

Functional Annotation Clustering

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Current Gene List: List_2

Current Background: Homo sapiens

282 DAVID IDs
 Options Classification Stringency Medium

58 Cluster(s)
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Annotation Cluster 1		Enrichment Score: 3.73	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	Actin-binding	RT	RT	15	2.1E-5	2.3E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	actin filament binding	RT	RT	10	2.0E-4	2.1E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	actin cytoskeleton	RT	RT	11	1.5E-3	5.4E-2
Annotation Cluster 2		Enrichment Score: 3.4	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_DIRECT	cell-cell adherens junction	RT	RT	15	3.3E-4	2.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell-cell adhesion	RT	RT	14	3.5E-4	2.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	cadherin binding involved in cell-cell adhesion	RT	RT	14	5.4E-4	4.6E-2
Annotation Cluster 3		Enrichment Score: 2.5	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH3	RT	RT	10	7.1E-4	7.7E-1
<input type="checkbox"/>	UP_KEYWORDS	SH3 domain	RT	RT	10	2.6E-3	7.3E-2
<input type="checkbox"/>	INTERPRO	Src homology-3 domain	RT	RT	10	4.6E-3	6.5E-1
<input type="checkbox"/>	SMART	SH3	RT	RT	10	1.1E-2	5.4E-1
Annotation Cluster 4		Enrichment Score: 2.27	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	Cell membrane	RT	RT	62	2.0E-3	6.3E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	plasma membrane	RT	RT	82	2.5E-3	6.7E-2
<input type="checkbox"/>	UP_KEYWORDS	Membrane	RT	RT	117	3.0E-2	3.8E-1
Annotation Cluster 5		Enrichment Score: 2.19	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	Calcium	RT	RT	26	3.4E-4	1.8E-2
<input type="checkbox"/>	INTERPRO	EF-hand-like domain	RT	RT	13	8.1E-4	3.7E-1
<input type="checkbox"/>	INTERPRO	EF-hand domain	RT	RT	11	1.9E-3	3.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium ion binding	RT	RT	22	3.4E-3	2.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 1	RT	RT	9	4.1E-3	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 2	RT	RT	9	4.1E-3	1.0E0
<input type="checkbox"/>	SMART	EFh	RT	RT	8	1.4E-2	5.4E-1
<input type="checkbox"/>	INTERPRO	EF-Hand 1, calcium-binding site	RT	RT	8	1.5E-2	8.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	calcium-binding region:1	RT	RT	5	1.0E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	calcium-binding region:2	RT	RT	4	2.2E-1	1.0E0
Annotation Cluster 6		Enrichment Score: 2.07	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	S100/Calbindin-D9k, conserved site	RT	RT	4	5.5E-3	6.5E-1
<input type="checkbox"/>	INTERPRO	S100/CaBP-9k-type, calcium binding, subdomain	RT	RT	4	8.3E-3	7.4E-1
<input type="checkbox"/>	SMART	SM01394	RT	RT	4	1.3E-2	5.4E-1
Annotation Cluster 7		Enrichment Score: 1.9	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium-dependent protein binding	RT	RT	8	2.8E-5	7.2E-3
<input type="checkbox"/>	UP_KEYWORDS	Annexin	RT	RT	3	1.5E-2	2.8E-1
<input type="checkbox"/>	UP_KEYWORDS	Calcium/phospholipid-binding	RT	RT	3	1.7E-2	2.8E-1
<input type="checkbox"/>	INTERPRO	Annexin	RT	RT	3	1.7E-2	8.4E-1
<input type="checkbox"/>	INTERPRO	Annexin repeat, conserved site	RT	RT	3	1.7E-2	8.4E-1
<input type="checkbox"/>	INTERPRO	Annexin repeat	RT	RT	3	1.7E-2	8.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Annexin 4	RT	RT	3	1.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Annexin 1	RT	RT	3	1.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Annexin 2	RT	RT	3	1.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Annexin 3	RT	RT	3	1.7E-2	1.0E0
<input type="checkbox"/>	SMART	ANX	RT	RT	3	2.5E-2	7.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium-dependent phospholipid binding	RT	RT	3	2.2E-1	1.0E0
Annotation Cluster 8		Enrichment Score: 1.74	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_DIRECT	brush border	RT	RT	6	1.9E-3	6.1E-2
<input type="checkbox"/>	UP_KEYWORDS	Calmodulin-binding	RT	RT	8	4.5E-3	1.2E-1
<input type="checkbox"/>	INTERPRO	IQ motif, EF-hand binding site	RT	RT	6	8.7E-3	7.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	calmodulin binding	RT	RT	9	8.7E-3	4.1E-1
<input type="checkbox"/>	SMART	IQ	RT	RT	5	1.4E-2	5.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Myosin head-like	RT	RT	4	1.4E-2	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	actin-dependent ATPase activity	RT	RT	3	1.6E-2	5.2E-1
<input type="checkbox"/>	INTERPRO	Myosin, N-terminal, SH3-like	RT	RT	3	1.9E-2	8.5E-1
<input type="checkbox"/>	INTERPRO	Myosin head, motor domain	RT	RT	4	2.0E-2	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	actin filament-based movement	RT	RT	3	2.8E-2	1.0E0
<input type="checkbox"/>	INTERPRO	Myosin-like IQ motif-containing domain	RT	RT	3	3.0E-2	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Myosin	RT	RT	4	3.1E-2	3.8E-1
<input type="checkbox"/>	SMART	MYSc	RT	RT	4	3.4E-2	8.4E-1
<input type="checkbox"/>	UP_KEYWORDS	Motor protein	RT	RT	6	3.6E-2	4.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	microfilament motor activity	RT	RT	3	3.7E-2	5.8E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	myosin complex	RT	RT	4	3.7E-2	3.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	motor activity	RT	RT	4	8.0E-2	1.0E0
Annotation Cluster 9		Enrichment Score: 1.71	G	RT	Count	P_Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	Regulation of actin cytoskeleton	RT	RT	13	2.2E-4	1.3E-2

Annotation Cluster 1	Enrichment Score: 3.73	G			Count	P_Value	Benjamini
KEGG_PATHWAY	Adherens junction	RT			6	7.0E-3	1.8E-1
KEGG_PATHWAY	Viral carcinogenesis	RT			8	6.0E-2	6.5E-1
KEGG_PATHWAY	Focal adhesion	RT			7	1.4E-1	7.7E-1
BIOCARTA	Integrin Signaling Pathway	RT			3	2.1E-1	1.0E0
Annotation Cluster 10	Enrichment Score: 1.68	G			Count	P_Value	Benjamini
UP_KEYWORDS	Calmodulin-binding	RT			8	4.5E-3	1.2E-1
INTERPRO	IQ motif, EF-hand binding site	RT			6	8.7E-3	7.4E-1
SMART	IQ	RT			5	1.4E-2	5.4E-1
UP_SEQ_FEATURE	domain:IQ 4	RT			3	1.7E-2	1.0E0
UP_SEQ_FEATURE	domain:IQ 3	RT			3	3.6E-2	1.0E0
UP_SEQ_FEATURE	domain:IQ 1	RT			3	7.5E-2	1.0E0
UP_SEQ_FEATURE	domain:IQ 2	RT			3	7.5E-2	1.0E0
Annotation Cluster 11	Enrichment Score: 1.63	G			Count	P_Value	Benjamini
KEGG_PATHWAY	Tight junction	RT			9	1.1E-4	1.3E-2
GOTERM_CC_DIRECT	bicellular tight junction	RT			7	6.6E-3	1.2E-1
KEGG_PATHWAY	Leukocyte transendothelial migration	RT			7	1.3E-2	3.1E-1
INTERPRO	Claudin, conserved site	RT			3	4.0E-2	1.0E0
GOTERM_BP_DIRECT	calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molecules	RT			3	4.2E-2	1.0E0
INTERPRO	Claudin	RT			3	4.3E-2	1.0E0
UP_KEYWORDS	Tight junction	RT			4	1.1E-1	6.1E-1
INTERPRO	PMP-22/EMP/MP20/Claudin	RT			3	1.4E-1	1.0E0
KEGG_PATHWAY	Hepatitis C	RT			5	1.9E-1	8.5E-1
Annotation Cluster 12	Enrichment Score: 1.45	G			Count	P_Value	Benjamini
INTERPRO	Insulin-like growth factor binding protein-related protein (IGFBP-rP), MAC25	RT			3	1.2E-3	3.7E-1
UP_SEQ_FEATURE	domain:IGFBP N-terminal	RT			3	3.0E-2	1.0E0
GOTERM_MF_DIRECT	insulin-like growth factor binding	RT			3	3.0E-2	5.5E-1
INTERPRO	Insulin-like growth factor-binding protein, IGFBP	RT			3	3.3E-2	1.0E0
INTERPRO	Insulin-like growth factor binding protein, N-terminal	RT			5	1.4E-1	1.0E0
GOTERM_BP_DIRECT	regulation of cell growth	RT			3	3.6E-1	1.0E0
Annotation Cluster 13	Enrichment Score: 1.33	G			Count	P_Value	Benjamini
GOTERM_BP_DIRECT	transcription from RNA polymerase II promoter	RT			16	1.5E-2	1.0E0
GOTERM_MF_DIRECT	transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	RT			9	2.9E-2	5.5E-1
UP_KEYWORDS	Transcription	RT			41	8.6E-2	5.5E-1
GOTERM_BP_DIRECT	positive regulation of transcription from RNA polymerase II promoter	RT			21	1.3E-1	1.0E0
Annotation Cluster 14	Enrichment Score: 1.31	G			Count	P_Value	Benjamini
UP_KEYWORDS	Alzheimer disease	RT			4	1.2E-3	4.1E-2
UP_KEYWORDS	Amyloidosis	RT			3	5.4E-2	4.5E-1
KEGG_PATHWAY	Alzheimer's disease	RT			6	1.6E-1	8.3E-1
UP_KEYWORDS	Neurodegeneration	RT			5	5.5E-1	1.0E0
Annotation Cluster 15	Enrichment Score: 1.19	G			Count	P_Value	Benjamini
GOTERM_CC_DIRECT	actin filament	RT			6	2.7E-3	6.7E-2
INTERPRO	Calponin homology domain	RT			3	3.0E-1	1.0E0
SMART	CH	RT			3	3.3E-1	1.0E0
Annotation Cluster 16	Enrichment Score: 1.18	G			Count	P_Value	Benjamini
GOTERM_BP_DIRECT	interferon-gamma-mediated signaling pathway	RT			6	5.0E-3	9.8E-1
GOTERM_BP_DIRECT	T cell costimulation	RT			6	7.4E-3	1.0E0
GOTERM_CC_DIRECT	trans-Golgi network membrane	RT			6	7.7E-3	1.2E-1
UP_KEYWORDS	MHC II	RT			3	2.1E-2	3.4E-1
GOTERM_MF_DIRECT	MHC class II receptor activity	RT			3	2.1E-2	5.3E-1
GOTERM_BP_DIRECT	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	RT			3	2.8E-2	1.0E0
INTERPRO	MHC class II, alpha/beta chain, N-terminal	RT			3	3.7E-2	1.0E0
GOTERM_CC_DIRECT	MHC class II protein complex	RT			3	4.1E-2	4.1E-1
INTERPRO	Immunoglobulin/major histocompatibility complex, conserved site	RT			4	5.6E-2	1.0E0
UP_KEYWORDS	Lysosome	RT			8	6.5E-2	4.8E-1
GOTERM_CC_DIRECT	integral component of luminal side of endoplasmic reticulum membrane	RT			3	6.8E-2	5.6E-1
GOTERM_CC_DIRECT	transport vesicle membrane	RT			3	1.1E-1	6.9E-1
GOTERM_CC_DIRECT	clathrin-coated endocytic vesicle membrane	RT			3	1.2E-1	7.1E-1
INTERPRO	MHC classes I/II-like antigen recognition protein	RT			3	1.4E-1	1.0E0
GOTERM_BP_DIRECT	antigen processing and presentation of exogenous peptide antigen via MHC class II	RT			4	1.7E-1	1.0E0
GOTERM_CC_DIRECT	ER to Golgi transport vesicle membrane	RT			3	1.8E-1	8.5E-1
GOTERM_CC_DIRECT	lysosomal membrane	RT			7	2.2E-1	9.3E-1
GOTERM_CC_DIRECT	endocytic vesicle membrane	RT			3	2.5E-1	1.0E0
INTERPRO	Immunoglobulin C1-set	RT			3	2.6E-1	1.0E0
SMART	IGc1	RT			3	3.2E-1	1.0E0
KEGG_PATHWAY	Antigen processing and presentation	RT			3	3.7E-1	1.0E0
Annotation Cluster 17	Enrichment Score: 1.09	G			Count	P_Value	Benjamini
UP_KEYWORDS	Immunity	RT			13	3.8E-2	4.1E-1
UP_KEYWORDS	Innate immunity	RT			8	6.3E-2	4.8E-1
GOTERM_BP_DIRECT	innate immune response	RT			10	2.3E-1	1.0E0
Annotation Cluster 18	Enrichment Score: 1.03	G			Count	P_Value	Benjamini
KEGG_PATHWAY	B cell receptor signaling pathway	RT			6	6.2E-3	1.8E-1

Annotation Cluster 1	Enrichment Score: 3.73	G		Count	P_Value	Benjamini
GOTERM_BP_DIRECT	stimulatory C-type lectin receptor signaling pathway	RT		5	8.2E-2	1.0E0
GOTERM_BP_DIRECT	Fc-epsilon receptor signaling pathway	RT		6	1.5E-1	1.0E0
BIOCARTA	Fc Epsilon Receptor I Signaling in Mast Cells	RT		3	2.3E-1	1.0E0
KEGG_PATHWAY	NF-kappa B signaling pathway	RT		3	4.4E-1	1.0E0
Annotation Cluster 19	Enrichment Score: 1.02	G		Count	P_Value	Benjamini
UP_KEYWORDS	Guanine-nucleotide releasing factor	RT		9	9.2E-4	3.6E-2
GOTERM_BP_DIRECT	positive regulation of GTPase activity	RT		17	1.6E-2	1.0E0
INTERPRO	Guanine-nucleotide dissociation stimulator, CDC24, conserved site	RT		3	3.7E-2	1.0E0
UP_SEQ_FEATURE	domain:PH	RT		8	5.3E-2	1.0E0
UP_SEQ_FEATURE	domain:DH	RT		4	6.7E-2	1.0E0
INTERPRO	Dbl homology (DH) domain	RT		4	8.4E-2	1.0E0
INTERPRO	Pleckstrin homology domain	RT		8	1.0E-1	1.0E0
GOTERM_MF_DIRECT	guanyl-nucleotide exchange factor activity	RT		5	1.1E-1	1.0E0
GOTERM_MF_DIRECT	Rho guanyl-nucleotide exchange factor activity	RT		4	1.1E-1	1.0E0
SMART	RhoGEF	RT		4	1.2E-1	1.0E0
GOTERM_BP_DIRECT	regulation of Rho protein signal transduction	RT		4	1.3E-1	1.0E0
GOTERM_BP_DIRECT	regulation of small GTPase mediated signal transduction	RT		5	1.6E-1	1.0E0
SMART	PH	RT		8	1.9E-1	1.0E0
INTERPRO	Pleckstrin homology-like domain	RT		9	2.8E-1	1.0E0
GOTERM_MF_DIRECT	GTPase activator activity	RT		6	4.2E-1	1.0E0
UP_KEYWORDS	GTPase activation	RT		4	4.9E-1	1.0E0
GOTERM_BP_DIRECT	intracellular signal transduction	RT		6	7.6E-1	1.0E0
Annotation Cluster 20	Enrichment Score: 1.02	G		Count	P_Value	Benjamini
UP_KEYWORDS	Inflammatory response	RT		6	5.4E-2	4.5E-1
UP_KEYWORDS	Innate immunity	RT		8	6.3E-2	4.8E-1
GOTERM_BP_DIRECT	regulation of inflammatory response	RT		3	2.6E-1	1.0E0
Annotation Cluster 21	Enrichment Score: 0.95	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	domain:WW	RT		3	3.6E-2	1.0E0
INTERPRO	WW domain	RT		3	1.8E-1	1.0E0
SMART	WW	RT		3	2.2E-1	1.0E0
Annotation Cluster 22	Enrichment Score: 0.94	G		Count	P_Value	Benjamini
GOTERM_CC_DIRECT	integral component of plasma membrane	RT		33	1.0E-2	1.6E-1
UP_KEYWORDS	Membrane	RT		117	3.0E-2	3.8E-1
UP_KEYWORDS	Glycoprotein	RT		75	3.6E-2	4.1E-1
UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT		58	7.3E-2	1.0E0
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		69	8.1E-2	1.0E0
UP_SEQ_FEATURE	signal peptide	RT		56	8.2E-2	1.0E0
UP_KEYWORDS	Disulfide bond	RT		56	8.7E-2	5.5E-1
UP_SEQ_FEATURE	disulfide bond	RT		47	1.7E-1	1.0E0
UP_SEQ_FEATURE	topological domain:Extracellular	RT		45	1.8E-1	1.0E0
UP_KEYWORDS	Signal	RT		63	1.9E-1	8.0E-1
UP_KEYWORDS	Transmembrane helix	RT		81	2.9E-1	9.9E-1
UP_KEYWORDS	Transmembrane	RT		81	3.0E-1	1.0E0
UP_SEQ_FEATURE	transmembrane region	RT		74	3.2E-1	1.0E0
GOTERM_CC_DIRECT	integral component of membrane	RT		71	8.2E-1	1.0E0
Annotation Cluster 23	Enrichment Score: 0.89	G		Count	P_Value	Benjamini
GOTERM_BP_DIRECT	lipopolysaccharide-mediated signaling pathway	RT		3	8.9E-2	1.0E0
GOTERM_BP_DIRECT	Fc-gamma receptor signaling pathway involved in phagocytosis	RT		5	1.4E-1	1.0E0
KEGG_PATHWAY	Fc gamma R-mediated phagocytosis	RT		4	1.7E-1	8.5E-1
Annotation Cluster 24	Enrichment Score: 0.89	G		Count	P_Value	Benjamini
KEGG_PATHWAY	Platelet activation	RT		7	2.3E-2	4.7E-1
BIOCARTA	Influence of Ras and Rho proteins on G1 to S Transition	RT		4	2.3E-2	1.0E0
KEGG_PATHWAY	Sphingolipid signaling pathway	RT		6	5.3E-2	6.5E-1
GOTERM_BP_DIRECT	platelet activation	RT		5	1.1E-1	1.0E0
BIOCARTA	Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia	RT		3	1.1E-1	1.0E0
KEGG_PATHWAY	Oxytocin signaling pathway	RT		6	1.1E-1	7.4E-1
KEGG_PATHWAY	Vascular smooth muscle contraction	RT		5	1.4E-1	7.7E-1
KEGG_PATHWAY	Focal adhesion	RT		7	1.4E-1	7.7E-1
KEGG_PATHWAY	cGMP-PKG signaling pathway	RT		5	2.8E-1	1.0E0
KEGG_PATHWAY	Colorectal cancer	RT		3	2.8E-1	1.0E0
KEGG_PATHWAY	Thyroid hormone signaling pathway	RT		4	3.1E-1	1.0E0
KEGG_PATHWAY	Axon guidance	RT		4	3.7E-1	1.0E0
UP_KEYWORDS	Magnesium	RT		9	4.6E-1	1.0E0
Annotation Cluster 25	Enrichment Score: 0.87	G		Count	P_Value	Benjamini
GOTERM_MF_DIRECT	transcription factor activity, sequence-specific DNA binding	RT		23	3.9E-2	5.8E-1
UP_KEYWORDS	DNA-binding	RT		36	8.1E-2	5.5E-1
UP_KEYWORDS	Transcription	RT		41	8.6E-2	5.5E-1
UP_KEYWORDS	Transcription regulation	RT		40	8.6E-2	5.5E-1
UP_KEYWORDS	Nucleus	RT		81	1.0E-1	6.1E-1
GOTERM_MF_DIRECT	DNA binding	RT		33	1.1E-1	1.0E0
GOTERM_BP_DIRECT	regulation of transcription, DNA-templated	RT		24	5.7E-1	1.0E0
GOTERM_BP_DIRECT	transcription, DNA-templated	RT		29	7.1E-1	1.0E0
Annotation Cluster 26	Enrichment Score: 0.86	G		Count	P_Value	Benjamini
UP_KEYWORDS	Phospholipid biosynthesis	RT		3	1.2E-1	6.2E-1

Annotation Cluster 1	Enrichment Score: 3.73	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	phospholipid biosynthetic process	RT		3	1.3E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS	Phospholipid metabolism	RT		3	1.4E-1	6.7E-1
<input type="checkbox"/> UP_KEYWORDS	Lipid biosynthesis	RT		5	1.6E-1	7.2E-1
Annotation Cluster 27	Enrichment Score: 0.84	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	triglyceride biosynthetic process	RT		3	6.2E-2	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	phosphatidic acid biosynthetic process	RT		3	1.0E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Glycerophospholipid metabolism	RT		3	4.8E-1	1.0E0
Annotation Cluster 28	Enrichment Score: 0.83	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_BP_DIRECT	embryonic skeletal system morphogenesis	RT		4	2.3E-2	1.0E0
<input type="checkbox"/> INTERPRO	Homeodomain-like	RT		10	5.7E-2	1.0E0
<input type="checkbox"/> UP_KEYWORDS	Homeobox	RT		8	6.4E-2	4.8E-1
<input type="checkbox"/> INTERPRO	Homeodomain	RT		8	8.0E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	DNA-binding region:Homeobox	RT		6	1.2E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	anterior/posterior pattern specification	RT		4	1.3E-1	1.0E0
<input type="checkbox"/> INTERPRO	Homeodomain, metazoa	RT		4	1.5E-1	1.0E0
<input type="checkbox"/> SMART	HOX	RT		7	2.9E-1	1.0E0
<input type="checkbox"/> INTERPRO	Homeobox, conserved site	RT		5	3.0E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	chromatin binding	RT		7	5.5E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	sequence-specific DNA binding	RT		5	9.6E-1	1.0E0
Annotation Cluster 29	Enrichment Score: 0.83	G		Count	P_Value	Benjamini
<input type="checkbox"/> KEGG_PATHWAY	Cell cycle	RT		6	6.0E-2	6.5E-1
<input type="checkbox"/> BIOCARTA	Cyclins and Cell Cycle Regulation	RT		3	1.1E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	G1/S transition of mitotic cell cycle	RT		3	4.7E-1	1.0E0
Annotation Cluster 30	Enrichment Score: 0.83	G		Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_MF_DIRECT	transmembrane receptor protein tyrosine phosphatase activity	RT		3	2.7E-2	5.5E-1
<input type="checkbox"/> INTERPRO	Protein-tyrosine phosphatase, catalytic	RT		4	6.3E-2	1.0E0
<input type="checkbox"/> SMART	PTPc motif	RT		4	1.0E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS	Protein phosphatase	RT		5	1.0E-1	6.1E-1
<input type="checkbox"/> INTERPRO	Protein-tyrosine phosphatase, receptor/non-receptor type	RT		3	1.0E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	active site:Phosphocysteine intermediate	RT		4	1.1E-1	1.0E0
<input type="checkbox"/> INTERPRO	Protein-tyrosine/Dual specificity phosphatase	RT		4	1.2E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	protein dephosphorylation	RT		5	1.3E-1	1.0E0
<input type="checkbox"/> SMART	PTPc	RT		3	1.4E-1	1.0E0
<input type="checkbox"/> INTERPRO	Fibronectin, type III	RT		6	1.8E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	peptidyl-tyrosine dephosphorylation	RT		4	2.0E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:Fibronectin type-III 4	RT		3	2.1E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:Fibronectin type-III 2	RT		4	2.8E-1	1.0E0
<input type="checkbox"/> SMART	FN3	RT		5	2.8E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:Fibronectin type-III 1	RT		4	2.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	Protein-tyrosine phosphatase, active site	RT		3	3.0E-1	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:Fibronectin type-III 3	RT		3	3.2E-1	1.0E0
Annotation Cluster 31	Enrichment Score: 0.81	G		Count	P_Value	Benjamini
<input type="checkbox"/> BIOCARTA	Influence of Ras and Rho proteins on G1 to S Transition	RT		4	2.3E-2	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Acute myeloid leukemia	RT		4	6.9E-2	6.7E-1
<input type="checkbox"/> KEGG_PATHWAY	Hepatitis B	RT		6	1.0E-1	7.1E-1
<input type="checkbox"/> KEGG_PATHWAY	Pathways in cancer	RT		11	1.3E-1	7.7E-1
<input type="checkbox"/> KEGG_PATHWAY	Ras signaling pathway	RT		7	1.9E-1	8.5E-1
<input type="checkbox"/> KEGG_PATHWAY	FoxO signaling pathway	RT		5	1.9E-1	8.5E-1
<input type="checkbox"/> KEGG_PATHWAY	PI3K-Akt signaling pathway	RT		9	2.3E-1	9.8E-1
<input type="checkbox"/> KEGG_PATHWAY	Pancreatic cancer	RT		3	3.0E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Chronic myeloid leukemia	RT		3	3.5E-1	1.0E0
<input type="checkbox"/> KEGG_PATHWAY	Prostate cancer	RT		3	4.4E-1	1.0E0
Annotation Cluster 32	Enrichment Score: 0.77	G		Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	GPCR, family 2, secretin-like, conserved site	RT		4	1.4E-2	8.4E-1
<input type="checkbox"/> UP_SEQ_FEATURE	site:Cleavage	RT		5	1.6E-2	1.0E0
<input type="checkbox"/> INTERPRO	GPCR, family 2, secretin-like	RT		4	3.6E-2	1.0E0
<input type="checkbox"/> INTERPRO	GPCR, family 2-like	RT		4	5.9E-2	1.0E0
<input type="checkbox"/> INTERPRO	GPCR, family 2, extracellular hormone receptor domain	RT		3	6.2E-2	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	cell surface receptor signaling pathway	RT		9	6.6E-2	1.0E0
<input type="checkbox"/> SMART	HormR	RT		3	7.2E-2	1.0E0
<input type="checkbox"/> UP_SEQ_FEATURE	domain:GPS	RT		3	8.7E-2	1.0E0
<input type="checkbox"/> INTERPRO	GPS domain	RT		3	9.6E-2	1.0E0
<input type="checkbox"/> SMART	GPS	RT		3	1.1E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS	Transducer	RT		11	7.7E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS	Receptor	RT		18	9.0E-1	1.0E0
<input type="checkbox"/> GOTERM_BP_DIRECT	G-protein coupled receptor signaling pathway	RT		11	9.0E-1	1.0E0
<input type="checkbox"/> UP_KEYWORDS	G-protein coupled receptor	RT		8	9.4E-1	1.0E0
<input type="checkbox"/> GOTERM_MF_DIRECT	G-protein coupled receptor activity	RT		7	9.6E-1	1.0E0
<input type="checkbox"/> INTERPRO	G_protein-coupled receptor, rhodopsin-like	RT		4	1.0E0	1.0E0
<input type="checkbox"/> INTERPRO	GPCR, rhodopsin-like, 7TM	RT		4	1.0E0	1.0E0
Annotation Cluster 33	Enrichment Score: 0.71	G		Count	P_Value	Benjamini
<input type="checkbox"/> UP_KEYWORDS	Lectin	RT		7	2.8E-2	3.8E-1
<input type="checkbox"/> GOTERM_MF_DIRECT	carbohydrate binding	RT		6	1.8E-1	1.0E0
<input type="checkbox"/> INTERPRO	C-type lectin-like	RT		4	1.9E-1	1.0E0
<input type="checkbox"/> INTERPRO	C-type lectin fold	RT		4	2.2E-1	1.0E0

Annotation Cluster 1	Enrichment Score: 3.73	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	domain:C-type lectin	RT		3	3.1E-1	1.0E0
INTERPRO	C-type lectin	RT		3	3.7E-1	1.0E0
SMART	CLECT	RT		3	4.5E-1	1.0E0
Annotation Cluster 34	Enrichment Score: 0.7	G		Count	P_Value	Benjamini
KEGG_PATHWAY	Neurotrophin_signaling_pathway	RT		5	1.5E-1	8.0E-1
KEGG_PATHWAY	Ras_signaling_pathway	RT		7	1.9E-1	8.5E-1
KEGG_PATHWAY	Rap1_signaling_pathway	RT		6	2.9E-1	1.0E0
Annotation Cluster 35	Enrichment Score: 0.69	G		Count	P_Value	Benjamini
UP_KEYWORDS	Sushi	RT		3	1.7E-1	7.4E-1
INTERPRO	Sushi/SCR/CCP	RT		3	2.0E-1	1.0E0
SMART	CCP	RT		3	2.5E-1	1.0E0
Annotation Cluster 36	Enrichment Score: 0.68	G		Count	P_Value	Benjamini
GOTERM_CC_DIRECT	extrinsic component of cytoplasmic side of plasma membrane	RT		6	3.3E-3	7.5E-2
GOTERM_BP_DIRECT	transmembrane receptor protein tyrosine kinase signaling_pathway	RT		6	1.7E-2	1.0E0
GOTERM_MF_DIRECT	non-membrane spanning protein tyrosine kinase activity	RT		4	3.3E-2	5.6E-1
UP_KEYWORDS	Proto-oncogene	RT		8	4.0E-2	4.1E-1
UP_KEYWORDS	Tyrosine-protein kinase	RT		5	6.4E-2	4.8E-1
UP_KEYWORDS	Kinase	RT		16	7.1E-2	5.0E-1
UP_SEQ_FEATURE	active site:Proton acceptor	RT		15	7.9E-2	1.0E0
UP_SEQ_FEATURE	binding site:ATP	RT		13	8.2E-2	1.0E0
UP_KEYWORDS	ATP-binding	RT		25	1.2E-1	6.2E-1
UP_SEQ_FEATURE	domain:Protein kinase	RT		11	1.3E-1	1.0E0
INTERPRO	Tyrosine-protein kinase_catalytic_domain	RT		4	1.3E-1	1.0E0
GOTERM_BP_DIRECT	peptidyl-tyrosine autophosphorylation	RT		3	1.3E-1	1.0E0
GOTERM_MF_DIRECT	protein tyrosine kinase activity	RT		5	1.5E-1	1.0E0
KEGG_PATHWAY	Neurotrophin_signaling_pathway	RT		5	1.5E-1	8.0E-1
UP_KEYWORDS	Transferase	RT		29	1.6E-1	7.2E-1
UP_KEYWORDS	Nucleotide-binding	RT		30	1.6E-1	7.2E-1
INTERPRO	Protein kinase_catalytic_domain	RT		11	1.7E-1	1.0E0
GOTERM_BP_DIRECT	protein phosphorylation	RT		11	1.8E-1	1.0E0
INTERPRO	Protein kinase_ATP_binding_site	RT		9	1.9E-1	1.0E0
SMART	TyrKc	RT		4	1.9E-1	1.0E0
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT		18	2.1E-1	1.0E0
INTERPRO	Protein kinase-like_domain	RT		11	2.4E-1	1.0E0
KEGG_PATHWAY	MAPK_signaling_pathway	RT		7	2.6E-1	1.0E0
UP_KEYWORDS	Myristate	RT		5	2.7E-1	9.5E-1
GOTERM_MF_DIRECT	ATP binding	RT		27	2.7E-1	1.0E0
BIOCARTA	Keratinocyte Differentiation	RT		3	3.1E-1	1.0E0
INTERPRO	Serine-threonine_tyrosine_protein_kinase_catalytic_domain	RT		4	3.3E-1	1.0E0
UP_SEQ_FEATURE	domain:SH2	RT		3	3.8E-1	1.0E0
INTERPRO	Tyrosine-protein kinase_active_site	RT		3	4.0E-1	1.0E0
UP_KEYWORDS	SH2_domain	RT		3	4.3E-1	1.0E0
GOTERM_BP_DIRECT	peptidyl-tyrosine phosphorylation	RT		4	4.3E-1	1.0E0
UP_KEYWORDS	Magnesium	RT		9	4.6E-1	1.0E0
INTERPRO	Serine/threonine_protein_kinase_active_site	RT		6	4.6E-1	1.0E0
UP_SEQ_FEATURE	lipid moiety-binding region:N-myristoyl glycine	RT		3	4.7E-1	1.0E0
INTERPRO	SH2_domain	RT		3	4.9E-1	1.0E0
KEGG_PATHWAY	TNF_signaling_pathway	RT		3	5.5E-1	1.0E0
SMART	SH2	RT		3	5.5E-1	1.0E0
BIOCARTA	MAPKinase Signaling Pathway	RT		3	6.1E-1	1.0E0
SMART	S_TKc	RT		7	6.2E-1	1.0E0
GOTERM_MF_DIRECT	protein kinase activity	RT		6	6.4E-1	1.0E0
GOTERM_BP_DIRECT	positive regulation of cell proliferation	RT		7	7.4E-1	1.0E0
GOTERM_BP_DIRECT	protein autophosphorylation	RT		3	7.5E-1	1.0E0
UP_KEYWORDS	Serine/threonine_protein_kinase	RT		5	7.8E-1	1.0E0
GOTERM_MF_DIRECT	protein serine_threonine_kinase activity	RT		4	9.3E-1	1.0E0
Annotation Cluster 37	Enrichment Score: 0.65	G		Count	P_Value	Benjamini
UP_KEYWORDS	Metal-binding	RT		64	1.7E-2	2.8E-1
UP_SEQ_FEATURE	zinc finger region:C2H2-type 16	RT		5	5.3E-2	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 13	RT		7	6.3E-2	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 14	RT		6	6.4E-2	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 9	RT		10	8.6E-2	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 17	RT		4	1.0E-1	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 7	RT		11	1.1E-1	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 15	RT		5	1.1E-1	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 11	RT		8	1.2E-1	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 8	RT		10	1.3E-1	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 12	RT		7	1.4E-1	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 6	RT		11	1.5E-1	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 3	RT		13	1.7E-1	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 19	RT		3	1.7E-1	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 10	RT		8	1.9E-1	1.0E0
INTERPRO	Zinc_finger_C2H2-like	RT		15	2.2E-1	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 18	RT		3	2.2E-1	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 5	RT		11	2.3E-1	1.0E0

Annotation Cluster 1	Enrichment Score: 3.73	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	RT		11	3.4E-1	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	RT		10	3.5E-1	1.0E0
INTERPRO	<u>Zinc_finger_C2H2</u>	RT		14	3.7E-1	1.0E0
UP_KEYWORDS	Zinc	RT		34	4.1E-1	1.0E0
GOTERM_MF_DIRECT	nucleic acid binding	RT		17	4.4E-1	1.0E0
INTERPRO	Zinc_finger_C2H2-type/integrase DNA-binding domain	RT		12	4.6E-1	1.0E0
SMART	ZnF_C2H2	RT		15	4.9E-1	1.0E0
UP_KEYWORDS	Zinc-finger	RT		25	5.2E-1	1.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 4	RT		9	5.6E-1	1.0E0
UP_SEQ_FEATURE	domain:KRAB	RT		5	6.9E-1	1.0E0
GOTERM_BP_DIRECT	transcription_DNA-templated	RT		29	7.1E-1	1.0E0
GOTERM_MF_DIRECT	metal ion binding	RT		30	7.2E-1	1.0E0
INTERPRO	Krueppel-associated box	RT		5	8.4E-1	1.0E0
SMART	KRAB	RT		5	9.2E-1	1.0E0
Annotation Cluster 38	Enrichment Score: 0.65	G		Count	P_Value	Benjamini
KEGG_PATHWAY	Toxoplasmosis	RT		6	3.9E-2	6.0E-1
KEGG_PATHWAY	Influenza A	RT		5	3.4E-1	1.0E0
KEGG_PATHWAY	Herpes simplex infection	RT		3	8.2E-1	1.0E0
Annotation Cluster 39	Enrichment Score: 0.64	G		Count	P_Value	Benjamini
KEGG_PATHWAY	Viral myocarditis	RT		4	7.2E-2	6.7E-1
KEGG_PATHWAY	Influenza A	RT		5	3.4E-1	1.0E0
KEGG_PATHWAY	Phagosome	RT		4	4.7E-1	1.0E0
Annotation Cluster 40	Enrichment Score: 0.59	G		Count	P_Value	Benjamini
UP_KEYWORDS	Immunoglobulin domain	RT		13	6.5E-2	4.8E-1
INTERPRO	Immunoglobulin subtype	RT		12	1.1E-1	1.0E0
INTERPRO	Immunoglobulin I-set	RT		5	1.5E-1	1.0E0
INTERPRO	Immunoglobulin-like domain	RT		16	1.5E-1	1.0E0
UP_SEQ_FEATURE	domain:Ig-like C2-type 5	RT		3	1.7E-1	1.0E0
INTERPRO	Immunoglobulin-like fold	RT		18	2.2E-1	1.0E0
SMART	IG	RT		12	2.7E-1	1.0E0
UP_SEQ_FEATURE	domain:Ig-like C2-type 4	RT		3	2.8E-1	1.0E0
UP_SEQ_FEATURE	domain:Ig-like C2-type 1	RT		5	3.0E-1	1.0E0
UP_SEQ_FEATURE	domain:Ig-like C2-type 2	RT		5	3.0E-1	1.0E0
INTERPRO	Immunoglobulin subtype 2	RT		5	4.9E-1	1.0E0
UP_SEQ_FEATURE	domain:Ig-like C2-type 3	RT		3	5.3E-1	1.0E0
SMART	IGc2	RT		5	6.5E-1	1.0E0
INTERPRO	Immunoglobulin V-set	RT		5	8.6E-1	1.0E0
Annotation Cluster 41	Enrichment Score: 0.56	G		Count	P_Value	Benjamini
UP_KEYWORDS	Lipid metabolism	RT		10	1.3E-1	6.3E-1
UP_KEYWORDS	Lipid biosynthesis	RT		5	1.6E-1	7.2E-1
KEGG_PATHWAY	Metabolic pathways	RT		13	9.9E-1	1.0E0
Annotation Cluster 42	Enrichment Score: 0.56	G		Count	P_Value	Benjamini
UP_KEYWORDS	Cell division	RT		10	7.8E-2	5.4E-1
UP_KEYWORDS	Cell cycle	RT		12	2.6E-1	9.4E-1
GOTERM_BP_DIRECT	cell division	RT		8	3.0E-1	1.0E0
UP_KEYWORDS	Mitosis	RT		5	4.7E-1	1.0E0
GOTERM_BP_DIRECT	mitotic nuclear division	RT		5	5.4E-1	1.0E0
Annotation Cluster 43	Enrichment Score: 0.53	G		Count	P_Value	Benjamini
INTERPRO	EGF-like calcium-binding_conserved site	RT		4	1.8E-1	1.0E0
UP_SEQ_FEATURE	domain:EGF-like 2; calcium-binding	RT		3	1.9E-1	1.0E0
INTERPRO	EGF-type aspartate/asparagine hydroxylation site	RT		4	2.0E-1	1.0E0
UP_KEYWORDS	EGF-like domain	RT		6	2.2E-1	8.3E-1
INTERPRO	Epidermal growth factor-like domain	RT		6	2.4E-1	1.0E0
INTERPRO	EGF-like calcium-binding	RT		4	2.8E-1	1.0E0
SMART	EGF CA	RT		4	3.9E-1	1.0E0
SMART	EGF	RT		5	4.3E-1	1.0E0
UP_SEQ_FEATURE	domain:EGF-like 1	RT		3	4.9E-1	1.0E0
INTERPRO	EGF-like_conserved site	RT		4	5.5E-1	1.0E0
Annotation Cluster 44	Enrichment Score: 0.53	G		Count	P_Value	Benjamini
UP_KEYWORDS	LIM domain	RT		3	2.5E-1	9.4E-1
INTERPRO	Zinc_finger_LIM-type	RT		3	2.8E-1	1.0E0
SMART	LIM	RT		3	3.7E-1	1.0E0
Annotation Cluster 45	Enrichment Score: 0.4	G		Count	P_Value	Benjamini
GOTERM_CC_DIRECT	microtubule	RT		7	3.1E-1	1.0E0
UP_KEYWORDS	Microtubule	RT		6	3.3E-1	1.0E0
GOTERM_MF_DIRECT	microtubule binding	RT		4	6.2E-1	1.0E0
Annotation Cluster 46	Enrichment Score: 0.37	G		Count	P_Value	Benjamini
UP_KEYWORDS	Prenylation	RT		4	3.9E-1	1.0E0
UP_SEQ_FEATURE	propeptide:Removed in mature form	RT		5	4.0E-1	1.0E0
GOTERM_MF_DIRECT	GTPase activity	RT		5	4.9E-1	1.0E0
Annotation Cluster 47	Enrichment Score: 0.28	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	domain:Helix-loop-helix motif	RT		3	4.7E-1	1.0E0
INTERPRO	Myc-type_basic helix-loop-helix_(bHLH)_domain	RT		3	5.0E-1	1.0E0
SMART	HLH	RT		3	6.0E-1	1.0E0
Annotation Cluster 48	Enrichment Score: 0.27	G		Count	P_Value	Benjamini
GOTERM_MF_DIRECT	metallopeptidase activity	RT		3	3.5E-1	1.0E0
UP_KEYWORDS	Metalloprotease	RT		3	6.1E-1	1.0E0

Annotation Cluster 1	Enrichment Score: 3.73	G		Count	P_Value	Benjamini
UP_KEYWORDS	Protease	RT		7	7.4E-1	1.0E0
Annotation Cluster 49	Enrichment Score: 0.23	G		Count	P_Value	Benjamini
GOTERM_MF_DIRECT	GTP binding	RT		8	3.7E-1	1.0E0
GOTERM_MF_DIRECT	GTPase activity	RT		5	4.9E-1	1.0E0
UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	RT		4	8.0E-1	1.0E0
UP_KEYWORDS	GTP-binding	RT		4	8.4E-1	1.0E0
Annotation Cluster 50	Enrichment Score: 0.22	G		Count	P_Value	Benjamini
UP_KEYWORDS	RNA-binding	RT		10	5.4E-1	1.0E0
GOTERM_MF_DIRECT	poly(A) RNA binding	RT		18	5.6E-1	1.0E0
GOTERM_MF_DIRECT	RNA binding	RT		8	7.3E-1	1.0E0
Annotation Cluster 51	Enrichment Score: 0.17	G		Count	P_Value	Benjamini
INTERPRO	G-protein beta WD-40 repeat	RT		3	3.9E-1	1.0E0
INTERPRO	WD40 repeat, conserved site	RT		4	4.3E-1	1.0E0
UP_SEQ_FEATURE	repeat:WD 7	RT		3	6.2E-1	1.0E0
INTERPRO	WD40-repeat-containing domain	RT		5	6.5E-1	1.0E0
UP_SEQ_FEATURE	repeat:WD 4	RT		4	6.8E-1	1.0E0
INTERPRO	WD40/YVTN repeat-like-containing domain	RT		5	7.1E-1	1.0E0
UP_SEQ_FEATURE	repeat:WD 3	RT		4	7.2E-1	1.0E0
UP_KEYWORDS	WD repeat	RT		4	7.3E-1	1.0E0
UP_SEQ_FEATURE	repeat:WD 1	RT		4	7.4E-1	1.0E0
UP_SEQ_FEATURE	repeat:WD 2	RT		4	7.4E-1	1.0E0
INTERPRO	WD40 repeat	RT		4	7.5E-1	1.0E0
UP_SEQ_FEATURE	repeat:WD 6	RT		3	7.5E-1	1.0E0
UP_SEQ_FEATURE	repeat:WD 5	RT		3	8.4E-1	1.0E0
SMART	WD40	RT		4	8.6E-1	1.0E0
Annotation Cluster 52	Enrichment Score: 0.13	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	domain:Ig-like V-type	RT		3	5.3E-1	1.0E0
INTERPRO	Immunoglobulin V-set	RT		5	8.6E-1	1.0E0
SMART	IgV	RT		4	8.7E-1	1.0E0
Annotation Cluster 53	Enrichment Score: 0.11	G		Count	P_Value	Benjamini
INTERPRO	BTB/POZ-like	RT		3	7.4E-1	1.0E0
INTERPRO	BTB/POZ fold	RT		3	7.6E-1	1.0E0
SMART	BTB	RT		3	8.2E-1	1.0E0
Annotation Cluster 54	Enrichment Score: 0.11	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	zinc finger region:RING-type	RT		4	6.1E-1	1.0E0
INTERPRO	Zinc finger, RING-type, conserved site	RT		3	7.1E-1	1.0E0
INTERPRO	Zinc finger, RING-type	RT		4	8.0E-1	1.0E0
INTERPRO	Zinc finger, RING/FYVE/PHD-type	RT		5	9.0E-1	1.0E0
SMART	RING	RT		3	9.3E-1	1.0E0
Annotation Cluster 55	Enrichment Score: 0.07	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	repeat:3	RT		3	8.2E-1	1.0E0
UP_SEQ_FEATURE	repeat:1	RT		3	8.7E-1	1.0E0
UP_SEQ_FEATURE	repeat:2	RT		3	8.7E-1	1.0E0
Annotation Cluster 56	Enrichment Score: 0.06	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	repeat:ANK 3	RT		3	7.8E-1	1.0E0
UP_SEQ_FEATURE	repeat:ANK 1	RT		3	8.5E-1	1.0E0
UP_SEQ_FEATURE	repeat:ANK 2	RT		3	8.5E-1	1.0E0
UP_KEYWORDS	ANK repeat	RT		3	8.7E-1	1.0E0
INTERPRO	Ankyrin repeat	RT		3	8.9E-1	1.0E0
INTERPRO	Ankyrin repeat-containing domain	RT		3	9.0E-1	1.0E0
SMART	ANK	RT		3	9.4E-1	1.0E0
Annotation Cluster 57	Enrichment Score: 0.02	G		Count	P_Value	Benjamini
GOTERM_BP_DIRECT	protein ubiquitination	RT		4	9.2E-1	1.0E0
UP_KEYWORDS	Ubl conjugation pathway	RT		6	9.5E-1	1.0E0
GOTERM_MF_DIRECT	ubiquitin-protein transferase activity	RT		3	9.6E-1	1.0E0
Annotation Cluster 58	Enrichment Score: 0.01	G		Count	P_Value	Benjamini
UP_SEQ_FEATURE	transit peptide:Mitochondrion	RT		4	9.6E-1	1.0E0
UP_KEYWORDS	Mitochondrion	RT		10	9.7E-1	1.0E0
UP_KEYWORDS	Transit peptide	RT		4	9.8E-1	1.0E0

433 terms were not clustered.