Category	Annotation Cluster 1	Enrichment Score: 7.984500598278341				
	Category	Term	Count	%	PValue	Proteins
mitochondria	GOTERM_CC_FAT	GO:0005739-mitochondrion	52	21.31	7.00236E-12	P54071, Q60597, Q9DB10, Q9R1Z7, Q9CQV7, Q99L43, Q8BH59, Q9DCW4, Q8BWF0, P97450, Q9CPW2, P84091, Q9CQ85, Q66GT5, P56382, Q8CC88, Q05920, Q9ERS2, P47802, P56375, O35683, P52196, Q9ESW4, Q4KMM3, P19096, Q80Y14, Q9CZU6, Q9QUH0, Q791T5, Q9CPP6, Q924L1, P28271, P97493, Q9CQX8, Q8BIJ6, Q91V92, Q9D051, Q9D8S9, Q9D8T7, P19246, Q9D1L0, Q9JKL4, P58059, Q9D0L7, Q9WVL0, P26638, Q9CQ69, Q9EQ80, P05063, P58281, Q9CZD3, P03893
mitochondria	GOTERM_CC_FAT	GO:0044429-mitochondrial part	28	11.48	4.0111E-09	Q791T5, Q9CPP6, P54071, Q60597, Q9CQX8, Q8BIJ6, Q9D051, Q9CQV7, Q8BH59, Q99L43, Q9DCW4, Q9JKL4, P58059, P97450, Q9CPW2, Q9CQ85, Q66GT5, Q9CQ69, P56382, Q05920, P58281, Q9ERS2, P47802, O35683, P52196, Q9ESW4, Q9CZU6, P03893
mitochondria	GOTERM_CC_FAT	GO:0031967-organelle envelope	28	11.48	7.62946E-09	Q791T5, Q9CPP6, P54071, P21619, Q60597, Q8BKC5, Q9CQV7, Q8BH59, Q99L43, Q9JKL4, P58059, P97450, Q07076, Q9CQ85, Q66GT5, Q9CQ69, P56382, Q91YE6, Q05920, P58281, Q9ERS2, P47802, O35683, P52196, Q9ESW4, Q9ERU9, Q9CXW3, P03893
mitochondria	SP_PIR_KEYWORDS	mitochondrion	34	13.93	7.87809E-09	Q791T5, Q9CPP6, P54071, P97493, Q60597, Q9DB10, Q9CQX8, Q8BIJ6, Q9D051, Q9CQV7, Q8BH59, Q99L43, Q9D8T7, Q9DCW4, Q9D1L0, Q8BWF0, Q9JKL4, P58059, P97450, Q9CPW2, Q9CQ85, Q66GT5, P56382, Q9CQ69, Q05920, P58281, Q9ERS2, P47802, O35683, P52196, Q9ESW4, Q4KMM3, Q9CZU6, P03893
mitochondria	GOTERM_CC_FAT	GO:0031975-envelope	28	11.48	8.25312E-09	Q791T5, Q9CPP6, P54071, P21619, Q60597, Q8BKC5, Q9CQV7, Q8BH59, Q99L43, Q9JKL4, P58059, P97450, Q07076, Q9CQ85, Q66GT5, Q9CQ69, P56382, Q91YE6, Q05920, P58281, Q9ERS2, P47802, O35683, P52196, Q9ESW4, Q9ERU9, Q9CXW3, P03893
mitochondria	GOTERM_CC_FAT	GO:0019866-organelle inner membrane	21	8.61	1.39463E-08	Q791T5, Q9CPP6, P97450, P54071, P21619, Q9CQ85, Q66GT5, P56382, Q9CQ69, Q05920, Q9CQV7, Q8BH59, Q99L43, P58281, Q9ERS2, P47802, O35683, P52196, Q9JKL4, P03893, P58059
mitochondria	GOTERM_CC_FAT	GO:0031090-organelle membrane	34	13.93	2.12705E-08	Q791T5, Q9CPP6, P54071, P21619, Q60597, Q9CR95, Q9CQV7, Q99L43, Q8BH59, P17047, Q8K3H0, Q9JKL4, P58059, Q810B6, Q811D0, P97450, Q9Z2I2, O08585, Q9CQ85, O35609, Q66GT5, P56382, Q9CQ69, Q9JKD3, Q05920, P58281, Q62277, Q9ERS2, P47802, O35683, Q6NVE8, P52196, Q9ESW4, P03893
mitochondria	GOTERM_CC_FAT	GO:0005743-mitochondrial inner membrane	20	8.20	3.21884E-08	Q791T5, Q9CPP6, P97450, P54071, Q9CQ85, Q66GT5, P56382, Q9CQ69, Q05920, Q9CQV7, Q8BH59, Q99L43, P58281, Q9ERS2, P47802, O35683, P52196, Q9JKL4, P03893, P58059
mitochondria	GOTERM_CC_FAT	GO:0031966-mitochondrial membrane	22	9.02	4.48598E-08	Q791T5, Q9CPP6, P97450, P54071, Q9CQ85, Q66GT5, Q60597, P56382, Q9CQ69, Q05920, Q9CQV7, Q8BH59, Q99L43, P58281, Q9ERS2, P47802, O35683, P52196, Q9ESW4, Q9JKL4, P03893, P58059
mitochondria	GOTERM_CC_FAT	GO:0005740-mitochondrial envelope	22	9.02	1.25771E-07	Q791T5, Q9CPP6, P97450, P54071, Q9CQ85, Q66GT5, Q60597, P56382, Q9CQ69, Q05920, Q9CQV7, Q8BH59, Q99L43, P58281, Q9ERS2, P47802, O35683, P52196, Q9ESW4, Q9JKL4, P03893, P58059
mitochondria	SP_PIR_KEYWORDS	mitochondrion inner membrane	15	6.15	1.97278E-07	Q791T5, Q9CPP6, P97450, Q9CQ85, Q66GT5, Q9CQ69, P56382, Q9CQV7, Q8BH59, Q99L43, P58281, Q9ERS2, O35683, Q9JKL4, P03893
	Annotation Cluster 2	Enrichment Score: 5.76289866237697				
	Category	Term	Count	%	PValue	Genes
Transcription	GOTERM_BP_FAT	GO:0006418-tRNA aminoacylation for protein translation	10	4.10	8.58779E-09	Q9CZD3, P32921, Q61035, Q8BLY2, Q3U0V1, P26638, Q8BIJ6, Q8BGQ7, Q8BU30, Q9D0R2
Transcription	GOTERM_BP_FAT	GO:0043039-tRNA aminoacylation	10	4.10	8.58779E-09	Q9CZD3, P32921, Q61035, Q8BLY2, Q3U0V1, P26638, Q8BIJ6, Q8BGQ7, Q8BU30, Q9D0R2
Transcription	GOTERM_BP_FAT	GO:0043038-amino acid activation	10	4.10	8.58779E-09	Q9CZD3, P32921, Q61035, Q8BLY2, Q3U0V1, P26638, Q8BIJ6, Q8BGQ7, Q8BU30, Q9D0R2
Transcription	GOTERM_MF_FAT	GO:0004812-aminoacyl-tRNA ligase activity	10	4.10	1.04631E-08	Q9CZD3, P32921, Q61035, Q8BLY2, Q3U0V1, P26638, Q8BIJ6, Q8BGQ7, Q8BU30, Q9D0R2
Transcription	GOTERM_MF_FAT	GO:0016875-ligase activity, forming carbon-oxygen bonds	10	4.10	1.04631E-08	Q9CZD3, P32921, Q61035, Q8BLY2, Q3U0V1, P26638, Q8BIJ6, Q8BGQ7, Q8BU30, Q9D0R2
Transcription	GOTERM_MF_FAT	GO:0016876-ligase activity, forming aminoacyl-tRNA and related compounds	10	4.10	1.04631E-08	Q9CZD3, P32921, Q61035, Q8BLY2, Q3U0V1, P26638, Q8BIJ6, Q8BGQ7, Q8BU30, Q9D0R2
Transcription	SP_PIR_KEYWORDS	Aminoacyl-tRNA synthetase	9	3.69	4.20788E-08	Q9CZD3, P32921, Q61035, Q8BLY2, P26638, Q8BIJ6, Q8BGQ7, Q8BU30, Q9D0R2
Transcription	KEGG_PATHWAY	mmu00970:Aminoacyl-tRNA biosynthesis	9	3.69	4.29753E-07	Q9CZD3, P32921, Q61035, Q8BLY2, P26638, Q8BIJ6, Q8BGQ7, Q8BU30, Q9D0R2
Transcription	INTERPRO	IPR002314:Aminoacyl-tRNA synthetase, class II (G, H, P and S), conserved region	5	2.05	8.70783E-06	Q9CZD3, Q61035, Q8BLY2, P26638, Q9D0R2
Transcription	SP_PIR_KEYWORDS	protein biosynthesis	11	4.51	1.93808E-05	Q9CZD3, P32921, Q61035, Q8BLY2, P26638, Q8BIJ6, P14115, P23116, Q8BGQ7, Q8BU30, Q9D0R2
Transcription	GOTERM_BP_FAT	GO:0006399-tRNA metabolic process	10	4.10	2.14637E-05	Q9CZD3, P32921, Q61035, Q8BLY2, Q3U0V1, P26638, Q8BIJ6, Q8BGQ7, Q8BU30, Q9D0R2
Transcription	GOTERM_BP_FAT	GO:0006412-translation	16	6.56	2.73732E-05	P32921, Q61035, Q9CPR4, P26638, Q8BIJ6, Q8BGQ7, P23116, P14115, P14206, Q9CZD3, Q8BLY2, Q3U0V1, Q8BU30, Q9D8E6, Q9D0R2, P58059
Transcription	INTERPRO	IPR006195:Aminoacyl-tRNA synthetase, class II, conserved region	5	2.05	5.90434E-05	Q9CZD3, Q61035, Q8BLY2, P26638, Q9D0R2
Transcription	INTERPRO	IPR004154:Anticodon-binding	4	1.64	0.00017432	Q9CZD3, Q61035, Q8BLY2, Q9D0R2
Transcription	GOTERM_BP_FAT	GO:0034660-ncRNA metabolic process	11	4.51	0.000410825	Q9CZD3, P32921, Q61035, Q8BLY2, Q3U0V1, P26638, Q8BIJ6, Q8BGQ7, Q8BU30, Q9D0R2, Q923D5
Transcription	INTERPRO	IPR001412:Aminoacyl-tRNA synthetase, class I, conserved site	5	2.05	0.000966728	P32921, P17047, Q3U0V1, Q8BIJ6, Q8BU30
Transcription	SP_PIR_KEYWORDS	ligase	12	4.92	0.002018475	Q9CZD3, P32921, Q61035, Q8BLY2, P26638, Q8BIJ6, Q8BGQ7, Q8BU30, Q05920, Q64737, Q3U487, Q9D0R2
	Annotation Cluster 3	Enrichment Score: 4.4598344410174295				
	Category	Term	Count	%	PValue	Genes
mitochondria	SP_PIR_KEYWORDS	mitochondrion	34	13.93	7.87809E-09	Q791T5, Q9CPP6, P54071, P97493, Q60597, Q9DB10, Q9CQX8, Q8BIJ6, Q9D051, Q9CQV7, Q8BH59, Q99L43, Q9D8T7, Q9DCW4, Q9D1L0, Q8BWF0, Q9JKL4, P58059, P97450, Q9CPW2, Q9CQ85, Q66GT5, P56382, Q9CQ69, Q05920, P58281, Q9ERS2, P47802, O35683, P52196, Q9ESW4, Q4KMM3, Q9CZU6, P03893

mitochondria	SP_PIR_KEYWORDS	transit peptide	16	6.56	0.001442618	P54071, P97450, Q9CPW2, P97493, Q9DB10, Q60597, Q66GT5, Q8BIJ6, Q05920, Q9D051, P58281, Q9D8T7, Q9D1L0, Q9ESW4, Q8BWF0, Q9CZU6
mitochondria	UP_SEQ_FEATURE	transit peptide:Mitochondrion	16	6.56	0.003672184	P54071, P97450, Q9CPW2, P97493, Q9DB10, Q60597, Q66GT5, Q8BIJ6, Q05920, Q9D051, P58281, Q9D8T7, Q9D1L0, Q9ESW4, Q8BWF0, Q9CZU6
	Annotation Cluster 4	Enrichment Score: 4.143337264351797				
	Category	Term	Count	%	PValue	Genes
mitochondria	GOTERM_BP_FAT	GO:0006091-generation of precursor metabolites and energy	22	9.02	4.83949E-11	Q9CPP6, P97450, P54071, P05201, Q9CPW2, P28271, P97493, Q60597, P56382, Q9CQ69, P06745, Q9D051, Q8BH59, P05063, Q9ERS2, Q9DCW4, Q8C0L0, O35683, Q8BWF0, Q9CZU6, Q9QUH0, P03893
mitochondria	GOTERM_BP_FAT	GO:0022900-electron transport chain	12	4.92	3.15522E-07	Q9CPP6, Q9ERS2, Q9DCW4, Q8C0L0, Q9CPW2, O35683, P97493, Q9CQ69, Q8BWF0, Q8BH59, P03893, Q9QUH0
mitochondria	SP_PIR_KEYWORDS	electron transport	10	4.10	8.38447E-06	Q9CPP6, Q9ERS2, Q9DCW4, Q8C0L0, Q9CPW2, O35683, P97493, Q9CQ69, P03893, Q9QUH0
mitochondria	GOTERM_BP_FAT	GO:0055114-oxidation reduction	19	7.79	0.004214331	Q9CPP6, P54071, Q9CPW2, P97493, Q60597, Q9CQ69, Q9D051, O88712, Q8BH59, Q9CY27, Q9ERS2, Q9DCW4, Q8C0L0, O35683, Q00612, Q8BWF0, P19096, Q9QUH0, P03893
mitochondria	SP_PIR_KEYWORDS	respiratory chain	5	2.05	0.009799168	Q9CPP6, Q9ERS2, O35683, Q9CQ69, P03893
mitochondria	GOTERM_CC_FAT	GO:0070469-respiratory chain	5	2.05	0.012940514	Q9CPP6, Q9ERS2, O35683, Q9CQ69, P03893
mitochondria	GOTERM_MF_FAT	GO:0016651-oxidoreductase activity, acting on NADH or NADPH	3	1.23	0.145032146	Q9CPP6, Q9ERS2, P03893
	Annotation Cluster 5	Enrichment Score: 3.529247705841288				
	Category	Term	Count	%	PValue	Genes
cytoskeleton	GOTERM_BP_FAT	GO:0030036-actin cytoskeleton organization	11	4.51	7.89061E-05	Q811D0, P70336, Q3UHD9, Q9Z2H5, P08556, Q0GNC1, Q9JL26, Q3UH68, P63001, Q8BPM0, Q03173
cytoskeleton	GOTERM_BP_FAT	GO:0030029-actin filament-based process	11	4.51	0.000135133	Q811D0, P70336, Q3UHD9, Q9Z2H5, P08556, Q0GNC1, Q9JL26, Q3UH68, P63001, Q8BPM0, Q03173
cytoskeleton	GOTERM_BP_FAT	GO:0007010-cytoskeleton organization	14	5.74	0.000472138	P70336, Q811D0, Q9Z2H5, P08556, Q3UU96, Q3UH68, P63001, Q03173, P54227, Q3UHD9, Q0GNC1, P19246, Q9JL26, Q8BPM0
cytoskeleton	GOTERM_MF_FAT	GO:0003779-actin binding	12	4.92	0.001517286	Q9CQI3, Q7TMB8, Q9QYB5, Q9Z2H5, Q3V0K9, Q0GNC1, Q9JL26, Q9CPW4, Q3UH68, Q8BPM0, Q9JKK7, Q03173
	Annotation Cluster 6	Enrichment Score: 3.174013563079447				
	Category	Term	Count	%	PValue	Genes
	INTERPRO	IPR001023:Heat shock protein Hsp70	4	1.64	0.00033585	P48722, Q9JKR6, Q61699, Q61316
	INTERPRO	IPR013126:Heat shock protein 70	4	1.64	0.00033585	P48722, Q9JKR6, Q61699, Q61316
	INTERPRO	IPR018181:Heat shock protein 70, conserved site	4	1.64	0.000570994	P48722, Q9JKR6, Q61699, Q61316
	SP_PIR_KEYWORDS	stress response	5	2.05	0.003126243	P54071, P48722, Q9JKR6, Q61699, Q61316
	Annotation Cluster 7	Enrichment Score: 3.12038267063547				
	Category	Term	Count	%	PValue	Genes
cytoskeleton	SP_PIR_KEYWORDS	microtubule	12	4.92	0.000214824	P54227, P28740, Q9ERD7, Q9QXL2, Q6A065, P39054, P27546, Q8BRT1, O08788, Q80U49, P62627, Q8C1B1
cytoskeleton	SP_PIR_KEYWORDS	cytoskeleton	20	8.20	0.00037062	P28740, Q9Z2H5, Q9QWI6, Q6A065, Q9CPW4, Q8R5J9, P39054, Q80U49, P23116, O08788, Q03173, Q6PDI5, Q61301, Q91VR8, Q9QYB5, P19246, Q8CHH9, Q8BRT1, Q9JKK7, Q9JMH9
cytoskeleton	GOTERM_CC_FAT	GO:0005856-cytoskeleton	31	12.70	0.000401775	Q9Z2H5, P21619, P23116, O08788, Q03173, Q6PDI5, Q9QXL2, P19246, Q8CHH9, Q9JMH9, Q811D0, P70336, P28740, Q9QWI6, Q6A065, Q9CPW4, Q8R5J9, P39054, Q6PFD5, Q80U49, P62627, Q4ACU6, Q61301, P54227, Q91VR8, Q9QYB5, Q9ERD7, P27546, Q8BRT1, Q9JKK7, Q8C1B1
cytoskeleton	GOTERM_CC_FAT	GO:0044430-cytoskeletal part	24	9.84	0.000493992	Q811D0, P70336, P28740, P21619, Q6A065, Q9CPW4, P39054, Q6PFD5, Q80U49, P62627, P23116, O08788, Q03173, Q4ACU6, Q6PDI5, P54227, Q9ERD7, Q9QXL2, P19246, Q8CHH9, Q8BRT1, P27546, Q9JMH9, Q8C1B1
cytoskeleton	GOTERM_CC_FAT	GO:0005874-microtubule	12	4.92	0.00055506	P54227, P28740, Q9ERD7, Q9QXL2, Q6A065, P39054, P27546, Q8BRT1, O08788, Q80U49, P62627, Q8C1B1
cytoskeleton	GOTERM_CC_FAT	GO:0043228-non-membrane-bounded organelle	43	17.62	0.001692811	Q9Z2H5, P21619, Q9CPR4, O54962, Q9CQX8, O08788, P23116, Q03173, Q6PDI5, Q923D5, P14206, Q60668, Q9QXL2, P19246, Q8CHH9, Q9D8E6, Q9JMH9, P58059, Q811D0, P70336, P28740, P10922, Q9QWI6, Q6A065, Q9CPW4, P39054, Q8R5J9, Q6PFD5, Q8BTY2, Q80U49, P62627, P14115, Q4ACU6, Q61301, P54227, Q91VR8, Q9QYB5, Q9ERD7, Q8BRT1, P27546, Q4KMM3, Q9JKK7, Q8C1B1
cytoskeleton	GOTERM_CC_FAT	GO:0043232-intracellular non-membrane-bounded organelle	43	17.62	0.001692811	Q9Z2H5, P21619, Q9CPR4, O54962, Q9CQX8, O08788, P23116, Q03173, Q6PDI5, Q923D5, P14206, Q60668, Q9QXL2, P19246, Q8CHH9, Q9D8E6, Q9JMH9, P58059, Q811D0, P70336, P28740, P10922, Q9QWI6, Q6A065, Q9CPW4, P39054, Q8R5J9, Q6PFD5, Q8BTY2, Q80U49, P62627, P14115, Q4ACU6, Q61301, P54227, Q91VR8, Q9QYB5, Q9ERD7, Q8BRT1, P27546, Q4KMM3, Q9JKK7, Q8C1B1
cytoskeleton	GOTERM_CC_FAT	GO:0015630-microtubule cytoskeleton	15	6.15	0.004331794	P70336, P28740, Q6A065, P39054, Q80U49, P23116, O08788, P62627, Q6PDI5, P54227, Q9ERD7, Q9QXL2, P27546, Q8BRT1, Q8C1B1
	Annotation Cluster 8	Enrichment Score: 2.559623030917132				
	Category	Term	Count	%	PValue	Genes
cytoskeleton	GOTERM_MF_FAT	GO:0008092-cytoskeletal protein binding	15	6.15	0.0011633	Q9CQI3, Q9Z2H5, Q3V0K9, Q9CPW4, Q3UH68, Q03173, P54227, Q9QYB5, Q7TMB8, Q58A65, Q0GNC1, Q9JL26, Q8BRT1, Q8BPM0, Q9JKK7
cytoskeleton	GOTERM_MF_FAT	GO:0003779-actin binding	12	4.92	0.001517286	Q9CQI3, Q7TMB8, Q9QYB5, Q9Z2H5, Q3V0K9, Q0GNC1, Q9JL26, Q9CPW4, Q3UH68, Q8BPM0, Q9JKK7, Q03173
cytoskeleton	SP_PIR_KEYWORDS	actin-binding	9	3.69	0.011867841	Q7TMB8, Q9QYB5, Q9Z2H5, Q3V0K9, Q0GNC1, Q9CPW4, Q8BPM0, Q9JKK7, Q03173

	Annotation Cluster 9	Enrichment Score: 2.361678413877474				
	Category	Term	Count	%	PValue	Genes
nucleus	GOTERM_MF_FAT	GO:0000166-nucleotide binding	49	20.08	0.000151795	P54071, P32921, Q64737, Q60668, P59708, Q80ZJ1, Q9JKR6, Q8CHH9, Q9Z130, Q8BU30, Q9JMH9, P70336, Q99020, P63001, O35609, Q8CC88, Q05920, Q9ERS2, Q3UHD9, P54775, P12367, Q9ESW4, P36536, Q9D0R2, Q5F2E8, Q8BIJ6, Q8BGR6, Q91V92, Q61316, Q9D8T7, Q9QXL2, Q8BLY2, Q8K310, O70161, P28740, P48722, Q61035, P08556, Q3UU96, P39054, P26638, Q8BGQ7, O88712, P58281, Q5XJV6, Q9CZD3, Q9ERD7, Q3U0V1, Q61699
nucleus	GOTERM_MF_FAT	GO:0032555-purine ribonucleotide binding	41	16.80	0.000492838	P32921, Q5F2E8, Q8BIJ6, Q91V92, Q8BGR6, Q64737, Q61316, Q9QXL2, Q80ZJ1, Q8BLY2, Q9JKR6, Q8CHH9, Q8BU30, O70161, Q9JMH9, P70336, P28740, Q61035, P48722, P08556, Q3UU96, P26638, P39054, O35609, P63001, Q8CC88, Q8BGQ7, Q05920, P58281, Q9CZD3, Q5XJV6, Q3UHD9, Q9ERS2, P54775, P12367, Q9ERD7, Q3U0V1, Q9ESW4, P36536, Q61699, Q9D0R2
nucleus	GOTERM_MF_FAT	GO:0032553-ribonucleotide binding	41	16.80	0.000492838	P32921, Q5F2E8, Q8BIJ6, Q91V92, Q8BGR6, Q64737, Q61316, Q9QXL2, Q80ZJ1, Q8BLY2, Q9JKR6, Q8CHH9, Q8BU30, O70161, Q9JMH9, P70336, P28740, Q61035, P48722, P08556, Q3UU96, P26638, P39054, O35609, P63001, Q8CC88, Q8BGQ7, Q05920, P58281, Q9CZD3, Q5XJV6, Q3UHD9, Q9ERS2, P54775, P12367, Q9ERD7, Q3U0V1, Q9ESW4, P36536, Q61699, Q9D0R2
nucleus	GOTERM_MF_FAT	GO:0017076-purine nucleotide binding	41	16.80	0.001110125	P32921, Q5F2E8, Q8BIJ6, Q91V92, Q8BGR6, Q64737, Q61316, Q9QXL2, Q80ZJ1, Q8BLY2, Q9JKR6, Q8CHH9, Q8BU30, O70161, Q9JMH9, P70336, P28740, Q61035, P48722, P08556, Q3UU96, P26638, P39054, O35609, P63001, Q8CC88, Q8BGQ7, Q05920, P58281, Q9CZD3, Q5XJV6, Q3UHD9, Q9ERS2, P54775, P12367, Q9ERD7, Q3U0V1, Q9ESW4, P36536, Q61699, Q9D0R2
nucleus	SP_PIR_KEYWORDS	nucleotide-binding	38	15.57	0.001195881	P32921, Q5F2E8, Q8BIJ6, Q91V92, Q8BGR6, Q64737, Q61316, Q80ZJ1, Q9QXL2, Q8BLY2, Q9JKR6, Q8CHH9, Q8BU30, O70161, Q9JMH9, P70336, P28740, Q61035, P48722, P08556, Q3UU96, P26638, P39054, P63001, Q8CC88, Q8BGQ7, Q05920, P58281, Q9CZD3, Q5XJV6, Q3UHD9, P54775, P12367, Q9ERD7, Q9ESW4, P36536, Q61699, Q9D0R2
nucleus	GOTERM_MF_FAT	GO:0032559-adenyl ribonucleotide binding	32	13.11	0.004884217	P32921, Q5F2E8, Q8BIJ6, Q91V92, Q64737, Q61316, Q9QXL2, Q8BLY2, Q9JKR6, Q8BU30, O70161, Q9JMH9, P70336, P28740, Q61035, P48722, Q3UU96, P26638, O35609, Q8CC88, Q8BGQ7, Q05920, Q9CZD3, Q5XJV6, Q3UHD9, Q9ERS2, P54775, P12367, Q3U0V1, Q9ESW4, Q61699, Q9D0R2
nucleus	GOTERM_MF_FAT	GO:0005524-ATP binding	31	12.70	0.007579659	P32921, Q5F2E8, Q8BIJ6, Q91V92, Q64737, Q61316, Q9QXL2, Q8BLY2, Q9JKR6, Q8BU30, O70161, Q9JMH9, P70336, P28740, Q61035, P48722, Q3UU96, P26638, O35609, Q8CC88, Q8BGQ7, Q05920, Q9CZD3, Q5XJV6, Q3UHD9, Q9ERS2, P54775, Q3U0V1, Q9ESW4, Q61699, Q9D0R2
nucleus	GOTERM_MF_FAT	GO:0030554-adenyl nucleotide binding	32	13.11	0.009943467	P32921, Q5F2E8, Q8BIJ6, Q91V92, Q64737, Q61316, Q9QXL2, Q8BLY2, Q9JKR6, Q8BU30, O70161, Q9JMH9, P70336, P28740, Q61035, P48722, Q3UU96, P26638, O35609, Q8CC88, Q8BGQ7, Q05920, Q9CZD3, Q5XJV6, Q3UHD9, Q9ERS2, P54775, P12367, Q3U0V1, Q9ESW4, Q61699, Q9D0R2
nucleus	GOTERM_MF_FAT	GO:0001883-purine nucleoside binding	32	13.11	0.011156858	P32921, Q5F2E8, Q8BIJ6, Q91V92, Q64737, Q61316, Q9QXL2, Q8BLY2, Q9JKR6, Q8BU30, O70161, Q9JMH9, P70336, P28740, Q61035, P48722, Q3UU96, P26638, O35609, Q8CC88, Q8BGQ7, Q05920, Q9CZD3, Q5XJV6, Q3UHD9, Q9ERS2, P54775, P12367, Q3U0V1, Q9ESW4, Q61699, Q9D0R2
nucleus	GOTERM_MF_FAT	GO:0001882-nucleoside binding	32	13.11	0.012171139	P32921, Q5F2E8, Q8BIJ6, Q91V92, Q64737, Q61316, Q9QXL2, Q8BLY2, Q9JKR6, Q8BU30, O70161, Q9JMH9, P70336, P28740, Q61035, P48722, Q3UU96, P26638, O35609, Q8CC88, Q8BGQ7, Q05920, Q9CZD3, Q5XJV6, Q3UHD9, Q9ERS2, P54775, P12367, Q3U0V1, Q9ESW4, Q61699, Q9D0R2
nucleus	SP_PIR_KEYWORDS	atp-binding	27	11.07	0.025655606	P32921, Q5F2E8, Q8BIJ6, Q91V92, Q64737, Q61316, Q9QXL2, Q8BLY2, Q9JKR6, O70161, Q8BU30, Q9JMH9, P70336, P28740, Q61035, P48722, Q3UU96, P26638, Q8CC88, Q8BGQ7, Q05920, Q5XJV6, Q9CZD3, P54775, Q9ESW4, Q61699, Q9D0R2
nucleus	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	13	5.33	0.727943076	P70336, P28740, Q3UU96, Q5F2E8, P26638, Q8CC88, Q91V92, Q64737, Q5XJV6, Q9CZD3, P54775, Q9QXL2, Q9JMH9
	Annotation Cluster 10	Enrichment Score: 2.3084847897649343				
	Category	Term	Count	%	PValue	Genes
?	GOTERM_MF_FAT	GO:0019899-enzyme binding	12	4.92	0.000226292	Q811D0, Q8BVQ5, Q7TMB8, Q3UHD9, Q9D5V5, Q58A65, Q8QZZ7, Q0GNC1, Q9JL26, Q8BMI3, Q8BPM0, Q91YE6
?	GOTERM_MF_FAT	GO:0031267-small GTPase binding	6	2.46	0.001054313	Q7TMB8, Q0GNC1, Q9JL26, Q8BMI3, Q8BPM0, Q91YE6
?	GOTERM_MF_FAT	GO:0051020-GTPase binding	6	2.46	0.001320235	Q7TMB8, Q0GNC1, Q9JL26, Q8BMI3, Q8BPM0, Q91YE6
?	GOTERM_MF_FAT	GO:0017048-Rho GTPase binding	4	1.64	0.003707759	Q7TMB8, Q0GNC1, Q9JL26, Q8BPM0
?	INTERPRO	IPR010472:Diaphanous FH3	3	1.23	0.005755969	Q0GNC1, Q9JL26, Q8BPM0
?	INTERPRO	IPR010473:Diaphanous GTPase-binding	3	1.23	0.005755969	Q0GNC1, Q9JL26, Q8BPM0
?	GOTERM_MF_FAT	GO:0017016-Ras GTPase binding	5	2.05	0.00667251	Q7TMB8, Q0GNC1, Q9JL26, Q8BPM0, Q91YE6
?	SMART	SM00498:FH2	3	1.23	0.008095074	Q0GNC1, Q9JL26, Q8BPM0
?	INTERPRO	IPR014768:GTPase-binding/formin homology 3	3	1.23	0.008643849	Q0GNC1, Q9JL26, Q8BPM0
?	UP_SEQ_FEATURE	domain:GBD/FH3	3	1.23	0.011513986	Q0GNC1, Q9JL26, Q8BPM0
?	INTERPRO	IPR003104:Actin-binding FH2 and DRF autoregulatory	3	1.23	0.013938269	Q0GNC1, Q9JL26, Q8BPM0
?	INTERPRO	IPR015425:Actin-binding FH2	3	1.23	0.015945537	Q0GNC1, Q9JL26, Q8BPM0
?	UP_SEQ_FEATURE	domain:FH2	3	1.23	0.021123641	Q0GNC1, Q9JL26, Q8BPM0
	Annotation Cluster 11	Enrichment Score: 2.2614695977784343				
	Category	Term	Count	%	PValue	Genes
vescicle	GOTERM_BP_FAT	GO:0016192-vesicle-mediated transport	20	8.20	1.71788E-05	Q810B6, O54774, Q6PAR5, Q9QWI6, P08556, P84091, O08585, P63001, P39054, Q9CQW1, Q9JKD3, Q9CR95, Q62277, Q9CZD3, Q3UHD9, Q3UPL0, Q60902, Q8BMI3, P84086, P36536
vescicle	GOTERM_BP_FAT	GO:0016044-membrane organization	10	4.10	0.011470941	Q62277, Q810B6, Q811D0, Q6PAR5, P08556, Q60902, P63001, P39054, Q9CR95, P58281
vescicle	GOTERM_BP_FAT	GO:0010324-membrane invagination	8	3.28	0.013808932	Q62277, Q810B6, Q6PAR5, P08556, Q60902, P63001, P39054, Q9CR95
vescicle	GOTERM_BP_FAT	GO:0006897-endocytosis	8	3.28	0.013808932	Q62277, Q810B6, Q6PAR5, P08556, Q60902, P63001, P39054, Q9CR95

vescicle	SP_PIR_KEYWORDS	Endocytosis	4	1.64	0.131141263	Q6PAR5, Q60902, P39054, Q9CR95
	Annotation Cluster 12	Enrichment Score: 2.1497048119978475				
	Category	Term	Count	%	PValue	Genes
mitochondria	KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	7	2.87	1.1765E-05	P54071, P28271, Q60597, Q91V92, Q05920, Q9CZU6, Q9D051
mitochondria	GOTERM_BP_FAT	GO:0045333-cellular respiration	7	2.87	0.000137001	Q9CPP6, P54071, P28271, Q8BWF0, Q9CZU6, Q8BH59, P03893
mitochondria	GOTERM_BP_FAT	GO:0015980-energy derivation by oxidation of organic compounds	8	3.28	0.000353351	Q9CPP6, P54071, P05201, P28271, Q8BWF0, Q9CZU6, Q8BH59, P03893
mitochondria	GOTERM_BP_FAT	GO:0022904-respiratory electron transport chain	4	1.64	0.006145474	Q9CPP6, Q8BWF0, Q8BH59, P03893
mitochondria	GOTERM_BP_FAT	GO:0006084-acetyl-CoA metabolic process	4	1.64	0.008187358	P54071, P28271, Q91V92, Q9CZU6
mitochondria	GOTERM_BP_FAT	GO:0006732-coenzyme metabolic process	7	2.87	0.012868992	Q9CQ60, P54071, P28271, Q00612, Q8BWF0, Q91V92, Q9CZU6
mitochondria	SP_PIR_KEYWORDS	tricarboxylic acid cycle	3	1.23	0.026678973	P54071, P28271, Q9CZU6
mitochondria	GOTERM_BP_FAT	GO:0051186-cofactor metabolic process	7	2.87	0.036662093	Q9CQ60, P54071, P28271, Q00612, Q8BWF0, Q91V92, Q9CZU6
mitochondria	GOTERM_BP_FAT	GO:0006099-tricarboxylic acid cycle	3	1.23	0.03792115	P54071, P28271, Q9CZU6
mitochondria	GOTERM_BP_FAT	GO:0046356-acetyl-CoA catabolic process	3	1.23	0.041009496	P54071, P28271, Q9CZU6
mitochondria	GOTERM_BP_FAT	GO:0009060-aerobic respiration	3	1.23	0.050810278	P54071, P28271, Q9CZU6
mitochondria	GOTERM_BP_FAT	GO:0009109-coenzyme catabolic process	3	1.23	0.057761477	P54071, P28271, Q9CZU6
mitochondria	GOTERM_BP_FAT	GO:0051187-cofactor catabolic process	3	1.23	0.068758818	P54071, P28271, Q9CZU6
	Annotation Cluster 13	Enrichment Score: 2.019674351083093				
	Category	Term	Count	%	PValue	Genes
	INTERPRO	IPR001412:Aminoacyl-tRNA synthetase, class I, conserved site	5	2.05	0.000966728	P32921, P17047, Q3U0V1, Q8BIJ6, Q8BU30
	INTERPRO	IPR014729:Rossmann-like alpha/beta/alpha sandwich fold	4	1.64	0.015230699	P32921, Q9DCW4, Q8BIJ6, Q8BU30
	UP_SEQ_FEATURE	short sequence motif:"KMSKS" region	3	1.23	0.021123641	P32921, Q8BIJ6, Q8BU30
	UP_SEQ_FEATURE	short sequence motif:"HIGH" region	3	1.23	0.026823141	P32921, Q8BIJ6, Q8BU30
	Annotation Cluster 14	Enrichment Score: 1.9459507548476633				
	Category	Term	Count	%	PValue	Genes
transport	SP_PIR_KEYWORDS	transport	42	17.21	3.09961E-05	Q9CPP6, Q791T5, P97441, O54774, Q9D1C8, P97493, Q8BKC5, Q8BY89, Q9CR95, Q9CQV7, Q8BH59, Q9DCW4, P63080, P61971, Q9EPR4, Q8JZR6, P97450, Q9CPW2, P84091, P54285, Q9CQ85, Q9CQW1, O35609, P56382, Q9CQ69, Q8BTY2, Q91YE6, Q9JKD3, P61620, Q9DCP2, Q9ERS2, Q8C0L0, P47802, O35683, Q3UPL0, Q3U0V1, Q8BMI3, P84086, P36536, Q9ERU9, Q9QUH0, P03893
transport	SP_PIR_KEYWORDS	protein transport	18	7.38	0.000183925	O54774, Q9D1C8, P84091, Q9CQ85, O35609, Q9CQW1, Q91YE6, Q9JKD3, Q8BKC5, P61620, Q9CR95, Q9CQV7, P47802, Q3UPL0, Q8BMI3, Q9ERU9, P36536, P61971
transport	GOTERM_BP_FAT	GO:0046907-intracellular transport	17	6.97	0.000239885	O54774, Q9Z2I2, P84091, O08585, O35609, Q9CQW1, Q91YE6, Q8BKC5, P61620, Q03173, Q8BH59, Q3UHD9, P47802, Q8BMI3, Q9ERU9, P36536, P61971
transport	GOTERM_BP_FAT	GO:0015031-protein transport	20	8.20	0.001252975	O54774, Q9D1C8, P84091, O08585, Q9CQ85, O35609, Q9CQW1, Q91YE6, Q9JKD3, Q8BKC5, P61620, Q9CR95, Q9CQV7, P50396, P47802, Q3UPL0, Q8BMI3, Q9ERU9, P36536, P61971
transport	GOTERM_BP_FAT	GO:0045184-establishment of protein localization	20	8.20	0.001369251	O54774, Q9D1C8, P84091, O08585, Q9CQ85, O35609, Q9CQW1, Q91YE6, Q9JKD3, Q8BKC5, P61620, Q9CR95, Q9CQV7, P50396, P47802, Q3UPL0, Q8BMI3, Q9ERU9, P36536, P61971
transport	GOTERM_MF_FAT	GO:0008565-protein transporter activity	6	2.46	0.001747965	O54774, Q9CQ85, Q91YE6, Q8BKC5, P61971, P61620
transport	GOTERM_BP_FAT	GO:0008104-protein localization	21	8.61	0.002842801	Q811D0, O54774, Q9D1C8, P84091, O08585, Q9CQ85, O35609, Q9CQW1, Q91YE6, Q9JKD3, Q8BKC5, P61620, Q9CR95, Q9CQV7, P50396, P47802, Q3UPL0, Q8BMI3, Q9ERU9, P36536, P61971
transport	GOTERM_BP_FAT	GO:0006886-intracellular protein transport	11	4.51	0.004229125	O54774, P47802, P84091, O08585, O35609, Q8BMI3, Q91YE6, Q8BKC5, P61971, P36536, P61620
transport	GOTERM_BP_FAT	GO:0034613-cellular protein localization	11	4.51	0.007363292	O54774, P47802, P84091, O08585, O35609, Q8BMI3, Q91YE6, Q8BKC5, P61971, P36536, P61620
transport	GOTERM_BP_FAT	GO:0070727-cellular macromolecule localization	11	4.51	0.007674998	O54774, P47802, P84091, O08585, O35609, Q8BMI3, Q91YE6, Q8BKC5, P61971, P36536, P61620
transport	GOTERM_BP_FAT	GO:0017038-protein import	4	1.64	0.098672146	P47802, Q91YE6, Q8BKC5, P61971
transport	GOTERM_BP_FAT	GO:0033365-protein localization in organelle	4	1.64	0.142674735	P47802, Q91YE6, Q8BKC5, P61971
transport	GOTERM_BP_FAT	GO:0006606-protein import into nucleus	3	1.23	0.174053675	Q91YE6, Q8BKC5, P61971
transport	GOTERM_BP_FAT	GO:0051170-nuclear import	3	1.23	0.183722534	Q91YE6, Q8BKC5, P61971
transport	GOTERM_BP_FAT	GO:0034504-protein localization in nucleus	3	1.23	0.198365303	Q91YE6, Q8BKC5, P61971
transport	GOTERM_BP_FAT	GO:0006605-protein targeting	4	1.64	0.266345259	P47802, Q91YE6, Q8BKC5, P61971
transport	GOTERM_BP_FAT	GO:0006913-nucleocytoplasmic transport	3	1.23	0.371717581	Q91YE6, Q8BKC5, P61971
transport	GOTERM_BP_FAT	GO:0051169-nuclear transport	3	1.23	0.381346352	Q91YE6, Q8BKC5, P61971
	Annotation Cluster 15	Enrichment Score: 1.8048666178879997				
	Category	Term	Count	%	PValue	Genes
metabolism	GOTERM_BP_FAT	GO:0006006-glucose metabolic process	8	3.28	0.002863061	Q9CQ60, Q60597, Q00612, P06745, Q8BWF0, Q05920, Q9D051, P05063

metabolism	GOTERM_BP_FAT	GO:0019320-hexose catabolic process	5	2.05	0.005208823	Q9CQ60, Q60597, P06745, Q9D051, P05063
metabolism	GOTERM_BP_FAT	GO:0006007-glucose catabolic process	5	2.05	0.005208823	Q9CQ60, Q60597, P06745, Q9D051, P05063
metabolism	GOTERM_BP_FAT	GO:0046365-monosaccharide catabolic process	5	2.05	0.005959671	Q9CQ60, Q60597, P06745, Q9D051, P05063
metabolism	GOTERM_BP_FAT	GO:0019318-hexose metabolic process	8	3.28	0.007952654	Q9CQ60, Q60597, Q00612, P06745, Q8BWF0, Q05920, Q9D051, P05063
metabolism	GOTERM_BP_FAT	GO:0044275-cellular carbohydrate catabolic process	5	2.05	0.008635188	Q9CQ60, Q60597, P06745, Q9D051, P05063
metabolism	KEGG_PATHWAY	mmu00030:Pentose phosphate pathway	4	1.64	0.009713434	Q9CQ60, Q00612, P06745, P05063
metabolism	GOTERM_BP_FAT	GO:0046164-alcohol catabolic process	5	2.05	0.011385105	Q9CQ60, Q60597, P06745, Q9D051, P05063
metabolism	GOTERM_BP_FAT	GO:0005996-monosaccharide metabolic process	8	3.28	0.014790091	Q9CQ60, Q60597, Q00612, P06745, Q8BWF0, Q05920, Q9D051, P05063
metabolism	SP_PIR_KEYWORDS	glycolysis	4	1.64	0.018937662	Q60597, P06745, Q9D051, P05063
metabolism	GOTERM_BP_FAT	GO:0006096-glycolysis	4	1.64	0.021246031	Q60597, P06745, Q9D051, P05063
metabolism	SP_PIR_KEYWORDS	gluconeogenesis	3	1.23	0.021595623	P06745, Q05920, P05063
metabolism	GOTERM_BP_FAT	GO:0016052-carbohydrate catabolic process	5	2.05	0.023730749	Q9CQ60, Q60597, P06745, Q9D051, P05063
metabolism	UP_SEQ_FEATURE	binding site:Substrate	7	2.87	0.23994563	Q9CZD3, P54071, P52196, Q00612, Q8BWF0, Q05920, P05063
metabolism	KEGG_PATHWAY	mmu00010:Glycolysis / Gluconeogenesis	3	1.23	0.328556443	P06745, Q9D051, P05063
neuron	Annotation Cluster 16	Enrichment Score: 1.7607233191133849				
neuron	Category	Term	Count	%	PValue	Genes
neuron	SP_PIR_KEYWORDS	synapse	11	4.51	0.000653926	Q62277, P97441, Q811D0, Q7TMB8, Q80U40, P39054, Q6PFD5, P63080, Q9JKD3, Q03173, Q4ACU6
neuron	SP_PIR_KEYWORDS	cell junction	14	5.74	0.002681595	P97441, Q811D0, Q8BIW1, P39054, Q6PFD5, Q9JKD3, Q03173, Q61301, Q4ACU6, Q62277, Q7TMB8, Q80U40, P63080, O70161
neuron	GOTERM_CC_FAT	GO:0045202-synapse	12	4.92	0.005268321	Q62277, P97441, Q811D0, Q7TMB8, Q80U40, P39054, Q6PFD5, P63080, P84086, Q9JKD3, Q03173, Q4ACU6
neuron	GOTERM_CC_FAT	GO:0030054-cell junction	15	6.15	0.006310061	P97441, Q811D0, Q8BIW1, P39054, Q6PFD5, Q9JKD3, Q03173, Q61301, Q4ACU6, Q62277, Q9QYB5, Q7TMB8, Q80U40, P63080, O70161
neuron	GOTERM_CC_FAT	GO:0014069-postsynaptic density	4	1.64	0.03438038	Q811D0, P39054, Q6PFD5, Q4ACU6
neuron	SP_PIR_KEYWORDS	postsynaptic cell membrane	5	2.05	0.061898307	Q811D0, P39054, Q6PFD5, P63080, Q4ACU6
neuron	GOTERM_CC_FAT	GO:0044456-synapse part	7	2.87	0.077504403	Q62277, Q811D0, P39054, Q6PFD5, P63080, Q9JKD3, Q4ACU6
neuron	GOTERM_CC_FAT	GO:0045211-postsynaptic membrane	5	2.05	0.10054284	Q811D0, P39054, Q6PFD5, P63080, Q4ACU6
	GOTERM_CC_FAT	GO:0044459-plasma membrane part	29	11.89	0.147297655	O54774, P97441, Q640R3, Q03173, Q80ZJ1, P63080, O70161, Q9EPR4, Q811D0, Q8BIW1, P08556, P84091, O08585, P54285, P63001, P39054, Q9CQW1, Q6PFD5, Q8BTY2, Q9JKD3, Q4ACU6, Q61301, Q9DCP2, Q62277, Q9QYB5, Q7TMB8, Q80U40, Q3UPL0, O88653
	Annotation Cluster 17	Enrichment Score: 1.6437148860724222				
	Category	Term	Count	%	PValue	Genes
vescicle	GOTERM_BP_FAT	GO:0033043-regulation of organelle organization	9	3.69	0.001139755	P54227, Q811D0, P70336, Q9CPW4, P63001, P27546, Q8BRT1, Q3U487, Q7TSC1
cytoskeleton	GOTERM_BP_FAT	GO:0051493-regulation of cytoskeleton organization	7	2.87	0.00218769	P54227, Q811D0, P70336, Q9CPW4, P63001, P27546, Q8BRT1
vescicle	GOTERM_BP_FAT	GO:0010638-positive regulation of organelle organization	4	1.64	0.032806223	Q811D0, P70336, P63001, Q7TSC1
vescicle	GOTERM_BP_FAT	GO:0051130-positive regulation of cellular component organization	4	1.64	0.226748912	Q811D0, P70336, P63001, Q7TSC1
	GOTERM_BP_FAT	GO:0051726-regulation of cell cycle	5	2.05	0.325931904	Q811D0, P70336, P08556, Q3U487, Q7TSC1
	Annotation Cluster 18	Enrichment Score: 1.5702384614450258				
	Category	Term	Count	%	PValue	Genes
	INTERPRO	IPR011989:Armadillo-like helical	8	3.28	0.001607437	O54774, P98203, Q9D0L7, Q148V7, Q8BRT1, Q91YE6, Q8BKC5, Q6PDI5
	UP_SEQ_FEATURE	repeat:HEAT 3	4	1.64	0.024057444	Q148V7, Q8BRT1, Q8BKC5, Q6PDI5
	INTERPRO	IPR000357:HEAT	4	1.64	0.024718434	Q148V7, Q8BRT1, Q8BKC5, Q6PDI5
	UP_SEQ_FEATURE	repeat:HEAT 1	4	1.64	0.036153008	Q148V7, Q8BRT1, Q8BKC5, Q6PDI5
	UP_SEQ_FEATURE	repeat:HEAT 2	4	1.64	0.036153008	Q148V7, Q8BRT1, Q8BKC5, Q6PDI5
	UP_SEQ_FEATURE	repeat:HEAT 5	3	1.23	0.075517389	Q8BRT1, Q8BKC5, Q6PDI5
	UP_SEQ_FEATURE	repeat:HEAT 4	3	1.23	0.108041453	Q8BRT1, Q8BKC5, Q6PDI5
	Annotation Cluster 19	Enrichment Score: 1.5317195433539386				
	Category	Term	Count	%	PValue	Genes
vescicle	GOTERM_CC_FAT	GO:0030117-membrane coat	5	2.05	0.008741949	O54774, P84091, O08585, Q8BMI3, Q9CR95
vescicle	GOTERM_CC_FAT	GO:0048475-coated membrane	5	2.05	0.008741949	O54774, P84091, O08585, Q8BMI3, Q9CR95
vescicle	GOTERM_CC_FAT	GO:0005905-coated pit	4	1.64	0.009922536	Q60902, P84091, O08585, Q9CR95
vescicle	GOTERM_CC_FAT	GO:0030118-clathrin coat	4	1.64	0.011730014	P84091, O08585, Q8BMI3, Q9CR95
vescicle	GOTERM_CC_FAT	GO:0044431-Golgi apparatus part	6	2.46	0.214649849	O54774, O08585, O35609, Q8BMI3, Q9JKD3, Q8CDG3

vescicle	KEGG_PATHWAY	mmu04142:Lysosome	4	1.64	0.337920379	O54774, P17047, O08585, Q8BMI3
	Annotation Cluster 20	Enrichment Score: 1.4929887354234659				
	Category	Term	Count	%	PValue	Genes
?	SMART	SM00233:PH	11	4.51	0.000234219	Q8K394, P70336, Q3UHD9, Q5DU25, Q3UU96, P39054, Q8R4H2, Q8K3H0, Q7SIG6, Q3TES0, Q9QWY8
?	UP_SEQ_FEATURE	domain:PH	11	4.51	0.0010517	Q8K394, P70336, Q3UHD9, Q5DU25, Q3UU96, P39054, Q8R4H2, Q8K3H0, Q7SIG6, Q3TES0, Q9QWY8
?	GOTERM_BP_FAT	GO:0032012-regulation of ARF protein signal transduction	5	2.05	0.001643336	Q3UHD9, Q5DU25, Q7SIG6, Q3TES0, Q9QWY8
?	INTERPRO	IPR001849:Pleckstrin homology	11	4.51	0.002341219	Q8K394, P70336, Q3UHD9, Q5DU25, Q3UU96, P39054, Q8R4H2, Q8K3H0, Q7SIG6, Q3TES0, Q9QWY8
?	SP_PIR_KEYWORDS	GTPase activation	8	3.28	0.002502672	Q6PAR5, Q3UHD9, P50396, Q8R4H2, Q5SSM3, Q7SIG6, Q80UJ7, Q9QWY8
?	KEGG_PATHWAY	mmu04144:Endocytosis	10	4.10	0.007763966	Q3UHD9, Q9D1C8, Q5DU25, P84091, O08585, P39054, O70161, Q7SIG6, Q3TES0, Q9QWY8
?	GOTERM_MF_FAT	GO:0005083-small GTPase regulator activity	9	3.69	0.009435403	Q3UHD9, P50396, Q5DU25, Q3UU96, Q8R4H2, Q7SIG6, Q3TES0, Q80UJ7, Q9QWY8
?	GOTERM_MF_FAT	GO:0005096-GTPase activator activity	8	3.28	0.013640736	Q6PAR5, Q3UHD9, P50396, Q8R4H2, Q5SSM3, Q7SIG6, Q80UJ7, Q9QWY8
?	GOTERM_MF_FAT	GO:0008047-enzyme activator activity	9	3.69	0.017428527	Q6PAR5, Q3UHD9, P50396, O88653, Q8R4H2, Q5SSM3, Q7SIG6, Q80UJ7, Q9QWY8
cytoskeleton	SMART	SM00326:SH3	7	2.87	0.017693808	Q811D0, Q80U40, P54285, Q6P9K8, Q4ACU6, Q7SIG6, Q9QWY8
?	SMART	SM00105:ArfGap	3	1.23	0.021251929	Q3UHD9, Q7SIG6, Q9QWY8
?	GOTERM_MF_FAT	GO:0030695-GTPase regulator activity	11	4.51	0.021285012	Q6PAR5, Q3UHD9, P50396, Q5DU25, Q3UU96, Q8R4H2, Q5SSM3, Q7SIG6, Q3TES0, Q80UJ7, Q9QWY8
cytoskeleton	SMART	SM00248:ANK	7	2.87	0.02255775	Q810B6, Q3UHD9, Q6P9K8, Q4ACU6, Q7SIG6, Q9DBR7, Q9QWY8
?	GOTERM_MF_FAT	GO:0060589-nucleoside-triphosphatase regulator activity	11	4.51	0.023532628	Q6PAR5, Q3UHD9, P50396, Q5DU25, Q3UU96, Q8R4H2, Q5SSM3, Q7SIG6, Q3TES0, Q80UJ7, Q9QWY8
?	GOTERM_BP_FAT	GO:0051056-regulation of small GTPase mediated signal transduction	8	3.28	0.03495363	Q6PAR5, Q3UHD9, P08556, Q5DU25, Q8R4H2, Q7SIG6, Q3TES0, Q9QWY8
?	GOTERM_BP_FAT	GO:0046578-regulation of Ras protein signal transduction	7	2.87	0.035840007	Q3UHD9, P08556, Q5DU25, Q8R4H2, Q7SIG6, Q3TES0, Q9QWY8
?	INTERPRO	IPR001164:Arf GTPase activating protein	3	1.23	0.035890214	Q3UHD9, Q7SIG6, Q9QWY8
?	GOTERM_MF_FAT	GO:0008060-ARF GTPase activator activity	3	1.23	0.036403669	Q3UHD9, Q7SIG6, Q9QWY8
?	INTERPRO	IPR011993:Pleckstrin homology-type	9	3.69	0.036499024	P70336, Q9Z2H5, P39054, Q8R4H2, Q9ERU9, Q8K3H0, Q03173, Q7SIG6, Q9QWY8
?	GOTERM_BP_FAT	GO:0032312-regulation of ARF GTPase activity	3	1.23	0.03792115	Q3UHD9, Q7SIG6, Q9QWY8
?	UP_SEQ_FEATURE	domain:Arf-GAP	3	1.23	0.039814296	Q3UHD9, Q7SIG6, Q9QWY8
cytoskeleton	SP_PIR_KEYWORDS	sh3 domain	7	2.87	0.058815594	Q811D0, Q80U40, P54285, Q6P9K8, Q4ACU6, Q7SIG6, Q9QWY8
cytoskeleton	INTERPRO	IPR001452:Src homology-3 domain	7	2.87	0.058937003	Q811D0, Q80U40, P54285, Q6P9K8, Q4ACU6, Q7SIG6, Q9QWY8
cytoskeleton	UP_SEQ_FEATURE	repeat:ANK 1	7	2.87	0.071302013	Q810B6, Q3UHD9, Q6P9K8, Q4ACU6, Q7SIG6, Q9DBR7, Q9QWY8
cytoskeleton	UP_SEQ_FEATURE	repeat:ANK 2	7	2.87	0.071302013	Q810B6, Q3UHD9, Q6P9K8, Q4ACU6, Q7SIG6, Q9DBR7, Q9QWY8
cytoskeleton	INTERPRO	IPR002110:Ankyrin	7	2.87	0.072740926	Q810B6, Q3UHD9, Q6P9K8, Q4ACU6, Q7SIG6, Q9DBR7, Q9QWY8
cytoskeleton	SP_PIR_KEYWORDS	ank repeat	7	2.87	0.080962301	Q810B6, Q3UHD9, Q6P9K8, Q4ACU6, Q7SIG6, Q9DBR7, Q9QWY8
cytoskeleton	UP_SEQ_FEATURE	domain:SH3	6	2.46	0.102724546	Q811D0, P54285, Q6P9K8, Q4ACU6, Q7SIG6, Q9QWY8
cytoskeleton	UP_SEQ_FEATURE	repeat:ANK 6	4	1.64	0.115078564	Q810B6, Q6P9K8, Q4ACU6, Q9DBR7
?	GOTERM_BP_FAT	GO:0043087-regulation of GTPase activity	4	1.64	0.130360779	Q3UHD9, P50396, Q7SIG6, Q9QWY8
cytoskeleton	UP_SEQ_FEATURE	repeat:ANK 5	4	1.64	0.221481614	Q810B6, Q6P9K8, Q4ACU6, Q9DBR7
?	GOTERM_BP_FAT	GO:0051336-regulation of hydrolase activity	5	2.05	0.273944968	Q791T5, Q3UHD9, P50396, Q7SIG6, Q9QWY8
?	GOTERM_BP_FAT	GO:0032318-regulation of Ras GTPase activity	3	1.23	0.292952292	Q3UHD9, Q7SIG6, Q9QWY8
cytoskeleton	UP_SEQ_FEATURE	repeat:ANK 4	4	1.64	0.298978557	Q810B6, Q6P9K8, Q4ACU6, Q9DBR7
?	GOTERM_MF_FAT	GO:0005085-guanyl-nucleotide exchange factor activity	4	1.64	0.305755858	Q6PAR5, Q5DU25, Q8R4H2, Q3TES0
cytoskeleton	UP_SEQ_FEATURE	repeat:ANK 3	4	1.64	0.434669975	Q810B6, Q6P9K8, Q4ACU6, Q9DBR7
	Annotation Cluster 21	Enrichment Score: 1.4753414628725434				
	Category	Term	Count	%	PValue	Genes
protein modif	GOTERM_BP_FAT	GO:0006457-protein folding	7	2.87	0.0074196	P48722, Q9Z2I2, Q62446, Q8BGQ7, Q9ERU9, Q61699, Q9D832
protein modif	GOTERM_MF_FAT	GO:0016859-cis-trans isomerase activity	4	1.64	0.012564676	Q9Z2I2, Q9WVL0, Q62446, Q9ERU9
protein modif	SP_PIR_KEYWORDS	Isomerase	5	2.05	0.075870622	Q9Z2I2, Q9WVL0, P06745, Q62446, Q9ERU9
protein modif	SP_PIR_KEYWORDS	Rotamase	3	1.23	0.076788184	Q9Z2I2, Q62446, Q9ERU9
protein modif	GOTERM_MF_FAT	GO:0003755-peptidyl-prolyl cis-trans isomerase activity	3	1.23	0.077337984	Q9Z2I2, Q62446, Q9ERU9
	Annotation Cluster 22	Enrichment Score: 1.464689888398678				
	Category	Term	Count	%	PValue	Genes
cytoskeleton	GOTERM_CC_FAT	GO:0015630-microtubule cytoskeleton	15	6.15	0.004331794	P70336, P28740, Q6A065, P39054, Q80U49, P23116, O08788, P62627, Q6PDI5, P54227, Q9ERD7, Q9QXL2, P27546, Q8BRT1, Q8C1B1
cytoskeleton	GOTERM_CC_FAT	GO:0005813-centrosome	6	2.46	0.073898982	P70336, P28740, Q6A065, Q8BRT1, P23116, Q6PDI5

cytoskeleton	GOTERM_CC_FAT	GO:0005815-microtubule organizing center	6	2.46	0.126073592	P70336, P28740, Q6A065, Q8BRT1, P23116, Q6PDI5
	Annotation Cluster 23	Enrichment Score: 1.4003148956402045				
	Category	Term	Count	%	PValue	Genes
cytoskeleton	GOTERM_BP_FAT	GO:0051493-regulation of cytoskeleton organization	7	2.87	0.00218769	P54227, Q811D0, P70336, Q9CPW4, P63001, P27546, Q8BRT1
cytoskeleton	GOTERM_BP_FAT	GO:0070507-regulation of microtubule cytoskeleton organization	4	1.64	0.01238342	P54227, P70336, P27546, Q8BRT1
cytoskeleton	GOTERM_BP_FAT	GO:0031111-negative regulation of microtubule polymerization or depolymerization	3	1.23	0.019123264	P54227, P27546, Q8BRT1
cytoskeleton	GOTERM_BP_FAT	GO:0032886-regulation of microtubule-based process	4	1.64	0.022543367	P54227, P70336, P27546, Q8BRT1
cytoskeleton	GOTERM_BP_FAT	GO:0031110-regulation of microtubule polymerization or depolymerization	3	1.23	0.054246032	P54227, P27546, Q8BRT1
cytoskeleton	GOTERM_BP_FAT	GO:0051494-negative regulation of cytoskeleton organization	3	1.23	0.136378358	P54227, P27546, Q8BRT1
cytoskeleton	GOTERM_BP_FAT	GO:0010639-negative regulation of organelle organization	3	1.23	0.203277994	P54227, P27546, Q8BRT1
cytoskeleton	GOTERM_BP_FAT	GO:0051129-negative regulation of cellular component organization	3	1.23	0.357165788	P54227, P27546, Q8BRT1
	Annotation Cluster 24	Enrichment Score: 1.3644929386492004				
	Category	Term	Count	%	PValue	Genes
metabolism	GOTERM_BP_FAT	GO:0046165-alcohol biosynthetic process	4	1.64	0.013344974	P05201, Q00612, P06745, Q05920
metabolism	GOTERM_BP_FAT	GO:0034637-cellular carbohydrate biosynthetic process	4	1.64	0.039589674	P05201, Q00612, P06745, Q05920
metabolism	GOTERM_BP_FAT	GO:0046364-monosaccharide biosynthetic process	3	1.23	0.065020526	Q00612, P06745, Q05920
metabolism	GOTERM_BP_FAT	GO:0016051-carbohydrate biosynthetic process	4	1.64	0.101409377	P05201, Q00612, P06745, Q05920
	Annotation Cluster 25	Enrichment Score: 1.3096258709079858				
	Category	Term	Count	%	PValue	Genes
mitochondria	GOTERM_MF_FAT	GO:0015035-protein disulfide oxidoreductase activity	3	1.23	0.008772591	P97493, Q80Y14, Q9QUH0
mitochondria	GOTERM_MF_FAT	GO:0015036-disulfide oxidoreductase activity	3	1.23	0.016179908	P97493, Q80Y14, Q9QUH0
mitochondria	INTERPRO	IPR012335:Thioredoxin fold	5	2.05	0.050276692	Q8C0L0, Q9WVL0, P97493, Q80Y14, Q9QUH0
mitochondria	GOTERM_BP_FAT	GO:0045454-cell redox homeostasis	4	1.64	0.05098457	Q8C0L0, P97493, Q80Y14, Q9QUH0
mitochondria	GOTERM_MF_FAT	GO:0016667-oxidoreductase activity, acting on sulfur group of donors	3	1.23	0.069795314	P97493, Q80Y14, Q9QUH0
mitochondria	SP_PIR_KEYWORDS	Redox-active center	3	1.23	0.09714624	Q8C0L0, P97493, Q9QUH0
mitochondria	GOTERM_MF_FAT	GO:0009055-electron carrier activity	5	2.05	0.275713001	Q9DCW4, Q9CPW2, P97493, Q80Y14, Q9QUH0
	Annotation Cluster 26	Enrichment Score: 1.3046333259581324				
	Category	Term	Count	%	PValue	Genes
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	10	4.10	0.024247762	Q3UHD9, Q9ERD7, P08556, Q80ZJ1, P63001, P39054, Q8CHH9, Q8BGR6, P36536, P58281
	SP_PIR_KEYWORDS	gtp-binding	10	4.10	0.026636756	Q3UHD9, Q9ERD7, P08556, Q80ZJ1, P63001, P39054, Q8CHH9, Q8BGR6, P36536, P58281
	GOTERM_MF_FAT	GO:0003924-GTPase activity	6	2.46	0.027079551	Q3UHD9, Q9ERD7, P08556, P63001, P39054, P58281
	GOTERM_MF_FAT	GO:0005525-GTP binding	10	4.10	0.044775355	Q3UHD9, Q9ERD7, P08556, Q80ZJ1, P63001, P39054, Q8CHH9, Q8BGR6, P36536, P58281
	GOTERM_MF_FAT	GO:0019001-guanyl nucleotide binding	10	4.10	0.051002365	Q3UHD9, Q9ERD7, P08556, Q80ZJ1, P63001, P39054, Q8CHH9, Q8BGR6, P36536, P58281
	GOTERM_MF_FAT	GO:0032561-guanyl ribonucleotide binding	10	4.10	0.051002365	Q3UHD9, Q9ERD7, P08556, Q80ZJ1, P63001, P39054, Q8CHH9, Q8BGR6, P36536, P58281
	INTERPRO	IPR005225:Small GTP-binding protein	4	1.64	0.361870006	P08556, Q80ZJ1, P63001, P36536
	Annotation Cluster 27	Enrichment Score: 1.2293121471156916				
	Category	Term	Count	%	PValue	Genes
	SMART	SM00033:CH	4	1.64	0.029298712	Q3V0K9, Q3UH68, Q69ZW3, Q5SXY1
	INTERPRO	IPR001715:Calponin-like actin-binding	4	1.64	0.059380087	Q3V0K9, Q3UH68, Q69ZW3, Q5SXY1
	UP_SEQ_FEATURE	domain:CH	3	1.23	0.117916398	Q3UH68, Q69ZW3, Q5SXY1
	Annotation Cluster 28	Enrichment Score: 1.2285525064729441				

	Category	Term	Count	%	PValue	Genes
protein modif	SP_PIR_KEYWORDS	isopeptide bond	9	3.69	0.034866925	Q9D5V5, Q80U40, Q60597, Q9CQ69, Q80U49, Q9ERU9, O88712, Q8CDG3, Q9D0R2
protein modif	SP_PIR_KEYWORDS	ubl conjugation	13	5.33	0.05237948	Q60597, Q9CQ69, O08788, Q80U49, O88712, Q8CDG3, Q62277, Q9QYB5, Q9D5V5, Q80U40, Q8BMI3, Q9ERU9, Q9D0R2
protein modif	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin)	6	2.46	0.112919161	Q80U40, Q60597, Q9CQ69, Q80U49, Q8CDG3, Q9D0R2
	Annotation Cluster 29	Enrichment Score: 1.1858016170156027				
	Category	Term	Count	%	PValue	Genes
neural disease	KEGG_PATHWAY	mmu05016:Huntington's disease	11	4.51	0.001130808	Q9CPP6, P97450, Q9Z1B3, O35683, Q3UVX5, P84091, O08585, Q9CQ69, P56382, Q05A62, O08788
neural disease	SP_PIR_KEYWORDS	respiratory chain	5	2.05	0.009799168	Q9CPP6, Q9ERS2, O35683, Q9CQ69, P03893
neural disease	GOTERM_CC_FAT	GO:0070469-respiratory chain	5	2.05	0.012940514	Q9CPP6, Q9ERS2, O35683, Q9CQ69, P03893
neural disease	KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	6	2.46	0.073248313	Q9CPP6, P97450, O35683, Q9CQ69, P56382, P03893
neural disease	KEGG_PATHWAY	mmu05012:Parkinson's disease	6	2.46	0.079061354	Q9CPP6, P97450, O35683, Q9CQ69, P56382, P03893
neural disease	GOTERM_BP_FAT	GO:0006119-oxidative phosphorylation	3	1.23	0.174053675	P97450, P56382, P03893
neural disease	KEGG_PATHWAY	mmu05010:Alzheimer's disease	6	2.46	0.204958188	Q9CPP6, P97450, Q9Z1B3, O35683, Q9CQ69, P56382
neural disease	GOTERM_MF_FAT	GO:0015078-hydrogen ion transmembrane transporter activity	3	1.23	0.293877919	P97450, Q9CQ69, P56382
neural disease	GOTERM_MF_FAT	GO:0015077-monovalent inorganic cation transmembrane transporter activity	3	1.23	0.318197917	P97450, Q9CQ69, P56382
neural disease	GOTERM_MF_FAT	GO:0022890-inorganic cation transmembrane transporter activity	3	1.23	0.500587206	P97450, Q9CQ69, P56382
	Annotation Cluster 30	Enrichment Score: 1.1121899823955164				
	Category	Term	Count	%	PValue	Genes
mitochondria	GOTERM_CC_FAT	GO:0005759-mitochondrial matrix	9	3.69	0.002078179	Q9DCW4, Q9CPW2, P52196, Q60597, Q9CQX8, Q8BIJ6, Q05920, Q9CZU6, Q9D051
mitochondria	GOTERM_CC_FAT	GO:0031980-mitochondrial lumen	9	3.69	0.002078179	Q9DCW4, Q9CPW2, P52196, Q60597, Q9CQX8, Q8BIJ6, Q05920, Q9CZU6, Q9D051
mitochondria	GOTERM_CC_FAT	GO:0031974-membrane-enclosed lumen	20	8.20	0.28628442	Q8CGF7, Q9CPW2, P21619, Q9CQX8, Q60597, Q8BIJ6, Q05920, Q9D051, O88712, Q923D5, P58281, Q9ERS2, Q9DCW4, Q9JKR6, P52196, Q4KMM3, Q8K310, Q8K3H0, Q9CZU6, Q9CXW3
mitochondria	GOTERM_CC_FAT	GO:0070013-intracellular organelle lumen	18	7.38	0.418906721	Q8CGF7, Q9CPW2, P21619, Q9CQX8, Q60597, Q8BIJ6, Q05920, Q9D051, O88712, Q923D5, Q9ERS2, Q9DCW4, Q9JKR6, P52196, Q4KMM3, Q8K310, Q8K3H0, Q9CZU6
mitochondria	GOTERM_CC_FAT	GO:0043233-organelle lumen	18	7.38	0.423301864	Q8CGF7, Q9CPW2, P21619, Q9CQX8, Q60597, Q8BIJ6, Q05920, Q9D051, O88712, Q923D5, Q9ERS2, Q9DCW4, Q9JKR6, P52196, Q4KMM3, Q8K310, Q8K3H0, Q9CZU6
mitochondria	GOTERM_CC_FAT	GO:0031981-nuclear lumen	8	3.28	0.968119809	Q8CGF7, Q9ERS2, P21619, Q4KMM3, Q8K310, O88712, Q8K3H0, Q923D5
	Annotation Cluster 31	Enrichment Score: 1.1079338678590984				
	Category	Term	Count	%	PValue	Genes
cytoskeleton	GOTERM_MF_FAT	GO:0003774-motor activity	6	2.46	0.03578498	P28740, Q9QXL2, P39054, O08788, P62627, Q9JMH9
cytoskeleton	SP_PIR_KEYWORDS	motor protein	5	2.05	0.085341726	P28740, Q9QXL2, P39054, P62627, Q9JMH9
cytoskeleton	GOTERM_BP_FAT	GO:0007018-microtubule-based movement	4	1.64	0.155358919	P28740, Q9ERD7, Q9QXL2, P62627
	Annotation Cluster 32	Enrichment Score: 1.096236483192459				
	Category	Term	Count	%	PValue	Genes
cytoskeleton	GOTERM_BP_FAT	GO:0051493-regulation of cytoskeleton organization	7	2.87	0.00218769	P54227, Q811D0, P70336, Q9CPW4, P63001, P27546, Q8BRT1
cytoskeleton	GOTERM_BP_FAT	GO:0032271-regulation of protein polymerization	4	1.64	0.041388225	P54227, Q811D0, Q9CPW4, P63001
cytoskeleton	GOTERM_BP_FAT	GO:0043254-regulation of protein complex assembly	4	1.64	0.057214447	P54227, Q811D0, Q9CPW4, P63001
cytoskeleton	GOTERM_BP_FAT	GO:0044087-regulation of cellular component biogenesis	4	1.64	0.118449694	P54227, Q811D0, Q9CPW4, P63001
cytoskeleton	GOTERM_BP_FAT	GO:0030833-regulation of actin filament polymerization	3	1.23	0.122778952	Q811D0, Q9CPW4, P63001
cytoskeleton	GOTERM_BP_FAT	GO:0008064-regulation of actin polymerization or depolymerization	3	1.23	0.145621919	Q811D0, Q9CPW4, P63001
cytoskeleton	GOTERM_BP_FAT	GO:0030832-regulation of actin filament length	3	1.23	0.150291628	Q811D0, Q9CPW4, P63001
cytoskeleton	GOTERM_BP_FAT	GO:0032535-regulation of cellular component size	5	2.05	0.172335004	Q811D0, Q7TMB8, Q9ERS2, Q9CPW4, P63001
cytoskeleton	GOTERM_BP_FAT	GO:0032956-regulation of actin cytoskeleton organization	3	1.23	0.193467614	Q811D0, Q9CPW4, P63001
cytoskeleton	GOTERM_BP_FAT	GO:0032970-regulation of actin filament-based process	3	1.23	0.198365303	Q811D0, Q9CPW4, P63001

	Annotation Cluster 33	Enrichment Score: 1.0181158533217032				
	Category	Term	Count	%	PValue	Genes
cytoskeleton	GOTERM_CC_FAT	GO:0016323-basolateral plasma membrane	7	2.87	0.014317736	Q811D0, Q8BIW1, Q8BTY2, Q03173, O70161, Q9EPR4, Q61301
cytoskeleton	GOTERM_CC_FAT	GO:0005912-adherens junction	5	2.05	0.061473422	Q811D0, Q8BIW1, Q03173, O70161, Q61301
cytoskeleton	GOTERM_CC_FAT	GO:0070161-anchoring junction	5	2.05	0.094079524	Q811D0, Q8BIW1, Q03173, O70161, Q61301
cytoskeleton	GOTERM_CC_FAT	GO:0005925-focal adhesion	3	1.23	0.189696691	Q8BIW1, Q03173, O70161
cytoskeleton	GOTERM_CC_FAT	GO:0005924-cell-substrate adherens junction	3	1.23	0.210109336	Q8BIW1, Q03173, O70161
cytoskeleton	GOTERM_CC_FAT	GO:0030055-cell-substrate junction	3	1.23	0.235908143	Q8BIW1, Q03173, O70161

	Annotation Cluster 34	Enrichment Score: 0.9618049208641112				
	Category	Term	Count	%	PValue	Genes
signaling	GOTERM_BP_FAT	GO:0033674-positive regulation of kinase activity	6	2.46	0.031201134	Q811D0, Q3UHD9, Q58A65, O88653, P63001, Q9ESW4
signaling	GOTERM_BP_FAT	GO:0051347-positive regulation of transferase activity	6	2.46	0.035849111	Q811D0, Q3UHD9, Q58A65, O88653, P63001, Q9ESW4
signaling	GOTERM_MF_FAT	GO:0019901-protein kinase binding	4	1.64	0.067041984	Q811D0, Q3UHD9, Q58A65, Q8QZZ7
signaling	GOTERM_BP_FAT	GO:0045860-positive regulation of protein kinase activity	5	2.05	0.086534886	Q811D0, Q3UHD9, Q58A65, O88653, Q9ESW4
signaling	GOTERM_BP_FAT	GO:0042325-regulation of phosphorylation	8	3.28	0.096279726	Q811D0, Q3UHD9, Q58A65, P12367, O88653, P63001, Q9ESW4, P61148
signaling	GOTERM_MF_FAT	GO:0019900-kinase binding	4	1.64	0.101739823	Q811D0, Q3UHD9, Q58A65, Q8QZZ7
signaling	GOTERM_BP_FAT	GO:0019220-regulation of phosphate metabolic process	8	3.28	0.112737877	Q811D0, Q3UHD9, Q58A65, P12367, O88653, P63001, Q9ESW4, P61148
signaling	GOTERM_BP_FAT	GO:0051174-regulation of phosphorus metabolic process	8	3.28	0.112737877	Q811D0, Q3UHD9, Q58A65, P12367, O88653, P63001, Q9ESW4, P61148
signaling	GOTERM_BP_FAT	GO:0043549-regulation of kinase activity	6	2.46	0.117675876	Q811D0, Q3UHD9, Q58A65, O88653, P63001, Q9ESW4
signaling	GOTERM_BP_FAT	GO:0051338-regulation of transferase activity	6	2.46	0.132485503	Q811D0, Q3UHD9, Q58A65, O88653, P63001, Q9ESW4
signaling	GOTERM_BP_FAT	GO:0043085-positive regulation of catalytic activity	7	2.87	0.141186377	Q791T5, Q811D0, Q3UHD9, Q58A65, O88653, P63001, Q9ESW4
signaling	GOTERM_BP_FAT	GO:0032147-activation of protein kinase activity	3	1.23	0.150291628	Q811D0, O88653, Q9ESW4
signaling	GOTERM_BP_FAT	GO:0044093-positive regulation of molecular function	7	2.87	0.231549398	Q791T5, Q811D0, Q3UHD9, Q58A65, O88653, P63001, Q9ESW4
signaling	GOTERM_BP_FAT	GO:0045859-regulation of protein kinase activity	5	2.05	0.241880298	Q811D0, Q3UHD9, Q58A65, O88653, Q9ESW4
signaling	GOTERM_MF_FAT	GO:0019207-kinase regulator activity	3	1.23	0.249888499	Q3UHD9, P12367, O88653

	Annotation Cluster 35	Enrichment Score: 0.9421042912410842				
	Category	Term	Count	%	PValue	Genes
vescicle	GOTERM_BP_FAT	GO:0006887-exocytosis	5	2.05	0.061305958	Q9CZD3, Q9QWI6, Q9CQW1, P84086, Q9JKD3
vescicle	GOTERM_BP_FAT	GO:0032940-secretion by cell	6	2.46	0.106687202	Q9CZD3, Q9QWI6, Q9Z2I2, Q9CQW1, P84086, Q9JKD3
vescicle	SP_PIR_KEYWORDS	exocytosis	3	1.23	0.146201495	Q9QWI6, P84086, Q9JKD3
vescicle	GOTERM_BP_FAT	GO:0046903-secretion	6	2.46	0.178244449	Q9CZD3, Q9QWI6, Q9Z2I2, Q9CQW1, P84086, Q9JKD3

	Annotation Cluster 36	Enrichment Score: 0.9409167298695106				
	Category	Term	Count	%	PValue	Genes
vescicle	GOTERM_CC_FAT	GO:0031982-vesicle	14	5.74	0.030518847	P97441, Q07076, P84091, O08585, Q9CQW1, P63001, Q9JKD3, Q9CR95, Q9CZD3, Q62277, P17047, Q3UPL0, Q8BHN3, P19096
vescicle	GOTERM_CC_FAT	GO:0031410-cytoplasmic vesicle	13	5.33	0.053337412	P97441, P84091, O08585, Q9CQW1, P63001, Q9JKD3, Q9CR95, Q9CZD3, Q62277, P17047, Q3UPL0, Q8BHN3, P19096
vescicle	GOTERM_CC_FAT	GO:0030665-clathrin coated vesicle membrane	3	1.23	0.090069153	Q62277, O08585, Q9CR95
vescicle	SP_PIR_KEYWORDS	cytoplasmic vesicle	7	2.87	0.095042972	Q62277, P97441, Q3UPL0, O08585, Q9CQW1, Q9JKD3, Q9CR95
vescicle	GOTERM_CC_FAT	GO:0030659-cytoplasmic vesicle membrane	4	1.64	0.122524208	Q62277, P17047, O08585, Q9CR95
vescicle	GOTERM_CC_FAT	GO:0016023-cytoplasmic membrane-bounded vesicle	10	4.10	0.127157002	Q62277, Q9CZD3, P17047, P84091, O08585, Q8BHN3, P63001, P19096, Q9JKD3, Q9CR95
vescicle	GOTERM_CC_FAT	GO:0031988-membrane-bounded vesicle	10	4.10	0.135321607	Q62277, Q9CZD3, P17047, P84091, O08585, Q8BHN3, P63001, P19096, Q9JKD3, Q9CR95
vescicle	GOTERM_CC_FAT	GO:0044433-cytoplasmic vesicle part	4	1.64	0.148023972	Q62277, P17047, O08585, Q9CR95
vescicle	GOTERM_CC_FAT	GO:0012506-vesicle membrane	4	1.64	0.154651167	Q62277, P17047, O08585, Q9CR95
vescicle	GOTERM_CC_FAT	GO:0030662-coated vesicle membrane	3	1.23	0.169585181	Q62277, O08585, Q9CR95
vescicle	GOTERM_CC_FAT	GO:0030136-clathrin-coated vesicle	4	1.64	0.178539069	Q62277, O08585, Q9JKD3, Q9CR95
vescicle	GOTERM_CC_FAT	GO:0030135-coated vesicle	4	1.64	0.251285452	Q62277, O08585, Q9JKD3, Q9CR95

neuron	Annotation Cluster 37	Enrichment Score: 0.9375696001381684				
neuron	Category	Term	Count	%	PValue	Genes
neuron	GOTERM_BP_FAT	GO:0048169-regulation of long-term neuronal synaptic plasticity	3	1.23	0.026542552	Q62277, P08556, Q3UVX5
neuron	GOTERM_BP_FAT	GO:0048168-regulation of neuronal synaptic plasticity	3	1.23	0.050810278	Q62277, P08556, Q3UVX5
neuron	GOTERM_BP_FAT	GO:0048167-regulation of synaptic plasticity	3	1.23	0.136378358	Q62277, P08556, Q3UVX5
neuron	GOTERM_BP_FAT	GO:0050804-regulation of synaptic transmission	4	1.64	0.152154949	Q62277, P08556, Q3UVX5, Q7TSC1
neuron	GOTERM_BP_FAT	GO:0051969-regulation of transmission of nerve impulse	4	1.64	0.175008184	Q62277, P08556, Q3UVX5, Q7TSC1
neuron	GOTERM_BP_FAT	GO:0031644-regulation of neurological system process	4	1.64	0.195308575	Q62277, P08556, Q3UVX5, Q7TSC1
neuron	GOTERM_BP_FAT	GO:0044057-regulation of system process	5	2.05	0.285961349	Q62277, P08556, Q9Z2I2, Q3UVX5, Q7TSC1
	Annotation Cluster 38	Enrichment Score: 0.9229611258296337				
	Category	Term	Count	%	PValue	Genes
Transcription	GOTERM_MF_FAT	GO:0005198-structural molecule activity	13	5.33	0.016020858	Q811D0, Q9Z2H5, P21619, O08585, Q9CPR4, P14115, Q61301, P14206, Q9QYB5, Q9ERD7, P02468, Q9D8E6, P58059
Transcription	SP_PIR_KEYWORDS	ribonucleoprotein	8	3.28	0.069622144	Q99020, Q9CPR4, Q9CQX8, P14115, Q9D8E6, P14206, P58059, Q60668
Transcription	SP_PIR_KEYWORDS	ribosomal protein	6	2.46	0.092157929	Q9CPR4, Q9CQX8, P14115, Q9D8E6, P14206, P58059
Transcription	GOTERM_CC_FAT	GO:0005840-ribosome	6	2.46	0.132111221	Q9CPR4, Q9CQX8, P14115, Q9D8E6, P14206, P58059
Transcription	GOTERM_MF_FAT	GO:0003735-structural constituent of ribosome	5	2.05	0.13856844	Q9CPR4, P14115, Q9D8E6, P14206, P58059
Transcription	KEGG_PATHWAY	mmu03010:Ribosome	4	1.64	0.198119842	Q9CPR4, P14115, Q9D8E6, P14206
Transcription	GOTERM_CC_FAT	GO:0033279-ribosomal subunit	3	1.23	0.235908143	Q9CPR4, Q9CQX8, P14206
Transcription	GOTERM_CC_FAT	GO:0030529-ribonucleoprotein complex	8	3.28	0.469970051	Q99020, Q9CPR4, Q9CQX8, P14115, Q9D8E6, P14206, P58059, Q60668
neuron	Annotation Cluster 39	Enrichment Score: 0.8438373029560156				
neuron	Category	Term	Count	%	PValue	Genes
neuron	GOTERM_CC_FAT	GO:0030027-lamellipodium	5	2.05	0.011631897	Q7TMB8, Q9CPW4, P63001, Q03173, Q61301
neuron	GOTERM_CC_FAT	GO:0031252-cell leading edge	6	2.46	0.020481963	Q7TMB8, Q9CPW4, P63001, O08788, Q03173, Q61301
cytoskeleton	GOTERM_CC_FAT	GO:0005912-adherens junction	5	2.05	0.061473422	Q811D0, Q8BIW1, Q03173, O70161, Q61301
neuron	GOTERM_BP_FAT	GO:0000904-cell morphogenesis involved in differentiation	7	2.87	0.067194923	P54227, Q7TMB8, Q99020, P63001, Q03173, O70161, Q61301
neuron	GOTERM_BP_FAT	GO:0007409-axonogenesis	6	2.46	0.069490404	P54227, Q7TMB8, P63001, Q03173, O70161, Q61301
neuron	GOTERM_BP_FAT	GO:0048812-neuron projection morphogenesis	6	2.46	0.089442805	P54227, Q7TMB8, P63001, Q03173, O70161, Q61301
cytoskeleton	GOTERM_CC_FAT	GO:0070161-anchoring junction	5	2.05	0.094079524	Q811D0, Q8BIW1, Q03173, O70161, Q61301
neuron	GOTERM_BP_FAT	GO:0048667-cell morphogenesis involved in neuron differentiation	6	2.46	0.099647063	P54227, Q7TMB8, P63001, Q03173, O70161, Q61301
neuron	GOTERM_CC_FAT	GO:0042995-cell projection	13	5.33	0.108716678	Q811D0, Q9CPW4, P63001, Q8BTY2, Q61330, Q03173, Q61301, P58281, Q7TMB8, Q9ERD7, Q60865, P63080, P84086
neuron	GOTERM_BP_FAT	GO:0000902-cell morphogenesis	8	3.28	0.121343886	P54227, Q7TMB8, Q99020, P63001, Q8BRT1, Q03173, O70161, Q61301
neuron	SP_PIR_KEYWORDS	cell projection	6	2.46	0.126661011	Q7TMB8, Q9CPW4, Q60865, Q8BTY2, Q03173, Q61301
neuron	GOTERM_BP_FAT	GO:0048858-cell projection morphogenesis	6	2.46	0.137344715	P54227, Q7TMB8, P63001, Q03173, O70161, Q61301
neuron	GOTERM_BP_FAT	GO:0032990-cell part morphogenesis	6	2.46	0.158374963	P54227, Q7TMB8, P63001, Q03173, O70161, Q61301
neuron	GOTERM_BP_FAT	GO:0031175-neuron projection development	6	2.46	0.171461221	P54227, Q7TMB8, P63001, Q03173, O70161, Q61301
neuron	GOTERM_BP_FAT	GO:0032989-cellular component morphogenesis	8	3.28	0.195585382	P54227, Q7TMB8, Q99020, P63001, Q8BRT1, Q03173, O70161, Q61301
neuron	SP_PIR_KEYWORDS	neurogenesis	4	1.64	0.307920296	P54227, Q7TMB8, P28740, Q03173
cytoskeleton	GOTERM_CC_FAT	GO:0015629-actin cytoskeleton	5	2.05	0.321046463	Q9QWI6, Q9CPW4, Q03173, Q61301, Q9JMH9
neuron	GOTERM_BP_FAT	GO:0048666-neuron development	6	2.46	0.356676374	P54227, Q7TMB8, P63001, Q03173, O70161, Q61301
neuron	GOTERM_BP_FAT	GO:0030030-cell projection organization	6	2.46	0.429891387	P54227, Q7TMB8, P63001, Q03173, O70161, Q61301
neuron	GOTERM_BP_FAT	GO:0030182-neuron differentiation	7	2.87	0.450676172	P54227, Q7TMB8, Q9ERD7, P63001, Q03173, O70161, Q61301
neuron	SP_PIR_KEYWORDS	differentiation	7	2.87	0.591024754	P54227, Q7TMB8, P28740, O88712, Q03173, Q61301, P61148
neuron	SP_PIR_KEYWORDS	developmental protein	7	2.87	0.966131272	P54227, Q7TMB8, P28740, Q03173, Q61301, P61148, Q7TQ95
	Annotation Cluster 40	Enrichment Score: 0.8407151501893866				
	Category	Term	Count	%	PValue	Genes
Transcription	PIR_SUPERFAMILY	PIRSF002072:helix-destabilizing protein	3	1.23	0.007613879	Q99020, Q9Z130, Q60668
Transcription	SMART	SM00360:RRM	6	2.46	0.057966459	Q9D8T7, Q99020, Q8K310, Q9Z130, P59708, Q60668

Transcription	INTERPRO	IPR000504:RNA recognition motif, RNP-1	6	2.46	0.145032146	Q9D8T7, Q99020, Q8K310, Q9Z130, P59708, Q60668
Transcription	INTERPRO	IPR012677:Nucleotide-binding, alpha-beta plait	6	2.46	0.147034531	Q9D8T7, Q99020, Q8K310, Q9Z130, P59708, Q60668
Transcription	UP_SEQ_FEATURE	domain:RRM 2	4	1.64	0.149319143	Q99020, Q8K310, Q9Z130, Q60668
Transcription	UP_SEQ_FEATURE	domain:RRM 1	4	1.64	0.149319143	Q99020, Q8K310, Q9Z130, Q60668
Transcription	SP_PIR_KEYWORDS	rna-binding	9	3.69	0.333144059	Q9D8T7, Q99020, P28271, Q3U0V1, Q8K310, Q9Z130, Q8BGQ7, P59708, Q60668
Transcription	GOTERM_BP_FAT	GO:0016071-mRNA metabolic process	5	2.05	0.583241476	Q3U0V1, Q9Z130, Q923D5, P59708, Q60668
Transcription	GOTERM_MF_FAT	GO:0003723-RNA binding	9	3.69	0.665557928	Q9DB27, Q9D8T7, Q99020, P28271, Q3U0V1, Q8K310, Q9Z130, P59708, Q60668
	Annotation Cluster 41	Enrichment Score: 0.819735596539				
	Category	Term	Count	%	PValue	Genes
nucleus	GOTERM_CC_FAT	GO:0005635-nuclear envelope	6	2.46	0.063832326	Q07076, P21619, Q91YE6, Q8BKC5, Q9ERU9, Q9CXW3
nucleus	GOTERM_CC_FAT	GO:0005643-nuclear pore	3	1.23	0.199871394	Q91YE6, Q8BKC5, Q9ERU9
nucleus	GOTERM_CC_FAT	GO:0046930-pore complex	3	1.23	0.27227132	Q91YE6, Q8BKC5, Q9ERU9
	Annotation Cluster 42	Enrichment Score: 0.7439171422679404				
	Category	Term	Count	%	PValue	Genes
	GOTERM_BP_FAT	GO:0043933-macromolecular complex subunit organization	10	4.10	0.060495238	P54227, Q58A65, Q9ERD7, P10922, P61458, P02468, Q91YE6, Q8BKC5, P23116, Q03173
	GOTERM_BP_FAT	GO:0034621-cellular macromolecular complex subunit organization	7	2.87	0.11385891	P54227, Q9ERD7, P10922, Q91YE6, Q8BKC5, P23116, Q03173
	GOTERM_BP_FAT	GO:0065003-macromolecular complex assembly	8	3.28	0.171989608	Q58A65, Q9ERD7, P10922, P61458, P02468, Q91YE6, Q8BKC5, P23116
	GOTERM_BP_FAT	GO:0006461-protein complex assembly	6	2.46	0.190943405	Q58A65, Q9ERD7, P61458, P02468, Q91YE6, Q8BKC5
	GOTERM_BP_FAT	GO:0070271-protein complex biogenesis	6	2.46	0.190943405	Q58A65, Q9ERD7, P61458, P02468, Q91YE6, Q8BKC5
	GOTERM_BP_FAT	GO:0034622-cellular macromolecular complex assembly	5	2.05	0.335152986	Q9ERD7, P10922, Q91YE6, Q8BKC5, P23116
	GOTERM_BP_FAT	GO:0043623-cellular protein complex assembly	3	1.23	0.428486525	Q9ERD7, Q91YE6, Q8BKC5
neuron	Annotation Cluster 43	Enrichment Score: 0.7021491323380084				
neuron	Category	Term	Count	%	PValue	Genes
neuron	KEGG_PATHWAY	mmu04720:Long-term potentiation	4	1.64	0.119591213	Q9Z1B3, P08556, Q3UVX5, Q9DBR7
neuron	KEGG_PATHWAY	mmu04540:Gap junction	4	1.64	0.184942067	Q9Z1B3, Q9ERD7, P08556, Q3UVX5
neuron	KEGG_PATHWAY	mmu04730:Long-term depression	3	1.23	0.353848716	Q9Z1B3, P08556, Q3UVX5
	Annotation Cluster 44	Enrichment Score: 0.6758294605578368				
	Category	Term	Count	%	PValue	Genes
transport	GOTERM_BP_FAT	GO:0046942-carboxylic acid transport	4	1.64	0.148972588	Q8R5J9, Q9EPR4, Q8BH59, Q9DCP2
transport	GOTERM_BP_FAT	GO:0015849-organic acid transport	4	1.64	0.152154949	Q8R5J9, Q9EPR4, Q8BH59, Q9DCP2
transport	GOTERM_BP_FAT	GO:0006865-amino acid transport	3	1.23	0.24796566	Q8R5J9, Q8BH59, Q9DCP2
transport	GOTERM_BP_FAT	GO:0015837-amine transport	3	1.23	0.352288261	Q8R5J9, Q8BH59, Q9DCP2
	Annotation Cluster 45	Enrichment Score: 0.6620334661135747				
	Category	Term	Count	%	PValue	Genes
	UP_SEQ_FEATURE	repeat:2	6	2.46	0.08015986	Q07076, P19246, Q3U0V1, P23116, Q9ERU9, Q03173
	UP_SEQ_FEATURE	repeat:1	5	2.05	0.1876468	Q07076, P19246, Q3U0V1, Q9ERU9, Q03173
	UP_SEQ_FEATURE	repeat:4	4	1.64	0.197901429	P19246, Q3U0V1, P23116, Q03173
	UP_SEQ_FEATURE	repeat:3	4	1.64	0.270083256	Q07076, P19246, Q3U0V1, Q03173
	UP_SEQ_FEATURE	repeat:7	3	1.23	0.270250117	P19246, P23116, Q03173
	UP_SEQ_FEATURE	repeat:6	3	1.23	0.292763832	P19246, P23116, Q03173
	UP_SEQ_FEATURE	repeat:5	3	1.23	0.364953657	P19246, P23116, Q03173
	Annotation Cluster 46	Enrichment Score: 0.6087089968661792				
	Category	Term	Count	%	PValue	Genes
ion transport/channels	UP_SEQ_FEATURE	domain:IQ	3	1.23	0.191926871	Q5DU25, Q9JMH9, Q3TES0
ion transport/channels	SMART	SM00015:IQ	3	1.23	0.229638579	Q5DU25, Q9JMH9, Q3TES0

ion transport/channels	INTERPRO	IPR000048:IQ calmodulin-binding region	3	1.23	0.338604227	Q5DU25, Q9JMH9, Q3TES0
neuron	Annotation Cluster 47	Enrichment Score: 0.5986232641183005				
neuron	Category	Term	Count	%	PValue	Genes
neuron	GOTERM_BP_FAT	GO:0007267-cell-cell signaling	8	3.28	0.096279726	Q62277, Q9Z2I2, Q6PFD5, P63080, Q9JKK7, Q8BWF0, Q61301, P61148
neuron	GOTERM_BP_FAT	GO:0019226-transmission of nerve impulse	6	2.46	0.191296233	Q62277, Q9Z2I2, P63080, Q9JKK7, Q8BWF0, Q61301
neuron	GOTERM_BP_FAT	GO:0007268-synaptic transmission	5	2.05	0.218949392	Q62277, P63080, Q9JKK7, Q8BWF0, Q61301
neuron	GOTERM_BP_FAT	GO:0050877-neurological system process	10	4.10	0.999820267	Q62277, P08556, Q9Z2I2, Q3UVX5, P63080, Q9JKK7, Q8BWF0, Q8BGQ7, Q61301, P58281
	Annotation Cluster 48	Enrichment Score: 0.5774367792002517				
	Category	Term	Count	%	PValue	Genes
transport	GOTERM_BP_FAT	GO:0051223-regulation of protein transport	3	1.23	0.218093401	Q6PAR5, Q9JKD3, Q7TSC1
transport	GOTERM_BP_FAT	GO:0070201-regulation of establishment of protein localization	3	1.23	0.24796566	Q6PAR5, Q9JKD3, Q7TSC1
transport	GOTERM_BP_FAT	GO:0032880-regulation of protein localization	3	1.23	0.342496072	Q6PAR5, Q9JKD3, Q7TSC1
	Annotation Cluster 49	Enrichment Score: 0.5666146167329914				
	Category	Term	Count	%	PValue	Genes
	UP_SEQ_FEATURE	lipid moiety-binding region:S-farnesyl cysteine	4	1.64	0.032431227	P08556, Q80ZJ1, P21619, Q9CQW1
	SP_PIR_KEYWORDS	prenylation	5	2.05	0.133229126	P08556, Q80ZJ1, P21619, Q9CQW1, P63001
	GOTERM_BP_FAT	GO:0007264-small GTPase mediated signal transduction	7	2.87	0.133680851	P70336, Q3UHD9, P50396, P08556, Q80ZJ1, P63001, Q8K2C9
	SP_PIR_KEYWORDS	methylation	6	2.46	0.179680807	Q99020, P08556, Q80ZJ1, P63001, Q9Z130, Q60668
	INTERPRO	IPR005225:Small GTP-binding protein	4	1.64	0.361870006	P08556, Q80ZJ1, P63001, P36536
	UP_SEQ_FEATURE	short sequence motif:Effector region	3	1.23	0.408009168	P08556, Q80ZJ1, P63001
	INTERPRO	IPR013753:Ras	3	1.23	0.470579359	P08556, Q80ZJ1, P63001
	INTERPRO	IPR001806:Ras GTPase	3	1.23	0.508319263	P08556, Q80ZJ1, P63001
	UP_SEQ_FEATURE	propeptide:Removed in mature form	4	1.64	0.651767096	P08556, Q80ZJ1, P63001, Q61330
	SP_PIR_KEYWORDS	lipoprotein	6	2.46	0.902892395	P08556, Q80ZJ1, P21619, Q9CQW1, P63001, Q61330
	Annotation Cluster 50	Enrichment Score: 0.5547713779771216				
	Category	Term	Count	%	PValue	Genes
ion transport/channels	GOTERM_MF_FAT	GO:0031402-sodium ion binding	4	1.64	0.154459762	Q8JZR6, Q8BTY2, Q9EPR4, Q9DCP2
ion transport/channels	SP_PIR_KEYWORDS	Sodium	4	1.64	0.162729435	Q8JZR6, Q8BTY2, Q9EPR4, Q9DCP2
ion transport/channels	GOTERM_MF_FAT	GO:0015297-antiporter activity	3	1.23	0.163444988	Q8JZR6, Q8BTY2, Q9DCP2
ion transport/channels	GOTERM_BP_FAT	GO:0006811-ion transport	14	5.74	0.164059503	Q8JZR6, P97441, P97450, Q9Z2I2, P54285, Q8R5J9, Q8BTY2, P56382, Q8BH59, Q9CY27, Q9DCP2, P52196, P63080, Q9EPR4
ion transport/channels	SP_PIR_KEYWORDS	Sodium transport	4	1.64	0.189462324	Q8JZR6, Q8BTY2, Q9EPR4, Q9DCP2
ion transport/channels	GOTERM_BP_FAT	GO:0006814-sodium ion transport	4	1.64	0.237441956	Q8JZR6, Q8BTY2, Q9EPR4, Q9DCP2
ion transport/channels	GOTERM_BP_FAT	GO:0006812-cation transport	10	4.10	0.258911708	Q8JZR6, P97441, P97450, Q9Z2I2, P54285, Q8BTY2, P56382, Q9EPR4, Q9CY27, Q9DCP2
ion transport/channels	GOTERM_BP_FAT	GO:0030001-metal ion transport	8	3.28	0.385876431	Q8JZR6, P97441, Q9Z2I2, P54285, Q8BTY2, Q9EPR4, Q9CY27, Q9DCP2

ion transport/channels	GOTERM_BP_FAT	GO:0015672-monovalent inorganic cation transport	6	2.46	0.387082945	Q8JZR6, P97450, Q8BTY2, P56382, Q9EPR4, Q9DCP2
ion transport/channels	SP_PIR_KEYWORDS	Symport	3	1.23	0.434089547	Q8BTY2, Q9EPR4, Q9DCP2
ion transport/channels	SP_PIR_KEYWORDS	ion transport	9	3.69	0.450971887	Q8JZR6, P97441, P97450, P54285, Q8BTY2, P56382, P63080, Q9EPR4, Q9DCP2
ion transport/channels	GOTERM_MF_FAT	GO:0031420-alkali metal ion binding	4	1.64	0.512980444	Q8JZR6, Q8BTY2, Q9EPR4, Q9DCP2
ion transport/channels	GOTERM_MF_FAT	GO:0015293-symporter activity	3	1.23	0.521199156	Q8BTY2, Q9EPR4, Q9DCP2
	Annotation Cluster 51	Enrichment Score: 0.554140939431224				
	Category	Term	Count	%	PValue	Genes
	SMART	SM00320:WD40	6	2.46	0.112098397	Q3UPL0, Q9QXL2, Q6NVE8, Q9ERG2, P62881, Q8CCN5
	INTERPRO	IPR019775:WD40 repeat, conserved site	7	2.87	0.12297326	Q3UPL0, Q9QXL2, Q6NVE8, Q9ERG2, P61971, P62881, Q8CCN5
	UP_SEQ_FEATURE	repeat:WD 6	5	2.05	0.22894276	Q3UPL0, Q9QXL2, Q6NVE8, Q9ERG2, P62881
	INTERPRO	IPR001680:WD40 repeat	6	2.46	0.250463581	Q3UPL0, Q9QXL2, Q6NVE8, Q9ERG2, P62881, Q8CCN5
	UP_SEQ_FEATURE	repeat:WD 3	6	2.46	0.271086411	Q3UPL0, Q9QXL2, Q6NVE8, Q9ERG2, P62881, Q8CCN5
	SP_PIR_KEYWORDS	wd repeat	6	2.46	0.279841302	Q3UPL0, Q9QXL2, Q6NVE8, Q9ERG2, P62881, Q8CCN5
	UP_SEQ_FEATURE	repeat:WD 1	6	2.46	0.286039074	Q3UPL0, Q9QXL2, Q6NVE8, Q9ERG2, P62881, Q8CCN5
	UP_SEQ_FEATURE	repeat:WD 2	6	2.46	0.286039074	Q3UPL0, Q9QXL2, Q6NVE8, Q9ERG2, P62881, Q8CCN5
	UP_SEQ_FEATURE	repeat:WD 7	4	1.64	0.290698295	Q3UPL0, Q9QXL2, Q6NVE8, P62881
	INTERPRO	IPR019782:WD40 repeat 2	5	2.05	0.306469422	Q3UPL0, Q9QXL2, Q6NVE8, Q9ERG2, P62881
	INTERPRO	IPR017986:WD40 repeat, region	5	2.05	0.347318194	Q3UPL0, Q9QXL2, Q6NVE8, Q9ERG2, P62881
	UP_SEQ_FEATURE	repeat:WD 5	5	2.05	0.367987953	Q3UPL0, Q9QXL2, Q6NVE8, Q9ERG2, P62881
	INTERPRO	IPR019781:WD40 repeat, subgroup	5	2.05	0.368595685	Q3UPL0, Q9QXL2, Q6NVE8, Q9ERG2, P62881
	UP_SEQ_FEATURE	repeat:WD 4	5	2.05	0.418014464	Q3UPL0, Q9QXL2, Q6NVE8, Q9ERG2, P62881
	INTERPRO	IPR015943:WD40/YVTN repeat-like	5	2.05	0.566241516	Q9QXL2, Q6NVE8, Q9ERG2, Q80UG2, P62881
	Annotation Cluster 52	Enrichment Score: 0.5451744255490383				
	Category	Term	Count	%	PValue	Genes
	SMART	SM00228:PDZ	4	1.64	0.179080809	Q811D0, Q8R4H2, Q4ACU6, Q9JMH9
	INTERPRO	IPR001478:PDZ/DHR/GLGF	4	1.64	0.304981001	Q811D0, Q8R4H2, Q4ACU6, Q9JMH9
	UP_SEQ_FEATURE	domain:PDZ	3	1.23	0.423794083	Q8R4H2, Q4ACU6, Q9JMH9
	Annotation Cluster 53	Enrichment Score: 0.4980857191174188				
	Category	Term	Count	%	PValue	Genes
ion transport/channels	GOTERM_BP_FAT	GO:0019725-cellular homeostasis	9	3.69	0.092652314	Q811D0, Q07076, Q8C0L0, Q9Z2I2, P28271, P97493, Q80Y14, Q9CY27, Q9QUH0
ion transport/channels	GOTERM_BP_FAT	GO:0042592-homeostatic process	12	4.92	0.164999625	Q811D0, P05201, Q07076, Q8C0L0, Q9Z2I2, P28271, P97493, P63001, Q00612, Q80Y14, Q9CY27, Q9QUH0
	GOTERM_BP_FAT	GO:0008283-cell proliferation	6	2.46	0.239890612	Q811D0, Q07076, P08556, Q9Z2I2, P63001, Q8K3H0
ion transport/channels	GOTERM_BP_FAT	GO:0030005-cellular di-, tri-valent inorganic cation homeostasis	4	1.64	0.26999017	Q07076, Q9Z2I2, P28271, Q9CY27
ion transport/channels	GOTERM_BP_FAT	GO:0055066-di-, tri-valent inorganic cation homeostasis	4	1.64	0.314062694	Q07076, Q9Z2I2, P28271, Q9CY27
ion transport/channels	GOTERM_BP_FAT	GO:0030003-cellular cation homeostasis	4	1.64	0.336096069	Q07076, Q9Z2I2, P28271, Q9CY27
ion transport/channels	GOTERM_BP_FAT	GO:0055080-cation homeostasis	4	1.64	0.451925357	Q07076, Q9Z2I2, P28271, Q9CY27

ion transport/channels	GOTERM_BP_FAT	GO:0006873-cellular ion homeostasis	5	2.05	0.468800282	Q811D0, Q07076, Q9Z2I2, P28271, Q9CY27
ion transport/channels	GOTERM_BP_FAT	GO:0055082-cellular chemical homeostasis	5	2.05	0.489181203	Q811D0, Q07076, Q9Z2I2, P28271, Q9CY27
ion transport/channels	GOTERM_BP_FAT	GO:0048878-chemical homeostasis	6	2.46	0.547915072	Q811D0, P05201, Q07076, Q9Z2I2, P28271, Q9CY27
ion transport/channels	GOTERM_BP_FAT	GO:0050801-ion homeostasis	5	2.05	0.55929288	Q811D0, Q07076, Q9Z2I2, P28271, Q9CY27
	Annotation Cluster 54	Enrichment Score: 0.38966211157716224				
	Category	Term	Count	%	PValue	Genes
metabolism	GOTERM_BP_FAT	GO:0006650-glycerophospholipid metabolic process	3	1.23	0.332658224	Q66GT5, Q8BWF0, O70161
metabolism	GOTERM_BP_FAT	GO:0006644-phospholipid metabolic process	4	1.64	0.37665877	Q66GT5, Q8BWF0, O70161, Q99L43
metabolism	GOTERM_BP_FAT	GO:0019637-organophosphate metabolic process	4	1.64	0.423339875	Q66GT5, Q8BWF0, O70161, Q99L43
metabolism	GOTERM_BP_FAT	GO:0046486-glycerolipid metabolic process	3	1.23	0.52085403	Q66GT5, Q8BWF0, O70161
	Annotation Cluster 55	Enrichment Score: 0.35476417773487856				
	Category	Term	Count	%	PValue	Genes
nucleus	GOTERM_BP_FAT	GO:0044271-nitrogen compound biosynthetic process	7	2.87	0.222507822	P97450, P05201, P61458, Q00612, P56382, Q9R1Z7, Q64737
nucleus	GOTERM_BP_FAT	GO:0009165-nucleotide biosynthetic process	4	1.64	0.416518023	P97450, Q00612, P56382, Q64737
nucleus	GOTERM_BP_FAT	GO:0009152-purine ribonucleotide biosynthetic process	3	1.23	0.423854353	P97450, P56382, Q64737
nucleus	GOTERM_BP_FAT	GO:0034654-nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	4	1.64	0.437892582	P97450, Q00612, P56382, Q64737
nucleus	GOTERM_BP_FAT	GO:0034404-nucleobase, nucleoside and nucleotide biosynthetic process	4	1.64	0.437892582	P97450, Q00612, P56382, Q64737
nucleus	GOTERM_BP_FAT	GO:0009260-ribonucleotide biosynthetic process	3	1.23	0.44226486	P97450, P56382, Q64737
nucleus	GOTERM_BP_FAT	GO:0009150-purine ribonucleotide metabolic process	3	1.23	0.478090326	P97450, P56382, Q64737
nucleus	GOTERM_BP_FAT	GO:0009259-ribonucleotide metabolic process	3	1.23	0.50402803	P97450, P56382, Q64737
nucleus	GOTERM_BP_FAT	GO:0006164-purine nucleotide biosynthetic process	3	1.23	0.553350511	P97450, P56382, Q64737
nucleus	GOTERM_BP_FAT	GO:0006163-purine nucleotide metabolic process	3	1.23	0.63794013	P97450, P56382, Q64737
	Annotation Cluster 56	Enrichment Score: 0.30667996102688244				
	Category	Term	Count	%	PValue	Genes
extracellular matrix/adhesion	GOTERM_BP_FAT	GO:0016477-cell migration	6	2.46	0.222626348	P02468, Q9JL26, P63001, Q8BRT1, Q61330, Q61301
extracellular matrix/adhesion	GOTERM_BP_FAT	GO:0048870-cell motility	6	2.46	0.335509471	P02468, Q9JL26, P63001, Q8BRT1, Q61330, Q61301
extracellular matrix/adhesion	GOTERM_BP_FAT	GO:0051674-localization of cell	6	2.46	0.335509471	P02468, Q9JL26, P63001, Q8BRT1, Q61330, Q61301
extracellular matrix/adhesion	GOTERM_BP_FAT	GO:0006928-cell motion	7	2.87	0.373726588	P02468, Q9JL26, P63001, Q8BRT1, Q61330, Q03173, Q61301
extracellular matrix/adhesion	SP_PIR_KEYWORDS	cell adhesion	5	2.05	0.757632024	P98203, Q640R3, P02468, Q61330, Q61301
extracellular matrix/adhesion	GOTERM_BP_FAT	GO:0007155-cell adhesion	7	2.87	0.772189749	Q811D0, P98203, Q640R3, P02468, P63001, Q61330, Q61301
extracellular matrix/adhesion	GOTERM_BP_FAT	GO:0022610-biological adhesion	7	2.87	0.77364754	Q811D0, P98203, Q640R3, P02468, P63001, Q61330, Q61301

extracellular matrix/adhesion	GOTERM_BP_FAT	GO:0016337-cell-cell adhesion	3	1.23	0.830414034	Q811D0, P98203, Q61301
	Annotation Cluster 57	Enrichment Score: 0.3057821581573837				
	Category	Term	Count	%	PValue	Genes
	GOTERM_CC_FAT	GO:0000267-cell fraction	10	4.10	0.456420595	Q62277, Q7TMB8, P50396, Q07076, Q9CPU4, P08556, P17047, P63001, Q05920, P14206
	GOTERM_CC_FAT	GO:0005626-insoluble fraction	9	3.69	0.460738236	Q62277, Q7TMB8, P50396, Q07076, Q9CPU4, P08556, P17047, P63001, P14206
	GOTERM_CC_FAT	GO:0005624-membrane fraction	8	3.28	0.575220079	Q62277, Q7TMB8, P50396, Q9CPU4, P08556, P17047, P63001, P14206
	Annotation Cluster 58	Enrichment Score: 0.25685232404041797				
	Category	Term	Count	%	PValue	Genes
immune	GOTERM_BP_FAT	GO:0002443-leukocyte mediated immunity	3	1.23	0.337582558	Q811D0, P84086, P98086
immune	GOTERM_BP_FAT	GO:0002252-immune effector process	3	1.23	0.508269998	Q811D0, P84086, P98086
immune	GOTERM_BP_FAT	GO:0006955-immune response	3	1.23	0.988481518	Q811D0, P84086, P98086
	Annotation Cluster 59	Enrichment Score: 0.24551935737046382				
	Category	Term	Count	%	PValue	Genes
development	SP_PIR_KEYWORDS	angiogenesis	3	1.23	0.204006356	P32921, P06745, P61148
development	GOTERM_BP_FAT	GO:0001525-angiogenesis	3	1.23	0.537297072	P32921, P06745, P61148
development	GOTERM_BP_FAT	GO:0048514-blood vessel morphogenesis	3	1.23	0.749562831	P32921, P06745, P61148
development	GOTERM_BP_FAT	GO:0001568-blood vessel development	3	1.23	0.844127186	P32921, P06745, P61148
development	GOTERM_BP_FAT	GO:0001944-vasculature development	3	1.23	0.853746841	P32921, P06745, P61148
	Annotation Cluster 60	Enrichment Score: 0.23843932597601025				
	Category	Term	Count	%	PValue	Genes
ion transport/channels	INTERPRO	IPR011992:EF-Hand type	5	2.05	0.343444183	Q8K394, Q9Z1B3, Q60902, Q3V0K9, Q8BH59
ion transport/channels	SMART	SM00054:EFh	3	1.23	0.392416259	Q60902, Q3V0K9, Q8BH59
ion transport/channels	INTERPRO	IPR018247:EF-HAND 1	4	1.64	0.521888042	P56375, Q60902, Q3V0K9, Q8BH59
ion transport/channels	INTERPRO	IPR002048:Calcium-binding EF-hand	3	1.23	0.536439301	Q60902, Q3V0K9, Q8BH59
ion transport/channels	INTERPRO	IPR018249:EF-HAND 2	3	1.23	0.751032478	Q60902, Q3V0K9, Q8BH59
ion transport/channels	SP_PIR_KEYWORDS	calcium	8	3.28	0.868315034	Q62277, Q9Z1B3, Q07076, Q60902, Q3V0K9, O08585, P54285, Q8BH59
ion transport/channels	GOTERM_MF_FAT	GO:0005509-calcium ion binding	9	3.69	0.870738179	Q62277, Q8K394, Q9Z1B3, Q07076, Q60902, Q3V0K9, O08585, P54285, Q8BH59
	Annotation Cluster 61	Enrichment Score: 0.19281743199543191				
	Category	Term	Count	%	PValue	Genes
ubiquitin	GOTERM_BP_FAT	GO:0030163-protein catabolic process	9	3.69	0.475557622	P35123, Q9D5V5, P54775, A2RT62, Q9ERU9, Q8CDG3, Q8BY87, Q9CXW3, Q3U487
ubiquitin	SP_PIR_KEYWORDS	ubl conjugation pathway	8	3.28	0.482424322	P35123, Q9D5V5, A2RT62, Q9ERU9, Q8CDG3, Q8BY87, Q9CXW3, Q3U487
metabolism	SP_PIR_KEYWORDS	thiol protease	3	1.23	0.487809466	P35123, Q8CDG3, Q8BY87
ubiquitin	GOTERM_BP_FAT	GO:0043632-modification-dependent macromolecule catabolic process	8	3.28	0.529724435	P35123, Q9D5V5, A2RT62, Q9ERU9, Q8CDG3, Q8BY87, Q9CXW3, Q3U487
ubiquitin	GOTERM_BP_FAT	GO:0019941-modification-dependent protein catabolic process	8	3.28	0.529724435	P35123, Q9D5V5, A2RT62, Q9ERU9, Q8CDG3, Q8BY87, Q9CXW3, Q3U487
ubiquitin	GOTERM_BP_FAT	GO:0006511-ubiquitin-dependent protein catabolic process	3	1.23	0.569009457	P35123, Q9D5V5, Q8BY87
metabolism	GOTERM_MF_FAT	GO:0008234-cysteine-type peptidase activity	3	1.23	0.575833757	P35123, Q8CDG3, Q8BY87
ubiquitin	GOTERM_BP_FAT	GO:0051603-proteolysis involved in cellular protein catabolic process	8	3.28	0.583076419	P35123, Q9D5V5, A2RT62, Q9ERU9, Q8CDG3, Q8BY87, Q9CXW3, Q3U487

ubiquitin	GOTERM_BP_FAT	GO:0044257-cellular protein catabolic process	8	3.28	0.589047209	P35123, Q9D5V5, A2RT62, Q9ERU9, Q8CDG3, Q8BY87, Q9CXW3, Q3U487
ubiquitin	GOTERM_BP_FAT	GO:0009057-macromolecule catabolic process	9	3.69	0.660079123	P35123, Q9D5V5, P54775, A2RT62, Q9ERU9, Q8CDG3, Q8BY87, Q9CXW3, Q3U487
ubiquitin	GOTERM_BP_FAT	GO:0044265-cellular macromolecule catabolic process	8	3.28	0.718234516	P35123, Q9D5V5, A2RT62, Q9ERU9, Q8CDG3, Q8BY87, Q9CXW3, Q3U487
ubiquitin	GOTERM_BP_FAT	GO:0006508-proteolysis	11	4.51	0.897894059	P35123, Q8VCT3, Q11011, Q9D5V5, A2RT62, Q9ERU9, Q8CDG3, Q8BY87, P98086, Q9CXW3, Q3U487
metabolism	SP_PIR_KEYWORDS	Protease	5	2.05	0.91579008	P35123, Q8VCT3, Q11011, Q8CDG3, Q8BY87
metabolism	GOTERM_MF_FAT	GO:0070011-peptidase activity, acting on L-amino acid peptides	5	2.05	0.960149221	P35123, Q8VCT3, Q11011, Q8CDG3, Q8BY87
metabolism	GOTERM_MF_FAT	GO:0008233-peptidase activity	5	2.05	0.968816934	P35123, Q8VCT3, Q11011, Q8CDG3, Q8BY87
neuron	Annotation Cluster 62	Enrichment Score: 0.18964112086943943				
neuron	Category	Term	Count	%	PValue	Genes
neuron	GOTERM_BP_FAT	GO:0007611-learning or memory	3	1.23	0.337582558	P08556, Q3UVX5, Q9JKK7
neuron	GOTERM_BP_FAT	GO:0007610-behavior	5	2.05	0.799275884	P08556, Q3UVX5, P63001, Q9JKK7, P62627
neuron	GOTERM_BP_FAT	GO:0050890-cognition	4	1.64	0.999999835	P08556, Q3UVX5, Q9JKK7, P58281
	Annotation Cluster 63	Enrichment Score: 0.14960602912802945				
	Category	Term	Count	%	PValue	Genes
development	GOTERM_BP_FAT	GO:0060562-epithelial tube morphogenesis	3	1.23	0.44226486	Q811D0, Q03173, Q4ACU6
development	GOTERM_BP_FAT	GO:0035239-tube morphogenesis	3	1.23	0.673756257	Q811D0, Q03173, Q4ACU6
development	GOTERM_BP_FAT	GO:0002009-morphogenesis of an epithelium	3	1.23	0.679952409	Q811D0, Q03173, Q4ACU6
development	GOTERM_BP_FAT	GO:0035295-tube development	4	1.64	0.693942686	Q811D0, Q03173, Q4ACU6, P61148
development	GOTERM_BP_FAT	GO:0048729-tissue morphogenesis	3	1.23	0.833940271	Q811D0, Q03173, Q4ACU6
development	GOTERM_BP_FAT	GO:0048598-embryonic morphogenesis	4	1.64	0.866002285	Q811D0, Q03173, Q4ACU6, Q7TQ95
development	GOTERM_BP_FAT	GO:0060429-epithelium development	3	1.23	0.883316712	Q811D0, Q03173, Q4ACU6
	Annotation Cluster 64	Enrichment Score: 0.12656767506069933				
	Category	Term	Count	%	PValue	Genes
	SP_PIR_KEYWORDS	membrane	81	33.20	0.232920648	P97441, O54774, Q6PAR5, Q64310, P21619, Q9D1C8, Q3UVX5, Q9DB10, Q61330, Q8BY89, Q9CQV7, Q8BH59, Q9CY27, Q99L43, Q9QWY8, Q80ZJ1, P17047, Q7TQ95, Q810B6, P70336, P97450, P84091, Q9CQ85, O08585, Q9CQW1, P63001, Q66GT5, O35609, Q8BTY2, P56382, Q6PFD5, Q8R4H2, Q9JKD3, Q61301, Q4ACU6, Q9DCP2, Q8BI08, Q62277, Q9QYB5, Q9ERS2, P47802, O35683, Q6NVE8, Q9ESW4, Q9CPP6, Q791T5, Q640R3, Q924L1, Q8K2C9, Q9CR95, P14206, Q80TR1, P63080, Q9ERG2, Q68FD9, Q9JKL4, Q8K3H0, O70161, Q9EPR4, Q7SIG6, Q8BWQ6, Q8JZR6, Q811D0, Q9D0L7, P08556, Q9CPU4, P39054, Q8R5J9, Q9CQ69, Q80UG2, P61620, P58281, Q5XJV6, Q80U40, Q8C0L0, Q3UPL0, Q60902, O88653, Q8BMI3, Q69ZW3, P03893
	UP_SEQ_FEATURE	transmembrane region	40	16.39	0.999893895	Q791T5, P97441, Q64310, Q640R3, Q924L1, Q3UVX5, Q9DB10, Q8K2C9, Q8BY89, Q9CQV7, Q9CY27, Q99L43, Q8BH59, Q80TR1, P17047, P63080, Q68FD9, Q9EPR4, Q7TQ95, Q8BWQ6, Q8JZR6, Q9D0L7, Q9CPU4, Q9CQ85, Q8R5J9, O35609, Q8BTY2, Q80UG2, Q9JKD3, P61620, Q8BI08, Q9DCP2, P58281, Q62277, Q5XJV6, Q9ERS2, Q8C0L0, P47802, O35683, P03893
	SP_PIR_KEYWORDS	transmembrane	40	16.39	0.999999373	Q791T5, P97441, Q64310, Q640R3, Q924L1, Q3UVX5, Q9DB10, Q8K2C9, Q8BY89, Q9CQV7, Q9CY27, Q99L43, Q8BH59, Q80TR1, P17047, P63080, Q68FD9, Q9EPR4, Q7TQ95, Q8BWQ6, Q8JZR6, Q9D0L7, Q9CPU4, Q9CQ85, Q8R5J9, O35609, Q8BTY2, Q80UG2, Q9JKD3, P61620, Q8BI08, Q9DCP2, P58281, Q62277, Q5XJV6, Q9ERS2, Q8C0L0, P47802, O35683, P03893
	GOTERM_CC_FAT	GO:0016021-integral to membrane	46	18.85	0.999999986	Q791T5, P97441, Q64310, Q640R3, Q924L1, Q3UVX5, Q9DB10, Q8BKC5, Q8K2C9, Q8BY89, Q9CQV7, Q9CY27, Q99L43, Q8BH59, Q7TSC1, Q80TR1, P17047, P63080, Q68FD9, Q9EPR4, Q7TQ95, Q8BWQ6, Q8JZR6, Q9D0L7, Q9CPU4, P54285, Q9CQ85, Q9CQW1, Q8R5J9, O35609, Q8BTY2, Q91YE6, Q80UG2, Q9JKD3, P61620, Q8BI08, Q9DCP2, P58281, Q62277, Q5XJV6, Q9ERS2, Q8C0L0, P47802, O35683, Q9ERU9, P03893
	GOTERM_CC_FAT	GO:0031224-intrinsic to membrane	48	19.67	0.999999992	Q791T5, P97441, Q64310, Q640R3, Q924L1, Q3UVX5, Q9DB10, Q61330, Q8BKC5, Q8K2C9, Q8BY89, Q9CQV7, Q9CY27, Q99L43, Q8BH59, Q7TSC1, Q80TR1, P17047, P63080, Q68FD9, Q9EPR4, Q7TQ95, Q8BWQ6, Q8JZR6, Q9D0L7, P08556, Q9CPU4, P54285, Q9CQ85, Q9CQW1, Q8R5J9, O35609, Q8BTY2, Q91YE6, Q80UG2, Q9JKD3, P61620, Q8BI08, Q9DCP2, P58281, Q62277, Q5XJV6, Q9ERS2, Q8C0L0, P47802, O35683, Q9ERU9, P03893
	Annotation Cluster 65	Enrichment Score: 0.11367067751158477				
	Category	Term	Count	%	PValue	Genes
signaling	GOTERM_BP_FAT	GO:0006793-phosphorus metabolic process	14	5.74	0.383916228	P70336, P97450, Q3UU96, Q5F2E8, O35609, Q66GT5, P56382, Q9EPW0, Q5XJV6, Q58A65, O88653, Q9ESW4, P03893, Q9DBR7
signaling	GOTERM_BP_FAT	GO:0006796-phosphate metabolic process	14	5.74	0.383916228	P70336, P97450, Q3UU96, Q5F2E8, O35609, Q66GT5, P56382, Q9EPW0, Q5XJV6, Q58A65, O88653, Q9ESW4, P03893, Q9DBR7
signaling	GOTERM_BP_FAT	GO:0016310-phosphorylation	11	4.51	0.503040089	Q5XJV6, P70336, P97450, Q58A65, O88653, Q3UU96, Q5F2E8, O35609, Q9ESW4, P56382, P03893
signaling	SMART	SM00220:S_TKc	3	1.23	0.740973629	P70336, Q3UU96, Q5F2E8
signaling	GOTERM_MF_FAT	GO:0004674-protein serine/threonine kinase activity	5	2.05	0.809676528	Q5XJV6, P70336, Q3UU96, Q5F2E8, O35609
signaling	UP_SEQ_FEATURE	binding site:ATP	7	2.87	0.838653594	Q5XJV6, P70336, Q3UU96, Q5F2E8, Q8BIJ6, Q8BU30, Q05920

signaling	INTERPRO	IPR008271:Serine/threonine protein kinase, active site	4	1.64	0.852418921	P70336, Q3UU96, Q5F2E8, O35609
signaling	INTERPRO	IPR002290:Serine/threonine protein kinase	3	1.23	0.863688074	P70336, Q3UU96, Q5F2E8
signaling	GOTERM_BP_FAT	GO:0006468-protein amino acid phosphorylation	7	2.87	0.867080595	Q5XJV6, P70336, Q58A65, O88653, Q3UU96, Q5F2E8, O35609
signaling	INTERPRO	IPR017442:Serine/threonine protein kinase-related	4	1.64	0.869744676	P70336, Q3UU96, Q5F2E8, O35609
signaling	UP_SEQ_FEATURE	active site:Proton acceptor	8	3.28	0.879539137	Q5XJV6, P70336, Q3UU96, Q5F2E8, Q00612, Q9R1Z7, Q8BWF0, P05063
signaling	INTERPRO	IPR000719:Protein kinase, core	5	2.05	0.887027402	Q5XJV6, P70336, Q3UU96, Q5F2E8, O35609
signaling	SP_PIR_KEYWORDS	serine/threonine-protein kinase	4	1.64	0.894163027	Q5XJV6, P70336, Q3UU96, Q5F2E8
signaling	SP_PIR_KEYWORDS	kinase	7	2.87	0.919240149	Q5XJV6, P70336, P12367, Q3UU96, Q5F2E8, Q9ESW4, O70161
signaling	INTERPRO	IPR017441:Protein kinase, ATP binding site	4	1.64	0.945665686	Q5XJV6, P70336, Q3UU96, Q5F2E8
signaling	GOTERM_MF_FAT	GO:0004672-protein kinase activity	5	2.05	0.952030621	Q5XJV6, P70336, Q3UU96, Q5F2E8, O35609
signaling	UP_SEQ_FEATURE	domain:Protein kinase	4	1.64	0.977098474	Q5XJV6, P70336, Q3UU96, Q5F2E8
	Annotation Cluster 66	Enrichment Score: 0.10924070055997286				
	Category	Term	Count	%	PValue	Genes
Transcription	GOTERM_BP_FAT	GO:0016071-mRNA metabolic process	5	2.05	0.583241476	Q3U0V1, Q9Z130, Q923D5, P59708, Q60668
Transcription	SP_PIR_KEYWORDS	mrna splicing	3	1.23	0.732123995	Q3U0V1, Q923D5, P59708
Transcription	GOTERM_BP_FAT	GO:0008380-RNA splicing	3	1.23	0.756983016	Q3U0V1, Q923D5, P59708
Transcription	SP_PIR_KEYWORDS	mrna processing	3	1.23	0.837729576	Q3U0V1, Q923D5, P59708
Transcription	GOTERM_BP_FAT	GO:0006397-mRNA processing	3	1.23	0.87138728	Q3U0V1, Q923D5, P59708
Transcription	GOTERM_BP_FAT	GO:0006396-RNA processing	4	1.64	0.936961087	Q3U0V1, Q8BGQ7, Q923D5, P59708
	Annotation Cluster 67	Enrichment Score: 0.08905784755672848				
	Category	Term	Count	%	PValue	Genes
protein modif	GOTERM_MF_FAT	GO:0042803-protein homodimerization activity	3	1.23	0.725454755	Q9D7X8, Q00612, Q9R1Z7
protein modif	GOTERM_MF_FAT	GO:0046983-protein dimerization activity	4	1.64	0.82939239	Q9D7X8, Q00612, Q9R1Z7, Q80UJ7
protein modif	GOTERM_MF_FAT	GO:0042802-identical protein binding	3	1.23	0.898371735	Q9D7X8, Q00612, Q9R1Z7
	Annotation Cluster 68	Enrichment Score: 0.0849823566502917				
	Category	Term	Count	%	PValue	Genes
apoptosis	GOTERM_BP_FAT	GO:0043523-regulation of neuron apoptosis	3	1.23	0.292952292	P08556, Q8BGQ7, Q7TSC1
apoptosis	GOTERM_BP_FAT	GO:0043065-positive regulation of apoptosis	3	1.23	0.850601711	Q791T5, Q9ERS2, Q7TSC1
apoptosis	GOTERM_BP_FAT	GO:0043068-positive regulation of programmed cell death	3	1.23	0.853746841	Q791T5, Q9ERS2, Q7TSC1
apoptosis	GOTERM_BP_FAT	GO:0010942-positive regulation of cell death	3	1.23	0.85683182	Q791T5, Q9ERS2, Q7TSC1
apoptosis	GOTERM_BP_FAT	GO:0006915-apoptosis	5	2.05	0.876820806	Q791T5, Q9ERS2, Q9D7X8, Q7TSC1, P58281
apoptosis	GOTERM_BP_FAT	GO:0012501-programmed cell death	5	2.05	0.884920111	Q791T5, Q9ERS2, Q9D7X8, Q7TSC1, P58281
apoptosis	GOTERM_BP_FAT	GO:0008219-cell death	5	2.05	0.914403097	Q791T5, Q9ERS2, Q9D7X8, Q7TSC1, P58281
apoptosis	GOTERM_BP_FAT	GO:0016265-death	5	2.05	0.923089674	Q791T5, Q9ERS2, Q9D7X8, Q7TSC1, P58281
apoptosis	GOTERM_BP_FAT	GO:0042981-regulation of apoptosis	5	2.05	0.943585611	Q791T5, Q9ERS2, P08556, Q8BGQ7, Q7TSC1
apoptosis	SP_PIR_KEYWORDS	Apoptosis	3	1.23	0.944047971	Q791T5, Q9ERS2, P58281
apoptosis	GOTERM_BP_FAT	GO:0043067-regulation of programmed cell death	5	2.05	0.947135157	Q791T5, Q9ERS2, P08556, Q8BGQ7, Q7TSC1
apoptosis	GOTERM_BP_FAT	GO:0010941-regulation of cell death	5	2.05	0.948593292	Q791T5, Q9ERS2, P08556, Q8BGQ7, Q7TSC1
	Annotation Cluster 69	Enrichment Score: 0.07145885996834248				
	Category	Term	Count	%	PValue	Genes
	SP_PIR_KEYWORDS	repressor	6	2.46	0.610600382	Q8CGF7, Q9D8T7, Q99020, Q91WV0, Q9Z130, O88712
	GOTERM_MF_FAT	GO:0003700-transcription factor activity	3	1.23	0.999701445	Q8CGF7, Q99020, O88712
	GOTERM_MF_FAT	GO:0030528-transcription regulator activity	4	1.64	0.999990856	Q8CGF7, Q99020, P61458, O88712
	Annotation Cluster 70	Enrichment Score: 0.06689470027656456				
	Category	Term	Count	%	PValue	Genes
cell cycle	GOTERM_BP_FAT	GO:0007049-cell cycle	8	3.28	0.721401538	P54227, Q9DB27, Q9ERD7, Q640R3, Q8CHH9, Q8BRT1, Q8K3H0, P84089
cell cycle	GOTERM_BP_FAT	GO:0000278-mitotic cell cycle	3	1.23	0.844127186	P54227, Q9ERD7, Q8BRT1
cell cycle	GOTERM_BP_FAT	GO:0000279-M phase	3	1.23	0.897640891	P54227, Q9ERD7, Q8BRT1
cell cycle	GOTERM_BP_FAT	GO:0022402-cell cycle process	4	1.64	0.902852894	P54227, Q9ERD7, Q640R3, Q8BRT1
cell cycle	GOTERM_BP_FAT	GO:0022403-cell cycle phase	3	1.23	0.938041223	P54227, Q9ERD7, Q8BRT1

	Annotation Cluster 71	Enrichment Score: 0.04894286341993925				
	Category	Term	Count	%	PValue	Genes
Transcription	SP_PIR_KEYWORDS	repressor	6	2.46	0.610600382	Q8CGF7, Q9D8T7, Q99020, Q91WV0, Q9Z130, O88712
Transcription	GOTERM_MF_FAT	GO:0003723-RNA binding	9	3.69	0.665557928	Q9DB27, Q9D8T7, Q99020, P28271, Q3U0V1, Q8K310, Q9Z130, P59708, Q60668
Transcription	SP_PIR_KEYWORDS	transcription regulation	10	4.10	0.999228051	Q9DB27, Q8CGF7, Q9D8T7, Q99020, Q91WV0, Q3U0V1, Q9Z130, O88712, Q64152, Q60668
Transcription	SP_PIR_KEYWORDS	dna-binding	7	2.87	0.999904897	Q99020, P10922, Q91WV0, Q3U0V1, O54962, Q9Z130, Q60668
Transcription	GOTERM_MF_FAT	GO:0003677-DNA binding	10	4.10	0.999907867	Q8CGF7, Q99020, P10922, Q91WV0, Q3U0V1, O54962, Q9Z130, Q8VD37, O88712, Q60668
Transcription	SP_PIR_KEYWORDS	Transcription	10	4.10	0.999915688	Q9DB27, Q8CGF7, Q9D8T7, Q99020, Q91WV0, Q3U0V1, Q9Z130, O88712, Q64152, Q60668
Transcription	GOTERM_BP_FAT	GO:0006350-transcription	10	4.10	0.999930733	Q9DB27, Q8CGF7, Q9D8T7, Q99020, Q91WV0, Q3U0V1, Q9Z130, O88712, Q64152, Q60668
Transcription	GOTERM_BP_FAT	GO:0045449-regulation of transcription	12	4.92	0.99999439	Q9DB27, Q8CGF7, Q9D8T7, Q9ERS2, Q99020, P61458, Q91WV0, Q3U0V1, Q9Z130, O88712, Q64152, Q60668

	Annotation Cluster 72	Enrichment Score: 0.013319303816877494				
	Category	Term	Count	%	PValue	Genes
	GOTERM_BP_FAT	GO:0045892-negative regulation of transcription, DNA-dependent	3	1.23	0.922398689	Q9ERS2, Q99020, O88712
	GOTERM_BP_FAT	GO:0051253-negative regulation of RNA metabolic process	3	1.23	0.924115634	Q9ERS2, Q99020, O88712
	GOTERM_BP_FAT	GO:0016481-negative regulation of transcription	3	1.23	0.962613102	Q9ERS2, Q99020, O88712
	GOTERM_BP_FAT	GO:0010605-negative regulation of macromolecule metabolic process	4	1.64	0.968999363	Q9ERS2, Q99020, Q9D1C8, O88712
	GOTERM_BP_FAT	GO:0045934-negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	3	1.23	0.972092082	Q9ERS2, Q99020, O88712
	GOTERM_BP_FAT	GO:0051172-negative regulation of nitrogen compound metabolic process	3	1.23	0.973376521	Q9ERS2, Q99020, O88712
	GOTERM_BP_FAT	GO:0010629-negative regulation of gene expression	3	1.23	0.976062163	Q9ERS2, Q99020, O88712
	GOTERM_BP_FAT	GO:0010558-negative regulation of macromolecule biosynthetic process	3	1.23	0.978229005	Q9ERS2, Q99020, O88712
	GOTERM_BP_FAT	GO:0031327-negative regulation of cellular biosynthetic process	3	1.23	0.981128847	Q9ERS2, Q99020, O88712
	GOTERM_BP_FAT	GO:0009890-negative regulation of biosynthetic process	3	1.23	0.982009843	Q9ERS2, Q99020, O88712
	GOTERM_BP_FAT	GO:0051252-regulation of RNA metabolic process	4	1.64	0.999999853	Q9ERS2, Q99020, O88712, Q60668
	GOTERM_BP_FAT	GO:0006355-regulation of transcription, DNA-dependent	3	1.23	0.999999983	Q9ERS2, Q99020, O88712

	Annotation Cluster 73	Enrichment Score: 0.006724244229075689				
	Category	Term	Count	%	PValue	Genes
nucleus	GOTERM_CC_FAT	GO:0031981-nuclear lumen	8	3.28	0.968119809	Q8CGF7, Q9ERS2, P21619, Q4KMM3, Q8K310, O88712, Q8K3H0, Q923D5
nucleus	GOTERM_CC_FAT	GO:0005654-nucleoplasm	4	1.64	0.991343193	Q9ERS2, O88712, Q8K3H0, Q923D5
nucleus	GOTERM_CC_FAT	GO:0044451-nucleoplasm part	3	1.23	0.994658806	O88712, Q8K3H0, Q923D5

	Annotation Cluster 74	Enrichment Score: 0.003751763296613519				
	Category	Term	Count	%	PValue	Genes
	GOTERM_MF_FAT	GO:0046872-metal ion binding	40	16.39	0.981692563	P97441, P54071, Q11011, Q8VCT3, Q3UH68, P28271, Q8BIJ6, Q9R1Z7, Q91V92, Q8VD37, Q64737, Q9CY27, Q8BH59, Q9QWY8, Q9Z1B3, Q8K310, Q8BU30, Q9EPR4, Q7SIG6, Q9JI46, Q8JZR6, Q810B6, Q8K394, P70336, Q07076, Q9CPW2, Q8BIW1, Q3V0K9, Q3UU96, P54285, O08585, Q8BTY2, Q05920, Q9DCP2, Q62277, Q3UHD9, Q9QYB5, Q60902, P19096, Q9ERU9
	GOTERM_MF_FAT	GO:0043167-ion binding	41	16.80	0.981850544	P97441, P54071, Q11011, Q8VCT3, Q3UH68, P28271, Q8BIJ6, Q9R1Z7, Q91V92, Q8VD37, Q64737, Q9CY27, Q8BH59, Q9QWY8, Q9Z1B3, P63080, Q8K310, Q8BU30, Q9EPR4, Q7SIG6, Q9JI46, Q8JZR6, Q810B6, Q8K394, P70336, Q07076, Q9CPW2, Q8BIW1, Q3V0K9, Q3UU96, P54285, O08585, Q8BTY2, Q05920, Q9DCP2, Q62277, Q3UHD9, Q9QYB5, Q60902, P19096, Q9ERU9
	GOTERM_MF_FAT	GO:0043169-cation binding	40	16.39	0.984815269	P97441, P54071, Q11011, Q8VCT3, Q3UH68, P28271, Q8BIJ6, Q9R1Z7, Q91V92, Q8VD37, Q64737, Q9CY27, Q8BH59, Q9QWY8, Q9Z1B3, Q8K310, Q8BU30, Q9EPR4, Q7SIG6, Q9JI46, Q8JZR6, Q810B6, Q8K394, P70336, Q07076, Q9CPW2, Q8BIW1, Q3V0K9, Q3UU96, P54285, O08585, Q8BTY2, Q05920, Q9DCP2, Q62277, Q3UHD9, Q9QYB5, Q60902, P19096, Q9ERU9
	GOTERM_MF_FAT	GO:0046914-transition metal ion binding	24	9.84	0.991002582	Q810B6, P70336, P97441, P54071, Q8VCT3, Q11011, Q9CPW2, Q8BIW1, P28271, Q3UU96, Q3UH68, Q9R1Z7, Q8BIJ6, Q05920, Q8VD37, Q64737, Q9CY27, Q9QWY8, Q3UHD9, Q8K310, P19096, Q9ERU9, Q8BU30, Q7SIG6
	GOTERM_MF_FAT	GO:0008270-zinc ion binding	17	6.97	0.996645569	Q810B6, P70336, P97441, Q11011, Q8VCT3, Q3UU96, Q3UH68, Q9R1Z7, Q8BIJ6, Q8VD37, Q9QWY8, Q3UHD9, Q8K310, P19096, Q9ERU9, Q8BU30, Q7SIG6
	SP_PIR_KEYWORDS	zinc-finger	8	3.28	0.99745826	Q810B6, P70336, Q3UHD9, Q3UU96, Q8K310, Q9ERU9, Q8VD37, Q9QWY8

	SP_PIR_KEYWORDS	zinc	14	5.74	0.998503309	Q810B6, P70336, P97441, Q11011, Q8VCT3, Q3UU96, Q3UH68, Q9R1Z7, Q8VD37, Q9QWY8, Q3UHD9, Q8K310, Q9ERU9, Q7SIG6
	SP_PIR_KEYWORDS	metal-binding	21	8.61	0.999425597	Q810B6, P70336, P54071, Q8VCT3, Q11011, Q9CPW2, Q8BIW1, P28271, Q3UU96, Q3UH68, Q9R1Z7, Q91V92, Q05920, Q8VD37, Q64737, Q9QWY8, Q3UHD9, Q8K310, Q9ERU9, Q7SIG6, Q9JI46
	Annotation Cluster 75	Enrichment Score: 7.09913148354024E-4				
	Category	Term	Count	%	PValue	Genes
extracellular matrix/adhesion	GOTERM_CC_FAT	GO:0005615-extracellular space	3	1.23	0.994519213	Q8VCT3, P06745, P61148
extracellular matrix/adhesion	GOTERM_CC_FAT	GO:0044421-extracellular region part	4	1.64	0.998961401	Q8VCT3, P02468, P06745, P61148
extracellular matrix/adhesion	SP_PIR_KEYWORDS	Secreted	5	2.05	0.999996701	Q8VCT3, P02468, P06745, Q8CC88, P98086
extracellular matrix/adhesion	GOTERM_CC_FAT	GO:0005576-extracellular region	6	2.46	0.999999757	Q8VCT3, P02468, P06745, Q8CC88, P61148, P98086
	Annotation Cluster 76	Enrichment Score: 1.538419080175349E-7				
	Category	Term	Count	%	PValue	Genes
	SP_PIR_KEYWORDS	disulfide bond	13	5.33	0.999998109	Q9EQQ9, Q640R3, P97493, Q80UG2, Q61330, Q80TR1, Q8C0L0, P17047, P02468, P63080, Q8BWF0, P98086, Q9QUH0
	UP_SEQ_FEATURE	disulfide bond	13	5.33	0.999999802	Q9EQQ9, Q640R3, P97493, Q80UG2, Q61330, Q80TR1, Q8C0L0, P17047, P02468, P63080, Q8BWF0, P98086, Q9QUH0
	SP_PIR_KEYWORDS	signal	14	5.74	0.999999975	Q640R3, Q3UVX5, Q8CC88, Q80UG2, Q61330, Q5XJV6, Q80TR1, Q8C0L0, P17047, P02468, Q8BHN3, Q9JKR6, P63080, P98086
	SP_PIR_KEYWORDS	glycoprotein	19	7.79	0.999999989	Q640R3, Q924L1, Q3UVX5, Q8BTY2, Q80UG2, Q61330, Q8BY89, Q9DCP2, Q8BI08, Q9CY27, Q62277, Q80TR1, P17047, P02468, Q8BHN3, Q9JKR6, P63080, Q9EPR4, P98086
	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	19	7.79	1	Q640R3, Q924L1, Q3UVX5, Q8BTY2, Q80UG2, Q61330, Q8BY89, Q9DCP2, Q8BI08, Q9CY27, Q62277, Q80TR1, P17047, P02468, Q8BHN3, Q9JKR6, P63080, Q9EPR4, P98086
	UP_SEQ_FEATURE	signal peptide	14	5.74	1	Q640R3, Q3UVX5, Q8CC88, Q80UG2, Q61330, Q5XJV6, Q80TR1, Q8C0L0, P17047, P02468, Q8BHN3, Q9JKR6, P63080, P98086
	Unclustered terms					
	SP_PIR_KEYWORDS	phosphoprotein	164	67.21	8.33551E-25	O54774, P97441, P32921, P21619, Q8VBV7, O54962, P23116, Q8BKC5, Q64737, Q8BY87, P59708, Q8CCN5, P98203, Q8CHH9, Q6P9K8, Q8BWF0, Q9JMH9, Q5SSM3, P70336, Q99020, Q6A065, O35609, Q8R4H2, P14115, Q9QYB5, Q80X50, P54775, P52196, P19096, Q8C1B1, Q9CXW3, Q148V7, Q8QZZ7, Q5DU25, Q3UH68, Q9CQX8, Q8BIJ6, Q91V92, Q8K2C9, O08788, Q9D051, Q8CGY8, Q9CR95, Q9D8S9, Q80UJ7, Q9D8T7, Q58A65, Q00612, Q9D1L0, Q9EPR4, Q7SIG6, Q5SXY1, P28740, P48722, Q9QWI6, P08556, P54285, Q8BGQ7, O88712, P58281, P05063, Q9CZD3, P50396, Q8C0L0, Q3UPL0, Q8BRT1, P27546, Q8BMI3, Q9ERU9, Q9DB70, P03893, Q9DBR7, Q9CQI3, Q9EQQ9, Q6PAR5, Q9Z2H5, Q9CPR4, Q9R1Z7, Q03173, Q8VD37, Q99L43, Q9D832, Q60668, Q7TSC1, Q9QWY8, Q9Z1B3, Q60865, Q6Y7W8, Q9Z130, Q9D8E6, Q7TQ95, Q8K394, Q3V0K9, P84091, O08585, Q91WV0, P63001, Q8BTY2, Q6PFD5, P06745, Q05920, Q61301, Q4ACU6, Q9DCP2, Q62277, P54227, Q91VR8, Q7TMB8, Q3UHD9, P12367, Q0GNC1, Q9JL26, Q6NVE8, P84086, Q4KMM3, P36536, Q64152, Q9D0R2, Q791T5, Q8CGF7, Q640R3, A2AG50, Q5F2E8, Q62446, Q6PDI5, Q8CDG3, Q923D5, P14206, Q61316, P35123, Q8BVQ5, Q80TR1, Q9QXL2, P19246, Q9ERG2, Q8K310, Q68FD9, Q8K3H0, O70161, Q9DB27, Q8JZR6, Q8BWQ6, Q811D0, Q9D0L7, P05201, P10922, Q3TDD9, Q3UU96, P26638, P39054, Q80UG2, Q80U49, Q9EPW0, Q3TES0, Q5XJV6, Q9D5V5, Q80U40, P60469, Q60902, Q3U0V1,
	SP_PIR_KEYWORDS	acetylation	92	37.70	1.17312E-22	Q9CQI3, P54071, Q11011, Q6PAR5, P21619, Q60597, Q8BKC5, P23116, Q9CQV7, Q8BY87, Q9CY27, Q64737, Q7TSC1, P59708, Q60668, Q9Z1B3, Q9DCW4, P61458, Q8CHH9, Q8BWF0, P61971, Q9Z130, Q8BU30, Q9D8E6, Q8K394, Q810B6, P97450, Q99020, O35127, Q07076, Q91WV0, P06745, P56382, Q91YE6, P62627, P14115, Q05920, Q61301, P54227, Q91VR8, Q7TMB8, Q9ERS2, P54775, Q80X50, P12367, P52196, Q8BGS2, Q6NVE8, P84086, Q9ESW4, P19096, Q9CZU6, P84089, Q9QUH0, Q9CXW3, Q9D0R2, Q9CPP6, Q8VCT3, Q148V7, P97493, Q8BIJ6, Q62446, Q91V92, O08788, Q8CGY8, Q8CDG3, Q923D5, P14206, Q61316, Q8BVQ5, Q58A65, Q8BLY2, Q00612, Q8K310, Q9DB27, Q9CQ60, P48722, Q61035, P26638, P39054, Q8R5J9, Q80UG2, Q8BGQ7, Q9EQ80, P58281, P05063, Q9CZD3, Q9ERD7, Q60902, Q3U0V1, P27546, Q9ERU9
	SP_PIR_KEYWORDS	cytoplasm	95	38.93	2.64391E-16	Q9EQQ9, O54774, Q11011, P32921, Q9Z2H5, Q8VBV7, O54962, Q8BKC5, P23116, Q03173, Q7TSC1, Q60668, Q9QWY8, P61458, Q60865, Q8CHH9, Q8BPM0, Q6P9K8, Q9Z130, P61971, Q8BU30, Q9JMH9, Q810B6, Q8K394, P70336, Q99020, Q3V0K9, Q8BIW1, Q6A065, Q9CPW4, Q9CQW1, P06745, Q8R4H2, Q91YE6, P62627, Q61301, Q4ACU6, P54227, Q91VR8, Q3UHD9, Q9QYB5, Q7TMB8, P54775, Q9JL26, Q6NVE8, P84086, P19096, Q9QUH0, Q9CXW3, Q9D0R2, Q640R3, Q8QZZ7, Q5DU25, P28271, Q5F2E8, Q91V92, O08788, Q8CGY8, Q6PDI5, P14206, Q923D5, Q80UJ7, Q61316, Q58A65, Q9QXL2, Q8BLY2, Q9ERG2, Q7SIG6, Q9JI46, Q9DB27, Q9CQ60, P05201, P28740, P48722, Q9QWI6, Q9WVL0, Q3UU96, P26638, Q8R5J9, P39054, Q80U49, Q8BGQ7, O88712, Q9EQ80, Q3TES0, P50396, Q3UPL0, P60469, Q3U0V1, Q8BRT1, Q9JKK7, O88851, Q61699, Q69ZW3, Q9DBR7
	SP_PIR_KEYWORDS	alternative splicing	94	38.52	2.28687E-06	Q9EQQ9, P32921, Q6PAR5, Q9Z2H5, P21619, Q3UVX5, Q60597, Q8BKC5, Q8BY89, Q8VD37, Q03173, Q9CQV7, Q8BY87, Q64737, Q60668, Q9QWY8, Q8CCN5, Q9Z1B3, P98203, Q80ZJ1, P17047, Q6Y7W8, Q8CHH9, Q8BPM0, Q6P9K8, Q9JMH9, Q5SSM3, Q810B6, Q9CPW2, Q6A065, Q8BTY2, Q8CC88, Q61301, Q3UHD9, Q9QYB5, Q7TMB8, Q80X50, Q0GNC1, Q9JL26, Q8BGS2, Q6NVE8, Q4KMM3, Q9ESW4, Q64152, Q8C1B1, Q791T5, Q8CGF7, Q148V7, Q924L1, A2AG50, Q3UH68, O08788, Q8CGY8, Q6PDI5, Q8CDG3, Q3U487, Q9D8T7, Q80TR1, Q58A65, Q9QXL2, Q8BHN3, Q68FD9, O70161, Q9EPR4, Q7SIG6, Q5SXY1, Q8BWQ6, Q8JZR6, Q9DB27, Q811D0, Q9D0L7, P28740, P48722, Q9QWI6, Q3TDD9, P54285, Q3UU96, P39054, Q80U49, O88712, Q9EPW0, P58281, Q80U40, Q3UPL0, Q60902, P27546, Q8BRT1, Q9JKK7, Q05A62, Q8BWR2, P62881, Q61699, Q69ZW3, Q9DBR7

	SP_PIR_KEYWORDS	coiled coil	47	19.26	5.84578E-06	Q8CGF7, P21619, Q148V7, A2AG50, Q5DU25, Q5F2E8, Q3UH68, O08788, Q8K2C9, P23116, Q03173, Q923D5, P98203, Q58A65, Q9QXL2, P19246, Q8BLY2, Q60865, Q8CHH9, Q8BPM0, Q9ERG2, Q8K3H0, Q7SIG6, Q9JMH9, Q7TQ95, Q5SXY1, P70336, P28740, Q9QWI6, Q6A065, Q3TDD9, Q3UU96, Q9CQW1, Q8R4H2, Q4ACU6, P58281, Q3TES0, P54227, Q91VR8, Q60902, P60469, Q0GNC1, P02468, Q6NVE8, Q8BRT1, P84086, Q69ZW3
	UP_SEQ_FEATURE	splice variant	93	38.11	0.000369031	Q9EQQ9, P32921, Q6PAR5, Q9Z2H5, P21619, Q3UVX5, Q60597, Q8BKC5, Q8BY89, Q8VD37, Q03173, Q9CQV7, Q8BY87, Q64737, Q60668, Q9QWY8, Q8CCN5, Q9Z1B3, P98203, Q80ZJ1, P17047, Q6Y7W8, Q8CHH9, Q8BPM0, Q6P9K8, Q9JMH9, Q5SSM3, Q810B6, Q9CPW2, Q6A065, Q8BTY2, Q8CC88, Q61301, Q3UHD9, Q9QYB5, Q7TMB8, Q80X50, Q0GNC1, Q9JL26, Q8BGS2, Q6NVE8, Q4KMM3, Q9ESW4, Q64152, Q8C1B1, Q791T5, Q8CGF7, Q148V7, Q924L1, A2AG50, Q3UH68, O08788, Q8CGY8, Q6PDI5, Q8CDG3, Q3U487, Q9D8T7, Q80TR1, Q58A65, Q9QXL2, Q8BHN3, Q68FD9, O70161, Q9EPR4, Q7SIG6, Q5SXY1, Q8BWQ6, Q8JZR6, Q9DB27, Q811D0, Q9D0L7, P28740, P48722, Q9QWI6, Q3TDD9, Q3UU96, P39054, Q80U49, O88712, Q9EPW0, P58281, Q80U40, Q3UPL0, Q60902, P27546, Q8BRT1, Q9JKK7, Q05A62, Q8BWR2, P62881, Q61699, Q69ZW3, Q9DBR7
	UP_SEQ_FEATURE	compositionally biased region:Pro-rich	24	9.84	0.000486687	Q8CGF7, Q5DU25, P39054, Q03173, Q8VD37, Q4ACU6, Q8CDG3, Q3TES0, Q923D5, Q9QWY8, Q5XJV6, Q60902, Q3UPL0, Q0GNC1, Q9JL26, Q6Y7W8, Q6NVE8, Q8BMI3, Q8BPM0, Q6P9K8, Q69ZW3, Q5SSM3, Q7SIG6, Q7TQ95
	GOTERM_CC_FAT	GO:0005768-endosome	12	4.92	0.00083931	Q810B6, Q6PAR5, Q3UHD9, Q3UPL0, P17047, Q9D1C8, O88653, Q6NVE8, Q8BMI3, Q9JKD3, Q8K3H0, Q6PDI5
	UP_SEQ_FEATURE	domain:WHEP-TRS	3	1.23	0.001347319	Q9CZD3, P32921, Q61035
	SP_PIR_KEYWORDS	endosome	10	4.10	0.001512208	Q810B6, Q6PAR5, P17047, Q9D1C8, O88653, Q6NVE8, Q8BMI3, Q9JKD3, Q8K3H0, Q6PDI5
	GOTERM_CC_FAT	GO:0009898-internal side of plasma membrane	12	4.92	0.002367904	O54774, Q9QYB5, Q3UPL0, Q640R3, P08556, Q80ZJ1, P84091, O88653, O08585, Q9CQW1, P63001, Q61301
	INTERPRO	IPR000738:WHEP-TRS	3	1.23	0.002461186	Q9CZD3, P32921, Q61035
	INTERPRO	IPR012947:Threonyl/alanyl tRNA synthetase, SAD	3	1.23	0.002461186	Q8BLY2, Q8BGQ7, Q9D0R2
	GOTERM_MF_FAT	GO:0005522-profilin binding	3	1.23	0.002498445	Q7TMB8, Q9JL26, Q03173
	GOTERM_CC_FAT	GO:0012505-endomembrane system	17	6.97	0.003436707	Q811D0, Q07076, P21619, Q9Z2I2, P84091, O08585, O35609, Q91YE6, Q9JKD3, Q8BKC5, Q9CR95, Q62277, P17047, Q60902, Q9ERU9, O70161, Q9CXW3
	KEGG_PATHWAY	mmu04810:Regulation of actin cytoskeleton	11	4.51	0.003985384	Q91VR8, P70336, Q7TMB8, P08556, Q9CPW4, P63001, Q8R4H2, Q03173, O70161, P61148, Q9DBR7
	SP_PIR_KEYWORDS	multifunctional enzyme	5	2.05	0.007770003	Q9EQQ9, Q9WVL0, P19096, Q05920, Q64737
	BIOCARTA	m_malatexPathway:Shuttle for transfer of acetyl groups from mitochondria to the cytosol	3	1.23	0.008815091	Q91V92, Q05920, Q9CZU6
	KEGG_PATHWAY	mmu00480:Glutathione metabolism	5	2.05	0.011984823	P54071, Q9CPU4, Q9D7X8, Q9WVL0, Q00612
	KEGG_PATHWAY	mmu00290:Valine, leucine and isoleucine biosynthesis	3	1.23	0.014645204	Q8BIJ6, Q8BU30, Q9D051
	GOTERM_CC_FAT	GO:0019898-extrinsic to membrane	14	5.74	0.015358958	Q810B6, P70336, Q811D0, Q6PAR5, Q9Z2H5, Q9D1C8, P63001, Q6PFD5, Q3UPL0, Q60902, Q8BMI3, Q9ERG2, Q8K3H0, Q7SIG6
	INTERPRO	IPR012675:Beta-grasp fold, ferredoxin-type	3	1.23	0.015945537	Q9CPW2, Q8BLY2, Q9D0R2
	GOTERM_CC_FAT	GO:0005829-cytosol	15	6.15	0.02207591	Q6PAR5, P05201, Q07076, Q9D1C8, Q9D7X8, P28271, Q9WVL0, P63001, Q9CQW1, O88712, P54775, Q9JL26, Q60865, Q6NVE8, P84086
	SP_PIR_KEYWORDS	lyase	6	2.46	0.024947971	P61458, P28271, Q9R1Z7, P19096, Q91V92, P05063
	KEGG_PATHWAY	mmu04666:Fc gamma R-mediated phagocytosis	6	2.46	0.026566676	Q9CPW4, P63001, P39054, O70161, Q7SIG6, Q9QWY8
	GOTERM_BP_FAT	GO:0043648-dicarboxylic acid metabolic process	3	1.23	0.029234612	P05201, Q8BWF0, Q05920
	GOTERM_CC_FAT	GO:0044455-mitochondrial membrane part	4	1.64	0.03103387	P97450, Q9ERS2, P56382, P58281
	INTERPRO	IPR013816:ATP-grasp fold, subdomain 2	3	1.23	0.033048556	Q91V92, Q05920, Q64737
	SP_PIR_KEYWORDS	translocation	4	1.64	0.057631737	Q9CQ85, Q9ERU9, P61620, Q9CQV7
	UP_SEQ_FEATURE	compositionally biased region:Poly-Glu	11	4.51	0.060407935	Q8JZR6, Q8BVQ5, Q3UVX5, Q5DU25, Q9JKR6, Q5F2E8, Q9ERU9, Q8VD37, Q69ZW3, Q7TSC1, Q3TES0
	SP_PIR_KEYWORDS	coated pit	3	1.23	0.061642569	Q60902, P84091, O08585
	GOTERM_BP_FAT	GO:0007017-microtubule-based process	7	2.87	0.065678086	P54227, P28740, Q9ERD7, Q9QXL2, P19246, Q3UU96, P62627
	GOTERM_CC_FAT	GO:0044440-endosomal part	3	1.23	0.085827234	Q810B6, Q6NVE8, Q8K3H0
	GOTERM_CC_FAT	GO:0010008-endosome membrane	3	1.23	0.085827234	Q810B6, Q6NVE8, Q8K3H0
	GOTERM_CC_FAT	GO:0005794-Golgi apparatus	15	6.15	0.097051786	O54774, Q64310, P08556, P28271, O08585, O35609, Q9CQW1, Q9JKD3, Q8CDG3, Q8BHN3, Q6NVE8, Q8BRT1, Q8BMI3, P36536, Q7SIG6
	COG_ONTOLOGY	Cell division and chromosome partitioning	4	1.64	0.098115822	P70336, Q3UU96, Q91YE6, Q5SXY1
ion transport/channels	GOTERM_BP_FAT	GO:0006820-anion transport	5	2.05	0.098673831	Q8JZR6, P52196, Q8R5J9, Q8BTY2, Q8BH59
	GOTERM_MF_FAT	GO:0016836-hydro-lyase activity	3	1.23	0.105536854	P61458, P28271, P19096
	KEGG_PATHWAY	mmu04310:Wnt signaling pathway	6	2.46	0.114076442	P70336, Q9Z1B3, P63001, Q8BPM0, O88712, Q9CXW3
	UP_SEQ_FEATURE	active site:Proton donor	6	2.46	0.123579485	Q8VCT3, Q11011, Q8BHN3, P06745, O88712, Q64737
	GOTERM_CC_FAT	GO:0005783-endoplasmic reticulum	17	6.97	0.127315576	Q811D0, Q9D0L7, Q64310, Q9CPU4, Q9Z2I2, P28271, Q8R5J9, Q9CQW1, P61620, Q6PDI5, Q8CDG3, Q99L43, Q9CY27, Q3UPL0, Q8BHN3, Q9JKR6, P36536
neuron	GOTERM_CC_FAT	GO:0043005-neuron projection	7	2.87	0.129695489	Q9ERD7, Q60865, P63080, P84086, Q61330, Q61301, P58281

	SP_PIR_KEYWORDS	golgi apparatus	12	4.92	0.129714639	O54774, Q64310, P08556, Q6NVE8, Q8BHN3, Q9CQW1, Q8BRT1, Q8BMI3, Q9JKD3, P36536, Q8CDG3, Q7SIG6
	KEGG_PATHWAY	mmu04070:Phosphatidylinositol signaling system	4	1.64	0.138984775	Q9Z1B3, O70161, Q9EPW0, Q99L43
	SP_PIR_KEYWORDS	growth regulation	3	1.23	0.14154955	Q9DB27, Q9D0L7, Q640R3
	SP_PIR_KEYWORDS	lipid synthesis	4	1.64	0.149825964	P19096, Q91V92, Q05920, Q9CY27
	GOTERM_CC_FAT	GO:0034399-nuclear periphery	3	1.23	0.149877526	Q8CGF7, P21619, Q8K310
	UP_SEQ_FEATURE	short sequence motif:Nuclear localization signal	8	3.28	0.150576575	Q8CGF7, P35123, P98203, Q11011, P21619, Q91WV0, Q8K310, Q8CGY8
	KEGG_PATHWAY	mmu00620:Pyruvate metabolism	3	1.23	0.157081662	P56375, Q05920, Q9D051
	COG_ONTOLOGY	Translation, ribosomal structure and biogenesis	3	1.23	0.169092775	Q9DB27, Q9CZD3, Q61035
	GOTERM_BP_FAT	GO:0007265-Ras protein signal transduction	3	1.23	0.188586241	P70336, P08556, Q8K2C9
neuron development signaling	GOTERM_CC_FAT	GO:0030424-axon	4	1.64	0.189072765	Q9ERD7, P63080, Q61330, Q61301
	KEGG_PATHWAY	mmu04360:Axon guidance	5	2.05	0.189524567	P70336, P08556, P63001, Q8R4H2, Q80UG2
	GOTERM_BP_FAT	GO:0000165-MAPKKK cascade	4	1.64	0.198747782	Q58A65, O88653, Q8K2C9, Q4ACU6
	GOTERM_MF_FAT	GO:0016407-acetyltransferase activity	3	1.23	0.201343872	Q9EQQ9, P19096, Q8CGY8
	SP_PIR_KEYWORDS	endoplasmic reticulum	13	5.33	0.207171409	Q811D0, Q9D0L7, Q64310, Q9CPU4, Q8R5J9, P61620, Q6PDI5, Q8CDG3, Q9CY27, Q3UPL0, Q8BHN3, Q9JKR6, P36536
	SMART	SM00454:SAM	3	1.23	0.21148459	P60469, Q6P9K8, Q4ACU6
	GOTERM_MF_FAT	GO:0019842-vitamin binding	4	1.64	0.213771471	P05201, Q60597, P19096, Q05920
	SP_PIR_KEYWORDS	nucleotide binding	3	1.23	0.21389347	P28740, P63001, P36536
	SP_PIR_KEYWORDS	P-loop	3	1.23	0.21885416	P28740, P63001, P36536
	KEGG_PATHWAY	mmu00562:Inositol phosphate metabolism	3	1.23	0.238747171	Q9Z1B3, O70161, Q9EPW0
	GOTERM_BP_FAT	GO:0007242-intracellular signaling cascade	16	6.56	0.25112417	Q8K394, P70336, P08556, Q3UU96, P63001, Q8R4H2, Q8K2C9, Q4ACU6, Q7TSC1, P54227, Q9Z1B3, Q3UHD9, P50396, Q58A65, Q80ZJ1, O88653
	GOTERM_BP_FAT	GO:0010564-regulation of cell cycle process	3	1.23	0.257962433	P70336, Q3U487, Q7TSC1
	GOTERM_BP_FAT	GO:0040008-regulation of growth	6	2.46	0.263507118	Q9DB27, Q811D0, Q9ERS2, Q9D0L7, Q640R3, Q00612
	UP_SEQ_FEATURE	domain:C2	3	1.23	0.275883197	Q8K394, Q9Z1B3, Q9EPW0
	GOTERM_BP_FAT	GO:0055085-transmembrane transport	9	3.69	0.280482293	P97441, P97450, Q9CQ85, P56382, Q9ERU9, P61620, Q9EPR4, Q9CQV7, Q8BH59
	SP_PIR_KEYWORDS	er-golgi transport	3	1.23	0.288844212	Q3UPL0, Q9CQW1, P36536
	GOTERM_CC_FAT	GO:0005886-plasma membrane	45	18.44	0.301079006	P97441, O54774, Q8VCT3, Q640R3, Q9D1C8, Q3UVX5, Q61330, Q03173, Q9CR95, P14206, P98203, Q80TR1, P17047, Q80ZJ1, P63080, O70161, Q9EPR4, Q7SIG6, P70336, Q811D0, Q07076, P08556, Q8BIW1, P84091, P54285, O08585, Q9CQW1, P39054, P63001, Q6PFD5, Q8BTY2, Q80UG2, Q9JKD3, Q61301, Q4ACU6, Q8BI08, Q9DCP2, Q62277, Q7TMB8, Q9QYB5, Q80U40, Q3UPL0, Q60902, O88653, P62881
	KEGG_PATHWAY	mmu04010:MAPK signaling pathway	7	2.87	0.306913369	P54227, P08556, O88653, P54285, Q5F2E8, P63001, P61148
	GOTERM_MF_FAT	GO:0030145-manganese ion binding	4	1.64	0.309361966	P54071, Q8BIW1, Q05920, Q64737
	SP_PIR_KEYWORDS	manganese	4	1.64	0.311610954	P54071, Q8BIW1, Q05920, Q64737
	INTERPRO	IPR001660:Sterile alpha motif SAM	3	1.23	0.314669842	P60469, Q6P9K8, Q4ACU6
	INTERPRO	IPR016040:NAD(P)-binding domain	4	1.64	0.315693714	Q00612, P19096, Q91V92, O88712
	SP_PIR_KEYWORDS	Proto-oncogene	3	1.23	0.323706453	P35123, P08556, Q924L1
	SP_PIR_KEYWORDS	Chaperone	4	1.64	0.330077042	P48722, Q9JKR6, Q9CQV7, Q9D832
	GOTERM_CC_FAT	GO:0042470-melanosome	3	1.23	0.334315709	Q8BHN3, P63001, P19096
	GOTERM_CC_FAT	GO:0048770-pigment granule	3	1.23	0.334315709	Q8BHN3, P63001, P19096
	GOTERM_BP_FAT	GO:0008610-lipid biosynthetic process	6	2.46	0.338829753	Q8VCT3, P19096, Q91V92, Q05920, Q9CY27, Q99L43
	KEGG_PATHWAY	mmu04270:Vascular smooth muscle contraction	4	1.64	0.342677479	P70336, Q9Z1B3, Q8R4H2, Q9DBR7
	GOTERM_MF_FAT	GO:0048037-cofactor binding	5	2.05	0.346630681	P54071, P05201, Q60597, P19096, O88712
	SP_PIR_KEYWORDS	cell membrane	26	10.66	0.370944869	Q9D1C8, Q3UVX5, Q61330, Q9CR95, P14206, Q80TR1, Q80ZJ1, P17047, P63080, Q7SIG6, Q811D0, P70336, P08556, P84091, P63001, P39054, Q8BTY2, Q6PFD5, Q9JKD3, Q4ACU6, Q61301, Q9DCP2, Q8BI08, Q9QYB5, Q80U40, Q60902
	GOTERM_BP_FAT	GO:0007346-regulation of mitotic cell cycle	3	1.23	0.371717581	Q811D0, Q3U487, Q7TSC1
	GOTERM_BP_FAT	GO:0007005-mitochondrion organization	3	1.23	0.376539536	P47802, Q9D7X8, P58281
	KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	5	2.05	0.384826944	P70336, Q9Z1B3, P08556, P63001, P62881
	SP_PIR_KEYWORDS	nad	4	1.64	0.399892697	Q8BWF0, P19096, O88712, P03893
	COG_ONTOLOGY	Posttranslational modification, protein turnover, chaperones	3	1.23	0.402334583	P54775, Q8CGY8, Q9D832
	UP_SEQ_FEATURE	mutagenesis site	13	5.33	0.413104523	Q9EQQ9, Q66GT5, P63001, Q03173, Q9CR95, Q9QWY8, Q80ZJ1, Q0GNC1, Q8BRT1, O70161, Q7SIG6, Q9QUH0, Q9JI46
	GOTERM_MF_FAT	GO:0016790-thiolester hydrolase activity	3	1.23	0.417389461	P35123, P19096, Q8BY87
	GOTERM_BP_FAT	GO:0000226-microtubule cytoskeleton organization	3	1.23	0.44226486	P54227, P19246, Q3UU96
	KEGG_PATHWAY	mmu04510:Focal adhesion	5	2.05	0.447499497	P70336, P02468, P63001, O70161, Q9DBR7
	GOTERM_BP_FAT	GO:0009628-response to abiotic stimulus	5	2.05	0.449606509	Q07076, P08556, P63001, P62627, Q7TSC1
neuron	GOTERM_CC_FAT	GO:0030425-dendrite	3	1.23	0.457337075	Q60865, P84086, P58281
	KEGG_PATHWAY	mmu05200:Pathways in cancer	7	2.87	0.487131671	P08556, P02468, P63001, O88712, Q8K3H0, Q61301, P61148

	GOTERM_CC_FAT	GO:0030141-secretory granule	3	1.23	0.489460587	Q9CZD3, P17047, P84091
	SP_PIR_KEYWORDS	oxidoreductase	9	3.69	0.509657342	P54071, Q60597, Q00612, Q8BWF0, P19096, Q9D051, O88712, Q9CY27, P03893
	UP_SEQ_FEATURE	compositionally biased region:Ser-rich	7	2.87	0.511196675	Q8BWQ6, Q3UU96, Q8BRT1, Q68FD9, O08788, Q9DBR7, Q5SXY1
ion transport/channels	GOTERM_MF_FAT	GO:0008509-anion transmembrane transporter activity	3	1.23	0.513022236	Q8JZR6, Q8BTY2, P63080
	SP_PIR_KEYWORDS	growth factor	3	1.23	0.513457241	Q9CQI3, P06745, P61148
	UP_SEQ_FEATURE	compositionally biased region:Glu-rich	5	2.05	0.514781207	Q8CGF7, Q8C0L0, Q3UH68, Q6Y7W8, P23116
	GOTERM_CC_FAT	GO:0005938-cell cortex	3	1.23	0.528979072	Q9QYB5, Q8CHH9, Q8BRT1
	UP_SEQ_FEATURE	compositionally biased region:Gly-rich	4	1.64	0.543138083	Q8K394, Q99020, Q3U0V1, Q9Z130
nucleus	SP_PIR_KEYWORDS	chromosomal protein	3	1.23	0.550314142	P10922, O54962, Q60668
	GOTERM_BP_FAT	GO:0022613-ribonucleoprotein complex biogenesis	3	1.23	0.553350511	Q91YE6, P23116, Q923D5
	GOTERM_MF_FAT	GO:0008083-growth factor activity	3	1.23	0.55685083	Q9CQI3, P06745, P61148
	UP_SEQ_FEATURE	region of interest:Substrate binding	3	1.23	0.568038478	Q9CZD3, P54071, Q05920
	GOTERM_BP_FAT	GO:0016053-organic acid biosynthetic process	3	1.23	0.569009457	Q8VCT3, P05201, P19096
	GOTERM_BP_FAT	GO:0046394-carboxylic acid biosynthetic process	3	1.23	0.569009457	Q8VCT3, P05201, P19096
	SP_PIR_KEYWORDS	nadp	3	1.23	0.573777955	P54071, Q00612, P19096
	GOTERM_CC_FAT	GO:0000139-Golgi membrane	3	1.23	0.574406681	O08585, O35609, Q9JKD3
	GOTERM_BP_FAT	GO:0009100-glycoprotein metabolic process	3	1.23	0.591751391	Q811D0, Q8BHN3, Q8CGY8
	GOTERM_BP_FAT	GO:0010608-posttranscriptional regulation of gene expression	3	1.23	0.595454268	P28271, Q91YE6, Q60668
signaling	SP_PIR_KEYWORDS	transferase	19	7.79	0.602085869	Q9EQQ9, P70336, P05201, Q9D7X8, Q9CPU4, Q9WVL0, Q3UU96, Q5F2E8, Q9CQW1, Q91V92, Q8CGY8, Q64737, Q99L43, Q5XJV6, P52196, Q9ESW4, P19096, O70161, Q9CZU6
	KEGG_PATHWAY	mmu04670:Leukocyte transendothelial migration	3	1.23	0.613488863	P70336, P63001, Q61301
signaling	GOTERM_BP_FAT	GO:0007243-protein kinase cascade	4	1.64	0.619411372	Q58A65, O88653, Q8K2C9, Q4ACU6
	SP_PIR_KEYWORDS	Acyltransferase	3	1.23	0.621525861	Q9EQQ9, Q9D7X8, P19096
	UP_SEQ_FEATURE	compositionally biased region:Poly-Gly	4	1.64	0.623738071	Q9ERG2, Q80Y14, Q8BWR2, Q7TSC1
	GOTERM_MF_FAT	GO:0050662-coenzyme binding	3	1.23	0.625811989	P54071, Q60597, O88712
	GOTERM_CC_FAT	GO:0044432-endoplasmic reticulum part	4	1.64	0.631083397	Q811D0, Q9Z2I2, Q9JKR6, Q8BHN3
	KEGG_PATHWAY	mmu03040:Spliceosome	3	1.23	0.636026032	Q8CGF7, Q923D5, P59708
	GOTERM_BP_FAT	GO:0015674-di-, tri-valent inorganic cation transport	3	1.23	0.641318887	Q9Z2I2, P54285, Q9CY27
	GOTERM_BP_FAT	GO:0060341-regulation of cellular localization	3	1.23	0.641318887	Q9Z2I2, Q9JKD3, Q9DBR7
immune	GOTERM_BP_FAT	GO:0001775-cell activation	4	1.64	0.647357067	Q811D0, Q9Z2I2, P84086, Q7TSC1
	GOTERM_BP_FAT	GO:0031399-regulation of protein modification process	3	1.23	0.65458728	P12367, Q9D1C8, P61148
signaling	GOTERM_BP_FAT	GO:0009967-positive regulation of signal transduction	3	1.23	0.676866341	P08556, Q9JKK7, Q7TSC1
	KEGG_PATHWAY	mmu04530:Tight junction	3	1.23	0.682010992	Q9Z2H5, P08556, Q61301
	KEGG_PATHWAY	mmu04910:Insulin signaling pathway	3	1.23	0.693710343	P12367, P08556, P19096
	GOTERM_CC_FAT	GO:0005911-cell-cell junction	3	1.23	0.700421149	Q811D0, Q9QYB5, Q61301
	GOTERM_BP_FAT	GO:0006631-fatty acid metabolic process	3	1.23	0.712338079	Q8VCT3, Q8BWF0, P19096
signaling	GOTERM_BP_FAT	GO:0010647-positive regulation of cell communication	3	1.23	0.726133733	P08556, Q9JKK7, Q7TSC1
	UP_SEQ_FEATURE	active site:Nucleophile	3	1.23	0.726415548	P97493, Q8BHN3, Q8BWF0
	GOTERM_BP_FAT	GO:0032268-regulation of cellular protein metabolic process	4	1.64	0.731353665	P12367, Q9D1C8, P28271, P61148
	SP_PIR_KEYWORDS	hydrolase	19	7.79	0.73350952	Q9CQ60, Q9EQQ9, Q8VCT3, Q11011, Q8BIW1, P39054, Q66GT5, P56382, Q8CDG3, Q9EPW0, Q8BY87, P35123, Q8BVQ5, Q9Z1B3, P56375, Q8BHN3, P19096, O88851, Q9JI46
	GOTERM_CC_FAT	GO:0048471-perinuclear region of cytoplasm	3	1.23	0.745727642	Q7TMB8, Q58A65, Q6NVE8
	UP_SEQ_FEATURE	compositionally biased region:Poly-Pro	5	2.05	0.753381991	Q8CGF7, Q80X50, Q80TR1, Q4ACU6, Q7TSC1
immune	GOTERM_BP_FAT	GO:0002684-positive regulation of immune system process	3	1.23	0.768930396	O54774, P54285, P98086
nucleus	GOTERM_CC_FAT	GO:0005694-chromosome	5	2.05	0.779741338	Q9QYB5, P10922, O54962, Q8BRT1, Q60668
immune	GOTERM_BP_FAT	GO:0045321-leukocyte activation	3	1.23	0.797638108	Q811D0, Q9Z2I2, P84086
	GOTERM_MF_FAT	GO:0016791-phosphatase activity	3	1.23	0.82458255	Q66GT5, Q9EPW0, Q9DBR7
	GOTERM_MF_FAT	GO:0008289-lipid binding	4	1.64	0.836749665	P70336, Q07076, P84091, Q3UU96

cell cycle	SP_PIR_KEYWORDS	cell cycle	5	2.05	0.85692979	Q9DB27, Q640R3, Q8BRT1, Q8K3H0, P84089
	SP_PIR_KEYWORDS	nucleus	45	18.44	0.896252453	Q8CGF7, Q9EQQ9, Q11011, P21619, Q8VBV7, Q8QZZ7, O54962, Q62446, Q8BKC5, P23116, Q8CGY8, Q6PDI5, Q7TSC1, Q8CCN5, P14206, Q923D5, Q60668, P59708, P35123, Q9D8T7, P61458, Q8K310, Q9Z130, Q9JKL4, Q8K3H0, Q5SXY1, Q99020, P48722, Q8BIW1, P10922, Q91WV0, Q9CQZ1, Q91YE6, O88712, Q3UHD9, Q9ERS2, P54775, Q60902, Q3U0V1, Q4KMM3, Q9ERU9, O88851, Q61699, Q64152, Q9CXW3
	GOTERM_BP_FAT	GO:0008284-positive regulation of cell proliferation	3	1.23	0.898758	Q811D0, P08556, P61148
	SP_PIR_KEYWORDS	magnesium	4	1.64	0.911808249	P54071, P70336, Q91V92, Q9JI46
	UP_SEQ_FEATURE	compositionally biased region:Poly-Ala	3	1.23	0.921525471	Q99020, Q80Y14, Q4ACU6
	GOTERM_BP_FAT	GO:0043009-chordate embryonic development	4	1.64	0.926079213	Q811D0, P54775, Q03173, Q64152
	GOTERM_BP_FAT	GO:0009792-embryonic development ending in birth or egg hatching	4	1.64	0.928949694	Q811D0, P54775, Q03173, Q64152
	GOTERM_MF_FAT	GO:0005506-iron ion binding	3	1.23	0.943113942	Q9CPW2, P28271, Q9CY27
	GOTERM_MF_FAT	GO:0000287-magnesium ion binding	3	1.23	0.973100318	P54071, Q91V92, Q9JI46
	GOTERM_BP_FAT	GO:0033554-cellular response to stress	3	1.23	0.974302391	Q9DB27, Q8K2C9, Q8BGQ7
	UP_SEQ_FEATURE	sequence variant	3	1.23	0.975116407	Q8CGF7, Q9Z1B3, Q80X50
	GOTERM_BP_FAT	GO:0042127-regulation of cell proliferation	4	1.64	0.977945123	Q811D0, P08556, P61148, Q7TSC1
	UP_SEQ_FEATURE	compositionally biased region:Poly-Ser	3	1.23	0.980147716	Q3UVX5, Q9ERU9, Q3TES0
	UP_SEQ_FEATURE	topological domain:Lumenal	3	1.23	0.987598222	P17047, P61620, Q8BI08
immune	GOTERM_BP_FAT	GO:0010033-response to organic substance	3	1.23	0.992394697	P48722, Q9Z2I2, Q8BGQ7
	GOTERM_MF_FAT	GO:0043565-sequence-specific DNA binding	3	1.23	0.99530688	Q99020, Q91WV0, Q60668
immune	INTERPRO	IPR013783:Immunoglobulin-like fold	3	1.23	0.998231362	P10922, Q640R3, Q61330
	GOTERM_BP_FAT	GO:0010604-positive regulation of macromolecule metabolic process	3	1.23	0.998467768	Q99020, P61458, P61148
	SP_PIR_KEYWORDS	transducer	5	2.05	0.999998179	Q8K394, Q9Z1B3, Q80TR1, Q3UVX5, P62881
	UP_SEQ_FEATURE	topological domain:Cytoplasmic	17	6.97	0.999999809	Q8JZR6, P97441, Q640R3, Q3UVX5, O35609, Q8R5J9, Q8BTY2, Q80UG2, Q9JKD3, Q8BY89, P61620, Q8BI08, Q62277, Q80TR1, P17047, P63080, Q7TQ95
	GOTERM_BP_FAT	GO:0007186-G-protein coupled receptor protein signaling pathway	6	2.46	0.999999954	Q80TR1, Q3UVX5, Q9ESW4, P63080, Q8R4H2, P62881
	UP_SEQ_FEATURE	topological domain:Extracellular	10	4.10	0.999999957	Q8JZR6, Q80TR1, Q640R3, Q3UVX5, Q8BTY2, P63080, Q80UG2, Q9JKD3, Q8BY89, Q7TQ95
	GOTERM_BP_FAT	GO:0007166-cell surface receptor linked signal transduction	8	3.28	1	Q80TR1, Q3UVX5, P54285, Q9ESW4, P63080, Q8R4H2, P62881, P61148
	SP_PIR_KEYWORDS	receptor	6	2.46	1	Q80TR1, Q60902, Q3UVX5, P63080, Q80UG2, P14206