

Functional Annotation Clustering

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Current Gene List: condition_specific_genes_

Current Background: Homo sapiens

2052 DAVID IDs
Options Classification Stringency Medium ▾

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342 Cluster(s)

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Annotation Cluster 1		Enrichment Score: 54.91	 		Count P_Value Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE		CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO2)	 	325	4.9E-64 4.4E-60
<input type="checkbox"/> UP_KW_PTM	Ubl conjugation		 	584	1.6E-52 1.6E-51
<input type="checkbox"/> UP_KW_PTM	Isopeptide bond		 	448	2.4E-50 1.8E-49
Annotation Cluster 2		Enrichment Score: 38.59	 		Count P_Value Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	cytoplasmic translation		 	77	1.1E-61 5.9E-58
<input type="checkbox"/> GOTERM_CC_DIRECT	cytosolic ribosome		 	71	2.6E-51 4.3E-49
<input type="checkbox"/> GOTERM_BP_DIRECT	translation		 	97	1.3E-39 3.4E-36
<input type="checkbox"/> GOTERM_CC_DIRECT	ribonucleoprotein complex		 	109	5.4E-38 7.7E-36
<input type="checkbox"/> GOTERM_CC_DIRECT	cytosolic large ribosomal subunit		 	49	8.4E-38 1.0E-35
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Ribosomal protein		 	91	5.6E-37 3.2E-35
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Ribonucleoprotein		 	118	6.5E-37 3.2E-35
<input type="checkbox"/> GOTERM_CC_DIRECT	ribosome		 	82	3.4E-36 3.8E-34
<input type="checkbox"/> GOTERM_MF_DIRECT	structural constituent of ribosome		 	88	5.3E-36 2.6E-33
<input type="checkbox"/> KEGG_PATHWAY	Ribosome		 	82	8.2E-30 2.8E-27
<input type="checkbox"/> KEGG_PATHWAY	Coronavirus disease - COVID-19		 	96	3.2E-28 5.5E-26
Annotation Cluster 3		Enrichment Score: 13.43	 		Count P_Value Benjamini
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	RNA-binding		 	183	1.5E-28 4.9E-27
<input type="checkbox"/> INTERPRO	Nucleotide-bd a/b plait_sf		 	76	4.6E-17 2.0E-13
<input type="checkbox"/> INTERPRO	RBD_domain_sf		 	73	9.1E-16 2.0E-12
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:RRM		 	67	2.0E-15 4.5E-12
<input type="checkbox"/> SMART	RRM		 	63	4.9E-15 2.4E-12
<input type="checkbox"/> INTERPRO	RRM_dom		 	65	2.3E-14 3.3E-11
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:RRM 1		 	32	2.0E-8 1.6E-5
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:RRM 2		 	32	2.0E-8 1.6E-5
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:RRM 3		 	15	2.5E-4 6.7E-2
Annotation Cluster 4		Enrichment Score: 12.42	 		Count P_Value Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	cytosolic small ribosomal subunit		 	30	1.3E-18 8.9E-17
<input type="checkbox"/> GOTERM_BP_DIRECT	ribosomal small subunit biogenesis		 	30	5.3E-11 2.8E-8
<input type="checkbox"/> GOTERM_CC_DIRECT	small-subunit processome		 	28	7.9E-10 2.8E-8
Annotation Cluster 5		Enrichment Score: 12.16	 		Count P_Value Benjamini
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	mRNA_processing		 	118	4.7E-23 3.2E-21
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	mRNA_splicing		 	97	6.1E-21 2.8E-19
<input type="checkbox"/> GOTERM_BP_DIRECT	RNA_splicing		 	61	3.2E-14 4.2E-11
<input type="checkbox"/> GOTERM_BP_DIRECT	mRNA_splicing_via_spliceosome		 	59	4.1E-14 4.4E-11
<input type="checkbox"/> GOTERM_BP_DIRECT	mRNA_processing		 	61	3.0E-12 2.0E-9
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Spliceosome		 	45	2.9E-10 3.2E-9
<input type="checkbox"/> GOTERM_CC_DIRECT	spliceosomal_complex		 	37	1.9E-8 5.5E-7
<input type="checkbox"/> GOTERM_CC_DIRECT	catalytic_step_2_spliceosome		 	28	1.1E-7 3.0E-6
<input type="checkbox"/> KEGG_PATHWAY	Spliceosome		 	49	5.1E-5 4.1E-4
Annotation Cluster 6		Enrichment Score: 10.78	 		Count P_Value Benjamini
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Chaperone		 	67	1.2E-13 2.8E-12
<input type="checkbox"/> GOTERM_BP_DIRECT	protein_folding		 	50	1.5E-11 9.0E-9
<input type="checkbox"/> GOTERM_MF_DIRECT	unfolded_protein_binding		 	39	2.5E-9 4.0E-7
Annotation Cluster 7		Enrichment Score: 8.95	 		Count P_Value Benjamini
<input type="checkbox"/> KEGG_PATHWAY	Th17_cell_differentiation		 	47	4.9E-15 4.1E-13
<input type="checkbox"/> KEGG_PATHWAY	PD-L1_expression_and_PD-1_checkpoint_pathway_in_cancer		 	35	6.4E-10 2.4E-8
<input type="checkbox"/> KEGG_PATHWAY	Th1_and_Th2_cell_differentiation		 	35	1.8E-9 5.1E-8
<input type="checkbox"/> KEGG_PATHWAY	Inflammatory_bowel_disease		 	20	2.7E-4 1.7E-3
Annotation Cluster 8		Enrichment Score: 7.11	 		Count P_Value Benjamini
<input type="checkbox"/> KEGG_PATHWAY	PD-L1_expression_and_PD-1_checkpoint_pathway_in_cancer		 	35	6.4E-10 2.4E-8
<input type="checkbox"/> KEGG_PATHWAY	T_cell_receptor_signaling_pathway		 	40	1.1E-8 2.1E-7
<input type="checkbox"/> BIOCARTA	T_Cell_Receptor_Signaling_Pathway		 	21	7.0E-5 4.6E-3
Annotation Cluster 9		Enrichment Score: 7.08	 		Count P_Value Benjamini

		Enrichment Score:	G	Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY	Human immunodeficiency virus 1 infection	RT		58	1.0E-8	2.1E-7
<input type="checkbox"/> KEGG_PATHWAY	Kaposi sarcoma-associated herpesvirus infection	RT		54	1.8E-8	3.3E-7
<input type="checkbox"/> KEGG_PATHWAY	Human cytomegalovirus infection	RT		54	3.1E-6	3.6E-5
Annotation Cluster 10	Enrichment Score: 5.98	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	translational initiation	RT		27	2.1E-12	1.6E-9
<input type="checkbox"/> GOTERM_CC_DIRECT	eukaryotic translation initiation factor 3 complex	RT		13	2.9E-9	9.8E-8
<input type="checkbox"/> GOTERM_BP_DIRECT	formation of cytoplasmic translation initiation complex	RT		12	7.5E-8	1.3E-5
<input type="checkbox"/> GOTERM_CC_DIRECT	eukaryotic 43S preinitiation complex	RT		12	2.7E-7	6.1E-6
<input type="checkbox"/> GOTERM_CC_DIRECT	eukaryotic 48S preinitiation complex	RT		11	1.6E-6	3.2E-5
<input type="checkbox"/> GOTERM_MF_DIRECT	translation initiation factor activity	RT		21	2.3E-6	1.7E-4
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Initiation factor	RT		20	4.6E-6	5.5E-5
<input type="checkbox"/> GOTERM_CC_DIRECT	eukaryotic translation initiation factor 3 complex, eIF3m	RT		6	1.6E-4	2.1E-3
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Protein biosynthesis	RT		33	5.7E-4	4.3E-3
<input type="checkbox"/> GOTERM_BP_DIRECT	viral translational termination-reinitiation	RT		4	8.8E-3	1.9E-1
Annotation Cluster 11	Enrichment Score: 5.73	G		Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY	Measles	RT		45	1.8E-9	5.1E-8
<input type="checkbox"/> KEGG_PATHWAY	Kaposi sarcoma-associated herpesvirus infection	RT		54	1.8E-8	3.3E-7
<input type="checkbox"/> KEGG_PATHWAY	Hepatitis B	RT		45	3.6E-7	4.9E-6
<input type="checkbox"/> KEGG_PATHWAY	Hepatitis C	RT		37	2.4E-4	1.5E-3
<input type="checkbox"/> KEGG_PATHWAY	Human papillomavirus infection	RT		58	7.6E-3	3.4E-2
Annotation Cluster 12	Enrichment Score: 4.64	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Cell cycle	RT		126	8.4E-8	1.9E-6
<input type="checkbox"/> GOTERM_BP_DIRECT	cell division	RT		71	8.5E-7	1.2E-4
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Cell division	RT		75	1.0E-4	9.7E-4
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Mitosis	RT		45	4.0E-2	1.8E-1
Annotation Cluster 13	Enrichment Score: 4.55	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Ubl conjugation pathway	RT		131	8.9E-7	1.7E-5
<input type="checkbox"/> GOTERM_BP_DIRECT	protein ubiquitination	RT		77	2.1E-5	1.9E-3
<input type="checkbox"/> GOTERM_MF_DIRECT	ubiquitin_protein ligase activity	RT		57	1.2E-3	3.2E-2
Annotation Cluster 14	Enrichment Score: 4.26	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	innate immune response	RT		89	1.6E-6	2.0E-4
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Innate immunity	RT		81	4.9E-6	7.4E-5
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Immunity	RT		132	2.2E-2	1.1E-1
Annotation Cluster 15	Enrichment Score: 4.04	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	multivesicular body assembly	RT		19	1.3E-10	5.8E-8
<input type="checkbox"/> GOTERM_BP_DIRECT	ESCRT III complex disassembly	RT		10	9.7E-9	2.1E-6
<input type="checkbox"/> GOTERM_BP_DIRECT	autophagosome maturation	RT		21	2.6E-8	5.1E-6
<input type="checkbox"/> GOTERM_BP_DIRECT	multivesicular body sorting_pathway	RT		13	1.6E-6	2.0E-4
<input type="checkbox"/> GOTERM_BP_DIRECT	macroautophagy	RT		23	1.7E-6	2.1E-4
<input type="checkbox"/> GOTERM_BP_DIRECT	membrane fission	RT		16	5.4E-6	5.7E-4
<input type="checkbox"/> GOTERM_CC_DIRECT	nuclear_pore	RT		26	5.6E-6	1.0E-4
<input type="checkbox"/> GOTERM_BP_DIRECT	nucleus_organization	RT		12	7.7E-6	7.8E-4
<input type="checkbox"/> GOTERM_BP_DIRECT	viral budding via host ESCRT complex	RT		12	7.7E-6	7.8E-4
<input type="checkbox"/> GOTERM_BP_DIRECT	ubiquitin-dependent protein catabolic process via the multivesicular body sorting_pathway	RT		14	8.9E-6	8.8E-4
<input type="checkbox"/> GOTERM_BP_DIRECT	regulation of mitotic spindle assembly	RT		12	1.2E-5	1.2E-3
<input type="checkbox"/> GOTERM_BP_DIRECT	regulation of centrosome duplication	RT		11	1.3E-5	1.2E-3
<input type="checkbox"/> GOTERM_CC_DIRECT	multivesicular body	RT		16	1.8E-5	3.0E-4
<input type="checkbox"/> GOTERM_BP_DIRECT	nuclear_envelope_reassembly	RT		10	6.3E-5	4.5E-3
<input type="checkbox"/> GOTERM_BP_DIRECT	viral budding from plasma membrane	RT		9	6.5E-5	4.5E-3
<input type="checkbox"/> GOTERM_BP_DIRECT	plasma membrane repair	RT		11	1.8E-4	1.0E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	mitotic metaphase plate congression	RT		14	2.8E-4	1.5E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	vesicle fusion with vacuole	RT		7	3.1E-4	1.6E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	multivesicular body-lysosome fusion	RT		7	3.1E-4	1.6E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	late endosome to lysosome transport	RT		9	4.4E-4	2.0E-2
<input type="checkbox"/> UP_SEQ_FEATURE	MOTIF:MIT-interacting motif	RT		5	1.1E-3	1.9E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	amphisome_membrane	RT		7	1.3E-3	1.2E-2
<input type="checkbox"/> INTERPRO	Snf7_fam	RT		7	1.4E-3	1.4E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	multivesicular body_membrane	RT		10	2.2E-3	2.0E-2
<input type="checkbox"/> GOTERM_CC_DIRECT	ESCRT III complex	RT		6	2.5E-3	2.2E-2
<input type="checkbox"/> UP_SEQ_FEATURE	REGION:Interaction with VTA1	RT		4	3.4E-3	4.4E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	kinetochore_microtubule	RT		8	5.1E-3	4.1E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	late endosome to vacuole transport	RT		5	8.6E-3	1.9E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	membrane budding	RT		6	1.3E-2	2.6E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	endosome transport via multivesicular body	RT		5	1.3E-2	2.6E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	sorting_pathway	RT		4	1.9E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	exit from mitosis	RT		6	3.4E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	establishment of protein localization	RT		Count	P_Value	Benjamini
Annotation Cluster 16	Enrichment Score: 3.92	G		197	1.9E-6	1.5E-5
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Mitochondrion	RT		81	2.8E-5	4.3E-4
<input type="checkbox"/> UP_KW_DOMAIN	Transit_peptide	RT		78	9.6E-4	1.8E-1
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSIT:Mitochondrion	RT		58	4.2E-3	3.4E-2
<input type="checkbox"/> GOTERM_CC_DIRECT	mitochondrial_matrix	RT		Count	P_Value	Benjamini
Annotation Cluster 17	Enrichment Score: 3.77	G		9	3.6E-5	2.8E-3
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation of cytoplasmic translation	RT		7	6.7E-5	4.5E-3
<input type="checkbox"/> GOTERM_BP_DIRECT	negative regulation of nuclear-transcribed mRNA catabolic_process, deadenylation-dependent decay	RT		7	3.1E-4	1.6E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	CRD-mediated mRNA stabilization	RT		7	3.1E-4	1.6E-2
<input type="checkbox"/> GOTERM_CC_DIRECT	CRD-mediated mRNA stability_complex	RT		5	1.2E-3	1.1E-2
Annotation Cluster 18	Enrichment Score: 3.64	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	SAP_dom_sf	RT		11	1.5E-4	3.4E-2
<input type="checkbox"/> SMART	SAP	RT		10	1.9E-4	2.3E-2
<input type="checkbox"/> INTERPRO	SAP_dom	RT		10	2.8E-4	4.8E-2
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:SAP	RT		10	3.6E-4	8.4E-2
Annotation Cluster 19	Enrichment Score: 3.59	G		Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY	Amyotrophic lateral sclerosis	RT		88	9.1E-10	3.1E-8
<input type="checkbox"/> KEGG_PATHWAY	Huntington_disease	RT		72	1.2E-7	2.0E-6
<input type="checkbox"/> KEGG_PATHWAY	Parkinson_disease	RT		65	1.3E-7	2.0E-6
<input type="checkbox"/> KEGG_PATHWAY	Pathways_of_neurodegeneration - multiple diseases	RT		99	2.7E-7	3.8E-6
<input type="checkbox"/> KEGG_PATHWAY	Prion_disease	RT		62	3.2E-6	3.6E-5
<input type="checkbox"/> KEGG_PATHWAY	Oxidative_phosphorylation	RT		37	5.4E-6	5.6E-5

		Enrichment Score:	G	RT	Count	P_Value	Benjamini	
Annotation Cluster 1		54.91			78	1.5E-5	1.4E-4	
<input type="checkbox"/> KEGG_PATHWAY	Alzheimer disease				30	1.6E-5	1.7E-4	
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Electron transport				51	2.5E-5	2.2E-4	
<input type="checkbox"/> KEGG_PATHWAY	Chemical carcinogenesis - reactive oxygen species				47	3.9E-5	3.2E-4	
<input type="checkbox"/> KEGG_PATHWAY	Diabetic cardiomyopathy				38	6.9E-5	5.3E-4	
<input type="checkbox"/> KEGG_PATHWAY	Non-alcoholic fatty liver disease				20	1.4E-4	1.2E-3	
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Respiratory chain				8	1.6E-4	5.4E-3	
<input type="checkbox"/> UP_KW_DISEASE	Leber hereditary optic neuropathy				18	1.8E-4	1.0E-2	
<input type="checkbox"/> GOTERM_BP_DIRECT	mitochondrial ATP synthesis coupled proton transport				11	6.7E-4	7.1E-3	
<input type="checkbox"/> GOTERM_CC_DIRECT	respiratory chain				17	9.8E-4	3.8E-2	
<input type="checkbox"/> GOTERM_BP_DIRECT	aerobic respiration				13	1.2E-3	3.4E-2	
<input type="checkbox"/> GOTERM_MF_DIRECT	NADH dehydrogenase (ubiquinone) activity				13	3.7E-3	3.1E-2	
<input type="checkbox"/> GOTERM_CC_DIRECT	mitochondrial respiratory chain complex I				10	7.0E-3	9.3E-2	
<input type="checkbox"/> UP_KW_LIGAND	Ubiquinone				11	1.5E-2	2.9E-1	
<input type="checkbox"/> GOTERM_BP_DIRECT	mitochondrial electron transport, NADH to ubiquinone				36	1.6E-2	2.3E-1	
<input type="checkbox"/> UP_KW_DISEASE	Primary mitochondrial disease				48	4.0E-2	1.3E-1	
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Mitochondrion inner membrane				38	7.4E-2	2.4E-1	
<input type="checkbox"/> KEGG_PATHWAY	Thermogenesis				4	1.0E-1	8.3E-1	
<input type="checkbox"/> GOTERM_MF_DIRECT	NADH dehydrogenase activity				16	1.4E-1	6.7E-1	
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Translocase				10	2.3E-1	1.0E0	
<input type="checkbox"/> GOTERM_BP_DIRECT	mitochondrial respiratory chain complex I assembly				18	6.9E-1	1.0E0	
<input type="checkbox"/> KEGG_PATHWAY	Retrograde endocannabinoid signaling				Annotation Cluster 20			
	Enrichment Score: 3.53					Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Ubiquitin-like				19	2.5E-5	1.0E-2	
<input type="checkbox"/> INTERPRO	Ubiquitin-like_dom_sf				38	5.3E-5	2.0E-2	
<input type="checkbox"/> INTERPRO	Ubiquitin-like_dom				16	6.7E-4	9.2E-2	
<input type="checkbox"/> SMART	UBQ				11	9.0E-3	1.7E-1	
Annotation Cluster 21	Enrichment Score: 3.49					Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	proteasome complex				19	6.0E-6	1.1E-4	
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Proteasome				16	4.0E-4	2.5E-3	
<input type="checkbox"/> KEGG_PATHWAY	Proteasome				15	1.1E-3	5.9E-3	
<input type="checkbox"/> GOTERM_CC_DIRECT	proteasome accessory complex				7	4.1E-3	3.4E-2	
Annotation Cluster 22	Enrichment Score: 3.46					Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	MOTIF:Q motif				15	9.0E-6	4.5E-3	
<input type="checkbox"/> INTERPRO	RNA-helicase DEAD-box_CS				12	2.4E-5	1.3E-2	
<input type="checkbox"/> UP_SEQ_FEATURE	MOTIF:DEAD box				13	4.8E-5	1.7E-2	
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:DEAD-box RNA helicase Q				12	1.3E-4	4.0E-2	
<input type="checkbox"/> INTERPRO	RNA_helicase_DEAD_Q_motif				12	2.8E-4	4.8E-2	
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Helicase C-terminal				24	3.1E-4	7.5E-2	
<input type="checkbox"/> SMART	HELICc				24	3.2E-4	2.9E-2	
<input type="checkbox"/> INTERPRO	Helicase_C				24	3.4E-4	5.5E-2	
<input type="checkbox"/> SMART	DEXDc				24	4.2E-4	2.9E-2	
<input type="checkbox"/> INTERPRO	DEAD/DEAH_box_helicase_dom				18	4.2E-4	6.4E-2	
<input type="checkbox"/> INTERPRO	Helicase_ATP-bd				24	5.1E-4	7.2E-2	
<input type="checkbox"/> GOTERM_MF_DIRECT	RNA helicase activity				19	6.5E-4	2.1E-2	
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Helicase ATP-binding				24	9.9E-4	1.8E-1	
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Helicase				29	1.5E-3	1.5E-2	
<input type="checkbox"/> GOTERM_MF_DIRECT	hydrolase activity				47	1.6E-3	4.2E-2	
<input type="checkbox"/> GOTERM_MF_DIRECT	helicase activity				18	2.5E-2	3.4E-1	
Annotation Cluster 23	Enrichment Score: 3.44					Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Znf_PHD-finger				21	4.9E-5	2.0E-2	
<input type="checkbox"/> SMART	PHD				23	5.2E-5	1.3E-2	
<input type="checkbox"/> INTERPRO	Znf_PHD				23	5.6E-5	2.0E-2	
<input type="checkbox"/> INTERPRO	Znf_FYVE_PHD				30	8.7E-5	2.7E-2	
<input type="checkbox"/> INTERPRO	Zinc_finger_PHD-type_CS				19	1.6E-4	3.6E-2	
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:PHD-type				19	2.8E-4	7.0E-2	
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:PHD-type				13	2.5E-3	3.3E-1	
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:PHD-type 2				10	7.6E-3	8.2E-1	
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:PHD-type 1				10	1.1E-2	1.0E0	
Annotation Cluster 24	Enrichment Score: 3.43					Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:PCI				11	6.0E-5	2.0E-2	
<input type="checkbox"/> INTERPRO	PCI_dom				10	2.8E-4	4.8E-2	
<input type="checkbox"/> SMART	PINT				7	3.0E-3	7.5E-2	
Annotation Cluster 25	Enrichment Score: 3.17					Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	RNA polymerase II transcription factor complex				30	8.0E-6	1.4E-4	
<input type="checkbox"/> UP_SEQ_FEATURE	REGION:Leucine-zipper				26	1.4E-4	4.2E-2	
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:BZIP				14	3.1E-4	7.5E-2	
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:bZIP				15	5.9E-4	1.2E-1	
<input type="checkbox"/> INTERPRO	bZIP_sf				15	6.9E-4	9.2E-2	
<input type="checkbox"/> INTERPRO	bZIP				15	8.4E-4	1.1E-1	
<input type="checkbox"/> SMART	BRLZ				14	1.5E-3	6.6E-2	
<input type="checkbox"/> UP_SEQ_FEATURE	REGION:Basic motif				14	2.3E-3	3.3E-1	
<input type="checkbox"/> INTERPRO	TF_DNA-bd_sf				5	7.9E-2	1.0E0	
Annotation Cluster 26	Enrichment Score: 3.16					Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	LIPID:S-geranylgeranyl cysteine				29	2.1E-6	1.3E-3	
<input type="checkbox"/> UP_SEQ_FEATURE	MOTIF:Effector region				25	1.6E-5	6.7E-3	
<input type="checkbox"/> GOTERM_MF_DIRECT	GDP_binding				21	8.6E-5	4.5E-3	
<input type="checkbox"/> SMART	RAN				22	1.5E-4	2.3E-2	
<input type="checkbox"/> INTERPRO	Small_GTP-bd_dom				34	2.2E-4	4.6E-2	
<input type="checkbox"/> GOTERM_MF_DIRECT	GTPase activity				58	7.3E-4	2.2E-2	
<input type="checkbox"/> SMART	RAB				30	7.6E-4	4.1E-2	
<input type="checkbox"/> UP_KW_LIGAND	GTP-binding				58	1.1E-3	2.3E-2	
<input type="checkbox"/> INTERPRO	P-loop_NTPase				119	1.3E-3	1.4E-1	
<input type="checkbox"/> SMART	RHO				25	2.2E-3	7.0E-2	
<input type="checkbox"/> SMART	RAS				26	3.1E-3	7.5E-2	
<input type="checkbox"/> GOTERM_MF_DIRECT	GTP binding				62	3.4E-3	7.6E-2	
<input type="checkbox"/> INTERPRO	Small_GTPase				25	7.2E-3	4.6E-1	
<input type="checkbox"/> UP_KW_PTM	Prenylation				34	8.4E-3	3.2E-2	
<input type="checkbox"/> UP_SEQ_FEATURE	PROPEP:Removed in mature form				40	3.0E-2	1.0E0	
Annotation Cluster 27	Enrichment Score: 2.97					Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Thioredoxin-like_sf	</						

		Enrichment Score:	G		Count	P_Value	Benjamini
Annotation Cluster 1							
<input type="checkbox"/> INTERPRO	Thioredoxin_CS	RT			9	9.4E-5	2.7E-2
<input type="checkbox"/> UP_KW_DOMAIN	Redox-active center	RT			15	1.8E-4	1.9E-3
<input type="checkbox"/> GOTERM_MF_DIRECT	protein disulfide oxidoreductase activity	RT			10	3.3E-4	1.3E-2
<input type="checkbox"/> UP_SEQ_FEATURE	DISULFID:Redox-active	RT			15	3.9E-4	9.0E-2
<input type="checkbox"/> GOTERM_MF_DIRECT	disulfide oxidoreductase activity	RT			5	3.3E-3	7.5E-2
<input type="checkbox"/> GOTERM_MF_DIRECT	protein disulfide isomerase activity	RT			6	4.3E-2	5.0E-1
<input type="checkbox"/> INTERPRO	PDI_thioredoxin-like_dom	RT			3	7.9E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Thioredoxin 1	RT			3	2.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Thioredoxin 2	RT			3	2.1E-1	1.0E0
Annotation Cluster 28		Enrichment Score: 2.93	G				
<input type="checkbox"/> GOTERM_MF_DIRECT	ubiquitin ligase inhibitor activity	RT			7	8.7E-5	4.5E-3
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation of signal transduction by p53 class mediator	RT			7	1.5E-4	9.0E-3
<input type="checkbox"/> GOTERM_MF_DIRECT	MDM2/MDM4 family protein binding	RT			4	1.3E-1	9.2E-1
Annotation Cluster 29		Enrichment Score: 2.83	G				
<input type="checkbox"/> GOTERM_BP_DIRECT	mitophagy	RT			15	6.7E-5	4.5E-3
<input type="checkbox"/> UP_SEQ_FEATURE	LIPID:Phosphatidylethanolamine amidated glycine; alternate	RT			6	1.5E-4	4.2E-2
<input type="checkbox"/> UP_SEQ_FEATURE	LIPID:Phosphatidylserine amidated glycine; alternate	RT			6	1.5E-4	4.2E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	autophagosome assembly	RT			19	1.8E-4	1.0E-2
<input type="checkbox"/> INTERPRO	Atg8-like	RT			6	4.0E-4	6.3E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	cellular response to nitrogen starvation	RT			7	5.7E-4	2.4E-2
<input type="checkbox"/> UP_SEQ_FEATURE	SITE:Cleavage; by ATG4B	RT			5	2.4E-3	3.3E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	phosphatidylethanolamine binding	RT			7	6.1E-3	1.2E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	autophagosome	RT			16	7.0E-3	5.4E-2
<input type="checkbox"/> KEGG_PATHWAY	Autophagy - other	RT			8	9.8E-2	3.0E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	GABA receptor binding	RT			5	1.1E-1	9.1E-1
Annotation Cluster 30		Enrichment Score: 2.81	G				
<input type="checkbox"/> INTERPRO	Znf_RING/FYVE/PHD	RT			79	1.4E-5	1.1E-2
<input type="checkbox"/> GOTERM_MF_DIRECT	ubiquitin-protein transferase activity	RT			43	4.1E-4	1.4E-2
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:RING-type	RT			37	5.3E-4	1.1E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	ubiquitin protein ligase activity	RT			57	1.2E-3	3.2E-2
<input type="checkbox"/> INTERPRO	Znf_RING	RT			48	2.3E-3	1.9E-1
<input type="checkbox"/> SMART	RING	RT			41	2.6E-3	7.0E-2
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:RING-type	RT			33	1.2E-2	1.0E0
<input type="checkbox"/> INTERPRO	Znf_RING_CS	RT			24	1.3E-1	1.0E0
Annotation Cluster 31		Enrichment Score: 2.75	G				
<input type="checkbox"/> GOTERM_MF_DIRECT	ubiquitin ligase inhibitor activity	RT			7	8.7E-5	4.5E-3
<input type="checkbox"/> GOTERM_BP_DIRECT	negative regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	RT			9	9.3E-4	3.6E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	negative regulation of ubiquitin protein ligase activity	RT			4	7.2E-2	7.7E-1
Annotation Cluster 32		Enrichment Score: 2.69	G				
<input type="checkbox"/> SMART	ZnF_RBZ	RT			9	3.6E-4	2.9E-2
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:RanBP2-type	RT			8	4.1E-4	9.0E-2
<input type="checkbox"/> INTERPRO	Znf_RanBP2_sf	RT			9	1.1E-3	1.3E-1
<input type="checkbox"/> INTERPRO	Znf_RanBP2	RT			9	2.0E-3	1.9E-1
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:RanBP2-type	RT			7	7.4E-3	8.2E-1
<input type="checkbox"/> INTERPRO	TET_fam	RT			3	2.7E-2	9.9E-1
Annotation Cluster 33		Enrichment Score: 2.69	G				
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:ARID	RT			7	1.9E-3	2.9E-1
<input type="checkbox"/> SMART	ARID	RT			7	2.0E-3	7.0E-2
<input type="checkbox"/> SMART	BRIGHT	RT			7	2.0E-3	7.0E-2
<input type="checkbox"/> INTERPRO	ARID_dom_sf	RT			7	2.1E-3	1.9E-1
<input type="checkbox"/> INTERPRO	ARID_dom	RT			7	2.1E-3	1.9E-1
Annotation Cluster 34		Enrichment Score: 2.62	G				
<input type="checkbox"/> GOTERM_MF_DIRECT	ATPase activity	RT			71	1.4E-4	6.2E-3
<input type="checkbox"/> UP_KW_LIGAND	Nucleotide-binding	RT			233	1.6E-4	6.4E-3
<input type="checkbox"/> UP_KW_LIGAND	ATP-binding	RT			169	2.5E-2	2.5E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	ATP binding	RT			182	6.0E-2	6.3E-1
Annotation Cluster 35		Enrichment Score: 2.59	G				
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	RT			8	3.3E-4	1.6E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	3'-UTR-mediated mRNA destabilization	RT			8	1.8E-3	6.0E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation of intracellular mRNA localization	RT			3	2.8E-2	4.3E-1
Annotation Cluster 36		Enrichment Score: 2.49	G				
<input type="checkbox"/> GOTERM_BP_DIRECT	antigen processing and presentation	RT			23	1.3E-	5.8E-8
<input type="checkbox"/> KEGG_PATHWAY	Antigen_processing_and_presentation	RT			31	5.4E-9	1.3E-7
<input type="checkbox"/> GOTERM_CC_DIRECT	ER to Golgi transport vesicle membrane	RT			23	6.4E-9	2.0E-7
<input type="checkbox"/> GOTERM_CC_DIRECT	lumenal side of endoplasmic reticulum membrane	RT			16	1.4E-8	4.2E-7
<input type="checkbox"/> GOTERM_MF_DIRECT	MHC class II protein complex binding	RT			15	1.1E-7	1.2E-5
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Immunoglobulin C1-set	RT			11	3.3E-7	2.3E-4
<input type="checkbox"/> KEGG_PATHWAY	Viral_myocarditis	RT			24	3.4E-6	3.7E-5
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Ig-like C1-type	RT			15	1.3E-5	5.7E-3
<input type="checkbox"/> GOTERM_CC_DIRECT	MHC class II protein complex	RT			12	1.5E-5	2.5E-4
<input type="checkbox"/> INTERPRO	MHC_I_a_C	RT			7	2.1E-5	1.3E-2
<input type="checkbox"/> KEGG_PATHWAY	Allograft_rejection	RT			16	2.6E-5	2.2E-4
<input type="checkbox"/> KEGG_PATHWAY	Type_I_diabetes_mellitus	RT			17	3.3E-5	2.8E-4
<input type="checkbox"/> UP_SEQ_FEATURE	REGION:Alpha-1	RT			9	4.9E-5	1.7E-2
<input type="checkbox"/> UP_SEQ_FEATURE	REGION:Alpha-2	RT			9	4.9E-5	1.7E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation of T cell activation	RT			13	5.0E-5	3.9E-3
<input type="checkbox"/> INTERPRO	MHC_I_a_a1/a2	RT			8	9.0E-5	2.7E-2
<input type="checkbox"/> KEGG_PATHWAY	Graft-versus-host_disease	RT			16	1.0E-4	7.3E-4
<input type="checkbox"/> GOTERM_CC_DIRECT	clathrin-coated endocytic vesicle membrane	RT			19	1.2E-4	1.7E-3
<input type="checkbox"/> GOTERM_MF_DIRECT	MHC class II receptor activity	RT			8	1.4E-4	6.2E-3
<input type="checkbox"/> UP_SEQ_FEATURE	REGION:Connecting peptide	RT			13	1.6E-4	4.4E-2
<input type="checkbox"/> KEGG_PATHWAY	Inflammatory_bowel_disease	RT			20	2.7E-4	1.7E-3
<input type="checkbox"/> INTERPRO	MHC_II_a/b_N	RT			10	2.8E-4	4.8E-2
<input type="checkbox"/> GOTERM_MF_DIRECT	peptide antigen binding	RT			15	3.1E-4	1.2E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	antigen_processing_and_presentation_of_peptide_or polysaccharide_antigen_via_MHC_class_II	RT			9	4.4E-4	2.0E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	peptide_antigen_assembly_with_MHC_class_II_protein_complex	RT			8	5.3E-4	2.3E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	Autoimmune_thyroid_disease	RT			17	5.5E-4	3.2E-3
<input type="checkbox"/> KEGG_PATHWAY							

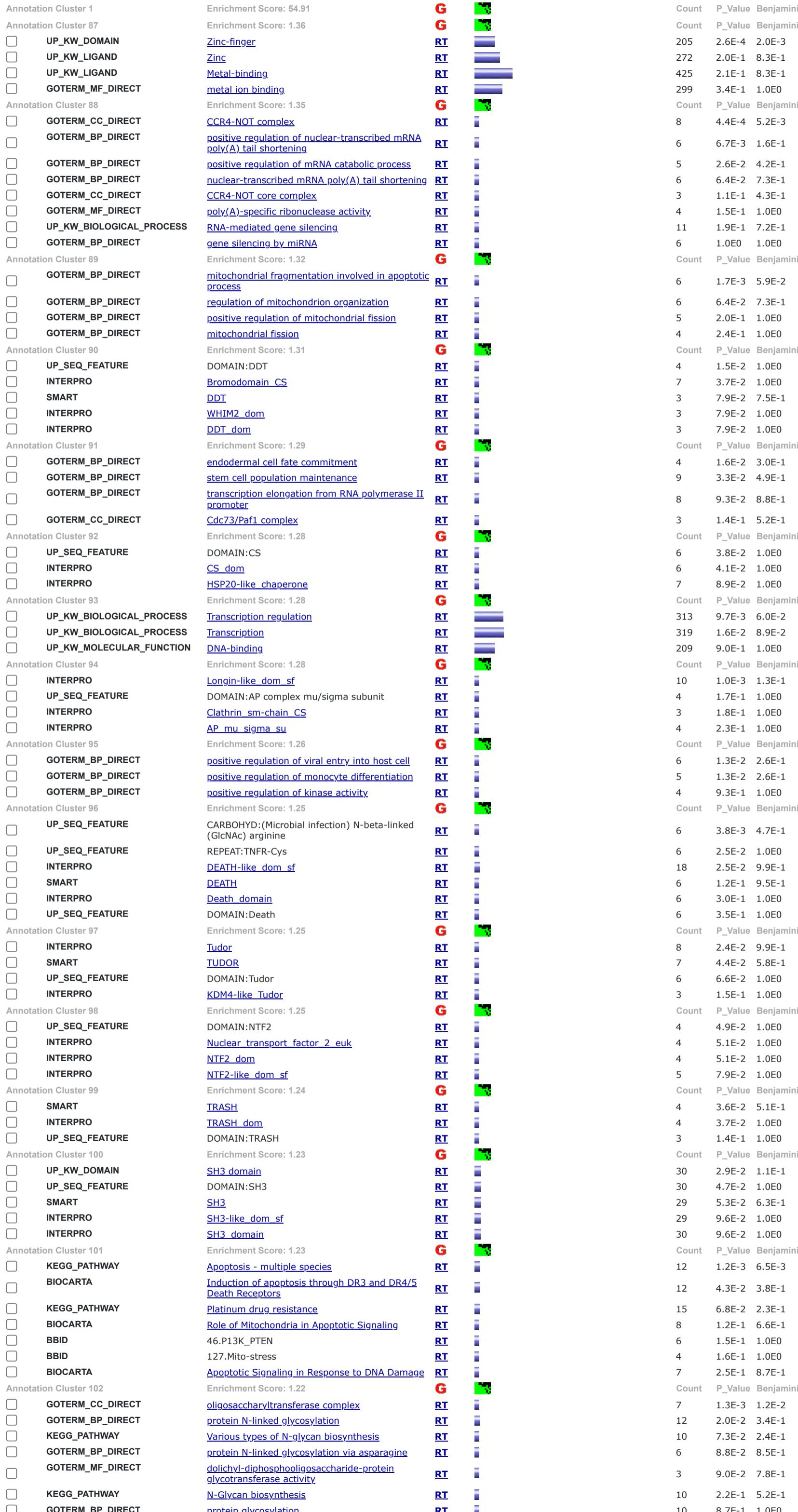
		Enrichment Score: 54.91	G			Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	MHC II	RT			9	5.8E-4	3.2E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	antigen_processing_and_presentation_of_exogenous_peptide_antigen_via_MHC_class_II	RT			11	6.5E-4	2.7E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	MHC class I protein complex	RT			6	8.0E-4	8.0E-3
<input type="checkbox"/>	KEGG_PATHWAY	Rheumatoid arthritis	RT			24	9.4E-4	5.1E-3
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	MHC I	RT			6	1.1E-3	5.2E-3
<input type="checkbox"/>	BIOCARTA	Antigen Processing and Presentation	RT			8	1.7E-3	4.9E-2
<input type="checkbox"/>	SMART	MHC II_alpha	RT			5	2.5E-3	7.0E-2
<input type="checkbox"/>	INTERPRO	MHC_II_a_N	RT			5	2.6E-3	1.9E-1
<input type="checkbox"/>	INTERPRO	MHC_I/II-like_Ag-recog	RT			12	5.1E-3	3.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:MHC class II alpha chain N-terminal	RT			4	7.8E-3	8.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:Alpha-3	RT			5	1.1E-2	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	protection_from_natural_killer_cell-mediated_cytotoxicity	RT			4	1.6E-2	3.0E-1
<input type="checkbox"/>	INTERPRO	MHC_I-like_Ag-recog	RT			8	2.0E-2	9.2E-1
<input type="checkbox"/>	INTERPRO	MHC_I-like_Ag-recog_sf	RT			8	2.0E-2	9.2E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	transport Vesicle membrane	RT			10	2.1E-2	1.3E-1
<input type="checkbox"/>	SMART	MHC_II_beta	RT			6	2.6E-2	4.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:MHC class I alpha chain C-terminal	RT			3	2.6E-2	1.0E0
<input type="checkbox"/>	INTERPRO	MHC_II_b_N	RT			6	2.7E-2	9.9E-1
<input type="checkbox"/>	SMART	IGc1	RT			14	3.0E-2	4.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	TAP binding	RT			3	3.1E-2	4.0E-1
<input type="checkbox"/>	INTERPRO	Ig/MHC_CS	RT			13	3.6E-2	1.0E0
<input type="checkbox"/>	INTERPRO	Ig_C1-set	RT			14	4.1E-2	1.0E0
<input type="checkbox"/>	BBID	70.Signal_peptides_(MHC)_class_I_molecules	RT			4	4.8E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:VL9 epitope	RT			3	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:MHC class II beta chain N-terminal	RT			5	5.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:MHC class I-like antigen recognition-like	RT			6	5.6E-2	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Hematopoietic cell lineage	RT			19	6.7E-2	2.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	antigen_processing_and_presentation_of_endogenous_peptide_antigen_via_MHC_class_Ib	RT			5	7.0E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	antigen_processing_and_presentation_of_endogenous_peptide_antigen_via_MHC_class_I_via_ER_pathway,_TAP-independent	RT			5	7.0E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation_of_T_cell-mediated_cytotoxicity	RT			8	7.4E-2	7.9E-1
<input type="checkbox"/>	KEGG_PATHWAY	Intestinal immune network for IgA production	RT			11	8.1E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation_of_immune_response	RT			8	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	endocytic vesicle membrane	RT			12	1.0E-1	4.3E-1
<input type="checkbox"/>	KEGG_PATHWAY	Cell adhesion molecules	RT			26	1.3E-1	3.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Asthma	RT			7	1.9E-1	4.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	beta-2-microglobulin_binding	RT			3	2.0E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:Beta-1	RT			3	2.1E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:Beta-2	RT			3	2.1E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	detection_of_bacterium	RT			3	3.5E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Immunoglobulin V-set	RT			5	5.7E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Staphylococcus_aureus_infection	RT			10	8.7E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Ig-like V-type	RT			9	9.7E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Systemic_lupus erythematosus	RT			8	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Ig-like	RT			30	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Ig-like_fold	RT			63	1.0E0	1.0E0
<input type="checkbox"/>	SMART	IGv	RT			6	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Ig-like_dom_sf	RT			37	1.0E0	1.0E0
<input type="checkbox"/>	UP_KW_DOMAIN	Immunoglobulin_domain	RT			26	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Ig-like_dom	RT			28	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Ig_sub	RT			14	1.0E0	1.0E0
<input type="checkbox"/>	SMART	IG	RT			14	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Ig_V-set	RT			11	1.0E0	1.0E0
Annotation Cluster 37		Enrichment Score: 2.39	G			Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 6	RT			42	1.0E-3	1.8E-1
<input type="checkbox"/>	UP_KW_DOMAIN	WD_repeat	RT			42	1.1E-3	7.1E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD	RT			36	1.6E-3	2.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 5	RT			42	1.7E-3	2.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 4	RT			42	2.1E-3	3.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 3	RT			42	2.4E-3	3.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 1	RT			42	4.1E-3	5.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 2	RT			42	4.1E-3	5.0E-1
<input type="checkbox"/>	SMART	WD40	RT			42	4.7E-3	1.0E-1
<input type="checkbox"/>	INTERPRO	WD40_rpt	RT			42	5.4E-3	3.6E-1
<input type="checkbox"/>	INTERPRO	G-protein_beta_WD-40_rep	RT			19	6.9E-3	4.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 7	RT			32	7.4E-3	8.2E-1
<input type="checkbox"/>	INTERPRO	WD40_repeat_dom_sf	RT			45	9.2E-3	5.0E-1
<input type="checkbox"/>	INTERPRO	WD40_repeat_CS	RT			25	1.1E-2	5.8E-1
<input type="checkbox"/>	INTERPRO	WD40/YVTN_repeat-like_dom_sf	RT			47	3.9E-2	1.0E0
Annotation Cluster 38		Enrichment Score: 2.36	G			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation_of_telomere_maintenance	RT			9	1.1E-4	7.0E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein_localization_to_chromosome,_telomeric_region	RT			7	3.1E-4	1.6E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	nuclear_telomere_cap_complex	RT			6	8.0E-4	8.0E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	telomeric_DNA_binding	RT			9	8.6E-3	1.5E-1
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Telomere	RT			12	1.3E-2	4.9E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	shelterin_complex	RT			4	2.4E-2	1.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	telomere_capping	RT			5	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation_of_telomere_maintenance_via_telomerase	RT			6	6.4E-2	7.3E-1
Annotation Cluster 39		Enrichment Score: 2.32	G			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation_of_ER-associated ubiquitin-dependent_protein_catabolic_process	RT			6	4.5E-4	2.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation_of_ERAD_pathway	RT			7	4.9E-3	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation_of_protein_ubiquitination_involved_in_ubiquitin-dependent_protein_catabolic_process	RT			7	4.9E-2	6.2E-1
Annotation Cluster 40		Enrichment Score: 2.31	G			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	tumor_necrosis_factor-mediated_signaling_pathway	RT			18	6.1E-5	4.4E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	tumor_necrosis_factor-activated_receptor_activity	RT			7	2.0E-4	8.2E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:TNFR-Cys	RT			7	4.0E-3	4.9E-1
<input type="checkbox"/>	SMART	TNFR	RT			8	5.2E-3	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:TNFR-Cys 1	RT			8	8.0E-3	8.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:TNFR-Cys 2	RT			8	8.0E-3	8.3E-1

		Enrichment Score:	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	TNFR/NGFR_Cys rich_reg	54.91	■	■	8	8.7E-3	4.8E-1
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:TNFR-Cys 3		■	■	7	2.0E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:TNFR-Cys		■	■	6	2.5E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:TNFR-Cys 4		■	■	4	1.2E-1	1.0E0
Annotation Cluster 41	Enrichment Score: 2.27	G	■	■	Count	P_Value	Benjamini
<input type="checkbox"/> BIOCARTA	CTL mediated immune response against target cells		■	■	11	3.5E-5	4.0E-3
<input type="checkbox"/> BIOCARTA	The Co-Stimulatory Signal During T-cell Activation		■	■	13	3.5E-5	4.0E-3
<input type="checkbox"/> BIOCARTA	Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor		■	■	14	4.5E-5	4.0E-3
<input type="checkbox"/> BIOCARTA	Lck and Fyn tyrosine kinases in initiation of TCR Activation		■	■	9	1.9E-4	1.0E-2
<input type="checkbox"/> BIOCARTA	T Cytotoxic Cell Surface Molecules		■	■	9	4.7E-4	1.8E-2
<input type="checkbox"/> BIOCARTA	T Helper Cell Surface Molecules		■	■	9	4.7E-4	1.8E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	alpha-beta T cell activation		■	■	6	9.3E-4	3.6E-2
<input type="checkbox"/> BIOCARTA	Stathmin and breast cancer resistance to antimicrotubule agents		■	■	12	3.0E-3	7.9E-2
<input type="checkbox"/> BIOCARTA	HIV Induced T Cell Apoptosis		■	■	7	5.6E-3	1.2E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	alpha-beta T cell receptor complex		■	■	6	5.8E-3	4.6E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	positive thymic T cell selection		■	■	6	6.7E-3	1.6E-1
<input type="checkbox"/> BIOCARTA	IL 17 Signaling Pathway		■	■	8	1.6E-2	2.2E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	gamma-delta T cell activation		■	■	5	1.9E-2	3.3E-1
<input type="checkbox"/> BIOCARTA	T Cell Receptor and CD3 Complex		■	■	4	2.6E-2	3.1E-1
<input type="checkbox"/> BIOCARTA	NO2-dependent IL 12 Pathway in NK cells		■	■	8	3.3E-2	3.5E-1
<input type="checkbox"/> SMART	ITAM		■	■	4	5.1E-2	6.3E-1
<input type="checkbox"/> INTERPRO	CD3_esu/gsu/dsu		■	■	3	5.1E-2	1.0E0
<input type="checkbox"/> BIOCARTA	Role of Tob in T-cell activation		■	■	8	6.0E-2	4.4E-1
<input type="checkbox"/> INTERPRO	Phos_immunorcpt_sig_ITAM		■	■	4	6.8E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:ITAM		■	■	4	8.3E-2	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT	gamma-delta T cell receptor complex		■	■	3	1.4E-1	5.2E-1
<input type="checkbox"/> BIOCARTA	IL12 and Stat4 Dependent Signaling Pathway in Th1 Development		■	■	7	2.1E-1	8.6E-1
Annotation Cluster 42	Enrichment Score: 2.27	G	■	■	Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Translation_prot_SH3-like_sf		■	■	8	4.6E-4	6.7E-2
<input type="checkbox"/> INTERPRO	Rib_uL2_dom2		■	■	9	1.1E-3	1.3E-1
<input type="checkbox"/> INTERPRO	KOW		■	■	6	2.6E-3	1.9E-1
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:KOW		■	■	4	2.4E-2	1.0E0
<input type="checkbox"/> SMART	KOW		■	■	3	1.5E-1	1.0E0
Annotation Cluster 43	Enrichment Score: 2.27	G	■	■	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:RHD		■	■	7	1.2E-4	3.9E-2
<input type="checkbox"/> INTERPRO	RHD_dimer		■	■	7	1.3E-4	3.3E-2
<input type="checkbox"/> INTERPRO	RHD_DNA_bind_dom		■	■	7	1.3E-4	3.3E-2
<input type="checkbox"/> INTERPRO	RHD_DNA_bind_dom_sf		■	■	7	1.3E-4	3.3E-2
<input type="checkbox"/> INTERPRO	p53-like_TF_DNA-bd_sf		■	■	12	3.0E-3	2.2E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	NIK/NF-kappaB_signaling		■	■	9	5.2E-3	1.3E-1
<input type="checkbox"/> INTERPRO	NFkB/Dor		■	■	4	8.2E-3	4.7E-1
<input type="checkbox"/> INTERPRO	RHD_CS		■	■	4	8.2E-3	4.7E-1
<input type="checkbox"/> INTERPRO	IPT_NFKappaB		■	■	4	8.2E-3	4.7E-1
<input type="checkbox"/> INTERPRO	IPT_dom		■	■	9	8.7E-3	4.8E-1
<input type="checkbox"/> SMART	IPT		■	■	8	1.6E-2	2.9E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	cellular_response_to_stress		■	■	6	2.3E-2	3.9E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	calcineurin-NFAT_signaling_cascade		■	■	5	5.7E-2	6.6E-1
<input type="checkbox"/> INTERPRO	NFAT		■	■	3	7.9E-2	1.0E0
<input type="checkbox"/> INTERPRO	Ig_E-set		■	■	17	8.8E-2	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	cytokine_production		■	■	3	1.5E-1	1.0E0
Annotation Cluster 44	Enrichment Score: 2.25	G	■	■	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	kinetochore		■	■	33	4.0E-5	6.3E-4
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Centromere		■	■	24	3.4E-2	1.2E-1
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Kinetochore		■	■	16	1.3E-1	3.8E-1
Annotation Cluster 45	Enrichment Score: 2.17	G	■	■	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation_of_transcription_initiation_from_RNA_polymerase_II_promoter		■	■	15	1.8E-3	6.2E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation_of_transcription_elongation_from_RNA_polymerase_II_promoter		■	■	13	3.4E-3	9.9E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	RNA_polymerase_II_transcriptional_preinitiation_complex_assembly		■	■	14	7.0E-3	1.7E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	core_mediator_complex		■	■	8	1.0E-2	7.6E-2
<input type="checkbox"/> GOTERM_CC_DIRECT	mediator_complex		■	■	9	3.2E-2	1.8E-1
Annotation Cluster 46	Enrichment Score: 2.15	G	■	■	Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Ribosomal_eL8/eL30/eS12/Gad45		■	■	6	2.6E-3	1.9E-1
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Ribosomal protein eL8/eL30/eS12/Gadd45		■	■	5	1.1E-2	1.0E0
<input type="checkbox"/> INTERPRO	Ribosomal_eL30-like_sf		■	■	6	1.2E-2	6.0E-1
Annotation Cluster 47	Enrichment Score: 2.11	G	■	■	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	TOPO_DOM:Mitochondrial intermembrane		■	■	26	2.4E-3	3.3E-1
<input type="checkbox"/> UP_SEQ_FEATURE	TOPO_DOM:Mitochondrial matrix		■	■	19	4.7E-3	5.6E-1
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Mitochondrion_inner_membrane		■	■	48	4.0E-2	1.3E-1
Annotation Cluster 48	Enrichment Score: 2.05	G	■	■	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	tricarboxylic_acid_cycle		■	■	12	5.9E-4	2.5E-2
<input type="checkbox"/> KEGG_PATHWAY	Citrate_cycle_(TCA_cycle)		■	■	12	6.6E-4	3.8E-3
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Tricarboxylic_acid_cycle		■	■	10	1.3E-3	9.2E-3
<input type="checkbox"/> KEGG_PATHWAY	2-Oxocarboxylic_acid_metabolism		■	■	9	4.8E-2	1.7E-1
<input type="checkbox"/> KEGG_PATHWAY	Carbon_metabolism		■	■	22	4.9E-2	1.7E-1
<input type="checkbox"/> KEGG_PATHWAY	Lipoic_acid_metabolism		■	■	4	4.3E-1	8.6E-1
Annotation Cluster 49	Enrichment Score: 2.05	G	■	■	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:ADF-H		■	■	6	2.4E-3	3.3E-1
<input type="checkbox"/> SMART	ADF		■	■	6	2.5E-3	7.0E-2
<input type="checkbox"/> INTERPRO	ADF-H		■	■	6	2.6E-3	1.9E-1
<input type="checkbox"/> INTERPRO	ADF-H/Gelsolin-like_dom_sf		■	■	8	1.1E-2	5.8E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	actin_filament_depolymerization		■	■	3	3.5E-1	1.0E0
Annotation Cluster 50	Enrichment Score: 2.05	G	■	■	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	F-actin_capping_protein_complex		■	■	6	3.9E-4	4.7E-3
<input type="checkbox"/> GOTERM_BP_DIRECT	barbed-end_actin_filament_capping		■	■	9	4.4E-4	2.0E-2
<input type="checkbox"/> INTERPRO	CapZ_alpha/beta		■	■	3	5.1E-2	1.0E0
<input type="checkbox"/> INTERPRO	CapZ_alpha/beta_2		■	■	3	5.1E-2	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Actin_capping		■	■	5	1.4E-1	6.6E-1

Annotation Cluster 1		Enrichment Score: 54.91			Count	P_Value	Benjamini
Annotation Cluster 51		Enrichment Score: 2.04			Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO		HSP70_C_sf			7	1.4E-3	1.4E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		protein refolding			9	4.1E-3	1.1E-1
<input type="checkbox"/> INTERPRO		HSP70_peptide-bd_sf			6	6.0E-3	3.9E-1
<input type="checkbox"/> INTERPRO		Hsp_70_fam			6	1.2E-2	6.0E-1
<input type="checkbox"/> INTERPRO		Heat_shock_70_CS			6	1.2E-2	6.0E-1
<input type="checkbox"/> INTERPRO		ATPase_NBD			15	1.4E-2	6.8E-1
<input type="checkbox"/> UP_SEQ_FEATURE		MUTAGEN:K->R: Complete loss of in vitro methylation by METTL21A.			3	7.7E-2	1.0E0
Annotation Cluster 52		Enrichment Score: 2			Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:1-4			8	4.1E-4	9.0E-2
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:1-3			8	9.7E-4	1.8E-1
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:1-2			9	1.8E-3	2.9E-1
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:1-1			9	2.4E-3	3.3E-1
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:2-1			8	8.0E-3	8.3E-1
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:2-2			8	1.2E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:1-5			4	2.4E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:2-3			5	7.5E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:3-2			3	1.8E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:3-1			3	1.8E-1	1.0E0
Annotation Cluster 53		Enrichment Score: 1.99			Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE		MOTIF:Cx9C motif 1			7	7.4E-3	8.2E-1
<input type="checkbox"/> UP_SEQ_FEATURE		MOTIF:Cx9C motif 2			7	7.4E-3	8.2E-1
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:CHCH			7	2.0E-2	1.0E0
Annotation Cluster 54		Enrichment Score: 1.96			Count	P_Value	Benjamini
<input type="checkbox"/> SMART		BROMO			11	6.4E-3	1.3E-1
<input type="checkbox"/> UP_KW_DOMAIN		Bromodomain			10	7.0E-3	3.6E-2
<input type="checkbox"/> INTERPRO		Bromodomain			11	7.8E-3	4.7E-1
<input type="checkbox"/> INTERPRO		Bromodomain-like_sf			11	9.2E-3	5.0E-1
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:Bromo			10	1.5E-2	1.0E0
<input type="checkbox"/> INTERPRO		Bromodomain_CS			7	3.7E-2	1.0E0
Annotation Cluster 55		Enrichment Score: 1.9			Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT		transcription_factor_AP-1_complex			5	4.2E-4	5.0E-3
<input type="checkbox"/> INTERPRO		JNK			3	2.7E-2	9.9E-1
<input type="checkbox"/> INTERPRO		Leuzip_Jun			3	2.7E-2	9.9E-1
<input type="checkbox"/> INTERPRO		TF_DNA-bd_sf			5	7.9E-2	1.0E0
Annotation Cluster 56		Enrichment Score: 1.89			Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		positive_regulation_of_erythrocyte_differentiation			11	1.4E-3	5.2E-2
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:STAT transcription factor protein interaction			5	2.4E-3	3.3E-1
<input type="checkbox"/> SMART		STAT_int			5	2.5E-3	7.0E-2
<input type="checkbox"/> INTERPRO		STAT_N_sf			5	2.6E-3	1.9E-1
<input type="checkbox"/> INTERPRO		STAT_linker			5	2.6E-3	1.9E-1
<input type="checkbox"/> INTERPRO		STAT			5	2.6E-3	1.9E-1
<input type="checkbox"/> INTERPRO		STAT_TF_coiled-coil			5	2.6E-3	1.9E-1
<input type="checkbox"/> INTERPRO		STAT_TF_DNA-bd_N			5	2.6E-3	1.9E-1
<input type="checkbox"/> INTERPRO		STAT_TF_prot_interaction			5	2.6E-3	1.9E-1
<input type="checkbox"/> INTERPRO		STAT_TF_alpha			5	2.6E-3	1.9E-1
<input type="checkbox"/> INTERPRO		STAT_TF_DNA-bd			5	2.6E-3	1.9E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		interleukin-9-mediated_signaling_pathway			5	2.8E-3	8.4E-2
<input type="checkbox"/> GOTERM_BP_DIRECT		interleukin-15-mediated_signaling_pathway			6	2.9E-3	8.4E-2
<input type="checkbox"/> INTERPRO		p53-like_TF_DNA-bd_sf			12	3.0E-3	2.2E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		interleukin-2-mediated_signaling_pathway			5	5.2E-3	1.3E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		JAK-STAT cascade involved in growth hormone signaling_pathway			5	1.3E-2	2.6E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		JAK-STAT cascade			11	1.5E-2	2.9E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		response_to_peptide_hormone			11	1.5E-2	2.9E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		interleukin-4-mediated_signaling_pathway			4	2.6E-2	4.2E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		regulation_of_multicellular_organism_growth			7	2.9E-2	4.3E-1
<input type="checkbox"/> BIOCARTA		IL22_Soluble_Receptor_Signaling_Pathway			6	9.1E-2	5.4E-1
<input type="checkbox"/> BBID		48.mice_minus_JAKs_and_STATs			6	1.1E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		cellular_response_to_organic_substance			6	2.4E-1	1.0E0
<input type="checkbox"/> BIOCARTA		IL-10_Anti-inflammatory_Signaling_Pathway			5	2.4E-1	8.7E-1
<input type="checkbox"/> BBID		12.IL-6_type_cytokine-signal-transduct			5	6.9E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		cellular_response_to_hormone_stimulus			4	7.8E-1	1.0E0
<input type="checkbox"/> BIOCARTA		Bioactive_Peptide_Induced_Signaling_Pathway			7	7.9E-1	1.0E0
Annotation Cluster 57		Enrichment Score: 1.83			Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		DNA_repair			45	8.2E-3	1.9E-1
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS		DNA_damage			66	1.8E-2	9.3E-2
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS		DNA_repair			56	2.3E-2	1.1E-1
Annotation Cluster 58		Enrichment Score: 1.82			Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT		membrane_coat			10	1.8E-4	2.4E-3
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:Clathrin/coatomer adaptor adaptin-like N-terminal			4	1.2E-1	1.0E0
<input type="checkbox"/> INTERPRO		Clathrin/coatomer_adapt-like_N			4	1.5E-1	1.0E0
Annotation Cluster 59		Enrichment Score: 1.81			Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT		K63-linked_polyubiquitin_binding			9	3.2E-3	7.4E-2
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:CCHC_NOA-type			3	2.6E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		ZN_FING:CCHC_NOA-type			3	2.6E-2	1.0E0
<input type="checkbox"/> INTERPRO		NEMO_ZF			3	2.7E-2	9.9E-1
Annotation Cluster 60		Enrichment Score: 1.79			Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		lysosomal_lumen_acidification			11	5.5E-5	4.1E-3
<input type="checkbox"/> KEGG_PATHWAY		Vibrio_cholerae_infection			17	2.6E-4	1.7E-3
<input type="checkbox"/> GOTERM_BP_DIRECT		regulation_of_macroautophagy			15	1.3E-3	4.7E-2
<input type="checkbox"/> GOTERM_BP_DIRECT		vacuolar_acidification			9	1.3E-3	4.7E-2
<input type="checkbox"/> GOTERM_BP_DIRECT		Golgi_lumen_acidification			6	1.7E-3	5.9E-2
<input type="checkbox"/> GOTERM_CC_DIRECT		clathrin-coated_vesicle_membrane			10	3.5E-3	2.9E-2
<input type="checkbox"/> GOTERM_CC_DIRECT		proton-transporting_V-type_ATPase_complex			6	8.4E-3	6.1E-2
<input type="checkbox"/> GOTERM_BP_DIRECT		endosomal_lumen_acidification			6	9.6E-3	2.1E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		intracellular_pH_reduction			6	9.6E-3	2.1E-1
<input type="checkbox"/> KEGG_PATHWAY		Epithelial_cell_signaling_in_Helicobacter_pylo ri_infection			17	1.2E-2	5.2E-2
<input type="checkbox"/> GOTERM_MF_DIRECT		proton-transporting_ATPase_activity,_rotational_mechanism			8	1.3E-2	2.1E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		synaptic_vesicle_lumen_acidification			6	2.3E-2	3.9E-1
<input type="checkbox"/> GOTERM_CC_DIRECT		proton-transporting_V-type_ATPase,_V0_domain			4	6.6E-2	3.0E

		Enrichment Score: 54.91	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_DIRECT	vacuolar proton-transporting V-type ATPase, V0 domain	RT		4	6.6E-2	3.0E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	extrinsic component of synaptic vesicle membrane	RT		4	8.5E-2	3.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	vacuolar proton-transporting V-type ATPase, V1 domain	RT		4	1.1E-1	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	hydrogen ion transmembrane transport	RT		20	1.1E-1	9.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	proton-transporting V-type ATPase, V1 domain	RT		3	1.1E-1	4.3E-1
<input type="checkbox"/>	KEGG_PATHWAY	Collecting duct acid secretion	RT		7	1.1E-1	3.4E-1
<input type="checkbox"/>	KEGG_PATHWAY	Synaptic vesicle cycle	RT		14	1.8E-1	4.6E-1
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Hydrogen ion transport	RT		10	2.2E-1	7.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	transmembrane transporter complex	RT		6	4.3E-1	1.0E0
Annotation Cluster 61							
<input type="checkbox"/>	UP_SEQ_FEATURE	Enrichment Score: 1.75	G		Count	P_Value	Benjamini
<input type="checkbox"/>	DOMAIN:CXXC-type	RT		5	1.1E-2	1.0E0	
<input type="checkbox"/>	GOTERM_MF_DIRECT	unmethylated CpG binding	RT		5	1.5E-2	2.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	ZN_FING:CXXC-type	RT		5	1.7E-2	1.0E0
<input type="checkbox"/>	INTERPRO	Znf_CXXC	RT		5	3.3E-2	1.0E0
Annotation Cluster 62							
<input type="checkbox"/>	GOTERM_MF_DIRECT	Enrichment Score: 1.74	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	cysteine-type endopeptidase activity	RT		19	1.4E-4	6.2E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	protein deubiquitination	RT		21	3.4E-4	1.7E-2
<input type="checkbox"/>	INTERPRO	DOMAIN:DUSP	RT		5	1.1E-3	1.9E-1
<input type="checkbox"/>	INTERPRO	DUSP-like_sf	RT		5	2.6E-3	1.9E-1
<input type="checkbox"/>	INTERPRO	Pept_C19_DUSP	RT		5	2.6E-3	1.9E-1
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Thiol_protease	RT		28	3.9E-3	3.4E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	thiol-dependent ubiquitin-specific protease activity	RT		21	1.3E-2	2.1E-1
<input type="checkbox"/>	SMART	DUSP	RT		4	1.5E-2	2.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitinyl hydrolase activity	RT		6	2.1E-2	3.0E-1
<input type="checkbox"/>	INTERPRO	Papain-like_cys_pep_sf	RT		23	3.3E-2	1.0E0
<input type="checkbox"/>	INTERPRO	USP_CS	RT		13	3.6E-2	1.0E0
<input type="checkbox"/>	INTERPRO	Peptidase_C19_UCH	RT		13	5.2E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:USP	RT		13	5.7E-2	1.0E0
<input type="checkbox"/>	INTERPRO	USP_dom	RT		13	6.2E-2	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	Lys48-specific deubiquitinase activity	RT		6	6.3E-2	6.3E-1
<input type="checkbox"/>	INTERPRO	Ub_USP-typ	RT		3	7.9E-2	1.0E0
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Protease	RT		60	5.1E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	ACT_SITE:Nucleophile	RT		37	5.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	proteolysis	RT		60	5.7E-1	1.0E0
Annotation Cluster 63							
<input type="checkbox"/>	GOTERM_CC_DIRECT	Enrichment Score: 1.72	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_DIRECT	histone acetyltransferase complex	RT		9	3.3E-3	2.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	NSL_complex	RT		5	1.7E-2	1.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	positive regulation of histone H3-K4 methylation	RT		5	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	MLL1_complex	RT		7	8.7E-2	3.7E-1
Annotation Cluster 64							
<input type="checkbox"/>	SMART	Enrichment Score: 1.71	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	ZnF_AN1	RT		5	4.7E-3	1.0E-1
<input type="checkbox"/>	INTERPRO	Znf_AN1	RT		5	4.7E-3	3.2E-1
<input type="checkbox"/>	INTERPRO	AN1-like_Znf	RT		5	4.7E-3	3.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:A20-type	RT		4	1.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:AN1-type	RT		4	2.4E-2	1.0E0
<input type="checkbox"/>	SMART	ZnF_A20	RT		4	3.6E-2	5.1E-1
<input type="checkbox"/>	INTERPRO	Znf_A20	RT		4	3.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	ZN_FING:AN1-type	RT		3	7.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	ZN_FING:A20-type	RT		3	1.1E-1	1.0E0
Annotation Cluster 65							
<input type="checkbox"/>	BIOCARTA	Enrichment Score: 1.7	G		Count	P_Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	Lck and Fyn tyrosine kinases in initiation of TCR Activation	RT		9	1.9E-4	1.0E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	Primary immunodeficiency	RT		10	4.2E-2	1.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	T cell receptor complex	RT		9	9.7E-1	1.0E0
Annotation Cluster 66							
<input type="checkbox"/>	GOTERM_BP_DIRECT	Enrichment Score: 1.67	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	positive regulation of telomere maintenance via telomerase	RT		11	1.8E-3	6.2E-2
<input type="checkbox"/>	INTERPRO	Chaperone_TCP-1	RT		6	4.0E-3	2.9E-1
<input type="checkbox"/>	INTERPRO	Chaperonin_TCP-1_CS	RT		5	7.9E-3	4.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of telomerase RNA localization to Cajal body	RT		6	1.3E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of establishment of protein localization to telomere	RT		5	1.3E-2	2.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	chaperonin-containing_T-complex	RT		5	1.7E-2	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of protein localization to Cajal body	RT		5	1.9E-2	3.3E-1
<input type="checkbox"/>	INTERPRO	GROEL-like_equatorial_sf	RT		6	2.1E-2	9.5E-1
<input type="checkbox"/>	INTERPRO	GroEL-like_apical_dom_sf	RT		6	2.7E-2	9.9E-1
<input type="checkbox"/>	INTERPRO	TCP-1-like_intermed_sf	RT		6	2.7E-2	9.9E-1
<input type="checkbox"/>	INTERPRO	Cpn60/GroEL/TCP-1	RT		6	2.7E-2	9.9E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	zona_pellucida_receptor_complex	RT		4	3.6E-2	1.9E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	cell_body	RT		10	3.0E-1	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	binding_of_sperm_to_zona_pellucida	RT		6	3.2E-1	1.0E0
Annotation Cluster 67							
<input type="checkbox"/>	UP_SEQ_FEATURE	Enrichment Score: 1.66	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	DOMAIN:Serine/threonine specific protein phosphatases	RT		7	7.8E-4	1.5E-1
<input type="checkbox"/>	INTERPRO	PP2Ac	RT		7	1.3E-3	6.5E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	Ser/Thr-sp_prot-phosphatase	RT		7	1.4E-3	1.4E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	protein_dephosphorylation	RT		24	1.5E-3	5.3E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	PTW/PP1_phosphatase_complex	RT		5	2.5E-3	2.2E-2
<input type="checkbox"/>	INTERPRO	protein_serine/threonine_phosphatase_activity	RT		15	2.8E-3	6.9E-2
<input type="checkbox"/>	INTERPRO	Metallo-dependent_PP-like	RT		8	2.4E-2	9.9E-1
<input type="checkbox"/>	INTERPRO	Calcineurin-like_PHP_ApaH	RT		8	2.4E-2	9.9E-1
<input type="checkbox"/>	INTERPRO	STPPase_N	RT		3	2.7E-2	9.9E-1
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Protein_phosphatase	RT		24	3.0E-2	1.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	myosin_phosphatase_activity	RT		15	7.1E-2	6.9E-1
<input type="checkbox"/>	INTERPRO	PPA2-like	RT		3	7.9E-2	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptidyl-threonine_dephosphorylation	RT		5	1.0E-1	9.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	entrainment_of_circadian_clock_by_photoperiod	RT		6	1.0E-1	9.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	glycogen_metabolic_process	RT		7	1.2E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	phosphoprotein_phosphatase_activity	RT		8	1.8E-1	1.0E0
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Glycogen_metabolism	RT				

Annotation Cluster 1	Enrichment Score: 54.91	G	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	AMP salvage	RT	4	8.8E-3	1.9E-1
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Purine salvage	RT	4	1.3E-2	7.6E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	purine ribonucleoside salvage	RT	4	2.6E-2	4.2E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	GMP salvage	RT	3	8.3E-2	8.3E-1
Annotation Cluster 69	Enrichment Score: 1.65	G	Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	PTBP1-like RRM2	RT	4	8.2E-3	4.7E-1
<input type="checkbox"/> INTERPRO	HnRNP-L/PTB	RT	4	8.2E-3	4.7E-1
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:RRM 4	RT	4	1.7E-1	1.0E0
Annotation Cluster 70	Enrichment Score: 1.63	G	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	nuclear telomere cap complex	RT	6	8.0E-4	8.0E-3
<input type="checkbox"/> GOTERM_MF_DIRECT	double-stranded telomeric DNA binding	RT	4	6.1E-2	6.3E-1
<input type="checkbox"/> BIOCARTA	Telomeres, Telomerase, Cellular Aging, and Immortality	RT	6	2.7E-1	9.2E-1
Annotation Cluster 71	Enrichment Score: 1.62	G	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:DED	RT	4	2.4E-2	1.0E0
<input type="checkbox"/> SMART	DED	RT	4	2.5E-2	4.1E-1
<input type="checkbox"/> INTERPRO	DED_dom	RT	4	2.5E-2	9.9E-1
Annotation Cluster 72	Enrichment Score: 1.6	G	Count	P_Value	Benjamini
<input type="checkbox"/> BIOCARTA	D4-GDI Signaling Pathway	RT	8	6.0E-3	1.2E-1
<input type="checkbox"/> BIOCARTA	HIV-I Nef	RT	21	9.1E-3	1.6E-1
<input type="checkbox"/> BIOCARTA	Caspase Cascade in Apoptosis	RT	11	1.0E-2	1.6E-1
<input type="checkbox"/> BIOCARTA	FAS signaling_pathway_(CD95_)	RT	11	7.8E-2	4.8E-1
<input type="checkbox"/> BIOCARTA	TNFR1 Signaling Pathway	RT	9	2.2E-1	8.7E-1
Annotation Cluster 73	Enrichment Score: 1.6	G	Count	P_Value	Benjamini
<input type="checkbox"/> UP_KW_DOMAIN	SH2 domain	RT	19	8.2E-3	3.7E-2
<input type="checkbox"/> INTERPRO	SH2_dom_sf	RT	20	1.9E-2	8.7E-1
<input type="checkbox"/> INTERPRO	SH2	RT	19	2.4E-2	9.9E-1
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:SH2	RT	18	3.1E-2	1.0E0
<input type="checkbox"/> SMART	SH2	RT	16	8.9E-2	8.3E-1
Annotation Cluster 74	Enrichment Score: 1.59	G	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	mitochondrial fragmentation involved in apoptotic process	RT	6	1.7E-3	5.9E-2
<input type="checkbox"/> GOTERM_BP_DIRECT	release of cytochrome c from mitochondria	RT	6	7.5E-2	8.0E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	mitochondrial fusion	RT	5	1.4E-1	1.0E0
Annotation Cluster 75	Enrichment Score: 1.58	G	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C3H1-type	RT	15	1.5E-3	2.5E-1
<input type="checkbox"/> INTERPRO	Znf_CCCH	RT	14	7.6E-3	4.7E-1
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:C3H1-type	RT	12	8.6E-3	8.9E-1
<input type="checkbox"/> INTERPRO	Znf_CCCH_sf	RT	10	1.2E-2	6.0E-1
<input type="checkbox"/> SMART	Znf_C3H1	RT	11	2.5E-2	4.1E-1
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C3H1-type 1	RT	7	1.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C3H1-type 2	RT	7	1.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C3H1-type 3	RT	3	6.7E-1	1.0E0
Annotation Cluster 76	Enrichment Score: 1.57	G	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:BAT2 N-terminal	RT	3	2.6E-2	1.0E0
<input type="checkbox"/> INTERPRO	BAT2_N	RT	3	2.7E-2	9.9E-1
<input type="checkbox"/> INTERPRO	PRRC2	RT	3	2.7E-2	9.9E-1
Annotation Cluster 77	Enrichment Score: 1.54	G	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C4-type	RT	16	8.2E-4	1.6E-1
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Arf-GAP	RT	7	5.6E-2	1.0E0
<input type="checkbox"/> SMART	ArfGap	RT	7	5.9E-2	6.7E-1
<input type="checkbox"/> INTERPRO	ARFGAP/RecO	RT	7	6.0E-2	1.0E0
<input type="checkbox"/> INTERPRO	ArfGAP_dom_sf	RT	7	6.0E-2	1.0E0
<input type="checkbox"/> INTERPRO	ArfGAP_dom	RT	7	6.0E-2	1.0E0
Annotation Cluster 78	Enrichment Score: 1.48	G	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	RT	11	5.3E-3	1.4E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	exon-exon junction complex	RT	6	4.8E-2	2.4E-1
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Nonsense-mediated mRNA decay	RT	7	1.4E-1	5.6E-1
Annotation Cluster 79	Enrichment Score: 1.47	G	Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	OS9-like_dom	RT	3	2.7E-2	9.9E-1
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:MRH	RT	4	3.5E-2	1.0E0
<input type="checkbox"/> INTERPRO	Man6P_isomerase_rcpt-bd_dom_sf	RT	4	3.7E-2	1.0E0
<input type="checkbox"/> INTERPRO	MRH_dom	RT	4	3.7E-2	1.0E0
Annotation Cluster 80	Enrichment Score: 1.45	G	Count	P_Value	Benjamini
<input type="checkbox"/> SMART	ARF	RT	14	6.7E-4	4.1E-2
<input type="checkbox"/> SMART	SAR	RT	7	7.8E-2	7.5E-1
<input type="checkbox"/> INTERPRO	Small_GTPase_ARF/SAR	RT	7	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	Small_GTPase_ARF	RT	5	2.1E-1	1.0E0
Annotation Cluster 81	Enrichment Score: 1.44	G	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT	Lys63-specific deubiquitinase activity	RT	7	4.3E-3	9.0E-2
<input type="checkbox"/> GOTERM_MF_DIRECT	Lys48-specific deubiquitinase activity	RT	6	6.3E-2	6.3E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	protein K63-linked deubiquitination	RT	6	1.8E-1	1.0E0
Annotation Cluster 82	Enrichment Score: 1.42	G	Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	ENTH_VHS	RT	8	1.7E-2	7.9E-1
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:VHS	RT	4	4.9E-2	1.0E0
<input type="checkbox"/> SMART	VHS	RT	4	5.1E-2	6.3E-1
<input type="checkbox"/> INTERPRO	VHS_dom	RT	4	5.1E-2	1.0E0
Annotation Cluster 83	Enrichment Score: 1.4	G	Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Di19_Zn-bd	RT	4	2.5E-2	9.9E-1
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2HC RNF-type	RT	3	4.9E-2	1.0E0
<input type="checkbox"/> INTERPRO	ZF_C2HC_RNF	RT	3	5.1E-2	1.0E0
Annotation Cluster 84	Enrichment Score: 1.4	G	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	cellular respiration	RT	11	6.4E-3	1.6E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	mitochondrial electron transport, ubiquinol to cytochrome c	RT	5	4.5E-2	5.9E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	mitochondrial respiratory chain complex III	RT	5	5.2E-2	2.5E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	ubiquinol-cytochrome-c reductase activity	RT	3	1.6E-1	1.0E0
Annotation Cluster 85	Enrichment Score: 1.39	G	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	telomere maintenance	RT	15	2.2E-3	6.9E-2
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	DNA recombination	RT	16	1.1E-1	4.3E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	DNA recombination	RT	11	3.0E-1	1.0E0
Annotation Cluster 86	Enrichment Score: 1.37	G	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	histone acetyltransferase complex	RT	9	3.3E-3	2.9E-2
<input type="checkbox"/> GOTERM_MF_DIRECT	histone acetyltransferase activity	RT	7	1.1E-1	9.1E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	H3 histone acetyltransferase activity	RT	3	2.0E-1	1.0E0



Annotation Cluster 1		Enrichment Score: 54.91	G	██████████	Count	P_Value	Benjamini
Annotation Cluster 103		Enrichment Score: 1.22	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		nucleophagy	RT	██████████	4	2.6E-2	4.2E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		glycophagy	RT	██████████	5	2.6E-2	4.2E-1
<input type="checkbox"/> GOTERM_CC_DIRECT		pre-autophagosomal structure	RT	██████████	8	2.7E-2	1.6E-1
<input type="checkbox"/> GOTERM_CC_DIRECT		pre-autophagosomal structure membrane	RT	██████████	5	1.6E-1	5.7E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		pexophagy	RT	██████████	3	2.7E-1	1.0E0
Annotation Cluster 104		Enrichment Score: 1.21	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:WW	RT	██████████	10	4.4E-2	1.0E0
<input type="checkbox"/> SMART		WW	RT	██████████	10	5.3E-2	6.3E-1
<input type="checkbox"/> INTERPRO		WW_dom	RT	██████████	10	6.6E-2	1.0E0
<input type="checkbox"/> INTERPRO		WW_dom_sf	RT	██████████	9	9.5E-2	1.0E0
Annotation Cluster 105		Enrichment Score: 1.21	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		positive regulation of histone acetylation	RT	██████████	5	1.9E-2	3.3E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		positive regulation of transcription from RNA polymerase I promoter	RT	██████████	7	4.1E-2	5.5E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		positive regulation of transcription from RNA polymerase III promoter	RT	██████████	4	3.0E-1	1.0E0
Annotation Cluster 106		Enrichment Score: 1.2	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		cellular sphingolipid homeostasis	RT	██████████	4	8.8E-3	1.9E-1
<input type="checkbox"/> INTERPRO		ORMDL	RT	██████████	3	2.7E-2	9.9E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		ceramide metabolic process	RT	██████████	7	3.5E-2	5.0E-1
<input type="checkbox"/> PIR_SUPERFAMILY		ORMDL	RT	██████████	3	4.6E-2	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT		SPOTS complex	RT	██████████	3	5.0E-2	2.4E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		negative regulation of ceramide biosynthetic process	RT	██████████	3	5.3E-2	6.3E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		regulation of ceramide biosynthetic process	RT	██████████	3	8.3E-2	8.3E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		cellular lipid metabolic process	RT	██████████	4	3.0E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		sphingolipid biosynthetic process	RT	██████████	6	6.1E-1	1.0E0
Annotation Cluster 107		Enrichment Score: 1.18	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT		U2-type spliceosomal complex	RT	██████████	8	1.9E-2	1.2E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		U2-type prespliceosome assembly	RT	██████████	7	3.5E-2	5.0E-1
<input type="checkbox"/> GOTERM_CC_DIRECT		U2 snRNP	RT	██████████	7	5.0E-2	2.4E-1
<input type="checkbox"/> GOTERM_CC_DIRECT		U12-type spliceosomal complex	RT	██████████	4	5.5E-1	1.0E0
Annotation Cluster 108		Enrichment Score: 1.18	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT		peptide-lysine-N-acetyltransferase activity	RT	██████████	5	1.5E-2	2.3E-1
<input type="checkbox"/> GOTERM_MF_DIRECT		acetyltransferase activity	RT	██████████	5	6.5E-2	6.4E-1
<input type="checkbox"/> GOTERM_MF_DIRECT		histone acetyltransferase activity	RT	██████████	7	1.1E-1	9.1E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		protein acetylation	RT	██████████	4	1.6E-1	1.0E0
Annotation Cluster 109		Enrichment Score: 1.13	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE		TRANSMEM:Helical; Anchor for type IV membrane protein	RT	██████████	14	1.1E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:V-SNARE coiled-coil homology	RT	██████████	5	2.3E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:v-SNARE coiled-coil homology	RT	██████████	5	2.3E-2	1.0E0
<input type="checkbox"/> INTERPRO		V_SNARE_CC	RT	██████████	5	3.3E-2	1.0E0
<input type="checkbox"/> INTERPRO		Synaptobrevin-like	RT	██████████	4	5.1E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:Longin	RT	██████████	3	7.7E-2	1.0E0
<input type="checkbox"/> SMART		Longin	RT	██████████	3	7.9E-2	7.5E-1
<input type="checkbox"/> INTERPRO		Longin_dom	RT	██████████	3	7.9E-2	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT		SNARE complex	RT	██████████	9	9.2E-2	3.9E-1
<input type="checkbox"/> GOTERM_MF_DIRECT		SNAP receptor activity	RT	██████████	8	1.0E-1	8.3E-1
<input type="checkbox"/> KEGG_PATHWAY		SNARE interactions in vesicular transport	RT	██████████	8	1.1E-1	3.3E-1
<input type="checkbox"/> UP_SEQ_FEATURE		TOPO_DOM:Vesicular	RT	██████████	5	5.5E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		vesicle fusion	RT	██████████	3	7.5E-1	1.0E0
Annotation Cluster 110		Enrichment Score: 1.12	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:MRG	RT	██████████	3	4.9E-2	1.0E0
<input type="checkbox"/> INTERPRO		MRG	RT	██████████	3	5.1E-2	1.0E0
<input type="checkbox"/> INTERPRO		MRG_C_sf	RT	██████████	3	5.1E-2	1.0E0
<input type="checkbox"/> INTERPRO		MRG_dom	RT	██████████	3	5.1E-2	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT		NuA4 histone acetyltransferase complex	RT	██████████	5	3.8E-1	9.9E-1
Annotation Cluster 111		Enrichment Score: 1.12	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		cellular respiration	RT	██████████	11	6.4E-3	1.6E-1
<input type="checkbox"/> UP_SEQ_FEATURE		TRANSMEM:Helical; Name=I	RT	██████████	3	4.9E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		TRANSMEM:Helical; Name=II	RT	██████████	3	4.9E-2	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT		respiratory chain complex IV	RT	██████████	4	8.5E-2	3.6E-1
<input type="checkbox"/> GOTERM_MF_DIRECT		cytochrome-c oxidase activity	RT	██████████	5	9.7E-2	8.2E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		mitochondrial electron transport_cytochrome c to oxygen	RT	██████████	6	1.0E-1	9.2E-1
<input type="checkbox"/> GOTERM_CC_DIRECT		mitochondrial respiratory chain complex IV	RT	██████████	5	2.2E-1	7.0E-1
<input type="checkbox"/> KEGG_PATHWAY		Cardiac muscle contraction	RT	██████████	13	4.1E-1	8.3E-1
Annotation Cluster 112		Enrichment Score: 1.11	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT		actin filament binding	RT	██████████	36	6.2E-3	1.2E-1
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION		Actin-binding	RT	██████████	36	2.4E-1	9.6E-1
<input type="checkbox"/> GOTERM_MF_DIRECT		actin binding	RT	██████████	40	3.1E-1	1.0E0
Annotation Cluster 113		Enrichment Score: 1.1	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		protein peptidyl-prolyl isomerase	RT	██████████	8	9.9E-3	2.1E-1
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION		Rotamase	RT	██████████	11	1.5E-2	1.2E-1
<input type="checkbox"/> GOTERM_MF_DIRECT		peptidyl-prolyl cis-trans isomerase activity	RT	██████████	11	2.3E-2	3.2E-1
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:PPIase cyclophilin-type	RT	██████████	6	7.7E-2	1.0E0
<input type="checkbox"/> INTERPRO		Cyclophilin-like_dom_sf	RT	██████████	6	8.1E-2	1.0E0
<input type="checkbox"/> INTERPRO		Cyclophilin-type_PPIase_dom	RT	██████████	6	8.1E-2	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION		Isomerase	RT	██████████	23	1.0E-1	5.5E-1
<input type="checkbox"/> INTERPRO		Cyclophilin-type_PPIase_CS	RT	██████████	5	1.5E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT		cyclosporin A binding	RT	██████████	5	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO		Cyclophilin-type_PPIase	RT	██████████	3	4.1E-1	1.0E0
<input type="checkbox"/> PIR_SUPERFAMILY		Peptidylpro_isomse	RT	██████████	3	5.6E-1	1.0E0
Annotation Cluster 114		Enrichment Score: 1.09	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT		cyclin-dependent protein kinase holoenzyme complex	RT	██████████	13	6.3E-4	6.9E-3
<input type="checkbox"/> GOTERM_MF_DIRECT		cyclin-dependent protein serine/threonine kinase regulator activity	RT	██████████	9	1.6E-2	2.4E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		regulation of cyclin-dependent protein serine/threonine kinase activity	RT	██████████	11	2.0E-2	3.4E-1
<input type="checkbox"/> SMART		CYCLIN	RT	██████████	9	2.9E-2	4.5E-1
<input type="checkbox"/> INTERPRO		Cyclin-like_dom	RT	██████████	9	2.9E-2	1.0E0
<input type="checkbox"/> INTERPRO		Cyclin/Ssn8	RT	██████████	4	3.7E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:Cyclin-like	RT	██████████	7	6.5E-2	1.0E0
<input type="checkbox"/> INTERPRO		Cyclin-like_sf	RT	██████████	9	8.7E-2	1.0E0

		Enrichment Score: 54.91	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	Cyclin_N	RT	██████████	7	1.5E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Cyclin N-terminal	RT	██████████	5	1.8E-1	1.0E0
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Cyclin	RT	██████████	7	1.9E-1	8.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	cyclin-dependent protein serine/threonine kinase activator activity	RT	██████████	4	2.3E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Cyclin C-terminal	RT	██████████	4	2.5E-1	1.0E0
<input type="checkbox"/>	SMART	Cyclin_C	RT	██████████	4	3.4E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Cyclin_C-dom	RT	██████████	4	3.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitotic cell cycle phase transition	RT	██████████	4	3.9E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Cyclin	RT	██████████	3	6.3E-1	1.0E0
Annotation Cluster 115		Enrichment Score: 1.09	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:RNA-binding S4	RT	██████████	3	4.9E-2	1.0E0
<input type="checkbox"/>	SMART	S4	RT	██████████	3	7.9E-2	7.5E-1
<input type="checkbox"/>	INTERPRO	S4_RNA-bd	RT	██████████	3	7.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:S4 RNA-binding	RT	██████████	3	1.1E-1	1.0E0
<input type="checkbox"/>	INTERPRO	S4_RNA-bd_sf	RT	██████████	3	1.1E-1	1.0E0
Annotation Cluster 116		Enrichment Score: 1.08	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of DNA repair	RT	██████████	11	7.0E-2	7.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	SAGA complex	RT	██████████	6	9.1E-2	3.9E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	transcription factor TFTC complex	RT	██████████	5	9.2E-2	3.9E-1
Annotation Cluster 117		Enrichment Score: 1.08	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of release of cytochrome c from mitochondria	RT	██████████	7	2.9E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of intrinsic apoptotic signaling pathway	RT	██████████	8	7.4E-2	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	release of cytochrome c from mitochondria	RT	██████████	6	7.5E-2	8.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	MOTIF:BH3	RT	██████████	4	3.1E-1	1.0E0
Annotation Cluster 118		Enrichment Score: 1.05	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 15	RT	██████████	5	2.3E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 16	RT	██████████	5	2.3E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 17	RT	██████████	5	2.3E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 10	RT	██████████	5	3.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 11	RT	██████████	5	3.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 12	RT	██████████	5	3.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 13	RT	██████████	5	3.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 14	RT	██████████	5	3.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 18	RT	██████████	4	3.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 19	RT	██████████	4	3.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 20	RT	██████████	4	3.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 7	RT	██████████	5	4.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 8	RT	██████████	5	4.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 9	RT	██████████	5	4.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 5	RT	██████████	5	5.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 6	RT	██████████	5	5.0E-2	1.0E0
<input type="checkbox"/>	INTERPRO	Actinin_actin-bd_CS	RT	██████████	6	6.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 21	RT	██████████	3	1.1E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 22	RT	██████████	3	1.1E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Calponin-homology (CH) 1	RT	██████████	6	1.1E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Calponin-homology (CH) 2	RT	██████████	6	1.1E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 3	RT	██████████	5	1.6E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 4	RT	██████████	5	1.6E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Spectrin_repeat	RT	██████████	5	2.1E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 1	RT	██████████	5	2.4E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 2	RT	██████████	5	2.4E-1	1.0E0
<input type="checkbox"/>	SMART	SPEC	RT	██████████	5	3.2E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Spectrin/alpha-actinin	RT	██████████	5	3.4E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Calponin-homology (CH)	RT	██████████	10	3.4E-1	1.0E0
<input type="checkbox"/>	INTERPRO	CH_dom	RT	██████████	10	4.0E-1	1.0E0
<input type="checkbox"/>	INTERPRO	CH_dom_sf	RT	██████████	10	4.3E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:Actin-binding	RT	██████████	7	5.8E-1	1.0E0
<input type="checkbox"/>	SMART	CH	RT	██████████	7	6.4E-1	1.0E0
Annotation Cluster 119		Enrichment Score: 1.05	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_DIRECT	clathrin-coated endocytic vesicle	RT	██████████	8	8.4E-3	6.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	clathrin-dependent endocytosis	RT	██████████	8	1.9E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	postsynaptic neurotransmitter receptor internalization	RT	██████████	4	3.9E-2	5.3E-1
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Coated_pit	RT	██████████	10	1.2E-1	3.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	Endocrine and other factor-regulated calcium reabsorption	RT	██████████	11	1.2E-1	3.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	endolysosome membrane	RT	██████████	5	1.2E-1	4.8E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	AP-2 adaptor complex	RT	██████████	3	2.9E-1	8.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	clathrin adaptor activity	RT	██████████	4	2.9E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	synaptic vesicle endocytosis	RT	██████████	6	4.0E-1	1.0E0
Annotation Cluster 120		Enrichment Score: 1.03	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	Chromo-like_dom_sf	RT	██████████	9	1.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Tudor-knot	RT	██████████	4	1.5E-2	1.0E0
<input type="checkbox"/>	INTERPRO	Tudor-knot	RT	██████████	4	1.5E-2	7.4E-1
<input type="checkbox"/>	SMART	CHROMO	RT	██████████	8	4.4E-2	5.8E-1
<input type="checkbox"/>	INTERPRO	Chromo/chromo_shadow_dom	RT	██████████	8	4.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Chromo 1	RT	██████████	4	1.0E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Chromo	RT	██████████	7	1.1E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Chromo 2	RT	██████████	3	2.1E-1	1.0E0
<input type="checkbox"/>	INTERPRO	SNF2_N	RT	██████████	6	2.2E-1	1.0E0
<input type="checkbox"/>	INTERPRO	SNF2-like_sf	RT	██████████	6	2.2E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Chromo_domain	RT	██████████	5	2.7E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Chromodomain_CS	RT	██████████	4	3.1E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	MOTIF:DEAH box	RT	██████████	5	7.0E-1	1.0E0
Annotation Cluster 121		Enrichment Score: 1.03	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	ENTH_VHS	RT	██████████	8	1.7E-2	7.9E-1
<input type="checkbox"/>	SMART	RPR	RT	██████████	3	1.5E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:CID	RT	██████████	3	1.8E-1	1.0E0
<input type="checkbox"/>	INTERPRO	CID_dom	RT	██████████	3	1.8E-1	1.0E0
Annotation Cluster 122		Enrichment Score: 1.02	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_DIRECT	chromatin silencing complex	RT	██████████	4	6.6E-2	3.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	heterochromatin assembly	RT	██████████	7	8.6E-2	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	chromatin silencing at rDNA	RT	██████████	3	1.5E-1	1.0E0

Annotation Cluster 1	Enrichment Score: 54.91	G	██████████	Count	P_Value	Benjamini
Annotation Cluster 123	Enrichment Score: 1.01	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Rotamase	RT	██████████	11	1.5E-2	1.2E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	peptidyl-prolyl cis-trans isomerase activity	RT	██████████	11	2.3E-2	3.2E-1
<input type="checkbox"/> INTERPRO	PPIase_dom_sf	RT	██████████	5	1.3E-1	1.0E0
<input type="checkbox"/> INTERPRO	PPIase_FKBP_dom	RT	██████████	4	2.3E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:PPIase FKBP-type	RT	██████████	4	2.5E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	FK506 binding	RT	██████████	3	3.3E-1	1.0E0
Annotation Cluster 124	Enrichment Score: 1.01	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	translational elongation	RT	██████████	8	1.2E-3	4.6E-2
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Elongation factor	RT	██████████	8	2.9E-2	1.8E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	translation elongation factor activity	RT	██████████	8	4.6E-2	5.2E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	eukaryotic translation elongation factor 1 complex	RT	██████████	3	5.0E-2	2.4E-1
<input type="checkbox"/> INTERPRO	G_TR_CS	RT	██████████	4	6.8E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REGION:G1	RT	██████████	5	1.2E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REGION:G2	RT	██████████	5	1.2E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REGION:G4	RT	██████████	5	1.2E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REGION:G5	RT	██████████	5	1.2E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REGION:G3	RT	██████████	5	1.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	Transl_elong_EFTu/EF1A_C	RT	██████████	3	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	Transl_B-barrel_sf	RT	██████████	6	1.7E-1	1.0E0
<input type="checkbox"/> INTERPRO	EFTu-like_2	RT	██████████	4	2.0E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Tr-type G	RT	██████████	4	2.2E-1	1.0E0
<input type="checkbox"/> INTERPRO	Transl_elong_EF1A/Init_IF2_C	RT	██████████	3	3.0E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:tr-type G	RT	██████████	4	3.1E-1	1.0E0
<input type="checkbox"/> INTERPRO	T_Tr_GTP-bd_dom	RT	██████████	4	3.4E-1	1.0E0
Annotation Cluster 125	Enrichment Score: 1.01	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	ZFP36-like	RT	██████████	3	2.7E-2	9.9E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	RT	██████████	4	5.4E-2	6.3E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	cellular response to fibroblast growth factor stimulus	RT	██████████	7	9.7E-2	9.1E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	response to wounding	RT	██████████	7	6.5E-1	1.0E0
Annotation Cluster 126	Enrichment Score: 1	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> SMART	MIF4G	RT	██████████	4	6.7E-2	7.2E-1
<input type="checkbox"/> INTERPRO	MIF4G-like_typ-3	RT	██████████	4	6.8E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:MIF4G	RT	██████████	3	2.1E-1	1.0E0
Annotation Cluster 127	Enrichment Score: 0.99	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:Matrin-type	RT	██████████	5	4.0E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Matrin-type	RT	██████████	3	1.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	Matrin/U1-C_Znf_C2H2	RT	██████████	3	1.8E-1	1.0E0
Annotation Cluster 128	Enrichment Score: 0.98	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Pept_asp_AS	RT	██████████	4	6.8E-2	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	cysteine-type peptidase activity	RT	██████████	9	7.0E-2	6.8E-1
<input type="checkbox"/> INTERPRO	Pept_his_AS	RT	██████████	4	8.6E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Peptidase C1A papain C-terminal	RT	██████████	4	1.0E-1	1.0E0
<input type="checkbox"/> SMART	Pept_C1	RT	██████████	4	1.3E-1	9.9E-1
<input type="checkbox"/> INTERPRO	Peptidase_C1A	RT	██████████	4	1.3E-1	1.0E0
<input type="checkbox"/> INTERPRO	Peptidase_C1A_C	RT	██████████	4	1.3E-1	1.0E0
<input type="checkbox"/> INTERPRO	Pept_cys_AS	RT	██████████	5	1.5E-1	1.0E0
Annotation Cluster 129	Enrichment Score: 0.98	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY	Pancreatic cancer	RT	██████████	21	8.6E-4	4.8E-3
<input type="checkbox"/> KEGG_PATHWAY	Colorectal cancer	RT	██████████	22	1.8E-3	9.1E-3
<input type="checkbox"/> KEGG_PATHWAY	Non-small cell lung cancer	RT	██████████	19	2.8E-3	1.4E-2
<input type="checkbox"/> KEGG_PATHWAY	Chronic myeloid leukemia	RT	██████████	19	5.3E-3	2.4E-2
<input type="checkbox"/> KEGG_PATHWAY	Prostate cancer	RT	██████████	20	3.1E-2	1.2E-1
<input type="checkbox"/> BIOCARTA	Influence of Ras and Rho proteins on G1 to S Transition	RT	██████████	10	6.4E-2	4.5E-1
<input type="checkbox"/> KEGG_PATHWAY	FoxO signaling pathway	RT	██████████	23	9.4E-2	2.9E-1
<input type="checkbox"/> KEGG_PATHWAY	Endometrial cancer	RT	██████████	12	1.1E-1	3.2E-1
<input type="checkbox"/> KEGG_PATHWAY	Small cell lung cancer	RT	██████████	16	1.8E-1	4.6E-1
<input type="checkbox"/> KEGG_PATHWAY	Glioma	RT	██████████	13	2.3E-1	5.4E-1
<input type="checkbox"/> KEGG_PATHWAY	Hepatocellular carcinoma	RT	██████████	25	2.8E-1	6.4E-1
<input type="checkbox"/> KEGG_PATHWAY	AGE-RAGE signaling pathway in diabetic complications	RT	██████████	15	3.8E-1	8.0E-1
<input type="checkbox"/> KEGG_PATHWAY	ErBb signaling pathway	RT	██████████	13	3.8E-1	8.0E-1
<input type="checkbox"/> KEGG_PATHWAY	Bladder cancer	RT	██████████	7	4.1E-1	8.3E-1
<input type="checkbox"/> KEGG_PATHWAY	Endocrine resistance	RT	██████████	14	4.6E-1	9.0E-1
<input type="checkbox"/> KEGG_PATHWAY	Melanoma	RT	██████████	10	5.6E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Choline metabolism in cancer	RT	██████████	13	5.9E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	EGFR tyrosine kinase inhibitor resistance	RT	██████████	10	6.8E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Breast cancer	RT	██████████	17	7.7E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Gastric cancer	RT	██████████	15	9.1E-1	1.0E0
Annotation Cluster 130	Enrichment Score: 0.98	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	protein K11-linked ubiquitination	RT	██████████	9	1.2E-2	2.5E-1
<input type="checkbox"/> UP_SEQ_FEATURE	ACT_SITE:Glycyl thioester intermediate	RT	██████████	13	5.2E-2	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	postreplication repair	RT	██████████	4	5.4E-2	6.3E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	ubiquitin-like protein transferase activity	RT	██████████	7	1.0E-1	8.3E-1
<input type="checkbox"/> SMART	UBCc	RT	██████████	8	1.1E-1	9.2E-1
<input type="checkbox"/> INTERPRO	UBQ-conjugating_enzyme/RWD	RT	██████████	10	1.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:UBC core	RT	██████████	8	1.2E-1	1.0E0
<input type="checkbox"/> INTERPRO	UBQ-conjugat_E2	RT	██████████	8	1.3E-1	1.0E0
<input type="checkbox"/> INTERPRO	UBQ-conjugating_AS	RT	██████████	5	2.7E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	ubiquitin_conjugating_enzyme_activity	RT	██████████	6	3.1E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	protein_modification_by_small_protein_conjugation	RT	██████████	5	3.4E-1	1.0E0
Annotation Cluster 131	Enrichment Score: 0.95	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> SMART	btg1	RT	██████████	3	1.1E-1	9.1E-1
<input type="checkbox"/> INTERPRO	BTG-like_sf	RT	██████████	3	1.1E-1	1.0E0
<input type="checkbox"/> INTERPRO	Anti_prolifrtn	RT	██████████	3	1.1E-1	1.0E0
Annotation Cluster 132	Enrichment Score: 0.95	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	proteasomal protein catabolic process	RT	██████████	9	2.9E-2	4.3E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	proteasome_core_complex,_beta-subunit_complex	RT	██████████	4	8.5E-2	3.6E-1
<input type="checkbox"/> INTERPRO	Proteasome_subB-type	RT	██████████	4	8.6E-2	1.0E0
<input type="checkbox"/> INTERPRO	Proteasome_bsu_CS	RT	██████████	4	1.1E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT	proteasome core complex	RT	██████████	5	1.2E-1	4.8E-1
<input type="checkbox"/> INTERPRO	Proteasome_sua/b	RT	██████████	5	1.9E-1	1.0E0

Annotation Cluster 1	Enrichment Score: 54.91	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Ntn_hydrolases_N	RT		6	4.2E-1	1.0E0
Annotation Cluster 133	Enrichment Score: 0.94	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:PA	RT		5	1.1E-1	1.0E0
<input type="checkbox"/> INTERPRO	PA_domain	RT		5	1.1E-1	1.0E0
<input type="checkbox"/> INTERPRO	PA_dom_sf	RT		5	1.3E-1	1.0E0
Annotation Cluster 134	Enrichment Score: 0.94	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DNA_BIND:A.T hook 1	RT		4	8.3E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DNA_BIND:A.T hook 2	RT		4	8.3E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DNA_BIND:A.T hook 3	RT		3	2.1E-1	1.0E0
Annotation Cluster 135	Enrichment Score: 0.92	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	Sin3_complex	RT		6	4.8E-2	2.4E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	negative regulation of stem cell population maintenance	RT		6	5.4E-2	6.3E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation of stem cell population maintenance	RT		9	8.7E-2	8.5E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	negative regulation of cell migration	RT		14	9.4E-1	1.0E0
Annotation Cluster 136	Enrichment Score: 0.92	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT	kinase activity	RT		38	1.1E-2	1.8E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	phosphorylation	RT		81	1.4E-2	2.8E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	protein phosphorylation	RT		52	2.0E-2	3.5E-1
<input type="checkbox"/> UP_SEQ_FEATURE	ACT_SITE:Proton acceptor	RT		102	3.6E-2	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Kinase	RT		93	8.0E-2	4.6E-1
<input type="checkbox"/> INTERPRO	Ser/Thr_kinase_AS	RT		39	1.2E-1	1.0E0
<input type="checkbox"/> SMART	S_TKc	RT		44	1.2E-1	9.5E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	peptidyl-serine phosphorylation	RT		22	1.3E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	protein serine/threonine kinase activity	RT		49	1.3E-1	9.6E-1
<input type="checkbox"/> INTERPRO	Protein_kinase_ATP_BS	RT		43	3.0E-1	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Serine/threonine-protein kinase	RT		46	3.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Protein kinase	RT		51	4.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	Prot_kinase_dom	RT		51	4.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	Kinase-like_dom_sf	RT		55	5.1E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	protein kinase activity	RT		39	6.9E-1	1.0E0
Annotation Cluster 137	Enrichment Score: 0.92	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	proteasome accessory complex	RT		7	4.1E-3	3.4E-2
<input type="checkbox"/> INTERPRO	AAA_lid_3	RT		7	3.7E-2	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT	proteasome regulatory particle	RT		4	6.6E-2	3.0E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	proteasome regulatory particle, base subcomplex	RT		4	1.1E-1	4.3E-1
<input type="checkbox"/> INTERPRO	Prot_ATP_ID_OB_2nd	RT		3	1.1E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	proteasome-activating ATPase activity	RT		3	1.3E-1	9.2E-1
<input type="checkbox"/> INTERPRO	ATPase_AAA_CS	RT		6	1.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:AAA+ ATPase	RT		9	1.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:ATPase AAA-type core	RT		5	2.0E-1	1.0E0
<input type="checkbox"/> INTERPRO	ATPase_AAA_core	RT		8	2.5E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation of proteasomal protein catabolic process	RT		4	3.3E-1	1.0E0
<input type="checkbox"/> SMART	AAA	RT		15	5.2E-1	1.0E0
<input type="checkbox"/> INTERPRO	AAA+_ATPase	RT		15	5.2E-1	1.0E0
Annotation Cluster 138	Enrichment Score: 0.92	G		Count	P_Value	Benjamini
<input type="checkbox"/> SMART	DnaJ	RT		9	1.0E-1	9.0E-1
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:J	RT		9	1.2E-1	1.0E0
<input type="checkbox"/> INTERPRO	DnaJ_domain_CS	RT		6	1.2E-1	1.0E0
<input type="checkbox"/> INTERPRO	DnaJ_domain	RT		9	1.2E-1	1.0E0
<input type="checkbox"/> INTERPRO	J_dom_sf	RT		9	1.5E-1	1.0E0
Annotation Cluster 139	Enrichment Score: 0.91	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	Lst4-Lst7 complex	RT		4	6.6E-2	3.0E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	cellular response to amino acid stimulus	RT		11	9.9E-2	9.2E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	Ragulator complex	RT		3	1.1E-1	4.3E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	TORC1 signaling	RT		4	1.1E-1	9.8E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation of TOR signaling	RT		6	3.6E-1	1.0E0
Annotation Cluster 140	Enrichment Score: 0.9	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	GTP-bd	RT		5	9.4E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:CP-type G	RT		3	1.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	G_CP_dom	RT		3	1.5E-1	1.0E0
Annotation Cluster 141	Enrichment Score: 0.88	G		Count	P_Value	Benjamini
<input type="checkbox"/> BIOCARTA	T Cell Receptor Signaling Pathway	RT		21	7.0E-5	4.6E-3
<input type="checkbox"/> BIOCARTA	Signaling Pathway from G-Protein Families	RT		12	5.3E-2	4.2E-1
<input type="checkbox"/> KEGG_PATHWAY	B_cell receptor_signaling_pathway	RT		17	5.7E-2	2.0E-1
<input type="checkbox"/> BIOCARTA	Role of MEF2D in T-cell Apoptosis	RT		7	1.2E-1	6.6E-1
<input type="checkbox"/> BIOCARTA	BCR Signaling Pathway	RT		10	2.1E-1	8.6E-1
<input type="checkbox"/> BIOCARTA	NFAT and Hypertrophy of the heart (Transcription in the broken heart)	RT		14	2.5E-1	8.7E-1
<input type="checkbox"/> BIOCARTA	fMLP induced chemokine gene expression in HMC-1 cells	RT		10	2.9E-1	9.4E-1
<input type="checkbox"/> BIOCARTA	Fc Epsilon Receptor I Signaling in Mast Cells	RT		10	3.5E-1	9.7E-1
<input type="checkbox"/> KEGG_PATHWAY	VEGF signaling_pathway	RT		9	4.7E-1	9.1E-1
<input type="checkbox"/> BIOCARTA	Effects of calcineurin in Keratinocyte Differentiation	RT		5	5.3E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK)	RT		5	8.5E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Regulation of PGC-1a	RT		4	8.8E-1	1.0E0
Annotation Cluster 142	Enrichment Score: 0.88	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	microtubule	RT		43	3.9E-2	2.1E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	microtubule binding	RT		34	2.2E-1	1.0E0
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Microtubule	RT		36	2.6E-1	6.7E-1
Annotation Cluster 143	Enrichment Score: 0.88	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:MPN	RT		5	9.0E-2	1.0E0
<input type="checkbox"/> INTERPRO	MPN	RT		5	9.4E-2	1.0E0
<input type="checkbox"/> SMART	JAB_MPN	RT		4	1.1E-1	9.1E-1
<input type="checkbox"/> INTERPRO	JAMM/MPN+_dom	RT		4	1.3E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	metallopeptidase activity	RT		10	3.5E-1	1.0E0
Annotation Cluster 144	Enrichment Score: 0.88	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	eukaryotic translation initiation factor 4F complex	RT		5	3.2E-2	1.8E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	translation factor activity, RNA binding	RT		6	7.5E-2	7.1E-1
<input type="checkbox"/> BIOCARTA	mTOR Signaling Pathway	RT		9	1.2E-1	6.6E-1
<input type="checkbox"/> BIOCARTA	Internal Ribosome entry_pathway	RT		4	1.4E-1	7.4E-1
<input type="checkbox"/> BIOCARTA	Eukaryotic protein translation	RT		6	1.9E-1	8.1E-1
<input type="checkbox"/> BIOCARTA	Regulation of eIF4e and p70 S6 Kinase	RT		5	7.2E-1	1.0E0

Annotation Cluster 1	Enrichment Score: 54.91	G	██████████	Count	P_Value	Benjamini
Annotation Cluster 145	Enrichment Score: 0.88	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:Matrin-type	RT	██████████	5	4.0E-2	1.0E0
<input type="checkbox"/> INTERPRO	Znf_C2H2_jaz	RT	██████████	4	6.8E-2	1.0E0
<input type="checkbox"/> SMART	ZnF_U1	RT	██████████	5	3.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	Matrin/U1-like-C_Znf_C2H2	RT	██████████	5	3.4E-1	1.0E0
Annotation Cluster 146	Enrichment Score: 0.87	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Phosphoribosyltransferase	RT	██████████	3	7.7E-2	1.0E0
<input type="checkbox"/> INTERPRO	PRTase-like	RT	██████████	4	1.1E-1	1.0E0
<input type="checkbox"/> INTERPRO	PRibTrfase_dom	RT	██████████	3	3.0E-1	1.0E0
Annotation Cluster 147	Enrichment Score: 0.87	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	regulation_of_macromolecule_metabolic_process	RT	██████████	6	8.8E-2	8.5E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	regulation_of_nitrogen_compound_metabolic_process	RT	██████████	6	1.1E-1	9.8E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	regulation_of_primary_metabolic_process	RT	██████████	7	2.5E-1	1.0E0
Annotation Cluster 148	Enrichment Score: 0.87	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> SMART	DSRM	RT	██████████	5	9.3E-2	8.4E-1
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:DRBM 1	RT	██████████	4	1.0E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:DRBM 2	RT	██████████	4	1.0E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:DRBM	RT	██████████	5	1.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	dsRBD_dom	RT	██████████	5	1.7E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	small RNA loading onto RISC	RT	██████████	3	2.7E-1	1.0E0
Annotation Cluster 149	Enrichment Score: 0.84	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	UIM_dom	RT	██████████	6	4.9E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:UIM 1	RT	██████████	4	2.0E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:UIM 2	RT	██████████	4	2.0E-1	1.0E0
<input type="checkbox"/> SMART	UIM	RT	██████████	4	2.3E-1	1.0E0
Annotation Cluster 150	Enrichment Score: 0.83	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	protein_K69-linked_ufmylation	RT	██████████	3	8.3E-2	8.3E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	protein_ufmylation	RT	██████████	3	1.2E-1	9.8E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	reticulophagy	RT	██████████	4	3.3E-1	1.0E0
Annotation Cluster 151	Enrichment Score: 0.83	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	protein_depalmitoylation	RT	██████████	4	3.9E-2	5.3E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	palmitoyl-(protein)_hydrolase_activity	RT	██████████	4	1.0E-1	8.3E-1
<input type="checkbox"/> INTERPRO	AB_hydrolase	RT	██████████	11	8.0E-1	1.0E0
Annotation Cluster 152	Enrichment Score: 0.83	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	WWE_dom_sf	RT	██████████	5	3.3E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:PARP catalytic	RT	██████████	5	7.5E-2	1.0E0
<input type="checkbox"/> INTERPRO	Poly(ADP-ribose)pol_cat_dom	RT	██████████	5	7.9E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:WWE	RT	██████████	4	8.3E-2	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	NAD+ ADP-ribosyltransferase_activity	RT	██████████	6	1.0E-1	8.3E-1
<input type="checkbox"/> INTERPRO	WWE-dom	RT	██████████	4	1.3E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	protein_poly-ADP-ribosylation	RT	██████████	3	1.5E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	protein ADP-ribosylase_activity	RT	██████████	4	2.6E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	nucleotidyltransferase_activity	RT	██████████	6	5.6E-1	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Nucleotidyltransferase	RT	██████████	7	9.8E-1	1.0E0
Annotation Cluster 153	Enrichment Score: 0.83	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:14-3-3	RT	██████████	3	1.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	SITE:Interaction with phosphoserine on interacting protein	RT	██████████	3	1.4E-1	1.0E0
<input type="checkbox"/> SMART	14_3_3	RT	██████████	3	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	14-3_3	RT	██████████	3	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	14-3-3_CS	RT	██████████	3	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	14-3-3_domain	RT	██████████	3	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	14-3-3_dom_sf	RT	██████████	3	1.5E-1	1.0E0
<input type="checkbox"/> PIR_SUPERFAMILY	14-3-3	RT	██████████	3	2.3E-1	1.0E0
Annotation Cluster 154	Enrichment Score: 0.83	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	purine_nucleotide_biosynthetic_process	RT	██████████	6	2.9E-2	4.3E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	'de novo' XMP biosynthetic_process	RT	██████████	3	1.5E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	GMP_biosynthetic_process	RT	██████████	3	2.7E-1	1.0E0
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Purine_biosynthesis	RT	██████████	3	4.1E-1	1.0E0
Annotation Cluster 155	Enrichment Score: 0.82	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY	cGMP-PKG_signaling_pathway	RT	██████████	30	4.0E-2	1.5E-1
<input type="checkbox"/> KEGG_PATHWAY	Adrenergic_signaling_in_cardiomyocytes	RT	██████████	24	2.2E-1	5.2E-1
<input type="checkbox"/> KEGG_PATHWAY	cAMP_signaling_pathway	RT	██████████	31	3.9E-1	8.1E-1
Annotation Cluster 156	Enrichment Score: 0.81	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> SMART	HAT	RT	██████████	4	6.7E-2	7.2E-1
<input type="checkbox"/> INTERPRO	HAT	RT	██████████	4	6.8E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:HAT 8	RT	██████████	3	7.7E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:HAT 7	RT	██████████	3	1.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:HAT 6	RT	██████████	3	1.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:HAT 5	RT	██████████	3	2.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:HAT 4	RT	██████████	3	2.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:HAT 1	RT	██████████	3	2.9E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:HAT 2	RT	██████████	3	2.9E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:HAT 3	RT	██████████	3	2.9E-1	1.0E0
Annotation Cluster 157	Enrichment Score: 0.81	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	DNA-dependent_protein_kinase_complex	RT	██████████	3	7.8E-2	3.5E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	regulation_of_smooth_muscle_cell_proliferation	RT	██████████	4	9.1E-2	8.7E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	DNA-dependent_protein_kinase-DNA_ligase_4_complex	RT	██████████	3	1.4E-1	5.2E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	double-strand_break_repair_via_nonhomologous_end_joining	RT	██████████	7	1.5E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT	nonhomologous_end_joining_complex	RT	██████████	3	1.8E-1	6.0E-1
<input type="checkbox"/> KEGG_PATHWAY	Non-homologous_end-joining	RT	██████████	3	5.0E-1	9.3E-1
Annotation Cluster 158	Enrichment Score: 0.79	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:TPR	RT	██████████	19	6.5E-3	7.7E-1
<input type="checkbox"/> INTERPRO	TPR-like_helical_dom_sf	RT	██████████	34	1.8E-2	8.5E-1
<input type="checkbox"/> INTERPRO	TPR_1	RT	██████████	8	2.4E-2	9.9E-1
<input type="checkbox"/> UP_KW_DOMAIN	TPR_repeat	RT	██████████	23	4.9E-2	1.7E-1
<input type="checkbox"/> SMART	TPR	RT	██████████	20	5.8E-2	6.7E-1
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:TPR_3	RT	██████████	21	7.2E-2	1.0E0
<input type="checkbox"/> INTERPRO	TPR_repeat	RT	██████████	20	9.4E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:TPR_1	RT	██████████	21	1.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:TPR_2	RT	██████████	21	1.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:TPR_9	RT	██████████	6	2.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:TPR_12	RT	██████████	3	4.3E-1	1.0E0

		Enrichment Score:	G	RT	Count	P_Value	Benjamini
Annotation Cluster 1	<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:TPR 7		RT	8	4.6E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:TPR 11		RT	3	5.6E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:TPR 8		RT	6	6.3E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:TPR 6		RT	8	6.3E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:TPR 5		RT	8	6.9E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:TPR 10		RT	3	7.5E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:TPR 4		RT	9	7.7E-1	1.0E0
Annotation Cluster 159		Enrichment Score: 0.79		RT	Count	P_Value	Benjamini
	<input type="checkbox"/> UP_KW_LIGAND	Thiamine_pyrophosphate		RT	4	1.4E-1	8.3E-1
	<input type="checkbox"/> INTERPRO	THDP-binding		RT	4	1.5E-1	1.0E0
	<input type="checkbox"/> SMART	Transket_pyr		RT	3	1.8E-1	1.0E0
	<input type="checkbox"/> INTERPRO	Transketolase-like_Pyr-bd		RT	3	1.8E-1	1.0E0
Annotation Cluster 160		Enrichment Score: 0.78		RT	Count	P_Value	Benjamini
	<input type="checkbox"/> GOTERM_BP_DIRECT	anterograde axonal transport		RT	7	8.6E-2	8.5E-1
	<input type="checkbox"/> GOTERM_BP_DIRECT	anterograde synaptic vesicle transport		RT	4	2.1E-1	1.0E0
	<input type="checkbox"/> GOTERM_BP_DIRECT	melanosome organization		RT	5	2.4E-1	1.0E0
Annotation Cluster 161		Enrichment Score: 0.78		RT	Count	P_Value	Benjamini
	<input type="checkbox"/> GOTERM_CC_DIRECT	histone acetyltransferase complex		RT	9	3.3E-3	2.9E-2
	<input type="checkbox"/> GOTERM_CC_DIRECT	MOZ/MORF histone acetyltransferase complex		RT	3	1.4E-1	5.2E-1
	<input type="checkbox"/> GOTERM_MF_DIRECT	histone acetyltransferase activity (H3-K14 specific)		RT	3	2.4E-1	1.0E0
	<input type="checkbox"/> GOTERM_BP_DIRECT	regulation of hemopoiesis		RT	3	3.1E-1	1.0E0
	<input type="checkbox"/> GOTERM_BP_DIRECT	regulation of developmental process		RT	3	6.1E-1	1.0E0
	<input type="checkbox"/> GOTERM_CC_DIRECT	nucleosome		RT	8	9.9E-1	1.0E0
Annotation Cluster 162		Enrichment Score: 0.77		RT	Count	P_Value	Benjamini
	<input type="checkbox"/> GOTERM_MF_DIRECT	acetyl-CoA C-acyltransferase activity		RT	4	1.0E-2	1.7E-1
	<input type="checkbox"/> GOTERM_MF_DIRECT	acetyl-CoA C-myristoyltransferase activity		RT	3	3.1E-2	4.0E-1
	<input type="checkbox"/> INTERPRO	Thiolase_acyl_enz_int_AS		RT	3	7.9E-2	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Thiolase C-terminal		RT	3	1.1E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Thiolase N-terminal		RT	3	1.1E-1	1.0E0
	<input type="checkbox"/> INTERPRO	Thiolase		RT	3	1.1E-1	1.0E0
	<input type="checkbox"/> INTERPRO	Thiolase_CS		RT	3	1.1E-1	1.0E0
	<input type="checkbox"/> INTERPRO	Thiolase_N		RT	3	1.1E-1	1.0E0
	<input type="checkbox"/> INTERPRO	Thiolase_C		RT	3	1.1E-1	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	3-hydroxyacyl-CoA dehydrogenase activity		RT	3	1.3E-1	9.2E-1
	<input type="checkbox"/> GOTERM_MF_DIRECT	acetyl-CoA C-acetyltransferase activity		RT	3	1.3E-1	9.2E-1
	<input type="checkbox"/> GOTERM_MF_DIRECT	enoyl-CoA hydratase activity		RT	3	1.6E-1	1.0E0
	<input type="checkbox"/> PIR_SUPERFAMILY	Ac-CoA_Ac_transf		RT	3	1.8E-1	1.0E0
	<input type="checkbox"/> KEGG_PATHWAY	Fatty_acid_elongation		RT	6	2.5E-1	5.8E-1
	<input type="checkbox"/> INTERPRO	Thiolase-like		RT	3	2.6E-1	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	transferase_activity_transferring_acyl_groups_other_than_amino-acyl_groups		RT	4	3.2E-1	1.0E0
	<input type="checkbox"/> KEGG_PATHWAY	Fatty_acid_metabolism		RT	9	4.3E-1	8.6E-1
	<input type="checkbox"/> GOTERM_BP_DIRECT	fatty_acid_beta-oxidation		RT	6	5.8E-1	1.0E0
	<input type="checkbox"/> KEGG_PATHWAY	Valine_leucine_and_isoleucine_degradation		RT	6	7.4E-1	1.0E0
	<input type="checkbox"/> KEGG_PATHWAY	Fatty_acid_degradation		RT	5	8.1E-1	1.0E0
	<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Fatty_acid_metabolism		RT	10	1.0E0	1.0E0
Annotation Cluster 163		Enrichment Score: 0.77		RT	Count	P_Value	Benjamini
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:MIT		RT	4	4.9E-2	1.0E0
	<input type="checkbox"/> SMART	MIT		RT	3	2.6E-1	1.0E0
	<input type="checkbox"/> INTERPRO	MIT_dom_sf		RT	3	2.6E-1	1.0E0
	<input type="checkbox"/> INTERPRO	MIT_dom		RT	3	2.6E-1	1.0E0
Annotation Cluster 164		Enrichment Score: 0.77		RT	Count	P_Value	Benjamini
	<input type="checkbox"/> GOTERM_MF_DIRECT	death_receptor_binding		RT	6	2.1E-2	3.0E-1
	<input type="checkbox"/> GOTERM_CC_DIRECT	death-inducing_signaling_complex		RT	4	2.4E-2	1.4E-1
	<input type="checkbox"/> GOTERM_BP_DIRECT	pyroptosis		RT	7	1.1E-1	9.8E-1
	<input type="checkbox"/> GOTERM_MF_DIRECT	cysteine-type_endopeptidase_activity_involved_in_apoptotic_signaling_pathway		RT	3	1.3E-1	9.2E-1
	<input type="checkbox"/> SMART	CAsc		RT	4	1.5E-1	1.0E0
	<input type="checkbox"/> INTERPRO	Pept_C14A		RT	4	1.5E-1	1.0E0
	<input type="checkbox"/> INTERPRO	Pept_C14_p20		RT	4	1.8E-1	1.0E0
	<input type="checkbox"/> INTERPRO	Pept_C14_caspase		RT	4	1.8E-1	1.0E0
	<input type="checkbox"/> GOTERM_BP_DIRECT	Caspase-like_dom_sf		RT	4	1.8E-1	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	execution_phase_of_apoptosis		RT	5	2.0E-1	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	cysteine-type_endopeptidase_activity_involved_in_apoptotic_process		RT	3	2.0E-1	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	cysteine-type_endopeptidase_activity_involved_in_execution_phase_of_apoptosis		RT	3	2.0E-1	1.0E0
	<input type="checkbox"/> GOTERM_BP_DIRECT	positive_regulation_of_neuron_apoptotic_process		RT	10	2.1E-1	1.0E0
	<input type="checkbox"/> INTERPRO	Caspase_his_AS		RT	3	3.0E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Caspase family p20		RT	3	3.3E-1	1.0E0
	<input type="checkbox"/> INTERPRO	Pept_C14_p10		RT	3	3.7E-1	1.0E0
	<input type="checkbox"/> INTERPRO	Caspase_cys_AS		RT	3	3.7E-1	1.0E0
	<input type="checkbox"/> BBID	86.Apoptosis_Nematode&_Vert		RT	3	7.0E-1	1.0E0
Annotation Cluster 165		Enrichment Score: 0.77		RT	Count	P_Value	Benjamini
	<input type="checkbox"/> UP_SEQ_FEATURE	REGION:Membrane-binding amphipathic helix		RT	5	2.3E-2	1.0E0
	<input type="checkbox"/> GOTERM_CC_DIRECT	retromer_tubulation_complex		RT	3	5.0E-2	2.4E-1
	<input type="checkbox"/> INTERPRO	Vps5_C		RT	3	7.9E-2	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:BAR		RT	7	1.2E-1	1.0E0
	<input type="checkbox"/> INTERPRO	AH/BAR_dom_sf		RT	11	2.5E-1	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	phosphatidylinositol_binding		RT	15	2.7E-1	1.0E0
	<input type="checkbox"/> INTERPRO	PX_dom		RT	7	3.7E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:PX		RT	7	3.7E-1	1.0E0
	<input type="checkbox"/> SMART	PX		RT	6	4.6E-1	1.0E0
	<input type="checkbox"/> INTERPRO	PX_dom_sf		RT	7	4.6E-1	1.0E0
Annotation Cluster 166		Enrichment Score: 0.76		RT	Count	P_Value	Benjamini
	<input type="checkbox"/> GOTERM_MF_DIRECT	iron-sulfur_cluster_binding		RT	7	2.9E-2	3.9E-1
	<input type="checkbox"/> GOTERM_BP_DIRECT	protein_maturation_by_iron-sulfur_cluster_transfer		RT	4	9.1E-2	8.7E-1
	<input type="checkbox"/> GOTERM_BP_DIRECT	iron-sulfur_cluster_assembly		RT	7	1.1E-1	9.8E-1
	<input type="checkbox"/> UP_KW_LIGAND	Iron-sulfur		RT	8	5.6E-1	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	4_iron,_4_sulfur_cluster_binding		RT	3	9.6E-1	1.0E0
Annotation Cluster 167		Enrichment Score: 0.76		RT	Count	P_Value	Benjamini
	<input type="checkbox"/> SMART	HMG17		RT	3	7.9E-2	7.5E-1
	<input type="checkbox"/> INTERPRO	HMGN_fam		RT	3	7.9E-2	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	nucleosomal_DNA_binding		RT	6	8.4E-1	1.0E0
Annotation Cluster 168		Enrichment Score: 0.76		RT	Count	P_Value	Benjamini

		Enrichment Score:	G	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	cytoplasmic side of lysosomal membrane	RT		5	4.1E-2	2.1E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	BORC complex	RT		3	1.8E-1	6.0E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	regulation of endosome size	RT		3	3.1E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	organelle transport along microtubule	RT		3	4.2E-1	1.0E0
Annotation Cluster 169	Enrichment Score: 0.75	G		Count	P_Value	Benjamini
<input type="checkbox"/> BIOCARTA	IL 2 signaling pathway	RT		12	1.2E-3	4.1E-2
<input type="checkbox"/> KEGG_PATHWAY	Renal cell carcinoma	RT		19	1.7E-3	8.7E-3
<input type="checkbox"/> KEGG_PATHWAY	Non-small cell lung cancer	RT		19	2.8E-3	1.4E-2
<input type="checkbox"/> BIOCARTA	TPO Signaling Pathway	RT		11	1.0E-2	1.6E-1
<input type="checkbox"/> BIOCARTA	EGF Signaling Pathway	RT		11	2.6E-2	3.1E-1
<input type="checkbox"/> BIOCARTA	IL-2 Receptor Beta Chain in T cell Activation	RT		14	2.9E-2	3.3E-1
<input type="checkbox"/> BIOCARTA	PDGF Signaling Pathway	RT		11	3.3E-2	3.5E-1
<input type="checkbox"/> KEGG_PATHWAY	Acute myeloid leukemia	RT		15	3.7E-2	1.4E-1
<input type="checkbox"/> BIOCARTA	IL_6 signaling pathway	RT		9	3.8E-2	3.6E-1
<input type="checkbox"/> KEGG_PATHWAY	B cell receptor signaling pathway	RT		17	5.7E-2	2.0E-1
<input type="checkbox"/> BIOCARTA	EPO Signaling Pathway	RT		8	6.0E-2	4.4E-1
<input type="checkbox"/> BIOCARTA	Inhibition of Cellular Proliferation by Gleevec	RT		9	6.3E-2	4.5E-1
<input type="checkbox"/> BBID	67.Ikaros_and_signaling_inhibitors	RT		10	6.5E-2	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Prolactin signaling pathway	RT		14	9.5E-2	2.9E-1
<input type="checkbox"/> BIOCARTA	IL_3 signaling pathway	RT		6	1.5E-1	7.4E-1
<input type="checkbox"/> BIOCARTA	Nerve growth factor pathway (NGF)	RT		7	1.8E-1	8.1E-1
<input type="checkbox"/> BIOCARTA	BCR Signaling Pathway	RT		10	2.1E-1	8.6E-1
<input type="checkbox"/> BIOCARTA	IGF-1 Signaling Pathway	RT		7	2.1E-1	8.6E-1
<input type="checkbox"/> BIOCARTA	Insulin Signaling Pathway	RT		7	2.1E-1	8.6E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	insulin-like growth factor receptor signaling pathway	RT		6	2.2E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Cadmium induces DNA synthesis and proliferation in macrophages	RT		6	2.3E-1	8.7E-1
<input type="checkbox"/> BIOCARTA	Role of ERBB2 in Signal Transduction and Oncology	RT		7	2.9E-1	9.4E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	myelination	RT		9	3.0E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Fc Epsilon Receptor I Signaling in Mast Cells	RT		10	3.5E-1	9.7E-1
<input type="checkbox"/> KEGG_PATHWAY	ErbB signaling pathway	RT		13	3.8E-1	8.0E-1
<input type="checkbox"/> BIOCARTA	Signaling of Hepatocyte Growth Factor Receptor	RT		9	4.1E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Growth Hormone Signaling Pathway	RT		7	4.4E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Integrin Signaling Pathway	RT		9	4.4E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	Schwann cell development	RT		3	4.6E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Endocrine resistance	RT		14	4.6E-1	9.0E-1
<input type="checkbox"/> BIOCARTA	Links between Pyk2 and Map Kinases	RT		7	4.8E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation	RT		6	4.8E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Erk1/Erk2 MapK Signaling Pathway	RT		7	5.5E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Choline metabolism in cancer	RT		13	5.9E-1	1.0E0
<input type="checkbox"/> BBID	104.Insulin_signaling	RT		5	6.4E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling	RT		7	6.5E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	EGFR tyrosine kinase inhibitor resistance	RT		10	6.8E-1	1.0E0
<input type="checkbox"/> BIOCARTA	CXCR4 Signaling Pathway	RT		5	7.2E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia	RT		5	7.2E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Breast cancer	RT		17	7.7E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Bioactive Peptide Induced Signaling Pathway	RT		7	7.9E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Signaling pathways regulating pluripotency of stem cells	RT		16	8.1E-1	1.0E0
<input type="checkbox"/> BBID	100.MAPK_signaling_cascades	RT		5	8.4E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	GnRH signaling pathway	RT		10	8.4E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Sprouty regulation of tyrosine kinase signals	RT		3	9.0E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	GnRH secretion	RT		5	9.7E-1	1.0E0
Annotation Cluster 170	Enrichment Score: 0.75	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_KW_DOMAIN	Annexin	RT		4	1.2E-1	3.7E-1
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:Annexin 1	RT		4	1.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:Annexin 2	RT		4	1.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:Annexin 3	RT		4	1.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:Annexin 4	RT		4	1.5E-1	1.0E0
<input type="checkbox"/> SMART	ANX	RT		4	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	Annexin	RT		4	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	Annexin_repeat_CS	RT		4	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	Annexin_repeat	RT		4	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	Annexin_sf	RT		4	1.5E-1	1.0E0
<input type="checkbox"/> UP_KW_LIGAND	Calcium/phospholipid-binding	RT		4	1.9E-1	8.3E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	phosphatidylserine binding	RT		9	4.5E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	calcium-dependent phospholipid binding	RT		7	4.9E-1	1.0E0
Annotation Cluster 171	Enrichment Score: 0.74	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	protein neddylation	RT		4	9.1E-2	8.7E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	regulation of protein neddylation	RT		4	1.9E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	protein neddylation	RT		5	2.0E-1	1.0E0
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Signalosome	RT		3	3.2E-1	7.6E-1
Annotation Cluster 172	Enrichment Score: 0.74	G		Count	P_Value	Benjamini
<input type="checkbox"/> SMART	Mob1_phoein	RT		3	1.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	MOB kinase_act_sf	RT		3	1.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	MOB kinase_act_fam	RT		3	1.8E-1	1.0E0
Annotation Cluster 173	Enrichment Score: 0.74	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	ectopic germ cell programmed cell death	RT		5	1.0E-1	9.2E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	negative regulation of reproductive process	RT		3	2.3E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	negative regulation of developmental process	RT		3	2.7E-1	1.0E0
Annotation Cluster 174	Enrichment Score: 0.73	G		Count	P_Value	Benjamini
<input type="checkbox"/> SMART	JmjC	RT		7	7.8E-2	7.5E-1
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:JmjC	RT		7	1.2E-1	1.0E0
<input type="checkbox"/> INTERPRO	JmjC_dom	RT		7	1.2E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	histone demethylase activity	RT		5	1.5E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	dioxygenase activity	RT		5	3.2E-1	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Dioxygenase	RT		9	7.2E-1	1.0E0
Annotation Cluster 175	Enrichment Score: 0.7	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:LisH	RT		6	1.3E-1	1.0E0
<input type="checkbox"/> SMART	LisH	RT		5	1.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	LisH	RT		6	1.9E-1	1.0E0
<input type="checkbox"/> SMART	CTLH	RT		3	2.2E-1	1.0E0

Annotation Cluster 1		Enrichment Score: 54.91	G			Count	P_Value	Benjamini
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:CTLH	RT			3	2.5E-1	1.0E0
	<input type="checkbox"/> INTERPRO	<u>CTLH_C</u>	RT			3	2.6E-1	1.0E0
Annotation Cluster 176		Enrichment Score: 0.7	G			Count	P_Value	Benjamini
	<input type="checkbox"/> BIOCARTA	<u>The information-processing_pathway_at the IFN-beta enhancer</u>	RT			7	3.9E-2	3.6E-1
	<input type="checkbox"/> UP_SEQ_FEATURE	DNA_BIND:IRF tryptophan pentad repeat	RT			3	2.1E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:IRF tryptophan pentad repeat	RT			3	2.5E-1	1.0E0
	<input type="checkbox"/> SMART	<u>IRF</u>	RT			3	2.6E-1	1.0E0
	<input type="checkbox"/> INTERPRO	<u>Interferon_reg_fact_DNA-bd_dom</u>	RT			3	2.6E-1	1.0E0
	<input type="checkbox"/> INTERPRO	<u>Interferon_reg_fac_CS</u>	RT			3	2.6E-1	1.0E0
	<input type="checkbox"/> GOTERM_BP_DIRECT	<u>immune system_process</u>	RT			8	3.5E-1	1.0E0
Annotation Cluster 177		Enrichment Score: 0.7	G			Count	P_Value	Benjamini
	<input type="checkbox"/> BIOCARTA	<u>TNFR2_Signaling_Pathway</u>	RT			9	1.4E-2	2.0E-1
	<input type="checkbox"/> BIOCARTA	<u>Acetylation and Deacetylation of RelA in The Nucleus</u>	RT			7	7.4E-2	4.8E-1
	<input type="checkbox"/> BIOCARTA	<u>CD40L_Signaling_Pathway</u>	RT			6	1.5E-1	7.4E-1
	<input type="checkbox"/> BIOCARTA	<u>NF-kB_Signaling_Pathway</u>	RT			7	2.9E-1	9.4E-1
	<input type="checkbox"/> BIOCARTA	<u>TNF/Stress Related Signaling</u>	RT			7	3.6E-1	9.8E-1
	<input type="checkbox"/> BIOCARTA	<u>Toll-Like Receptor Pathway</u>	RT			9	4.7E-1	1.0E0
	<input type="checkbox"/> BIOCARTA	<u>Chaperones modulate interferon Signaling Pathway</u>	RT			5	5.3E-1	1.0E0
	<input type="checkbox"/> KEGG_PATHWAY	<u>Adipocytokine_signaling_pathway</u>	RT			9	6.7E-1	1.0E0
Annotation Cluster 178		Enrichment Score: 0.68	G			Count	P_Value	Benjamini
	<input type="checkbox"/> GOTERM_BP_DIRECT	<u>NLS-bearing_protein_import_into_nucleus</u>	RT			5	1.4E-1	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	<u>nuclear_import_signal_receptor_activity</u>	RT			5	1.5E-1	1.0E0
	<input type="checkbox"/> SMART	<u>ARM</u>	RT			7	2.1E-1	1.0E0
	<input type="checkbox"/> GOTERM_CC_DIRECT	<u>NLS-dependent_protein_nuclear_import_complex</u>	RT			3	2.6E-1	7.6E-1
	<input type="checkbox"/> INTERPRO	<u>Armadillo</u>	RT			7	2.6E-1	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	<u>nuclear_localization_sequence_binding</u>	RT			5	2.7E-1	1.0E0
Annotation Cluster 179		Enrichment Score: 0.68	G			Count	P_Value	Benjamini
	<input type="checkbox"/> UP_SEQ_FEATURE	CARBOHYD:(Microbial infection) O-alpha-linked (GlcNAc) threonine; by C.novyi toxin TcdA; alternate	RT			3	4.9E-2	1.0E0
	<input type="checkbox"/> INTERPRO	<u>Small_GTPase_Rho</u>	RT			5	2.3E-1	1.0E0
	<input type="checkbox"/> GOTERM_BP_DIRECT	<u>regulation_of_actin_cytoskeleton_organization</u>	RT			8	8.3E-1	1.0E0
Annotation Cluster 180		Enrichment Score: 0.67	G			Count	P_Value	Benjamini
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:STI1	RT			3	1.4E-1	1.0E0
	<input type="checkbox"/> SMART	<u>STI1</u>	RT			3	2.6E-1	1.0E0
	<input type="checkbox"/> INTERPRO	<u>STI1_HS-bd</u>	RT			3	2.6E-1	1.0E0
Annotation Cluster 181		Enrichment Score: 0.67	G			Count	P_Value	Benjamini
	<input type="checkbox"/> GOTERM_BP_DIRECT	<u>response_to_cholesterol</u>	RT			4	7.2E-2	7.7E-1
	<input type="checkbox"/> GOTERM_MF_DIRECT	<u>type_I_transforming_growth_factor_beta_receptor_binding</u>	RT			4	1.3E-1	9.2E-1
	<input type="checkbox"/> BIOCARTA	<u>TGF_beta_signaling_pathway</u>	RT			7	1.5E-1	7.4E-1
	<input type="checkbox"/> GOTERM_BP_DIRECT	<u>positive_regulation_of_epithelial_to_mesenchymal_transition</u>	RT			7	4.8E-1	1.0E0
	<input type="checkbox"/> GOTERM_BP_DIRECT	<u>aortic_valve_morphogenesis</u>	RT			4	7.2E-1	1.0E0
Annotation Cluster 182		Enrichment Score: 0.66	G			Count	P_Value	Benjamini
	<input type="checkbox"/> INTERPRO	<u>Prefoldin</u>	RT			4	5.1E-2	1.0E0
	<input type="checkbox"/> GOTERM_CC_DIRECT	<u>prefoldin_complex</u>	RT			3	1.4E-1	5.2E-1
	<input type="checkbox"/> GOTERM_BP_DIRECT	<u>negative_regulation_of_amyloid_fibrilFormation</u>	RT			3	4.2E-1	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	<u>beta-amylid_binding</u>	RT			9	7.1E-1	1.0E0
Annotation Cluster 183		Enrichment Score: 0.66	G			Count	P_Value	Benjamini
	<input type="checkbox"/> INTERPRO	<u>ITM2</u>	RT			3	2.7E-2	9.9E-1
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:BRICHOS	RT			3	2.5E-1	1.0E0
	<input type="checkbox"/> SMART	<u>BRICHOS</u>	RT			3	2.6E-1	1.0E0
	<input type="checkbox"/> INTERPRO	<u>BRICHOS_dom</u>	RT			3	2.6E-1	1.0E0
	<input type="checkbox"/> GOTERM_BP_DIRECT	<u>negative_regulation_of_amyloid_precursor_protein_biosynthetic_process</u>	RT			4	3.3E-1	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	<u>beta-amylid_binding</u>	RT			9	7.1E-1	1.0E0
Annotation Cluster 184		Enrichment Score: 0.66	G			Count	P_Value	Benjamini
	<input type="checkbox"/> GOTERM_MF_DIRECT	<u>SH3_domain_binding</u>	RT			18	1.7E-1	1.0E0
	<input type="checkbox"/> UP_KW_DOMAIN	<u>SH3-binding</u>	RT			9	2.0E-1	5.6E-1
	<input type="checkbox"/> UP_SEQ_FEATURE	MOTIF:SH3-binding	RT			8	3.0E-1	1.0E0
Annotation Cluster 185		Enrichment Score: 0.65	G			Count	P_Value	Benjamini
	<input type="checkbox"/> GOTERM_CC_DIRECT	<u>SNARE_complex</u>	RT			9	9.2E-2	3.9E-1
	<input type="checkbox"/> GOTERM_MF_DIRECT	<u>SNAP_receptor_activity</u>	RT			8	1.0E-1	8.3E-1
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:T-SNARE coiled-coil homology	RT			5	2.0E-1	1.0E0
	<input type="checkbox"/> INTERPRO	<u>T_SNARE_dom</u>	RT			5	3.0E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:t-SNARE coiled-coil homology	RT			4	3.6E-1	1.0E0
	<input type="checkbox"/> SMART	<u>t_SNARE</u>	RT			3	6.8E-1	1.0E0
Annotation Cluster 186		Enrichment Score: 0.65	G			Count	P_Value	Benjamini
	<input type="checkbox"/> UP_SEQ_FEATURE	REGION:GTPase domain (Globular)	RT			3	1.4E-1	1.0E0
	<input type="checkbox"/> INTERPRO	<u>GBP_C</u>	RT			3	1.5E-1	1.0E0
	<input type="checkbox"/> INTERPRO	<u>Guanylate-bd_ATL_C</u>	RT			3	2.2E-1	1.0E0
	<input type="checkbox"/> INTERPRO	<u>Guanylate-bd_C_sf</u>	RT			3	2.6E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:GB1/RHD3-type G	RT			3	2.9E-1	1.0E0
	<input type="checkbox"/> INTERPRO	<u>G_GB1_RHD3_dom</u>	RT			3	3.0E-1	1.0E0
	<input type="checkbox"/> INTERPRO	<u>Guanylate-bd_N</u>	RT			3	3.0E-1	1.0E0
Annotation Cluster 187		Enrichment Score: 0.64	G			Count	P_Value	Benjamini
	<input type="checkbox"/> GOTERM_BP_DIRECT	<u>viral_entry_into_host_cell</u>	RT			15	1.5E-1	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	<u>virus_receptor_activity</u>	RT			12	2.2E-1	1.0E0
	<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	<u>Host_cell_receptor_for_virus_entry</u>	RT			10	3.6E-1	1.0E0
Annotation Cluster 188		Enrichment Score: 0.63	G			Count	P_Value	Benjamini
	<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:PHD-type 3	RT			4	8.3E-2	1.0E0
	<input type="checkbox"/> INTERPRO	<u>Post-SET_dom</u>	RT			5	9.4E-2	1.0E0
	<input type="checkbox"/> SMART	<u>SET</u>	RT			8	1.0E-1	9.0E-1
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Post-SET	RT			5	1.1E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:AWS	RT			3	1.1E-1	1.0E0
	<input type="checkbox"/> SMART	<u>AWS</u>	RT			3	1.1E-1	9.1E-1
	<input type="checkbox"/> INTERPRO	<u>AWS_dom</u>	RT			3	1.1E-1	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	<u>histone_methyltransferase_activity_(H3-K36_specific)</u>	RT			4	1.5E-1	1.0E0
	<input type="checkbox"/> SMART	<u>PostSET</u>	RT			4	1.8E-1	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	<u>methyltransferase_activity</u>	RT			10	2.2E-1	1.0E0
	<input type="checkbox"/> GOTERM_BP_DIRECT	<u>methylation</u>	RT			19	2.5E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:SET	RT			8	2.7E-1	1.0E0
	<input type="checkbox"/> INTERPRO	<u>SET_dom</u>	RT			8	2.8E-1	1.0E0

		Enrichment Score:	G	RT	Count	P_Value	Benjamini
Annotation Cluster 1		54.91			8	3.0E-1	1.0E0
<input type="checkbox"/> INTERPRO	SET_dom_sf				10	4.0E-1	8.1E-1
<input type="checkbox"/> KEGG_PATHWAY	Lysine degradation				3	4.8E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K4 specific)				22	6.5E-1	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Methyltransferase				9	7.2E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	S-adenosylmethionine-dependent methyltransferase activity				12	8.0E-1	1.0E0
<input type="checkbox"/> INTERPRO	SAM-dependent MTases_sf				16	9.2E-1	1.0E0
<input type="checkbox"/> UP_KW_LIGAND	S-adenosyl-L-methionine				Count	P_Value	Benjamini
Annotation Cluster 189	Enrichment Score: 0.63				4	1.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REGION:TRIAD supradomain				4	1.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:IBR-type				4	1.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:RING-type 2; atypical				4	1.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	TRIAD_supradom				6	2.2E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	ubiquitin conjugating enzyme binding				3	2.6E-1	1.0E0
<input type="checkbox"/> INTERPRO	E3 Ub_ligase_RBR				4	2.8E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:RING-type 1				3	4.4E-1	1.0E0
<input type="checkbox"/> SMART	IBR				3	4.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	IBR_dom				Count	P_Value	Benjamini
Annotation Cluster 190	Enrichment Score: 0.62				18	3.4E-2	1.3E-1
<input type="checkbox"/> KEGG_PATHWAY	Nucleotide metabolism				8	6.1E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Pyrimidine metabolism				10	6.9E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Drug metabolism - other enzymes				Count	P_Value	Benjamini
Annotation Cluster 191	Enrichment Score: 0.62				3	1.2E-1	9.8E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	interleukin-11-mediated signaling_pathway				4	1.6E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	interleukin-6-mediated signaling_pathway				3	2.7E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	T-helper_17_cell lineage commitment				5	6.9E-1	1.0E0
<input type="checkbox"/> BBID	12.IL-6_type_cytokine-signal-transduct				Count	P_Value	Benjamini
Annotation Cluster 192	Enrichment Score: 0.61				10	6.5E-2	1.0E0
<input type="checkbox"/> BBID	67.Ikaros_and_signaling_inhibitors				8	2.0E-1	1.0E0
<input type="checkbox"/> BBID	3.T_cell_receptor				6	4.2E-1	1.0E0
<input type="checkbox"/> BBID	63.LAT_couples_T-cell_receptor				5	6.4E-1	1.0E0
<input type="checkbox"/> BBID	54.T-cell_anergy				Count	P_Value	Benjamini
Annotation Cluster 193	Enrichment Score: 0.61				6	8.1E-3	1.5E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	non-membrane spanning_protein tyrosine phosphatase activity				24	3.0E-2	1.8E-1
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Protein_phosphatase				12	2.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ACT_SITE:Phosphocysteine intermediate				9	2.8E-1	1.0E0
<input type="checkbox"/> SMART	PTPc_motif				9	2.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	Tyr_Pase_cat				14	3.3E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	dephosphorylation				13	3.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	Prot-tyrosine_phosphatase-like				10	3.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Tyrosine-protein phosphatase				10	3.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	Tyr_Pase_AS				10	3.5E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	protein_tyrosine_phosphatase_activity				5	3.8E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	peptidyl-tyrosine_dephosphorylation				6	4.0E-1	1.0E0
<input type="checkbox"/> INTERPRO	PTP_cat				5	5.0E-1	1.0E0
<input type="checkbox"/> SMART	PTPc				10	5.3E-1	1.0E0
<input type="checkbox"/> INTERPRO	Tyr_Pase_dom				7	6.8E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Tyrosine specific protein phosphatases				Count	P_Value	Benjamini
Annotation Cluster 194	Enrichment Score: 0.6				3	2.3E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	RNA_secondary_structure_unwinding				7	2.4E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	DNA_helicase_activity				9	2.9E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	DNA_duplex_unwinding				Count	P_Value	Benjamini
Annotation Cluster 195	Enrichment Score: 0.6				3	2.2E-1	1.0E0
<input type="checkbox"/> SMART	Alpha_adaptinC2				3	2.2E-1	1.0E0
<input type="checkbox"/> INTERPRO	Clathrin_a/b/g-adaptin_app_Ig				3	3.3E-1	1.0E0
<input type="checkbox"/> INTERPRO	Clathrin_app_Ig-like_sf				Count	P_Value	Benjamini
Annotation Cluster 196	Enrichment Score: 0.6				9	9.6E-2	9.1E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation_of DNA repair				9	9.6E-2	9.1E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	regulation_of embryonic development				4	2.3E-1	7.0E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	Ino80_complex				3	4.6E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation_of telomere maintenance in response_to DNA damage				3	4.9E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	regulation_of DNA strand elongation				3	5.5E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	regulation_of chromosome organization				Count	P_Value	Benjamini
Annotation Cluster 197	Enrichment Score: 0.59				3	2.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:MIR_3				3	2.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:MIR_1				3	2.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:MIR_2				3	2.6E-1	1.0E0
<input type="checkbox"/> SMART	MIR				3	2.6E-1	1.0E0
<input type="checkbox"/> INTERPRO	MIR_motif				3	2.6E-1	1.0E0
<input type="checkbox"/> INTERPRO	MIR_dom_sf				3	2.6E-1	1.0E0
Annotation Cluster 198	Enrichment Score: 0.57				Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY	Growth_hormone_synthesis,_secretion_and_action				23	4.3E-2	1.6E-1
<input type="checkbox"/> KEGG_PATHWAY	Estrogen_signaling_pathway				23	1.3E-1	3.7E-1
<input type="checkbox"/> KEGG_PATHWAY	Relaxin_signaling_pathway				21	1.9E-1	4.8E-1
<input type="checkbox"/> KEGG_PATHWAY	Chemical_carcinogenesis - receptor_activation				28	5.0E-1	9.3E-1
<input type="checkbox"/> KEGG_PATHWAY	Cholinergic_synapse				13	7.8E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Alcoholism				19	9.2E-1	1.0E0
Annotation Cluster 199	Enrichment Score: 0.56				Count	P_Value	Benjamini
<input type="checkbox"/> SMART	EFh				21	9.3E-2	8.4E-1
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:EF-hand_1				24	1.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:EF-hand_5				4	1.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:EF-hand				25	1.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:EF-hand_2				24	1.6E-1	1.0E0
<input type="checkbox"/> INTERPRO	EF-hand-dom_pair				33	1.9E-1	1.0E0
<input type="checkbox"/> INTERPRO	EF_Hand_1_Ca_BS				22	2.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:EF-hand_3				12	4.0E-1	1.0E0
<input type="checkbox"/> INTERPRO	EF_hand_dom				25	4.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:EF-hand_4				8	4.4E-1	1.0E0
<input type="checkbox"/> UP_KW_LIGAND	Calcium				66	1.0E0	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	calcium ion binding				48	1.0E0	1.0E0
Annotation Cluster 200	Enrichment Score: 0.56				Count	P_Value	Benjamini
<input type="checkbox"/> BBID	72.IAP_interaction_with_cell_death_pathways				7	1.4E-1	1.0E0
<input type="checkbox"/> BBID	150.caspase_and_NFKB_activation			<			

Annotation Cluster 1		Enrichment Score: 54.91	G	Count	P_Value	Benjamini
<input type="checkbox"/>	BBID	40.Deg_of_Chrom_DNA_TNF-ind_apoptosis	RT	3	7.0E-1	1.0E0
Annotation Cluster 201		Enrichment Score: 0.55	G	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:EH	RT	3	2.5E-1	1.0E0
<input type="checkbox"/>	SMART	EH	RT	3	3.0E-1	1.0E0
<input type="checkbox"/>	INTERPRO	EH_dom	RT	3	3.0E-1	1.0E0
Annotation Cluster 202		Enrichment Score: 0.54	G	Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	G_patch	RT	6	2.8E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:G-patch	RT	6	2.9E-1	1.0E0
<input type="checkbox"/>	INTERPRO	G_patch_dom	RT	6	3.0E-1	1.0E0
Annotation Cluster 203		Enrichment Score: 0.54	G	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Phorbol-ester/DAG-type	RT	10	1.1E-1	1.0E0
<input type="checkbox"/>	INTERPRO	PE/DAG-bd	RT	11	1.3E-1	1.0E0
<input type="checkbox"/>	INTERPRO	DAG/PE-bd	RT	5	2.3E-1	1.0E0
<input type="checkbox"/>	INTERPRO	C1-like_sf	RT	9	2.8E-1	1.0E0
<input type="checkbox"/>	SMART	C1	RT	9	3.2E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	ZN_FING:Phorbol-ester/DAG-type	RT	6	4.3E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	ZN_FING:Phorbol-ester/DAG-type 1	RT	3	6.4E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	ZN_FING:Phorbol-ester/DAG-type 2	RT	3	6.4E-1	1.0E0
Annotation Cluster 204		Enrichment Score: 0.53	G	Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_DIRECT	mitochondrial ribosome	RT	5	2.2E-1	7.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitochondrial translation	RT	13	2.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	mitochondrial large ribosomal subunit	RT	7	4.7E-1	1.0E0
Annotation Cluster 205		Enrichment Score: 0.53	G	Count	P_Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	Basal transcription factors	RT	9	1.8E-1	4.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription initiation from RNA polymerase II promoter	RT	7	3.2E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	transcription factor TFIID complex	RT	6	4.5E-1	1.0E0
Annotation Cluster 206		Enrichment Score: 0.52	G	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:1	RT	35	2.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:3	RT	32	3.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:4	RT	27	5.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:2	RT	34	5.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:7	RT	20	7.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:6	RT	20	1.4E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:5	RT	21	1.9E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:8	RT	16	2.4E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:10	RT	13	2.7E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:9	RT	14	2.8E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:12	RT	12	2.9E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:11	RT	12	3.1E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:17	RT	8	3.3E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:13	RT	11	3.3E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:14	RT	10	3.9E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:16	RT	8	4.0E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:15	RT	9	4.0E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:21	RT	6	4.6E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:20	RT	6	5.0E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:19	RT	6	5.4E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:18	RT	6	5.8E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:30	RT	3	6.2E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:22	RT	5	6.3E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:29	RT	3	6.9E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:24	RT	4	6.9E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:28	RT	3	7.3E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:27	RT	3	8.0E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:26	RT	3	8.3E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:25	RT	3	8.8E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:23	RT	3	9.0E-1	1.0E0
Annotation Cluster 207		Enrichment Score: 0.52	G	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:K Homology	RT	6	1.3E-1	1.0E0
<input type="checkbox"/>	INTERPRO	KH_dom_type_1	RT	7	1.7E-1	1.0E0
<input type="checkbox"/>	SMART	KH	RT	6	3.4E-1	1.0E0
<input type="checkbox"/>	INTERPRO	KH_dom	RT	6	3.4E-1	1.0E0
<input type="checkbox"/>	INTERPRO	KH_dom_type_1_sf	RT	7	3.5E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:KH_3	RT	3	4.0E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:KH_1	RT	4	4.7E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:KH_2	RT	4	4.7E-1	1.0E0
Annotation Cluster 208		Enrichment Score: 0.51	G	Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	UBX	RT	3	2.2E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:UBX	RT	3	3.6E-1	1.0E0
<input type="checkbox"/>	INTERPRO	UBX_dom	RT	3	3.7E-1	1.0E0
Annotation Cluster 209		Enrichment Score: 0.51	G	Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	ventricular septum development	RT	6	2.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	aorta development	RT	5	2.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	coronary vasculature development	RT	4	5.2E-1	1.0E0
Annotation Cluster 210		Enrichment Score: 0.51	G	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:CAP-Gly	RT	3	2.5E-1	1.0E0
<input type="checkbox"/>	SMART	CAP_GLY	RT	3	3.3E-1	1.0E0
<input type="checkbox"/>	INTERPRO	CAP-Gly_dom_sf	RT	3	3.3E-1	1.0E0
<input type="checkbox"/>	INTERPRO	CAP-Gly_domain	RT	3	3.3E-1	1.0E0
Annotation Cluster 211		Enrichment Score: 0.48	G	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Hydrogen ion transport	RT	10	2.2E-1	7.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	proton-transporting ATP synthase activity, rotational mechanism	RT	4	3.2E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	ATP synthesis coupled proton transport	RT	4	5.0E-1	1.0E0
Annotation Cluster 212		Enrichment Score: 0.48	G	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:RanBD1	RT	3	3.3E-1	1.0E0
<input type="checkbox"/>	SMART	RanBD	RT	3	3.3E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Ran_bind_dom	RT	3	3.3E-1	1.0E0
<input type="checkbox"/>	INTERPRO	RanBP1-like	RT	3	3.3E-1	1.0E0
Annotation Cluster 213		Enrichment Score: 0.48	G	Count	P_Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	Endometrial cancer	RT	12	1.1E-1	3.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	Thyroid cancer	RT	8	1.8E-1	4.6E-1
<input type="checkbox"/>	BIOCARTA	p53 Signaling Pathway	RT	4	6.8E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Basal cell carcinoma	RT	4	9.9E-1	1.0E0

Annotation Cluster 1		Enrichment Score: 54.91	G			Count	P_Value	Benjamini
Annotation Cluster 214		Enrichment Score: 0.46	G			Count	P_Value	Benjamini
<input type="checkbox"/> BIOCARTA		Role of PI3K subunit p85 in regulation of Actin Organization and Cell Migration	RT			6	1.9E-1	8.1E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		Arp2/3 complex-mediated actin nucleation	RT			5	2.2E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT		Arp2/3 protein complex	RT			3	2.9E-1	8.2E-1
<input type="checkbox"/> BIOCARTA		Rho cell motility signaling pathway	RT			8	4.8E-1	1.0E0
<input type="checkbox"/> BIOCARTA		How does salmonella hijack a cell	RT			4	4.8E-1	1.0E0
<input type="checkbox"/> BIOCARTA		Y branching of actin filaments	RT			5	6.1E-1	1.0E0
Annotation Cluster 215		Enrichment Score: 0.46	G			Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY		Circadian rhythm	RT			8	1.3E-1	3.6E-1
<input type="checkbox"/> BIOCARTA		Regulation of p27 Phosphorylation during Cell Cycle Progression	RT			4	4.8E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	RT			5	7.0E-1	1.0E0
Annotation Cluster 216		Enrichment Score: 0.45	G			Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT		mitogen-activated protein kinase binding	RT			5	2.0E-1	1.0E0
<input type="checkbox"/> INTERPRO		Rhodanese-like_dom_sf	RT			5	2.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:Rhodanese	RT			5	2.2E-1	1.0E0
<input type="checkbox"/> INTERPRO		Rhodanese-like_dom	RT			5	2.3E-1	1.0E0
<input type="checkbox"/> INTERPRO		MKP	RT			3	2.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		ACT_SITE:Phosphocysteine intermediate	RT			12	2.7E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT		MAP kinase tyrosine phosphatase activity	RT			3	2.9E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT		protein tyrosine/threonine phosphatase activity	RT			3	2.9E-1	1.0E0
<input type="checkbox"/> SMART		RHOD	RT			4	3.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:Tyrosine-protein phosphatase	RT			10	3.4E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		peptidyl-tyrosine dephosphorylation	RT			5	3.8E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT		MAP kinase tyrosine/serine/threonine phosphatase activity	RT			3	4.1E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		negative regulation of MAPK cascade	RT			6	4.6E-1	1.0E0
<input type="checkbox"/> INTERPRO		Tyr_Pase_dom	RT			10	5.3E-1	1.0E0
<input type="checkbox"/> INTERPRO		TYR_PHOSPHATASE_DUAL_dom	RT			5	6.2E-1	1.0E0
<input type="checkbox"/> SMART		DSPc	RT			4	7.4E-1	1.0E0
<input type="checkbox"/> INTERPRO		Dual-sp_phosphatase_cat-dom	RT			4	8.0E-1	1.0E0
Annotation Cluster 217		Enrichment Score: 0.45	G			Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		nucleocytoplasmic transport	RT			9	1.4E-1	1.0E0
<input type="checkbox"/> BIOCARTA		Mechanism of Protein Import into the Nucleus	RT			5	2.4E-1	8.7E-1
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT		Nuclear pore complex	RT			6	6.2E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT		structural constituent of nuclear pore	RT			3	7.8E-1	1.0E0
Annotation Cluster 218		Enrichment Score: 0.45	G			Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:MATH	RT			3	3.3E-1	1.0E0
<input type="checkbox"/> SMART		MATH	RT			3	3.3E-1	1.0E0
<input type="checkbox"/> INTERPRO		MATH/TRAFF_dom	RT			3	3.3E-1	1.0E0
<input type="checkbox"/> INTERPRO		TRAFF-like	RT			3	4.4E-1	1.0E0
Annotation Cluster 219		Enrichment Score: 0.44	G			Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:Nudix hydrolase	RT			5	3.1E-1	1.0E0
<input type="checkbox"/> INTERPRO		NUDIX_hydrolase_dom	RT			5	3.2E-1	1.0E0
<input type="checkbox"/> INTERPRO		NUDIX_hydrolase-like_dom_sf	RT			5	3.4E-1	1.0E0
<input type="checkbox"/> INTERPRO		NUDIX_hydrolase_CS	RT			3	4.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		MOTIF:Nudix box	RT			4	4.4E-1	1.0E0
Annotation Cluster 220		Enrichment Score: 0.44	G			Count	P_Value	Benjamini
<input type="checkbox"/> BIOCARTA		Bystander B Cell Activation	RT			5	8.0E-2	4.8E-1
<input type="checkbox"/> BIOCARTA		Antigen Dependent B Cell Activation	RT			5	2.4E-1	8.7E-1
<input type="checkbox"/> BIOCARTA		Th1/Th2 Differentiation	RT			5	5.7E-1	1.0E0
<input type="checkbox"/> BIOCARTA		IL_5 Signaling Pathway	RT			3	6.1E-1	1.0E0
<input type="checkbox"/> BIOCARTA		Cytokines and Inflammatory Response	RT			4	9.4E-1	1.0E0
Annotation Cluster 221		Enrichment Score: 0.43	G			Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		cholesterol biosynthetic process	RT			8	6.5E-2	7.3E-1
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS		Cholesterol biosynthesis	RT			5	2.4E-1	8.0E-1
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS		Cholesterol metabolism	RT			11	2.7E-1	8.3E-1
<input type="checkbox"/> KEGG_PATHWAY		Terpenoid backbone biosynthesis	RT			5	3.3E-1	7.3E-1
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS		Sterol biosynthesis	RT			5	4.1E-1	1.0E0
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS		Sterol metabolism	RT			11	4.1E-1	1.0E0
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS		Steroid metabolism	RT			12	7.0E-1	1.0E0
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS		Steroid biosynthesis	RT			5	7.9E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		cholesterol metabolic process	RT			6	9.4E-1	1.0E0
Annotation Cluster 222		Enrichment Score: 0.43	G			Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:MBD	RT			3	3.6E-1	1.0E0
<input type="checkbox"/> SMART		MBD	RT			3	3.7E-1	1.0E0
<input type="checkbox"/> INTERPRO		Methyl_CpG_DNA-bd	RT			3	3.7E-1	1.0E0
<input type="checkbox"/> INTERPRO		DNA-bd_dom_sf	RT			3	3.7E-1	1.0E0
Annotation Cluster 223		Enrichment Score: 0.43	G			Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO		Tetraspanin_CS	RT			5	1.7E-1	1.0E0
<input type="checkbox"/> INTERPRO		Tetraspanin_animals	RT			5	3.0E-1	1.0E0
<input type="checkbox"/> INTERPRO		Tetraspanin_EC2_sf	RT			5	3.9E-1	1.0E0
<input type="checkbox"/> INTERPRO		Tetraspanin/Peripherin	RT			5	4.3E-1	1.0E0
<input type="checkbox"/> PIR_SUPERFAMILY		Tetraspanin	RT			5	5.1E-1	1.0E0
<input type="checkbox"/> BBID		73.Integrins_and_other_cell-surface_receptors	RT			4	6.6E-1	1.0E0
Annotation Cluster 224		Enrichment Score: 0.43	G			Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT		aminopeptidase activity	RT			6	2.2E-1	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION		Aminopeptidase	RT			5	4.5E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT		metalloaminopeptidase activity	RT			4	5.3E-1	1.0E0
Annotation Cluster 225		Enrichment Score: 0.42	G			Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		regulation of meiotic cell cycle	RT			4	3.3E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT		anaphase-promoting complex	RT			4	3.9E-1	9.9E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		anaphase-promoting_complex-dependent catabolic process	RT			4	4.1E-1	1.0E0
Annotation Cluster 226		Enrichment Score: 0.42	G			Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO		Endo/exonu/phosph_ase_sf	RT			5	3.0E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:Endonuclease/exonuclease/phosphatase	RT			3	3.3E-1	1.0E0
<input type="checkbox"/> INTERPRO		Endo/exonuclease/phosphatase	RT			3	5.7E-1	1.0E0
Annotation Cluster 227		Enrichment Score: 0.41	G			Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE		DNA_BIND:HMG_box_1	RT			3	2.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		DNA_BIND:HMG_box_2	RT			3	2.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:HMG_box	RT			6	3.7E-1	1.0E0
<input type="checkbox"/> SMART		HMG	RT			7	4.4E-1	1.0E0
<input type="checkbox"/> INTERPRO		HMG_box_dom						

Annotation Cluster 1		Enrichment Score: 54.91	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO		HMG_box_dom_sf	RT		7	5.0E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		DNA_BIND:HMG box	RT		6	5.6E-1	1.0EO
Annotation Cluster 228		Enrichment Score: 0.41	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:ARM	RT		6	1.0E-1	1.0EO
<input type="checkbox"/> SMART		ARM	RT		7	2.1E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:ARM 9	RT		4	2.5E-1	1.0EO
<input type="checkbox"/> INTERPRO		Armadillo	RT		7	2.6E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:ARM 8	RT		4	4.2E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:ARM 5	RT		5	4.2E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:ARM 7	RT		4	4.7E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:ARM 4	RT		5	5.3E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:ARM 6	RT		4	5.7E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:ARM 3	RT		5	6.1E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:ARM 2	RT		5	6.5E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:ARM 1	RT		3	9.0E-1	1.0EO
Annotation Cluster 229		Enrichment Score: 0.4	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO		WW_dom_sf	RT		9	9.5E-2	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:WW 1	RT		3	8.0E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:WW 2	RT		3	8.0E-1	1.0EO
Annotation Cluster 230		Enrichment Score: 0.4	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 15	RT		4	1.7E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 14	RT		4	2.2E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 12	RT		4	2.5E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 13	RT		4	2.5E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 17	RT		3	2.5E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 18	RT		3	2.5E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 19	RT		3	2.5E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 16	RT		3	2.9E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 11	RT		4	3.1E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 10	RT		4	4.2E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 9	RT		4	4.4E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 6	RT		5	4.9E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 8	RT		4	5.2E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 5	RT		5	6.1E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 7	RT		4	6.1E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 4	RT		5	7.3E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 2	RT		6	7.9E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 1	RT		6	7.9E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REPEAT:HEAT 3	RT		5	8.3E-1	1.0EO
Annotation Cluster 231		Enrichment Score: 0.4	G		Count	P_Value	Benjamini
<input type="checkbox"/> BIOCARTA		Protein Kinase A at the Centrosome	RT		5	3.4E-1	9.5E-1
<input type="checkbox"/> BIOCARTA		AKAP95 role in mitosis and chromosome dynamics	RT		4	4.3E-1	1.0EO
<input type="checkbox"/> BIOCARTA		Regulation of ck1/cdk5 by type 1 glutamate receptors	RT		5	4.3E-1	1.0EO
Annotation Cluster 232		Enrichment Score: 0.4	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT		3'-5'-exoribonuclease activity	RT		7	7.9E-2	7.3E-1
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION		Exonuclease	RT		8	3.5E-1	1.0EO
<input type="checkbox"/> INTERPRO		RNaseH_sf	RT		4	9.5E-1	1.0EO
<input type="checkbox"/> INTERPRO		RNaseH-like_sf	RT		4	9.9E-1	1.0EO
Annotation Cluster 233		Enrichment Score: 0.4	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT		2 iron, 2 sulfur cluster binding	RT		6	1.9E-1	1.0EO
<input type="checkbox"/> UP_KW_LIGAND		Iron-sulfur	RT		8	5.6E-1	1.0EO
<input type="checkbox"/> UP_KW_LIGAND		2Fe-2S	RT		3	6.2E-1	1.0EO
Annotation Cluster 234		Enrichment Score: 0.4	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO		UBA-like_sf	RT		9	2.5E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:UBA	RT		7	4.1E-1	1.0EO
<input type="checkbox"/> INTERPRO		UBA	RT		6	4.6E-1	1.0EO
<input type="checkbox"/> SMART		UBA	RT		4	5.5E-1	1.0EO
Annotation Cluster 235		Enrichment Score: 0.39	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:G-alpha	RT		4	2.0E-1	1.0EO
<input type="checkbox"/> SMART		G_alpha	RT		4	2.0E-1	1.0EO
<input type="checkbox"/> INTERPRO		Gprotein_alpha_su	RT		4	2.0E-1	1.0EO
<input type="checkbox"/> INTERPRO		GproteinA_insert	RT		4	2.0E-1	1.0EO
<input type="checkbox"/> GOTERM_CC_DIRECT		heterotrimeric G-protein complex	RT		6	2.7E-1	7.8E-1
<input type="checkbox"/> UP_SEQ_FEATURE		REGION:G2 motif	RT		5	3.3E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REGION:G5 motif	RT		5	3.3E-1	1.0EO
<input type="checkbox"/> KEGG_PATHWAY		Long-term depression	RT		10	3.4E-1	7.5E-1
<input type="checkbox"/> GOTERM_MF_DIRECT		G-protein beta/gamma-subunit complex binding	RT		4	4.1E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REGION:G1 motif	RT		5	6.1E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REGION:G3 motif	RT		5	6.1E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		REGION:G4 motif	RT		5	6.1E-1	1.0EO
<input type="checkbox"/> KEGG_PATHWAY		Regulation of lipolysis in adipocytes	RT		6	8.7E-1	1.0EO
<input type="checkbox"/> GOTERM_BP_DIRECT		adenylate cyclase-modulating G-protein coupled receptor signaling pathway	RT		4	8.8E-1	1.0EO
<input type="checkbox"/> KEGG_PATHWAY		Morphine addiction	RT		7	9.8E-1	1.0EO
Annotation Cluster 236		Enrichment Score: 0.39	G		Count	P_Value	Benjamini
<input type="checkbox"/> BIOCARTA		Cadmium induces DNA synthesis and proliferation in macrophages	RT		6	2.3E-1	8.7E-1
<input type="checkbox"/> KEGG_PATHWAY		Pertussis	RT		12	3.6E-1	7.7E-1
<input type="checkbox"/> BBID		92.Ancient_Host_Defense_Pathways	RT		4	3.9E-1	1.0EO
<input type="checkbox"/> BIOCARTA		Toll-Like Receptor Pathway	RT		9	4.7E-1	1.0EO
<input type="checkbox"/> BIOCARTA		Role of EGF Receptor Transactivation by GPCRs in Cardiac Hypertrophy	RT		4	7.2E-1	1.0EO
Annotation Cluster 237		Enrichment Score: 0.39	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:PB1	RT		3	4.0E-1	1.0EO
<input type="checkbox"/> SMART		PB1	RT		3	4.1E-1	1.0EO
<input type="checkbox"/> INTERPRO		PB1_dom	RT		3	4.1E-1	1.0EO
Annotation Cluster 238		Enrichment Score: 0.39	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:Myb-like	RT		6	1.6E-1	1.0EO
<input type="checkbox"/> INTERPRO		SANT/Myb	RT		8	1.9E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:HTH myb-type	RT		3	3.6E-1	1.0EO
<input type="checkbox"/> INTERPRO		Myb_dom	RT		3	4.1E-1	1.0EO
<input type="checkbox"/> SMART		SANT	RT		6	4.2E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:SANT	RT		4	5.4E-1	1.0EO
<input type="checkbox"/> INTERPRO		SANT_dom	RT		3	7.6E-1	1.0EO

Annotation Cluster 1		Enrichment Score: 54.91	G			Count	P_Value	Benjamini
	<input type="checkbox"/> INTERPRO	Homeobox-like_sf	RT			17	1.0E0	1.0E0
Annotation Cluster 239		Enrichment Score: 0.39	G			Count	P_Value	Benjamini
	<input type="checkbox"/> GOTERM_MF_DIRECT	cyclin_binding	RT			8	6.1E-2	6.3E-1
	<input type="checkbox"/> GOTERM_BP_DIRECT	regulation_of_G2/M_transition_of_mitotic_cell_cycle	RT			3	3.8E-1	1.0E0
	<input type="checkbox"/> BBID	94.E2F_transcriptional_activity_cell_cycle	RT			3	5.5E-1	1.0E0
	<input type="checkbox"/> BIOCARTA	Cyclins_and_Cell_Cycle_Regulation	RT			6	5.6E-1	1.0E0
	<input type="checkbox"/> BBID	26.cyclin-CDK_complexes	RT			4	7.6E-1	1.0E0
	<input type="checkbox"/> BIOCARTA	Cell_Cycle	RT			5	8.7E-1	1.0E0
Annotation Cluster 240		Enrichment Score: 0.38	G			Count	P_Value	Benjamini
	<input type="checkbox"/> UP_SEQ_FEATURE	MOTIF:Box 1 motif	RT			6	7.7E-2	1.0E0
	<input type="checkbox"/> INTERPRO	Hempt_rcpt_S_F1_CS	RT			4	8.6E-2	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	cytokine_binding	RT			9	8.7E-2	7.8E-1
	<input type="checkbox"/> KEGG_PATHWAY	JAK-STAT_signaling_pathway	RT			28	9.5E-2	2.9E-1
	<input type="checkbox"/> UP_SEQ_FEATURE	MOTIF:WSXWS motif	RT			6	1.4E-1	1.0E0
	<input type="checkbox"/> GOTERM_BP_DIRECT	cytokine-mediated_signaling_pathway	RT			18	3.1E-1	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	cytokine_receptor_activity	RT			7	4.0E-1	1.0E0
	<input type="checkbox"/> GOTERM_BP_DIRECT	immunoglobulin-mediated_immune_response	RT			8	9.2E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Fibronectin type-III	RT			11	9.8E-1	1.0E0
	<input type="checkbox"/> INTERPRO	FN3_dom	RT			12	9.9E-1	1.0E0
	<input type="checkbox"/> INTERPRO	FN3_sf	RT			12	1.0E0	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Fibronectin type-III 3	RT			3	1.0E0	1.0E0
	<input type="checkbox"/> GOTERM_CC_DIRECT	receptor_complex	RT			9	1.0E0	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Fibronectin type-III 1	RT			4	1.0E0	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Fibronectin type-III 2	RT			4	1.0E0	1.0E0
	<input type="checkbox"/> SMART	FN3	RT			3	1.0E0	1.0E0
Annotation Cluster 241		Enrichment Score: 0.37	G			Count	P_Value	Benjamini
	<input type="checkbox"/> KEGG_PATHWAY	Endocrine_and_other_factor-regulated_calcium_reabsorption	RT			11	1.2E-1	3.5E-1
	<input type="checkbox"/> KEGG_PATHWAY	Pancreatic_secretion	RT			13	6.4E-1	1.0E0
	<input type="checkbox"/> KEGG_PATHWAY	Salivary_secretion	RT			7	9.8E-1	1.0E0
Annotation Cluster 242		Enrichment Score: 0.37	G			Count	P_Value	Benjamini
	<input type="checkbox"/> GOTERM_BP_DIRECT	alpha-linolenic_acid_metabolic_process	RT			3	2.7E-1	1.0E0
	<input type="checkbox"/> KEGG_PATHWAY	Fatty_acid_metabolism	RT			9	4.3E-1	8.6E-1
	<input type="checkbox"/> KEGG_PATHWAY	Biosynthesis_of_unsaturated_fatty_acids	RT			4	6.8E-1	1.0E0
Annotation Cluster 243		Enrichment Score: 0.37	G			Count	P_Value	Benjamini
	<input type="checkbox"/> BIOCARTA	Ras_Signaling_Pathway	RT			7	2.9E-1	9.4E-1
	<input type="checkbox"/> BBID	102.Cholesterol_Stress_Response	RT			3	3.6E-1	1.0E0
	<input type="checkbox"/> BIOCARTA	Role_of_MAL_in_Rho-Mediated_Activation_of_SRF	RT			4	7.5E-1	1.0E0
Annotation Cluster 244		Enrichment Score: 0.37	G			Count	P_Value	Benjamini
	<input type="checkbox"/> KEGG_PATHWAY	Endometrial_cancer	RT			12	1.1E-1	3.2E-1
	<input type="checkbox"/> GOTERM_BP_DIRECT	insulin-like_growth_factor_receptor_signaling_pathway	RT			6	2.2E-1	1.0E0
	<input type="checkbox"/> BBID	105.Signaling_glucose_uptake	RT			4	4.7E-1	1.0E0
	<input type="checkbox"/> BBID	106.Glycogen_synthase-synthesis	RT			3	6.3E-1	1.0E0
	<input type="checkbox"/> BBID	104.Insulin_signaling	RT			5	6.4E-1	1.0E0
	<input type="checkbox"/> BIOCARTA	PTEN-dependent_cell_cycle_arrest_and_apoptosis	RT			4	7.2E-1	1.0E0
	<input type="checkbox"/> BBID	107.mRNA_translation-protein_synthesis	RT			3	9.0E-1	1.0E0
Annotation Cluster 245		Enrichment Score: 0.36	G			Count	P_Value	Benjamini
	<input type="checkbox"/> GOTERM_BP_DIRECT	heparan_sulfate_proteoglycan_catabolic_process	RT			3	2.3E-1	1.0E0
	<input type="checkbox"/> UP_KW_DISEASE	Mucopolysaccharidosis	RT			3	5.2E-1	1.0E0
	<input type="checkbox"/> KEGG_PATHWAY	Glycosaminoglycan_degradation	RT			3	7.1E-1	1.0E0
Annotation Cluster 246		Enrichment Score: 0.35	G			Count	P_Value	Benjamini
	<input type="checkbox"/> BIOCARTA	AKT_Signaling_Pathway	RT			7	2.5E-1	8.7E-1
	<input type="checkbox"/> BIOCARTA	Inactivation_of_Gsk3_by_AKT_causes_accumulation_of_b-catenin_in_Alveolar_Macrophages	RT			7	4.4E-1	1.0E0
	<input type="checkbox"/> BIOCARTA	Skeletal_muscle_hypertrophy_is_regulated_via_AKT/mTOR_pathway	RT			4	7.8E-1	1.0E0
Annotation Cluster 247		Enrichment Score: 0.35	G			Count	P_Value	Benjamini
	<input type="checkbox"/> BIOCARTA	Ras_Signaling_Pathway	RT			7	2.9E-1	9.4E-1
	<input type="checkbox"/> BIOCARTA	Human_Cytomegalovirus_and_Map_Kinase_Pathways	RT			5	4.3E-1	1.0E0
	<input type="checkbox"/> BIOCARTA	CXCR4_Signaling_Pathway	RT			5	7.2E-1	1.0E0
Annotation Cluster 248		Enrichment Score: 0.35	G			Count	P_Value	Benjamini
	<input type="checkbox"/> GOTERM_BP_DIRECT	regulation_of_stem_cell_differentiation	RT			5	2.2E-1	1.0E0
	<input type="checkbox"/> GOTERM_BP_DIRECT	regulation_of_cell_fate_specification	RT			3	4.2E-1	1.0E0
	<input type="checkbox"/> GOTERM_CC_DIRECT	NuRD_complex	RT			3	5.4E-1	1.0E0
	<input type="checkbox"/> GOTERM_MF_DIRECT	nucleosomal_DNA_binding	RT			6	8.4E-1	1.0E0
Annotation Cluster 249		Enrichment Score: 0.34	G			Count	P_Value	Benjamini
	<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Sarcoplasmic_reticulum	RT			8	3.4E-1	7.6E-1
	<input type="checkbox"/> GOTERM_CC_DIRECT	sarcoplasmic_reticulum	RT			6	5.1E-1	1.0E0
	<input type="checkbox"/> GOTERM_CC_DIRECT	sarcoplasmic_reticulum_membrane	RT			5	5.4E-1	1.0E0
Annotation Cluster 250		Enrichment Score: 0.34	G			Count	P_Value	Benjamini
	<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Glucose_metabolism	RT			4	2.5E-1	8.0E-1
	<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Carbohydrate_metabolism	RT			12	5.9E-1	1.0E0
	<input type="checkbox"/> GOTERM_BP_DIRECT	glucose_metabolic_process	RT			7	6.5E-1	1.0E0
Annotation Cluster 251		Enrichment Score: 0.33	G			Count	P_Value	Benjamini
	<input type="checkbox"/> BIOCARTA	Cadmium_induces_DNA_synthesis_and_proliferation_in_macrophages	RT			6	2.3E-1	8.7E-1
	<input type="checkbox"/> BIOCARTA	TNF/Stress_Related_Signaling	RT			7	3.6E-1	9.8E-1
	<input type="checkbox"/> BIOCARTA	ATM_Signaling_Pathway	RT			6	4.0E-1	1.0E0
	<input type="checkbox"/> BIOCARTA	Toll-Like_Receptor_Pathway	RT			9	4.7E-1	1.0E0
	<input type="checkbox"/> BBID	77.IkBa_Kinase_JNK_MEKK1	RT			3	5.5E-1	1.0E0
	<input type="checkbox"/> BIOCARTA	Signal_transduction_through_IL1R	RT			7	6.5E-1	1.0E0
	<input type="checkbox"/> BIOCARTA	The_4-1BB-dependent immune_response	RT			3	9.0E-1	1.0E0
Annotation Cluster 252		Enrichment Score: 0.32	G			Count	P_Value	Benjamini
	<input type="checkbox"/> SMART	RasGAP	RT			3	4.1E-1	1.0E0
	<input type="checkbox"/> INTERPRO	RasGAP_CS	RT			3	4.1E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Ras-GAP	RT			3	4.3E-1	1.0E0
	<input type="checkbox"/> INTERPRO	RasGAP_dom	RT			3	4.4E-1	1.0E0
	<input type="checkbox"/> INTERPRO	Rho_GTPase_activation_prot	RT			9	7.5E-1	1.0E0
Annotation Cluster 253		Enrichment Score: 0.32	G			Count	P_Value	Benjamini
	<input type="checkbox"/> GOTERM_MF_DIRECT	calcium_ion_transmembrane_transporter_activity	RT			4	4.4E-2	5.0E-1
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Cation-transporting P-type ATPase C-terminal	RT			4	6.5E-2	1.0E0
	<input type="checkbox"/> INTERPRO	ATPase_P-type_cation-transporter	RT			4	2.0E-1	1.0E0
	<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Cation-transporting P-type ATPase N-terminal	RT			4	2.2E-1	1.0E0

		Enrichment Score: 54.91	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	Cation ATPase_N	RT	RT	4	2.3E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium-transporting ATPase activity	RT	RT	3	2.4E-1	1.0E0
<input type="checkbox"/>	INTERPRO	ATPase_P-typ_cation-transporter_N	RT	RT	4	2.9E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation_of_cardiac_conduction	RT	RT	3	6.7E-1	1.0E0
<input type="checkbox"/>	INTERPRO	ATPase_P-typ_transduc_dom_A_sf	RT	RT	4	7.2E-1	1.0E0
<input type="checkbox"/>	INTERPRO	P_typ_ATPase	RT	RT	4	7.2E-1	1.0E0
<input type="checkbox"/>	INTERPRO	ATPase_P-typ_P_site	RT	RT	4	7.2E-1	1.0E0
<input type="checkbox"/>	INTERPRO	P_typ_ATPase_HD_dom	RT	RT	4	7.2E-1	1.0E0
<input type="checkbox"/>	INTERPRO	ATPase_P-typ_cyto_dom_N	RT	RT	4	7.2E-1	1.0E0
<input type="checkbox"/>	INTERPRO	ATPase_P-typ_TM_dom_sf	RT	RT	4	7.4E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	ACT_SITE:4-aspartylphosphate intermediate	RT	RT	4	7.6E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Mineral_absorption	RT	RT	7	8.0E-1	1.0E0
<input type="checkbox"/>	INTERPRO	HAD_sf	RT	RT	6	9.1E-1	1.0E0
<input type="checkbox"/>	INTERPRO	HAD-like_sf	RT	RT	6	9.2E-1	1.0E0
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Calcium_transport	RT	RT	7	9.8E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Salivary_secretion	RT	RT	7	9.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	sperm_flagellum	RT	RT	4	9.9E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	ion_transmembrane_transport	RT	RT	7	1.0E0	1.0E0
Annotation Cluster 254							
<input type="checkbox"/>	UP_SEQ_FEATURE	Enrichment Score: 0.31	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	DOMAIN:ZZ-type	RT	RT	3	3.6E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Znf_ZZ	RT	RT	3	4.8E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Znf_ZZ_sf	RT	RT	3	5.7E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Znf_ZZ	RT	RT	3	5.7E-1	1.0E0
Annotation Cluster 255							
<input type="checkbox"/>	SMART	Enrichment Score: 0.31	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	H15	RT	RT	3	3.7E-1	1.0E0
<input type="checkbox"/>	INTERPRO	DOMAIN:H15	RT	RT	3	4.0E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	Histone_H1/H5_H15	RT	RT	3	4.1E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleosome	RT	RT	8	9.9E-1	1.0E0
Annotation Cluster 256							
<input type="checkbox"/>	SMART	Enrichment Score: 0.3	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	IBN_N	RT	RT	3	4.8E-1	1.0E0
<input type="checkbox"/>	INTERPRO	DOMAIN:Importin N-terminal	RT	RT	3	5.0E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Importin-beta_N	RT	RT	3	5.1E-1	1.0E0
Annotation Cluster 257							
<input type="checkbox"/>	INTERPRO	Enrichment Score: 0.3	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	S100/CaBP7/8-like_CS	RT	RT	4	4.5E-1	1.0E0
<input type="checkbox"/>	INTERPRO	S_100	RT	RT	4	5.3E-1	1.0E0
<input type="checkbox"/>	INTERPRO	S100_Ca-bd_sub	RT	RT	4	5.3E-1	1.0E0
Annotation Cluster 258							
<input type="checkbox"/>	GOTERM_BP_DIRECT	Enrichment Score: 0.3	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	alanine_transport	RT	RT	3	1.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	DOMAIN:Amino acid transporter transmembrane	RT	RT	3	4.3E-1	1.0E0
<input type="checkbox"/>	INTERPRO	L-amino_acid_transmembrane_transporter_activity	RT	RT	4	5.0E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	AA_transpt_TM	RT	RT	3	5.1E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	amino_acid_transmembrane_transport	RT	RT	4	5.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	neutral_amino_acid_transport	RT	RT	3	6.7E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	amino_acid_transmembrane_transporter_activity	RT	RT	4	6.9E-1	1.0E0
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Amino-acid_transport	RT	RT	4	9.6E-1	1.0E0
Annotation Cluster 259							
<input type="checkbox"/>	KEGG_PATHWAY	Enrichment Score: 0.29	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	Dopaminergic_synapse	RT	RT	24	6.4E-2	2.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	Cholinergic_synapse	RT	RT	13	7.8E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Melanogenesis	RT	RT	11	8.3E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Alcoholism	RT	RT	19	9.2E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Circadian entrainment	RT	RT	9	9.3E-1	1.0E0
Annotation Cluster 260							
<input type="checkbox"/>	GOTERM_BP_DIRECT	Enrichment Score: 0.29	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	glutamine_transport	RT	RT	3	2.3E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	L-glutamine_transmembrane_transporter_activity	RT	RT	3	2.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	amino_acid_transmembrane_transporter_activity	RT	RT	4	6.9E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	amino_acid_transport	RT	RT	3	9.5E-1	1.0E0
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Symport	RT	RT	8	9.9E-1	1.0E0
Annotation Cluster 261							
<input type="checkbox"/>	INTERPRO	Enrichment Score: 0.28	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	Actin/actin-like_CS	RT	RT	4	3.1E-1	1.0E0
<input type="checkbox"/>	SMART	Actin_CS	RT	RT	3	5.4E-1	1.0E0
<input type="checkbox"/>	INTERPRO	ACTIN	RT	RT	4	6.4E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Actin	RT	RT	4	6.8E-1	1.0E0
Annotation Cluster 262							
<input type="checkbox"/>	GOTERM_CC_DIRECT	Enrichment Score: 0.27	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	cytoplasmic_dynein_complex	RT	RT	4	3.9E-1	9.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	dynein_intermediate_chain_binding	RT	RT	5	5.6E-1	1.0E0
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Dynein	RT	RT	4	7.1E-1	1.0E0
Annotation Cluster 263							
<input type="checkbox"/>	GOTERM_CC_DIRECT	Enrichment Score: 0.27	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	chromatin	RT	RT	129	1.9E-2	1.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	transcription_factor_activity_sequence-specific_DNA_binding	RT	RT	59	8.2E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	transcriptional_activator_activity_RNA_polymerase_II_transcription_regulatory_region_sequence-specific_binding	RT	RT	46	8.7E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation_of_transcription_from_RNA_polymerase_II_promoter	RT	RT	139	9.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	sequence-specific_double-stranded_DNA_binding	RT	RT	39	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA_polymerase_II_core_promoter_proximal_region_sequence-specific_DNA_binding	RT	RT	86	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA_polymerase_II_transcription_factor_activity_sequence-specific_DNA_binding	RT	RT	71	1.0E0	1.0E0
Annotation Cluster 264							
<input type="checkbox"/>	GOTERM_BP_DIRECT	Enrichment Score: 0.27	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	phosphatidylinositol_biosynthetic_process	RT	RT	7	3.0E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	phosphatidylinositol-3-phosphatase_activity	RT	RT	3	4.1E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	phosphatidylinositol_dephosphorylation	RT	RT	4	6.0E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Phosphatidylinositol_signaling_system	RT	RT	12	6.9E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Inositol_phosphate_metabolism	RT	RT	7	9.1E-1	1.0E0
Annotation Cluster 265							

		Enrichment Score: 54.91	G		Count	P_Value	Benjamini
<input type="checkbox"/> BIOCARTA		Transcription factor CREB and its extracellular signals	RT		7	4.4E-1	1.0E0
<input type="checkbox"/> BIOCARTA		Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation	RT		6	4.8E-1	1.0E0
<input type="checkbox"/> BIOCARTA		Regulation of BAD phosphorylation	RT		4	9.1E-1	1.0E0
Annotation Cluster 268							
<input type="checkbox"/> BIOCARTA		Enrichment Score: 0.23	G		Count	P_Value	Benjamini
<input type="checkbox"/> BIOCARTA		Phospholipase C-epsilon pathway	RT		4	4.3E-1	1.0E0
<input type="checkbox"/> BIOCARTA		Transcription factor CREB and its extracellular signals	RT		7	4.4E-1	1.0E0
<input type="checkbox"/> BIOCARTA		How Progesterone Initiates the Oocyte Maturation	RT		8	5.1E-1	1.0E0
<input type="checkbox"/> BIOCARTA		Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway	RT		3	7.1E-1	1.0E0
<input type="checkbox"/> BIOCARTA		Attenuation of GPCR Signaling	RT		3	7.6E-1	1.0E0
<input type="checkbox"/> BIOCARTA		ChREBP regulation by carbohydrates and cAMP	RT		4	8.1E-1	1.0E0
Annotation Cluster 269							
<input type="checkbox"/> GOTERM_MF_DIRECT		Enrichment Score: 0.23	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		1-phosphatidylinositol-3-kinase regulator activity	RT		3	5.2E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT		phosphatidylinositol phosphorylation	RT		6	6.3E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT		phosphatidylinositol 3-kinase complex	RT		3	6.5E-1	1.0E0
Annotation Cluster 270							
<input type="checkbox"/> GOTERM_BP_DIRECT		Enrichment Score: 0.22	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		integrin-mediated signaling pathway	RT		13	4.5E-1	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION		cell-matrix adhesion	RT		11	6.6E-1	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION		Integrin	RT		5	7.4E-1	1.0E0
Annotation Cluster 271							
<input type="checkbox"/> INTERPRO		Enrichment Score: 0.22	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO		F-box_dom	RT		8	4.9E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:F-box	RT		8	5.4E-1	1.0E0
<input type="checkbox"/> INTERPRO		F-box-like_dom_sf	RT		7	6.9E-1	1.0E0
<input type="checkbox"/> SMART		FBOX	RT		4	7.5E-1	1.0E0
Annotation Cluster 272							
<input type="checkbox"/> BIOCARTA		Enrichment Score: 0.21	G		Count	P_Value	Benjamini
<input type="checkbox"/> BIOCARTA		Neuropeptides VIP and PACAP inhibit the apoptosis of activated T cells	RT		7	4.0E-1	1.0E0
<input type="checkbox"/> BIOCARTA		Nitric Oxide Signaling Pathway	RT		5	6.5E-1	1.0E0
<input type="checkbox"/> BIOCARTA		Actions of Nitric Oxide in the Heart	RT		5	8.7E-1	1.0E0
Annotation Cluster 273							
<input type="checkbox"/> INTERPRO		Enrichment Score: 0.21	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO		FERM_CS	RT		5	2.3E-1	1.0E0
<input type="checkbox"/> INTERPRO		Ez/rad/moesin-like	RT		3	5.4E-1	1.0E0
<input type="checkbox"/> SMART		B41	RT		6	6.2E-1	1.0E0
<input type="checkbox"/> INTERPRO		FERM_central	RT		6	6.3E-1	1.0E0
<input type="checkbox"/> INTERPRO		Band_41_domain	RT		6	6.3E-1	1.0E0
<input type="checkbox"/> INTERPRO		FERM_2	RT		6	6.3E-1	1.0E0
<input type="checkbox"/> INTERPRO		FERM/acyl-CoA-bd_prot_sf	RT		6	6.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		DOMAIN:FERM	RT		6	6.6E-1	1.0E0
<input type="checkbox"/> SMART		FERM_C	RT		3	7.6E-1	1.0E0
<input type="checkbox"/> INTERPRO		FERM_PH-like_C	RT		3	7.6E-1	1.0E0
<input type="checkbox"/> INTERPRO		FERM_N	RT		3	7.8E-1	1.0E0
<input type="checkbox"/> INTERPRO		FERM_domain	RT		5	8.0E-1	1.0E0
Annotation Cluster 274							
<input type="checkbox"/> BIOCARTA		Enrichment Score: 0.21	G		Count	P_Value	Benjamini
<input type="checkbox"/> BIOCARTA		WNT Signaling Pathway	RT		7	4.0E-1	1.0E0
<input type="checkbox"/> BIOCARTA		Multi-step Regulation of Transcription by Pitx2	RT		4	6.3E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		embryonic digit morphogenesis	RT		4	9.2E-1	1.0E0
Annotation Cluster 275							
<input type="checkbox"/> BIOCARTA		Enrichment Score: 0.21	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE		Electron Transport Reaction in Mitochondria	RT		5	1.5E-1	7.4E-1
<input type="checkbox"/> UP_KW_LIGAND		BINDING:axial binding residue	RT		7	9.7E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT		Heme	RT		7	1.0E0	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT		heme binding	RT		8	1.0E0	1.0E0
Annotation Cluster 276							
<input type="checkbox"/> GOTERM_MF_DIRECT		Enrichment Score: 0.2	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION		endopeptidase inhibitor activity	RT		6	5.2E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT		Thiol_protease inhibitor	RT		4	5.3E-1	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION		cysteine-type endopeptidase inhibitor activity	RT		5	5.6E-1	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION		Protease inhibitor	RT		8	9.9E-1	1.0E0
Annotation Cluster 277							
<input type="checkbox"/> KEGG_PATHWAY		Enrichment Score: 0.2	G		Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY		Long-term depression	RT		10	3.4E-1	7.5E-1
<input type="checkbox"/> KEGG_PATHWAY		Gap_junction	RT		10	7.9E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY		Serotonergic synapse	RT		11	9.3E-1	1.0E0
Annotation Cluster 278							
<input type="checkbox"/> GOTERM_MF_DIRECT		Enrichment Score: 0.2	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		glutathione peroxidase activity	RT		5	2.2E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		cellular oxidant detoxification	RT		9	5.1E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT		glutathione transferase activity	RT		4	5.8E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY		Metabolism of xenobiotics by cytochrome P450	RT		4	1.0E0	1.0E0
<input type="checkbox"/> KEGG_PATHWAY		Chemical carcinogenesis - DNA adducts	RT		3	1.0E0	1.0E0
<input type="checkbox"/> KEGG_PATHWAY		Drug metabolism - cytochrome P450	RT		3	1.0E0	1.0E0
Annotation Cluster 279							
<input type="checkbox"/> GOTERM_BP_DIRECT		Enrichment Score: 0.2	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		regulation of G1/S transition of mitotic cell cycle	RT		8	3.0E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		regulation of nucleotide-excision repair	RT		4	5.2E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		regulation of G0 to G1 transition	RT		3	7.3E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT		SWI/SNF complex	RT		3	8.1E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		positive regulation of double-strand break repair	RT		4	8.1E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		regulation of mitotic metaphase/anaphase transition	RT		3	8.7E-1	1.0E0
Annotation Cluster 280							
<input type="checkbox"/> KEGG_PATHWAY		Enrichment Score: 0.19	G		Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY		DNA replication	RT		6	4.8E-1	9.2E-1
<input type="checkbox"/> KEGG_PATHWAY		Mismatch repair	RT				

		Enrichment Score:	G	Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY	Insulin secretion	54.91		7	9.7E-1	1.0E0
Annotation Cluster 283		0.18		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	negative regulation by host of viral release from host cell	negative regulation by host of viral release from host cell		4	2.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:B30.2/SPRY	DOMAIN:B30.2/SPRY		11	5.2E-1	1.0E0
<input type="checkbox"/> INTERPRO	B30.2/SPRY	B30.2/SPRY		11	5.6E-1	1.0E0
<input type="checkbox"/> SMART	SPRY	SPRY		10	5.7E-1	1.0E0
<input type="checkbox"/> INTERPRO	SPRY_dom	SPRY_dom		10	6.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	B30.2/SPRY_sf	B30.2/SPRY_sf		11	6.8E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:B box-type	DOMAIN:B box-type		6	7.6E-1	1.0E0
<input type="checkbox"/> INTERPRO	Butyrophylin SPRY	Butyrophylin SPRY		7	7.7E-1	1.0E0
<input type="checkbox"/> SMART	PRY	PRY		5	7.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	PRY	PRY		5	7.8E-1	1.0E0
<input type="checkbox"/> SMART	BBOX	BBOX		7	8.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:B box-type	ZN_FING:B box-type		5	8.6E-1	1.0E0
<input type="checkbox"/> INTERPRO	Znf_B-box	Znf_B-box		7	8.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	ConA-like_dom_sf	ConA-like_dom_sf		18	9.4E-1	1.0E0
Annotation Cluster 284		0.17		Count	P_Value	Benjamini
<input type="checkbox"/> BIOCARTA	Control of Gene Expression by Vitamin D Receptor	Control of Gene Expression by Vitamin D Receptor		7	4.0E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Multi-step Regulation of Transcription by Pitx2	Multi-step Regulation of Transcription by Pitx2		4	6.3E-1	1.0E0
<input type="checkbox"/> BIOCARTA	CARM1 and Regulation of the Estrogen Receptor	CARM1 and Regulation of the Estrogen Receptor		5	8.9E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Notch signalling_pathway	Notch signalling_pathway		6	9.0E-1	1.0E0
Annotation Cluster 285		0.16		Count	P_Value	Benjamini
<input type="checkbox"/> SMART	FCH	FCH		3	6.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	FCH_dom	FCH_dom		3	6.8E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:F-BAR	DOMAIN:F-BAR		3	7.1E-1	1.0E0
<input type="checkbox"/> INTERPRO	F_BAR	F_BAR		3	7.2E-1	1.0E0
Annotation Cluster 286		0.16		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:ANK 15	REPEAT:ANK 15		3	4.0E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:ANK 13	REPEAT:ANK 13		3	4.0E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:ANK 14	REPEAT:ANK 14		3	4.0E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:ANK 12	REPEAT:ANK 12		3	5.0E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:ANK 11	REPEAT:ANK 11		3	6.9E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:ANK 10	REPEAT:ANK 10		3	7.9E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:ANK 9	REPEAT:ANK 9		3	9.2E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:ANK 7	REPEAT:ANK 7		5	9.2E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:ANK 8	REPEAT:ANK 8		3	9.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:ANK 4	REPEAT:ANK 4		13	9.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:ANK 6	REPEAT:ANK 6		6	9.9E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:ANK 5	REPEAT:ANK 5		9	9.9E-1	1.0E0
Annotation Cluster 287		0.16		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT	C-X-C chemokine receptor activity	C-X-C chemokine receptor activity		3	2.0E-1	1.0E0
<input type="checkbox"/> INTERPRO	Chemokine_rcpt	Chemokine_rcpt		4	2.0E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Selective expression of chemokine receptors during T-cell polarization	Selective expression of chemokine receptors during T-cell polarization		8	3.0E-1	9.5E-1
<input type="checkbox"/> BBID	14.chemokine_receptor-ligand	14.chemokine_receptor-ligand		4	3.9E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	C-C chemokine receptor activity	C-C chemokine receptor activity		4	4.4E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	C-C chemokine binding	C-C chemokine binding		4	4.4E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	calcium-mediated signaling	calcium-mediated signaling		12	4.8E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	cell chemotaxis	cell chemotaxis		7	7.7E-1	1.0E0
<input type="checkbox"/> BBID	15.T-cell_polarization-chemokine_receptors	15.T-cell_polarization-chemokine_receptors		4	8.4E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation of cytosolic calcium ion concentration	positive regulation of cytosolic calcium ion concentration		12	8.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	GPCR_Rhodopsn	GPCR_Rhodopsn		9	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	GPCR_Rhodopsn_7TM	GPCR_Rhodopsn_7TM		9	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=1	TRANSMEM:Helical; Name=1		28	1.0E0	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	G-protein_coupled_receptor	G-protein_coupled_receptor		10	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=2	TRANSMEM:Helical; Name=2		28	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=3	TRANSMEM:Helical; Name=3		28	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=4	TRANSMEM:Helical; Name=4		28	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=5	TRANSMEM:Helical; Name=5		24	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=6	TRANSMEM:Helical; Name=6		23	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=7	TRANSMEM:Helical; Name=7		19	1.0E0	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	G-protein coupled receptor activity	G-protein coupled receptor activity		10	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:G-protein coupled receptors family 1 profile	DOMAIN:G-protein coupled receptors family 1 profile		7	1.0E0	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Transducer	Transducer		16	1.0E0	1.0E0
Annotation Cluster 288		0.16		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Pkinase_C	Pkinase_C		5	4.6E-1	1.0E0
<input type="checkbox"/> SMART	S_TK_X	S_TK_X		5	7.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:AGC-kinase C-terminal	DOMAIN:AGC-kinase C-terminal		5	8.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	AGC-kinase_C	AGC-kinase_C		5	8.5E-1	1.0E0
Annotation Cluster 289		0.16		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	RGS_subdom1/3	RGS_subdom1/3		3	5.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	RGS_sf	RGS_sf		5	5.4E-1	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Signal transduction inhibitor	Signal transduction inhibitor		6	6.3E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	G-protein_alpha-subunit_binding	G-protein_alpha-subunit_binding		4	6.3E-1	1.0E0
<input type="checkbox"/> INTERPRO	RGS_subdomain_2	RGS_subdomain_2		4	7.4E-1	1.0E0
<input type="checkbox"/> SMART	RGS	RGS		3	8.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:RGS	DOMAIN:RGS		3	8.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	RGS	RGS		3	8.8E-1	1.0E0
Annotation Cluster 290		0.15		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	PH-like_dom_sf	PH-like_dom_sf		47	4.3E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:PH	DOMAIN:PH		26	7.1E-1	1.0E0
<input type="checkbox"/> INTERPRO	PH_domain	PH_domain		23	8.8E-1	1.0E0
<input type="checkbox"/> SMART	PH	PH		22	8.9E-1	1.0E0
Annotation Cluster 291		0.15		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	OxRdtase_FAD/NAD-bd	OxRdtase_FAD/NAD-bd		3	4.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:FAD-binding FR-type	DOMAIN:FAD-binding FR-type		3	6.2E-1	1.0E0
<input type="checkbox"/> INTERPRO	FAD-bd_FR_type	FAD-bd_FR_type		3	6.3E-1	1.0E0
<input type="checkbox"/> INTERPRO	FNR_nucleotide-bd	FNR_nucleotide-bd		3	6.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	Riboflavin_synthase-like_b-brl	Riboflavin_synthase-like_b-brl		3	6.5E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	flavin_adenine_dinucleotide_binding	flavin_adenine_dinucleotide_binding		5	9.4E-1	1.0E0
<input type="checkbox"/> UP_KW_LIGAND	FAD	FAD		8	9.6E-1	1.0E0
<input type="checkbox"/> UP_KW_LIGAND	Flavoprotein	Flavoprotein		8	9.8E-1	1.0E0

Annotation Cluster 1	Enrichment Score: 54.91	G	██████████	Count	P_Value	Benjamini
Annotation Cluster 292	Enrichment Score: 0.14	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	heterotrimeric G-protein complex	RT	██████████	6	2.7E-1	7.8E-1
<input type="checkbox"/> KEGG_PATHWAY	Renin secretion	RT	██████████	9	6.5E-1	1.0EO
<input type="checkbox"/> KEGG_PATHWAY	Serotonergic synapse	RT	██████████	11	9.3E-1	1.0EO
<input type="checkbox"/> KEGG_PATHWAY	Glutamatergic synapse	RT	██████████	11	9.3E-1	1.0EO
<input type="checkbox"/> KEGG_PATHWAY	Circadian entrainment	RT	██████████	9	9.3E-1	1.0EO
<input type="checkbox"/> KEGG_PATHWAY	Morphine addiction	RT	██████████	7	9.8E-1	1.0EO
Annotation Cluster 293	Enrichment Score: 0.13	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> BIOCARTA	Erk1/Erk2 MapK Signaling_pathway	RT	██████████	7	5.5E-1	1.0EO
<input type="checkbox"/> BIOCARTA	CCR3 signaling in Eosinophils	RT	██████████	5	6.9E-1	1.0EO
<input type="checkbox"/> BIOCARTA	Role of ?-arrestins in the activation and targeting of MAP kinases	RT	██████████	3	8.5E-1	1.0EO
<input type="checkbox"/> BIOCARTA	Roles of ?-arrestin-dependent Recruitment of Src Kinases in GPCR Signaling	RT	██████████	3	9.3E-1	1.0EO
Annotation Cluster 294	Enrichment Score: 0.13	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	BRCT_dom	RT	██████████	3	7.2E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:BRCT	RT	██████████	3	7.3E-1	1.0EO
<input type="checkbox"/> INTERPRO	BRCT_dom_sf	RT	██████████	3	7.8E-1	1.0EO
Annotation Cluster 295	Enrichment Score: 0.12	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Phospholipid biosynthesis	RT	██████████	7	4.4E-1	1.0EO
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Phospholipid metabolism	RT	██████████	7	7.9E-1	1.0EO
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Lipid biosynthesis	RT	██████████	17	8.5E-1	1.0EO
<input type="checkbox"/> GOTERM_BP_DIRECT	phospholipid biosynthetic_process	RT	██████████	3	8.7E-1	1.0EO
<input type="checkbox"/> KEGG_PATHWAY	Glycerophospholipid metabolism	RT	██████████	9	9.4E-1	1.0EO
Annotation Cluster 296	Enrichment Score: 0.12	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:ETS	RT	██████████	3	5.9E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE	DNA_BIND:ETS	RT	██████████	3	8.0E-1	1.0EO
<input type="checkbox"/> INTERPRO	ETS_fam	RT	██████████	3	8.1E-1	1.0EO
<input type="checkbox"/> SMART	ETS	RT	██████████	3	8.2E-1	1.0EO
<input type="checkbox"/> INTERPRO	Ets_dom	RT	██████████	3	8.2E-1	1.0EO
Annotation Cluster 297	Enrichment Score: 0.12	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:PSI	RT	██████████	3	6.7E-1	1.0EO
<input type="checkbox"/> SMART	PSI	RT	██████████	4	8.2E-1	1.0EO
<input type="checkbox"/> INTERPRO	PSI	RT	██████████	4	8.2E-1	1.0EO
Annotation Cluster 298	Enrichment Score: 0.11	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:HECT	RT	██████████	3	7.7E-1	1.0EO
<input type="checkbox"/> SMART	HECTc	RT	██████████	3	7.8E-1	1.0EO
<input type="checkbox"/> INTERPRO	HECT_dom	RT	██████████	3	7.8E-1	1.0EO
<input type="checkbox"/> INTERPRO	Hect_E3_ubiquitin_ligase	RT	██████████	3	7.8E-1	1.0EO
Annotation Cluster 299	Enrichment Score: 0.1	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT	non-membrane spanning_protein tyrosine kinase activity	RT	██████████	7	3.6E-1	1.0EO
<input type="checkbox"/> GOTERM_CC_DIRECT	extrinsic component of cytoplasmic side of plasma membrane	RT	██████████	4	7.2E-1	1.0EO
<input type="checkbox"/> INTERPRO	Ser-Thr/Tyr kinase_cat_dom	RT	██████████	14	7.4E-1	1.0EO
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Tyrosine-protein kinase	RT	██████████	10	8.8E-1	1.0EO
<input type="checkbox"/> SMART	TyrKc	RT	██████████	7	8.9E-1	1.0EO
<input type="checkbox"/> INTERPRO	Tyr_kinase_cat_dom	RT	██████████	7	9.0E-1	1.0EO
<input type="checkbox"/> GOTERM_MF_DIRECT	protein tyrosine kinase activity	RT	██████████	9	9.2E-1	1.0EO
<input type="checkbox"/> GOTERM_BP_DIRECT	peptidyl-tyrosine phosphorylation	RT	██████████	3	9.7E-1	1.0EO
<input type="checkbox"/> INTERPRO	Tyr_kinase_AS	RT	██████████	6	9.7E-1	1.0EO
Annotation Cluster 300	Enrichment Score: 0.1	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> UP_KW_DOMAIN	LIM_domain	RT	██████████	7	6.5E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:LIM zinc-binding	RT	██████████	7	7.0E-1	1.0EO
<input type="checkbox"/> SMART	LIM	RT	██████████	7	7.4E-1	1.0EO
<input type="checkbox"/> INTERPRO	Znf_LIM	RT	██████████	7	7.7E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:LIM zinc-binding 1	RT	██████████	3	9.6E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:LIM zinc-binding 2	RT	██████████	3	9.6E-1	1.0EO
Annotation Cluster 301	Enrichment Score: 0.1	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT	RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding	RT	██████████	7	5.1E-1	1.0EO
<input type="checkbox"/> INTERPRO	Znf_NHR/GATA	RT	██████████	6	6.7E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Nuclear receptor	RT	██████████	4	8.3E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:NR C4-type	RT	██████████	4	8.4E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE	DNA_BIND:Nuclear receptor	RT	██████████	4	8.4E-1	1.0EO
<input type="checkbox"/> SMART	ZnF_C4	RT	██████████	4	8.4E-1	1.0EO
<input type="checkbox"/> INTERPRO	Znf_hrmn_rcpt	RT	██████████	4	8.4E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:NR LBD	RT	██████████	4	8.6E-1	1.0EO
<input type="checkbox"/> SMART	HOI	RT	██████████	4	8.6E-1	1.0EO
<input type="checkbox"/> INTERPRO	Nucl_hrmn_rcpt_lig-bd	RT	██████████	4	8.6E-1	1.0EO
<input type="checkbox"/> INTERPRO	Nuclear_hrmn_rcpt	RT	██████████	4	8.6E-1	1.0EO
<input type="checkbox"/> INTERPRO	NHR-like_dom_sf	RT	██████████	4	8.6E-1	1.0EO
Annotation Cluster 302	Enrichment Score: 0.1	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:GST C-terminal	RT	██████████	4	7.1E-1	1.0EO
<input type="checkbox"/> INTERPRO	Glutathione-S-Trfase_C_sf	RT	██████████	4	8.0E-1	1.0EO
<input type="checkbox"/> INTERPRO	Glutathione_S-Trfase_N	RT	██████████	3	8.1E-1	1.0EO
<input type="checkbox"/> INTERPRO	Glutathione_S-Trfase	RT	██████████	3	8.2E-1	1.0EO
<input type="checkbox"/> INTERPRO	Glutathione-S-Trfase_C-like	RT	██████████	3	8.7E-1	1.0EO
Annotation Cluster 303	Enrichment Score: 0.09	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> SMART	FHA	RT	██████████	3	7.2E-1	1.0EO
<input type="checkbox"/> INTERPRO	SMAD_FHA_dom_sf	RT	██████████	5	8.2E-1	1.0EO
<input type="checkbox"/> INTERPRO	FHA_dom	RT	██████████	3	8.7E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:FHA	RT	██████████	3	8.8E-1	1.0EO
Annotation Cluster 304	Enrichment Score: 0.09	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Rho_GTPase_activation_prot	RT	██████████	9	7.5E-1	1.0EO
<input type="checkbox"/> SMART	RhoGAP	RT	██████████	6	8.4E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Rho-GAP	RT	██████████	6	8.5E-1	1.0EO
<input type="checkbox"/> INTERPRO	RhoGAP_dom	RT	██████████	6	8.5E-1	1.0EO
Annotation Cluster 305	Enrichment Score: 0.07	G	██████████	Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	C2_domain_sf	RT	██████████	16	7.7E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:C2	RT	██████████	11	8.5E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:C2_1	RT	██████████	5	8.6E-1	1.0EO
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:C2_2	RT	██████████	5	8.6E-1	1.0EO
<input type="checkbox"/> INTERPRO	C2_dom	RT	██████████	12	8.7E-1	1.0EO
<input type="checkbox"/> SMART	C2	RT	██████████	10	8.8E-1	1.0EO
Annotation Cluster 306	Enrichment Score: 0.07	G	██████████	Count	P_Value	Benjamini

Annotation Cluster	Enrichment Score	Category	Term	RT	Count	P_Value	Benjamini
Annotation Cluster 1	54.91		Pyridoxal_phosphate	G	6	7.8E-1	1.0E0
			PyrdxIP-dep_Trfase_major	RT	4	8.1E-1	1.0E0
			PyrdxIP-dep_Trfase	RT	4	8.3E-1	1.0E0
			PyrdxIP-dep_Trfase_small	RT	3	8.9E-1	1.0E0
			pyridoxal_phosphate_binding	RT	4	9.5E-1	1.0E0
Annotation Cluster 307	0.06			G	Count	P_Value	Benjamini
			Integrin	RT	5	7.4E-1	1.0E0
			Integrin_dom_sf	RT	3	7.4E-1	1.0E0
			integrin_complex	RT	3	7.7E-1	1.0E0
			cell_adhesion-mediated_by_integrin	RT	3	9.2E-1	1.0E0
			VWA	RT	5	9.4E-1	1.0E0
			vWFA_dom_sf	RT	7	9.4E-1	1.0E0
			VWF_A	RT	5	9.6E-1	1.0E0
			DOMAIN:VWFA	RT	5	9.7E-1	1.0E0
Annotation Cluster 308	0.06			G	Count	P_Value	Benjamini
			hydrolase_activity,_hydrolyzing_O-glycosyl_compounds	RT	3	7.4E-1	1.0E0
			Glycosidase	RT	7	9.2E-1	1.0E0
			Glycoside_hydrolase_SF	RT	3	9.8E-1	1.0E0
Annotation Cluster 309	0.05			G	Count	P_Value	Benjamini
			myosin_II_complex	RT	3	7.2E-1	1.0E0
			Myosin	RT	3	9.8E-1	1.0E0
			Motor_protein	RT	9	9.8E-1	1.0E0
Annotation Cluster 310	0.05			G	Count	P_Value	Benjamini
			DOMAIN:SAM	RT	8	8.4E-1	1.0E0
			SAM	RT	7	8.6E-1	1.0E0
			SAM	RT	7	9.2E-1	1.0E0
			SAM/pointed_sf	RT	8	9.7E-1	1.0E0
Annotation Cluster 311	0.05			G	Count	P_Value	Benjamini
			kinesin_complex	RT	6	5.3E-1	1.0E0
			Kinesin-like_fam	RT	3	9.0E-1	1.0E0
			Kinesin_motor_CS	RT	3	9.2E-1	1.0E0
			DOMAIN:Kinesin motor	RT	3	9.4E-1	1.0E0
			KISc	RT	3	9.4E-1	1.0E0
			Kinesin_motor_dom	RT	3	9.4E-1	1.0E0
			microtubule-based_movement	RT	5	9.7E-1	1.0E0
			Motor_protein	RT	9	9.8E-1	1.0E0
			microtubule_motor_activity	RT	3	9.9E-1	1.0E0
			Kinesin_motor_dom_sf	RT	4	9.9E-1	1.0E0
Annotation Cluster 312	0.04			G	Count	P_Value	Benjamini
			serine-type_peptidase_activity	RT	6	7.7E-1	1.0E0
			ACT_SITE:Charge relay system	RT	16	9.2E-1	1.0E0
			serine-type_endopeptidase_activity	RT	14	9.6E-1	1.0E0
			Serine_protease	RT	10	9.8E-1	1.0E0
Annotation Cluster 313	0.04			G	Count	P_Value	Benjamini
			DOMAIN:PID	RT	3	8.7E-1	1.0E0
			PTB	RT	3	9.2E-1	1.0E0
			PTB/PI_dom	RT	3	9.3E-1	1.0E0
Annotation Cluster 314	0.04			G	Count	P_Value	Benjamini
			DOMAIN:SOCS_box	RT	3	9.0E-1	1.0E0
			SOCS_box	RT	3	9.1E-1	1.0E0
			SOCS_box	RT	3	9.1E-1	1.0E0
Annotation Cluster 315	0.04			G	Count	P_Value	Benjamini
			PDZ_6	RT	3	6.5E-1	1.0E0
			PDZ_sf	RT	8	1.0E0	1.0E0
			DOMAIN:PDZ	RT	7	1.0E0	1.0E0
			PDZ	RT	7	1.0E0	1.0E0
			PDZ	RT	7	1.0E0	1.0E0
Annotation Cluster 316	0.03			G	Count	P_Value	Benjamini
			REPEAT:ANK 3	RT	19	8.2E-1	1.0E0
			REPEAT:ANK	RT	16	8.8E-1	1.0E0
			ANK_repeat	RT	20	8.9E-1	1.0E0
			REPEAT:ANK 1	RT	20	9.3E-1	1.0E0
			REPEAT:ANK 2	RT	20	9.3E-1	1.0E0
			Ankyrin_rpt	RT	20	9.5E-1	1.0E0
			ANK	RT	19	9.6E-1	1.0E0
			REPEAT:ANK 4	RT	13	9.6E-1	1.0E0
			Ankyrin_rpt-contain_sf	RT	20	9.6E-1	1.0E0
			REPEAT:ANK 5	RT	9	9.9E-1	1.0E0
Annotation Cluster 317	0.03			G	Count	P_Value	Benjamini
			DNA-directed_RNA_polymerase	RT	3	9.2E-1	1.0E0
			DNA-directed_RNA_polymerase	RT	3	9.2E-1	1.0E0
			RNA_polymerase	RT	3	9.4E-1	1.0E0
Annotation Cluster 318	0.03			G	Count	P_Value	Benjamini
			RhoGEF	RT	5	9.2E-1	1.0E0
			DOMAIN:DH	RT	5	9.3E-1	1.0E0
			DH-domain	RT	5	9.3E-1	1.0E0
			DBL_dom_sf	RT	5	9.4E-1	1.0E0
Annotation Cluster 319	0.03			G	Count	P_Value	Benjamini
			LIPID:GPI-anchor amidated serine	RT	5	8.4E-1	1.0E0
			side_of_membrane	RT	7	9.8E-1	1.0E0
			GPI-anchor	RT	7	1.0E0	1.0E0
Annotation Cluster 320	0.02			G	Count	P_Value	Benjamini
			Gastric_acid_secretion	RT	8	8.6E-1	1.0E0
			Salivary_secretion	RT	7	9.8E-1	1.0E0
			Bile_secretion	RT	3	1.0E0	1.0E0
Annotation Cluster 321	0.02			G	Count	P_Value	Benjamini
			Leu-rich_rpt_4	RT	4	4.0E-1	1.0E0
			LRR_SD22	RT	4	9.1E-1	1.0E0
			REPEAT:LRR 15	RT	3	9.5E-1	1.0E0
			REPEAT:LRR 14	RT	3	9.5E-1	1.0E0
			LRR_BAC	RT	3	9.8E-1	1.0E0
			REPEAT:LRR 13	RT	3	9.8E-1	1.0E0
			REPEAT:LRR 11	RT	4	1.0E0	1.0E0
			REPEAT:LRR 12	RT	3	1.0E0	1.0E0

		Enrichment Score:	G	RT	Count	P_Value	Benjamini
Annotation Cluster 1		54.91			14	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:LRR 4				4	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:LRR 10				14	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:LRR 3				14	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:LRR 2				14	1.0E0	1.0E0
<input type="checkbox"/> UP_KW_DOMAIN	Leucine-rich repeat				14	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:LRR 1				14	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	Leu-rich rpt typical-subtyp				7	1.0E0	1.0E0
<input type="checkbox"/> SMART	LRR_TYP				7	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:LRR 6				9	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:LRR 7				7	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:LRR 5				10	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:LRR 9				4	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	LRR_dom_sf				14	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	Leu-rich rpt				9	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:LRR 8				4	1.0E0	1.0E0
Annotation Cluster 322	Enrichment Score: 0.02				Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT	E-box binding				6	7.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:BHLH				4	9.8E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:bHLH				4	1.0E0	1.0E0
<input type="checkbox"/> SMART	HLH				4	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	HLH_DNA-bd_sf				4	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	bHLH_dom				4	1.0E0	1.0E0
Annotation Cluster 323	Enrichment Score: 0.02				Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	ABC_transporter-like_CS				3	9.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:ABC transporter				3	9.6E-1	1.0E0
<input type="checkbox"/> INTERPRO	ABC_transporter-like_ATP-bd				3	9.7E-1	1.0E0
Annotation Cluster 324	Enrichment Score: 0.02				Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:Solcar				3	9.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:Solcar 3				3	9.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:Solcar 1				3	9.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:Solcar 2				3	9.7E-1	1.0E0
<input type="checkbox"/> INTERPRO	Mt_carrier_dom_sf				3	9.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	Mitochondrial_sb/sol_carrier				3	9.8E-1	1.0E0
Annotation Cluster 325	Enrichment Score: 0.01				Count	P_Value	Benjamini
<input type="checkbox"/> SMART	BACK				4	9.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	BTB-kelch_protein				3	9.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	BACK				4	9.5E-1	1.0E0
<input type="checkbox"/> UP_KW_DOMAIN	Kelch_repeat				4	9.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:Kelch 5				4	9.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:BACK				3	9.6E-1	1.0E0
<input type="checkbox"/> INTERPRO	Kelch_1				4	9.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:Kelch 6				3	9.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:Kelch 4				4	9.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:Kelch 1				4	9.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:Kelch 2				4	9.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	REPEAT:Kelch 3				4	9.7E-1	1.0E0
<input type="checkbox"/> SMART	Kelch				3	9.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	Kelch-typ_b-propeller				4	9.8E-1	1.0E0
<input type="checkbox"/> PIR_SUPERFAMILY	Kelch-like_protein_gigaxonin				3	9.9E-1	1.0E0
Annotation Cluster 326	Enrichment Score: 0.01				Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Major facilitator superfamily (MFS) profile				5	9.0E-1	1.0E0
<input type="checkbox"/> INTERPRO	MFS				4	9.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	MFS_dom				5	9.9E-1	1.0E0
<input type="checkbox"/> INTERPRO	MFS_trans_sf				7	1.0E0	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	transmembrane transporter activity				6	1.0E0	1.0E0
Annotation Cluster 327	Enrichment Score: 0.01				Count	P_Value	Benjamini
<input type="checkbox"/> SMART	BACK				4	9.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	BACK				4	9.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:BTB				10	9.9E-1	1.0E0
<input type="checkbox"/> SMART	BTB				10	9.9E-1	1.0E0
<input type="checkbox"/> INTERPRO	SKP1/BTB/POZ_sf				11	9.9E-1	1.0E0
<input type="checkbox"/> INTERPRO	BTB/POZ_dom				10	9.9E-1	1.0E0
Annotation Cluster 328	Enrichment Score: 0.01				Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT	calcium_channel_activity				5	9.6E-1	1.0E0
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Calcium_transport				7	9.8E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	calcium ion transmembrane transport				7	9.9E-1	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Calcium_channel				3	1.0E0	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Ion_channel				6	1.0E0	1.0E0
Annotation Cluster 329	Enrichment Score: 0.01				Count	P_Value	Benjamini
<input type="checkbox"/> SMART	TBC				3	9.8E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Rab-GAP TBC				3	9.9E-1	1.0E0
<input type="checkbox"/> INTERPRO	Rab-GAP-TBC_dom				3	9.9E-1	1.0E0
<input type="checkbox"/> INTERPRO	Rab-GAP_TBC_sf				3	9.9E-1	1.0E0
Annotation Cluster 330	Enrichment Score: 0.01				Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_DIRECT	cilium				18	9.5E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	cilium_assembly				14	9.9E-1	1.0E0
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Cilium biogenesis/degradation				13	1.0E0	1.0E0
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Cilium				14	1.0E0	1.0E0
Annotation Cluster 331	Enrichment Score: 0.01				Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	PROPEP:Activation peptide				6	8.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	TRYPSIN_SER				3	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	TRYPSIN_HIS				3	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	Peptidase_S1_PA				4	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	Peptidase_S1A				3	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:Peptidase S1				3	1.0E0	1.0E0
<input type="checkbox"/> SMART	Tryp_SPc				3	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	Trypsin_dom				3	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	Peptidase_S1_PA_chymotrypsin				3	1.0E0	1.0E0
Annotation Cluster 332	Enrichment Score: 0				Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=9				5	9.9E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=10				4	9.9E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical; Name=8				5	9.9E-1	1.0E0
Annotation Cluster 333	Enrichment Score: 0				Count	P_Value	Benjamini
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Protease_inhibitor				8	9.9E-1	1.0E0

		Enrichment Score:	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Serine_protease_inhibitor	54.91			3	1.0E0	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	serine-type_endopeptidase_inhibitor_activity				3	1.0E0	1.0E0
Annotation Cluster 334	Enrichment Score: 0				Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	sodium_ion_transport				3	9.9E-1	1.0E0
<input type="checkbox"/> UP_KW_LIGAND	Sodium				7	1.0E0	1.0E0
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Sodium_transport				5	1.0E0	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Protein_digestion_and_absorption				3	1.0E0	1.0E0
Annotation Cluster 335	Enrichment Score: 0				Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY	Dilated_cardiomyopathy				6	1.0E0	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Hypertrophic_cardiomyopathy				5	1.0E0	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Arrhythmogenic_right_ventricular_cardiomyopathy				4	1.0E0	1.0E0
Annotation Cluster 336	Enrichment Score: 0				Count	P_Value	Benjamini
<input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	Differentiation				68	1.0E0	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Developmental_protein				53	1.0E0	1.0E0
<input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	Developmental_protein				53	1.0E0	1.0E0
Annotation Cluster 337	Enrichment Score: 0				Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:C2H2-type				29	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 1				23	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	Znf_C2H2_type				39	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 6				17	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 2				23	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 3				24	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 5				19	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	Znf_C2H2_sf				33	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 4				20	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 7				13	1.0E0	1.0E0
<input type="checkbox"/> SMART	ZnF_C2H2				30	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 12				3	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 9				8	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 8				9	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 10				5	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	ZN_FING:C2H2-type 11				3	1.0E0	1.0E0
Annotation Cluster 338	Enrichment Score: 0				Count	P_Value	Benjamini
<input type="checkbox"/> UP_KW_DOMAIN	Transmembrane_helix				450	1.0E0	1.0E0
<input type="checkbox"/> UP_KW_DOMAIN	Transmembrane				453	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TRANSMEM:Helical				425	1.0E0	1.0E0
<input type="checkbox"/> UP_KW_CELLULAR_COMPONENT	Membrane				750	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TOPO_DOM:Cytoplasmic				274	1.0E0	1.0E0
Annotation Cluster 339	Enrichment Score: 0				Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:EGF-like				5	1.0E0	1.0E0
<input type="checkbox"/> UP_KW_DOMAIN	EGF-like_domain				5	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	EGF-like_dom				3	1.0E0	1.0E0
Annotation Cluster 340	Enrichment Score: 0				Count	P_Value	Benjamini
<input type="checkbox"/> UP_KW_DOMAIN	Homeobox				5	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	Homeobox_dom				6	1.0E0	1.0E0
<input type="checkbox"/> SMART	HOX				5	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DNA_BIND:Homeobox				4	1.0E0	1.0E0
Annotation Cluster 341	Enrichment Score: 0				Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	TOPO_DOM:Cytoplasmic				274	1.0E0	1.0E0
<input type="checkbox"/> UP_KW_DOMAIN	Signal				268	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	CARBOHYD:N-linked (GlcNAc...) asparagine				217	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	TOPO_DOM:Extracellular				148	1.0E0	1.0E0
<input type="checkbox"/> UP_KW_PTM	Glycoprotein				254	1.0E0	1.0E0
<input type="checkbox"/> UP_KW_PTM	Disulfide_bond				198	1.0E0	1.0E0
Annotation Cluster 342	Enrichment Score: -0				Count	P_Value	Benjamini
<input type="checkbox"/> SMART	KRAB				3	1.0E0	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DOMAIN:KRAB				3	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	KRAB_dom_sf				3	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	KRAB				3	1.0E0	1.0E0

2686 terms were not clustered.

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