

Functional Annotation Clustering

[Help and Manual](#)

Current Gene List: List_1
Current Background: Homo sapiens
2998 DAVID IDs

Options


Classification Stringency












































Medium





Rerun using options




















































Create Sublist

341 Cluster(s)

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Annotation Cluster 1		Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	RT		525	0.0E0	5.8E0	0.0E0	0.0E0
<input type="checkbox"/>	INTERPRO	Zinc finger, C2H2-like	RT		637	0.0E0	5.2E0	0.0E0	0.0E0
<input type="checkbox"/>	INTERPRO	Zinc finger C2H2-type/integrase DNA-binding domain	RT		622	0.0E0	5.4E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 3	RT		556	0.0E0	6.0E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 4	RT		519	0.0E0	6.0E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_KEYWORDS	Nucleus	RT		1680	0.0E0	2.2E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 5	RT		496	0.0E0	6.1E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 6	RT		455	0.0E0	6.2E0	0.0E0	0.0E0
<input type="checkbox"/>	INTERPRO	Zinc finger, C2H2	RT		642	0.0E0	5.0E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 7	RT		427	3.2E-315	6.3E0	3.1E-312	2.9E-312
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	RT		473	2.6E-314	5.8E0	2.1E-311	2.0E-311
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 8	RT		393	2.7E-288	6.3E0	1.9E-285	1.8E-285
<input type="checkbox"/>	SMART	ZnF_C2H2	RT		637	4.2E-283	3.4E0	2.0E-280	1.8E-280
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 9	RT		355	3.2E-260	6.3E0	2.0E-257	1.9E-257
<input type="checkbox"/>	UP_KEYWORDS	Zinc-finger	RT		811	1.8E-243	3.1E0	4.3E-241	3.3E-241
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 10	RT		318	2.3E-236	6.4E0	1.3E-233	1.2E-233
<input type="checkbox"/>	GOTERM_MF_DIRECT	nucleic acid binding	RT		597	2.2E-227	3.6E0	2.8E-224	2.5E-224
<input type="checkbox"/>	UP_KEYWORDS	Transcription	RT		940	2.0E-226	2.7E0	3.3E-224	2.5E-224
<input type="checkbox"/>	UP_KEYWORDS	DNA-binding	RT		854	2.8E-224	2.9E0	3.4E-222	2.6E-222
<input type="checkbox"/>	INTERPRO	Krueppel-associated box	RT		350	8.1E-222	5.4E0	4.7E-219	4.3E-219
<input type="checkbox"/>	UP_KEYWORDS	Transcription regulation	RT		917	4.4E-221	2.7E0	3.5E-219	2.7E-219
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KRAB	RT		309	7.2E-218	6.1E0	3.7E-215	3.5E-215
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 11	RT		275	2.6E-197	6.2E0	1.2E-194	1.2E-194
<input type="checkbox"/>	UP_KEYWORDS	Metal-binding	RT		1153	8.1E-193	2.2E0	5.6E-191	4.3E-191
<input type="checkbox"/>	UP_KEYWORDS	Zinc	RT		877	1.9E-191	2.6E0	1.1E-189	8.7E-190
<input type="checkbox"/>	GOTERM_MF_DIRECT	metal ion binding	RT		863	2.9E-186	2.5E0	1.9E-183	1.7E-183
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 12	RT		237	7.5E-173	6.3E0	3.2E-170	3.1E-170
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription, DNA-templated	RT		813	8.0E-171	2.5E0	4.8E-167	4.6E-167
<input type="checkbox"/>	SMART	KRAB	RT		345	1.2E-161	3.6E0	2.9E-159	2.7E-159
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of transcription, DNA-templated	RT		671	2.0E-156	2.6E0	5.9E-153	5.7E-153
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA binding	RT		705	4.8E-150	2.5E0	1.5E-147	1.4E-147
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 13	RT		188	1.6E-135	6.3E0	6.1E-133	5.9E-133
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 14	RT		146	2.8E-107	6.4E0	1.0E-104	9.6E-105
<input type="checkbox"/>	GOTERM_CC_DIRECT	intracellular	RT		505	1.1E-93	2.4E0	3.2E-91	2.8E-91
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 15	RT		122	1.0E-86	6.2E0	3.1E-84	2.9E-84
<input type="checkbox"/>	GOTERM_MF_DIRECT	transcription factor activity, sequence-specific DNA binding	RT		401	1.9E-79	2.5E0	4.9E-77	4.4E-77
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 16	RT		93	2.2E-64	6.2E0	5.1E-62	4.9E-62
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 17	RT		74	4.8E-51	6.1E0	7.4E-49	7.1E-49
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 18	RT		58	2.8E-39	6.1E0	3.9E-37	3.8E-37
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 19	RT		48	2.9E-32	6.1E0	3.5E-30	3.4E-30
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 20	RT		32	2.2E-21	6.1E0	2.2E-19	2.1E-19
















































Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 21	RT	<div><div></div></div>	24	1.0E-16	6.3E0	8.6E-15	8.3E-15
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 22	RT	<div><div></div></div>	23	6.2E-16	6.3E0	5.0E-14	4.8E-14
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 23	RT	<div><div></div></div>	15	1.9E-10	6.4E0	1.2E-8	1.1E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 24	RT	<div><div></div></div>	13	6.7E-9	6.3E0	4.0E-7	3.8E-7
Annotation Cluster 2		Enrichment Score: 92.97	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_KEYWORDS	Nucleotide-binding	RT	<div><div></div></div>	786	2.0E-222	3.0E0	1.9E-220	1.5E-220
<input type="checkbox"/>	UP_KEYWORDS	ATP-binding	RT	<div><div></div></div>	640	7.5E-190	3.2E0	4.0E-188	3.1E-188
<input type="checkbox"/>	GOTERM_MF_DIRECT	ATP binding	RT	<div><div></div></div>	661	8.9E-153	2.6E0	3.8E-150	3.4E-150
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT	<div><div></div></div>	472	3.3E-142	3.2E0	1.3E-139	1.3E-139
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase	RT	<div><div></div></div>	267	2.4E-99	3.8E0	7.9E-97	7.6E-97
<input type="checkbox"/>	INTERPRO	Protein kinase-like domain	RT	<div><div></div></div>	294	7.9E-98	3.4E0	3.6E-95	3.3E-95
<input type="checkbox"/>	INTERPRO	Protein kinase, catalytic domain	RT	<div><div></div></div>	278	1.2E-96	3.5E0	4.4E-94	4.0E-94
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:ATP	RT	<div><div></div></div>	282	4.3E-91	3.4E0	1.3E-88	1.3E-88
<input type="checkbox"/>	INTERPRO	Protein kinase, ATP binding site	RT	<div><div></div></div>	232	2.9E-88	3.8E0	9.6E-86	8.8E-86
<input type="checkbox"/>	UP_KEYWORDS	Kinase	RT	<div><div></div></div>	323	3.0E-85	3.0E0	1.2E-83	9.3E-84
<input type="checkbox"/>	UP_KEYWORDS	Serine/threonine-protein kinase	RT	<div><div></div></div>	203	8.6E-68	3.5E0	2.8E-66	2.1E-66
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Proton acceptor	RT	<div><div></div></div>	272	1.3E-61	2.8E0	2.7E-59	2.6E-59
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein kinase activity	RT	<div><div></div></div>	190	6.6E-56	3.2E0	1.2E-53	1.1E-53
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein serine/threonine kinase activity	RT	<div><div></div></div>	193	4.6E-54	3.1E0	7.3E-52	6.5E-52
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein phosphorylation	RT	<div><div></div></div>	215	8.3E-52	2.8E0	8.3E-49	8.0E-49
<input type="checkbox"/>	INTERPRO	Serine/threonine-protein kinase, active site	RT	<div><div></div></div>	166	1.6E-51	3.3E0	2.9E-49	2.6E-49
<input type="checkbox"/>	UP_KEYWORDS	Transferase	RT	<div><div></div></div>	469	1.1E-47	1.9E0	2.7E-46	2.1E-46
<input type="checkbox"/>	SMART	S_TKc	RT	<div><div></div></div>	188	2.5E-30	2.1E0	2.4E-28	2.1E-28
Annotation Cluster 3		Enrichment Score: 57.69	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 4	RT	<div><div></div></div>	131	1.2E-73	5.2E0	3.3E-71	3.2E-71
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 5	RT	<div><div></div></div>	115	7.0E-69	5.5E0	1.8E-66	1.7E-66
<input type="checkbox"/>	UP_KEYWORDS	ANK repeat	RT	<div><div></div></div>	161	2.0E-67	4.2E0	6.1E-66	4.7E-66
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 3	RT	<div><div></div></div>	139	1.6E-65	4.6E0	3.9E-63	3.8E-63
<input type="checkbox"/>	INTERPRO	Ankyrin repeat	RT	<div><div></div></div>	159	2.9E-62	3.9E0	6.6E-60	6.0E-60
<input type="checkbox"/>	INTERPRO	Ankyrin repeat-containing domain	RT	<div><div></div></div>	162	1.1E-61	3.8E0	2.2E-59	2.1E-59
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 2	RT	<div><div></div></div>	146	7.5E-59	4.1E0	1.4E-56	1.4E-56
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 1	RT	<div><div></div></div>	145	3.2E-58	4.0E0	5.7E-56	5.5E-56
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 6	RT	<div><div></div></div>	83	6.8E-52	5.7E0	1.1E-49	1.0E-49
<input type="checkbox"/>	SMART	ANK	RT	<div><div></div></div>	157	4.9E-38	2.6E0	5.8E-36	5.2E-36
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 7	RT	<div><div></div></div>	55	3.8E-36	5.9E0	5.0E-34	4.8E-34
Annotation Cluster 4		Enrichment Score: 37.87	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	rRNA processing	RT	<div><div></div></div>	147	3.1E-63	4.1E0	6.1E-60	5.9E-60
<input type="checkbox"/>	UP_KEYWORDS	Ribonucleoprotein	RT	<div><div></div></div>	160	7.0E-57	3.7E0	1.9E-55	1.5E-55
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	RT	<div><div></div></div>	97	6.2E-53	4.8E0	7.4E-50	7.1E-50
<input type="checkbox"/>	GOTERM_BP_DIRECT	SRP-dependent cotranslational protein targeting to membrane	RT	<div><div></div></div>	80	2.3E-46	5.0E0	2.0E-43	1.9E-43
<input type="checkbox"/>	GOTERM_BP_DIRECT	translational initiation	RT	<div><div></div></div>	97	1.7E-43	4.2E0	1.3E-40	1.2E-40
<input type="checkbox"/>	KEGG_PATHWAY	Ribosome	RT	<div><div></div></div>	96	1.9E-38	3.7E0	2.4E-36	1.1E-36
<input type="checkbox"/>	GOTERM_BP_DIRECT	viral transcription	RT	<div><div></div></div>	81	2.0E-37	4.3E0	1.3E-34	1.3E-34
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosolic large ribosomal subunit	RT	<div><div></div></div>	58	2.5E-35	5.4E0	3.2E-33	2.8E-33
<input type="checkbox"/>	UP_KEYWORDS	Ribosomal protein	RT	<div><div></div></div>	98	5.8E-34	3.6E0	1.1E-32	8.4E-33
<input type="checkbox"/>	GOTERM_CC_DIRECT	ribosome	RT	<div><div></div></div>	93	3.6E-32	3.6E0	4.0E-30	3.5E-30
















































Annotation Cluster 1		Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	structural constituent of ribosome	RT		100	1.2E-22	2.7E0	1.0E-20	9.2E-21
<input type="checkbox"/>	GOTERM_BP_DIRECT	translation	RT		109	1.6E-22	2.6E0	5.7E-20	5.5E-20
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosolic small ribosomal subunit	RT		34	2.3E-16	4.5E0	1.4E-14	1.2E-14
Annotation Cluster 5		Enrichment Score: 34.73			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Leucine-rich repeat, typical subtype	RT		141	1.0E-76	4.9E0	3.0E-74	2.7E-74
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 5	RT		147	1.2E-64	4.3E0	2.9E-62	2.8E-62
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 4	RT		153	3.0E-62	4.1E0	6.5E-60	6.3E-60
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 6	RT		136	1.5E-61	4.4E0	3.1E-59	3.0E-59
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 7	RT		123	5.4E-61	4.8E0	1.0E-58	1.0E-58
<input type="checkbox"/>	INTERPRO	Leucine-rich repeat	RT		159	1.4E-59	3.7E0	2.6E-57	2.4E-57
<input type="checkbox"/>	UP_KEYWORDS	Leucine-rich repeat	RT		167	7.8E-59	3.7E0	2.2E-57	1.7E-57
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 3	RT		161	1.1E-55	3.6E0	1.9E-53	1.8E-53
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 1	RT		164	2.2E-53	3.5E0	3.7E-51	3.6E-51
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 2	RT		164	3.8E-53	3.5E0	6.3E-51	6.1E-51
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 8	RT		105	4.7E-53	4.8E0	7.6E-51	7.3E-51
<input type="checkbox"/>	SMART	LRR_TYP	RT		141	8.3E-53	3.2E0	1.3E-50	1.2E-50
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 9	RT		95	5.9E-48	4.8E0	8.6E-46	8.2E-46
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 10	RT		81	4.0E-40	4.8E0	5.7E-38	5.5E-38
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 11	RT		72	1.3E-36	4.9E0	1.7E-34	1.7E-34
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 12	RT		65	1.3E-33	4.9E0	1.6E-31	1.6E-31
<input type="checkbox"/>	INTERPRO	Cysteine-rich flanking region, C-terminal	RT		58	1.2E-26	4.3E0	1.4E-24	1.3E-24
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 13	RT		52	1.3E-25	4.7E0	1.4E-23	1.3E-23
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 14	RT		42	5.5E-21	4.8E0	5.4E-19	5.2E-19
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 15	RT		36	3.3E-18	4.8E0	3.0E-16	2.9E-16
<input type="checkbox"/>	SMART	LRRCT	RT		58	2.1E-17	2.8E0	1.1E-15	1.0E-15
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 16	RT		31	3.1E-15	4.7E0	2.4E-13	2.3E-13
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 17	RT		27	1.1E-14	5.1E0	8.3E-13	8.0E-13
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 18	RT		20	9.4E-11	5.0E0	6.2E-9	6.0E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 19	RT		19	1.6E-10	5.2E0	1.0E-8	1.0E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 20	RT		18	2.7E-10	5.3E0	1.7E-8	1.6E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 21	RT		14	5.9E-8	5.3E0	3.0E-6	2.9E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 22	RT		10	4.5E-6	5.7E0	1.8E-4	1.7E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 23	RT		8	1.2E-4	5.5E0	3.5E-3	3.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 24	RT		6	1.1E-3	5.8E0	2.9E-2	2.8E-2
Annotation Cluster 6		Enrichment Score: 29.55			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	mRNA splicing, via spliceosome	RT		142	3.7E-55	3.8E0	5.6E-52	5.4E-52
<input type="checkbox"/>	UP_KEYWORDS	Spliceosome	RT		82	5.3E-37	4.4E0	1.1E-35	8.6E-36
<input type="checkbox"/>	KEGG_PATHWAY	Spliceosome	RT		91	9.8E-35	3.5E0	8.0E-33	3.8E-33
<input type="checkbox"/>	GOTERM_CC_DIRECT	catalytic step 2 spliceosome	RT		64	7.6E-30	4.4E0	7.6E-28	6.6E-28
<input type="checkbox"/>	UP_KEYWORDS	mRNA splicing	RT		111	7.7E-28	2.9E0	1.2E-26	9.0E-27
<input type="checkbox"/>	UP_KEYWORDS	mRNA processing	RT		128	5.9E-27	2.6E0	8.3E-26	6.4E-26
<input type="checkbox"/>	GOTERM_CC_DIRECT	spliceosomal complex	RT		59	4.6E-24	4.0E0	4.1E-22	3.6E-22
<input type="checkbox"/>	GOTERM_BP_DIRECT	RNA splicing	RT		54	1.4E-6	1.9E0	7.3E-5	7.0E-5
Annotation Cluster 7		Enrichment Score: 27.38			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SCAN box	RT		51	2.3E-32	5.8E0	2.9E-30	2.8E-30
<input type="checkbox"/>	INTERPRO	Transcription regulator SCAN	RT		52	8.4E-32	5.4E0	1.1E-29	1.0E-29

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Retrovirus capsid, C-terminal	RT	<div><div></div><div></div></div>	52	6.3E-26	4.6E0	6.6E-24	6.0E-24
<input type="checkbox"/>	SMART	SCAN	RT	<div><div></div><div></div></div>	51	2.5E-22	3.5E0	1.7E-20	1.5E-20
Annotation Cluster 8		Enrichment Score: 21.42	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Ubiquitin mediated proteolysis	RT	<div><div></div><div></div></div>	97	5.0E-39	3.7E0	1.2E-36	5.8E-37
<input type="checkbox"/>	UP_KEYWORDS	Ubl conjugation pathway	RT	<div><div></div><div></div></div>	213	1.8E-29	2.2E0	3.0E-28	2.3E-28
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitin-protein transferase activity	RT	<div><div></div><div></div></div>	134	5.5E-25	2.4E0	5.5E-23	4.9E-23
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitin protein ligase activity	RT	<div><div></div><div></div></div>	80	1.0E-16	2.5E0	6.0E-15	5.4E-15
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein ubiquitination	RT	<div><div></div><div></div></div>	115	2.1E-12	1.9E0	3.0E-10	2.9E-10
<input type="checkbox"/>	GOTERM_MF_DIRECT	ligase activity	RT	<div><div></div><div></div></div>	88	2.8E-10	1.9E0	8.7E-9	7.7E-9
Annotation Cluster 9		Enrichment Score: 19.34	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Cell cycle	RT	<div><div></div><div></div></div>	211	1.5E-31	2.2E0	2.6E-30	2.0E-30
<input type="checkbox"/>	UP_KEYWORDS	Cell division	RT	<div><div></div><div></div></div>	133	1.7E-22	2.4E0	2.2E-21	1.7E-21
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell division	RT	<div><div></div><div></div></div>	125	1.3E-17	2.1E0	3.2E-15	3.1E-15
<input type="checkbox"/>	UP_KEYWORDS	Mitosis	RT	<div><div></div><div></div></div>	92	2.4E-16	2.4E0	2.8E-15	2.2E-15
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitotic nuclear division	RT	<div><div></div><div></div></div>	88	2.4E-12	2.1E0	3.3E-10	3.2E-10
Annotation Cluster 10		Enrichment Score: 18.32	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Tyrosine-protein kinase	RT	<div><div></div><div></div></div>	83	1.5E-44	5.1E0	3.4E-43	2.6E-43
<input type="checkbox"/>	INTERPRO	Serine-threonine/tyrosine-protein kinase catalytic domain	RT	<div><div></div><div></div></div>	97	6.4E-44	4.3E0	1.0E-41	9.6E-42
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, catalytic domain	RT	<div><div></div><div></div></div>	69	1.2E-38	5.0E0	1.8E-36	1.6E-36
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, active site	RT	<div><div></div><div></div></div>	70	1.8E-34	4.6E0	2.6E-32	2.4E-32
<input type="checkbox"/>	SMART	TyrKc	RT	<div><div></div><div></div></div>	69	5.6E-27	3.3E0	4.4E-25	4.0E-25
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein tyrosine kinase activity	RT	<div><div></div><div></div></div>	77	3.6E-26	3.4E0	3.9E-24	3.4E-24
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptidyl-tyrosine phosphorylation	RT	<div><div></div><div></div></div>	81	7.3E-24	3.1E0	3.1E-21	3.0E-21
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptidyl-tyrosine autophosphorylation	RT	<div><div></div><div></div></div>	32	5.2E-17	4.7E0	1.1E-14	1.1E-14
<input type="checkbox"/>	GOTERM_MF_DIRECT	non-membrane spanning protein tyrosine kinase activity	RT	<div><div></div><div></div></div>	34	2.1E-16	4.4E0	1.2E-14	1.1E-14
<input type="checkbox"/>	GOTERM_MF_DIRECT	transmembrane receptor protein tyrosine kinase activity	RT	<div><div></div><div></div></div>	26	2.1E-11	4.1E0	7.4E-10	6.6E-10
<input type="checkbox"/>	GOTERM_BP_DIRECT	transmembrane receptor protein tyrosine kinase signaling pathway	RT	<div><div></div><div></div></div>	43	5.8E-10	2.7E0	6.5E-8	6.2E-8
<input type="checkbox"/>	GOTERM_CC_DIRECT	extrinsic component of cytoplasmic side of plasma membrane	RT	<div><div></div><div></div></div>	33	1.2E-9	3.1E0	4.3E-8	3.8E-8
<input type="checkbox"/>	UP_KEYWORDS	SH2 domain	RT	<div><div></div><div></div></div>	36	2.1E-6	2.3E0	1.5E-5	1.1E-5
<input type="checkbox"/>	INTERPRO	SH2 domain	RT	<div><div></div><div></div></div>	39	3.6E-6	2.1E0	8.2E-5	7.5E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2	RT	<div><div></div><div></div></div>	31	2.9E-5	2.2E0	9.6E-4	9.2E-4
<input type="checkbox"/>	SMART	SH2	RT	<div><div></div><div></div></div>	35	3.3E-2	1.4E0	2.6E-1	2.3E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	receptor binding	RT	<div><div></div><div></div></div>	49	9.6E-1	8.3E-1	1.0E0	9.6E-1
Annotation Cluster 11		Enrichment Score: 16.22	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	GTP-binding	RT	<div><div></div><div></div></div>	145	1.3E-35	2.9E0	2.5E-34	1.9E-34
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	RT	<div><div></div><div></div></div>	133	3.6E-33	2.9E0	4.5E-31	4.3E-31
<input type="checkbox"/>	GOTERM_MF_DIRECT	GTP binding	RT	<div><div></div><div></div></div>	155	2.7E-28	2.4E0	3.2E-26	2.8E-26
<input type="checkbox"/>	GOTERM_MF_DIRECT	GTPase activity	RT	<div><div></div><div></div></div>	107	8.1E-25	2.7E0	7.4E-23	6.6E-23
<input type="checkbox"/>	INTERPRO	Small GTP-binding protein domain	RT	<div><div></div><div></div></div>	76	1.1E-18	2.8E0	1.0E-16	9.4E-17
<input type="checkbox"/>	INTERPRO	Small GTPase superfamily, Ras type	RT	<div><div></div><div></div></div>	32	3.6E-18	5.1E0	3.3E-16	3.1E-16
<input type="checkbox"/>	INTERPRO	Small GTPase superfamily	RT	<div><div></div><div></div></div>	60	1.4E-13	2.7E0	8.9E-12	8.1E-12
<input type="checkbox"/>	GOTERM_BP_DIRECT	small GTPase mediated signal transduction	RT	<div><div></div><div></div></div>	83	1.9E-10	2.0E0	2.2E-8	2.1E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Effector region	RT	<div><div></div><div></div></div>	39	1.1E-8	2.6E0	6.4E-7	6.1E-7
<input type="checkbox"/>	UP_KEYWORDS	Prenylation	RT	<div><div></div><div></div></div>	46	2.5E-5	1.9E0	1.5E-4	1.2E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	propeptide:Removed in mature form	RT	<div><div></div><div></div></div>	52	2.8E-3	1.5E0	6.7E-2	6.4E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	lipid moiety-binding region:S-geranylgeranyl cysteine	RT	<div><div></div><div></div></div>	28	3.2E-3	1.8E0	7.7E-2	7.4E-2

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 12		Enrichment Score: 16.09	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	RT	<div><div></div><div></div></div>	55	4.7E-31	5.3E0	5.6E-29	5.4E-29
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HECT	RT	<div><div></div><div></div></div>	23	6.6E-14	5.6E0	4.8E-12	4.7E-12
<input type="checkbox"/>	INTERPRO	HECT	RT	<div><div></div><div></div></div>	23	4.8E-13	5.1E0	3.0E-11	2.7E-11
<input type="checkbox"/>	SMART	HECTc	RT	<div><div></div><div></div></div>	23	2.8E-9	3.3E0	7.9E-8	7.2E-8
Annotation Cluster 13		Enrichment Score: 15.77	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Helicase	RT	<div><div></div><div></div></div>	82	1.0E-31	3.9E0	1.8E-30	1.4E-30
<input type="checkbox"/>	INTERPRO	Helicase, superfamily 1/2, ATP-binding domain	RT	<div><div></div><div></div></div>	68	1.9E-26	3.8E0	2.1E-24	2.0E-24
<input type="checkbox"/>	INTERPRO	Helicase, C-terminal	RT	<div><div></div><div></div></div>	67	3.4E-26	3.8E0	3.7E-24	3.4E-24
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Helicase C-terminal	RT	<div><div></div><div></div></div>	64	8.9E-26	4.0E0	9.6E-24	9.3E-24
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Helicase ATP-binding	RT	<div><div></div><div></div></div>	65	6.9E-25	3.9E0	7.3E-23	7.0E-23
<input type="checkbox"/>	GOTERM_MF_DIRECT	helicase activity	RT	<div><div></div><div></div></div>	50	1.3E-17	3.5E0	8.6E-16	7.7E-16
<input type="checkbox"/>	SMART	DEXDc	RT	<div><div></div><div></div></div>	67	1.2E-15	2.5E0	5.7E-14	5.2E-14
<input type="checkbox"/>	SMART	HELICc	RT	<div><div></div><div></div></div>	66	1.6E-15	2.5E0	7.0E-14	6.4E-14
<input type="checkbox"/>	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT	<div><div></div><div></div></div>	41	2.8E-15	3.7E0	2.1E-13	1.9E-13
<input type="checkbox"/>	GOTERM_MF_DIRECT	ATP-dependent RNA helicase activity	RT	<div><div></div><div></div></div>	38	2.4E-13	3.5E0	1.0E-11	8.9E-12
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:DEAH box	RT	<div><div></div><div></div></div>	28	6.7E-13	4.4E0	4.6E-11	4.4E-11
<input type="checkbox"/>	GOTERM_BP_DIRECT	RNA secondary structure unwinding	RT	<div><div></div><div></div></div>	26	2.2E-9	3.5E0	2.1E-7	2.0E-7
<input type="checkbox"/>	INTERPRO	RNA helicase, DEAD-box type, Q motif	RT	<div><div></div><div></div></div>	22	2.0E-8	3.7E0	6.2E-7	5.7E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Q motif	RT	<div><div></div><div></div></div>	21	1.4E-7	3.6E0	7.2E-6	6.9E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:DEAD box	RT	<div><div></div><div></div></div>	19	6.0E-7	3.6E0	2.6E-5	2.5E-5
<input type="checkbox"/>	INTERPRO	RNA helicase, ATP-dependent, DEAD-box, conserved site	RT	<div><div></div><div></div></div>	16	3.1E-6	3.7E0	7.3E-5	6.7E-5
Annotation Cluster 14		Enrichment Score: 15.47	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Protein phosphatase	RT	<div><div></div><div></div></div>	66	4.5E-21	3.4E0	5.7E-20	4.4E-20
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein dephosphorylation	RT	<div><div></div><div></div></div>	58	9.1E-14	2.7E0	1.4E-11	1.4E-11
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein serine/threonine phosphatase activity	RT	<div><div></div><div></div></div>	36	9.5E-14	3.7E0	4.4E-12	3.9E-12
Annotation Cluster 15		Enrichment Score: 15.15	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	RT	<div><div></div><div></div></div>	55	4.7E-31	5.3E0	5.6E-29	5.4E-29
<input type="checkbox"/>	INTERPRO	Ubiquitin-conjugating enzyme, active site	RT	<div><div></div><div></div></div>	24	8.5E-16	5.7E0	6.7E-14	6.2E-14
<input type="checkbox"/>	INTERPRO	Ubiquitin-conjugating enzyme, E2	RT	<div><div></div><div></div></div>	31	2.1E-15	4.6E0	1.6E-13	1.5E-13
<input type="checkbox"/>	INTERPRO	Ubiquitin-conjugating enzyme/RWD-like	RT	<div><div></div><div></div></div>	33	2.9E-12	3.7E0	1.6E-10	1.5E-10
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitin conjugating enzyme activity	RT	<div><div></div><div></div></div>	23	3.8E-12	4.7E0	1.4E-10	1.3E-10
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein K48-linked ubiquitination	RT	<div><div></div><div></div></div>	26	1.4E-8	3.3E0	1.2E-6	1.1E-6
Annotation Cluster 16		Enrichment Score: 12.35	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	DNA repair	RT	<div><div></div><div></div></div>	98	6.9E-16	2.3E0	7.8E-15	6.0E-15
<input type="checkbox"/>	UP_KEYWORDS	DNA damage	RT	<div><div></div><div></div></div>	110	2.3E-15	2.1E0	2.5E-14	1.9E-14
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA repair	RT	<div><div></div><div></div></div>	74	5.3E-8	1.9E0	4.1E-6	4.0E-6
Annotation Cluster 17		Enrichment Score: 12.02	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	proteasome-mediated ubiquitin-dependent protein catabolic process	RT	<div><div></div><div></div></div>	99	1.9E-25	2.9E0	8.9E-23	8.6E-23
<input type="checkbox"/>	GOTERM_BP_DIRECT	anaphase-promoting complex-dependent catabolic process	RT	<div><div></div><div></div></div>	54	3.5E-23	4.0E0	1.4E-20	1.3E-20
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	RT	<div><div></div><div></div></div>	52	2.3E-22	4.1E0	7.5E-20	7.2E-20
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	RT	<div><div></div><div></div></div>	48	2.4E-20	4.0E0	6.5E-18	6.2E-18
<input type="checkbox"/>	GOTERM_BP_DIRECT	stimulatory C-type lectin receptor signaling pathway	RT	<div><div></div><div></div></div>	60	5.3E-20	3.4E0	1.4E-17	1.3E-17
<input type="checkbox"/>	GOTERM_BP_DIRECT	T cell receptor signaling pathway	RT	<div><div></div><div></div></div>	68	5.6E-16	2.7E0	1.1E-13	1.0E-13
<input type="checkbox"/>	GOTERM_BP_DIRECT	NIK/NF-kappaB signaling	RT	<div><div></div><div></div></div>	41	1.6E-15	3.7E0	2.9E-13	2.8E-13
<input type="checkbox"/>	GOTERM_BP_DIRECT	Fc-epsilon receptor signaling pathway	RT	<div><div></div><div></div></div>	73	6.3E-14	2.4E0	1.0E-11	9.8E-12
















































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of canonical Wnt signaling pathway	RT		53	8.5E-12	2.6E0	1.1E-9	1.1E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of mRNA stability	RT		46	1.5E-10	2.6E0	1.7E-8	1.7E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	RT		18	2.5E-9	4.6E0	2.4E-7	2.3E-7
<input type="checkbox"/>	UP_KEYWORDS	Proteasome	RT		27	2.7E-9	3.5E0	2.4E-8	1.8E-8
<input type="checkbox"/>	GOTERM_CC_DIRECT	proteasome complex	RT		29	1.6E-8	3.1E0	5.0E-7	4.4E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of cellular amino acid metabolic process	RT		26	1.2E-7	3.0E0	8.3E-6	8.0E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of canonical Wnt signaling pathway	RT		55	2.9E-7	2.0E0	1.9E-5	1.8E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	Wnt signaling pathway, planar cell polarity pathway	RT		35	3.0E-6	2.3E0	1.5E-4	1.5E-4
<input type="checkbox"/>	KEGG_PATHWAY	Proteasome	RT		23	4.1E-6	2.7E0	1.2E-5	5.8E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	RT		24	1.4E-4	2.3E0	4.3E-3	4.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	tumor necrosis factor-mediated signaling pathway	RT		36	4.0E-4	1.8E0	1.0E-2	1.0E-2
Annotation Cluster 18		Enrichment Score: 11.69	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Actin-related protein	RT		29	2.8E-17	5.3E0	2.4E-15	2.2E-15
<input type="checkbox"/>	SMART	ACTIN	RT		29	4.9E-13	3.6E0	1.8E-11	1.6E-11
<input type="checkbox"/>	INTERPRO	Actin/actin-like conserved site	RT		18	1.0E-10	5.3E0	4.3E-9	3.9E-9
<input type="checkbox"/>	INTERPRO	Actin, conserved site	RT		15	1.3E-8	5.2E0	4.2E-7	3.9E-7
Annotation Cluster 19		Enrichment Score: 11.41	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein K11-linked ubiquitination	RT		25	4.5E-16	5.5E0	8.9E-14	8.6E-14
<input type="checkbox"/>	GOTERM_CC_DIRECT	anaphase-promoting complex	RT		19	5.0E-11	5.2E0	2.1E-9	1.9E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	RT		18	2.5E-9	4.6E0	2.4E-7	2.3E-7
Annotation Cluster 20		Enrichment Score: 11.35	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 3	RT		61	6.9E-27	4.3E0	7.6E-25	7.3E-25
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 2	RT		76	5.4E-18	2.8E0	4.9E-16	4.7E-16
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 4	RT		38	3.5E-16	4.2E0	2.9E-14	2.8E-14
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 1	RT		72	1.7E-15	2.7E0	1.3E-13	1.3E-13
<input type="checkbox"/>	UP_SEQ_FEATURE	calcium-binding region:1	RT		55	4.0E-14	2.9E0	3.0E-12	2.9E-12
<input type="checkbox"/>	UP_SEQ_FEATURE	calcium-binding region:3	RT		27	2.2E-13	4.7E0	1.6E-11	1.5E-11
<input type="checkbox"/>	UP_SEQ_FEATURE	calcium-binding region:2	RT		51	2.8E-13	2.9E0	2.0E-11	1.9E-11
<input type="checkbox"/>	INTERPRO	EF-Hand 1, calcium-binding site	RT		67	9.0E-12	2.3E0	4.5E-10	4.1E-10
<input type="checkbox"/>	INTERPRO	EF-hand domain	RT		79	1.4E-11	2.1E0	6.7E-10	6.1E-10
<input type="checkbox"/>	INTERPRO	EF-hand-like domain	RT		90	3.9E-11	2.0E0	1.7E-9	1.6E-9
<input type="checkbox"/>	SMART	EFh	RT		72	9.8E-11	2.0E0	3.1E-9	2.8E-9
<input type="checkbox"/>	COG_ONTOLOGY	Signal transduction mechanisms / Cytoskeleton / Cell division and chromosome partitioning / General function prediction only	RT		31	4.9E-5	1.8E0	7.6E-4	7.6E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium ion binding	RT		110	8.9E-1	9.1E-1	1.0E0	8.9E-1
<input type="checkbox"/>	UP_KEYWORDS	Calcium	RT		107	9.9E-1	8.4E-1	1.0E0	9.9E-1
Annotation Cluster 21		Enrichment Score: 11.32	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Motor protein	RT		84	3.8E-36	4.3E0	7.7E-35	5.9E-35
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Kinesin-motor	RT		33	5.9E-18	5.1E0	5.2E-16	5.0E-16
<input type="checkbox"/>	GOTERM_CC_DIRECT	kinesin complex	RT		37	1.8E-17	4.4E0	1.2E-15	1.0E-15
<input type="checkbox"/>	INTERPRO	Kinesin, motor region, conserved site	RT		32	4.7E-17	4.8E0	4.0E-15	3.6E-15
<input type="checkbox"/>	INTERPRO	Kinesin, motor domain	RT		33	2.9E-16	4.5E0	2.4E-14	2.2E-14
<input type="checkbox"/>	GOTERM_MF_DIRECT	microtubule motor activity	RT		42	1.4E-12	3.1E0	5.4E-11	4.8E-11
<input type="checkbox"/>	GOTERM_CC_DIRECT	microtubule	RT		96	3.1E-11	2.0E0	1.4E-9	1.3E-9
<input type="checkbox"/>	SMART	KISc	RT		33	6.1E-11	3.0E0	2.1E-9	1.9E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	microtubule-based movement	RT		38	1.4E-9	2.8E0	1.4E-7	1.3E-7

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Microtubule	RT		76	6.1E-8	1.9E0	4.8E-7	3.7E-7
<input type="checkbox"/>	GOTERM_MF_DIRECT	ATP-dependent microtubule motor activity, plus-end-directed	RT		13	1.3E-6	4.6E0	2.9E-5	2.6E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Globular	RT		12	1.4E-6	5.1E0	6.0E-5	5.8E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	microtubule binding	RT		61	9.1E-6	1.7E0	1.8E-4	1.6E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	antigen processing and presentation of exogenous peptide antigen via MHC class II	RT		25	1.7E-2	1.6E0	2.1E-1	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	retrograde vesicle-mediated transport, Golgi to ER	RT		21	5.2E-2	1.5E0	4.8E-1	4.6E-1
Annotation Cluster 22		Enrichment Score: 11.08	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:AGC-kinase C-terminal	RT		33	2.1E-13	4.0E0	1.5E-11	1.5E-11
<input type="checkbox"/>	INTERPRO	Protein kinase, C-terminal	RT		24	3.5E-13	5.0E0	2.2E-11	2.0E-11
<input type="checkbox"/>	INTERPRO	AGC-kinase, C-terminal	RT		33	2.9E-12	3.7E0	1.6E-10	1.5E-10
<input type="checkbox"/>	SMART	S TK X	RT		32	2.1E-8	2.6E0	5.3E-7	4.8E-7
Annotation Cluster 23		Enrichment Score: 11.06	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	T cell receptor signaling pathway	RT		66	7.4E-24	3.4E0	2.0E-22	9.5E-23
<input type="checkbox"/>	KEGG_PATHWAY	Prostate cancer	RT		56	3.4E-19	3.3E0	5.9E-18	2.8E-18
<input type="checkbox"/>	KEGG_PATHWAY	Pancreatic cancer	RT		43	1.1E-15	3.4E0	1.3E-14	5.9E-15
<input type="checkbox"/>	KEGG_PATHWAY	ErbB signaling pathway	RT		51	2.2E-15	3.0E0	2.4E-14	1.1E-14
<input type="checkbox"/>	KEGG_PATHWAY	Acute myeloid leukemia	RT		39	2.3E-15	3.6E0	2.4E-14	1.1E-14
<input type="checkbox"/>	KEGG_PATHWAY	Chronic myeloid leukemia	RT		44	3.2E-14	3.2E0	3.1E-13	1.4E-13
<input type="checkbox"/>	KEGG_PATHWAY	Endometrial cancer	RT		35	3.8E-13	3.5E0	3.3E-12	1.6E-12
<input type="checkbox"/>	KEGG_PATHWAY	Glioma	RT		40	4.2E-13	3.2E0	3.5E-12	1.7E-12
<input type="checkbox"/>	KEGG_PATHWAY	B cell receptor signaling pathway	RT		41	1.0E-12	3.1E0	8.0E-12	3.8E-12
<input type="checkbox"/>	KEGG_PATHWAY	VEGF signaling pathway	RT		38	1.0E-12	3.2E0	8.1E-12	3.8E-12
<input type="checkbox"/>	KEGG_PATHWAY	Prolactin signaling pathway	RT		41	3.6E-12	3.0E0	2.7E-11	1.3E-11
<input type="checkbox"/>	KEGG_PATHWAY	Non-small cell lung cancer	RT		34	5.4E-11	3.1E0	3.5E-10	1.7E-10
<input type="checkbox"/>	KEGG_PATHWAY	Fc epsilon RI signaling pathway	RT		38	9.4E-11	2.9E0	5.6E-10	2.7E-10
<input type="checkbox"/>	KEGG_PATHWAY	Bladder cancer	RT		27	6.4E-10	3.4E0	3.2E-9	1.5E-9
<input type="checkbox"/>	KEGG_PATHWAY	Melanoma	RT		37	2.2E-9	2.7E0	1.0E-8	4.7E-9
<input type="checkbox"/>	KEGG_PATHWAY	Sphingolipid signaling pathway	RT		52	3.3E-9	2.2E0	1.4E-8	6.6E-9
<input type="checkbox"/>	KEGG_PATHWAY	Renal cell carcinoma	RT		35	3.7E-9	2.8E0	1.5E-8	7.2E-9
<input type="checkbox"/>	KEGG_PATHWAY	Central carbon metabolism in cancer	RT		31	4.5E-7	2.5E0	1.6E-6	7.5E-7
<input type="checkbox"/>	KEGG_PATHWAY	Choline metabolism in cancer	RT		40	4.2E-6	2.1E0	1.2E-5	5.8E-6
<input type="checkbox"/>	KEGG_PATHWAY	Signaling pathways regulating pluripotency of stem cells	RT		44	7.1E-4	1.6E0	1.6E-3	7.6E-4
<input type="checkbox"/>	KEGG_PATHWAY	Natural killer cell mediated cytotoxicity	RT		38	2.1E-3	1.6E0	4.5E-3	2.1E-3
Annotation Cluster 24		Enrichment Score: 11.05	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	lipid moiety-binding region:N-myristoyl glycine	RT		57	6.6E-18	3.3E0	5.8E-16	5.5E-16
<input type="checkbox"/>	UP_KEYWORDS	Myristate	RT		72	2.6E-14	2.5E0	2.7E-13	2.1E-13
<input type="checkbox"/>	UP_KEYWORDS	Lipoprotein	RT		153	4.0E-3	1.2E0	1.9E-2	1.5E-2
Annotation Cluster 25		Enrichment Score: 9.95	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of protein kinase activity	RT		53	5.0E-16	3.2E0	9.7E-14	9.3E-14
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein kinase inhibitor activity	RT		32	3.9E-12	3.7E0	1.4E-10	1.3E-10
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of JAK-STAT cascade	RT		25	1.0E-9	3.7E0	1.0E-7	1.0E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	cytokine-mediated signaling pathway	RT		41	7.9E-5	1.9E0	2.6E-3	2.5E-3
Annotation Cluster 26		Enrichment Score: 9.83	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Chagas disease (American trypanosomiasis)	RT		58	4.9E-16	2.9E0	5.7E-15	2.7E-15
<input type="checkbox"/>	KEGG_PATHWAY	Toxoplasmosis	RT		58	1.3E-14	2.7E0	1.3E-13	5.9E-14
<input type="checkbox"/>	KEGG_PATHWAY	Toll-like receptor signaling pathway	RT		49	7.2E-10	2.4E0	3.4E-9	1.6E-9



Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Leishmaniasis	RT		32	2.0E-6	2.3E0	6.3E-6	3.0E-6
<input type="checkbox"/>	KEGG_PATHWAY	Pertussis	RT		32	8.0E-6	2.2E0	2.3E-5	1.1E-5
Annotation Cluster 27		Enrichment Score: 9.7	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Motor protein	RT		84	3.8E-36	4.3E0	7.7E-35	5.9E-35
<input type="checkbox"/>	UP_KEYWORDS	Myosin	RT		44	1.5E-28	5.9E0	2.3E-27	1.8E-27
<input type="checkbox"/>	INTERPRO	Myosin head, motor domain	RT		34	3.4E-20	5.3E0	3.3E-18	3.1E-18
<input type="checkbox"/>	GOTERM_CC_DIRECT	myosin complex	RT		38	6.2E-20	4.8E0	4.2E-18	3.7E-18
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Myosin head-like	RT		31	3.0E-19	5.7E0	2.8E-17	2.7E-17
<input type="checkbox"/>	GOTERM_MF_DIRECT	motor activity	RT		41	1.3E-15	3.7E0	6.5E-14	5.8E-14
<input type="checkbox"/>	SMART	MYSc	RT		34	1.9E-14	3.5E0	7.5E-13	6.8E-13
<input type="checkbox"/>	INTERPRO	IQ motif, EF-hand binding site	RT		43	2.6E-12	3.1E0	1.5E-10	1.4E-10
<input type="checkbox"/>	GOTERM_MF_DIRECT	microfilament motor activity	RT		18	4.3E-11	5.4E0	1.5E-9	1.3E-9
<input type="checkbox"/>	UP_KEYWORDS	Muscle protein	RT		32	4.4E-11	3.5E0	4.3E-10	3.3E-10
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Actin-binding	RT		21	5.3E-11	4.9E0	3.6E-9	3.4E-9
<input type="checkbox"/>	UP_KEYWORDS	Calmodulin-binding	RT		55	9.2E-11	2.5E0	8.7E-10	6.8E-10
<input type="checkbox"/>	INTERPRO	Myosin, N-terminal, SH3-like	RT		15	1.0E-10	6.2E0	4.3E-9	3.9E-9
<input type="checkbox"/>	INTERPRO	Myosin-like IQ motif-containing domain	RT		17	1.2E-10	5.5E0	5.0E-9	4.6E-9
<input type="checkbox"/>	GOTERM_CC_DIRECT	muscle myosin complex	RT		15	4.8E-10	6.0E0	1.9E-8	1.6E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ	RT		28	2.7E-8	3.1E0	1.5E-6	1.4E-6
<input type="checkbox"/>	INTERPRO	Myosin tail	RT		15	4.1E-8	4.9E0	1.3E-6	1.1E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	calmodulin binding	RT		60	6.6E-7	1.9E0	1.6E-5	1.4E-5
<input type="checkbox"/>	UP_KEYWORDS	Actin-binding	RT		71	1.1E-6	1.8E0	8.2E-6	6.3E-6
<input type="checkbox"/>	GOTERM_CC_DIRECT	myosin filament	RT		12	2.9E-6	4.8E0	6.4E-5	5.7E-5
<input type="checkbox"/>	SMART	IQ	RT		29	5.5E-6	2.3E0	9.6E-5	8.7E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 1	RT		16	2.3E-5	3.3E0	7.9E-4	7.6E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 2	RT		16	2.3E-5	3.3E0	7.9E-4	7.6E-4
<input type="checkbox"/>	UP_KEYWORDS	Thick filament	RT		11	3.1E-5	4.4E0	1.9E-4	1.4E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 3	RT		12	9.8E-5	3.7E0	3.0E-3	2.9E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	actin filament-based movement	RT		11	1.1E-4	3.8E0	3.5E-3	3.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 4	RT		9	5.2E-4	4.1E0	1.4E-2	1.4E-2
<input type="checkbox"/>	KEGG_PATHWAY	Tight junction	RT		30	1.3E-3	1.8E0	2.8E-3	1.3E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 5	RT		6	1.4E-2	3.7E0	2.7E-1	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	muscle contraction	RT		27	3.1E-2	1.5E0	3.4E-1	3.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 6	RT		3	3.3E-1	2.6E0	1.0E0	9.6E-1
Annotation Cluster 28		Enrichment Score: 9.43	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	termination of RNA polymerase II transcription	RT		42	3.7E-17	3.9E0	8.4E-15	8.1E-15
<input type="checkbox"/>	GOTERM_BP_DIRECT	mRNA 3'-end processing	RT		35	1.3E-15	4.1E0	2.4E-13	2.3E-13
<input type="checkbox"/>	GOTERM_BP_DIRECT	RNA export from nucleus	RT		27	1.6E-7	2.9E0	1.1E-5	1.1E-5
<input type="checkbox"/>	KEGG_PATHWAY	mRNA surveillance pathway	RT		36	1.4E-5	2.1E0	3.8E-5	1.8E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	mRNA export from nucleus	RT		34	6.1E-5	2.0E0	2.1E-3	2.0E-3
Annotation Cluster 29		Enrichment Score: 8.93	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 6	RT		83	6.8E-52	5.7E0	1.1E-49	1.0E-49
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 7	RT		55	3.8E-36	5.9E0	5.0E-34	4.8E-34
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 8	RT		41	1.3E-27	6.1E0	1.5E-25	1.5E-25
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 9	RT		36	9.9E-24	6.0E0	1.0E-21	9.8E-22
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 10	RT		26	1.7E-17	6.1E0	1.4E-15	1.4E-15

















































Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 11	RT	<div><div></div><div></div></div>	23	6.2E-16	6.3E0	5.0E-14	4.8E-14
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 12	RT	<div><div></div><div></div></div>	16	1.6E-10	6.1E0	1.0E-8	1.0E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 13	RT	<div><div></div><div></div></div>	13	2.9E-8	5.9E0	1.5E-6	1.5E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 14	RT	<div><div></div><div></div></div>	13	2.9E-8	5.9E0	1.5E-6	1.5E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 15	RT	<div><div></div><div></div></div>	13	2.9E-8	5.9E0	1.5E-6	1.5E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 16	RT	<div><div></div><div></div></div>	11	8.5E-7	5.8E0	3.6E-5	3.5E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 17	RT	<div><div></div><div></div></div>	10	4.5E-6	5.7E0	1.8E-4	1.7E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 18	RT	<div><div></div><div></div></div>	10	4.5E-6	5.7E0	1.8E-4	1.7E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 19	RT	<div><div></div><div></div></div>	10	4.5E-6	5.7E0	1.8E-4	1.7E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 20	RT	<div><div></div><div></div></div>	9	2.3E-5	5.6E0	7.9E-4	7.6E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 21	RT	<div><div></div><div></div></div>	9	2.3E-5	5.6E0	7.9E-4	7.6E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 22	RT	<div><div></div><div></div></div>	8	1.2E-4	5.5E0	3.5E-3	3.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 23	RT	<div><div></div><div></div></div>	8	1.2E-4	5.5E0	3.5E-3	3.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 24	RT	<div><div></div><div></div></div>	6	2.6E-3	5.1E0	6.2E-2	6.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 25	RT	<div><div></div><div></div></div>	5	1.1E-2	4.9E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 26	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 27	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein targeting to plasma membrane	RT	<div><div></div><div></div></div>	9	5.9E-2	2.0E0	5.2E-1	5.0E-1
<input type="checkbox"/>	INTERPRO	ZU5	RT	<div><div></div><div></div></div>	4	3.0E-1	2.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	DEATH	RT	<div><div></div><div></div></div>	9	3.4E-1	1.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:ZU5	RT	<div><div></div><div></div></div>	3	3.9E-1	2.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	ZU5	RT	<div><div></div><div></div></div>	3	6.9E-1	1.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	cytoskeletal adaptor activity	RT	<div><div></div><div></div></div>	3	7.8E-1	1.1E0	1.0E0	8.9E-1
Annotation Cluster 30		Enrichment Score: 8.33	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BTB	RT	<div><div></div><div></div></div>	58	2.1E-13	2.7E0	1.5E-11	1.5E-11
<input type="checkbox"/>	INTERPRO	BTB/POZ-like	RT	<div><div></div><div></div></div>	63	1.2E-9	2.2E0	4.5E-8	4.1E-8
<input type="checkbox"/>	INTERPRO	BTB/POZ fold	RT	<div><div></div><div></div></div>	65	1.9E-9	2.1E0	6.7E-8	6.1E-8
<input type="checkbox"/>	SMART	BTB	RT	<div><div></div><div></div></div>	63	9.5E-4	1.5E0	1.2E-2	1.1E-2
Annotation Cluster 31		Enrichment Score: 8	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Estrogen signaling pathway	RT	<div><div></div><div></div></div>	58	1.8E-17	3.0E0	2.4E-16	1.1E-16
<input type="checkbox"/>	KEGG_PATHWAY	Chemokine signaling pathway	RT	<div><div></div><div></div></div>	68	4.2E-8	1.9E0	1.6E-7	7.4E-8
<input type="checkbox"/>	KEGG_PATHWAY	Melanogenesis	RT	<div><div></div><div></div></div>	41	1.1E-6	2.1E0	3.8E-6	1.8E-6
<input type="checkbox"/>	KEGG_PATHWAY	Cholinergic synapse	RT	<div><div></div><div></div></div>	42	8.8E-6	2.0E0	2.5E-5	1.2E-5
<input type="checkbox"/>	KEGG_PATHWAY	cAMP signaling pathway	RT	<div><div></div><div></div></div>	64	1.3E-5	1.7E0	3.5E-5	1.7E-5
Annotation Cluster 32		Enrichment Score: 7.87	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Viral nucleoprotein	RT	<div><div></div><div></div></div>	20	2.2E-10	4.9E0	2.0E-9	1.5E-9
<input type="checkbox"/>	GOTERM_CC_DIRECT	viral nucleocapsid	RT	<div><div></div><div></div></div>	20	8.5E-10	4.5E0	3.1E-8	2.8E-8
<input type="checkbox"/>	UP_KEYWORDS	Virion	RT	<div><div></div><div></div></div>	20	1.4E-5	2.9E0	8.5E-5	6.6E-5
Annotation Cluster 33		Enrichment Score: 7.86	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Chronic myeloid leukemia	RT	<div><div></div><div></div></div>	44	3.2E-14	3.2E0	3.1E-13	1.4E-13
<input type="checkbox"/>	KEGG_PATHWAY	Small cell lung cancer	RT	<div><div></div><div></div></div>	35	7.0E-6	2.1E0	2.0E-5	9.4E-6
<input type="checkbox"/>	BIOCARTA	Influence of Ras and Rho proteins on G1 to S Transition	RT	<div><div></div><div></div></div>	21	1.1E-5	2.4E0	5.6E-4	4.0E-4
Annotation Cluster 34		Enrichment Score: 7.48	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Tubulin/FtsZ, C-terminal	RT	<div><div></div><div></div></div>	20	3.8E-12	5.4E0	2.0E-10	1.8E-10
<input type="checkbox"/>	INTERPRO	Tubulin, C-terminal	RT	<div><div></div><div></div></div>	20	3.8E-12	5.4E0	2.0E-10	1.8E-10
<input type="checkbox"/>	INTERPRO	Tubulin, conserved site	RT	<div><div></div><div></div></div>	20	3.8E-12	5.4E0	2.0E-10	1.8E-10



Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Tubulin	RT	<div><div></div><div></div></div>	20	1.6E-11	5.2E0	7.4E-10	6.8E-10
<input type="checkbox"/>	INTERPRO	Tubulin/FtsZ, 2-layer sandwich domain	RT	<div><div></div><div></div></div>	19	2.0E-11	5.4E0	9.2E-10	8.4E-10
<input type="checkbox"/>	INTERPRO	Tubulin/FtsZ, GTPase domain	RT	<div><div></div><div></div></div>	20	5.5E-11	5.0E0	2.4E-9	2.2E-9
<input type="checkbox"/>	SMART	SM00865	RT	<div><div></div><div></div></div>	19	2.6E-8	3.5E0	6.3E-7	5.7E-7
<input type="checkbox"/>	SMART	SM00864	RT	<div><div></div><div></div></div>	20	2.9E-8	3.4E0	6.5E-7	5.9E-7
<input type="checkbox"/>	KEGG_PATHWAY	Pathogenic Escherichia coli infection	RT	<div><div></div><div></div></div>	27	3.4E-7	2.7E0	1.2E-6	5.7E-7
<input type="checkbox"/>	GOTERM_MF_DIRECT	structural constituent of cytoskeleton	RT	<div><div></div><div></div></div>	40	1.6E-6	2.2E0	3.6E-5	3.2E-5
<input type="checkbox"/>	INTERPRO	Beta tubulin	RT	<div><div></div><div></div></div>	9	3.5E-6	6.2E0	8.0E-5	7.3E-5
<input type="checkbox"/>	INTERPRO	Beta tubulin, autoregulation binding site	RT	<div><div></div><div></div></div>	9	3.5E-6	6.2E0	8.0E-5	7.3E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	microtubule-based process	RT	<div><div></div><div></div></div>	19	4.8E-6	3.1E0	2.4E-4	2.3E-4
<input type="checkbox"/>	INTERPRO	Alpha tubulin	RT	<div><div></div><div></div></div>	7	3.9E-3	3.9E0	4.3E-2	4.0E-2
<input type="checkbox"/>	KEGG_PATHWAY	Phagosome	RT	<div><div></div><div></div></div>	27	7.6E-1	9.3E-1	1.0E0	7.6E-1
Annotation Cluster 35		Enrichment Score: 6.92	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein serine/threonine phosphatase activity	RT	<div><div></div><div></div></div>	36	9.5E-14	3.7E0	4.4E-12	3.9E-12
<input type="checkbox"/>	INTERPRO	Protein phosphatase 2C (PP2C)-like	RT	<div><div></div><div></div></div>	17	5.1E-10	5.3E0	2.1E-8	1.9E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Manganese 1; via carbonyl oxygen	RT	<div><div></div><div></div></div>	13	1.1E-9	6.8E0	6.7E-8	6.4E-8
<input type="checkbox"/>	INTERPRO	Protein phosphatase 2C	RT	<div><div></div><div></div></div>	14	6.1E-8	5.1E0	1.8E-6	1.7E-6
<input type="checkbox"/>	INTERPRO	Protein phosphatase 2C, manganese/magnesium aspartate binding site	RT	<div><div></div><div></div></div>	11	1.1E-7	6.2E0	3.2E-6	3.0E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptidyl-threonine dephosphorylation	RT	<div><div></div><div></div></div>	11	1.7E-7	5.9E0	1.2E-5	1.1E-5
<input type="checkbox"/>	SMART	PP2Cc	RT	<div><div></div><div></div></div>	17	3.0E-7	3.5E0	5.8E-6	5.3E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Manganese 1	RT	<div><div></div><div></div></div>	15	6.3E-6	3.8E0	2.4E-4	2.3E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Manganese 2	RT	<div><div></div><div></div></div>	15	6.3E-6	3.8E0	2.4E-4	2.3E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PP2C-like	RT	<div><div></div><div></div></div>	10	1.3E-5	5.2E0	4.5E-4	4.3E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	cation binding	RT	<div><div></div><div></div></div>	7	8.2E-3	3.5E0	6.9E-2	6.2E-2
Annotation Cluster 36		Enrichment Score: 6.28	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Protein phosphatase	RT	<div><div></div><div></div></div>	66	4.5E-21	3.4E0	5.7E-20	4.4E-20
<input type="checkbox"/>	INTERPRO	Dual specificity phosphatase, catalytic domain	RT	<div><div></div><div></div></div>	31	6.1E-15	4.5E0	4.4E-13	4.0E-13
<input type="checkbox"/>	INTERPRO	Dual specificity phosphatase, subgroup, catalytic domain	RT	<div><div></div><div></div></div>	28	7.6E-15	4.8E0	5.3E-13	4.8E-13
<input type="checkbox"/>	INTERPRO	Dual specificity phosphatase	RT	<div><div></div><div></div></div>	24	1.2E-12	4.8E0	7.0E-11	6.4E-11
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein tyrosine/serine/threonine phosphatase activity	RT	<div><div></div><div></div></div>	25	8.5E-11	4.0E0	2.8E-9	2.5E-9
<input type="checkbox"/>	SMART	DSPc	RT	<div><div></div><div></div></div>	28	2.7E-10	3.2E0	8.1E-9	7.3E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Tyrosine-protein phosphatase	RT	<div><div></div><div></div></div>	31	5.1E-10	3.4E0	3.1E-8	3.0E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Rhodanese	RT	<div><div></div><div></div></div>	15	8.7E-8	4.9E0	4.4E-6	4.3E-6
<input type="checkbox"/>	INTERPRO	Protein-tyrosine/Dual specificity phosphatase	RT	<div><div></div><div></div></div>	34	1.5E-7	2.6E0	4.2E-6	3.8E-6
<input type="checkbox"/>	INTERPRO	Mitogen-activated protein (MAP) kinase phosphatase	RT	<div><div></div><div></div></div>	10	6.2E-7	6.2E0	1.7E-5	1.6E-

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein tyrosine/threonine phosphatase activity	RT		3	7.5E-2	6.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	endoderm formation	RT		5	1.3E-1	2.5E0	8.2E-1	7.9E-1
<input type="checkbox"/>	SMART	PTPc motif	RT		18	3.8E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Protein-tyrosine phosphatase, receptor/non-receptor type	RT		6	7.6E-1	9.8E-1	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	PTPc	RT		6	9.7E-1	6.6E-1	1.0E0	9.7E-1
Annotation Cluster 37		Enrichment Score: 6.15	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription-coupled nucleotide-excision repair	RT		39	1.0E-11	3.1E0	1.3E-9	1.3E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	telomere maintenance via recombination	RT		21	9.4E-9	3.9E0	8.3E-7	7.9E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA damage response, detection of DNA damage	RT		22	2.3E-8	3.6E0	1.9E-6	1.8E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, preincision complex assembly	RT		19	6.1E-8	3.9E0	4.7E-6	4.5E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision, 5'-to lesion	RT		21	2.8E-7	3.4E0	1.8E-5	1.8E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision	RT		21	4.9E-7	3.3E0	3.0E-5	2.9E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	error-prone translesion synthesis	RT		14	8.7E-7	4.4E0	4.9E-5	4.7E-5
<input type="checkbox"/>	KEGG_PATHWAY	Nucleotide excision repair	RT		24	4.0E-6	2.6E0	1.2E-5	5.7E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA gap filling	RT		15	5.3E-6	3.7E0	2.5E-4	2.4E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	error-free translesion synthesis	RT		13	8.2E-6	4.1E0	3.6E-4	3.5E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	translesion synthesis	RT		18	2.3E-5	3.0E0	8.9E-4	8.5E-4
<input type="checkbox"/>	KEGG_PATHWAY	Mismatch repair	RT		13	4.1E-4	2.9E0	9.6E-4	4.5E-4
<input type="checkbox"/>	KEGG_PATHWAY	DNA replication	RT		17	4.8E-4	2.4E0	1.1E-3	5.3E-4
Annotation Cluster 38		Enrichment Score: 6.12	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	ATP-dependent RNA helicase activity	RT		38	2.4E-13	3.5E0	1.0E-11	8.9E-12
<input type="checkbox"/>	INTERPRO	Domain of unknown function DUF1605	RT		13	8.4E-7	4.7E0	2.3E-5	2.1E-5
<input type="checkbox"/>	INTERPRO	Helicase-associated domain	RT		13	2.2E-6	4.5E0	5.2E-5	4.8E-5
<input type="checkbox"/>	INTERPRO	DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site	RT		14	5.7E-6	3.9E0	1.2E-4	1.1E-4
<input type="checkbox"/>	SMART	SM00847	RT		13	1.9E-4	2.9E0	2.9E-3	2.6E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	ATP-dependent helicase activity	RT		14	3.8E-4	2.9E0	4.9E-3	4.4E-3
Annotation Cluster 39		Enrichment Score: 5.93	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SET	RT		32	9.6E-15	4.4E0	7.4E-13	7.1E-13
<input type="checkbox"/>	INTERPRO	SET domain	RT		33	7.6E-14	4.0E0	5.1E-12	4.7E-12
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone-lysine N-methyltransferase activity	RT		24	3.2E-9	3.7E0	9.6E-8	8.6E-8
<input type="checkbox"/>	SMART	SET	RT		26	9.1E-8	2.8E0	2.0E-6	1.8E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Post-SET	RT		12	1.4E-6	5.1E0	6.0E-5	5.8E-5
<input type="checkbox"/>	INTERPRO	Post-SET domain	RT		11	3.7E-5	4.3E0	6.6E-4	6.0E-4
<input type="checkbox"/>	UP_KEYWORDS	S-adenosyl-L-methionine	RT		46	6.3E-5	1.8E0	3.6E-4	2.8E-4
<input type="checkbox"/>	UP_KEYWORDS	Methyltransferase	RT		47	4.1E-4	1.7E0	2.2E-3	1.7E-3
<input type="checkbox"/>	SMART	PostSET	RT		9	5.0E-3	2.8E0	5.1E-2	4.6E-2
<input type="checkbox"/>	KEGG_PATHWAY	Lysine degradation	RT		18	1.5E-2	1.8E0	2.8E-2	1.5E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	methyltransferase activity	RT		19	3.1E-1	1.2E0	1.0E0	8.9E-1
Annotation Cluster 40		Enrichment Score: 5.45	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of telomere maintenance via telomerase	RT		22	1.1E-9	4.1E0	1.1E-7	1.0E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of telomerase activity	RT		16	1.8E-5	3.3E0	7.0E-4	6.7E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of telomere capping	RT		9	2.3E-3	3.3E0	4.7E-2	4.5E-2
Annotation Cluster 41		Enrichment Score: 5.23	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	ATPase, AAA-type, conserved site	RT		19	5.6E-9	4.4E0	1.9E-7	1.8E-7
<input type="checkbox"/>	INTERPRO	ATPase, AAA-type, core	RT		24	1.0E-6	2.9E0	2.7E-5	2.5E-5
<input type="checkbox"/>	INTERPRO	AAA+ ATPase domain	RT		44	5.3E-6	2.0E0	1.1E-4	1.0E-4

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	SMART	AAA	RT	<div><div></div><div></div></div>	44	3.7E-2	1.3E0	2.7E-1	2.4E-1
Annotation Cluster 42		Enrichment Score: 5.05	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PI3K/PI4K	RT	<div><div></div><div></div></div>	16	1.6E-10	6.1E0	1.0E-8	1.0E-8
<input type="checkbox"/>	INTERPRO	Phosphatidylinositol 3-/4-kinase, catalytic domain	RT	<div><div></div><div></div></div>	16	2.5E-9	5.2E0	9.0E-8	8.2E-8
<input type="checkbox"/>	INTERPRO	Phosphatidylinositol 3/4-kinase, conserved site	RT	<div><div></div><div></div></div>	14	1.7E-8	5.4E0	5.4E-7	5.0E-7
<input type="checkbox"/>	SMART	PI3Kc	RT	<div><div></div><div></div></div>	15	9.0E-7	3.6E0	1.7E-5	1.6E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FAT	RT	<div><div></div><div></div></div>	6	3.6E-4	6.8E0	9.9E-3	9.5E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FATC	RT	<div><div></div><div></div></div>	6	3.6E-4	6.8E0	9.9E-3	9.5E-3
<input type="checkbox"/>	INTERPRO	PIK-related kinase, FATC	RT	<div><div></div><div></div></div>	6	5.7E-4	6.2E0	7.8E-3	7.1E-3
<input type="checkbox"/>	INTERPRO	PIK-related kinase	RT	<div><div></div><div></div></div>	6	5.7E-4	6.2E0	7.8E-3	7.1E-3
<input type="checkbox"/>	INTERPRO	PIK-related kinase, FAT	RT	<div><div></div><div></div></div>	5	2.9E-3	6.2E0	3.3E-2	3.1E-2
<input type="checkbox"/>	SMART	SM01343	RT	<div><div></div><div></div></div>	6	4.3E-3	4.1E0	4.5E-2	4.1E-2
Annotation Cluster 43		Enrichment Score: 5.01	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-binding oligomerization domain containing signaling pathway	RT	<div><div></div><div></div></div>	17	1.8E-7	4.0E0	1.2E-5	1.2E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	I-kappaB kinase/NF-kappaB signaling	RT	<div><div></div><div></div></div>	27	1.3E-6	2.7E0	7.3E-5	7.0E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of tumor necrosis factor-mediated signaling pathway	RT	<div><div></div><div></div></div>	15	1.4E-4	3.0E0	4.4E-3	4.2E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	TRIF-dependent toll-like receptor signaling pathway	RT	<div><div></div><div></div></div>	14	2.6E-4	3.0E0	7.3E-3	7.0E-3
Annotation Cluster 44		Enrichment Score: 4.99	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	WD40 repeat, conserved site	RT	<div><div></div><div></div></div>	55	1.2E-7	2.1E0	3.6E-6	3.3E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 5	RT	<div><div></div><div></div></div>	66	2.4E-7	1.9E0	1.1E-5	1.0E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 4	RT	<div><div></div><div></div></div>	69	3.9E-7	1.8E0	1.8E-5	1.7E-5
<input type="checkbox"/>	INTERPRO	G-protein beta WD-40 repeat	RT	<div><div></div><div></div></div>	36	4.3E-7	2.4E0	1.2E-5	1.1E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 7	RT	<div><div></div><div></div></div>	47	5.5E-7	2.1E0	2.4E-5	2.3E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 6	RT	<div><div></div><div></div></div>	55	2.1E-6	1.9E0	8.5E-5	8.2E-5
<input type="checkbox"/>	UP_KEYWORDS	WD repeat	RT	<div><div></div><div></div></div>	71	3.0E-6	1.7E0	2.0E-5	1.5E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 3	RT	<div><div></div><div></div></div>	69	3.1E-6	1.7E0	1.3E-4	1.2E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 2	RT	<div><div></div><div></div></div>	69	1.0E-5	1.7E0	3.7E-4	3.5E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 1	RT	<div><div></div><div></div></div>	69	1.0E-5	1.7E0	3.7E-4	3.5E-4
<input type="checkbox"/>	INTERPRO	WD40-repeat-containing domain	RT	<div><div></div><div></div></div>	76	9.2E-5	1.5E0	1.6E-3	1.4E-3
<input type="checkbox"/>	INTERPRO	WD40 repeat	RT	<div><div></div><div></div></div>	67	2.0E-4	1.5E0	3.1E-3	2.9E-3
<input type="checkbox"/>	INTERPRO	WD40/YVTN repeat-like-containing domain	RT	<div><div></div><div></div></div>	74	2.7E-3	1.4E0	3.2E-2	2.9E-2
<input type="checkbox"/>	SMART	WD40	RT	<div><div></div><div></div></div>	67	5.1E-1	1.0E0	1.0E0	9.1E-1
Annotation Cluster 45		Enrichment Score: 4.92	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:TXY	RT	<div><div></div><div></div></div>	11	2.3E-7	6.2E0	1.0E-5	1.0E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	MAP kinase activity	RT	<div><div></div><div></div></div>	12	6.4E-7	5.1E0	1.6E-5	1.4E-5
<input type="checkbox"/>	INTERPRO	Mitogen-activated protein (MAP) kinase, conserved site	RT	<div><div></div><div></div></div>	10	1.0E-5	5.2E0	2.0E-4	1.8E-4
<input type="checkbox"/>	INTERPRO	Mitogen-activated protein (MAP) kinase, p38	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
Annotation Cluster 46		Enrichment Score: 4.88	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	cadherin binding involved in cell-cell adhesion	RT	<div><div></div><div></div></div>	80	4.3E-6	1.6E0	8.7E-5	7.8E-5
<input type="checkbox"/>	GOTERM_CC_DIRECT	cell-cell adherens junction	RT	<div><div></div><div></div></div>	82	8.2E-6	1.6E0	1.5E-4	1.3E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell-cell adhesion	RT	<div><div></div><div></div></div>	72	6.4E-5	1.6E0	2.1E-3	2.1E-3
Annotation Cluster 47		Enrichment Score: 4.87	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Actinin-type, actin-binding, conserved site	RT	<div><div></div><div></div></div>	18	1.2E-9	4.9E0	4.5E-8	4.1E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Actin-binding	RT	<div><div></div><div></div></div>	16	2.3E-9	5.5E0	1.4E-7	1.3E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 4	RT	<div><div></div><div></div></div>	16	6.9E-9	5.2E0	4.0E-7	3.9E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CH 1	RT	<div><div></div><div></div></div>	18	1.3E-8	4.5E0	7.1E-7	6.9E-7





Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CH 2	RT	<div><div></div><div></div></div>	18	1.3E-8	4.5E0	7.1E-7	6.9E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 3	RT	<div><div></div><div></div></div>	16	1.9E-8	5.0E0	1.0E-6	1.0E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 6	RT	<div><div></div><div></div></div>	12	3.9E-8	6.3E0	2.0E-6	2.0E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 7	RT	<div><div></div><div></div></div>	12	3.9E-8	6.3E0	2.0E-6	2.0E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 8	RT	<div><div></div><div></div></div>	12	3.9E-8	6.3E0	2.0E-6	2.0E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 9	RT	<div><div></div><div></div></div>	12	3.9E-8	6.3E0	2.0E-6	2.0E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 5	RT	<div><div></div><div></div></div>	12	1.6E-7	5.8E0	7.9E-6	7.6E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 10	RT	<div><div></div><div></div></div>	11	2.3E-7	6.2E0	1.0E-5	1.0E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 11	RT	<div><div></div><div></div></div>	11	2.3E-7	6.2E0	1.0E-5	1.0E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 12	RT	<div><div></div><div></div></div>	11	2.3E-7	6.2E0	1.0E-5	1.0E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 13	RT	<div><div></div><div></div></div>	11	2.3E-7	6.2E0	1.0E-5	1.0E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 14	RT	<div><div></div><div></div></div>	11	2.3E-7	6.2E0	1.0E-5	1.0E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 15	RT	<div><div></div><div></div></div>	11	2.3E-7	6.2E0	1.0E-5	1.0E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 16	RT	<div><div></div><div></div></div>	11	2.3E-7	6.2E0	1.0E-5	1.0E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 17	RT	<div><div></div><div></div></div>	11	2.3E-7	6.2E0	1.0E-5	1.0E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 1	RT	<div><div></div><div></div></div>	16	4.7E-7	4.2E0	2.1E-5	2.0E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 2	RT	<div><div></div><div></div></div>	16	4.7E-7	4.2E0	2.1E-5	2.0E-5
<input type="checkbox"/>	INTERPRO	Spectrin repeat	RT	<div><div></div><div></div></div>	15	5.9E-6	3.7E0	1.2E-4	1.1E-4
<input type="checkbox"/>	INTERPRO	Spectrin/alpha-actinin	RT	<div><div></div><div></div></div>	16	1.0E-5	3.4E0	2.0E-4	1.8E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 18	RT	<div><div></div><div></div></div>	8	4.0E-5	6.1E0	1.3E-3	1.2E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 19	RT	<div><div></div><div></div></div>	7	2.1E-4	6.0E0	6.2E-3	5.9E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 20	RT	<div><div></div><div></div></div>	7	2.1E-4	6.0E0	6.2E-3	5.9E-3
<input type="checkbox"/>	INTERPRO	Calponin homology domain	RT	<div><div></div><div></div></div>	25	6.1E-4	2.0E0	8.3E-3	7.6E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	spectrin	RT	<div><div></div><div></div></div>	7	8.2E-4	4.9E0	8.6E-3	7.5E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 21	RT	<div><div></div><div></div></div>	6	1.1E-3	5.8E0	2.9E-2	2.8E-2
<input type="checkbox"/>	SMART	SPEC	RT	<div><div></div><div></div></div>	16	1.5E-3	2.2E0	1.7E-2	1.5E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 22	RT	<div><div></div><div></div></div>	5	5.4E-3	5.7E0	1.2E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	actin filament capping	RT	<div><div></div><div></div></div>	7	1.3E-2	3.2E0	1.8E-1	1.7E-1
<input type="checkbox"/>	INTERPRO	Spectrin, beta subunit	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	spectrin, beta subunit	RT	<div><div></div><div></div></div>	4	2.1E-2	5.4E0	2.9E-1	2.9E-1
<input type="checkbox"/>	SMART	CH	RT	<div><div></div><div></div></div>	25	2.2E-2	1.5E0	1.8E-1	1.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 23	RT	<div><div></div><div></div></div>	4	2.5E-2	5.5E0	4.4E-1	4.3E-1
<input type="checkbox"/>	UP_KEYWORDS	Actin capping	RT	<div><div></div><div></div></div>	7	4.7E-2	2.5E0	1.7E-1	1.3E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	ankyrin binding	RT	<div><div></div><div></div></div>	7	1.0E-1	2.1E0	5.0E-1	4.4E-1
<input type="checkbox"/>	INTERPRO	Pleckstrin homology domain, spectrin-type	RT	<div><div></div><div></div></div>	4	1.2E-1	3.1E0	6.4E-1	5.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	phospholipid binding	RT	<div><div></div><div></div></div>	11	9.3E-1	7.6E-1	1.0E0	9.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	ER to Golgi vesicle-mediated transport	RT	<div><div></div><div></div></div>	17	1.0E0	6.3E-1	1.0E0	1.0E0
Annotation Cluster 48		Enrichment Score: 4.73	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, preincision complex assembly	RT	<div><div></div><div></div></div>	19	6.1E-8	3.9E0	4.7E-6	4.5E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	global genome nucleotide-excision repair	RT	<div><div></div><div></div></div>	20	7.3E-8	3.7E0	5.4E-6	5.2E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision, 5'-to lesion	RT	<div><div></div><div></div></div>	21	2.8E-7	3.4E0	1.8E-5	1.8E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision	RT	<div><div></div><div></div></div>	21	4.9E-7	3.3E0	3.0E-5	2.9E-5
<input type="checkbox"/>	KEGG_PATHWAY	Nucleotide excision repair	RT	<div><div></div><div></div></div>	24	4.0E-6	2.6E0	1.2E-5	5.7E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA duplex unwinding	RT	<div><div></div><div></div></div>	14	9.6E-6	3.8E0	4.2E-4	4.0E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA damage recognition	RT	<div><div></div><div></div></div>	12	5.8E-4	3.1E0	1.5E-2	1.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, preincision complex stabilization	RT	<div><div></div><div></div></div>	11	1.1E-3	3.1E0	2.5E-2	2.4E-2






Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision, 3'-to lesion	RT		11	2.5E-3	2.8E0	5.0E-2	4.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair	RT		11	1.4E-1	1.6E0	8.3E-1	8.0E-1
Annotation Cluster 49		Enrichment Score: 4.66	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Biological rhythms	RT		40	1.7E-6	2.2E0	1.2E-5	9.1E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of circadian rhythm	RT		21	6.3E-5	2.5E0	2.1E-3	2.0E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	rhythmic process	RT		22	9.6E-5	2.4E0	3.1E-3	3.0E-3
Annotation Cluster 50		Enrichment Score: 4.65	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	gene expression	RT		31	1.8E-12	3.8E0	2.6E-10	2.5E-10
<input type="checkbox"/>	GOTERM_CC_DIRECT	DNA-directed RNA polymerase II, core complex	RT		14	1.4E-7	4.9E0	3.7E-6	3.3E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	7-methylguanosine mRNA capping	RT		20	1.4E-7	3.6E0	1.0E-5	9.7E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of viral transcription	RT		18	4.6E-7	3.7E0	2.9E-5	2.8E-5
<input type="checkbox"/>	KEGG_PATHWAY	Pyrimidine metabolism	RT		41	1.5E-6	2.1E0	4.9E-6	2.3E-6
<input type="checkbox"/>	UP_KEYWORDS	DNA-directed RNA polymerase	RT		19	2.4E-6	3.3E0	1.6E-5	1.2E-5
<input type="checkbox"/>	KEGG_PATHWAY	RNA polymerase	RT		19	3.6E-6	3.1E0	1.1E-5	5.1E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription initiation from RNA polymerase I promoter	RT		18	5.3E-6	3.2E0	2.5E-4	2.4E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription elongation from RNA polymerase I promoter	RT		17	5.6E-6	3.4E0	2.6E-4	2.5E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	termination of RNA polymerase I transcription	RT		17	9.7E-6	3.2E0	4.2E-4	4.0E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-directed RNA polymerase activity	RT		19	1.2E-5	3.0E0	2.2E-4	2.0E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase I activity	RT		10	1.4E-5	5.0E0	2.6E-4	2.3E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription elongation from RNA polymerase II promoter	RT		32	1.4E-5	2.2E0	5.8E-4	5.6E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase II activity	RT		9	2.0E-5	5.4E0	3.5E-4	3.2E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	DNA-directed RNA polymerase I complex	RT		10	2.3E-5	4.9E0	3.8E-4	3.3E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of type I interferon production	RT		21	1.2E-4	2.4E0	3.7E-3	3.6E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription initiation from RNA polymerase II promoter	RT		44	2.9E-4	1.7E0	8.0E-3	7.7E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	snRNA transcription from RNA polymerase II promoter	RT		24	8.1E-4	2.0E0	1.9E-2	1.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of gene expression, epigenetic	RT		22	8.6E-4	2.1E0	2.0E-2	2.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription from RNA polymerase III promoter	RT		14	1.8E-3	2.5E0	3.7E-2	3.5E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	gene silencing by RNA	RT		31	4.7E-3	1.7E0	8.3E-2	8.0E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	DNA-directed RNA polymerase III complex	RT		8	2.1E-2	2.7E0	1.3E-1	1.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase III activity	RT		8	2.1E-2	2.6E0	1.4E-1	1.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	Cytosolic DNA-sensing pathway	RT		19	5.4E-2	1.5E0	9.5E-2	5.4E-2
Annotation Cluster 51		Enrichment Score: 4.63	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Purine metabolism	RT		67	8.4E-9	2.0E0	3.4E-8	1.6E-8
<input type="checkbox"/>	KEGG_PATHWAY	Pyrimidine metabolism	RT		41	1.5E-6	2.1E0	4.9E-6	2.3E-6
<input type="checkbox"/>	KEGG_PATHWAY	Metabolic pathways	RT		98	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 52		Enrichment Score: 4.62	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA synthesis involved in DNA repair	RT		20	5.1E-7	3.4E0	3.0E-5	2.9E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	strand displacement	RT		15	1.9E-5	3.4E0	7.3E-4	7.0E-4
<input type="checkbox"/>	KEGG_PATHWAY	Homologous recombination	RT		14	1.5E-3	2.5E0	3.2E-3	1.5E-3
Annotation Cluster 53		Enrichment Score: 4.49	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Heat shock protein 70 family	RT		12	1.4E-6	5.0E0	3.5E-5	3.2E-5
<input type="checkbox"/>	INTERPRO	Heat shock protein 70, conserved site	RT		12	1.4E-6	5.0E0	3.5E-5	3.2E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	response to unfolded protein	RT		14	1.8E-2	2.0E0	2.2E-1	2.1E-1
Annotation Cluster 54		Enrichment Score: 4.46	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Gap junction	RT		60	8.4E-23	3.5E0	1.9E-21	8.8E-22
<input type="checkbox"/>	GOTERM_MF_DIRECT	adenylate cyclase activity	RT		19	1.7E-13	6.0E0	7.5E-12	6.7E-12
<input type="checkbox"/>	INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase	RT		18	4.0E-12	5.9E0	2.0E-10	1.9E-10













































Annotation Cluster 1		Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase, conserved site	RT	<div><div></div></div>	17	2.2E-11	5.9E0	1.0E-9	9.4E-10
<input type="checkbox"/>	KEGG_PATHWAY	GnRH signaling pathway	RT	<div><div></div></div>	45	2.7E-10	2.6E0	1.5E-9	7.0E-10
<input type="checkbox"/>	KEGG_PATHWAY	Vascular smooth muscle contraction	RT	<div><div></div></div>	53	3.2E-10	2.4E0	1.7E-9	8.2E-10
<input type="checkbox"/>	SMART	CYCc	RT	<div><div></div></div>	17	1.6E-8	3.8E0	4.1E-7	3.8E-7
<input type="checkbox"/>	UP_KEYWORDS	cAMP biosynthesis	RT	<div><div></div></div>	10	2.5E-7	6.9E0	1.9E-6	1.5E-6
<input type="checkbox"/>	KEGG_PATHWAY	Inflammatory mediator regulation of TRP channels	RT	<div><div></div></div>	41	5.9E-7	2.2E0	2.1E-6	9.7E-7
<input type="checkbox"/>	KEGG_PATHWAY	Regulation of lipolysis in adipocytes	RT	<div><div></div></div>	28	8.5E-7	2.6E0	2.9E-6	1.4E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	cyclic nucleotide biosynthetic process	RT	<div><div></div></div>	11	8.8E-7	5.4E0	4.9E-5	4.7E-5
<input type="checkbox"/>	KEGG_PATHWAY	Melanogenesis	RT	<div><div></div></div>	41	1.1E-6	2.1E0	3.8E-6	1.8E-6
<input type="checkbox"/>	KEGG_PATHWAY	Adrenergic signaling in cardiomyocytes	RT	<div><div></div></div>	51	1.8E-6	1.9E0	5.8E-6	2.7E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	activation of protein kinase A activity	RT	<div><div></div></div>	13	3.6E-6	4.3E0	1.8E-4	1.7E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Magnesium 2; via carbonyl oxygen	RT	<div><div></div></div>	10	4.5E-6	5.7E0	1.8E-4	1.7E-4
<input type="checkbox"/>	KEGG_PATHWAY	Cholinergic synapse	RT	<div><div></div></div>	42	8.8E-6	2.0E0	2.5E-5	1.2E-5
<input type="checkbox"/>	KEGG_PATHWAY	Gastric acid secretion	RT	<div><div></div></div>	31	1.3E-5	2.2E0	3.5E-5	1.6E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	phosphorus-oxygen lyase activity	RT	<div><div></div></div>	10	1.4E-5	5.0E0	2.6E-4	2.3E-4
<input type="checkbox"/>	KEGG_PATHWAY	Dopaminergic synapse	RT	<div><div></div></div>	46	1.5E-5	1.9E0	3.8E-5	1.8E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Magnesium 1	RT	<div><div></div></div>	18	2.9E-5	3.0E0	9.6E-4	9.2E-4
<input type="checkbox"/>	KEGG_PATHWAY	Circadian entrainment	RT	<div><div></div></div>	36	4.2E-5	2.0E0	1.1E-4	5.0E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Magnesium 2	RT	<div><div></div></div>	17	8.3E-5	2.9E0	2.6E-3	2.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	cAMP biosynthetic process	RT	<div><div></div></div>	11	1.1E-4	3.8E0	3.5E-3	3.4E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	renal water homeostasis	RT	<div><div></div></div>	15	3.3E-4	2.8E0	9.0E-3	8.6E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular response to glucagon stimulus	RT	<div><div></div></div>	17	4.4E-4	2.5E0	1.1E-2	1.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular response to forskolin	RT	<div><div></div></div>	7	4.7E-4	5.2E0	1.2E-2	1.2E-2
<input type="checkbox"/>	INTERPRO	Adenylate cyclase-like	RT	<div><div></div></div>	6	5.7E-4	6.2E0	7.8E-3	7.1E-3
<input type="checkbox"/>	KEGG_PATHWAY	Thyroid hormone synthesis	RT	<div><div></div></div>	25	2.1E-3	1.9E0	4.5E-3	2.1E-3
<input type="checkbox"/>	KEGG_PATHWAY	Endocrine and other factor-regulated calcium reabsorption	RT	<div><div></div></div>	18	2.9E-3	2.1E0	6.1E-3	2.9E-3
<input type="checkbox"/>	KEGG_PATHWAY	Aldosterone synthesis and secretion	RT	<div><div></div></div>	27	3.9E-3	1.7E0	8.2E-3	3.9E-3
<input type="checkbox"/>	KEGG_PATHWAY	Salivary secretion	RT	<div><div></div></div>	28	4.7E-3	1.7E0	9.7E-3	4.7E-3
<input type="checkbox"/>	KEGG_PATHWAY	Retrograde endocannabinoid signaling	RT	<div><div></div></div>	31	7.3E-3	1.6E0	1.5E-2	7.3E-3
<input type="checkbox"/>	KEGG_PATHWAY	Glutamatergic synapse	RT	<div><div></div></div>	34	7.7E-3	1.5E0	1.5E-2	7.7E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway	RT	<div><div></div></div>	16	8.4E-3	2.0E0	1.3E-1	1.3E-1
<input type="checkbox"/>	KEGG_PATHWAY	Ovarian steroidogenesis	RT	<div><div></div></div>	16	3.8E-2	1.7E0	6.8E-2	3.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	cAMP-mediated signaling	RT	<div><div></div></div>	12	4.5E-2	1.9E0	4.3E-1	4.1E-1
<input type="checkbox"/>	KEGG_PATHWAY	GABAergic synapse	RT	<div><div></div></div>	24	4.9E-2	1.5E0	8.7E-2	4.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	activation of adenylate cyclase activity	RT	<div><div></div></div>	12	6.3E-2	1.8E0	5.5E-1	5.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	Pancreatic secretion	RT	<div><div></div></div>	25	7.3E-2	1.4E0	1.3E-1	7.3E-2
<input type="checkbox"/>	KEGG_PATHWAY	Insulin secretion	RT	<div><div></div></div>	23	8.1E-2	1.4E0	1.4E-1	8.1E-2
<input type="checkbox"/>	KEGG_PATHWAY	Calcium signaling pathway	RT	<div><div></div></div>	43	9.1E-2	1.2E0	1.5E-1	9.1E-2
<input type="checkbox"/>	KEGG_PATHWAY	Dilated cardiomyopathy	RT	<div><div></div></div>	22	1.2E-1	1.4E0	1.9E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	adenylate cyclase-activating G-protein coupled receptor signaling pathway	RT	<div><div></div></div>	13	1.3E-1	1.5E0	8.2E-1	7.9E-1
<input type="checkbox"/>	KEGG_PATHWAY	Morphine addiction	RT	<div><div></div></div>	23	1.4E-1	1.3E0	2.4E-1	1.4E-1
<input type="checkbox"/>	KEGG_PATHWAY	Bile secretion	RT	<div><div></div></div>	17	2.4E-1	1.3E0	3.8E-1	2.4E-1
<input type="checkbox"/>	KEGG_PATHWAY	Serotonergic synapse	RT	<div><div></div></div>	25	3.0E-1	1.2E0	4.6E-1	3.0E-1
<input type="checkbox"/>	KEGG_PATHWAY	Taste transduction	RT	<div><div></div></div>	6	9.5E-1	6.9E-1	1.0E0	9.5E-1
Annotation Cluster 55					Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	ADP-ribosylation	RT	<div><div></div></div>	30	2.2E-9	3.3E0	2.0E-8	1.5E-8

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div>G</div></div>	<div><div></div><div>RT</div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	G-protein beta/gamma-subunit complex binding	RT	<div><div></div><div>RT</div></div>	16	1.5E-8	4.8E0	4.2E-7	3.8E-7
<input type="checkbox"/>	INTERPRO	Guanine nucleotide binding protein (G-protein), alpha subunit	RT	<div><div></div><div>RT</div></div>	14	1.7E-8	5.4E0	5.4E-7	5.0E-7
<input type="checkbox"/>	INTERPRO	G protein alpha subunit, helical insertion	RT	<div><div></div><div>RT</div></div>	14	1.7E-8	5.4E0	5.4E-7	5.0E-7
<input type="checkbox"/>	SMART	SM00275	RT	<div><div></div><div>RT</div></div>	14	3.0E-6	3.6E0	5.6E-5	5.0E-5
<input type="checkbox"/>	INTERPRO	G-protein alpha subunit, group I	RT	<div><div></div><div>RT</div></div>	8	1.9E-5	6.2E0	3.6E-4	3.3E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	guanyl nucleotide binding	RT	<div><div></div><div>RT</div></div>	8	9.8E-5	5.3E0	1.5E-3	1.3E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	heterotrimeric G-protein complex	RT	<div><div></div><div>RT</div></div>	12	9.6E-3	2.3E0	7.0E-2	6.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	adenylate cyclase-modulating G-protein coupled receptor signaling pathway	RT	<div><div></div><div>RT</div></div>	13	1.5E-2	2.1E0	2.0E-1	1.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	G-protein coupled serotonin receptor binding	RT	<div><div></div><div>RT</div></div>	4	1.6E-2	6.0E0	1.2E-1	1.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	G-protein coupled receptor binding	RT	<div><div></div><div>RT</div></div>	16	3.4E-2	1.7E0	2.1E-1	1.9E-1
<input type="checkbox"/>	UP_KEYWORDS	Transducer	RT	<div><div></div><div>RT</div></div>	29	1.0E0	2.2E-1	1.0E0	1.0E0
Annotation Cluster 56		Enrichment Score: 4.44	<div><div></div><div>G</div></div>	<div><div></div><div>RT</div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 23	RT	<div><div></div><div>RT</div></div>	15	1.9E-10	6.4E0	1.2E-8	1.1E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 24	RT	<div><div></div><div>RT</div></div>	13	6.7E-9	6.3E0	4.0E-7	3.8E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 26	RT	<div><div></div><div>RT</div></div>	8	4.0E-5	6.1E0	1.3E-3	1.2E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 25	RT	<div><div></div><div>RT</div></div>	7	2.1E-4	6.0E0	6.2E-3	5.9E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 27	RT	<div><div></div><div>RT</div></div>	7	2.1E-4	6.0E0	6.2E-3	5.9E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 28	RT	<div><div></div><div>RT</div></div>	6	3.6E-4	6.8E0	9.9E-3	9.5E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 30	RT	<div><div></div><div>RT</div></div>	6	1.1E-3	5.8E0	2.9E-2	2.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 29	RT	<div><div></div><div>RT</div></div>	6	1.1E-3	5.8E0	2.9E-2	2.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 21; degenerate	RT	<div><div></div><div>RT</div></div>	3	1.1E-1	5.1E0	1.0E0	9.6E-1
Annotation Cluster 57		Enrichment Score: 4.34	<div><div></div><div>G</div></div>	<div><div></div><div>RT</div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	TPR repeat	RT	<div><div></div><div>RT</div></div>	53	3.7E-8	2.2E0	2.9E-7	2.3E-7
<input type="checkbox"/>	INTERPRO	Tetratricopeptide repeat-containing domain	RT	<div><div></div><div>RT</div></div>	48	3.7E-8	2.3E0	1.2E-6	1.1E-6
<input type="checkbox"/>	INTERPRO	Tetratricopeptide repeat	RT	<div><div></div><div>RT</div></div>	47	4.8E-7	2.1E0	1.3E-5	1.2E-5
<input type="checkbox"/>	INTERPRO	Tetratricopeptide-like helical	RT	<div><div></div><div>RT</div></div>	62	6.2E-6	1.8E0	1.3E-4	1.2E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 1	RT	<div><div></div><div>RT</div></div>	47	6.8E-6	2.0E0	2.6E-4	2.5E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 2	RT	<div><div></div><div>RT</div></div>	47	6.8E-6	2.0E0	2.6E-4	2.5E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 3	RT	<div><div></div><div>RT</div></div>	43	1.7E-5	2.0E0	6.2E-4	6.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 5	RT	<div><div></div><div>RT</div></div>	27	2.8E-5	2.4E0	9.3E-4	9.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 6	RT	<div><div></div><div>RT</div></div>	25	3.3E-5	2.4E0	1.1E-3	1.0E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 7	RT	<div><div></div><div>RT</div></div>	21	2.9E-4	2.3E0	8.2E-3	7.9E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 4	RT	<div><div></div><div>RT</div></div>	29	4.1E-4	2.0E0	1.1E-2	1.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 8	RT	<div><div></div><div>RT</div></div>	17	1.5E-3	2.3E0	3.9E-2	3.7E-2
<input type="checkbox"/>	SMART	TPR	RT	<div><div></div><div>RT</div></div>	47	4.3E-3	1.5E0	4.5E-2	





Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Winged helix-turn-helix DNA-binding domain	RT	<div><div></div><div></div></div>	65	9.8E-6	1.7E0	2.0E-4	1.8E-4
<input type="checkbox"/>	INTERPRO	Transcription factor, fork head, conserved site	RT	<div><div></div><div></div></div>	14	1.6E-3	2.6E0	2.0E-2	1.8E-2
<input type="checkbox"/>	SMART	FH	RT	<div><div></div><div></div></div>	22	3.8E-3	1.8E0	4.2E-2	3.8E-2
Annotation Cluster 60		Enrichment Score: 4.13	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	adenylate cyclase activity	RT	<div><div></div><div></div></div>	19	1.7E-13	6.0E0	7.5E-12	6.7E-12
<input type="checkbox"/>	INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase	RT	<div><div></div><div></div></div>	18	4.0E-12	5.9E0	2.0E-10	1.9E-10
<input type="checkbox"/>	INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase, conserved site	RT	<div><div></div><div></div></div>	17	2.2E-11	5.9E0	1.0E-9	9.4E-10
<input type="checkbox"/>	SMART	CYCc	RT	<div><div></div><div></div></div>	17	1.6E-8	3.8E0	4.1E-7	3.8E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Guanylate cyclase	RT	<div><div></div><div></div></div>	8	1.0E-5	6.8E0	3.7E-4	3.5E-4
<input type="checkbox"/>	UP_KEYWORDS	cGMP biosynthesis	RT	<div><div></div><div></div></div>	8	3.8E-5	6.1E0	2.2E-4	1.7E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	guanylate cyclase complex, soluble	RT	<div><div></div><div></div></div>	8	6.4E-5	5.6E0	8.7E-4	7.6E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	guanylate cyclase activity	RT	<div><div></div><div></div></div>	8	9.8E-5	5.3E0	1.5E-3	1.3E-3
<input type="checkbox"/>	INTERPRO	Haem NO binding associated	RT	<div><div></div><div></div></div>	6	1.7E-3	5.3E0	2.1E-2	1.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	cGMP biosynthetic process	RT	<div><div></div><div></div></div>	8	1.1E-2	3.0E0	1.5E-1	1.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	receptor guanylyl cyclase signaling pathway	RT	<div><div></div><div></div></div>	6	1.6E-2	3.6E0	2.1E-1	2.0E-1
<input type="checkbox"/>	UP_KEYWORDS	Lyase	RT	<div><div></div><div></div></div>	32	2.6E-2	1.5E0	1.0E-1	8.0E-2
<input type="checkbox"/>	INTERPRO	Heme-NO binding	RT	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.4E-1	5.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of cGMP biosynthetic process	RT	<div><div></div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	NO signalling/Golgi transport ligand-binding domain	RT	<div><div></div><div></div></div>	3	4.4E-1	2.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	BIOCARTA	Ion Channels and Their Functional Role in Vascular Endothelium	RT	<div><div></div><div></div></div>	7	6.3E-1	1.1E0	9.5E-1	6.8E-1
<input type="checkbox"/>	INTERPRO	Extracellular ligand-binding receptor	RT	<div><div></div><div></div></div>	5	8.5E-1	8.6E-1	1.0E0	9.1E-1
Annotation Cluster 61		Enrichment Score: 4.05	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	phosphatidylinositol-mediated signaling	RT	<div><div></div><div></div></div>	42	6.9E-8	2.3E0	5.1E-6	4.9E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	phosphatidylinositol-3-phosphate biosynthetic process	RT	<div><div></div><div></div></div>	20	2.1E-4	2.4E0	6.1E-3	5.9E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	phosphatidylinositol phosphorylation	RT	<div><div></div><div></div></div>	31	2.5E-4	2.0E0	7.0E-3	6.7E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	phosphatidylinositol-4,5-bisphosphate 3-kinase activity	RT	<div><div></div><div></div></div>	23	2.9E-4	2.2E0	3.9E-3	3.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of phosphatidylinositol 3-kinase signaling	RT	<div><div></div><div></div></div>	27	3.0E-4	2.0E0	8.0E-3	7.7E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	1-phosphatidylinositol-3-kinase activity	RT	<div><div></div><div></div></div>	18	3.2E-4	2.5E0	4.4E-3	3.9E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	Ras guanyl-nucleotide exchange factor activity	RT	<div><div></div><div></div></div>	35	4.5E-4	1.8E0	5.6E-3	5.0E-3
Annotation Cluster 62		Enrichment Score: 4.02	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Ubiquitin	RT	<div><div></div><div></div></div>	26	1.5E-6	2.7E0	3.8E-5	3.5E-5
<input type="checkbox"/>	INTERPRO	Ubiquitin subgroup	RT	<div><div></div><div></div></div>	9	2.7E-4	4.3E0	4.0E-3	3.6E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ubiquitin-like	RT	<div><div></div><div></div></div>	17	4.1E-4	2.6E0	1.1E-2	1.1E-2
<input type="checkbox"/>	SMART	UBQ	RT	<div><div></div><div></div></div>	22	4.8E-4	2.1E0	6.6E-3	6.0E-3
Annotation Cluster 63		Enrichment Score: 4	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Alcoholism	RT	<div><div></div><div></div></div>	70	5.5E-10	2.1E0	2.8E-9	1.3E-9
<input type="checkbox"/>	INTERPRO	Histone core	RT	<div><div></div><div></div></div>	31	4.6E-8	2.8E0	1.4E-6	1.3E-6
<input type="checkbox"/>	UP_KEYWORDS	Nucleosome core	RT	<div><div></div><div></div></div>	32	1.4E-6	2.5E0	1.0E-5	7.9E-6
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleosome	RT	<div><div></div><div></div></div>	34	3.1E-6	2.3E0	6.8E-5	6.0E-5
<input type="checkbox"/>	INTERPRO	Histone-fold	RT	<div><div></div><div></div></div>	35	1.2E-4	1.9E0	1.9E-3	1.7E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	nuclear nucleosome	RT	<div><div></div><div></div></div>	18	2.0E-4	2.6E0	2.4E-3	2.1E-3
<input type="checkbox"/>	INTERPRO	Histone H2B	RT	<div><div></div><div></div></div>	12	6.0E-4	3.1E0	8.2E-3	7.5E-3
<input type="checkbox"/>	KEGG_PATHWAY	Systemic lupus erythematosus	RT	<div><div></div><div></div></div>	42	1.0E-3	1.6E0	2.3E-3	1.1E-3
<input type="checkbox"/>	INTERPRO	Histone H2A	RT	<div><div></div><div></div></div>	12	1.4E-3	2.9E0	1.7E-2	1.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	chromatin silencing	RT	<div><div></div><div></div></div>	16	5.4E-3	2.1E0	9.2E-2	8.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleosome assembly	RT	<div><div></div><div></div></div>	31	1.3E-2	1.5E0	1.8E-1	1.7E-1
















































Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	SMART	H2B	RT	<div><div></div><div></div></div>	12	1.9E-2	2.0E0	1.6E-1	1.4E-1
<input type="checkbox"/>	SMART	H2A	RT	<div><div></div><div></div></div>	12	3.6E-2	1.9E0	2.6E-1	2.3E-1
Annotation Cluster 64		Enrichment Score: 3.98	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SOCS box	RT	<div><div></div><div></div></div>	20	2.9E-7	3.6E0	1.3E-5	1.3E-5
<input type="checkbox"/>	INTERPRO	SOCS protein, C-terminal	RT	<div><div></div><div></div></div>	20	2.1E-6	3.2E0	5.2E-5	4.8E-5
<input type="checkbox"/>	SMART	SM00969	RT	<div><div></div><div></div></div>	20	9.3E-4	2.1E0	1.2E-2	1.1E-2
<input type="checkbox"/>	SMART	SOCS	RT	<div><div></div><div></div></div>	8	2.0E-1	1.6E0	8.5E-1	7.7E-1
Annotation Cluster 65		Enrichment Score: 3.89	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of telomere maintenance via telomerase	RT	<div><div></div><div></div></div>	22	1.1E-9	4.1E0	1.1E-7	1.0E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of telomerase RNA localization to Cajal body	RT	<div><div></div><div></div></div>	12	2.2E-6	4.7E0	1.2E-4	1.1E-4
<input type="checkbox"/>	INTERPRO	Chaperonin Cpn60/TCP-1	RT	<div><div></div><div></div></div>	12	3.7E-6	4.6E0	8.3E-5	7.6E-5
<input type="checkbox"/>	INTERPRO	GroEL-like apical domain	RT	<div><div></div><div></div></div>	12	3.7E-6	4.6E0	8.3E-5	7.6E-5
<input type="checkbox"/>	INTERPRO	GroEL-like equatorial domain	RT	<div><div></div><div></div></div>	11	1.6E-5	4.5E0	3.1E-4	2.9E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of protein localization to Cajal body	RT	<div><div></div><div></div></div>	8	2.7E-5	5.9E0	9.7E-4	9.3E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	chaperonin-containing T-complex	RT	<div><div></div><div></div></div>	8	6.4E-5	5.6E0	8.7E-4	7.6E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	zona pellucida receptor complex	RT	<div><div></div><div></div></div>	8	6.4E-5	5.6E0	8.7E-4	7.6E-4
<input type="checkbox"/>	INTERPRO	Chaperonin TCP-1, conserved site	RT	<div><div></div><div></div></div>	8	7.5E-5	5.5E0	1.3E-3	1.2E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of establishment of protein localization to telomere	RT	<div><div></div><div></div></div>	8	1.0E-4	5.3E0	3.2E-3	3.1E-3
<input type="checkbox"/>	INTERPRO	Chaperone tailless complex polypeptide 1 (TCP-1)	RT	<div><div></div><div></div></div>	9	1.2E-4	4.6E0	1.9E-3	1.7E-3
<input type="checkbox"/>	INTERPRO	TCP-1-like chaperonin intermediate domain	RT	<div><div></div><div></div></div>	9	1.2E-4	4.6E0	1.9E-3	1.7E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	toxin transport	RT	<div><div></div><div></div></div>	11	7.0E-2	1.8E0	5.8E-1	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	scaRNA localization to Cajal body	RT	<div><div></div><div></div></div>	3	1.3E-1	4.4E0	8.2E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	binding of sperm to zona pellucida	RT	<div><div></div><div></div></div>	9	2.3E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein binding involved in protein folding	RT	<div><div></div><div></div></div>	4	4.3E-1	1.7E0	1.0E0	8.9E-1
Annotation Cluster 66		Enrichment Score: 3.85	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_CC_DIRECT	precatalytic spliceosome	RT	<div><div></div><div></div></div>	17	6.6E-8	4.3E0	1.9E-6	1.7E-6
<input type="checkbox"/>	GOTERM_CC_DIRECT	U2 snRNP	RT	<div><div></div><div></div></div>	15	8.3E-8	4.8E0	2.3E-6	2.0E-6
<input type="checkbox"/>	GOTERM_CC_DIRECT	U4/U6 x U5 tri-snRNP complex	RT	<div><div></div><div></div></div>	15	1.1E-6	4.1E0	2.6E-5	2.3E-5
<input type="checkbox"/>	GOTERM_CC_DIRECT	U12-type spliceosomal complex	RT	<div><div></div><div></div></div>	16	1.2E-6	3.9E0	2.7E-5	2.4E-5
<input type="checkbox"/>	INTERPRO	Ribonucleoprotein LSM domain	RT	<div><div></div><div></div></div>	14	2.7E-6	4.1E0	6.5E-5	6.0E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	spliceosomal complex assembly	RT	<div><div></div><div></div></div>	16	3.0E-6	3.6E0	1.5E-4	1.5E-4
<input type="checkbox"/>	INTERPRO	Like-Sm (LSM) domain	RT	<div><div></div><div></div></div>	14	2.1E-5	3.6E0	3.9E-4	3.5E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	U5 snRNP	RT	<div><div></div><div></div></div>	11	6.1E-5	4.1E0	8.7E-4	7.6E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	small nuclear ribonucleoprotein complex	RT	<div><div></div><div></div></div>	11	6.1E-5	4.1E0	8.7E-4	7.6E-4
<input type="checkbox"/>	BIOCARTA	Spliceosomal Assembly	RT	<div><div></div><div></div></div>	13	6.4E-5	2.8E0	1.4E-3	1.0E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	U1 snRNP binding	RT	<div><div></div><div></div></div>	7	1.3E-4	6.0E0	1.9E-3	1.7E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	U1 snRNP	RT	<div><div></div><div></div></div>	11	2.1E-4	3.7E0	2.5E-3	2.2E-3
<input type="checkbox"/>	SMART	Sm	RT	<div><div></div><div></div></div>	14	3.1E-4	2.7E0	4.4E-3	4.0E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	U4 snRNP	RT	<div><div></div><div></div></div>	8	4.3E-4	4.6E0	4.7E-3	4.1E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	methylosome	RT	<div><div></div><div></div></div>	8	9.0E-4	4.2E0	9.1E-3	8.0E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone mRNA metabolic process	RT	<div><div></div><div></div></div>	8	1.4E-3	3.9E0	3.0E-2	2.9E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	spliceosomal tri-snRNP complex	RT	<div><div></div><div></div></div>	5	2.7E-3	6.4E0	2.5E-2	2.2E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	pICln-Sm protein complex	RT	<div><div></div><div></div></div>	5	7.0E-3	5.3E0	5.3E-2	4.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	spliceosomal snRNP assembly	RT	<div><div></div><div></div></div>	11	1.3E-2	2.3E0	1.8E-1	1.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear import	RT	<div><div></div><div></div></div>	7	6.9E-2	2.3E0	5.8E-1	5.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	U7 snRNP	RT	<div><div></div><div></div></div>	4	8.3E-2	3.6E0	4.0E-1	3.5E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_CC_DIRECT	SMN-Sm protein complex	RT	<div><div></div><div></div></div>	6	1.2E-1	2.2E0	4.9E-1	4.3E-1
Annotation Cluster 67		Enrichment Score: 3.79	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of cellular amino acid metabolic process	RT	<div><div></div><div></div></div>	26	1.2E-7	3.0E0	8.3E-6	8.0E-6
<input type="checkbox"/>	GOTERM_CC_DIRECT	proteasome regulatory particle, base subcomplex	RT	<div><div></div><div></div></div>	11	4.4E-7	5.8E0	1.1E-5	9.9E-6
<input type="checkbox"/>	GOTERM_CC_DIRECT	proteasome accessory complex	RT	<div><div></div><div></div></div>	12	7.0E-6	4.5E0	1.3E-4	1.1E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	nuclear proteasome complex	RT	<div><div></div><div></div></div>	8	1.6E-5	6.4E0	2.7E-4	2.4E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	proteasome regulatory particle	RT	<div><div></div><div></div></div>	9	3.9E-5	5.2E0	6.2E-4	5.5E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	RT	<div><div></div><div></div></div>	24	1.4E-4	2.3E0	4.3E-3	4.1E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosolic proteasome complex	RT	<div><div></div><div></div></div>	8	1.8E-4	5.1E0	2.2E-3	2.0E-3
<input type="checkbox"/>	INTERPRO	26S proteasome subunit P45	RT	<div><div></div><div></div></div>	6	5.7E-4	6.2E0	7.8E-3	7.1E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	proteasome-activating ATPase activity	RT	<div><div></div><div></div></div>	6	6.8E-4	6.0E0	7.8E-3	7.0E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	TBP-class protein binding	RT	<div><div></div><div></div></div>	11	1.0E-3	3.1E0	1.1E-2	9.9E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of RNA polymerase II transcriptional preinitiation complex assembly	RT	<div><div></div><div></div></div>	7	1.2E-3	4.6E0	2.8E-2	2.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein catabolic process	RT	<div><div></div><div></div></div>	16	1.9E-3	2.3E0	4.0E-2	3.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of proteasomal protein catabolic process	RT	<div><div></div><div></div></div>	8	1.1E-2	3.0E0	1.5E-1	1.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	ER-associated ubiquitin-dependent protein catabolic process	RT	<div><div></div><div></div></div>	15	1.2E-1	1.5E0	8.2E-1	7.8E-1
Annotation Cluster 68		Enrichment Score: 3.72	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, receptor class V, conserved site	RT	<div><div></div><div></div></div>	14	5.8E-10	6.2E0	2.2E-8	2.0E-8
<input type="checkbox"/>	INTERPRO	Ephrin receptor ligand binding domain	RT	<div><div></div><div></div></div>	14	5.8E-10	6.2E0	2.2E-8	2.0E-8
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, ephrin receptor	RT	<div><div></div><div></div></div>	14	5.8E-10	6.2E0	2.2E-8	2.0E-8
<input type="checkbox"/>	PIR_SUPERFAMILY	tyrosine-protein kinase, ephrin receptor type	RT	<div><div></div><div></div></div>	14	2.5E-9	5.4E0	4.9E-7	4.8E-7
<input type="checkbox"/>	SMART	EPH_Ibd	RT	<div><div></div><div></div></div>	14	1.3E-7	4.1E0	2.6E-6	2.4E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	ephrin receptor activity	RT	<div><div></div><div></div></div>	11	1.6E-7	6.0E0	4.2E-6	3.7E-6
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase ephrin type A/B receptor-like	RT	<div><div></div><div></div></div>	15	5.9E-6	3.7E0	1.2E-4	1.1E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	ephrin receptor signaling pathway	RT	<div><div></div><div></div></div>	32	1.4E-5	2.2E0	5.8E-4	5.6E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SAM	RT	<div><div></div><div></div></div>	26	2.4E-4	2.1E0	7.0E-3	6.8E-3
<input type="checkbox"/>	INTERPRO	Sterile alpha motif domain	RT	<div><div></div><div></div></div>	30	2.7E-4	2.0E0	4.0E-3	3.6E-3
<input type="checkbox"/>	INTERPRO	Sterile alpha motif/pointed domain	RT	<div><div></div><div></div></div>	34	6.7E-4	1.8E0	9.0E-3	8.2E-3
<input type="checkbox"/>	SMART	SM01411	RT	<div><div></div><div></div></div>	15	7.6E-4	2.4E0	1.0E-2	9.1E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	transmembrane-ephrin receptor activity	RT	<div><div></div><div></div></div>	6	9.2E-3	4.0E0	7.5E-2	6.7E-2
<input type="checkbox"/>	INTERPRO	Galactose-binding domain-like	RT	<div><div></div><div></div></div>	23	9.2E-3	1.7E0	9.2E-2	8.4E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	GPI-linked ephrin receptor activity	RT	<div><div></div><div></div></div>	5	1.8E-2	4.3E0	1.2E-1	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:PDZ-binding	RT	<div><div></div><div></div></div>	19	2.8E-2	1.7E0	4.9E-1	4.8E-1
<input type="checkbox"/>	SMART	SAM	RT	<div><div></div><div></div></div>	28	8.1E-2	1.3E0	4.7E-1	4.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Cys-rich	RT	<div><div></div><div></div></div>	30	1.2E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Fibronectin type-III 2	RT	<div><div></div><div></div></div>	25	1.6E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Fibronectin type-III 1	RT	<div><div></div><div></div></div>	25	1.7E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Insulin-like growth factor binding protein, N-terminal	RT	<div><div></div><div></div></div>	27	2.3E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Fibronectin, type III	RT	<div><div></div><div></div></div>	38	2.7E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	FN3	RT	<div><div></div><div></div></div>	30	9.5E-1	8.1E-1	1.0E0	9.5E-1
Annotation Cluster 69		Enrichment Score: 3.68	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	BIOCARTA	Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation	RT	<div><div></div><div></div></div>	18	5.8E-5	2.4E0	1.4E-3	1.0E-3
<input type="checkbox"/>	BIOCARTA	Regulation of BAD phosphorylation	RT	<div><div></div><div></div></div>	19	1.4E-4	2.2E0	2.4E-3	1.7E-3
<input type="checkbox"/>	BIOCARTA	Transcription factor CREB and its extracellular signals	RT	<div><div></div><div></div></div>	18	1.1E-3	2.0E0	1.1E-2	7.7E-3
Annotation Cluster 70		Enrichment Score: 3.67	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_MF_DIRECT	phosphoprotein phosphatase activity	RT	<div><div></div><div></div></div>	26	3.7E-9	3.4E0	1.1E-7	9.7E-8

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase	RT		12	1.1E-7	5.7E0	3.2E-6	2.9E-6
<input type="checkbox"/>	SMART	PP2Ac	RT		12	9.2E-6	3.8E0	1.6E-4	1.4E-4
<input type="checkbox"/>	INTERPRO	Metallophosphoesterase domain	RT		12	2.8E-3	2.7E0	3.3E-2	3.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Manganese	RT		11	2.1E-2	2.2E0	3.9E-1	3.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Iron	RT		12	9.5E-2	1.7E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Proton donor	RT		21	9.8E-1	7.2E-1	1.0E0	9.8E-1
Annotation Cluster 71		Enrichment Score: 3.67	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Bromodomain	RT		20	4.3E-7	3.5E0	3.3E-6	2.5E-6
<input type="checkbox"/>	INTERPRO	Bromodomain, conserved site	RT		16	1.6E-6	3.8E0	4.0E-5	3.7E-5
<input type="checkbox"/>	INTERPRO	Bromodomain	RT		20	1.3E-5	2.9E0	2.6E-4	2.3E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Bromo	RT		12	1.8E-3	2.8E0	4.5E-2	4.4E-2
<input type="checkbox"/>	SMART	BROMO	RT		20	2.8E-3	1.9E0	3.1E-2	2.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Bromo 1	RT		7	4.1E-3	4.0E0	9.8E-2	9.4E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Bromo 2	RT		7	4.1E-3	4.0E0	9.8E-2	9.4E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	lysine-acetylated histone binding	RT		9	5.5E-3	3.0E0	4.9E-2	4.4E-2
Annotation Cluster 72		Enrichment Score: 3.41	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	extrinsic component of cytoplasmic side of plasma membrane	RT		33	1.2E-9	3.1E0	4.3E-8	3.8E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2	RT		31	2.9E-5	2.2E0	9.6E-4	9.2E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH3	RT		44	3.6E-4	1.7E0	1.0E-2	9.7E-3
<input type="checkbox"/>	UP_KEYWORDS	SH3 domain	RT		46	7.0E-3	1.5E0	3.3E-2	2.5E-2
<input type="checkbox"/>	INTERPRO	Src homology-3 domain	RT		46	4.5E-2	1.3E0	3.3E-1	3.0E-1
<input type="checkbox"/>	SMART	SH3	RT		45	8.8E-1	8.9E-1	1.0E0	9.1E-1
Annotation Cluster 73		Enrichment Score: 3.4	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	nucleotide binding	RT		97	2.3E-7	1.7E0	5.7E-6	5.1E-6
<input type="checkbox"/>	INTERPRO	RNA recognition motif domain	RT		64	5.1E-6	1.8E0	1.1E-4	1.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:RRM	RT		39	3.8E-5	2.0E0	1.2E-3	1.2E-3
<input type="checkbox"/>	INTERPRO	Nucleotide-binding, alpha-beta plait	RT		68	7.0E-5	1.6E0	1.2E-3	1.1E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:RRM 1	RT		30	7.3E-3	1.6E0	1.6E-1	1.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:RRM 2	RT		30	7.3E-3	1.6E0	1.6E-1	1.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:RRM 3	RT		15	5.6E-2	1.7E0	8.4E-1	8.1E-1
<input type="checkbox"/>	SMART	RRM	RT		63	6.8E-2	1.2E0	4.0E-1	3.6E-1
Annotation Cluster 74		Enrichment Score: 3.24	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PI3K/PI4K	RT		16	1.6E-10	6.1E0	1.0E-8	1.0E-8
<input type="checkbox"/>	INTERPRO	Phosphatidylinositol 3-/4-kinase, catalytic domain	RT		16	2.5E-9	5.2E0	9.0E-8	8.2E-8
<input type="checkbox"/>	INTERPRO	Phosphatidylinositol 3/4-kinase, conserved site	RT		14	1.7E-8	5.4E0	5.4E-7	5.0E-7
<input type="checkbox"/>	SMART	PI3Kc	RT		15	9.0E-7	3.6E0	1.7E-5	1.6E-5
<input type="checkbox"/>	INTERPRO	Phosphoinositide 3-kinase, accessory (PIK) domain	RT		9	1.5E-5	5.6E0	2.9E-4	2.7E-4
<input type="checkbox"/>	INTERPRO	Phosphatidylinositol 3-kinase C2 (PI3K C2) domain	RT		8	1.9E-5	6.2E0	3.6E-4	3.3E-4
<input type="checkbox"/>	SMART	PI3Ka	RT		9	9.4E-5	4.1E0	1.4E-3	1.3E-3
<input type="checkbox"/>	INTERPRO	Phosphatidylinositol 3-kinase Ras-binding (PI3K RBD) domain	RT		7	1.1E-4	6.2E0	1.7E-3	1.6E-3
<input type="checkbox"/>	INTERPRO	Phosphatidylinositol Kinase	RT		9	1.2E-4	4.6E0	1.9E-3	1.7E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	1-phosphatidylinositol-4-phosphate 3-kinase activity	RT		7	1.3E-4	6.0E0	1.9E-3	1.7E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	phosphatidylinositol-3-phosphate biosynthetic process	RT		20	2.1E-4	2.4E0	6.1E-3	5.9E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	1-phosphatidylinositol-3-kinase activity	RT		18	3.2E-4	2.5E0	4.4E-3	3.9E-3
<input type="checkbox"/>	SMART	PI3K C2	RT		8	3.4E-4	4.1E0	4.7E-3	4.3E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	phosphatidylinositol 3-kinase complex	RT		9	4.6E-4	4.1E0	4.9E-3	4.3E-3

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	phosphatidylinositol 3-kinase activity	RT	<div><div></div><div></div></div>	5	3.4E-3	6.0E0	3.2E-2	2.9E-2
<input type="checkbox"/>	SMART	PI3K_rbd	RT	<div><div></div><div></div></div>	6	4.3E-3	4.1E0	4.5E-2	4.1E-2
<input type="checkbox"/>	INTERPRO	Phosphatidylinositol 3-kinase adaptor-binding (PI3K ABD) domain	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	phosphatidylinositol biosynthetic process	RT	<div><div></div><div></div></div>	17	2.8E-2	1.7E0	3.1E-1	3.0E-1
<input type="checkbox"/>	SMART	PI3K_p85B	RT	<div><div></div><div></div></div>	3	1.5E-1	4.1E0	6.9E-1	6.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	Inositol phosphate metabolism	RT	<div><div></div><div></div></div>	14	6.3E-1	1.0E0	9.0E-1	6.3E-1
<input type="checkbox"/>	KEGG_PATHWAY	Phosphatidylinositol signaling system	RT	<div><div></div><div></div></div>	19	6.3E-1	1.0E0	9.0E-1	6.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PX	RT	<div><div></div><div></div></div>	4	9.8E-1	5.7E-1	1.0E0	9.8E-1
<input type="checkbox"/>	INTERPRO	Phox homologous domain	RT	<div><div></div><div></div></div>	5	9.8E-1	5.6E-1	1.0E0	9.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	phosphatidylinositol binding	RT	<div><div></div><div></div></div>	7	1.0E0	4.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	PX	RT	<div><div></div><div></div></div>	4	1.0E0	3.6E-1	1.0E0	1.0E0
Annotation Cluster 75		Enrichment Score: 3.19	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	receptor signaling protein tyrosine kinase activity	RT	<div><div></div><div></div></div>	10	8.8E-7	6.0E0	2.1E-5	1.8E-5
<input type="checkbox"/>	INTERPRO	EGF receptor, L domain	RT	<div><div></div><div></div></div>	7	1.1E-4	6.2E0	1.7E-3	1.6E-3
<input type="checkbox"/>	INTERPRO	Furin-like cysteine-rich domain	RT	<div><div></div><div></div></div>	7	1.1E-4	6.2E0	1.7E-3	1.6E-3
<input type="checkbox"/>	INTERPRO	Furin-like repeat	RT	<div><div></div><div></div></div>	10	8.8E-4	3.4E0	1.2E-2	1.1E-2
<input type="checkbox"/>	INTERPRO	Tyrosine protein kinase, EGF/ERB/Xmrk receptor	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	SMART	FU	RT	<div><div></div><div></div></div>	10	1.7E-2	2.3E0	1.5E-1	1.4E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	tyrosine-protein kinase, EGF receptor type	RT	<div><div></div><div></div></div>	4	2.1E-2	5.4E0	2.9E-1	2.9E-1
Annotation Cluster 76		Enrichment Score: 3.09	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	ligase activity	RT	<div><div></div><div></div></div>	88	2.8E-10	1.9E0	8.7E-9	7.7E-9
<input type="checkbox"/>	UP_KEYWORDS	Ligase	RT	<div><div></div><div></div></div>	91	1.7E-8	1.8E0	1.4E-7	1.1E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:RING-type	RT	<div><div></div><div></div></div>	48	1.1E-2	1.4E0	2.2E-1	2.1E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, RING-type	RT	<div><div></div><div></div></div>	60	4.3E-2	1.3E0	3.2E-1	2.9E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, RING/FYVE/PHD-type	RT	<div><div></div><div></div></div>	82	1.7E-1	1.1E0	8.4E-1	7.7E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, RING-type, conserved site	RT	<div><div></div><div></div></div>	27	6.4E-1	9.9E-1	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	RING	RT	<div><div></div><div></div></div>	46	9.9E-1	7.7E-1	1.0E0	9.9E-1
Annotation Cluster 77		Enrichment Score: 3.08	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Cell Cycle	RT	<div><div></div><div></div></div>	20	1.0E-5	2.4E0	5.6E-4	4.0E-4
<input type="checkbox"/>	BIOCARTA	cdc25 and chk1 Regulatory Pathway in response to DNA damage	RT	<div><div></div><div></div></div>	8	7.3E-3	2.7E0	3.7E-2	2.6E-2
<input type="checkbox"/>	BIOCARTA	RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage	RT	<div><div></div><div></div></div>	10	7.6E-3	2.3E0	3.7E-2	2.6E-2
Annotation Cluster 78		Enrichment Score: 3.04	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone deacetylase activity	RT	<div><div></div><div></div></div>	22	1.4E-7	3.4E0	3.6E-6	3.2E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone deacetylation	RT	<div><div></div><div></div></div>	22	5.1E-6	2.8E0	2.5E-4	2.4E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Histone deacetylase	RT	<div><div></div><div></div></div>	9	7.3E-6	6.1E0	2.7E-4	2.6E-4
<input type="checkbox"/>	INTERPRO	Histone deacetylase domain	RT	<div><div></div><div></div></div>	10	1.0E-5	5.2E0	2.0E-4	1.8E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	NAD-dependent histone deacetylase activity (H3-K14 specific)	RT	<div><div></div><div></div></div>	10	1.4E-5	5.0E0	2.6E-4	2.3E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein deacetylase activity	RT	<div><div></div><div></div></div>	9	2.0E-5	5.4E0	3.5E-4	3.2E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H3 deacetylation	RT	<div><div></div><div></div></div>	13	3.4E-5	3.7E0	1.2E-3	1.2E-3
<input type="checkbox"/>	INTERPRO	Histone deacetylase superfamily	RT	<div><div></div><div></div></div>	10	6.7E-5	4.4E0	1.2E-3	1.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein deacetylation	RT	<div><div></div><div></div></div>	8	2.9E-4	4.7E0	7.9E-3	7.6E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	histone deacetylase complex	RT	<div><div></div><div></div></div>	15	6.7E-4	2.6E0	7.1E-3	6.2E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H4 deacetylation	RT	<div><div></div><div></div></div>	6	9.4E-3	3.9E0	1.4E-1	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptidyl-lysine deacetylation	RT	<div><div></div><div></div></div>	5	1.8E-2	4.2E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of gene expression, epigenetic	RT	<div><div></div><div></div></div>	7	2.0E-2	3.0E0	2.4E-1	2.3E-1
<input type="checkbox"/>	INTERPRO	Histone deacetylase class II, eukaryotic	RT	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of myotube differentiation	RT	<div><div></div><div></div></div>	7	4.0E-2	2.6E0	3.9E-1	3.8E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	PIR_SUPERFAMILY	histone deacetylase class II, eukaryotic type	RT	<div><div></div><div></div></div>	4	4.6E-2	4.4E0	5.6E-1	5.5E-1
<input type="checkbox"/>	COG_ONTOLOGY	Chromatin structure and dynamics / Secondary metabolites biosynthesis, transport, and catabolism	RT	<div><div></div><div></div></div>	7	4.7E-2	2.2E0	4.8E-1	4.8E-1
<input type="checkbox"/>	INTERPRO	Histone deacetylase, glutamine rich N-terminal domain	RT	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.4E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	Histone deacetylase	RT	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.4E-1	5.8E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	histone deacetylase class I, eukaryotic type	RT	<div><div></div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	1.0E0
Annotation Cluster 79		Enrichment Score: 2.99	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	BIOCARTA	IL-2 Receptor Beta Chain in T cell Activation	RT	<div><div></div><div></div></div>	28	2.7E-6	2.2E0	3.9E-4	2.8E-4
<input type="checkbox"/>	BIOCARTA	Inhibition of Cellular Proliferation by Gleevec	RT	<div><div></div><div></div></div>	19	8.8E-6	2.5E0	5.6E-4	4.0E-4
<input type="checkbox"/>	BIOCARTA	EGF Signaling Pathway	RT	<div><div></div><div></div></div>	21	1.1E-5	2.4E0	5.6E-4	4.0E-4
<input type="checkbox"/>	BIOCARTA	PDGF Signaling Pathway	RT	<div><div></div><div></div></div>	21	2.8E-5	2.3E0	9.1E-4	6.5E-4
<input type="checkbox"/>	BIOCARTA	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling	RT	<div><div></div><div></div></div>	23	5.9E-5	2.1E0	1.4E-3	1.0E-3
<input type="checkbox"/>	BIOCARTA	Growth Hormone Signaling Pathway	RT	<div><div></div><div></div></div>	20	6.3E-5	2.3E0	1.4E-3	1.0E-3
<input type="checkbox"/>	BIOCARTA	IL 2 signaling pathway	RT	<div><div></div><div></div></div>	17	1.3E-4	2.4E0	2.4E-3	1.7E-3
<input type="checkbox"/>	BIOCARTA	TPO Signaling Pathway	RT	<div><div></div><div></div></div>	18	1.4E-4	2.3E0	2.4E-3	1.7E-3
<input type="checkbox"/>	BIOCARTA	IGF-1 Signaling Pathway	RT	<div><div></div><div></div></div>	16	3.0E-4	2.3E0	4.1E-3	2.9E-3
<input type="checkbox"/>	BIOCARTA	Role of ERBB2 in Signal Transduction and Oncology	RT	<div><div></div><div></div></div>	16	1.3E-3	2.1E0	1.2E-2	8.8E-3
<input type="checkbox"/>	BIOCARTA	IL 6 signaling pathway	RT	<div><div></div><div></div></div>	15	1.4E-3	2.2E0	1.2E-2	8.8E-3
<input type="checkbox"/>	BIOCARTA	Insulin Signaling Pathway	RT	<div><div></div><div></div></div>	15	1.4E-3	2.2E0	1.2E-2	8.8E-3
<input type="checkbox"/>	BIOCARTA	EPO Signaling Pathway	RT	<div><div></div><div></div></div>	14	1.5E-3	2.2E0	1.3E-2	8.9E-3
<input type="checkbox"/>	BIOCARTA	Links between Pyk2 and Map Kinases	RT	<div><div></div><div></div></div>	18	2.0E-3	2.0E0	1.6E-2	1.2E-2
<input type="checkbox"/>	BIOCARTA	Signaling of Hepatocyte Growth Factor Receptor	RT	<div><div></div><div></div></div>	21	3.7E-3	1.8E0	2.3E-2	1.6E-2
<input type="checkbox"/>	BIOCARTA	BCR Signaling Pathway	RT	<div><div></div><div></div></div>	20	4.3E-3	1.8E0	2.6E-2	1.8E-2
<input type="checkbox"/>	BIOCARTA	Fc Epsilon Receptor I Signaling in Mast Cells	RT	<div><div></div><div></div></div>	22	4.9E-3	1.7E0	2.9E-2	2.0E-2
<input type="checkbox"/>	BIOCARTA	T Cell Receptor Signaling Pathway	RT	<div><div></div><div></div></div>	24	5.3E-3	1.7E0	3.0E-2	2.1E-2
<input type="checkbox"/>	BIOCARTA	Integrin Signaling Pathway	RT	<div><div></div><div></div></div>	21	5.6E-3	1.7E0	3.1E-2	2.2E-2
<input type="checkbox"/>	BIOCARTA	IL 3 signaling pathway	RT	<div><div></div><div></div></div>	11	7.2E-3	2.2E0	3.7E-2	2.6E-2
<input type="checkbox"/>	BIOCARTA	Bioactive Peptide Induced Signaling Pathway	RT	<div><div></div><div></div></div>	21	8.3E-3	1.7E0	3.9E-2	2.7E-2
<input type="checkbox"/>	BIOCARTA	Nerve growth factor pathway (NGF)	RT	<div><div></div><div></div></div>	13	1.1E-2	2.0E0	4.9E-2	3.5E-2
<input type="checkbox"/>	BIOCARTA	fMLP induced chemokine gene expression in HMC-1 cells	RT	<div><div></div><div></div></div>	20	1.4E-2	1.6E0	5.9E-2	4.2E-2
<input type="checkbox"/>	BIOCARTA	Erk1/Erk2 Mapk Signaling pathway	RT	<div><div></div><div></div></div>	17	1.5E-2	1.7E0	6.3E-2	4.5E-2
<input type="checkbox"/>	BIOCARTA	Sprouty regulation of tyrosine kinase signals	RT	<div><div></div><div></div></div>	11	3.8E-2	1.9E0	1.2E-1	8.8E-2
<input type="checkbox"/>	BIOCARTA	Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia	RT	<div><div></div><div></div></div>	12	1.3E-1	1.5E0	3.1E-1	2.2E-1
Annotation Cluster 80		Enrichment Score: 2.95	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	GOTERM_MF_DIRECT	U1 snRNP binding	RT	<div><div></div><div></div></div>	7	1.3E-4	6.0E0	1.9E-3	1.7E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	commitment complex	RT	<div><div></div><div></div></div>	6	1.5E-3	5.4E0	1.5E-2	1.3E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	prespliceosome	RT	<div><div></div><div></div></div>	5	7.0E-3	5.3E0	5.3E-2	4.7E-2
Annotation Cluster 81		Enrichment Score: 2.9	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	INTERPRO	14-3-3 protein	RT	<div><div></div><div></div></div>	7	1.1E-4	6.2E0	1.7E-3	1.6E-3
<input type="checkbox"/>	INTERPRO	14-3-3 protein, conserved site	RT	<div><div></div><div></div></div>	7	1.1E-4	6.2E0	1.7E-3	1.6E-3
<input type="checkbox"/>	INTERPRO	14-3-3 domain	RT	<div><div></div><div></div></div>	7	1.1E-4	6.2E0	1.7E-3	1.6E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Interaction with phosphoserine on interacting protein	RT	<div><div></div><div></div></div>	7	2.1E-4	6.0E0	6.2E-3	5.9E-3
<input type="checkbox"/>	PIR_SUPERFAMILY	14-3-3 protein	RT	<div><div></div><div></div></div>	7	2.2E-4	5.4E0	1.4E-2	1.4E-2
<input type="checkbox"/>	SMART	14 3 3	RT	<div><div></div><div></div></div>	7	1.2E-3	4.1E0	1.5E-2	1.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	RT	<div><div></div><div></div></div>	13	2.3E-3	2.6E0	4.5E-2	4.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein targeting	RT	<div><div></div><div></div></div>	10	2.0E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	membrane organization	RT	<div><div></div><div></div></div>	8	2.9E-1	1.5E0	1.0E0	9.6E-1

Annotation Cluster 1			Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
Annotation Cluster 82			Enrichment Score: 2.79	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	MyD88-dependent toll-like receptor signaling pathway	RT		24	2.5E-11	4.3E0	3.1E-9	2.9E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 20	RT		18	2.7E-10	5.3E0	1.7E-8	1.6E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 21	RT		14	5.9E-8	5.3E0	3.0E-6	2.9E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of cytokine secretion	RT		10	4.4E-6	5.4E0	2.2E-4	2.1E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 22	RT		10	4.5E-6	5.7E0	1.8E-4	1.7E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	toll-like receptor signaling pathway	RT		16	5.6E-6	3.5E0	2.6E-4	2.5E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 23	RT		8	1.2E-4	5.5E0	3.5E-3	3.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 24	RT		6	1.1E-3	5.8E0	2.9E-2	2.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	I-kappaB phosphorylation	RT		8	1.4E-3	3.9E0	3.0E-2	2.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:TIR	RT		11	1.8E-3	3.0E0	4.5E-2	4.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of chemokine production	RT		9	3.8E-3	3.1E0	6.9E-2	6.6E-2
<input type="checkbox"/>	INTERPRO	Toll/interleukin-1 receptor homology (TIR) domain	RT		11	5.1E-3	2.6E0	5.6E-2	5.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 25	RT		5	5.4E-3	5.7E0	1.2E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interleukin-8 production	RT		11	7.2E-3	2.5E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Toll-like receptor	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of NF-kappaB import into nucleus	RT		9	1.7E-2	2.5E0	2.1E-1	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interferon-alpha biosynthetic process	RT		4	1.7E-2	5.9E0	2.1E-1	2.0E-1
<input type="checkbox"/>	SMART	TIR	RT		11	1.8E-2	2.1E0	1.6E-1	1.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interferon-beta biosynthetic process	RT		5	1.8E-2	4.2E0	2.2E-1	2.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	toll-like receptor, 1/2/4/6/10 types [Parent=PIRSF800008]	RT		4	2.1E-2	5.4E0	2.9E-1	2.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 26	RT		4	2.5E-2	5.5E0	4.4E-1	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of toll-like receptor signaling pathway	RT		4	3.7E-2	4.7E0	3.7E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interleukin-6 production	RT		13	6.6E-2	1.7E0	5.6E-1	5.3E-1
<input type="checkbox"/>	UP_KEYWORDS	Inflammatory response	RT		30	7.5E-2	1.4E0	2.6E-1	2.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 27	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interferon-gamma biosynthetic process	RT		5	1.3E-1	2.5E0	8.2E-1	7.9E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	endolysosome membrane	RT		4	2.9E-1	2.1E0	8.6E-1	7.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	lipopeptide binding	RT		3	4.0E-1	2.2E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	phagocytic vesicle membrane	RT		8	8.4E-1	8.6E-1	1.0E0	8.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	transmembrane signaling receptor activity	RT		17	1.0E0	4.7E-1	1.0E0	1.0E0
Annotation Cluster 83			Enrichment Score: 2.78	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Ala/Asp-rich (DA-box)	RT		8	1.0E-5	6.8E0	3.7E-4	3.5E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Flexible hinge	RT		7	6.1E-5	6.8E0	1.9E-3	1.8E-3
<input type="checkbox"/>	INTERPRO	RecF/RecN/SMC	RT		7	1.1E-4	6.2E0	1.7E-3	1.6E-3
<input type="checkbox"/>	INTERPRO	Structural maintenance of chromosomes protein	RT		5	2.9E-3	6.2E0	3.3E-2	3.1E-2
<input type="checkbox"/>	PIR_SUPERFAMILY	structural maintenance of chromosomes protein	RT		5	4.7E-3	5.4E0	2.3E-1	2.3E-1
<input type="checkbox"/>	INTERPRO	SMCs flexible hinge	RT		5	7.7E-3	5.2E0	7.7E-2	7.1E-2
<input type="checkbox"/>	SMART	SM00968	RT		5	3.5E-2	3.4E0	2.6E-1	2.3E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	meiotic cohesin complex	RT		3	2.4E-1	3.2E0	8.3E-1	7.3E-1
Annotation Cluster 84			Enrichment Score: 2.76	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	INTERPRO	SNF2-related	RT		22	4.5E-10	4.3E0	1.8E-8	1.7E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Chromo 2	RT		8	4.0E-5	6.1E0	1.3E-3	1.2E-3
<input type="checkbox"/>	INTERPRO	Chromo domain-like	RT		14	8.1E-4	2.7E0	1.1E-2	9.9E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Chromo 1	RT		8	1.1E-3	4.2E0	2.9E-2	2.8E-2
<input type="checkbox"/>	INTERPRO	Chromo domain/shadow	RT		14	1.1E-3	2.6E0	1.4E-2	1.3E-2

















































Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	BRK domain	RT	<div><div></div><div></div></div>	5	7.7E-3	5.2E0	7.7E-2	7.1E-2
<input type="checkbox"/>	INTERPRO	Chromo domain	RT	<div><div></div><div></div></div>	10	1.7E-2	2.4E0	1.4E-1	1.3E-1
<input type="checkbox"/>	SMART	BRK	RT	<div><div></div><div></div></div>	5	3.5E-2	3.4E0	2.6E-1	2.3E-1
<input type="checkbox"/>	SMART	CHROMO	RT	<div><div></div><div></div></div>	14	4.3E-2	1.7E0	3.0E-1	2.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	hydrolase activity, acting on acid anhydrides	RT	<div><div></div><div></div></div>	3	2.7E-1	3.0E0	9.9E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	Chromo domain, conserved site	RT	<div><div></div><div></div></div>	5	4.1E-1	1.5E0	1.0E0	9.1E-1
Annotation Cluster 85		Enrichment Score: 2.74	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	sister chromatid cohesion	RT	<div><div></div><div></div></div>	35	4.7E-5	2.0E0	1.7E-3	1.6E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	kinetochore	RT	<div><div></div><div></div></div>	28	6.8E-5	2.2E0	9.2E-4	8.0E-4
<input type="checkbox"/>	UP_KEYWORDS	Centromere	RT	<div><div></div><div></div></div>	35	1.0E-3	1.8E0	5.3E-3	4.1E-3
<input type="checkbox"/>	UP_KEYWORDS	Kinetochore	RT	<div><div></div><div></div></div>	22	4.6E-2	1.5E0	1.7E-1	1.3E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	condensed chromosome kinetochore	RT	<div><div></div><div></div></div>	19	1.3E-1	1.4E0	5.3E-1	4.7E-1
Annotation Cluster 86		Enrichment Score: 2.74	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:S-adenosyl-L-methionine binding	RT	<div><div></div><div></div></div>	15	2.3E-4	2.9E0	6.6E-3	6.3E-3
<input type="checkbox"/>	INTERPRO	Bacterial Fmu (Sun)/eukaryotic nucleolar NOL1/Nop2p	RT	<div><div></div><div></div></div>	7	9.4E-4	4.8E0	1.2E-2	1.1E-2
<input type="checkbox"/>	INTERPRO	RNA (C5-cytosine) methyltransferase	RT	<div><div></div><div></div></div>	6	4.0E-3	4.6E0	4.4E-2	4.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:S-adenosyl-L-methionine	RT	<div><div></div><div></div></div>	15	1.3E-2	2.0E0	2.5E-1	2.4E-1
Annotation Cluster 87		Enrichment Score: 2.74	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Post-SET	RT	<div><div></div><div></div></div>	12	1.4E-6	5.1E0	6.0E-5	5.8E-5
<input type="checkbox"/>	INTERPRO	Post-SET domain	RT	<div><div></div><div></div></div>	11	3.7E-5	4.3E0	6.6E-4	6.0E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K36 specific)	RT	<div><div></div><div></div></div>	5	8.9E-3	5.0E0	7.3E-2	6.5E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:AWS	RT	<div><div></div><div></div></div>	4	2.5E-2	5.5E0	4.4E-1	4.3E-1
<input type="checkbox"/>	INTERPRO	AWS	RT	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	SMART	AWS	RT	<div><div></div><div></div></div>	4	9.9E-2	3.3E0	5.3E-1	4.8E-1
Annotation Cluster 88		Enrichment Score: 2.7	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase 1	RT	<div><div></div><div></div></div>	11	6.7E-6	5.0E0	2.6E-4	2.5E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase 2	RT	<div><div></div><div></div></div>	11	6.7E-6	5.0E0	2.6E-4	2.5E-4
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, non-receptor Jak/Tyk2	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	tyrosine-protein kinase, Jak/Tyk2 type	RT	<div><div></div><div></div></div>	4	2.1E-2	5.4E0	2.9E-1	2.9E-1
<input type="checkbox"/>	INTERPRO	Ribosomal protein S6 kinase II	RT	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	4.0E-1	3.7E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	ribosomal protein S6 kinase II	RT	<div><div></div><div></div></div>	4	7.9E-2	3.6E0	6.9E-1	6.8E-1
Annotation Cluster 89		Enrichment Score: 2.63	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein peptidyl-prolyl isomerization	RT	<div><div></div><div></div></div>	20	2.5E-5	2.8E0	9.4E-4	9.0E-4
<input type="checkbox"/>	UP_KEYWORDS	Rotamase	RT	<div><div></div><div></div></div>	17	3.6E-5	3.1E0	2.1E-4	1.6E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	peptidyl-prolyl cis-trans isomerase activity	RT	<div><div></div><div></div></div>	20	7.2E-5	2.6E0	1.2E-3	1.0E-3
<input type="checkbox"/>	INTERPRO	Cyclophilin-like peptidyl-prolyl cis-trans isomerase domain	RT	<div><div></div><div></div></div>	11	2.6E-3	2.8E0	3.1E-2	2.8E-2
<input type="checkbox"/>	INTERPRO	Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site	RT	<div><div></div><div></div></div>	10	3.4E-3	3.0E0	3.8E-2	3.5E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PPIase cyclophilin-type	RT	<div><div></div><div></div></div>	10	5.0E-3	2.8E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Cyclophilin-type peptidyl-prolyl cis-trans isomerase	RT	<div><div></div><div></div></div>	10	6.9E-3	2.7E0	7.4E-2	6.8E-2
<input type="checkbox"/>	UP_KEYWORDS	Cyclosporin	RT	<div><div></div><div></div></div>	5	1.1E-2	4.9E0	4.6E-2	3.6E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	cyclosporin A binding	RT	<div><div></div><div></div></div>	5	1.8E-2	4.3E0	1.2E-1	1.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	peptidyl-prolyl cis-trans isomerase	RT	<div><div></div><div></div></div>	6	5.2E-2	2.7E0	5.9E-1	5.9E-1
<input type="checkbox"/>	INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain	RT	<div><div></div><div></div></div>	7	5.7E-2	2.4E0	4.0E-1	3.7E-1
Annotation Cluster 90		Enrichment Score: 2.61	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein peptidyl-prolyl isomerization	RT	<div><div></div><div></div></div>	20	2.5E-5	2.8E0	9.4E-4	9.0E-4
<input type="checkbox"/>	UP_KEYWORDS	Rotamase	RT	<div><div></div><div></div></div>	17	3.6E-5	3.1E0	2.1E-4	1.6E-4

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	peptidyl-prolyl cis-trans isomerase activity	RT	<div><div></div><div></div></div>	20	7.2E-5	2.6E0	1.2E-3	1.0E-3
<input type="checkbox"/>	UP_KEYWORDS	Isomerase	RT	<div><div></div><div></div></div>	34	2.3E-4	1.9E0	1.3E-3	1.0E-3
<input type="checkbox"/>	INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type	RT	<div><div></div><div></div></div>	8	3.2E-2	2.5E0	2.4E-1	2.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	chaperone-mediated protein folding	RT	<div><div></div><div></div></div>	12	3.7E-2	1.9E0	3.8E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	FK506 binding	RT	<div><div></div><div></div></div>	8	3.8E-2	2.4E0	2.3E-1	2.0E-1
<input type="checkbox"/>	INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain	RT	<div><div></div><div></div></div>	7	5.7E-2	2.4E0	4.0E-1	3.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PPIase FKBP-type	RT	<div><div></div><div></div></div>	5	8.6E-2	2.8E0	1.0E0	9.6E-1
Annotation Cluster 91		Enrichment Score: 2.56	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	U6 snRNP	RT	<div><div></div><div></div></div>	7	9.1E-5	6.4E0	1.2E-3	1.0E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	Lsm1-7-Pat1 complex	RT	<div><div></div><div></div></div>	4	1.4E-2	6.4E0	9.3E-2	8.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay	RT	<div><div></div><div></div></div>	11	1.7E-2	2.2E0	2.1E-1	2.0E-1
Annotation Cluster 92		Enrichment Score: 2.55	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Arg/Ser-rich (RS domain)	RT	<div><div></div><div></div></div>	11	6.4E-5	4.2E0	2.0E-3	1.9E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Gly-rich (hinge region)	RT	<div><div></div><div></div></div>	6	1.1E-3	5.8E0	2.9E-2	2.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of mRNA splicing, via spliceosome	RT	<div><div></div><div></div></div>	9	1.7E-2	2.5E0	2.1E-1	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	mRNA splice site selection	RT	<div><div></div><div></div></div>	7	5.3E-2	2.4E0	4.9E-1	4.7E-1
Annotation Cluster 93		Enrichment Score: 2.47	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	UTP biosynthetic process	RT	<div><div></div><div></div></div>	9	1.7E-4	4.4E0	5.0E-3	4.8E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	CTP biosynthetic process	RT	<div><div></div><div></div></div>	9	1.7E-4	4.4E0	5.0E-3	4.8E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Pros-phosphohistidine intermediate	RT	<div><div></div><div></div></div>	7	2.1E-4	6.0E0	6.2E-3	5.9E-3
<input type="checkbox"/>	INTERPRO	Nucleoside diphosphate kinase	RT	<div><div></div><div></div></div>	8	5.1E-4	4.5E0	7.3E-3	6.7E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	nucleoside diphosphate kinase activity	RT	<div><div></div><div></div></div>	11	6.3E-4	3.3E0	7.3E-3	6.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleoside diphosphate phosphorylation	RT	<div><div></div><div></div></div>	10	1.2E-3	3.3E0	2.8E-2	2.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleobase-containing small molecule interconversion	RT	<div><div></div><div></div></div>	12	1.4E-3	2.8E0	3.0E-2	2.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	GTP biosynthetic process	RT	<div><div></div><div></div></div>	8	2.6E-3	3.6E0	5.0E-2	4.8E-2
<input type="checkbox"/>	SMART	NDK	RT	<div><div></div><div></div></div>	8	6.8E-3	3.0E0	6.8E-2	6.1E-2
<input type="checkbox"/>	INTERPRO	Nucleoside diphosphate kinase, active site	RT	<div><div></div><div></div></div>	5	1.6E-2	4.4E0	1.3E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	pyrimidine nucleotide metabolic process	RT	<div><div></div><div></div></div>	5	5.0E-2	3.3E0	4.7E-1	4.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleoside triphosphate biosynthetic process	RT	<div><div></div><div></div></div>	6	7.2E-2	2.5E0	5.8E-1	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	purine nucleotide metabolic process	RT	<div><div></div><div></div></div>	5	7.3E-2	3.0E0	5.8E-1	5.5E-1
<input type="checkbox"/>	UP_KEYWORDS	Nucleotide metabolism	RT	<div><div></div><div></div></div>	8	1.0E-1	2.0E0	3.4E-1	2.6E-1
Annotation Cluster 94		Enrichment Score: 2.41	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein K6-linked ubiquitination	RT	<div><div></div><div></div></div>	7	4.7E-4	5.2E0	1.2E-2	1.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein K29-linked ubiquitination	RT	<div><div></div><div></div></div>	5	3.5E-3	5.9E0	6.6E-2	6.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein K27-linked ubiquitination	RT	<div><div></div><div></div></div>	4	3.7E-2	4.7E0	3.7E-1	3.6E-1
Annotation Cluster 95		Enrichment Score: 2.4	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	INTERPRO	Ribosomal protein S1, RNA-binding domain	RT	<div><div></div><div></div></div>	7	9.4E-4	4.8E0	1.2E-2	1.1E-2
<input type="checkbox"/>	INTERPRO	RNA-binding domain, S1	RT	<div><div></div><div></div></div>	7	9.4E-4	4.8E0	1.2E-2	1.1E-2
<input type="checkbox"/>	SMART	SM00316	RT	<div><div></div><div></div></div>	7	9.2E-3	3.2E0	8.7E-2	7.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:S1 motif	RT	<div><div></div><div></div></div>	5	3.1E-2	3.8E0	5.4E-1	5.2E-1
Annotation Cluster 96		Enrichment Score: 2.31	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	RT	<div><div></div><div></div></div>	9	5.0E-6	5.9E0	2.5E-4	2.4E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	RT	<div><div></div><div></div></div>	4	1.7E-2	5.9E0	2.1E-1	2.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Sufficient for nucleolar localization	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	PeBoW complex	RT	<div><div></div><div></div></div>	3	1.2E-1	4.8E0	4.9E-1	4.3E-1

















































Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 97		Enrichment Score: 2.31	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	UP_KEYWORDS	Exonuclease	RT	<div><div></div><div></div></div>	18	6.0E-4	2.4E0	3.2E-3	2.4E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	3'-5'-exoribonuclease activity	RT	<div><div></div><div></div></div>	11	6.3E-4	3.3E0	7.3E-3	6.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	RNA phosphodiester bond hydrolysis, exonucleolytic	RT	<div><div></div><div></div></div>	11	1.3E-2	2.3E0	1.8E-1	1.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	nuclear exosome (RNase complex)	RT	<div><div></div><div></div></div>	7	2.1E-2	3.0E0	1.3E-1	1.1E-1
<input type="checkbox"/>	UP_KEYWORDS	Nuclease	RT	<div><div></div><div></div></div>	29	2.9E-2	1.5E0	1.1E-1	8.8E-2
Annotation Cluster 98		Enrichment Score: 2.3	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of axonogenesis	RT	<div><div></div><div></div></div>	13	1.1E-4	3.3E0	3.5E-3	3.4E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	Roundabout binding	RT	<div><div></div><div></div></div>	7	1.2E-3	4.6E0	1.3E-2	1.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	Roundabout signaling pathway	RT	<div><div></div><div></div></div>	6	3.8E-2	3.0E0	3.8E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	axon extension involved in axon guidance	RT	<div><div></div><div></div></div>	5	1.3E-1	2.5E0	8.2E-1	7.9E-1
Annotation Cluster 99		Enrichment Score: 2.24	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	BIOCARTA	Cadmium induces DNA synthesis and proliferation in macrophages	RT	<div><div></div><div></div></div>	14	2.6E-4	2.5E0	4.0E-3	2.9E-3
<input type="checkbox"/>	BIOCARTA	Links between Pyk2 and Map Kinases	RT	<div><div></div><div></div></div>	18	2.0E-3	2.0E0	1.6E-2	1.2E-2
<input type="checkbox"/>	BIOCARTA	CXCR4 Signaling Pathway	RT	<div><div></div><div></div></div>	16	2.5E-3	2.0E0	1.8E-2	1.3E-2
<input type="checkbox"/>	BIOCARTA	CCR3 signaling in Eosinophils	RT	<div><div></div><div></div></div>	13	4.2E-2	1.7E0	1.3E-1	9.3E-2
<input type="checkbox"/>	BIOCARTA	Aspirin Blocks Signaling Pathway Involved in Platelet Activation	RT	<div><div></div><div></div></div>	11	1.1E-1	1.6E0	2.9E-1	2.0E-1
Annotation Cluster 100		Enrichment Score: 2.19	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Cullin, N-terminal	RT	<div><div></div><div></div></div>	8	2.1E-4	5.0E0	3.3E-3	3.0E-3
<input type="checkbox"/>	INTERPRO	Cullin homology	RT	<div><div></div><div></div></div>	7	9.4E-4	4.8E0	1.2E-2	1.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in NEDD8)	RT	<div><div></div><div></div></div>	6	1.1E-3	5.8E0	2.9E-2	2.8E-2
<input type="checkbox"/>	INTERPRO	Cullin protein, neddylation domain	RT	<div><div></div><div></div></div>	6	4.0E-3	4.6E0	4.4E-2	4.0E-2
<input type="checkbox"/>	SMART	CULLIN	RT	<div><div></div><div></div></div>	6	1.2E-2	3.5E0	1.1E-1	9.9E-2
<input type="checkbox"/>	INTERPRO	Cullin, conserved site	RT	<div><div></div><div></div></div>	5	1.6E-2	4.4E0	1.3E-1	1.2E-1
<input type="checkbox"/>	SMART	SM00884	RT	<div><div></div><div></div></div>	6	2.5E-2	3.0E0	2.0E-1	1.9E-1
<input type="checkbox"/>	INTERPRO	Cullin repeat-like-containing domain	RT	<div><div></div><div></div></div>	6	3.2E-2	3.1E0	2.4E-1	2.2E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	cullin-RING ubiquitin ligase complex	RT	<div><div></div><div></div></div>	4	1.6E-1	2.8E0	6.2E-1	5.4E-1
Annotation Cluster 101		Enrichment Score: 2.16	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	guanyl nucleotide binding	RT	<div><div></div><div></div></div>	8	9.8E-5	5.3E0	1.5E-3	1.3E-3
<input type="checkbox"/>	INTERPRO	G-protein alpha subunit, group Q	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	phospholipase C-activating dopamine receptor signaling pathway	RT	<div><div></div><div></div></div>	4	2.3E-1	2.4E0	1.0E0	9.6E-1
Annotation Cluster 102		Enrichment Score: 2.14	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Thioredoxin 1	RT	<div><div></div><div></div></div>	9	7.3E-6	6.1E0	2.7E-4	2.6E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Thioredoxin 2	RT	<div><div></div><div></div></div>	9	7.3E-6	6.1E0	2.7E-4	2.6E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	response to endoplasmic reticulum stress	RT	<div><div></div><div></div></div>	29	1.7E-5	2.3E0	6.8E-4	6.6E-4
<input type="checkbox"/>	INTERPRO	Thioredoxin domain	RT	<div><div></div><div></div></div>	18	9.8E-5	2.7E0	1.7E-3	1.5E-3
<input type="checkbox"/>	INTERPRO	Thioredoxin, conserved site	RT	<div><div></div><div></div></div>	10	5.1E-4	3.6E0	7.3E-3	6.7E-3
<input type="checkbox"/>	INTERPRO	Disulphide isomerase	RT	<div><div></div><div></div></div>	5	2.9E-3	6.2E0	3.3E-2	3.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell redox homeostasis	RT	<div><div></div><div></div></div>	24	3.3E-3	1.8E0	6.3E-2	6.0E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein disulfide isomerase activity	RT	<div><div></div><div></div></div>	10	6.4E-3	2.7E0	5.6E-2	5.0E-2
<input type="checkbox"/>	UP_KEYWORDS	Redox-active center	RT	<div><div></div><div></div></div>	15	8.4E-3	2.1E0	3.8E-2	2.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Contributes to redox potential value	RT	<div><div></div><div></div></div>	5	1.1E-2	4.9E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Lowers pKa of C-terminal Cys of first active site	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Lowers pKa of C-terminal Cys of second active site	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	INTERPRO	Protein disulphide isomerase	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Thioredoxin 3	RT	<div><div></div><div></div></div>	4	2.5E-2	5.5E0	4.4E-1	4.3E-1




Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Thioredoxin	RT	<div><div></div><div></div></div>	10	4.4E-2	2.1E0	7.3E-1	7.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Prevents secretion from ER	RT	<div><div></div><div></div></div>	13	1.8E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	disulfide oxidoreductase activity	RT	<div><div></div><div></div></div>	3	2.7E-1	3.0E0	9.9E-1	8.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	isomerase activity	RT	<div><div></div><div></div></div>	6	2.7E-1	1.7E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	cell	RT	<div><div></div><div></div></div>	18	4.0E-1	1.1E0	1.0E0	8.8E-1
<input type="checkbox"/>	INTERPRO	Thioredoxin-like fold	RT	<div><div></div><div></div></div>	23	4.4E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	endoplasmic reticulum lumen	RT	<div><div></div><div></div></div>	19	1.0E0	6.3E-1	1.0E0	1.0E0
Annotation Cluster 103		Enrichment Score: 1.97	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Ribosomal protein S5 domain 2-type fold, subgroup	RT	<div><div></div><div></div></div>	12	6.0E-4	3.1E0	8.2E-3	7.5E-3
<input type="checkbox"/>	INTERPRO	Translation elongation factor EFTu/EF1A, domain 2	RT	<div><div></div><div></div></div>	9	1.0E-3	3.7E0	1.3E-2	1.2E-2
<input type="checkbox"/>	INTERPRO	Translation elongation/initiation factor/Ribosomal, beta-barrel	RT	<div><div></div><div></div></div>	13	1.5E-3	2.7E0	1.9E-2	1.7E-2
<input type="checkbox"/>	INTERPRO	Elongation factor, GTP-binding domain	RT	<div><div></div><div></div></div>	10	2.2E-3	3.1E0	2.7E-2	2.4E-2
<input type="checkbox"/>	INTERPRO	Translation elongation factor EFG, V domain	RT	<div><div></div><div></div></div>	5	7.7E-3	5.2E0	7.7E-2	7.1E-2
<input type="checkbox"/>	INTERPRO	Elongation factor G, III-V domain	RT	<div><div></div><div></div></div>	5	7.7E-3	5.2E0	7.7E-2	7.1E-2
<input type="checkbox"/>	SMART	SM00838	RT	<div><div></div><div></div></div>	5	1.5E-2	4.1E0	1.3E-1	1.2E-1
<input type="checkbox"/>	INTERPRO	Translation elongation factor EFG/EF2, domain IV	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	UP_KEYWORDS	Elongation factor	RT	<div><div></div><div></div></div>	10	2.3E-2	2.3E0	9.3E-2	7.2E-2
<input type="checkbox"/>	SMART	SM00889	RT	<div><div></div><div></div></div>	4	4.9E-2	4.1E0	3.0E-1	2.7E-1
<input type="checkbox"/>	INTERPRO	Translation elongation factor EF1A/initiation factor IF2gamma, C-terminal	RT	<div><div></div><div></div></div>	4	2.6E-1	2.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Translation elongation factor EFTu/EF1A, C-terminal	RT	<div><div></div><div></div></div>	3	3.2E-1	2.7E0	1.0E0	9.1E-1
Annotation Cluster 104		Enrichment Score: 1.95	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 14	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 15	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 2	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 3	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 4	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 5	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 6	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 7	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 8	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 9	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 1	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 2	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 3	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 4	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 1	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 10	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 11	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 12	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 13	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
Annotation Cluster 105		Enrichment Score: 1.95	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	four-way junction DNA binding	RT	<div><div></div><div></div></div>	10	9.2E-5	4.3E0	1.5E-3	1.3E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitotic recombination	RT	<div><div></div><div></div></div>	8	2.6E-3	3.6E0	5.0E-2	4.8E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	recombinase activity	RT	<div><div></div><div></div></div>	6	4.7E-3	4.5E0	4.3E-2	3.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	reciprocal meiotic recombination	RT	<div><div></div><div></div></div>	12	7.4E-3	2.4E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	DNA recombination and repair protein, RecA-like	RT	<div><div></div><div></div></div>	5	7.7E-3	5.2E0	7.7E-2	7.1E-2

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	PIR_SUPERFAMILY	DNA repair and recombination protein, Rad51 type	RT	<div><div></div><div></div></div>	5	1.2E-2	4.5E0	2.9E-1	2.9E-1
<input type="checkbox"/>	INTERPRO	DNA recombination and repair protein Rad51, C-terminal	RT	<div><div></div><div></div></div>	5	1.6E-2	4.4E0	1.3E-1	1.2E-1
<input type="checkbox"/>	INTERPRO	DNA recombination/repair protein RecA/RadB, ATP-binding domain	RT	<div><div></div><div></div></div>	5	1.6E-2	4.4E0	1.3E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	chromosome organization involved in meiotic cell cycle	RT	<div><div></div><div></div></div>	4	1.7E-2	5.9E0	2.1E-1	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	strand invasion	RT	<div><div></div><div></div></div>	5	1.8E-2	4.2E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	endodeoxyribonuclease activity	RT	<div><div></div><div></div></div>	9	2.2E-2	2.4E0	1.4E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA recombinase assembly	RT	<div><div></div><div></div></div>	4	3.7E-2	4.7E0	3.7E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	DNA repair Rad51/transcription factor NusA, alpha-helical	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	Rad51B-Rad51C-Rad51D-XRCC2 complex	RT	<div><div></div><div></div></div>	3	1.8E-1	3.8E0	6.7E-1	5.9E-1
Annotation Cluster 106		Enrichment Score: 1.92	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 18	RT	<div><div></div><div></div></div>	8	4.0E-5	6.1E0	1.3E-3	1.2E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 20	RT	<div><div></div><div></div></div>	7	2.1E-4	6.0E0	6.2E-3	5.9E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 19	RT	<div><div></div><div></div></div>	7	2.1E-4	6.0E0	6.2E-3	5.9E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 21	RT	<div><div></div><div></div></div>	6	1.1E-3	5.8E0	2.9E-2	2.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 22	RT	<div><div></div><div></div></div>	5	5.4E-3	5.7E0	1.2E-1	1.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 23	RT	<div><div></div><div></div></div>	4	2.5E-2	5.5E0	4.4E-1	4.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 30	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 31	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 24	RT	<div><div></div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 25	RT	<div><div></div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 26	RT	<div><div></div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 27	RT	<div><div></div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 28	RT	<div><div></div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 29	RT	<div><div></div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.6E-1
Annotation Cluster 107		Enrichment Score: 1.9	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	rRNA-binding	RT	<div><div></div><div></div></div>	14	6.6E-6	4.0E0	4.3E-5	3.3E-5
<input type="checkbox"/>	INTERPRO	KOW	RT	<div><div></div><div></div></div>	7	9.4E-4	4.8E0	1.2E-2	1.1E-2
<input type="checkbox"/>	INTERPRO	RNA-binding S4 domain	RT	<div><div></div><div></div></div>	5	7.7E-3	5.2E0	7.7E-2	7.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:S4 RNA-binding	RT	<div><div></div><div></div></div>	5	2.0E-2	4.3E0	3.7E-1	3.6E-1
<input type="checkbox"/>	SMART	S4	RT	<div><div></div><div></div></div>	4	4.9E-2	4.1E0	3.0E-1	2.7E-1
<input type="checkbox"/>	INTERPRO	Ribosomal protein S4e	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Ribosomal protein S4e, N-terminal	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Ribosomal protein S4e, central region	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Ribosomal protein S4e, N-terminal, conserved site	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	ribosomal protein S4a/S4e	RT	<div><div></div><div></div></div>	3	8.8E-2	5.4E0	6.9E-1	6.8E-1
Annotation Cluster 108		Enrichment Score: 1.89	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Initiation factor	RT	<div><div></div><div></div></div>	19	1.1E-3	2.2E0	5.5E-3	4.3E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of translational initiation	RT	<div><div></div><div></div></div>	15	1.4E-3	2.5E0	3.0E-2	2.9E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	translation initiation factor activity	RT	<div><div></div><div></div></div>	21	1.6E-3	2.1E0	1.7E-2	1.5E-2
<input type="checkbox"/>	UP_KEYWORDS	Protein biosynthesis	RT	<div><div></div><div></div></div>	37	1.8E-3	1.7E0	9.1E-3	7.1E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	eukaryotic translation initiation factor 3 complex	RT	<div><div></div><div></div></div>	9	2.4E-3	3.4E0	2.2E-2	2.0E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	eukaryotic 48S preinitiation complex	RT	<div><div></div><div></div></div>	8	4.7E-3	3.4E0	4.0E-2	3.5E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	eukaryotic translation initiation factor 3 complex, eIF3m	RT	<div><div></div><div></div></div>	5	1.4E-2	4.5E0	9.4E-2	8.2E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	translation initiation factor binding	RT	<div><div></div><div></div></div>	9	1.6E-2	2.6E0	1.2E-1	1.0E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	eukaryotic 43S preinitiation complex	RT	<div><div></div><div></div></div>	7	2.1E-2	3.0E0	1.3E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	formation of translation preinitiation complex	RT	<div><div></div><div></div></div>	9	2.9E-2	2.3E0	3.2E-1	3.1E-1

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	RNA transport	RT		42	7.7E-2	1.3E0	1.3E-1	7.7E-2
<input type="checkbox"/>	INTERPRO	Proteasome component (PCI) domain	RT		6	1.3E-1	2.2E0	6.4E-1	5.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PCI	RT		6	1.3E-1	2.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	PINT	RT		6	3.6E-1	1.5E0	1.0E0	9.1E-1
Annotation Cluster 109		Enrichment Score: 1.89	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:C2 tensin-type	RT		6	5.1E-3	4.5E0	1.2E-1	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Phosphatase tensin-type	RT		6	9.0E-3	4.1E0	2.0E-1	1.9E-1
<input type="checkbox"/>	INTERPRO	Tensin phosphatase, C2 domain	RT		6	1.3E-2	3.7E0	1.3E-1	1.1E-1
<input type="checkbox"/>	SMART	SM01326	RT		6	4.6E-2	2.7E0	3.0E-1	2.7E-1
Annotation Cluster 110		Enrichment Score: 1.83	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Mini-chromosome maintenance, DNA-dependent ATPase	RT		7	9.4E-4	4.8E0	1.2E-2	1.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MCM	RT		6	2.6E-3	5.1E0	6.2E-2	6.0E-2
<input type="checkbox"/>	SMART	MCM	RT		7	9.2E-3	3.2E0	8.7E-2	7.9E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	MCM complex	RT		5	4.0E-2	3.5E0	2.3E-1	2.0E-1
<input type="checkbox"/>	INTERPRO	Mini-chromosome maintenance, conserved site	RT		4	5.7E-2	4.1E0	4.0E-1	3.7E-1
<input type="checkbox"/>	BIOCARTA	CDK Regulation of DNA Replication	RT		9	2.1E-1	1.5E0	4.4E-1	3.1E-1
Annotation Cluster 111		Enrichment Score: 1.8	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Post-SET	RT		12	1.4E-6	5.1E0	6.0E-5	5.8E-5
<input type="checkbox"/>	INTERPRO	Post-SET domain	RT		11	3.7E-5	4.3E0	6.6E-4	6.0E-4
<input type="checkbox"/>	SMART	PostSET	RT		9	5.0E-3	2.8E0	5.1E-2	4.6E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K4 specific)	RT		9	5.5E-3	3.0E0	4.9E-2	4.4E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	histone methyltransferase complex	RT		10	5.8E-3	2.8E0	4.8E-2	4.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H3-K4 methylation	RT		9	1.2E-2	2.7E0	1.7E-1	1.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type 3	RT		5	4.7E-2	3.4E0	7.7E-1	7.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type 2	RT		9	6.3E-2	2.0E0	9.0E-1	8.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type 1	RT		9	1.0E-1	1.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	FY-rich, N-terminal	RT		3	1.9E-1	3.7E0	8.9E-1	8.1E-1
<input type="checkbox"/>	INTERPRO	FY-rich, C-terminal	RT		3	1.9E-1	3.7E0	8.9E-1	8.1E-1
<input type="checkbox"/>	SMART	FYRC	RT		3	3.6E-1	2.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	FYRN	RT		3	3.6E-1	2.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	Set1C/COMPASS complex	RT		3	5.4E-1	1.7E0	1.0E0	8.8E-1
Annotation Cluster 112		Enrichment Score: 1.79	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	transcription factor activity, RNA polymerase II transcription factor recruiting	RT		7	4.6E-4	5.2E0	5.6E-3	5.0E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HTH myb-type 1	RT		5	2.0E-3	6.8E0	5.0E-2	4.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HTH myb-type 2	RT		5	2.0E-3	6.8E0	5.0E-2	4.8E-2
<input type="checkbox"/>	INTERPRO	SANT/Myb domain	RT		16	2.1E-3	2.3E0	2.5E-2	2.3E-2
<input type="checkbox"/>	INTERPRO	Myb-like domain	RT		6	4.0E-3	4.6E0	4.4E-2	4.0E-2
<input type="checkbox"/>	INTERPRO	Myb domain	RT		6	7.7E-3	4.1E0	7.7E-2	7.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HTH myb-type 3	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Myb-like 1	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Myb-like 2	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	INTERPRO	C-myb, C-terminal	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	SMART	SANT	RT		16	8.5E-2	1.5E0	4.9E-1	4.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:H-T-H motif	RT		7	1.7E-1	1.8E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Homeodomain-like	RT		19	1.0E0	3.5E-1	1.0E0	1.0E0
Annotation Cluster 113		Enrichment Score: 1.76	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Phototransduction	RT		13	2.4E-3	2.5E0	5.2E-3	2.5E-3

Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	photoreceptor disc membrane	RT	<div><div></div></div>	8	2.1E-2	2.7E0	1.3E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of rhodopsin mediated signaling pathway	RT	<div><div></div></div>	9	1.0E-1	1.8E0	7.1E-1	6.8E-1
Annotation Cluster 114		Enrichment Score: 1.76	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Death domain	RT	<div><div></div></div>	14	2.1E-3	2.5E0	2.6E-2	2.4E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Death	RT	<div><div></div></div>	13	3.0E-3	2.5E0	7.2E-2	7.0E-2
<input type="checkbox"/>	INTERPRO	Death-like domain	RT	<div><div></div></div>	23	4.2E-2	1.5E0	3.1E-1	2.9E-1
<input type="checkbox"/>	SMART	DEATH	RT	<div><div></div></div>	9	3.4E-1	1.4E0	1.0E0	9.1E-1
Annotation Cluster 115		Enrichment Score: 1.73	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	EGF receptor, L domain	RT	<div><div></div></div>	7	1.1E-4	6.2E0	1.7E-3	1.6E-3
<input type="checkbox"/>	INTERPRO	Furin-like cysteine-rich domain	RT	<div><div></div></div>	7	1.1E-4	6.2E0	1.7E-3	1.6E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	insulin receptor substrate binding	RT	<div><div></div></div>	8	6.5E-4	4.3E0	7.5E-3	6.7E-3
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, insulin-like receptor	RT	<div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	insulin receptor	RT	<div><div></div></div>	3	8.8E-2	5.4E0	6.9E-1	6.8E-1
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, receptor class II, conserved site	RT	<div><div></div></div>	3	5.5E-1	1.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	receptor complex	RT	<div><div></div></div>	20	6.3E-1	1.0E0	1.0E0	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Fibronectin type-III 3	RT	<div><div></div></div>	6	1.0E0	4.9E-1	1.0E0	1.0E0
Annotation Cluster 116		Enrichment Score: 1.69	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	mRNA cleavage	RT	<div><div></div></div>	8	1.4E-3	3.9E0	3.0E-2	2.9E-2
<input type="checkbox"/>	BIOCARTA	Polyadenylation of mRNA	RT	<div><div></div></div>	7	7.1E-2	2.1E0	2.0E-1	1.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	mRNA polyadenylation	RT	<div><div></div></div>	9	8.6E-2	1.9E0	6.4E-1	6.2E-1
Annotation Cluster 117		Enrichment Score: 1.67	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Cyclins and Cell Cycle Regulation	RT	<div><div></div></div>	18	3.0E-4	2.2E0	4.1E-3	2.9E-3
<input type="checkbox"/>	BBID	26.cyclin-CDK complexes	RT	<div><div></div></div>	11	1.6E-2	2.0E0	8.5E-1	8.5E-1
<input type="checkbox"/>	BBID	1.RBphosphoE2F	RT	<div><div></div></div>	9	9.2E-2	1.7E0	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	cyclin-dependent protein serine/threonine kinase inhibitor activity	RT	<div><div></div></div>	5	9.7E-2	2.7E0	4.7E-1	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of phosphorylation	RT	<div><div></div></div>	7	1.1E-1	2.1E0	7.3E-1	7.0E-1
Annotation Cluster 118		Enrichment Score: 1.67	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	POLO box duplicated domain	RT	<div><div></div></div>	5	2.9E-3	6.2E0	3.3E-2	3.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:POLO box 1	RT	<div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:POLO box 2	RT	<div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
Annotation Cluster 119		Enrichment Score: 1.66	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Glutamine amidotransferase	RT	<div><div></div></div>	6	5.7E-4	6.2E0	7.8E-3	7.1E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Glutamine amidotransferase type-1	RT	<div><div></div></div>	5	2.0E-3	6.8E0	5.0E-2	4.8E-2
<input type="checkbox"/>	UP_KEYWORDS	Pyrimidine biosynthesis	RT	<div><div></div></div>	4	6.8E-2	3.9E0	2.4E-1	1.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:For GATase activity	RT	<div><div></div></div>	4	1.0E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	glutamine metabolic process	RT	<div><div></div></div>	7	1.1E-1	2.1E0	7.3E-1	7.0E-1
<input type="checkbox"/>	UP_KEYWORDS	Glutamine amidotransferase	RT	<div><div></div></div>	4	1.3E-1	3.1E0	4.2E-1	3.3E-1
Annotation Cluster 120		Enrichment Score: 1.65	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Protein kinase inhibitor	RT	<div><div></div></div>	7	1.0E-2	3.4E0	4.4E-2	3.4E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	mitogen-activated protein kinase kinase binding	RT	<div><div></div></div>	8	1.0E-2	3.0E0	8.2E-2	7.3E-2
<input type="checkbox"/>	INTERPRO	Pseudokinase tribbles family/serine-threonine-protein kinase 40	RT	<div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of MAP kinase activity	RT	<div><div></div></div>	5	5.0E-2	3.3E0	4.7E-1	4.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitin-protein transferase regulator activity	RT	<div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
Annotation Cluster 121		Enrichment Score: 1.63	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Pre-SET	RT	<div><div></div></div>	5	1.1E-2	4.9E0	2.2E-1	2.1E-1
<input type="checkbox"/>	INTERPRO	Pre-SET domain	RT	<div><div></div></div>	5	1.6E-2	4.4E0	1.3E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H3-K9 methylation	RT	<div><div></div></div>	4	1.7E-2	5.9E0	2.1E-1	2.0E-1




























Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K9 specific)	RT		4	3.6E-2	4.8E0	2.2E-1	1.9E-1
<input type="checkbox"/>	SMART	PreSET	RT		5	6.7E-2	2.9E0	4.0E-1	3.6E-1
Annotation Cluster 122		Enrichment Score: 1.63	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Shigellosis	RT		29	5.9E-6	2.4E0	1.7E-5	8.0E-6
<input type="checkbox"/>	BIOCARTA	The 4-1BB-dependent immune response	RT		14	6.7E-4	2.4E0	7.4E-3	5.3E-3
<input type="checkbox"/>	BIOCARTA	Toll-Like Receptor Pathway	RT		23	1.1E-3	1.8E0	1.1E-2	7.7E-3
<input type="checkbox"/>	BIOCARTA	Signal transduction through IL1R	RT		20	2.7E-3	1.8E0	1.8E-2	1.3E-2
<input type="checkbox"/>	KEGG_PATHWAY	Epithelial cell signaling in Helicobacter pylori infection	RT		23	5.7E-3	1.8E0	1.2E-2	5.7E-3
<input type="checkbox"/>	BIOCARTA	NFkB activation by Nontypeable Hemophilus influenzae	RT		15	8.4E-3	1.9E0	3.9E-2	2.7E-2
<input type="checkbox"/>	BIOCARTA	NF-kB Signaling Pathway	RT		14	1.6E-2	1.9E0	6.4E-2	4.5E-2
<input type="checkbox"/>	BIOCARTA	CD40L Signaling Pathway	RT		10	2.7E-2	2.0E0	1.0E-1	7.1E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	I-kappaB/NF-kappaB complex	RT		4	3.0E-2	5.1E0	1.8E-1	1.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	RIG-I-like receptor signaling pathway	RT		21	3.8E-2	1.6E0	6.8E-2	3.8E-2
<input type="checkbox"/>	BIOCARTA	Activation of PKC through G protein coupled receptor	RT		6	4.2E-2	2.6E0	1.3E-1	9.3E-2
<input type="checkbox"/>	BBID	77.IkBa Kinase JNK MEKK1	RT		6	6.5E-2	2.3E0	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	Acetylation and Deacetylation of RelA in The Nucleus	RT		9	1.2E-1	1.7E0	2.9E-1	2.1E-1
<input type="checkbox"/>	BIOCARTA	Double Stranded RNA Induced Gene Expression	RT		6	2.0E-1	1.8E0	4.3E-1	3.1E-1
<input type="checkbox"/>	BIOCARTA	TNF/Stress Related Signaling	RT		11	2.8E-1	1.3E0	5.5E-1	3.9E-1
<input type="checkbox"/>	BIOCARTA	Erythropoietin mediated neuroprotection through NF-kB	RT		7	2.9E-1	1.5E0	5.7E-1	4.0E-1
<input type="checkbox"/>	BIOCARTA	TNFR2 Signaling Pathway	RT		8	3.7E-1	1.4E0	6.8E-1	4.8E-1
<input type="checkbox"/>	BBID	90.IB_and-cat-Arm_processing_of_Ci	RT		4	3.8E-1	1.8E0	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	TACI and BCMA stimulation of B cell immune responses.	RT		6	5.8E-1	1.2E0	9.0E-1	6.4E-1
Annotation Cluster 123		Enrichment Score: 1.6	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK)	RT		20	2.8E-4	2.1E0	4.0E-3	2.9E-3
<input type="checkbox"/>	BIOCARTA	Signal Dependent Regulation of Myogenesis by Corepressor MITR	RT		9	8.3E-4	3.0E0	8.4E-3	6.0E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MADS-box	RT		5	5.4E-3	5.7E0	1.2E-1	1.2E-1
<input type="checkbox"/>	INTERPRO	Transcription factor, MADS-box	RT		5	7.7E-3	5.2E0	7.7E-2	7.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:Mef2-type	RT		4	2.5E-2	5.5E0	4.4E-1	4.3E-1
<input type="checkbox"/>	SMART	MADS	RT		5	3.5E-2	3.4E0	2.6E-1	2.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Beta domain	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	INTERPRO	Holliday junction regulator protein family C-terminal	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
<input type="checkbox"/>	BIOCARTA	Regulation of PGC-1a	RT		12	1.3E-1	1.5E0	3.1E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Lys-rich (basic)	RT		3	3.9E-1	2.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Cleavage	RT		9	8.2E-1	8.8E-1	1.0E0	9.6E-1
Annotation Cluster 124		Enrichment Score: 1.6	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:TEA	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	INTERPRO	TEA/ATTS	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Transcriptional enhancer factor	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	transcriptional enhancer factor	RT		4	2.1E-2	5.4E0	2.9E-1	2.9E-1
<input type="checkbox"/>	SMART	TEA	RT		4	4.9E-2	4.1E0	3.0E-1	2.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Transcriptional activation	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1
Annotation Cluster 125		Enrichment Score: 1.57	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Magnesium	RT		36	2.3E-5	2.1E0	7.9E-4	7.6E-4
<input type="checkbox"/>	INTERPRO	P-type ATPase, transmembrane domain	RT		11	3.7E-5	4.3E0	6.6E-4	6.0E-4
<input type="checkbox"/>	INTERPRO	Cation-transporting P-type ATPase, C-terminal	RT		11	7.6E-5	4.0E0	1.3E-3	1.2E-3
<input type="checkbox"/>	INTERPRO	Cation-transporting P-type ATPase, N-terminal	RT		11	1.5E-4	3.8E0	2.3E-3	2.1E-3
<input type="checkbox"/>	INTERPRO	P-type ATPase, A domain	RT		16	2.3E-4	2.8E0	3.5E-3	3.2E-3
















































Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	INTERPRO	Cation-transporting P-type ATPase	RT	<div><div></div><div></div></div>	16	2.3E-4	2.8E0	3.5E-3	3.2E-3
<input type="checkbox"/>	INTERPRO	P-type ATPase, phosphorylation site	RT	<div><div></div><div></div></div>	16	2.3E-4	2.8E0	3.5E-3	3.2E-3
<input type="checkbox"/>	INTERPRO	P-type ATPase, cytoplasmic domain N	RT	<div><div></div><div></div></div>	16	2.3E-4	2.8E0	3.5E-3	3.2E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:4-aspartylphosphate intermediate	RT	<div><div></div><div></div></div>	16	3.2E-4	2.7E0	9.1E-3	8.7E-3
<input type="checkbox"/>	INTERPRO	Sodium/potassium-transporting P-type ATPase, subfamily IIC	RT	<div><div></div><div></div></div>	6	5.7E-4	6.2E0	7.8E-3	7.1E-3
<input type="checkbox"/>	SMART	SM00831	RT	<div><div></div><div></div></div>	11	1.4E-3	2.8E0	1.7E-2	1.5E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular sodium ion homeostasis	RT	<div><div></div><div></div></div>	10	2.0E-3	3.1E0	4.1E-2	3.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	establishment or maintenance of transmembrane electrochemical gradient	RT	<div><div></div><div></div></div>	8	2.6E-3	3.6E0	5.0E-2	4.8E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	sodium:potassium-exchanging ATPase activity	RT	<div><div></div><div></div></div>	6	1.6E-2	3.6E0	1.2E-1	1.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	sodium ion export from cell	RT	<div><div></div><div></div></div>	6	1.6E-2	3.6E0	2.1E-1	2.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	steroid hormone binding	RT	<div><div></div><div></div></div>	4	3.6E-2	4.8E0	2.2E-1	1.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular potassium ion homeostasis	RT	<div><div></div><div></div></div>	6	3.8E-2	3.0E0	3.8E-1	3.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Interaction with phosphoinositide-3 kinase	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular response to steroid hormone stimulus	RT	<div><div></div><div></div></div>	5	7.3E-2	3.0E0	5.8E-1	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	response to glycoside	RT	<div><div></div><div></div></div>	3	7.6E-2	5.9E0	5.8E-1	5.5E-1
<input type="checkbox"/>	UP_KEYWORDS	Sodium/potassium transport	RT	<div><div></div><div></div></div>	4	9.8E-2	3.4E0	3.3E-1	2.5E-1
<input type="checkbox"/>	INTERPRO	HAD-like domain	RT	<div><div></div><div></div></div>	17	2.3E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	sodium:potassium-exchanging ATPase complex	RT	<div><div></div><div></div></div>	4	2.4E-1	2.3E0	8.3E-1	7.3E-1
<input type="checkbox"/>	KEGG_PATHWAY	Carbohydrate digestion and absorption	RT	<div><div></div><div></div></div>	11	2.8E-1	1.4E0	4.4E-1	2.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	ATP hydrolysis coupled proton transport	RT	<div><div></div><div></div></div>	8	2.9E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of cardiac conduction	RT	<div><div></div><div></div></div>	12	3.4E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell communication by electrical coupling, involved in cardiac conduction	RT	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	potassium ion import	RT	<div><div></div><div></div></div>	6	5.2E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Proximal tubule bicarbonate reclamation	RT	<div><div></div><div></div></div>	4	8.5E-1	9.0E-1	1.0E0	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	ion transmembrane transport	RT	<div><div></div><div></div></div>	30	9.0E-1	8.5E-1	1.0E0	9.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Cardiac muscle contraction	RT	<div><div></div><div></div></div>	11	9.3E-1	7.6E-1	1.0E0	9.3E-1
<input type="checkbox"/>	UP_KEYWORDS	Potassium	RT	<div><div></div><div></div></div>	12	9.9E-1	6.4E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_KEYWORDS	Potassium transport	RT	<div><div></div><div></div></div>	10	9.9E-1	5.9E-1	1.0E0	9.9E-1
<input type="checkbox"/>	KEGG_PATHWAY	Mineral absorption	RT	<div><div></div><div></div></div>	4	9.9E-1	4.7E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_KEYWORDS	Sodium transport	RT	<div><div></div><div></div></div>	4	1.0E0	2.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Protein digestion and absorption	RT	<div><div></div><div></div></div>	4	1.0E0	2.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Sodium	RT	<div><div></div><div></div></div>	4	1.0E0	2.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain:Lumenal	RT	<div><div></div><div></div></div>	22	1.0E0	3.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Ion transport	RT	<div><div></div><div></div></div>	31	1.0E0	3.3E-1	1.0E0	1.0E0
Annotation Cluster 126		Enrichment Score: 1.51	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	GOTERM_MF_DIRECT	single-stranded DNA-dependent ATPase activity	RT	<div><div></div><div></div></div>	7	2.5E-3	4.2E0	2.5E-2	2.2E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	DNA replication factor C complex	RT	<div><div></div><div></div></div>	5	7.0E-3	5.3E0	5.3E-2	4.7E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA clamp loader activity	RT	<div><div></div><div></div></div>	5	3.1E-2	3.7E0	1.9E-1	1.7E-1
<input type="checkbox"/>	INTERPRO	DNA polymerase III, clamp loader complex, gamma/delta/delta subunit, C-terminal	RT	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	4.0E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Replication factor C, C-terminal domain	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of DNA-directed DNA polymerase activity	RT	<div><div></div><div></div></div>	4	9.9E-2	3.4E0	6.9E-1	6.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	Ctf18 RFC-like complex	RT	<div><div></div><div></div></div>	4	1.2E-1	3.2E0	4.9E-1	4.3E-1
Annotation Cluster 127		Enrichment Score: 1.49	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Bromo	RT	<div><div></div><div></div></div>	12	1.8E-3	2.8E0	4.5E-2	4.4E-2
<input type="checkbox"/>	INTERPRO	DDT domain superfamily	RT	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DDT	RT	<div><div></div><div></div></div>	4	4.5E-2	4.5E0	7.4E-1	7.2E-1
<input type="checkbox"/>	SMART	DDT	RT	<div><div></div><div></div></div>	4	9.9E-2	3.3E0	5.3E-1	4.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type	RT	<div><div></div><div></div></div>	12	1.3E-1	1.6E0	1.0E0	9.6E-1







Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 128		Enrichment Score: 1.49	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	MLL5-L complex	RT	<div><div></div><div></div></div>	6	3.5E-3	4.8E0	3.1E-2	2.7E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	PTW/PP1_phosphatase complex	RT	<div><div></div><div></div></div>	5	1.4E-2	4.5E0	9.4E-2	8.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	entrainment of circadian clock by photoperiod	RT	<div><div></div><div></div></div>	4	6.8E-1	1.2E0	1.0E0	9.6E-1
Annotation Cluster 129		Enrichment Score: 1.49	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Dynamin, GTPase domain	RT	<div><div></div><div></div></div>	6	1.7E-3	5.3E0	2.1E-2	1.9E-2
<input type="checkbox"/>	INTERPRO	Dynamin, GTPase region, conserved site	RT	<div><div></div><div></div></div>	5	7.7E-3	5.2E0	7.7E-2	7.1E-2
<input type="checkbox"/>	INTERPRO	Dynamin central domain	RT	<div><div></div><div></div></div>	5	7.7E-3	5.2E0	7.7E-2	7.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:GED	RT	<div><div></div><div></div></div>	5	1.1E-2	4.9E0	2.2E-1	2.1E-1
<input type="checkbox"/>	SMART	DYNc	RT	<div><div></div><div></div></div>	6	1.2E-2	3.5E0	1.1E-1	9.9E-2
<input type="checkbox"/>	INTERPRO	Dynamin GTPase effector	RT	<div><div></div><div></div></div>	5	1.6E-2	4.4E0	1.3E-1	1.2E-1
<input type="checkbox"/>	SMART	GED	RT	<div><div></div><div></div></div>	5	3.5E-2	3.4E0	2.6E-1	2.3E-1
<input type="checkbox"/>	INTERPRO	GTPase effector domain, GED	RT	<div><div></div><div></div></div>	5	4.3E-2	3.4E0	3.2E-1	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	dynamin polymerization involved in mitochondrial fission	RT	<div><div></div><div></div></div>	4	9.9E-2	3.4E0	6.9E-1	6.6E-1
<input type="checkbox"/>	INTERPRO	Dynamin	RT	<div><div></div><div></div></div>	6	1.3E-1	2.2E0	6.4E-1	5.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitochondrial fission	RT	<div><div></div><div></div></div>	5	4.0E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	membrane fusion	RT	<div><div></div><div></div></div>	6	8.9E-1	8.1E-1	1.0E0	9.6E-1
Annotation Cluster 130		Enrichment Score: 1.47	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitin-ubiquitin ligase activity	RT	<div><div></div><div></div></div>	7	1.3E-2	3.2E0	9.9E-2	8.9E-2
<input type="checkbox"/>	INTERPRO	U box domain	RT	<div><div></div><div></div></div>	6	1.3E-2	3.7E0	1.3E-1	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:U-box	RT	<div><div></div><div></div></div>	4	7.0E-2	3.9E0	9.7E-1	9.3E-1
<input type="checkbox"/>	SMART	Ubox	RT	<div><div></div><div></div></div>	5	1.1E-1	2.5E0	5.6E-1	5.1E-1
Annotation Cluster 131		Enrichment Score: 1.47	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase II transcription factor binding	RT	<div><div></div><div></div></div>	20	1.0E-4	2.5E0	1.5E-3	1.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:GATA-type 1	RT	<div><div></div><div></div></div>	6	3.6E-4	6.8E0	9.9E-3	9.5E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:GATA-type 2	RT	<div><div></div><div></div></div>	6	3.6E-4	6.8E0	9.9E-3	9.5E-3
<input type="checkbox"/>	INTERPRO	Zinc finger, GATA-type	RT	<div><div></div><div></div></div>	7	2.4E-2	2.9E0	1.9E-1	1.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	anatomical structure formation involved in morphogenesis	RT	<div><div></div><div></div></div>	6	2.6E-2	3.2E0	2.9E-1	2.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	enhancer sequence-specific DNA binding	RT	<div><div></div><div></div></div>	8	3.8E-2	2.4E0	2.3E-1	2.0E-1
<input type="checkbox"/>	SMART	ZnF_GATA	RT	<div><div></div><div></div></div>	7	5.1E-2	2.4E0	3.1E-1	2.8E-1
<input type="checkbox"/>	INTERPRO	GATA-type transcription activator, N-terminal	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	intestinal epithelial cell differentiation	RT	<div><div></div><div></div></div>	4	9.9E-2	3.4E0	6.9E-1	6.6E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, NHR/GATA-type	RT	<div><div></div><div></div></div>	13	2.2E-1	1.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	tissue development	RT	<div><div></div><div></div></div>	4	4.8E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell development	RT	<div><div></div><div></div></div>	8	5.2E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell fate commitment	RT	<div><div></div><div></div></div>	9	5.2E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular response to BMP stimulus	RT	<div><div></div><div></div></div>	3	9.7E-1	5.9E-1	1.0E0	9.7E-1
Annotation Cluster 132		Enrichment Score: 1.47	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein kinase C activity	RT	<div><div></div><div></div></div>	10	2.0E-4	4.0E0	2.8E-3	2.5E-3
<input type="checkbox"/>	INTERPRO	Diacylglycerol/phorbol-ester binding	RT	<div><div></div><div></div></div>	11	3.7E-3	2.7E0	4.1E-2	3.8E-2
<input type="checkbox"/>	INTERPRO	Protein kinase C, delta/epsilon/eta/theta types	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	protein kinase C, delta/epsilon/eta/theta types	RT	<div><div></div><div></div></div>	4	2.1E-2	5.4E0	2.9E-1	2.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 1	RT	<div><div></div><div></div></div>	8	3.3E-2	2.5E0	5.7E-1	5.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 2	RT	<div><div></div><div></div></div>	8	3.3E-2	2.5E0	5.7E-1	5.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium-independent protein kinase C activity	RT	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	INTERPRO	Protein kinase C-like, phorbol ester/diacylglycerol binding	RT	<div><div></div><div></div></div>	15	1.7E-1	1.4E0	8.3E-1	7.6E-1














































Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	SMART	C1	RT	<div><div></div><div></div></div>	15	7.6E-1	9.4E-1	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type	RT	<div><div></div><div></div></div>	5	9.1E-1	7.6E-1	1.0E0	9.6E-1
Annotation Cluster 133		Enrichment Score: 1.46	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitotic cell cycle	RT	<div><div></div><div></div></div>	16	1.9E-3	2.3E0	4.0E-2	3.8E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	receptor signaling protein serine/threonine kinase activity	RT	<div><div></div><div></div></div>	17	1.1E-2	1.9E0	8.7E-2	7.7E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CRIB	RT	<div><div></div><div></div></div>	7	4.9E-2	2.5E0	8.0E-1	7.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:GTPase-binding	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Autoregulatory region	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	INTERPRO	PAK-box/P21-Rho-binding	RT	<div><div></div><div></div></div>	7	9.0E-2	2.2E0	5.0E-1	4.5E-1
<input type="checkbox"/>	SMART	PBD	RT	<div><div></div><div></div></div>	7	1.8E-1	1.8E0	7.6E-1	6.9E-1
Annotation Cluster 134		Enrichment Score: 1.46	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	cardiac muscle contraction	RT	<div><div></div><div></div></div>	16	5.4E-3	2.1E0	9.2E-2	8.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of the force of heart contraction	RT	<div><div></div><div></div></div>	9	8.5E-3	2.8E0	1.3E-1	1.3E-1
<input type="checkbox"/>	KEGG_PATHWAY	Cardiac muscle contraction	RT	<div><div></div><div></div></div>	11	9.3E-1	7.6E-1	1.0E0	9.3E-1
Annotation Cluster 135		Enrichment Score: 1.45	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	SCF ubiquitin ligase complex	RT	<div><div></div><div></div></div>	17	3.2E-3	2.2E0	2.8E-2	2.5E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:F-box	RT	<div><div></div><div></div></div>	18	3.3E-2	1.7E0	5.7E-1	5.5E-1
<input type="checkbox"/>	INTERPRO	F-box domain, cyclin-like	RT	<div><div></div><div></div></div>	19	4.4E-2	1.6E0	3.3E-1	3.0E-1
<input type="checkbox"/>	SMART	FBOX	RT	<div><div></div><div></div></div>	12	3.6E-1	1.3E0	1.0E0	9.1E-1
Annotation Cluster 136		Enrichment Score: 1.44	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Threonine protease	RT	<div><div></div><div></div></div>	9	4.9E-3	3.1E0	2.3E-2	1.8E-2
<input type="checkbox"/>	INTERPRO	Proteasome, subunit alpha/beta	RT	<div><div></div><div></div></div>	9	6.4E-3	2.9E0	7.0E-2	6.4E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	proteasome core complex	RT	<div><div></div><div></div></div>	9	1.1E-2	2.7E0	7.7E-2	6.8E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	threonine-type endopeptidase activity	RT	<div><div></div><div></div></div>	9	1.6E-2	2.6E0	1.2E-1	1.0E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	proteasome core complex, alpha-subunit complex	RT	<div><div></div><div></div></div>	5	2.5E-2	4.0E0	1.5E-1	1.3E-1
<input type="checkbox"/>	INTERPRO	Proteasome, alpha-subunit, N-terminal domain	RT	<div><div></div><div></div></div>	5	2.7E-2	3.9E0	2.2E-1	2.0E-1
<input type="checkbox"/>	INTERPRO	Proteasome A-type subunit	RT	<div><div></div><div></div></div>	5	2.7E-2	3.9E0	2.2E-1	2.0E-1
<input type="checkbox"/>	SMART	SM00948	RT	<div><div></div><div></div></div>	5	1.1E-1	2.5E0	5.6E-1	5.1E-1
<input type="checkbox"/>	INTERPRO	Proteasome, beta-type subunit, conserved site	RT	<div><div></div><div></div></div>	5	1.1E-1	2.6E0	6.3E-1	5.7E-1
<input type="checkbox"/>	INTERPRO	Proteasome B-type subunit	RT	<div><div></div><div></div></div>	4	2.6E-1	2.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	proteolysis involved in cellular protein catabolic process	RT	<div><div></div><div></div></div>	10	4.2E-1	1.2E0	1.0E0	9.6E-1
Annotation Cluster 137		Enrichment Score: 1.43	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA topological change	RT	<div><div></div><div></div></div>	6	9.4E-3	3.9E0	1.4E-1	1.3E-1
<input type="checkbox"/>	UP_KEYWORDS	Topoisomerase	RT	<div><div></div><div></div></div>	4	4.4E-2	4.6E0	1.6E-1	1.3E-1
<input type="checkbox"/>	INTERPRO	Toprim domain	RT	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.4E-1	5.8E-1
Annotation Cluster 138		Enrichment Score: 1.43	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	2'-5'-oligoadenylate synthase	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	2-5-oligoadenylate synthetase, conserved site	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	2'-5'-oligoadenylate synthetase 1, domain 2/C-terminal	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	2'-5'-oligoadenylate synthetase activity	RT	<div><div></div><div></div></div>	4	1.6E-2	6.0E0	1.2E-1	1.0E-1
<input type="checkbox"/>	INTERPRO	2-5-oligoadenylate synthetase, N-terminal	RT	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	Nucleotidyl transferase domain	RT	<div><div></div><div></div></div>	4	2.1E-1	2.5E0	9.9E-1	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	nucleotidyltransferase activity	RT	<div><div></div><div></div></div>	7	2.9E-1	1.5E0	1.0E0	8.9E-1
Annotation Cluster 139		Enrichment Score: 1.42	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	ROC GTPase	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Roc	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1

















































Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Mitochondrial Rho-like	RT	<div><div></div><div></div></div>	5	6.3E-2	3.1E0	4.1E-1	3.7E-1
Annotation Cluster 140		Enrichment Score: 1.42	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of translational initiation	RT	<div><div></div><div></div></div>	9	1.4E-3	3.6E0	3.0E-2	2.9E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	translation activator activity	RT	<div><div></div><div></div></div>	5	4.9E-2	3.3E0	2.8E-1	2.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	3'-UTR-mediated mRNA stabilization	RT	<div><div></div><div></div></div>	7	5.3E-2	2.4E0	4.9E-1	4.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	mRNA 3'-UTR binding	RT	<div><div></div><div></div></div>	9	5.9E-1	1.1E0	1.0E0	8.9E-1
Annotation Cluster 141		Enrichment Score: 1.42	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process	RT	<div><div></div><div></div></div>	8	2.6E-3	3.6E0	5.0E-2	4.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear mRNA surveillance	RT	<div><div></div><div></div></div>	5	5.0E-2	3.3E0	4.7E-1	4.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone mRNA catabolic process	RT	<div><div></div><div></div></div>	4	4.3E-1	1.7E0	1.0E0	9.6E-1
Annotation Cluster 142		Enrichment Score: 1.42	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:A.T hook 3	RT	<div><div></div><div></div></div>	6	9.0E-3	4.1E0	2.0E-1	1.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:A.T hook 1	RT	<div><div></div><div></div></div>	6	3.1E-2	3.1E0	5.4E-1	5.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:A.T hook 2	RT	<div><div></div><div></div></div>	6	3.1E-2	3.1E0	5.4E-1	5.2E-1
<input type="checkbox"/>	INTERPRO	AT hook, DNA-binding motif	RT	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	4.0E-1	3.7E-1
<input type="checkbox"/>	SMART	AT_hook	RT	<div><div></div><div></div></div>	4	1.6E-1	2.7E0	7.0E-1	6.4E-1
Annotation Cluster 143		Enrichment Score: 1.4	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	RNA-processing protein, HAT helix	RT	<div><div></div><div></div></div>	6	1.3E-2	3.7E0	1.3E-1	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 4	RT	<div><div></div><div></div></div>	6	2.2E-2	3.4E0	4.0E-1	3.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 9	RT	<div><div></div><div></div></div>	4	2.5E-2	5.5E0	4.4E-1	4.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 1	RT	<div><div></div><div></div></div>	6	3.1E-2	3.1E0	5.4E-1	5.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 2	RT	<div><div></div><div></div></div>	6	3.1E-2	3.1E0	5.4E-1	5.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 3	RT	<div><div></div><div></div></div>	6	3.1E-2	3.1E0	5.4E-1	5.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 8	RT	<div><div></div><div></div></div>	4	4.5E-2	4.5E0	7.4E-1	7.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 5	RT	<div><div></div><div></div></div>	5	6.5E-2	3.1E0	9.2E-1	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 7	RT	<div><div></div><div></div></div>	4	7.0E-2	3.9E0	9.7E-1	9.3E-1
<input type="checkbox"/>	SMART	HAT	RT	<div><div></div><div></div></div>	6	7.3E-2	2.4E0	4.3E-1	3.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 6	RT	<div><div></div><div></div></div>	4	1.3E-1	3.0E0	1.0E0	9.6E-1
Annotation Cluster 144		Enrichment Score: 1.39	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Leucine-rich repeat-containing protein 8, N-terminal	RT	<div><div></div><div></div></div>	5	2.9E-3	6.2E0	3.3E-2	3.1E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	volume-sensitive anion channel activity	RT	<div><div></div><div></div></div>	4	1.6E-2	6.0E0	1.2E-1	1.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of anion transport	RT	<div><div></div><div></div></div>	5	7.3E-2	3.0E0	5.8E-1	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	anion transmembrane transport	RT	<div><div></div><div></div></div>	5	7.7E-1	9.9E-1	1.0E0	9.6E-1
Annotation Cluster 145		Enrichment Score: 1.35	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone serine kinase activity	RT	<div><div></div><div></div></div>	5	3.4E-3	6.0E0	3.2E-2	2.9E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	chromosome passenger complex	RT	<div><div></div><div></div></div>	4	3.0E-2	5.1E0	1.8E-1	1.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	condensed nuclear chromosome, centromeric region	RT	<div><div></div><div></div></div>	4	2.0E-1	2.5E0	7.3E-1	6.4E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	spindle pole centrosome	RT	<div><div></div><div></div></div>	4	2.0E-1	2.5E0	7.3E-1	6.4E-1
Annotation Cluster 146		Enrichment Score: 1.35	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	ESC/E(Z) complex	RT	<div><div></div><div></div></div>	9	1.5E-3	3.6E0	1.4E-2	1.2E-2
<input type="checkbox"/>	BIOCARTA	The PRC2 Complex Sets Long-term Gene Silencing Through Modification of Histone Tails	RT	<div><div></div><div></div></div>	8	1.9E-1	1.6E0	4.1E-1	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of gene expression, epigenetic	RT	<div><div></div><div></div></div>	11	3.3E-1	1.3E0	1.0E0	9.6E-1
Annotation Cluster 147		Enrichment Score: 1.34	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	HRDC domain	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	HRDC-like	RT	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HRDC	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	SMART	HRDC	RT		3	1.5E-1	4.1E0	6.9E-1	6.2E-1
Annotation Cluster 148		Enrichment Score: 1.33	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	fibroblast growth factor-activated receptor activity	RT		5	3.4E-3	6.0E0	3.2E-2	2.9E-2
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, fibroblast growth factor receptor	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	fibroblast growth factor receptor	RT		4	2.1E-2	5.4E0	2.9E-1	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of phospholipase activity	RT		4	1.4E-1	3.0E0	8.2E-1	7.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	fibroblast growth factor binding	RT		7	1.8E-1	1.8E0	7.5E-1	6.7E-1
<input type="checkbox"/>	UP_KEYWORDS	Craniosynostosis	RT		5	4.0E-1	1.6E0	1.0E0	7.8E-1
Annotation Cluster 149		Enrichment Score: 1.3	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of guanylate cyclase activity	RT		7	4.9E-3	3.8E0	8.5E-2	8.1E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium sensitive guanylate cyclase activator activity	RT		4	3.6E-2	4.8E0	2.2E-1	1.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	phototransduction	RT		5	6.9E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 150		Enrichment Score: 1.3	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Ubiquitin subgroup	RT		9	2.7E-4	4.3E0	4.0E-3	3.6E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of necrotic cell death	RT		8	1.4E-3	3.9E0	3.0E-2	2.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of type I interferon production	RT		7	1.3E-2	3.2E0	1.8E-1	1.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	MyD88-independent toll-like receptor signaling pathway	RT		7	1.3E-2	3.2E0	1.8E-1	1.7E-1
<input type="checkbox"/>	INTERPRO	Ubiquitin conserved site	RT		6	2.1E-2	3.4E0	1.7E-1	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of epidermal growth factor receptor signaling pathway	RT		12	3.1E-2	2.0E0	3.4E-1	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of transcription from RNA polymerase II promoter in response to hypoxia	RT		10	3.6E-2	2.1E0	3.7E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of epidermal growth factor receptor signaling pathway	RT		9	3.8E-2	2.2E0	3.8E-1	3.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)	RT		7	3.8E-2	2.6E0	6.4E-1	6.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of type I interferon production	RT		10	5.4E-2	2.0E0	4.9E-1	4.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	viral life cycle	RT		10	6.5E-2	1.9E0	5.5E-1	5.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:40S ribosomal protein S27a	RT		4	7.0E-2	3.9E0	9.7E-1	9.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Essential for function	RT		4	7.0E-2	3.9E0	9.7E-1	9.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Lys-rich (highly basic)	RT		4	7.0E-2	3.9E0	9.7E-1	9.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Ubiquitin	RT		4	7.0E-2	3.9E0	9.7E-1	9.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:Activating enzyme	RT		4	1.0E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	virion assembly	RT		5	1.3E-1	2.5E0	8.2E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	glycogen biosynthetic process	RT		8	1.4E-1	1.8E0	8.2E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	interstrand cross-link repair	RT		12	1.9E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	intracellular transport of virus	RT		11	3.6E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	endocytic vesicle membrane	RT		8	9.1E-1	7.7E-1	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	endosomal transport	RT		5	1.0E0	4.5E-1	1.0E0	1.0E0
Annotation Cluster 151		Enrichment Score: 1.27	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	dendritic spine development	RT		7	1.3E-2	3.2E0	1.8E-1	1.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	central nervous system projection neuron axonogenesis	RT		5	3.2E-2	3.7E0	3.4E-1	3.3E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	axon guidance receptor activity	RT		4	9.7E-2	3.4E0	4.7E-1	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	retinal ganglion cell axon guidance	RT		6	2.1E-1	1.9E0	1.0E0	9.6E-1
Annotation Cluster 152		Enrichment Score: 1.26	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	OMIM_DISEASE	Schimmelpenning-Feuerstein-Mims syndrome, somatic mosaic	RT		3	4.5E-2	7.8E0	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Hypervariable region	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	BBID	65.Integrin affinity modulation	RT		5	6.2E-2	2.7E0	1.0E0	1.0E0
Annotation Cluster 153		Enrichment Score: 1.26	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:I-domain	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	INTERPRO	5'-3' exonuclease, C-terminal domain	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1

















































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Helix-hairpin-helix motif, class 2	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	XPG/Rad2 endonuclease	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	XPG-I domain	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:N-domain	RT		4	4.5E-2	4.5E0	7.4E-1	7.2E-1
<input type="checkbox"/>	INTERPRO	XPG N-terminal	RT		4	5.7E-2	4.1E0	4.0E-1	3.7E-1
<input type="checkbox"/>	SMART	HhH2	RT		4	9.9E-2	3.3E0	5.3E-1	4.8E-1
<input type="checkbox"/>	SMART	XPGI	RT		4	9.9E-2	3.3E0	5.3E-1	4.8E-1
<input type="checkbox"/>	SMART	XPGN	RT		4	9.9E-2	3.3E0	5.3E-1	4.8E-1
<input type="checkbox"/>	INTERPRO	XPG conserved site	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	nuclease activity	RT		7	1.8E-1	1.8E0	7.5E-1	6.7E-1
Annotation Cluster 154		Enrichment Score: 1.26	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptidyl-lysine monomethylation	RT		5	3.2E-2	3.7E0	3.4E-1	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptidyl-lysine dimethylation	RT		4	3.7E-2	4.7E0	3.7E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein-lysine N-methyltransferase activity	RT		6	1.4E-1	2.1E0	6.1E-1	5.5E-1
Annotation Cluster 155		Enrichment Score: 1.25	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	rRNA catabolic process	RT		8	6.8E-4	4.3E0	1.7E-2	1.6E-2
<input type="checkbox"/>	INTERPRO	Ribonuclease II/R, conserved site	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	nuclear exosome (RNase complex)	RT		7	2.1E-2	3.0E0	1.3E-1	1.1E-1
<input type="checkbox"/>	UP_KEYWORDS	Exosome	RT		6	3.0E-2	3.2E0	1.2E-1	9.2E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytoplasmic exosome (RNase complex)	RT		6	4.1E-2	2.9E0	2.3E-1	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear mRNA surveillance	RT		5	5.0E-2	3.3E0	4.7E-1	4.5E-1
<input type="checkbox"/>	INTERPRO	Exoribonuclease, phosphorolytic domain 1	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	exosome (RNase complex)	RT		6	9.3E-2	2.4E0	4.3E-1	3.8E-1
<input type="checkbox"/>	INTERPRO	Exoribonuclease, phosphorolytic domain 2	RT		4	1.2E-1	3.1E0	6.4E-1	5.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5'	RT		4	1.8E-1	2.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	exoribonuclease activity	RT		5	2.0E-1	2.1E0	7.8E-1	7.0E-1
<input type="checkbox"/>	INTERPRO	PNPase/RNase PH domain	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	U4 snRNA 3'-end processing	RT		3	4.0E-1	2.2E0	1.0E0	9.6E-1
Annotation Cluster 156		Enrichment Score: 1.25	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Heat shock factor (HSF)-type, DNA-binding	RT		5	2.7E-2	3.9E0	2.2E-1	2.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Hydrophobic repeat HR-A/B	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Hydrophobic repeat HR-C	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	SMART	HSF	RT		5	1.1E-1	2.5E0	5.6E-1	5.1E-1
Annotation Cluster 157		Enrichment Score: 1.25	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Guanylate kinase, conserved site	RT		9	1.7E-3	3.5E0	2.1E-2	1.9E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	ionotropic glutamate receptor complex	RT		6	3.5E-3	4.8E0	3.1E-2	2.7E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	ionotropic glutamate receptor binding	RT		10	4.4E-3	2.8E0	4.1E-2	3.7E-2
<input type="checkbox"/>	INTERPRO	Guanylate kinase	RT		10	4.9E-3	2.8E0	5.3E-2	4.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Guanylate kinase-like	RT		10	5.0E-3	2.8E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	GMP metabolic process	RT		8	7.1E-3	3.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	guanylate kinase activity	RT		7	8.2E-3	3.5E0	6.9E-2	6.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	establishment or maintenance of epithelial cell apical/basal polarity	RT		7	1.3E-2	3.2E0	1.8E-1	1.7E-1
<input type="checkbox"/>	INTERPRO	PDZ-associated domain of NMDA receptors	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Membrane-associated guanylate kinase (MAGUK), PEST domain, N-terminal	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Membrane-associated guanylate kinase (MAGUK) scaffold protein	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Guanylate kinase/L-type calcium channel	RT		10	1.7E-2	2.4E0	1.4E-1	1.3E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	GDP metabolic process	RT	<div><div></div><div></div></div>	6	2.6E-2	3.2E0	2.9E-1	2.8E-1
<input type="checkbox"/>	SMART	SM01277	RT	<div><div></div><div></div></div>	4	4.9E-2	4.1E0	3.0E-1	2.7E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	membrane-associated guanylate kinase (MAGUK) scaffold protein	RT	<div><div></div><div></div></div>	3	8.8E-2	5.4E0	6.9E-1	6.8E-1
<input type="checkbox"/>	SMART	GuKc	RT	<div><div></div><div></div></div>	10	1.4E-1	1.6E0	6.9E-1	6.2E-1
<input type="checkbox"/>	INTERPRO	Variant SH3	RT	<div><div></div><div></div></div>	14	1.7E-1	1.4E0	8.6E-1	7.9E-1
<input type="checkbox"/>	INTERPRO	L27	RT	<div><div></div><div></div></div>	5	1.8E-1	2.2E0	8.7E-1	8.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	receptor localization to synapse	RT	<div><div></div><div></div></div>	4	1.8E-1	2.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	BIOCARTA	Synaptic Proteins at the Synaptic Junction	RT	<div><div></div><div></div></div>	9	2.1E-1	1.5E0	4.4E-1	3.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	receptor clustering	RT	<div><div></div><div></div></div>	6	2.4E-1	1.8E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:L27 1	RT	<div><div></div><div></div></div>	3	2.7E-1	2.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:L27 2	RT	<div><div></div><div></div></div>	3	2.7E-1	2.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PDZ 3	RT	<div><div></div><div></div></div>	6	4.6E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	L27, C-terminal	RT	<div><div></div><div></div></div>	3	5.0E-1	1.9E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	L27	RT	<div><div></div><div></div></div>	4	6.0E-1	1.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PDZ 1	RT	<div><div></div><div></div></div>	6	7.6E-1	9.7E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PDZ 2	RT	<div><div></div><div></div></div>	6	7.6E-1	9.7E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	ligand-gated ion channel activity	RT	<div><div></div><div></div></div>	4	9.5E-1	6.6E-1	1.0E0	9.5E-1
Annotation Cluster 158		Enrichment Score: 1.25	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, receptor class III, conserved site	RT	<div><div></div><div></div></div>	8	1.9E-5	6.2E0	3.6E-4	3.3E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of phospholipase C activity	RT	<div><div></div><div></div></div>	8	1.0E-4	5.3E0	3.2E-3	3.1E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	vascular endothelial growth factor-activated receptor activity	RT	<div><div></div><div></div></div>	5	1.8E-2	4.3E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, CSF-1/PDGF receptor	RT	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	tyrosine-protein kinase, CSF-1/PDGF receptor type	RT	<div><div></div><div></div></div>	4	4.6E-2	4.4E0	5.6E-1	5.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	growth factor binding	RT	<div><div></div><div></div></div>	7	2.9E-1	1.5E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 7	RT	<div><div></div><div></div></div>	5	4.1E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 5	RT	<div><div></div><div></div></div>	10	4.2E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 3	RT	<div><div></div><div></div></div>	18	7.1E-1	9.6E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 4	RT	<div><div></div><div></div></div>	10	8.0E-1	9.0E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 6	RT	<div><div></div><div></div></div>	5	8.1E-1	9.2E-1	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Immunoglobulin	RT	<div><div></div><div></div></div>	10	9.3E-1	7.6E-1	1.0E0	9.3E-1
Annotation Cluster 159		Enrichment Score: 1.25	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	vagina development	RT	<div><div></div><div></div></div>	6	9.4E-3	3.9E0	1.4E-1	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	natural killer cell differentiation	RT	<div><div></div><div></div></div>	6	3.8E-2	3.0E0	3.8E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of lymphocyte activation	RT	<div><div></div><div></div></div>	3	7.6E-2	5.9E0	5.8E-1	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	apoptotic cell clearance	RT	<div><div></div><div></div></div>	6	9.4E-2	2.4E0	6.8E-1	6.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	secretion by cell	RT	<div><div></div><div></div></div>	4	2.3E-1	2.4E0	1.0E0	9.6E-1
Annotation Cluster 160		Enrichment Score: 1.23	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:PC 1	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:PC 2	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:PC 3	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:PC 4	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
Annotation Cluster 161		Enrichment Score: 1.22	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleotide-activated protein kinase complex	RT	<div><div></div><div></div></div>	6	1.9E-2	3.5E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	cAMP-dependent protein kinase regulator activity	RT	<div><div></div><div></div></div>	4	9.7E-2	3.4E0	4.7E-1	4.2E-1
<input type="checkbox"/>	BIOCARTA	ChREBP regulation by carbohydrates and cAMP	RT	<div><div></div><div></div></div>	11	1.1E-1	1.6E0	2.9E-1	2.0E-1
Annotation Cluster 162		Enrichment Score: 1.22	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	

















































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Apoptosis	RT		28	9.7E-6	2.3E0	2.7E-5	1.2E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c	RT		6	9.4E-3	3.9E0	1.4E-1	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	glial cell apoptotic process	RT		4	3.7E-2	4.7E0	3.7E-1	3.6E-1
<input type="checkbox"/>	BIOCARTA	HIV-I Nef	RT		28	3.8E-2	1.4E0	1.2E-1	8.8E-2
<input type="checkbox"/>	BIOCARTA	Role of Mitochondria in Apoptotic Signaling	RT		12	7.0E-2	1.7E0	2.0E-1	1.4E-1
<input type="checkbox"/>	BIOCARTA	D4-GDI Signaling Pathway	RT		8	9.5E-2	1.9E0	2.5E-1	1.8E-1
<input type="checkbox"/>	BIOCARTA	Induction of apoptosis through DR3 and DR4/5 Death Receptors	RT		15	1.6E-1	1.4E0	3.6E-1	2.6E-1
<input type="checkbox"/>	BBID	86.Apoptosis Nematode& Vert	RT		6	2.0E-1	1.8E0	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	Caspase Cascade in Apoptosis	RT		10	3.8E-1	1.3E0	7.0E-1	4.9E-1
<input type="checkbox"/>	BBID	127.Mito-stress	RT		4	3.8E-1	1.8E0	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	Stress Induction of HSP Regulation	RT		6	6.4E-1	1.1E0	9.6E-1	6.8E-1
<input type="checkbox"/>	BBID	46.P13K PTEN	RT		4	8.8E-1	9.0E-1	1.0E0	1.0E0
Annotation Cluster 163		Enrichment Score: 1.22	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Signaling of Hepatocyte Growth Factor Receptor	RT		21	3.7E-3	1.8E0	2.3E-2	1.6E-2
<input type="checkbox"/>	BIOCARTA	Role of MAL in Rho-Mediated Activation of SRF	RT		13	6.1E-3	2.1E0	3.3E-2	2.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	Bergmann glial cell differentiation	RT		6	9.4E-3	3.9E0	1.4E-1	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of Golgi inheritance	RT		4	1.7E-2	5.9E0	2.1E-1	2.0E-1
<input type="checkbox"/>	BIOCARTA	Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway	RT		9	3.1E-2	2.1E0	1.1E-1	7.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of early endosome to late endosome transport	RT		5	3.2E-2	3.7E0	3.4E-1	3.3E-1
<input type="checkbox"/>	BIOCARTA	Sprouty regulation of tyrosine kinase signals	RT		11	3.8E-2	1.9E0	1.2E-1	8.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	trachea formation	RT		4	6.4E-2	3.9E0	5.5E-1	5.2E-1
<input type="checkbox"/>	BIOCARTA	Roles of ?-arrestin-dependent Recruitment of Src Kinases in GPCR Signaling	RT		11	8.2E-2	1.7E0	2.2E-1	1.6E-1
<input type="checkbox"/>	BIOCARTA	Aspirin Blocks Signaling Pathway Involved in Platelet Activation	RT		11	1.1E-1	1.6E0	2.9E-1	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	thyroid gland development	RT		8	1.2E-1	1.9E0	7.7E-1	7.4E-1
<input type="checkbox"/>	BIOCARTA	Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia	RT		12	1.3E-1	1.5E0	3.1E-1	2.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of stress-activated MAPK cascade	RT		4	1.4E-1	3.0E0	8.2E-1	7.9E-1
<input type="checkbox"/>	BIOCARTA	Regulation of Splicing through Sam68	RT		5	1.6E-1	2.2E0	3.7E-1	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	ERK1 and ERK2 cascade	RT		6	3.8E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	BIOCARTA	Pelp1 Modulation of Estrogen Receptor Activity	RT		4	4.2E-1	1.7E0	7.3E-1	5.2E-1
<input type="checkbox"/>	BIOCARTA	Role of ?-arrestins in the activation and targeting of MAP kinases	RT		7	4.3E-1	1.3E0	7.3E-1	5.2E-1
Annotation Cluster 164		Enrichment Score: 1.21	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Xeroderma pigmentosum	RT		5	3.1E-2	3.8E0	1.2E-1	9.2E-2
<input type="checkbox"/>	UP_KEYWORDS	Cockayne syndrome	RT		4	4.4E-2	4.6E0	1.6E-1	1.3E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	holo TFIIH complex	RT		5	8.0E-2	2.9E0	3.9E-1	3.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	UV protection	RT		5	1.3E-1	2.5E0	8.2E-1	7.9E-1
Annotation Cluster 165		Enrichment Score: 1.2	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of chemokine production	RT		9	3.8E-3	3.1E0	6.9E-2	6.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interferon-beta production	RT		10	2.8E-2	2.2E0	3.2E-1	3.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interleukin-6 production	RT		13	6.6E-2	1.7E0	5.6E-1	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interleukin-12 production	RT		8	1.2E-1	1.9E0	7.7E-1	7.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of tumor necrosis factor production	RT		12	1.6E-1	1.5E0	9.1E-1	8.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular response to lipoteichoic acid	RT		3	4.6E-1	2.0E0	1.0E0	9.6E-1
Annotation Cluster 166		Enrichment Score: 1.2	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Rho-like	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BTB 1	RT		5	6.5E-2	3.1E0	9.2E-1	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BTB 2	RT		5	6.5E-2	3.1E0	9.2E-1	8.9E-1
Annotation Cluster 167		Enrichment Score: 1.2	G		Count	P_Value	Fold Change	Benjamini	FDR

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Regulation of cell cycle progression by Plk3	RT		7	1.8E-2	2.7E0	7.0E-2	5.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	replicative senescence	RT		6	3.8E-2	3.0E0	3.8E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA damage checkpoint	RT		10	5.4E-2	2.0E0	4.9E-1	4.7E-1
<input type="checkbox"/>	BIOCARTA	Role of BRCA1, BRCA2 and ATR in Cancer Susceptibility	RT		9	4.4E-1	1.2E0	7.3E-1	5.2E-1
Annotation Cluster 168		Enrichment Score: 1.18	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 4	RT		5	2.0E-3	6.8E0	5.0E-2	4.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 3	RT		6	2.6E-3	5.1E0	6.2E-2	6.0E-2
<input type="checkbox"/>	INTERPRO	WW domain	RT		16	1.8E-2	1.9E0	1.5E-1	1.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 1	RT		10	1.9E-2	2.3E0	3.7E-1	3.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 2	RT		10	1.9E-2	2.3E0	3.7E-1	3.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of potassium ion transmembrane transporter activity	RT		4	6.4E-2	3.9E0	5.5E-1	5.2E-1
<input type="checkbox"/>	SMART	WW	RT		16	2.1E-1	1.3E0	8.6E-1	7.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW	RT		6	2.1E-1	1.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of membrane potential	RT		8	9.8E-1	6.3E-1	1.0E0	9.8E-1
<input type="checkbox"/>	SMART	C2	RT		18	1.0E0	5.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of ion transmembrane transport	RT		3	1.0E0	1.6E-1	1.0E0	1.0E0
Annotation Cluster 169		Enrichment Score: 1.17	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H3-K27 methylation	RT		4	1.7E-2	5.9E0	2.1E-1	2.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K27 specific)	RT		3	7.5E-2	6.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA methylation	RT		8	1.2E-1	1.9E0	7.7E-1	7.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein-lysine N-methyltransferase activity	RT		6	1.4E-1	2.1E0	6.1E-1	5.5E-1
Annotation Cluster 170		Enrichment Score: 1.16	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	UBA/THIF-type NAD/FAD binding fold	RT		6	1.3E-2	3.7E0	1.3E-1	1.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitin activating enzyme activity	RT		4	3.6E-2	4.8E0	2.2E-1	1.9E-1
<input type="checkbox"/>	INTERPRO	Ubiquitin-activating enzyme e1, C-terminal	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Ubiquitin-activating enzyme, E1	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	small protein activating enzyme activity	RT		4	9.7E-2	3.4E0	4.7E-1	4.2E-1
<input type="checkbox"/>	INTERPRO	Ubiquitin-activating enzyme	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	Ubiquitin/SUMO-activating enzyme E1	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
<input type="checkbox"/>	SMART	SM00985	RT		3	1.5E-1	4.1E0	6.9E-1	6.2E-1
Annotation Cluster 171		Enrichment Score: 1.16	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Ribosomal protein L1, 2-layer alpha/beta-sandwich	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Ribosomal protein L1, 3-layer alpha/beta-sandwich	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Ribosomal protein L1, superfamily	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
Annotation Cluster 172		Enrichment Score: 1.16	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Pseudouridine synthase, RsuA/RluB/C/D/E/F	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Pseudouridine synthase, catalytic domain	RT		6	4.5E-2	2.9E0	3.3E-1	3.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	pseudouridine synthase activity	RT		6	5.2E-2	2.8E0	3.0E-1	2.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	tRNA pseudouridine synthesis	RT		4	6.4E-2	3.9E0	5.5E-1	5.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	deaminase activity	RT		4	1.4E-1	3.0E0	5.9E-1	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	pseudouridine synthesis	RT		4	3.8E-1	1.8E0	1.0E0	9.6E-1
Annotation Cluster 173		Enrichment Score: 1.15	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	RNA polymerase Rpb2, domain 3	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	DNA-directed RNA polymerase, subunit 2	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	DNA-directed RNA polymerase, subunit 2, domain 6	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	RNA polymerase, beta subunit, conserved site	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	RNA polymerase Rpb2, OB-fold	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
















































Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	RNA polymerase Rpb2, domain 7	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	RNA polymerase Rpb2, domain 2	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	RNA polymerase, beta subunit, protrusion	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	ribonucleoside binding	RT	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
Annotation Cluster 174		Enrichment Score: 1.14	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2HC-type	RT	<div><div></div><div></div></div>	6	2.6E-3	5.1E0	6.2E-2	6.0E-2
<input type="checkbox"/>	INTERPRO	MOZ/SAS-like protein	RT	<div><div></div><div></div></div>	5	2.9E-3	6.2E0	3.3E-2	3.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone acetylation	RT	<div><div></div><div></div></div>	11	4.9E-2	1.9E0	4.7E-1	4.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone acetyltransferase activity	RT	<div><div></div><div></div></div>	13	9.5E-2	1.6E0	4.7E-1	4.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	acetyltransferase activity	RT	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	Acyl-CoA N-acyltransferase	RT	<div><div></div><div></div></div>	7	7.7E-1	9.4E-1	1.0E0	9.1E-1
<input type="checkbox"/>	UP_KEYWORDS	Acyltransferase	RT	<div><div></div><div></div></div>	12	1.0E0	4.8E-1	1.0E0	1.0E0
Annotation Cluster 175		Enrichment Score: 1.13	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	extrinsic apoptotic signaling pathway in absence of ligand	RT	<div><div></div><div></div></div>	15	7.0E-4	2.6E0	1.7E-2	1.7E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	BH3 domain binding	RT	<div><div></div><div></div></div>	4	1.6E-2	6.0E0	1.2E-1	1.0E-1
<input type="checkbox"/>	INTERPRO	Apoptosis regulator, Bcl-2, BH1 motif, conserved site	RT	<div><div></div><div></div></div>	5	2.7E-2	3.9E0	2.2E-1	2.0E-1
<input type="checkbox"/>	INTERPRO	Apoptosis regulator, Bcl-2, BH2 motif, conserved site	RT	<div><div></div><div></div></div>	5	2.7E-2	3.9E0	2.2E-1	2.0E-1
<input type="checkbox"/>	INTERPRO	Apoptosis regulator, Bcl-2, BH3 motif, conserved site	RT	<div><div></div><div></div></div>	5	2.7E-2	3.9E0	2.2E-1	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of protein heterodimerization activity	RT	<div><div></div><div></div></div>	5	3.2E-2	3.7E0	3.4E-1	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of mitochondrial membrane potential	RT	<div><div></div><div></div></div>	10	3.6E-2	2.1E0	3.7E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of anoikis	RT	<div><div></div><div></div></div>	7	5.3E-2	2.4E0	4.9E-1	4.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:BH1	RT	<div><div></div><div></div></div>	5	6.5E-2	3.1E0	9.2E-1	8.9E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	Bcl-2 family protein complex	RT	<div><div></div><div></div></div>	3	6.6E-2	6.4E0	3.3E-1	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of mitochondrial membrane permeability	RT	<div><div></div><div></div></div>	5	7.3E-2	3.0E0	5.8E-1	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	release of cytochrome c from mitochondria	RT	<div><div></div><div></div></div>	8	7.9E-2	2.1E0	6.0E-1	5.7E-1
<input type="checkbox"/>	INTERPRO	Blc2 family	RT	<div><div></div><div></div></div>	5	8.7E-2	2.8E0	4.9E-1	4.5E-1
<input type="checkbox"/>	INTERPRO	Bcl2-like	RT	<div><div></div><div></div></div>	5	8.7E-2	2.8E0	4.9E-1	4.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:BH2	RT	<div><div></div><div></div></div>	5	1.1E-1	2.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:BH3	RT	<div><div></div><div></div></div>	5	2.3E-1	2.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	endoplasmic reticulum calcium ion homeostasis	RT	<div><div></div><div></div></div>	5	2.4E-1	2.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of intrinsic apoptotic signaling pathway	RT	<div><div></div><div></div></div>	8	3.2E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of protein homodimerization activity	RT	<div><div></div><div></div></div>	3	3.4E-1	2.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	BBID	127.Mito-stress	RT	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	152.altered synaptic signalling-neurodegenerative disorders	RT	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	pore complex	RT	<div><div></div><div></div></div>	3	4.3E-1	2.1E0	1.0E0	8.8E-1
Annotation Cluster 176		Enrichment Score: 1.13	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	eukaryotic translation initiation factor 4F complex	RT	<div><div></div><div></div></div>	5	4.0E-2	3.5E0	2.3E-1	2.0E-1
<input type="checkbox"/>	BIOCARTA	Eukaryotic protein translation	RT	<div><div></div><div></div></div>	10	4.4E-2	1.9E0	1.4E-1	9.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear-transcribed mRNA poly(A) tail shortening	RT	<div><div></div><div></div></div>	9	1.0E-1	1.8E0	7.1E-1	6.8E-1
<input type="checkbox"/>	BIOCARTA	Internal Ribosome entry pathway	RT	<div><div></div><div></div></div>	5	1.6E-1	2.2E0	3.7E-1	2.6E-1
Annotation Cluster 177		Enrichment Score: 1.13	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 5	RT	<div><div></div><div></div></div>	6	1.4E-2	3.7E0	2.7E-1	2.6E-1
<input type="checkbox"/>	INTERPRO	Dilute	RT	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.9E-1	4.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Dilute	RT	<div><div></div><div></div></div>	4	1.0E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	SM01132	RT	<div><div></div><div></div></div>	4	2.4E-1	2.3E0	9.5E-1	8.6E-1
Annotation Cluster 178		Enrichment Score: 1.12	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Bridging helix	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	RNA polymerase Rpb1, domain 1	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	RNA polymerase Rpb1, domain 5	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	RNA polymerase Rpb1, domain 4	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	RNA polymerase, N-terminal	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	RNA polymerase, alpha subunit	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	RNA polymerase Rpb1, domain 3	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	SMART	RPOLA_N	RT		3	1.5E-1	4.1E0	6.9E-1	6.2E-1
Annotation Cluster 179		Enrichment Score: 1.12	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Proprotein convertase, P	RT		6	1.7E-3	5.3E0	2.1E-2	1.9E-2
<input type="checkbox"/>	INTERPRO	Peptidase S8, subtilisin, Asp-active site	RT		5	7.7E-3	5.2E0	7.7E-2	7.1E-2
<input type="checkbox"/>	INTERPRO	Peptidase S8, subtilisin, Ser-active site	RT		6	7.7E-3	4.1E0	7.7E-2	7.1E-2
<input type="checkbox"/>	INTERPRO	Peptidase S8, subtilisin, His-active site	RT		6	7.7E-3	4.1E0	7.7E-2	7.1E-2
<input type="checkbox"/>	INTERPRO	Peptidase S8, subtilisin-related	RT		6	1.3E-2	3.7E0	1.3E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Peptidase S8/S53 domain	RT		6	2.1E-2	3.4E0	1.7E-1	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptide biosynthetic process	RT		4	3.7E-2	4.7E0	3.7E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	Proteinase inhibitor, propeptide	RT		6	1.3E-1	2.2E0	6.4E-1	5.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptide hormone processing	RT		5	2.8E-1	1.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein processing	RT		11	8.0E-1	9.0E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	signal peptide processing	RT		4	8.2E-1	9.5E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Serine protease	RT		8	1.0E0	3.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Charge relay system	RT		8	1.0E0	2.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	serine-type endopeptidase activity	RT		10	1.0E0	2.3E-1	1.0E0	1.0E0
Annotation Cluster 180		Enrichment Score: 1.11	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	MAP kinase kinase activity	RT		7	8.2E-3	3.5E0	6.9E-2	6.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Cleavage; by anthrax lethal factor	RT		3	2.2E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	proteolysis in other organism	RT		3	2.7E-1	3.0E0	1.0E0	9.6E-1
Annotation Cluster 181		Enrichment Score: 1.1	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:TFIIB-type	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	INTERPRO	Transcription factor TFIIB	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, TFIIB-type	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
Annotation Cluster 182		Enrichment Score: 1.07	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	rRNA methylation	RT		7	2.9E-2	2.8E0	3.2E-1	3.1E-1
<input type="checkbox"/>	INTERPRO	Ribosomal RNA adenine methylase transferase	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Ribosomal RNA adenine methylase transferase, N-terminal	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	SMART	rADc	RT		3	1.5E-1	4.1E0	6.9E-1	6.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	rRNA (adenine-N6,N6-)-dimethyltransferase activity	RT		3	2.0E-1	3.6E0	7.8E-1	7.0E-1
Annotation Cluster 183		Enrichment Score: 1.07	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote	RT		15	7.4E-3	2.1E0	7.7E-2	7.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:UBA	RT		13	1.0E-2	2.2E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of proteasomal ubiquitin-dependent protein catabolic process	RT		6	3.8E-2	3.0E0	3.8E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	Ubiquilin	RT		4	5.7E-2	4.1E0	4.0E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Heat shock chaperonin-binding	RT		5	6.3E-2	3.1E0	4.1E-1	3.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	polyubiquitin binding	RT		8	7.7E-2	2.1E0	3.9E-1	3.5E-1
<input type="checkbox"/>	SMART	STI1	RT		5	2.1E-1	2.0E0	8.9E-1	8.1E-1
<input type="checkbox"/>	SMART	UBA	RT		10	2.7E-1	1.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	UBA-like	RT		11	4.9E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	autophagosome	RT		7	9.5E-1	6.9E-1	1.0E0	9.5E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 184		Enrichment Score: 1.06	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	actomyosin	RT	<div><div></div><div></div></div>	7	5.9E-3	3.7E0	4.8E-2	4.2E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	myosin II filament	RT	<div><div></div><div></div></div>	3	6.6E-2	6.4E0	3.3E-1	2.9E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	myosin II complex	RT	<div><div></div><div></div></div>	4	8.3E-2	3.6E0	4.0E-1	3.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	actomyosin structure organization	RT	<div><div></div><div></div></div>	7	3.0E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Cell shape	RT	<div><div></div><div></div></div>	5	5.0E-1	1.4E0	1.0E0	7.8E-1
Annotation Cluster 185		Enrichment Score: 1.06	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H2A monoubiquitination	RT	<div><div></div><div></div></div>	6	3.8E-2	3.0E0	3.8E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	UV-damage excision repair	RT	<div><div></div><div></div></div>	5	9.9E-2	2.7E0	6.9E-1	6.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	Cul4B-RING E3 ubiquitin ligase complex	RT	<div><div></div><div></div></div>	3	1.8E-1	3.8E0	6.7E-1	5.9E-1
Annotation Cluster 186		Enrichment Score: 1.05	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	activation of JNKK activity	RT	<div><div></div><div></div></div>	4	6.4E-2	3.9E0	5.5E-1	5.2E-1
<input type="checkbox"/>	INTERPRO	Mitogen-activated protein (MAP) kinase kinase kinase, 9/10/11	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	JUN kinase kinase kinase activity	RT	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	mitogen-activated protein kinase kinase kinase, types 9/10/11	RT	<div><div></div><div></div></div>	3	8.8E-2	5.4E0	6.9E-1	6.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Leucine-zipper 1	RT	<div><div></div><div></div></div>	4	1.3E-1	3.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Leucine-zipper 2	RT	<div><div></div><div></div></div>	4	1.3E-1	3.0E0	1.0E0	9.6E-1
Annotation Cluster 187		Enrichment Score: 1.03	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of interferon-gamma-mediated signaling pathway	RT	<div><div></div><div></div></div>	9	3.8E-4	4.1E0	1.0E-2	9.6E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	JAK-STAT cascade involved in growth hormone signaling pathway	RT	<div><div></div><div></div></div>	9	1.4E-3	3.6E0	3.0E-2	2.9E-2
<input type="checkbox"/>	BIOCARTA	Stat3 Signaling Pathway	RT	<div><div></div><div></div></div>	8	2.3E-3	3.0E0	1.7E-2	1.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2; atypical	RT	<div><div></div><div></div></div>	5	5.4E-3	5.7E0	1.2E-1	1.2E-1
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, non-receptor Jak/Tyk2	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	tyrosine-protein kinase, Jak/Tyk2 type	RT	<div><div></div><div></div></div>	4	2.1E-2	5.4E0	2.9E-1	2.9E-1
<input type="checkbox"/>	BIOCARTA	IL22 Soluble Receptor Signaling Pathway	RT	<div><div></div><div></div></div>	9	3.1E-2	2.1E0	1.1E-1	7.8E-2
<input type="checkbox"/>	INTERPRO	MyTH4 domain	RT	<div><div></div><div></div></div>	5	4.3E-2	3.4E0	3.2E-1	2.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MyTH4 1	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MyTH4 2	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	BBID	48.mice minus JAKs and STATs	RT	<div><div></div><div></div></div>	8	6.1E-2	2.0E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	75.Stats activators of Apoptosis	RT	<div><div></div><div></div></div>	4	1.4E-1	2.7E0	1.0E0	1.0E0
<input type="checkbox"/>	SMART	MyTH4	RT	<div><div></div><div></div></div>	5	1.6E-1	2.3E0	7.0E-1	6.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	growth hormone receptor binding	RT	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	7.8E-1	7.0E-1
<input type="checkbox"/>	BIOCARTA	IL-10 Anti-inflammatory Signaling Pathway	RT	<div><div></div><div></div></div>	7	2.3E-1	1.6E0	4.7E-1	3.4E-1
<input type="checkbox"/>	BIOCARTA	IFN gamma signaling pathway	RT	<div><div></div><div></div></div>	4	3.1E-1	2.0E0	5.9E-1	4.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	CCR5 chemokine receptor binding	RT	<div><div></div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	FERM domain	RT	<div><div></div><div></div></div>	10	4.4E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Band 4.1 domain	RT	<div><div></div><div></div></div>	10	4.4E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	BBID	12.IL-6 type cytok-signal-transduct	RT	<div><div></div><div></div></div>	8	5.1E-1	1.2E0	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	FERM central domain	RT	<div><div></div><div></div></div>	9	5.9E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	BBID	11.IL-6 gp130-Jak-STAT	RT	<div><div></div><div></div></div>	3	6.0E-1	1.6E0	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FERM	RT	<div><div></div><div></div></div>	7	7.4E-1	9.7E-1	1.0E0	9.6E-1
<input type="checkbox"/>	BIOCARTA	IFN alpha signaling pathway	RT	<div><div></div><div></div></div>	3	8.5E-1	1.0E0	1.0E0	8.5E-1
<input type="checkbox"/>	SMART	B41	RT	<div><div></div><div></div></div>	10	9.1E-1	8.0E-1	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	FERM/acyl-CoA-binding protein, 3-helical bundle	RT	<div><div></div><div></div></div>	5	9.7E-1	6.2E-1	1.0E0	9.7E-1
Annotation Cluster 188		Enrichment Score: 1.03	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Non-homologous end-joining	RT	<div><div></div><div></div></div>	7	2.5E-2	2.8E0	4.6E-2	2.5E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	nonhomologous end joining complex	RT	<div><div></div><div></div></div>	4	1.2E-1	3.2E0	4.9E-1	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	establishment of integrated proviral latency	RT	<div><div></div><div></div></div>	4	1.4E-1	3.0E0	8.2E-1	7.9E-1















































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of smooth muscle cell proliferation	RT		4	1.8E-1	2.6E0	1.0E0	9.6E-1
Annotation Cluster 189		Enrichment Score: 1.03	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Elongation factor	RT		10	2.3E-2	2.3E0	9.3E-2	7.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	translational elongation	RT		6	1.7E-1	2.0E0	9.8E-1	9.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	translation elongation factor activity	RT		9	2.0E-1	1.6E0	7.9E-1	7.0E-1
Annotation Cluster 190		Enrichment Score: 1.01	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Innate immunity	RT		53	1.1E-2	1.4E0	4.6E-2	3.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	innate immune response	RT		82	1.5E-1	1.1E0	8.8E-1	8.4E-1
<input type="checkbox"/>	UP_KEYWORDS	Immunity	RT		73	5.6E-1	1.0E0	1.0E0	7.8E-1
Annotation Cluster 191		Enrichment Score: 1.01	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	E2F1 Destruction Pathway	RT		7	7.1E-2	2.1E0	2.0E-1	1.4E-1
<input type="checkbox"/>	BIOCARTA	Regulation of p27 Phosphorylation during Cell Cycle Progression	RT		8	9.5E-2	1.9E0	2.5E-1	1.8E-1
<input type="checkbox"/>	BIOCARTA	Cyclin E Destruction Pathway	RT		6	1.4E-1	2.0E0	3.3E-1	2.4E-1
Annotation Cluster 192		Enrichment Score: 1	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:C2	RT		21	1.4E-2	1.7E0	2.6E-1	2.5E-1
<input type="checkbox"/>	INTERPRO	C2 calcium-dependent membrane targeting	RT		35	7.5E-2	1.3E0	4.3E-1	4.0E-1
<input type="checkbox"/>	SMART	C2	RT		18	1.0E0	5.8E-1	1.0E0	1.0E0
Annotation Cluster 193		Enrichment Score: 0.98	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	IL22 Soluble Receptor Signaling Pathway	RT		9	3.1E-2	2.1E0	1.1E-1	7.8E-2
<input type="checkbox"/>	BBID	48.mice minus JAKs and STATs	RT		8	6.1E-2	2.0E0	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	JAK-STAT cascade	RT		10	7.8E-2	1.9E0	5.9E-1	5.6E-1
<input type="checkbox"/>	INTERPRO	STAT transcription factor, coiled coil	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
<input type="checkbox"/>	INTERPRO	STAT transcription factor, protein interaction	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
<input type="checkbox"/>	INTERPRO	STAT transcription factor, DNA-binding, subdomain	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
<input type="checkbox"/>	INTERPRO	STAT transcription factor, all-alpha	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
<input type="checkbox"/>	INTERPRO	STAT transcription factor, DNA-binding	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
<input type="checkbox"/>	INTERPRO	STAT transcription factor, core	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
<input type="checkbox"/>	BIOCARTA	IL-10 Anti-inflammatory Signaling Pathway	RT		7	2.3E-1	1.6E0	4.7E-1	3.4E-1
<input type="checkbox"/>	SMART	SM00964	RT		4	2.4E-1	2.3E0	9.5E-1	8.6E-1
<input type="checkbox"/>	INTERPRO	p53-like transcription factor, DNA-binding	RT		9	4.2E-1	1.3E0	1.0E0	9.1E-1
Annotation Cluster 194		Enrichment Score: 0.98	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of protein metabolic process	RT		5	3.2E-2	3.7E0	3.4E-1	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular response to laminar fluid shear stress	RT		4	1.4E-1	3.0E0	8.2E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of heterotypic cell-cell adhesion	RT		4	1.4E-1	3.0E0	8.2E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of response to cytokine stimulus	RT		3	2.0E-1	3.6E0	1.0E0	9.6E-1
Annotation Cluster 195		Enrichment Score: 0.97	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	Swr1 complex	RT		5	4.0E-2	3.5E0	2.3E-1	2.0E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	NuA4 histone acetyltransferase complex	RT		7	5.1E-2	2.5E0	2.8E-1	2.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H2A acetylation	RT		5	2.4E-1	2.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H4 acetylation	RT		8	2.6E-1	1.5E0	1.0E0	9.6E-1
Annotation Cluster 196		Enrichment Score: 0.97	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:REM 1	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:REM 2	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:REM 3	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	INTERPRO	HR1 rho-binding repeat	RT		4	1.2E-1	3.1E0	6.4E-1	5.8E-1
<input type="checkbox"/>	SMART	Hr1	RT		4	2.4E-1	2.3E0	9.5E-1	8.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	epithelial cell migration	RT		3	2.7E-1	3.0E0	1.0E0	9.6E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 197		Enrichment Score: 0.95	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	INTERPRO	Zinc finger, PHD-finger	RT	<div><div></div><div></div></div>	21	2.4E-2	1.6E0	1.9E-1	1.7E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, PHD-type	RT	<div><div></div><div></div></div>	23	2.4E-2	1.6E0	1.9E-1	1.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type 2	RT	<div><div></div><div></div></div>	9	6.3E-2	2.0E0	9.0E-1	8.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type 1	RT	<div><div></div><div></div></div>	9	1.0E-1	1.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type	RT	<div><div></div><div></div></div>	12	1.3E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, FYVE/PHD-type	RT	<div><div></div><div></div></div>	27	2.6E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, PHD-type, conserved site	RT	<div><div></div><div></div></div>	13	3.9E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	PHD	RT	<div><div></div><div></div></div>	23	5.3E-1	1.1E0	1.0E0	9.1E-1
Annotation Cluster 198		Enrichment Score: 0.95	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Histone H2B	RT	<div><div></div><div></div></div>	12	6.0E-4	3.1E0	8.2E-3	7.5E-3
<input type="checkbox"/>	SMART	H2B	RT	<div><div></div><div></div></div>	12	1.9E-2	2.0E0	1.6E-1	1.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	innate immune response in mucosa	RT	<div><div></div><div></div></div>	7	2.4E-1	1.7E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	antibacterial humoral response	RT	<div><div></div><div></div></div>	7	7.8E-1	9.4E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Antibiotic	RT	<div><div></div><div></div></div>	4	1.0E0	2.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Antimicrobial	RT	<div><div></div><div></div></div>	4	1.0E0	2.5E-1	1.0E0	1.0E0
Annotation Cluster 199		Enrichment Score: 0.95	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Domain A	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Domain B	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	INTERPRO	Domain of unknown function DUF3452, retinoblastoma-associated	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Retinoblastoma-associated protein, B-box	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Retinoblastoma-associated protein, A-box	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Rb C-terminal	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	SMART	SM01367	RT	<div><div></div><div></div></div>	3	1.5E-1	4.1E0	6.9E-1	6.2E-1
<input type="checkbox"/>	SMART	SM01368	RT	<div><div></div><div></div></div>	3	1.5E-1	4.1E0	6.9E-1	6.2E-1
<input type="checkbox"/>	SMART	SM01369	RT	<div><div></div><div></div></div>	3	1.5E-1	4.1E0	6.9E-1	6.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of lipid kinase activity	RT	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Spacer	RT	<div><div></div><div></div></div>	4	7.1E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 200		Enrichment Score: 0.94	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	nucleosomal DNA binding	RT	<div><div></div><div></div></div>	15	1.6E-2	1.9E0	1.2E-1	1.0E-1
<input type="checkbox"/>	INTERPRO	Histone H3	RT	<div><div></div><div></div></div>	6	1.8E-1	2.0E0	8.8E-1	8.0E-1
<input type="checkbox"/>	SMART	H3	RT	<div><div></div><div></div></div>	6	5.2E-1	1.3E0	1.0E0	9.1E-1
Annotation Cluster 201		Enrichment Score: 0.92	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of actin polymerization or depolymerization	RT	<div><div></div><div></div></div>	4	9.9E-2	3.4E0	6.9E-1	6.6E-1
<input type="checkbox"/>	INTERPRO	DEK, C-terminal	RT	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.4E-1	5.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of lamellipodium assembly	RT	<div><div></div><div></div></div>	4	1.4E-1	3.0E0	8.2E-1	7.9E-1
Annotation Cluster 202		Enrichment Score: 0.91	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	cysteine-type endopeptidase inhibitor activity involved in apoptotic process	RT	<div><div></div><div></div></div>	9	2.8E-2	2.3E0	1.8E-1	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of nucleotide-binding, oligomerization domain containing signaling pathway	RT	<div><div></div><div></div></div>	3	7.6E-2	5.9E0	5.8E-1	5.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:BIR 1	RT	<div><div></div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:BIR 2	RT	<div><div></div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:BIR 3	RT	<div><div></div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Baculoviral inhibition of apoptosis protein repeat	RT	<div><div></div><div></div></div>	4	1.2E-1	3.1E0	6.4E-1	5.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	inhibition of cysteine-type endopeptidase activity involved in apoptotic process	RT	<div><div></div><div></div></div>	4	1.8E-1	2.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	BIR	RT	<div><div></div><div></div></div>	4	3.1E-1	2.0E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of innate immune response	RT	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	9.6E-1
Annotation Cluster 203		Enrichment Score: 0.9	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	Rap protein signal transduction	RT		6	1.6E-2	3.6E0	2.1E-1	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	microvillus assembly	RT		6	1.5E-1	2.1E0	8.5E-1	8.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	recycling endosome membrane	RT		6	8.4E-1	8.7E-1	1.0E0	8.8E-1
Annotation Cluster 204		Enrichment Score: 0.9	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Brix domain	RT		4	5.7E-2	4.1E0	4.0E-1	3.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Brix	RT		4	7.0E-2	3.9E0	9.7E-1	9.3E-1
<input type="checkbox"/>	SMART	SM00879	RT		4	1.6E-1	2.7E0	7.0E-1	6.4E-1
<input type="checkbox"/>	INTERPRO	Anticodon-binding	RT		4	4.0E-1	1.8E0	1.0E0	9.1E-1
Annotation Cluster 205		Enrichment Score: 0.89	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PDZ	RT		26	2.1E-2	1.6E0	4.0E-1	3.9E-1
<input type="checkbox"/>	INTERPRO	PDZ domain	RT		32	1.2E-1	1.3E0	6.3E-1	5.8E-1
<input type="checkbox"/>	SMART	PDZ	RT		32	8.8E-1	8.7E-1	1.0E0	9.1E-1
Annotation Cluster 206		Enrichment Score: 0.88	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	endoplasmic reticulum chaperone complex	RT		5	8.0E-2	2.9E0	3.9E-1	3.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein folding in endoplasmic reticulum	RT		5	1.6E-1	2.3E0	9.3E-1	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Prevents secretion from ER	RT		13	1.8E-1	1.5E0	1.0E0	9.6E-1
Annotation Cluster 207		Enrichment Score: 0.88	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Autoinhibitory domain	RT		4	4.5E-2	4.5E0	7.4E-1	7.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	calmodulin-dependent protein kinase activity	RT		8	6.2E-2	2.2E0	3.5E-1	3.1E-1
<input type="checkbox"/>	BIOCARTA	Ca+ +/ Calmodulin-dependent Protein Kinase Activation	RT		4	8.5E-1	9.4E-1	1.0E0	8.5E-1
Annotation Cluster 208		Enrichment Score: 0.86	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitin conjugating enzyme binding	RT		10	6.3E-2	1.9E0	3.5E-1	3.1E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, C6HC-type	RT		6	8.0E-2	2.5E0	4.6E-1	4.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:RING-type 1; atypical	RT		4	1.0E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:IBR-type	RT		5	1.1E-1	2.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:RING-type 2	RT		4	2.5E-1	2.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	IBR	RT		5	4.6E-1	1.5E0	1.0E0	9.1E-1
Annotation Cluster 209		Enrichment Score: 0.86	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KEN	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	INTERPRO	KEN domain	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	PUB domain	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	PUG	RT		3	3.6E-1	2.4E0	1.0E0	9.1E-1
Annotation Cluster 210		Enrichment Score: 0.85	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	spectrin-associated cytoskeleton	RT		5	2.5E-2	4.0E0	1.5E-1	1.3E-1
<input type="checkbox"/>	UP_KEYWORDS	Elliptocytosis	RT		3	3.3E-1	2.6E0	9.1E-1	7.1E-1
<input type="checkbox"/>	UP_KEYWORDS	Hereditary hemolytic anemia	RT		7	3.5E-1	1.5E0	9.5E-1	7.3E-1
Annotation Cluster 211		Enrichment Score: 0.84	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Glycolysis	RT		11	1.0E-2	2.4E0	4.4E-2	3.4E-2
<input type="checkbox"/>	INTERPRO	Enolase, C-terminal	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	phosphopyruvate hydratase complex	RT		4	5.4E-2	4.2E0	2.9E-1	2.5E-1
<input type="checkbox"/>	INTERPRO	Enolase	RT		4	5.7E-2	4.1E0	4.0E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Enolase, N-terminal	RT		4	5.7E-2	4.1E0	4.0E-1	3.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	canonical glycolysis	RT		9	5.9E-2	2.0E0	5.2E-1	5.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	phosphopyruvate hydratase activity	RT		4	6.3E-2	4.0E0	3.5E-1	3.1E-1
<input type="checkbox"/>	INTERPRO	Enolase, conserved site	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	SMART	SM01192	RT		4	9.9E-2	3.3E0	5.3E-1	4.8E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	glycolytic process	RT	<div><div></div></div>	10	1.1E-1	1.7E0	7.3E-1	7.0E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	enolase	RT	<div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	1.0E0
<input type="checkbox"/>	SMART	SM01193	RT	<div><div></div></div>	4	1.6E-1	2.7E0	7.0E-1	6.4E-1
<input type="checkbox"/>	BIOCARTA	Glycolysis Pathway	RT	<div><div></div></div>	5	4.3E-1	1.5E0	7.3E-1	5.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	gluconeogenesis	RT	<div><div></div></div>	8	6.3E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Biosynthesis of amino acids	RT	<div><div></div></div>	12	8.4E-1	8.6E-1	1.0E0	8.4E-1
<input type="checkbox"/>	KEGG_PATHWAY	Glycolysis / Gluconeogenesis	RT	<div><div></div></div>	11	8.6E-1	8.5E-1	1.0E0	8.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Carbon metabolism	RT	<div><div></div></div>	15	9.8E-1	6.9E-1	1.0E0	9.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:Substrate	RT	<div><div></div></div>	20	1.0E0	4.5E-1	1.0E0	1.0E0
Annotation Cluster 212		Enrichment Score: 0.83	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:CXXC-type	RT	<div><div></div></div>	5	4.7E-2	3.4E0	7.7E-1	7.4E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, CXXC-type	RT	<div><div></div></div>	5	1.1E-1	2.6E0	6.3E-1	5.7E-1
<input type="checkbox"/>	INTERPRO	Leucine-rich repeat, cysteine-containing subtype	RT	<div><div></div></div>	6	1.8E-1	2.0E0	8.8E-1	8.0E-1
<input type="checkbox"/>	SMART	LRR_CC	RT	<div><div></div></div>	6	5.2E-1	1.3E0	1.0E0	9.1E-1
Annotation Cluster 213		Enrichment Score: 0.83	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HSA	RT	<div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Helicase/SANT-associated, DNA binding	RT	<div><div></div></div>	3	1.2E-1	4.6E0	6.4E-1	5.8E-1
<input type="checkbox"/>	SMART	HSA	RT	<div><div></div></div>	3	2.5E-1	3.0E0	9.9E-1	9.0E-1
Annotation Cluster 214		Enrichment Score: 0.82	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	JAB1/Mov34/MPN/PAD-1	RT	<div><div></div></div>	7	6.7E-3	3.6E0	7.2E-2	6.6E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MPN	RT	<div><div></div></div>	6	2.2E-2	3.4E0	4.0E-1	3.9E-1
<input type="checkbox"/>	SMART	JAB_MPN	RT	<div><div></div></div>	7	3.2E-2	2.6E0	2.5E-1	2.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:JAMM motif	RT	<div><div></div></div>	4	7.0E-2	3.9E0	9.7E-1	9.3E-1
<input type="checkbox"/>	INTERPRO	Rpn11/EIF3F C-terminal domain	RT	<div><div></div></div>	3	1.2E-1	4.6E0	6.4E-1	5.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	metallopeptidase activity	RT	<div><div></div></div>	6	1.0E0	4.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	thiol-dependent ubiquitin-specific protease activity	RT	<div><div></div></div>	5	1.0E0	3.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Zinc; catalytic	RT	<div><div></div></div>	4	1.0E0	2.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Metalloprotease	RT	<div><div></div></div>	5	1.0E0	2.3E-1	1.0E0	1.0E0
Annotation Cluster 215		Enrichment Score: 0.82	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of cyclin-dependent protein serine/threonine kinase activity	RT	<div><div></div></div>	9	3.8E-2	2.2E0	3.8E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	cyclin-dependent protein serine/threonine kinase regulator activity	RT	<div><div></div></div>	5	2.4E-1	2.0E0	9.0E-1	8.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of phosphorylation of RNA polymerase II C-terminal domain	RT	<div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	9.6E-1
Annotation Cluster 216		Enrichment Score: 0.81	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Adenylate kinase, active site lid domain	RT	<div><div></div></div>	3	1.2E-1	4.6E0	6.4E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	Adenylate kinase	RT	<div><div></div></div>	4	1.7E-1	2.8E0	8.2E-1	7.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	adenylate kinase activity	RT	<div><div></div></div>	4	1.8E-1	2.6E0	7.5E-1	6.7E-1
Annotation Cluster 217		Enrichment Score: 0.8	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of cell adhesion mediated by integrin	RT	<div><div></div></div>	7	1.3E-2	3.2E0	1.8E-1	1.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2 1	RT	<div><div></div></div>	3	5.4E-1	1.7E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2 2	RT	<div><div></div></div>	3	5.4E-1	1.7E0	1.0E0	9.6E-1
Annotation Cluster 218		Enrichment Score: 0.8	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A2	RT	<div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A3	RT	<div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Putative uncharacterized protein C21orf81	RT	<div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A1	RT	<div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.6E-1
Annotation Cluster 219		Enrichment Score: 0.8	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Phosphoserine intermediate	RT	<div><div></div></div>	6	9.0E-3	4.1E0	2.0E-1	1.9E-1
<input type="checkbox"/>	INTERPRO	Alkaline phosphatase, active site	RT	<div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1


Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Alkaline phosphatase	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	SMART	alkPPc	RT	<div><div></div><div></div></div>	4	4.9E-2	4.1E0	3.0E-1	2.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	alkaline phosphatase activity	RT	<div><div></div><div></div></div>	4	6.3E-2	4.0E0	3.5E-1	3.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	lipid moiety-binding region:GPI-anchor amidated aspartate	RT	<div><div></div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Folate biosynthesis	RT	<div><div></div><div></div></div>	5	2.8E-1	1.9E0	4.3E-1	2.8E-1
<input type="checkbox"/>	INTERPRO	Alkaline phosphatase-like, alpha/beta/alpha	RT	<div><div></div><div></div></div>	4	9.0E-1	8.0E-1	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Alkaline-phosphatase-like, core domain	RT	<div><div></div><div></div></div>	4	9.1E-1	7.7E-1	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	lipid moiety-binding region:GPI-anchor amidated serine	RT	<div><div></div><div></div></div>	4	9.9E-1	5.0E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_KEYWORDS	GPI-anchor	RT	<div><div></div><div></div></div>	8	1.0E0	4.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	anchored component of membrane	RT	<div><div></div><div></div></div>	6	1.0E0	3.4E-1	1.0E0	1.0E0
Annotation Cluster 220		Enrichment Score: 0.79	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of establishment of endothelial barrier	RT	<div><div></div><div></div></div>	5	1.8E-2	4.2E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of bicellular tight junction assembly	RT	<div><div></div><div></div></div>	3	1.3E-1	4.4E0	8.2E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of myosin-light-chain-phosphatase activity	RT	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cortical actin cytoskeleton organization	RT	<div><div></div><div></div></div>	6	3.8E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	establishment of protein localization to plasma membrane	RT	<div><div></div><div></div></div>	8	5.8E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 221		Enrichment Score: 0.79	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	isotype switching	RT	<div><div></div><div></div></div>	7	2.9E-2	2.8E0	3.2E-1	3.1E-1
<input type="checkbox"/>	OMIM_DISEASE	Mismatch repair cancer syndrome	RT	<div><div></div><div></div></div>	3	8.2E-2	5.9E0	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	guanine/thymine mispair binding	RT	<div><div></div><div></div></div>	3	1.3E-1	4.5E0	5.9E-1	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	somatic hypermutation of immunoglobulin genes	RT	<div><div></div><div></div></div>	5	2.8E-1	1.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Hereditary nonpolyposis colorectal cancer	RT	<div><div></div><div></div></div>	3	3.9E-1	2.3E0	1.0E0	7.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	mismatched DNA binding	RT	<div><div></div><div></div></div>	3	5.7E-1	1.6E0	1.0E0	8.9E-1
Annotation Cluster 222		Enrichment Score: 0.78	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 8	RT	<div><div></div><div></div></div>	15	4.9E-2	1.7E0	8.1E-1	7.8E-1
<input type="checkbox"/>	INTERPRO	Quinonprotein alcohol dehydrogenase-like superfamily	RT	<div><div></div><div></div></div>	13	7.5E-2	1.7E0	4.4E-1	4.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 9	RT	<div><div></div><div></div></div>	11	1.0E-1	1.7E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 11	RT	<div><div></div><div></div></div>	8	1.4E-1	1.8E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 10	RT	<div><div></div><div></div></div>	8	1.6E-1	1.8E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 13	RT	<div><div></div><div></div></div>	5	2.7E-1	1.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 12	RT	<div><div></div><div></div></div>	5	4.1E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 14	RT	<div><div></div><div></div></div>	3	6.3E-1	1.5E0	1.0E0	9.6E-1
Annotation Cluster 223		Enrichment Score: 0.78	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	sulfate assimilation	RT	<div><div></div><div></div></div>	5	3.2E-2	3.7E0	3.4E-1	3.3E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor	RT	<div><div></div><div></div></div>	4	1.4E-1	3.0E0	5.9E-1	5.3E-1
<input type="checkbox"/>	INTERPRO	Thioredoxin	RT	<div><div></div><div></div></div>	3	1.9E-1	3.7E0	8.9E-1	8.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	glycerol ether metabolic process	RT	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein disulfide oxidoreductase activity	RT	<div><div></div><div></div></div>	4	7.9E-1	9.9E-1	1.0E0	8.9E-1
Annotation Cluster 224		Enrichment Score: 0.76	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	beta-catenin destruction complex disassembly	RT	<div><div></div><div></div></div>	7	1.5E-1	1.9E0	8.9E-1	8.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	beta-catenin destruction complex	RT	<div><div></div><div></div></div>	5	1.7E-1	2.3E0	6.5E-1	5.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	beta-catenin destruction complex assembly	RT	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	1.0E0	9.6E-1
Annotation Cluster 225		Enrichment Score: 0.76	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	PIR_SUPERFAMILY	heat shock protein, HSP90/HTPG types	RT	<div><div></div><div></div></div>	4	2.1E-2	5.4E0	2.9E-1	2.9E-1
<input type="checkbox"/>	INTERPRO	Heat shock protein Hsp90, conserved site	RT	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.4E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	Heat shock protein Hsp90, N-terminal	RT	<div><div></div><div></div></div>	4	1.7E-1	2.8E0	8.2E-1	7.5E-1
<input type="checkbox"/>	INTERPRO	Heat shock protein Hsp90	RT	<div><div></div><div></div></div>	4	2.6E-1	2.3E0	1.0E0	9.1E-1

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Histidine kinase-like ATPase, ATP-binding domain	RT		7	4.5E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	HATPase_c	RT		4	5.3E-1	1.5E0	1.0E0	9.1E-1
Annotation Cluster 226		Enrichment Score: 0.76	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 7	RT		4	1.0E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Regulator of chromosome condensation, RCC1	RT		7	1.1E-1	2.1E0	6.0E-1	5.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 5	RT		6	1.1E-1	2.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II	RT		7	1.3E-1	2.0E0	6.6E-1	6.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 4	RT		6	1.3E-1	2.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 1	RT		6	1.6E-1	2.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 2	RT		6	1.6E-1	2.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 3	RT		6	1.6E-1	2.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 6	RT		4	3.0E-1	2.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	COG_ONTOLOGY	Cell division and chromosome partitioning / Cytoskeleton	RT		5	1.0E0	5.1E-1	1.0E0	1.0E0
Annotation Cluster 227		Enrichment Score: 0.74	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Carbamoyl-phosphate synthetase large subunit-like, ATP-binding domain	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
<input type="checkbox"/>	INTERPRO	ATP-grasp fold, subdomain 2	RT		7	9.0E-2	2.2E0	5.0E-1	4.5E-1
<input type="checkbox"/>	INTERPRO	ATP-grasp fold	RT		5	1.4E-1	2.4E0	7.3E-1	6.7E-1
<input type="checkbox"/>	INTERPRO	Pre-ATP-grasp domain	RT		5	1.8E-1	2.2E0	8.7E-1	8.0E-1
<input type="checkbox"/>	INTERPRO	ATP-grasp fold, subdomain 1	RT		5	2.1E-1	2.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Rudiment single hybrid motif	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:ATP-grasp	RT		3	5.9E-1	1.6E0	1.0E0	9.6E-1
Annotation Cluster 228		Enrichment Score: 0.74	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Hedgehog signaling pathway	RT		12	8.1E-3	2.3E0	1.6E-2	8.1E-3
<input type="checkbox"/>	BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM	RT		10	1.5E-2	2.2E0	6.3E-2	4.5E-2
<input type="checkbox"/>	BIOCARTA	Sonic Hedgehog (Shh) Pathway	RT		10	4.4E-2	1.9E0	1.4E-1	9.7E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	ciliary base	RT		8	1.2E-1	1.9E0	4.9E-1	4.3E-1
<input type="checkbox"/>	BIOCARTA	Regulation of ck1/cdk5 by type 1 glutamate receptors	RT		9	1.6E-1	1.6E0	3.6E-1	2.6E-1
<input type="checkbox"/>	UP_KEYWORDS	cAMP	RT		8	2.6E-1	1.5E0	7.6E-1	5.9E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	cAMP-dependent protein kinase complex	RT		3	3.0E-1	2.7E0	8.8E-1	7.7E-1
<input type="checkbox"/>	BIOCARTA	Transcription Regulation by Methyltransferase of CARM1	RT		6	3.5E-1	1.5E0	6.5E-1	4.6E-1
<input type="checkbox"/>	BIOCARTA	Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway	RT		6	3.5E-1	1.5E0	6.5E-1	4.6E-1
<input type="checkbox"/>	BIOCARTA	Phospholipase C-epsilon pathway	RT		6	3.5E-1	1.5E0	6.5E-1	4.6E-1
<input type="checkbox"/>	BIOCARTA	Attenuation of GPCR Signaling	RT		6	4.3E-1	1.4E0	7.3E-1	5.2E-1
<input type="checkbox"/>	BIOCARTA	GATA3 participate in activating the Th2 cytokine genes expression	RT		7	4.3E-1	1.3E0	7.3E-1	5.2E-1
<input type="checkbox"/>	BIOCARTA	mCalpain and friends in Cell motility	RT		9	4.4E-1	1.2E0	7.3E-1	5.2E-1
<input type="checkbox"/>	BIOCARTA	Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor	RT		9	4.4E-1	1.2E0	7.3E-1	5.2E-1
<input type="checkbox"/>	BIOCARTA	Stathmin and breast cancer resistance to antimicrotubule agents	RT		9	6.1E-1	1.1E0	9.4E-1	6.7E-1
Annotation Cluster 229		Enrichment Score: 0.72	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Presenilin action in Notch and Wnt signaling	RT		8	1.4E-1	1.7E0	3.3E-1	2.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	beta-catenin destruction complex disassembly	RT		7	1.5E-1	1.9E0	8.9E-1	8.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	Wnt signalosome	RT		4	2.4E-1	2.3E0	8.3E-1	7.3E-1
<input type="checkbox"/>	BIOCARTA	Multi-step Regulation of Transcription by Pitx2	RT		8	2.5E-1	1.5E0	5.0E-1	3.6E-1
Annotation Cluster 230		Enrichment Score: 0.72	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	TATA-box binding protein	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Beta2-adaptin/TBP, C-terminal domain	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA-templated transcription, initiation	RT	<div><div></div><div></div></div>	8	4.1E-1	1.3E0	1.0E0	9.6E-1
Annotation Cluster 231		Enrichment Score: 0.71	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 1	RT	<div><div></div><div></div></div>	8	3.3E-2	2.5E0	5.7E-1	5.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 2	RT	<div><div></div><div></div></div>	8	3.3E-2	2.5E0	5.7E-1	5.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium-transporting ATPase activity	RT	<div><div></div><div></div></div>	5	4.9E-2	3.3E0	2.8E-1	2.5E-1
<input type="checkbox"/>	INTERPRO	Protein kinase C, alpha/beta/gamma types	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	protein kinase C, alpha/beta/gamma types	RT	<div><div></div><div></div></div>	3	8.8E-2	5.4E0	6.9E-1	6.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of glial cell apoptotic process	RT	<div><div></div><div></div></div>	4	9.9E-2	3.4E0	6.9E-1	6.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 2; via carbonyl oxygen	RT	<div><div></div><div></div></div>	10	1.1E-1	1.7E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium-dependent protein kinase C activity	RT	<div><div></div><div></div></div>	3	1.3E-1	4.5E0	5.9E-1	5.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 2	RT	<div><div></div><div></div></div>	11	3.2E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 1	RT	<div><div></div><div></div></div>	9	3.8E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 3; via carbonyl oxygen	RT	<div><div></div><div></div></div>	4	6.1E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 1; via carbonyl oxygen	RT	<div><div></div><div></div></div>	4	8.7E-1	8.5E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 3	RT	<div><div></div><div></div></div>	4	8.7E-1	8.5E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular calcium ion homeostasis	RT	<div><div></div><div></div></div>	11	9.6E-1	7.0E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Calcium transport	RT	<div><div></div><div></div></div>	5	1.0E0	3.5E-1	1.0E0	1.0E0
Annotation Cluster 232		Enrichment Score: 0.7	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	rDNA heterochromatin	RT	<div><div></div><div></div></div>	3	1.2E-1	4.8E0	4.9E-1	4.3E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	chromatin silencing complex	RT	<div><div></div><div></div></div>	4	1.6E-1	2.8E0	6.2E-1	5.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	chromatin silencing at rDNA	RT	<div><div></div><div></div></div>	8	4.4E-1	1.3E0	1.0E0	9.6E-1
Annotation Cluster 233		Enrichment Score: 0.69	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Btk-type	RT	<div><div></div><div></div></div>	4	1.3E-1	3.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, Btk motif	RT	<div><div></div><div></div></div>	4	1.7E-1	2.8E0	8.2E-1	7.5E-1
<input type="checkbox"/>	SMART	BTK	RT	<div><div></div><div></div></div>	4	3.9E-1	1.8E0	1.0E0	9.1E-1
Annotation Cluster 234		Enrichment Score: 0.69	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	AKAP95 role in mitosis and chromosome dynamics	RT	<div><div></div><div></div></div>	8	6.1E-2	2.0E0	1.8E-1	1.3E-1
<input type="checkbox"/>	BIOCARTA	Protein Kinase A at the Centrosome	RT	<div><div></div><div></div></div>	8	1.9E-1	1.6E0	4.1E-1	2.9E-1
<input type="checkbox"/>	BIOCARTA	Rho-Selective Guanine Exchange Factor AKAP13 Mediates Stress Fiber Formation	RT	<div><div></div><div></div></div>	4	7.6E-1	1.1E0	1.0E0	7.6E-1
Annotation Cluster 235		Enrichment Score: 0.69	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of chemokine biosynthetic process	RT	<div><div></div><div></div></div>	7	2.6E-3	4.1E0	5.0E-2	4.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of calcidiol 1-monooxygenase activity	RT	<div><div></div><div></div></div>	3	7.6E-2	5.9E0	5.8E-1	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of membrane protein ectodomain proteolysis	RT	<div><div></div><div></div></div>	4	4.8E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Graft-versus-host disease	RT	<div><div></div><div></div></div>	5	9.0E-1	7.9E-1	1.0E0	9.0E-1
<input type="checkbox"/>	KEGG_PATHWAY	Type I diabetes mellitus	RT	<div><div></div><div></div></div>	6	9.3E-1	7.4E-1	1.0E0	9.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of insulin secretion	RT	<div><div></div><div></div></div>	8	9.5E-1	7.1E-1	1.0E0	9.6E-1
Annotation Cluster 236		Enrichment Score: 0.67	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1-2	RT	<div><div></div><div></div></div>	10	4.4E-2	2.1E0	7.3E-1	7.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1-1	RT	<div><div></div><div></div></div>	10	5.2E-2	2.0E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:2 X 16 AA Gly-rich approximate repeats	RT	<div><div></div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:2 X 19 AA perfect repeats	RT	<div><div></div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:2-1	RT	<div><div></div><div></div></div>	7	3.3E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:2-2	RT	<div><div></div><div></div></div>	7	3.8E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1-4	RT	<div><div></div><div></div></div>	4	5.4E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1-3	RT	<div><div></div><div></div></div>	4	5.8E-1	1.4E0	1.0E0	9.6E-1
Annotation Cluster 237		Enrichment Score: 0.67	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Aspartic peptidase, DDI1-type	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	aspartic-type endopeptidase activity	RT	<div><div></div><div></div></div>	10	8.9E-2	1.8E0	4.5E-1	4.0E-1
<input type="checkbox"/>	INTERPRO	Aspartic peptidase	RT	<div><div></div><div></div></div>	8	1.3E-1	1.8E0	6.7E-1	6.1E-1
<input type="checkbox"/>	INTERPRO	Peptidase A1	RT	<div><div></div><div></div></div>	4	2.1E-1	2.5E0	9.9E-1	9.1E-1
<input type="checkbox"/>	INTERPRO	Propeptide, peptidase A1	RT	<div><div></div><div></div></div>	3	3.2E-1	2.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_KEYWORDS	Aspartyl protease	RT	<div><div></div><div></div></div>	4	6.1E-1	1.3E0	1.0E0	7.8E-1
<input type="checkbox"/>	INTERPRO	Peptidase aspartic, active site	RT	<div><div></div><div></div></div>	4	6.8E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	propeptide:Activation peptide	RT	<div><div></div><div></div></div>	4	1.0E0	3.6E-1	1.0E0	1.0E0
Annotation Cluster 238		Enrichment Score: 0.66	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Purine biosynthesis	RT	<div><div></div><div></div></div>	5	1.1E-1	2.6E0	3.6E-1	2.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	purine nucleobase biosynthetic process	RT	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	'de novo' IMP biosynthetic process	RT	<div><div></div><div></div></div>	3	2.7E-1	3.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	purine ribonucleoside monophosphate biosynthetic process	RT	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	9.6E-1
Annotation Cluster 239		Enrichment Score: 0.66	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PDZ	RT	<div><div></div><div></div></div>	26	2.1E-2	1.6E0	4.0E-1	3.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:LD motif 1	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:LD motif 2	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:LD motif 3	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding 3	RT	<div><div></div><div></div></div>	6	3.0E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding	RT	<div><div></div><div></div></div>	5	3.0E-1	1.8E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	LIM domain	RT	<div><div></div><div></div></div>	13	3.5E-1	1.2E0	9.6E-1	7.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding 4	RT	<div><div></div><div></div></div>	3	5.0E-1	1.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, LIM-type	RT	<div><div></div><div></div></div>	13	5.0E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding 1	RT	<div><div></div><div></div></div>	8	6.1E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding 2	RT	<div><div></div><div></div></div>	8	6.1E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	LIM	RT	<div><div></div><div></div></div>	13	9.6E-1	7.3E-1	1.0E0	9.6E-1
Annotation Cluster 240		Enrichment Score: 0.65	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PUA	RT	<div><div></div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Pseudouridine synthase/archaeosine transglycosylase	RT	<div><div></div><div></div></div>	3	1.9E-1	3.7E0	8.9E-1	8.1E-1
<input type="checkbox"/>	INTERPRO	PUA-like domain	RT	<div><div></div><div></div></div>	5	3.7E-1	1.6E0	1.0E0	9.1E-1
Annotation Cluster 241		Enrichment Score: 0.65	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	calcineurin complex	RT	<div><div></div><div></div></div>	3	1.2E-1	4.8E0	4.9E-1	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of NFAT protein import into nucleus	RT	<div><div></div><div></div></div>	4	2.3E-1	2.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	calcineurin-NFAT signaling cascade	RT	<div><div></div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	9.6E-1
Annotation Cluster 242		Enrichment Score: 0.65	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Small Leucine-rich Proteoglycan (SLRP) molecules	RT	<div><div></div><div></div></div>	6	1.6E-2	3.0E0	6.6E-2	4.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	keratan sulfate catabolic process	RT	<div><div></div><div></div></div>	6	3.8E-2	3.0E0	3.8E-1	3.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...) (keratan sulfate)	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of sodium ion transport	RT	<div><div></div><div></div></div>	5	4.0E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	sodium channel regulator activity	RT	<div><div></div><div></div></div>	7	4.5E-1	1.3E0	1.0E0	8.9E-1
Annotation Cluster 244		Enrichment Score: 0.64	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	GKAP/Homer scaffold activity	RT	<div><div></div><div></div></div>	3	1.3E-1	4.5E0	5.9E-1	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	vocalization behavior	RT	<div><div></div><div></div></div>	5	2.0E-1	2.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	adult behavior	RT	<div><div></div><div></div></div>	6	4.5E-1	1.4E0	1.0E0	9.6E-1
Annotation Cluster 245		Enrichment Score: 0.63	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	type I interferon signaling pathway	RT	<div><div></div><div></div></div>	15	1.8E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Antiviral defense	RT	<div><div></div><div></div></div>	21	2.4E-1	1.2E0	7.1E-1	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	defense response to virus	RT	<div><div></div><div></div></div>	32	2.9E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 246		Enrichment Score: 0.63	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	lung-associated mesenchyme development	RT	<div><div></div><div></div></div>	5	7.3E-2	3.0E0	5.8E-1	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	branching involved in salivary gland morphogenesis	RT	<div><div></div><div></div></div>	4	2.8E-1	2.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	midbrain development	RT	<div><div></div><div></div></div>	6	6.2E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 247		Enrichment Score: 0.63	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Circadian rhythm	RT	<div><div></div><div></div></div>	13	9.3E-3	2.2E0	1.8E-2	9.3E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	AMP-activated protein kinase activity	RT	<div><div></div><div></div></div>	5	1.8E-2	4.3E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleotide-activated protein kinase complex	RT	<div><div></div><div></div></div>	6	1.9E-2	3.5E0	1.2E-1	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CBS 3	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CBS 4	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	BIOCARTA	Reversal of Insulin Resistance by Leptin	RT	<div><div></div><div></div></div>	7	1.1E-1	1.9E0	2.9E-1	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	carnitine shuttle	RT	<div><div></div><div></div></div>	4	1.8E-1	2.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Fatty acid biosynthesis	RT	<div><div></div><div></div></div>	10	3.4E-1	1.3E0	9.4E-1	7.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	fatty acid biosynthetic process	RT	<div><div></div><div></div></div>	9	6.7E-1	1.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CBS 1	RT	<div><div></div><div></div></div>	3	7.6E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CBS 2	RT	<div><div></div><div></div></div>	3	7.6E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	CBS domain	RT	<div><div></div><div></div></div>	3	8.1E-1	1.0E0	1.0E0	8.1E-1
<input type="checkbox"/>	INTERPRO	Cystathionine beta-synthase, core	RT	<div><div></div><div></div></div>	3	8.6E-1	9.3E-1	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	CBS	RT	<div><div></div><div></div></div>	3	8.9E-1	8.7E-1	1.0E0	9.1E-1
<input type="checkbox"/>	UP_KEYWORDS	Fatty acid metabolism	RT	<div><div></div><div></div></div>	13	9.6E-1	7.2E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Lipid biosynthesis	RT	<div><div></div><div></div></div>	11	1.0E0	4.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Lipid metabolism	RT	<div><div></div><div></div></div>	19	1.0E0	3.0E-1	1.0E0	1.0E0
Annotation Cluster 248		Enrichment Score: 0.63	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interleukin-12 production	RT	<div><div></div><div></div></div>	8	1.2E-1	1.9E0	7.7E-1	7.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interleukin-10 production	RT	<div><div></div><div></div></div>	7	1.8E-1	1.8E0	1.0E0	9.6E-1
<input type="checkbox"/>	BIOCARTA	Dendritic cells in regulating TH1 and TH2 Development	RT	<div><div></div><div></div></div>	8	6.2E-1	1.1E0	9.5E-1	6.7E-1
Annotation Cluster 249		Enrichment Score: 0.63	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Dorso-ventral axis formation	RT	<div><div></div><div></div></div>	12	8.1E-3	2.3E0	1.6E-2	8.1E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LNR 3	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	INTERPRO	Notch, NOD domain	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Notch, NODP domain	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.3E-1	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LNR 1	RT	<div><div></div><div></div></div>	4	2.5E-2	5.5E0	4.4E-1	4.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LNR 2	RT	<div><div></div><div></div></div>	4	2.5E-2	5.5E0	4.4E-1	4.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 28	RT	<div><div></div><div></div></div>	4	2.5E-2	5.5E0	4.4E-1	4.3E-1
<input type="checkbox"/>	SMART	SM01338	RT	<div><div></div><div></div></div>	4	4.9E-2	4.1E0	3.0E-1	2.7E-1
<input type="checkbox"/>	SMART	SM01339	RT	<div><div></div><div></div></div>	4	4.9E-2	4.1E0	3.0E-1	2.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 29	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 33	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 34	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.4E-1	8.1E-1
<input type="checkbox"/>	INTERPRO	Domain of unknown function DUF3454, notch	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Notch domain	RT	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.9E-1	4.5E-1
<input type="checkbox"/>	SMART	SM01334	RT	<div><div></div><div></div></div>	3	1.5E-1	4.1E0	6.9E-1	6.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 20	RT	<div><div></div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 24	RT	<div><div></div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 26	RT	<div><div></div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 27	RT	<div><div></div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 13; calcium-binding	RT	<div><div></div><div></div></div>	4	2.1E-1	2.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 17; calcium-binding	RT	<div><div></div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 21; calcium-binding	RT	<div><div></div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 22	RT	<div><div></div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 23; calcium-binding	RT	<div><div></div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	NL	RT	<div><div></div><div></div></div>	4	2.4E-1	2.3E0	9.5E-1	8.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 14; calcium-binding	RT	<div><div></div><div></div></div>	4	2.5E-1	2.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 15; calcium-binding	RT	<div><div></div><div></div></div>	4	2.5E-1	2.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Notch signaling pathway	RT	<div><div></div><div></div></div>	12	3.1E-1	1.3E0	4.8E-1	3.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 19	RT	<div><div></div><div></div></div>	3	3.3E-1	2.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 11; calcium-binding	RT	<div><div></div><div></div></div>	4	3.4E-1	1.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 12; calcium-binding	RT	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Notch signaling pathway	RT	<div><div></div><div></div></div>	9	4.7E-1	1.2E0	1.0E0	7.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 8; calcium-binding	RT	<div><div></div><div></div></div>	5	4.8E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 16; calcium-binding	RT	<div><div></div><div></div></div>	3	5.0E-1	1.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 9; calcium-binding	RT	<div><div></div><div></div></div>	3	7.0E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 9	RT	<div><div></div><div></div></div>	4	7.1E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 10	RT	<div><div></div><div></div></div>	3	7.4E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 6	RT	<div><div></div><div></div></div>	6	7.9E-1	9.3E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 7; calcium-binding	RT	<div><div></div><div></div></div>	4	8.0E-1	9.7E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 3	RT	<div><div></div><div></div></div>	9	8.9E-1	8.1E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 7	RT	<div><div></div><div></div></div>	3	9.3E-1	7.3E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 4	RT	<div><div></div><div></div></div>	6	9.5E-1	6.9E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 5	RT	<div><div></div><div></div></div>	4	9.6E-1	6.5E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 5; calcium-binding	RT	<div><div></div><div></div></div>	3	9.8E-1	5.4E-1	1.0E0	9.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 2	RT	<div><div></div><div></div></div>	8	9.8E-1	6.1E-1	1.0E0	9.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 1	RT	<div><div></div><div></div></div>	9	1.0E0	5.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	EGF-like calcium-binding, conserved site	RT	<div><div></div><div></div></div>	7	1.0E0	4.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	EGF-type aspartate/asparagine hydroxylation site	RT	<div><div></div><div></div></div>	7	1.0E0	4.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	EGF-like calcium-binding	RT	<div><div></div><div></div></div>	7	1.0E0	3.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	EGF-like, conserved site	RT	<div><div></div><div></div></div>	10	1.0E0	3.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Epidermal growth factor-like domain	RT	<div><div></div><div></div></div>	12	1.0E0	3.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	EGF-like domain	RT	<div><div></div><div></div></div>	10	1.0E0	2.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	EGF_CA	RT	<div><div></div><div></div></div>	7	1.0E0	2.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	EGF	RT	<div><div></div><div></div></div>	11	1.0E0	2.4E-1	1.0E0	1.0E0
Annotation Cluster 250		Enrichment Score: 0.61	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	INTERPRO	High mobility group (HMG) box domain	RT	<div><div></div><div></div></div>	15	6.6E-2	1.6E0	4.1E-1	3.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:HMG box 1	RT	<div><div></div><div></div></div>	5	2.7E-1	1.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:HMG box 2	RT	<div><div></div><div></div></div>	5	2.7E-1	1.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:HMG box	RT	<div><div></div><div></div></div>	9	3.1E-1	1.4E0	1.0E0	9.6E-1























































Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	SMART	HMG	RT	<div><div></div><div></div></div>	14	5.9E-1	1.1E0	1.0E0	9.1E-1
Annotation Cluster 251		Enrichment Score: 0.61	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Actin-related protein 3 (Arp3)	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	Arp2/3 protein complex	RT	<div><div></div><div></div></div>	4	2.9E-1	2.1E0	8.6E-1	7.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	Arp2/3 complex-mediated actin nucleation	RT	<div><div></div><div></div></div>	4	7.4E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 252		Enrichment Score: 0.6	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Natriuretic peptide receptor	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	natriuretic peptide receptor activity	RT	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	hormone binding	RT	<div><div></div><div></div></div>	4	2.8E-1	2.2E0	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	Extracellular ligand-binding receptor	RT	<div><div></div><div></div></div>	5	8.5E-1	8.6E-1	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	peptide hormone binding	RT	<div><div></div><div></div></div>	4	8.5E-1	8.8E-1	1.0E0	8.9E-1
Annotation Cluster 253		Enrichment Score: 0.59	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BBID	108.Regulating glucose transport	RT	<div><div></div><div></div></div>	7	1.1E-1	1.9E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	104.Insulin signaling	RT	<div><div></div><div></div></div>	9	2.5E-1	1.4E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	105.Signaling glucose uptake	RT	<div><div></div><div></div></div>	6	2.8E-1	1.6E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	106.Glycogen synthase-synthesis	RT	<div><div></div><div></div></div>	5	3.3E-1	1.7E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	107.mRNA translation-protein synthesis	RT	<div><div></div><div></div></div>	7	4.1E-1	1.4E0	1.0E0	1.0E0
Annotation Cluster 254		Enrichment Score: 0.58	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	execution phase of apoptosis	RT	<div><div></div><div></div></div>	7	4.0E-2	2.6E0	3.9E-1	3.8E-1
<input type="checkbox"/>	BIOCARTA	Role of Mitochondria in Apoptotic Signaling	RT	<div><div></div><div></div></div>	12	7.0E-2	1.7E0	2.0E-1	1.4E-1
<input type="checkbox"/>	BIOCARTA	D4-GDI Signaling Pathway	RT	<div><div></div><div></div></div>	8	9.5E-2	1.9E0	2.5E-1	1.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	death receptor binding	RT	<div><div></div><div></div></div>	6	1.2E-1	2.2E0	5.5E-1	4.9E-1
<input type="checkbox"/>	INTERPRO	Peptidase C14, caspase precursor p45, core	RT	<div><div></div><div></div></div>	5	1.8E-1	2.2E0	8.7E-1	8.0E-1
<input type="checkbox"/>	BBID	86.Apoptosis Nematode& Vert	RT	<div><div></div><div></div></div>	6	2.0E-1	1.8E0	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Peptidase C14, ICE, catalytic subunit p20, active site	RT	<div><div></div><div></div></div>	4	2.1E-1	2.5E0	9.9E-1	9.1E-1
<input type="checkbox"/>	INTERPRO	Peptidase C14, ICE, catalytic subunit p20	RT	<div><div></div><div></div></div>	5	2.1E-1	2.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	response to cobalt ion	RT	<div><div></div><div></div></div>	3	2.7E-1	3.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Peptidase C14, caspase non-catalytic subunit p10	RT	<div><div></div><div></div></div>	4	3.0E-1	2.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	death-inducing signaling complex	RT	<div><div></div><div></div></div>	3	3.0E-1	2.7E0	8.8E-1	7.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	cysteine-type endopeptidase activity involved in apoptotic process	RT	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	8.9E-1
<input type="checkbox"/>	BIOCARTA	Caspase Cascade in Apoptosis	RT	<div><div></div><div></div></div>	10	3.8E-1	1.3E0	7.0E-1	4.9E-1
<input type="checkbox"/>	SMART	CASC	RT	<div><div></div><div></div></div>	5	4.0E-1	1.6E0	1.0E0	9.1E-1
<input type="checkbox"/>	BBID	72.IAP interaction with cell death pathways	RT	<div><div></div><div></div></div>	6	7.0E-1	1.1E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	150.caspase and NFkB activation	RT	<div><div></div><div></div></div>	6	8.1E-1	9.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	cysteine-type endopeptidase activity	RT	<div><div></div><div></div></div>	9	8.3E-1	8.8E-1	1.0E0	8.9E-1
<input type="checkbox"/>	UP_KEYWORDS	Thiol protease	RT	<div><div></div><div></div></div>	9	1.0E0	4.0E-1	1.0E0	1.0E0
Annotation Cluster 255		Enrichment Score: 0.58	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	beta-catenin destruction complex disassembly	RT	<div><div></div><div></div></div>	7	1.5E-1	1.9E0	8.9E-1	8.5E-1
<input type="checkbox"/>	INTERPRO	DIX domain	RT	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DIX	RT	<div><div></div><div></div></div>	3	2.7E-1	2.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	DAX	RT	<div><div></div><div></div></div>	3	4.6E-1	2.0E0	1.0E0	9.1E-1
Annotation Cluster 256		Enrichment Score: 0.57	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase II transcription factor activity, TBP-class protein binding, involved in preinitiation complex assembly	RT	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	transcription factor TFIID complex	RT	<div><div></div><div></div></div>	9	2.0E-1	1.6E0	7.3E-1	6.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	transcription factor activity, RNA polymerase II core promoter sequence-specific binding involved in preinitiation complex assembly	RT	<div><div></div><div></div></div>	3	4.6E-1	2.0E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	RNA polymerase II transcriptional preinitiation complex assembly	RT	<div><div></div><div></div></div>	3	7.5E-1	1.2E0	1.0E0	9.6E-1
Annotation Cluster 257		Enrichment Score: 0.57	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:CR-type	RT	<div><div></div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:CXXCXGXG motif	RT	<div><div></div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.6E-1



















































Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Chaperone DnaJ	RT	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.4E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	HSP40/DnaJ peptide-binding	RT	<div><div></div><div></div></div>	4	1.7E-1	2.8E0	8.2E-1	7.5E-1
<input type="checkbox"/>	INTERPRO	Chaperone DnaJ, C-terminal	RT	<div><div></div><div></div></div>	4	1.7E-1	2.8E0	8.2E-1	7.5E-1
<input type="checkbox"/>	INTERPRO	Heat shock protein DnaJ, cysteine-rich domain	RT	<div><div></div><div></div></div>	3	1.9E-1	3.7E0	8.9E-1	8.1E-1
<input type="checkbox"/>	INTERPRO	DnaJ domain, conserved site	RT	<div><div></div><div></div></div>	5	6.5E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:J	RT	<div><div></div><div></div></div>	8	6.6E-1	1.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	DnaJ domain	RT	<div><div></div><div></div></div>	8	7.4E-1	9.7E-1	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	DnaJ	RT	<div><div></div><div></div></div>	8	9.7E-1	6.8E-1	1.0E0	9.7E-1
Annotation Cluster 258		Enrichment Score: 0.56	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	embryonic skeletal limb joint morphogenesis	RT	<div><div></div><div></div></div>	3	7.6E-2	5.9E0	5.8E-1	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	embryonic hindlimb morphogenesis	RT	<div><div></div><div></div></div>	7	3.3E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	embryonic forelimb morphogenesis	RT	<div><div></div><div></div></div>	5	8.1E-1	9.3E-1	1.0E0	9.6E-1
Annotation Cluster 259		Enrichment Score: 0.56	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	telomerase RNA binding	RT	<div><div></div><div></div></div>	6	1.2E-1	2.2E0	5.5E-1	4.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	telomere maintenance via telomerase	RT	<div><div></div><div></div></div>	5	3.6E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Dyskeratosis congenita	RT	<div><div></div><div></div></div>	3	4.9E-1	1.9E0	1.0E0	7.8E-1
Annotation Cluster 260		Enrichment Score: 0.56	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	BRCT domain	RT	<div><div></div><div></div></div>	8	1.5E-1	1.8E0	7.7E-1	7.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BRCT 1	RT	<div><div></div><div></div></div>	4	2.5E-1	2.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BRCT 2	RT	<div><div></div><div></div></div>	4	2.5E-1	2.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	BRCT	RT	<div><div></div><div></div></div>	7	2.7E-1	1.6E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BRCT	RT	<div><div></div><div></div></div>	3	6.3E-1	1.5E0	1.0E0	9.6E-1
Annotation Cluster 261		Enrichment Score: 0.56	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	DNA-directed DNA polymerase, family B, exonuclease domain	RT	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.4E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	DNA-directed DNA polymerase, family B, multifunctional domain	RT	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.4E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	DNA-directed DNA polymerase, family B	RT	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.4E-1	5.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	3'-5' exonuclease activity	RT	<div><div></div><div></div></div>	6	2.0E-1	1.9E0	7.9E-1	7.1E-1
<input type="checkbox"/>	SMART	POLBc	RT	<div><div></div><div></div></div>	3	2.5E-1	3.0E0	9.9E-1	9.0E-1
<input type="checkbox"/>	UP_KEYWORDS	DNA-directed DNA polymerase	RT	<div><div></div><div></div></div>	6	2.7E-1	1.7E0	7.6E-1	5.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-directed DNA polymerase activity	RT	<div><div></div><div></div></div>	7	3.6E-1	1.4E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_KEYWORDS	4Fe-4S	RT	<div><div></div><div></div></div>	7	4.6E-1	1.3E0	1.0E0	7.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	4 iron, 4 sulfur cluster binding	RT	<div><div></div><div></div></div>	7	7.3E-1	9.9E-1	1.0E0	8.9E-1
<input type="checkbox"/>	UP_KEYWORDS	Iron-sulfur	RT	<div><div></div><div></div></div>	7	8.9E-1	8.0E-1	1.0E0	8.9E-1
Annotation Cluster 262		Enrichment Score: 0.55	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Nitric Oxide Signaling Pathway	RT	<div><div></div><div></div></div>	11	1.5E-1	1.5E0	3.5E-1	2.5E-1
<input type="checkbox"/>	BIOCARTA	Effects of calcineurin in Keratinocyte Differentiation	RT	<div><div></div><div></div></div>	9	2.6E-1	1.4E0	5.2E-1	3.7E-1
<input type="checkbox"/>	BIOCARTA	Role of MEF2D in T-cell Apoptosis	RT	<div><div></div><div></div></div>	7	5.7E-1	1.2E0	8.9E-1	6.3E-1
Annotation Cluster 263		Enrichment Score: 0.55	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	I-kappaB/NF-kappaB complex	RT	<div><div></div><div></div></div>	4	3.0E-2	5.1E0	1.8E-1	1.6E-1
<input type="checkbox"/>	INTERPRO	NF-kappa-B/Rel/Dorsal	RT	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	Rel homology domain	RT	<div><div></div><div></div></div>	4	2.1E-1	2.5E0	9.9E-1	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:RHD	RT	<div><div></div><div></div></div>	3	3.9E-1	2.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	p53-like transcription factor, DNA-binding	RT	<div><div></div><div></div></div>	9	4.2E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Cell surface receptor IPT/TIG	RT	<div><div></div><div></div></div>	6	5.8E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	transcriptional activator activity, RNA polymerase II distal enhancer sequence-specific binding	RT	<div><div></div><div></div></div>	5	6.2E-1	1.2E0	1.0E0	8.9E-1
<input type="checkbox"/>	SMART	IPT	RT	<div><div></div><div></div></div>	5	9.3E-1	7.5E-1	1.0E0	9.3E-1

















































Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Immunoglobulin E-set	RT	<div><div></div></div>	12	9.7E-1	7.0E-1	1.0E0	9.7E-1
Annotation Cluster 264		Enrichment Score: 0.54	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BRO1	RT	<div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	BRO1 domain	RT	<div><div></div></div>	3	2.5E-1	3.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	SM01041	RT	<div><div></div></div>	3	4.6E-1	2.0E0	1.0E0	9.1E-1
Annotation Cluster 265		Enrichment Score: 0.51	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Glycogen metabolism	RT	<div><div></div></div>	8	7.3E-2	2.1E0	2.5E-1	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	glycogen metabolic process	RT	<div><div></div></div>	8	2.1E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	entrainment of circadian clock by photoperiod	RT	<div><div></div></div>	4	6.8E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Carbohydrate metabolism	RT	<div><div></div></div>	11	8.9E-1	8.0E-1	1.0E0	8.9E-1
Annotation Cluster 266		Enrichment Score: 0.5	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Zinc finger, TFIIS-type	RT	<div><div></div></div>	3	2.5E-1	3.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:TFIIS-type	RT	<div><div></div></div>	3	2.7E-1	2.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	ZnF_C2C2	RT	<div><div></div></div>	3	4.6E-1	2.0E0	1.0E0	9.1E-1
Annotation Cluster 267		Enrichment Score: 0.48	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	social behavior	RT	<div><div></div></div>	12	1.8E-1	1.5E0	9.8E-1	9.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of excitatory postsynaptic potential	RT	<div><div></div></div>	5	4.4E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	adult behavior	RT	<div><div></div></div>	6	4.5E-1	1.4E0	1.0E0	9.6E-1
Annotation Cluster 268		Enrichment Score: 0.46	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KH	RT	<div><div></div></div>	6	7.3E-2	2.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	K Homology domain	RT	<div><div></div></div>	10	1.5E-1	1.6E0	7.4E-1	6.8E-1
<input type="checkbox"/>	INTERPRO	K Homology domain, type 1	RT	<div><div></div></div>	10	2.7E-1	1.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	KH	RT	<div><div></div></div>	10	6.1E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KH 3	RT	<div><div></div></div>	3	6.7E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KH 1	RT	<div><div></div></div>	4	7.1E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KH 2	RT	<div><div></div></div>	4	7.1E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 269		Enrichment Score: 0.44	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MATH	RT	<div><div></div></div>	4	2.5E-1	2.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	MATH	RT	<div><div></div></div>	4	3.0E-1	2.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	TRAF-like	RT	<div><div></div></div>	6	3.8E-1	1.5E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	MATH	RT	<div><div></div></div>	4	6.0E-1	1.4E0	1.0E0	9.1E-1
Annotation Cluster 270		Enrichment Score: 0.44	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SWIRM	RT	<div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	SWIRM domain	RT	<div><div></div></div>	3	2.5E-1	3.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	SANT domain	RT	<div><div></div></div>	6	4.1E-1	1.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SANT	RT	<div><div></div></div>	3	7.9E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 271		Enrichment Score: 0.42	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of guanylate cyclase activity	RT	<div><div></div></div>	7	4.9E-3	3.8E0	8.5E-2	8.1E-2
<input type="checkbox"/>	INTERPRO	Nitric oxide synthase, oxygenase domain	RT	<div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	nitric-oxide synthase activity	RT	<div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Flavodoxin-like	RT	<div><div></div></div>	4	1.0E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Flavodoxin/nitric oxide synthase	RT	<div><div></div></div>	4	1.2E-1	3.1E0	6.4E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	Flavodoxin	RT	<div><div></div></div>	4	1.2E-1	3.1E0	6.4E-1	5.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	tetrahydrobiopterin binding	RT	<div><div></div></div>	3	1.3E-1	4.5E0	5.9E-1	5.3E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	NADP binding	RT	<div><div></div></div>	9	2.2E-1	1.5E0	8.7E-1	7.8E-1
<input type="checkbox"/>	INTERPRO	FAD-binding, type 1	RT	<div><div></div></div>	3	2.5E-1	3.1E0	1.0E0	9.1E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	NADPH-cytochrome p450 reductase, FAD-binding, alpha-helical domain-3	RT	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:FMN	RT	<div><div></div><div></div></div>	4	3.0E-1	2.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Oxidoreductase FAD/NAD(P)-binding	RT	<div><div></div><div></div></div>	4	3.0E-1	2.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	arginine binding	RT	<div><div></div><div></div></div>	3	3.3E-1	2.6E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of vasodilation	RT	<div><div></div><div></div></div>	7	3.6E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	nitric oxide biosynthetic process	RT	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	arginine catabolic process	RT	<div><div></div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	nitric oxide mediated signal transduction	RT	<div><div></div><div></div></div>	5	4.0E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Flavoprotein pyridine nucleotide cytochrome reductase	RT	<div><div></div><div></div></div>	3	4.4E-1	2.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	FMN binding	RT	<div><div></div><div></div></div>	4	4.7E-1	1.6E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FAD-binding FR-type	RT	<div><div></div><div></div></div>	4	5.4E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Arginine biosynthesis	RT	<div><div></div><div></div></div>	5	5.6E-1	1.3E0	8.3E-1	5.6E-1
<input type="checkbox"/>	UP_KEYWORDS	FMN	RT	<div><div></div><div></div></div>	4	6.1E-1	1.3E0	1.0E0	7.8E-1
<input type="checkbox"/>	INTERPRO	Ferredoxin reductase-type FAD-binding domain	RT	<div><div></div><div></div></div>	4	6.1E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Riboflavin synthase-like beta-barrel	RT	<div><div></div><div></div></div>	4	6.1E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of blood pressure	RT	<div><div></div><div></div></div>	4	9.0E-1	7.9E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:FAD	RT	<div><div></div><div></div></div>	7	9.1E-1	7.7E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:NADP	RT	<div><div></div><div></div></div>	8	9.3E-1	7.4E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	RT	<div><div></div><div></div></div>	8	9.9E-1	5.5E-1	1.0E0	9.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	heme binding	RT	<div><div></div><div></div></div>	13	1.0E0	5.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Arginine and proline metabolism	RT	<div><div></div><div></div></div>	4	1.0E0	4.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	COG_ONTOLOGY	Inorganic ion transport and metabolism	RT	<div><div></div><div></div></div>	5	1.0E0	4.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	flavin adenine dinucleotide binding	RT	<div><div></div><div></div></div>	4	1.0E0	3.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Heme	RT	<div><div></div><div></div></div>	9	1.0E0	4.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	FAD	RT	<div><div></div><div></div></div>	6	1.0E0	3.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Flavoprotein	RT	<div><div></div><div></div></div>	6	1.0E0	3.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	NADP	RT	<div><div></div><div></div></div>	10	1.0E0	3.7E-1	1.0E0	1.0E0
Annotation Cluster 272		Enrichment Score: 0.42	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium-transporting ATPase activity	RT	<div><div></div><div></div></div>	5	4.9E-2	3.3E0	2.8E-1	2.5E-1
<input type="checkbox"/>	INTERPRO	Calcium-transporting P-type ATPase, subfamily IIA, SERCA-type	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	4.1E-1	3.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 2; via carbonyl oxygen	RT	<div><div></div><div></div></div>	10	1.1E-1	1.7E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	platelet dense tubular network membrane	RT	<div><div></div><div></div></div>	3	4.3E-1	2.1E0	1.0E0	8.8E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	sarcoplasmic reticulum membrane	RT	<div><div></div><div></div></div>	7	4.5E-1	1.3E0	1.0E0	8.8E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	sarcoplasmic reticulum	RT	<div><div></div><div></div></div>	7	4.5E-1	1.3E0	1.0E0	8.8E-1
<input type="checkbox"/>	UP_KEYWORDS	Sarcoplasmic reticulum	RT	<div><div></div><div></div></div>	6	7.1E-1	1.0E0	1.0E0	7.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular calcium ion homeostasis	RT	<div><div></div><div></div></div>	11	9.6E-1	7.0E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	calcium ion transport	RT	<div><div></div><div></div></div>	6	1.0E0	4.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	calcium ion transmembrane transport	RT	<div><div></div><div></div></div>	10	1.0E0	5.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Calcium transport	RT	<div><div></div><div></div></div>	5	1.0E0	3.5E-1	1.0E0	1.0E0
Annotation Cluster 273		Enrichment Score: 0.41	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	actin crosslink formation	RT	<div><div></div><div></div></div>	4	2.8E-1	2.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	actin filament bundle assembly	RT	<div><div></div><div></div></div>	7	4.0E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	actin filament network formation	RT	<div><div></div><div></div></div>	3	5.2E-1	1.8E0	1.0E0	9.6E-1
Annotation Cluster 274		Enrichment Score: 0.4	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SANT 1	RT	<div><div></div><div></div></div>	3	3.9E-1	2.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SANT 2	RT	<div><div></div><div></div></div>	3	3.9E-1	2.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	SANT domain	RT	<div><div></div><div></div></div>	6	4.1E-1	1.4E0	1.0E0	9.1E-1
Annotation Cluster 275		Enrichment Score: 0.4	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Postsynaptic cell membrane	RT	<div><div></div><div></div></div>	33	1.3E-1	1.3E0	4.1E-1	3.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	postsynaptic membrane	RT	<div><div></div><div></div></div>	39	2.0E-1	1.2E0	7.4E-1	6.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	postsynaptic density	RT	<div><div></div><div></div></div>	34	2.3E-1	1.2E0	8.2E-1	7.2E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Synapse	RT	<div><div></div><div></div></div>	48	8.0E-1	9.2E-1	1.0E0	8.0E-1
<input type="checkbox"/>	UP_KEYWORDS	Cell junction	RT	<div><div></div><div></div></div>	88	9.1E-1	8.9E-1	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	cell junction	RT	<div><div></div><div></div></div>	62	9.4E-1	8.6E-1	1.0E0	9.4E-1
Annotation Cluster 276		Enrichment Score: 0.4	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BBID	68.Mitogen signaling in growth control	RT	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	2.Cytokine Receptors	RT	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	54.T-cell anergy	RT	<div><div></div><div></div></div>	8	4.3E-1	1.3E0	1.0E0	1.0E0
Annotation Cluster 277		Enrichment Score: 0.39	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Sirtuin family, catalytic core small domain	RT	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Deacetylase sirtuin-type	RT	<div><div></div><div></div></div>	3	2.7E-1	2.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Sirtuin family, catalytic core domain	RT	<div><div></div><div></div></div>	3	3.2E-1	2.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Sirtuin family	RT	<div><div></div><div></div></div>	3	3.2E-1	2.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	NAD+ binding	RT	<div><div></div><div></div></div>	3	6.7E-1	1.4E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:NAD	RT	<div><div></div><div></div></div>	7	9.8E-1	6.0E-1	1.0E0	9.8E-1
Annotation Cluster 278		Enrichment Score: 0.39	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	RISC complex	RT	<div><div></div><div></div></div>	4	2.4E-1	2.3E0	8.3E-1	7.3E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	RISC-loading complex	RT	<div><div></div><div></div></div>	3	3.0E-1	2.7E0	8.8E-1	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	miRNA loading onto RISC involved in gene silencing by miRNA	RT	<div><div></div><div></div></div>	3	3.4E-1	2.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	pre-miRNA processing	RT	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	production of miRNAs involved in gene silencing by miRNA	RT	<div><div></div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PAZ	RT	<div><div></div><div></div></div>	3	4.4E-1	2.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Argonaute/Dicer protein, PAZ	RT	<div><div></div><div></div></div>	3	5.0E-1	1.9E0	1.0E0	9.1E-1
<input type="checkbox"/>	BIOCARTA	Dicer Pathway	RT	<div><div></div><div></div></div>	3	5.3E-1	1.8E0	8.4E-1	6.0E-1
<input type="checkbox"/>	SMART	SM00949	RT	<div><div></div><div></div></div>	3	6.9E-1	1.4E0	1.0E0	9.1E-1
Annotation Cluster 279		Enrichment Score: 0.39	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DOC	RT	<div><div></div><div></div></div>	3	3.3E-1	2.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Anaphase-promoting complex, subunit 10/DOC domain	RT	<div><div></div><div></div></div>	3	3.8E-1	2.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	SM01337	RT	<div><div></div><div></div></div>	3	5.5E-1	1.7E0	1.0E0	9.1E-1
Annotation Cluster 280		Enrichment Score: 0.39	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein ADP-ribosylation	RT	<div><div></div><div></div></div>	7	1.3E-1	2.0E0	8.2E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of telomere maintenance via telomere lengthening	RT	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	NAD+ ADP-ribosyltransferase activity	RT	<div><div></div><div></div></div>	7	3.3E-1	1.5E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PARP catalytic	RT	<div><div></div><div></div></div>	3	7.4E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Poly(ADP-ribose) polymerase, catalytic domain	RT	<div><div></div><div></div></div>	3	7.9E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_KEYWORDS	Glycosyltransferase	RT	<div><div></div><div></div></div>	5	1.0E0	1.5E-1	1.0E0	1.0E0
Annotation Cluster 281		Enrichment Score: 0.37	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:RanBP2-type	RT	<div><div></div><div></div></div>	5	2.7E-1	1.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, RanBP2-type	RT	<div><div></div><div></div></div>	6	3.8E-1	1.5E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	ZnF_RBZ	RT	<div><div></div><div></div></div>	5	7.6E-1	1.0E0	1.0E0	9.1E-1
Annotation Cluster 282		Enrichment Score: 0.37	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Bernard Soulier syndrome	RT	<div><div></div><div></div></div>	3	5.7E-2	6.9E0	2.1E-1	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	blood coagulation, intrinsic pathway	RT	<div><div></div><div></div></div>	5	3.6E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Blood coagulation	RT	<div><div></div><div></div></div>	6	8.5E-1	8.6E-1	1.0E0	8.5E-1
<input type="checkbox"/>	UP_KEYWORDS	Hemostasis	RT	<div><div></div><div></div></div>	6	8.5E-1	8.6E-1	1.0E0	8.5E-1
<input type="checkbox"/>	KEGG_PATHWAY	ECM-receptor interaction	RT	<div><div></div><div></div></div>	7	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 283		Enrichment Score: 0.36	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 9	RT	<div><div></div><div></div></div>	5	1.7E-1	2.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 10	RT	<div><div></div><div></div></div>	5	1.7E-1	2.3E0	1.0E0	9.6E-1

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 7	RT		6	2.7E-1	1.7E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 8	RT		5	3.0E-1	1.8E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	HEAT, type 2	RT		5	3.7E-1	1.6E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 6	RT		6	4.6E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 11	RT		3	5.0E-1	1.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 5	RT		6	6.0E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 1	RT		8	7.7E-1	9.4E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 2	RT		8	7.7E-1	9.4E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 4	RT		6	7.8E-1	9.5E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 3	RT		6	8.8E-1	8.2E-1	1.0E0	9.6E-1
Annotation Cluster 284		Enrichment Score: 0.36	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Interaction with KCND2	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 1; degenerate	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of potassium ion transmembrane transport	RT		4	4.8E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cardiac conduction	RT		6	9.0E-1	7.9E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	voltage-gated ion channel activity	RT		3	9.8E-1	5.6E-1	1.0E0	9.8E-1
<input type="checkbox"/>	UP_KEYWORDS	Potassium	RT		12	9.9E-1	6.4E-1	1.0E0	9.9E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	voltage-gated potassium channel complex	RT		8	9.9E-1	5.8E-1	1.0E0	9.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	potassium channel activity	RT		3	9.9E-1	4.8E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_KEYWORDS	Potassium transport	RT		10	9.9E-1	5.9E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_KEYWORDS	Potassium channel	RT		4	1.0E0	3.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	potassium ion transmembrane transport	RT		5	1.0E0	2.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Voltage-gated channel	RT		4	1.0E0	1.8E-1	1.0E0	1.0E0
Annotation Cluster 285		Enrichment Score: 0.34	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of chemokine biosynthetic process	RT		7	2.6E-3	4.1E0	5.0E-2	4.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of MHC class II biosynthetic process	RT		5	3.2E-2	3.7E0	3.4E-1	3.3E-1
<input type="checkbox"/>	KEGG_PATHWAY	African trypanosomiasis	RT		12	4.0E-2	1.9E0	7.0E-2	4.0E-2
<input type="checkbox"/>	KEGG_PATHWAY	Malaria	RT		15	7.4E-2	1.6E0	1.3E-1	7.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	defense response to protozoan	RT		7	8.7E-2	2.2E0	6.4E-1	6.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	Inflammatory bowel disease (IBD)	RT		18	9.5E-2	1.5E0	1.6E-1	9.5E-2
<input type="checkbox"/>	BBID	111.Stress influences immunity	RT		5	1.3E-1	2.3E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	112.StressandCRHinfluence	RT		5	1.3E-1	2.3E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	19.Cytokine_microglia	RT		7	1.7E-1	1.7E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	18.Cytokine_astocytes	RT		9	1.9E-1	1.5E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	56.Macrophage regulation of CD4+T cells	RT		6	2.8E-1	1.6E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	58.(CD40L)_ immnosurveillance	RT		8	3.6E-1	1.4E0	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of isotype switching to IgG isotypes	RT		3	4.0E-1	2.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	BBID	22.Cytokine-chemokine_CNS	RT		6	4.6E-1	1.4E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	20.Cytokine_oligodendrocytes	RT		3	4.7E-1	2.0E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	21.Cytokine_neurons	RT		3	4.7E-1	2.0E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	113.Th1andTh2cells	RT		4	5.0E-1	1.6E0	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of growth of symbiont in host	RT		4	5.2E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	BBID	80.T_cell Activation	RT		10	6.0E-1	1.1E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	35.Chemokines_EAE Autoreactive T Cells	RT		4	6.1E-1	1.4E0	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	Dendritic cells in regulating TH1 and TH2 Development	RT		8	6.2E-1	1.1E0	9.5E-1	6.7E-1
<input type="checkbox"/>	BBID	88.Alternatively Activated APC	RT		5	6.2E-1	1.2E0	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Rheumatoid arthritis	RT		17	6.4E-1	1.0E0	9.2E-1	6.4E-1
<input type="checkbox"/>	INTERPRO	Four-helical cytokine_core	RT		8	7.4E-1	9.7E-1	1.0E0	9.1E-1
<input type="checkbox"/>	BIOCARTA	Regulation of hematopoiesis by cytokines	RT		5	7.8E-1	1.0E0	1.0E0	7.8E-1
<input type="checkbox"/>	BIOCARTA	Cytokine Network	RT		7	7.8E-1	9.7E-1	1.0E0	7.8E-1
<input type="checkbox"/>	BIOCARTA	Cytokines and Inflammatory Response	RT		9	7.9E-1	9.4E-1	1.0E0	7.9E-1
<input type="checkbox"/>	INTERPRO	Four-helical cytokine-like_core	RT		8	7.9E-1	9.2E-1	1.0E0	9.1E-1
<input type="checkbox"/>	BBID	76.Sig_trans_Ca2_Calcineurin_NF-AT	RT		3	7.9E-1	1.2E0	1.0E0	1.0E0

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Intestinal immune network for IgA production	RT		8	8.3E-1	8.8E-1	1.0E0	8.3E-1
<input type="checkbox"/>	BIOCARTA	Antigen Dependent B Cell Activation	RT		4	8.5E-1	9.4E-1	1.0E0	8.5E-1
<input type="checkbox"/>	BBID	59.L-type Ca2+ Tat immune cells	RT		3	8.6E-1	1.0E0	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Allograft rejection	RT		6	8.7E-1	8.4E-1	1.0E0	8.7E-1
<input type="checkbox"/>	BBID	97.Immune injury MS-lesions MS antigen	RT		5	9.0E-1	8.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Graft-versus-host disease	RT		5	9.0E-1	7.9E-1	1.0E0	9.0E-1
<input type="checkbox"/>	BIOCARTA	Adhesion and Diapedesis of Granulocytes	RT		4	9.2E-1	8.1E-1	1.0E0	9.2E-1
<input type="checkbox"/>	UP_KEYWORDS	Growth factor	RT		15	9.2E-1	7.9E-1	1.0E0	9.2E-1
<input type="checkbox"/>	BBID	15.T-cell polarization-chemokine receptors	RT		5	9.2E-1	8.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	Selective expression of chemokine receptors during T-cell polarization	RT		7	9.4E-1	7.6E-1	1.0E0	9.4E-1
<input type="checkbox"/>	KEGG_PATHWAY	Asthma	RT		4	9.5E-1	6.9E-1	1.0E0	9.5E-1
<input type="checkbox"/>	BIOCARTA	Cells and Molecules involved in local acute inflammatory response	RT		4	9.5E-1	7.2E-1	1.0E0	9.5E-1
<input type="checkbox"/>	BBID	5.B7 CD40 B-cell activa	RT		3	9.7E-1	6.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	Role of Tob in T-cell activation	RT		4	9.7E-1	6.4E-1	1.0E0	9.7E-1
<input type="checkbox"/>	BIOCARTA	Th1/Th2 Differentiation	RT		4	9.8E-1	6.1E-1	1.0E0	9.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	growth factor activity	RT		19	9.8E-1	7.0E-1	1.0E0	9.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	Autoimmune thyroid disease	RT		4	1.0E0	4.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	cytokine activity	RT		14	1.0E0	4.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Cytokine	RT		12	1.0E0	4.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Cytokine-cytokine receptor interaction	RT		16	1.0E0	3.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	immune response	RT		31	1.0E0	4.4E-1	1.0E0	1.0E0
Annotation Cluster 286		Enrichment Score: 0.33	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Caspase Cascade in Apoptosis	RT		10	3.8E-1	1.3E0	7.0E-1	4.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CARD	RT		6	4.2E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Caspase Recruitment	RT		6	5.1E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	CARD	RT		4	6.0E-1	1.4E0	1.0E0	9.1E-1
Annotation Cluster 287		Enrichment Score: 0.32	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Exportin-1/Importin-beta-like	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	Ran GTPase binding	RT		7	3.9E-1	1.4E0	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	Importin-beta, N-terminal	RT		4	5.3E-1	1.5E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Importin N-terminal	RT		3	6.3E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	SM00913	RT		4	7.9E-1	1.0E0	1.0E0	9.1E-1
Annotation Cluster 288		Enrichment Score: 0.32	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Filamin/ABP280 repeat-like	RT		4	3.0E-1	2.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Filamin/ABP280 repeat	RT		3	5.0E-1	1.9E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	IG_FLMN	RT		3	7.5E-1	1.2E0	1.0E0	9.1E-1
Annotation Cluster 289		Enrichment Score: 0.28	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Immunoglobulin I-set	RT		37	2.7E-3	1.6E0	3.2E-2	2.9E-2
<input type="checkbox"/>	INTERPRO	Immunoglobulin subtype 2	RT		42	4.8E-1	1.0E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 3	RT		18	7.1E-1	9.6E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 1	RT		24	9.3E-1	8.1E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 2	RT		24	9.3E-1	8.1E-1	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	IGc2	RT		42	1.0E0	6.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Immunoglobulin domain	RT		49	1.0E0	6.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Immunoglobulin subtype	RT		47	1.0E0	5.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Immunoglobulin-like fold	RT		85	1.0E0	5.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Immunoglobulin-like domain	RT		51	1.0E0	4.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	IG	RT		47	1.0E0	3.8E-1	1.0E0	1.0E0
Annotation Cluster 290		Enrichment Score: 0.27	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	SMAD protein complex assembly	RT		3	4.0E-1	2.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	type I transforming growth factor beta receptor binding	RT		3	4.6E-1	2.0E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	transforming growth factor beta receptor binding	RT		6	8.6E-1	8.5E-1	1.0E0	8.9E-1

Annotation Cluster 1			Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 291			Enrichment Score: 0.24	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:"KMSKS" region	RT		5	2.0E-1	2.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:"HIGH" region	RT		5	2.7E-1	1.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Aminoacyl-tRNA synthetase, class I, conserved site	RT		4	4.4E-1	1.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Glutathione S-transferase, C-terminal	RT		5	5.2E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Rossmann-like alpha/beta/alpha sandwich fold	RT		8	5.3E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	aminoacyl-tRNA ligase activity	RT		4	5.6E-1	1.4E0	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	Aminoacyl-tRNA synthetase, class 1a, anticodon-binding	RT		3	6.4E-1	1.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_KEYWORDS	Aminoacyl-tRNA synthetase	RT		5	8.2E-1	9.0E-1	1.0E0	8.2E-1
<input type="checkbox"/>	INTERPRO	Glutathione S-transferase, C-terminal-like	RT		5	9.2E-1	7.6E-1	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:GST C-terminal	RT		4	9.2E-1	7.4E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	tRNA aminoacylation for protein translation	RT		5	9.2E-1	7.4E-1	1.0E0	9.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Aminoacyl-tRNA biosynthesis	RT		5	1.0E0	3.9E-1	1.0E0	1.0E0
Annotation Cluster 292			Enrichment Score: 0.23	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MIF4G	RT		3	4.4E-1	2.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	MIF4G-like, type 3	RT		3	5.0E-1	1.9E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	MIF4-like, type 1/2/3	RT		3	7.2E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	MIF4G	RT		3	7.5E-1	1.2E0	1.0E0	9.1E-1
Annotation Cluster 293			Enrichment Score: 0.23	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MBD	RT		3	5.0E-1	1.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Methyl-CpG DNA binding	RT		3	5.5E-1	1.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	DNA-binding, integrase-type	RT		3	5.5E-1	1.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	MBD	RT		3	7.9E-1	1.1E0	1.0E0	9.1E-1
Annotation Cluster 294			Enrichment Score: 0.23	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Heparin-binding	RT		5	3.4E-1	1.7E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	organ induction	RT		3	6.3E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Heparin-binding	RT		8	9.8E-1	6.2E-1	1.0E0	9.8E-1
Annotation Cluster 295			Enrichment Score: 0.23	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Importin subunit alpha	RT		3	3.2E-1	2.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IBB	RT		3	3.3E-1	2.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	NLS-bearing protein import into nucleus	RT		6	3.5E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	importin subunit alpha	RT		3	3.8E-1	2.3E0	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 8	RT		5	4.1E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Importin-alpha, importin-beta-binding domain	RT		3	4.4E-1	2.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 7	RT		5	4.8E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 6	RT		5	5.4E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 5	RT		5	6.3E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 4	RT		5	6.9E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	nuclear localization sequence binding	RT		5	7.1E-1	1.1E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 9	RT		3	7.6E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 3	RT		5	7.9E-1	9.5E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 2	RT		5	8.1E-1	9.2E-1	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Armadillo	RT		5	9.3E-1	7.2E-1	1.0E0	9.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 1	RT		3	9.5E-1	6.6E-1	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	ARM	RT		5	9.9E-1	5.2E-1	1.0E0	9.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein transporter activity	RT		6	1.0E0	5.0E-1	1.0E0	1.0E0
Annotation Cluster 296			Enrichment Score: 0.23	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR































Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:ZZ-type	RT	<div><div></div><div></div></div>	4	4.6E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, ZZ-type	RT	<div><div></div><div></div></div>	4	5.7E-1	1.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	ZnF_ZZ	RT	<div><div></div><div></div></div>	4	7.9E-1	1.0E0	1.0E0	9.1E-1
Annotation Cluster 297		Enrichment Score: 0.23	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein-hormone receptor activity	RT	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	INTERPRO	G protein-coupled receptor, rhodopsin-like	RT	<div><div></div><div></div></div>	7	1.0E0	6.0E-2	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	GPCR, rhodopsin-like, 7TM	RT	<div><div></div><div></div></div>	7	1.0E0	5.9E-2	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	G-protein coupled receptor activity	RT	<div><div></div><div></div></div>	10	1.0E0	8.4E-2	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	G-protein coupled receptor	RT	<div><div></div><div></div></div>	11	1.0E0	9.0E-2	1.0E0	1.0E0
Annotation Cluster 298		Enrichment Score: 0.22	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Cyclic nucleotide-binding, conserved site	RT	<div><div></div><div></div></div>	5	2.5E-1	1.9E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Cyclic nucleotide-binding domain	RT	<div><div></div><div></div></div>	7	5.1E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Cyclic nucleotide-binding-like	RT	<div><div></div><div></div></div>	7	5.9E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_KEYWORDS	cAMP-binding	RT	<div><div></div><div></div></div>	3	7.3E-1	1.2E0	1.0E0	7.8E-1
<input type="checkbox"/>	INTERPRO	RmlC-like jelly roll fold	RT	<div><div></div><div></div></div>	7	7.9E-1	9.2E-1	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	cAMP binding	RT	<div><div></div><div></div></div>	4	7.9E-1	9.9E-1	1.0E0	8.9E-1
<input type="checkbox"/>	SMART	cNMP	RT	<div><div></div><div></div></div>	7	8.1E-1	9.2E-1	1.0E0	9.1E-1
Annotation Cluster 299		Enrichment Score: 0.21	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	nuclear pore	RT	<div><div></div><div></div></div>	14	3.4E-1	1.2E0	9.5E-1	8.3E-1
<input type="checkbox"/>	UP_KEYWORDS	Nuclear pore complex	RT	<div><div></div><div></div></div>	7	7.6E-1	9.6E-1	1.0E0	7.8E-1
<input type="checkbox"/>	UP_KEYWORDS	Translocation	RT	<div><div></div><div></div></div>	9	9.4E-1	7.4E-1	1.0E0	9.4E-1
Annotation Cluster 300		Enrichment Score: 0.2	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Histone H2A type 1-D	RT	<div><div></div><div></div></div>	3	6.3E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Histone H3.1	RT	<div><div></div><div></div></div>	3	6.3E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Histone H3.2	RT	<div><div></div><div></div></div>	3	6.3E-1	1.5E0	1.0E0	9.6E-1
Annotation Cluster 301		Enrichment Score: 0.19	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Vision	RT	<div><div></div><div></div></div>	20	3.1E-1	1.2E0	8.8E-1	6.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	visual perception	RT	<div><div></div><div></div></div>	29	8.9E-1	8.5E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Sensory transduction	RT	<div><div></div><div></div></div>	22	1.0E0	2.5E-1	1.0E0	1.0E0
Annotation Cluster 302		Enrichment Score: 0.18	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Forkhead-associated (FHA) domain	RT	<div><div></div><div></div></div>	7	5.6E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FHA	RT	<div><div></div><div></div></div>	6	6.0E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	SMAD/FHA domain	RT	<div><div></div><div></div></div>	9	6.4E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	FHA	RT	<div><div></div><div></div></div>	5	8.5E-1	8.8E-1	1.0E0	9.1E-1
Annotation Cluster 303		Enrichment Score: 0.18	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:NAD; via carbonyl oxygen	RT	<div><div></div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	NAD binding	RT	<div><div></div><div></div></div>	5	9.0E-1	7.8E-1	1.0E0	9.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:NAD	RT	<div><div></div><div></div></div>	5	9.7E-1	6.3E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:NAD	RT	<div><div></div><div></div></div>	7	9.8E-1	6.0E-1	1.0E0	9.8E-1
Annotation Cluster 304		Enrichment Score: 0.18	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	ATP hydrolysis coupled proton transport	RT	<div><div></div><div></div></div>	8	2.9E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Hydrogen ion transport	RT	<div><div></div><div></div></div>	4	9.8E-1	5.6E-1	1.0E0	9.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	Oxidative phosphorylation	RT	<div><div></div><div></div></div>	5	1.0E0	2.0E-1	1.0E0	1.0E0
Annotation Cluster 305		Enrichment Score: 0.17	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	TACI and BCMA stimulation of B cell immune responses.	RT	<div><div></div><div></div></div>	6	5.8E-1	1.2E0	9.0E-1	6.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	membrane protein intracellular domain proteolysis	RT	<div><div></div><div></div></div>	4	6.1E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	BIOCARTA	Bone Remodelling	RT	<div><div></div><div></div></div>	5	7.3E-1	1.1E0	1.0E0	7.3E-1
<input type="checkbox"/>	BBID	99.NF-kB activation	RT	<div><div></div><div></div></div>	6	8.1E-1	9.6E-1	1.0E0	1.0E0
Annotation Cluster 306		Enrichment Score: 0.17	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Steroid-binding	RT	<div><div></div><div></div></div>	5	1.9E-1	2.1E0	5.9E-1	4.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Steroid-binding	RT	<div><div></div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, NHR/GATA-type	RT	<div><div></div><div></div></div>	13	2.2E-1	1.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Modulating	RT	<div><div></div><div></div></div>	3	6.3E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	steroid binding	RT	<div><div></div><div></div></div>	5	6.9E-1	1.1E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:NR C4-type	RT	<div><div></div><div></div></div>	6	8.1E-1	9.1E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:Nuclear receptor	RT	<div><div></div><div></div></div>	6	8.1E-1	9.1E-1	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, nuclear hormone receptor-type	RT	<div><div></div><div></div></div>	6	8.8E-1	8.1E-1	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Steroid hormone receptor	RT	<div><div></div><div></div></div>	6	9.0E-1	7.9E-1	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Nuclear hormone receptor, ligand-binding, core	RT	<div><div></div><div></div></div>	6	9.1E-1	7.7E-1	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Hinge	RT	<div><div></div><div></div></div>	3	9.3E-1	7.3E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Ligand-binding	RT	<div><div></div><div></div></div>	3	9.5E-1	6.8E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding	RT	<div><div></div><div></div></div>	4	9.5E-1	6.6E-1	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	steroid hormone receptor activity	RT	<div><div></div><div></div></div>	6	9.7E-1	6.4E-1	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	steroid hormone mediated signaling pathway	RT	<div><div></div><div></div></div>	5	9.9E-1	5.2E-1	1.0E0	9.9E-1
<input type="checkbox"/>	SMART	ZnF_C4	RT	<div><div></div><div></div></div>	6	9.9E-1	5.3E-1	1.0E0	9.9E-1
<input type="checkbox"/>	SMART	HOLI	RT	<div><div></div><div></div></div>	6	1.0E0	5.1E-1	1.0E0	1.0E0
Annotation Cluster 307		Enrichment Score: 0.16	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:OPR	RT	<div><div></div><div></div></div>	3	5.4E-1	1.7E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Phox/Bem1p	RT	<div><div></div><div></div></div>	3	6.9E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	PB1	RT	<div><div></div><div></div></div>	3	8.9E-1	8.7E-1	1.0E0	9.1E-1
Annotation Cluster 308		Enrichment Score: 0.15	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	mitochondrial small ribosomal subunit	RT	<div><div></div><div></div></div>	5	5.7E-1	1.3E0	1.0E0	8.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitochondrial translational elongation	RT	<div><div></div><div></div></div>	14	7.0E-1	9.8E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitochondrial translation	RT	<div><div></div><div></div></div>	6	7.5E-1	9.9E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitochondrial translational termination	RT	<div><div></div><div></div></div>	13	8.1E-1	9.0E-1	1.0E0	9.6E-1
Annotation Cluster 309		Enrichment Score: 0.15	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Patatin/Phospholipase A2-related	RT	<div><div></div><div></div></div>	3	4.4E-1	2.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Acyl transferase/acyl hydrolase/lysophospholipase	RT	<div><div></div><div></div></div>	3	8.1E-1	1.0E0	1.0E0	9.1E-1
<input type="checkbox"/>	KEGG_PATHWAY	Glycerophospholipid metabolism	RT	<div><div></div><div></div></div>	5	1.0E0	2.7E-1	1.0E0	1.0E0
Annotation Cluster 310		Enrichment Score: 0.14	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Role of PI3K subunit p85 in regulation of Actin Organization and Cell Migration	RT	<div><div></div><div></div></div>	7	4.3E-1	1.3E0	7.3E-1	5.2E-1
<input type="checkbox"/>	BIOCARTA	How does salmonella hijack a cell	RT	<div><div></div><div></div></div>	4	8.5E-1	9.4E-1	1.0E0	8.5E-1
<input type="checkbox"/>	BIOCARTA	Y branching of actin filaments	RT	<div><div></div><div></div></div>	3	1.0E0	4.3E-1	1.0E0	1.0E0
Annotation Cluster 311		Enrichment Score: 0.13	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H4-K16 acetylation	RT	<div><div></div><div></div></div>	4	6.8E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	histone acetyltransferase complex	RT	<div><div></div><div></div></div>	4	7.2E-1	1.1E0	1.0E0	8.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H4-K5 acetylation	RT	<div><div></div><div></div></div>	3	7.8E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H4-K8 acetylation	RT	<div><div></div><div></div></div>	3	7.8E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 312		Enrichment Score: 0.12	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	One carbon pool by folate	RT	<div><div></div><div></div></div>	5	5.6E-1	1.3E0	8.3E-1	5.6E-1
<input type="checkbox"/>	UP_KEYWORDS	One-carbon metabolism	RT	<div><div></div><div></div></div>	3	7.3E-1	1.2E0	1.0E0	7.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	folic acid metabolic process	RT	<div><div></div><div></div></div>	3	8.3E-1	9.9E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	one-carbon metabolic process	RT	<div><div></div><div></div></div>	3	9.7E-1	5.9E-1	1.0E0	9.7E-1
Annotation Cluster 313		Enrichment Score: 0.11	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of viral transcription	RT	<div><div></div><div></div></div>	3	6.7E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of viral release from host cell	RT	<div><div></div><div></div></div>	3	7.8E-1	1.1E0	1.0E0	9.6E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:B box-type	RT	<div><div></div><div></div></div>	8	8.9E-1	8.0E-1	1.0E0	9.6E-1
Annotation Cluster 314		Enrichment Score: 0.11	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Phospholipid-transporting P-type ATPase, subfamily IV	RT	<div><div></div><div></div></div>	3	6.9E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	phospholipid-translocating ATPase activity	RT	<div><div></div><div></div></div>	3	7.1E-1	1.3E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	phospholipid translocation	RT	<div><div></div><div></div></div>	4	7.4E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Lipid transport	RT	<div><div></div><div></div></div>	4	1.0E0	2.9E-1	1.0E0	1.0E0
Annotation Cluster 315		Enrichment Score: 0.11	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	cAMP response element binding	RT	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	Basic-leucine zipper domain	RT	<div><div></div><div></div></div>	5	9.8E-1	5.7E-1	1.0E0	9.8E-1
<input type="checkbox"/>	SMART	BRLZ	RT	<div><div></div><div></div></div>	5	1.0E0	4.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:Basic motif	RT	<div><div></div><div></div></div>	10	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 316		Enrichment Score: 0.1	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SAP	RT	<div><div></div><div></div></div>	4	7.1E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	SAP domain	RT	<div><div></div><div></div></div>	4	7.7E-1	1.0E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	SAP	RT	<div><div></div><div></div></div>	4	9.5E-1	7.1E-1	1.0E0	9.5E-1
Annotation Cluster 317		Enrichment Score: 0.09	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CS	RT	<div><div></div><div></div></div>	3	7.0E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	CS-like domain	RT	<div><div></div><div></div></div>	3	7.9E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	HSP20-like chaperone	RT	<div><div></div><div></div></div>	3	9.5E-1	6.6E-1	1.0E0	9.5E-1
Annotation Cluster 318		Enrichment Score: 0.06	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Nuclear pore complex	RT	<div><div></div><div></div></div>	7	7.6E-1	9.6E-1	1.0E0	7.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	tRNA export from nucleus	RT	<div><div></div><div></div></div>	4	9.2E-1	7.4E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of glucose transport	RT	<div><div></div><div></div></div>	4	9.3E-1	7.2E-1	1.0E0	9.6E-1
Annotation Cluster 319		Enrichment Score: 0.05	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like 3	RT	<div><div></div><div></div></div>	3	7.9E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like 1	RT	<div><div></div><div></div></div>	3	9.4E-1	7.0E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like 2	RT	<div><div></div><div></div></div>	3	9.4E-1	7.0E-1	1.0E0	9.6E-1
Annotation Cluster 320		Enrichment Score: 0.05	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	3',5'-cyclic-nucleotide phosphodiesterase activity	RT	<div><div></div><div></div></div>	4	7.7E-1	1.0E0	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	3'5'-cyclic nucleotide phosphodiesterase	RT	<div><div></div><div></div></div>	3	8.4E-1	9.8E-1	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	3'5'-cyclic nucleotide phosphodiesterase, conserved site	RT	<div><div></div><div></div></div>	3	8.7E-1	8.9E-1	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	3'5'-cyclic nucleotide phosphodiesterase, catalytic domain	RT	<div><div></div><div></div></div>	3	8.9E-1	8.5E-1	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	HD/PDEase domain	RT	<div><div></div><div></div></div>	3	9.1E-1	8.1E-1	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 1	RT	<div><div></div><div></div></div>	3	9.3E-1	7.3E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 2	RT	<div><div></div><div></div></div>	3	9.3E-1	7.3E-1	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	HDc	RT	<div><div></div><div></div></div>	3	9.9E-1	5.3E-1	1.0E0	9.9E-1
Annotation Cluster 321		Enrichment Score: 0.05	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DEP	RT	<div><div></div><div></div></div>	3	7.9E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	DEP domain	RT	<div><div></div><div></div></div>	3	9.1E-1	8.1E-1	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	DEP	RT	<div><div></div><div></div></div>	3	9.8E-1	5.5E-1	1.0E0	9.8E-1
Annotation Cluster 322		Enrichment Score: 0.04	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Kelch-like protein, gigaxonin	RT	<div><div></div><div></div></div>	7	6.9E-1	1.0E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	Cul3-RING ubiquitin ligase complex	RT	<div><div></div><div></div></div>	10	7.5E-1	9.5E-1	1.0E0	8.8E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	kelch-like protein, gigaxonin type	RT	<div><div></div><div></div></div>	7	8.1E-1	9.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Galactose oxidase, beta-propeller	RT	<div><div></div><div></div></div>	4	8.7E-1	8.5E-1	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 6	RT	<div><div></div><div></div></div>	6	9.0E-1	7.9E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 5	RT	<div><div></div><div></div></div>	7	9.4E-1	7.2E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BACK	RT	<div><div></div><div></div></div>	3	9.5E-1	6.8E-1	1.0E0	9.6E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	BTB/Kelch-associated	RT	<div><div></div></div>	7	9.5E-1	7.0E-1	1.0E0	9.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 4	RT	<div><div></div></div>	7	9.6E-1	6.8E-1	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Kelch repeat type 1	RT	<div><div></div></div>	7	9.6E-1	6.8E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 1	RT	<div><div></div></div>	7	9.6E-1	6.7E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 2	RT	<div><div></div></div>	7	9.6E-1	6.7E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 3	RT	<div><div></div></div>	7	9.6E-1	6.7E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Kelch repeat	RT	<div><div></div></div>	7	9.6E-1	6.7E-1	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Kelch-type beta propeller	RT	<div><div></div></div>	4	9.9E-1	4.7E-1	1.0E0	9.9E-1
<input type="checkbox"/>	SMART	Kelch	RT	<div><div></div></div>	7	1.0E0	4.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	SM00875	RT	<div><div></div></div>	7	1.0E0	4.7E-1	1.0E0	1.0E0
Annotation Cluster 323		Enrichment Score: 0.03	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Heparin-binding growth factor/Fibroblast growth factor	RT	<div><div></div></div>	3	8.9E-1	8.5E-1	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Cytokine, IL-1-like	RT	<div><div></div></div>	4	9.2E-1	7.5E-1	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	FGF	RT	<div><div></div></div>	3	9.8E-1	5.5E-1	1.0E0	9.8E-1
Annotation Cluster 324		Enrichment Score: 0.02	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:G-patch	RT	<div><div></div></div>	3	8.7E-1	8.9E-1	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	G-patch domain	RT	<div><div></div></div>	3	9.7E-1	5.8E-1	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	G_patch	RT	<div><div></div></div>	3	1.0E0	3.9E-1	1.0E0	1.0E0
Annotation Cluster 325		Enrichment Score: 0.02	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Host cell receptor for virus entry	RT	<div><div></div></div>	7	9.2E-1	7.5E-1	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	viral entry into host cell	RT	<div><div></div></div>	10	9.4E-1	7.4E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	virus receptor activity	RT	<div><div></div></div>	7	9.8E-1	6.0E-1	1.0E0	9.8E-1
Annotation Cluster 326		Enrichment Score: 0.02	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Cilium biogenesis/degradation	RT	<div><div></div></div>	17	9.3E-1	7.9E-1	1.0E0	9.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cilium morphogenesis	RT	<div><div></div></div>	18	9.4E-1	7.8E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cilium assembly	RT	<div><div></div></div>	14	9.8E-1	6.7E-1	1.0E0	9.8E-1
Annotation Cluster 327		Enrichment Score: 0.02	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LisH	RT	<div><div></div></div>	3	9.3E-1	7.3E-1	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	LisH dimerisation motif	RT	<div><div></div></div>	3	9.5E-1	6.6E-1	1.0E0	9.5E-1
<input type="checkbox"/>	SMART	LisH	RT	<div><div></div></div>	3	9.9E-1	5.3E-1	1.0E0	9.9E-1
Annotation Cluster 328		Enrichment Score: 0.01	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Zinc finger, B-box	RT	<div><div></div></div>	11	8.7E-1	8.3E-1	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:B box-type	RT	<div><div></div></div>	8	8.9E-1	8.0E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:B30.2/SPRY	RT	<div><div></div></div>	10	9.6E-1	7.0E-1	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	SP1a/Ryanodine receptor SPRY	RT	<div><div></div></div>	10	9.8E-1	6.6E-1	1.0E0	9.8E-1
<input type="checkbox"/>	INTERPRO	B30.2/SPRY domain	RT	<div><div></div></div>	10	9.9E-1	6.3E-1	1.0E0	9.9E-1
<input type="checkbox"/>	INTERPRO	SPRY-associated	RT	<div><div></div></div>	4	9.9E-1	5.0E-1	1.0E0	9.9E-1
<input type="checkbox"/>	SMART	BBOX	RT	<div><div></div></div>	10	1.0E0	5.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Butyrophilin-like	RT	<div></div>	5	1.0E0	4.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	PRY	RT	<div><div></div></div>	4	1.0E0	3.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	SPRY	RT	<div><div></div></div>	10	1.0E0	4.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Concanavalin A-like lectin/glucanase, subgroup	RT	<div><div></div></div>	13	1.0E0	3.5E-1	1.0E0	1.0E0
Annotation Cluster 329		Enrichment Score: 0.01	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:FYVE-type	RT	<div><div></div></div>	4	9.4E-1	7.0E-1	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, FYVE-type	RT	<div><div></div></div>	3	9.6E-1	6.4E-1	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, FYVE-related	RT	<div><div></div></div>	3	9.8E-1	5.5E-1	1.0E0	9.8E-1
<input type="checkbox"/>	SMART	FYVE	RT	<div><div></div></div>	3	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 330		Enrichment Score: 0.01	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone demethylase activity	RT	<div><div></div></div>	3	9.2E-1	7.8E-1	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:JmjC	RT	<div><div></div></div>	3	9.6E-1	6.4E-1	1.0E0	9.6E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div><div><div></div><div></div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	INTERPRO	JmjC domain	RT	<div><div></div><div></div></div>	3	9.8E-1	5.6E-1	1.0E0	9.8E-1
<input type="checkbox"/>	SMART	JmjC	RT	<div><div></div><div></div></div>	3	1.0E0	4.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Dioxygenase	RT	<div><div></div><div></div></div>	5	1.0E0	4.1E-1	1.0E0	1.0E0
Annotation Cluster 331		Enrichment Score: 0.01	<div><div>G</div><div><div></div><div></div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	INTERPRO	Ras-association	RT	<div><div></div><div></div></div>	4	9.7E-1	6.2E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ras-associating	RT	<div><div></div><div></div></div>	3	9.7E-1	6.0E-1	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	RA	RT	<div><div></div><div></div></div>	3	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 332		Enrichment Score: 0	<div><div>G</div><div><div></div><div></div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:22	RT	<div><div></div><div></div></div>	4	9.5E-1	6.6E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:21	RT	<div><div></div><div></div></div>	4	9.6E-1	6.3E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:24	RT	<div><div></div><div></div></div>	3	9.7E-1	6.0E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:20	RT	<div><div></div><div></div></div>	4	9.7E-1	5.9E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:19	RT	<div><div></div><div></div></div>	4	9.8E-1	5.7E-1	1.0E0	9.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:18	RT	<div><div></div><div></div></div>	4	9.8E-1	5.6E-1	1.0E0	9.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1	RT	<div><div></div><div></div></div>	27	9.9E-1	7.2E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:2	RT	<div><div></div><div></div></div>	27	9.9E-1	7.1E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:17	RT	<div><div></div><div></div></div>	4	9.9E-1	4.9E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:16	RT	<div><div></div><div></div></div>	4	1.0E0	4.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:8	RT	<div><div></div><div></div></div>	10	1.0E0	5.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:9	RT	<div><div></div><div></div></div>	8	1.0E0	5.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:6	RT	<div><div></div><div></div></div>	12	1.0E0	5.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:10	RT	<div><div></div><div></div></div>	7	1.0E0	4.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:11	RT	<div><div></div><div></div></div>	6	1.0E0	4.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:7	RT	<div><div></div><div></div></div>	10	1.0E0	5.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:3	RT	<div><div></div><div></div></div>	19	1.0E0	5.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:12	RT	<div><div></div><div></div></div>	5	1.0E0	4.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:15	RT	<div><div></div><div></div></div>	4	1.0E0	3.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:4	RT	<div><div></div><div></div></div>	15	1.0E0	5.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:14	RT	<div><div></div><div></div></div>	4	1.0E0	3.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:5	RT	<div><div></div><div></div></div>	11	1.0E0	4.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:13	RT	<div><div></div><div></div></div>	4	1.0E0	3.2E-1	1.0E0	1.0E0
Annotation Cluster 333		Enrichment Score: 0	<div><div>G</div><div><div></div><div></div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PH	RT	<div><div></div><div></div></div>	25	9.9E-1	7.0E-1	1.0E0	9.9E-1
<input type="checkbox"/>	INTERPRO	Pleckstrin homology domain	RT	<div><div></div><div></div></div>	25	1.0E0	5.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Pleckstrin homology-like domain	RT	<div><div></div><div></div></div>	40	1.0E0	5.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	PH	RT	<div><div></div><div></div></div>	24	1.0E0	3.7E-1	1.0E0	1.0E0
Annotation Cluster 334		Enrichment Score: 0	<div><div>G</div><div><div></div><div></div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_CC_DIRECT	peroxisome	RT	<div><div></div><div></div></div>	9	1.0E0	5.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Peroxisome	RT	<div><div></div><div></div></div>	6	1.0E0	4.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Peroxisome	RT	<div><div></div><div></div></div>	6	1.0E0	3.8E-1	1.0E0	1.0E0
Annotation Cluster 335		Enrichment Score: 0	<div><div>G</div><div><div></div><div></div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_CC_DIRECT	mitochondrial matrix	RT	<div><div></div><div></div></div>	37	9.9E-1	7.2E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	transit peptide:Mitochondrion	RT	<div><div></div><div></div></div>	39	1.0E0	5.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	mitochondrial inner membrane	RT	<div><div></div><div></div></div>	37	1.0E0	5.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Transit peptide	RT	<div><div></div><div></div></div>	43	1.0E0	5.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Mitochondrion	RT	<div><div></div><div></div></div>	109	1.0E0	6.7E-1	1.0E0	1.0E0
Annotation Cluster 336		Enrichment Score: 0	<div><div>G</div><div><div></div><div></div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	INTERPRO	Chemokine interleukin-8-like domain	RT	<div><div></div><div></div></div>	3	1.0E0	4.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	chemokine activity	RT	<div><div></div><div></div></div>	3	1.0E0	3.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	chemokine-mediated signaling pathway	RT	<div><div></div><div></div></div>	4	1.0E0	3.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	SCY	RT	<div><div></div><div></div></div>	3	1.0E0	2.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	BBID	109.Chemokine families	RT	<div><div></div><div></div></div>	3	1.0E0	3.0E-1	1.0E0	1.0E0
Annotation Cluster 337		Enrichment Score: 0	<div><div>G</div><div><div></div><div></div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DH	RT	<div><div></div><div></div></div>	4	1.0E0	4.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of Rho protein signal transduction	RT	<div><div></div><div></div></div>	6	1.0E0	4.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Dbl homology (DH) domain	RT	<div><div></div><div></div></div>	4	1.0E0	3.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	Rho guanyl-nucleotide exchange factor activity	RT	<div><div></div><div></div></div>	4	1.0E0	3.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	guanyl-nucleotide exchange factor activity	RT	<div><div></div><div></div></div>	6	1.0E0	3.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	RhoGEF	RT	<div><div></div><div></div></div>	4	1.0E0	2.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Guanine-nucleotide releasing factor	RT	<div><div></div><div></div></div>	5	1.0E0	2.3E-1	1.0E0	1.0E0
Annotation Cluster 338		Enrichment Score: 0	<div><div>G</div><div><div></div><div></div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Rho-GAP	RT	<div><div></div><div></div></div>	3	1.0E0	3.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Rho GTPase activation protein	RT	<div><div></div><div></div></div>	5	1.0E0	3.4E-1	1.0E0	1.0E0

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Rho GTPase-activating protein domain	RT		3	1.0E0	2.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	GTPase activation	RT		9	1.0E0	3.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	RhoGAP	RT		3	1.0E0	1.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	GTPase activator activity	RT		15	1.0E0	3.2E-1	1.0E0	1.0E0
Annotation Cluster 339		Enrichment Score: 0	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:Basic motif	RT		10	1.0E0	4.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Helix-loop-helix motif	RT		5	1.0E0	3.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Myc-type, basic helix-loop-helix (bHLH) domain	RT		5	1.0E0	2.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	HLH	RT		5	1.0E0	1.8E-1	1.0E0	1.0E0
Annotation Cluster 340		Enrichment Score: -0	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Cell membrane	RT		320	1.0E0	6.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	plasma membrane	RT		457	1.0E0	7.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Membrane	RT		612	1.0E0	5.6E-1	1.0E0	1.0E0
Annotation Cluster 341		Enrichment Score: -0	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Glycoprotein	RT		276	1.0E0	4.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Signal	RT		267	1.0E0	4.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	integral component of membrane	RT		288	1.0E0	3.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	signal peptide	RT		219	1.0E0	4.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Receptor	RT		108	1.0E0	4.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		217	1.0E0	3.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	disulfide bond	RT		161	1.0E0	3.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT		175	1.0E0	3.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain:Extracellular	RT		145	1.0E0	3.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	transmembrane region	RT		226	1.0E0	3.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	integral component of plasma membrane	RT		100	1.0E0	4.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Disulfide bond	RT		204	1.0E0	4.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Transmembrane	RT		312	1.0E0	3.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Transmembrane helix	RT		309	1.0E0	3.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Membrane	RT		612	1.0E0	5.6E-1	1.0E0	1.0E0

3237 terms were not clustered.