster 44	Enrichment Score: 2.48	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">vesicle lumen</a>	<b>RT</b>		8	1.9E-4	1.5E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">platelet alpha granule lumen</a>	<b>RT</b>		7	6.9E-4	4.2E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">cytoplasmic membrane-bounded vesicle lumen</a>	<b>RT</b>		7	1.0E-3	5.6E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">platelet alpha granule</a>	<b>RT</b>		7	3.6E-3	1.7E-2
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">fibrinogen complex</a>	<b>RT</b>		3	1.4E-2	5.5E-2
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">secretory granule</a>	<b>RT</b>		11	2.2E-2	8.7E-2
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">cytoplasmic vesicle part</a>	<b>RT</b>		11	2.8E-2	1.1E-1
Annotation Cluster 45	Enrichment Score: 2.45	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">trimer</a>	<b>RT</b>		8	4.3E-7	6.2E-6
<input type="checkbox"/> SMART	<a href="#">TSPN</a>	<b>RT</b>		3	6.0E-2	3.5E-1
<input type="checkbox"/> UP_SEQ_FEATURE	domain:TSP N-terminal	<b>RT</b>		3	7.2E-2	7.7E-1
<input type="checkbox"/> INTERPRO	<a href="#">Laminin G, thrombospondin-type, N-terminal</a>	<b>RT</b>		3	8.1E-2	6.3E-1
Annotation Cluster 46	Enrichment Score: 2.22	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">membrane organization</a>	<b>RT</b>		22	5.2E-4	1.2E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">endocytosis</a>	<b>RT</b>		12	2.1E-2	2.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">membrane invagination</a>	<b>RT</b>		12	2.1E-2	2.0E-1
Annotation Cluster 47	Enrichment Score: 2.19	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">glycosaminoglycan binding</a>	<b>RT</b>		11	3.5E-3	5.2E-2
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">heparin binding</a>	<b>RT</b>		9	5.2E-3	7.4E-2
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">polysaccharide binding</a>	<b>RT</b>		11	6.8E-3	8.5E-2
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">pattern binding</a>	<b>RT</b>		11	6.8E-3	8.5E-2
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">heparin-binding</a>	<b>RT</b>		6	8.2E-3	4.1E-2
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">carbohydrate binding</a>	<b>RT</b>		18	1.1E-2	1.1E-1
Annotation Cluster 48	Enrichment Score: 2.17	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">actomyosin</a>	<b>RT</b>		7	6.3E-5	5.7E-4
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">actin filament bundle</a>	<b>RT</b>		6	5.4E-4	3.5E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cytokinesis</a>	<b>RT</b>		6	3.2E-3	4.8E-2
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">stress fiber</a>	<b>RT</b>		5	3.4E-3	1.7E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell division</a>	<b>RT</b>		9	4.4E-1	9.5E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">spindle</a>	<b>RT</b>		5	5.5E-1	8.6E-1
Annotation Cluster 49	Enrichment Score: 2.08	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">cell fraction</a>	<b>RT</b>		51	8.0E-5	7.1E-4
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">insoluble fraction</a>	<b>RT</b>		32	4.0E-2	1.4E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">membrane fraction</a>	<b>RT</b>		27	1.8E-1	4.7E-1
Annotation Cluster 50	Enrichment Score: 2.05	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">organelle lumen</a>	<b>RT</b>		71	7.6E-4	4.5E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">membrane-enclosed lumen</a>	<b>RT</b>		71	1.3E-3	6.7E-3
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">intracellular organelle lumen</a>	<b>RT</b>		65	6.5E-3	2.9E-2
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">nuclear lumen</a>	<b>RT</b>		27	9.9E-1	1.0E0
Annotation Cluster 51	Enrichment Score: 2	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein complex biogenesis</a>	<b>RT</b>		25	1.7E-3	3.0E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein complex assembly</a>	<b>RT</b>		25	1.7E-3	3.0E-2

	Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
<b>Annotation Cluster 1</b>						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular protein complex assembly</a>	<a href="#">RT</a>		12	2.3E-3	3.8E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein oligomerization</a>	<a href="#">RT</a>		11	1.1E-2	1.3E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">macromolecular complex assembly</a>	<a href="#">RT</a>		27	1.4E-2	1.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">macromolecular complex subunit organization</a>	<a href="#">RT</a>		28	1.7E-2	1.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular macromolecular complex subunit organization</a>	<a href="#">RT</a>		15	6.0E-2	4.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular macromolecular complex assembly</a>	<a href="#">RT</a>		13	9.6E-2	5.4E-1
<b>Annotation Cluster 52</b>						
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">isopeptide bond</a>	<a href="#">RT</a>		16	1.4E-3	8.9E-3
<input type="checkbox"/> UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin)	<a href="#">RT</a>		12	1.7E-3	6.0E-2
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">ubl conjugation</a>	<a href="#">RT</a>		13	4.5E-1	8.5E-1
<b>Annotation Cluster 53</b>						
<input type="checkbox"/> UP_SEQ_FEATURE	domain:GST C-terminal	<a href="#">RT</a>		5	3.6E-3	1.1E-1
<input type="checkbox"/> INTERPRO	<a href="#">Glutathione S-transferase, C-terminal-like</a>	<a href="#">RT</a>		4	2.4E-2	3.0E-1
<input type="checkbox"/> INTERPRO	<a href="#">Glutathione S-transferase/chloride channel, C-terminal</a>	<a href="#">RT</a>		4	2.7E-2	3.1E-1
<b>Annotation Cluster 54</b>						
<input type="checkbox"/> UP_SEQ_FEATURE	domain:ADF-H	<a href="#">RT</a>		3	9.6E-3	2.4E-1
<input type="checkbox"/> SMART	<a href="#">ADF</a>	<a href="#">RT</a>		3	1.4E-2	1.5E-1
<input type="checkbox"/> INTERPRO	<a href="#">Actin-binding, cofilin/tropomyosin type</a>	<a href="#">RT</a>		3	1.9E-2	2.5E-1
<b>Annotation Cluster 55</b>						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">response to inorganic substance</a>	<a href="#">RT</a>		17	5.0E-5	2.0E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">response to reactive oxygen species</a>	<a href="#">RT</a>		8	2.5E-3	4.0E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">response to hydrogen peroxide</a>	<a href="#">RT</a>		7	2.5E-3	4.0E-2
<input type="checkbox"/> INTERPRO	<a href="#">Peroxiredoxin, C-terminal</a>	<a href="#">RT</a>		3	4.5E-3	8.2E-2
<input type="checkbox"/> UP_SEQ_FEATURE	active site:Cysteine sulfenic acid (-SOH) intermediate	<a href="#">RT</a>		3	5.3E-3	1.5E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">antioxidant activity</a>	<a href="#">RT</a>		6	7.1E-3	8.3E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">response to oxidative stress</a>	<a href="#">RT</a>		11	7.6E-3	9.6E-2
<input type="checkbox"/> INTERPRO	<a href="#">Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen</a>	<a href="#">RT</a>		3	9.2E-3	1.5E-1
<input type="checkbox"/> PIR_SUPERFAMILY	PIRSF000239:alkyl hydroperoxide reductase C22 protein	<a href="#">RT</a>		3	1.2E-2	2.4E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">antioxidant</a>	<a href="#">RT</a>		3	1.2E-2	5.6E-2
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">peroxiredoxin activity</a>	<a href="#">RT</a>		3	1.7E-2	1.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">hydrogen peroxide metabolic process</a>	<a href="#">RT</a>		4	2.3E-2	2.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">oxygen and reactive oxygen species metabolic process</a>	<a href="#">RT</a>		6	2.5E-2	2.2E-1
<input type="checkbox"/> UP_SEQ_FEATURE	domain:Thioredoxin	<a href="#">RT</a>		4	2.5E-2	4.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular response to reactive oxygen species</a>	<a href="#">RT</a>		4	3.7E-2	2.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">hydrogen peroxide catabolic process</a>	<a href="#">RT</a>		3	6.5E-2	4.2E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular response to hydrogen peroxide</a>	<a href="#">RT</a>		3	7.2E-2	4.5E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">peroxidase</a>	<a href="#">RT</a>		3	8.2E-2	3.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular response to oxidative stress</a>	<a href="#">RT</a>		4	8.9E-2	5.1E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">oxidoreductase activity, acting on peroxide as acceptor</a>	<a href="#">RT</a>		3	2.0E-1	7.7E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">peroxidase activity</a>	<a href="#">RT</a>		3	2.0E-1	7.7E-1
<b>Annotation Cluster 56</b>						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell junction organization</a>	<a href="#">RT</a>		6	1.3E-2	1.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell junction assembly</a>	<a href="#">RT</a>		5	1.8E-2	1.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell-substrate junction assembly</a>	<a href="#">RT</a>		4	1.8E-2	1.8E-1
<b>Annotation Cluster 57</b>						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of cell adhesion</a>	<a href="#">RT</a>		13	1.5E-4	4.4E-3
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of cell-substrate adhesion</a>	<a href="#">RT</a>		5	2.6E-2	2.3E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">positive regulation of cell-substrate adhesion</a>	<a href="#">RT</a>		4	3.1E-2	2.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">positive regulation of cell adhesion</a>	<a href="#">RT</a>		5	6.1E-2	4.1E-1

	Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
Annotation Cluster 1						
UP_SEQ_FEATURE	domain:EGF-like 1	<a href="#">RT</a>		5	2.0E-1	9.8E-1
Annotation Cluster 58		<b>G</b>				
UP_SEQ_FEATURE	domain:Fibronectin type-III 14	<a href="#">RT</a>		4	3.7E-4	1.6E-2
UP_SEQ_FEATURE	domain:Fibronectin type-III 15	<a href="#">RT</a>		4	3.7E-4	1.6E-2
UP_SEQ_FEATURE	domain:Fibronectin type-III 13	<a href="#">RT</a>		4	7.7E-4	3.0E-2
UP_SEQ_FEATURE	domain:Fibronectin type-III 10	<a href="#">RT</a>		4	7.7E-4	3.0E-2
UP_SEQ_FEATURE	domain:Fibronectin type-III 11	<a href="#">RT</a>		4	7.7E-4	3.0E-2
UP_SEQ_FEATURE	domain:Fibronectin type-III 9	<a href="#">RT</a>		4	4.0E-3	1.2E-1
UP_SEQ_FEATURE	domain:Fibronectin type-III 16	<a href="#">RT</a>		3	7.3E-3	1.9E-1
UP_SEQ_FEATURE	domain:Fibronectin type-III 7	<a href="#">RT</a>		4	1.1E-2	2.5E-1
UP_SEQ_FEATURE	domain:Fibronectin type-III 8	<a href="#">RT</a>		4	1.1E-2	2.5E-1
UP_SEQ_FEATURE	domain:Fibronectin type-III 12	<a href="#">RT</a>		3	1.2E-2	2.7E-1
UP_SEQ_FEATURE	domain:Fibronectin type-III 6	<a href="#">RT</a>		4	2.2E-2	4.1E-1
UP_SEQ_FEATURE	domain:Fibronectin type-III 5	<a href="#">RT</a>		4	5.6E-2	6.9E-1
UP_SEQ_FEATURE	domain:Fibronectin type-III 4	<a href="#">RT</a>		4	1.2E-1	9.0E-1
UP_SEQ_FEATURE	domain:Fibronectin type-III 3	<a href="#">RT</a>		4	2.2E-1	9.8E-1
UP_SEQ_FEATURE	domain:Fibronectin type-III 2	<a href="#">RT</a>		4	4.6E-1	1.0E0
UP_SEQ_FEATURE	domain:Fibronectin type-III 1	<a href="#">RT</a>		4	4.7E-1	1.0E0
INTERPRO	<a href="#">Fibronectin, type III-like fold</a>	<a href="#">RT</a>		5	5.7E-1	1.0E0
SMART	<a href="#">FN3</a>	<a href="#">RT</a>		4	6.8E-1	9.9E-1
INTERPRO	<a href="#">Fibronectin, type III</a>	<a href="#">RT</a>		4	7.8E-1	1.0E0
Annotation Cluster 59		<b>G</b>				
GOTERM_CC_FAT	<a href="#">growth cone</a>	<a href="#">RT</a>		6	1.4E-2	5.7E-2
GOTERM_CC_FAT	<a href="#">site of polarized growth</a>	<a href="#">RT</a>		6	1.5E-2	6.1E-2
GOTERM_CC_FAT	<a href="#">neuron projection</a>	<a href="#">RT</a>		16	4.0E-2	1.4E-1
Annotation Cluster 60		<b>G</b>				
INTERPRO	<a href="#">Heat shock protein Hsp90, conserved site</a>	<a href="#">RT</a>		4	9.8E-5	2.5E-3
PIR_SUPERFAMILY	PIRSF002583:heat shock protein, HSP90/HTPG types	<a href="#">RT</a>		4	1.5E-3	5.0E-2
INTERPRO	<a href="#">Heat shock protein Hsp90</a>	<a href="#">RT</a>		4	1.9E-3	3.9E-2
SMART	<a href="#">HATPase_c</a>	<a href="#">RT</a>		4	1.7E-2	1.6E-1
INTERPRO	<a href="#">ATP-binding region, ATPase-like</a>	<a href="#">RT</a>		4	2.7E-2	3.1E-1
PIR_SUPERFAMILY	PIRSF002583:Hsp90	<a href="#">RT</a>		3	5.8E-2	6.4E-1
KEGG_PATHWAY	<a href="#">Prostate cancer</a>	<a href="#">RT</a>		6	3.1E-1	7.3E-1
KEGG_PATHWAY	<a href="#">NOD-like receptor signaling pathway</a>	<a href="#">RT</a>		4	4.8E-1	8.4E-1
KEGG_PATHWAY	<a href="#">Progesterone-mediated oocyte maturation</a>	<a href="#">RT</a>		4	7.0E-1	9.4E-1
Annotation Cluster 61		<b>G</b>				
GOTERM_BP_FAT	<a href="#">regulation of endocytosis</a>	<a href="#">RT</a>		8	7.3E-4	1.5E-2
GOTERM_BP_FAT	<a href="#">regulation of vesicle-mediated transport</a>	<a href="#">RT</a>		8	9.6E-3	1.1E-1
GOTERM_BP_FAT	<a href="#">positive regulation of endocytosis</a>	<a href="#">RT</a>		4	3.4E-2	2.7E-1
GOTERM_BP_FAT	<a href="#">positive regulation of phagocytosis</a>	<a href="#">RT</a>		3	3.4E-2	2.7E-1
GOTERM_BP_FAT	<a href="#">regulation of phagocytosis</a>	<a href="#">RT</a>		3	5.8E-2	4.0E-1
GOTERM_BP_FAT	<a href="#">positive regulation of transport</a>	<a href="#">RT</a>		8	3.1E-1	8.8E-1
Annotation Cluster 62		<b>G</b>				
UP_SEQ_FEATURE	domain:EH	<a href="#">RT</a>		3	3.6E-3	1.1E-1
SMART	<a href="#">EH</a>	<a href="#">RT</a>		3	1.6E-2	1.6E-1
INTERPRO	<a href="#">EPS15 homology (EH)</a>	<a href="#">RT</a>		3	2.3E-2	2.8E-1
SMART	<a href="#">DYNc</a>	<a href="#">RT</a>		3	2.3E-2	1.9E-1
INTERPRO	<a href="#">Dynamamin, GTPase region</a>	<a href="#">RT</a>		3	3.1E-2	3.4E-1
UP_SEQ_FEATURE	domain:EF-hand	<a href="#">RT</a>		4	4.4E-2	6.2E-1
SP_PIR_KEYWORDS	<a href="#">endosome</a>	<a href="#">RT</a>		8	1.1E-1	3.7E-1
Annotation Cluster 63		<b>G</b>				
GOTERM_BP_FAT	<a href="#">actomyosin structure organization</a>	<a href="#">RT</a>		6	5.5E-4	1.2E-2
GOTERM_BP_FAT	<a href="#">myofibril assembly</a>	<a href="#">RT</a>		5	1.6E-3	2.9E-2

	Annotation Cluster	Enrichment Score			Count	P_Value	Benjamini
<input type="checkbox"/>	Annotation Cluster 1	Enrichment Score: 22.09	<b>G</b>				
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular component assembly involved in morphogenesis</a>	<a href="#">RT</a>		6	1.8E-3	3.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">striated muscle cell development</a>	<a href="#">RT</a>		6	9.0E-3	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">muscle cell development</a>	<a href="#">RT</a>		6	1.2E-2	1.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">striated muscle cell differentiation</a>	<a href="#">RT</a>		7	2.2E-2	2.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">muscle cell differentiation</a>	<a href="#">RT</a>		8	3.0E-2	2.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">sarcomere organization</a>	<a href="#">RT</a>		3	3.4E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">muscle organ development</a>	<a href="#">RT</a>		11	3.7E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">muscle tissue development</a>	<a href="#">RT</a>		7	8.9E-2	5.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cardiac muscle cell differentiation</a>	<a href="#">RT</a>		3	1.1E-1	5.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cardiac cell differentiation</a>	<a href="#">RT</a>		3	1.5E-1	6.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cardiac muscle tissue development</a>	<a href="#">RT</a>		4	1.7E-1	7.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">striated muscle tissue development</a>	<a href="#">RT</a>		6	1.7E-1	7.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">heart development</a>	<a href="#">RT</a>		8	2.8E-1	8.5E-1
<input type="checkbox"/>	Annotation Cluster 64	Enrichment Score: 1.56	<b>G</b>				
<input type="checkbox"/>	INTERPRO	<a href="#">Alpha crystallin/Heat shock protein</a>	<a href="#">RT</a>		3	1.2E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to heat</a>	<a href="#">RT</a>		6	1.2E-2	1.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Heat shock protein Hsp20</a>	<a href="#">RT</a>		3	1.5E-2	2.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to temperature stimulus</a>	<a href="#">RT</a>		6	5.4E-2	3.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to abiotic stimulus</a>	<a href="#">RT</a>		14	1.2E-1	6.1E-1
<input type="checkbox"/>	Annotation Cluster 65	Enrichment Score: 1.5	<b>G</b>				
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">circulatory system process</a>	<a href="#">RT</a>		11	1.7E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">blood circulation</a>	<a href="#">RT</a>		11	1.7E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of blood pressure</a>	<a href="#">RT</a>		7	3.7E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of blood vessel size</a>	<a href="#">RT</a>		5	4.1E-2	3.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of tube size</a>	<a href="#">RT</a>		5	4.1E-2	3.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">vascular process in circulatory system</a>	<a href="#">RT</a>		5	5.5E-2	3.8E-1
<input type="checkbox"/>	Annotation Cluster 66	Enrichment Score: 1.42	<b>G</b>				
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1-2	<a href="#">RT</a>		4	1.3E-2	2.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1-1	<a href="#">RT</a>		4	1.5E-2	3.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1-4	<a href="#">RT</a>		3	4.2E-2	6.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1-3	<a href="#">RT</a>		3	4.6E-2	6.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:2-1	<a href="#">RT</a>		3	8.3E-2	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:2-2	<a href="#">RT</a>		3	9.5E-2	8.5E-1
<input type="checkbox"/>	Annotation Cluster 67	Enrichment Score: 1.41	<b>G</b>				
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribonucleoside metabolic process</a>	<a href="#">RT</a>		5	2.6E-2	2.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine nucleoside metabolic process</a>	<a href="#">RT</a>		4	3.4E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine ribonucleoside metabolic process</a>	<a href="#">RT</a>		4	3.4E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleoside metabolic process</a>	<a href="#">RT</a>		5	7.3E-2	4.6E-1
<input type="checkbox"/>	Annotation Cluster 68	Enrichment Score: 1.4	<b>G</b>				
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">establishment of organelle localization</a>	<a href="#">RT</a>		7	7.0E-3	9.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">organelle localization</a>	<a href="#">RT</a>		8	7.7E-3	9.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">establishment of vesicle localization</a>	<a href="#">RT</a>		3	2.0E-1	7.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">vesicle localization</a>	<a href="#">RT</a>		3	2.3E-1	8.0E-1
<input type="checkbox"/>	Annotation Cluster 69	Enrichment Score: 1.38	<b>G</b>				
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">myristate</a>	<a href="#">RT</a>		7	2.7E-2	1.1E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">myristylation</a>	<a href="#">RT</a>		4	3.8E-2	1.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	lipid moiety-binding region:N-myristoyl glycine	<a href="#">RT</a>		6	7.0E-2	7.6E-1
<input type="checkbox"/>	Annotation Cluster 70	Enrichment Score: 1.36	<b>G</b>				
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">protein polymerization</a>	<a href="#">RT</a>		8	1.8E-4	4.9E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Tubulin/FtsZ, 2-layer sandwich domain</a>	<a href="#">RT</a>		4	1.1E-2	1.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Tubulin, conserved site</a>	<a href="#">RT</a>		4	1.3E-2	1.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Tubulin/FtsZ, GTPase domain</a>	<a href="#">RT</a>		4	1.5E-2	2.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Tubulin</a>	<a href="#">RT</a>		4	1.5E-2	2.1E-1

Annotation Cluster 1		Enrichment Score: 22.09	G		Count	P_Value	Benjamini
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF002306:tubulin	RT		4	4.3E-2	5.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">microtubule-based movement</a>	RT		7	6.1E-2	4.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">microtubule-based process</a>	RT		11	9.7E-2	5.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">microtubule cytoskeleton</a>	RT		20	1.5E-1	4.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">microtubule cytoskeleton organization</a>	RT		7	1.6E-1	6.8E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">microtubule</a>	RT		7	2.9E-1	6.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Gap junction</a>	RT		6	3.1E-1	7.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">microtubule</a>	RT		8	6.0E-1	8.9E-1
Annotation Cluster 71		Enrichment Score: 1.36	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Cell attachment site	RT		12	1.0E-6	9.2E-5
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">basement membrane</a>	RT		9	1.1E-3	5.8E-3
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">cell adhesion</a>	RT		18	3.4E-3	2.0E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">basement membrane</a>	RT		5	6.5E-3	3.4E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 4	RT		5	2.6E-2	4.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 2	RT		6	2.8E-2	4.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 3	RT		5	5.7E-2	6.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">EGF</a>	RT		7	5.8E-2	5.1E-1
<input type="checkbox"/>	SMART	<a href="#">EGF</a>	RT		8	7.6E-2	3.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">EGF-like, type 3</a>	RT		8	1.3E-1	7.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">EGF-like</a>	RT		8	1.5E-1	8.2E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">egf-like domain</a>	RT		8	1.6E-1	4.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">EGF-like region, conserved site</a>	RT		10	1.9E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 6	RT		3	2.0E-1	9.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 1	RT		5	2.0E-1	9.8E-1
<input type="checkbox"/>	SMART	<a href="#">EGF_CA</a>	RT		3	5.3E-1	9.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">EGF-like calcium-binding</a>	RT		3	6.2E-1	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">EGF-like calcium-binding, conserved site</a>	RT		3	6.2E-1	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">EGF-type aspartate/asparagine hydroxylation conserved site</a>	RT		3	6.2E-1	1.0E0
Annotation Cluster 72		Enrichment Score: 1.34	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Alcohol dehydrogenase GroES-like</a>	RT		3	3.6E-2	3.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Alcohol dehydrogenase superfamily, zinc-containing</a>	RT		3	5.1E-2	4.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Alcohol dehydrogenase, zinc-binding</a>	RT		3	5.1E-2	4.8E-1
Annotation Cluster 73		Enrichment Score: 1.33	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	<a href="#">PINT</a>	RT		3	3.8E-2	2.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PCI	RT		3	5.1E-2	6.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Proteasome component region PCI</a>	RT		3	5.1E-2	4.8E-1
Annotation Cluster 74		Enrichment Score: 1.29	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cellular component organization</a>	RT		12	5.3E-3	7.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cytoskeleton organization</a>	RT		5	2.5E-2	2.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of actin filament polymerization</a>	RT		3	3.4E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of protein polymerization</a>	RT		3	1.3E-1	6.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of organelle organization</a>	RT		5	1.5E-1	6.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of protein complex assembly</a>	RT		3	2.1E-1	7.7E-1
Annotation Cluster 75		Enrichment Score: 1.26	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribosome biogenesis</a>	RT		9	1.1E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribosomal large subunit biogenesis</a>	RT		3	2.4E-2	2.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">rRNA processing</a>	RT		7	2.6E-2	2.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribosomal small subunit biogenesis</a>	RT		3	2.9E-2	2.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">rRNA metabolic process</a>	RT		7	3.1E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ncRNA metabolic process</a>	RT		11	6.0E-2	4.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribonucleoprotein complex biogenesis</a>	RT		9	7.8E-2	4.8E-1

	Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
<b>Annotation Cluster 1</b>						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">ncRNA processing</a>	<a href="#">RT</a>		8	1.8E-1	7.2E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">RNA processing</a>	<a href="#">RT</a>		11	8.7E-1	1.0E0
<b>Annotation Cluster 76</b>	<b>Enrichment Score: 1.19</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">negative regulation of endothelial cell proliferation</a>	<a href="#">RT</a>		4	9.2E-3	1.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of endothelial cell proliferation</a>	<a href="#">RT</a>		4	4.4E-2	3.2E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">negative regulation of cell proliferation</a>	<a href="#">RT</a>		9	6.7E-1	9.9E-1
<b>Annotation Cluster 77</b>	<b>Enrichment Score: 1.17</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">response to extracellular stimulus</a>	<a href="#">RT</a>		12	2.1E-2	2.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">response to nutrient levels</a>	<a href="#">RT</a>		10	5.7E-2	3.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">response to nutrient</a>	<a href="#">RT</a>		6	2.6E-1	8.3E-1
<b>Annotation Cluster 78</b>	<b>Enrichment Score: 1.13</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">neuron projection</a>	<a href="#">RT</a>		16	4.0E-2	1.4E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">dendrite</a>	<a href="#">RT</a>		9	7.0E-2	2.3E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">cell soma</a>	<a href="#">RT</a>		9	8.0E-2	2.5E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">axon</a>	<a href="#">RT</a>		8	1.3E-1	3.8E-1
<b>Annotation Cluster 79</b>	<b>Enrichment Score: 1.13</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of cell projection organization</a>	<a href="#">RT</a>		9	1.6E-3	2.8E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of cell morphogenesis</a>	<a href="#">RT</a>		9	1.6E-2	1.7E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of neuron projection development</a>	<a href="#">RT</a>		6	2.9E-2	2.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of neuron differentiation</a>	<a href="#">RT</a>		8	4.7E-2	3.4E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of nervous system development</a>	<a href="#">RT</a>		9	1.0E-1	5.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of neurogenesis</a>	<a href="#">RT</a>		8	1.2E-1	6.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of cell morphogenesis involved in differentiation</a>	<a href="#">RT</a>		5	1.2E-1	6.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">negative regulation of axonogenesis</a>	<a href="#">RT</a>		3	1.3E-1	6.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of cell development</a>	<a href="#">RT</a>		9	1.4E-1	6.4E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">negative regulation of cell projection organization</a>	<a href="#">RT</a>		3	1.5E-1	6.7E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of axonogenesis</a>	<a href="#">RT</a>		4	1.7E-1	7.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">negative regulation of neurogenesis</a>	<a href="#">RT</a>		3	3.1E-1	8.7E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">negative regulation of cell development</a>	<a href="#">RT</a>		3	3.3E-1	8.9E-1
<b>Annotation Cluster 80</b>	<b>Enrichment Score: 1.12</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> BIOCARTA	<a href="#">Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia</a>	<a href="#">RT</a>		6	2.7E-3	1.1E-1
<input type="checkbox"/> BIOCARTA	<a href="#">Ras-Independent pathway in NK cell-mediated cytotoxicity</a>	<a href="#">RT</a>		4	5.5E-2	6.6E-1
<input type="checkbox"/> BIOCARTA	<a href="#">Integrin Signaling Pathway</a>	<a href="#">RT</a>		5	7.0E-2	7.1E-1
<input type="checkbox"/> BIOCARTA	<a href="#">Signaling of Hepatocyte Growth Factor Receptor</a>	<a href="#">RT</a>		4	2.1E-1	9.0E-1
<input type="checkbox"/> BIOCARTA	<a href="#">Aspirin Blocks Signaling Pathway Involved in Platelet Activation</a>	<a href="#">RT</a>		3	2.2E-1	8.9E-1
<input type="checkbox"/> BIOCARTA	<a href="#">Erk1/Erk2 Mapk Signaling pathway</a>	<a href="#">RT</a>		3	4.0E-1	9.6E-1
<b>Annotation Cluster 81</b>	<b>Enrichment Score: 1.12</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">pyruvate metabolic process</a>	<a href="#">RT</a>		6	3.6E-3	5.3E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">monosaccharide biosynthetic process</a>	<a href="#">RT</a>		4	6.3E-2	4.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">alcohol biosynthetic process</a>	<a href="#">RT</a>		4	9.4E-2	5.3E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">carbohydrate biosynthetic process</a>	<a href="#">RT</a>		6	1.3E-1	6.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">gluconeogenesis</a>	<a href="#">RT</a>		3	1.3E-1	6.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">hexose biosynthetic process</a>	<a href="#">RT</a>		3	1.8E-1	7.2E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular carbohydrate biosynthetic process</a>	<a href="#">RT</a>		4	2.4E-1	8.1E-1
<b>Annotation Cluster 82</b>	<b>Enrichment Score: 1.08</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">exocytosis</a>	<a href="#">RT</a>		7	6.5E-2	4.2E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">secretion by cell</a>	<a href="#">RT</a>		10	7.2E-2	4.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">secretion</a>	<a href="#">RT</a>		12	1.2E-1	6.1E-1
<b>Annotation Cluster 83</b>	<b>Enrichment Score: 1.06</b>	<b>G</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
<input type="checkbox"/> SMART	<a href="#">RAS</a>	<a href="#">RT</a>		3	6.5E-2	3.5E-1

	Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> Annotation Cluster 1						
<input type="checkbox"/> INTERPRO	<a href="#">Ras small GTPase, Ras type</a>	<a href="#">RT</a>		3	8.8E-2	6.5E-1
<input type="checkbox"/> PIR_SUPERFAMILY	PIRSF037165:ras protein	<a href="#">RT</a>		3	1.1E-1	8.5E-1
<input type="checkbox"/> Annotation Cluster 84	Enrichment Score: 1.06	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">myofibril assembly</a>	<a href="#">RT</a>		5	1.6E-3	2.9E-2
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Hypertrophic cardiomyopathy (HCM)</a>	<a href="#">RT</a>		6	2.8E-1	6.9E-1
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Dilated cardiomyopathy</a>	<a href="#">RT</a>		6	3.4E-1	7.5E-1
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Arrhythmogenic right ventricular cardiomyopathy (ARVC)</a>	<a href="#">RT</a>		5	3.9E-1	7.8E-1
<input type="checkbox"/> Annotation Cluster 85	Enrichment Score: 1.05	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">natural killer cell mediated cytotoxicity</a>	<a href="#">RT</a>		3	1.5E-2	1.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">natural killer cell mediated immunity</a>	<a href="#">RT</a>		3	1.5E-2	1.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell killing</a>	<a href="#">RT</a>		4	2.1E-2	2.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">leukocyte mediated cytotoxicity</a>	<a href="#">RT</a>		3	2.4E-2	2.2E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">leukocyte mediated immunity</a>	<a href="#">RT</a>		6	6.1E-2	4.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">lymphocyte mediated immunity</a>	<a href="#">RT</a>		5	9.5E-2	5.3E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">immune effector process</a>	<a href="#">RT</a>		7	1.1E-1	5.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">defense response</a>	<a href="#">RT</a>		15	6.6E-1	9.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">innate immune response</a>	<a href="#">RT</a>		4	6.7E-1	9.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">immune response</a>	<a href="#">RT</a>		10	9.9E-1	1.0E0
<input type="checkbox"/> Annotation Cluster 86	Enrichment Score: 1.04	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">response to acid</a>	<a href="#">RT</a>		4	2.1E-2	2.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">response to amino acid stimulus</a>	<a href="#">RT</a>		3	6.5E-2	4.2E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">response to organic nitrogen</a>	<a href="#">RT</a>		4	2.0E-1	7.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">response to amine stimulus</a>	<a href="#">RT</a>		3	2.5E-1	8.2E-1
<input type="checkbox"/> Annotation Cluster 87	Enrichment Score: 1.01	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">programmed cell death</a>	<a href="#">RT</a>		22	7.9E-2	4.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell death</a>	<a href="#">RT</a>		25	8.2E-2	4.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">death</a>	<a href="#">RT</a>		25	8.5E-2	5.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">apoptosis</a>	<a href="#">RT</a>		20	1.6E-1	6.9E-1
<input type="checkbox"/> Annotation Cluster 88	Enrichment Score: 1	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> SMART	<a href="#">LIM</a>	<a href="#">RT</a>		5	4.4E-2	2.8E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">LIM domain</a>	<a href="#">RT</a>		5	4.8E-2	1.9E-1
<input type="checkbox"/> INTERPRO	<a href="#">Zinc finger, LIM-type</a>	<a href="#">RT</a>		5	7.4E-2	6.0E-1
<input type="checkbox"/> UP_SEQ_FEATURE	domain:LIM zinc-binding 1	<a href="#">RT</a>		3	2.5E-1	9.9E-1
<input type="checkbox"/> UP_SEQ_FEATURE	domain:LIM zinc-binding 2	<a href="#">RT</a>		3	2.5E-1	9.9E-1
<input type="checkbox"/> Annotation Cluster 89	Enrichment Score: 1	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">identical protein binding</a>	<a href="#">RT</a>		26	2.6E-2	2.1E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">protein homodimerization activity</a>	<a href="#">RT</a>		13	1.6E-1	6.9E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">protein dimerization activity</a>	<a href="#">RT</a>		18	2.4E-1	8.2E-1
<input type="checkbox"/> Annotation Cluster 90	Enrichment Score: 1	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">myosin</a>	<a href="#">RT</a>		5	1.6E-2	7.3E-2
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">actin-dependent ATPase activity</a>	<a href="#">RT</a>		3	1.7E-2	1.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">actin filament-based movement</a>	<a href="#">RT</a>		4	1.8E-2	1.8E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">myosin complex</a>	<a href="#">RT</a>		5	9.4E-2	2.9E-1
<input type="checkbox"/> UP_SEQ_FEATURE	domain:Myosin head-like	<a href="#">RT</a>		3	1.5E-1	9.4E-1
<input type="checkbox"/> SMART	<a href="#">MYSc</a>	<a href="#">RT</a>		3	1.5E-1	5.8E-1
<input type="checkbox"/> INTERPRO	<a href="#">Myosin head, motor region</a>	<a href="#">RT</a>		3	2.0E-1	8.9E-1
<input type="checkbox"/> SMART	<a href="#">IQ</a>	<a href="#">RT</a>		4	2.1E-1	6.5E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">motor protein</a>	<a href="#">RT</a>		5	2.5E-1	6.2E-1
<input type="checkbox"/> INTERPRO	<a href="#">IQ calmodulin-binding region</a>	<a href="#">RT</a>		4	2.9E-1	9.6E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">motor activity</a>	<a href="#">RT</a>		6	3.1E-1	8.8E-1
<input type="checkbox"/> Annotation Cluster 91	Enrichment Score: 1	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein homooligomerization</a>	<a href="#">RT</a>		7	3.0E-2	2.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein homotetramerization</a>	<a href="#">RT</a>		3	1.3E-1	6.4E-1

	Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
Annotation Cluster 1						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein tetramerization</a>	<a href="#">RT</a>		3	2.5E-1	8.2E-1
Annotation Cluster 92	Enrichment Score: 0.97	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">mitochondrial membrane part</a>	<a href="#">RT</a>		10	6.2E-3	2.7E-2
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">electron transport</a>	<a href="#">RT</a>		5	1.3E-1	4.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">electron transport chain</a>	<a href="#">RT</a>		6	1.5E-1	6.7E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">respiratory chain</a>	<a href="#">RT</a>		4	1.6E-1	4.6E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">mitochondrial respiratory chain</a>	<a href="#">RT</a>		4	2.4E-1	5.6E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">respiratory chain</a>	<a href="#">RT</a>		4	3.2E-1	6.7E-1
Annotation Cluster 93	Enrichment Score: 0.94	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">carboxylic acid biosynthetic process</a>	<a href="#">RT</a>		8	9.0E-2	5.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">organic acid biosynthetic process</a>	<a href="#">RT</a>		8	9.0E-2	5.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">aspartate family amino acid metabolic process</a>	<a href="#">RT</a>		3	1.2E-1	6.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular amino acid biosynthetic process</a>	<a href="#">RT</a>		4	1.3E-1	6.3E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">glutamine family amino acid metabolic process</a>	<a href="#">RT</a>		4	1.4E-1	6.4E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">amine biosynthetic process</a>	<a href="#">RT</a>		5	1.4E-1	6.5E-1
Annotation Cluster 94	Enrichment Score: 0.93	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	<a href="#">Fibrinogen, alpha/beta/gamma chain, C-terminal globular, subdomain 1</a>	<a href="#">RT</a>		3	8.8E-2	6.5E-1
<input type="checkbox"/> SMART	<a href="#">FBG</a>	<a href="#">RT</a>		3	1.2E-1	5.1E-1
<input type="checkbox"/> UP_SEQ_FEATURE	domain:Fibrinogen C-terminal	<a href="#">RT</a>		3	1.3E-1	9.1E-1
<input type="checkbox"/> INTERPRO	<a href="#">Fibrinogen, alpha/beta/gamma chain, C-terminal globular</a>	<a href="#">RT</a>		3	1.5E-1	8.2E-1
Annotation Cluster 95	Enrichment Score: 0.89	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">Aminoacyl-tRNA synthetase</a>	<a href="#">RT</a>		4	3.8E-2	1.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">ncRNA metabolic process</a>	<a href="#">RT</a>		11	6.0E-2	4.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">tRNA aminoacylation</a>	<a href="#">RT</a>		4	1.0E-1	5.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">amino acid activation</a>	<a href="#">RT</a>		4	1.0E-1	5.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">tRNA aminoacylation for protein translation</a>	<a href="#">RT</a>		4	1.0E-1	5.6E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">ligase activity, forming carbon-oxygen bonds</a>	<a href="#">RT</a>		4	1.2E-1	6.0E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">aminoacyl-tRNA ligase activity</a>	<a href="#">RT</a>		4	1.2E-1	6.0E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">ligase activity, forming aminoacyl-tRNA and related compounds</a>	<a href="#">RT</a>		4	1.2E-1	6.0E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">ligase</a>	<a href="#">RT</a>		9	2.3E-1	6.0E-1
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Aminoacyl-tRNA biosynthesis</a>	<a href="#">RT</a>		4	2.4E-1	6.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">tRNA metabolic process</a>	<a href="#">RT</a>		4	5.6E-1	9.8E-1
Annotation Cluster 96	Enrichment Score: 0.89	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">endosome</a>	<a href="#">RT</a>		8	1.1E-1	3.7E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">endosome</a>	<a href="#">RT</a>		13	1.4E-1	3.9E-1
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Endocytosis</a>	<a href="#">RT</a>		12	1.4E-1	5.5E-1
Annotation Cluster 97	Enrichment Score: 0.88	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Amino sugar and nucleotide sugar metabolism</a>	<a href="#">RT</a>		6	3.5E-2	2.4E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">carbohydrate biosynthetic process</a>	<a href="#">RT</a>		6	1.3E-1	6.1E-1
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Starch and sucrose metabolism</a>	<a href="#">RT</a>		3	5.3E-1	8.7E-1
Annotation Cluster 98	Enrichment Score: 0.87	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular component morphogenesis</a>	<a href="#">RT</a>		20	4.6E-3	6.4E-2
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell projection organization</a>	<a href="#">RT</a>		17	2.1E-2	2.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell morphogenesis</a>	<a href="#">RT</a>		16	3.1E-2	2.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell projection morphogenesis</a>	<a href="#">RT</a>		10	1.5E-1	6.7E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">neuron projection development</a>	<a href="#">RT</a>		10	1.8E-1	7.3E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell part morphogenesis</a>	<a href="#">RT</a>		10	1.8E-1	7.3E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">neuron development</a>	<a href="#">RT</a>		12	2.2E-1	7.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell morphogenesis involved in differentiation</a>	<a href="#">RT</a>		9	2.6E-1	8.3E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">neuron projection morphogenesis</a>	<a href="#">RT</a>		8	2.7E-1	8.4E-1

	Annotation Cluster	Enrichment Score			Count	P_Value	Benjamini
<input type="checkbox"/>	<b>Annotation Cluster 1</b>	<b>Enrichment Score: 22.09</b>	<b>G</b>				
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">neuron differentiation</a>	<a href="#">RT</a>		14	2.9E-1	8.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">axonogenesis</a>	<a href="#">RT</a>		7	3.4E-1	9.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cell morphogenesis involved in neuron differentiation</a>	<a href="#">RT</a>		7	4.1E-1	9.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">axon guidance</a>	<a href="#">RT</a>		4	4.9E-1	9.7E-1
<input type="checkbox"/>	<b>Annotation Cluster 99</b>	<b>Enrichment Score: 0.85</b>	<b>G</b>				
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">protein kinase C binding</a>	<a href="#">RT</a>		4	1.8E-2	1.6E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">protein kinase binding</a>	<a href="#">RT</a>		7	1.8E-1	7.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">kinase binding</a>	<a href="#">RT</a>		7	3.2E-1	8.8E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">enzyme binding</a>	<a href="#">RT</a>		16	3.8E-1	9.3E-1
<input type="checkbox"/>	<b>Annotation Cluster 100</b>	<b>Enrichment Score: 0.82</b>	<b>G</b>				
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 1	<a href="#">RT</a>		3	1.2E-1	9.0E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Armadillo-like helical</a>	<a href="#">RT</a>		6	1.5E-1	8.2E-1
<input type="checkbox"/>	SMART	<a href="#">ARM</a>	<a href="#">RT</a>		3	1.5E-1	5.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 3	<a href="#">RT</a>		3	1.5E-1	9.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 2	<a href="#">RT</a>		3	1.6E-1	9.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Armadillo</a>	<a href="#">RT</a>		3	1.9E-1	8.8E-1
<input type="checkbox"/>	<b>Annotation Cluster 101</b>	<b>Enrichment Score: 0.8</b>	<b>G</b>				
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">vesicular fraction</a>	<a href="#">RT</a>		11	1.2E-1	3.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">membrane fraction</a>	<a href="#">RT</a>		27	1.8E-1	4.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">microsome</a>	<a href="#">RT</a>		10	1.8E-1	4.7E-1
<input type="checkbox"/>	<b>Annotation Cluster 102</b>	<b>Enrichment Score: 0.75</b>	<b>G</b>				
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of cell growth</a>	<a href="#">RT</a>		6	7.7E-2	4.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of cell size</a>	<a href="#">RT</a>		6	9.8E-2	5.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of growth</a>	<a href="#">RT</a>		6	1.4E-1	6.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell growth</a>	<a href="#">RT</a>		8	2.0E-1	7.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell size</a>	<a href="#">RT</a>		8	2.5E-1	8.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of growth</a>	<a href="#">RT</a>		9	6.1E-1	9.9E-1
<input type="checkbox"/>	<b>Annotation Cluster 103</b>	<b>Enrichment Score: 0.72</b>	<b>G</b>				
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">Aminopeptidase</a>	<a href="#">RT</a>		4	1.3E-2	6.1E-2
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">aminopeptidase activity</a>	<a href="#">RT</a>		4	4.2E-2	2.9E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">exopeptidase activity</a>	<a href="#">RT</a>		5	1.4E-1	6.5E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">metalloprotease</a>	<a href="#">RT</a>		5	3.3E-1	7.3E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">Protease</a>	<a href="#">RT</a>		12	3.3E-1	7.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">metallopeptidase activity</a>	<a href="#">RT</a>		6	5.1E-1	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Peptidase M, neutral zinc metallopeptidases, zinc-binding site</a>	<a href="#">RT</a>		3	6.2E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Zinc; catalytic	<a href="#">RT</a>		3	6.9E-1	1.0E0
<input type="checkbox"/>	<b>Annotation Cluster 104</b>	<b>Enrichment Score: 0.71</b>	<b>G</b>				
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">epithelial cell differentiation</a>	<a href="#">RT</a>		7	1.2E-1	6.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">keratinocyte differentiation</a>	<a href="#">RT</a>		4	2.2E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">epidermal cell differentiation</a>	<a href="#">RT</a>		4	2.6E-1	8.3E-1
<input type="checkbox"/>	<b>Annotation Cluster 105</b>	<b>Enrichment Score: 0.71</b>	<b>G</b>				
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine nucleoside monophosphate metabolic process</a>	<a href="#">RT</a>		3	8.6E-2	5.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">purine ribonucleoside monophosphate metabolic process</a>	<a href="#">RT</a>		3	8.6E-2	5.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ribonucleoside monophosphate metabolic process</a>	<a href="#">RT</a>		3	1.3E-1	6.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">nucleoside monophosphate metabolic process</a>	<a href="#">RT</a>		3	4.9E-1	9.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Purine metabolism</a>	<a href="#">RT</a>		7	6.2E-1	9.1E-1
<input type="checkbox"/>	<b>Annotation Cluster 106</b>	<b>Enrichment Score: 0.71</b>	<b>G</b>				
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">skeletal system development</a>	<a href="#">RT</a>		13	9.8E-2	5.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ossification</a>	<a href="#">RT</a>		6	1.6E-1	6.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">bone development</a>	<a href="#">RT</a>		6	1.9E-1	7.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">skeletal system morphogenesis</a>	<a href="#">RT</a>		4	5.3E-1	9.7E-1

	Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
Annotation Cluster 1	Enrichment Score: 22.09	<b>G</b>				
Annotation Cluster 107	Enrichment Score: 0.69	<b>G</b>				
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">integrin complex</a>	<b>RT</b>		3	1.8E-1	4.7E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">receptor complex</a>	<b>RT</b>		6	2.0E-1	4.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">integrin-mediated signaling pathway</a>	<b>RT</b>		4	2.5E-1	8.2E-1
Annotation Cluster 108	Enrichment Score: 0.68	<b>G</b>				
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">wound healing</a>	<b>RT</b>		10	4.8E-2	3.4E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of body fluid levels</a>	<b>RT</b>		7	1.4E-1	6.4E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">hemostasis</a>	<b>RT</b>		5	2.8E-1	8.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">blood coagulation</a>	<b>RT</b>		4	4.6E-1	9.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">coagulation</a>	<b>RT</b>		4	4.6E-1	9.6E-1
Annotation Cluster 109	Enrichment Score: 0.66	<b>G</b>				
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">Rotamase</a>	<b>RT</b>		3	1.6E-1	4.6E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">peptidyl-prolyl cis-trans isomerase activity</a>	<b>RT</b>		3	2.5E-1	8.3E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">cis-trans isomerase activity</a>	<b>RT</b>		3	2.7E-1	8.4E-1
Annotation Cluster 110	Enrichment Score: 0.64	<b>G</b>				
<input type="checkbox"/> INTERPRO	<a href="#">Ubiquitin conserved site</a>	<b>RT</b>		3	1.7E-1	8.5E-1
<input type="checkbox"/> SMART	<a href="#">UBQ</a>	<b>RT</b>		3	2.1E-1	6.5E-1
<input type="checkbox"/> INTERPRO	<a href="#">Ubiquitin</a>	<b>RT</b>		3	2.6E-1	9.5E-1
<input type="checkbox"/> INTERPRO	<a href="#">Ubiquitin supergroup</a>	<b>RT</b>		3	3.1E-1	9.7E-1
Annotation Cluster 111	Enrichment Score: 0.62	<b>G</b>				
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular response to starvation</a>	<b>RT</b>		3	1.9E-1	7.4E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular response to extracellular stimulus</a>	<b>RT</b>		4	2.1E-1	7.7E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">response to starvation</a>	<b>RT</b>		3	2.8E-1	8.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular response to nutrient levels</a>	<b>RT</b>		3	3.0E-1	8.6E-1
Annotation Cluster 112	Enrichment Score: 0.62	<b>G</b>				
<input type="checkbox"/> UP_SEQ_FEATURE	metal ion-binding site:Magnesium	<b>RT</b>		7	2.5E-2	4.5E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">magnesium</a>	<b>RT</b>		9	6.2E-1	9.4E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">magnesium ion binding</a>	<b>RT</b>		9	9.0E-1	1.0E0
Annotation Cluster 113	Enrichment Score: 0.61	<b>G</b>				
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of synaptic plasticity</a>	<b>RT</b>		5	7.3E-2	4.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of nervous system development</a>	<b>RT</b>		9	1.0E-1	5.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of cell development</a>	<b>RT</b>		9	1.4E-1	6.4E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of neuronal synaptic plasticity</a>	<b>RT</b>		3	2.2E-1	7.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of synaptic transmission</a>	<b>RT</b>		5	4.3E-1	9.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of transmission of nerve impulse</a>	<b>RT</b>		5	4.9E-1	9.7E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of system process</a>	<b>RT</b>		9	5.0E-1	9.7E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of neurological system process</a>	<b>RT</b>		5	5.2E-1	9.7E-1
Annotation Cluster 114	Enrichment Score: 0.6	<b>G</b>				
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">epithelium development</a>	<b>RT</b>		12	2.6E-2	2.2E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">epithelial tube morphogenesis</a>	<b>RT</b>		5	8.4E-2	5.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">tissue morphogenesis</a>	<b>RT</b>		8	1.6E-1	6.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">primary neural tube formation</a>	<b>RT</b>		3	2.0E-1	7.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">tube morphogenesis</a>	<b>RT</b>		6	2.1E-1	7.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">neural tube development</a>	<b>RT</b>		4	2.4E-1	8.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">morphogenesis of an epithelium</a>	<b>RT</b>		5	2.4E-1	8.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">neural tube formation</a>	<b>RT</b>		3	2.6E-1	8.3E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">embryonic epithelial tube formation</a>	<b>RT</b>		3	2.9E-1	8.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">tube lumen formation</a>	<b>RT</b>		3	3.0E-1	8.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">morphogenesis of embryonic epithelium</a>	<b>RT</b>		3	4.2E-1	9.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">branching morphogenesis of a tube</a>	<b>RT</b>		3	4.8E-1	9.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">morphogenesis of a branching structure</a>	<b>RT</b>		3	5.5E-1	9.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">tube development</a>	<b>RT</b>		6	6.4E-1	9.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">embryonic morphogenesis</a>	<b>RT</b>		7	7.7E-1	1.0E0
Annotation Cluster 115	Enrichment Score: 0.58	<b>G</b>				

Annotation Cluster 1		Enrichment Score: 22.09	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to endogenous stimulus</a>	RT		15	1.3E-1	6.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to steroid hormone stimulus</a>	RT		7	3.4E-1	9.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to hormone stimulus</a>	RT		11	4.2E-1	9.4E-1
Annotation Cluster 116		Enrichment Score: 0.53	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">homeostasis of number of cells</a>	RT		6	1.0E-1	5.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">erythrocyte homeostasis</a>	RT		4	1.2E-1	6.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">myeloid cell differentiation</a>	RT		5	2.0E-1	7.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">erythrocyte differentiation</a>	RT		3	2.9E-1	8.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">immune system development</a>	RT		9	3.7E-1	9.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">hemopoietic or lymphoid organ development</a>	RT		8	4.6E-1	9.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">hemopoiesis</a>	RT		7	5.3E-1	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">leukocyte differentiation</a>	RT		3	8.4E-1	1.0E0
Annotation Cluster 117		Enrichment Score: 0.53	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell projection assembly</a>	RT		4	9.2E-3	1.1E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Ras Signaling Pathway</a>	RT		5	1.2E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cell projection organization</a>	RT		5	2.8E-2	2.4E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Role of MAL in Rho-Mediated Activation of SRF</a>	RT		4	5.5E-2	6.6E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Ras-Independent pathway in NK cell-mediated cytotoxicity</a>	RT		4	5.5E-2	6.6E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Agrin in Postsynaptic Differentiation</a>	RT		4	1.3E-1	8.4E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Renal cell carcinoma</a>	RT		6	1.7E-1	5.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Pancreatic cancer</a>	RT		6	1.8E-1	5.7E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">p38 MAPK Signaling Pathway</a>	RT		4	2.0E-1	9.1E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">VEGF signaling pathway</a>	RT		6	2.0E-1	6.1E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">fMLP induced chemokine gene expression in HMC-1 cells</a>	RT		3	3.3E-1	9.5E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">BCR Signaling Pathway</a>	RT		3	3.4E-1	9.5E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Links between Pyk2 and Map Kinases</a>	RT		3	3.4E-1	9.5E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling</a>	RT		3	3.6E-1	9.5E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">MAPK signaling pathway</a>	RT		13	4.4E-1	8.1E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Axon guidance</a>	RT		7	4.5E-1	8.2E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">T Cell Receptor Signaling Pathway</a>	RT		3	4.8E-1	9.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Long-term potentiation</a>	RT		4	5.4E-1	8.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">B cell receptor signaling pathway</a>	RT		4	6.1E-1	9.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">locomotory behavior</a>	RT		7	6.7E-1	9.9E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">MAPKinase Signaling Pathway</a>	RT		4	7.3E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">chemotaxis</a>	RT		4	7.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">taxis</a>	RT		4	7.6E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">GnRH signaling pathway</a>	RT		4	7.8E-1	9.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Toll-like receptor signaling pathway</a>	RT		4	8.0E-1	9.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">T cell receptor signaling pathway</a>	RT		4	8.4E-1	9.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Fc epsilon RI signaling pathway</a>	RT		3	8.4E-1	9.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Colorectal cancer</a>	RT		3	8.7E-1	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">behavior</a>	RT		9	9.0E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Chemokine signaling pathway</a>	RT		6	9.0E-1	9.9E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Natural killer cell mediated cytotoxicity</a>	RT		4	9.2E-1	9.9E-1
Annotation Cluster 118		Enrichment Score: 0.52	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">enzyme inhibitor activity</a>	RT		12	9.2E-2	5.2E-1
<input type="checkbox"/>	SMART	<a href="#">SERPIN</a>	RT		3	1.7E-1	5.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Protease inhibitor I4, serpin</a>	RT		3	2.1E-1	9.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF001630:serpin	RT		3	3.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">endopeptidase inhibitor activity</a>	RT		5	5.2E-1	9.7E-1

	Enrichment Score: 22.09	G		Count	P_Value	Benjamini
Annotation Cluster 1						
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">peptidase inhibitor activity</a>	RT		5	5.6E-1	9.8E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">serine-type endopeptidase inhibitor activity</a>	RT		3	6.9E-1	1.0E0
Annotation Cluster 119	Enrichment Score: 0.5	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of response to external stimulus</a>	RT		7	2.0E-1	7.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">negative regulation of response to external stimulus</a>	RT		3	3.5E-1	9.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">negative regulation of response to stimulus</a>	RT		4	4.5E-1	9.6E-1
Annotation Cluster 120	Enrichment Score: 0.49	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">growth factor binding</a>	RT		7	5.5E-2	3.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">transforming growth factor beta receptor signaling pathway</a>	RT		3	4.4E-1	9.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">transmembrane receptor protein serine/threonine kinase signaling pathway</a>	RT		4	4.7E-1	9.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">enzyme linked receptor protein signaling pathway</a>	RT		6	9.3E-1	1.0E0
Annotation Cluster 121	Enrichment Score: 0.49	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">fatty acid binding</a>	RT		3	2.6E-1	8.4E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">carboxylic acid binding</a>	RT		6	3.2E-1	8.9E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">monocarboxylic acid binding</a>	RT		3	4.1E-1	9.4E-1
Annotation Cluster 122	Enrichment Score: 0.49	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">microtubule cytoskeleton organization</a>	RT		7	1.6E-1	6.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">spindle organization</a>	RT		3	3.1E-1	8.7E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">M phase</a>	RT		8	7.1E-1	1.0E0
Annotation Cluster 123	Enrichment Score: 0.47	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cerebral cortex development</a>	RT		3	2.0E-1	7.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">telencephalon development</a>	RT		4	2.2E-1	7.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">pallium development</a>	RT		3	3.1E-1	8.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">neuron migration</a>	RT		3	4.7E-1	9.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">forebrain development</a>	RT		4	7.3E-1	1.0E0
Annotation Cluster 124	Enrichment Score: 0.46	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	metal ion-binding site:Magnesium	RT		7	2.5E-2	4.5E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">potassium</a>	RT		3	7.0E-1	9.7E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">potassium ion binding</a>	RT		3	8.5E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">alkali metal ion binding</a>	RT		3	9.8E-1	1.0E0
Annotation Cluster 125	Enrichment Score: 0.43	G		Count	P_Value	Benjamini
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">mitochondrion outer membrane</a>	RT		4	1.5E-1	4.6E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">mitochondrial outer membrane</a>	RT		4	4.3E-1	7.8E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">organelle outer membrane</a>	RT		4	5.3E-1	8.5E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">outer membrane</a>	RT		4	5.5E-1	8.6E-1
Annotation Cluster 126	Enrichment Score: 0.42	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">chordate embryonic development</a>	RT		12	2.0E-1	7.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">embryonic development ending in birth or egg hatching</a>	RT		12	2.1E-1	7.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">in utero embryonic development</a>	RT		5	6.4E-1	9.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">embryonic morphogenesis</a>	RT		7	7.7E-1	1.0E0
Annotation Cluster 127	Enrichment Score: 0.41	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of response to external stimulus</a>	RT		7	2.0E-1	7.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of inflammatory response</a>	RT		4	2.9E-1	8.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">G-protein coupled receptor protein signaling pathway</a>	RT		4	1.0E0	1.0E0
Annotation Cluster 128	Enrichment Score: 0.41	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">microtubule cytoskeleton</a>	RT		20	1.5E-1	4.1E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">centrosome</a>	RT		8	3.9E-1	7.5E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">microtubule organizing center</a>	RT		8	5.2E-1	8.5E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">microtubule associated complex</a>	RT		3	7.6E-1	9.6E-1
Annotation Cluster 129	Enrichment Score: 0.4	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">steroid hormone receptor binding</a>	RT		3	2.6E-1	8.4E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">hormone receptor binding</a>	RT		4	4.0E-1	9.3E-1

	Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
Annotation Cluster 1						
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">nuclear hormone receptor binding</a>	<a href="#">RT</a>		3	6.0E-1	9.9E-1
Annotation Cluster 130	Enrichment Score: 0.39	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of caspase activity</a>	<a href="#">RT</a>		4	3.1E-1	8.7E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of endopeptidase activity</a>	<a href="#">RT</a>		4	3.3E-1	8.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of peptidase activity</a>	<a href="#">RT</a>		4	3.6E-1	9.1E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">activation of caspase activity</a>	<a href="#">RT</a>		3	3.9E-1	9.3E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">positive regulation of peptidase activity</a>	<a href="#">RT</a>		3	4.3E-1	9.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">positive regulation of caspase activity</a>	<a href="#">RT</a>		3	4.3E-1	9.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">positive regulation of hydrolase activity</a>	<a href="#">RT</a>		6	4.5E-1	9.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of hydrolase activity</a>	<a href="#">RT</a>		9	6.0E-1	9.9E-1
Annotation Cluster 131	Enrichment Score: 0.38	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">cell membrane</a>	<a href="#">RT</a>		50	1.5E-1	4.6E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">plasma membrane</a>	<a href="#">RT</a>		102	5.0E-1	8.3E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">membrane</a>	<a href="#">RT</a>		101	9.9E-1	1.0E0
Annotation Cluster 132	Enrichment Score: 0.37	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">anatomical structure homeostasis</a>	<a href="#">RT</a>		5	2.7E-1	8.3E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">tissue homeostasis</a>	<a href="#">RT</a>		3	4.6E-1	9.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">multicellular organismal homeostasis</a>	<a href="#">RT</a>		3	6.2E-1	9.9E-1
Annotation Cluster 133	Enrichment Score: 0.37	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of protein localization</a>	<a href="#">RT</a>		6	2.6E-1	8.2E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of protein transport</a>	<a href="#">RT</a>		4	5.4E-1	9.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of establishment of protein localization</a>	<a href="#">RT</a>		4	5.8E-1	9.8E-1
Annotation Cluster 134	Enrichment Score: 0.36	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Pancreatic cancer</a>	<a href="#">RT</a>		6	1.8E-1	5.7E-1
<input type="checkbox"/> BIOCARTA	<a href="#">Inhibition of Cellular Proliferation by Gleevec</a>	<a href="#">RT</a>		3	2.2E-1	8.9E-1
<input type="checkbox"/> BIOCARTA	<a href="#">TPO Signaling Pathway</a>	<a href="#">RT</a>		3	2.4E-1	9.0E-1
<input type="checkbox"/> BIOCARTA	<a href="#">PDGF Signaling Pathway</a>	<a href="#">RT</a>		3	3.3E-1	9.5E-1
<input type="checkbox"/> BIOCARTA	<a href="#">EGF Signaling Pathway</a>	<a href="#">RT</a>		3	3.4E-1	9.5E-1
<input type="checkbox"/> BIOCARTA	<a href="#">MAPKinase Signaling Pathway</a>	<a href="#">RT</a>		4	7.3E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Toll-like receptor signaling pathway</a>	<a href="#">RT</a>		4	8.0E-1	9.7E-1
<input type="checkbox"/> KEGG_PATHWAY	<a href="#">Chemokine signaling pathway</a>	<a href="#">RT</a>		6	9.0E-1	9.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein amino acid phosphorylation</a>	<a href="#">RT</a>		7	1.0E0	1.0E0
Annotation Cluster 135	Enrichment Score: 0.32	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">Ras GTPase binding</a>	<a href="#">RT</a>		4	4.2E-1	9.4E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">small GTPase binding</a>	<a href="#">RT</a>		4	4.9E-1	9.7E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">GTPase binding</a>	<a href="#">RT</a>		4	5.4E-1	9.8E-1
Annotation Cluster 136	Enrichment Score: 0.3	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">heme</a>	<a href="#">RT</a>		6	8.4E-2	3.0E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">iron</a>	<a href="#">RT</a>		6	6.4E-1	9.5E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">iron ion binding</a>	<a href="#">RT</a>		7	8.1E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">heme binding</a>	<a href="#">RT</a>		3	8.2E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">tetrapyrrole binding</a>	<a href="#">RT</a>		3	8.5E-1	1.0E0
Annotation Cluster 137	Enrichment Score: 0.3	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">voltage-gated anion channel activity</a>	<a href="#">RT</a>		4	1.8E-2	1.6E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">anion transmembrane transporter activity</a>	<a href="#">RT</a>		7	1.8E-1	7.4E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">anion channel activity</a>	<a href="#">RT</a>		4	3.3E-1	8.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">chloride transport</a>	<a href="#">RT</a>		3	4.5E-1	9.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">anion transport</a>	<a href="#">RT</a>		5	4.7E-1	9.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">inorganic anion transport</a>	<a href="#">RT</a>		3	6.7E-1	9.9E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">voltage-gated ion channel activity</a>	<a href="#">RT</a>		4	8.8E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">voltage-gated channel activity</a>	<a href="#">RT</a>		4	8.8E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">gated channel activity</a>	<a href="#">RT</a>		4	9.9E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">ion channel activity</a>	<a href="#">RT</a>		4	1.0E0	1.0E0

Annotation Cluster 1		Enrichment Score: 22.09	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">substrate specific channel activity</a>	RT		4	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">channel activity</a>	RT		4	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">passive transmembrane transporter activity</a>	RT		4	1.0E0	1.0E0
Annotation Cluster 138		Enrichment Score: 0.29	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of nitric oxide biosynthetic process</a>	RT		4	1.4E-2	1.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of nitric oxide biosynthetic process</a>	RT		4	2.8E-2	2.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of macromolecule metabolic process</a>	RT		16	9.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of nitrogen compound metabolic process</a>	RT		11	9.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cellular biosynthetic process</a>	RT		11	9.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of biosynthetic process</a>	RT		11	9.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	RT		7	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of RNA metabolic process</a>	RT		4	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of macromolecule biosynthetic process</a>	RT		6	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of transcription, DNA-dependent</a>	RT		3	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of transcription</a>	RT		4	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of gene expression</a>	RT		4	1.0E0	1.0E0
Annotation Cluster 139		Enrichment Score: 0.27	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">signal</a>	RT		69	2.3E-1	6.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	signal peptide	RT		69	2.5E-1	9.9E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">Secreted</a>	RT		37	2.8E-1	6.7E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">disulfide bond</a>	RT		50	8.7E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	disulfide bond	RT		48	8.8E-1	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">glycoprotein</a>	RT		68	9.8E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		55	1.0E0	1.0E0
Annotation Cluster 140		Enrichment Score: 0.27	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of oxygen and reactive oxygen species metabolic process</a>	RT		3	2.9E-2	2.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of immune system process</a>	RT		5	1.5E-1	6.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of protein kinase activity</a>	RT		4	3.6E-1	9.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of kinase activity</a>	RT		4	3.8E-1	9.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of transferase activity</a>	RT		4	4.2E-1	9.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of MAP kinase activity</a>	RT		5	4.6E-1	9.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of signal transduction</a>	RT		7	4.7E-1	9.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of cell communication</a>	RT		7	5.8E-1	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">activation of MAPK activity</a>	RT		3	6.0E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of phosphorus metabolic process</a>	RT		12	6.6E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of phosphate metabolic process</a>	RT		12	6.6E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of kinase activity</a>	RT		9	6.6E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">MAPKKK cascade</a>	RT		5	6.7E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of transferase activity</a>	RT		9	7.0E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of MAP kinase activity</a>	RT		3	7.2E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of leukocyte activation</a>	RT		4	7.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of phosphorylation</a>	RT		10	8.2E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of kinase activity</a>	RT		5	8.3E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of transferase activity</a>	RT		5	8.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of protein kinase activity</a>	RT		7	8.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">protein kinase cascade</a>	RT		7	9.0E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of protein kinase activity</a>	RT		3	9.8E-1	1.0E0

	Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> Annotation Cluster 1						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein amino acid phosphorylation</a>	<a href="#">RT</a>		7	1.0E0	1.0E0
<input type="checkbox"/> Annotation Cluster 141						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">skeletal system morphogenesis</a>	<a href="#">RT</a>		4	5.3E-1	9.7E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cartilage development</a>	<a href="#">RT</a>		3	5.5E-1	9.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">embryonic skeletal system development</a>	<a href="#">RT</a>		3	5.7E-1	9.8E-1
<input type="checkbox"/> Annotation Cluster 142						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">meiosis I</a>	<a href="#">RT</a>		3	2.8E-1	8.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">meiosis</a>	<a href="#">RT</a>		3	7.0E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">M phase of meiotic cell cycle</a>	<a href="#">RT</a>		3	7.0E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">M phase</a>	<a href="#">RT</a>		8	7.1E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">meiotic cell cycle</a>	<a href="#">RT</a>		3	7.1E-1	1.0E0
<input type="checkbox"/> Annotation Cluster 143						
<input type="checkbox"/> SMART	<a href="#">PDZ</a>	<a href="#">RT</a>		4	5.2E-1	9.5E-1
<input type="checkbox"/> INTERPRO	<a href="#">PDZ/DHR/GLGF</a>	<a href="#">RT</a>		4	6.3E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:PDZ	<a href="#">RT</a>		3	6.3E-1	1.0E0
<input type="checkbox"/> Annotation Cluster 144						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">eye development</a>	<a href="#">RT</a>		5	4.1E-1	9.4E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">eye morphogenesis</a>	<a href="#">RT</a>		3	5.1E-1	9.7E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">camera-type eye development</a>	<a href="#">RT</a>		3	7.5E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">sensory organ development</a>	<a href="#">RT</a>		5	8.2E-1	1.0E0
<input type="checkbox"/> Annotation Cluster 145						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">nucleocytoplasmic transport</a>	<a href="#">RT</a>		5	5.4E-1	9.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">nuclear transport</a>	<a href="#">RT</a>		5	5.5E-1	9.8E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein import into nucleus</a>	<a href="#">RT</a>		3	6.3E-1	9.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein import</a>	<a href="#">RT</a>		4	6.3E-1	9.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">nuclear import</a>	<a href="#">RT</a>		3	6.4E-1	9.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein localization in nucleus</a>	<a href="#">RT</a>		3	6.8E-1	9.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein localization in organelle</a>	<a href="#">RT</a>		4	7.0E-1	1.0E0
<input type="checkbox"/> Annotation Cluster 146						
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">Golgi apparatus part</a>	<a href="#">RT</a>		9	5.3E-1	8.5E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">vesicle membrane</a>	<a href="#">RT</a>		5	5.7E-1	8.8E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">cytoplasmic vesicle membrane</a>	<a href="#">RT</a>		4	7.2E-1	9.5E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">Golgi membrane</a>	<a href="#">RT</a>		5	7.3E-1	9.5E-1
<input type="checkbox"/> Annotation Cluster 147						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">positive regulation of I-kappaB kinase/NF-kappaB cascade</a>	<a href="#">RT</a>		4	4.3E-1	9.5E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of I-kappaB kinase/NF-kappaB cascade</a>	<a href="#">RT</a>		4	4.9E-1	9.7E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">positive regulation of cell communication</a>	<a href="#">RT</a>		8	7.1E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of protein kinase cascade</a>	<a href="#">RT</a>		6	7.4E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">positive regulation of signal transduction</a>	<a href="#">RT</a>		7	7.4E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">positive regulation of protein kinase cascade</a>	<a href="#">RT</a>		4	7.8E-1	1.0E0
<input type="checkbox"/> Annotation Cluster 148						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">neuron projection morphogenesis</a>	<a href="#">RT</a>		8	2.7E-1	8.4E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">locomotory behavior</a>	<a href="#">RT</a>		7	6.7E-1	9.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of small GTPase mediated signal transduction</a>	<a href="#">RT</a>		4	9.5E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of Ras protein signal transduction</a>	<a href="#">RT</a>		3	9.7E-1	1.0E0
<input type="checkbox"/> Annotation Cluster 149						
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">neurogenesis</a>	<a href="#">RT</a>		5	3.1E-1	7.0E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">differentiation</a>	<a href="#">RT</a>		7	8.8E-1	1.0E0
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">developmental protein</a>	<a href="#">RT</a>		8	9.9E-1	1.0E0
<input type="checkbox"/> Annotation Cluster 150						
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:2	<a href="#">RT</a>		6	5.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:1	<a href="#">RT</a>		5	6.9E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:3	<a href="#">RT</a>		4	7.9E-1	1.0E0

Annotation Cluster 1		Enrichment Score: 22.09	G		Count	P_Value	Benjamini
Annotation Cluster 151		Enrichment Score: 0.16	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of macromolecule metabolic process</a>	RT		29	1.5E-2	1.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	RT		14	5.0E-1	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of nitrogen compound metabolic process</a>	RT		14	5.2E-1	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of RNA metabolic process</a>	RT		10	5.4E-1	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of biosynthetic process</a>	RT		15	5.6E-1	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of transcription</a>	RT		11	7.0E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of macromolecule biosynthetic process</a>	RT		13	7.0E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of cellular biosynthetic process</a>	RT		13	7.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of transcription, DNA-dependent</a>	RT		8	7.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of gene expression</a>	RT		11	8.0E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of transcription from RNA polymerase II promoter</a>	RT		4	9.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">transcription repressor activity</a>	RT		4	9.9E-1	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">activator</a>	RT		3	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of RNA metabolic process</a>	RT		20	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of transcription, DNA-dependent</a>	RT		18	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">transcription regulator activity</a>	RT		14	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">transcription factor activity</a>	RT		5	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of transcription</a>	RT		25	1.0E0	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">transcription regulation</a>	RT		9	1.0E0	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">Transcription</a>	RT		9	1.0E0	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">dna-binding</a>	RT		7	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">transcription</a>	RT		11	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">DNA binding</a>	RT		13	1.0E0	1.0E0
Annotation Cluster 152		Enrichment Score: 0.15	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of nucleotide metabolic process</a>	RT		4	5.5E-1	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of nucleotide biosynthetic process</a>	RT		3	7.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cyclic nucleotide biosynthetic process</a>	RT		3	7.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cyclic nucleotide metabolic process</a>	RT		3	7.7E-1	1.0E0
Annotation Cluster 153		Enrichment Score: 0.15	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	<a href="#">TPR</a>	RT		3	6.3E-1	9.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Tetratricopeptide-like helical</a>	RT		4	6.6E-1	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Tetratricopeptide repeat</a>	RT		3	7.2E-1	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Tetratricopeptide region</a>	RT		3	7.4E-1	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">tpr repeat</a>	RT		3	8.2E-1	9.9E-1
Annotation Cluster 154		Enrichment Score: 0.12	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cell activation</a>	RT		8	5.7E-1	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">T cell activation</a>	RT		3	8.2E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">leukocyte activation</a>	RT		5	8.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">lymphocyte activation</a>	RT		4	8.7E-1	1.0E0
Annotation Cluster 155		Enrichment Score: 0.1	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell activation</a>	RT		5	6.3E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">activation of immune response</a>	RT		3	6.8E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of leukocyte activation</a>	RT		3	7.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cell activation</a>	RT		3	7.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of leukocyte activation</a>	RT		4	7.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of T cell activation</a>	RT		3	7.9E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of response to stimulus</a>	RT		5	8.4E-1	1.0E0

	Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> Annotation Cluster 1						
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">positive regulation of immune response</a>	<a href="#">RT</a>		3	8.8E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">regulation of lymphocyte activation</a>	<a href="#">RT</a>		3	8.8E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">positive regulation of immune system process</a>	<a href="#">RT</a>		4	9.4E-1	1.0E0
<input type="checkbox"/> Annotation Cluster 156	Enrichment Score: 0.1	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein modification by small protein conjugation or removal</a>	<a href="#">RT</a>		4	7.6E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein ubiquitination</a>	<a href="#">RT</a>		3	8.0E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">protein modification by small protein conjugation</a>	<a href="#">RT</a>		3	8.4E-1	1.0E0
<input type="checkbox"/> Annotation Cluster 157	Enrichment Score: 0.1	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">kinetochore</a>	<a href="#">RT</a>		3	6.1E-1	9.0E-1
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell cycle phase</a>	<a href="#">RT</a>		10	7.0E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">M phase</a>	<a href="#">RT</a>		8	7.1E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">mitosis</a>	<a href="#">RT</a>		5	8.0E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">nuclear division</a>	<a href="#">RT</a>		5	8.0E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">M phase of mitotic cell cycle</a>	<a href="#">RT</a>		5	8.1E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">organelle fission</a>	<a href="#">RT</a>		5	8.2E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">chromosome, centromeric region</a>	<a href="#">RT</a>		3	8.5E-1	9.9E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">chromosomal part</a>	<a href="#">RT</a>		5	9.9E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">chromosome</a>	<a href="#">RT</a>		5	1.0E0	1.0E0
<input type="checkbox"/> Annotation Cluster 158	Enrichment Score: 0.08	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">di-, tri-valent inorganic cation homeostasis</a>	<a href="#">RT</a>		6	7.1E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cation homeostasis</a>	<a href="#">RT</a>		7	7.1E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular cation homeostasis</a>	<a href="#">RT</a>		6	7.6E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular di-, tri-valent inorganic cation homeostasis</a>	<a href="#">RT</a>		5	8.2E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular ion homeostasis</a>	<a href="#">RT</a>		8	8.2E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular chemical homeostasis</a>	<a href="#">RT</a>		8	8.3E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular calcium ion homeostasis</a>	<a href="#">RT</a>		4	8.3E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">calcium ion homeostasis</a>	<a href="#">RT</a>		4	8.5E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cellular metal ion homeostasis</a>	<a href="#">RT</a>		4	8.7E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">ion homeostasis</a>	<a href="#">RT</a>		8	8.8E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">metal ion homeostasis</a>	<a href="#">RT</a>		4	8.9E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">chemical homeostasis</a>	<a href="#">RT</a>		8	9.7E-1	1.0E0
<input type="checkbox"/> Annotation Cluster 159	Enrichment Score: 0.07	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">Ras GTPase activator activity</a>	<a href="#">RT</a>		3	6.9E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">enzyme activator activity</a>	<a href="#">RT</a>		8	7.7E-1	1.0E0
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">GTPase activation</a>	<a href="#">RT</a>		3	8.1E-1	9.9E-1
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">GTPase activator activity</a>	<a href="#">RT</a>		5	8.3E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">small GTPase regulator activity</a>	<a href="#">RT</a>		5	9.3E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">nucleoside-triphosphatase regulator activity</a>	<a href="#">RT</a>		7	9.6E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_FAT	<a href="#">GTPase regulator activity</a>	<a href="#">RT</a>		6	9.8E-1	1.0E0
<input type="checkbox"/> Annotation Cluster 160	Enrichment Score: 0.05	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cyclic-nucleotide-mediated signaling</a>	<a href="#">RT</a>		3	8.3E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">second-messenger-mediated signaling</a>	<a href="#">RT</a>		5	8.4E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">G-protein coupled receptor protein signaling pathway</a>	<a href="#">RT</a>		4	1.0E0	1.0E0
<input type="checkbox"/> Annotation Cluster 161	Enrichment Score: 0.05	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">synaptic transmission</a>	<a href="#">RT</a>		7	7.5E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">transmission of nerve impulse</a>	<a href="#">RT</a>		7	8.7E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">cell-cell signaling</a>	<a href="#">RT</a>		10	9.6E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	<a href="#">neurological system process</a>	<a href="#">RT</a>		15	1.0E0	1.0E0
<input type="checkbox"/> Annotation Cluster 162	Enrichment Score: 0.05	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/> SP_PIR_KEYWORDS	<a href="#">lysosome</a>	<a href="#">RT</a>		3	7.8E-1	9.9E-1
<input type="checkbox"/> GOTERM_CC_FAT	<a href="#">lytic vacuole</a>	<a href="#">RT</a>		4	9.2E-1	1.0E0

	Annotation Cluster	Enrichment Score			Count	P_Value	Benjamini
<input type="checkbox"/>	Annotation Cluster 1	Enrichment Score: 22.09	<b>G</b>				
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">lysosome</a>	<a href="#">RT</a>		4	9.2E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">vacuole</a>	<a href="#">RT</a>		4	9.7E-1	1.0E0
<input type="checkbox"/>	Annotation Cluster 163	Enrichment Score: 0.04	<b>G</b>				
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH3	<a href="#">RT</a>		3	8.6E-1	1.0E0
<input type="checkbox"/>	SMART	<a href="#">SH3</a>	<a href="#">RT</a>		3	9.1E-1	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">sh3 domain</a>	<a href="#">RT</a>		3	9.1E-1	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Src homology-3 domain</a>	<a href="#">RT</a>		3	9.5E-1	1.0E0
<input type="checkbox"/>	Annotation Cluster 164	Enrichment Score: 0.04	<b>G</b>				
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">transmembrane protein</a>	<a href="#">RT</a>		14	4.6E-1	8.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">intrinsic to plasma membrane</a>	<a href="#">RT</a>		15	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">integral to plasma membrane</a>	<a href="#">RT</a>		14	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain:Cytoplasmic	<a href="#">RT</a>		19	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain:Extracellular	<a href="#">RT</a>		11	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	transmembrane region	<a href="#">RT</a>		31	1.0E0	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">transmembrane</a>	<a href="#">RT</a>		31	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">integral to membrane</a>	<a href="#">RT</a>		40	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">intrinsic to membrane</a>	<a href="#">RT</a>		50	1.0E0	1.0E0
<input type="checkbox"/>	Annotation Cluster 165	Enrichment Score: 0.03	<b>G</b>				
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">calcium ion transport</a>	<a href="#">RT</a>		3	8.7E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">di-, tri-valent inorganic cation transport</a>	<a href="#">RT</a>		3	9.3E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">metal ion transport</a>	<a href="#">RT</a>		5	1.0E0	1.0E0
<input type="checkbox"/>	Annotation Cluster 166	Enrichment Score: 0.01	<b>G</b>				
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 5	<a href="#">RT</a>		3	9.4E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 4	<a href="#">RT</a>		3	9.6E-1	1.0E0
<input type="checkbox"/>	SMART	<a href="#">WD40</a>	<a href="#">RT</a>		3	9.6E-1	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">WD40 repeat 2</a>	<a href="#">RT</a>		3	9.6E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 3	<a href="#">RT</a>		3	9.7E-1	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">WD40 repeat, region</a>	<a href="#">RT</a>		3	9.7E-1	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">WD40 repeat, subgroup</a>	<a href="#">RT</a>		3	9.7E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 2	<a href="#">RT</a>		3	9.7E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 1	<a href="#">RT</a>		3	9.7E-1	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">wd repeat</a>	<a href="#">RT</a>		3	9.7E-1	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">WD40 repeat</a>	<a href="#">RT</a>		3	9.8E-1	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">WD40 repeat, conserved site</a>	<a href="#">RT</a>		3	9.8E-1	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">WD40/YVTN repeat-like</a>	<a href="#">RT</a>		3	9.9E-1	1.0E0
<input type="checkbox"/>	Annotation Cluster 167	Enrichment Score: 0.01	<b>G</b>				
<input type="checkbox"/>	INTERPRO	<a href="#">Immunoglobulin</a>	<a href="#">RT</a>		3	9.4E-1	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">Immunoglobulin domain</a>	<a href="#">RT</a>		3	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Immunoglobulin-like</a>	<a href="#">RT</a>		3	1.0E0	1.0E0
<input type="checkbox"/>	Annotation Cluster 168	Enrichment Score: 0.01	<b>G</b>				
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">DNA metabolic process</a>	<a href="#">RT</a>		8	9.7E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">DNA repair</a>	<a href="#">RT</a>		4	9.7E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to DNA damage stimulus</a>	<a href="#">RT</a>		4	1.0E0	1.0E0
<input type="checkbox"/>	Annotation Cluster 169	Enrichment Score: 0.01	<b>G</b>				
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">transcription, DNA-dependent</a>	<a href="#">RT</a>		4	9.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">RNA biosynthetic process</a>	<a href="#">RT</a>		4	9.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">transcription</a>	<a href="#">RT</a>		11	1.0E0	1.0E0
<input type="checkbox"/>	Annotation Cluster 170	Enrichment Score: 0.01	<b>G</b>				
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">visual perception</a>	<a href="#">RT</a>		3	9.7E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">sensory perception of light stimulus</a>	<a href="#">RT</a>		3	9.7E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cognition</a>	<a href="#">RT</a>		6	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">sensory perception</a>	<a href="#">RT</a>		4	1.0E0	1.0E0
<input type="checkbox"/>	Annotation Cluster 171	Enrichment Score: 0	<b>G</b>				
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">male gamete generation</a>	<a href="#">RT</a>		4	9.8E-1	1.0E0

Annotation Cluster 1		Enrichment Score: 22.09	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">spermatogenesis</a>	<a href="#">RT</a>		4	9.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">gamete generation</a>	<a href="#">RT</a>		5	9.9E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">sexual reproduction</a>	<a href="#">RT</a>		6	9.9E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">reproductive process in a multicellular organism</a>	<a href="#">RT</a>		6	9.9E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">multicellular organism reproduction</a>	<a href="#">RT</a>		6	9.9E-1	1.0E0
Annotation Cluster 172		Enrichment Score: 0	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">metal-binding</a>	<a href="#">RT</a>		40	1.0E0	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">zinc</a>	<a href="#">RT</a>		15	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">transition metal ion binding</a>	<a href="#">RT</a>		32	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">zinc ion binding</a>	<a href="#">RT</a>		18	1.0E0	1.0E0

419 terms were not clustered.

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