

Functional Annotation Clustering

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Current Gene List: List_3

Current Background: Homo sapiens

790 DAVID IDs
 Options Classification Stringency Medium

132 Cluster(s)
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Annotation Cluster 1		Enrichment Score: 4.36	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	Innate immunity	RT	RT	29	8.8E-7	7.6E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	defense response to virus	RT	RT	22	1.2E-5	7.8E-3
<input type="checkbox"/>	UP_KEYWORDS	Immunity	RT	RT	40	2.1E-5	1.0E-3
<input type="checkbox"/>	UP_KEYWORDS	Antiviral defense	RT	RT	15	1.4E-4	5.3E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	innate immune response	RT	RT	32	5.2E-3	5.6E-1
Annotation Cluster 2		Enrichment Score: 4.09	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_DIRECT	cell-cell adherens junction	RT	RT	34	1.9E-6	2.0E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	cadherin binding involved in cell-cell adhesion	RT	RT	29	6.3E-5	2.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell-cell adhesion	RT	RT	23	4.5E-3	5.0E-1
Annotation Cluster 3		Enrichment Score: 2.87	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	Death-like domain	RT	RT	14	1.1E-4	1.5E-1
<input type="checkbox"/>	INTERPRO	Caspase Recruitment	RT	RT	7	9.4E-4	5.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CARD	RT	RT	5	2.5E-2	1.0E0
Annotation Cluster 4		Enrichment Score: 2.23	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	phospholipase inhibitor activity	RT	RT	5	9.0E-4	2.0E-1
<input type="checkbox"/>	UP_KEYWORDS	Annexin	RT	RT	5	1.5E-3	3.3E-2
<input type="checkbox"/>	INTERPRO	Annexin	RT	RT	5	2.0E-3	5.4E-1
<input type="checkbox"/>	INTERPRO	Annexin repeat, conserved site	RT	RT	5	2.0E-3	5.4E-1
<input type="checkbox"/>	INTERPRO	Annexin repeat	RT	RT	5	2.0E-3	5.4E-1
<input type="checkbox"/>	UP_KEYWORDS	Calcium/phospholipid-binding	RT	RT	5	2.0E-3	4.1E-2
<input type="checkbox"/>	SMART	ANX	RT	RT	5	2.6E-3	8.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Annexin 1	RT	RT	4	1.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Annexin 2	RT	RT	4	1.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Annexin 3	RT	RT	4	1.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Annexin 4	RT	RT	4	1.9E-2	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium-dependent phospholipid binding	RT	RT	5	2.4E-1	1.0E0
Annotation Cluster 5		Enrichment Score: 2.06	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CN hydrolase	RT	RT	4	2.9E-3	1.0E0
<input type="checkbox"/>	INTERPRO	Carbon-nitrogen hydrolase	RT	RT	4	3.2E-3	6.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	nitrogen compound metabolic process	RT	RT	4	2.2E-2	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	RT	RT	4	3.0E-2	1.0E0
Annotation Cluster 6		Enrichment Score: 1.98	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	Calmodulin-binding	RT	RT	15	2.1E-3	4.1E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	calmodulin binding	RT	RT	17	8.1E-3	5.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Calmodulin-binding	RT	RT	6	6.7E-2	1.0E0
Annotation Cluster 7		Enrichment Score: 1.82	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of activated T cell proliferation	RT	RT	6	5.9E-3	5.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	tumor necrosis factor receptor superfamily binding	RT	RT	3	1.7E-2	7.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	tumor necrosis factor receptor binding	RT	RT	5	3.5E-2	1.0E0
Annotation Cluster 8		Enrichment Score: 1.78	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	Nucleotide-binding	RT	RT	98	2.6E-4	8.5E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Proton acceptor	RT	RT	46	3.0E-4	3.8E-1
<input type="checkbox"/>	UP_KEYWORDS	ATP-binding	RT	RT	77	9.7E-4	2.8E-2
<input type="checkbox"/>	UP_KEYWORDS	Kinase	RT	RT	46	1.3E-3	2.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:ATP	RT	RT	36	4.0E-3	1.0E0
<input type="checkbox"/>	INTERPRO	Protein kinase, ATP binding site	RT	RT	26	1.3E-2	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	ATP binding	RT	RT	82	2.0E-2	8.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase	RT	RT	29	2.2E-2	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Transferase	RT	RT	82	2.4E-2	2.5E-1
<input type="checkbox"/>	INTERPRO	Protein kinase, catalytic domain	RT	RT	30	2.6E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT	RT	52	2.7E-2	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein kinase activity	RT	RT	24	3.9E-2	1.0E0
<input type="checkbox"/>	INTERPRO	Protein kinase-like domain	RT	RT	30	6.5E-2	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein phosphorylation	RT	RT	28	7.5E-2	1.0E0
<input type="checkbox"/>	INTERPRO	Serine/threonine-protein kinase, active site	RT	RT	19	8.7E-2	1.0E0
<input type="checkbox"/>	SMART	S_TKc	RT	RT	21	1.7E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Serine/threonine-protein kinase	RT	RT	20	1.7E-1	8.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein serine/threonine kinase activity	RT	RT	17	5.6E-1	1.0E0
Annotation Cluster 9		Enrichment Score: 1.73	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	Flavoprotein	RT	RT	13	2.4E-3	4.6E-2
<input type="checkbox"/>	UP_KEYWORDS	FAD	RT	RT	12	3.2E-3	5.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:FAD	RT	RT	8	1.0E-2	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	oxidoreductase activity	RT	RT	14	9.4E-2	1.0E0

Annotation Cluster 1	Enrichment Score: 4.36	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT	flavin adenine dinucleotide binding	RT		5	3.0E-1	1.0E0
Annotation Cluster 10	Enrichment Score: 1.54	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_KEYWORDS	Oxidoreductase	RT		35	9.5E-3	1.4E-1
<input type="checkbox"/> UP_KEYWORDS	NADP	RT		14	2.6E-2	2.6E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	oxidoreductase activity	RT		14	9.4E-2	1.0E0
Annotation Cluster 11	Enrichment Score: 1.36	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_KEYWORDS	Mitochondrion	RT		59	1.1E-2	1.5E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	mitochondrial matrix	RT		22	3.3E-2	4.9E-1
<input type="checkbox"/> UP_KEYWORDS	Transit peptide	RT		30	3.9E-2	3.3E-1
<input type="checkbox"/> UP_SEQ_FEATURE	transit peptide:Mitochondrion	RT		23	2.5E-1	1.0E0
Annotation Cluster 12	Enrichment Score: 1.34	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	domain:PARP catalytic	RT		4	2.7E-2	1.0E0
<input type="checkbox"/> INTERPRO	Poly(ADP-ribose) polymerase, catalytic domain	RT		4	3.0E-2	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	NAD+ ADP-ribosyltransferase activity	RT		4	1.2E-1	1.0E0
Annotation Cluster 13	Enrichment Score: 1.32	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	transmembrane receptor protein tyrosine kinase signaling pathway	RT		12	3.3E-3	4.5E-1
<input type="checkbox"/> UP_KEYWORDS	Tyrosine-protein kinase	RT		11	1.1E-2	1.5E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	non-membrane spanning protein tyrosine kinase activity	RT		7	1.4E-2	7.0E-1
<input type="checkbox"/> UP_SEQ_FEATURE	domain:Protein kinase	RT		29	2.2E-2	1.0E0
<input type="checkbox"/> INTERPRO	Tyrosine-protein kinase, catalytic domain	RT		9	2.2E-2	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT	extrinsic component of cytoplasmic side of plasma membrane	RT		8	2.2E-2	3.9E-1
<input type="checkbox"/> INTERPRO	Protein kinase, catalytic domain	RT		30	2.6E-2	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	peptidyl-tyrosine autophosphorylation	RT		6	3.0E-2	1.0E0
<input type="checkbox"/> SMART	TyrKc	RT		9	3.3E-2	1.0E0
<input type="checkbox"/> INTERPRO	Tyrosine-protein kinase, active site	RT		9	3.9E-2	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	protein autophosphorylation	RT		14	4.1E-2	1.0E0
<input type="checkbox"/> UP_KEYWORDS	SH2 domain	RT		9	5.4E-2	4.0E-1
<input type="checkbox"/> INTERPRO	Protein kinase-like domain	RT		30	6.5E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:SH2	RT		8	8.1E-2	1.0E0
<input type="checkbox"/> SMART	SH2	RT		9	8.4E-2	1.0E0
<input type="checkbox"/> INTERPRO	SH2 domain	RT		9	8.9E-2	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	protein tyrosine kinase activity	RT		10	1.2E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	peptidyl-tyrosine phosphorylation	RT		11	1.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	Serine-threonine/tyrosine-protein kinase catalytic domain	RT		9	2.1E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	transmembrane receptor protein tyrosine kinase activity	RT		4	2.3E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	Fc-gamma receptor signaling pathway involved in phagocytosis	RT		7	4.9E-1	1.0E0
Annotation Cluster 14	Enrichment Score: 1.32	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	domain:SH3	RT		14	2.0E-2	1.0E0
<input type="checkbox"/> UP_KEYWORDS	SH3 domain	RT		15	3.7E-2	3.2E-1
<input type="checkbox"/> INTERPRO	Src homology-3 domain	RT		15	6.2E-2	1.0E0
<input type="checkbox"/> SMART	SH3	RT		14	1.2E-1	1.0E0
Annotation Cluster 15	Enrichment Score: 1.3	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	integrin-mediated signaling pathway	RT		14	4.0E-4	1.6E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	integrin complex	RT		6	4.6E-3	1.3E-1
<input type="checkbox"/> UP_SEQ_FEATURE	short sequence motif:GFFKR motif	RT		4	1.9E-2	1.0E0
<input type="checkbox"/> INTERPRO	Integrin alpha chain, C-terminal cytoplasmic region, conserved site	RT		4	2.5E-2	1.0E0
<input type="checkbox"/> INTERPRO	Integrin alpha-2	RT		4	3.5E-2	1.0E0
<input type="checkbox"/> INTERPRO	Integrin alpha chain	RT		4	3.5E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:FG-GAP 2	RT		4	3.6E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:FG-GAP 3	RT		4	3.6E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:FG-GAP 4	RT		4	3.6E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:FG-GAP 5	RT		4	3.6E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:FG-GAP 6	RT		4	3.6E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:FG-GAP 7	RT		4	3.6E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:FG-GAP 1	RT		4	3.6E-2	1.0E0
<input type="checkbox"/> INTERPRO	FG-GAP repeat	RT		4	4.0E-2	1.0E0
<input type="checkbox"/> INTERPRO	Integrin alpha beta-propellor	RT		4	4.0E-2	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	cell-matrix adhesion	RT		9	4.5E-2	1.0E0
<input type="checkbox"/> SMART	Int_alpha	RT		4	4.9E-2	1.0E0
<input type="checkbox"/> UP_KEYWORDS	Integrin	RT		5	9.2E-2	6.1E-1
<input type="checkbox"/> KEGG_PATHWAY	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	RT		6	2.8E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Regulation of actin cytoskeleton	RT		13	4.3E-1	1.0E0
<input type="checkbox"/> INTERPRO	von Willebrand factor, type A	RT		5	5.6E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Hypertrophic cardiomyopathy (HCM)	RT		4	7.9E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Dilated cardiomyopathy	RT		3	9.4E-1	1.0E0
Annotation Cluster 16	Enrichment Score: 1.29	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	short sequence motif:BH3	RT		4	2.7E-2	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation of release of cytochrome c from mitochondria	RT		5	3.3E-2	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	RT		5	4.1E-2	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation of protein homooligomerization	RT		3	5.7E-2	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	positive regulation of intrinsic apoptotic signaling pathway	RT		4	1.8E-1	1.0E0

Annotation Cluster 1		Enrichment Score: 4.36	G		Count	P_Value	Benjamini
Annotation Cluster 17		Enrichment Score: 1.21	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	Domain of unknown function DUF1899	RT		3	3.9E-2	1.0E0
<input type="checkbox"/>	INTERPRO	Coronin	RT		3	3.9E-2	1.0E0
<input type="checkbox"/>	SMART	SM01166	RT		3	4.5E-2	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	actin cytoskeleton organization	RT		9	2.2E-1	1.0E0
Annotation Cluster 18		Enrichment Score: 1.14	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	Glycosidase	RT		8	3.7E-2	3.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	Other glycan degradation	RT		4	6.6E-2	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	oligosaccharide catabolic process	RT		3	8.2E-2	1.0E0
<input type="checkbox"/>	INTERPRO	Glycosyl hydrolase, family 13, all-beta	RT		3	1.4E-1	1.0E0
Annotation Cluster 19		Enrichment Score: 1.12	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	LIM domain	RT		8	2.0E-2	2.2E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, LIM-type	RT		8	2.7E-2	1.0E0
<input type="checkbox"/>	SMART	LIM	RT		8	3.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding 1	RT		5	1.3E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding 2	RT		5	1.3E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding	RT		3	1.7E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding 3	RT		3	2.5E-1	1.0E0
Annotation Cluster 20		Enrichment Score: 1.09	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	PAS fold-3	RT		4	1.1E-2	1.0E0
<input type="checkbox"/>	SMART	PAS	RT		5	2.3E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PAS 1	RT		4	3.6E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PAS 2	RT		4	3.6E-2	1.0E0
<input type="checkbox"/>	INTERPRO	PAS fold	RT		4	4.0E-2	1.0E0
<input type="checkbox"/>	INTERPRO	PAS domain	RT		5	4.8E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PAC	RT		4	7.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:Basic motif	RT		11	1.1E-1	1.0E0
<input type="checkbox"/>	INTERPRO	PAC motif	RT		3	1.5E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Helix-loop-helix motif	RT		8	1.6E-1	1.0E0
<input type="checkbox"/>	SMART	PAC	RT		3	1.7E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Myc-type, basic helix-loop-helix (bHLH) domain	RT		8	1.9E-1	1.0E0
<input type="checkbox"/>	SMART	HLH	RT		8	2.3E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein dimerization activity	RT		7	6.3E-1	1.0E0
Annotation Cluster 21		Enrichment Score: 1.05	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	Calmodulin-binding	RT		15	2.1E-3	4.1E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	brush border	RT		8	1.2E-2	2.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	microfilament motor activity	RT		4	5.3E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Myosin head-like	RT		5	5.5E-2	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	motor activity	RT		7	6.5E-2	1.0E0
<input type="checkbox"/>	SMART	IQ	RT		6	7.8E-2	1.0E0
<input type="checkbox"/>	INTERPRO	Myosin head, motor domain	RT		5	7.8E-2	1.0E0
<input type="checkbox"/>	SMART	MYSc	RT		5	9.8E-2	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	actin-dependent ATPase activity	RT		3	1.1E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Myosin, N-terminal, SH3-like	RT		3	1.2E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Myosin	RT		5	1.3E-1	7.2E-1
<input type="checkbox"/>	INTERPRO	IQ motif, EF-hand binding site	RT		7	1.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	myosin complex	RT		5	1.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	actin filament-based movement	RT		3	1.7E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Myosin-like IQ motif-containing domain	RT		3	1.8E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Motor protein	RT		6	5.9E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ	RT		3	6.9E-1	1.0E0
Annotation Cluster 22		Enrichment Score: 1.04	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	WD40/YVTN repeat-like-containing domain	RT		22	3.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 3	RT		18	3.5E-2	1.0E0
<input type="checkbox"/>	INTERPRO	WD40 repeat, conserved site	RT		13	3.9E-2	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	WD repeat	RT		18	4.2E-2	3.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 4	RT		17	4.2E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 1	RT		18	4.6E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 2	RT		18	4.6E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 5	RT		15	8.1E-2	1.0E0
<input type="checkbox"/>	INTERPRO	WD40 repeat	RT		17	8.1E-2	1.0E0
<input type="checkbox"/>	INTERPRO	WD40-repeat-containing domain	RT		18	1.2E-1	1.0E0
<input type="checkbox"/>	SMART	WD40	RT		17	1.3E-1	1.0E0
<input type="checkbox"/>	INTERPRO	G-protein beta WD-40 repeat	RT		6	3.3E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 6	RT		8	6.5E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 7	RT		5	8.4E-1	1.0E0
Annotation Cluster 23		Enrichment Score: 1	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of endopeptidase activity	RT		12	1.8E-2	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Protease inhibitor	RT		11	2.0E-2	2.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Reactive bond	RT		6	3.0E-2	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Serine protease inhibitor	RT		7	1.1E-1	6.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	serine-type endopeptidase inhibitor activity	RT		8	1.3E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Protease inhibitor I4, serpin, conserved site	RT		4	1.5E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Proteinase inhibitor I2, Kunitz, conserved site	RT		3	1.6E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Proteinase inhibitor I2, Kunitz metazoa	RT				

Annotation Cluster 1		Enrichment Score: 4.36	G		Count	P_Value	Benjamini
<input type="checkbox"/> SMART		SERPIN	RT		4	2.2E-1	1.0E0
Annotation Cluster 24		Enrichment Score: 0.97	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT		tumor necrosis factor receptor binding	RT		5	3.5E-2	1.0E0
<input type="checkbox"/> INTERPRO		Tumour necrosis factor, conserved site	RT		3	8.3E-2	1.0E0
<input type="checkbox"/> SMART		TNF	RT		3	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO		Tumour necrosis factor	RT		3	1.6E-1	1.0E0
<input type="checkbox"/> INTERPRO		Tumour necrosis factor-like domain	RT		5	1.8E-1	1.0E0
Annotation Cluster 25		Enrichment Score: 0.94	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_KEYWORDS		Protein biosynthesis	RT		12	3.1E-2	3.0E-1
<input type="checkbox"/> GOTERM_CC_DIRECT		eukaryotic translation initiation factor 3 complex, eIF3m	RT		3	3.1E-2	4.8E-1
<input type="checkbox"/> UP_KEYWORDS		Initiation factor	RT		6	7.0E-2	4.9E-1
<input type="checkbox"/> GOTERM_BP_DIRECT		regulation of translational initiation	RT		5	7.3E-2	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT		translation initiation factor activity	RT		6	1.2E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT		eukaryotic 48S preinitiation complex	RT		3	1.3E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT		eukaryotic 43S preinitiation complex	RT		3	1.3E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT		eukaryotic translation initiation factor 3 complex	RT		3	1.6E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		formation of translation preinitiation complex	RT		3	2.7E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		translational initiation	RT		4	9.4E-1	1.0E0
Annotation Cluster 26		Enrichment Score: 0.94	G		Count	P_Value	Benjamini
<input type="checkbox"/> BBID		59.L-type Ca2+ Tat immune cells	RT		4	1.5E-2	6.9E-1
<input type="checkbox"/> BBID		58.(CD40L) immnosurveillance	RT		3	3.2E-1	1.0E0
<input type="checkbox"/> BBID		97.Immune injury_MS-lesions MS antigen	RT		3	3.2E-1	1.0E0
Annotation Cluster 27		Enrichment Score: 0.93	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_KEYWORDS		Protein phosphatase	RT		12	1.3E-2	1.7E-1
<input type="checkbox"/> INTERPRO		Protein-tyrosine phosphatase_catalytic	RT		7	4.2E-2	1.0E0
<input type="checkbox"/> INTERPRO		Protein-tyrosine/Dual specificity phosphatase	RT		8	4.9E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		active site:Phosphocysteine intermediate	RT		8	5.0E-2	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		protein dephosphorylation	RT		11	5.2E-2	1.0E0
<input type="checkbox"/> SMART		PTPc_motif	RT		7	5.8E-2	1.0E0
<input type="checkbox"/> INTERPRO		Protein-tyrosine phosphatase_active site	RT		7	8.8E-2	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		peptidyl-tyrosine dephosphorylation	RT		8	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO		Protein-tyrosine phosphatase_receptor/non-receptor type	RT		4	2.0E-1	1.0E0
<input type="checkbox"/> SMART		PTPc	RT		4	2.2E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		domain:Tyrosine-protein phosphatase	RT		5	2.3E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT		protein tyrosine phosphatase activity	RT		7	2.6E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT		phosphoprotein phosphatase activity	RT		4	3.1E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT		protein tyrosine/serine/threonine phosphatase activity	RT		3	4.8E-1	1.0E0
<input type="checkbox"/> INTERPRO		Dual specificity phosphatase_catalytic domain	RT		3	5.3E-1	1.0E0
Annotation Cluster 28		Enrichment Score: 0.89	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		glial cell apoptotic process	RT		3	1.8E-2	1.0E0
<input type="checkbox"/> BBID		86.Apoptosis_Nematode& Vert	RT		4	2.1E-2	6.9E-1
<input type="checkbox"/> GOTERM_MF_DIRECT		death receptor binding	RT		4	3.0E-2	1.0E0
<input type="checkbox"/> KEGG_PATHWAY		Amyotrophic lateral sclerosis (ALS)	RT		6	1.2E-1	1.0E0
<input type="checkbox"/> BIOCARTA		Induction of apoptosis through DR3 and DR4/5 Death Receptors	RT		5	1.9E-1	1.0E0
<input type="checkbox"/> BIOCARTA		Apoptotic Signaling in Response to DNA Damage	RT		4	1.9E-1	1.0E0
<input type="checkbox"/> BIOCARTA		Role of Mitochondria in Apoptotic Signaling	RT		4	1.9E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY		Apoptosis	RT		6	2.3E-1	1.0E0
<input type="checkbox"/> BIOCARTA		HIV-I Nef	RT		7	2.4E-1	1.0E0
<input type="checkbox"/> BBID		150.caspase_and_NFKB_activation	RT		3	3.5E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		aging	RT		6	8.6E-1	1.0E0
Annotation Cluster 29		Enrichment Score: 0.88	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO		Cysteine_peptidase_asparagine active site	RT		3	6.0E-2	1.0E0
<input type="checkbox"/> INTERPRO		Cysteine_peptidase_histidine active site	RT		3	7.1E-2	1.0E0
<input type="checkbox"/> INTERPRO		Peptidase C1A_papain C-terminal	RT		3	9.6E-2	1.0E0
<input type="checkbox"/> INTERPRO		Peptidase C1A_papain	RT		3	1.1E-1	1.0E0
<input type="checkbox"/> SMART		Pept_C1	RT		3	1.1E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT		cysteine-type endopeptidase activity	RT		6	1.2E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		proteolysis involved in cellular protein catabolic process	RT		5	1.6E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS		Thiol protease	RT		9	2.3E-1	9.4E-1
<input type="checkbox"/> GOTERM_MF_DIRECT		cysteine-type peptidase activity	RT		3	4.9E-1	1.0E0
Annotation Cluster 30		Enrichment Score: 0.88	G		Count	P_Value	Benjamini
<input type="checkbox"/> SMART		IQ	RT		6	7.8E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		domain:IQ 4	RT		3	1.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		domain:IQ 1	RT		4	1.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		domain:IQ 2	RT		4	1.4E-1	1.0E0
<input type="checkbox"/> INTERPRO		IQ motif_EF-hand binding site	RT		7	1.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE		domain:IQ 3	RT		3	2.1E-1	1.0E0
Annotation Cluster 31		Enrichment Score: 0.87	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT		histone H4-K16 acetylation	RT		4	5.6E-2	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		histone H4-K8 acetylation	RT		3	1.6E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT		histone H4-K5 acetylation	RT		3	1.6E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT		histone acetyltransferase complex	RT		3	2.5E-1	1.0E0
Annotation Cluster 32		Enrichment Score: 0.79	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_KEYWORDS		Lipid biosynthesis	RT		12	3.7E-2	3.2E-1
<input type="checkbox"/> UP_KEYWORDS		Phospholipid biosynthesis	RT		4	2.5E-1	9.5E-1

Annotation Cluster 1	Enrichment Score: 4.36	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	phospholipid biosynthetic process	RT		4	2.6E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS	Phospholipid metabolism	RT		4	2.9E-1	1.0E0
Annotation Cluster 33	Enrichment Score: 0.78	G		Count	P_Value	Benjamini
<input type="checkbox"/> SMART	CY	RT		3	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	Proteinase inhibitor I25_cystatin	RT		3	1.6E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	cysteine-type endopeptidase inhibitor activity	RT		4	1.8E-1	1.0E0
Annotation Cluster 34	Enrichment Score: 0.77	G		Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY	Legionellosis	RT		7	6.4E-2	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Pertussis	RT		8	1.0E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Leishmaniasis	RT		4	7.3E-1	1.0E0
Annotation Cluster 35	Enrichment Score: 0.77	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_KEYWORDS	Steroid metabolism	RT		7	1.1E-1	6.5E-1
<input type="checkbox"/> UP_KEYWORDS	Cholesterol metabolism	RT		5	1.7E-1	8.2E-1
<input type="checkbox"/> UP_KEYWORDS	Sterol metabolism	RT		5	2.5E-1	9.6E-1
Annotation Cluster 36	Enrichment Score: 0.77	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	DNA-binding region:ETS	RT		4	8.6E-2	1.0E0
<input type="checkbox"/> INTERPRO	Ets domain	RT		4	1.0E-1	1.0E0
<input type="checkbox"/> SMART	ETS	RT		4	1.2E-1	1.0E0
<input type="checkbox"/> INTERPRO	Winged helix-turn-helix DNA-binding domain	RT		9	7.4E-1	1.0E0
Annotation Cluster 37	Enrichment Score: 0.77	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	domain:HECT	RT		4	9.4E-2	1.0E0
<input type="checkbox"/> INTERPRO	HECT	RT		4	1.0E-1	1.0E0
<input type="checkbox"/> SMART	HECTc	RT		4	1.2E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	protein ubiquitination involved in ubiquitin-dependent protein catabolic process	RT		10	2.3E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	RT		4	5.3E-1	1.0E0
Annotation Cluster 38	Enrichment Score: 0.76	G		Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY	Lysosome	RT		11	1.1E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	proteolysis involved in cellular protein catabolic process	RT		5	1.6E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS	Zymogen	RT		11	3.0E-1	1.0E0
Annotation Cluster 39	Enrichment Score: 0.75	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_KEYWORDS	Lectin	RT		11	1.2E-1	6.8E-1
<input type="checkbox"/> INTERPRO	C-type lectin-like	RT		8	1.3E-1	1.0E0
<input type="checkbox"/> INTERPRO	C-type lectin	RT		7	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	C-type lectin fold	RT		8	1.7E-1	1.0E0
<input type="checkbox"/> SMART	CLECT	RT		7	1.8E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:C-type lectin	RT		6	2.2E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	carbohydrate binding	RT		11	3.4E-1	1.0E0
Annotation Cluster 40	Enrichment Score: 0.75	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	K Homology domain_type 1	RT		5	1.0E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:KH 3	RT		3	1.1E-1	1.0E0
<input type="checkbox"/> INTERPRO	K Homology domain	RT		4	2.0E-1	1.0E0
<input type="checkbox"/> SMART	KH	RT		4	2.3E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:KH 1	RT		3	2.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:KH 2	RT		3	2.4E-1	1.0E0
Annotation Cluster 41	Enrichment Score: 0.74	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT	transcriptional activator activity_RNA polymerase II core_promoter proximal region sequence-specific binding	RT		17	5.1E-2	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	RNA polymerase II core_promoter proximal region sequence-specific DNA binding	RT		20	2.0E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	transcription from RNA polymerase II promoter	RT		23	5.9E-1	1.0E0
Annotation Cluster 42	Enrichment Score: 0.73	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Sterile alpha motif/pointed domain	RT		10	4.9E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:SAM	RT		6	2.2E-1	1.0E0
<input type="checkbox"/> SMART	SAM	RT		6	3.2E-1	1.0E0
<input type="checkbox"/> INTERPRO	Sterile alpha motif domain	RT		6	3.3E-1	1.0E0
Annotation Cluster 43	Enrichment Score: 0.72	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_KEYWORDS	GTP-binding	RT		22	2.3E-2	2.4E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	GTP binding	RT		25	4.6E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	RT		18	1.0E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	small GTPase mediated signal transduction	RT		15	2.0E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	GTPase activity	RT		14	2.2E-1	1.0E0
<input type="checkbox"/> INTERPRO	Small GTP-binding_protein domain	RT		10	2.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	Small GTPase superfamily	RT		8	3.4E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS	Prenylation	RT		8	4.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	short sequence motif:Effector region	RT		5	5.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	lipid moiety-binding region:S-geranylgeranyl cysteine	RT		5	6.1E-1	1.0E0
Annotation Cluster 44	Enrichment Score: 0.72	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	fat cell differentiation	RT		7	1.0E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DNA-binding region:Basic motif	RT		11	1.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:Leucine-zipper	RT		8	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	Basic-leucine zipper domain	RT		4	3.8E-1	1.0E0
<input type="checkbox"/> SMART	BRLZ	RT		4	3.9E-1	1.0E0
Annotation Cluster 45	Enrichment Score: 0.71	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	PDZ domain	RT		11	1.0E-1	1.0E0
<input type="checkbox"/> SMART	PDZ	RT		11	1.2E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:PDZ 1	RT		4	2.2E-1	1.0E0

Annotation Cluster 1	Enrichment Score: 4.36	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	domain:PDZ 2	RT		4	2.2E-1	1.0E0
UP_SEQ_FEATURE	domain:PDZ	RT		7	2.8E-1	1.0E0
UP_SEQ_FEATURE	domain:PDZ 3	RT		3	3.3E-1	1.0E0
Annotation Cluster 46	Enrichment Score: 0.69	G		Count	P_Value	Benjamini
KEGG_PATHWAY	ECM-receptor interaction	RT		9	8.8E-2	1.0E0
KEGG_PATHWAY	Focal adhesion	RT		16	1.3E-1	1.0E0
KEGG_PATHWAY	PI3K-Akt signaling pathway	RT		17	7.5E-1	1.0E0
Annotation Cluster 47	Enrichment Score: 0.68	G		Count	P_Value	Benjamini
INTERPRO	S100/Calbindin-D9k, conserved site	RT		5	1.7E-2	1.0E0
INTERPRO	S100/CaBP-9k-type, calcium binding, subdomain	RT		5	2.9E-2	1.0E0
SMART	SM01394	RT		5	3.3E-2	1.0E0
INTERPRO	EF-hand-like domain	RT		16	1.7E-1	1.0E0
UP_SEQ_FEATURE	calcium-binding region:1; low affinity	RT		3	1.7E-1	1.0E0
INTERPRO	EF-Hand 1, calcium-binding site	RT		11	1.9E-1	1.0E0
UP_SEQ_FEATURE	calcium-binding region:2; high affinity	RT		3	2.1E-1	1.0E0
INTERPRO	EF-hand domain	RT		13	2.2E-1	1.0E0
UP_SEQ_FEATURE	domain:EF-hand 2	RT		10	3.0E-1	1.0E0
UP_SEQ_FEATURE	calcium-binding region:2	RT		7	3.1E-1	1.0E0
UP_SEQ_FEATURE	calcium-binding region:1	RT		7	3.8E-1	1.0E0
UP_SEQ_FEATURE	domain:EF-hand 1	RT		9	4.3E-1	1.0E0
UP_SEQ_FEATURE	calcium-binding region:3	RT		3	4.5E-1	1.0E0
GOTERM_MF_DIRECT	calcium ion binding	RT		33	4.7E-1	1.0E0
UP_SEQ_FEATURE	domain:EF-hand 3	RT		5	5.2E-1	1.0E0
SMART	EFh	RT		7	6.1E-1	1.0E0
UP_SEQ_FEATURE	domain:EF-hand 4	RT		3	7.0E-1	1.0E0
Annotation Cluster 48	Enrichment Score: 0.67	G		Count	P_Value	Benjamini
GOTERM_BP_DIRECT	extracellular matrix organization	RT		15	5.2E-2	1.0E0
GOTERM_BP_DIRECT	cell adhesion	RT		23	3.9E-1	1.0E0
UP_KEYWORDS	Cell adhesion	RT		20	4.7E-1	1.0E0
Annotation Cluster 49	Enrichment Score: 0.67	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	RT		8	9.2E-2	1.0E0
UP_KEYWORDS	Heme	RT		9	1.3E-1	7.3E-1
GOTERM_MF_DIRECT	heme binding	RT		8	3.8E-1	1.0E0
UP_KEYWORDS	Iron	RT		14	4.7E-1	1.0E0
Annotation Cluster 50	Enrichment Score: 0.65	G		Count	P_Value	Benjamini
GOTERM_MF_DIRECT	nucleoside kinase activity	RT		3	6.7E-2	1.0E0
GOTERM_BP_DIRECT	pyrimidine nucleoside salvage	RT		3	9.6E-2	1.0E0
KEGG_PATHWAY	Pyrimidine metabolism	RT		6	6.3E-1	1.0E0
GOTERM_BP_DIRECT	phosphorylation	RT		5	6.5E-1	1.0E0
Annotation Cluster 51	Enrichment Score: 0.65	G		Count	P_Value	Benjamini
KEGG_PATHWAY	Cytokine-cytokine receptor interaction	RT		19	9.2E-2	1.0E0
UP_KEYWORDS	Cytokine	RT		12	1.1E-1	6.5E-1
GOTERM_MF_DIRECT	cytokine activity	RT		12	1.4E-1	1.0E0
INTERPRO	Four-helical cytokine, core	RT		4	3.4E-1	1.0E0
KEGG_PATHWAY	Jak-STAT signaling pathway	RT		10	3.6E-1	1.0E0
INTERPRO	Four-helical cytokine-like, core	RT		4	3.8E-1	1.0E0
KEGG_PATHWAY	Inflammatory bowel disease (IBD)	RT		5	4.4E-1	1.0E0
Annotation Cluster 52	Enrichment Score: 0.64	G		Count	P_Value	Benjamini
INTERPRO	WW domain	RT		5	1.7E-1	1.0E0
SMART	WW	RT		5	1.7E-1	1.0E0
UP_SEQ_FEATURE	domain:WW 1	RT		3	3.1E-1	1.0E0
UP_SEQ_FEATURE	domain:WW 2	RT		3	3.1E-1	1.0E0
Annotation Cluster 53	Enrichment Score: 0.63	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	domain:DAPIN	RT		3	2.1E-1	1.0E0
INTERPRO	DAPIN domain	RT		3	2.4E-1	1.0E0
SMART	SM01289	RT		3	2.5E-1	1.0E0
Annotation Cluster 54	Enrichment Score: 0.63	G		Count	P_Value	Benjamini
GOTERM_BP_DIRECT	ER to Golgi vesicle-mediated transport	RT		11	1.7E-1	1.0E0
GOTERM_CC_DIRECT	endoplasmic reticulum-Golgi intermediate compartment membrane	RT		5	2.7E-1	1.0E0
GOTERM_BP_DIRECT	COPII vesicle coating	RT		5	2.8E-1	1.0E0
Annotation Cluster 55	Enrichment Score: 0.6	G		Count	P_Value	Benjamini
INTERPRO	Sugar transporter, conserved site	RT		4	1.3E-1	1.0E0
INTERPRO	Major facilitator superfamily domain	RT		9	2.0E-1	1.0E0
GOTERM_MF_DIRECT	transmembrane transporter activity	RT		4	3.6E-1	1.0E0
INTERPRO	General substrate transporter	RT		3	4.5E-1	1.0E0
Annotation Cluster 56	Enrichment Score: 0.6	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	domain:IGFBP N-terminal	RT		3	1.8E-1	1.0E0
SMART	IB	RT		3	1.9E-1	1.0E0
INTERPRO	Insulin-like growth factor-binding protein, IGFBP	RT		3	1.9E-1	1.0E0
INTERPRO	Insulin-like growth factor binding protein, N-terminal	RT		8	3.4E-1	1.0E0
GOTERM_BP_DIRECT	regulation of cell growth	RT		5	4.7E-1	1.0E0
Annotation Cluster 57	Enrichment Score: 0.59	G		Count	P_Value	Benjamini
GOTERM_MF_DIRECT	3'-5'-exoribonuclease activity	RT		4	5.3E-2	1.0E0
GOTERM_BP_DIRECT	RNA phosphodiester bond hydrolysis, exonucleolytic	RT		3	3.5E-1	1.0E0
UP_KEYWORDS	Nuclease	RT		7	4.0E-1	1.0E0
UP_KEYWORDS	Exonuclease	RT		3	5.8E-1	1.0E0

Annotation Cluster 1	Enrichment Score: 4.36	G		Count	P_Value	Benjamini
Annotation Cluster 58	Enrichment Score: 0.58	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	L-amino acid transport	RT		3	9.6E-2	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	L-amino acid transmembrane transporter activity	RT		3	1.1E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS	Amino-acid transport	RT		3	4.5E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	amino acid transport	RT		3	4.6E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	amino acid transmembrane transporter activity	RT		3	6.1E-1	1.0E0
Annotation Cluster 59	Enrichment Score: 0.58	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_KEYWORDS	Metal-binding	RT		158	4.7E-2	3.6E-1
<input type="checkbox"/> UP_KEYWORDS	Zinc	RT		91	5.1E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	metal ion binding	RT		84	7.9E-1	1.0E0
Annotation Cluster 60	Enrichment Score: 0.55	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:TNFR-Cys 3	RT		3	2.4E-1	1.0E0
<input type="checkbox"/> SMART	TNFR	RT		3	2.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:TNFR-Cys 1	RT		3	2.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:TNFR-Cys 2	RT		3	2.7E-1	1.0E0
<input type="checkbox"/> INTERPRO	TNFR/NGFR cysteine-rich region	RT		3	2.7E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	tumor necrosis factor-activated receptor activity	RT		3	2.8E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	tumor necrosis factor-mediated signaling pathway	RT		7	4.2E-1	1.0E0
Annotation Cluster 61	Enrichment Score: 0.54	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Glutathione S-transferase, C-terminal-like	RT		4	2.3E-1	1.0E0
<input type="checkbox"/> INTERPRO	Glutathione S-transferase, C-terminal	RT		3	2.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:GST C-terminal	RT		3	4.3E-1	1.0E0
Annotation Cluster 62	Enrichment Score: 0.53	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	domain:C2	RT		6	2.2E-1	1.0E0
<input type="checkbox"/> SMART	C2	RT		8	3.3E-1	1.0E0
<input type="checkbox"/> INTERPRO	C2 calcium-dependent membrane targeting	RT		9	3.6E-1	1.0E0
Annotation Cluster 63	Enrichment Score: 0.53	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	semaphorin-plexin signaling pathway	RT		4	1.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	Plexin-like fold	RT		4	2.6E-1	1.0E0
<input type="checkbox"/> SMART	PSI	RT		4	2.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	Plexin	RT		3	2.9E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:Sema	RT		3	3.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	Semaphorin/CD100 antigen	RT		3	3.6E-1	1.0E0
<input type="checkbox"/> SMART	Sema	RT		3	4.0E-1	1.0E0
Annotation Cluster 64	Enrichment Score: 0.53	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Tetraspanin/Peripherin	RT		4	1.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	Tetraspanin	RT		3	3.5E-1	1.0E0
<input type="checkbox"/> PIR_SUPERFAMILY	tetraspanin	RT		3	5.0E-1	1.0E0
Annotation Cluster 65	Enrichment Score: 0.53	G		Count	P_Value	Benjamini
<input type="checkbox"/> SMART	CH	RT		6	1.6E-1	1.0E0
<input type="checkbox"/> INTERPRO	Calponin homology domain	RT		6	2.0E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:CH 2	RT		3	2.8E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:CH 1	RT		3	2.8E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:CH	RT		3	4.9E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT	Z disc	RT		6	5.5E-1	1.0E0
Annotation Cluster 66	Enrichment Score: 0.51	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_KEYWORDS	Neurotransmitter transport	RT		4	1.7E-1	8.1E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	synaptic vesicle	RT		7	1.8E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Synaptic vesicle cycle	RT		5	4.3E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT	synaptic vesicle membrane	RT		3	6.7E-1	1.0E0
Annotation Cluster 67	Enrichment Score: 0.51	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:Spectrin 1	RT		3	2.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:Spectrin 2	RT		3	2.7E-1	1.0E0
<input type="checkbox"/> INTERPRO	Spectrin/alpha-actinin	RT		3	3.3E-1	1.0E0
<input type="checkbox"/> SMART	SPEC	RT		3	3.7E-1	1.0E0
Annotation Cluster 68	Enrichment Score: 0.5	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Protein phosphatase 2C (PP2C)-like	RT		3	1.9E-1	1.0E0
<input type="checkbox"/> SMART	PP2Cc	RT		3	2.2E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	protein serine/threonine phosphatase activity	RT		3	7.2E-1	1.0E0
Annotation Cluster 69	Enrichment Score: 0.5	G		Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY	Glucagon signaling pathway	RT		9	1.5E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	glycogen catabolic process	RT		3	2.4E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Insulin signaling pathway	RT		6	8.6E-1	1.0E0
Annotation Cluster 70	Enrichment Score: 0.5	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Pleckstrin homology-like domain	RT		24	1.0E-1	1.0E0
<input type="checkbox"/> INTERPRO	Pleckstrin homology domain	RT		13	4.2E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:PH	RT		11	4.8E-1	1.0E0
<input type="checkbox"/> SMART	PH	RT		13	5.0E-1	1.0E0
Annotation Cluster 71	Enrichment Score: 0.49	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	inositol phosphate metabolic process	RT		5	1.5E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Phosphatidylinositol signaling system	RT		7	4.2E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Inositol phosphate metabolism	RT		5	5.2E-1	1.0E0
Annotation Cluster 72	Enrichment Score: 0.49	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_KEYWORDS	Fatty acid metabolism	RT		9	1.0E-1	6.5E-1
<input type="checkbox"/> KEGG_PATHWAY	Fatty acid degradation	RT		4	3.9E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Fatty acid metabolism	RT		4	4.7E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	fatty acid beta-oxidation	RT		3	5.8E-1	1.0E0

Annotation Cluster 1		Enrichment Score: 4.36	G		Count	P_Value	Benjamini
Annotation Cluster 73		Enrichment Score: 0.49	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H3 acetylation	RT		5	1.2E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Zinc finger, PHD-finger	RT		6	2.2E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Zinc finger, PHD-type, conserved site	RT		5	2.9E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Zinc finger, PHD-type	RT		6	2.9E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type	RT		4	3.3E-1	1.0E0
<input type="checkbox"/>	SMART	PHD	RT		6	3.6E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Zinc finger, FYVE/PHD-type	RT		7	5.1E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Zinc finger, RING/FYVE/PHD-type	RT		15	8.8E-1	1.0E0
Annotation Cluster 74		Enrichment Score: 0.48	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone deacetylase activity	RT		4	2.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone deacetylation	RT		4	3.3E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone deacetylase binding	RT		6	4.5E-1	1.0E0
Annotation Cluster 75		Enrichment Score: 0.48	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	Laminin G domain	RT		5	2.3E-1	1.0E0
<input type="checkbox"/>	SMART	LamG	RT		4	2.8E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Laminin G-like 1	RT		3	3.3E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Laminin G-like 2	RT		3	3.3E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Concanavalin A-like lectin/glucanase, subgroup	RT		10	6.0E-1	1.0E0
Annotation Cluster 76		Enrichment Score: 0.48	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Manganese 1	RT		3	2.8E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Manganese 2	RT		3	2.8E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Manganese	RT		9	4.6E-1	1.0E0
Annotation Cluster 77		Enrichment Score: 0.48	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	Galactose oxidase, beta-propeller	RT		5	2.9E-2	1.0E0
<input type="checkbox"/>	INTERPRO	Kelch-like protein, gigaxonin	RT		4	2.4E-1	1.0E0
<input type="checkbox"/>	INTERPRO	BTB/Kelch-associated	RT		5	2.4E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Kelch repeat type_1	RT		5	2.6E-1	1.0E0
<input type="checkbox"/>	SMART	SM00875	RT		5	2.7E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 4	RT		5	2.9E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Kelch repeat	RT		5	2.9E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 1	RT		5	3.0E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 2	RT		5	3.0E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 3	RT		5	3.0E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BACK	RT		3	3.3E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 6	RT		4	3.3E-1	1.0E0
<input type="checkbox"/>	PIR_SUPERFAMILY	kelch-like protein, gigaxonin type	RT		4	4.5E-1	1.0E0
<input type="checkbox"/>	SMART	Kelch	RT		4	4.7E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 5	RT		4	4.8E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BTB	RT		7	4.9E-1	1.0E0
<input type="checkbox"/>	INTERPRO	BTB/POZ-like	RT		8	6.0E-1	1.0E0
<input type="checkbox"/>	INTERPRO	BTB/POZ fold	RT		8	6.6E-1	1.0E0
<input type="checkbox"/>	SMART	BTB	RT		8	6.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	Cul3-RING ubiquitin ligase complex	RT		3	7.7E-1	1.0E0
Annotation Cluster 78		Enrichment Score: 0.47	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	Glycolysis	RT		4	1.1E-1	6.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	canonical glycolysis	RT		3	3.2E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Carbon metabolism	RT		8	3.9E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	glycolytic process	RT		3	4.5E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Glycolysis / Gluconeogenesis	RT		4	7.0E-1	1.0E0
Annotation Cluster 79		Enrichment Score: 0.46	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	release of sequestered calcium ion into cytosol	RT		6	3.3E-2	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	ion channel activity	RT		5	1.1E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Calcium channel	RT		4	4.6E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Ligand-gated ion channel	RT		4	5.9E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Calcium transport	RT		4	7.3E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Ion transport domain	RT		4	8.1E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Ion channel	RT		10	9.3E-1	1.0E0
Annotation Cluster 80		Enrichment Score: 0.43	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	signal peptide	RT		143	1.4E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Signal	RT		170	1.9E-1	8.4E-1
<input type="checkbox"/>	UP_KEYWORDS	Glycoprotein	RT		179	3.5E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		165	5.5E-1	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Disulfide bond	RT		130	5.9E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	disulfide bond	RT		105	8.5E-1	1.0E0
Annotation Cluster 81		Enrichment Score: 0.43	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	glutathione metabolic process	RT		7	3.6E-2	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	glutathione derivative biosynthetic process	RT		3	2.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular oxidant detoxification	RT		5	3.7E-1	1.0E0
<input type="checkbox"/>	INTERPRO	Thioredoxin-like fold	RT		7	4.3E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	glutathione transferase activity	RT		3	4.5E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Glutathione metabolism	RT		4	5.1E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Metabolism of xenobiotics by cytochrome P450	RT		5	5.6E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Chemical carcinogenesis	RT		4	8.0E-1	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Drug metabolism - cytochrome P450	RT		3	8.8E-1	1.0E0
Annotation Cluster 82		Enrichment Score: 0.42	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	DEATH	RT		3	3.4E-1	1.0E0

Annotation Cluster 1	Enrichment Score: 4.36	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	domain:Death	RT		3	4.0E-1	1.0E0
INTERPRO	<u>Death domain</u>	RT		3	4.2E-1	1.0E0
Annotation Cluster 83	Enrichment Score: 0.42	G		Count	P_Value	Benjamini
UP_KEYWORDS	<u>GPI-anchor</u>	RT		8	2.7E-1	9.6E-1
UP_SEQ_FEATURE	propeptide:Removed in mature form	RT		12	3.2E-1	1.0E0
UP_SEQ_FEATURE	lipid moiety-binding region:GPI-anchor amidated serine	RT		4	3.6E-1	1.0E0
GOTERM_CC_DIRECT	<u>anchored component of membrane</u>	RT		5	7.0E-1	1.0E0
Annotation Cluster 84	Enrichment Score: 0.41	G		Count	P_Value	Benjamini
SMART	<u>SOCS</u>	RT		3	2.2E-1	1.0E0
UP_SEQ_FEATURE	domain:SOCS box	RT		3	4.4E-1	1.0E0
INTERPRO	<u>SOCS protein, C-terminal</u>	RT		3	4.7E-1	1.0E0
SMART	<u>SM00969</u>	RT		3	5.2E-1	1.0E0
Annotation Cluster 85	Enrichment Score: 0.39	G		Count	P_Value	Benjamini
GOTERM_MF_DIRECT	<u>dipeptidyl-peptidase activity</u>	RT		3	1.1E-1	1.0E0
GOTERM_MF_DIRECT	<u>metallopeptidase activity</u>	RT		6	2.7E-1	1.0E0
UP_KEYWORDS	<u>Metalloprotease</u>	RT		7	5.2E-1	1.0E0
UP_SEQ_FEATURE	metal ion-binding site:Zinc; catalytic	RT		5	7.5E-1	1.0E0
GOTERM_MF_DIRECT	<u>metalloendopeptidase activity</u>	RT		3	9.6E-1	1.0E0
Annotation Cluster 86	Enrichment Score: 0.39	G		Count	P_Value	Benjamini
UP_KEYWORDS	<u>Repressor</u>	RT		36	7.2E-3	1.1E-1
UP_KEYWORDS	<u>Transcription regulation</u>	RT		88	6.1E-1	1.0E0
UP_KEYWORDS	<u>Transcription</u>	RT		90	6.3E-1	1.0E0
GOTERM_BP_DIRECT	<u>transcription, DNA-templated</u>	RT		77	9.0E-1	1.0E0
UP_KEYWORDS	<u>DNA-binding</u>	RT		69	9.1E-1	1.0E0
GOTERM_MF_DIRECT	<u>transcription factor activity, sequence-specific DNA binding</u>	RT		35	9.1E-1	1.0E0
GOTERM_BP_DIRECT	<u>regulation of transcription, DNA-templated</u>	RT		57	9.3E-1	1.0E0
Annotation Cluster 87	Enrichment Score: 0.39	G		Count	P_Value	Benjamini
GOTERM_BP_DIRECT	<u>tricarboxylic acid cycle</u>	RT		3	3.7E-1	1.0E0
KEGG_PATHWAY	<u>Carbon metabolism</u>	RT		8	3.9E-1	1.0E0
KEGG_PATHWAY	<u>Citrate cycle (TCA cycle)</u>	RT		3	4.8E-1	1.0E0
Annotation Cluster 88	Enrichment Score: 0.39	G		Count	P_Value	Benjamini
KEGG_PATHWAY	<u>SNARE interactions in vesicular transport</u>	RT		4	2.7E-1	1.0E0
GOTERM_MF_DIRECT	<u>SNARE binding</u>	RT		4	3.2E-1	1.0E0
GOTERM_MF_DIRECT	<u>SNAP receptor activity</u>	RT		3	5.1E-1	1.0E0
GOTERM_CC_DIRECT	<u>SNARE complex</u>	RT		3	6.5E-1	1.0E0
Annotation Cluster 89	Enrichment Score: 0.38	G		Count	P_Value	Benjamini
GOTERM_BP_DIRECT	<u>semaphorin-plexin signaling pathway</u>	RT		4	1.8E-1	1.0E0
INTERPRO	<u>Immunoglobulin E-set</u>	RT		5	6.4E-1	1.0E0
GOTERM_BP_DIRECT	<u>regulation of cell migration</u>	RT		4	6.4E-1	1.0E0
Annotation Cluster 90	Enrichment Score: 0.38	G		Count	P_Value	Benjamini
KEGG_PATHWAY	<u>Pathogenic Escherichia coli infection</u>	RT		5	2.8E-1	1.0E0
KEGG_PATHWAY	<u>Shigellosis</u>	RT		5	4.4E-1	1.0E0
KEGG_PATHWAY	<u>Bacterial invasion of epithelial cells</u>	RT		5	6.0E-1	1.0E0
Annotation Cluster 91	Enrichment Score: 0.37	G		Count	P_Value	Benjamini
INTERPRO	<u>Immunoglobulin</u>	RT		8	4.9E-2	1.0E0
UP_SEQ_FEATURE	domain:Ig-like C2-type 3	RT		9	1.3E-1	1.0E0
UP_SEQ_FEATURE	domain:Ig-like C2-type 4	RT		6	1.7E-1	1.0E0
UP_SEQ_FEATURE	domain:Ig-like C2-type 1	RT		11	2.6E-1	1.0E0
UP_SEQ_FEATURE	domain:Ig-like C2-type 2	RT		11	2.7E-1	1.0E0
UP_SEQ_FEATURE	domain:Ig-like C2-type 5	RT		4	3.6E-1	1.0E0
UP_KEYWORDS	<u>Immunoglobulin domain</u>	RT		23	4.2E-1	1.0E0
UP_SEQ_FEATURE	domain:Ig-like C2-type 6	RT		3	4.3E-1	1.0E0
INTERPRO	<u>Immunoglobulin subtype 2</u>	RT		10	6.9E-1	1.0E0
INTERPRO	<u>Immunoglobulin subtype</u>	RT		19	7.3E-1	1.0E0
SMART	<u>IGc2</u>	RT		10	7.8E-1	1.0E0
INTERPRO	<u>Immunoglobulin I-set</u>	RT		5	8.3E-1	1.0E0
SMART	<u>IG</u>	RT		19	8.4E-1	1.0E0
INTERPRO	<u>Immunoglobulin-like domain</u>	RT		23	9.7E-1	1.0E0
INTERPRO	<u>Immunoglobulin-like fold</u>	RT		29	9.7E-1	1.0E0
INTERPRO	<u>Immunoglobulin V-set</u>	RT		8	1.0E0	1.0E0
Annotation Cluster 92	Enrichment Score: 0.36	G		Count	P_Value	Benjamini
KEGG_PATHWAY	<u>Malaria</u>	RT		5	2.6E-1	1.0E0
KEGG_PATHWAY	<u>Toxoplasmosis</u>	RT		8	3.6E-1	1.0E0
KEGG_PATHWAY	<u>African trypanosomiasis</u>	RT		3	5.3E-1	1.0E0
KEGG_PATHWAY	<u>Leishmaniasis</u>	RT		4	7.3E-1	1.0E0
Annotation Cluster 93	Enrichment Score: 0.36	G		Count	P_Value	Benjamini
GOTERM_CC_DIRECT	<u>integral component of plasma membrane</u>	RT		77	1.2E-2	2.5E-1
UP_KEYWORDS	<u>Membrane</u>	RT		297	2.4E-1	9.4E-1
UP_KEYWORDS	<u>Glycoprotein</u>	RT		179	3.5E-1	1.0E0
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		165	5.5E-1	1.0E0
UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT		131	6.9E-1	1.0E0
UP_SEQ_FEATURE	topological domain:Extracellular	RT		103	7.7E-1	1.0E0
UP_KEYWORDS	<u>Transmembrane helix</u>	RT		196	9.5E-1	1.0E0
UP_KEYWORDS	<u>Transmembrane</u>	RT		196	9.6E-1	1.0E0
UP_SEQ_FEATURE	transmembrane region	RT		177	9.7E-1	1.0E0
GOTERM_CC_DIRECT	<u>integral component of membrane</u>	RT		176	1.0E0	1.0E0

Annotation Cluster 1	Enrichment Score: 4.36	G		Count	P_Value	Benjamini
Annotation Cluster 94	Enrichment Score: 0.35	G		Count	P_Value	Benjamini
<input type="checkbox"/> BIOCARTA	Fc Epsilon Receptor I Signaling in Mast Cells	RT		5	2.8E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Effects of calcineurin in Keratinocyte Differentiation	RT		3	3.8E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Signaling Pathway from G-Protein Families	RT		4	4.2E-1	1.0E0
<input type="checkbox"/> BIOCARTA	BCR Signaling Pathway	RT		4	4.2E-1	1.0E0
<input type="checkbox"/> BIOCARTA	Neuropeptides VIP and PACAP inhibit the apoptosis of activated T cells	RT		3	5.5E-1	1.0E0
<input type="checkbox"/> BIOCARTA	T Cell Receptor Signaling Pathway	RT		3	8.2E-1	1.0E0
Annotation Cluster 95	Enrichment Score: 0.33	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Guanine-nucleotide dissociation stimulator, CDC24, conserved site	RT		3	2.1E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS	Guanine-nucleotide releasing factor	RT		9	2.1E-1	8.9E-1
<input type="checkbox"/> UP_SEQ_FEATURE	domain:DH	RT		4	5.0E-1	1.0E0
<input type="checkbox"/> INTERPRO	Dbl homology (DH) domain	RT		4	5.6E-1	1.0E0
<input type="checkbox"/> SMART	RhoGEF	RT		4	5.8E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	Rho guanyl-nucleotide exchange factor activity	RT		4	6.5E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	regulation of Rho protein signal transduction	RT		4	7.0E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	guanyl-nucleotide exchange factor activity	RT		5	7.6E-1	1.0E0
Annotation Cluster 96	Enrichment Score: 0.32	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	FERM conserved site	RT		3	2.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	FERM, N-terminal	RT		3	3.3E-1	1.0E0
<input type="checkbox"/> INTERPRO	FERM/acyl-CoA-binding protein, 3-helical bundle	RT		4	3.3E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:FERM	RT		3	5.7E-1	1.0E0
<input type="checkbox"/> INTERPRO	FERM domain	RT		3	6.2E-1	1.0E0
<input type="checkbox"/> INTERPRO	FERM central domain	RT		3	6.2E-1	1.0E0
<input type="checkbox"/> INTERPRO	Band 4.1 domain	RT		3	6.2E-1	1.0E0
<input type="checkbox"/> SMART	B41	RT		3	6.6E-1	1.0E0
Annotation Cluster 97	Enrichment Score: 0.32	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:ARM 1	RT		3	3.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:ARM 3	RT		3	4.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:ARM 2	RT		3	4.3E-1	1.0E0
<input type="checkbox"/> INTERPRO	Armadillo-like helical	RT		7	9.0E-1	1.0E0
Annotation Cluster 98	Enrichment Score: 0.31	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT	protein binding, bridging	RT		6	2.4E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_DIRECT	cornified envelope	RT		3	5.8E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	peptide cross-linking	RT		3	6.5E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	keratinocyte differentiation	RT		4	6.6E-1	1.0E0
Annotation Cluster 99	Enrichment Score: 0.29	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT	endonuclease activity	RT		4	3.9E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS	Nuclease	RT		7	4.0E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS	Endonuclease	RT		3	8.4E-1	1.0E0
Annotation Cluster 100	Enrichment Score: 0.28	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	regulation of small GTPase mediated signal transduction	RT		9	2.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	Rho GTPase activation protein	RT		6	3.1E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS	GTPase activation	RT		8	6.3E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:Rho-GAP	RT		3	7.5E-1	1.0E0
<input type="checkbox"/> INTERPRO	Rho GTPase-activating protein domain	RT		3	7.6E-1	1.0E0
<input type="checkbox"/> SMART	RhoGAP	RT		3	7.9E-1	1.0E0
Annotation Cluster 101	Enrichment Score: 0.27	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 15	RT		5	1.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 14	RT		5	2.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 16	RT		4	2.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 13	RT		5	3.4E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 17	RT		3	4.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 6	RT		10	4.3E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 12	RT		5	4.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 10	RT		6	4.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 5	RT		10	5.5E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 11	RT		5	5.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 9	RT		6	6.0E-1	1.0E0
<input type="checkbox"/> INTERPRO	Cysteine-rich flanking region, C-terminal	RT		4	6.6E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 4	RT		10	6.7E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 7	RT		7	6.9E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 8	RT		6	6.9E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 1	RT		12	7.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 2	RT		12	7.1E-1	1.0E0
<input type="checkbox"/> SMART	LRRCT	RT		4	7.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:LRR 3	RT		11	7.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	Leucine-rich repeat	RT		9	8.4E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS	Leucine-rich repeat	RT		10	8.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	Leucine-rich repeat, typical subtype	RT		6	8.5E-1	1.0E0
<input type="checkbox"/> SMART	LRR_TYP	RT		6	9.0E-1	1.0E0
Annotation Cluster 102	Enrichment Score: 0.27	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Transforming growth factor-beta, C-terminal	RT		3	4.5E-1	1.0E0
<input type="checkbox"/> SMART	TGFb	RT		3	4.8E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS	Growth factor	RT		6	5.6E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	growth factor activity	RT		7	7.1E-1	1.0E0

Annotation Cluster 1		Enrichment Score: 4.36	G		Count	P_Value	Benjamini
Annotation Cluster 103		Enrichment Score: 0.25	G		Count	P_Value	Benjamini
	KEGG_PATHWAY	Glucagon_signaling_pathway	RT		9	1.5E-1	1.0E0
	KEGG_PATHWAY	Renin secretion	RT		6	2.5E-1	1.0E0
	KEGG_PATHWAY	Long-term_potentiation	RT		6	2.7E-1	1.0E0
	KEGG_PATHWAY	Amphetamine_addiction	RT		6	2.7E-1	1.0E0
	KEGG_PATHWAY	Gastric_acid_secretion	RT		6	3.4E-1	1.0E0
	KEGG_PATHWAY	Inflammatory mediator regulation of TRP channels	RT		7	4.2E-1	1.0E0
	KEGG_PATHWAY	Phosphatidylinositol_signaling_system	RT		7	4.2E-1	1.0E0
	BIOCARTA	Signaling_Pathway_from_G-Protein_Families	RT		4	4.2E-1	1.0E0
	KEGG_PATHWAY	Aldosterone_synthesis_and_secretion	RT		6	4.3E-1	1.0E0
	KEGG_PATHWAY	Salivary_secretion	RT		6	4.8E-1	1.0E0
	BIOCARTA	Bioactive_Peptide_Induced_Signaling_Pathway	RT		4	4.9E-1	1.0E0
	BIOCARTA	Regulation_of_PGC-1a	RT		3	5.0E-1	1.0E0
	KEGG_PATHWAY	Gap_junction	RT		6	5.0E-1	1.0E0
	KEGG_PATHWAY	Oocyte_meiosis	RT		7	5.4E-1	1.0E0
	KEGG_PATHWAY	Glutamatergic_synapse	RT		7	5.7E-1	1.0E0
	KEGG_PATHWAY	Calcium_signaling_pathway	RT		10	6.1E-1	1.0E0
	KEGG_PATHWAY	Long-term_depression	RT		4	6.2E-1	1.0E0
	KEGG_PATHWAY	Dopaminergic_synapse	RT		7	6.8E-1	1.0E0
	KEGG_PATHWAY	Oxytocin_signaling_pathway	RT		8	6.9E-1	1.0E0
	KEGG_PATHWAY	Serotonergic_synapse	RT		6	7.1E-1	1.0E0
	KEGG_PATHWAY	Thyroid_hormone_synthesis	RT		4	7.2E-1	1.0E0
	BIOCARTA	NFAT_and_Hypertrophy_of_the_heart_(Transcription_in_the_broken_heart)	RT		4	7.3E-1	1.0E0
	KEGG_PATHWAY	Cocaine_addiction	RT		3	7.4E-1	1.0E0
	KEGG_PATHWAY	Circadian entrainment	RT		5	7.5E-1	1.0E0
	KEGG_PATHWAY	Vascular_smooth_muscle_contraction	RT		6	7.5E-1	1.0E0
	KEGG_PATHWAY	Estrogen_signaling_pathway	RT		5	7.8E-1	1.0E0
	KEGG_PATHWAY	cGMP-PKG_signaling_pathway	RT		7	8.5E-1	1.0E0
	KEGG_PATHWAY	Retrograde_endocannabinoid_signaling	RT		4	9.1E-1	1.0E0
	KEGG_PATHWAY	Alcoholism	RT		7	9.1E-1	1.0E0
	KEGG_PATHWAY	Cholinergic_synapse	RT		4	9.4E-1	1.0E0
	KEGG_PATHWAY	GnRH_signaling_pathway	RT		3	9.6E-1	1.0E0
	KEGG_PATHWAY	Adrenergic_signaling_in_cardiomyocytes	RT		3	1.0E0	1.0E0
Annotation Cluster 104		Enrichment Score: 0.24	G		Count	P_Value	Benjamini
	GOTERM_BP_DIRECT	chemotaxis	RT		8	2.9E-1	1.0E0
	GOTERM_BP_DIRECT	cellular calcium ion homeostasis	RT		4	7.8E-1	1.0E0
	GOTERM_BP_DIRECT	chemokine-mediated_signaling_pathway	RT		3	8.3E-1	1.0E0
Annotation Cluster 105		Enrichment Score: 0.24	G		Count	P_Value	Benjamini
	GOTERM_BP_DIRECT	viral_entry_into_host_cell	RT		5	4.7E-1	1.0E0
	GOTERM_MF_DIRECT	virus_receptor_activity	RT		4	5.9E-1	1.0E0
	UP_KEYWORDS	Host_cell_receptor_for_virus_entry	RT		3	7.1E-1	1.0E0
Annotation Cluster 106		Enrichment Score: 0.23	G		Count	P_Value	Benjamini
	GOTERM_BP_DIRECT	mitotic_nuclear_division	RT		13	4.1E-1	1.0E0
	UP_KEYWORDS	Cell_cycle	RT		26	5.1E-1	1.0E0
	UP_KEYWORDS	Cell_division	RT		15	6.2E-1	1.0E0
	GOTERM_BP_DIRECT	cell_division	RT		15	6.9E-1	1.0E0
	UP_KEYWORDS	Mitosis	RT		9	7.9E-1	1.0E0
Annotation Cluster 107		Enrichment Score: 0.22	G		Count	P_Value	Benjamini
	GOTERM_MF_DIRECT	ubiquitin-protein_transferase_activity	RT		16	4.6E-1	1.0E0
	GOTERM_MF_DIRECT	ligase_activity	RT		13	5.0E-1	1.0E0
	GOTERM_BP_DIRECT	protein_ubiquitination	RT		15	7.2E-1	1.0E0
	UP_KEYWORDS	Ubl_conjugation_pathway	RT		23	8.2E-1	1.0E0
Annotation Cluster 108		Enrichment Score: 0.21	G		Count	P_Value	Benjamini
	GOTERM_BP_DIRECT	RNA_export_from_nucleus	RT		4	4.4E-1	1.0E0
	GOTERM_BP_DIRECT	mRNA_export_from_nucleus	RT		5	6.5E-1	1.0E0
	GOTERM_BP_DIRECT	mRNA_3'-end_processing	RT		3	6.5E-1	1.0E0
	GOTERM_BP_DIRECT	termination_of_RNA_polymerase_II_transcription	RT		3	7.8E-1	1.0E0
Annotation Cluster 109		Enrichment Score: 0.21	G		Count	P_Value	Benjamini
	UP_KEYWORDS	Thiol_protease	RT		9	2.3E-1	9.4E-1
	GOTERM_MF_DIRECT	thiol-dependent_ubiquitin-specific_protease_activity	RT		5	4.6E-1	1.0E0
	GOTERM_BP_DIRECT	protein_deubiquitination	RT		4	8.2E-1	1.0E0
	INTERPRO	Peptidase_C19,_ubiquitin_carboxyl-terminal_hydrolase_2,_conserved_site	RT		3	8.2E-1	1.0E0
	INTERPRO	Peptidase_C19,_ubiquitin_carboxyl-terminal_hydrolase_2	RT		3	8.4E-1	1.0E0
	GOTERM_BP_DIRECT	ubiquitin-dependent_protein_catabolic_process	RT		5	9.6E-1	1.0E0
Annotation Cluster 110		Enrichment Score: 0.2	G		Count	P_Value	Benjamini
	UP_SEQ_FEATURE	active_site:4-aspartylphosphate_intermediate	RT		3	4.7E-1	1.0E0
	INTERPRO	HAD-like_domain	RT		4	6.4E-1	1.0E0
	UP_SEQ_FEATURE	metal_ion-binding_site:Magnesium	RT		4	8.4E-1	1.0E0
Annotation Cluster 111		Enrichment Score: 0.2	G		Count	P_Value	Benjamini
	UP_KEYWORDS	Nonsense-mediated_mRNA_decay	RT		3	3.0E-1	1.0E0
	KEGG_PATHWAY	mRNA_surveillance_pathway	RT		4	8.7E-1	1.0E0
	GOTERM_BP_DIRECT	nuclear-transcribed_mRNA_catabolic_process,_nonsense-mediated_decay	RT		3	9.7E-1	1.0E0
Annotation Cluster 112		Enrichment Score: 0.19	G		Count	P_Value	Benjamini
	UP_SEQ_FEATURE	domain:EGF-like_2; calcium-binding	RT		4	3.9E-1	1.0E0
	UP_SEQ_FEATURE	domain:EGF-like_3; calcium-binding	RT		3	4.4E-1	1.0E0</

Annotation Cluster 1	Enrichment Score: 4.36	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	domain:EGF-like 1	RT		6	5.0E-1	1.0E0
INTERPRO	EGF-like calcium-binding, conserved site	RT		5	6.0E-1	1.0E0
UP_KEYWORDS	EGF-like domain	RT		9	6.9E-1	1.0E0
INTERPRO	EGF-like, conserved site	RT		8	7.0E-1	1.0E0
INTERPRO	Epidermal growth factor-like domain	RT		9	7.3E-1	1.0E0
INTERPRO	EGF-like calcium-binding	RT		5	7.6E-1	1.0E0
INTERPRO	EGF-type aspartate/asparagine hydroxylation site	RT		4	8.1E-1	1.0E0
SMART	EGF CA	RT		5	8.2E-1	1.0E0
SMART	EGF	RT		7	8.4E-1	1.0E0
Annotation Cluster 113	Enrichment Score: 0.19	G		Count	P_Value	Benjamini
INTERPRO	SMAD/FHA domain	RT		4	3.7E-1	1.0E0
INTERPRO	Forkhead-associated (FHA) domain	RT		3	4.5E-1	1.0E0
UP_KEYWORDS	DNA damage	RT		12	7.9E-1	1.0E0
UP_KEYWORDS	DNA repair	RT		9	8.7E-1	1.0E0
GOTERM_BP_DIRECT	DNA repair	RT		6	9.8E-1	1.0E0
Annotation Cluster 114	Enrichment Score: 0.19	G		Count	P_Value	Benjamini
UP_KEYWORDS	Hydroxylation	RT		5	4.9E-1	1.0E0
GOTERM_BP_DIRECT	collagen catabolic process	RT		4	5.4E-1	1.0E0
INTERPRO	Collagen triple helix repeat	RT		4	6.5E-1	1.0E0
UP_KEYWORDS	Collagen	RT		4	7.3E-1	1.0E0
GOTERM_CC_DIRECT	collagen trimer	RT		3	9.0E-1	1.0E0
Annotation Cluster 115	Enrichment Score: 0.18	G		Count	P_Value	Benjamini
UP_KEYWORDS	mRNA splicing	RT		12	4.1E-1	1.0E0
GOTERM_BP_DIRECT	RNA splicing	RT		8	6.0E-1	1.0E0
UP_KEYWORDS	mRNA processing	RT		13	6.2E-1	1.0E0
UP_KEYWORDS	Spliceosome	RT		5	7.2E-1	1.0E0
GOTERM_BP_DIRECT	mRNA splicing, via spliceosome	RT		8	8.6E-1	1.0E0
KEGG_PATHWAY	Spliceosome	RT		5	9.3E-1	1.0E0
Annotation Cluster 116	Enrichment Score: 0.15	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	repeat:Solcar 3	RT		3	6.0E-1	1.0E0
UP_SEQ_FEATURE	repeat:Solcar 1	RT		3	6.3E-1	1.0E0
UP_SEQ_FEATURE	repeat:Solcar 2	RT		3	6.3E-1	1.0E0
INTERPRO	Mitochondrial substrate/solute carrier	RT		3	6.4E-1	1.0E0
INTERPRO	Mitochondrial carrier domain	RT		3	6.4E-1	1.0E0
UP_KEYWORDS	Mitochondrion inner membrane	RT		9	8.1E-1	1.0E0
GOTERM_MF_DIRECT	structural constituent of ribosome	RT		8	8.5E-1	1.0E0
GOTERM_BP_DIRECT	translation	RT		6	9.9E-1	1.0E0
Annotation Cluster 117	Enrichment Score: 0.14	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	domain:SCAN box	RT		3	6.8E-1	1.0E0
INTERPRO	Transcription regulator SCAN	RT		3	7.1E-1	1.0E0
SMART	SCAN	RT		3	7.4E-1	1.0E0
INTERPRO	Retrovirus capsid, C-terminal	RT		3	7.8E-1	1.0E0
Annotation Cluster 118	Enrichment Score: 0.13	G		Count	P_Value	Benjamini
UP_KEYWORDS	Symport	RT		5	6.3E-1	1.0E0
GOTERM_BP_DIRECT	sodium ion transport	RT		4	7.0E-1	1.0E0
UP_KEYWORDS	Sodium transport	RT		4	8.3E-1	1.0E0
UP_KEYWORDS	Sodium	RT		4	8.6E-1	1.0E0
Annotation Cluster 119	Enrichment Score: 0.12	G		Count	P_Value	Benjamini
INTERPRO	ATPase, AAA-type, core	RT		3	6.2E-1	1.0E0
INTERPRO	AAA+ ATPase domain	RT		5	8.1E-1	1.0E0
SMART	AAA	RT		5	8.6E-1	1.0E0
Annotation Cluster 120	Enrichment Score: 0.09	G		Count	P_Value	Benjamini
GOTERM_CC_DIRECT	chromosome, centromeric region	RT		3	6.9E-1	1.0E0
UP_KEYWORDS	Centromere	RT		5	7.7E-1	1.0E0
UP_KEYWORDS	Chromosome	RT		8	9.9E-1	1.0E0
Annotation Cluster 121	Enrichment Score: 0.08	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	domain:Ig-like V-type	RT		6	5.7E-1	1.0E0
INTERPRO	Immunoglobulin V-set	RT		8	1.0E-0	1.0E0
SMART	IGV	RT		5	1.0E-0	1.0E0
Annotation Cluster 122	Enrichment Score: 0.07	G		Count	P_Value	Benjamini
COG_ONTOLOGY	DNA replication, recombination, and repair	RT		4	6.9E-1	1.0E0
GOTERM_MF_DIRECT	helicase activity	RT		4	7.2E-1	1.0E0
UP_SEQ_FEATURE	domain:Helicase ATP-binding	RT		4	8.3E-1	1.0E0
INTERPRO	Helicase, superfamily 1/2, ATP-binding domain	RT		4	8.3E-1	1.0E0
UP_KEYWORDS	Helicase	RT		4	9.1E-1	1.0E0
UP_SEQ_FEATURE	domain:Helicase C-terminal	RT		3	9.3E-1	1.0E0
INTERPRO	Helicase, C-terminal	RT		3	9.4E-1	1.0E0
SMART	HELICc	RT		3	9.5E-1	1.0E0
SMART	DEXDc	RT		3	9.6E-1	1.0E0
Annotation Cluster 123	Enrichment Score: 0.06	G		Count	P_Value	Benjamini
GOTERM_BP_DIRECT	mitochondrial translational elongation	RT		4	7.3E-1	1.0E0
GOTERM_MF_DIRECT	structural constituent of ribosome	RT		8	8.5E-1	1.0E0
UP_KEYWORDS	Ribonucleoprotein	RT		9	8.8E-1	1.0E0
GOTERM_BP_DIRECT	mitochondrial translational termination	RT		3	9.0E-1	1.0E0
UP_KEYWORDS	Ribosomal protein	RT		3	9.9E-1	1.0E0
Annotation Cluster 124	Enrichment Score: 0.05	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	repeat:17	RT		3	6.5E-1	1.0E0

Annotation Cluster 1		Enrichment Score: 4.36	G		Count	P_Value	Benjamini
	UP_SEQ_FEATURE	repeat:16	RT		3	6.9E-1	1.0E0
	UP_SEQ_FEATURE	repeat:15	RT		3	7.9E-1	1.0E0
	UP_SEQ_FEATURE	repeat:14	RT		3	8.2E-1	1.0E0
	UP_SEQ_FEATURE	repeat:13	RT		3	8.4E-1	1.0E0
	UP_SEQ_FEATURE	repeat:12	RT		3	8.5E-1	1.0E0
	UP_SEQ_FEATURE	repeat:11	RT		3	8.7E-1	1.0E0
	UP_SEQ_FEATURE	repeat:10	RT		3	9.0E-1	1.0E0
	UP_SEQ_FEATURE	repeat:9	RT		3	9.2E-1	1.0E0
	UP_SEQ_FEATURE	repeat:7	RT		3	9.7E-1	1.0E0
	UP_SEQ_FEATURE	repeat:1	RT		6	9.7E-1	1.0E0
	UP_SEQ_FEATURE	repeat:2	RT		6	9.8E-1	1.0E0
	UP_SEQ_FEATURE	repeat:6	RT		3	9.8E-1	1.0E0
	UP_SEQ_FEATURE	repeat:5	RT		3	9.9E-1	1.0E0
	UP_SEQ_FEATURE	repeat:3	RT		4	9.9E-1	1.0E0
	UP_SEQ_FEATURE	repeat:4	RT		3	1.0E0	1.0E0
Annotation Cluster 125		Enrichment Score: 0.05	G		Count	P_Value	Benjamini
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 5	RT		20	7.4E-1	1.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 7	RT		16	8.0E-1	1.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 13	RT		7	8.1E-1	1.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 3	RT		22	8.1E-1	1.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 6	RT		17	8.3E-1	1.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	RT		21	8.3E-1	1.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 14	RT		5	8.6E-1	1.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 12	RT		8	8.8E-1	1.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 9	RT		12	8.9E-1	1.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 15	RT		4	9.0E-1	1.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 11	RT		9	9.0E-1	1.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 8	RT		13	9.1E-1	1.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 16	RT		3	9.1E-1	1.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	RT		17	9.2E-1	1.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 10	RT		10	9.2E-1	1.0E0
	INTERPRO	<u>Zinc finger, C2H2</u>	RT		26	9.3E-1	1.0E0
	GOTERM_MF_DIRECT	<u>nucleic acid binding</u>	RT		35	9.3E-1	1.0E0
	INTERPRO	<u>Zinc finger, C2H2-like</u>	RT		24	9.5E-1	1.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 4	RT		17	9.5E-1	1.0E0
	INTERPRO	<u>Zinc finger C2H2-type/integrase DNA-binding domain</u>	RT		22	9.5E-1	1.0E0
	UP_KEYWORDS	<u>Zinc-finger</u>	RT		54	9.8E-1	1.0E0
	UP_SEQ_FEATURE	domain:KRAB	RT		8	9.8E-1	1.0E0
	SMART	<u>ZnF_C2H2</u>	RT		24	9.8E-1	1.0E0
	INTERPRO	<u>Krueppel-associated box</u>	RT		10	9.8E-1	1.0E0
	SMART	<u>KRAB</u>	RT		10	9.9E-1	1.0E0
Annotation Cluster 126		Enrichment Score: 0.04	G		Count	P_Value	Benjamini
	UP_SEQ_FEATURE	repeat:ANK 1	RT		8	8.4E-1	1.0E0
	UP_SEQ_FEATURE	repeat:ANK 2	RT		8	8.5E-1	1.0E0
	UP_KEYWORDS	<u>ANK repeat</u>	RT		8	8.8E-1	1.0E0
	INTERPRO	<u>Ankyrin repeat</u>	RT		8	9.0E-1	1.0E0
	UP_SEQ_FEATURE	repeat:ANK 3	RT		6	9.1E-1	1.0E0
	INTERPRO	<u>Ankyrin repeat-containing domain</u>	RT		8	9.2E-1	1.0E0
	SMART	<u>ANK</u>	RT		8	9.3E-1	1.0E0
	UP_SEQ_FEATURE	repeat:ANK 4	RT		4	9.6E-1	1.0E0
	UP_SEQ_FEATURE	repeat:ANK 5	RT		3	9.8E-1	1.0E0
Annotation Cluster 127		Enrichment Score: 0.04	G		Count	P_Value	Benjamini
	GOTERM_MF_DIRECT	<u>nucleotide binding</u>	RT		13	8.3E-1	1.0E0
	INTERPRO	<u>Nucleotide-binding, alpha-beta plait</u>	RT		9	8.5E-1	1.0E0
	UP_SEQ_FEATURE	domain:RRM	RT		4	9.0E-1	1.0E0
	INTERPRO	<u>RNA recognition motif domain</u>	RT		6	9.5E-1	1.0E0
	UP_SEQ_FEATURE	domain:RRM 1	RT		3	9.6E-1	1.0E0
	UP_SEQ_FEATURE	domain:RRM 2	RT		3	9.6E-1	1.0E0
	SMART	<u>RRM</u>	RT		6	9.6E-1	1.0E0
Annotation Cluster 128		Enrichment Score: 0.03	G		Count	P_Value	Benjamini
	INTERPRO	<u>Zinc finger, RING/FYVE/PHD-type</u>	RT		15	8.8E-1	1.0E0
	UP_SEQ_FEATURE	zinc finger region:RING-type	RT		7	8.9E-1	1.0E0
	INTERPRO	<u>Zinc finger, RING-type</u>	RT		8	9.6E-1	1.0E0
	SMART	<u>RING</u>	RT		7	9.6E-1	1.0E0
	INTERPRO	<u>Zinc finger, RING-type, conserved site</u>	RT		4	9.7E-1	1.0E0
Annotation Cluster 129		Enrichment Score: 0.02	G		Count	P_Value	Benjamini
	INTERPRO	<u>Homeodomain-like</u>	RT		10	9.3E-1	1.0E0
	UP_KEYWORDS	<u>Homeobox</u>	RT		7	9.4E-1	1.0E0
	INTERPRO	<u>Homeodomain</u>	RT		7	9.5E-1	1.0E0
	SMART	<u>HOX</u>	RT		7	9.7E-1	1.0E0
	UP_SEQ_FEATURE	DNA-binding region:Homeobox	RT		3	1.0E0	1.0E0
Annotation Cluster 130		Enrichment Score: 0.01	G		Count	P_Value	Benjamini
	UP_KEYWORDS	<u>Postsynaptic cell membrane</u>	RT		4	9.7E-1	1.0E0
	UP_KEYWORDS	<u>Synapse</u>	RT		8	9.8E-1	1.0E0
	GOTERM_CC_DIRECT	<u>postsynaptic membrane</u>	RT		4	9.9E-1	1.0E0
Annotation Cluster 131		Enrichment Score: 0.01	G		Count	P_Value	Benjamini
	INTERPRO	<u>Tetratricopeptide repeat</u>	RT		3	9.8E-1	1.0E0

Annotation Cluster 1	Enrichment Score: 4.36	G		Count	P_Value	Benjamini
<input type="checkbox"/> SMART	TPR	RT		3	9.8E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:TPR 3	RT		3	9.8E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS	TPR repeat	RT		3	9.9E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:TPR 1	RT		3	9.9E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	repeat:TPR 2	RT		3	9.9E-1	1.0E0
<input type="checkbox"/> INTERPRO	Tetratricopeptide-like helical	RT		4	9.9E-1	1.0E0
Annotation Cluster 132	Enrichment Score: 0	G		Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY	Neuroactive ligand-receptor interaction	RT		6	1.0E0	1.0E0
<input type="checkbox"/> UP_KEYWORDS	Transducer	RT		10	1.0E0	1.0E0
<input type="checkbox"/> UP_KEYWORDS	G-protein coupled receptor	RT		7	1.0E0	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	G-protein coupled receptor activity	RT		6	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	G_protein-coupled receptor, rhodopsin-like	RT		5	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	GPCR, rhodopsin-like, 7TM	RT		5	1.0E0	1.0E0

1213 terms were not clustered.