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

Functional Annotation Clustering

Help and Manual

Current Gene List: List_1
Current Background: Mus musculus
453 DAVID IDs

Options **Classification Stringency** Medium

Rerun using options Create Sublist

30 Cluster(s)

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	Annotation Cluster 1	Enrichment Score: 4.77	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	transcription regulation	RT	72	1.2E-7	1.9E-5
☐	SP_PIR_KEYWORDS	Transcription	RT	72	1.6E-5	1.7E-3
☐	SP_PIR_KEYWORDS	nucleus	RT	128	5.1E-5	4.0E-3
☐	SP_PIR_KEYWORDS	dna-binding	RT	54	9.0E-4	2.6E-2
	Annotation Cluster 2	**Enrichment Score: 3.31**	**G**	**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	isopeptide bond	RT	18	4.6E-4	2.1E-2
☐	SP_PIR_KEYWORDS	ubl conjugation	RT	27	5.0E-4	2.0E-2
☐	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO)	RT	10	5.1E-4	1.4E-1
	Annotation Cluster 3	**Enrichment Score: 2.17**	**G**	**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT	64	1.5E-4	9.6E-3
☐	SP_PIR_KEYWORDS	atp-binding	RT	51	6.8E-4	2.1E-2
☐	SP_PIR_KEYWORDS	transferase	RT	53	1.1E-3	2.8E-2
☐	SP_PIR_KEYWORDS	kinase	RT	28	1.4E-2	1.9E-1
☐	UP_SEQ_FEATURE	domain:Protein kinase	RT	22	1.5E-2	6.9E-1
☐	UP_SEQ_FEATURE	binding site:ATP	RT	24	1.8E-2	7.2E-1
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT	35	2.4E-2	7.5E-1
☐	SP_PIR_KEYWORDS	serine/threonine-protein kinase	RT	17	2.6E-2	2.3E-1
☐	UP_SEQ_FEATURE	active site:Proton acceptor	RT	24	1.1E-1	9.3E-1
	Annotation Cluster 4	**Enrichment Score: 2.05**	**G**	**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	golgi apparatus	RT	28	5.0E-4	1.8E-2
☐	UP_SEQ_FEATURE	topological domain:Lumenal	RT	20	1.4E-2	7.2E-1
☐	SP_PIR_KEYWORDS	glycosyltransferase	RT	11	2.4E-2	2.3E-1
☐	SP_PIR_KEYWORDS	Signal-anchor	RT	17	3.9E-2	2.9E-1
	Annotation Cluster 5	**Enrichment Score: 2**	**G**	**Count**	**P_Value**	**Benjamini**
☐	UP_SEQ_FEATURE	domain:W2	RT	5	1.6E-5	2.3E-2
☐	SP_PIR_KEYWORDS	Initiation factor	RT	4	1.5E-1	6.0E-1
☐	SP_PIR_KEYWORDS	protein biosynthesis	RT	5	4.4E-1	8.7E-1
	Annotation Cluster 6	**Enrichment Score: 1.83**	**G**	**Count**	**P_Value**	**Benjamini**
☐	UP_SEQ_FEATURE	repeat:LDL-receptor class B 5	RT	5	2.0E-4	9.3E-2
☐	UP_SEQ_FEATURE	repeat:LDL-receptor class B 1	RT	5	2.8E-4	9.8E-2
☐	UP_SEQ_FEATURE	repeat:LDL-receptor class B 2	RT	5	2.8E-4	9.8E-2
☐	UP_SEQ_FEATURE	repeat:LDL-receptor class B 3	RT	5	2.8E-4	9.8E-2
☐	UP_SEQ_FEATURE	repeat:LDL-receptor class B 4	RT	5	2.8E-4	9.8E-2
☐	UP_SEQ_FEATURE	repeat:LDL-receptor class B 6	RT	4	1.4E-3	2.5E-1
☐	UP_SEQ_FEATURE	repeat:LDL-receptor class B 10	RT	3	9.7E-3	7.0E-1
☐	UP_SEQ_FEATURE	repeat:LDL-receptor class B 14	RT	3	9.7E-3	7.0E-1
☐	UP_SEQ_FEATURE	repeat:LDL-receptor class B 13	RT	3	9.7E-3	7.0E-1

☐	**UP_SEQ_FEATURE**	repeat:LDL-receptor class B 12	RT		3	9.7E-3	7.0E-1
☐	**UP_SEQ_FEATURE**	repeat:LDL-receptor class B 11	RT		3	9.7E-3	7.0E-1
☐	**UP_SEQ_FEATURE**	repeat:LDL-receptor class B 18	RT		3	9.7E-3	7.0E-1
☐	**UP_SEQ_FEATURE**	repeat:LDL-receptor class B 17	RT		3	9.7E-3	7.0E-1
☐	**UP_SEQ_FEATURE**	repeat:LDL-receptor class B 16	RT		3	9.7E-3	7.0E-1
☐	**UP_SEQ_FEATURE**	repeat:LDL-receptor class B 15	RT		3	9.7E-3	7.0E-1
☐	**UP_SEQ_FEATURE**	repeat:LDL-receptor class B 19	RT		3	9.7E-3	7.0E-1
☐	**UP_SEQ_FEATURE**	repeat:LDL-receptor class B 20	RT		3	9.7E-3	7.0E-1
☐	**UP_SEQ_FEATURE**	repeat:LDL-receptor class B 9	RT		3	9.7E-3	7.0E-1
☐	**UP_SEQ_FEATURE**	repeat:LDL-receptor class B 7	RT		3	1.3E-2	7.3E-1
☐	**UP_SEQ_FEATURE**	repeat:LDL-receptor class B 8	RT		3	1.3E-2	7.3E-1
☐	**UP_SEQ_FEATURE**	domain:LDL-receptor class A 3	RT		4	1.5E-2	7.1E-1
☐	**UP_SEQ_FEATURE**	domain:LDL-receptor class A 8	RT		3	1.7E-2	7.3E-1
☐	**UP_SEQ_FEATURE**	domain:LDL-receptor class A 1	RT		4	2.2E-2	7.6E-1
☐	**UP_SEQ_FEATURE**	domain:LDL-receptor class A 2	RT		4	2.4E-2	7.3E-1
☐	**UP_SEQ_FEATURE**	domain:LDL-receptor class A 7	RT		3	2.7E-2	7.3E-1
☐	**UP_SEQ_FEATURE**	domain:LDL-receptor class A 6	RT		3	2.7E-2	7.3E-1
☐	**UP_SEQ_FEATURE**	domain:EGF-like 3	RT		6	3.0E-2	7.5E-1
☐	**UP_SEQ_FEATURE**	domain:LDL-receptor class A 5	RT		3	3.3E-2	7.7E-1
☐	**UP_SEQ_FEATURE**	domain:EGF-like 4	RT		5	4.2E-2	8.3E-1
☐	**UP_SEQ_FEATURE**	domain:LDL-receptor class A 4	RT		3	5.1E-2	8.6E-1
☐	**UP_SEQ_FEATURE**	short sequence motif:Endocytosis signal	RT		3	5.1E-2	8.6E-1
☐	**UP_SEQ_FEATURE**	domain:EGF-like 1	RT		7	6.1E-2	8.7E-1
☐	**UP_SEQ_FEATURE**	domain:EGF-like 6	RT		4	7.3E-2	9.0E-1
☐	**SP_PIR_KEYWORDS**	Endocytosis	RT		6	7.6E-2	4.2E-1
☐	**SP_PIR_KEYWORDS**	egf-like domain	RT		10	9.3E-2	4.8E-1
☐	**UP_SEQ_FEATURE**	domain:EGF-like 7	RT		3	1.4E-1	9.5E-1
☐	**UP_SEQ_FEATURE**	domain:EGF-like 8	RT		3	1.5E-1	9.6E-1
☐	**UP_SEQ_FEATURE**	domain:EGF-like 5	RT		3	2.7E-1	9.9E-1
☐	**UP_SEQ_FEATURE**	domain:EGF-like 2	RT		4	3.5E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:EGF-like 2; calcium-binding	RT		3	4.0E-1	1.0E0
	Annotation Cluster 7	**Enrichment Score: 1.56**	G		**Count**	**P_Value**	**Benjamini**
☐	**SP_PIR_KEYWORDS**	nucleotide binding	RT		6	2.0E-2	2.2E-1
☐	**SP_PIR_KEYWORDS**	P-loop	RT		6	2.1E-2	2.2E-1
☐	**SP_PIR_KEYWORDS**	GTP binding	RT		4	5.3E-2	3.5E-1
	Annotation Cluster 8	**Enrichment Score: 1.37**	G		**Count**	**P_Value**	**Benjamini**
☐	**UP_SEQ_FEATURE**	calcium-binding region:2	RT		9	8.6E-3	6.9E-1
☐	**UP_SEQ_FEATURE**	calcium-binding region:1	RT		9	1.4E-2	7.1E-1
☐	**UP_SEQ_FEATURE**	domain:EF-hand 2	RT		10	2.6E-2	7.3E-1
☐	**UP_SEQ_FEATURE**	domain:EF-hand 1	RT		9	6.3E-2	8.8E-1
☐	**UP_SEQ_FEATURE**	domain:EF-hand 3	RT		5	1.7E-1	9.7E-1
☐	**SP_PIR_KEYWORDS**	calcium	RT		23	1.8E-1	6.5E-1
	Annotation Cluster 9	**Enrichment Score: 1.35**	G		**Count**	**P_Value**	**Benjamini**
☐	**SP_PIR_KEYWORDS**	cell division	RT		13	2.3E-2	2.3E-1
☐	**SP_PIR_KEYWORDS**	cell cycle	RT		19	2.6E-2	2.2E-1
☐	**SP_PIR_KEYWORDS**	mitosis	RT		8	1.5E-1	6.0E-1
	Annotation Cluster 10	**Enrichment Score: 1.12**	G		**Count**	**P_Value**	**Benjamini**
☐	**UP_SEQ_FEATURE**	short sequence motif:DEAD box	RT		4	4.4E-2	8.3E-1
☐	**UP_SEQ_FEATURE**	short sequence motif:Q motif	RT		4	5.5E-2	8.7E-1
☐	**UP_SEQ_FEATURE**	domain:Helicase C-terminal	RT		6	7.7E-2	9.1E-1
☐	**UP_SEQ_FEATURE**	domain:Helicase ATP-binding	RT		6	8.6E-2	9.1E-1

☐	SP_PIR_KEYWORDS	helicase	RT		6	1.7E-1	6.2E-1
	Annotation Cluster 11	Enrichment Score: 1.1	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:WW 3	RT		3	1.7E-2	7.3E-1
☐	UP_SEQ_FEATURE	domain:WW 2	RT		3	1.7E-1	9.7E-1
☐	UP_SEQ_FEATURE	domain:WW 1	RT		3	1.7E-1	9.7E-1
	Annotation Cluster 12	Enrichment Score: 0.99	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	lipoprotein	RT		24	1.8E-2	2.2E-1
☐	SP_PIR_KEYWORDS	palmitate	RT		10	6.4E-2	4.0E-1
☐	UP_SEQ_FEATURE	lipid moiety-binding region:S-palmitoyl cysteine	RT		9	9.2E-2	9.1E-1
☐	SP_PIR_KEYWORDS	transducer	RT		9	1.0E0	1.0E0
	Annotation Cluster 13	Enrichment Score: 0.92	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:IQ 3	RT		3	5.8E-2	8.8E-1
☐	UP_SEQ_FEATURE	domain:IQ 2	RT		3	1.7E-1	9.7E-1
☐	UP_SEQ_FEATURE	domain:IQ 1	RT		3	1.8E-1	9.7E-1
	Annotation Cluster 14	Enrichment Score: 0.89	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	metal ion-binding site:Calcium 2; via carbonyl oxygen	RT		4	7.3E-2	9.0E-1
☐	UP_SEQ_FEATURE	metal ion-binding site:Calcium 3; via carbonyl oxygen	RT		3	1.0E-1	9.3E-1
☐	UP_SEQ_FEATURE	metal ion-binding site:Calcium 2	RT		4	1.8E-1	9.7E-1
☐	UP_SEQ_FEATURE	metal ion-binding site:Calcium 3	RT		3	2.0E-1	9.8E-1
	Annotation Cluster 15	Enrichment Score: 0.63	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 7; atypical	RT		3	2.0E-3	3.1E-1
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 3	RT		11	1.3E-1	9.5E-1
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	RT		11	1.3E-1	9.5E-1
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	RT		11	1.5E-1	9.6E-1
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 6	RT		6	3.7E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 5	RT		7	3.7E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 4	RT		7	4.6E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 10	RT		3	6.9E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 9	RT		3	7.4E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 8	RT		3	8.2E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 7	RT		3	8.5E-1	1.0E0
	Annotation Cluster 16	Enrichment Score: 0.62	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	repeat:ANK 9	RT		4	6.0E-2	8.8E-1
☐	UP_SEQ_FEATURE	repeat:ANK 8	RT		4	8.3E-2	9.1E-1
☐	UP_SEQ_FEATURE	repeat:ANK 10	RT		3	1.3E-1	9.5E-1
☐	UP_SEQ_FEATURE	repeat:ANK 7	RT		4	1.6E-1	9.7E-1
☐	SP_PIR_KEYWORDS	ank repeat	RT		8	3.0E-1	7.7E-1
☐	UP_SEQ_FEATURE	repeat:ANK 6	RT		4	3.4E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 1	RT		7	3.9E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 2	RT		7	3.9E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 3	RT		6	4.1E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 4	RT		5	4.3E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 5	RT		4	5.4E-1	1.0E0
	Annotation Cluster 17	Enrichment Score: 0.57	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	region of interest:Actin-binding	RT		3	1.3E-1	9.5E-1
☐	UP_SEQ_FEATURE	domain:Myosin head-like	RT		3	1.8E-1	9.7E-1
☐	SP_PIR_KEYWORDS	calmodulin-binding	RT		5	2.4E-1	7.2E-1
☐	SP_PIR_KEYWORDS	myosin	RT		3	3.2E-1	7.9E-1
☐	SP_PIR_KEYWORDS	motor protein	RT		3	8.0E-1	9.8E-1
	Annotation Cluster 18	Enrichment Score: 0.54	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	tyrosine-protein kinase	RT		6	1.5E-1	6.0E-1

☐	UP_SEQ_FEATURE	domain:Fibronectin type-III 2	RT		5	3.9E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Fibronectin type-III 1	RT		5	4.0E-1	1.0E0
	Annotation Cluster 19	**Enrichment Score: 0.51**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	UP_SEQ_FEATURE	repeat:WD 13	RT		3	8.8E-2	9.1E-1
☐	UP_SEQ_FEATURE	repeat:WD 12	RT		3	1.0E-1	9.3E-1
☐	UP_SEQ_FEATURE	repeat:WD 8	RT		4	1.3E-1	9.5E-1
☐	UP_SEQ_FEATURE	repeat:WD 11	RT		3	1.6E-1	9.6E-1
☐	UP_SEQ_FEATURE	repeat:WD 10	RT		3	1.6E-1	9.6E-1
☐	UP_SEQ_FEATURE	repeat:WD 9	RT		3	2.3E-1	9.9E-1
☐	UP_SEQ_FEATURE	repeat:WD 7	RT		6	2.3E-1	9.9E-1
☐	UP_SEQ_FEATURE	repeat:WD 6	RT		6	4.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 5	RT		6	6.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	wd repeat	RT		7	6.2E-1	9.4E-1
☐	UP_SEQ_FEATURE	repeat:WD 4	RT		6	6.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 3	RT		6	7.3E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 1	RT		6	7.5E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 2	RT		6	7.5E-1	1.0E0
	Annotation Cluster 20	**Enrichment Score: 0.47**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	voltage-gated channel	RT		6	2.3E-1	7.2E-1
☐	SP_PIR_KEYWORDS	potassium channel	RT		4	2.4E-1	7.2E-1
☐	SP_PIR_KEYWORDS	potassium transport	RT		5	2.6E-1	7.5E-1
☐	SP_PIR_KEYWORDS	potassium	RT		5	3.2E-1	7.9E-1
☐	SP_PIR_KEYWORDS	ion transport	RT		14	5.6E-1	9.2E-1
☐	SP_PIR_KEYWORDS	ionic channel	RT		8	6.0E-1	9.3E-1
	Annotation Cluster 21	**Enrichment Score: 0.43**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	zinc-finger	RT		35	2.0E-1	6.8E-1
☐	SP_PIR_KEYWORDS	metal-binding	RT		68	4.2E-1	8.6E-1
☐	SP_PIR_KEYWORDS	zinc	RT		46	5.8E-1	9.3E-1
	Annotation Cluster 22	**Enrichment Score: 0.42**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	UP_SEQ_FEATURE	domain:BACK	RT		3	1.6E-1	9.6E-1
☐	UP_SEQ_FEATURE	domain:BTB	RT		5	3.5E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:Kelch 5	RT		3	4.0E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:Kelch 4	RT		3	4.3E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:Kelch 3	RT		3	4.5E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:Kelch 2	RT		3	4.5E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:Kelch 1	RT		3	4.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	kelch repeat	RT		3	4.9E-1	9.0E-1
	Annotation Cluster 23	**Enrichment Score: 0.38**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	UP_SEQ_FEATURE	lipid moiety-binding region:GPI-anchor amidated serine	RT		4	1.8E-1	9.7E-1
☐	SP_PIR_KEYWORDS	gpi-anchor	RT		4	5.8E-1	9.3E-1
☐	UP_SEQ_FEATURE	propeptide:Removed in mature form	RT		6	6.9E-1	1.0E0
	Annotation Cluster 24	**Enrichment Score: 0.36**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	protein phosphatase	RT		5	3.3E-1	8.0E-1
☐	UP_SEQ_FEATURE	domain:Tyrosine-protein phosphatase	RT		3	4.2E-1	1.0E0
☐	UP_SEQ_FEATURE	active site:Phosphocysteine intermediate	RT		3	5.9E-1	1.0E0
	Annotation Cluster 25	**Enrichment Score: 0.34**	G	🟩	**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	glycoprotein	RT		96	2.0E-1	6.8E-1
☐	SP_PIR_KEYWORDS	disulfide bond	RT		63	4.1E-1	8.5E-1
☐	SP_PIR_KEYWORDS	signal	RT		75	4.3E-1	8.7E-1
☐	SP_PIR_KEYWORDS	Secreted	RT		36	5.1E-1	9.0E-1
☐	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		91	5.5E-1	1.0E0
	UP_SEQ_FEATURE	disulfide bond	RT		62	6.1E-1	1.0E0

☐						
☐	UP_SEQ_FEATURE	signal peptide	RT	75	7.2E-1	1.0E0
	Annotation Cluster 26	**Enrichment Score: 0.33**	G	**Count**	**P_Value**	**Benjamini**
☐	UP_SEQ_FEATURE	domain:Ig-like C2-type 1	RT	5	4.5E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Ig-like C2-type 2	RT	5	4.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	Immunoglobulin domain	RT	12	5.0E-1	9.0E-1
	Annotation Cluster 27	**Enrichment Score: 0.19**	G	**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	glycoprotein	RT	96	2.0E-1	6.8E-1
☐	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT	91	5.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	membrane	RT	134	5.5E-1	9.2E-1
☐	UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT	67	8.4E-1	1.0E0
☐	UP_SEQ_FEATURE	topological domain:Extracellular	RT	42	9.9E-1	1.0E0
☐	UP_SEQ_FEATURE	transmembrane region	RT	88	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	transmembrane	RT	91	1.0E0	1.0E0
	Annotation Cluster 28	**Enrichment Score: 0.18**	G	**Count**	**P_Value**	**Benjamini**
☐	UP_SEQ_FEATURE	repeat:LRR 11	RT	4	4.1E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 10	RT	4	5.1E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 13	RT	3	5.1E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 12	RT	3	6.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 5	RT	6	6.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 9	RT	4	6.3E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 8	RT	4	6.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 4	RT	6	7.0E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 6	RT	5	7.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 3	RT	6	7.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 7	RT	4	7.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	leucine-rich repeat	RT	6	8.0E-1	9.8E-1
☐	UP_SEQ_FEATURE	repeat:LRR 1	RT	6	8.3E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 2	RT	6	8.3E-1	1.0E0
	Annotation Cluster 29	**Enrichment Score: 0.07**	G	**Count**	**P_Value**	**Benjamini**
☐	UP_SEQ_FEATURE	repeat:TPR 1	RT	3	8.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 2	RT	3	8.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	tpr repeat	RT	3	8.6E-1	9.9E-1
	Annotation Cluster 30	**Enrichment Score: 0.01**	G	**Count**	**P_Value**	**Benjamini**
☐	SP_PIR_KEYWORDS	transit peptide	RT	7	9.7E-1	1.0E0
☐	UP_SEQ_FEATURE	transit peptide:Mitochondrion	RT	7	9.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	mitochondrion	RT	11	9.9E-1	1.0E0

161 terms were not clustered.

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