

Functional Annotation Clustering

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Current Gene List: List\_1  
Current Background: Homo sapiens  
2998 DAVID IDs

Options

Classification Stringency























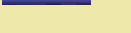




















Medium

Rerun using options



















































Create Sublist

336 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	<a href="#">RT</a>		536	0.0E0	5.9E0	0.0E0	0.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, C2H2</a>	<a href="#">RT</a>		653	0.0E0	5.1E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 3	<a href="#">RT</a>		565	0.0E0	6.1E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 4	<a href="#">RT</a>		526	0.0E0	6.1E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 5	<a href="#">RT</a>		503	0.0E0	6.2E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 6	<a href="#">RT</a>		460	0.0E0	6.3E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 7	<a href="#">RT</a>		432	0.0E0	6.4E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	<a href="#">RT</a>		483	0.0E0	5.9E0	0.0E0	0.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, C2H2-like</a>	<a href="#">RT</a>		648	0.0E0	5.3E0	0.0E0	0.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger C2H2-type/integrase DNA-binding domain</a>	<a href="#">RT</a>		634	0.0E0	5.5E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Nucleus</a>	<a href="#">RT</a>		1662	6.6E-320	2.2E0	3.1E-317	2.4E-317
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 8	<a href="#">RT</a>		399	9.0E-300	6.4E0	6.3E-297	6.1E-297
<input type="checkbox"/>	SMART	<a href="#">ZnF_C2H2</a>	<a href="#">RT</a>		648	4.9E-299	3.5E0	2.3E-296	2.0E-296
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 9	<a href="#">RT</a>		361	9.7E-272	6.4E0	6.0E-269	5.8E-269
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Zinc-finger</a>	<a href="#">RT</a>		843	9.4E-270	3.2E0	2.2E-267	1.7E-267
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 10	<a href="#">RT</a>		324	2.7E-248	6.5E0	1.5E-245	1.4E-245
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">nucleic acid binding</a>	<a href="#">RT</a>		609	1.8E-239	3.7E0	2.3E-236	2.1E-236
<input type="checkbox"/>	INTERPRO	<a href="#">Krueppel-associated box</a>	<a href="#">RT</a>		355	7.4E-230	5.5E0	4.2E-227	3.8E-227
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KRAB	<a href="#">RT</a>		314	8.3E-227	6.2E0	4.2E-224	4.1E-224
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transcription</a>	<a href="#">RT</a>		932	7.8E-221	2.7E0	1.2E-218	9.6E-219
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transcription regulation</a>	<a href="#">RT</a>		908	8.1E-215	2.7E0	9.6E-213	7.5E-213
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">DNA-binding</a>	<a href="#">RT</a>		838	1.2E-212	2.8E0	1.1E-210	8.9E-211
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Zinc</a>	<a href="#">RT</a>		904	1.6E-209	2.6E0	1.1E-207	8.5E-208
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 11	<a href="#">RT</a>		280	1.4E-206	6.3E0	6.6E-204	6.4E-204
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Metal-binding</a>	<a href="#">RT</a>		1174	3.8E-205	2.2E0	2.3E-203	1.8E-203
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">metal ion binding</a>	<a href="#">RT</a>		881	7.7E-199	2.5E0	5.0E-196	4.4E-196
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 12	<a href="#">RT</a>		242	1.8E-182	6.4E0	7.6E-180	7.3E-180
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">transcription, DNA-templated</a>	<a href="#">RT</a>		813	2.9E-171	2.5E0	1.7E-167	1.6E-167
<input type="checkbox"/>	SMART	<a href="#">KRAB</a>	<a href="#">RT</a>		350	2.1E-169	3.6E0	4.8E-167	4.3E-167
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of transcription, DNA-templated</a>	<a href="#">RT</a>		674	7.3E-159	2.7E0	2.1E-155	2.0E-155
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">DNA binding</a>	<a href="#">RT</a>		708	2.8E-152	2.5E0	1.2E-149	1.1E-149
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 13	<a href="#">RT</a>		192	4.9E-143	6.4E0	1.9E-140	1.9E-140
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 14	<a href="#">RT</a>		148	3.9E-111	6.5E0	1.4E-108	1.3E-108
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">intracellular</a>	<a href="#">RT</a>		513	2.1E-98	2.4E0	6.3E-96	5.5E-96
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 15	<a href="#">RT</a>		125	3.3E-92	6.4E0	1.1E-89	1.0E-89
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">transcription factor activity, sequence-specific DNA binding</a>	<a href="#">RT</a>		390	3.8E-73	2.4E0	9.8E-71	8.7E-71
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 16	<a href="#">RT</a>		96	1.2E-69	6.3E0	3.0E-67	2.9E-67
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 17	<a href="#">RT</a>		76	1.8E-54	6.3E0	2.7E-52	2.6E-52
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 18	<a href="#">RT</a>		60	1.3E-42	6.3E0	1.8E-40	1.7E-40
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 19	<a href="#">RT</a>		50	1.5E-35	6.3E0	1.8E-33	1.7E-33
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 20	<a href="#">RT</a>		32	2.2E-21	6.1E0	2.1E-19	2.0E-19















































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 2		Enrichment Score: 80.34	<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	<a href="#">Nucleotide-binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	769	1.5E-209	3.0E0	1.1E-207	8.5E-208
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">ATP-binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	619	9.8E-174	3.1E0	5.2E-172	4.0E-172
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ATP binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	640	5.1E-139	2.6E0	1.6E-136	1.5E-136
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	<a href="#">RT</a>	<div><div></div><div></div></div>	447	2.8E-123	3.1E0	1.0E-120	1.0E-120
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase	<a href="#">RT</a>	<div><div></div><div></div></div>	249	8.4E-84	3.5E0	2.6E-81	2.5E-81
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase-like domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	275	2.0E-82	3.2E0	9.2E-80	8.4E-80
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase, catalytic domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	259	8.9E-81	3.3E0	3.4E-78	3.1E-78
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:ATP	<a href="#">RT</a>	<div><div></div><div></div></div>	264	4.2E-77	3.2E0	1.2E-74	1.2E-74
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase, ATP binding site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	214	3.0E-72	3.5E0	8.6E-70	7.9E-70
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Kinase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	301	1.7E-70	2.8E0	5.8E-69	4.5E-69
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Serine/threonine-protein kinase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	187	2.7E-55	3.3E0	6.8E-54	5.3E-54
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Proton acceptor	<a href="#">RT</a>	<div><div></div><div></div></div>	255	2.2E-51	2.6E0	3.2E-49	3.0E-49
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein kinase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	180	1.4E-48	3.0E0	2.3E-46	2.1E-46
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein serine/threonine kinase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	180	6.1E-45	2.9E0	7.9E-43	7.0E-43
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein phosphorylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	201	5.6E-43	2.6E0	4.1E-40	3.9E-40
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transferase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	454	4.7E-42	1.8E0	9.7E-41	7.5E-41
<input type="checkbox"/>	INTERPRO	<a href="#">Serine/threonine-protein kinase, active site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	150	1.1E-39	3.0E0	1.9E-37	1.7E-37
<input type="checkbox"/>	SMART	<a href="#">S_TKc</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	171	5.7E-22	1.9E0	3.0E-20	2.7E-20
Annotation Cluster 3		Enrichment Score: 59.99	<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:ANK 4	<a href="#">RT</a>	<div><div></div><div></div></div>	133	2.9E-76	5.3E0	8.0E-74	7.7E-74
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 5	<a href="#">RT</a>	<div><div></div><div></div></div>	117	1.1E-71	5.6E0	2.7E-69	2.6E-69
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">ANK repeat</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	164	2.2E-70	4.3E0	7.0E-69	5.5E-69
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 3	<a href="#">RT</a>	<div><div></div><div></div></div>	141	1.0E-67	4.6E0	2.3E-65	2.3E-65
<input type="checkbox"/>	INTERPRO	<a href="#">Ankyrin repeat-containing domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	165	1.7E-64	3.9E0	3.4E-62	3.1E-62
<input type="checkbox"/>	INTERPRO	<a href="#">Ankyrin repeat</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	161	3.5E-64	3.9E0	6.6E-62	6.1E-62
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 2	<a href="#">RT</a>	<div><div></div><div></div></div>	148	9.4E-61	4.1E0	1.7E-58	1.7E-58
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 1	<a href="#">RT</a>	<div><div></div><div></div></div>	147	4.0E-60	4.1E0	7.2E-58	6.9E-58
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 6	<a href="#">RT</a>	<div><div></div><div></div></div>	85	7.5E-55	5.8E0	1.2E-52	1.1E-52
<input type="checkbox"/>	SMART	<a href="#">ANK</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	159	9.3E-40	2.6E0	1.1E-37	9.7E-38
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 7	<a href="#">RT</a>	<div><div></div><div></div></div>	56	1.0E-37	6.1E0	1.3E-35	1.3E-35
Annotation Cluster 4		Enrichment Score: 41.28	<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	<a href="#">rRNA processing</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	150	1.7E-66	4.2E0	3.3E-63	3.2E-63
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Ribonucleoprotein</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	169	8.4E-65	3.9E0	2.3E-63	1.8E-63
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nuclear-transcribed mRNA catabolic process, nonsense-mediated decay</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	99	1.1E-55	4.9E0	1.6E-52	1.6E-52
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">SRP-dependent cotranslational protein targeting to membrane</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	81	7.7E-48	5.1E0	9.1E-45	8.6E-45
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">translational initiation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	100	7.7E-47	4.3E0	7.6E-44	7.2E-44
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Ribosome</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	101	5.0E-44	3.9E0	6.2E-42	2.8E-42
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Ribosomal protein</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	104	4.5E-39	3.9E0	9.0E-38	7.0E-38
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">viral transcription</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	81	1.8E-37	4.3E0	1.2E-34	1.1E-34
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">cytosolic large ribosomal subunit</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	59	8.4E-37	5.5E0	1.1E-34	9.3E-35
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">ribosome</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	97	1.3E-35	3.7E0	1.4E-33	1.3E-33
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">structural constituent of ribosome</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	107	3.5E-27	2.9E0	3.2E-25	2.9E-25
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">translation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	116	8.8E-27	2.7E0	3.7E-24	3.5E-24
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">cytosolic small ribosomal subunit</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	35	1.9E-17	4.6E0	1.2E-15	1.0E-15
Annotation Cluster 5		Enrichment Score: 36.85	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR

Annotation Cluster 1		Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Ubl conjugation pathway</a>	<a href="#">RT</a>		269	3.8E-59	2.7E0	1.0E-57	7.8E-58
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Ubiquitin mediated proteolysis</a>	<a href="#">RT</a>		107	2.3E-50	4.1E0	5.7E-48	2.6E-48
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ubiquitin-protein transferase activity</a>	<a href="#">RT</a>		168	1.1E-46	3.0E0	1.5E-44	1.4E-44
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein ubiquitination</a>	<a href="#">RT</a>		147	2.1E-27	2.4E0	9.6E-25	9.1E-25
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ubiquitin protein ligase activity</a>	<a href="#">RT</a>		92	2.9E-24	2.9E0	2.3E-22	2.1E-22
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ligase activity</a>	<a href="#">RT</a>		104	1.4E-17	2.3E0	7.3E-16	6.5E-16
Annotation Cluster 6		Enrichment Score: 32.06			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Leucine-rich repeat, typical subtype</a>	<a href="#">RT</a>		144	1.1E-80	5.0E0	3.7E-78	3.4E-78
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 5	<a href="#">RT</a>		151	8.9E-69	4.5E0	2.1E-66	2.0E-66
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 4	<a href="#">RT</a>		158	4.2E-67	4.2E0	8.9E-65	8.6E-65
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 7	<a href="#">RT</a>		128	8.2E-67	5.0E0	1.7E-64	1.6E-64
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 6	<a href="#">RT</a>		140	8.7E-66	4.6E0	1.7E-63	1.7E-63
<input type="checkbox"/>	INTERPRO	<a href="#">Leucine-rich repeat</a>	<a href="#">RT</a>		165	3.4E-65	3.9E0	7.6E-63	7.0E-63
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Leucine-rich repeat</a>	<a href="#">RT</a>		174	6.5E-65	3.8E0	1.9E-63	1.5E-63
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 3	<a href="#">RT</a>		167	7.9E-61	3.8E0	1.5E-58	1.5E-58
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 1	<a href="#">RT</a>		170	2.8E-58	3.6E0	4.8E-56	4.7E-56
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 2	<a href="#">RT</a>		170	5.0E-58	3.6E0	8.5E-56	8.2E-56
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 8	<a href="#">RT</a>		108	1.4E-56	5.0E0	2.4E-54	2.3E-54
<input type="checkbox"/>	SMART	<a href="#">LRR_TYP</a>	<a href="#">RT</a>		144	2.5E-56	3.3E0	3.9E-54	3.5E-54
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 9	<a href="#">RT</a>		98	1.8E-51	5.0E0	2.8E-49	2.7E-49
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 10	<a href="#">RT</a>		84	1.5E-43	4.9E0	2.1E-41	2.0E-41
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 11	<a href="#">RT</a>		73	9.0E-38	4.9E0	1.2E-35	1.1E-35
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 12	<a href="#">RT</a>		66	8.7E-35	5.0E0	1.0E-32	9.7E-33
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 13	<a href="#">RT</a>		53	1.0E-26	4.8E0	1.1E-24	1.0E-24
<input type="checkbox"/>	INTERPRO	<a href="#">Cysteine-rich flanking region, C-terminal</a>	<a href="#">RT</a>		58	1.2E-26	4.3E0	1.2E-24	1.1E-24
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 14	<a href="#">RT</a>		43	4.2E-22	4.9E0	4.1E-20	3.9E-20
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 15	<a href="#">RT</a>		37	2.5E-19	4.9E0	2.3E-17	2.2E-17
<input type="checkbox"/>	SMART	<a href="#">LRRCT</a>	<a href="#">RT</a>		58	1.7E-17	2.9E0	7.3E-16	6.5E-16
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 16	<a href="#">RT</a>		32	2.3E-16	4.8E0	1.9E-14	1.8E-14
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 17	<a href="#">RT</a>		28	6.5E-16	5.3E0	5.0E-14	4.8E-14
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 18	<a href="#">RT</a>		20	9.4E-11	5.0E0	6.1E-9	5.9E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 19	<a href="#">RT</a>		19	1.6E-10	5.2E0	1.0E-8	9.9E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 20	<a href="#">RT</a>		18	2.7E-10	5.3E0	1.7E-8	1.6E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 21	<a href="#">RT</a>		14	5.9E-8	5.3E0	3.1E-6	3.0E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 22	<a href="#">RT</a>		10	4.5E-6	5.7E0	1.9E-4	1.9E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 23	<a href="#">RT</a>		8	1.2E-4	5.5E0	3.7E-3	3.6E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 24	<a href="#">RT</a>		6	1.1E-3	5.8E0	3.1E-2	3.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 25	<a href="#">RT</a>		5	5.4E-3	5.7E0	1.3E-1	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of interferon-alpha biosynthetic process</a>	<a href="#">RT</a>		4	1.7E-2	5.9E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of interferon-beta biosynthetic process</a>	<a href="#">RT</a>		5	1.8E-2	4.2E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 26	<a href="#">RT</a>		4	2.5E-2	5.5E0	4.8E-1	4.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 27	<a href="#">RT</a>		3	1.1E-1	5.1E0	1.0E0	9.7E-1
Annotation Cluster 7		Enrichment Score: 30.14			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SCAN box	<a href="#">RT</a>		53	2.3E-35	6.0E0	2.7E-33	2.6E-33
<input type="checkbox"/>	INTERPRO	<a href="#">Transcription regulator SCAN</a>	<a href="#">RT</a>		54	7.8E-35	5.6E0	9.8E-33	9.0E-33
<input type="checkbox"/>	INTERPRO	<a href="#">Retrovirus capsid, C-terminal</a>	<a href="#">RT</a>		54	2.8E-28	4.8E0	3.2E-26	2.9E-26

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	<a href="#">SCAN</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	53	5.7E-25	3.7E0	4.4E-23	3.9E-23
Annotation Cluster 8		Enrichment Score: 25.16	<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	<a href="#">mRNA splicing, via spliceosome</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	132	3.9E-46	3.5E0	3.3E-43	3.1E-43
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Spliceosome</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	88	3.7E-32	3.5E0	2.2E-30	1.0E-30
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Spliceosome</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	77	4.5E-32	4.2E0	7.1E-31	5.5E-31
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">catalytic step 2 spliceosome</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	60	9.7E-26	4.1E0	9.6E-24	8.3E-24
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">mRNA splicing</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	105	4.3E-24	2.8E0	6.2E-23	4.8E-23
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">mRNA processing</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	121	4.5E-23	2.5E0	6.2E-22	4.8E-22
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">spliceosomal complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	52	6.1E-18	3.5E0	4.1E-16	3.6E-16
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">RNA splicing</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	52	7.0E-6	1.9E0	3.1E-4	3.0E-4
Annotation Cluster 9		Enrichment Score: 21.2	<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	<a href="#">Helicase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	94	2.3E-43	4.5E0	5.2E-42	4.0E-42
<input type="checkbox"/>	INTERPRO	<a href="#">Helicase, superfamily 1/2, ATP-binding domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	77	2.2E-35	4.3E0	3.1E-33	2.8E-33
<input type="checkbox"/>	INTERPRO	<a href="#">Helicase, C-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	76	3.5E-35	4.4E0	4.7E-33	4.3E-33
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Helicase C-terminal	<a href="#">RT</a>	<div><div></div><div></div></div>	73	1.0E-34	4.6E0	1.1E-32	1.1E-32
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Helicase ATP-binding	<a href="#">RT</a>	<div><div></div><div></div></div>	74	2.0E-33	4.4E0	2.2E-31	2.1E-31
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">helicase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	57	5.5E-24	4.0E0	4.1E-22	3.7E-22
<input type="checkbox"/>	SMART	<a href="#">DEXDc</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	76	1.2E-22	2.8E0	7.6E-21	6.8E-21
<input type="checkbox"/>	SMART	<a href="#">HELICc</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	75	1.4E-22	2.9E0	7.9E-21	7.1E-21
<input type="checkbox"/>	INTERPRO	<a href="#">DNA/RNA helicase, DEAD/DEAH box type, N-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	46	5.9E-20	4.1E0	5.4E-18	4.9E-18
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ATP-dependent RNA helicase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	43	7.2E-18	3.9E0	4.0E-16	3.5E-16
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:DEAH box	<a href="#">RT</a>	<div><div></div><div></div></div>	32	3.0E-17	5.1E0	2.5E-15	2.4E-15
<input type="checkbox"/>	INTERPRO	<a href="#">SNF2-related</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	26	1.5E-14	5.0E0	9.1E-13	8.3E-13
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">RNA secondary structure unwinding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	29	5.0E-12	3.9E0	6.3E-10	6.0E-10
<input type="checkbox"/>	INTERPRO	<a href="#">RNA helicase, DEAD-box type, Q motif</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	25	3.6E-11	4.2E0	1.5E-9	1.4E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Q motif	<a href="#">RT</a>	<div><div></div><div></div></div>	24	4.3E-10	4.1E0	2.6E-8	2.5E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:DEAD box	<a href="#">RT</a>	<div><div></div><div></div></div>	22	1.7E-9	4.2E0	1.0E-7	9.8E-8
<input type="checkbox"/>	INTERPRO	<a href="#">RNA helicase, ATP-dependent, DEAD-box, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	19	5.6E-9	4.4E0	1.8E-7	1.7E-7
Annotation Cluster 10		Enrichment Score: 19.83	<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	<a href="#">Cell cycle</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	216	6.2E-34	2.3E0	1.0E-32	8.1E-33
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Cell division</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	132	5.3E-22	2.3E0	7.0E-21	5.4E-21
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cell division</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	124	3.3E-17	2.1E0	6.9E-15	6.6E-15
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Mitosis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	92	2.4E-16	2.4E0	2.7E-15	2.1E-15
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitotic nuclear division</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	90	2.8E-13	2.2E0	4.1E-11	3.9E-11
Annotation Cluster 11		Enrichment Score: 19.26	<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	active site:Glycyl thioester intermediate	<a href="#">RT</a>	<div><div></div><div></div></div>	60	8.0E-38	5.8E0	1.1E-35	1.0E-35
<input type="checkbox"/>	INTERPRO	<a href="#">Ubiquitin-conjugating enzyme, active site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	26	3.1E-19	6.2E0	2.6E-17	2.4E-17
<input type="checkbox"/>	INTERPRO	<a href="#">Ubiquitin-conjugating enzyme, E2</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	34	5.7E-19	5.0E0	4.6E-17	4.2E-17
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ubiquitin conjugating enzyme activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	26	4.2E-16	5.3E0	2.1E-14	1.9E-14
<input type="checkbox"/>	INTERPRO	<a href="#">Ubiquitin-conjugating enzyme/RWD-like</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	37	7.1E-16	4.1E0	4.9E-14	4.5E-14
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein K48-linked ubiquitination</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	30	6.5E-12	3.8E0	7.9E-10	7.6E-10
Annotation Cluster 12		Enrichment Score: 18.73	<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	active site:Glycyl thioester intermediate	<a href="#">RT</a>	<div><div></div><div></div></div>	60	8.0E-38	5.8E0	1.1E-35	1.0E-35
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HECT	<a href="#">RT</a>	<div><div></div><div></div></div>	24	2.9E-15	5.8E0	2.2E-13	2.2E-13
<input type="checkbox"/>	INTERPRO	<a href="#">HECT</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	24	2.4E-14	5.3E0	1.4E-12	1.3E-12
<input type="checkbox"/>	SMART	<a href="#">HECTc</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	24	2.2E-10	3.5E0	7.1E-9	6.4E-9






Annotation Cluster 1		Enrichment Score: ?	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 13		Enrichment Score: 18	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Tyrosine-protein kinase</a>	<a href="#">RT</a>	<div></div>	81	3.5E-42	5.0E0	7.6E-41	5.9E-41
<input type="checkbox"/>	INTERPRO	<a href="#">Serine-threonine/tyrosine-protein kinase catalytic domain</a>	<a href="#">RT</a>	<div></div>	95	8.1E-42	4.2E0	1.4E-39	1.3E-39
<input type="checkbox"/>	INTERPRO	<a href="#">Tyrosine-protein kinase, catalytic domain</a>	<a href="#">RT</a>	<div></div>	68	2.3E-37	5.0E0	3.5E-35	3.2E-35
<input type="checkbox"/>	INTERPRO	<a href="#">Tyrosine-protein kinase, active site</a>	<a href="#">RT</a>	<div></div>	69	2.5E-33	4.5E0	3.0E-31	2.7E-31
<input type="checkbox"/>	SMART	<a href="#">TyrKc</a>	<a href="#">RT</a>	<div></div>	68	5.1E-26	3.3E0	4.8E-24	4.3E-24
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein tyrosine kinase activity</a>	<a href="#">RT</a>	<div></div>	76	2.2E-25	3.4E0	1.9E-23	1.7E-23
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein autophosphorylation</a>	<a href="#">RT</a>	<div></div>	88	1.5E-24	3.0E0	5.8E-22	5.5E-22
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">peptidyl-tyrosine phosphorylation</a>	<a href="#">RT</a>	<div></div>	79	1.9E-22	3.1E0	7.1E-20	6.7E-20
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">non-membrane spanning protein tyrosine kinase activity</a>	<a href="#">RT</a>	<div></div>	34	2.1E-16	4.4E0	1.1E-14	9.4E-15
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">peptidyl-tyrosine autophosphorylation</a>	<a href="#">RT</a>	<div></div>	31	7.6E-16	4.6E0	1.5E-13	1.4E-13
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">transmembrane receptor protein tyrosine kinase activity</a>	<a href="#">RT</a>	<div></div>	25	1.9E-10	3.9E0	6.0E-9	5.4E-9
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">extrinsic component of cytoplasmic side of plasma membrane</a>	<a href="#">RT</a>	<div></div>	34	2.4E-10	3.2E0	9.6E-9	8.4E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">transmembrane receptor protein tyrosine kinase signaling pathway</a>	<a href="#">RT</a>	<div></div>	42	2.2E-9	2.6E0	1.9E-7	1.8E-7
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">SH2 domain</a>	<a href="#">RT</a>	<div></div>	37	7.2E-7	2.4E0	5.0E-6	3.9E-6
<input type="checkbox"/>	INTERPRO	<a href="#">SH2 domain</a>	<a href="#">RT</a>	<div></div>	39	3.6E-6	2.1E0	7.7E-5	7.1E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2	<a href="#">RT</a>	<div></div>	31	2.9E-5	2.2E0	1.0E-3	1.0E-3
<input type="checkbox"/>	SMART	<a href="#">SH2</a>	<a href="#">RT</a>	<div></div>	36	1.9E-2	1.4E0	1.5E-1	1.3E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">receptor binding</a>	<a href="#">RT</a>	<div></div>	47	9.8E-1	7.9E-1	1.0E0	9.8E-1
Annotation Cluster 14		Enrichment Score: 17.62	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">GTP-binding</a>	<a href="#">RT</a>	<div></div>	149	3.1E-38	3.0E0	5.9E-37	4.5E-37
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	<a href="#">RT</a>	<div></div>	137	8.1E-36	3.0E0	1.0E-33	9.6E-34
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">GTP binding</a>	<a href="#">RT</a>	<div></div>	159	1.5E-30	2.5E0	1.6E-28	1.5E-28
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">GTPase activity</a>	<a href="#">RT</a>	<div></div>	111	2.0E-27	2.8E0	2.0E-25	1.8E-25
<input type="checkbox"/>	INTERPRO	<a href="#">Small GTP-binding protein domain</a>	<a href="#">RT</a>	<div></div>	78	5.4E-20	2.9E0	5.1E-18	4.7E-18
<input type="checkbox"/>	INTERPRO	<a href="#">Small GTPase superfamily, Ras type</a>	<a href="#">RT</a>	<div></div>	33	1.7E-19	5.2E0	1.5E-17	1.4E-17
<input type="checkbox"/>	INTERPRO	<a href="#">Small GTPase superfamily</a>	<a href="#">RT</a>	<div></div>	62	8.3E-15	2.8E0	5.2E-13	4.8E-13
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">small GTPase mediated signal transduction</a>	<a href="#">RT</a>	<div></div>	85	2.6E-11	2.0E0	3.0E-9	2.9E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Effector region	<a href="#">RT</a>	<div></div>	41	7.7E-10	2.8E0	4.6E-8	4.5E-8
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Prenylation</a>	<a href="#">RT</a>	<div></div>	49	2.0E-6	2.0E0	1.3E-5	1.0E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	lipid moiety-binding region:S-geranylgeranyl cysteine	<a href="#">RT</a>	<div></div>	28	3.2E-3	1.8E0	8.3E-2	8.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	propeptide:Removed in mature form	<a href="#">RT</a>	<div></div>	51	4.6E-3	1.5E0	1.2E-1	1.1E-1
Annotation Cluster 15		Enrichment Score: 17.43	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 19	<a href="#">RT</a>	<div></div>	50	1.5E-35	6.3E0	1.8E-33	1.7E-33
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 20	<a href="#">RT</a>	<div></div>	32	2.2E-21	6.1E0	2.1E-19	2.0E-19
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 21	<a href="#">RT</a>	<div></div>	24	1.0E-16	6.3E0	8.4E-15	8.1E-15
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 22	<a href="#">RT</a>	<div></div>	23	6.2E-16	6.3E0	4.9E-14	4.7E-14
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 23	<a href="#">RT</a>	<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	<a href="#">RT</a>	<div></div>	13	6.7E-9	6.3E0	3.7E-7	3.6E-7
Annotation Cluster 16		Enrichment Score: 15.74	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Protein phosphatase</a>	<a href="#">RT</a>	<div></div>	67	7.7E-22	3.5E0	9.8E-21	7.6E-21
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein dephosphorylation</a>	<a href="#">RT</a>	<div></div>	58	8.5E-14	2.7E0	1.3E-11	1.3E-11
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein serine/threonine phosphatase activity</a>	<a href="#">RT</a>	<div></div>	36	9.2E-14	3.7E0	3.9E-12	3.5E-12
Annotation Cluster 17		Enrichment Score: 15.13	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">DNA repair</a>	<a href="#">RT</a>	<div></div>	104	5.2E-19	2.4E0	6.1E-18	4.7E-18
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">DNA damage</a>	<a href="#">RT</a>	<div></div>	115	8.6E-18	2.2E0	9.7E-17	7.5E-17
















































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">DNA repair</a>	RT		81	9.3E-11	2.0E0	1.0E-8	9.5E-9
Annotation Cluster 18		Enrichment Score: 15.12	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BTB	RT		71	3.2E-22	3.4E0	3.1E-20	3.0E-20
<input type="checkbox"/>	INTERPRO	<a href="#">BTB/POZ-like</a>	RT		77	4.5E-17	2.7E0	3.4E-15	3.1E-15
<input type="checkbox"/>	INTERPRO	<a href="#">BTB/POZ fold</a>	RT		79	1.2E-16	2.6E0	8.5E-15	7.8E-15
<input type="checkbox"/>	SMART	<a href="#">BTB</a>	RT		75	1.9E-7	1.7E0	4.0E-6	3.6E-6
Annotation Cluster 19		Enrichment Score: 13.83	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein K11-linked ubiquitination</a>	RT		27	1.6E-19	5.9E0	4.3E-17	4.1E-17
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">anaphase-promoting complex</a>	RT		20	2.4E-12	5.5E0	1.1E-10	9.8E-11
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle</a>	RT		20	8.6E-12	5.2E0	1.0E-9	9.8E-10
Annotation Cluster 20		Enrichment Score: 13.04	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Actin-related protein</a>	RT		30	1.1E-18	5.5E0	8.5E-17	7.7E-17
<input type="checkbox"/>	SMART	<a href="#">ACTIN</a>	RT		30	2.4E-14	3.7E0	8.5E-13	7.7E-13
<input type="checkbox"/>	INTERPRO	<a href="#">Actin/actin-like conserved site</a>	RT		19	4.2E-12	5.6E0	2.1E-10	1.9E-10
<input type="checkbox"/>	INTERPRO	<a href="#">Actin, conserved site</a>	RT		16	6.3E-10	5.5E0	2.2E-8	2.0E-8
Annotation Cluster 21		Enrichment Score: 11.05	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">proteasome-mediated ubiquitin-dependent protein catabolic process</a>	RT		105	1.1E-29	3.1E0	5.3E-27	5.0E-27
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">anaphase-promoting complex-dependent catabolic process</a>	RT		53	3.2E-22	4.0E0	1.0E-19	9.9E-20
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition</a>	RT		50	1.9E-20	3.9E0	6.0E-18	5.7E-18
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle</a>	RT		47	2.1E-19	3.9E0	5.4E-17	5.1E-17
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">stimulatory C-type lectin receptor signaling pathway</a>	RT		57	1.1E-17	3.2E0	2.5E-15	2.4E-15
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">T cell receptor signaling pathway</a>	RT		64	1.4E-13	2.6E0	2.0E-11	1.9E-11
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">NIK/NF-kappaB signaling</a>	RT		38	5.4E-13	3.4E0	7.4E-11	7.0E-11
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle</a>	RT		20	8.6E-12	5.2E0	1.0E-9	9.8E-10
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">Fc-epsilon receptor signaling pathway</a>	RT		68	2.1E-11	2.3E0	2.5E-9	2.4E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of canonical Wnt signaling pathway</a>	RT		50	4.0E-10	2.5E0	4.0E-8	3.8E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of mRNA stability</a>	RT		44	2.1E-9	2.5E0	1.9E-7	1.8E-7
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">proteasome complex</a>	RT		28	7.6E-8	3.0E0	2.2E-6	2.0E-6
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Proteasome</a>	RT		25	7.9E-8	3.2E0	6.1E-7	4.7E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of canonical Wnt signaling pathway</a>	RT		53	1.7E-6	1.9E0	9.0E-5	8.6E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">Wnt signaling pathway, planar cell polarity pathway</a>	RT		34	8.4E-6	2.2E0	3.6E-4	3.4E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of cellular amino acid metabolic process</a>	RT		23	9.3E-6	2.7E0	3.9E-4	3.7E-4
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Proteasome</a>	RT		21	5.9E-5	2.5E0	1.5E-4	7.0E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent</a>	RT		21	2.7E-3	2.0E0	5.3E-2	5.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">tumor necrosis factor-mediated signaling pathway</a>	RT		32	6.3E-3	1.6E0	1.0E-1	1.0E-1
Annotation Cluster 22		Enrichment Score: 11.02	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">T cell receptor signaling pathway</a>	RT		64	2.9E-22	3.3E0	6.4E-21	2.9E-21
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Prostate cancer</a>	RT		59	4.8E-22	3.5E0	9.2E-21	4.2E-21
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Pancreatic cancer</a>	RT		43	8.7E-16	3.5E0	1.2E-14	5.4E-15
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Acute myeloid leukemia</a>	RT		38	1.6E-14	3.5E0	1.9E-13	8.5E-14
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Chronic myeloid leukemia</a>	RT		44	2.4E-14	3.2E0	2.7E-13	1.2E-13
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Endometrial cancer</a>	RT		36	3.5E-14	3.6E0	3.3E-13	1.5E-13
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">ErbB signaling pathway</a>	RT		49	5.3E-14	2.9E0	4.8E-13	2.2E-13
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Glioma</a>	RT		40	3.2E-13	3.2E0	2.8E-12	1.3E-12
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">VEGF signaling pathway</a>	RT		38	8.2E-13	3.3E0	6.7E-12	3.1E-12

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Prolactin signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	41	2.8E-12	3.0E0	2.1E-11	9.8E-12
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">B cell receptor signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	40	4.6E-12	3.0E0	3.4E-11	1.5E-11
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Renal cell carcinoma</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	38	2.3E-11	3.0E0	1.5E-10	7.1E-11
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Non-small cell lung cancer</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	34	4.4E-11	3.2E0	2.8E-10	1.3E-10
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Fc epsilon RI signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	38	7.4E-11	2.9E0	4.6E-10	2.1E-10
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Melanoma</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	37	1.8E-9	2.7E0	9.2E-9	4.2E-9
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Sphingolipid signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	52	2.5E-9	2.3E0	1.1E-8	5.2E-9
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Bladder cancer</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	25	2.5E-8	3.2E0	1.0E-7	4.6E-8
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Osteoclast differentiation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	53	2.9E-8	2.1E0	1.1E-7	5.1E-8
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Central carbon metabolism in cancer</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	32	9.6E-8	2.6E0	3.6E-7	1.6E-7
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Choline metabolism in cancer</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	40	3.5E-6	2.1E0	1.1E-5	4.8E-6
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Thyroid cancer</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	8.0E-5	2.9E0	2.0E-4	9.1E-5
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Natural killer cell mediated cytotoxicity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	38	1.8E-3	1.6E0	3.8E-3	1.8E-3
Annotation Cluster 23		Enrichment Score: 10.73	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	lipid moiety-binding region:N-myristoyl glycine	<a href="#">RT</a>	<div><div></div><div></div></div>	56	3.6E-17	3.3E0	3.0E-15	2.9E-15
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Myristate</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	72	2.6E-14	2.5E0	2.6E-13	2.0E-13
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Lipoprotein</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	151	6.9E-3	1.2E0	3.1E-2	2.4E-2
Annotation Cluster 24		Enrichment Score: 10.49	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase, C-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	24	3.5E-13	5.0E0	2.0E-11	1.9E-11
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:AGC-kinase C-terminal	<a href="#">RT</a>	<div><div></div><div></div></div>	32	1.6E-12	3.9E0	1.1E-10	1.1E-10
<input type="checkbox"/>	INTERPRO	<a href="#">AGC-kinase, C-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	32	2.0E-11	3.5E0	8.8E-10	8.1E-10
<input type="checkbox"/>	SMART	<a href="#">S_TK_X</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	31	9.4E-8	2.5E0	2.2E-6	1.9E-6
Annotation Cluster 25		Enrichment Score: 9.8	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of protein kinase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	53	4.8E-16	3.2E0	9.4E-14	8.9E-14
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein kinase inhibitor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	32	3.8E-12	3.7E0	1.4E-10	1.3E-10
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of JAK-STAT cascade</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	25	9.8E-10	3.7E0	9.5E-8	9.0E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cytokine-mediated signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	39	3.6E-4	1.8E0	9.7E-3	9.2E-3
Annotation Cluster 26		Enrichment Score: 9.57	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">SCF ubiquitin ligase complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	31	1.3E-12	3.9E0	6.5E-11	5.7E-11
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:F-box	<a href="#">RT</a>	<div><div></div><div></div></div>	37	2.6E-12	3.5E0	1.8E-10	1.8E-10
<input type="checkbox"/>	INTERPRO	<a href="#">F-box domain, cyclin-like</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	38	1.4E-11	3.2E0	6.4E-10	5.8E-10
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">SCF-dependent proteasomal ubiquitin-dependent protein catabolic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	18	7.2E-9	4.4E0	6.0E-7	5.7E-7
<input type="checkbox"/>	SMART	<a href="#">FBOX</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	24	4.5E-6	2.5E0	7.0E-5	6.3E-5
Annotation Cluster 27		Enrichment Score: 8.89	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 3	<a href="#">RT</a>	<div><div></div><div></div></div>	58	5.3E-24	4.1E0	5.5E-22	5.3E-22
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 4	<a href="#">RT</a>	<div><div></div><div></div></div>	36	2.6E-14	4.0E0	2.0E-12	1.9E-12
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 2	<a href="#">RT</a>	<div><div></div><div></div></div>	69	7.7E-14	2.5E0	5.7E-12	5.5E-12
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 1	<a href="#">RT</a>	<div><div></div><div></div></div>	65	9.4E-12	2.4E0	6.5E-10	6.3E-10
<input type="checkbox"/>	UP_SEQ_FEATURE	calcium-binding region:3	<a href="#">RT</a>	<div><div></div><div></div></div>	25	2.4E-11	4.4E0	1.6E-9	1.6E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	calcium-binding region:1	<a href="#">RT</a>	<div><div></div><div></div></div>	49	1.5E-10	2.6E0	9.9E-9	9.6E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	calcium-binding region:2	<a href="#">RT</a>	<div><div></div><div></div></div>	45	1.1E-9	2.6E0	6.4E-8	6.2E-8
<input type="checkbox"/>	INTERPRO	<a href="#">EF-hand domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	72	1.1E-8	2.0E0	3.6E-7	3.3E-7
<input type="checkbox"/>	INTERPRO	<a href="#">EF-Hand 1, calcium-binding site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	60	1.5E-8	2.1E0	4.8E-7	4.4E-7
<input type="checkbox"/>	INTERPRO	<a href="#">EF-hand-like domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	82	3.6E-8	1.8E0	1.0E-6	9.5E-7
<input type="checkbox"/>	SMART	<a href="#">EFh</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	64	2.8E-7	1.8E0	5.4E-6	4.9E-6
<input type="checkbox"/>	COG_ONTOLOGY	<a href="#">Signal transduction mechanisms / Cytoskeleton / Cell division and chromosome partitioning / General function prediction only</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	31	5.8E-5	1.8E0	9.0E-4	9.0E-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"/>	GOTERM_MF_DIRECT	<a href="#">calcium ion binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	101	9.8E-1	8.4E-1	1.0E0	9.8E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Calcium</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	95	1.0E0	7.4E-1	1.0E0	1.0E0
Annotation Cluster 28		Enrichment Score: 8.81	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Viral nucleoprotein</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	21	1.7E-11	5.1E0	1.5E-10	1.2E-10
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">viral nucleocapsid</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	21	6.9E-11	4.8E0	2.9E-9	2.6E-9
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Virion</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	21	3.2E-6	3.1E0	2.0E-5	1.6E-5
Annotation Cluster 29		Enrichment Score: 8.51	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Myosin</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	44	1.5E-28	5.9E0	2.3E-27	1.8E-27
<input type="checkbox"/>	INTERPRO	<a href="#">Myosin head, motor domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	34	3.4E-20	5.3E0	3.3E-18	3.0E-18
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">myosin complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	38	6.1E-20	4.8E0	4.9E-18	4.3E-18
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Myosin head-like	<a href="#">RT</a>	<div><div></div><div></div></div>	31	3.0E-19	5.7E0	2.7E-17	2.6E-17
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Motor protein</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	63	1.8E-18	3.2E0	2.1E-17	1.6E-17
<input type="checkbox"/>	SMART	<a href="#">MYSc</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	34	1.7E-14	3.5E0	6.5E-13	5.9E-13
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">motor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	37	2.8E-12	3.3E0	1.1E-10	9.6E-11
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Muscle protein</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	33	7.2E-12	3.7E0	6.8E-11	5.3E-11
<input type="checkbox"/>	INTERPRO	<a href="#">IQ motif, EF-hand binding site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	42	1.2E-11	3.0E0	6.0E-10	5.5E-10
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">microfilament motor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	18	4.2E-11	5.4E0	1.5E-9	1.3E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Actin-binding	<a href="#">RT</a>	<div><div></div><div></div></div>	21	5.3E-11	4.9E0	3.6E-9	3.4E-9
<input type="checkbox"/>	INTERPRO	<a href="#">Myosin, N-terminal, SH3-like</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	1.0E-10	6.2E0	4.1E-9	3.8E-9
<input type="checkbox"/>	INTERPRO	<a href="#">Myosin-like IQ motif-containing domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	1.2E-10	5.5E0	4.8E-9	4.4E-9
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">muscle myosin complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	4.8E-10	6.0E0	1.7E-8	1.5E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ	<a href="#">RT</a>	<div><div></div><div></div></div>	28	2.7E-8	3.1E0	1.5E-6	1.4E-6
<input type="checkbox"/>	INTERPRO	<a href="#">Myosin tail</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	4.1E-8	4.9E0	1.1E-6	1.0E-6
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Calmodulin-binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	49	7.4E-8	2.2E0	5.8E-7	4.5E-7
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">myosin filament</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	2.9E-6	4.8E0	6.4E-5	5.6E-5
<input type="checkbox"/>	SMART	<a href="#">IQ</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	28	1.8E-5	2.2E0	2.5E-4	2.3E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 1	<a href="#">RT</a>	<div><div></div><div></div></div>	16	2.3E-5	3.3E0	8.4E-4	8.1E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 2	<a href="#">RT</a>	<div><div></div><div></div></div>	16	2.3E-5	3.3E0	8.4E-4	8.1E-4
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Thick filament</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	3.1E-5	4.4E0	1.8E-4	1.4E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">calmodulin binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	54	6.6E-5	1.7E0	9.9E-4	8.8E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 3	<a href="#">RT</a>	<div><div></div><div></div></div>	12	9.8E-5	3.7E0	3.2E-3	3.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">actin filament-based movement</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.1E-4	3.8E0	3.5E-3	3.3E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 4	<a href="#">RT</a>	<div><div></div><div></div></div>	9	5.2E-4	4.1E0	1.5E-2	1.5E-2
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Actin-binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	60	1.1E-3	1.5E0	5.5E-3	4.3E-3
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Tight junction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	28	5.0E-3	1.7E0	1.0E-2	5.0E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 5	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.4E-2	3.7E0	2.9E-1	2.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">muscle contraction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	28	1.8E-2	1.6E0	2.3E-1	2.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">actin binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	59	4.1E-2	1.3E0	2.5E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 6	<a href="#">RT</a>	<div><div></div><div></div></div>	3	3.3E-1	2.6E0	1.0E0	9.7E-1
Annotation Cluster 30		Enrichment Score: 8.4	<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:DEAH box	<a href="#">RT</a>	<div><div></div><div></div></div>	32	3.0E-17	5.1E0	2.5E-15	2.4E-15
<input type="checkbox"/>	INTERPRO	<a href="#">Domain of unknown function DUF1605</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	3.3E-9	5.5E0	1.1E-7	1.0E-7
<input type="checkbox"/>	INTERPRO	<a href="#">Helicase-associated domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	1.3E-8	5.2E0	4.0E-7	3.7E-7
<input type="checkbox"/>	INTERPRO	<a href="#">DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	6.9E-8	4.5E0	1.8E-6	1.7E-6
<input type="checkbox"/>	SMART	<a href="#">SM00847</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	3.0E-6	3.4E0	4.9E-5	4.4E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ATP-dependent helicase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	1.6E-5	3.3E0	2.9E-4	2.6E-4
Annotation Cluster 31		Enrichment Score: 8.12	<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>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 6	<a href="#">RT</a>	<div><div></div></div>	85	7.5E-55	5.8E0	1.2E-52	1.1E-52
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 7	<a href="#">RT</a>	<div><div></div></div>	56	1.0E-37	6.1E0	1.3E-35	1.3E-35
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 8	<a href="#">RT</a>	<div><div></div></div>	41	1.3E-27	6.1E0	1.4E-25	1.4E-25
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 9	<a href="#">RT</a>	<div><div></div></div>	36	9.9E-24	6.0E0	1.0E-21	9.7E-22
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 10	<a href="#">RT</a>	<div><div></div></div>	26	1.7E-17	6.1E0	1.4E-15	1.4E-15
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 11	<a href="#">RT</a>	<div><div></div></div>	23	6.2E-16	6.3E0	4.9E-14	4.7E-14
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 12	<a href="#">RT</a>	<div><div></div></div>	16	1.6E-10	6.1E0	1.0E-8	9.9E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 13	<a href="#">RT</a>	<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	<a href="#">RT</a>	<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	<a href="#">RT</a>	<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	<a href="#">RT</a>	<div><div></div></div>	11	8.5E-7	5.8E0	4.1E-5	3.9E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 17	<a href="#">RT</a>	<div><div></div></div>	10	4.5E-6	5.7E0	1.9E-4	1.9E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 18	<a href="#">RT</a>	<div><div></div></div>	10	4.5E-6	5.7E0	1.9E-4	1.9E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 19	<a href="#">RT</a>	<div><div></div></div>	10	4.5E-6	5.7E0	1.9E-4	1.9E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 20	<a href="#">RT</a>	<div><div></div></div>	9	2.3E-5	5.6E0	8.4E-4	8.2E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 21	<a href="#">RT</a>	<div><div></div></div>	9	2.3E-5	5.6E0	8.4E-4	8.2E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 22	<a href="#">RT</a>	<div><div></div></div>	8	1.2E-4	5.5E0	3.7E-3	3.6E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 23	<a href="#">RT</a>	<div><div></div></div>	8	1.2E-4	5.5E0	3.7E-3	3.6E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 24	<a href="#">RT</a>	<div><div></div></div>	6	2.6E-3	5.1E0	6.6E-2	6.4E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Death domain</a>	<a href="#">RT</a>	<div><div></div></div>	13	6.6E-3	2.3E0	6.8E-2	6.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Death	<a href="#">RT</a>	<div><div></div></div>	12	9.3E-3	2.3E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 25	<a href="#">RT</a>	<div><div></div></div>	5	1.1E-2	4.9E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 26	<a href="#">RT</a>	<div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 27	<a href="#">RT</a>	<div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Death-like domain</a>	<a href="#">RT</a>	<div><div></div></div>	21	1.1E-1	1.4E0	6.0E-1	5.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein targeting to plasma membrane</a>	<a href="#">RT</a>	<div><div></div></div>	8	1.3E-1	1.8E0	8.1E-1	7.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">spectrin binding</a>	<a href="#">RT</a>	<div><div></div></div>	7	2.6E-1	1.6E0	9.5E-1	8.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">ZU5</a>	<a href="#">RT</a>	<div><div></div></div>	4	3.0E-1	2.1E0	9.8E-1	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:ZU5	<a href="#">RT</a>	<div><div></div></div>	3	3.9E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">DEATH</a>	<a href="#">RT</a>	<div><div></div></div>	8	5.1E-1	1.2E0	1.0E0	9.0E-1
<input type="checkbox"/>	SMART	<a href="#">ZU5</a>	<a href="#">RT</a>	<div><div></div></div>	3	6.9E-1	1.4E0	1.0E0	9.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">cytoskeletal adaptor activity</a>	<a href="#">RT</a>	<div><div></div></div>	3	7.8E-1	1.1E0	1.0E0	8.9E-1
Annotation Cluster 32		Enrichment Score: 7.81	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Chronic myeloid leukemia</a>	<a href="#">RT</a>	<div><div></div></div>	44	2.4E-14	3.2E0	2.7E-13	1.2E-13
<input type="checkbox"/>	BIOCARTA	<a href="#">Influence of Ras and Rho proteins on G1 to S Transition</a>	<a href="#">RT</a>	<div><div></div></div>	21	9.1E-6	2.4E0	2.9E-4	2.0E-4
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Small cell lung cancer</a>	<a href="#">RT</a>	<div><div></div></div>	34	1.7E-5	2.1E0	4.8E-5	2.2E-5
Annotation Cluster 33		Enrichment Score: 7.68	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SET	<a href="#">RT</a>	<div><div></div></div>	35	5.8E-18	4.9E0	5.1E-16	4.9E-16
<input type="checkbox"/>	INTERPRO	<a href="#">SET domain</a>	<a href="#">RT</a>	<div><div></div></div>	36	6.9E-17	4.4E0	5.0E-15	4.6E-15
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">histone-lysine N-methyltransferase activity</a>	<a href="#">RT</a>	<div><div></div></div>	27	5.2E-12	4.1E0	1.9E-10	1.7E-10
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Post-SET	<a href="#">RT</a>	<div><div></div></div>	15	1.9E-10	6.4E0	1.2E-8	1.1E-8
<input type="checkbox"/>	SMART	<a href="#">SET</a>	<a href="#">RT</a>	<div><div></div></div>	29	2.3E-10	3.1E0	7.1E-9	6.4E-9
<input type="checkbox"/>	INTERPRO	<a href="#">Post-SET domain</a>	<a href="#">RT</a>	<div><div></div></div>	14	1.7E-8	5.4E0	5.0E-7	4.6E-7
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">S-adenosyl-L-methionine</a>	<a href="#">RT</a>	<div><div></div></div>	49	5.8E-6	1.9E0	3.6E-5	2.8E-5
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Methyltransferase</a>	<a href="#">RT</a>	<div><div></div></div>	50	5.1E-5	1.8E0	2.9E-4	2.3E-4
<input type="checkbox"/>	SMART	<a href="#">PostSET</a>	<a href="#">RT</a>	<div><div></div></div>	11	1.0E-4	3.5E0	1.3E-3	1.1E-3
















































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Lysine degradation</a>	RT		21	8.8E-4	2.1E0	1.9E-3	8.8E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">histone methyltransferase activity (H3-K4 specific)</a>	RT		10	1.2E-3	3.3E0	1.2E-2	1.1E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">methyltransferase activity</a>	RT		21	1.5E-1	1.3E0	6.3E-1	5.6E-1
Annotation Cluster 34		Enrichment Score: 7.44	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Bromodomain, conserved site</a>	RT		21	1.1E-11	5.0E0	5.6E-10	5.1E-10
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Bromodomain</a>	RT		25	2.0E-11	4.4E0	1.9E-10	1.4E-10
<input type="checkbox"/>	INTERPRO	<a href="#">Bromodomain</a>	RT		25	3.0E-9	3.6E0	1.0E-7	9.5E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Bromo	RT		17	4.5E-7	4.0E0	2.2E-5	2.1E-5
<input type="checkbox"/>	SMART	<a href="#">BROMO</a>	RT		25	6.1E-6	2.4E0	9.1E-5	8.1E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">lysine-acetylated histone binding</a>	RT		10	1.2E-3	3.3E0	1.2E-2	1.1E-2
Annotation Cluster 35		Enrichment Score: 7.23	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">termination of RNA polymerase II transcription</a>	RT		40	2.7E-15	3.7E0	4.8E-13	4.6E-13
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mRNA 3'-end processing</a>	RT		32	1.0E-12	3.8E0	1.3E-10	1.3E-10
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">RNA export from nucleus</a>	RT		26	7.0E-7	2.8E0	4.4E-5	4.2E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mRNA export from nucleus</a>	RT		35	2.3E-5	2.1E0	8.7E-4	8.2E-4
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">mRNA surveillance pathway</a>	RT		35	3.3E-5	2.0E0	8.9E-5	4.1E-5
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">mRNA transport</a>	RT		24	3.0E-2	1.6E0	1.2E-1	9.0E-2
Annotation Cluster 36		Enrichment Score: 7.04	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SOCS box	RT		25	1.1E-11	4.5E0	7.4E-10	7.2E-10
<input type="checkbox"/>	INTERPRO	<a href="#">SOCS protein, C-terminal</a>	RT		25	1.8E-10	4.0E0	7.3E-9	6.6E-9
<input type="checkbox"/>	SMART	<a href="#">SM00969</a>	RT		25	9.5E-7	2.6E0	1.7E-5	1.5E-5
<input type="checkbox"/>	SMART	<a href="#">SOCS</a>	RT		10	3.6E-2	2.0E0	2.4E-1	2.1E-1
Annotation Cluster 37		Enrichment Score: 7.01	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Tubulin/FtsZ, C-terminal</a>	RT		20	3.8E-12	5.4E0	2.0E-10	1.8E-10
<input type="checkbox"/>	INTERPRO	<a href="#">Tubulin, C-terminal</a>	RT		20	3.8E-12	5.4E0	2.0E-10	1.8E-10
<input type="checkbox"/>	INTERPRO	<a href="#">Tubulin, conserved site</a>	RT		20	3.8E-12	5.4E0	2.0E-10	1.8E-10
<input type="checkbox"/>	INTERPRO	<a href="#">Tubulin</a>	RT		20	1.6E-11	5.2E0	7.2E-10	6.6E-10
<input type="checkbox"/>	INTERPRO	<a href="#">Tubulin/FtsZ, 2-layer sandwich domain</a>	RT		19	2.0E-11	5.4E0	8.8E-10	8.1E-10
<input type="checkbox"/>	INTERPRO	<a href="#">Tubulin/FtsZ, GTPase domain</a>	RT		20	5.5E-11	5.0E0	2.3E-9	2.1E-9
<input type="checkbox"/>	SMART	<a href="#">SM00865</a>	RT		19	2.5E-8	3.5E0	6.4E-7	5.7E-7
<input type="checkbox"/>	SMART	<a href="#">SM00864</a>	RT		20	2.7E-8	3.4E0	6.5E-7	5.9E-7
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Pathogenic Escherichia coli infection</a>	RT		26	1.3E-6	2.7E0	4.1E-6	1.9E-6
<input type="checkbox"/>	INTERPRO	<a href="#">Beta tubulin</a>	RT		9	3.5E-6	6.2E0	7.6E-5	7.0E-5
<input type="checkbox"/>	INTERPRO	<a href="#">Beta tubulin, autoregulation binding site</a>	RT		9	3.5E-6	6.2E0	7.6E-5	7.0E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">microtubule-based process</a>	RT		19	4.7E-6	3.1E0	2.3E-4	2.2E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">structural constituent of cytoskeleton</a>	RT		37	3.0E-5	2.0E0	4.9E-4	4.4E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Alpha tubulin</a>	RT		7	3.9E-3	3.9E0	4.1E-2	3.8E-2
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Microtubule</a>	RT		55	1.8E-2	1.3E0	7.3E-2	5.7E-2
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Phagosome</a>	RT		27	7.4E-1	9.4E-1	1.0E0	7.4E-1
Annotation Cluster 38		Enrichment Score: 6.93	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein serine/threonine phosphatase activity</a>	RT		36	9.2E-14	3.7E0	3.9E-12	3.5E-12
<input type="checkbox"/>	INTERPRO	<a href="#">Protein phosphatase 2C (PP2C)-like</a>	RT		17	5.1E-10	5.3E0	2.0E-8	1.8E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Manganese 1; via carbonyl oxygen	RT		13	1.1E-9	6.8E0	6.4E-8	6.2E-8
<input type="checkbox"/>	INTERPRO	<a href="#">Protein phosphatase 2C</a>	RT		14	6.1E-8	5.1E0	1.6E-6	1.5E-6
<input type="checkbox"/>	INTERPRO	<a href="#">Protein phosphatase 2C, manganese/magnesium aspartate binding site</a>	RT		11	1.1E-7	6.2E0	2.8E-6	2.6E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">peptidyl-threonine dephosphorylation</a>	RT		11	1.7E-7	5.9E0	1.2E-5	1.1E-5

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	<a href="#">PP2Cc</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	2.8E-7	3.5E0	5.4E-6	4.9E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Manganese 1	<a href="#">RT</a>	<div><div></div><div></div></div>	15	6.3E-6	3.8E0	2.7E-4	2.6E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Manganese 2	<a href="#">RT</a>	<div><div></div><div></div></div>	15	6.3E-6	3.8E0	2.7E-4	2.6E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PP2C-like	<a href="#">RT</a>	<div><div></div><div></div></div>	10	1.3E-5	5.2E0	4.8E-4	4.7E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">cation binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	8.1E-3	3.5E0	6.8E-2	6.0E-2
Annotation Cluster 39		Enrichment Score: 6.83	<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	<a href="#">Protein phosphatase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	67	7.7E-22	3.5E0	9.8E-21	7.6E-21
<input type="checkbox"/>	INTERPRO	<a href="#">Dual specificity phosphatase, catalytic domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	31	6.1E-15	4.5E0	4.1E-13	3.7E-13
<input type="checkbox"/>	INTERPRO	<a href="#">Dual specificity phosphatase, subgroup, catalytic domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	28	7.6E-15	4.8E0	4.9E-13	4.5E-13
<input type="checkbox"/>	INTERPRO	<a href="#">Dual specificity phosphatase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	24	1.2E-12	4.8E0	6.5E-11	5.9E-11
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein tyrosine/serine/threonine phosphatase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	25	8.3E-11	4.0E0	2.7E-9	2.4E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Tyrosine-protein phosphatase	<a href="#">RT</a>	<div><div></div><div></div></div>	32	9.1E-11	3.5E0	6.1E-9	5.9E-9
<input type="checkbox"/>	SMART	<a href="#">DSPc</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	28	2.5E-10	3.2E0	7.1E-9	6.4E-9
<input type="checkbox"/>	INTERPRO	<a href="#">Protein-tyrosine/Dual specificity phosphatase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	35	4.0E-8	2.6E0	1.1E-6	1.0E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Rhodanese	<a href="#">RT</a>	<div><div></div><div></div></div>	15	8.7E-8	4.9E0	4.5E-6	4.4E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Phosphocysteine intermediate	<a href="#">RT</a>	<div><div></div><div></div></div>	33	2.1E-7	2.6E0	1.0E-5	1.0E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein tyrosine phosphatase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	39	2.9E-7	2.3E0	6.8E-6	6.1E-6
<input type="checkbox"/>	INTERPRO	<a href="#">Mitogen-activated protein (MAP) kinase phosphatase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	6.2E-7	6.2E0	1.5E-5	1.4E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">peptidyl-tyrosine dephosphorylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	38	7.7E-7	2.3E0	4.8E-5	4.6E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">MAP kinase tyrosine/serine/threonine phosphatase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	3.0E-6	5.0E0	6.2E-5	5.5E-5
<input type="checkbox"/>	INTERPRO	<a href="#">Rhodanese-like domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	3.1E-6	3.9E0	6.8E-5	6.2E-5
<input type="checkbox"/>	INTERPRO	<a href="#">Protein-tyrosine phosphatase, active site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	29	9.6E-6	2.4E0	1.8E-4	1.7E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">inactivation of MAPK activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	1.0E-5	3.6E0	4.0E-4	3.8E-4
<input type="checkbox"/>	SMART	<a href="#">RHOD</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	5.2E-5	2.9E0	6.9E-4	6.2E-4
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">dual specificity protein phosphatase (MAP kinase phosphatase)</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.4E-4	5.3E0	1.5E-2	1.5E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">Regulation of MAP Kinase Pathways Through Dual Specificity Phosphatases</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	7.5E-4	3.1E0	6.2E-3	4.2E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">phosphatase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	1.3E-3	2.4E0	1.4E-2	1.2E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Protein-tyrosine phosphatase, catalytic</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	19	9.0E-3	1.9E0	8.7E-2	7.9E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein tyrosine/threonine phosphatase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">endoderm formation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.3E-1	2.5E0	8.1E-1	7.7E-1
<input type="checkbox"/>	SMART	<a href="#">PTPc motif</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	19	2.7E-1	1.2E0	9.7E-1	8.7E-1
Annotation Cluster 40		Enrichment Score: 6.19	<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	<a href="#">ligase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	104	1.4E-17	2.3E0	7.3E-16	6.5E-16
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Ligase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	108	5.7E-15	2.1E0	5.8E-14	4.5E-14
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:RING-type	<a href="#">RT</a>	<div><div></div><div></div></div>	59	1.7E-5	1.7E0	6.5E-4	6.3E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, RING-type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	72	2.5E-4	1.5E0	3.5E-3	3.2E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, RING/FYVE/PHD-type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	99	1.1E-3	1.4E0	1.4E-2	1.3E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, RING-type, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	34	1.4E-1	1.2E0	6.6E-1	6.0E-1
<input type="checkbox"/>	SMART	<a href="#">RING</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	54	8.6E-1	9.0E-1	1.0E0	9.0E-1
Annotation Cluster 41		Enrichment Score: 6.18	<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	<a href="#">transcription-coupled nucleotide-excision repair</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	41	3.1E-13	3.3E0	4.4E-11	4.2E-11
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">DNA damage response, detection of DNA damage</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	22	2.2E-8	3.6E0	1.8E-6	1.7E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleotide-excision repair, preincision complex assembly</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	19	6.0E-8	3.9E0	4.5E-6	4.3E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">telomere maintenance via recombination</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	20	7.1E-8	3.7E0	5.2E-6	5.0E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleotide-excision repair, DNA incision, 5'-to lesion</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	21	2.7E-7	3.4E0	1.8E-5	1.8E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleotide-excision repair, DNA incision</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	21	4.8E-7	3.3E0	3.2E-5	3.0E-5

Annotation Cluster 1		Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">translesion synthesis</a>	<a href="#">RT</a>		19	4.7E-6	3.1E0	2.3E-4	2.2E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleotide-excision repair, DNA gap filling</a>	<a href="#">RT</a>		15	5.2E-6	3.7E0	2.5E-4	2.3E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">error-free translesion synthesis</a>	<a href="#">RT</a>		13	8.0E-6	4.1E0	3.5E-4	3.3E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">error-prone translesion synthesis</a>	<a href="#">RT</a>		13	8.0E-6	4.1E0	3.5E-4	3.3E-4
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Nucleotide excision repair</a>	<a href="#">RT</a>		23	1.4E-5	2.6E0	4.0E-5	1.8E-5
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">DNA replication</a>	<a href="#">RT</a>		18	1.2E-4	2.6E0	2.9E-4	1.3E-4
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Mismatch repair</a>	<a href="#">RT</a>		13	3.8E-4	3.0E0	8.9E-4	4.1E-4
Annotation Cluster 42		Enrichment Score: 5.63			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">WD40 repeat, conserved site</a>	<a href="#">RT</a>		57	1.8E-8	2.1E0	5.2E-7	4.7E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 7	<a href="#">RT</a>		50	2.6E-8	2.3E0	1.5E-6	1.4E-6
<input type="checkbox"/>	INTERPRO	<a href="#">G-protein beta WD-40 repeat</a>	<a href="#">RT</a>		38	3.8E-8	2.5E0	1.1E-6	9.7E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 5	<a href="#">RT</a>		68	4.4E-8	2.0E0	2.3E-6	2.2E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 4	<a href="#">RT</a>		70	1.8E-7	1.9E0	9.1E-6	8.8E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 6	<a href="#">RT</a>		57	3.7E-7	2.0E0	1.8E-5	1.8E-5
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">WD repeat</a>	<a href="#">RT</a>		73	7.1E-7	1.8E0	5.0E-6	3.9E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 3	<a href="#">RT</a>		71	7.2E-7	1.8E0	3.5E-5	3.4E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 1	<a href="#">RT</a>		71	2.6E-6	1.7E0	1.2E-4	1.2E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 2	<a href="#">RT</a>		71	2.6E-6	1.7E0	1.2E-4	1.2E-4
<input type="checkbox"/>	INTERPRO	<a href="#">WD40-repeat-containing domain</a>	<a href="#">RT</a>		78	2.9E-5	1.6E0	5.0E-4	4.6E-4
<input type="checkbox"/>	INTERPRO	<a href="#">WD40 repeat</a>	<a href="#">RT</a>		69	6.3E-5	1.6E0	1.1E-3	9.6E-4
<input type="checkbox"/>	INTERPRO	<a href="#">WD40/YVTN repeat-like-containing domain</a>	<a href="#">RT</a>		76	1.1E-3	1.4E0	1.3E-2	1.2E-2
<input type="checkbox"/>	SMART	<a href="#">WD40</a>	<a href="#">RT</a>		69	3.8E-1	1.1E0	1.0E0	9.0E-1
Annotation Cluster 43		Enrichment Score: 5.46			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of telomere maintenance via telomerase</a>	<a href="#">RT</a>		22	1.0E-9	4.1E0	9.9E-8	9.4E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of telomerase activity</a>	<a href="#">RT</a>		16	1.8E-5	3.3E0	6.8E-4	6.5E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of telomere capping</a>	<a href="#">RT</a>		9	2.3E-3	3.3E0	4.6E-2	4.4E-2
Annotation Cluster 44		Enrichment Score: 5.36			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">gene expression</a>	<a href="#">RT</a>		33	2.1E-14	4.1E0	3.4E-12	3.3E-12
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">DNA-directed RNA polymerase II, core complex</a>	<a href="#">RT</a>		14	1.4E-7	4.9E0	3.8E-6	3.3E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">7-methylguanosine mRNA capping</a>	<a href="#">RT</a>		20	1.4E-7	3.6E0	9.9E-6	9.4E-6
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">DNA-directed RNA polymerase</a>	<a href="#">RT</a>		20	4.3E-7	3.5E0	3.2E-6	2.5E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of viral transcription</a>	<a href="#">RT</a>		18	4.6E-7	3.7E0	3.0E-5	2.9E-5
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">RNA polymerase</a>	<a href="#">RT</a>		20	5.3E-7	3.3E0	1.8E-6	8.3E-7
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">RNA polymerase I activity</a>	<a href="#">RT</a>		11	8.2E-7	5.5E0	1.8E-5	1.6E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">transcription elongation from RNA polymerase I promoter</a>	<a href="#">RT</a>		18	8.9E-7	3.6E0	5.1E-5	4.9E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">transcription initiation from RNA polymerase I promoter</a>	<a href="#">RT</a>		19	9.1E-7	3.4E0	5.1E-5	4.9E-5
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Pyrimidine metabolism</a>	<a href="#">RT</a>		41	1.2E-6	2.1E0	4.1E-6	1.9E-6
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">DNA-directed RNA polymerase I complex</a>	<a href="#">RT</a>		11	1.6E-6	5.4E0	3.8E-5	3.4E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">termination of RNA polymerase I transcription</a>	<a href="#">RT</a>		18	1.7E-6	3.4E0	9.0E-5	8.6E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">DNA-directed RNA polymerase activity</a>	<a href="#">RT</a>		20	2.4E-6	3.1E0	5.0E-5	4.5E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">transcription elongation from RNA polymerase II promoter</a>	<a href="#">RT</a>		32	1.4E-5	2.2E0	5.5E-4	5.3E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">RNA polymerase II activity</a>	<a href="#">RT</a>		9	2.0E-5	5.4E0	3.4E-4	3.0E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of gene expression, epigenetic</a>	<a href="#">RT</a>		25	3.3E-5	2.4E0	1.2E-3	1.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">snRNA transcription from RNA polymerase II promoter</a>	<a href="#">RT</a>		24	8.0E-4	2.0E0	1.9E-2	1.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">transcription initiation from RNA polymerase II promoter</a>	<a href="#">RT</a>		40	3.8E-3	1.6E0	6.9E-2	6.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">gene silencing by RNA</a>	<a href="#">RT</a>		30	8.8E-3	1.6E0	1.4E-1	1.3E-1



















































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">DNA-directed RNA polymerase III complex</a>	<a href="#">RT</a>		8	2.1E-2	2.7E0	1.4E-1	1.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">RNA polymerase III activity</a>	<a href="#">RT</a>		8	2.1E-2	2.7E0	1.4E-1	1.3E-1
Annotation Cluster 45		Enrichment Score: 5.36	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Cyclin</a>	<a href="#">RT</a>		22	2.0E-8	3.8E0	1.6E-7	1.2E-7
<input type="checkbox"/>	INTERPRO	<a href="#">Cyclin-like</a>	<a href="#">RT</a>		24	3.4E-8	3.4E0	9.8E-7	9.0E-7
<input type="checkbox"/>	SMART	<a href="#">CYCLIN</a>	<a href="#">RT</a>		23	3.2E-6	2.6E0	5.1E-5	4.6E-5
<input type="checkbox"/>	INTERPRO	<a href="#">Cyclin, N-terminal</a>	<a href="#">RT</a>		18	4.7E-6	3.3E0	9.7E-5	8.9E-5
<input type="checkbox"/>	INTERPRO	<a href="#">Cyclin, C-terminal domain</a>	<a href="#">RT</a>		11	1.5E-4	3.8E0	2.1E-3	2.0E-3
<input type="checkbox"/>	SMART	<a href="#">SM01332</a>	<a href="#">RT</a>		11	4.6E-3	2.5E0	4.3E-2	3.8E-2
Annotation Cluster 46		Enrichment Score: 5.31	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Toll-like receptor signaling pathway</a>	<a href="#">RT</a>		46	2.3E-8	2.3E0	9.4E-8	4.3E-8
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">NOD-like receptor signaling pathway</a>	<a href="#">RT</a>		27	2.9E-6	2.5E0	8.8E-6	4.0E-6
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Leishmaniasis</a>	<a href="#">RT</a>		29	5.3E-5	2.1E0	1.4E-4	6.4E-5
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Pertussis</a>	<a href="#">RT</a>		29	1.6E-4	2.0E0	3.9E-4	1.8E-4
Annotation Cluster 47		Enrichment Score: 5.24	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">ATPase, AAA-type, conserved site</a>	<a href="#">RT</a>		19	5.6E-9	4.4E0	1.8E-7	1.7E-7
<input type="checkbox"/>	INTERPRO	<a href="#">ATPase, AAA-type, core</a>	<a href="#">RT</a>		24	1.0E-6	2.9E0	2.5E-5	2.3E-5
<input type="checkbox"/>	INTERPRO	<a href="#">AAA+ ATPase domain</a>	<a href="#">RT</a>		44	5.3E-6	2.0E0	1.1E-4	9.9E-5
<input type="checkbox"/>	SMART	<a href="#">AAA</a>	<a href="#">RT</a>		44	3.5E-2	1.3E0	2.4E-1	2.1E-1
Annotation Cluster 48		Enrichment Score: 4.97	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Tetratricopeptide repeat-containing domain</a>	<a href="#">RT</a>		50	4.0E-9	2.3E0	1.3E-7	1.2E-7
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">TPR repeat</a>	<a href="#">RT</a>		55	4.6E-9	2.3E0	3.9E-8	3.0E-8
<input type="checkbox"/>	INTERPRO	<a href="#">Tetratricopeptide repeat</a>	<a href="#">RT</a>		49	6.2E-8	2.2E0	1.6E-6	1.5E-6
<input type="checkbox"/>	INTERPRO	<a href="#">Tetratricopeptide-like helical</a>	<a href="#">RT</a>		65	6.2E-7	1.8E0	1.5E-5	1.4E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 1	<a href="#">RT</a>		49	1.2E-6	2.0E0	5.4E-5	5.2E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 2	<a href="#">RT</a>		49	1.2E-6	2.0E0	5.4E-5	5.2E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 3	<a href="#">RT</a>		45	3.0E-6	2.0E0	1.3E-4	1.3E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 5	<a href="#">RT</a>		28	8.8E-6	2.4E0	3.5E-4	3.4E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 6	<a href="#">RT</a>		26	1.0E-5	2.5E0	3.9E-4	3.8E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 4	<a href="#">RT</a>		31	6.7E-5	2.1E0	2.2E-3	2.2E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 7	<a href="#">RT</a>		22	9.4E-5	2.5E0	3.1E-3	3.0E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 8	<a href="#">RT</a>		18	5.0E-4	2.5E0	1.5E-2	1.4E-2
<input type="checkbox"/>	SMART	<a href="#">TPR</a>	<a href="#">RT</a>		49	1.2E-3	1.5E0	1.3E-2	1.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 9	<a href="#">RT</a>		10	3.6E-2	2.1E0	6.6E-1	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 10	<a href="#">RT</a>		7	9.2E-2	2.2E0	1.0E0	9.7E-1
Annotation Cluster 49		Enrichment Score: 4.92	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:TXY	<a href="#">RT</a>		11	2.3E-7	6.2E0	1.1E-5	1.1E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">MAP kinase activity</a>	<a href="#">RT</a>		12	6.4E-7	5.1E0	1.4E-5	1.3E-5
<input type="checkbox"/>	INTERPRO	<a href="#">Mitogen-activated protein (MAP) kinase, conserved site</a>	<a href="#">RT</a>		10	1.0E-5	5.2E0	1.9E-4	1.7E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Mitogen-activated protein (MAP) kinase, p38</a>	<a href="#">RT</a>		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
Annotation Cluster 50		Enrichment Score: 4.85	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Purine metabolism</a>	<a href="#">RT</a>		68	2.3E-9	2.0E0	1.1E-8	4.9E-9
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Pyrimidine metabolism</a>	<a href="#">RT</a>		41	1.2E-6	2.1E0	4.1E-6	1.9E-6
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Metabolic pathways</a>	<a href="#">RT</a>		92	1.0E0	3.9E-1	1.0E0	1.0E0
Annotation Cluster 51		Enrichment Score: 4.84	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Gap junction</a>	<a href="#">RT</a>		60	5.6E-23	3.6E0	1.5E-21	7.0E-22
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Estrogen signaling pathway</a>	<a href="#">RT</a>		57	7.2E-17	3.0E0	1.0E-15	4.7E-16





Annotation Cluster 1		Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Oxytocin signaling pathway</a>	<a href="#">RT</a>		70	3.3E-14	2.4E0	3.3E-13	1.5E-13
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">adenylate cyclase activity</a>	<a href="#">RT</a>		19	1.7E-13	6.0E0	6.9E-12	6.1E-12
<input type="checkbox"/>	INTERPRO	<a href="#">Adenylyl cyclase class-3/4/guanylyl cyclase</a>	<a href="#">RT</a>		18	4.0E-12	5.9E0	2.1E-10	1.9E-10
<input type="checkbox"/>	INTERPRO	<a href="#">Adenylyl cyclase class-3/4/guanylyl cyclase, conserved site</a>	<a href="#">RT</a>		17	2.2E-11	5.9E0	9.7E-10	8.9E-10
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">GnRH signaling pathway</a>	<a href="#">RT</a>		45	2.1E-10	2.6E0	1.2E-9	5.6E-10
<input type="checkbox"/>	SMART	<a href="#">CYCc</a>	<a href="#">RT</a>		17	1.5E-8	3.9E0	4.0E-7	3.6E-7
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Vascular smooth muscle contraction</a>	<a href="#">RT</a>		49	2.9E-8	2.2E0	1.1E-7	5.1E-8
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Melanogenesis</a>	<a href="#">RT</a>		43	9.6E-8	2.2E0	3.6E-7	1.6E-7
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Chemokine signaling pathway</a>	<a href="#">RT</a>		66	1.8E-7	1.9E0	6.7E-7	3.1E-7
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">cAMP biosynthesis</a>	<a href="#">RT</a>		10	2.5E-7	6.9E0	1.9E-6	1.5E-6
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Inflammatory mediator regulation of TRP channels</a>	<a href="#">RT</a>		41	4.8E-7	2.2E0	1.7E-6	7.7E-7
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Regulation of lipolysis in adipocytes</a>	<a href="#">RT</a>		28	7.2E-7	2.6E0	2.4E-6	1.1E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cyclic nucleotide biosynthetic process</a>	<a href="#">RT</a>		11	8.7E-7	5.4E0	5.1E-5	4.9E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">activation of protein kinase A activity</a>	<a href="#">RT</a>		13	3.5E-6	4.3E0	1.8E-4	1.7E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Magnesium 2; via carbonyl oxygen	<a href="#">RT</a>		10	4.5E-6	5.7E0	1.9E-4	1.9E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Magnesium 1	<a href="#">RT</a>		19	6.4E-6	3.2E0	2.7E-4	2.6E-4
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Circadian entrainment</a>	<a href="#">RT</a>		37	1.3E-5	2.0E0	3.9E-5	1.8E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">phosphorus-oxygen lyase activity</a>	<a href="#">RT</a>		10	1.4E-5	5.0E0	2.6E-4	2.3E-4
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Cholinergic synapse</a>	<a href="#">RT</a>		41	1.9E-5	1.9E0	5.2E-5	2.4E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Magnesium 2	<a href="#">RT</a>		18	1.9E-5	3.1E0	7.3E-4	7.0E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cAMP biosynthetic process</a>	<a href="#">RT</a>		11	1.1E-4	3.8E0	3.5E-3	3.3E-3
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Gastric acid secretion</a>	<a href="#">RT</a>		28	2.5E-4	2.0E0	6.0E-4	2.7E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">renal water homeostasis</a>	<a href="#">RT</a>		15	3.3E-4	2.8E0	8.9E-3	8.4E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to glucagon stimulus</a>	<a href="#">RT</a>		17	4.3E-4	2.5E0	1.1E-2	1.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to forskolin</a>	<a href="#">RT</a>		7	4.7E-4	5.2E0	1.2E-2	1.2E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Adenylate cyclase-like</a>	<a href="#">RT</a>		6	5.7E-4	6.2E0	7.2E-3	6.6E-3
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Endocrine and other factor-regulated calcium reabsorption</a>	<a href="#">RT</a>		19	9.2E-4	2.2E0	2.0E-3	9.2E-4
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Thyroid hormone synthesis</a>	<a href="#">RT</a>		25	1.9E-3	1.9E0	3.9E-3	1.9E-3
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Salivary secretion</a>	<a href="#">RT</a>		28	4.2E-3	1.7E0	8.6E-3	4.2E-3
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Retrograde endocannabinoid signaling</a>	<a href="#">RT</a>		31	6.5E-3	1.6E0	1.3E-2	6.5E-3
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Glutamatergic synapse</a>	<a href="#">RT</a>		34	6.9E-3	1.6E0	1.3E-2	6.9E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway</a>	<a href="#">RT</a>		16	8.3E-3	2.0E0	1.3E-1	1.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Aldosterone synthesis and secretion</a>	<a href="#">RT</a>		25	1.4E-2	1.6E0	2.7E-2	1.4E-2
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Lyase</a>	<a href="#">RT</a>		32	2.6E-2	1.5E0	1.0E-1	7.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">activation of adenylate cyclase activity</a>	<a href="#">RT</a>		13	2.8E-2	1.9E0	3.3E-1	3.1E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Ovarian steroidogenesis</a>	<a href="#">RT</a>		16	3.6E-2	1.7E0	6.3E-2	3.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cAMP-mediated signaling</a>	<a href="#">RT</a>		12	4.5E-2	1.9E0	4.3E-1	4.1E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">GABAergic synapse</a>	<a href="#">RT</a>		24	4.6E-2	1.5E0	8.0E-2	4.6E-2
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Pancreatic secretion</a>	<a href="#">RT</a>		25	6.8E-2	1.4E0	1.2E-1	6.8E-2
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Insulin secretion</a>	<a href="#">RT</a>		23	7.6E-2	1.4E0	1.3E-1	7.6E-2
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Dilated cardiomyopathy</a>	<a href="#">RT</a>		22	1.1E-1	1.4E0	1.8E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">adenylate cyclase-activating G-protein coupled receptor signaling pathway</a>	<a href="#">RT</a>		13	1.2E-1	1.5E0	8.1E-1	7.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Morphine addiction</a>	<a href="#">RT</a>		23	1.4E-1	1.3E0	2.2E-1	1.4E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Bile secretion</a>	<a href="#">RT</a>		17	2.3E-1	1.3E0	3.7E-1	2.3E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Serotonergic synapse</a>	<a href="#">RT</a>		25	2.8E-1	1.2E0	4.4E-1	2.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Calcium signaling pathway</a>	<a href="#">RT</a>		38	3.2E-1	1.1E0	5.0E-1	3.2E-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"/>	KEGG_PATHWAY	<a href="#">Taste transduction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	9.5E-1	7.0E-1	1.0E0	9.5E-1
Annotation Cluster 52		Enrichment Score: 4.8	<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	<a href="#">cadherin binding involved in cell-cell adhesion</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	79	7.9E-6	1.6E0	1.5E-4	1.4E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">cell-cell adherens junction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	81	1.5E-5	1.6E0	2.7E-4	2.4E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cell-cell adhesion</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	73	3.3E-5	1.6E0	1.2E-3	1.1E-3
Annotation Cluster 53		Enrichment Score: 4.8	<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	<a href="#">RT</a>	<div><div></div><div></div></div>	15	3.6E-9	5.7E0	2.0E-7	2.0E-7
<input type="checkbox"/>	INTERPRO	<a href="#">Phosphatidylinositol 3/4-kinase, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	1.7E-8	5.4E0	5.0E-7	4.6E-7
<input type="checkbox"/>	INTERPRO	<a href="#">Phosphatidylinositol 3-/4-kinase, catalytic domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	4.1E-8	4.9E0	1.1E-6	1.0E-6
<input type="checkbox"/>	SMART	<a href="#">PI3Kc</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	8.6E-7	3.6E0	1.6E-5	1.4E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FAT	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.6E-4	6.8E0	1.1E-2	1.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FATC	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.6E-4	6.8E0	1.1E-2	1.0E-2
<input type="checkbox"/>	INTERPRO	<a href="#">PIK-related kinase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	5.7E-4	6.2E0	7.2E-3	6.6E-3
<input type="checkbox"/>	INTERPRO	<a href="#">PIK-related kinase, FATC</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	5.7E-4	6.2E0	7.2E-3	6.6E-3
<input type="checkbox"/>	INTERPRO	<a href="#">PIK-related kinase, FAT</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.9E-3	6.2E0	3.2E-2	2.9E-2
<input type="checkbox"/>	SMART	<a href="#">SM01343</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	4.2E-3	4.1E0	4.0E-2	3.6E-2
Annotation Cluster 54		Enrichment Score: 4.77	<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	<a href="#">global genome nucleotide-excision repair</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	21	9.2E-9	3.9E0	7.6E-7	7.2E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleotide-excision repair, preincision complex assembly</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	19	6.0E-8	3.9E0	4.5E-6	4.3E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleotide-excision repair, DNA incision, 5'-to lesion</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	21	2.7E-7	3.4E0	1.8E-5	1.8E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleotide-excision repair, DNA incision</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	21	4.8E-7	3.3E0	3.2E-5	3.0E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleotide-excision repair, DNA duplex unwinding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	9.5E-6	3.8E0	3.9E-4	3.7E-4
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Nucleotide excision repair</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	23	1.4E-5	2.6E0	4.0E-5	1.8E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleotide-excision repair, DNA damage recognition</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	5.7E-4	3.1E0	1.4E-2	1.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleotide-excision repair, preincision complex stabilization</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.1E-3	3.1E0	2.5E-2	2.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleotide-excision repair, DNA incision, 3'-to lesion</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	2.5E-3	2.8E0	5.0E-2	4.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleotide-excision repair</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.4E-1	1.6E0	8.2E-1	7.8E-1
Annotation Cluster 55		Enrichment Score: 4.63	<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	<a href="#">DNA synthesis involved in DNA repair</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	20	5.0E-7	3.4E0	3.2E-5	3.1E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">strand displacement</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	1.8E-5	3.4E0	7.1E-4	6.8E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">DNA double-strand break processing</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	2.4E-5	4.3E0	9.0E-4	8.5E-4
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Homologous recombination</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	1.4E-3	2.5E0	2.9E-3	1.4E-3
Annotation Cluster 56		Enrichment Score: 4.49	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Heat shock protein 70, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	1.4E-6	5.0E0	3.1E-5	2.9E-5
<input type="checkbox"/>	INTERPRO	<a href="#">Heat shock protein 70 family</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	1.4E-6	5.0E0	3.1E-5	2.9E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to unfolded protein</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	1.8E-2	2.0E0	2.3E-1	2.2E-1
Annotation Cluster 57		Enrichment Score: 4.44	<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:C2H2-type 23	<a href="#">RT</a>	<div><div></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	<a href="#">RT</a>	<div><div></div><div></div></div>	13	6.7E-9	6.3E0	3.7E-7	3.6E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 26	<a href="#">RT</a>	<div><div></div><div></div></div>	8	4.0E-5	6.1E0	1.4E-3	1.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 27	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.1E-4	6.0E0	6.6E-3	6.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 25	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.1E-4	6.0E0	6.6E-3	6.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 28	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.6E-4	6.8E0	1.1E-2	1.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 29	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.1E-3	5.8E0	3.1E-2	3.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 30	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.1E-3	5.8E0	3.1E-2	3.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 21; degenerate	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.7E-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 58		Enrichment Score: 4.33	<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	<a href="#">precatalytic spliceosome</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	6.6E-8	4.3E0	2.0E-6	1.8E-6
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">U4/U6 x U5 tri-snRNP complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	1.2E-7	4.4E0	3.4E-6	3.0E-6
<input type="checkbox"/>	INTERPRO	<a href="#">Ribonucleoprotein LSM domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	2.9E-7	4.4E0	7.2E-6	6.6E-6
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">U5 snRNP</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	13	6.4E-7	4.9E0	1.7E-5	1.5E-5
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">U12-type spliceosomal complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	1.2E-6	3.9E0	2.8E-5	2.4E-5
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">U4 snRNP</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	2.4E-6	5.8E0	5.4E-5	4.7E-5
<input type="checkbox"/>	INTERPRO	<a href="#">Like-Sm (LSM) domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	3.1E-6	3.9E0	6.8E-5	6.2E-5
<input type="checkbox"/>	BIOCARTA	<a href="#">Spliceosomal Assembly</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	3.8E-6	3.1E0	2.4E-4	1.6E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">U2 snRNP</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	13	8.1E-6	4.1E0	1.6E-4	1.4E-4
<input type="checkbox"/>	SMART	<a href="#">Sm</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	5.2E-5	2.9E0	6.9E-4	6.2E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">small nuclear ribonucleoprotein complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	6.1E-5	4.1E0	9.4E-4	8.2E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">methylosome</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.0E-4	4.8E0	1.4E-3	1.2E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">U1 snRNP binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.3E-4	6.0E0	1.8E-3	1.6E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">histone mRNA metabolic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.7E-4	4.4E0	5.0E-3	4.7E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">U1 snRNP</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	2.1E-4	3.7E0	2.6E-3	2.3E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">spliceosomal tri-snRNP complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.7E-3	6.4E0	2.4E-2	2.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nuclear import</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	5.7E-3	3.0E0	9.5E-2	9.0E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">pICln-Sm protein complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	7.0E-3	5.3E0	5.2E-2	4.6E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">SMN-Sm protein complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.1E-2	3.0E0	7.6E-2	6.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">spliceosomal snRNP assembly</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.3E-2	2.3E0	1.8E-1	1.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">U7 snRNP</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.4E-2	4.5E0	9.8E-2	8.6E-2
Annotation Cluster 59		Enrichment Score: 4.3	<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	<a href="#">adenylate cyclase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	19	1.7E-13	6.0E0	6.9E-12	6.1E-12
<input type="checkbox"/>	INTERPRO	<a href="#">Adenylyl cyclase class-3/4/guanylyl cyclase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	18	4.0E-12	5.9E0	2.1E-10	1.9E-10
<input type="checkbox"/>	INTERPRO	<a href="#">Adenylyl cyclase class-3/4/guanylyl cyclase, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	2.2E-11	5.9E0	9.7E-10	8.9E-10
<input type="checkbox"/>	SMART	<a href="#">CYCc</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	1.5E-8	3.9E0	4.0E-7	3.6E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Guanylate cyclase	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.0E-5	6.8E0	3.9E-4	3.8E-4
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">cGMP biosynthesis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	3.8E-5	6.1E0	2.2E-4	1.7E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">guanylate cyclase complex, soluble</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	6.3E-5	5.7E0	9.4E-4	8.2E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">guanylate cyclase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	9.7E-5	5.3E0	1.4E-3	1.2E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Haem NO binding associated</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.7E-3	5.3E0	2.0E-2	1.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cGMP biosynthetic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.1E-2	3.0E0	1.5E-1	1.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">receptor guanylyl cyclase signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.6E-2	3.6E0	2.2E-1	2.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Heme-NO binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.1E-1	5.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of cGMP biosynthetic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	9.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">NO signalling/Golgi transport ligand-binding domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.4E-1	2.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Ion Channels and Their Functional Role in Vascular Endothelium</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	6.2E-1	1.1E0	9.3E-1	6.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Extracellular ligand-binding receptor</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	8.5E-1	8.6E-1	1.0E0	9.1E-1
Annotation Cluster 60		Enrichment Score: 4.28	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Alcoholism</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	68	3.0E-9	2.0E0	1.4E-8	6.2E-9
<input type="checkbox"/>	INTERPRO	<a href="#">Histone core</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	30	1.9E-7	2.7E0	4.8E-6	4.4E-6
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Nucleosome core</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	31	4.5E-6	2.4E0	2.8E-5	2.2E-5
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">nucleosome</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	33	9.1E-6	2.2E0	1.8E-4	1.5E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">nuclear nucleosome</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	18	2.0E-4	2.6E0	2.5E-3	2.2E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Histone-fold</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	34	2.8E-4	1.9E0	3.9E-3	3.5E-3



Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Histone H2B</a>	RT		12	6.0E-4	3.1E0	7.5E-3	6.9E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleosome assembly</a>	RT		34	2.0E-3	1.7E0	4.0E-2	3.8E-2
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Systemic lupus erythematosus</a>	RT		39	5.7E-3	1.5E0	1.1E-2	5.7E-3
<input type="checkbox"/>	SMART	<a href="#">H2B</a>	RT		12	1.8E-2	2.0E0	1.4E-1	1.3E-1
Annotation Cluster 61		Enrichment Score: 4.07	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Adrenergic signaling in cardiomyocytes</a>	RT		51	1.4E-6	1.9E0	4.5E-6	2.1E-6
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Dopaminergic synapse</a>	RT		44	6.4E-5	1.8E0	1.7E-4	7.6E-5
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Retrograde endocannabinoid signaling</a>	RT		31	6.5E-3	1.6E0	1.3E-2	6.5E-3
Annotation Cluster 62		Enrichment Score: 4.04	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">G-protein beta/gamma-subunit complex binding</a>	RT		16	1.5E-8	4.8E0	4.2E-7	3.8E-7
<input type="checkbox"/>	INTERPRO	<a href="#">G protein alpha subunit, helical insertion</a>	RT		14	1.7E-8	5.4E0	5.0E-7	4.6E-7
<input type="checkbox"/>	INTERPRO	<a href="#">Guanine nucleotide binding protein (G-protein), alpha subunit</a>	RT		14	1.7E-8	5.4E0	5.0E-7	4.6E-7
<input type="checkbox"/>	SMART	<a href="#">SM00275</a>	RT		14	2.9E-6	3.6E0	4.9E-5	4.4E-5
<input type="checkbox"/>	INTERPRO	<a href="#">G-protein alpha subunit, group I</a>	RT		8	1.9E-5	6.2E0	3.4E-4	3.1E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">guanyl nucleotide binding</a>	RT		8	9.7E-5	5.3E0	1.4E-3	1.2E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">heterotrimeric G-protein complex</a>	RT		12	9.6E-3	2.3E0	7.0E-2	6.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">adenylate cyclase-modulating G-protein coupled receptor signaling pathway</a>	RT		13	1.5E-2	2.1E0	2.1E-1	2.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">G-protein coupled serotonin receptor binding</a>	RT		4	1.6E-2	6.0E0	1.1E-1	1.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">G-protein coupled receptor binding</a>	RT		15	6.6E-2	1.6E0	3.7E-1	3.3E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transducer</a>	RT		29	1.0E0	2.2E-1	1.0E0	1.0E0
Annotation Cluster 63		Enrichment Score: 3.94	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">DNA helicase activity</a>	RT		17	7.0E-8	4.2E0	1.8E-6	1.6E-6
<input type="checkbox"/>	INTERPRO	<a href="#">Mini-chromosome maintenance, DNA-dependent ATPase</a>	RT		9	3.5E-6	6.2E0	7.6E-5	7.0E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MCM	RT		8	1.0E-5	6.8E0	3.9E-4	3.8E-4
<input type="checkbox"/>	SMART	<a href="#">MCM</a>	RT		9	9.1E-5	4.1E0	1.1E-3	1.0E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Mini-chromosome maintenance, conserved site</a>	RT		6	5.7E-4	6.2E0	7.2E-3	6.6E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">MCM complex</a>	RT		7	8.2E-4	4.9E0	8.2E-3	7.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">DNA replication initiation</a>	RT		14	1.2E-3	2.6E0	2.8E-2	2.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">DNA unwinding involved in DNA replication</a>	RT		7	2.6E-3	4.2E0	5.1E-2	4.8E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">CDK Regulation of DNA Replication</a>	RT		12	1.1E-2	2.1E0	4.7E-2	3.2E-2
Annotation Cluster 64		Enrichment Score: 3.91	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">phosphatidylinositol-mediated signaling</a>	RT		42	6.6E-8	2.3E0	4.9E-6	4.7E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">phosphatidylinositol-3-phosphate biosynthetic process</a>	RT		21	6.1E-5	2.5E0	2.0E-3	1.9E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">1-phosphatidylinositol-3-kinase activity</a>	RT		19	8.9E-5	2.6E0	1.3E-3	1.2E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">phosphatidylinositol-4,5-bisphosphate 3-kinase activity</a>	RT		23	2.8E-4	2.2E0	3.6E-3	3.2E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of phosphatidylinositol 3-kinase signaling</a>	RT		27	2.9E-4	2.1E0	8.1E-3	7.7E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">phosphatidylinositol phosphorylation</a>	RT		30	5.8E-4	1.9E0	1.5E-2	1.4E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">Ras guanyl-nucleotide exchange factor activity</a>	RT		29	2.3E-2	1.5E0	1.5E-1	1.4E-1
Annotation Cluster 65		Enrichment Score: 3.9	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	<a href="#">Cell Cycle</a>	RT		22	1.2E-7	2.7E0	2.9E-5	2.0E-5
<input type="checkbox"/>	BIOCARTA	<a href="#">RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage</a>	RT		12	1.5E-4	2.8E0	2.0E-3	1.3E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">Regulation of cell cycle progression by PIK3</a>	RT		8	2.1E-3	3.1E0	1.4E-2	9.5E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">cdc25 and chk1 Regulatory Pathway in response to DNA damage</a>	RT		8	6.8E-3	2.7E0	3.3E-2	2.2E-2
Annotation Cluster 66		Enrichment Score: 3.89	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of telomere maintenance via telomerase</a>	RT		22	1.0E-9	4.1E0	9.9E-8	9.4E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of telomerase RNA localization to Cajal body</a>	RT		12	2.2E-6	4.7E0	1.1E-4	1.1E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Chaperonin Cpn60/TCP-1</a>	RT		12	3.7E-6	4.6E0	7.9E-5	7.2E-5
















































Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	INTERPRO	<a href="#">GroEL-like apical domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	3.7E-6	4.6E0	7.9E-5	7.2E-5
<input type="checkbox"/>	INTERPRO	<a href="#">GroEL-like equatorial domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.6E-5	4.5E0	2.9E-4	2.7E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein localization to Cajal body</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	2.6E-5	5.9E0	9.6E-4	9.1E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">zona pellucida receptor complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	6.3E-5	5.7E0	9.4E-4	8.2E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">chaperonin-containing T-complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	6.3E-5	5.7E0	9.4E-4	8.2E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Chaperonin TCP-1, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	7.5E-5	5.5E0	1.2E-3	1.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of establishment of protein localization to telomere</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.0E-4	5.3E0	3.2E-3	3.0E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Chaperone tailless complex polypeptide 1 (TCP-1)</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.2E-4	4.6E0	1.8E-3	1.7E-3
<input type="checkbox"/>	INTERPRO	<a href="#">TCP-1-like chaperonin intermediate domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.2E-4	4.6E0	1.8E-3	1.7E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">toxin transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	6.9E-2	1.8E0	5.7E-1	5.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">scaRNA localization to Cajal body</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.3E-1	4.4E0	8.1E-1	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">binding of sperm to zona pellucida</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	2.3E-1	1.5E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein binding involved in protein folding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	4.2E-1	1.7E0	1.0E0	8.9E-1
Annotation Cluster 67		Enrichment Score: 3.88	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">phosphoprotein phosphatase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	27	5.5E-10	3.6E0	1.7E-8	1.5E-8
<input type="checkbox"/>	INTERPRO	<a href="#">Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	1.1E-7	5.7E0	2.8E-6	2.5E-6
<input type="checkbox"/>	SMART	<a href="#">PP2Ac</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	8.8E-6	3.8E0	1.3E-4	1.1E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Metallophosphoesterase domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	13	7.2E-4	2.9E0	9.0E-3	8.2E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Manganese	<a href="#">RT</a>	<div><div></div><div></div></div>	11	2.1E-2	2.2E0	4.1E-1	4.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Iron	<a href="#">RT</a>	<div><div></div><div></div></div>	12	9.5E-2	1.7E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Proton donor	<a href="#">RT</a>	<div><div></div><div></div></div>	23	9.5E-1	7.8E-1	1.0E0	9.7E-1
Annotation Cluster 68		Enrichment Score: 3.83	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR	
<input type="checkbox"/>	INTERPRO	<a href="#">Tyrosine-protein kinase, receptor class V, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	5.8E-10	6.2E0	2.1E-8	1.9E-8
<input type="checkbox"/>	INTERPRO	<a href="#">Ephrin receptor ligand binding domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	5.8E-10	6.2E0	2.1E-8	1.9E-8
<input type="checkbox"/>	INTERPRO	<a href="#">Tyrosine-protein kinase, ephrin receptor</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	5.8E-10	6.2E0	2.1E-8	1.9E-8
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">tyrosine-protein kinase, ephrin receptor type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	3.2E-9	5.3E0	6.2E-7	6.1E-7
<input type="checkbox"/>	SMART	<a href="#">EPH_Ibd</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	1.2E-7	4.1E0	2.7E-6	2.4E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ephrin receptor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.6E-7	6.0E0	3.9E-6	3.5E-6
<input type="checkbox"/>	INTERPRO	<a href="#">Tyrosine-protein kinase ephrin type A/B receptor-like</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	5.9E-6	3.7E0	1.2E-4	1.1E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ephrin receptor signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	31	3.9E-5	2.1E0	1.4E-3	1.3E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Galactose-binding domain-like</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	29	4.8E-5	2.2E0	8.2E-4	7.5E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SAM	<a href="#">RT</a>	<div><div></div><div></div></div>	27	9.1E-5	2.2E0	3.0E-3	2.9E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Sterile alpha motif domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	31	1.1E-4	2.0E0	1.7E-3	1.5E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Sterile alpha motif/pointed domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	35	3.0E-4	1.9E0	4.2E-3	3.8E-3
<input type="checkbox"/>	SMART	<a href="#">SM01411</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	7.3E-4	2.4E0	8.2E-3	7.4E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">transmembrane-ephrin receptor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	9.1E-3	4.0E0	7.2E-2	6.4E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">GPI-linked ephrin receptor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.8E-2	4.3E0	1.2E-1	1.1E-1
<input type="checkbox"/>	SMART	<a href="#">SAM</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	29	4.9E-2	1.4E0	2.9E-1	2.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:PDZ-binding	<a href="#">RT</a>	<div><div></div><div></div></div>	18	5.2E-2	1.6E0	9.1E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Cys-rich	<a href="#">RT</a>	<div><div></div><div></div></div>	30	1.2E-1	1.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Fibronectin type-III 2	<a href="#">RT</a>	<div><div></div><div></div></div>	24	2.3E-1	1.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Fibronectin type-III 1	<a href="#">RT</a>	<div><div></div><div></div></div>	24	2.4E-1	1.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Fibronectin, type III</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	38	2.7E-1	1.1E0	9.6E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Insulin-like growth factor binding protein, N-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	26	3.1E-1	1.2E0	9.9E-1	9.1E-1
<input type="checkbox"/>	SMART	<a href="#">FN3</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	29	9.6E-1	7.9E-1	1.0E0	9.6E-1
Annotation Cluster 69		Enrichment Score: 3.76	<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"/>	BIOCARTA	<a href="#">Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation</a>	RT		18	4.7E-5	2.4E0	9.2E-4	6.2E-4
<input type="checkbox"/>	BIOCARTA	<a href="#">Regulation of BAD phosphorylation</a>	RT		19	1.1E-4	2.3E0	1.6E-3	1.1E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">Transcription factor CREB and its extracellular signals</a>	RT		18	9.7E-4	2.1E0	7.8E-3	5.3E-3
Annotation Cluster 70		Enrichment Score: 3.59	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleotide-binding oligomerization domain containing signaling pathway</a>	RT		15	1.0E-5	3.6E0	4.0E-4	3.8E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">I-kappaB kinase/NF-kappaB signaling</a>	RT		23	1.8E-4	2.3E0	5.3E-3	5.0E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">TRIF-dependent toll-like receptor signaling pathway</a>	RT		13	1.1E-3	2.8E0	2.5E-2	2.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of tumor necrosis factor-mediated signaling pathway</a>	RT		13	2.2E-3	2.6E0	4.5E-2	4.3E-2
Annotation Cluster 71		Enrichment Score: 3.49	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein peptidyl-prolyl isomerization</a>	RT		21	5.8E-6	2.9E0	2.7E-4	2.5E-4
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Rotamase</a>	RT		18	7.6E-6	3.3E0	4.6E-5	3.6E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">peptidyl-prolyl cis-trans isomerase activity</a>	RT		21	1.9E-5	2.7E0	3.3E-4	2.9E-4
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Isomerase</a>	RT		35	1.0E-4	2.0E0	5.4E-4	4.2E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site</a>	RT		12	1.4E-4	3.5E0	2.0E-3	1.9E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Cyclophilin-like peptidyl-prolyl cis-trans isomerase domain</a>	RT		12	6.0E-4	3.1E0	7.5E-3	6.9E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PPIase cyclophilin-type	RT		11	1.2E-3	3.1E0	3.4E-2	3.3E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Cyclophilin-type peptidyl-prolyl cis-trans isomerase</a>	RT		11	1.8E-3	3.0E0	2.0E-2	1.8E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">cyclosporin A binding</a>	RT		6	2.1E-3	5.1E0	2.0E-2	1.8E-2
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Cyclosporin</a>	RT		5	1.1E-2	4.9E0	4.6E-2	3.6E-2
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">peptidyl-prolyl cis-trans isomerase</a>	RT		7	1.4E-2	3.1E0	3.6E-1	3.5E-1
Annotation Cluster 72		Enrichment Score: 3.33	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">nucleotide binding</a>	RT		96	4.2E-7	1.6E0	9.7E-6	8.6E-6
<input type="checkbox"/>	INTERPRO	<a href="#">RNA recognition motif domain</a>	RT		63	1.0E-5	1.7E0	1.9E-4	1.8E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Nucleotide-binding, alpha-beta plait</a>	RT		67	1.3E-4	1.6E0	1.9E-3	1.7E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:RRM	RT		36	4.3E-4	1.8E0	1.3E-2	1.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:RRM 1	RT		32	1.9E-3	1.7E0	5.2E-2	5.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:RRM 2	RT		32	1.9E-3	1.7E0	5.2E-2	5.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:RRM 3	RT		16	2.8E-2	1.8E0	5.3E-1	5.2E-1
<input type="checkbox"/>	SMART	<a href="#">RRM</a>	RT		62	8.5E-2	1.2E0	4.6E-1	4.2E-1
Annotation Cluster 73		Enrichment Score: 3.27	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ATP-dependent chromatin remodeling</a>	RT		13	1.1E-4	3.4E0	3.5E-3	3.3E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">RNA polymerase II distal enhancer sequence-specific DNA binding</a>	RT		23	6.0E-4	2.1E0	7.0E-3	6.2E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">nucleosomal DNA binding</a>	RT		17	2.3E-3	2.2E0	2.3E-2	2.0E-2
Annotation Cluster 74		Enrichment Score: 3.17	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">nuclear proteasome complex</a>	RT		8	1.6E-5	6.4E0	2.9E-4	2.5E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">proteasome regulatory particle, base subcomplex</a>	RT		9	1.0E-4	4.8E0	1.4E-3	1.2E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">cytosolic proteasome complex</a>	RT		8	1.8E-4	5.1E0	2.4E-3	2.1E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">proteasome accessory complex</a>	RT		10	4.2E-4	3.7E0	4.6E-3	4.0E-3
<input type="checkbox"/>	INTERPRO	<a href="#">26S proteasome subunit P45</a>	RT		6	5.7E-4	6.2E0	7.2E-3	6.6E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein catabolic process</a>	RT		17	6.0E-4	2.5E0	1.5E-2	1.4E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">proteasome-activating ATPase activity</a>	RT		6	6.8E-4	6.0E0	7.6E-3	6.7E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">TBP-class protein binding</a>	RT		11	1.0E-3	3.1E0	1.1E-2	9.7E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of RNA polymerase II transcriptional preinitiation complex assembly</a>	RT		7	1.2E-3	4.6E0	2.8E-2	2.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of proteasomal protein catabolic process</a>	RT		8	1.1E-2	3.0E0	1.5E-1	1.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ER-associated ubiquitin-dependent protein catabolic process</a>	RT		17	3.7E-2	1.7E0	3.8E-1	3.6E-1
Annotation Cluster 75		Enrichment Score: 3.17	G		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	domain:PI3K/PI4K	<a href="#">RT</a>	<div><div></div><div></div></div>	15	3.6E-9	5.7E0	2.0E-7	2.0E-7
<input type="checkbox"/>	INTERPRO	<a href="#">Phosphatidylinositol 3/4-kinase, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	1.7E-8	5.4E0	5.0E-7	4.6E-7
<input type="checkbox"/>	INTERPRO	<a href="#">Phosphatidylinositol 3-/4-kinase, catalytic domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	4.1E-8	4.9E0	1.1E-6	1.0E-6
<input type="checkbox"/>	SMART	<a href="#">PI3Kc</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	8.6E-7	3.6E0	1.6E-5	1.4E-5
<input type="checkbox"/>	INTERPRO	<a href="#">Phosphoinositide 3-kinase, accessory (PIK) domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.5E-5	5.6E0	2.8E-4	2.5E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Phosphatidylinositol 3-kinase C2 (PI3K C2) domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.9E-5	6.2E0	3.4E-4	3.1E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">phosphatidylinositol-3-phosphate biosynthetic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	21	6.1E-5	2.5E0	2.0E-3	1.9E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">1-phosphatidylinositol-3-kinase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	19	8.9E-5	2.6E0	1.3E-3	1.2E-3
<input type="checkbox"/>	SMART	<a href="#">PI3Ka</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	9.1E-5	4.1E0	1.1E-3	1.0E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Phosphatidylinositol 3-kinase Ras-binding (PI3K RBD) domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.1E-4	6.2E0	1.6E-3	1.5E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Phosphatidylinositol Kinase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.2E-4	4.6E0	1.8E-3	1.7E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">1-phosphatidylinositol-4-phosphate 3-kinase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.3E-4	6.0E0	1.8E-3	1.6E-3
<input type="checkbox"/>	SMART	<a href="#">PI3K_C2</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	3.3E-4	4.1E0	3.9E-3	3.5E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">phosphatidylinositol 3-kinase complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	4.5E-4	4.1E0	4.9E-3	4.2E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">phosphatidylinositol 3-kinase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	3.4E-3	6.0E0	3.2E-2	2.8E-2
<input type="checkbox"/>	SMART	<a href="#">PI3K_rbd</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	4.2E-3	4.1E0	4.0E-2	3.6E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Phosphatidylinositol 3-kinase adaptor-binding (PI3K ABD) domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">phosphatidylinositol biosynthetic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	5.4E-2	1.6E0	4.8E-1	4.6E-1
<input type="checkbox"/>	SMART	<a href="#">PI3K_p85B</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.5E-1	4.1E0	6.5E-1	5.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Phosphatidylinositol signaling system</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	18	7.1E-1	9.6E-1	1.0E0	7.1E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Inositol phosphate metabolism</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	13	7.3E-1	9.6E-1	1.0E0	7.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PX	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.8E-1	5.7E-1	1.0E0	9.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Phox homologous domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	9.8E-1	5.6E-1	1.0E0	9.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">phosphatidylinositol binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.0E0	4.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	<a href="#">PX</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	3.6E-1	1.0E0	1.0E0
Annotation Cluster 76		Enrichment Score: 3.17	<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	<a href="#">protein K6-linked ubiquitination</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	2.6E-5	5.9E0	9.6E-4	9.1E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein K29-linked ubiquitination</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	3.5E-3	5.9E0	6.5E-2	6.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein K27-linked ubiquitination</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	3.5E-3	5.9E0	6.5E-2	6.2E-2
Annotation Cluster 77		Enrichment Score: 3.13	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	<a href="#">Inhibition of Cellular Proliferation by Gleevec</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	19	7.1E-6	2.5E0	2.9E-4	2.0E-4
<input type="checkbox"/>	BIOCARTA	<a href="#">EGF Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	21	9.1E-6	2.4E0	2.9E-4	2.0E-4
<input type="checkbox"/>	BIOCARTA	<a href="#">PDGF Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	21	2.2E-5	2.3E0	5.9E-4	4.0E-4
<input type="checkbox"/>	BIOCARTA	<a href="#">IL-2 Receptor Beta Chain in T cell Activation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	26	3.8E-5	2.1E0	9.2E-4	6.2E-4
<input type="checkbox"/>	BIOCARTA	<a href="#">IGF-1 Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	4.3E-5	2.5E0	9.2E-4	6.2E-4
<input type="checkbox"/>	BIOCARTA	<a href="#">Growth Hormone Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	20	5.1E-5	2.3E0	9.2E-4	6.2E-4
<input type="checkbox"/>	BIOCARTA	<a href="#">IL 2 signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	1.1E-4	2.4E0	1.6E-3	1.1E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">TPO Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	18	1.1E-4	2.3E0	1.6E-3	1.1E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	22	1.9E-4	2.1E0	2.4E-3	1.6E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">Insulin Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	2.6E-4	2.3E0	2.7E-3	1.8E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">IL 6 signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	2.6E-4	2.3E0	2.7E-3	1.8E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">Signaling of Hepatocyte Growth Factor Receptor</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	23	3.2E-4	2.0E0	3.1E-3	2.1E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">Role of ERBB2 in Signal Transduction and Oncology</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	1.2E-3	2.1E0	9.0E-3	6.1E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">EPO Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	1.3E-3	2.3E0	9.8E-3	6.7E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">Links between Pyk2 and Map Kinases</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	18	1.7E-3	2.0E0	1.3E-2	8.5E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">Bioactive Peptide Induced Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	22	2.7E-3	1.8E0	1.6E-2	1.1E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">BCR Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	20	3.6E-3	1.8E0	2.1E-2	1.4E-2


















































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"/>	BIOCARTA	<a href="#">Fc Epsilon Receptor I Signaling in Mast Cells</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	22	4.1E-3	1.7E0	2.3E-2	1.6E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">T Cell Receptor Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	24	4.4E-3	1.7E0	2.4E-2	1.7E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">IL 3 signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	6.5E-3	2.3E0	3.2E-2	2.2E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">Nerve growth factor pathway (NGF)</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	13	9.7E-3	2.0E0	4.2E-2	2.9E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">Integrin Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	20	1.2E-2	1.7E0	5.0E-2	3.4E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">fMLP induced chemokine gene expression in HMC-1 cells</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	19	2.7E-2	1.6E0	9.1E-2	6.1E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">Sprouty regulation of tyrosine kinase signals</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	3.5E-2	1.9E0	1.0E-1	7.0E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	2.2E-1	1.4E0	4.5E-1	3.1E-1
Annotation Cluster 78		Enrichment Score: 3.11	<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)	<a href="#">RT</a>	<div><div></div><div></div></div>	12	7.8E-6	4.5E0	3.1E-4	3.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Gly-rich (hinge region)	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.1E-3	5.8E0	3.1E-2	3.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mRNA splice site selection</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	5.3E-2	2.4E0	4.8E-1	4.5E-1
Annotation Cluster 79		Enrichment Score: 3.07	<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	<a href="#">histone deacetylase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	22	1.3E-7	3.4E0	3.3E-6	2.9E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">histone deacetylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	22	5.0E-6	2.8E0	2.4E-4	2.2E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Histone deacetylase	<a href="#">RT</a>	<div><div></div><div></div></div>	9	7.3E-6	6.1E0	3.0E-4	2.9E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Histone deacetylase domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	1.0E-5	5.2E0	1.9E-4	1.7E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">NAD-dependent histone deacetylase activity (H3-K14 specific)</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	1.4E-5	5.0E0	2.6E-4	2.3E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein deacetylase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	2.0E-5	5.4E0	3.4E-4	3.0E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">histone H3 deacetylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	13	3.4E-5	3.7E0	1.2E-3	1.1E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Histone deacetylase superfamily</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	6.7E-5	4.4E0	1.1E-3	1.0E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein deacetylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	2.9E-4	4.7E0	8.0E-3	7.6E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">histone deacetylase complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	6.7E-4	2.6E0	7.0E-3	6.2E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of gene expression, epigenetic</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	4.4E-3	3.4E0	7.7E-2	7.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">histone H4 deacetylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	9.4E-3	4.0E0	1.4E-1	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">peptidyl-lysine deacetylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.8E-2	4.2E0	2.3E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Histone deacetylase class II, eukaryotic</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of myotube differentiation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	4.0E-2	2.6E0	3.9E-1	3.7E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">histone deacetylase class II, eukaryotic type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	4.8E-2	4.3E0	6.2E-1	6.1E-1
<input type="checkbox"/>	COG_ONTOLOGY	<a href="#">Chromatin structure and dynamics / Secondary metabolites biosynthesis, transport, and catabolism</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	4.8E-2	2.2E0	5.0E-1	5.0E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Histone deacetylase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.1E-1	5.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Histone deacetylase, glutamine rich N-terminal domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.1E-1	5.6E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">histone deacetylase class I, eukaryotic type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.6E-1	4.0E0	1.0E0	9.9E-1
Annotation Cluster 80		Enrichment Score: 3.07	<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:Pre-SET	<a href="#">RT</a>	<div><div></div><div></div></div>	7	6.1E-5	6.8E0	2.1E-3	2.0E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Pre-SET domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.1E-4	6.2E0	1.6E-3	1.5E-3
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Lysine degradation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	21	8.8E-4	2.1E0	1.9E-3	8.8E-4
<input type="checkbox"/>	SMART	<a href="#">PreSET</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.2E-3	4.1E0	1.3E-2	1.2E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">histone methyltransferase activity (H3-K9 specific)</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	3.4E-3	6.0E0	3.2E-2	2.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">histone H3-K9 methylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.7E-2	5.9E0	2.2E-1	2.1E-1
Annotation Cluster 81		Enrichment Score: 3.06	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Post-SET	<a href="#">RT</a>	<div><div></div><div></div></div>	15	1.9E-10	6.4E0	1.2E-8	1.1E-8
<input type="checkbox"/>	INTERPRO	<a href="#">Post-SET domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	1.7E-8	5.4E0	5.0E-7	4.6E-7
<input type="checkbox"/>	SMART	<a href="#">PostSET</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.0E-4	3.5E0	1.3E-3	1.1E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">histone methyltransferase complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	3.1E-4	3.3E0	3.5E-3	3.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">histone H3-K4 methylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	6.5E-4	3.3E0	1.6E-2	1.5E-2












































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">histone methyltransferase activity (H3-K4 specific)</a>	RT		10	1.2E-3	3.3E0	1.2E-2	1.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type 2	RT		11	8.2E-3	2.5E0	2.0E-1	1.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type 3	RT		6	9.0E-3	4.1E0	2.1E-1	2.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type 1	RT		11	1.7E-2	2.3E0	3.4E-1	3.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">FY-rich, N-terminal</a>	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">FY-rich, C-terminal</a>	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	SMART	<a href="#">FYRN</a>	RT		4	9.8E-2	3.3E0	4.9E-1	4.4E-1
<input type="checkbox"/>	SMART	<a href="#">FYRC</a>	RT		4	9.8E-2	3.3E0	4.9E-1	4.4E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">MLL3/4 complex</a>	RT		4	1.6E-1	2.8E0	6.4E-1	5.6E-1
Annotation Cluster 82		Enrichment Score: 3.01	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">proteasome regulatory particle, base subcomplex</a>	RT		9	1.0E-4	4.8E0	1.4E-3	1.2E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent</a>	RT		21	2.7E-3	2.0E0	5.3E-2	5.0E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">proteasome regulatory particle</a>	RT		7	3.4E-3	4.0E0	2.9E-2	2.5E-2
Annotation Cluster 83		Enrichment Score: 3	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:S-adenosyl-L-methionine binding	RT		16	5.3E-5	3.1E0	1.9E-3	1.8E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Bacterial Fmu (Sun)/eukaryotic nucleolar NOL1/Nop2p</a>	RT		7	9.4E-4	4.8E0	1.1E-2	1.0E-2
<input type="checkbox"/>	INTERPRO	<a href="#">RNA (C5-cytosine) methyltransferase</a>	RT		6	4.0E-3	4.6E0	4.2E-2	3.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:S-adenosyl-L-methionine	RT		16	5.2E-3	2.1E0	1.3E-1	1.3E-1
Annotation Cluster 84		Enrichment Score: 2.99	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Translation protein SH3-like domain</a>	RT		11	6.3E-6	4.9E0	1.2E-4	1.1E-4
<input type="checkbox"/>	INTERPRO	<a href="#">KOW</a>	RT		8	7.5E-5	5.5E0	1.2E-3	1.1E-3
<input type="checkbox"/>	SMART	<a href="#">KOW</a>	RT		5	3.5E-2	3.4E0	2.4E-1	2.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ribosomal protein L24/L26, conserved site</a>	RT		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
Annotation Cluster 85		Enrichment Score: 2.86	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Nucleosome core</a>	RT		31	4.5E-6	2.4E0	2.8E-5	2.2E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">chromatin silencing</a>	RT		17	1.9E-3	2.2E0	4.0E-2	3.8E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Histone H2A</a>	RT		11	5.1E-3	2.6E0	5.3E-2	4.9E-2
<input type="checkbox"/>	SMART	<a href="#">H2A</a>	RT		11	8.1E-2	1.7E0	4.5E-1	4.0E-1
Annotation Cluster 86		Enrichment Score: 2.86	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein peptidyl-prolyl isomerization</a>	RT		21	5.8E-6	2.9E0	2.7E-4	2.5E-4
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Rotamase</a>	RT		18	7.6E-6	3.3E0	4.6E-5	3.6E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">peptidyl-prolyl cis-trans isomerase activity</a>	RT		21	1.9E-5	2.7E0	3.3E-4	2.9E-4
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Isomerase</a>	RT		35	1.0E-4	2.0E0	5.4E-4	4.2E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Peptidyl-prolyl cis-trans isomerase, FKBP-type</a>	RT		8	3.2E-2	2.5E0	2.4E-1	2.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">chaperone-mediated protein folding</a>	RT		12	3.7E-2	1.9E0	3.8E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">FK506 binding</a>	RT		8	3.8E-2	2.4E0	2.3E-1	2.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain</a>	RT		7	5.7E-2	2.4E0	3.9E-1	3.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PPIase FKBP-type	RT		5	8.6E-2	2.8E0	1.0E0	9.7E-1
Annotation Cluster 87		Enrichment Score: 2.77	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Ala/Asp-rich (DA-box)	RT		8	1.0E-5	6.8E0	3.9E-4	3.8E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Flexible hinge	RT		7	6.1E-5	6.8E0	2.1E-3	2.0E-3
<input type="checkbox"/>	INTERPRO	<a href="#">RecF/RecN/SMC</a>	RT		7	1.1E-4	6.2E0	1.6E-3	1.5E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Structural maintenance of chromosomes protein</a>	RT		5	2.9E-3	6.2E0	3.2E-2	2.9E-2
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">structural maintenance of chromosomes protein</a>	RT		5	5.1E-3	5.3E0	2.0E-1	1.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">SMCs flexible hinge</a>	RT		5	7.7E-3	5.2E0	7.5E-2	6.9E-2
<input type="checkbox"/>	SMART	<a href="#">SM00968</a>	RT		5	3.5E-2	3.4E0	2.4E-1	2.1E-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"/>	GOTERM_CC_DIRECT	<a href="#">meiotic cohesin complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.4E-1	3.2E0	8.4E-1	7.4E-1
Annotation Cluster 88		Enrichment Score: 2.76	<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:Chromo 2	<a href="#">RT</a>	<div><div></div><div></div></div>	8	4.0E-5	6.1E0	1.4E-3	1.4E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Chromo domain-like</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	2.0E-4	2.9E0	2.9E-3	2.7E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Chromo domain/shadow</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	3.0E-4	2.8E0	4.1E-3	3.8E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Chromo 1	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.1E-3	4.2E0	3.1E-2	3.0E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Chromo domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	5.1E-3	2.6E0	5.3E-2	4.9E-2
<input type="checkbox"/>	SMART	<a href="#">CHROMO</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	1.8E-2	1.9E0	1.4E-1	1.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Chromo domain, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	2.1E-1	1.9E0	9.5E-1	8.7E-1
Annotation Cluster 89		Enrichment Score: 2.72	<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	<a href="#">U6 snRNP</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	9.1E-5	6.4E0	1.3E-3	1.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	5.4E-3	2.5E0	9.3E-2	8.8E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">Lsm1-7-Pat1 complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.4E-2	6.4E0	9.7E-2	8.5E-2
Annotation Cluster 90		Enrichment Score: 2.71	<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:Chromo 2	<a href="#">RT</a>	<div><div></div><div></div></div>	8	4.0E-5	6.1E0	1.4E-3	1.4E-3
<input type="checkbox"/>	INTERPRO	<a href="#">BRK domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	5.7E-4	6.2E0	7.2E-3	6.6E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Chromo 1	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.1E-3	4.2E0	3.1E-2	3.0E-2
<input type="checkbox"/>	SMART	<a href="#">BRK</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	4.2E-3	4.1E0	4.0E-2	3.6E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">hydrolase activity, acting on acid anhydrides</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.7E-1	3.0E0	9.5E-1	8.4E-1
Annotation Cluster 91		Enrichment Score: 2.67	<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	<a href="#">Protein biosynthesis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	43	2.1E-5	1.9E0	1.2E-4	9.6E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of translational initiation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	9.9E-5	2.8E0	3.2E-3	3.0E-3
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Initiation factor</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	21	1.2E-4	2.5E0	6.4E-4	4.9E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">IRES-dependent viral translational initiation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.4E-4	5.9E0	4.2E-3	4.0E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">translation initiation factor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	23	2.2E-4	2.2E0	2.8E-3	2.5E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">eukaryotic translation initiation factor 3 complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	4.2E-4	3.7E0	4.6E-3	4.0E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">eukaryotic 43S preinitiation complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	8.4E-4	3.8E0	8.2E-3	7.1E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">eukaryotic 48S preinitiation complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	8.4E-4	3.8E0	8.2E-3	7.1E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">eukaryotic translation initiation factor 3 complex, eIF3m</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.5E-3	5.4E0	1.4E-2	1.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">formation of translation preinitiation complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	9.2E-3	2.6E0	1.4E-1	1.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Proteasome component (PCI) domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.3E-1	2.2E0	6.1E-1	5.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PCI	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.3E-1	2.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">viral translational termination-reinitiation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	SMART	<a href="#">PINT</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.5E-1	1.5E0	1.0E0	9.0E-1
Annotation Cluster 92		Enrichment Score: 2.66	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Thioredoxin domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	21	1.1E-6	3.2E0	2.7E-5	2.4E-5







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	site:Lowers pKa of C-terminal Cys of first active site	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Lowers pKa of C-terminal Cys of second active site	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Protein disulphide isomerase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Thioredoxin 3	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.5E-2	5.5E0	4.8E-1	4.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">isomerase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.3E-1	2.0E0	5.8E-1	5.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Thioredoxin-like fold</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	27	1.4E-1	1.3E0	6.8E-1	6.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Prevents secretion from ER	<a href="#">RT</a>	<div><div></div><div></div></div>	13	1.8E-1	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">cell</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	20	2.2E-1	1.3E0	7.9E-1	6.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">disulfide oxidoreductase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.7E-1	3.0E0	9.5E-1	8.4E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">endoplasmic reticulum lumen</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	19	1.0E0	6.3E-1	1.0E0	1.0E0
Annotation Cluster 93		Enrichment Score: 2.66	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">U1 snRNP binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.3E-4	6.0E0	1.8E-3	1.6E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">commitment complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.5E-3	5.4E0	1.4E-2	1.2E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">prespliceosome</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.4E-2	4.2E0	2.9E-1	2.5E-1
Annotation Cluster 94		Enrichment Score: 2.64	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH3	<a href="#">RT</a>	<div><div></div><div></div></div>	48	1.9E-5	1.9E0	7.1E-4	6.9E-4
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">SH3 domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	51	4.3E-4	1.6E0	2.2E-3	1.7E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Src homology-3 domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	51	5.3E-3	1.5E0	5.5E-2	5.0E-2
<input type="checkbox"/>	SMART	<a href="#">SH3</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	50	6.2E-1	9.9E-1	1.0E0	9.0E-1
Annotation Cluster 95		Enrichment Score: 2.59	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	INTERPRO	<a href="#">14-3-3 protein, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.1E-4	6.2E0	1.6E-3	1.5E-3
<input type="checkbox"/>	INTERPRO	<a href="#">14-3-3 domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.1E-4	6.2E0	1.6E-3	1.5E-3
<input type="checkbox"/>	INTERPRO	<a href="#">14-3-3 protein</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.1E-4	6.2E0	1.6E-3	1.5E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Interaction with phosphoserine on interacting protein	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.1E-4	6.0E0	6.6E-3	6.4E-3
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">14-3-3 protein</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.4E-4	5.3E0	1.5E-2	1.5E-2
<input type="checkbox"/>	SMART	<a href="#">14 3 3</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.2E-3	4.1E0	1.3E-2	1.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	13	2.2E-3	2.6E0	4.5E-2	4.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">membrane organization</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	2.9E-1	1.5E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein targeting</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	3.3E-1	1.4E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">cytoplasmic vesicle membrane</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	8.6E-1	8.6E-1	1.0E0	8.7E-1
Annotation Cluster 96		Enrichment Score: 2.52	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">UTP biosynthetic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.7E-4	4.4E0	5.0E-3	4.7E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">CTP biosynthetic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.7E-4	4.4E0	5.0E-3	4.7E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Pros-phosphohistidine intermediate	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.1E-4	6.0E0	6.6E-3	6.4E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleobase-containing small molecule interconversion</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	13	3.1E-4	3.1E0	8.4E-3	8.0E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Nucleoside diphosphate kinase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	5.1E-4	4.5E0	6.8E-3	6.3E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">nucleoside diphosphate kinase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	6.2E-4	3.3E0	7.1E-3	6.3E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleoside diphosphate phosphorylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	1.2E-3	3.3E0	2.8E-2	2.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">GTP biosynthetic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	2.6E-3	3.6E0	5.0E-2	4.8E-2
<input type="checkbox"/>	SMART	<a href="#">NDK</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	6.7E-3	3.0E0	6.1E-2	5.5E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Nucleoside diphosphate kinase, active site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.6E-2	4.4E0	1.3E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">pyrimidine nucleotide metabolic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	5.0E-2	3.3E0	4.6E-1	4.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleoside triphosphate biosynthetic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	7.2E-2	2.5E0	5.7E-1	5.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">purine nucleotide metabolic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	7.2E-2	3.0E0	5.7E-1	5.4E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Nucleotide metabolism</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.0E-1	2.0E0	3.4E-1	2.6E-1
Annotation Cluster 97		Enrichment Score: 2.52	<div><div>G</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"/>	INTERPRO	<a href="#">Translation elongation factor EFTu/EF1A, domain 2</a>	RT		11	1.6E-5	4.5E0	2.9E-4	2.7E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Translation elongation/initiation factor/Ribosomal, beta-barrel</a>	RT		16	1.7E-5	3.3E0	3.1E-4	2.8E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Elongation factor, GTP-binding domain</a>	RT		12	7.6E-5	3.7E0	1.2E-3	1.1E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Ribosomal protein S5 domain 2-type fold, subgroup</a>	RT		12	6.0E-4	3.1E0	7.5E-3	6.9E-3
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Elongation factor</a>	RT		12	2.3E-3	2.7E0	1.1E-2	8.6E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Translation elongation factor EFG, V domain</a>	RT		5	7.7E-3	5.2E0	7.5E-2	6.9E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Elongation factor G, III-V domain</a>	RT		5	7.7E-3	5.2E0	7.5E-2	6.9E-2
<input type="checkbox"/>	SMART	<a href="#">SM00838</a>	RT		5	1.4E-2	4.1E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Translation elongation factor EFG/EF2, domain IV</a>	RT		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Translation elongation factor EFTu/EF1A, C-terminal</a>	RT		5	1.6E-2	4.4E0	1.3E-1	1.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Translation elongation factor EF1A/initiation factor IF2gamma, C-terminal</a>	RT		6	2.1E-2	3.4E0	1.7E-1	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">translational elongation</a>	RT		8	2.2E-2	2.6E0	2.7E-1	2.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">translation elongation factor activity</a>	RT		11	4.7E-2	1.9E0	2.8E-1	2.5E-1
<input type="checkbox"/>	SMART	<a href="#">SM00889</a>	RT		4	4.8E-2	4.1E0	2.8E-1	2.6E-1
Annotation Cluster 98		Enrichment Score: 2.44	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of type I interferon production</a>	RT		23	9.3E-6	2.7E0	3.9E-4	3.7E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">transcription from RNA polymerase III promoter</a>	RT		14	1.7E-3	2.5E0	3.7E-2	3.5E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">DNA-directed RNA polymerase III complex</a>	RT		8	2.1E-2	2.7E0	1.4E-1	1.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">RNA polymerase III activity</a>	RT		8	2.1E-2	2.7E0	1.4E-1	1.3E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Cytosolic DNA-sensing pathway</a>	RT		18	9.0E-2	1.5E0	1.5E-1	9.0E-2
Annotation Cluster 99		Enrichment Score: 2.43	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Shigellosis</a>	RT		26	1.6E-4	2.1E0	3.8E-4	1.7E-4
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Epithelial cell signaling in Helicobacter pylori infection</a>	RT		23	5.2E-3	1.8E0	1.0E-2	5.2E-3
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">RIG-I-like receptor signaling pathway</a>	RT		20	6.3E-2	1.5E0	1.1E-1	6.3E-2
Annotation Cluster 100		Enrichment Score: 2.41	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">four-way junction DNA binding</a>	RT		10	9.2E-5	4.3E0	1.3E-3	1.2E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">replication fork</a>	RT		10	4.2E-4	3.7E0	4.6E-3	4.0E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">recombinase activity</a>	RT		7	4.5E-4	5.2E0	5.5E-3	4.9E-3
<input type="checkbox"/>	INTERPRO	<a href="#">DNA recombination and repair protein, RecA-like</a>	RT		6	5.7E-4	6.2E0	7.2E-3	6.6E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">reciprocal meiotic recombination</a>	RT		14	6.0E-4	2.8E0	1.5E-2	1.4E-2
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">DNA repair and recombination protein, Rad51 type</a>	RT		6	1.1E-3	5.3E0	5.4E-2	5.4E-2
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Homologous recombination</a>	RT		14	1.4E-3	2.5E0	2.9E-3	1.4E-3
<input type="checkbox"/>	INTERPRO	<a href="#">DNA recombination and repair protein Rad51, C-terminal</a>	RT		6	1.7E-3	5.3E0	2.0E-2	1.8E-2
<input type="checkbox"/>	INTERPRO	<a href="#">DNA recombination/repair protein RecA/RadB, ATP-binding domain</a>	RT		6	1.7E-3	5.3E0	2.0E-2	1.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">strand invasion</a>	RT		6	2.1E-3	5.1E0	4.3E-2	4.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitotic recombination</a>	RT		8	2.6E-3	3.6E0	5.0E-2	4.8E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">endodeoxyribonuclease activity</a>	RT		10	6.3E-3	2.7E0	5.5E-2	4.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">chromosome organization involved in meiotic cell cycle</a>	RT		4	1.7E-2	5.9E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">Rad51B-Rad51C-Rad51D-XRCC2 complex</a>	RT		4	3.0E-2	5.1E0	1.9E-1	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to ionizing radiation</a>	RT		14	5.8E-2	1.7E0	5.1E-1	4.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">DNA repair Rad51/transcription factor NusA, alpha-helical</a>	RT		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">meiotic DNA recombinase assembly</a>	RT		3	1.3E-1	4.4E0	8.1E-1	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">DNA recombinase assembly</a>	RT		3	2.0E-1	3.6E0	1.0E0	9.5E-1
Annotation Cluster 101		Enrichment Score: 2.4	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Ribosomal protein S1, RNA-binding domain</a>	RT		7	9.4E-4	4.8E0	1.1E-2	1.0E-2
<input type="checkbox"/>	INTERPRO	<a href="#">RNA-binding domain, S1</a>	RT		7	9.4E-4	4.8E0	1.1E-2	1.0E-2

















































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	SMART	<a href="#">SM00316</a>	<a href="#">RT</a>		7	9.0E-3	3.2E0	8.0E-2	7.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:S1 motif	<a href="#">RT</a>		5	3.1E-2	3.8E0	5.8E-1	5.6E-1
Annotation Cluster 102		Enrichment Score: 2.36	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase 1	<a href="#">RT</a>		10	6.7E-5	4.5E0	2.2E-3	2.2E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase 2	<a href="#">RT</a>		10	6.7E-5	4.5E0	2.2E-3	2.2E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Tyrosine-protein kinase, non-receptor Jak/Tyk2</a>	<a href="#">RT</a>		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">tyrosine-protein kinase, Jak/Tyk2 type</a>	<a href="#">RT</a>		4	2.2E-2	5.3E0	3.6E-1	3.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ribosomal protein S6 kinase II</a>	<a href="#">RT</a>		4	5.7E-2	4.1E0	3.9E-1	3.6E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">ribosomal protein S6 kinase II</a>	<a href="#">RT</a>		4	8.3E-2	3.6E0	7.7E-1	7.6E-1
Annotation Cluster 103		Enrichment Score: 2.31	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)</a>	<a href="#">RT</a>		9	5.0E-6	5.9E0	2.4E-4	2.2E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)</a>	<a href="#">RT</a>		4	1.7E-2	5.9E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Sufficient for nucleolar localization	<a href="#">RT</a>		3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">PeBoW complex</a>	<a href="#">RT</a>		3	1.2E-1	4.8E0	5.0E-1	4.4E-1
Annotation Cluster 104		Enrichment Score: 2.29	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Guanylate kinase, conserved site</a>	<a href="#">RT</a>		13	2.9E-7	5.0E0	7.2E-6	6.6E-6
<input type="checkbox"/>	INTERPRO	<a href="#">Guanylate kinase</a>	<a href="#">RT</a>		14	5.7E-6	3.9E0	1.1E-4	1.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Guanylate kinase-like	<a href="#">RT</a>		14	7.2E-6	4.0E0	3.0E-4	2.9E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">GMP metabolic process</a>	<a href="#">RT</a>		11	2.4E-5	4.3E0	9.0E-4	8.5E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:L27 1	<a href="#">RT</a>		7	6.1E-5	6.8E0	2.1E-3	2.0E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:L27 2	<a href="#">RT</a>		7	6.1E-5	6.8E0	2.1E-3	2.0E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Guanylate kinase/L-type calcium channel</a>	<a href="#">RT</a>		14	6.3E-5	3.3E0	1.1E-3	9.6E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">guanylate kinase activity</a>	<a href="#">RT</a>		9	1.6E-4	4.5E0	2.2E-3	1.9E-3
<input type="checkbox"/>	INTERPRO	<a href="#">L27</a>	<a href="#">RT</a>		9	5.4E-4	4.0E0	7.2E-3	6.6E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">GDP metabolic process</a>	<a href="#">RT</a>		8	6.7E-4	4.3E0	1.6E-2	1.6E-2
<input type="checkbox"/>	INTERPRO	<a href="#">L27, C-terminal</a>	<a href="#">RT</a>		7	2.0E-3	4.3E0	2.3E-2	2.1E-2
<input type="checkbox"/>	SMART	<a href="#">GuKc</a>	<a href="#">RT</a>		14	2.7E-3	2.3E0	2.8E-2	2.5E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">ionotropic glutamate receptor complex</a>	<a href="#">RT</a>		6	3.5E-3	4.8E0	2.9E-2	2.6E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ionotropic glutamate receptor binding</a>	<a href="#">RT</a>		10	4.4E-3	2.8E0	3.9E-2	3.5E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PDZ	<a href="#">RT</a>		27	1.2E-2	1.6E0	2.4E-1	2.3E-1
<input type="checkbox"/>	SMART	<a href="#">L27</a>	<a href="#">RT</a>		8	1.3E-2	2.7E0	1.1E-1	9.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">establishment or maintenance of epithelial cell apical/basal polarity</a>	<a href="#">RT</a>		7	1.3E-2	3.2E0	1.9E-1	1.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">PDZ-associated domain of NMDA receptors</a>	<a href="#">RT</a>		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Membrane-associated guanylate kinase (MAGUK), PEST domain, N-terminal</a>	<a href="#">RT</a>		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Membrane-associated guanylate kinase (MAGUK) scaffold protein</a>	<a href="#">RT</a>		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Variant SH3</a>	<a href="#">RT</a>		17	3.0E-2	1.7E0	2.3E-1	2.1E-1
<input type="checkbox"/>	SMART	<a href="#">SM01277</a>	<a href="#">RT</a>		4	4.8E-2	4.1E0	2.8E-1	2.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">PDZ domain</a>	<a href="#">RT</a>		33	8.0E-2	1.3E0	4.4E-1	4.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">membrane-associated guanylate kinase (MAGUK) scaffold protein</a>	<a href="#">RT</a>		3	9.1E-2	5.3E0	7.7E-1	7.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">receptor localization to synapse</a>	<a href="#">RT</a>		4	1.8E-1	2.6E0	9.9E-1	9.4E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Synaptic Proteins at the Synaptic Junction</a>	<a href="#">RT</a>		9	2.0E-1	1.5E0	4.1E-1	2.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">receptor clustering</a>	<a href="#">RT</a>		5	4.4E-1	1.5E0	1.0E0	9.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PDZ 3	<a href="#">RT</a>		6	4.6E-1	1.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PDZ 1	<a href="#">RT</a>		6	7.6E-1	9.7E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PDZ 2	<a href="#">RT</a>		6	7.6E-1	9.7E-1	1.0E0	9.7E-1

Annotation Cluster 1		Enrichment Score: ?	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	SMART	<a href="#">PDZ</a>	<a href="#">RT</a>	<div></div>	33	8.3E-1	9.0E-1	1.0E0	9.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ligand-gated ion channel activity</a>	<a href="#">RT</a>	<div></div>	4	9.5E-1	6.6E-1	1.0E0	9.5E-1
Annotation Cluster 105		Enrichment Score: 2.21	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">DDT domain superfamily</a>	<a href="#">RT</a>	<div></div>	5	2.9E-3	6.2E0	3.2E-2	2.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DDT	<a href="#">RT</a>	<div></div>	5	5.4E-3	5.7E0	1.3E-1	1.3E-1
<input type="checkbox"/>	SMART	<a href="#">DDT</a>	<a href="#">RT</a>	<div></div>	5	1.4E-2	4.1E0	1.2E-1	1.1E-1
Annotation Cluster 106		Enrichment Score: 2.19	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Cullin, N-terminal</a>	<a href="#">RT</a>	<div></div>	8	2.1E-4	5.0E0	3.1E-3	2.8E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Cullin homology</a>	<a href="#">RT</a>	<div></div>	7	9.4E-4	4.8E0	1.1E-2	1.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in NEDD8)	<a href="#">RT</a>	<div></div>	6	1.1E-3	5.8E0	3.1E-2	3.0E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Cullin protein, neddylation domain</a>	<a href="#">RT</a>	<div></div>	6	4.0E-3	4.6E0	4.2E-2	3.8E-2
<input type="checkbox"/>	SMART	<a href="#">CULLIN</a>	<a href="#">RT</a>	<div></div>	6	1.2E-2	3.5E0	1.0E-1	9.0E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Cullin, conserved site</a>	<a href="#">RT</a>	<div></div>	5	1.6E-2	4.4E0	1.3E-1	1.2E-1
<input type="checkbox"/>	SMART	<a href="#">SM00884</a>	<a href="#">RT</a>	<div></div>	6	2.5E-2	3.1E0	1.9E-1	1.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Cullin repeat-like-containing domain</a>	<a href="#">RT</a>	<div></div>	6	3.2E-2	3.1E0	2.4E-1	2.2E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">cullin-RING ubiquitin ligase complex</a>	<a href="#">RT</a>	<div></div>	4	1.6E-1	2.8E0	6.4E-1	5.6E-1
Annotation Cluster 107		Enrichment Score: 2.16	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">guanyl nucleotide binding</a>	<a href="#">RT</a>	<div></div>	8	9.7E-5	5.3E0	1.4E-3	1.2E-3
<input type="checkbox"/>	INTERPRO	<a href="#">G-protein alpha subunit, group Q</a>	<a href="#">RT</a>	<div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">phospholipase C-activating dopamine receptor signaling pathway</a>	<a href="#">RT</a>	<div></div>	4	2.3E-1	2.4E0	1.0E0	9.5E-1
Annotation Cluster 108		Enrichment Score: 2.1	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">rRNA-binding</a>	<a href="#">RT</a>	<div></div>	15	8.6E-7	4.3E0	5.9E-6	4.6E-6
<input type="checkbox"/>	INTERPRO	<a href="#">KOW</a>	<a href="#">RT</a>	<div></div>	8	7.5E-5	5.5E0	1.2E-3	1.1E-3
<input type="checkbox"/>	INTERPRO	<a href="#">RNA-binding S4 domain</a>	<a href="#">RT</a>	<div></div>	5	7.7E-3	5.2E0	7.5E-2	6.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:S4 RNA-binding	<a href="#">RT</a>	<div></div>	5	2.0E-2	4.3E0	3.9E-1	3.8E-1
<input type="checkbox"/>	SMART	<a href="#">S4</a>	<a href="#">RT</a>	<div></div>	4	4.8E-2	4.1E0	2.8E-1	2.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ribosomal protein S4e</a>	<a href="#">RT</a>	<div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ribosomal protein S4e, N-terminal</a>	<a href="#">RT</a>	<div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ribosomal protein S4e, central region</a>	<a href="#">RT</a>	<div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ribosomal protein S4e, N-terminal, conserved site</a>	<a href="#">RT</a>	<div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">ribosomal protein S4a/S4e</a>	<a href="#">RT</a>	<div></div>	3	9.1E-2	5.3E0	7.7E-1	7.6E-1
Annotation Cluster 109		Enrichment Score: 2.09	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Phototransduction</a>	<a href="#">RT</a>	<div></div>	14	5.9E-4	2.7E0	1.3E-3	6.1E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">photoreceptor disc membrane</a>	<a href="#">RT</a>	<div></div>	8	2.1E-2	2.7E0	1.4E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of rhodopsin mediated signaling pathway</a>	<a href="#">RT</a>	<div></div>	10	4.4E-2	2.0E0	4.2E-1	4.0E-1
Annotation Cluster 110		Enrichment Score: 2.02	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	<a href="#">Cadmium induces DNA synthesis and proliferation in macrophages</a>	<a href="#">RT</a>	<div></div>	14	2.3E-4	2.5E0	2.6E-3	1.8E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">Links between Pyk2 and Map Kinases</a>	<a href="#">RT</a>	<div></div>	18	1.7E-3	2.0E0	1.3E-2	8.5E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">CXCR4 Signaling Pathway</a>	<a href="#">RT</a>	<div></div>	16	2.2E-3	2.1E0	1.4E-2	9.5E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">CCR3 signaling in Eosinophils</a>	<a href="#">RT</a>	<div></div>	13	3.8E-2	1.7E0	1.1E-1	7.4E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">Aspirin Blocks Signaling Pathway Involved in Platelet Activation</a>	<a href="#">RT</a>	<div></div>	11	1.0E-1	1.6E0	2.6E-1	1.7E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia</a>	<a href="#">RT</a>	<div></div>	11	2.2E-1	1.4E0	4.5E-1	3.1E-1
Annotation Cluster 111		Enrichment Score: 1.97	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">SANT/Myb domain</a>	<a href="#">RT</a>	<div></div>	18	2.0E-4	2.6E0	2.9E-3	2.6E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">transcription factor activity, RNA polymerase II transcription factor recruiting</a>	<a href="#">RT</a>	<div></div>	7	4.5E-4	5.2E0	5.5E-3	4.9E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Myb domain</a>	<a href="#">RT</a>	<div></div>	6	7.7E-3	4.1E0	7.5E-2	6.9E-2

Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	SMART	<a href="#">SANT</a>	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	18	2.1E-2	1.7E0	1.6E-1	1.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">SANT domain</a>	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	8	1.1E-1	1.9E0	5.9E-1	5.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Homeodomain-like</a>	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	22	1.0E0	4.1E-1	1.0E0	1.0E0
Annotation Cluster 112		Enrichment Score: 1.96	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">transcription factor activity, RNA polymerase II transcription factor recruiting</a>	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	7	4.5E-4	5.2E0	5.5E-3	4.9E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HTH myb-type 1	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	5	2.0E-3	6.8E0	5.4E-2	5.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HTH myb-type 2	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	5	2.0E-3	6.8E0	5.4E-2	5.2E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Myb-like domain</a>	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	6	4.0E-3	4.6E0	4.2E-2	3.8E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Myb domain</a>	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	6	7.7E-3	4.1E0	7.5E-2	6.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HTH myb-type 3	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Myb-like 1	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Myb-like 2	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">C-myb, C-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:H-T-H motif	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	7	1.7E-1	1.8E0	1.0E0	9.7E-1
Annotation Cluster 113		Enrichment Score: 1.95	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 1	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 2	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 1	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 3	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 10	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 4	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 11	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 12	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 13	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 14	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 15	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 2	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 3	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 4	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 5	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 6	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 7	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 8	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 9	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
Annotation Cluster 114		Enrichment Score: 1.95	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of interferon-gamma-mediated signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	10	4.0E-5	4.6E0	1.4E-3	1.3E-3
<input type="checkbox"/>	BBID	<a href="#">75.Stats activators of Apoptosis</a>	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	1.2E-1	2.9E0	9.8E-1	9.8E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">IFN gamma signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	4	3.0E-1	2.1E0	5.5E-1	3.8E-1
Annotation Cluster 115		Enrichment Score: 1.95	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FBA	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	5	5.4E-3	5.7E0	1.3E-1	1.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">F-box associated (FBA) domain</a>	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	5	7.7E-3	5.2E0	7.5E-2	6.9E-2
<input type="checkbox"/>	SMART	<a href="#">SM01198</a>	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	5	3.5E-2	3.4E0	2.4E-1	2.1E-1
Annotation Cluster 116		Enrichment Score: 1.93	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">MyD88-dependent toll-like receptor signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	22	2.4E-9	4.0E0	2.1E-7	2.0E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of cytokine secretion</a>	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	10	4.3E-6	5.4E0	2.1E-4	2.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 22	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	10	4.5E-6	5.7E0	1.9E-4	1.9E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">toll-like receptor signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div><div></div></div>	14	1.7E-4	3.1E0	5.0E-3	4.7E-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"/>	UP_SEQ_FEATURE	repeat:LRR 24	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.1E-3	5.8E0	3.1E-2	3.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">I-kappaB phosphorylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.4E-3	4.0E0	3.0E-2	2.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of chemokine production</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	3.7E-3	3.1E0	6.8E-2	6.5E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:TIR	<a href="#">RT</a>	<div><div></div><div></div></div>	10	6.9E-3	2.7E0	1.6E-1	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of interleukin-8 production</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	7.1E-3	2.5E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Toll-like receptor</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of NF-kappaB import into nucleus</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.7E-2	2.5E0	2.2E-1	2.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Toll/interleukin-1 receptor homology (TIR) domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	1.7E-2	2.4E0	1.4E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of interferon-alpha biosynthetic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.7E-2	5.9E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of interferon-beta biosynthetic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.8E-2	4.2E0	2.3E-1	2.2E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">toll-like receptor, 1/2/4/6/10 types [Parent=PIRSF800008]</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.2E-2	5.3E0	3.6E-1	3.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of interferon-beta production</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	2.8E-2	2.2E0	3.3E-1	3.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">toll-like receptor 9 signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.9E-2	2.8E0	3.3E-1	3.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of toll-like receptor signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.7E-2	4.7E0	3.8E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">microglial cell activation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.8E-2	3.0E0	3.8E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of interleukin-12 production</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	4.7E-2	2.1E0	4.5E-1	4.3E-1
<input type="checkbox"/>	SMART	<a href="#">TIR</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	5.0E-2	1.9E0	2.9E-1	2.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">endolysosome membrane</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.1E-1	2.6E0	4.9E-1	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of interleukin-6 production</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	1.2E-1	1.6E0	8.1E-1	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of interferon-gamma biosynthetic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.3E-1	2.5E0	8.1E-1	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of tumor necrosis factor production</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	2.6E-1	1.4E0	1.0E0	9.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Inflammatory response</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	26	2.9E-1	1.2E0	8.1E-1	6.3E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">lipopeptide binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of inflammatory response</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	4.6E-1	1.1E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to lipoteichoic acid</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.6E-1	2.0E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">phagocytic vesicle membrane</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	8.4E-1	8.6E-1	1.0E0	8.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">transmembrane signaling receptor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	1.0E0	4.5E-1	1.0E0	1.0E0
Annotation Cluster 117		Enrichment Score: 1.9	<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	<a href="#">regulation of axonogenesis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	5.7E-4	3.1E0	1.4E-2	1.4E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">Roundabout binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	9.1E-3	4.0E0	7.2E-2	6.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">Roundabout signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.8E-2	3.0E0	3.8E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">axon extension involved in axon guidance</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.3E-1	2.5E0	8.1E-1	7.7E-1
Annotation Cluster 118		Enrichment Score: 1.89	<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:C2 tensin-type	<a href="#">RT</a>	<div><div></div><div></div></div>	6	5.1E-3	4.5E0	1.3E-1	1.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Phosphatase tensin-type	<a href="#">RT</a>	<div><div></div><div></div></div>	6	9.0E-3	4.1E0	2.1E-1	2.0E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Tensin phosphatase, C2 domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.3E-2	3.7E0	1.2E-1	1.1E-1
<input type="checkbox"/>	SMART	<a href="#">SM01326</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	4.5E-2	2.7E0	2.8E-1	2.6E-1
Annotation Cluster 119		Enrichment Score: 1.86	<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	<a href="#">protein refolding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	2.0E-4	4.0E0	6.0E-3	5.7E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to unfolded protein</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	1.8E-2	2.0E0	2.3E-1	2.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Antigen processing and presentation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	7.2E-1	9.6E-1	1.0E0	7.2E-1
Annotation Cluster 120		Enrichment Score: 1.85	<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	<a href="#">receptor signaling protein tyrosine kinase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	2.0E-5	5.4E0	3.4E-4	3.0E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">insulin receptor substrate binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	6.3E-5	4.9E0	9.6E-4	8.5E-4
<input type="checkbox"/>	INTERPRO	<a href="#">EGF receptor, L domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.7E-3	5.3E0	2.0E-2	1.8E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Furin-like cysteine-rich domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.7E-3	5.3E0	2.0E-2	1.8E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Furin-like repeat</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	4.3E-3	3.1E0	4.5E-2	4.1E-2



Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	SMART	<a href="#">FU</a>	<a href="#">RT</a>		9	5.1E-2	2.0E0	2.9E-1	2.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Tyrosine-protein kinase, insulin-like receptor</a>	<a href="#">RT</a>		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">insulin receptor</a>	<a href="#">RT</a>		3	9.1E-2	5.3E0	7.7E-1	7.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Tyrosine protein kinase, EGF/ERB/XmrK receptor</a>	<a href="#">RT</a>		3	1.2E-1	4.6E0	6.1E-1	5.6E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">tyrosine-protein kinase, EGF receptor type</a>	<a href="#">RT</a>		3	1.6E-1	4.0E0	1.0E0	9.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Tyrosine-protein kinase, receptor class II, conserved site</a>	<a href="#">RT</a>		3	5.5E-1	1.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Fibronectin type-III 3	<a href="#">RT</a>		6	1.0E0	4.9E-1	1.0E0	1.0E0
Annotation Cluster 121		Enrichment Score: 1.85	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">sister chromatid cohesion</a>	<a href="#">RT</a>		33	2.7E-4	1.9E0	7.6E-3	7.2E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">kinetochore</a>	<a href="#">RT</a>		24	2.7E-3	1.9E0	2.4E-2	2.1E-2
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Centromere</a>	<a href="#">RT</a>		32	7.4E-3	1.6E0	3.3E-2	2.6E-2
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Kinetochore</a>	<a href="#">RT</a>		18	2.7E-1	1.2E0	7.8E-1	6.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">condensed chromosome kinetochore</a>	<a href="#">RT</a>		16	3.9E-1	1.2E0	1.0E0	8.7E-1
Annotation Cluster 122		Enrichment Score: 1.84	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Apoptosis</a>	<a href="#">RT</a>		26	8.5E-5	2.2E0	2.1E-4	9.7E-5
<input type="checkbox"/>	BIOCARTA	<a href="#">HIV-I Nef</a>	<a href="#">RT</a>		26	9.4E-2	1.3E0	2.3E-1	1.6E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Induction of apoptosis through DR3 and DR4/5 Death Receptors</a>	<a href="#">RT</a>		13	3.7E-1	1.2E0	6.4E-1	4.3E-1
Annotation Cluster 123		Enrichment Score: 1.79	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	<a href="#">p53 Signaling Pathway</a>	<a href="#">RT</a>		13	1.3E-3	2.4E0	9.8E-3	6.7E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">cyclin-dependent protein kinase holoenzyme complex</a>	<a href="#">RT</a>		7	2.1E-2	3.0E0	1.4E-1	1.2E-1
<input type="checkbox"/>	BBID	<a href="#">4.cyclins &amp; p27 cell cycle</a>	<a href="#">RT</a>		5	4.9E-2	2.9E0	7.6E-1	7.6E-1
<input type="checkbox"/>	BBID	<a href="#">94.E2F transcriptional activity cell cycle</a>	<a href="#">RT</a>		6	4.9E-2	2.5E0	7.6E-1	7.6E-1
Annotation Cluster 124		Enrichment Score: 1.78	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	<a href="#">Regulation of cell cycle progression by Plk3</a>	<a href="#">RT</a>		8	2.1E-3	3.1E0	1.4E-2	9.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">replicative senescence</a>	<a href="#">RT</a>		7	8.4E-3	3.5E0	1.3E-1	1.2E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Role of BRCA1, BRCA2 and ATR in Cancer Susceptibility</a>	<a href="#">RT</a>		10	2.6E-1	1.4E0	5.1E-1	3.4E-1
Annotation Cluster 125		Enrichment Score: 1.7	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HSA	<a href="#">RT</a>		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Helicase/SANT-associated, DNA binding</a>	<a href="#">RT</a>		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	SMART	<a href="#">HSA</a>	<a href="#">RT</a>		4	4.8E-2	4.1E0	2.8E-1	2.6E-1
Annotation Cluster 126		Enrichment Score: 1.67	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">POLO box duplicated domain</a>	<a href="#">RT</a>		5	2.9E-3	6.2E0	3.2E-2	2.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:POLO box 1	<a href="#">RT</a>		3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:POLO box 2	<a href="#">RT</a>		3	5.8E-2	6.8E0	9.1E-1	8.8E-1
Annotation Cluster 127		Enrichment Score: 1.66	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Ubiquitin</a>	<a href="#">RT</a>		25	5.7E-6	2.6E0	1.1E-4	1.0E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Ubiquitin subgroup</a>	<a href="#">RT</a>		10	2.8E-5	4.8E0	4.9E-4	4.4E-4
<input type="checkbox"/>	SMART	<a href="#">UBQ</a>	<a href="#">RT</a>		22	4.6E-4	2.1E0	5.3E-3	4.8E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)	<a href="#">RT</a>		9	2.3E-3	3.4E0	6.1E-2	5.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of necrotic cell death</a>	<a href="#">RT</a>		7	8.4E-3	3.5E0	1.3E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of type I interferon production</a>	<a href="#">RT</a>		7	1.3E-2	3.2E0	1.9E-1	1.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:Activating enzyme	<a href="#">RT</a>		5	2.0E-2	4.3E0	3.9E-1	3.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of type I interferon production</a>	<a href="#">RT</a>		11	2.1E-2	2.2E0	2.6E-1	2.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ubiquitin conserved site</a>	<a href="#">RT</a>		6	2.1E-2	3.4E0	1.7E-1	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of epidermal growth factor receptor signaling pathway</a>	<a href="#">RT</a>		12	3.1E-2	2.0E0	3.5E-1	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of epidermal growth factor receptor signaling pathway</a>	<a href="#">RT</a>		9	3.8E-2	2.2E0	3.8E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">MyD88-independent toll-like receptor signaling pathway</a>	<a href="#">RT</a>		6	5.3E-2	2.7E0	4.8E-1	4.5E-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
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Essential for function	<a href="#">RT</a>	<div><div></div><div></div></div>	4	7.0E-2	3.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Ubiquitin	<a href="#">RT</a>	<div><div></div><div></div></div>	4	7.0E-2	3.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Lys-rich (highly basic)	<a href="#">RT</a>	<div><div></div><div></div></div>	4	7.0E-2	3.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:40S ribosomal protein S27a	<a href="#">RT</a>	<div><div></div><div></div></div>	4	7.0E-2	3.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">virion assembly</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.3E-1	2.5E0	8.1E-1	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">glycogen biosynthetic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.3E-1	1.8E0	8.1E-1	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">viral life cycle</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.4E-1	1.7E0	8.1E-1	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">intracellular transport of virus</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	5.0E-1	1.2E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">endocytic vesicle membrane</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	9.1E-1	7.7E-1	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">endosomal transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.0E0	4.5E-1	1.0E0	1.0E0
Annotation Cluster 128		Enrichment Score: 1.66	<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	<a href="#">Exonuclease</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	20	5.3E-5	2.7E0	3.0E-4	2.3E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">3'-5'-exoribonuclease activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	6.2E-4	3.3E0	7.1E-3	6.3E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">rRNA catabolic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	6.7E-4	4.3E0	1.6E-2	1.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">RNA phosphodiester bond hydrolysis, exonucleolytic</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	4.0E-3	2.5E0	7.2E-2	6.9E-2
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Nuclease</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	31	9.7E-3	1.6E0	4.3E-2	3.3E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Ribonuclease II/R, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">nuclear exosome (RNase complex)</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.1E-2	3.0E0	1.4E-1	1.2E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Exosome</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.0E-2	3.2E0	1.2E-1	9.0E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">cytoplasmic exosome (RNase complex)</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	4.1E-2	2.9E0	2.4E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nuclear mRNA surveillance</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	5.0E-2	3.3E0	4.6E-1	4.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Exoribonuclease, phosphorolytic domain 1</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.3E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">exosome (RNase complex)</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	9.3E-2	2.4E0	4.5E-1	3.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Exoribonuclease, phosphorolytic domain 2</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.2E-1	3.1E0	6.1E-1	5.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5'</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.8E-1	2.6E0	9.9E-1	9.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">exoribonuclease activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.0E-1	2.1E0	7.6E-1	6.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">PNPase/RNase PH domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	9.6E-1	8.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">U4 snRNA 3'-end processing</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	9.5E-1
Annotation Cluster 129		Enrichment Score: 1.66	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Glutamine amidotransferase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	5.7E-4	6.2E0	7.2E-3	6.6E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Glutamine amidotransferase type-1	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.0E-3	6.8E0	5.4E-2	5.2E-2
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Pyrimidine biosynthesis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	6.8E-2	3.9E0	2.4E-1	1.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:For GATase activity	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">glutamine metabolic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.1E-1	2.1E0	7.2E-1	6.9E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Glutamine amidotransferase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.3E-1	3.1E0	4.3E-1	3.3E-1
Annotation Cluster 130		Enrichment Score: 1.65	<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	<a href="#">Protein kinase inhibitor</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.0E-2	3.4E0	4.3E-2	3.3E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">mitogen-activated protein kinase kinase binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.0E-2	3.0E0	7.9E-2	7.0E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Pseudokinase tribbles family/serine-threonine-protein kinase 40</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of MAP kinase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	5.0E-2	3.3E0	4.6E-1	4.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ubiquitin-protein transferase regulator activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
Annotation Cluster 131		Enrichment Score: 1.65	<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	<a href="#">Hedgehog signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	7.7E-3	2.3E0	1.4E-2	7.7E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">Sonic Hedgehog (Shh) Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.2E-2	2.1E0	5.1E-2	3.5E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">ciliary base</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.2E-1	1.9E0	5.0E-1	4.4E-1
Annotation Cluster 132		Enrichment Score: 1.64	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, PHD-finger</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	24	2.6E-3	1.9E0	3.0E-2	2.7E-2

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, PHD-type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	26	3.0E-3	1.8E0	3.3E-2	3.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type 2	<a href="#">RT</a>	<div><div></div><div></div></div>	11	8.2E-3	2.5E0	2.0E-1	1.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type 1	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.7E-2	2.3E0	3.4E-1	3.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type	<a href="#">RT</a>	<div><div></div><div></div></div>	14	3.4E-2	1.8E0	6.3E-1	6.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, FYVE/PHD-type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	32	4.1E-2	1.4E0	3.0E-1	2.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, PHD-type, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	1.8E-1	1.4E0	8.6E-1	7.8E-1
<input type="checkbox"/>	SMART	<a href="#">PHD</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	26	2.5E-1	1.2E0	9.4E-1	8.4E-1
Annotation Cluster 133		Enrichment Score: 1.59	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	<a href="#">E2F1 Destruction Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.6E-2	2.5E0	6.2E-2	4.2E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">Regulation of p27 Phosphorylation during Cell Cycle Progression</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	2.9E-2	2.1E0	9.1E-2	6.1E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">Cyclin E Destruction Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	3.6E-2	2.4E0	1.1E-1	7.3E-2
Annotation Cluster 134		Enrichment Score: 1.55	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">P-type ATPase, transmembrane domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	3.7E-5	4.3E0	6.3E-4	5.7E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Cation-transporting P-type ATPase, C-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	7.6E-5	4.0E0	1.2E-3	1.1E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Cation-transporting P-type ATPase, N-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.5E-4	3.8E0	2.1E-3	2.0E-3
<input type="checkbox"/>	INTERPRO	<a href="#">P-type ATPase, cytoplasmic domain N</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	2.3E-4	2.8E0	3.3E-3	3.0E-3
<input type="checkbox"/>	INTERPRO	<a href="#">P-type ATPase, A domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	2.3E-4	2.8E0	3.3E-3	3.0E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Cation-transporting P-type ATPase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	2.3E-4	2.8E0	3.3E-3	3.0E-3
<input type="checkbox"/>	INTERPRO	<a href="#">P-type ATPase, phosphorylation site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	2.3E-4	2.8E0	3.3E-3	3.0E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:4-aspartylphosphate intermediate	<a href="#">RT</a>	<div><div></div><div></div></div>	16	3.2E-4	2.7E0	9.9E-3	9.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular sodium ion homeostasis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	3.8E-4	3.4E0	1.0E-2	9.6E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Sodium/potassium-transporting P-type ATPase, subfamily IIC</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	5.7E-4	6.2E0	7.2E-3	6.6E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Magnesium	<a href="#">RT</a>	<div><div></div><div></div></div>	32	7.0E-4	1.8E0	2.0E-2	2.0E-2
<input type="checkbox"/>	SMART	<a href="#">SM00831</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.4E-3	2.8E0	1.4E-2	1.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">establishment or maintenance of transmembrane electrochemical gradient</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	2.6E-3	3.6E0	5.0E-2	4.8E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">sodium:potassium-exchanging ATPase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.6E-2	3.6E0	1.1E-1	1.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">sodium ion export from cell</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.6E-2	3.6E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">steroid hormone binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.6E-2	4.8E0	2.2E-1	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular potassium ion homeostasis</a>	<a href="#">RT</a>	<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	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to steroid hormone stimulus</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	7.2E-2	3.0E0	5.7E-1	5.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to glycoside</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.6E-2	5.9E0	5.7E-1	5.4E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Sodium/potassium transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.8E-2	3.4E0	3.3E-1	2.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of cardiac conduction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	13	2.3E-1	1.4E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">sodium:potassium-exchanging ATPase complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.4E-1	2.3E0	8.4E-1	7.4E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Carbohydrate digestion and absorption</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	2.7E-1	1.4E0	4.3E-1	2.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ATP hydrolysis coupled proton transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	2.9E-1	1.5E0	1.0E0	9.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">HAD-like domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	3.2E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cell communication by electrical coupling involved in cardiac conduction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">potassium ion import</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	5.2E-1	1.3E0	1.0E0	9.5E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Proximal tubule bicarbonate reclamation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	8.4E-1	9.1E-1	1.0E0	8.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ion transmembrane transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	30	9.0E-1	8.5E-1	1.0E0	9.5E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Cardiac muscle contraction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	9.3E-1	7.7E-1	1.0E0	9.3E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Potassium</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	9.9E-1	6.4E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Potassium transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	9.9E-1	5.9E-1	1.0E0	9.9E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Mineral absorption</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.9E-1	4.8E-1	1.0E0	9.9E-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_KEYWORDS	<a href="#">Sodium transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	2.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Protein digestion and absorption</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	2.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Sodium</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	2.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain:Luminal	<a href="#">RT</a>	<div><div></div><div></div></div>	22	1.0E0	3.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Ion transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	32	1.0E0	3.4E-1	1.0E0	1.0E0
Annotation Cluster 135		Enrichment Score: 1.54	<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	<a href="#">histone methyltransferase activity (H3-K36 specific)</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	8.9E-3	5.0E0	7.2E-2	6.4E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:AWS	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.5E-2	5.5E0	4.8E-1	4.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">AWS</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	SMART	<a href="#">AWS</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.8E-2	3.3E0	4.9E-1	4.4E-1
Annotation Cluster 136		Enrichment Score: 1.51	<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	<a href="#">single-stranded DNA-dependent ATPase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.5E-3	4.2E0	2.4E-2	2.1E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">DNA replication factor C complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	7.0E-3	5.3E0	5.2E-2	4.6E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">DNA clamp loader activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	3.1E-2	3.7E0	2.0E-1	1.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">DNA polymerase III, clamp loader complex, gamma/delta/delta subunit, C-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Replication factor C, C-terminal domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of DNA-directed DNA polymerase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.8E-2	3.4E0	6.8E-1	6.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">Ctf18 RFC-like complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.2E-1	3.2E0	5.0E-1	4.4E-1
Annotation Cluster 137		Enrichment Score: 1.5	<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	<a href="#">positive regulation of translational initiation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.4E-3	3.6E0	3.0E-2	2.8E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">translation activator activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	4.9E-2	3.3E0	2.9E-1	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">3'-UTR-mediated mRNA stabilization</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	5.3E-2	2.4E0	4.8E-1	4.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">mRNA 3'-UTR binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	3.0E-1	1.3E0	9.5E-1	8.5E-1
Annotation Cluster 138		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	<a href="#">Dynamin, GTPase domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.7E-3	5.3E0	2.0E-2	1.8E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Dynamin, GTPase region, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	7.7E-3	5.2E0	7.5E-2	6.9E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Dynamin central domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	7.7E-3	5.2E0	7.5E-2	6.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:GED	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.1E-2	4.9E0	2.3E-1	2.2E-1
<input type="checkbox"/>	SMART	<a href="#">DYNc</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.2E-2	3.5E0	1.0E-1	9.0E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Dynamin GTPase effector</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.6E-2	4.4E0	1.3E-1	1.2E-1
<input type="checkbox"/>	SMART	<a href="#">GED</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	3.5E-2	3.4E0	2.4E-1	2.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">GTPase effector domain, GED</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	4.3E-2	3.4E0	3.1E-1	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">dynamin polymerization involved in mitochondrial fission</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.8E-2	3.4E0	6.8E-1	6.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Dynamin</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.3E-1	2.2E0	6.1E-1	5.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitochondrial fission</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	4.0E-1	1.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">membrane fusion</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	8.9E-1	8.1E-1	1.0E0	9.5E-1
Annotation Cluster 139		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"/>	BBID	<a href="#">26.cyclin-CDK complexes</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	1.9E-3	2.3E0	1.0E-1	1.0E-1
<input type="checkbox"/>	BBID	<a href="#">1.RBphosphoE2F</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	6.4E-2	1.9E0	8.2E-1	8.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">cyclin-dependent protein serine/threonine kinase inhibitor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	9.7E-2	2.7E0	4.6E-1	4.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of phosphorylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.1E-1	2.1E0	7.2E-1	6.9E-1
Annotation Cluster 140		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_BP_DIRECT	<a href="#">mitotic cell cycle</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	1.9E-3	2.3E0	4.0E-2	3.8E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">receptor signaling protein serine/threonine kinase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	1.1E-2	1.9E0	8.3E-2	7.4E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CRIB	<a href="#">RT</a>	<div><div></div><div></div></div>	7	4.9E-2	2.5E0	8.6E-1	8.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Autoregulatory region	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:GTPase-binding	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">PAK-box/P21-Rho-binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	9.0E-2	2.2E0	4.8E-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
<input type="checkbox"/>	SMART	<a href="#">PBD</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.8E-1	1.8E0	7.1E-1	6.4E-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"/>	INTERPRO	<a href="#">ROC GTPase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Roc	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Mitochondrial Rho-like</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	6.3E-2	3.1E0	3.9E-1	3.6E-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"/>	GOTERM_BP_DIRECT	<a href="#">nuclear-transcribed mRNA catabolic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	2.6E-3	3.6E0	5.0E-2	4.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nuclear mRNA surveillance</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	5.0E-2	3.3E0	4.6E-1	4.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">histone mRNA catabolic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	4.3E-1	1.7E0	1.0E0	9.5E-1
Annotation Cluster 143		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	<a href="#">RT</a>	<div><div></div><div></div></div>	6	9.0E-3	4.1E0	2.1E-1	2.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:A.T hook 1	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.1E-2	3.1E0	5.8E-1	5.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:A.T hook 2	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.1E-2	3.1E0	5.8E-1	5.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">AT hook, DNA-binding motif</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	3.9E-1	3.6E-1
<input type="checkbox"/>	SMART	<a href="#">AT_hook</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.6E-1	2.7E0	6.6E-1	5.9E-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	<a href="#">Leucine-rich repeat-containing protein 8, N-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.9E-3	6.2E0	3.2E-2	2.9E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">volume-sensitive anion channel activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.6E-2	6.0E0	1.1E-1	1.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of anion transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	7.2E-2	3.0E0	5.7E-1	5.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">anion transmembrane transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	7.7E-1	9.9E-1	1.0E0	9.5E-1
Annotation Cluster 145		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"/>	GOTERM_CC_DIRECT	<a href="#">MLL5-L complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.5E-3	4.8E0	2.9E-2	2.6E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">PTW/PP1 phosphatase complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	8.3E-2	3.6E0	4.0E-1	3.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">entrainment of circadian clock by photoperiod</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	2.4E-1	1.8E0	1.0E0	9.5E-1
Annotation Cluster 146		Enrichment Score: 1.38	<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	<a href="#">protein kinase C activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	2.0E-4	4.0E0	2.6E-3	2.3E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Diacylglycerol/phorbol-ester binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	3.7E-3	2.7E0	4.0E-2	3.6E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase C, delta/epsilon/eta/theta types</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">protein kinase C, delta/epsilon/eta/theta types</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.2E-2	5.3E0	3.6E-1	3.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 1	<a href="#">RT</a>	<div><div></div><div></div></div>	8	3.3E-2	2.5E0	6.1E-1	5.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 2	<a href="#">RT</a>	<div><div></div><div></div></div>	8	3.3E-2	2.5E0	6.1E-1	5.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">calcium-independent protein kinase C activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase C-like, phorbol ester/diacylglycerol binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	1.7E-1	1.4E0	8.0E-1	7.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of glial cell apoptotic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	3.4E-1	2.5E0	1.0E0	9.5E-1
<input type="checkbox"/>	SMART	<a href="#">C1</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	7.5E-1	9.4E-1	1.0E0	9.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type	<a href="#">RT</a>	<div><div></div><div></div></div>	5	9.1E-1	7.6E-1	1.0E0	9.7E-



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	<a href="#">HRDC</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.5E-1	4.1E0	6.5E-1	5.8E-1
Annotation Cluster 149		Enrichment Score: 1.33	<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	<a href="#">fibroblast growth factor-activated receptor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	3.4E-3	6.0E0	3.2E-2	2.8E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Tyrosine-protein kinase, fibroblast growth factor receptor</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">fibroblast growth factor receptor</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.2E-2	5.3E0	3.6E-1	3.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of phospholipase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.4E-1	3.0E0	8.1E-1	7.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">fibroblast growth factor binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.8E-1	1.8E0	7.2E-1	6.4E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Craniosynostosis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	4.0E-1	1.6E0	1.0E0	7.8E-1
Annotation Cluster 150		Enrichment Score: 1.33	<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	<a href="#">regulation of the force of heart contraction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	8.4E-3	2.8E0	1.3E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cardiac muscle contraction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	1.3E-2	2.0E0	1.9E-1	1.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Cardiac muscle contraction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	9.3E-1	7.7E-1	1.0E0	9.3E-1
Annotation Cluster 151		Enrichment Score: 1.31	<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	<a href="#">positive regulation of guanylate cyclase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	4.9E-3	3.8E0	8.4E-2	8.0E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">calcium sensitive guanylate cyclase activator activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.6E-2	4.8E0	2.2E-1	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">phototransduction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	6.9E-1	1.1E0	1.0E0	9.5E-1
Annotation Cluster 152		Enrichment Score: 1.3	<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	<a href="#">ubiquitin-ubiquitin ligase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.3E-2	3.2E0	9.7E-2	8.6E-2
<input type="checkbox"/>	INTERPRO	<a href="#">U box domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	6.3E-2	3.1E0	3.9E-1	3.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:U-box	<a href="#">RT</a>	<div><div></div><div></div></div>	4	7.0E-2	3.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">Ubox</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.1E-1	2.5E0	5.2E-1	4.7E-1
Annotation Cluster 153		Enrichment Score: 1.3	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	OMIM_DISEASE	<a href="#">Schimmelpenning-Feuerstein-Mims syndrome, somatic mosaic</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.3E-2	8.0E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	<a href="#">65.Integrin affinity modulation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	4.9E-2	2.9E0	7.6E-1	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Hypervariable region	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
Annotation Cluster 154		Enrichment Score: 1.3	<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:I-domain	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Helix-hairpin-helix motif, class 2</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">XPG/Rad2 endonuclease</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">XPG-I domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">5'-3' exonuclease, C-terminal domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:N-domain	<a href="#">RT</a>	<div><div></div><div></div></div>	4	4.5E-2	4.5E0	8.0E-1	7.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">XPG N-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">nuclease activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	7.7E-2	2.1E0	3.9E-1	3.5E-1
<input type="checkbox"/>	SMART	<a href="#">HhH2</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.8E-2	3.3E0	4.9E-1	4.4E-1
<input type="checkbox"/>	SMART	<a href="#">XPGI</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.8E-2	3.3E0	4.9E-1	4.4E-1
<input type="checkbox"/>	SMART	<a href="#">XPGN</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.8E-2	3.3E0	4.9E-1	4.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">XPG conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.1E-1	5.6E-1
Annotation Cluster 155		Enrichment Score: 1.28	<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	<a href="#">histone H2A monoubiquitination</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	8.4E-3	3.5E0	1.3E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">UV-damage excision repair</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	9.9E-2	2.7E0	6.8E-1	6.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">Cul4B-RING E3 ubiquitin ligase complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.8E-1	3.8E0	6.8E-1	5.9E-1
Annotation Cluster 156		Enrichment Score: 1.27	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	<a href="#">NFkB activation by Nontypeable Hemophilus influenzae</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	18	1.1E-4	2.3E0	1.6E-3	1.1E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">The 4-1BB-dependent immune response</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	5.8E-4	2.4E0	5.0E-3	3.4E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">Signal transduction through IL1R</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	18	1.7E-2	1.7E0	6.2E-2	4.2E-2

















































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"/>	BIOCARTA	<a href="#">Toll-Like Receptor Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	20	1.7E-2	1.6E0	6.2E-2	4.2E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">I-kappaB/NF-kappaB complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.0E-2	5.1E0	1.9E-1	1.6E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Activation of PKC through G protein coupled receptor</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	4.0E-2	2.6E0	1.1E-1	7.7E-2
<input type="checkbox"/>	BBID	<a href="#">77.IkBa_Kinase_JNK_MEKK1</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	4.9E-2	2.5E0	7.6E-1	7.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">RIG-I-like receptor signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	20	6.3E-2	1.5E0	1.1E-1	6.3E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">Double Stranded RNA Induced Gene Expression</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	6.7E-2	2.2E0	1.7E-1	1.2E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Acetylation and Deacetylation of RelA in The Nucleus</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.1E-1	1.7E0	2.6E-1	1.8E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">NF-kB Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.8E-1	1.5E0	3.8E-1	2.6E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">CD40L Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.8E-1	1.6E0	3.8E-1	2.6E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Erythropoietin mediated neuroprotection through NF-kB</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.8E-1	1.5E0	5.4E-1	3.6E-1
<input type="checkbox"/>	BBID	<a href="#">90.IB_and-cat-Arm_processing_of_Ci</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.4E-1	1.9E0	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	<a href="#">TNF/Stress Related Signaling</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	4.2E-1	1.2E0	6.6E-1	4.5E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">TNFR2 Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	5.5E-1	1.2E0	8.4E-1	5.7E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">TACI and BCMA stimulation of B cell immune responses.</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	7.7E-1	1.0E0	1.0E0	7.7E-1
Annotation Cluster 157		Enrichment Score: 1.27	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	2.7E-3	2.3E0	3.0E-2	2.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:UBA	<a href="#">RT</a>	<div><div></div><div></div></div>	13	1.0E-2	2.2E0	2.3E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Heat shock chaperonin-binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.3E-2	3.7E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">polyubiquitin binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	2.8E-2	2.3E0	1.9E-1	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of proteasomal ubiquitin-dependent protein catabolic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.8E-2	3.0E0	3.8E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ubiquilin</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	3.9E-1	3.6E-1
<input type="checkbox"/>	SMART	<a href="#">STI1</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	7.2E-2	2.4E0	4.0E-1	3.6E-1
<input type="checkbox"/>	SMART	<a href="#">UBA</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	2.7E-1	1.4E0	9.7E-1	8.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:UBA 1	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.7E-1	2.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:UBA 2	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.7E-1	2.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">UBA-like</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	3.5E-1	1.3E0	1.0E0	9.1E-1
Annotation Cluster 158		Enrichment Score: 1.26	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">UBA/THIF-type NAD/FAD binding fold</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.0E-3	4.3E0	2.3E-2	2.1E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ubiquitin activating enzyme activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.6E-2	4.8E0	2.2E-1	2.0E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ubiquitin-activating enzyme, E1</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ubiquitin-activating enzyme e1, C-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">small protein activating enzyme activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.7E-2	3.4E0	4.6E-1	4.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ubiquitin/SUMO-activating enzyme E1</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.1E-1	5.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ubiquitin-activating enzyme</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.1E-1	5.6E-1
<input type="checkbox"/>	SMART	<a href="#">SM00985</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.5E-1	4.1E0	6.5E-1	5.8E-1
Annotation Cluster 159		Enrichment Score: 1.26	<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	<a href="#">peptidyl-lysine monomethylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	3.2E-2	3.7E0	3.5E-1	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">peptidyl-lysine dimethylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.7E-2	4.7E0	3.8E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein-lysine N-methyltransferase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.4E-1	2.1E0	6.0E-1	5.3E-1
Annotation Cluster 160		Enrichment Score: 1.26	<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	<a href="#">Pwp2p-containing subcomplex of 90S preribosome</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.5E-3	5.4E0	1.4E-2	1.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 8	<a href="#">RT</a>	<div><div></div><div></div></div>	16	2.4E-2	1.8E0	4.8E-1	4.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Quinonprotein alcohol dehydrogenase-like superfamily</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	3.7E-2	1.8E0	2.7E-1	2.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 9	<a href="#">RT</a>	<div><div></div><div></div></div>	12	4.9E-2	1.9E0	8.6E-1	8.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 11	<a href="#">RT</a>	<div><div></div><div></div></div>	9	6.3E-2	2.0E0	9.7E-1	9.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 10	<a href="#">RT</a>	<div><div></div><div></div></div>	9	7.4E-2	2.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 13	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.1E-1	2.3E0	1.0E0	9.7E-1

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 12	RT		6	2.1E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 14	RT		3	6.3E-1	1.5E0	1.0E0	9.7E-1
Annotation Cluster 161		Enrichment Score: 1.26	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">Bergmann glial cell differentiation</a>	RT		7	1.2E-3	4.6E0	2.8E-2	2.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of Golgi inheritance</a>	RT		4	1.7E-2	5.9E0	2.2E-1	2.1E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway</a>	RT		9	2.9E-2	2.1E0	9.1E-2	6.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of stress-activated MAPK cascade</a>	RT		5	3.2E-2	3.7E0	3.5E-1	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of early endosome to late endosome transport</a>	RT		5	3.2E-2	3.7E0	3.5E-1	3.3E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Sprouty regulation of tyrosine kinase signals</a>	RT		11	3.5E-2	1.9E0	1.0E-1	7.0E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">Pelp1 Modulation of Estrogen Receptor Activity</a>	RT		6	4.0E-2	2.6E0	1.1E-1	7.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">trachea formation</a>	RT		4	6.4E-2	4.0E0	5.3E-1	5.1E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Roles of ?-arrestin-dependent Recruitment of Src Kinases in GPCR Signaling</a>	RT		11	7.6E-2	1.7E0	2.0E-1	1.3E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Aspirin Blocks Signaling Pathway Involved in Platelet Activation</a>	RT		11	1.0E-1	1.6E0	2.6E-1	1.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">thyroid gland development</a>	RT		8	1.1E-1	1.9E0	7.7E-1	7.3E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Regulation of Splicing through Sam68</a>	RT		5	1.6E-1	2.2E0	3.5E-1	2.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ERK1 and ERK2 cascade</a>	RT		7	2.1E-1	1.7E0	1.0E0	9.5E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia</a>	RT		11	2.2E-1	1.4E0	4.5E-1	3.1E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Role of ?-arrestins in the activation and targeting of MAP kinases</a>	RT		7	4.2E-1	1.3E0	6.6E-1	4.5E-1
Annotation Cluster 162		Enrichment Score: 1.25	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Heat shock factor (HSF)-type, DNA-binding</a>	RT		5	2.7E-2	3.9E0	2.1E-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	9.1E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Hydrophobic repeat HR-C	RT		3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	SMART	<a href="#">HSE</a>	RT		5	1.1E-1	2.5E0	5.2E-1	4.7E-1
Annotation Cluster 163		Enrichment Score: 1.25	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">histone H3-K27 methylation</a>	RT		4	1.7E-2	5.9E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">histone methyltransferase activity (H3-K27 specific)</a>	RT		3	7.5E-2	6.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein-lysine N-methyltransferase activity</a>	RT		6	1.4E-1	2.1E0	6.0E-1	5.3E-1
Annotation Cluster 164		Enrichment Score: 1.24	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">eukaryotic translation initiation factor 4F complex</a>	RT		5	4.0E-2	3.5E0	2.3E-1	2.0E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Eukaryotic protein translation</a>	RT		10	4.1E-2	1.9E0	1.1E-1	7.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nuclear-transcribed mRNA poly(A) tail shortening</a>	RT		10	4.4E-2	2.0E0	4.2E-1	4.0E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Internal Ribosome entry pathway</a>	RT		5	1.6E-1	2.2E0	3.5E-1	2.4E-1
Annotation Cluster 165		Enrichment Score: 1.24	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">nucleotide-activated protein kinase complex</a>	RT		6	1.9E-2	3.5E0	1.3E-1	1.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">cAMP-dependent protein kinase regulator activity</a>	RT		4	9.7E-2	3.4E0	4.6E-1	4.1E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">ChREBP regulation by carbohydrates and cAMP</a>	RT		11	1.0E-1	1.6E0	2.6E-1	1.7E-1
Annotation Cluster 166		Enrichment Score: 1.22	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">nucleosomal DNA binding</a>	RT		17	2.3E-3	2.2E0	2.3E-2	2.0E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Histone H3</a>	RT		6	1.8E-1	2.0E0	8.5E-1	7.7E-1
<input type="checkbox"/>	SMART	<a href="#">H3</a>	RT		6	5.1E-1	1.3E0	1.0E0	9.0E-1
Annotation Cluster 167		Enrichment Score: 1.21	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Xeroderma pigmentosum</a>	RT		5	3.1E-2	3.8E0	1.2E-1	9.0E-2
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Cockayne syndrome</a>	RT		4	4.4E-2	4.6E0	1.6E-1	1.3E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">holo TFIIH complex</a>	RT		5	8.0E-2	2.9E0	4.0E-1	3.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">UV protection</a>	RT		5	1.3E-1	2.5E0	8.1E-1	7.7E-1
Annotation Cluster 168		Enrichment Score: 1.21	G		Count	P_Value	Fold Change	Benjamini	FDR

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">extrinsic apoptotic signaling pathway in absence of ligand</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	6.9E-4	2.6E0	1.7E-2	1.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of mitochondrial membrane permeability</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.6E-2	3.6E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">BH3 domain binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.6E-2	6.0E0	1.1E-1	1.0E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Apoptosis regulator, Bcl-2, BH1 motif, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.7E-2	3.9E0	2.1E-1	2.0E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Apoptosis regulator, Bcl-2, BH2 motif, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.7E-2	3.9E0	2.1E-1	2.0E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Apoptosis regulator, Bcl-2, BH3 motif, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.7E-2	3.9E0	2.1E-1	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of protein heterodimerization activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	3.2E-2	3.7E0	3.5E-1	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of mitochondrial membrane potential</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	3.5E-2	2.1E0	3.8E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of anoikis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	5.3E-2	2.4E0	4.8E-1	4.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:BH1	<a href="#">RT</a>	<div><div></div><div></div></div>	5	6.5E-2	3.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">Bcl-2 family protein complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	6.6E-2	6.4E0	3.5E-1	3.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">release of cytochrome c from mitochondria</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	7.9E-2	2.1E0	5.9E-1	5.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Bcl2-like</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	8.7E-2	2.8E0	4.7E-1	4.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Blc2 family</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	8.7E-2	2.8E0	4.7E-1	4.3E-1
<input type="checkbox"/>	BBID	<a href="#">152.altered synaptic signalling-neurodegenerative disorders</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.1E-1	2.4E0	9.7E-1	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:BH2	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.1E-1	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Role of Mitochondria in Apoptotic Signaling</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.4E-1	1.5E0	3.1E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:BH3	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.3E-1	2.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">endoplasmic reticulum calcium ion homeostasis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.4E-1	2.0E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of protein homodimerization activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	3.4E-1	2.5E0	1.0E0	9.5E-1
<input type="checkbox"/>	BBID	<a href="#">127.Mito-stress</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.4E-1	1.9E0	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">pore complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.3E-1	2.1E0	1.0E0	8.7E-1
Annotation Cluster 169		Enrichment Score: 1.2	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Rho-like	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BTB 2	<a href="#">RT</a>	<div><div></div><div></div></div>	5	6.5E-2	3.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BTB 1	<a href="#">RT</a>	<div><div></div><div></div></div>	5	6.5E-2	3.1E0	1.0E0	9.6E-1
Annotation Cluster 170		Enrichment Score: 1.2	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Non-homologous end-joining</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	5.3E-3	3.2E0	1.1E-2	5.3E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">nonhomologous end joining complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.2E-1	3.2E0	5.0E-1	4.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">establishment of integrated proviral latency</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.4E-1	3.0E0	8.1E-1	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of smooth muscle cell proliferation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.8E-1	2.6E0	9.9E-1	9.4E-1
Annotation Cluster 171		Enrichment Score: 1.19	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)	<a href="#">RT</a>	<div><div></div><div></div></div>	9	2.3E-3	3.4E0	6.1E-2	5.9E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein tag</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.4E-1	3.0E0	5.8E-1	5.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Small ubiquitin-related modifier, SUMO</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.9E-1	3.7E0	8.6E-1	7.8E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Basic Mechanisms of SUMOylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.0E-1	2.1E0	5.5E-1	3.8E-1
Annotation Cluster 172		Enrichment Score: 1.19	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Tyrosine-protein kinase, receptor class III, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.9E-5	6.2E0	3.4E-4	3.1E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of phospholipase C activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.0E-4	5.3E0	3.2E-3	3.0E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">vascular endothelial growth factor-activated receptor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.8E-2	4.3E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Tyrosine-protein kinase, CSF-1/PDGF receptor</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">tyrosine-protein kinase, CSF-1/PDGF receptor type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	4.8E-2	4.3E0	6.2E-1	6.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">vascular endothelial growth factor signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	6.4E-2	4.0E0	5.3E-1	5.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">vascular endothelial growth factor binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	7.6E-1	6.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">growth factor binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.9E-1	1.5E0	9.5E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 7	<a href="#">RT</a>	<div><div></div><div></div></div>	5	4.1E-1	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 5	<a href="#">RT</a>	<div><div></div><div></div></div>	9	5.7E-1	1.1E0	1.0E0	9.7E-1

Annotation Cluster 1		Enrichment Score: ?	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 3	<a href="#">RT</a>	<div><div></div></div>	17	7.9E-1	9.0E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 6	<a href="#">RT</a>	<div><div></div></div>	5	8.1E-1	9.2E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 4	<a href="#">RT</a>	<div><div></div></div>	9	8.9E-1	8.1E-1	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Immunoglobulin</a>	<a href="#">RT</a>	<div><div></div></div>	10	9.3E-1	7.6E-1	1.0E0	9.3E-1
Annotation Cluster 173		Enrichment Score: 1.18	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:ZZ-type	<a href="#">RT</a>	<div><div></div></div>	7	2.9E-2	2.8E0	5.5E-1	5.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, ZZ-type</a>	<a href="#">RT</a>	<div><div></div></div>	7	5.7E-2	2.4E0	3.9E-1	3.6E-1
<input type="checkbox"/>	SMART	<a href="#">ZnF_ZZ</a>	<a href="#">RT</a>	<div><div></div></div>	7	1.8E-1	1.8E0	7.1E-1	6.4E-1
Annotation Cluster 174		Enrichment Score: 1.17	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Threonine protease</a>	<a href="#">RT</a>	<div><div></div></div>	8	1.9E-2	2.7E0	7.7E-2	6.0E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Proteasome, subunit alpha/beta</a>	<a href="#">RT</a>	<div><div></div></div>	8	2.4E-2	2.6E0	1.9E-1	1.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">proteasome core complex, alpha-subunit complex</a>	<a href="#">RT</a>	<div><div></div></div>	5	2.5E-2	4.0E0	1.6E-1	1.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Proteasome A-type subunit</a>	<a href="#">RT</a>	<div><div></div></div>	5	2.7E-2	3.9E0	2.1E-1	2.0E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Proteasome, alpha-subunit, N-terminal domain</a>	<a href="#">RT</a>	<div><div></div></div>	5	2.7E-2	3.9E0	2.1E-1	2.0E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">proteasome core complex</a>	<a href="#">RT</a>	<div><div></div></div>	8	3.6E-2	2.4E0	2.2E-1	1.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">threonine-type endopeptidase activity</a>	<a href="#">RT</a>	<div><div></div></div>	8	4.9E-2	2.3E0	2.9E-1	2.6E-1
<input type="checkbox"/>	SMART	<a href="#">SM00948</a>	<a href="#">RT</a>	<div><div></div></div>	5	1.1E-1	2.5E0	5.2E-1	4.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Proteasome, beta-type subunit, conserved site</a>	<a href="#">RT</a>	<div><div></div></div>	4	3.0E-1	2.1E0	9.8E-1	8.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Proteasome B-type subunit</a>	<a href="#">RT</a>	<div><div></div></div>	3	5.5E-1	1.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">proteolysis involved in cellular protein catabolic process</a>	<a href="#">RT</a>	<div><div></div></div>	9	5.7E-1	1.1E0	1.0E0	9.5E-1
Annotation Cluster 175		Enrichment Score: 1.16	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Ribosomal protein L1, 2-layer alpha/beta-sandwich</a>	<a href="#">RT</a>	<div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ribosomal protein L1, 3-layer alpha/beta-sandwich</a>	<a href="#">RT</a>	<div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ribosomal protein L1, superfamily</a>	<a href="#">RT</a>	<div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
Annotation Cluster 176		Enrichment Score: 1.16	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Pseudouridine synthase, RsuA/RluB/C/D/E/F</a>	<a href="#">RT</a>	<div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Pseudouridine synthase, catalytic domain</a>	<a href="#">RT</a>	<div><div></div></div>	6	4.5E-2	2.9E0	3.2E-1	3.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">pseudouridine synthase activity</a>	<a href="#">RT</a>	<div><div></div></div>	6	5.2E-2	2.8E0	3.0E-1	2.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">tRNA pseudouridine synthesis</a>	<a href="#">RT</a>	<div><div></div></div>	4	6.4E-2	4.0E0	5.3E-1	5.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">deaminase activity</a>	<a href="#">RT</a>	<div><div></div></div>	4	1.4E-1	3.0E0	5.8E-1	5.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">pseudouridine synthesis</a>	<a href="#">RT</a>	<div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	9.5E-1
Annotation Cluster 177		Enrichment Score: 1.15	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">DNA-directed RNA polymerase, subunit 2, domain 6</a>	<a href="#">RT</a>	<div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">RNA polymerase, beta subunit, conserved site</a>	<a href="#">RT</a>	<div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">DNA-directed RNA polymerase, subunit 2</a>	<a href="#">RT</a>	<div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">RNA polymerase Rpb2, OB-fold</a>	<a href="#">RT</a>	<div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">RNA polymerase Rpb2, domain 7</a>	<a href="#">RT</a>	<div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">RNA polymerase Rpb2, domain 2</a>	<a href="#">RT</a>	<div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">RNA polymerase, beta subunit, protrusion</a>	<a href="#">RT</a>	<div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">RNA polymerase Rpb2, domain 3</a>	<a href="#">RT</a>	<div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ribonucleoside binding</a>	<a href="#">RT</a>	<div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
Annotation Cluster 178		Enrichment Score: 1.13	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 5	<a href="#">RT</a>	<div><div></div></div>	6	1.4E-2	3.7E0	2.9E-1	2.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Dilute</a>	<a href="#">RT</a>	<div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Dilute	<a href="#">RT</a>	<div><div></div></div>	4	1.0E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">SM01132</a>	<a href="#">RT</a>	<div><div></div></div>	4	2.3E-1	2.3E0	9.0E-1	8.1E-1





















































Annotation Cluster 1			Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
Annotation Cluster 179			Enrichment Score: 1.13	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:GATA-type 1	<a href="#">RT</a>		6	3.6E-4	6.8E0	1.1E-2	1.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:GATA-type 2	<a href="#">RT</a>		6	3.6E-4	6.8E0	1.1E-2	1.0E-2
<input type="checkbox"/>	INTERPRO	<a href="#">GATA-type transcription activator, N-terminal</a>	<a href="#">RT</a>		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, GATA-type</a>	<a href="#">RT</a>		6	8.0E-2	2.5E0	4.4E-1	4.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">intestinal epithelial cell differentiation</a>	<a href="#">RT</a>		4	9.8E-2	3.4E0	6.8E-1	6.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">anatomical structure formation involved in morphogenesis</a>	<a href="#">RT</a>		5	9.9E-2	2.7E0	6.8E-1	6.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">enhancer sequence-specific DNA binding</a>	<a href="#">RT</a>		7	1.0E-1	2.1E0	4.9E-1	4.4E-1
<input type="checkbox"/>	SMART	<a href="#">ZnF_GATA</a>	<a href="#">RT</a>		6	1.5E-1	2.0E0	6.5E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, NHR/GATA-type</a>	<a href="#">RT</a>		11	4.6E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cell fate commitment</a>	<a href="#">RT</a>		7	8.1E-1	9.0E-1	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cell development</a>	<a href="#">RT</a>		6	8.3E-1	8.9E-1	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to BMP stimulus</a>	<a href="#">RT</a>		4	9.0E-1	7.9E-1	1.0E0	9.5E-1
Annotation Cluster 180			Enrichment Score: 1.13	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Bridging helix	<a href="#">RT</a>		3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">RNA polymerase, N-terminal</a>	<a href="#">RT</a>		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">RNA polymerase, alpha subunit</a>	<a href="#">RT</a>		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">RNA polymerase Rpb1, domain 3</a>	<a href="#">RT</a>		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">RNA polymerase Rpb1, domain 1</a>	<a href="#">RT</a>		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">RNA polymerase Rpb1, domain 5</a>	<a href="#">RT</a>		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">RNA polymerase Rpb1, domain 4</a>	<a href="#">RT</a>		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	SMART	<a href="#">RPOLA_N</a>	<a href="#">RT</a>		3	1.5E-1	4.1E0	6.5E-1	5.8E-1
Annotation Cluster 181			Enrichment Score: 1.12	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">2-5-oligoadenylate synthetase, conserved site</a>	<a href="#">RT</a>		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">2'-5'-oligoadenylate synthase</a>	<a href="#">RT</a>		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">2'-5'-oligoadenylate synthetase 1, domain 2/C-terminal</a>	<a href="#">RT</a>		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">2'-5'-oligoadenylate synthetase activity</a>	<a href="#">RT</a>		4	1.6E-2	6.0E0	1.1E-1	1.0E-1
<input type="checkbox"/>	INTERPRO	<a href="#">2-5-oligoadenylate synthetase, N-terminal</a>	<a href="#">RT</a>		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Nucleotidyl transferase domain</a>	<a href="#">RT</a>		4	2.1E-1	2.5E0	9.5E-1	8.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">nucleotidyltransferase activity</a>	<a href="#">RT</a>		7	2.9E-1	1.5E0	9.5E-1	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">interferon-gamma-mediated signaling pathway</a>	<a href="#">RT</a>		11	7.8E-1	9.2E-1	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">transferase activity</a>	<a href="#">RT</a>		12	9.4E-1	7.5E-1	1.0E0	9.4E-1
Annotation Cluster 182			Enrichment Score: 1.12	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Proprotein convertase, P</a>	<a href="#">RT</a>		6	1.7E-3	5.3E0	2.0E-2	1.8E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Peptidase S8, subtilisin, Asp-active site</a>	<a href="#">RT</a>		5	7.7E-3	5.2E0	7.5E-2	6.9E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Peptidase S8, subtilisin, His-active site</a>	<a href="#">RT</a>		6	7.7E-3	4.1E0	7.5E-2	6.9E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Peptidase S8, subtilisin, Ser-active site</a>	<a href="#">RT</a>		6	7.7E-3	4.1E0	7.5E-2	6.9E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Peptidase S8, subtilisin-related</a>	<a href="#">RT</a>		6	1.3E-2	3.7E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Peptidase S8/S53 domain</a>	<a href="#">RT</a>		6	2.1E-2	3.4E0	1.7E-1	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">peptide biosynthetic process</a>	<a href="#">RT</a>		4	3.7E-2	4.7E0	3.8E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Proteinase inhibitor, propeptide</a>	<a href="#">RT</a>		6	1.3E-1	2.2E0	6.1E-1	5.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">peptide hormone processing</a>	<a href="#">RT</a>		5	2.8E-1	1.9E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein processing</a>	<a href="#">RT</a>		12	6.9E-1	9.9E-1	1.0E0	9.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Zymogen</a>	<a href="#">RT</a>		17	1.0E0	5.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Serine protease</a>	<a href="#">RT</a>		9	1.0E0	4.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Charge relay system	<a href="#">RT</a>		8	1.0E0	2.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">serine-type endopeptidase activity</a>	<a href="#">RT</a>		10	1.0E0	2.3E-1	1.0E0	1.0E0
Annotation Cluster 183			Enrichment Score: 1.11	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR










Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, C6HC-type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.4E-2	2.9E0	1.9E-1	1.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:IBR-type	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.1E-2	3.1E0	5.8E-1	5.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:RING-type 2	<a href="#">RT</a>	<div><div></div><div></div></div>	5	8.6E-2	2.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:RING-type 1; atypical	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ubiquitin conjugating enzyme binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.3E-1	1.7E0	5.8E-1	5.2E-1
<input type="checkbox"/>	SMART	<a href="#">IBR</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	2.4E-1	1.7E0	9.3E-1	8.4E-1
Annotation Cluster 184		Enrichment Score: 1.11	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mRNA cleavage</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.8E-2	3.0E0	3.8E-1	3.6E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Polyadenylation of mRNA</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	6.7E-2	2.2E0	1.7E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mRNA polyadenylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	8.6E-2	1.9E0	6.3E-1	6.0E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">mRNA cleavage and polyadenylation specificity factor complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.7E-1	2.3E0	6.6E-1	5.8E-1
Annotation Cluster 185		Enrichment Score: 1.11	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">MAP kinase kinase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	8.1E-3	3.5E0	6.8E-2	6.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Cleavage; by anthrax lethal factor	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">proteolysis in other organism</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.7E-1	3.0E0	1.0E0	9.5E-1
Annotation Cluster 186		Enrichment Score: 1.11	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">dendritic spine development</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.3E-2	3.2E0	1.9E-1	1.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">axon guidance receptor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.7E-2	3.4E0	4.6E-1	4.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">central nervous system projection neuron axonogenesis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.4E-1	3.0E0	8.1E-1	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">retinal ganglion cell axon guidance</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	2.1E-1	1.9E0	1.0E0	9.5E-1
Annotation Cluster 187		Enrichment Score: 1.1	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:TFIIB-type	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Transcription factor TFIIB</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, TFIIB-type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.1E-1	5.6E-1
Annotation Cluster 188		Enrichment Score: 1.1	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	INTERPRO	<a href="#">Kelch-like protein, gigaxonin</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	1.2E-2	2.1E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">BTB/Kelch-associated</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	18	1.7E-2	1.8E0	1.4E-1	1.2E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">Cul3-RING ubiquitin ligase complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	18	2.8E-2	1.7E0	1.7E-1	1.5E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">kelch-like protein, gigaxonin type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	3.7E-2	1.8E0	5.4E-1	5.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Kelch repeat type 1</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	4.5E-2	1.6E0	3.2E-1	2.9E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Kelch repeat</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	5.2E-2	1.6E0	1.9E-1	1.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 5	<a href="#">RT</a>	<div><div></div><div></div></div>	16	5.3E-2	1.7E0	9.1E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 4	<a href="#">RT</a>	<div><div></div><div></div></div>	16	8.1E-2	1.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 1	<a href="#">RT</a>	<div><div></div><div></div></div>	16	8.9E-2	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 2	<a href="#">RT</a>	<div><div></div><div></div></div>	16	8.9E-2	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 3	<a href="#">RT</a>	<div><div></div><div></div></div>	16	8.9E-2	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 6	<a href="#">RT</a>	<div><div></div><div></div></div>	12	1.3E-1	1.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BACK	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.4E-1	1.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Galactose oxidase, beta-propeller</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.8E-1	1.7E0	8.3E-1	7.6E-1
<input type="checkbox"/>	SMART	<a href="#">Kelch</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	3.4E-1	1.2E0	1.0E0	9.0E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Kelch-type beta propeller</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	3.5E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	<a href="#">SM00875</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	4.0E-1	1.2E0	1.0E0	9.0E-1
Annotation Cluster 189		Enrichment Score: 1.09	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Nop	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Nop domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">NOSIC</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-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	<a href="#">SM00931</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.5E-1	4.1E0	6.5E-1	5.8E-1
Annotation Cluster 190		Enrichment Score: 1.08	<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	<a href="#">rRNA methylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.9E-2	2.8E0	3.3E-1	3.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ribosomal RNA adenine methylase transferase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ribosomal RNA adenine methylase transferase, N-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	SMART	<a href="#">rADc</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.5E-1	4.1E0	6.5E-1	5.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">rRNA (adenine-N6,N6-)-dimethyltransferase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	7.6E-1	6.7E-1
Annotation Cluster 191		Enrichment Score: 1.07	<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	<a href="#">SWI/SNF complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.1E-2	3.0E0	1.4E-1	1.2E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">npBAF complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.1E-1	2.6E0	4.9E-1	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleosome disassembly</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.4E-1	2.1E0	8.4E-1	8.0E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">nBAF complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.7E-1	2.3E0	6.6E-1	5.8E-1
Annotation Cluster 192		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_CC_DIRECT	<a href="#">actomyosin</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	5.9E-3	3.7E0	4.5E-2	4.0E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">myosin II filament</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	6.6E-2	6.4E0	3.5E-1	3.0E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">myosin II complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	8.3E-2	3.6E0	4.0E-1	3.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">actomyosin structure organization</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	3.0E-1	1.5E0	1.0E0	9.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Cell shape</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	5.0E-1	1.4E0	1.0E0	7.8E-1
Annotation Cluster 193		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"/>	UP_SEQ_FEATURE	domain:WW 4	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.0E-3	6.8E0	5.4E-2	5.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 3	<a href="#">RT</a>	<div><div></div><div></div></div>	6	2.6E-3	5.1E0	6.6E-2	6.4E-2
<input type="checkbox"/>	INTERPRO	<a href="#">WW domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	3.8E-2	1.8E0	2.8E-1	2.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 2	<a href="#">RT</a>	<div><div></div><div></div></div>	9	5.2E-2	2.1E0	9.1E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 1	<a href="#">RT</a>	<div><div></div><div></div></div>	9	5.2E-2	2.1E0	9.1E-1	8.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of potassium ion transmembrane transporter activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	6.4E-2	4.0E0	5.3E-1	5.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW	<a href="#">RT</a>	<div><div></div><div></div></div>	6	2.1E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">WW</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	3.0E-1	1.2E0	1.0E0	9.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of membrane potential</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	9.8E-1	6.3E-1	1.0E0	9.8E-1
<input type="checkbox"/>	SMART	<a href="#">C2</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	18	1.0E0	5.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of ion transmembrane transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.0E0	1.6E-1	1.0E0	1.0E0
Annotation Cluster 194		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_CC_DIRECT	<a href="#">beta-catenin destruction complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	5.6E-2	2.7E0	3.0E-1	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">beta-catenin destruction complex disassembly</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	6.4E-2	2.2E0	5.3E-1	5.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">beta-catenin destruction complex assembly</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	1.0E0	9.5E-1
Annotation Cluster 195		Enrichment Score: 1.04	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">activation of JNKK activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	6.4E-2	4.0E0	5.3E-1	5.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Mitogen-activated protein (MAP) kinase kinase kinase, 9/10/11</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">JUN kinase kinase kinase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">mitogen-activated protein kinase kinase kinase, types 9/10/11</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	9.1E-2	5.3E0	7.7E-1	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Leucine-zipper 1	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.3E-1	3.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Leucine-zipper 2	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.3E-1	3.0E0	1.0E0	9.7E-1
Annotation Cluster 196		Enrichment Score: 1.04	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">histone acetylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	13	7.3E-3	2.3E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">MOZ/SAS-like protein</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">histone acetyltransferase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	4.8E-2	1.7E0	2.9E-1	2.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">acetyltransferase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	5.2E-2	2.8E0	3.0E-1	2.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2HC-type	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E-1	3.4E0	1.0E0	9.7E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Acyl-CoA N-acyltransferase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	8.8E-1	8.1E-1	1.0E0	9.1E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Acyltransferase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	13	1.0E0	5.2E-1	1.0E0	1.0E0
Annotation Cluster 197		Enrichment Score: 1.02	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">JAK-STAT cascade involved in growth hormone signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.4E-3	3.6E0	3.0E-2	2.8E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">Stat3 Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	2.1E-3	3.1E0	1.4E-2	9.5E-3
<input type="checkbox"/>	BIOCARTA	<a href="#">IL22 Soluble Receptor Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	2.9E-2	2.1E0	9.1E-2	6.1E-2
<input type="checkbox"/>	BBID	<a href="#">48.mice minus JAKs and STATs</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	4.3E-2	2.1E0	7.6E-1	7.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">JAK-STAT cascade</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	7.7E-2	1.9E0	5.8E-1	5.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">STAT transcription factor, DNA-binding, subdomain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">STAT transcription factor, protein interaction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">STAT transcription factor, all-alpha</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">STAT transcription factor, DNA-binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">STAT transcription factor, core</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">STAT transcription factor, coiled coil</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.3E-1
<input type="checkbox"/>	SMART	<a href="#">SM00964</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.3E-1	2.3E0	9.0E-1	8.1E-1
<input type="checkbox"/>	BBID	<a href="#">12.IL-6 type cytok-signal-transduct</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	2.5E-1	1.4E0	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of type I interferon-mediated signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.7E-1	1.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">p53-like transcription factor, DNA-binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	2.7E-1	1.4E0	9.6E-1	8.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">CCR5 chemokine receptor binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	8.9E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">IL-10 Anti-inflammatory Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	4.2E-1	1.4E0	6.6E-1	4.5E-1
<input type="checkbox"/>	BBID	<a href="#">11.IL-6 gp130-Jak-STAT</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.6E-1	1.7E0	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	<a href="#">IFN alpha signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	8.4E-1	1.0E0	1.0E0	8.4E-1
Annotation Cluster 198		Enrichment Score: 1	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">kinesin complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	19	8.2E-4	2.3E0	8.2E-3	7.1E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">microtubule motor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	21	3.9E-2	1.6E0	2.4E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Kinesin-motor	<a href="#">RT</a>	<div><div></div><div></div></div>	12	4.9E-2	1.9E0	8.6E-1	8.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Kinesin, motor region, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	5.6E-2	1.8E0	3.9E-1	3.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Globular	<a href="#">RT</a>	<div><div></div><div></div></div>	6	7.3E-2	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Kinesin, motor domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	9.8E-2	1.7E0	5.2E-1	4.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">microtubule-based movement</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	18	2.0E-1	1.3E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">antigen processing and presentation of exogenous peptide antigen via MHC class II</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	4.9E-1	1.1E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">retrograde vesicle-mediated transport, Golgi to ER</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	5.3E-1	1.1E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ATP-dependent microtubule motor activity, plus-end-directed</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.6E-1	1.4E0	1.0E0	8.9E-1
<input type="checkbox"/>	SMART	<a href="#">KISc</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	5.6E-1	1.1E0	1.0E0	9.0E-1
Annotation Cluster 199		Enrichment Score: 1	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:C2	<a href="#">RT</a>	<div><div></div><div></div></div>	21	1.4E-2	1.7E0	2.8E-1	2.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">C2 calcium-dependent membrane targeting</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	35	7.5E-2	1.3E0	4.2E-1	3.8E-1
<input type="checkbox"/>	SMART	<a href="#">C2</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	18	1.0E0	5.8E-1	1.0E0	1.0E0
Annotation Cluster 200		Enrichment Score: 0.99	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	<a href="#">Stat3 Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	2.1E-3	3.1E0	1.4E-2	9.5E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Tyrosine-protein kinase, non-receptor Jak/Tyk2</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">tyrosine-protein kinase, Jak/Tyk2 type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.2E-2	5.3E0	3.6E-1	3.5E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">IL22 Soluble Receptor Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	2.9E-2	2.1E0	9.1E-2	6.1E-2
<input type="checkbox"/>	BBID	<a href="#">48.mice minus JAKs and STATs</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	4.3E-2	2.1E0	7.6E-1	7.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">MyTH4 domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	4.3E-2	3.4E0	3.1E-1	2.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2; atypical	<a href="#">RT</a>	<div><div></div><div></div></div>	4	4.5E-2	4.5E0	8.0E-1	7.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MyTH4 1	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MyTH4 2	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1

Annotation Cluster 1		Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	SMART	<a href="#">MyTH4</a>	<a href="#">RT</a>		5	1.6E-1	2.3E0	6.6E-1	5.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">growth hormone receptor binding</a>	<a href="#">RT</a>		3	2.0E-1	3.6E0	7.6E-1	6.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">FERM domain</a>	<a href="#">RT</a>		10	4.4E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Band 4.1 domain</a>	<a href="#">RT</a>		10	4.4E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">FERM central domain</a>	<a href="#">RT</a>		9	5.9E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FERM	<a href="#">RT</a>		7	7.4E-1	9.7E-1	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">B41</a>	<a href="#">RT</a>		10	9.1E-1	8.0E-1	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">FERM/acyl-CoA-binding protein, 3-helical bundle</a>	<a href="#">RT</a>		5	9.7E-1	6.2E-1	1.0E0	9.7E-1
Annotation Cluster 201		Enrichment Score: 0.98			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">sulfate assimilation</a>	<a href="#">RT</a>		6	4.8E-3	4.4E0	8.4E-2	8.0E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor</a>	<a href="#">RT</a>		5	3.1E-2	3.7E0	2.0E-1	1.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Thioredoxin</a>	<a href="#">RT</a>		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">glycerol ether metabolic process</a>	<a href="#">RT</a>		4	3.7E-2	4.7E0	3.8E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein-disulfide reductase activity</a>	<a href="#">RT</a>		3	2.7E-1	3.0E0	9.5E-1	8.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">thioredoxin-disulfide reductase activity</a>	<a href="#">RT</a>		3	5.2E-1	1.8E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein disulfide oxidoreductase activity</a>	<a href="#">RT</a>		5	5.9E-1	1.2E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular oxidant detoxification</a>	<a href="#">RT</a>		8	9.6E-1	6.8E-1	1.0E0	9.6E-1
Annotation Cluster 202		Enrichment Score: 0.97			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 19	<a href="#">RT</a>		5	2.0E-2	4.3E0	3.9E-1	3.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 20	<a href="#">RT</a>		5	2.0E-2	4.3E0	3.9E-1	3.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 4	<a href="#">RT</a>		8	2.6E-2	2.6E0	4.9E-1	4.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 6	<a href="#">RT</a>		6	3.1E-2	3.1E0	5.8E-1	5.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 7	<a href="#">RT</a>		6	3.1E-2	3.1E0	5.8E-1	5.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 8	<a href="#">RT</a>		6	3.1E-2	3.1E0	5.8E-1	5.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 9	<a href="#">RT</a>		6	3.1E-2	3.1E0	5.8E-1	5.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 18	<a href="#">RT</a>		5	3.1E-2	3.8E0	5.8E-1	5.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 3	<a href="#">RT</a>		8	3.3E-2	2.5E0	6.1E-1	5.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 5	<a href="#">RT</a>		6	4.3E-2	2.9E0	7.8E-1	7.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 21	<a href="#">RT</a>		4	7.0E-2	3.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 1	<a href="#">RT</a>		8	7.6E-2	2.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 2	<a href="#">RT</a>		8	7.6E-2	2.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 10	<a href="#">RT</a>		5	8.6E-2	2.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 11	<a href="#">RT</a>		5	8.6E-2	2.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 12	<a href="#">RT</a>		5	8.6E-2	2.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 13	<a href="#">RT</a>		5	8.6E-2	2.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 14	<a href="#">RT</a>		5	8.6E-2	2.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 15	<a href="#">RT</a>		5	8.6E-2	2.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 16	<a href="#">RT</a>		5	8.6E-2	2.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 17	<a href="#">RT</a>		5	8.6E-2	2.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Actin-binding	<a href="#">RT</a>		6	1.6E-1	2.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Spectrin/alpha-actinin</a>	<a href="#">RT</a>		8	1.8E-1	1.7E0	8.3E-1	7.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Spectrin repeat</a>	<a href="#">RT</a>		7	2.1E-1	1.7E0	9.4E-1	8.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 22	<a href="#">RT</a>		3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">EF-hand, Ca insensitive</a>	<a href="#">RT</a>		3	2.5E-1	3.1E0	9.6E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Actinin-type, actin-binding, conserved site</a>	<a href="#">RT</a>		6	3.1E-1	1.6E0	9.9E-1	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CH 1	<a href="#">RT</a>		6	3.6E-1	1.5E0	1.0E0	9.7E-1


















































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	domain:CH 2	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.6E-1	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">filopodium membrane</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.1E-1	1.5E0	1.0E0	8.7E-1
<input type="checkbox"/>	SMART	<a href="#">SPEC</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	5.9E-1	1.1E0	1.0E0	9.0E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Calponin homology domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	7.0E-1	9.8E-1	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CH	<a href="#">RT</a>	<div><div></div><div></div></div>	6	7.6E-1	9.7E-1	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">CH</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	9.5E-1	7.4E-1	1.0E0	9.5E-1
Annotation Cluster 203		Enrichment Score: 0.96	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">chromatin silencing complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	4.0E-2	3.5E0	2.3E-1	2.0E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">rDNA heterochromatin</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.2E-1	4.8E0	5.0E-1	4.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">chromatin silencing at rDNA</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	2.8E-1	1.4E0	1.0E0	9.5E-1
Annotation Cluster 204		Enrichment Score: 0.95	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of cyclin-dependent protein serine/threonine kinase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	3.8E-2	2.2E0	3.8E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">cyclin-dependent protein serine/threonine kinase regulator activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	9.1E-2	2.4E0	4.6E-1	4.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of phosphorylation of RNA polymerase II C-terminal domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	9.5E-1
Annotation Cluster 205		Enrichment Score: 0.95	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SWIRM	<a href="#">RT</a>	<div><div></div><div></div></div>	4	4.5E-2	4.5E0	8.0E-1	7.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">SWIRM domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">SANT domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.1E-1	1.9E0	5.9E-1	5.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SANT	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.4E-1	1.4E0	1.0E0	9.7E-1
Annotation Cluster 206		Enrichment Score: 0.95	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:UBR-type	<a href="#">RT</a>	<div><div></div><div></div></div>	4	7.0E-2	3.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, N-recognin</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.3E-1
<input type="checkbox"/>	SMART	<a href="#">ZnF UBR1</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.3E-1	2.3E0	9.0E-1	8.1E-1
Annotation Cluster 207		Enrichment Score: 0.95	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Domain A	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Domain B	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Domain of unknown function DUF3452, retinoblastoma-associated</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Retinoblastoma-associated protein, B-box</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Retinoblastoma-associated protein, A-box</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Rb C-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	SMART	<a href="#">SM01367</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.5E-1	4.1E0	6.5E-1	5.8E-1
<input type="checkbox"/>	SMART	<a href="#">SM01368</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.5E-1	4.1E0	6.5E-1	5.8E-1
<input type="checkbox"/>	SMART	<a href="#">SM01369</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.5E-1	4.1E0	6.5E-1	5.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of lipid kinase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Spacer	<a href="#">RT</a>	<div><div></div><div></div></div>	4	7.1E-1	1.1E0	1.0E0	9.7E-1
Annotation Cluster 208		Enrichment Score: 0.93	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">lung-associated mesenchyme development</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	7.2E-2	3.0E0	5.7E-1	5.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mesenchymal cell proliferation involved in lung development</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.6E-2	5.9E0	5.7E-1	5.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">hair follicle morphogenesis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	3.0E-1	1.5E0	1.0E0	9.5E-1
Annotation Cluster 209		Enrichment Score: 0.92	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of actin polymerization or depolymerization</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.8E-2	3.4E0	6.8E-1	6.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">DEK, C-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.1E-1	5.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of lamellipodium assembly</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.4E-1	3.0E0	8.1E-1	7.7E-1
Annotation Cluster 210		Enrichment Score: 0.92	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">Swr1 complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	4.0E-2	3.5E0	2.3E-1	2.0E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">NuA4 histone acetyltransferase complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	5.1E-2	2.5E0	2.9E-1	2.5E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">histone H2A acetylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.4E-1	2.0E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">histone H4 acetylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	4.3E-1	1.3E0	1.0E0	9.5E-1
Annotation Cluster 211		Enrichment Score: 0.91	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	INTERPRO	<a href="#">RNA-processing_protein, HAT helix</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.3E-2	3.7E0	1.2E-1	1.1E-1
<input type="checkbox"/>	SMART	<a href="#">HAT</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	7.2E-2	2.4E0	4.0E-1	3.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 4	<a href="#">RT</a>	<div><div></div><div></div></div>	5	8.6E-2	2.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 1	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.1E-1	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 2	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.1E-1	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 3	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.1E-1	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 9	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 5	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.1E-1	2.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 8	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 7	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.7E-1	2.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 6	<a href="#">RT</a>	<div><div></div><div></div></div>	3	3.9E-1	2.3E0	1.0E0	9.7E-1
Annotation Cluster 212		Enrichment Score: 0.9	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">Rap_protein signal transduction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.6E-2	3.6E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">microvillus assembly</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.4E-1	2.1E0	8.4E-1	8.0E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">recycling endosome membrane</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	8.4E-1	8.7E-1	1.0E0	8.7E-1
Annotation Cluster 213		Enrichment Score: 0.9	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	INTERPRO	<a href="#">SANT domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.1E-1	1.9E0	5.9E-1	5.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SANT 1	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.3E-1	3.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SANT 2	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.3E-1	3.0E0	1.0E0	9.7E-1
Annotation Cluster 214		Enrichment Score: 0.9	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	INTERPRO	<a href="#">Brix domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	3.9E-1	3.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Brix	<a href="#">RT</a>	<div><div></div><div></div></div>	4	7.0E-2	3.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">SM00879</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.6E-1	2.7E0	6.6E-1	5.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Anticodon-binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	4.0E-1	1.8E0	1.0E0	9.1E-1
Annotation Cluster 215		Enrichment Score: 0.88	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">endoplasmic reticulum chaperone complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	8.0E-2	2.9E0	4.0E-1	3.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein folding in endoplasmic reticulum</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.6E-1	2.3E0	9.2E-1	8.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Prevents secretion from ER	<a href="#">RT</a>	<div><div></div><div></div></div>	13	1.8E-1	1.5E0	1.0E0	9.7E-1
Annotation Cluster 216		Enrichment Score: 0.86	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein metabolic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	3.2E-2	3.7E0	3.5E-1	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to laminar fluid shear stress</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.4E-1	3.0E0	8.1E-1	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of response to cytokine stimulus</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of heterotypic cell-cell adhesion</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	9.5E-1
Annotation Cluster 217		Enrichment Score: 0.86	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KEN	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">KEN domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">PUB domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	9.6E-1	8.8E-1
<input type="checkbox"/>	SMART	<a href="#">PUG</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	3.6E-1	2.4E0	1.0E0	9.0E-1
Annotation Cluster 218		Enrichment Score: 0.85	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DOC	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Anaphase-promoting complex, subunit 10/DOC domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.2E-1	3.1E0	6.1E-1	5.6E-1
<input type="checkbox"/>	SMART	<a href="#">SM01337</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.3E-1	2.3E0	9.0E-1	8.1E-1
Annotation Cluster 219		Enrichment Score: 0.84	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	

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	<a href="#">Glycolysis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.0E-2	2.4E0	4.3E-2	3.3E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Enolase, C-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">phosphopyruvate hydratase complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.4E-2	4.2E0	2.9E-1	2.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Enolase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Enolase, N-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">canonical glycolysis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	5.9E-2	2.1E0	5.1E-1	4.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">phosphopyruvate hydratase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	6.3E-2	4.0E0	3.5E-1	3.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Enolase, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	SMART	<a href="#">SM01192</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.8E-2	3.3E0	4.9E-1	4.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">glycolytic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	1.1E-1	1.7E0	7.2E-1	6.9E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">enolase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.6E-1	4.0E0	1.0E0	9.9E-1
<input type="checkbox"/>	SMART	<a href="#">SM01193</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.6E-1	2.7E0	6.6E-1	5.9E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Glycolysis Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	4.1E-1	1.5E0	6.6E-1	4.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">gluconeogenesis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	6.3E-1	1.1E0	1.0E0	9.5E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Biosynthesis of amino acids</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	8.4E-1	8.7E-1	1.0E0	8.4E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Glycolysis / Gluconeogenesis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	8.5E-1	8.6E-1	1.0E0	8.5E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Carbon metabolism</a>	<a href="#">RT</a>	<div><div></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	<a href="#">RT</a>	<div><div></div><div></div></div>	21	1.0E0	4.8E-1	1.0E0	1.0E0
Annotation Cluster 220		Enrichment Score: 0.83	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Histone H2B</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	6.0E-4	3.1E0	7.5E-3	6.9E-3
<input type="checkbox"/>	SMART	<a href="#">H2B</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	1.8E-2	2.0E0	1.4E-1	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">innate immune response in mucosa</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.4E-1	1.7E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">antibacterial humoral response</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	7.7E-1	9.4E-1	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">defense response to Gram-positive bacterium</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	13	7.9E-1	9.1E-1	1.0E0	9.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Antibiotic</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	2.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Antimicrobial</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	2.5E-1	1.0E0	1.0E0
Annotation Cluster 221		Enrichment Score: 0.83	<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:REM 1	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:REM 2	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:REM 3	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">epithelial cell migration</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.7E-1	3.0E0	1.0E0	9.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">HR1 rho-binding repeat</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	3.8E-1	2.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	<a href="#">Hr1</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.4E-1	1.7E0	1.0E0	9.0E-1
Annotation Cluster 222		Enrichment Score: 0.82	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">JAB1/Mov34/MPN/PAD-1</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	6.7E-3	3.6E0	6.8E-2	6.3E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MPN	<a href="#">RT</a>	<div><div></div><div></div></div>	6	2.2E-2	3.4E0	4.3E-1	4.2E-1
<input type="checkbox"/>	SMART	<a href="#">JAB_MPN</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	3.1E-2	2.6E0	2.3E-1	2.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:JAMM motif	<a href="#">RT</a>	<div><div></div><div></div></div>	4	7.0E-2	3.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Rpn11/EIF3F C-terminal domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.1E-1	5.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">thiol-dependent ubiquitin-specific protease activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.0E0	3.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">metallopeptidase activity</a>	<a href="#">RT</a>	<div><div></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	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	2.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Metalloprotease</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	1.8E-1	1.0E0	1.0E0
Annotation Cluster 223		Enrichment Score: 0.82	<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	<a href="#">positive regulation of cell adhesion mediated by integrin</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	5.3E-2	2.7E0	4.8E-1	4.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2 1	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.5E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2 2	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.5E-1	2.3E0	1.0E0	9.7E-1
Annotation Cluster 224		Enrichment Score: 0.81	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Adenylate kinase, active site lid domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.1E-1	5.6E-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"/>	INTERPRO	<a href="#">Adenylate kinase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.7E-1	2.8E0	7.9E-1	7.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">adenylate kinase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.8E-1	2.7E0	7.3E-1	6.5E-1
Annotation Cluster 225		Enrichment Score: 0.8	<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	chain:Putative uncharacterized protein C21orf81	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A1	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A2	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A3	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.7E-1
Annotation Cluster 226		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	<a href="#">isotype switching</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.9E-2	2.8E0	3.3E-1	3.1E-1
<input type="checkbox"/>	OMIM_DISEASE	<a href="#">Mismatch repair cancer syndrome</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.9E-2	6.0E0	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">guanine/thymine mispair binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.3E-1	4.5E0	5.8E-1	5.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">somatic hypermutation of immunoglobulin genes</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.8E-1	1.9E0	1.0E0	9.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Hereditary nonpolyposis colorectal cancer</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	3.9E-1	2.3E0	1.0E0	7.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">mismatched DNA binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.7E-1	1.6E0	1.0E0	8.9E-1
Annotation Cluster 227		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"/>	INTERPRO	<a href="#">TATA-box binding protein</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Beta2-adaptin/TBP, C-terminal domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	9.6E-1	8.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">DNA-templated transcription, initiation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	2.5E-1	1.5E0	1.0E0	9.5E-1
Annotation Cluster 228		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"/>	BBID	<a href="#">104.Insulin signaling</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	8.4E-2	1.7E0	8.2E-1	8.2E-1
<input type="checkbox"/>	BBID	<a href="#">108.Regulating glucose transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	8.4E-2	2.0E0	8.2E-1	8.2E-1
<input type="checkbox"/>	BBID	<a href="#">105.Signaling glucose uptake</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	2.3E-1	1.7E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	<a href="#">106.Glycogen synthase-synthesis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.8E-1	1.8E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	<a href="#">107.mRNA translation-protein synthesis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	3.4E-1	1.4E0	1.0E0	1.0E0
Annotation Cluster 229		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	<a href="#">type I interferon signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	1.1E-1	1.5E0	7.4E-1	7.1E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Antiviral defense</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	22	1.7E-1	1.3E0	5.3E-1	4.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">defense response to virus</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	33	2.2E-1	1.2E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of viral genome replication</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	2.2E-1	1.5E0	1.0E0	9.5E-1
Annotation Cluster 230		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	<a href="#">heat shock protein, HSP90/HTPG types</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.2E-2	5.3E0	3.6E-1	3.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Heat shock protein Hsp90, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.1E-1	5.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Heat shock protein Hsp90, N-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.7E-1	2.8E0	7.9E-1	7.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Heat shock protein Hsp90</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.6E-1	2.3E0	9.6E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Histidine kinase-like ATPase, ATP-binding domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	4.5E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	<a href="#">HATPase_c</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.3E-1	1.5E0	1.0E0	9.0E-1
Annotation Cluster 231		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"/>	UP_SEQ_FEATURE	repeat:RCC1 7	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Regulator of chromosome condensation, RCC1</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.1E-1	2.1E0	5.8E-1	5.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 5	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.1E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.3E-1	2.0E0	6.3E-1	5.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 4	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.3E-1	2.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 1	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.6E-1	2.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 2	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.6E-1	2.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 3	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.6E-1	2.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 6	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.0E-1	2.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	COG_ONTOLOGY	<a href="#">Cell division and chromosome partitioning / Cytoskeleton</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.0E0	5.0E-1	1.0E0	1.0E0
Annotation Cluster 232		Enrichment Score: 0.76	<div><div></div><div>G</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"/>	UP_SEQ_FEATURE	domain:PUA	RT		3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">PUA-like domain</a>	RT		6	1.8E-1	2.0E0	8.5E-1	7.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Pseudouridine synthase/archaeosine transglycosylase</a>	RT		3	1.9E-1	3.7E0	8.6E-1	7.8E-1
Annotation Cluster 233		Enrichment Score: 0.76	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Innate immunity</a>	RT		51	2.4E-2	1.3E0	9.5E-2	7.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">innate immune response</a>	RT		78	3.0E-1	1.1E0	1.0E0	9.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Immunity</a>	RT		69	7.5E-1	9.5E-1	1.0E0	7.8E-1
Annotation Cluster 234		Enrichment Score: 0.75	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Protein-tyrosine phosphatase, catalytic</a>	RT		19	9.0E-3	1.9E0	8.7E-2	7.9E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">non-membrane spanning protein tyrosine phosphatase activity</a>	RT		4	1.4E-1	3.0E0	5.8E-1	5.2E-1
<input type="checkbox"/>	SMART	<a href="#">PTPc motif</a>	RT		19	2.7E-1	1.2E0	9.7E-1	8.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Protein-tyrosine phosphatase, receptor/non-receptor type</a>	RT		7	5.9E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	<a href="#">PTPc</a>	RT		7	9.2E-1	7.7E-1	1.0E0	9.2E-1
Annotation Cluster 235		Enrichment Score: 0.74	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Carbamoyl-phosphate synthetase large subunit-like, ATP-binding domain</a>	RT		4	8.8E-2	3.5E0	4.7E-1	4.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">ATP-grasp fold, subdomain 2</a>	RT		7	9.0E-2	2.2E0	4.8E-1	4.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">ATP-grasp fold</a>	RT		5	1.4E-1	2.4E0	7.0E-1	6.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Pre-ATP-grasp domain</a>	RT		5	1.8E-1	2.2E0	8.4E-1	7.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">ATP-grasp fold, subdomain 1</a>	RT		5	2.1E-1	2.1E0	9.6E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Rudiment single hybrid motif</a>	RT		3	2.5E-1	3.1E0	9.6E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:ATP-grasp	RT		3	5.9E-1	1.6E0	1.0E0	9.7E-1
Annotation Cluster 236		Enrichment Score: 0.74	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Glycogen metabolism</a>	RT		8	7.3E-2	2.1E0	2.5E-1	2.0E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">PTW/PP1 phosphatase complex</a>	RT		4	8.3E-2	3.6E0	4.0E-1	3.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">glycogen metabolic process</a>	RT		8	2.1E-1	1.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Carbohydrate metabolism</a>	RT		11	8.9E-1	8.0E-1	1.0E0	8.9E-1
Annotation Cluster 237		Enrichment Score: 0.73	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">DNA topological change</a>	RT		5	5.0E-2	3.3E0	4.6E-1	4.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">DNA binding, bending</a>	RT		6	1.7E-1	2.0E0	7.1E-1	6.3E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Apoptotic DNA fragmentation and tissue homeostasis</a>	RT		4	7.5E-1	1.1E0	1.0E0	7.5E-1
Annotation Cluster 238		Enrichment Score: 0.71	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	<a href="#">AKAP95 role in mitosis and chromosome dynamics</a>	RT		8	5.7E-2	2.1E0	1.5E-1	1.0E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Protein Kinase A at the Centrosome</a>	RT		8	1.8E-1	1.6E0	3.8E-1	2.6E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Rho-Selective Guanine Exchange Factor AKAP13 Mediates Stress Fiber Formation</a>	RT		4	7.5E-1	1.1E0	1.0E0	7.5E-1
Annotation Cluster 239		Enrichment Score: 0.7	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 1	RT		8	3.3E-2	2.5E0	6.1E-1	5.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 2	RT		8	3.3E-2	2.5E0	6.1E-1	5.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase C, alpha/beta/gamma types</a>	RT		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">protein kinase C, alpha/beta/gamma types</a>	RT		3	9.1E-2	5.3E0	7.7E-1	7.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">calcium-dependent protein kinase C activity</a>	RT		3	1.3E-1	4.5E0	5.8E-1	5.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 2; via carbonyl oxygen	RT		9	2.0E-1	1.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">African trypanosomiasis</a>	RT		9	2.9E-1	1.4E0	4.5E-1	2.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 1	RT		8	5.5E-1	1.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 3; via carbonyl oxygen	RT		3	8.4E-1	9.7E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 1; via carbonyl oxygen	RT		4	8.7E-1	8.5E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 3	RT		3	9.6E-1	6.4E-1	1.0E0	9.7E-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 240		Enrichment Score: 0.69	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Btk-type	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.3E-1	3.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, Btk motif</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.7E-1	2.8E0	7.9E-1	7.2E-1
<input type="checkbox"/>	SMART	<a href="#">BTK</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.9E-1	1.8E0	1.0E0	9.0E-1
Annotation Cluster 241		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	<a href="#">Repression of Pain Sensation by the Transcriptional Regulator DREAM</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	1.4E-2	2.2E0	5.5E-2	3.7E-2
<input type="checkbox"/>	BIOCARTA	<a href="#">Transcription Regulation by Methyltransferase of CARM1</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	5.7E-2	2.1E0	1.5E-1	1.0E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">ciliary base</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.2E-1	1.9E0	5.0E-1	4.4E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Regulation of ck1/cdk5 by type 1 glutamate receptors</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.5E-1	1.6E0	3.3E-1	2.3E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">mCalpain and friends in Cell motility</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	2.6E-1	1.4E0	5.1E-1	3.4E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	2.6E-1	1.4E0	5.1E-1	3.4E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">cAMP</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	2.6E-1	1.5E0	7.7E-1	6.0E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">cAMP-dependent protein kinase complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	3.0E-1	2.7E0	8.7E-1	7.6E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR)_pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.4E-1	1.5E0	6.0E-1	4.1E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Phospholipase C-epsilon_pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.4E-1	1.5E0	6.0E-1	4.1E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Attenuation of GPCR Signaling</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	4.2E-1	1.4E0	6.6E-1	4.5E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">GATA3 participate in activating the Th2 cytokine genes expression</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	4.2E-1	1.3E0	6.6E-1	4.5E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Stathmin and breast cancer resistance to antimicrotubule agents</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	7.5E-1	9.9E-1	1.0E0	7.5E-1
Annotation Cluster 242		Enrichment Score: 0.68	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of transporter activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.8E-2	3.4E0	6.8E-1	6.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">calcium channel regulator activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.5E-1	1.8E0	6.4E-1	5.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">chloride channel regulator activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.3E-1	2.4E0	8.5E-1	7.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">sodium channel regulator activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	2.8E-1	1.5E0	9.5E-1	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of sodium ion transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	4.0E-1	1.6E0	1.0E0	9.5E-1
Annotation Cluster 243		Enrichment Score: 0.68	<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	<a href="#">ventral midline development</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.6E-2	5.9E0	5.7E-1	5.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">smoothened signaling pathway involved in regulation of cerebellar granule cell precursor cell proliferation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.3E-1	4.4E0	8.1E-1	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">smoothened signaling pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	9.1E-1	7.7E-1	1.0E0	9.5E-1
Annotation Cluster 244		Enrichment Score: 0.68	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">DIX domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">beta-catenin destruction complex disassembly</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	6.4E-2	2.2E0	5.3E-1	5.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Dishevelled C-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Dishevelled family</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Dishevelled protein domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DIX	<a href="#">RT</a>	<div><div></div><div></div></div>	4	7.0E-2	3.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Dishevelled-related protein</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.1E-1	5.6E-1
<input type="checkbox"/>	SMART	<a href="#">DAX</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.6E-1	2.7E0	6.6E-1	5.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cochlea morphogenesis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	3.1E-1	1.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">planar cell polarity pathway involved in neural tube closure</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.3E-1	2.0E0	1.0E0	9.5E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Basal cell carcinoma</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	4.6E-1	1.2E0	6.9E-1	4.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">Rac GTPase binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	5.2E-1	1.2E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DEP	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.4E-1	1.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">DEP domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	7.4E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	<a href="#">DEP</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.3E-1	7.4E-1	1.0E0	9.3E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">frizzled binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	9.9E-1	5.0E-1	1.0E0	9.9E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div></div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 245		Enrichment Score: 0.66	<div><div></div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Purine biosynthesis</a>	<a href="#">RT</a>	<div><div></div></div>	5	1.1E-1	2.6E0	3.6E-1	2.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">purine nucleobase biosynthetic process</a>	<a href="#">RT</a>	<div><div></div></div>	3	2.0E-1	3.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">'de novo' IMP biosynthetic process</a>	<a href="#">RT</a>	<div><div></div></div>	3	2.7E-1	3.0E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">purine ribonucleoside monophosphate biosynthetic process</a>	<a href="#">RT</a>	<div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	9.5E-1
Annotation Cluster 246		Enrichment Score: 0.66	<div><div></div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of interleukin-12 production</a>	<a href="#">RT</a>	<div><div></div></div>	9	4.7E-2	2.1E0	4.5E-1	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of nitric-oxide synthase biosynthetic process</a>	<a href="#">RT</a>	<div><div></div></div>	5	1.6E-1	2.3E0	9.2E-1	8.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of interleukin-10 production</a>	<a href="#">RT</a>	<div><div></div></div>	7	1.8E-1	1.8E0	9.9E-1	9.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">lipopolysaccharide binding</a>	<a href="#">RT</a>	<div><div></div></div>	6	3.0E-1	1.6E0	9.5E-1	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of interferon-alpha production</a>	<a href="#">RT</a>	<div><div></div></div>	4	3.3E-1	2.0E0	1.0E0	9.5E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Dendritic cells in regulating TH1 and TH2 Development</a>	<a href="#">RT</a>	<div><div></div></div>	7	7.7E-1	9.8E-1	1.0E0	7.7E-1
Annotation Cluster 247		Enrichment Score: 0.65	<div><div></div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">calcineurin complex</a>	<a href="#">RT</a>	<div><div></div></div>	3	1.2E-1	4.8E0	5.0E-1	4.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of NFAT protein import into nucleus</a>	<a href="#">RT</a>	<div><div></div></div>	4	2.3E-1	2.4E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">calcineurin-NFAT signaling cascade</a>	<a href="#">RT</a>	<div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	9.5E-1
Annotation Cluster 248		Enrichment Score: 0.63	<div><div></div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">lung-associated mesenchyme development</a>	<a href="#">RT</a>	<div><div></div></div>	5	7.2E-2	3.0E0	5.7E-1	5.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">branching involved in salivary gland morphogenesis</a>	<a href="#">RT</a>	<div><div></div></div>	4	2.8E-1	2.2E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">midbrain development</a>	<a href="#">RT</a>	<div><div></div></div>	6	6.2E-1	1.1E0	1.0E0	9.5E-1
Annotation Cluster 249		Enrichment Score: 0.63	<div><div></div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Circadian rhythm</a>	<a href="#">RT</a>	<div><div></div></div>	13	8.7E-3	2.2E0	1.6E-2	8.7E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">AMP-activated protein kinase activity</a>	<a href="#">RT</a>	<div><div></div></div>	5	1.8E-2	4.3E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">nucleotide-activated protein kinase complex</a>	<a href="#">RT</a>	<div><div></div></div>	6	1.9E-2	3.5E0	1.3E-1	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CBS 3	<a href="#">RT</a>	<div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CBS 4	<a href="#">RT</a>	<div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Reversal of Insulin Resistance by Leptin</a>	<a href="#">RT</a>	<div><div></div></div>	7	1.1E-1	2.0E0	2.6E-1	1.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">carnitine shuttle</a>	<a href="#">RT</a>	<div><div></div></div>	4	1.8E-1	2.6E0	9.9E-1	9.4E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Fatty acid biosynthesis</a>	<a href="#">RT</a>	<div><div></div></div>	10	3.4E-1	1.3E0	9.5E-1	7.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">fatty acid biosynthetic process</a>	<a href="#">RT</a>	<div><div></div></div>	9	6.7E-1	1.0E0	1.0E0	9.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CBS 1	<a href="#">RT</a>	<div><div></div></div>	3	7.6E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CBS 2	<a href="#">RT</a>	<div><div></div></div>	3	7.6E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">CBS domain</a>	<a href="#">RT</a>	<div><div></div></div>	3	8.1E-1	1.0E0	1.0E0	8.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Cystathionine beta-synthase, core</a>	<a href="#">RT</a>	<div><div></div></div>	3	8.6E-1	9.3E-1	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	<a href="#">CBS</a>	<a href="#">RT</a>	<div><div></div></div>	3	8.9E-1	8.7E-1	1.0E0	9.0E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Fatty acid metabolism</a>	<a href="#">RT</a>	<div><div></div></div>	12	9.8E-1	6.6E-1	1.0E0	9.8E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Lipid biosynthesis</a>	<a href="#">RT</a>	<div><div></div></div>	11	1.0E0	4.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Lipid metabolism</a>	<a href="#">RT</a>	<div><div></div></div>	18	1.0E0	2.9E-1	1.0E0	1.0E0
Annotation Cluster 250		Enrichment Score: 0.63	<div><div></div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Dorso-ventral axis formation</a>	<a href="#">RT</a>	<div><div></div></div>	12	7.7E-3	2.3E0	1.4E-2	7.7E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LNR 3	<a href="#">RT</a>	<div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Notch, NOD domain</a>	<a href="#">RT</a>	<div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Notch, NODP domain</a>	<a href="#">RT</a>	<div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 28	<a href="#">RT</a>	<div><div></div></div>	4	2.5E-2	5.5E0	4.8E-1	4.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LNR 1	<a href="#">RT</a>	<div><div></div></div>	4	2.5E-2	5.5E0	4.8E-1	4.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LNR 2	<a href="#">RT</a>	<div><div></div></div>	4	2.5E-2	5.5E0	4.8E-1	4.7E-1
<input type="checkbox"/>	SMART	<a href="#">SM01338</a>	<a href="#">RT</a>	<div><div></div></div>	4	4.8E-2	4.1E0	2.8E-1	2.6E-1

Annotation Cluster 1		Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	SMART	<a href="#">SM01339</a>	<a href="#">RT</a>	<div><div></div></div>	4	4.8E-2	4.1E0	2.8E-1	2.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 29	<a href="#">RT</a>	<div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 33	<a href="#">RT</a>	<div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 34	<a href="#">RT</a>	<div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Domain of unknown function DUF3454, notch</a>	<a href="#">RT</a>	<div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Notch domain</a>	<a href="#">RT</a>	<div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.3E-1
<input type="checkbox"/>	SMART	<a href="#">SM01334</a>	<a href="#">RT</a>	<div><div></div></div>	3	1.5E-1	4.1E0	6.5E-1	5.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 20	<a href="#">RT</a>	<div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 24	<a href="#">RT</a>	<div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 26	<a href="#">RT</a>	<div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 27	<a href="#">RT</a>	<div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 13; calcium-binding	<a href="#">RT</a>	<div><div></div></div>	4	2.1E-1	2.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 17; calcium-binding	<a href="#">RT</a>	<div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 21; calcium-binding	<a href="#">RT</a>	<div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 22	<a href="#">RT</a>	<div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 23; calcium-binding	<a href="#">RT</a>	<div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">NL</a>	<a href="#">RT</a>	<div><div></div></div>	4	2.3E-1	2.3E0	9.0E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 14; calcium-binding	<a href="#">RT</a>	<div><div></div></div>	4	2.5E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 15; calcium-binding	<a href="#">RT</a>	<div><div></div></div>	4	2.5E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 19	<a href="#">RT</a>	<div><div></div></div>	3	3.3E-1	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 11; calcium-binding	<a href="#">RT</a>	<div><div></div></div>	4	3.4E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 12; calcium-binding	<a href="#">RT</a>	<div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Notch signaling pathway</a>	<a href="#">RT</a>	<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	<a href="#">RT</a>	<div><div></div></div>	5	4.8E-1	1.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 16; calcium-binding	<a href="#">RT</a>	<div><div></div></div>	3	5.0E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 9; calcium-binding	<a href="#">RT</a>	<div><div></div></div>	3	7.0E-1	1.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 9	<a href="#">RT</a>	<div><div></div></div>	4	7.1E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 10	<a href="#">RT</a>	<div><div></div></div>	3	7.4E-1	1.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 6	<a href="#">RT</a>	<div><div></div></div>	6	7.9E-1	9.3E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 7; calcium-binding	<a href="#">RT</a>	<div><div></div></div>	4	8.0E-1	9.7E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 3	<a href="#">RT</a>	<div><div></div></div>	9	8.9E-1	8.1E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 7	<a href="#">RT</a>	<div><div></div></div>	3	9.3E-1	7.3E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 4	<a href="#">RT</a>	<div><div></div></div>	6	9.5E-1	6.9E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 5	<a href="#">RT</a>	<div><div></div></div>	4	9.6E-1	6.5E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 5; calcium-binding	<a href="#">RT</a>	<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	<a href="#">RT</a>	<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	<a href="#">RT</a>	<div><div></div></div>	9	1.0E0	5.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">EGF-like calcium-binding, conserved site</a>	<a href="#">RT</a>	<div><div></div></div>	7	1.0E0	4.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">EGF-type aspartate/asparagine hydroxylation site</a>	<a href="#">RT</a>	<div><div></div></div>	7	1.0E0	4.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">EGF-like calcium-binding</a>	<a href="#">RT</a>	<div><div></div></div>	7	1.0E0	3.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">EGF-like, conserved site</a>	<a href="#">RT</a>	<div><div></div></div>	10	1.0E0	3.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Epidermal growth factor-like domain</a>	<a href="#">RT</a>	<div><div></div></div>	12	1.0E0	3.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">EGF-like domain</a>	<a href="#">RT</a>	<div><div></div></div>	10	1.0E0	2.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	<a href="#">EGF_CA</a>	<a href="#">RT</a>	<div><div></div></div>	7	1.0E0	2.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	<a href="#">EGF</a>	<a href="#">RT</a>	<div><div></div></div>	11	1.0E0	2.4E-1	1.0E0	1.0E0
Annotation Cluster 251		Enrichment Score: 0.63			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	<a href="#">Small Leucine-rich Proteoglycan (SLRP) molecules</a>	<a href="#">RT</a>	<div><div></div></div>	6	1.5E-2	3.1E0	5.9E-2	4.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">keratan sulfate catabolic process</a>	<a href="#">RT</a>	<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)	<a href="#">RT</a>	<div><div></div></div>	3	5.8E-2	6.8E0	9.1E-1	8.8E-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_KEYWORDS	<a href="#">Proteoglycan</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	2.8E-1	1.4E0	8.0E-1	6.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">keratan sulfate biosynthetic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	5.2E-1	1.3E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">lysosomal lumen</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	13	7.0E-1	9.7E-1	1.0E0	8.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">Golgi lumen</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	7.6E-1	9.3E-1	1.0E0	8.7E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Sulfation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	8.8E-1	8.1E-1	1.0E0	8.8E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Extracellular matrix</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	18	1.0E0	4.8E-1	1.0E0	1.0E0
Annotation Cluster 252		Enrichment Score: 0.61	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Actin-related protein 3 (Arp3)</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">Arp2/3 protein complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.9E-1	2.1E0	8.4E-1	7.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">Arp2/3 complex-mediated actin nucleation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	7.4E-1	1.1E0	1.0E0	9.5E-1
Annotation Cluster 253		Enrichment Score: 0.6	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Natriuretic peptide receptor</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">natriuretic peptide receptor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">hormone binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.8E-1	2.2E0	9.5E-1	8.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">peptide hormone binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	8.5E-1	8.8E-1	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Extracellular ligand-binding receptor</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	8.5E-1	8.6E-1	1.0E0	9.1E-1
Annotation Cluster 254		Enrichment Score: 0.59	<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	<a href="#">GKAP/Homer scaffold activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.3E-1	4.5E0	5.8E-1	5.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">vocalization behavior</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.0E-1	2.1E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">adult behavior</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	6.6E-1	1.1E0	1.0E0	9.5E-1
Annotation Cluster 255		Enrichment Score: 0.58	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">SIAH-type domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.1E-1	2.6E0	6.0E-1	5.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">TRAF-like</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	2.1E-1	1.7E0	9.4E-1	8.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:TRAF-type	<a href="#">RT</a>	<div><div></div><div></div></div>	3	3.3E-1	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, TRAF-type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	6.0E-1	1.5E0	1.0E0	9.1E-1
Annotation Cluster 256		Enrichment Score: 0.57	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	<a href="#">Nitric Oxide Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.4E-1	1.5E0	3.1E-1	2.1E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Effects of calcineurin in Keratinocyte Differentiation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	2.5E-1	1.5E0	4.9E-1	3.4E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Role of MEF2D in T-cell Apoptosis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	5.5E-1	1.2E0	8.4E-1	5.7E-1
Annotation Cluster 257		Enrichment Score: 0.57	<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:CXXCXGXG motif	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:CR-type	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Chaperone DnaJ</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.1E-1	5.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Chaperone DnaJ, C-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.7E-1	2.8E0	7.9E-1	7.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">HSP40/DnaJ peptide-binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.7E-1	2.8E0	7.9E-1	7.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Heat shock protein DnaJ, cysteine-rich domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.9E-1	3.7E0	8.6E-1	7.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">DnaJ domain, conserved site</a>	<a href="#">RT</a>	<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	<a href="#">RT</a>	<div><div></div><div></div></div>	8	6.6E-1	1.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">DnaJ domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	7.4E-1	9.7E-1	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	<a href="#">DnaJ</a>	<a href="#">RT</a>	<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	<a href="#">embryonic skeletal limb joint morphogenesis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.6E-2	5.9E0	5.7E-1	5.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">embryonic hindlimb morphogenesis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	3.3E-1	1.5E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">embryonic forelimb morphogenesis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	8.1E-1	9.3E-1	1.0E0	9.5E-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	<a href="#">R-SMAD binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.6E-2	2.6E0	1.1E-1	1.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.7E-2	5.9E0	2.2E-1	2.1E-1

Annotation Cluster 1		Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">SMAD protein complex assembly</a>	<a href="#">RT</a>	<div><div></div></div>	5	3.2E-2	3.7E0	3.5E-1	3.3E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">TGF beta signaling pathway</a>	<a href="#">RT</a>	<div><div></div></div>	11	5.3E-2	1.8E0	1.5E-1	9.8E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">SMAD protein complex</a>	<a href="#">RT</a>	<div><div></div></div>	4	1.2E-1	3.2E0	5.0E-1	4.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">endoderm development</a>	<a href="#">RT</a>	<div><div></div></div>	6	2.7E-1	1.7E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of epithelial to mesenchymal transition</a>	<a href="#">RT</a>	<div><div></div></div>	8	3.2E-1	1.4E0	1.0E0	9.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MH1	<a href="#">RT</a>	<div><div></div></div>	3	3.3E-1	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MH2	<a href="#">RT</a>	<div><div></div></div>	3	3.3E-1	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">SMAD domain, Dwarfin-type</a>	<a href="#">RT</a>	<div><div></div></div>	3	3.8E-1	2.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Dwarfin</a>	<a href="#">RT</a>	<div><div></div></div>	3	3.8E-1	2.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">MAD homology,, MH1</a>	<a href="#">RT</a>	<div><div></div></div>	3	3.8E-1	2.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of transforming growth factor beta receptor signaling pathway</a>	<a href="#">RT</a>	<div><div></div></div>	5	4.4E-1	1.5E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">type I transforming growth factor beta receptor binding</a>	<a href="#">RT</a>	<div><div></div></div>	3	4.6E-1	2.0E0	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">SMAD domain-like</a>	<a href="#">RT</a>	<div><div></div></div>	4	4.9E-1	1.5E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">MAD homology 1, Dwarfin-type</a>	<a href="#">RT</a>	<div><div></div></div>	3	6.0E-1	1.5E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	<a href="#">DWB</a>	<a href="#">RT</a>	<div><div></div></div>	3	6.2E-1	1.5E0	1.0E0	9.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">transforming growth factor beta receptor binding</a>	<a href="#">RT</a>	<div><div></div></div>	7	7.3E-1	9.9E-1	1.0E0	8.9E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Role of Tob in T-cell activation</a>	<a href="#">RT</a>	<div><div></div></div>	6	7.9E-1	9.7E-1	1.0E0	7.9E-1
<input type="checkbox"/>	SMART	<a href="#">DWA</a>	<a href="#">RT</a>	<div><div></div></div>	3	8.3E-1	1.0E0	1.0E0	9.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">SMAD protein signal transduction</a>	<a href="#">RT</a>	<div><div></div></div>	8	9.2E-1	7.7E-1	1.0E0	9.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">SMAD/FHA domain</a>	<a href="#">RT</a>	<div><div></div></div>	6	9.4E-1	7.0E-1	1.0E0	9.4E-1
Annotation Cluster 260		Enrichment Score: 0.56			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">I-kappaB/NF-kappaB complex</a>	<a href="#">RT</a>	<div><div></div></div>	4	3.0E-2	5.1E0	1.9E-1	1.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">NF-kappa-B/Rel/Dorsal</a>	<a href="#">RT</a>	<div><div></div></div>	4	3.2E-2	5.0E0	2.4E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Rel homology domain</a>	<a href="#">RT</a>	<div><div></div></div>	4	2.1E-1	2.5E0	9.5E-1	8.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">p53-like transcription factor, DNA-binding</a>	<a href="#">RT</a>	<div><div></div></div>	10	2.7E-1	1.4E0	9.6E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:RHD	<a href="#">RT</a>	<div><div></div></div>	3	3.9E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Cell surface receptor IPT/TIG</a>	<a href="#">RT</a>	<div><div></div></div>	6	5.8E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">transcriptional activator activity, RNA polymerase II distal enhancer sequence-specific binding</a>	<a href="#">RT</a>	<div><div></div></div>	4	8.1E-1	9.5E-1	1.0E0	8.9E-1
<input type="checkbox"/>	SMART	<a href="#">IPT</a>	<a href="#">RT</a>	<div><div></div></div>	5	9.3E-1	7.6E-1	1.0E0	9.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Immunoglobulin E-set</a>	<a href="#">RT</a>	<div><div></div></div>	10	9.9E-1	5.8E-1	1.0E0	9.9E-1
Annotation Cluster 261		Enrichment Score: 0.56			Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">BRCT domain</a>	<a href="#">RT</a>	<div><div></div></div>	8	1.5E-1	1.8E0	7.4E-1	6.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BRCT 1	<a href="#">RT</a>	<div><div></div></div>	4	2.5E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BRCT 2	<a href="#">RT</a>	<div><div></div></div>	4	2.5E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">BRCT</a>	<a href="#">RT</a>	<div><div></div></div>	7	2.7E-1	1.6E0	9.7E-1	8.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BRCT	<a href="#">RT</a>	<div><div></div></div>	3	6.3E-1	1.5E0	1.0E0	9.7E-1
Annotation Cluster 262		Enrichment Score: 0.55			Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">3'-5' exonuclease activity</a>	<a href="#">RT</a>	<div><div></div></div>	7	8.4E-2	2.2E0	4.3E-1	3.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">DNA-directed DNA polymerase, family B, exonuclease domain</a>	<a href="#">RT</a>	<div><div></div></div>	3	1.2E-1	4.6E0	6.1E-1	5.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">DNA-directed DNA polymerase, family B, multifunctional domain</a>	<a href="#">RT</a>	<div><div></div></div>	3	1.2E-1	4.6E0	6.1E-1	5.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">DNA-directed DNA polymerase, family B</a>	<a href="#">RT</a>	<div><div></div></div>	3	1.2E-1	4.6E0	6.1E-1	5.6E-1
<input type="checkbox"/>	SMART	<a href="#">POLBc</a>	<a href="#">RT</a>	<div><div></div></div>	3	2.5E-1	3.1E0	9.4E-1	8.4E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">4Fe-4S</a>	<a href="#">RT</a>	<div><div></div></div>	7	4.6E-1	1.3E0	1.0E0	7.8E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">DNA-directed DNA polymerase</a>	<a href="#">RT</a>	<div><div></div></div>	5	4.7E-1	1.4E0	1.0E0	7.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">DNA-directed DNA polymerase activity</a>	<a href="#">RT</a>	<div><div></div></div>	6	5.5E-1	1.2E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">4 iron, 4 sulfur cluster binding</a>	<a href="#">RT</a>	<div><div></div></div>	7	7.3E-1	9.9E-1	1.0E0	8.9E-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	<a href="#">Iron-sulfur</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	8.9E-1	8.0E-1	1.0E0	8.9E-1
Annotation Cluster 263		Enrichment Score: 0.55	<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	repeat:1-2	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.0E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1-1	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.1E-1	1.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:2 X 19 AA perfect repeats	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:2 X 16 AA Gly-rich approximate repeats	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:2-1	<a href="#">RT</a>	<div><div></div><div></div></div>	7	3.3E-1	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:2-2	<a href="#">RT</a>	<div><div></div><div></div></div>	7	3.8E-1	1.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1-4	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.9E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1-3	<a href="#">RT</a>	<div><div></div><div></div></div>	3	8.1E-1	1.0E0	1.0E0	9.7E-1
Annotation Cluster 264		Enrichment Score: 0.55	<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	<a href="#">response to reactive oxygen species</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.1E-1	1.7E0	7.4E-1	7.0E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Alkyl hydroperoxide reductase subunit C/Thiol specific antioxidant</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.9E-1	3.7E0	8.6E-1	7.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Peroxiredoxin, C-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.9E-1	3.7E0	8.6E-1	7.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">thioredoxin peroxidase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	7.6E-1	6.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Cysteine sulfenic acid (-SOH) intermediate	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Antioxidant</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.3E-1	2.0E0	9.3E-1	7.2E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Peroxidase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	5.0E-1	1.4E0	1.0E0	7.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">antioxidant activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	6.8E-1	1.2E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">hydrogen peroxide catabolic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	6.8E-1	1.2E0	1.0E0	9.5E-1
Annotation Cluster 265		Enrichment Score: 0.54	<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:MADS-box	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Transcription factor, MADS-box</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	9.6E-1	8.8E-1
<input type="checkbox"/>	SMART	<a href="#">MADS</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.5E-1	2.0E0	1.0E0	9.0E-1
Annotation Cluster 266		Enrichment Score: 0.53	<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:MBD	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.1E-1	2.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Methyl-CpG DNA binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.6E-1	2.3E0	9.6E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">DNA-binding, integrase-type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.6E-1	2.3E0	9.6E-1	8.8E-1
<input type="checkbox"/>	SMART	<a href="#">MBD</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.3E-1	1.5E0	1.0E0	9.0E-1
Annotation Cluster 267		Enrichment Score: 0.53	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">RNA polymerase II transcription factor activity, TBP-class protein binding, involved in preinitiation complex assembly</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">transcription factor activity, RNA polymerase II core promoter sequence-specific binding, involved in preinitiation complex assembly</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.6E-1	2.0E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">RNA polymerase II transcriptional preinitiation complex assembly</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.5E-1	1.2E0	1.0E0	9.5E-1
Annotation Cluster 268		Enrichment Score: 0.52	<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	<a href="#">mitochondrial translational elongation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	19	1.8E-1	1.3E0	9.9E-1	9.4E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">mitochondrial large ribosomal subunit</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	2.1E-1	1.5E0	7.8E-1	6.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitochondrial translational termination</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	3.8E-1	1.2E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitochondrial translation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	5.8E-1	1.2E0	1.0E0	9.5E-1
Annotation Cluster 269		Enrichment Score: 0.52	<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	<a href="#">activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	9.4E-3	4.0E0	1.4E-1	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">glial cell apoptotic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.7E-2	4.7E0	3.8E-1	3.6E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">D4-GDI Signaling Pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	8.9E-2	1.9E0	2.2E-1	1.5E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Role of Mitochondria in Apoptotic Signaling</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.4E-1	1.5E0	3.1E-1	2.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Peptidase C14, ICE, catalytic subunit p20, active site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	2.1E-1	2.5E0	9.5E-1	8.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to cobalt ion</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.7E-1	3.0E0	1.0E0	9.5E-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	<a href="#">Peptidase C14, caspase non-catalytic subunit p10</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.0E-1	2.1E0	9.8E-1	8.9E-1
<input type="checkbox"/>	BBID	<a href="#">127.Mito-stress</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.4E-1	1.9E0	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	<a href="#">Induction of apoptosis through DR3 and DR4/5 Death Receptors</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	13	3.7E-1	1.2E0	6.4E-1	4.3E-1
<input type="checkbox"/>	BBID	<a href="#">86.Apoptosis Nematode&amp; Vert</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	3.7E-1	1.6E0	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">cysteine-type endopeptidase activity involved in apoptotic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Peptidase C14, caspase precursor p45, core</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	4.0E-1	1.8E0	1.0E0	9.1E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Stress Induction of HSP Regulation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	4.2E-1	1.3E0	6.6E-1	4.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Peptidase C14, ICE, catalytic subunit p20</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	4.4E-1	1.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Caspase Cascade in Apoptosis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	5.4E-1	1.2E0	8.3E-1	5.6E-1
<input type="checkbox"/>	BBID	<a href="#">72.IAP interaction with cell death pathways</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	6.3E-1	1.2E0	1.0E0	1.0E0
<input type="checkbox"/>	SMART	<a href="#">CASC</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	6.5E-1	1.3E0	1.0E0	9.0E-1
<input type="checkbox"/>	BBID	<a href="#">150.caspase and NFKB activation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	7.5E-1	1.0E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	<a href="#">46.P13K PTEN</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	8.4E-1	9.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">cysteine-type endopeptidase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	9.0E-1	7.8E-1	1.0E0	9.0E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Thiol protease</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.0E0	3.6E-1	1.0E0	1.0E0
Annotation Cluster 270		Enrichment Score: 0.5	<div><div>G</div><div><div></div><div></div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, TFIIS-type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	9.6E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:TFIIS-type	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.7E-1	2.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">ZnF_C2C2</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.5E-1	2.0E0	1.0E0	9.0E-1
Annotation Cluster 271		Enrichment Score: 0.46	<div><div>G</div><div><div></div><div></div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	BBID	<a href="#">68.Mitogen signaling in growth control</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.4E-1	1.9E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	<a href="#">2.Cytokine Receptors</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.4E-1	1.9E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	<a href="#">54.T-cell anergy</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	3.5E-1	1.4E0	1.0E0	1.0E0
Annotation Cluster 272		Enrichment Score: 0.46	<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:KH	<a href="#">RT</a>	<div><div></div><div></div></div>	6	7.3E-2	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">K Homology domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	1.5E-1	1.6E0	7.1E-1	6.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">K Homology domain, type 1</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	2.7E-1	1.4E0	9.6E-1	8.8E-1
<input type="checkbox"/>	SMART	<a href="#">KH</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	6.1E-1	1.1E0	1.0E0	9.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KH 3	<a href="#">RT</a>	<div><div></div><div></div></div>	3	6.7E-1	1.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KH 2	<a href="#">RT</a>	<div><div></div><div></div></div>	4	7.1E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KH 1	<a href="#">RT</a>	<div><div></div><div></div></div>	4	7.1E-1	1.1E0	1.0E0	9.7E-1
Annotation Cluster 273		Enrichment Score: 0.45	<div><div>G</div><div><div></div><div></div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of guanylate cyclase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	4.9E-3	3.8E0	8.4E-2	8.0E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Nitric oxide synthase, oxygenase domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">nitric-oxide synthase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nitric oxide mediated signal transduction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	8.6E-2	2.2E0	6.3E-1	6.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Flavodoxin-like	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Flavodoxin/nitric oxide synthase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.2E-1	3.1E0	6.1E-1	5.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Flavodoxin</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.2E-1	3.1E0	6.1E-1	5.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">tetrahydrobiopterin binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.3E-1	4.5E0	5.8E-1	5.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of vasodilation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	2.1E-1	1.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">NADP binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	2.2E-1	1.5E0	8.4E-1	7.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">NADPH-cytochrome p450 reductase, FAD-binding, alpha-helical domain-3</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	9.6E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">FAD-binding, type 1</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	9.6E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:FMN	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.0E-1	2.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Oxidoreductase FAD/NAD(P)-binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.0E-1	2.1E0	9.8E-1	8.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">arginine binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	3.3E-1	2.6E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nitric oxide biosynthetic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">arginine catabolic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	9.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Flavoprotein pyridine nucleotide cytochrome reductase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.4E-1	2.1E0	1.0E0	9.1E-1




















































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">FMN binding</a>	RT		4	4.7E-1	1.6E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FAD-binding FR-type	RT		4	5.4E-1	1.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Arginine biosynthesis</a>	RT		5	5.5E-1	1.3E0	8.1E-1	5.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">FMN</a>	RT		4	6.1E-1	1.3E0	1.0E0	7.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ferredoxin reductase-type FAD-binding domain</a>	RT		4	6.1E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Riboflavin synthase-like beta-barrel</a>	RT		4	6.1E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of blood pressure</a>	RT		4	9.0E-1	7.9E-1	1.0E0	9.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:FAD	RT		7	9.1E-1	7.7E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:NADP	RT		8	9.3E-1	7.4E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	RT		8	9.9E-1	5.5E-1	1.0E0	9.9E-1
<input type="checkbox"/>	COG_ONTOLOGY	<a href="#">Inorganic ion transport and metabolism</a>	RT		6	1.0E0	5.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">flavin adenine dinucleotide binding</a>	RT		5	1.0E0	4.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">heme binding</a>	RT		13	1.0E0	5.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Arginine and proline metabolism</a>	RT		4	1.0E0	4.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Heme</a>	RT		9	1.0E0	4.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">FAD</a>	RT		6	1.0E0	3.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Flavoprotein</a>	RT		6	1.0E0	3.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">NADP</a>	RT		10	1.0E0	3.7E-1	1.0E0	1.0E0
Annotation Cluster 274		Enrichment Score: 0.45	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">RISC complex</a>	RT		5	8.0E-2	2.9E0	4.0E-1	3.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">RISC-loading complex</a>	RT		3	3.0E-1	2.7E0	8.7E-1	7.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">miRNA loading onto RISC involved in gene silencing by miRNA</a>	RT		3	3.4E-1	2.5E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">pre-miRNA processing</a>	RT		4	3.8E-1	1.8E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">production of miRNAs involved in gene silencing by miRNA</a>	RT		3	4.0E-1	2.2E0	1.0E0	9.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PAZ	RT		3	4.4E-1	2.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Argonaute/Dicer protein, PAZ</a>	RT		3	5.0E-1	1.9E0	1.0E0	9.1E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Dicer Pathway</a>	RT		3	5.2E-1	1.9E0	8.1E-1	5.5E-1
<input type="checkbox"/>	SMART	<a href="#">SM00949</a>	RT		3	6.9E-1	1.4E0	1.0E0	9.0E-1
Annotation Cluster 275		Enrichment Score: 0.43	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">social behavior</a>	RT		12	1.7E-1	1.5E0	9.7E-1	9.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of excitatory postsynaptic potential</a>	RT		5	4.4E-1	1.5E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">adult behavior</a>	RT		5	6.6E-1	1.1E0	1.0E0	9.5E-1
Annotation Cluster 276		Enrichment Score: 0.43	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">MIF4G-like, type 3</a>	RT		4	2.1E-1	2.5E0	9.5E-1	8.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MIF4G	RT		3	4.4E-1	2.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">MIF4-like, type 1/2/3</a>	RT		4	4.4E-1	1.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	<a href="#">MIF4G</a>	RT		4	4.6E-1	1.6E0	1.0E0	9.0E-1
Annotation Cluster 277		Enrichment Score: 0.43	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">cysteine-type endopeptidase inhibitor activity involved in apoptotic process</a>	RT		7	1.8E-1	1.8E0	7.2E-1	6.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Baculoviral inhibition of apoptosis protein repeat</a>	RT		3	3.8E-1	2.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">inhibition of cysteine-type endopeptidase activity involved in apoptotic process</a>	RT		3	4.6E-1	2.0E0	1.0E0	9.5E-1
<input type="checkbox"/>	SMART	<a href="#">BIR</a>	RT		3	6.2E-1	1.5E0	1.0E0	9.0E-1
Annotation Cluster 278		Enrichment Score: 0.43	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 5	RT		3	2.7E-1	2.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 1	RT		5	3.7E-1	1.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 2	RT		5	3.7E-1	1.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 4	RT		3	3.9E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 3	RT		3	5.0E-1	1.9E0	1.0E0	9.7E-1
Annotation Cluster 279		Enrichment Score: 0.42	G		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"/>	GOTERM_MF_DIRECT	<a href="#">calcium-transporting ATPase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	4.9E-2	3.3E0	2.9E-1	2.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Calcium-transporting P-type ATPase, subfamily IIA, SERCA-type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 2; via carbonyl oxygen	<a href="#">RT</a>	<div><div></div><div></div></div>	9	2.0E-1	1.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">sarcoplasmic reticulum</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	2.8E-1	1.5E0	8.4E-1	7.4E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">sarcoplasmic reticulum membrane</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	2.8E-1	1.5E0	8.4E-1	7.4E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">platelet dense tubular network membrane</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.3E-1	2.1E0	1.0E0	8.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 2	<a href="#">RT</a>	<div><div></div><div></div></div>	10	4.6E-1	1.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Sarcoplasmic reticulum</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	5.4E-1	1.2E0	1.0E0	7.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 1	<a href="#">RT</a>	<div><div></div><div></div></div>	8	5.5E-1	1.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular calcium ion homeostasis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	9.6E-1	7.0E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">calcium ion transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	9.9E-1	5.5E-1	1.0E0	9.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">calcium ion transmembrane transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	1.0E0	5.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Calcium transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.0E0	3.5E-1	1.0E0	1.0E0
Annotation Cluster 280		Enrichment Score: 0.39	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Postsynaptic cell membrane</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	34	8.8E-2	1.3E0	3.0E-1	2.3E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">postsynaptic membrane</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	39	2.0E-1	1.2E0	7.6E-1	6.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">postsynaptic density</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	33	3.0E-1	1.1E0	8.6E-1	7.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Synapse</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	47	8.4E-1	9.0E-1	1.0E0	8.4E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">cell junction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	58	9.8E-1	8.0E-1	1.0E0	9.8E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Cell junction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	81	9.8E-1	8.2E-1	1.0E0	9.8E-1
Annotation Cluster 281		Enrichment Score: 0.39	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Sirtuin family, catalytic core small domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	9.6E-1	8.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Deacetylase sirtuin-type	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.7E-1	2.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Sirtuin family</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	3.2E-1	2.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Sirtuin family, catalytic core domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	3.2E-1	2.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">NAD+ binding</a>	<a href="#">RT</a>	<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	<a href="#">RT</a>	<div><div></div><div></div></div>	7	9.8E-1	6.0E-1	1.0E0	9.8E-1
Annotation Cluster 282		Enrichment Score: 0.39	<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	<a href="#">protein ADP-ribosylation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.3E-1	2.0E0	8.1E-1	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of telomere maintenance via telomere lengthening</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">NAD+ ADP-ribosyltransferase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	3.2E-1	1.5E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PARP catalytic	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.4E-1	1.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Poly(ADP-ribose) polymerase, catalytic domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.9E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Glycosyltransferase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.0E0	1.5E-1	1.0E0	1.0E0
Annotation Cluster 283		Enrichment Score: 0.37	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Bernard Soulier syndrome</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.7E-2	6.9E0	2.1E-1	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">blood coagulation, intrinsic pathway</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	3.6E-1	1.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Blood coagulation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	8.5E-1	8.6E-1	1.0E0	8.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Hemostasis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	8.5E-1	8.6E-1	1.0E0	8.5E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">ECM-receptor interaction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.0E0	3.6E-1	1.0E0	1.0E0
Annotation Cluster 284		Enrichment Score: 0.36	<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:HEAT 9	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.7E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 10	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.7E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 7	<a href="#">RT</a>	<div><div></div><div></div></div>	6	2.7E-1	1.7E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 8	<a href="#">RT</a>	<div><div></div><div></div></div>	5	3.0E-1	1.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">HEAT, type 2</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	3.7E-1	1.6E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 6	<a href="#">RT</a>	<div><div></div><div></div></div>	6	4.6E-1	1.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 11	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.0E-1	1.9E0	1.0E0	9.7E-1

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:HEAT 5	<a href="#">RT</a>	<div><div></div><div></div></div>	6	6.0E-1	1.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 1	<a href="#">RT</a>	<div><div></div><div></div></div>	8	7.7E-1	9.4E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 2	<a href="#">RT</a>	<div><div></div><div></div></div>	8	7.7E-1	9.4E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 4	<a href="#">RT</a>	<div><div></div><div></div></div>	6	7.8E-1	9.5E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 3	<a href="#">RT</a>	<div><div></div><div></div></div>	6	8.8E-1	8.2E-1	1.0E0	9.7E-1
Annotation Cluster 285		Enrichment Score: 0.36	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Interaction with KCND2	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 1; degenerate	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of potassium ion transmembrane transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	4.8E-1	1.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cardiac conduction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	9.6E-1	6.6E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">voltage-gated ion channel activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	9.8E-1	5.6E-1	1.0E0	9.8E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Potassium</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	9.9E-1	6.4E-1	1.0E0	9.9E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">voltage-gated potassium channel complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	9.9E-1	5.8E-1	1.0E0	9.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">potassium channel activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	9.9E-1	4.8E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Potassium transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	9.9E-1	5.9E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Potassium channel</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	3.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">potassium ion transmembrane transport</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.0E0	2.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Voltage-gated channel</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	1.8E-1	1.0E0	1.0E0
Annotation Cluster 286		Enrichment Score: 0.32	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">RWD domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.0E-1	2.1E0	9.8E-1	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:RWD	<a href="#">RT</a>	<div><div></div><div></div></div>	3	5.0E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">RWD</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.4E-1	1.2E0	1.0E0	9.0E-1
Annotation Cluster 287		Enrichment Score: 0.28	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Exportin-1/Importin-beta-like</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	9.6E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Importin-beta, N-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	5.3E-1	1.5E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">Ran GTPase binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	5.8E-1	1.2E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Importin N-terminal	<a href="#">RT</a>	<div><div></div><div></div></div>	3	6.3E-1	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">SM00913</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	7.9E-1	1.0E0	1.0E0	9.0E-1
Annotation Cluster 288		Enrichment Score: 0.27	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:"KMSKS" region	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.0E-1	2.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:"HIGH" region	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.7E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">aminoacyl-tRNA ligase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	3.2E-1	1.8E0	9.8E-1	8.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Aminoacyl-tRNA synthetase, class I, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	4.4E-1	1.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Glutathione S-transferase, C-terminal</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	5.2E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Rossmann-like alpha/beta/alpha sandwich fold</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	5.3E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Aminoacyl-tRNA synthetase, class 1a, anticodon-binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	6.4E-1	1.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Aminoacyl-tRNA synthetase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	6.7E-1	1.1E0	1.0E0	7.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">tRNA aminoacylation for protein translation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	6.9E-1	1.0E0	1.0E0	9.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Glutathione S-transferase, C-terminal-like</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	9.2E-1	7.6E-1	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:GST C-terminal	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.2E-1	7.4E-1	1.0E0	9.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Aminoacyl-tRNA biosynthesis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.0E0	4.8E-1	1.0E0	1.0E0
Annotation Cluster 289		Enrichment Score: 0.25	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CARD	<a href="#">RT</a>	<div><div></div><div></div></div>	6	4.2E-1	1.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Caspase Recruitment</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	5.1E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Caspase Cascade in Apoptosis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	5.4E-1	1.2E0	8.3E-1	5.6E-1
<input type="checkbox"/>	SMART	<a href="#">CARD</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	8.3E-1	1.0E0	1.0E0	9.0E-1
Annotation Cluster 290		Enrichment Score: 0.25	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Immunoglobulin I-set</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	36	5.0E-3	1.6E0	5.3E-2	4.8E-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	<a href="#">Immunoglobulin subtype 2</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	41	5.5E-1	1.0E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 3	<a href="#">RT</a>	<div><div></div><div></div></div>	17	7.9E-1	9.0E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 1	<a href="#">RT</a>	<div><div></div><div></div></div>	23	9.5E-1	7.8E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 2	<a href="#">RT</a>	<div><div></div><div></div></div>	23	9.6E-1	7.7E-1	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">IGc2</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	41	1.0E0	6.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Immunoglobulin domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	47	1.0E0	5.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Immunoglobulin subtype</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	45	1.0E0	5.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Immunoglobulin-like fold</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	82	1.0E0	5.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	<a href="#">IG</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	45	1.0E0	3.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Immunoglobulin-like domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	49	1.0E0	3.9E-1	1.0E0	1.0E0
Annotation Cluster 291		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"/>	UP_KEYWORDS	<a href="#">Vision</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	21	2.3E-1	1.3E0	6.8E-1	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">visual perception</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	29	8.9E-1	8.6E-1	1.0E0	9.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Sensory transduction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	23	1.0E0	2.6E-1	1.0E0	1.0E0
Annotation Cluster 292		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"/>	UP_SEQ_FEATURE	region of interest:Heparin-binding	<a href="#">RT</a>	<div><div></div><div></div></div>	5	3.4E-1	1.7E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">organ induction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	6.3E-1	1.5E0	1.0E0	9.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Heparin-binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	9.8E-1	6.2E-1	1.0E0	9.8E-1
Annotation Cluster 293		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	<a href="#">protein-hormone receptor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">GPCR, rhodopsin-like, 7TM</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.0E0	5.9E-2	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">G-protein coupled receptor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	1.0E0	8.4E-2	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">G protein-coupled receptor, rhodopsin-like</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.0E0	6.0E-2	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">G-protein coupled receptor</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.0E0	9.0E-2	1.0E0	1.0E0
Annotation Cluster 294		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	<a href="#">Cyclic nucleotide-binding, conserved site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	2.5E-1	1.9E0	9.6E-1	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Cyclic nucleotide-binding domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	5.1E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Cyclic nucleotide-binding-like</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	5.9E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">cAMP-binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.3E-1	1.2E0	1.0E0	7.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">RmlC-like jelly roll fold</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	7.9E-1	9.2E-1	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">cAMP binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	7.9E-1	9.9E-1	1.0E0	8.9E-1
<input type="checkbox"/>	SMART	<a href="#">cNMP</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	8.1E-1	9.2E-1	1.0E0	9.0E-1
Annotation Cluster 295		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"/>	UP_SEQ_FEATURE	domain:SAP	<a href="#">RT</a>	<div><div></div><div></div></div>	5	4.8E-1	1.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">SAP domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	5.6E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	<a href="#">SAP</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	8.5E-1	8.9E-1	1.0E0	9.0E-1
Annotation Cluster 296		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_BP_DIRECT	<a href="#">positive regulation of chemokine biosynthetic process</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.6E-2	3.6E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of calcidiol 1-monooxygenase activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.6E-2	5.9E0	5.7E-1	5.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">defense response to protozoan</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	2.1E-1	1.9E0	1.0E0	9.5E-1
<input type="checkbox"/>	BBID	<a href="#">111.Stress influences immunity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.4E-1	1.9E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	<a href="#">112.StressandCRHinfluence</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.4E-1	1.9E0	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of isotype switching to IgG isotypes</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	9.5E-1
<input type="checkbox"/>	BBID	<a href="#">20.Cytokine oligodendrocytes</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.2E-1	2.2E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	<a href="#">21.Cytokine neurons</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	4.2E-1	2.2E0	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Malaria</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	4.7E-1	1.2E0	7.0E-1	4.7E-1
<input type="checkbox"/>	BBID	<a href="#">56.Macrophage regulation of CD4+T cells</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	4.7E-1	1.4E0	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of membrane protein ectodomain proteolysis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	4.8E-1	1.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	BBID	<a href="#">18.Cytokine astocytes</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	7	4.9E-1	1.3E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	<a href="#">19.Cytokine microglia</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	5.6E-1	1.3E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	<a href="#">22.Cytokine-chemokine CNS</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	6.4E-1	1.2E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	<a href="#">80.T cell Activation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	6.7E-1	1.0E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	<a href="#">58.(CD40L) immnosurveillance</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	6.9E-1	1.1E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	<a href="#">113.Th1andTh2cells</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.6E-1	1.2E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	<a href="#">76.Sig_trans Ca2 Calcineurin NF-AT</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.6E-1	1.2E0	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	<a href="#">Regulation of hematopoiesis by cytokines</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	7.7E-1	1.0E0	1.0E0	7.7E-1

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	<a href="#">Role of Tob in T-cell activation</a>	<a href="#">RT</a>		6	7.9E-1	9.7E-1	1.0E0	7.9E-1
<input type="checkbox"/>	BBID	<a href="#">88.Alternatively Activated APC</a>	<a href="#">RT</a>		4	7.9E-1	1.1E0	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Rheumatoid arthritis</a>	<a href="#">RT</a>		15	8.2E-1	8.9E-1	1.0E0	8.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Intestinal immune network for IgA production</a>	<a href="#">RT</a>		8	8.2E-1	8.9E-1	1.0E0	8.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Four-helical cytokine, core</a>	<a href="#">RT</a>		7	8.5E-1	8.5E-1	1.0E0	9.1E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Cytokines and Inflammatory Response</a>	<a href="#">RT</a>		8	8.8E-1	8.5E-1	1.0E0	8.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Four-helical cytokine-like, core</a>	<a href="#">RT</a>		7	8.9E-1	8.0E-1	1.0E0	9.1E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Cytokine Network</a>	<a href="#">RT</a>		6	8.9E-1	8.4E-1	1.0E0	8.9E-1
<input type="checkbox"/>	BBID	<a href="#">15.T-cell polarization-chemokine receptors</a>	<a href="#">RT</a>		5	8.9E-1	8.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Graft-versus-host disease</a>	<a href="#">RT</a>		5	9.0E-1	7.9E-1	1.0E0	9.0E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Type I diabetes mellitus</a>	<a href="#">RT</a>		6	9.3E-1	7.5E-1	1.0E0	9.3E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Selective expression of chemokine receptors during T-cell polarization</a>	<a href="#">RT</a>		7	9.3E-1	7.7E-1	1.0E0	9.3E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Allograft rejection</a>	<a href="#">RT</a>		5	9.4E-1	7.1E-1	1.0E0	9.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of insulin secretion</a>	<a href="#">RT</a>		8	9.5E-1	7.1E-1	1.0E0	9.5E-1
<input type="checkbox"/>	BBID	<a href="#">97.Immune injury MS-lesions MS antigen</a>	<a href="#">RT</a>		4	9.5E-1	7.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	BBID	<a href="#">5.B7 CD40 B-cell activa</a>	<a href="#">RT</a>		3	9.6E-1	7.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	<a href="#">Antigen Dependent B Cell Activation</a>	<a href="#">RT</a>		3	9.6E-1	7.1E-1	1.0E0	9.6E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Adhesion and Diapedesis of Granulocytes</a>	<a href="#">RT</a>		3	9.8E-1	6.2E-1	1.0E0	9.8E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Th1/Th2 Differentiation</a>	<a href="#">RT</a>		4	9.8E-1	6.2E-1	1.0E0	9.8E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Cells and Molecules involved in local acute inflammatory response</a>	<a href="#">RT</a>		3	9.9E-1	5.4E-1	1.0E0	9.9E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Autoimmune thyroid disease</a>	<a href="#">RT</a>		3	1.0E0	3.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">cytokine activity</a>	<a href="#">RT</a>		13	1.0E0	4.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Cytokine</a>	<a href="#">RT</a>		11	1.0E0	4.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Cytokine-cytokine receptor interaction</a>	<a href="#">RT</a>		15	1.0E0	3.2E-1	1.0E0	1.0E0
Annotation Cluster 297		Enrichment Score: 0.2	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Histone H2A type 1-D	<a href="#">RT</a>		3	6.3E-1	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Histone H3.1	<a href="#">RT</a>		3	6.3E-1	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Histone H3.2	<a href="#">RT</a>		3	6.3E-1	1.5E0	1.0E0	9.7E-1
Annotation Cluster 298		Enrichment Score: 0.19	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:RanBP2-type	<a href="#">RT</a>		4	5.0E-1	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, RanBP2-type</a>	<a href="#">RT</a>		5	5.9E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	<a href="#">ZnF_RBZ</a>	<a href="#">RT</a>		4	9.0E-1	8.2E-1	1.0E0	9.0E-1
Annotation Cluster 299		Enrichment Score: 0.19	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	<a href="#">Role of PI3K subunit p85 in regulation of Actin Organization and Cell Migration</a>	<a href="#">RT</a>		7	4.2E-1	1.3E0	6.6E-1	4.5E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">How does salmonella hijack a cell</a>	<a href="#">RT</a>		5	6.5E-1	1.2E0	9.7E-1	6.6E-1
<input type="checkbox"/>	BIOCARTA	<a href="#">Y branching of actin filaments</a>	<a href="#">RT</a>		4	9.8E-1	5.9E-1	1.0E0	9.8E-1
Annotation Cluster 300		Enrichment Score: 0.18	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:NAD; via carbonyl oxygen	<a href="#">RT</a>		3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">NAD binding</a>	<a href="#">RT</a>		5	9.0E-1	7.8E-1	1.0E0	9.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:NAD	<a href="#">RT</a>		5	9.7E-1	6.3E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:NAD	<a href="#">RT</a>		7	9.8E-1	6.0E-1	1.0E0	9.8E-1
Annotation Cluster 301		Enrichment Score: 0.18	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ATP hydrolysis coupled proton transport</a>	<a href="#">RT</a>		8	2.9E-1	1.5E0	1.0E0	9.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Hydrogen ion transport</a>	<a href="#">RT</a>		4	9.8E-1	5.6E-1	1.0E0	9.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Oxidative phosphorylation</a>	<a href="#">RT</a>		6	1.0E0	2.4E-1	1.0E0	1.0E0
Annotation Cluster 302		Enrichment Score: 0.18	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">PWWP</a>	<a href="#">RT</a>		5	4.8E-1	1.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	<a href="#">PWWP</a>	<a href="#">RT</a>		5	7.6E-1	1.0E0	1.0E0	9.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PWWP	<a href="#">RT</a>		3	7.9E-1	1.1E0	1.0E0	9.7E-1
Annotation Cluster 303		Enrichment Score: 0.17	G		Count	P_Value	Fold Change	Benjamini	FDR

Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Importin subunit alpha</a>	<a href="#">RT</a>	3	3.2E-1	2.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IBB	<a href="#">RT</a>	3	3.3E-1	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">importin subunit alpha</a>	<a href="#">RT</a>	3	3.9E-1	2.3E0	1.0E0	9.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Importin-alpha, importin-beta-binding domain</a>	<a href="#">RT</a>	3	4.4E-1	2.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 8	<a href="#">RT</a>	4	6.5E-1	1.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 7	<a href="#">RT</a>	4	7.1E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">nuclear localization sequence binding</a>	<a href="#">RT</a>	5	7.1E-1	1.1E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 6	<a href="#">RT</a>	4	7.6E-1	1.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 9	<a href="#">RT</a>	3	7.6E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">NLS-bearing protein import into nucleus</a>	<a href="#">RT</a>	4	7.7E-1	1.0E0	1.0E0	9.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 5	<a href="#">RT</a>	4	8.2E-1	9.4E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 4	<a href="#">RT</a>	4	8.5E-1	8.8E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 3	<a href="#">RT</a>	4	9.1E-1	7.6E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 2	<a href="#">RT</a>	4	9.2E-1	7.4E-1	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Armadillo</a>	<a href="#">RT</a>	4	9.8E-1	5.8E-1	1.0E0	9.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein transporter activity</a>	<a href="#">RT</a>	6	1.0E0	5.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	<a href="#">ARM</a>	<a href="#">RT</a>	4	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 304		Enrichment Score: 0.16	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:OPR	<a href="#">RT</a>	3	5.4E-1	1.7E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Phox/Bem1p</a>	<a href="#">RT</a>	3	6.9E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	<a href="#">PB1</a>	<a href="#">RT</a>	3	8.9E-1	8.7E-1	1.0E0	9.0E-1
Annotation Cluster 305		Enrichment Score: 0.15	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Patatin/Phospholipase A2-related</a>	<a href="#">RT</a>	3	4.4E-1	2.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Acyl transferase/acyl hydrolase/lysophospholipase</a>	<a href="#">RT</a>	3	8.1E-1	1.0E0	1.0E0	9.1E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Glycerophospholipid metabolism</a>	<a href="#">RT</a>	3	1.0E0	1.7E-1	1.0E0	1.0E0
Annotation Cluster 306		Enrichment Score: 0.12	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">3'5'-cyclic nucleotide phosphodiesterase</a>	<a href="#">RT</a>	4	6.1E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">3'5'-cyclic nucleotide phosphodiesterase, conserved site</a>	<a href="#">RT</a>	4	6.8E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">3'5'-cyclic nucleotide phosphodiesterase, catalytic domain</a>	<a href="#">RT</a>	4	7.1E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">HD/PDEase domain</a>	<a href="#">RT</a>	4	7.4E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">3',5'-cyclic-nucleotide phosphodiesterase activity</a>	<a href="#">RT</a>	4	7.7E-1	1.0E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 1	<a href="#">RT</a>	4	8.0E-1	9.7E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 2	<a href="#">RT</a>	4	8.0E-1	9.7E-1	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">HDc</a>	<a href="#">RT</a>	4	9.5E-1	7.1E-1	1.0E0	9.5E-1
Annotation Cluster 307		Enrichment Score: 0.12	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">One carbon pool by folate</a>	<a href="#">RT</a>	5	5.5E-1	1.3E0	8.1E-1	5.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">One-carbon metabolism</a>	<a href="#">RT</a>	3	7.3E-1	1.2E0	1.0E0	7.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">folic acid metabolic process</a>	<a href="#">RT</a>	3	8.3E-1	9.9E-1	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">one-carbon metabolic process</a>	<a href="#">RT</a>	3	9.7E-1	5.9E-1	1.0E0	9.7E-1
Annotation Cluster 308		Enrichment Score: 0.11	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Phospholipid-transporting P-type ATPase, subfamily IV</a>	<a href="#">RT</a>	3	6.9E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">phospholipid-translocating ATPase activity</a>	<a href="#">RT</a>	3	7.1E-1	1.3E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">phospholipid translocation</a>	<a href="#">RT</a>	4	7.4E-1	1.1E0	1.0E0	9.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Lipid transport</a>	<a href="#">RT</a>	4	1.0E0	2.9E-1	1.0E0	1.0E0
Annotation Cluster 309		Enrichment Score: 0.11	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Peptidase A1</a>	<a href="#">RT</a>	3	5.0E-1	1.9E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">aspartic-type endopeptidase activity</a>	<a href="#">RT</a>	5	8.3E-1	9.0E-1	1.0E0	8.9E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Aspartyl protease</a>	<a href="#">RT</a>	3	8.3E-1	9.8E-1	1.0E0	8.3E-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
<input type="checkbox"/>	INTERPRO	<a href="#">Peptidase aspartic, active site</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	8.7E-1	8.9E-1	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Aspartic peptidase</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	9.5E-1	6.9E-1	1.0E0	9.5E-1
Annotation Cluster 310		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	<a href="#">cAMP response element binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Basic-leucine zipper domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	9.8E-1	5.7E-1	1.0E0	9.8E-1
<input type="checkbox"/>	SMART	<a href="#">BRLZ</a>	<a href="#">RT</a>	<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	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.0E0	3.8E-1	1.0E0	1.0E0
Annotation Cluster 311		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"/>	UP_SEQ_FEATURE	domain:B30.2/SPRY	<a href="#">RT</a>	<div><div></div><div></div></div>	16	4.6E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, B-box</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	14	5.7E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">B30.2/SPRY domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	16	6.5E-1	1.0E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">SP1a/Ryanodine receptor SPRY</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	6.7E-1	9.9E-1	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:B box-type	<a href="#">RT</a>	<div><div></div><div></div></div>	10	6.8E-1	1.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">SPRY-associated</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	9.2E-1	7.4E-1	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Butyrophilin-like</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	9.6E-1	6.9E-1	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	<a href="#">BBOX</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	13	9.7E-1	7.2E-1	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">SPRY</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	9.9E-1	6.7E-1	1.0E0	9.9E-1
<input type="checkbox"/>	SMART	<a href="#">PRY</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.0E0	5.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Concanavalin A-like lectin/glucanase, subgroup</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	19	1.0E0	5.1E-1	1.0E0	1.0E0
Annotation Cluster 312		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"/>	GOTERM_CC_DIRECT	<a href="#">nuclear pore</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	12	5.9E-1	1.1E0	1.0E0	8.7E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Nuclear pore complex</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	8.7E-1	8.2E-1	1.0E0	8.7E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Translocation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	8	9.7E-1	6.5E-1	1.0E0	9.7E-1
Annotation Cluster 313		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"/>	INTERPRO	<a href="#">High mobility group (HMG) box domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	10	5.8E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:HMG box	<a href="#">RT</a>	<div><div></div><div></div></div>	5	9.0E-1	7.7E-1	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">HMG</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	9.7E-1	6.8E-1	1.0E0	9.7E-1
Annotation Cluster 314		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	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.0E-1	1.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">CS-like domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.9E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">HSP20-like chaperone</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	9.5E-1	6.6E-1	1.0E0	9.5E-1
Annotation Cluster 315		Enrichment Score: 0.08	<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:HMG box 1	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.6E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:HMG box 2	<a href="#">RT</a>	<div><div></div><div></div></div>	3	7.6E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">HMG</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	9.7E-1	6.8E-1	1.0E0	9.7E-1
Annotation Cluster 316		Enrichment Score: 0.07	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Steroid-binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	4.2E-1	1.7E0	1.0E0	7.8E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, NHR/GATA-type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	4.6E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Modulating	<a href="#">RT</a>	<div><div></div><div></div></div>	3	6.3E-1	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">steroid binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	8.5E-1	8.8E-1	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:NR C4-type	<a href="#">RT</a>	<div><div></div><div></div></div>	5	9.1E-1	7.6E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:Nuclear receptor	<a href="#">RT</a>	<div><div></div><div></div></div>	5	9.1E-1	7.6E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Hinge	<a href="#">RT</a>	<div><div></div><div></div></div>	3	9.3E-1	7.3E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Ligand-binding	<a href="#">RT</a>	<div><div></div><div></div></div>	3	9.5E-1	6.8E-1	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, nuclear hormone receptor-type</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	9.5E-1	6.7E-1	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.5E-1	6.6E-1	1.0E0	9.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Steroid hormone receptor</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	9.6E-1	6.6E-1	1.0E0	9.6E-1

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Nuclear hormone receptor, ligand-binding, core</a>	RT		5	9.6E-1	6.5E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">steroid hormone receptor activity</a>	RT		5	9.9E-1	5.3E-1	1.0E0	9.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">steroid hormone mediated signaling pathway</a>	RT		4	1.0E0	4.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	<a href="#">ZnF_C4</a>	RT		5	1.0E0	4.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	<a href="#">HOLI</a>	RT		5	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 317		Enrichment Score: 0.07	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">histone demethylase activity</a>	RT		5	5.5E-1	1.3E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:JmjC	RT		4	8.7E-1	8.5E-1	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">JmjC domain</a>	RT		4	9.2E-1	7.5E-1	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	<a href="#">JmjC</a>	RT		4	9.8E-1	5.6E-1	1.0E0	9.8E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Dioxygenase</a>	RT		6	1.0E0	5.0E-1	1.0E0	1.0E0
Annotation Cluster 318		Enrichment Score: 0.06	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">peptidase activity</a>	RT		15	6.6E-1	9.9E-1	1.0E0	8.9E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Zymogen</a>	RT		17	1.0E0	5.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Protease</a>	RT		39	1.0E0	4.9E-1	1.0E0	1.0E0
Annotation Cluster 319		Enrichment Score: 0.05	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:Fork-head	RT		7	7.6E-1	9.5E-1	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Transcription factor, fork head</a>	RT		7	8.2E-1	8.9E-1	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Transcription factor, fork head, conserved site</a>	RT		3	9.8E-1	5.5E-1	1.0E0	9.8E-1
<input type="checkbox"/>	SMART	<a href="#">FH</a>	RT		7	9.9E-1	5.8E-1	1.0E0	9.9E-1
Annotation Cluster 320		Enrichment Score: 0.04	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding	RT		3	7.9E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding 3	RT		3	9.0E-1	8.2E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">LIM domain</a>	RT		8	9.2E-1	7.6E-1	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding 1	RT		5	9.5E-1	6.8E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding 2	RT		5	9.5E-1	6.8E-1	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, LIM-type</a>	RT		8	9.6E-1	6.9E-1	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	<a href="#">LIM</a>	RT		8	1.0E0	4.5E-1	1.0E0	1.0E0
Annotation Cluster 321		Enrichment Score: 0.03	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Heparin-binding growth factor/Fibroblast growth factor</a>	RT		3	8.9E-1	8.5E-1	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Cytokine, IL-1-like</a>	RT		4	9.2E-1	7.5E-1	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	<a href="#">FGF</a>	RT		3	9.8E-1	5.6E-1	1.0E0	9.8E-1
Annotation Cluster 322		Enrichment Score: 0.02	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LisH	RT		3	9.3E-1	7.3E-1	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">LisH dimerisation motif</a>	RT		3	9.5E-1	6.6E-1	1.0E0	9.5E-1
<input type="checkbox"/>	SMART	<a href="#">LisH</a>	RT		3	9.9E-1	5.3E-1	1.0E0	9.9E-1
Annotation Cluster 323		Enrichment Score: 0.01	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Growth factor</a>	RT		15	9.2E-1	7.9E-1	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">growth factor activity</a>	RT		19	9.8E-1	7.0E-1	1.0E0	9.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">cytokine activity</a>	RT		13	1.0E0	4.4E-1	1.0E0	1.0E0
Annotation Cluster 324		Enrichment Score: 0.01	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:FYVE-type	RT		4	9.4E-1	7.0E-1	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, FYVE-type</a>	RT		3	9.6E-1	6.4E-1	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, FYVE-related</a>	RT		3	9.8E-1	5.5E-1	1.0E0	9.8E-1
<input type="checkbox"/>	SMART	<a href="#">FYVE</a>	RT		3	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 325		Enrichment Score: 0.01	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C3H1-type 1	RT		3	9.5E-1	6.6E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C3H1-type 2	RT		3	9.5E-1	6.6E-1	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, CCCH-type</a>	RT		5	9.9E-1	5.3E-1	1.0E0	9.9E-1
<input type="checkbox"/>	SMART	<a href="#">ZnF_C3H1</a>	RT		5	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 326		Enrichment Score: 0.01	G		Count	P_Value	Fold Change	Benjamini	FDR



Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Host cell receptor for virus entry</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	9.7E-1	6.4E-1	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">viral entry into host cell</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	9.7E-1	6.7E-1	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">virus receptor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	9.9E-1	5.1E-1	1.0E0	9.9E-1
Annotation Cluster 327		Enrichment Score: 0.01	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	<a href="#">Ras-association</a>	<a href="#">RT</a>	<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	<a href="#">RT</a>	<div><div></div><div></div></div>	3	9.7E-1	6.0E-1	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	<a href="#">RA</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	3	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 328		Enrichment Score: 0.01	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:22	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.5E-1	6.6E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:21	<a href="#">RT</a>	<div><div></div><div></div></div>	4	9.6E-1	6.3E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1	<a href="#">RT</a>	<div><div></div><div></div></div>	29	9.7E-1	7.7E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:24	<a href="#">RT</a>	<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	<a href="#">RT</a>	<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:2	<a href="#">RT</a>	<div><div></div><div></div></div>	29	9.7E-1	7.6E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:19	<a href="#">RT</a>	<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	<a href="#">RT</a>	<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:17	<a href="#">RT</a>	<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:11	<a href="#">RT</a>	<div><div></div><div></div></div>	7	9.9E-1	5.4E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:16	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	4.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:8	<a href="#">RT</a>	<div><div></div><div></div></div>	10	1.0E0	5.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:3	<a href="#">RT</a>	<div><div></div><div></div></div>	21	1.0E0	6.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:15	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.0E0	4.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:12	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.0E0	4.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:9	<a href="#">RT</a>	<div><div></div><div></div></div>	8	1.0E0	5.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:6	<a href="#">RT</a>	<div><div></div><div></div></div>	12	1.0E0	5.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:10	<a href="#">RT</a>	<div><div></div><div></div></div>	7	1.0E0	4.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:14	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.0E0	4.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:7	<a href="#">RT</a>	<div><div></div><div></div></div>	10	1.0E0	5.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:4	<a href="#">RT</a>	<div><div></div><div></div></div>	16	1.0E0	5.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:13	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.0E0	4.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:5	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.0E0	4.7E-1	1.0E0	1.0E0
Annotation Cluster 329		Enrichment Score: 0	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cilium morphogenesis</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	9.9E-1	6.5E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Cilium biogenesis/degradation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	13	9.9E-1	6.0E-1	1.0E0	9.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cilium assembly</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	11	1.0E0	5.3E-1	1.0E0	1.0E0
Annotation Cluster 330		Enrichment Score: 0	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">mitochondrial matrix</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	38	9.9E-1	7.4E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	transit peptide:Mitochondrion	<a href="#">RT</a>	<div><div></div><div></div></div>	43	1.0E0	6.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transit peptide</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	47	1.0E0	6.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Mitochondrion</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	116	1.0E0	7.1E-1	1.0E0	1.0E0
Annotation Cluster 331		Enrichment Score: 0	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Rho-GAP	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	4.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Rho GTPase-activating protein domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	3.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Rho GTPase activation protein</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.0E0	4.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	<a href="#">RhoGAP</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	2.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">GTPase activation</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	9	1.0E0	3.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">GTPase activator activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	15	1.0E0	3.2E-1	1.0E0	1.0E0
Annotation Cluster 332		Enrichment Score: 0	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DH	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	4.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of Rho protein signal transduction</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.0E0	4.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Dbl homology (DH) domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	3.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">Rho guanyl-nucleotide exchange factor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	3.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">guanyl-nucleotide exchange factor activity</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	6	1.0E0	3.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	<a href="#">RhoGEF</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	4	1.0E0	2.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Guanine-nucleotide releasing factor</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	5	1.0E0	2.3E-1	1.0E0	1.0E0
Annotation Cluster 333		Enrichment Score: 0	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PH	<a href="#">RT</a>	<div><div></div><div></div></div>	19	1.0E0	5.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Pleckstrin homology domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	18	1.0E0	4.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Pleckstrin homology-like domain</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	33	1.0E0	4.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	<a href="#">PH</a>	<a href="#">RT</a>	<div><div></div><div></div></div>	17	1.0E0	2.6E-1	1.0E0	1.0E0

Annotation Cluster 1		Enrichment Score: ?	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 334		Enrichment Score: 0	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:Basic motif	<a href="#">RT</a>	<div></div>	9	1.0E0	3.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Helix-loop-helix motif	<a href="#">RT</a>	<div></div>	4	1.0E0	2.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Myc-type, basic helix-loop-helix (bHLH) domain</a>	<a href="#">RT</a>	<div></div>	4	1.0E0	2.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	<a href="#">HLH</a>	<a href="#">RT</a>	<div></div>	4	1.0E0	1.4E-1	1.0E0	1.0E0
Annotation Cluster 335		Enrichment Score: -0	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Cell membrane</a>	<a href="#">RT</a>	<div></div>	311	1.0E0	6.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Membrane</a>	<a href="#">RT</a>	<div></div>	602	1.0E0	5.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">plasma membrane</a>	<a href="#">RT</a>	<div></div>	445	1.0E0	6.9E-1	1.0E0	1.0E0
Annotation Cluster 336		Enrichment Score: -0	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain:Cytoplasmic	<a href="#">RT</a>	<div></div>	171	1.0E0	3.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain:Extracellular	<a href="#">RT</a>	<div></div>	142	1.0E0	3.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transmembrane</a>	<a href="#">RT</a>	<div></div>	306	1.0E0	3.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	transmembrane region	<a href="#">RT</a>	<div></div>	224	1.0E0	3.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transmembrane helix</a>	<a href="#">RT</a>	<div></div>	305	1.0E0	3.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Disulfide bond</a>	<a href="#">RT</a>	<div></div>	196	1.0E0	3.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Membrane</a>	<a href="#">RT</a>	<div></div>	602	1.0E0	5.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Signal</a>	<a href="#">RT</a>	<div></div>	262	1.0E0	4.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">integral component of plasma membrane</a>	<a href="#">RT</a>	<div></div>	98	1.0E0	4.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Glycoprotein</a>	<a href="#">RT</a>	<div></div>	267	1.0E0	4.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	disulfide bond	<a href="#">RT</a>	<div></div>	153	1.0E0	3.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	<a href="#">RT</a>	<div></div>	209	1.0E0	3.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Receptor</a>	<a href="#">RT</a>	<div></div>	108	1.0E0	4.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	signal peptide	<a href="#">RT</a>	<div></div>	212	1.0E0	4.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">integral component of membrane</a>	<a href="#">RT</a>	<div></div>	281	1.0E0	3.5E-1	1.0E0	1.0E0

3206 terms

 were not clustered.