

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

338 Cluster(s)
















































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Annotation Cluster 1		Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Zinc finger, C2H2	RT		655	0.0E0	5.1E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	RT		483	0.0E0	5.9E0	0.0E0	0.0E0
<input type="checkbox"/>	INTERPRO	Zinc finger, C2H2-like	RT		649	0.0E0	5.3E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	RT		536	0.0E0	5.9E0	0.0E0	0.0E0
<input type="checkbox"/>	INTERPRO	Zinc finger C2H2-type/integrase DNA-binding domain	RT		634	0.0E0	5.5E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 3	RT		565	0.0E0	6.0E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 4	RT		527	0.0E0	6.1E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 5	RT		504	0.0E0	6.2E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 6	RT		461	0.0E0	6.3E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 7	RT		433	0.0E0	6.4E0	0.0E0	0.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 8	RT		399	1.2E-299	6.4E0	8.5E-297	8.2E-297
<input type="checkbox"/>	SMART	ZnF_C2H2	RT		649	1.6E-297	3.4E0	7.1E-295	6.3E-295
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 9	RT		361	1.3E-271	6.4E0	7.9E-269	7.7E-269
<input type="checkbox"/>	UP_KEYWORDS	Zinc-finger	RT		842	6.5E-269	3.2E0	3.1E-266	2.5E-266
<input type="checkbox"/>	UP_KEYWORDS	Nucleus	RT		1582	2.4E-267	2.1E0	5.6E-265	4.5E-265
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 10	RT		324	3.4E-248	6.5E0	1.9E-245	1.8E-245
<input type="checkbox"/>	INTERPRO	Krueppel-associated box	RT		355	7.4E-230	5.5E0	3.9E-227	3.6E-227
<input type="checkbox"/>	UP_KEYWORDS	Transcription	RT		941	4.0E-227	2.7E0	6.3E-225	5.0E-225
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KRAB	RT		314	1.0E-226	6.2E0	5.4E-224	5.2E-224
<input type="checkbox"/>	UP_KEYWORDS	Transcription regulation	RT		923	2.6E-225	2.7E0	3.0E-223	2.4E-223
<input type="checkbox"/>	GOTERM_MF_DIRECT	nucleic acid binding	RT		585	2.1E-216	3.5E0	2.7E-213	2.5E-213
<input type="checkbox"/>	UP_KEYWORDS	DNA-binding	RT		841	8.4E-215	2.8E0	7.9E-213	6.3E-213
<input type="checkbox"/>	UP_KEYWORDS	Zinc	RT		904	1.6E-209	2.6E0	1.3E-207	1.0E-207
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 11	RT		280	1.7E-206	6.3E0	8.1E-204	7.8E-204
<input type="checkbox"/>	UP_KEYWORDS	Metal-binding	RT		1168	1.4E-201	2.2E0	9.3E-200	7.4E-200
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 12	RT		242	2.1E-182	6.4E0	9.1E-180	8.8E-180
<input type="checkbox"/>	GOTERM_MF_DIRECT	metal ion binding	RT		854	5.4E-181	2.5E0	3.5E-178	3.2E-178
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription, DNA-templated	RT		819	7.1E-175	2.5E0	4.2E-171	4.0E-171
<input type="checkbox"/>	SMART	KRAB	RT		350	6.0E-168	3.6E0	1.3E-165	1.2E-165
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of transcription, DNA-templated	RT		679	4.5E-162	2.7E0	1.3E-158	1.3E-158
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA binding	RT		700	2.3E-147	2.5E0	1.0E-144	9.1E-145
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 13	RT		192	5.5E-143	6.4E0	2.2E-140	2.2E-140
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 14	RT		148	4.3E-111	6.5E0	1.5E-108	1.5E-108
<input type="checkbox"/>	GOTERM_CC_DIRECT	intracellular	RT		533	2.6E-110	2.5E0	1.1E-107	1.0E-107
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 15	RT		125	3.6E-92	6.4E0	1.1E-89	1.1E-89
<input type="checkbox"/>	GOTERM_MF_DIRECT	transcription factor activity, sequence-specific DNA binding	RT		403	6.1E-81	2.5E0	1.6E-78	1.5E-78
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 16	RT		96	1.3E-69	6.3E0	3.0E-67	2.9E-67
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 17	RT		76	1.9E-54	6.3E0	2.8E-52	2.7E-52
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 18	RT		60	1.4E-42	6.3E0	1.9E-40	1.8E-40
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 19	RT		50	1.5E-35	6.3E0	2.0E-33	1.9E-33
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 20	RT		32	2.2E-21	6.1E0	2.2E-19	2.1E-19
















































Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 2		Enrichment Score: 87.1	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Nucleotide-binding	<div><div>RT</div><div></div></div>	730	2.7E-181	2.8E0	1.6E-179	1.3E-179
<input type="checkbox"/>	UP_KEYWORDS	ATP-binding	<div><div>RT</div><div></div></div>	586	1.0E-149	2.9E0	5.3E-148	4.2E-148
<input type="checkbox"/>	GOTERM_MF_DIRECT	ATP binding	<div><div>RT</div><div></div></div>	606	7.3E-118	2.4E0	2.4E-115	2.2E-115
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	<div><div>RT</div><div></div></div>	439	2.2E-117	3.0E0	8.5E-115	8.2E-115
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase	<div><div>RT</div><div></div></div>	273	9.7E-105	3.9E0	3.2E-102	3.1E-102
<input type="checkbox"/>	INTERPRO	Protein kinase-like domain	<div><div>RT</div><div></div></div>	300	5.9E-103	3.5E0	2.5E-100	2.3E-100
<input type="checkbox"/>	INTERPRO	Protein kinase, catalytic domain	<div><div>RT</div><div></div></div>	284	5.7E-102	3.6E0	2.0E-99	1.9E-99
<input type="checkbox"/>	INTERPRO	Protein kinase, ATP binding site	<div><div>RT</div><div></div></div>	239	6.5E-95	3.9E0	1.9E-92	1.8E-92
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:ATP	<div><div>RT</div><div></div></div>	278	8.0E-88	3.4E0	2.4E-85	2.3E-85
<input type="checkbox"/>	UP_KEYWORDS	Kinase	<div><div>RT</div><div></div></div>	319	1.8E-82	3.0E0	7.7E-81	6.1E-81
<input type="checkbox"/>	UP_KEYWORDS	Serine/threonine-protein kinase	<div><div>RT</div><div></div></div>	209	8.8E-73	3.7E0	3.4E-71	2.8E-71
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Proton acceptor	<div><div>RT</div><div></div></div>	274	8.1E-63	2.8E0	1.5E-60	1.5E-60
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein kinase activity	<div><div>RT</div><div></div></div>	194	3.6E-59	3.2E0	7.9E-57	7.2E-57
<input type="checkbox"/>	INTERPRO	Serine/threonine-protein kinase, active site	<div><div>RT</div><div></div></div>	174	5.4E-58	3.5E0	9.5E-56	8.8E-56
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein serine/threonine kinase activity	<div><div>RT</div><div></div></div>	197	3.2E-57	3.1E0	6.1E-55	5.5E-55
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein phosphorylation	<div><div>RT</div><div></div></div>	218	7.6E-54	2.8E0	1.5E-50	1.4E-50
<input type="checkbox"/>	UP_KEYWORDS	Transferase	<div><div>RT</div><div></div></div>	454	4.7E-42	1.8E0	1.2E-40	9.3E-41
<input type="checkbox"/>	SMART	S_TKc	<div><div>RT</div><div></div></div>	195	6.0E-34	2.2E0	5.3E-32	4.7E-32
Annotation Cluster 3		Enrichment Score: 59.63	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 4	<div><div>RT</div><div></div></div>	132	6.4E-75	5.3E0	1.8E-72	1.8E-72
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 5	<div><div>RT</div><div></div></div>	117	1.2E-71	5.6E0	2.9E-69	2.8E-69
<input type="checkbox"/>	UP_KEYWORDS	ANK repeat	<div><div>RT</div><div></div></div>	163	2.2E-69	4.2E0	7.9E-68	6.4E-68
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 3	<div><div>RT</div><div></div></div>	141	1.1E-67	4.6E0	2.3E-65	2.2E-65
<input type="checkbox"/>	INTERPRO	Ankyrin repeat	<div><div>RT</div><div></div></div>	161	3.5E-64	3.9E0	7.4E-62	6.8E-62
<input type="checkbox"/>	INTERPRO	Ankyrin repeat-containing domain	<div><div>RT</div><div></div></div>	164	1.5E-63	3.8E0	2.8E-61	2.6E-61
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 2	<div><div>RT</div><div></div></div>	148	1.0E-60	4.1E0	1.8E-58	1.7E-58
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 1	<div><div>RT</div><div></div></div>	147	4.4E-60	4.1E0	7.3E-58	7.0E-58
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 6	<div><div>RT</div><div></div></div>	85	7.9E-55	5.8E0	1.2E-52	1.2E-52
<input type="checkbox"/>	SMART	ANK	<div><div>RT</div><div></div></div>	159	3.2E-39	2.6E0	3.6E-37	3.2E-37
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 7	<div><div>RT</div><div></div></div>	56	1.1E-37	6.1E0	1.4E-35	1.4E-35
Annotation Cluster 4		Enrichment Score: 47.49	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Leucine-rich repeat, typical subtype	<div><div>RT</div><div></div></div>	144	1.1E-80	5.0E0	3.0E-78	2.8E-78
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 5	<div><div>RT</div><div></div></div>	154	6.3E-72	4.5E0	1.6E-69	1.6E-69
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 4	<div><div>RT</div><div></div></div>	161	4.6E-70	4.3E0	1.1E-67	1.0E-67
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 6	<div><div>RT</div><div></div></div>	143	5.0E-69	4.7E0	1.1E-66	1.0E-66
<input type="checkbox"/>	UP_KEYWORDS	Leucine-rich repeat	<div><div>RT</div><div></div></div>	178	1.6E-68	3.9E0	5.5E-67	4.4E-67
<input type="checkbox"/>	INTERPRO	Leucine-rich repeat	<div><div>RT</div><div></div></div>	168	4.2E-68	4.0E0	9.9E-66	9.1E-66
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 7	<div><div>RT</div><div></div></div>	129	5.6E-68	5.0E0	1.2E-65	1.1E-65
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 3	<div><div>RT</div><div></div></div>	171	2.5E-64	3.9E0	4.9E-62	4.8E-62
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 1	<div><div>RT</div><div></div></div>	174	1.3E-61	3.7E0	2.4E-59	2.3E-59
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 2	<div><div>RT</div><div></div></div>	174	2.4E-61	3.7E0	4.3E-59	4.1E-59
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 8	<div><div>RT</div><div></div></div>	109	9.7E-58	5.0E0	1.6E-55	1.5E-55
<input type="checkbox"/>	SMART	LRR_TYP	<div><div>RT</div><div></div></div>	144	8.9E-56	3.3E0	1.3E-53	1.2E-53
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 9	<div><div>RT</div><div></div></div>	98	2.0E-51	5.0E0	2.9E-49	2.8E-49
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 10	<div><div>RT</div><div></div></div>	84	1.6E-43	4.9E0	2.2E-41	2.1E-41
















































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:LRR 11	RT	<div><div></div><div></div></div>	73	9.4E-38	4.9E0	1.3E-35	1.2E-35
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 12	RT	<div><div></div><div></div></div>	66	9.0E-35	5.0E0	1.1E-32	1.0E-32
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 13	RT	<div><div></div><div></div></div>	53	1.1E-26	4.8E0	1.2E-24	1.1E-24
<input type="checkbox"/>	INTERPRO	Cysteine-rich flanking region, C-terminal	RT	<div><div></div><div></div></div>	58	1.2E-26	4.3E0	1.2E-24	1.1E-24
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 14	RT	<div><div></div><div></div></div>	43	4.4E-22	4.9E0	4.4E-20	4.2E-20
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 15	RT	<div><div></div><div></div></div>	37	2.6E-19	4.9E0	2.4E-17	2.3E-17
<input type="checkbox"/>	SMART	LRRCT	RT	<div><div></div><div></div></div>	58	2.7E-17	2.8E0	1.3E-15	1.2E-15
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 16	RT	<div><div></div><div></div></div>	32	2.4E-16	4.8E0	1.9E-14	1.9E-14
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 17	RT	<div><div></div><div></div></div>	28	6.6E-16	5.3E0	5.0E-14	4.8E-14
Annotation Cluster 5		Enrichment Score: 47.28	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Ubl conjugation pathway	RT	<div><div></div><div></div></div>	274	3.0E-62	2.8E0	8.9E-61	7.2E-61
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitin-protein transferase activity	RT	<div><div></div><div></div></div>	174	3.0E-51	3.2E0	4.9E-49	4.5E-49
<input type="checkbox"/>	KEGG_PATHWAY	Ubiquitin mediated proteolysis	RT	<div><div></div><div></div></div>	107	1.2E-50	4.1E0	3.0E-48	1.3E-48
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein ubiquitination	RT	<div><div></div><div></div></div>	148	6.7E-28	2.4E0	4.9E-25	4.7E-25
Annotation Cluster 6		Enrichment Score: 30.08	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SCAN box	RT	<div><div></div><div></div></div>	53	2.4E-35	6.0E0	3.0E-33	2.9E-33
<input type="checkbox"/>	INTERPRO	Transcription regulator SCAN	RT	<div><div></div><div></div></div>	54	7.8E-35	5.6E0	9.6E-33	8.9E-33
<input type="checkbox"/>	INTERPRO	Retrovirus capsid, C-terminal	RT	<div><div></div><div></div></div>	54	2.8E-28	4.8E0	3.3E-26	3.0E-26
<input type="checkbox"/>	SMART	SCAN	RT	<div><div></div><div></div></div>	53	9.0E-25	3.6E0	5.7E-23	5.1E-23
Annotation Cluster 7		Enrichment Score: 21.8	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Pathways in cancer	RT	<div><div></div><div></div></div>	169	2.8E-29	2.3E0	8.4E-28	3.7E-28
<input type="checkbox"/>	KEGG_PATHWAY	PI3K-Akt signaling pathway	RT	<div><div></div><div></div></div>	137	6.8E-20	2.1E0	1.0E-18	4.6E-19
<input type="checkbox"/>	KEGG_PATHWAY	Ras signaling pathway	RT	<div><div></div><div></div></div>	100	2.1E-18	2.3E0	2.6E-17	1.2E-17
Annotation Cluster 8		Enrichment Score: 19.22	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Cell cycle	RT	<div><div></div><div></div></div>	218	6.5E-35	2.3E0	1.4E-33	1.1E-33
<input type="checkbox"/>	UP_KEYWORDS	Cell division	RT	<div><div></div><div></div></div>	131	1.6E-21	2.3E0	2.4E-20	1.9E-20
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell division	RT	<div><div></div><div></div></div>	123	2.1E-16	2.1E0	5.1E-14	4.9E-14
<input type="checkbox"/>	UP_KEYWORDS	Mitosis	RT	<div><div></div><div></div></div>	90	2.0E-15	2.4E0	2.7E-14	2.2E-14
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitotic nuclear division	RT	<div><div></div><div></div></div>	86	1.7E-11	2.1E0	2.6E-9	2.5E-9
Annotation Cluster 9		Enrichment Score: 18.67	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Tyrosine-protein kinase	RT	<div><div></div><div></div></div>	84	8.7E-46	5.1E0	2.3E-44	1.8E-44
<input type="checkbox"/>	INTERPRO	Serine-threonine/tyrosine-protein kinase catalytic domain	RT	<div><div></div><div></div></div>	98	5.4E-45	4.3E0	8.7E-43	8.1E-43
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, catalytic domain	RT	<div><div></div><div></div></div>	69	1.2E-38	5.0E0	1.6E-36	1.5E-36
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, active site	RT	<div><div></div><div></div></div>	71	1.3E-35	4.6E0	1.7E-33	1.6E-33
<input type="checkbox"/>	SMART	TyrKc	RT	<div><div></div><div></div></div>	69	7.8E-27	3.3E0	5.7E-25	5.1E-25
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein tyrosine kinase activity	RT	<div><div></div><div></div></div>	76	2.1E-25	3.4E0	2.1E-23	1.9E-23
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptidyl-tyrosine phosphorylation	RT	<div><div></div><div></div></div>	79	2.1E-22	3.1E0	1.1E-19	1.0E-19
<input type="checkbox"/>	GOTERM_MF_DIRECT	non-membrane spanning protein tyrosine kinase activity	RT	<div><div></div><div></div></div>	36	1.0E-18	4.7E0	7.1E-17	6.5E-17
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptidyl-tyrosine autophosphorylation	RT	<div><div></div><div></div></div>	33	2.9E-18	4.9E0	9.9E-16	9.5E-16
<input type="checkbox"/>	GOTERM_CC_DIRECT	extrinsic component of cytoplasmic side of plasma membrane	RT	<div><div></div><div></div></div>	35	4.6E-11	3.3E0	2.8E-9	2.5E-9
<input type="checkbox"/>	GOTERM_MF_DIRECT	transmembrane receptor protein tyrosine kinase activity	RT	<div><div></div><div></div></div>	25	1.8E-10	3.9E0	7.1E-9	6.5E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	transmembrane receptor protein tyrosine kinase signaling pathway	RT	<div><div></div><div></div></div>	43	5.8E-10	2.7E0	6.9E-8	6.6E-8
<input type="checkbox"/>	UP_KEYWORDS	SH2 domain	RT	<div><div></div><div></div></div>	38	2.3E-7	2.4E0	1.7E-6	1.4E-6
<input type="checkbox"/>	INTERPRO	SH2 domain	RT	<div><div></div><div></div></div>	39	3.6E-6	2.1E0	7.4E-5	6.8E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2	RT	<div><div></div><div></div></div>	30	7.8E-5	2.1E0	2.8E-3	2.7E-3
<input type="checkbox"/>	SMART	SH2	RT	<div><div></div><div></div></div>	36	2.2E-2	1.4E0	1.6E-1	1.4E-1


































Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	receptor binding	RT	<div><div></div><div></div></div>	55	7.9E-1	9.3E-1	1.0E0	9.1E-1
Annotation Cluster 10		Enrichment Score: 18.33	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	RT	<div><div></div><div></div></div>	58	5.5E-35	5.6E0	6.8E-33	6.5E-33
<input type="checkbox"/>	INTERPRO	Ubiquitin-conjugating enzyme, E2	RT	<div><div></div><div></div></div>	34	5.7E-19	5.0E0	5.2E-17	4.8E-17
<input type="checkbox"/>	INTERPRO	Ubiquitin-conjugating enzyme, active site	RT	<div><div></div><div></div></div>	25	2.0E-17	6.0E0	1.6E-15	1.5E-15
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitin conjugating enzyme activity	RT	<div><div></div><div></div></div>	26	4.1E-16	5.4E0	2.5E-14	2.2E-14
<input type="checkbox"/>	INTERPRO	Ubiquitin-conjugating enzyme/RWD-like	RT	<div><div></div><div></div></div>	36	6.1E-15	4.0E0	3.7E-13	3.5E-13
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein K48-linked ubiquitination	RT	<div><div></div><div></div></div>	30	6.6E-12	3.8E0	1.1E-9	1.0E-9
Annotation Cluster 11		Enrichment Score: 17.69	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	mRNA splicing, via spliceosome	RT	<div><div></div><div></div></div>	119	1.7E-35	3.2E0	2.0E-32	1.9E-32
<input type="checkbox"/>	KEGG_PATHWAY	Spliceosome	RT	<div><div></div><div></div></div>	79	1.4E-24	3.1E0	2.8E-23	1.3E-23
<input type="checkbox"/>	UP_KEYWORDS	Spliceosome	RT	<div><div></div><div></div></div>	67	2.8E-23	3.6E0	4.4E-22	3.6E-22
<input type="checkbox"/>	GOTERM_CC_DIRECT	spliceosomal complex	RT	<div><div></div><div></div></div>	52	6.2E-18	3.5E0	9.1E-16	8.1E-16
<input type="checkbox"/>	UP_KEYWORDS	mRNA processing	RT	<div><div></div><div></div></div>	105	4.3E-15	2.2E0	5.8E-14	4.6E-14
<input type="checkbox"/>	UP_KEYWORDS	mRNA splicing	RT	<div><div></div><div></div></div>	88	1.1E-14	2.3E0	1.4E-13	1.1E-13
<input type="checkbox"/>	GOTERM_CC_DIRECT	catalytic step 2 spliceosome	RT	<div><div></div><div></div></div>	46	9.5E-14	3.2E0	9.2E-12	8.2E-12
<input type="checkbox"/>	GOTERM_BP_DIRECT	RNA splicing	RT	<div><div></div><div></div></div>	40	1.7E-2	1.4E0	2.3E-1	2.2E-1
Annotation Cluster 12		Enrichment Score: 17.54	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	GTP-binding	RT	<div><div></div><div></div></div>	143	2.5E-34	2.9E0	5.0E-33	4.0E-33
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	RT	<div><div></div><div></div></div>	132	1.7E-32	2.9E0	2.0E-30	1.9E-30
<input type="checkbox"/>	GOTERM_MF_DIRECT	GTPase activity	RT	<div><div></div><div></div></div>	110	8.2E-27	2.8E0	1.1E-24	9.8E-25
<input type="checkbox"/>	GOTERM_MF_DIRECT	GTP binding	RT	<div><div></div><div></div></div>	150	9.3E-26	2.3E0	1.0E-23	9.2E-24
<input type="checkbox"/>	INTERPRO	Small GTPase superfamily, Ras type	RT	<div><div></div><div></div></div>	33	1.7E-19	5.2E0	1.7E-17	1.6E-17
<input type="checkbox"/>	INTERPRO	Small GTP-binding protein domain	RT	<div><div></div><div></div></div>	77	2.4E-19	2.9E0	2.3E-17	2.2E-17
<input type="checkbox"/>	INTERPRO	Small GTPase superfamily	RT	<div><div></div><div></div></div>	62	8.3E-15	2.8E0	4.8E-13	4.5E-13
<input type="checkbox"/>	UP_KEYWORDS	Prenylation	RT	<div><div></div><div></div></div>	61	6.6E-12	2.5E0	7.2E-11	5.8E-11
<input type="checkbox"/>	GOTERM_BP_DIRECT	small GTPase mediated signal transduction	RT	<div><div></div><div></div></div>	85	2.8E-11	2.0E0	4.1E-9	3.9E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Effector region	RT	<div><div></div><div></div></div>	41	7.9E-10	2.8E0	4.8E-8	4.6E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	propeptide:Removed in mature form	RT	<div><div></div><div></div></div>	66	2.4E-7	1.9E0	1.3E-5	1.2E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	lipid moiety-binding region:S-geranylgeranyl cysteine	RT	<div><div></div><div></div></div>	35	7.3E-6	2.2E0	3.1E-4	3.0E-4
Annotation Cluster 13		Enrichment Score: 17.43	<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 19	RT	<div><div></div><div></div></div>	50	1.5E-35	6.3E0	2.0E-33	1.9E-33
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 20	RT	<div><div></div><div></div></div>	32	2.2E-21	6.1E0	2.2E-19	2.1E-19
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 21	RT	<div><div></div><div></div></div>	24	1.0E-16	6.3E0	8.6E-15	8.3E-15
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 22	RT	<div><div></div><div></div></div>	23	6.3E-16	6.3E0	4.8E-14	4.6E-14</

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 16	RT		32	2.4E-16	4.8E0	1.9E-14	1.9E-14
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 17	RT		28	6.6E-16	5.3E0	5.0E-14	4.8E-14
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 18	RT		20	9.5E-11	5.0E0	6.2E-9	6.0E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 19	RT		19	1.6E-10	5.2E0	1.0E-8	1.0E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 20	RT		18	2.7E-10	5.3E0	1.7E-8	1.6E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 21	RT		14	6.0E-8	5.3E0	3.2E-6	3.1E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 22	RT		10	4.5E-6	5.7E0	2.0E-4	2.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 23	RT		8	1.2E-4	5.4E0	4.0E-3	3.9E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 24	RT		6	1.1E-3	5.8E0	3.0E-2	2.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 25	RT		5	5.4E-3	5.7E0	1.3E-1	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interferon-alpha biosynthetic process	RT		4	1.7E-2	5.9E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interferon-beta biosynthetic process	RT		5	1.8E-2	4.2E0	2.4E-1	2.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 26	RT		4	2.5E-2	5.4E0	4.6E-1	4.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 27	RT		3	1.1E-1	5.1E0	1.0E0	9.7E-1
Annotation Cluster 15		Enrichment Score: 16.22	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	ErbB signaling pathway	RT		54	4.1E-18	3.3E0	4.7E-17	2.1E-17
<input type="checkbox"/>	KEGG_PATHWAY	Proteoglycans in cancer	RT		90	3.5E-17	2.4E0	3.4E-16	1.5E-16
<input type="checkbox"/>	KEGG_PATHWAY	Focal adhesion	RT		89	1.6E-15	2.3E0	1.2E-14	5.5E-15
Annotation Cluster 16		Enrichment Score: 16.19	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	RT		58	5.5E-35	5.6E0	6.8E-33	6.5E-33
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HECT	RT		22	1.2E-12	5.3E0	8.5E-11	8.2E-11
<input type="checkbox"/>	INTERPRO	HECT	RT		22	8.0E-12	4.9E0	3.6E-10	3.3E-10
<input type="checkbox"/>	SMART	HECTc	RT		22	3.1E-8	3.2E0	7.4E-7	6.5E-7
Annotation Cluster 17		Enrichment Score: 15.65	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BTB	RT		72	5.8E-23	3.4E0	6.0E-21	5.7E-21
<input type="checkbox"/>	INTERPRO	BTB/POZ-like	RT		78	1.2E-17	2.7E0	9.7E-16	9.0E-16
<input type="checkbox"/>	INTERPRO	BTB/POZ fold	RT		80	3.2E-17	2.6E0	2.4E-15	2.2E-15
<input type="checkbox"/>	SMART	BTB	RT		76	1.2E-7	1.7E0	2.6E-6	2.3E-6
Annotation Cluster 18		Enrichment Score: 15.63	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Gap junction	RT		62	4.5E-25	3.7E0	9.9E-24	4.4E-24
<input type="checkbox"/>	KEGG_PATHWAY	Estrogen signaling pathway	RT		64	9.3E-23	3.4E0	1.7E-21	7.6E-22
<input type="checkbox"/>	KEGG_PATHWAY	Cholinergic synapse	RT		59	2.4E-15	2.8E0	1.8E-14	8.2E-15
<input type="checkbox"/>	KEGG_PATHWAY	GnRH signaling pathway	RT		47	9.1E-12	2.7E0	4.1E-11	1.8E-11
<input type="checkbox"/>	KEGG_PATHWAY	Melanogenesis	RT		41	7.7E-7	2.2E0	2.3E-6	1.0E-6
Annotation Cluster 19		Enrichment Score: 13.6	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 3	RT		66	4.5E-32	4.7E0	5.2E-30	5.0E-30
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 2	RT		82	8.5E-22	3.0E0	8.5E-20	8.2E-20
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 1	RT		78	3.3E-19	2.9E0	3.0E-17	2.9E-17
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 4	RT		40	4.2E-18	4.4E0	3.8E-16	3.6E-16
<input type="checkbox"/>	UP_SEQ_FEATURE	calcium-binding region:1	RT		59	7.2E-17	3.1E0	6.0E-15	5.8E-15
<input type="checkbox"/>	UP_SEQ_FEATURE	calcium-binding region:2	RT		55	6.0E-16	3.2E0	4.7E-14	4.5E-14
<input type="checkbox"/>	INTERPRO	EF-Hand 1, calcium-binding site	RT		73	6.0E-15	2.5E0	3.7E-13	3.5E-13
<input type="checkbox"/>	INTERPRO	EF-hand domain	RT		86	6.5E-15	2.3E0	3.9E-13	3.6E-13
<input type="checkbox"/>	INTERPRO	EF-hand-like domain	RT		97	4.1E-14	2.2E0	2.3E-12	2.1E-12
<input type="checkbox"/>	UP_SEQ_FEATURE	calcium-binding region:3	RT		27	2.3E-13	4.7E0	1.6E-11	1.5E-11
<input type="checkbox"/>	SMART	EFh	RT		73	4.1E-11	2.0E0	1.5E-9	1.3E-9

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	COG_ONTOLOGY	Signal transduction mechanisms / Cytoskeleton / Cell division and chromosome partitioning / General function prediction only	RT		33	1.8E-6	2.0E0	2.8E-5	2.8E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium ion binding	RT		117	6.8E-1	9.7E-1	1.0E0	9.1E-1
<input type="checkbox"/>	UP_KEYWORDS	Calcium	RT		112	9.6E-1	8.8E-1	1.0E0	9.6E-1
Annotation Cluster 20		Enrichment Score: 13.32	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Oxytocin signaling pathway	RT		76	3.7E-18	2.7E0	4.4E-17	2.0E-17
<input type="checkbox"/>	KEGG_PATHWAY	cGMP-PKG signaling pathway	RT		71	1.6E-13	2.4E0	9.2E-13	4.1E-13
<input type="checkbox"/>	KEGG_PATHWAY	Vascular smooth muscle contraction	RT		53	1.9E-10	2.4E0	8.0E-10	3.5E-10
Annotation Cluster 21		Enrichment Score: 13.01	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Actin-related protein	RT		30	1.1E-18	5.5E0	9.5E-17	8.8E-17
<input type="checkbox"/>	SMART	ACTIN	RT		30	3.1E-14	3.7E0	1.4E-12	1.2E-12
<input type="checkbox"/>	INTERPRO	Actin/actin-like conserved site	RT		19	4.2E-12	5.6E0	1.9E-10	1.8E-10
<input type="checkbox"/>	INTERPRO	Actin, conserved site	RT		16	6.3E-10	5.5E0	2.1E-8	1.9E-8
Annotation Cluster 22		Enrichment Score: 12.97	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Neurotrophin signaling pathway	RT		76	3.8E-26	3.3E0	1.0E-24	4.5E-25
<input type="checkbox"/>	KEGG_PATHWAY	Prostate cancer	RT		62	4.5E-25	3.7E0	9.9E-24	4.4E-24
<input type="checkbox"/>	KEGG_PATHWAY	Hepatitis B	RT		79	2.4E-21	2.9E0	4.1E-20	1.8E-20
<input type="checkbox"/>	KEGG_PATHWAY	T cell receptor signaling pathway	RT		62	1.1E-20	3.3E0	1.7E-19	7.6E-20
<input type="checkbox"/>	KEGG_PATHWAY	Pancreatic cancer	RT		47	8.8E-20	3.8E0	1.2E-18	5.5E-19
<input type="checkbox"/>	KEGG_PATHWAY	ErbB signaling pathway	RT		54	4.1E-18	3.3E0	4.7E-17	2.1E-17
<input type="checkbox"/>	KEGG_PATHWAY	Chronic myeloid leukemia	RT		47	4.7E-17	3.4E0	4.4E-16	1.9E-16
<input type="checkbox"/>	KEGG_PATHWAY	Glioma	RT		44	7.4E-17	3.6E0	6.6E-16	2.9E-16
<input type="checkbox"/>	KEGG_PATHWAY	Acute myeloid leukemia	RT		39	1.4E-15	3.7E0	1.2E-14	5.3E-15
<input type="checkbox"/>	KEGG_PATHWAY	Sphingolipid signaling pathway	RT		62	2.5E-15	2.7E0	1.9E-14	8.3E-15
<input type="checkbox"/>	KEGG_PATHWAY	Endometrial cancer	RT		37	3.1E-15	3.7E0	2.3E-14	1.0E-14
<input type="checkbox"/>	KEGG_PATHWAY	VEGF signaling pathway	RT		40	1.3E-14	3.4E0	8.8E-14	3.9E-14
<input type="checkbox"/>	KEGG_PATHWAY	Colorectal cancer	RT		40	2.8E-14	3.4E0	1.9E-13	8.3E-14
<input type="checkbox"/>	KEGG_PATHWAY	Prolactin signaling pathway	RT		43	6.3E-14	3.2E0	4.0E-13	1.8E-13
<input type="checkbox"/>	KEGG_PATHWAY	Non-small cell lung cancer	RT		37	1.1E-13	3.5E0	6.4E-13	2.9E-13
<input type="checkbox"/>	KEGG_PATHWAY	B cell receptor signaling pathway	RT		41	6.3E-13	3.1E0	3.4E-12	1.5E-12
<input type="checkbox"/>	KEGG_PATHWAY	Renal cell carcinoma	RT		39	3.2E-12	3.1E0	1.6E-11	6.9E-12
<input type="checkbox"/>	KEGG_PATHWAY	Fc epsilon RI signaling pathway	RT		39	1.1E-11	3.0E0	5.1E-11	2.3E-11
<input type="checkbox"/>	KEGG_PATHWAY	Bladder cancer	RT		28	5.9E-11	3.6E0	2.5E-10	1.1E-10
<input type="checkbox"/>	KEGG_PATHWAY	Hepatitis C	RT		58	1.5E-10	2.3E0	6.3E-10	2.8E-10
<input type="checkbox"/>	KEGG_PATHWAY	Thyroid hormone signaling pathway	RT		52	3.2E-10	2.4E0	1.3E-9	5.6E-10
<input type="checkbox"/>	KEGG_PATHWAY	Insulin signaling pathway	RT		58	8.3E-10	2.2E0	3.2E-9	1.4E-9
<input type="checkbox"/>	KEGG_PATHWAY	Melanoma	RT		37	1.5E-9	2.7E0	5.5E-9	2.4E-9
<input type="checkbox"/>	KEGG_PATHWAY	Central carbon metabolism in cancer	RT		33	1.9E-8	2.7E0	6.4E-8	2.8E-8
<input type="checkbox"/>	KEGG_PATHWAY	Choline metabolism in cancer	RT		41	1.0E-6	2.1E0	3.0E-6	1.3E-6
<input type="checkbox"/>	KEGG_PATHWAY	Fc gamma R-mediated phagocytosis	RT		32	8.4E-5	2.0E0	2.1E-4	9.3E-5
<input type="checkbox"/>	KEGG_PATHWAY	Signaling pathways regulating pluripotency of stem cells	RT		45	2.6E-4	1.7E0	5.9E-4	2.6E-4
<input type="checkbox"/>	KEGG_PATHWAY	Natural killer cell mediated cytotoxicity	RT		38	1.6E-3	1.6E0	3.3E-3	1.6E-3
Annotation Cluster 23		Enrichment Score: 12.77	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein K11-linked ubiquitination	RT		26	1.1E-17	5.7E0	3.3E-15	3.2E-15
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	RT		20	8.8E-12	5.2E0	1.3E-9	1.3E-9
<input type="checkbox"/>	GOTERM_CC_DIRECT	anaphase-promoting complex	RT		19	5.1E-11	5.2E0	2.9E-9	2.6E-9
Annotation Cluster 24		Enrichment Score: 11.88	G		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:F-box	RT		43	2.4E-17	4.0E0	2.0E-15	2.0E-15
<input type="checkbox"/>	INTERPRO	F-box domain, cyclin-like	RT		44	2.0E-16	3.7E0	1.4E-14	1.3E-14
<input type="checkbox"/>	GOTERM_CC_DIRECT	SCF ubiquitin ligase complex	RT		31	1.3E-12	3.9E0	9.3E-11	8.3E-11
<input type="checkbox"/>	GOTERM_BP_DIRECT	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	RT		19	5.6E-10	4.7E0	6.9E-8	6.6E-8
<input type="checkbox"/>	SMART	FBOX	RT		25	1.1E-6	2.6E0	1.9E-5	1.7E-5
Annotation Cluster 25		Enrichment Score: 11.88	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Helicase	RT		67	1.1E-19	3.2E0	1.5E-18	1.2E-18
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Helicase C-terminal	RT		53	1.2E-16	3.3E0	9.6E-15	9.2E-15
<input type="checkbox"/>	INTERPRO	Helicase, superfamily 1/2, ATP-binding domain	RT		56	1.2E-16	3.2E0	8.9E-15	8.2E-15
<input type="checkbox"/>	INTERPRO	Helicase, C-terminal	RT		55	2.3E-16	3.2E0	1.6E-14	1.4E-14
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Helicase ATP-binding	RT		54	5.0E-16	3.2E0	4.0E-14	3.9E-14
<input type="checkbox"/>	INTERPRO	SNF2-related	RT		25	2.5E-13	4.8E0	1.4E-11	1.3E-11
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:DEAH box	RT		28	6.8E-13	4.4E0	4.7E-11	4.5E-11
<input type="checkbox"/>	GOTERM_MF_DIRECT	helicase activity	RT		40	3.3E-10	2.8E0	1.2E-8	1.1E-8
<input type="checkbox"/>	SMART	DEXDc	RT		55	1.7E-8	2.0E0	5.4E-7	4.8E-7
<input type="checkbox"/>	SMART	HELICc	RT		54	2.3E-8	2.0E0	6.6E-7	5.9E-7
<input type="checkbox"/>	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT		29	1.0E-6	2.6E0	2.4E-5	2.2E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	ATP-dependent RNA helicase activity	RT		27	6.9E-6	2.5E0	1.5E-4	1.4E-4
Annotation Cluster 26		Enrichment Score: 11.43	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Oxytocin signaling pathway	RT		76	3.7E-18	2.7E0	4.4E-17	2.0E-17
<input type="checkbox"/>	KEGG_PATHWAY	Long-term potentiation	RT		38	1.9E-11	3.0E0	8.2E-11	3.7E-11
<input type="checkbox"/>	KEGG_PATHWAY	Melanogenesis	RT		41	7.7E-7	2.2E0	2.3E-6	1.0E-6
Annotation Cluster 27		Enrichment Score: 11.29	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Chagas disease (American trypanosomiasis)	RT		60	6.4E-18	3.0E0	7.0E-17	3.1E-17
<input type="checkbox"/>	KEGG_PATHWAY	TNF signaling pathway	RT		54	6.6E-13	2.7E0	3.5E-12	1.5E-12
<input type="checkbox"/>	KEGG_PATHWAY	Toll-like receptor signaling pathway	RT		53	1.8E-12	2.6E0	8.8E-12	3.9E-12
<input type="checkbox"/>	KEGG_PATHWAY	Fc epsilon RI signaling pathway	RT		39	1.1E-11	3.0E0	5.1E-11	2.3E-11
<input type="checkbox"/>	KEGG_PATHWAY	Hepatitis C	RT		58	1.5E-10	2.3E0	6.3E-10	2.8E-10
<input type="checkbox"/>	KEGG_PATHWAY	Influenza A	RT		68	9.9E-10	2.1E0	3.7E-9	1.6E-9
<input type="checkbox"/>	KEGG_PATHWAY	Osteoclast differentiation	RT		54	7.8E-9	2.2E0	2.6E-8	1.2E-8
Annotation Cluster 28		Enrichment Score: 11.2	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein serine/threonine phosphatase activity	RT		36	8.9E-14	3.7E0	4.5E-12	4.1E-12
<input type="checkbox"/>	UP_KEYWORDS	Protein phosphatase	RT		53	3.1E-12	2.7E0	3.6E-11	2.9E-11
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein dephosphorylation	RT		51	9.1E-10	2.4E0	1.0E-7	9.6E-8
Annotation Cluster 29		Enrichment Score: 11.07	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:AGC-kinase C-terminal	RT		33	2.2E-13	4.0E0	1.5E-11	1.5E-11
<input type="checkbox"/>	INTERPRO	Protein kinase, C-terminal	RT		24	3.5E-13	5.0E0	1.9E-11	1.7E-11
<input type="checkbox"/>	INTERPRO	AGC-kinase, C-terminal	RT		33	2.9E-12	3.7E0	1.5E-10	1.4E-10
<input type="checkbox"/>	SMART	S TK X	RT		32	2.4E-8	2.6E0	6.6E-7	5.9E-7
Annotation Cluster 30		Enrichment Score: 10	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Chronic myeloid leukemia	RT		47	4.7E-17	3.4E0	4.4E-16	1.9E-16
<input type="checkbox"/>	BIOCARTA	Influence of Ras and Rho proteins on G1 to S Transition	RT		23	1.3E-7	2.7E0	1.3E-5	9.8E-6
<input type="checkbox"/>	KEGG_PATHWAY	Small cell lung cancer	RT		38	1.6E-7	2.4E0	5.0E-7	2.2E-7
Annotation Cluster 31		Enrichment Score: 9.5	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Cholinergic synapse	RT		59	2.4E-15	2.8E0	1.8E-14	8.2E-15
<input type="checkbox"/>	KEGG_PATHWAY	Circadian entrainment	RT		52	2.9E-14	2.9E0	1.9E-13	8.3E-14
















































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Dopaminergic synapse	RT		61	4.4E-13	2.5E0	2.4E-12	1.1E-12
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular response to glucagon stimulus	RT		26	1.3E-10	3.9E0	1.7E-8	1.6E-8
<input type="checkbox"/>	KEGG_PATHWAY	Glutamatergic synapse	RT		52	2.2E-10	2.4E0	8.8E-10	3.9E-10
<input type="checkbox"/>	KEGG_PATHWAY	Retrograde endocannabinoid signaling	RT		44	3.5E-8	2.3E0	1.1E-7	5.0E-8
<input type="checkbox"/>	KEGG_PATHWAY	GABAergic synapse	RT		38	1.6E-7	2.4E0	5.0E-7	2.2E-7
<input type="checkbox"/>	KEGG_PATHWAY	Morphine addiction	RT		38	1.2E-6	2.2E0	3.5E-6	1.5E-6
<input type="checkbox"/>	KEGG_PATHWAY	Serotonergic synapse	RT		42	6.2E-6	2.0E0	1.7E-5	7.4E-6
Annotation Cluster 32		Enrichment Score: 9.24	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	bitter taste receptor activity	RT		24	2.7E-16	5.7E0	1.7E-14	1.5E-14
<input type="checkbox"/>	INTERPRO	Mammalian taste receptor	RT		24	8.5E-16	5.7E0	5.6E-14	5.2E-14
<input type="checkbox"/>	KEGG_PATHWAY	Taste transduction	RT		32	3.4E-13	3.7E0	1.9E-12	8.6E-13
<input type="checkbox"/>	UP_KEYWORDS	Taste	RT		24	2.9E-12	4.8E0	3.4E-11	2.8E-11
<input type="checkbox"/>	GOTERM_BP_DIRECT	detection of chemical stimulus involved in sensory perception of bitter taste	RT		26	1.3E-10	3.9E0	1.7E-8	1.6E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	sensory perception of taste	RT		16	1.8E-5	3.3E0	7.6E-4	7.2E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	taste receptor activity	RT		11	2.3E-5	4.4E0	3.9E-4	3.6E-4
<input type="checkbox"/>	UP_KEYWORDS	Sensory transduction	RT		47	1.0E0	5.3E-1	1.0E0	1.0E0
Annotation Cluster 33		Enrichment Score: 9.21	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	proteasome-mediated ubiquitin-dependent protein catabolic process	RT		101	8.1E-27	2.9E0	5.3E-24	5.0E-24
<input type="checkbox"/>	GOTERM_BP_DIRECT	anaphase-promoting complex-dependent catabolic process	RT		50	2.3E-19	3.7E0	9.5E-17	9.1E-17
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	RT		47	1.1E-17	3.7E0	3.4E-15	3.2E-15
<input type="checkbox"/>	GOTERM_BP_DIRECT	stimulatory C-type lectin receptor signaling pathway	RT		56	6.4E-17	3.2E0	1.7E-14	1.6E-14
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	RT		44	1.3E-16	3.7E0	3.2E-14	3.1E-14
<input type="checkbox"/>	GOTERM_BP_DIRECT	T cell receptor signaling pathway	RT		64	1.4E-13	2.6E0	2.9E-11	2.8E-11
<input type="checkbox"/>	GOTERM_BP_DIRECT	NIK/NF-kappaB signaling	RT		37	3.4E-12	3.3E0	6.1E-10	5.8E-10
<input type="checkbox"/>	GOTERM_BP_DIRECT	Fc-epsilon receptor signaling pathway	RT		69	7.2E-12	2.3E0	1.1E-9	1.1E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	RT		20	8.8E-12	5.2E0	1.3E-9	1.3E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of canonical Wnt signaling pathway	RT		44	4.1E-7	2.2E0	3.0E-5	2.8E-5
<input type="checkbox"/>	GOTERM_CC_DIRECT	proteasome complex	RT		26	1.4E-6	2.8E0	4.8E-5	4.3E-5
<input type="checkbox"/>	UP_KEYWORDS	Proteasome	RT		23	1.7E-6	3.0E0	1.2E-5	9.4E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of mRNA stability	RT		37	6.7E-6	2.1E0	3.3E-4	3.2E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of cellular amino acid metabolic process	RT		21	1.2E-4	2.4E0	4.1E-3	3.9E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of canonical Wnt signaling pathway	RT		47	1.9E-4	1.7E0	6.3E-3	6.0E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	proteasome accessory complex	RT		10	4.2E-4	3.7E0	5.6E-3	5.0E-3
<input type="checkbox"/>	KEGG_PATHWAY	Proteasome	RT		19	6.2E-4	2.3E0	1.3E-3	6.2E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	Wnt signaling pathway, planar cell polarity pathway	RT		29	9.2E-4	1.9E0	2.4E-2	2.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	RT		19	1.4E-2	1.8E0	2.1E-1	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	tumor necrosis factor-mediated signaling pathway	RT		30	2.1E-2	1.5E0	2.6E-1	2.4E-1
Annotation Cluster 34		Enrichment Score: 8.96	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of protein kinase activity	RT		49	3.3E-13	2.9E0	6.4E-11	6.1E-11
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein kinase inhibitor activity	RT		31	2.6E-11	3.6E0	1.1E-9	9.8E-10
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of JAK-STAT cascade	RT		25	1.0E-9	3.7E0	1.1E-7	1.0E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	cytokine-mediated signaling pathway	RT		40	1.7E-4	1.8E0	5.7E-3	5.5E-3
Annotation Cluster 35		Enrichment Score: 8.93	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Motor protein	RT		75	7.3E-28	3.8E0	1.4E-26	1.1E-26
<input type="checkbox"/>	UP_KEYWORDS	Myosin	RT		43	4.2E-27	5.8E0	7.3E-26	5.9E-26
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Myosin head-like	RT		30	6.7E-18	5.5E0	5.9E-16	5.7E-16

Annotation Cluster 1		Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	myosin complex	RT		36	1.2E-17	4.6E0	1.4E-15	1.3E-15
<input type="checkbox"/>	INTERPRO	Myosin head, motor domain	RT		32	1.4E-17	5.0E0	1.1E-15	1.0E-15
<input type="checkbox"/>	GOTERM_MF_DIRECT	motor activity	RT		37	2.7E-12	3.3E0	1.2E-10	1.1E-10
<input type="checkbox"/>	SMART	MYSc	RT		32	3.2E-12	3.2E0	1.3E-10	1.1E-10
<input type="checkbox"/>	UP_KEYWORDS	Muscle protein	RT		33	7.2E-12	3.7E0	7.7E-11	6.1E-11
<input type="checkbox"/>	INTERPRO	IQ motif, EF-hand binding site	RT		42	1.2E-11	3.0E0	5.3E-10	4.9E-10
<input type="checkbox"/>	UP_KEYWORDS	Calmodulin-binding	RT		56	2.7E-11	2.5E0	2.7E-10	2.2E-10
<input type="checkbox"/>	GOTERM_MF_DIRECT	microfilament motor activity	RT		18	4.2E-11	5.4E0	1.7E-9	1.5E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Actin-binding	RT		21	5.4E-11	4.9E0	3.6E-9	3.4E-9
<input type="checkbox"/>	INTERPRO	Myosin, N-terminal, SH3-like	RT		15	1.0E-10	6.2E0	3.8E-9	3.5E-9
<input type="checkbox"/>	INTERPRO	Myosin-like IQ motif-containing domain	RT		17	1.2E-10	5.5E0	4.5E-9	4.2E-9
<input type="checkbox"/>	GOTERM_CC_DIRECT	muscle myosin complex	RT		15	4.9E-10	6.0E0	2.4E-8	2.1E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ	RT		28	2.7E-8	3.1E0	1.5E-6	1.5E-6
<input type="checkbox"/>	INTERPRO	Myosin tail	RT		15	4.1E-8	4.9E0	1.1E-6	1.0E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	calmodulin binding	RT		60	6.1E-7	1.9E0	1.6E-5	1.5E-5
<input type="checkbox"/>	GOTERM_CC_DIRECT	myosin filament	RT		12	2.9E-6	4.8E0	8.2E-5	7.3E-5
<input type="checkbox"/>	SMART	IQ	RT		29	6.1E-6	2.3E0	9.0E-5	8.0E-5
<input type="checkbox"/>	UP_KEYWORDS	Actin-binding	RT		67	1.8E-5	1.7E0	1.1E-4	9.2E-5
<input type="checkbox"/>	UP_KEYWORDS	Thick filament	RT		11	3.1E-5	4.4E0	1.9E-4	1.5E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 3	RT		12	9.8E-5	3.7E0	3.5E-3	3.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 1	RT		15	1.1E-4	3.1E0	3.8E-3	3.7E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 2	RT		15	1.1E-4	3.1E0	3.8E-3	3.7E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	actin filament-based movement	RT		11	1.1E-4	3.8E0	3.9E-3	3.7E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 4	RT		9	5.2E-4	4.1E0	1.6E-2	1.5E-2
<input type="checkbox"/>	KEGG_PATHWAY	Tight junction	RT		29	2.2E-3	1.8E0	4.5E-3	2.2E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 5	RT		6	1.5E-2	3.7E0	2.9E-1	2.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	muscle contraction	RT		27	3.1E-2	1.5E0	3.5E-1	3.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IQ 6	RT		3	3.3E-1	2.6E0	1.0E0	9.7E-1
Annotation Cluster 36					Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	DNA damage	RT		98	1.4E-10	1.9E0	1.4E-9	1.1E-9
<input type="checkbox"/>	UP_KEYWORDS	DNA repair	RT		85	2.9E-10	2.0E0	2.6E-9	2.1E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA repair	RT		71	5.8E-7	1.8E0	4.0E-5	3.8E-5



















































Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 19	RT	<div><div></div><div></div></div>	10	4.5E-6	5.7E0	2.0E-4	2.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 20	RT	<div><div></div><div></div></div>	9	2.3E-5	5.6E0	9.0E-4	8.7E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 21	RT	<div><div></div><div></div></div>	9	2.3E-5	5.6E0	9.0E-4	8.7E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 22	RT	<div><div></div><div></div></div>	8	1.2E-4	5.4E0	4.0E-3	3.9E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 23	RT	<div><div></div><div></div></div>	8	1.2E-4	5.4E0	4.0E-3	3.9E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 24	RT	<div><div></div><div></div></div>	6	2.6E-3	5.1E0	6.6E-2	6.3E-2
<input type="checkbox"/>	INTERPRO	Death domain	RT	<div><div></div><div></div></div>	13	6.6E-3	2.3E0	7.0E-2	6.4E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Death	RT	<div><div></div><div></div></div>	12	9.3E-3	2.3E0	2.1E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 25	RT	<div><div></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	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 27	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein targeting to plasma membrane	RT	<div><div></div><div></div></div>	9	5.9E-2	2.1E0	5.3E-1	5.0E-1
<input type="checkbox"/>	INTERPRO	Death-like domain	RT	<div><div></div><div></div></div>	22	7.1E-2	1.5E0	4.0E-1	3.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	spectrin binding	RT	<div><div></div><div></div></div>	8	1.3E-1	1.8E0	6.0E-1	5.5E-1
<input type="checkbox"/>	INTERPRO	ZU5	RT	<div><div></div><div></div></div>	4	3.0E-1	2.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:ZU5	RT	<div><div></div><div></div></div>	3	3.9E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	DEATH	RT	<div><div></div><div></div></div>	8	5.2E-1	1.2E0	1.0E0	8.9E-1
<input type="checkbox"/>	SMART	ZU5	RT	<div><div></div><div></div></div>	3	6.9E-1	1.3E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	cytoskeletal adaptor activity	RT	<div><div></div><div></div></div>	3	7.8E-1	1.1E0	1.0E0	9.1E-1
Annotation Cluster 38		Enrichment Score: 7.86	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Viral nucleoprotein	RT	<div><div></div><div></div></div>	20	2.2E-10	4.9E0	2.0E-9	1.6E-9
<input type="checkbox"/>	GOTERM_CC_DIRECT	viral nucleocapsid	RT	<div><div></div><div></div></div>	20	8.5E-10	4.5E0	3.9E-8	3.5E-8
<input type="checkbox"/>	UP_KEYWORDS	Virion	RT	<div><div></div><div></div></div>	20	1.4E-5	2.9E0	8.7E-5	7.0E-5
Annotation Cluster 39		Enrichment Score: 7.42	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Bromodomain, conserved site	RT	<div><div></div><div></div></div>	21	1.1E-11	5.0E0	5.0E-10	4.6E-10
<input type="checkbox"/>	UP_KEYWORDS	Bromodomain	RT	<div><div></div><div></div></div>	24	1.8E-10	4.2E0	1.7E-9	1.4E-9
<input type="checkbox"/>	INTERPRO	Bromodomain	RT	<div><div></div><div></div></div>	25	3.0E-9	3.6E0	9.4E-8	8.7E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Bromo	RT	<div><div></div><div></div></div>	18	5.8E-8	4.2E0	3.1E-6	3.0E-6
<input type="checkbox"/>	SMART	BROMO	RT	<div><div></div><div></div></div>	25	7.2E-6	2.4E0	1.0E-4	9.1E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	lysine-acetylated histone binding	RT	<div><div></div><div></div></div>	10	1.2E-3	3.3E0	1.4E-2	1.3E-2
Annotation Cluster 40		Enrichment Score: 7.38	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Tubulin, C-terminal	RT	<div><div></div><div></div></div>	20	3.8E-12	5.4E0	1.8E-10	1.7E-10
<input type="checkbox"/>	INTERPRO	Tubulin/FtsZ, C-terminal	RT	<div><div></div><div></div></div>	20	3.8E-12	5.4E0	1.8E-10	1.7E-10
<input type="checkbox"/>	INTERPRO	Tubulin, conserved site	RT	<div><div></div><div></div></div>	20	3.8E-12	5.4E0	1.8E-10	1.7E-10
<input type="checkbox"/>	INTERPRO	Tubulin	RT	<div><div></div><div></div></div>	20	1.6E-11	5.2E0	6.5E-10	6.0E-10
<input type="checkbox"/>	INTERPRO	Tubulin/FtsZ, 2-layer sandwich domain	RT	<div><div></div><div></div></div>	19	2.0E-11	5.4E0	8.1E-10	7.5E-10
<input type="checkbox"/>	INTERPRO	Tubulin/FtsZ, GTPase domain	RT	<div><div></div><div></div></div>	20	5.5E-11	5.0E0	2.2E-9	2.0E-9
<input type="checkbox"/>	SMART	SM00865	RT	<div><div></div><div></div></div>	19	2.9E-8	3.5E0	7.4E-7	6.5E-7
<input type="checkbox"/>	SMART	SM00864	RT	<div><div></div><div></div></div>	20	3.2E-8	3.4E0	7.4E-7	6.5E-7
<input type="checkbox"/>	KEGG_PATHWAY	Pathogenic Escherichia coli infection	RT	<div><div></div><div></div></div>	26	1.1E-6	2.7E0	3.2E-6	1.4E-6
<input type="checkbox"/>	INTERPRO	Beta tubulin, autoregulation binding site	RT	<div><div></div><div></div></div>	9	3.5E-6	6.2E0	7.3E-5	6.7E-5
<input type="checkbox"/>	INTERPRO	Beta tubulin	RT	<div><div></div><div></div></div>	9	3.5E-6	6.2E0	7.3E-5	6.7E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	microtubule-based process	RT	<div><div></div><div></div></div>	19	4.8E-6	3.1E0	2.6E-4	2.5E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	structural constituent of cytoskeleton	RT	<div><div></div><div></div></div>	38	1.1E-5	2.1E0	2.3E-4	2.1E-4
<input type="checkbox"/>	INTERPRO	Alpha tubulin	RT	<div><div></div><div></div></div>	7	3.9E-3	3.9E0	4.3E-2	4.0E-2
<input type="checkbox"/>	KEGG_PATHWAY	Phagosome	RT	<div><div></div><div></div></div>	26	8.0E-1	9.1E-1	1.0E0	8.0E-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 41		Enrichment Score: 7.21	<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	heterotrimeric G-protein complex	RT	<div><div></div><div></div></div>	23	6.6E-11	4.4E0	3.6E-9	3.2E-9
<input type="checkbox"/>	GOTERM_MF_DIRECT	G-protein beta/gamma-subunit complex binding	RT	<div><div></div><div></div></div>	17	9.0E-10	5.1E0	3.2E-8	2.9E-8
<input type="checkbox"/>	UP_KEYWORDS	ADP-ribosylation	RT	<div><div></div><div></div></div>	30	2.2E-9	3.3E0	1.9E-8	1.6E-8
<input type="checkbox"/>	INTERPRO	Guanine nucleotide binding protein (G-protein), alpha subunit	RT	<div><div></div><div></div></div>	14	1.7E-8	5.4E0	4.8E-7	4.5E-7
<input type="checkbox"/>	INTERPRO	G protein alpha subunit, helical insertion	RT	<div><div></div><div></div></div>	14	1.7E-8	5.4E0	4.8E-7	4.5E-7
<input type="checkbox"/>	SMART	SM00275	RT	<div><div></div><div></div></div>	14	3.2E-6	3.5E0	5.0E-5	4.4E-5
<input type="checkbox"/>	INTERPRO	G-protein alpha subunit, group I	RT	<div><div></div><div></div></div>	8	1.9E-5	6.2E0	3.5E-4	3.3E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	guanyl nucleotide binding	RT	<div><div></div><div></div></div>	8	9.6E-5	5.3E0	1.6E-3	1.4E-3
Annotation Cluster 42		Enrichment Score: 7.01	<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:SOCS box	RT	<div><div></div><div></div></div>	25	1.1E-11	4.5E0	7.4E-10	7.1E-10
<input type="checkbox"/>	INTERPRO	SOCS protein, C-terminal	RT	<div><div></div><div></div></div>	25	1.8E-10	4.0E0	6.7E-9	6.2E-9
<input type="checkbox"/>	SMART	SM00969	RT	<div><div></div><div></div></div>	25	1.1E-6	2.6E0	1.9E-5	1.7E-5
<input type="checkbox"/>	SMART	SOCS	RT	<div><div></div><div></div></div>	10	3.8E-2	2.0E0	2.5E-1	2.2E-1
Annotation Cluster 43		Enrichment Score: 6.92	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein serine/threonine phosphatase activity	RT	<div><div></div><div></div></div>	36	8.9E-14	3.7E0	4.5E-12	4.1E-12
<input type="checkbox"/>	INTERPRO	Protein phosphatase 2C (PP2C)-like	RT	<div><div></div><div></div></div>	17	5.1E-10	5.3E0	1.8E-8	1.7E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Manganese 1; via carbonyl oxygen	RT	<div><div></div><div></div></div>	13	1.1E-9	6.8E0	6.6E-8	6.4E-8
<input type="checkbox"/>	INTERPRO	Protein phosphatase 2C	RT	<div><div></div><div></div></div>	14	6.1E-8	5.1E0	1.6E-6	1.5E-6
<input type="checkbox"/>	INTERPRO	Protein phosphatase 2C, manganese/magnesium aspartate binding site	RT	<div><div></div><div></div></div>	11	1.1E-7	6.2E0	2.8E-6	2.6E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptidyl-threonine dephosphorylation	RT	<div><div></div><div></div></div>	11	1.7E-7	5.9E0	1.3E-5	1.3E-5
<input type="checkbox"/>	SMART	PP2Cc	RT	<div><div></div><div></div></div>	17	3.2E-7	3.4E0	6.1E-6	5.4E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Manganese 1	RT	<div><div></div><div></div></div>	15	6.3E-6	3.8E0	2.8E-4	2.7E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Manganese 2	RT	<div><div></div><div></div></div>	15	6.3E-6	3.8E0	2.8E-4	2.7E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PP2C-like	RT	<div><div></div><div></div></div>	10	1.3E-5	5.2E0	5.1E-4	4.9E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	cation binding	RT	<div><div></div><div></div></div>	7	8.1E-3	3.5E0	7.3E-2	6.6E-2
Annotation Cluster 44		Enrichment Score: 6.76	<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	ligase activity	RT	<div><div></div><div></div></div>	109	3.3E-20	2.4E0	2.6E-18	2.3E-18
<input type="checkbox"/>	UP_KEYWORDS	Ligase	RT	<div><div></div><div></div></div>	103	6.9E-13	2.0E0	8.4E-12	6.7E-12
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:RING-type	RT	<div><div></div><div></div></div>	62	1.9E-6	1.8E0	9.4E-5	9.1E-5
<input type="checkbox"/>	INTERPRO	Zinc finger, RING-type	RT	<div><div></div><div></div></div>	77	1.4E-5	1.6E0	2.6E-4	2.4E-4
<input type="checkbox"/>	INTERPRO	Zinc finger, RING/FYVE/PHD-type	RT	<div><div></div><div></div></div>	104	1.3E-4	1.4E0	2.1E-3	1.9E-3
<input type="checkbox"/>	INTERPRO	Zinc finger, RING-type, conserved site	RT	<div><div></div><div></div></div>	35	9.7E-2	1.3E0	5.2E-1	4.8E-1
<input type="checkbox"/>	SMART	RING	RT	<div><div></div><div></div></div>	60	6.0E-1	9.9E-1	1.0E0	8.9E-1
Annotation Cluster 45		Enrichment Score: 6.55	<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	RT	<div><div></div><div></div></div>	28	6.8E-13	4.4E0	4.7E-11	4.5E-11
<input type="checkbox"/>	INTERPRO	Domain of unknown function DUF1605	RT	<div><div></div><div></div></div>	14	6.1E-8	5.1E0	1.6E-6	1.5E-6
<input type="checkbox"/>	INTERPRO	DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site	RT	<div><div></div><div></div></div>	16	6.9E-8	4.5E0	1.8E-6	1.7E-6
<input type="checkbox"/>	INTERPRO	Helicase-associated domain	RT	<div><div></div><div></div></div>	14	1.9E-7	4.8E0	4.6E-6	4.3E-6
<input type="checkbox"/>	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT	<div><div></div><div></div></div>	29	1.0E-6	2.6E0	2.4E-5	2.2E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	ATP-dependent RNA helicase activity	RT	<div><div></div><div></div></div>	27	6.9E-6	2.5E0	1.5E-4	1.4E-4
<input type="checkbox"/>	SMART	SM00847	RT	<div><div></div><div></div></div>	14	3.0E-5	3.1E0	3.9E-4	3.4E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	ATP-dependent helicase activity	RT	<div><div></div><div></div></div>	14	3.7E-4	2.9E0	5.4E-3	4.9E-3
Annotation Cluster 46		Enrichment Score: 6.49	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	INTERPRO	Peptidase C2, calpain, catalytic domain	RT	<div><div></div><div></div></div>	15	1.0E-10	6.2E0	3.8E-9	3.5E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Calpain catalytic	RT	<div><div></div><div></div></div>	14	1.7E-10	6.8E0	1.1E-8	1.1E-8
















































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	Peptidase C2, calpain family	RT	<div><div></div><div></div></div>	14	5.8E-10	6.2E0	2.0E-8	1.8E-8
<input type="checkbox"/>	INTERPRO	Peptidase C2, calpain, large subunit, domain III	RT	<div><div></div><div></div></div>	13	3.4E-9	6.2E0	1.0E-7	9.6E-8
<input type="checkbox"/>	INTERPRO	Peptidase C2, calpain, domain III	RT	<div><div></div><div></div></div>	12	1.9E-8	6.2E0	5.5E-7	5.1E-7
<input type="checkbox"/>	SMART	CysPc	RT	<div><div></div><div></div></div>	15	3.6E-8	4.0E0	7.9E-7	7.0E-7
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium-dependent cysteine-type endopeptidase activity	RT	<div><div></div><div></div></div>	15	4.7E-7	4.3E0	1.3E-5	1.2E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Domain III	RT	<div><div></div><div></div></div>	10	1.3E-6	6.2E0	6.5E-5	6.3E-5
<input type="checkbox"/>	SMART	calpain III	RT	<div><div></div><div></div></div>	12	1.9E-6	4.0E0	3.0E-5	2.7E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Domain IV	RT	<div><div></div><div></div></div>	7	6.1E-5	6.8E0	2.2E-3	2.2E-3
<input type="checkbox"/>	INTERPRO	Cysteine peptidase, cysteine active site	RT	<div><div></div><div></div></div>	11	7.4E-4	3.2E0	9.9E-3	9.1E-3
<input type="checkbox"/>	UP_KEYWORDS	Thiol protease	RT	<div><div></div><div></div></div>	18	9.1E-1	8.1E-1	1.0E0	9.1E-1
Annotation Cluster 47		Enrichment Score: 5.88	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Biological rhythms	RT	<div><div></div><div></div></div>	43	6.8E-8	2.4E0	5.3E-7	4.3E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	rhythmic process	RT	<div><div></div><div></div></div>	25	2.0E-6	2.7E0	1.1E-4	1.1E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of circadian rhythm	RT	<div><div></div><div></div></div>	22	1.7E-5	2.7E0	7.3E-4	7.0E-4
Annotation Cluster 48		Enrichment Score: 5.75	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:TXY	RT	<div><div></div><div></div></div>	12	7.0E-9	6.8E0	4.0E-7	3.9E-7
<input type="checkbox"/>	GOTERM_MF_DIRECT	MAP kinase activity	RT	<div><div></div><div></div></div>	13	3.1E-8	5.5E0	9.4E-7	8.6E-7
<input type="checkbox"/>	INTERPRO	Mitogen-activated protein (MAP) kinase, conserved site	RT	<div><div></div><div></div></div>	11	5.7E-7	5.7E0	1.3E-5	1.2E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of sequence-specific DNA binding transcription factor activity	RT	<div><div></div><div></div></div>	15	1.0E-5	3.6E0	4.8E-4	4.6E-4
<input type="checkbox"/>	INTERPRO	Mitogen-activated protein (MAP) kinase, p38	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
Annotation Cluster 49		Enrichment Score: 5.63	<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	heterotrimeric G-protein complex	RT	<div><div></div><div></div></div>	23	6.6E-11	4.4E0	3.6E-9	3.2E-9
<input type="checkbox"/>	INTERPRO	G-protein, gamma subunit	RT	<div><div></div><div></div></div>	11	2.1E-6	5.2E0	4.5E-5	4.1E-5
<input type="checkbox"/>	INTERPRO	G-protein gamma-like domain	RT	<div><div></div><div></div></div>	11	7.6E-5	4.0E0	1.3E-3	1.2E-3
<input type="checkbox"/>	SMART	GGL	RT	<div><div></div><div></div></div>	11	2.8E-3	2.6E0	2.8E-2	2.5E-2
Annotation Cluster 50		Enrichment Score: 5.47	<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	positive regulation of telomere maintenance via telomerase	RT	<div><div></div><div></div></div>	22	1.1E-9	4.1E0	1.1E-7	1.1E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of telomerase activity	RT	<div><div></div><div></div></div>	15	9.0E-5	3.1E0	3.2E-3	3.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of telomere capping	RT	<div><div></div><div></div></div>	10	4.0E-4	3.7E0	1.2E-2	1.1E-2
Annotation Cluster 51		Enrichment Score: 5.45	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	kinesin complex	RT	<div><div></div><div></div></div>	30	7.1E-11	3.6E0	3.6E-9	3.2E-9
<input type="checkbox"/>	INTERPRO	Kinesin, motor region, conserved site	RT	<div><div></div><div></div></div>	25	7.9E-10	3.8E0	2.6E-8	2.4E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Kinesin-motor	RT	<div><div></div><div></div></div>	25	8.1E-10	3.9E0	4.9E-8	4.7E-8
<input type="checkbox"/>	INTERPRO	Kinesin, motor domain	RT	<div><div></div><div></div></div>	25	1.0E-8	3.4E0	3.1E-7	2.8E-7
<input type="checkbox"/>	GOTERM_CC_DIRECT	microtubule	RT	<div><div></div><div></div></div>	87	5.0E-8	1.8E0	2.0E-6	1.8E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	microtubule motor activity	RT	<div><div></div><div></div></div>	34	1.8E-7	2.5E0	5.0E-6	4.5E-6
<input type="checkbox"/>	UP_KEYWORDS	Microtubule	RT	<div><div></div><div></div></div>	69	1.0E-5	1.7E0	6.7E-5	5.4E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	microtubule-based movement	RT	<div><div></div><div></div></div>	30	3.1E-5	2.2E0	1.2E-3	1.2E-3
<input type="checkbox"/>	SMART	KISc	RT	<div><div></div><div></div></div>	25	3.5E-5	2.2E0	4.4E-4	3.9E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Globular	RT	<div><div></div><div></div></div>	10	1.3E-4	4.3E0	4.5E-3	4.4E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	ATP-dependent microtubule motor activity, plus-end-directed	RT	<div><div></div><div></div></div>	10	6.8E-4	3.5E0	9.0E-3	8.2E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	microtubule binding	RT	<div><div></div><div></div></div>	52	2.5E-3	1.5E0	2.6E-2	2.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	antigen processing and presentation of exogenous peptide antigen via MHC class II	RT	<div><div></div><div></div></div>	24	3.0E-2	1.5E0	3.4E-1	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	retrograde vesicle-mediated transport, Golgi to ER	RT	<div><div></div><div></div></div>	19	1.4E-1	1.4E0	8.4E-1	8.0E-1
Annotation Cluster 52		Enrichment Score: 5.04	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PI3K/PI4K	RT	<div><div></div><div></div></div>	16	1.6E-10	6.1E0	1.0E-8	1.0E-8
















































Annotation Cluster 1		Enrichment Score: ?	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Phosphatidylinositol 3-/4-kinase, catalytic domain	RT	<div></div>	16	2.5E-9	5.2E0	8.1E-8	7.5E-8
<input type="checkbox"/>	INTERPRO	Phosphatidylinositol 3/4-kinase, conserved site	RT	<div></div>	14	1.7E-8	5.4E0	4.8E-7	4.5E-7
<input type="checkbox"/>	SMART	PI3Kc	RT	<div></div>	15	9.7E-7	3.6E0	1.7E-5	1.5E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FAT	RT	<div></div>	6	3.6E-4	6.8E0	1.1E-2	1.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FATC	RT	<div></div>	6	3.6E-4	6.8E0	1.1E-2	1.1E-2
<input type="checkbox"/>	INTERPRO	PIK-related kinase	RT	<div></div>	6	5.7E-4	6.2E0	7.8E-3	7.2E-3
<input type="checkbox"/>	INTERPRO	PIK-related kinase, FATC	RT	<div></div>	6	5.7E-4	6.2E0	7.8E-3	7.2E-3
<input type="checkbox"/>	INTERPRO	PIK-related kinase, FAT	RT	<div></div>	5	2.9E-3	6.2E0	3.4E-2	3.1E-2
<input type="checkbox"/>	SMART	SM01343	RT	<div></div>	6	4.4E-3	4.0E0	4.0E-2	3.6E-2
Annotation Cluster 53		Enrichment Score: 4.93	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	TPR repeat	RT	<div></div>	54	1.3E-8	2.2E0	1.1E-7	8.7E-8
<input type="checkbox"/>	INTERPRO	Tetratricopeptide repeat-containing domain	RT	<div></div>	48	3.7E-8	2.3E0	1.0E-6	9.6E-7
<input type="checkbox"/>	INTERPRO	Tetratricopeptide repeat	RT	<div></div>	48	1.7E-7	2.2E0	4.3E-6	4.0E-6
<input type="checkbox"/>	INTERPRO	Tetratricopeptide-like helical	RT	<div></div>	64	1.4E-6	1.8E0	3.0E-5	2.8E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 5	RT	<div></div>	29	2.7E-6	2.5E0	1.3E-4	1.3E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 2	RT	<div></div>	48	2.9E-6	2.0E0	1.4E-4	1.3E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 1	RT	<div></div>	48	2.9E-6	2.0E0	1.4E-4	1.3E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 6	RT	<div></div>	27	3.0E-6	2.6E0	1.4E-4	1.4E-4
<input type="checkbox"/>	INTERPRO	Tetratricopeptide TPR-1	RT	<div></div>	16	5.7E-6	3.5E0	1.2E-4	1.1E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 3	RT	<div></div>	44	7.5E-6	2.0E0	3.1E-4	3.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 4	RT	<div></div>	32	2.6E-5	2.2E0	9.8E-4	9.5E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 7	RT	<div></div>	23	2.9E-5	2.6E0	1.1E-3	1.1E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 8	RT	<div></div>	19	1.5E-4	2.6E0	5.0E-3	4.9E-3
<input type="checkbox"/>	SMART	TPR	RT	<div></div>	48	2.7E-3	1.5E0	2.8E-2	2.4E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 9	RT	<div></div>	11	1.3E-2	2.3E0	2.7E-1	2.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 10	RT	<div></div>	7	9.2E-2	2.2E0	1.0E0	9.7E-1
Annotation Cluster 54		Enrichment Score: 4.86	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Alcoholism	RT	<div></div>	83	3.4E-17	2.5E0	3.4E-16	1.5E-16
<input type="checkbox"/>	INTERPRO	Histone core	RT	<div></div>	29	7.3E-7	2.6E0	1.7E-5	1.5E-5
<input type="checkbox"/>	UP_KEYWORDS	Nucleosome core	RT	<div></div>	30	1.4E-5	2.3E0	8.7E-5	7.0E-5
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleosome	RT	<div></div>	32	2.6E-5	2.2E0	5.3E-4	4.7E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	nuclear nucleosome	RT	<div></div>	18	2.0E-4	2.6E0	2.9E-3	2.6E-3
<input type="checkbox"/>	INTERPRO	Histone H2B	RT	<div></div>	12	6.0E-4	3.1E0	8.3E-3	7.6E-3
<input type="checkbox"/>	INTERPRO	Histone-fold	RT	<div></div>	33	6.3E-4	1.8E0	8.5E-3	7.9E-3
<input type="checkbox"/>	KEGG_PATHWAY	Systemic lupus erythematosus	RT	<div></div>	41	1.5E-3	1.6E0	3.1E-3	1.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleosome assembly	RT	<div></div>	31	1.3E-2	1.5E0	2.0E-1	1.9E-1
<input type="checkbox"/>	SMART	H2B	RT	<div></div>	12	2.0E-2	2.0E0	1.4E-1	1.3E-1
Annotation Cluster 55		Enrichment Score: 4.75	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SET	RT	<div></div>	31	9.4E-14	4.3E0	6.9E-12	6.7E-12
<input type="checkbox"/>	INTERPRO	SET domain	RT	<div></div>	32	6.4E-13	3.9E0	3.4E-11	3.1E-11
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone-lysine N-methyltransferase activity	RT	<div></div>	24	3.1E-9	3.7E0	1.0E-7	9.1E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Post-SET	RT	<div></div>	14	5.2E-9	6.0E0	3.1E-7	3.0E-7
<input type="checkbox"/>	INTERPRO	Post-SET domain	RT	<div></div>	13	2.9E-7	5.0E0	6.9E-6	6.3E-6
<input type="checkbox"/>	SMART	SET	RT	<div></div>	25	5.7E-7	2.7E0	1.1E-5	9.3E-6
<input type="checkbox"/>	SMART	PostSET	RT	<div></div>	10	9.0E-4	3.1E0	9.7E-3	8.6E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	histone methyltransferase complex	RT	<div></div>	11	1.4E-3	3.0E0	1.6E-2	1.4E-2

Annotation Cluster 1		Enrichment Score: ?	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H3-K4 methylation	RT	<div><div></div></div>	10	3.1E-3	3.0E0	6.6E-2	6.3E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K4 specific)	RT	<div><div></div></div>	9	5.5E-3	3.0E0	5.2E-2	4.7E-2
<input type="checkbox"/>	KEGG_PATHWAY	Lysine degradation	RT	<div><div></div></div>	19	5.6E-3	1.9E0	1.1E-2	5.6E-3
<input type="checkbox"/>	UP_KEYWORDS	S-adenosyl-L-methionine	RT	<div><div></div></div>	36	2.8E-2	1.4E0	1.2E-1	9.8E-2
<input type="checkbox"/>	UP_KEYWORDS	Methyltransferase	RT	<div><div></div></div>	36	9.7E-2	1.3E0	3.7E-1	2.9E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	MLL3/4 complex	RT	<div><div></div></div>	4	1.6E-1	2.8E0	6.7E-1	6.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	methyltransferase activity	RT	<div><div></div></div>	16	6.2E-1	1.0E0	1.0E0	9.1E-1
Annotation Cluster 56		Enrichment Score: 4.64	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Cyclin	RT	<div><div></div></div>	21	1.2E-7	3.6E0	9.5E-7	7.6E-7
<input type="checkbox"/>	INTERPRO	Cyclin-like	RT	<div><div></div></div>	23	1.9E-7	3.2E0	4.6E-6	4.3E-6
<input type="checkbox"/>	SMART	CYCLIN	RT	<div><div></div></div>	22	1.7E-5	2.5E0	2.3E-4	2.1E-4
<input type="checkbox"/>	INTERPRO	Cyclin, N-terminal	RT	<div><div></div></div>	17	2.4E-5	3.1E0	4.3E-4	4.0E-4
<input type="checkbox"/>	INTERPRO	Cyclin, C-terminal domain	RT	<div><div></div></div>	10	8.8E-4	3.4E0	1.2E-2	1.1E-2
<input type="checkbox"/>	SMART	SM01332	RT	<div><div></div></div>	10	1.8E-2	2.2E0	1.3E-1	1.2E-1
Annotation Cluster 57		Enrichment Score: 4.62	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	adenylate cyclase activity	RT	<div><div></div></div>	19	1.6E-13	6.0E0	7.9E-12	7.2E-12
<input type="checkbox"/>	INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase	RT	<div><div></div></div>	18	4.0E-12	5.9E0	1.9E-10	1.7E-10
<input type="checkbox"/>	INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase, conserved site	RT	<div><div></div></div>	17	2.2E-11	5.9E0	9.0E-10	8.3E-10
<input type="checkbox"/>	SMART	CYCc	RT	<div><div></div></div>	17	1.7E-8	3.8E0	5.4E-7	4.8E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Guanylate cyclase	RT	<div><div></div></div>	8	1.0E-5	6.8E0	4.1E-4	4.0E-4
<input type="checkbox"/>	UP_KEYWORDS	cGMP biosynthesis	RT	<div><div></div></div>	8	3.8E-5	6.1E0	2.3E-4	1.8E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	guanylate cyclase complex, soluble	RT	<div><div></div></div>	8	6.4E-5	5.6E0	1.0E-3	9.1E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	guanylate cyclase activity	RT	<div><div></div></div>	8	9.6E-5	5.3E0	1.6E-3	1.4E-3
<input type="checkbox"/>	INTERPRO	Haem NO binding associated	RT	<div><div></div></div>	6	1.7E-3	5.3E0	2.1E-2	2.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	cGMP biosynthetic process	RT	<div><div></div></div>	8	1.1E-2	3.0E0	1.7E-1	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	receptor guanylyl cyclase signaling pathway	RT	<div><div></div></div>	6	1.6E-2	3.6E0	2.2E-1	2.1E-1
<input type="checkbox"/>	INTERPRO	Heme-NO binding	RT	<div><div></div></div>	3	1.2E-1	4.6E0	6.2E-1	5.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of cGMP biosynthetic process	RT	<div><div></div></div>	4	1.4E-1	3.0E0	8.3E-1	7.9E-1
<input type="checkbox"/>	BIOCARTA	Ion Channels and Their Functional Role in Vascular Endothelium	RT	<div><div></div></div>	8	4.1E-1	1.3E0	6.8E-1	5.1E-1
<input type="checkbox"/>	INTERPRO	NO signalling/Golgi transport ligand-binding domain	RT	<div><div></div></div>	3	4.4E-1	2.1E0	1.0E0	9.2E-1
Annotation Cluster 58		Enrichment Score: 4.44	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 23	RT	<div><div></div></div>	15	1.9E-10	6.4E0	1.2E-8	1.1E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 24	RT	<div><div></div></div>	13	6.7E-9	6.3E0	3.9E-7	3.8E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 26	RT	<div><div></div></div>	8	4.0E-5	6.1E0	1.5E-3	1.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 25	RT	<div><div></div></div>	7	2.1E-4	6.0E0	6.8E-3	6.6E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 27	RT	<div><div></div></div>	7	2.1E-4	6.0E0	6.8E-3	6.6E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 28	RT	<div><div></div></div>	6	3.6E-4	6.8E0	1.1E-2	1.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 30	RT	<div><div></div></div>	6	1.1E-3	5.8E0	3.0E-2	2.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 29	RT	<div><div></div></div>	6	1.1E-3	5.8E0	3.0E-2	2.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2H2-type 21; degenerate	RT	<div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.7E-1
Annotation Cluster 59		Enrichment Score: 4.44	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	chemokine-mediated signaling pathway	RT	<div><div></div></div>	36	2.9E-10	3.0E0	3.7E-8	3.5E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	chemotaxis	RT	<div><div></div></div>	50	8.2E-10	2.4E0	9.2E-8	8.8E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell chemotaxis	RT	<div><div></div></div>	33	1.7E-9	3.0E0	1.8E-7	1.7E-7
<input type="checkbox"/>	UP_KEYWORDS	Chemotaxis	RT	<div><div></div></div>	38	9.0E-9	2.7E0	7.7E-8	6.1E-8
<input type="checkbox"/>	INTERPRO	CXC chemokine, conserved site	RT	<div><div></div></div>	12	1.1E-7	5.7E0	2.7E-6	2.5E-6
















































Annotation Cluster 1		Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	CXC chemokine	RT		12	1.1E-7	5.7E0	2.7E-6	2.5E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	chemokine activity	RT		23	3.7E-6	2.8E0	8.5E-5	7.7E-5
<input type="checkbox"/>	INTERPRO	Chemokine interleukin-8-like domain	RT		21	1.0E-5	2.8E0	2.0E-4	1.9E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	CXCR chemokine receptor binding	RT		8	9.6E-5	5.3E0	1.6E-3	1.4E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	CXCR3 chemokine receptor binding	RT		5	3.4E-3	6.0E0	3.4E-2	3.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of leukocyte chemotaxis	RT		9	5.8E-3	3.0E0	1.1E-1	1.0E-1
<input type="checkbox"/>	SMART	SCY	RT		19	1.0E-2	1.8E0	8.3E-2	7.4E-2
<input type="checkbox"/>	BBID	109.Chemokine families	RT		11	6.4E-1	1.0E0	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Cytokine-cytokine receptor interaction	RT		45	6.7E-1	9.7E-1	9.5E-1	6.7E-1
<input type="checkbox"/>	UP_KEYWORDS	Cytokine	RT		26	7.4E-1	9.4E-1	1.0E0	8.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	immune response	RT		60	9.5E-1	8.4E-1	1.0E0	9.6E-1
Annotation Cluster 60		Enrichment Score: 4.38			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	adenylate cyclase activity	RT		19	1.6E-13	6.0E0	7.9E-12	7.2E-12
<input type="checkbox"/>	INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase	RT		18	4.0E-12	5.9E0	1.9E-10	1.7E-10
<input type="checkbox"/>	INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase, conserved site	RT		17	2.2E-11	5.9E0	9.0E-10	8.3E-10
<input type="checkbox"/>	KEGG_PATHWAY	Vascular smooth muscle contraction	RT		53	1.9E-10	2.4E0	8.0E-10	3.5E-10
<input type="checkbox"/>	KEGG_PATHWAY	Inflammatory mediator regulation of TRP channels	RT		46	8.9E-10	2.5E0	3.4E-9	1.5E-9
<input type="checkbox"/>	SMART	CYCc	RT		17	1.7E-8	3.8E0	5.4E-7	4.8E-7
<input type="checkbox"/>	UP_KEYWORDS	cAMP biosynthesis	RT		10	2.5E-7	6.9E0	1.8E-6	1.5E-6
<input type="checkbox"/>	KEGG_PATHWAY	Melanogenesis	RT		41	7.7E-7	2.2E0	2.3E-6	1.0E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	cyclic nucleotide biosynthetic process	RT		11	8.8E-7	5.4E0	5.7E-5	5.5E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	activation of protein kinase A activity	RT		13	3.5E-6	4.3E0	2.0E-4	1.9E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Magnesium 2; via carbonyl oxygen	RT		10	4.5E-6	5.7E0	2.0E-4	2.0E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	phosphorus-oxygen lyase activity	RT		10	1.4E-5	5.0E0	2.7E-4	2.5E-4
<input type="checkbox"/>	KEGG_PATHWAY	Gastric acid secretion	RT		30	2.9E-5	2.2E0	7.4E-5	3.3E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	cAMP biosynthetic process	RT		11	1.1E-4	3.8E0	3.9E-3	3.7E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Magnesium 2	RT		16	3.2E-4	2.7E0	1.0E-2	9.7E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	renal water homeostasis	RT		15	3.3E-4	2.8E0	9.9E-3	9.5E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Magnesium 1	RT		16	4.4E-4	2.7E0	1.3E-2	1.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular response to forskolin	RT		7	4.7E-4	5.2E0	1.3E-2	1.3E-2
<input type="checkbox"/>	INTERPRO	Adenylate cyclase-like	RT		6	5.7E-4	6.2E0	7.8E-3	7.2E-3
<input type="checkbox"/>	KEGG_PATHWAY	Aldosterone synthesis and secretion	RT		28	1.5E-3	1.8E0	3.1E-3	1.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	adenylate cyclase-activating G-protein coupled receptor signaling pathway	RT		17	6.4E-3	2.0E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cAMP-mediated signaling	RT		14	7.3E-3	2.2E0	1.3E-1	1.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	Purine metabolism	RT		47	1.1E-2	1.4E0	2.1E-2	1.1E-2
<input type="checkbox"/>	KEGG_PATHWAY	Thyroid hormone synthesis	RT		22	1.7E-2	1.7E0	3.1E-2	1.7E-2
<input type="checkbox"/>	KEGG_PATHWAY	Salivary secretion	RT		25	2.8E-2	1.5E0	4.9E-2	2.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	activation of adenylate cyclase activity	RT		13	2.8E-2	1.9E0	3.3E-1	3.2E-1
<input type="checkbox"/>	UP_KEYWORDS	Lyase	RT		30	6.5E-2	1.4E0	2.6E-1	2.1E-1
<input type="checkbox"/>	KEGG_PATHWAY	Ovarian steroidogenesis	RT		15	6.8E-2	1.6E0	1.2E-1	6.8E-2
<input type="checkbox"/>	KEGG_PATHWAY	Dilated cardiomyopathy	RT		22	1.0E-1	1.4E0	1.7E-1	1.0E-1
<input type="checkbox"/>	KEGG_PATHWAY	Insulin secretion	RT		21	1.7E-1	1.3E0	2.8E-1	1.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	Pancreatic secretion	RT		22	2.2E-1	1.2E0	3.5E-1	2.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	Bile secretion	RT		14	5.6E-1	1.1E0	8.3E-1	5.6E-1
Annotation Cluster 61		Enrichment Score: 4.26			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation	RT		18	4.0E-5	2.4E0	5.7E-4	4.3E-4















































Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Transcription factor CREB and its extracellular signals	RT	<div><div></div><div></div></div>	20	4.2E-5	2.3E0	5.7E-4	4.3E-4
<input type="checkbox"/>	BIOCARTA	Regulation of BAD phosphorylation	RT	<div><div></div><div></div></div>	19	9.6E-5	2.3E0	1.0E-3	7.7E-4
Annotation Cluster 62		Enrichment Score: 4.26	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Ubiquitin	RT	<div><div></div><div></div></div>	26	1.5E-6	2.7E0	3.3E-5	3.0E-5
<input type="checkbox"/>	INTERPRO	Ubiquitin subgroup	RT	<div><div></div><div></div></div>	10	2.8E-5	4.8E0	5.0E-4	4.6E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ubiquitin-like	RT	<div><div></div><div></div></div>	17	4.1E-4	2.6E0	1.3E-2	1.2E-2
<input type="checkbox"/>	SMART	UBQ	RT	<div><div></div><div></div></div>	22	5.2E-4	2.1E0	5.9E-3	5.3E-3
Annotation Cluster 63		Enrichment Score: 4.22	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription-coupled nucleotide-excision repair	RT	<div><div></div><div></div></div>	35	5.3E-9	2.8E0	5.1E-7	4.9E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	error-prone translesion synthesis	RT	<div><div></div><div></div></div>	14	8.7E-7	4.4E0	5.7E-5	5.4E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, preincision complex assembly	RT	<div><div></div><div></div></div>	17	3.1E-6	3.5E0	1.8E-4	1.7E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA damage response, detection of DNA damage	RT	<div><div></div><div></div></div>	19	4.8E-6	3.1E0	2.6E-4	2.5E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	translesion synthesis	RT	<div><div></div><div></div></div>	19	4.8E-6	3.1E0	2.6E-4	2.5E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA gap filling	RT	<div><div></div><div></div></div>	15	5.3E-6	3.7E0	2.7E-4	2.6E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision, 5'-to lesion	RT	<div><div></div><div></div></div>	19	7.9E-6	3.0E0	3.9E-4	3.7E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	error-free translesion synthesis	RT	<div><div></div><div></div></div>	13	8.1E-6	4.1E0	3.9E-4	3.8E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision	RT	<div><div></div><div></div></div>	19	1.3E-5	3.0E0	5.8E-4	5.5E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	global genome nucleotide-excision repair	RT	<div><div></div><div></div></div>	17	1.6E-5	3.1E0	7.2E-4	6.9E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	telomere maintenance via recombination	RT	<div><div></div><div></div></div>	17	1.6E-5	3.1E0	7.2E-4	6.9E-4
<input type="checkbox"/>	KEGG_PATHWAY	DNA replication	RT	<div><div></div><div></div></div>	19	2.6E-5	2.8E0	6.6E-5	2.9E-5
<input type="checkbox"/>	KEGG_PATHWAY	Nucleotide excision repair	RT	<div><div></div><div></div></div>	21	1.7E-4	2.3E0	4.0E-4	1.8E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA duplex unwinding	RT	<div><div></div><div></div></div>	12	3.5E-4	3.2E0	1.0E-2	1.0E-2
<input type="checkbox"/>	KEGG_PATHWAY	Mismatch repair	RT	<div><div></div><div></div></div>	11	6.1E-3	2.5E0	1.2E-2	6.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA damage recognition	RT	<div><div></div><div></div></div>	10	9.3E-3	2.6E0	1.5E-1	1.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, preincision complex stabilization	RT	<div><div></div><div></div></div>	9	1.7E-2	2.5E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision, 3'-to lesion	RT	<div><div></div><div></div></div>	9	2.9E-2	2.3E0	3.4E-1	3.2E-1
<input type="checkbox"/>	UP_KEYWORDS	Xeroderma pigmentosum	RT	<div><div></div><div></div></div>	3	3.9E-1	2.3E0	1.0E0	8.0E-1
Annotation Cluster 64		Enrichment Score: 3.96	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	termination of RNA polymerase II transcription	RT	<div><div></div><div></div></div>	31	2.4E-8	2.9E0	2.0E-6	1.9E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	mRNA 3'-end processing	RT	<div><div></div><div></div></div>	24	1.5E-6	2.8E0	9.3E-5	8.9E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	RNA export from nucleus	RT	<div><div></div><div></div></div>	16	3.6E-2	1.7E0	3.8E-1	3.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	mRNA export from nucleus	RT	<div><div></div><div></div></div>	23	1.1E-1	1.4E0	7.6E-1	7.3E-1
Annotation Cluster 65		Enrichment Score: 3.95	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Cell Cycle	RT	<div><div></div><div></div></div>	22	9.5E-8	2.7E0	1.3E-5	9.8E-6
<input type="checkbox"/>	BIOCARTA	RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage	RT	<div><div></div><div></div></div>	12	1.3E-4	2.9E0	1.3E-3	9.8E-4
<input type="checkbox"/>	BIOCARTA	Regulation of cell cycle progression by Plk3	RT	<div><div></div><div></div></div>	8	1.9E-3	3.1E0	1.1E-2	8.6E-3
<input type="checkbox"/>	BIOCARTA	cdc25 and chk1 Regulatory Pathway in response to DNA damage	RT	<div><div></div><div></div></div>	8	6.3E-3	2.8E0	2.6E-2	1.9E-2
Annotation Cluster 66		Enrichment Score: 3.91	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, receptor class V, conserved site	RT	<div><div></div><div></div></div>	14	5.8E-10	6.2E0	2.0E-8	1.8E-8
<input type="checkbox"/>	INTERPRO	Ephrin receptor ligand binding domain	RT	<div><div></div><div></div></div>	14	5.8E-10	6.2E0	2.0E-8	1.8E-8
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, ephrin receptor	RT	<div><div></div><div></div></div>	14	5.8E-10	6.2E0	2.0E-8	1.8E-8
<input type="checkbox"/>	PIR_SUPERFAMILY	tyrosine-protein kinase, ephrin receptor type	RT	<div><div></div><div></div></div>	14	6.9E-10	6.0E0	1.2E-7	1.2E-7
<input type="checkbox"/>	SMART	EPH_lbd	RT	<div><div></div><div></div></div>	14	1.4E-7	4.0E0	2.7E-6	2.4E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	ephrin receptor activity	RT	<div><div></div><div></div></div>	11	1.6E-7	6.0E0	4.5E-6	4.1E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	ephrin receptor signaling pathway	RT	<div><div></div><div></div></div>	34	1.6E-6	2.3E0	9.3E-5	8.9E-5
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase ephrin type A/B receptor-like	RT	<div><div></div><div></div></div>	15	5.9E-6	3.7E0	1.2E-4	1.1E-4
















































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Galactose-binding domain-like	RT		29	4.8E-5	2.2E0	8.4E-4	7.8E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SAM	RT		26	2.5E-4	2.1E0	7.8E-3	7.6E-3
<input type="checkbox"/>	INTERPRO	Sterile alpha motif domain	RT		30	2.7E-4	2.0E0	4.1E-3	3.8E-3
<input type="checkbox"/>	INTERPRO	Sterile alpha motif/pointed domain	RT		34	6.7E-4	1.8E0	9.0E-3	8.3E-3
<input type="checkbox"/>	SMART	SM01411	RT		15	8.0E-4	2.4E0	8.9E-3	7.9E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	transmembrane-ephrin receptor activity	RT		6	9.1E-3	4.0E0	7.9E-2	7.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:PDZ-binding	RT		20	1.4E-2	1.8E0	2.8E-1	2.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	GPI-linked ephrin receptor activity	RT		5	1.8E-2	4.3E0	1.3E-1	1.2E-1
<input type="checkbox"/>	SMART	SAM	RT		29	5.4E-2	1.4E0	2.9E-1	2.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Cys-rich	RT		31	8.6E-2	1.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Fibronectin type-III 2	RT		25	1.6E-1	1.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Fibronectin type-III 1	RT		25	1.7E-1	1.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Fibronectin, type III	RT		39	2.1E-1	1.2E0	9.8E-1	9.1E-1
<input type="checkbox"/>	INTERPRO	Insulin-like growth factor binding protein, N-terminal	RT		26	3.1E-1	1.2E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	FN3	RT		30	9.5E-1	8.1E-1	1.0E0	9.5E-1
Annotation Cluster 67		Enrichment Score: 3.83	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA double-strand break processing	RT		11	2.4E-5	4.3E0	1.0E-3	9.6E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA synthesis involved in DNA repair	RT		17	6.6E-5	2.9E0	2.4E-3	2.3E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	strand displacement	RT		12	2.0E-3	2.7E0	4.5E-2	4.3E-2
Annotation Cluster 68		Enrichment Score: 3.77	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Shigellosis	RT		30	1.3E-6	2.5E0	3.5E-6	1.6E-6
<input type="checkbox"/>	KEGG_PATHWAY	Epithelial cell signaling in Helicobacter pylori infection	RT		27	1.2E-4	2.1E0	2.9E-4	1.3E-4
<input type="checkbox"/>	KEGG_PATHWAY	RIG-I-like receptor signaling pathway	RT		21	3.3E-2	1.6E0	5.8E-2	3.3E-2
Annotation Cluster 69		Enrichment Score: 3.74	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	I-kappaB kinase/NF-kappaB signaling	RT		26	5.0E-6	2.6E0	2.7E-4	2.5E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	TRIF-dependent toll-like receptor signaling pathway	RT		14	2.6E-4	3.0E0	8.1E-3	7.7E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of tumor necrosis factor-mediated signaling pathway	RT		14	6.0E-4	2.8E0	1.6E-2	1.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of necrotic cell death	RT		8	1.4E-3	3.9E0	3.3E-2	3.2E-2
Annotation Cluster 70		Enrichment Score: 3.64	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Inhibition of Cellular Proliferation by Gleevec	RT		20	6.9E-7	2.7E0	4.1E-5	3.1E-5
<input type="checkbox"/>	BIOCARTA	EGF Signaling Pathway	RT		22	1.1E-6	2.5E0	5.4E-5	4.1E-5
<input type="checkbox"/>	BIOCARTA	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling	RT		25	1.5E-6	2.4E0	6.3E-5	4.7E-5
<input type="checkbox"/>	BIOCARTA	PDGF Signaling Pathway	RT		22	3.1E-6	2.5E0	1.1E-4	8.6E-5
<input type="checkbox"/>	BIOCARTA	Bioactive Peptide Induced Signaling Pathway	RT		26	1.6E-5	2.1E0	3.3E-4	2.5E-4
<input type="checkbox"/>	BIOCARTA	TPO Signaling Pathway	RT		19	1.7E-5	2.5E0	3.3E-4	2.5E-4
<input type="checkbox"/>	BIOCARTA	Signaling of Hepatocyte Growth Factor Receptor	RT		25	1.7E-5	2.2E0	3.3E-4	2.5E-4
<input type="checkbox"/>	BIOCARTA	IL-2 Receptor Beta Chain in T cell Activation	RT		26	3.1E-5	2.1E0	5.4E-4	4.0E-4
<input type="checkbox"/>	BIOCARTA	IGF-1 Signaling Pathway	RT		17	3.7E-5	2.5E0	5.7E-4	4.3E-4
<input type="checkbox"/>	BIOCARTA	Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation	RT		18	4.0E-5	2.4E0	5.7E-4	4.3E-4
<input type="checkbox"/>	BIOCARTA	IL 2 signaling pathway	RT		17	9.5E-5	2.4E0	1.0E-3	7.7E-4
<input type="checkbox"/>	BIOCARTA	Integrin Signaling Pathway	RT		24	1.3E-4	2.0E0	1.3E-3	9.8E-4
<input type="checkbox"/>	BIOCARTA	Growth Hormone Signaling Pathway	RT		19	2.0E-4	2.2E0	1.8E-3	1.4E-3
<input type="checkbox"/>	BIOCARTA	Role of ERBB2 in Signal Transduction and Oncology	RT		17	2.2E-4	2.3E0	1.8E-3	1.4E-3
<input type="checkbox"/>	BIOCARTA	IL 6 signaling pathway	RT		16	2.2E-4	2.4E0	1.8E-3	1.4E-3
<input type="checkbox"/>	BIOCARTA	Insulin Signaling Pathway	RT		16	2.2E-4	2.4E0	1.8E-3	1.4E-3
<input type="checkbox"/>	BIOCARTA	Fc Epsilon Receptor I Signaling in Mast Cells	RT		23	1.2E-3	1.8E0	8.2E-3	6.1E-3

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	T Cell Receptor Signaling Pathway	RT		25	1.4E-3	1.8E0	9.1E-3	6.8E-3
<input type="checkbox"/>	BIOCARTA	fMLP induced chemokine gene expression in HMC-1 cells	RT		22	1.4E-3	1.9E0	9.1E-3	6.8E-3
<input type="checkbox"/>	BIOCARTA	Links between Pyk2 and Map Kinases	RT		18	1.5E-3	2.0E0	9.3E-3	7.0E-3
<input type="checkbox"/>	BIOCARTA	Nerve growth factor pathway (NGF)	RT		14	2.3E-3	2.2E0	1.3E-2	9.9E-3
<input type="checkbox"/>	BIOCARTA	BCR Signaling Pathway	RT		20	3.1E-3	1.8E0	1.5E-2	1.1E-2
<input type="checkbox"/>	BIOCARTA	EPO Signaling Pathway	RT		13	4.9E-3	2.1E0	2.2E-2	1.7E-2
<input type="checkbox"/>	BIOCARTA	Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia	RT		14	1.9E-2	1.8E0	6.6E-2	5.0E-2
<input type="checkbox"/>	BIOCARTA	IL 3 signaling pathway	RT		10	2.3E-2	2.1E0	7.5E-2	5.6E-2
<input type="checkbox"/>	BIOCARTA	Trka Receptor Signaling Pathway	RT		9	4.5E-2	2.0E0	1.2E-1	9.0E-2
<input type="checkbox"/>	BIOCARTA	Sprouty regulation of tyrosine kinase signals	RT		10	8.5E-2	1.7E0	2.1E-1	1.6E-1
Annotation Cluster 71		Enrichment Score: 3.53	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	ATP-dependent chromatin remodeling	RT		14	1.9E-5	3.6E0	7.8E-4	7.5E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase II distal enhancer sequence-specific DNA binding	RT		23	5.9E-4	2.1E0	8.1E-3	7.4E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	nucleosomal DNA binding	RT		17	2.3E-3	2.2E0	2.5E-2	2.3E-2
Annotation Cluster 72		Enrichment Score: 3.52	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Mini-chromosome maintenance, DNA-dependent ATPase	RT		9	3.5E-6	6.2E0	7.3E-5	6.7E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MCM	RT		8	1.0E-5	6.8E0	4.1E-4	4.0E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA replication initiation	RT		16	7.8E-5	3.0E0	2.8E-3	2.7E-3
<input type="checkbox"/>	SMART	MCM	RT		9	9.7E-5	4.0E0	1.2E-3	1.0E-3
<input type="checkbox"/>	INTERPRO	Mini-chromosome maintenance, conserved site	RT		6	5.7E-4	6.2E0	7.8E-3	7.2E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	MCM complex	RT		7	8.2E-4	4.9E0	9.8E-3	8.8E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA helicase activity	RT		12	8.4E-4	3.0E0	1.1E-2	9.6E-3
<input type="checkbox"/>	BIOCARTA	CDK Regulation of DNA Replication	RT		13	2.5E-3	2.3E0	1.3E-2	9.9E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA unwinding involved in DNA replication	RT		7	2.6E-3	4.1E0	5.7E-2	5.4E-2
<input type="checkbox"/>	INTERPRO	Nucleic acid-binding, OB-fold	RT		22	8.9E-3	1.8E0	8.6E-2	8.0E-2
Annotation Cluster 73		Enrichment Score: 3.48	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	U2 snRNP	RT		14	9.2E-7	4.4E0	3.5E-5	3.1E-5
<input type="checkbox"/>	GOTERM_CC_DIRECT	U4/U6 x U5 tri-snRNP complex	RT		15	1.1E-6	4.1E0	4.0E-5	3.6E-5
<input type="checkbox"/>	GOTERM_CC_DIRECT	U4 snRNP	RT		10	2.4E-6	5.8E0	6.9E-5	6.1E-5
<input type="checkbox"/>	GOTERM_CC_DIRECT	U1 snRNP	RT		12	3.2E-5	4.0E0	6.3E-4	5.6E-4
<input type="checkbox"/>	BIOCARTA	Spliceosomal Assembly	RT		13	4.8E-5	2.9E0	6.3E-4	4.7E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	small nuclear ribonucleoprotein complex	RT		11	6.1E-5	4.1E0	1.0E-3	9.1E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	U5 snRNP	RT		11	6.1E-5	4.1E0	1.0E-3	9.1E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	methylosome	RT		9	1.0E-4	4.8E0	1.5E-3	1.4E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	U1 snRNP binding	RT		7	1.3E-4	6.0E0	2.0E-3	1.8E-3
<input type="checkbox"/>	INTERPRO	Ribonucleoprotein LSM domain	RT		12	1.4E-4	3.5E0	2.1E-3	2.0E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	U2-type prespliceosome	RT		10	4.2E-4	3.7E0	5.6E-3	5.0E-3
<input type="checkbox"/>	INTERPRO	Like-Sm (LSM) domain	RT		12	6.0E-4	3.1E0	8.3E-3	7.6E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	spliceosomal snRNP assembly	RT		13	1.1E-3	2.8E0	2.8E-2	2.7E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	U12-type spliceosomal complex	RT		12	1.1E-3	2.9E0	1.3E-2	1.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear import	RT		9	5.8E-3	3.0E0	1.1E-1	1.0E-1
<input type="checkbox"/>	SMART	Sm	RT		12	5.8E-3	2.3E0	5.3E-2	4.7E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	pICln-Sm protein complex	RT		5	7.0E-3	5.3E0	6.0E-2	5.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone mRNA metabolic process	RT		7	8.4E-3	3.5E0	1.4E-1	1.4E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	SMN-Sm protein complex	RT		8	1.1E-2	3.0E0	8.7E-2	7.8E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	U7 snRNP	RT		5	1.4E-2	4.5E0	1.1E-1	9.5E-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"/>	GOTERM_CC_DIRECT	spliceosomal tri-snRNP complex	RT	<div><div></div><div></div></div>	4	3.0E-2	5.1E0	2.0E-1	1.8E-1
Annotation Cluster 74		Enrichment Score: 3.47	<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:Post-SET	RT	<div><div></div><div></div></div>	14	5.2E-9	6.0E0	3.1E-7	3.0E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Pre-SET	RT	<div><div></div><div></div></div>	6	1.1E-3	5.8E0	3.0E-2	2.9E-2
<input type="checkbox"/>	INTERPRO	Pre-SET domain	RT	<div><div></div><div></div></div>	6	1.7E-3	5.3E0	2.1E-2	2.0E-2
<input type="checkbox"/>	SMART	PreSET	RT	<div><div></div><div></div></div>	6	1.2E-2	3.5E0	9.7E-2	8.6E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K9 specific)	RT	<div><div></div><div></div></div>	4	3.6E-2	4.8E0	2.3E-1	2.0E-1
Annotation Cluster 75		Enrichment Score: 3.34	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase	RT	<div><div></div><div></div></div>	12	1.1E-7	5.7E0	2.7E-6	2.5E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	phosphoprotein phosphatase activity	RT	<div><div></div><div></div></div>	22	2.9E-6	2.9E0	6.8E-5	6.2E-5
<input type="checkbox"/>	SMART	PP2Ac	RT	<div><div></div><div></div></div>	12	9.7E-6	3.7E0	1.3E-4	1.2E-4
<input type="checkbox"/>	INTERPRO	Metallophosphoesterase domain	RT	<div><div></div><div></div></div>	13	7.2E-4	2.9E0	9.7E-3	9.0E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Manganese	RT	<div><div></div><div></div></div>	11	2.1E-2	2.2E0	4.0E-1	3.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Iron	RT	<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	RT	<div><div></div><div></div></div>	20	9.9E-1	6.8E-1	1.0E0	9.9E-1
Annotation Cluster 76		Enrichment Score: 3.28	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PI3K/PI4K	RT	<div><div></div><div></div></div>	16	1.6E-10	6.1E0	1.0E-8	1.0E-8
<input type="checkbox"/>	INTERPRO	Phosphatidylinositol 3-/4-kinase, catalytic domain	RT	<div><div></div><div></div></div>	16	2.5E-9	5.2E0	8.1E-8	7.5E-8
<input type="checkbox"/>	INTERPRO	Phosphatidylinositol 3/4-kinase, conserved site	RT	<div><div></div><div></div></div>	14	1.7E-8	5.4E0	4.8E-7	4.5E-7
<input type="checkbox"/>	SMART	PI3Kc	RT	<div><div></div><div></div></div>	15	9.7E-7	3.6E0	1.7E-5	1.5E-5
<input type="checkbox"/>	GOTERM_CC_DIRECT	phosphatidylinositol 3-kinase complex	RT	<div><div></div><div></div></div>	11	5.0E-6	5.0E0	1.2E-4	1.1E-4
<input type="checkbox"/>	INTERPRO	Phosphoinositide 3-kinase, accessory (PIK) domain	RT	<div><div></div><div></div></div>	9	1.5E-5	5.6E0	2.8E-4	2.6E-4
<input type="checkbox"/>	INTERPRO	Phosphatidylinositol 3-kinase C2 (PI3K C2) domain	RT	<div><div></div><div></div></div>	8	1.9E-5	6.2E0	3.5E-4	3.3E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	phosphatidylinositol-3-phosphate biosynthetic process	RT	<div><div></div><div></div></div>	21	6.2E-5	2.5E0	2.3E-3	2.2E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	1-phosphatidylinositol-3-kinase activity	RT	<div><div></div><div></div></div>	19	8.7E-5	2.6E0	1.5E-3	1.3E-3
<input type="checkbox"/>	SMART	PI3Ka	RT	<div><div></div><div></div></div>	9	9.7E-5	4.0E0	1.2E-3	1.0E-3
<input type="checkbox"/>	INTERPRO	Phosphatidylinositol 3-kinase Ras-binding (PI3K RBD) domain	RT	<div><div></div><div></div></div>	7	1.1E-4	6.2E0	1.7E-3	1.6E-3
<input type="checkbox"/>	INTERPRO	Phosphatidylinositol Kinase	RT	<div><div></div><div></div></div>	9	1.2E-4	4.6E0	1.9E-3	1.8E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	1-phosphatidylinositol-4-phosphate 3-kinase activity	RT	<div><div></div><div></div></div>	7	1.3E-4	6.0E0	2.0E-3	1.8E-3
<input type="checkbox"/>	SMART	PI3K_C2	RT	<div><div></div><div></div></div>	8	3.5E-4	4.0E0	4.1E-3	3.6E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	phosphatidylinositol 3-kinase activity	RT	<div><div></div><div></div></div>	5	3.4E-3	6.0E0	3.4E-2	3.1E-2
<input type="checkbox"/>	SMART	PI3K_rbd	RT	<div><div></div><div></div></div>	6	4.4E-3	4.0E0	4.0E-2	3.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	phosphatidylinositol biosynthetic process	RT	<div><div></div><div></div></div>	19	5.7E-3	1.9E0	1.1E-1	1.0E-1
<input type="checkbox"/>	INTERPRO	Phosphatidylinositol 3-kinase adaptor-binding (PI3K ABD) domain	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	SMART	PI3K_p85B	RT	<div><div></div><div></div></div>	3	1.5E-1	4.0E0	6.6E-1	5.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	Phosphatidylinositol signaling system	RT	<div><div></div><div></div></div>	21	4.0E-1	1.1E0	6.1E-1	4.0E-1
<input type="checkbox"/>	KEGG_PATHWAY	Carbohydrate digestion and absorption	RT	<div><div></div><div></div></div>	10	4.0E-1	1.3E0	6.1E-1	4.0E-1
<input type="checkbox"/>	KEGG_PATHWAY	Inositol phosphate metabolism	RT	<div><div></div><div></div></div>	13	7.2E-1	9.6E-1	1.0E0	7.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PX	RT	<div><div></div><div></div></div>	4	9.8E-1	5.7E-1	1.0E0	9.8E-1
<input type="checkbox"/>	INTERPRO	Phox homologous domain	RT	<div><div></div><div></div></div>	5	9.8E-1	5.6E-1	1.0E0	9.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	phosphatidylinositol binding	RT	<div><div></div><div></div></div>	8	9.9E-1	5.6E-1	1.0E0	9.9E-1
<input type="checkbox"/>	SMART	PX	RT	<div><div></div><div></div></div>	4	1.0E0	3.6E-1	1.0E0	1.0E0
Annotation Cluster 77		Enrichment Score: 3.24	<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	positive regulation of telomere maintenance via telomerase	RT	<div><div></div><div></div></div>	22	1.1E-9	4.1E0	1.1E-7	1.1E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of protein localization to Cajal body	RT	<div><div></div><div></div></div>	8	2.6E-5	5.9E0	1.1E-3	1.0E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	chaperonin-containing T-complex	RT	<div><div></div><div></div></div>	8	6.4E-5	5.6E0	1.0E-3	9.1E-4

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	zona pellucida receptor complex	RT		8	6.4E-5	5.6E0	1.0E-3	9.1E-4
<input type="checkbox"/>	INTERPRO	Chaperonin TCP-1, conserved site	RT		8	7.5E-5	5.5E0	1.3E-3	1.2E-3
<input type="checkbox"/>	INTERPRO	TCP-1-like chaperonin intermediate domain	RT		9	1.2E-4	4.6E0	1.9E-3	1.8E-3
<input type="checkbox"/>	INTERPRO	Chaperone tailless complex polypeptide 1 (TCP-1)	RT		9	1.2E-4	4.6E0	1.9E-3	1.8E-3
<input type="checkbox"/>	INTERPRO	Chaperonin Cpn60/TCP-1	RT		10	2.8E-4	3.9E0	4.2E-3	3.9E-3
<input type="checkbox"/>	INTERPRO	GroEL-like apical domain	RT		10	2.8E-4	3.9E0	4.2E-3	3.9E-3
<input type="checkbox"/>	INTERPRO	GroEL-like equatorial domain	RT		9	1.0E-3	3.7E0	1.3E-2	1.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of establishment of protein localization to telomere	RT		7	1.2E-3	4.6E0	3.0E-2	2.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of telomerase RNA localization to Cajal body	RT		8	7.1E-3	3.2E0	1.3E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	scaRNA localization to Cajal body	RT		3	1.3E-1	4.4E0	8.3E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	toxin transport	RT		10	1.4E-1	1.6E0	8.4E-1	8.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	binding of sperm to zona pellucida	RT		9	2.3E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein binding involved in protein folding	RT		4	4.2E-1	1.7E0	1.0E0	9.1E-1
Annotation Cluster 78		Enrichment Score: 3.2	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	CXCR4 Signaling Pathway	RT		19	1.7E-5	2.5E0	3.3E-4	2.5E-4
<input type="checkbox"/>	BIOCARTA	CCR3 signaling in Eosinophils	RT		16	1.0E-3	2.2E0	7.2E-3	5.4E-3
<input type="checkbox"/>	BIOCARTA	Aspirin Blocks Signaling Pathway Involved in Platelet Activation	RT		13	1.5E-2	1.9E0	5.4E-2	4.0E-2
Annotation Cluster 79		Enrichment Score: 3.1	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Heat shock protein 70, conserved site	RT		12	1.4E-6	5.0E0	3.0E-5	2.8E-5
<input type="checkbox"/>	INTERPRO	Heat shock protein 70 family	RT		12	1.4E-6	5.0E0	3.0E-5	2.8E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein refolding	RT		8	7.1E-3	3.2E0	1.3E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	response to unfolded protein	RT		13	4.1E-2	1.8E0	4.0E-1	3.9E-1
<input type="checkbox"/>	KEGG_PATHWAY	Antigen processing and presentation	RT		15	6.0E-1	1.0E0	8.7E-1	6.0E-1
Annotation Cluster 80		Enrichment Score: 3.09	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	phosphatidylinositol-mediated signaling	RT		40	6.4E-7	2.2E0	4.4E-5	4.2E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	phosphatidylinositol-3-phosphate biosynthetic process	RT		21	6.2E-5	2.5E0	2.3E-3	2.2E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	1-phosphatidylinositol-3-kinase activity	RT		19	8.7E-5	2.6E0	1.5E-3	1.3E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	phosphatidylinositol phosphorylation	RT		30	5.9E-4	1.9E0	1.6E-2	1.6E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	phosphatidylinositol-4,5-bisphosphate 3-kinase activity	RT		22	7.7E-4	2.1E0	9.8E-3	8.9E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of phosphatidylinositol 3-kinase signaling	RT		25	1.8E-3	1.9E0	4.1E-2	3.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	phosphatidylinositol biosynthetic process	RT		19	5.7E-3	1.9E0	1.1E-1	1.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	Ras guanyl-nucleotide exchange factor activity	RT		30	1.3E-2	1.6E0	1.1E-1	9.9E-2
<input type="checkbox"/>	KEGG_PATHWAY	Inositol phosphate metabolism	RT		13	7.2E-1	9.6E-1	1.0E0	7.2E-1
Annotation Cluster 81		Enrichment Score: 3.05	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone deacetylase activity	RT		22	1.3E-7	3.4E0	3.8E-6	3.5E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone deacetylation	RT		22	5.1E-6	2.8E0	2.7E-4	2.5E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Histone deacetylase	RT		9	7.3E-6	6.1E0	3.1E-4	3.0E-4
<input type="checkbox"/>	INTERPRO	Histone deacetylase domain	RT		10	1.0E-5	5.2E0	2.0E-4	1.8E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	NAD-dependent histone deacetylase activity (H3-K14 specific)	RT		10	1.4E-5	5.0E0	2.7E-4	2.5E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein deacetylase activity	RT		9	2.0E-5	5.4E0	3.5E-4	3.2E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H3 deacetylation	RT		13	3.4E-5	3.7E0	1.3E-3	1.3E-3
<input type="checkbox"/>	INTERPRO	Histone deacetylase superfamily	RT		10	6.7E-5	4.4E0	1.2E-3	1.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein deacetylation	RT		8	2.9E-4	4.7E0	8.7E-3	8.3E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	histone deacetylase complex	RT		15	6.7E-4	2.6E0	8.1E-3	7.3E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H4 deacetylation	RT		6	9.4E-3	3.9E0	1.5E-1	1.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptidyl-lysine deacetylation	RT		5	1.8E-2	4.2E0	2.4E-1	2.3E-1

















































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of gene expression, epigenetic	RT		7	2.0E-2	3.0E0	2.5E-1	2.4E-1
<input type="checkbox"/>	INTERPRO	Histone deacetylase class II, eukaryotic	RT		4	3.2E-2	5.0E0	2.3E-1	2.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	histone deacetylase class II, eukaryotic type	RT		4	3.5E-2	4.8E0	4.6E-1	4.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of myotube differentiation	RT		7	4.0E-2	2.6E0	4.0E-1	3.8E-1
<input type="checkbox"/>	COG_ONTOLOGY	Chromatin structure and dynamics / Secondary metabolites biosynthesis, transport, and catabolism	RT		7	4.2E-2	2.3E0	4.4E-1	4.4E-1
<input type="checkbox"/>	INTERPRO	Histone deacetylase	RT		3	1.2E-1	4.6E0	6.2E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	Histone deacetylase, glutamine rich N-terminal domain	RT		3	1.2E-1	4.6E0	6.2E-1	5.8E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	histone deacetylase class I, eukaryotic type	RT		3	1.3E-1	4.5E0	9.1E-1	9.1E-1
Annotation Cluster 82		Enrichment Score: 2.99	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	14-3-3 protein	RT		7	1.1E-4	6.2E0	1.7E-3	1.6E-3
<input type="checkbox"/>	INTERPRO	14-3-3 protein, conserved site	RT		7	1.1E-4	6.2E0	1.7E-3	1.6E-3
<input type="checkbox"/>	INTERPRO	14-3-3 domain	RT		7	1.1E-4	6.2E0	1.7E-3	1.6E-3
<input type="checkbox"/>	PIR_SUPERFAMILY	14-3-3 protein	RT		7	1.2E-4	6.0E0	1.0E-2	1.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Interaction with phosphoserine on interacting protein	RT		7	2.1E-4	6.0E0	6.8E-3	6.6E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	RT		14	6.0E-4	2.8E0	1.6E-2	1.6E-2
<input type="checkbox"/>	SMART	14_3_3	RT		7	1.3E-3	4.0E0	1.3E-2	1.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein targeting	RT		10	2.0E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	membrane organization	RT		8	2.9E-1	1.5E0	1.0E0	9.6E-1
Annotation Cluster 83		Enrichment Score: 2.96	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Actin-binding	RT		13	3.9E-6	4.4E0	1.8E-4	1.8E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 4	RT		13	7.9E-6	4.2E0	3.3E-4	3.1E-4
<input type="checkbox"/>	INTERPRO	Actinin-type, actin-binding, conserved site	RT		14	1.1E-5	3.8E0	2.1E-4	2.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 3	RT		13	1.5E-5	4.0E0	5.9E-4	5.7E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CH 1	RT		14	3.8E-5	3.5E0	1.4E-3	1.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CH 2	RT		14	3.8E-5	3.5E0	1.4E-3	1.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 1	RT		13	1.3E-4	3.4E0	4.3E-3	4.2E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 2	RT		13	1.3E-4	3.4E0	4.3E-3	4.2E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 6	RT		9	1.4E-4	4.7E0	4.6E-3	4.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 7	RT		9	1.4E-4	4.7E0	4.6E-3	4.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 8	RT		9	1.4E-4	4.7E0	4.6E-3	4.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 9	RT		9	1.4E-4	4.7E0	4.6E-3	4.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 5	RT		9	2.8E-4	4.4E0	8.8E-3	8.5E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 10	RT		8	5.9E-4	4.5E0	1.7E-2	1.6E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 11	RT		8	5.9E-4	4.5E0	1.7E-2	1.6E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 12	RT		8	5.9E-4	4.5E0	1.7E-2	1.6E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 13	RT		8	5.9E-4	4.5E0	1.7E-2	1.6E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 14	RT		8	5.9E-4	4.5E0	1.7E-2	1.6E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 15	RT		8	5.9E-4	4.5E0	1.7E-2	1.6E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 16	RT		8	5.9E-4	4.5E0	1.7E-2	1.6E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 17	RT		8	5.9E-4	4.5E0	1.7E-2	1.6E-2
<input type="checkbox"/>	INTERPRO	Spectrin repeat	RT		12	9.2E-4	3.0E0	1.2E-2	1.1E-2
<input type="checkbox"/>	INTERPRO	Spectrin/alpha-actinin	RT		13	1.1E-3	2.8E0	1.4E-2	1.3E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 19	RT		6	2.6E-3	5.1E0	6.6E-2	6.3E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 20	RT		6	2.6E-3	5.1E0	6.6E-2	6.3E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 18	RT		6	5.1E-3	4.5E0	1.3E-1	1.2E-1
















































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	EF-hand, Ca insensitive	RT		5	7.7E-3	5.2E0	7.5E-2	7.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 21	RT		5	1.1E-2	4.9E0	2.3E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	Calponin homology domain	RT		20	3.0E-2	1.6E0	2.3E-1	2.1E-1
<input type="checkbox"/>	SMART	SPEC	RT		13	3.6E-2	1.8E0	2.4E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 22	RT		4	4.5E-2	4.5E0	7.8E-1	7.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	spectrin	RT		4	1.6E-1	2.8E0	6.7E-1	6.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 23	RT		3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	CH	RT		20	2.6E-1	1.2E0	9.7E-1	8.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	actin filament capping	RT		4	3.8E-1	1.8E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Actin capping	RT		4	5.4E-1	1.4E0	1.0E0	8.0E-1
Annotation Cluster 84		Enrichment Score: 2.95	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	U1 snRNP binding	RT		7	1.3E-4	6.0E0	2.0E-3	1.8E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	commitment complex	RT		6	1.5E-3	5.4E0	1.7E-2	1.5E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	prespliceosome	RT		5	7.0E-3	5.3E0	6.0E-2	5.3E-2
Annotation Cluster 85		Enrichment Score: 2.95	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK)	RT		21	4.2E-5	2.3E0	5.7E-4	4.3E-4
<input type="checkbox"/>	BIOCARTA	Signal Dependent Regulation of Myogenesis by Corepressor MITR	RT		9	6.9E-4	3.1E0	5.2E-3	3.9E-3
<input type="checkbox"/>	BIOCARTA	Regulation of PGC-1a	RT		13	4.9E-2	1.7E0	1.3E-1	9.7E-2
Annotation Cluster 86		Enrichment Score: 2.9	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Chromo 2	RT		8	4.0E-5	6.1E0	1.5E-3	1.4E-3
<input type="checkbox"/>	INTERPRO	Chromo domain/shadow	RT		16	7.1E-5	3.0E0	1.2E-3	1.1E-3
<input type="checkbox"/>	INTERPRO	Chromo domain-like	RT		15	2.0E-4	2.9E0	3.1E-3	2.9E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Chromo 1	RT		8	1.1E-3	4.2E0	3.0E-2	2.9E-2
<input type="checkbox"/>	INTERPRO	Chromo domain	RT		11	5.1E-3	2.6E0	5.5E-2	5.1E-2
<input type="checkbox"/>	SMART	CHROMO	RT		16	7.5E-3	2.0E0	6.5E-2	5.8E-2
<input type="checkbox"/>	INTERPRO	Chromo domain, conserved site	RT		6	2.1E-1	1.9E0	9.7E-1	9.0E-1
Annotation Cluster 87		Enrichment Score: 2.74	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Chemokine receptor family	RT		13	2.9E-7	5.0E0	6.9E-6	6.3E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	C-C chemokine receptor activity	RT		10	1.4E-5	5.0E0	2.7E-4	2.5E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	chemokine receptor activity	RT		11	1.1E-4	3.9E0	1.7E-3	1.5E-3
<input type="checkbox"/>	BBID	14.chemokine_receptor-ligand	RT		8	1.9E-2	2.3E0	7.0E-1	7.0E-1
<input type="checkbox"/>	BBID	16.Chemokines-rec-T-cells	RT		7	8.3E-2	2.0E0	9.9E-1	9.9E-1
<input type="checkbox"/>	BBID	15.T-cell_polarization-chemokine_receptors	RT		10	1.6E-1	1.5E0	9.9E-1	9.9E-1
<input type="checkbox"/>	BIOCARTA	Selective expression of chemokine receptors during T-cell polarization	RT		10	5.7E-1	1.1E0	8.8E-1	6.6E-1
Annotation Cluster 88		Enrichment Score: 2.74	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	gene expression	RT		28	6.9E-10	3.5E0	7.9E-8	7.6E-8
<input type="checkbox"/>	GOTERM_CC_DIRECT	DNA-directed RNA polymerase II, core complex	RT		12	1.6E-5	4.2E0	3.3E-4	2.9E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of viral transcription	RT		16	1.8E-5	3.3E0	7.6E-4	7.2E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase II activity	RT		9	2.0E-5	5.4E0	3.5E-4	3.2E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription initiation from RNA polymerase I promoter	RT		15	4.9E-4	2.7E0	1.4E-2	1.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	7-methylguanosine mRNA capping	RT		15	4.9E-4	2.7E0	1.4E-2	1.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	termination of RNA polymerase I transcription	RT		14	8.8E-4	2.7E0	2.3E-2	2.2E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase I activity	RT		8	1.3E-3	4.0E0	1.5E-2	1.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription elongation from RNA polymerase II promoter	RT		27	1.5E-3	1.9E0	3.6E-2	3.5E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	DNA-directed RNA polymerase I complex	RT		8	1.7E-3	3.9E0	1.8E-2	1.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription elongation from RNA polymerase I promoter	RT		13	2.2E-3	2.6E0	5.0E-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"/>	UP_KEYWORDS	DNA-directed RNA polymerase	RT	<div><div></div><div></div></div>	14	2.6E-3	2.5E0	1.4E-2	1.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of type I interferon production	RT	<div><div></div><div></div></div>	18	3.1E-3	2.1E0	6.7E-2	6.4E-2
<input type="checkbox"/>	KEGG_PATHWAY	RNA polymerase	RT	<div><div></div><div></div></div>	14	3.7E-3	2.3E0	7.5E-3	3.7E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of gene expression, epigenetic	RT	<div><div></div><div></div></div>	20	5.3E-3	1.9E0	9.9E-2	9.5E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-directed RNA polymerase activity	RT	<div><div></div><div></div></div>	14	6.8E-3	2.2E0	6.3E-2	5.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription initiation from RNA polymerase II promoter	RT	<div><div></div><div></div></div>	39	6.8E-3	1.5E0	1.2E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription from RNA polymerase III promoter	RT	<div><div></div><div></div></div>	12	1.6E-2	2.2E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	snRNA transcription from RNA polymerase II promoter	RT	<div><div></div><div></div></div>	20	2.1E-2	1.7E0	2.6E-1	2.4E-1
<input type="checkbox"/>	KEGG_PATHWAY	Pyrimidine metabolism	RT	<div><div></div><div></div></div>	26	9.0E-2	1.4E0	1.5E-1	9.0E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	DNA-directed RNA polymerase III complex	RT	<div><div></div><div></div></div>	6	1.7E-1	2.0E0	7.0E-1	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	gene silencing by RNA	RT	<div><div></div><div></div></div>	24	1.7E-1	1.3E0	9.5E-1	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase III activity	RT	<div><div></div><div></div></div>	6	1.7E-1	2.0E0	7.3E-1	6.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Cytosolic DNA-sensing pathway	RT	<div><div></div><div></div></div>	16	2.2E-1	1.3E0	3.5E-1	2.2E-1
Annotation Cluster 89		Enrichment Score: 2.74	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase 1	RT	<div><div></div><div></div></div>	11	6.8E-6	5.0E0	2.9E-4	2.8E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase 2	RT	<div><div></div><div></div></div>	11	6.8E-6	5.0E0	2.9E-4	2.8E-4
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, non-receptor Jak/Tyk2	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	tyrosine-protein kinase, Jak/Tyk2 type	RT	<div><div></div><div></div></div>	4	1.6E-2	6.0E0	2.5E-1	2.5E-1
<input type="checkbox"/>	INTERPRO	Ribosomal protein S6 kinase II	RT	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	3.8E-1	3.5E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	ribosomal protein S6 kinase II	RT	<div><div></div><div></div></div>	4	6.1E-2	4.0E0	6.0E-1	6.0E-1
Annotation Cluster 90		Enrichment Score: 2.71	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Chromo 2	RT	<div><div></div><div></div></div>	8	4.0E-5	6.1E0	1.5E-3	1.4E-3
<input type="checkbox"/>	INTERPRO	BRK domain	RT	<div><div></div><div></div></div>	6	5.7E-4	6.2E0	7.8E-3	7.2E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Chromo 1	RT	<div><div></div><div></div></div>	8	1.1E-3	4.2E0	3.0E-2	2.9E-2
<input type="checkbox"/>	SMART	BRK	RT	<div><div></div><div></div></div>	6	4.4E-3	4.0E0	4.0E-2	3.6E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	hydrolase activity, acting on acid anhydrides	RT	<div><div></div><div></div></div>	3	2.6E-1	3.0E0	9.9E-1	9.0E-1
Annotation Cluster 91		Enrichment Score: 2.7	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	proteasome regulatory particle, base subcomplex	RT	<div><div></div><div></div></div>	9	1.0E-4	4.8E0	1.5E-3	1.4E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein catabolic process	RT	<div><div></div><div></div></div>	18	1.7E-4	2.6E0	5.7E-3	5.5E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	nuclear proteasome complex	RT	<div><div></div><div></div></div>	7	3.2E-4	5.6E0	4.4E-3	3.9E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	proteasome accessory complex	RT	<div><div></div><div></div></div>	10	4.2E-4	3.7E0	5.6E-3	5.0E-3
<input type="checkbox"/>	INTERPRO	ATPase, AAA-type, conserved site	RT	<div><div></div><div></div></div>	13	4.8E-4	3.0E0	7.1E-3	6.5E-3
<input type="checkbox"/>	INTERPRO	26S proteasome subunit P45	RT	<div><div></div><div></div></div>	6	5.7E-4	6.2E0	7.8E-3	7.2E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	proteasome-activating ATPase activity	RT	<div><div></div><div></div></div>	6	6.8E-4	6.0E0	9.0E-3	8.2E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	TBP-class protein binding	RT	<div><div></div><div></div></div>	11	1.0E-3	3.1E0	1.2E-2	1.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of RNA polymerase II transcriptional preinitiation complex assembly	RT	<div><div></div><div></div></div>	7	1.2E-3	4.6E0	3.0E-2	2.9E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosolic proteasome complex	RT	<div><div></div><div></div></div>	7	1.8E-3	4.4E0	1.9E-2	1.7E-2
<input type="checkbox"/>	INTERPRO	ATPase, AAA-type, core	RT	<div><div></div><div></div></div>	17	5.1E-3	2.1E0	5.5E-2	5.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of proteasomal protein catabolic process	RT	<div><div></div><div></div></div>	8	1.1E-2	3.0E0	1.7E-1	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	ER-associated ubiquitin-dependent protein catabolic process	RT	<div><div></div><div></div></div>	18	1.8E-2	1.8E0	2.4E-1	2.3E-1
<input type="checkbox"/>	INTERPRO	AAA+ ATPase domain	RT	<div><div></div><div></div></div>	31	4.2E-2	1.4E0	3.0E-1	2.8E-1
<input type="checkbox"/>	SMART	AAA	RT	<div><div></div><div></div></div>	31	7.9E-1	9.2E-1	1.0E0	8.9E-1
Annotation Cluster 92		Enrichment Score: 2.64	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	G-protein beta WD-40 repeat	RT	<div><div></div><div></div></div>	33	1.2E-5	2.2E0	2.3E-4	2.1E-4
<input type="checkbox"/>	INTERPRO	WD40 repeat, conserved site	RT	<div><div></div><div></div></div>	47	1.1E-4	1.8E0	1.7E-3	1.6E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 7	RT	<div><div></div><div></div></div>	41	1.1E-4	1.8E0	3.8E-3	3.7E-3
















































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	repeat:WD 5	RT	<div><div></div><div></div></div>	55	5.5E-4	1.6E0	1.6E-2	1.6E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 4	RT	<div><div></div><div></div></div>	58	6.4E-4	1.5E0	1.8E-2	1.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 6	RT	<div><div></div><div></div></div>	47	7.0E-4	1.6E0	2.0E-2	1.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 3	RT	<div><div></div><div></div></div>	59	1.4E-3	1.5E0	3.9E-2	3.7E-2
<input type="checkbox"/>	UP_KEYWORDS	WD repeat	RT	<div><div></div><div></div></div>	60	2.1E-3	1.5E0	1.2E-2	9.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 1	RT	<div><div></div><div></div></div>	59	3.2E-3	1.4E0	7.9E-2	7.7E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 2	RT	<div><div></div><div></div></div>	59	3.2E-3	1.4E0	7.9E-2	7.7E-2
<input type="checkbox"/>	INTERPRO	WD40 repeat	RT	<div><div></div><div></div></div>	57	2.3E-2	1.3E0	1.7E-1	1.6E-1
<input type="checkbox"/>	INTERPRO	WD40-repeat-containing domain	RT	<div><div></div><div></div></div>	63	3.1E-2	1.3E0	2.3E-1	2.1E-1
<input type="checkbox"/>	INTERPRO	WD40/YVTN repeat-like-containing domain	RT	<div><div></div><div></div></div>	62	1.4E-1	1.2E0	7.0E-1	6.5E-1
<input type="checkbox"/>	SMART	WD40	RT	<div><div></div><div></div></div>	57	9.4E-1	8.6E-1	1.0E0	9.4E-1
Annotation Cluster 93		Enrichment Score: 2.61	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:Fork-head	RT	<div><div></div><div></div></div>	19	1.5E-4	2.6E0	5.0E-3	4.9E-3
<input type="checkbox"/>	INTERPRO	Transcription factor, fork head	RT	<div><div></div><div></div></div>	19	3.8E-4	2.4E0	5.6E-3	5.2E-3
<input type="checkbox"/>	INTERPRO	Transcription factor, fork head, conserved site	RT	<div><div></div><div></div></div>	12	1.5E-2	2.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	SMART	FH	RT	<div><div></div><div></div></div>	19	4.1E-2	1.6E0	2.6E-1	2.3E-1
Annotation Cluster 94		Enrichment Score: 2.53	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Protein phosphatase	RT	<div><div></div><div></div></div>	53	3.1E-12	2.7E0	3.6E-11	2.9E-11
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein tyrosine/serine/threonine phosphatase activity	RT	<div><div></div><div></div></div>	17	1.4E-4	2.7E0	2.1E-3	1.9E-3
<input type="checkbox"/>	INTERPRO	Dual specificity phosphatase, catalytic domain	RT	<div><div></div><div></div></div>	18	2.0E-4	2.6E0	3.0E-3	2.8E-3
<input type="checkbox"/>	INTERPRO	Dual specificity phosphatase, subgroup, catalytic domain	RT	<div><div></div><div></div></div>	15	8.7E-4	2.6E0	1.1E-2	1.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Tyrosine-protein phosphatase	RT	<div><div></div><div></div></div>	17	1.8E-2	1.8E0	3.5E-1	3.4E-1
<input type="checkbox"/>	INTERPRO	Dual specificity phosphatase	RT	<div><div></div><div></div></div>	11	2.0E-2	2.2E0	1.5E-1	1.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein tyrosine phosphatase activity	RT	<div><div></div><div></div></div>	26	2.2E-2	1.6E0	1.6E-1	1.4E-1
<input type="checkbox"/>	INTERPRO	Protein-tyrosine/Dual specificity phosphatase	RT	<div><div></div><div></div></div>	21	3.4E-2	1.6E0	2.4E-1	2.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptidyl-tyrosine dephosphorylation	RT	<div><div></div><div></div></div>	25	3.8E-2	1.5E0	3.9E-1	3.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Phosphocysteine intermediate	RT	<div><div></div><div></div></div>	20	4.2E-2	1.6E0	7.5E-1	7.2E-1
<input type="checkbox"/>	SMART	DSPc	RT	<div><div></div><div></div></div>	15	4.2E-2	1.7E0	2.7E-1	2.4E-1
<input type="checkbox"/>	INTERPRO	Protein-tyrosine phosphatase, active site	RT	<div><div></div><div></div></div>	19	5.6E-2	1.5E0	3.8E-1	3.5E-1
<input type="checkbox"/>	INTERPRO	Protein-tyrosine phosphatase, catalytic	RT	<div><div></div><div></div></div>	16	7.3E-2	1.6E0	4.1E-1	3.8E-1
<input type="checkbox"/>	SMART	PTPc motif	RT	<div><div></div><div></div></div>	16	6.2E-1	1.0E0	1.0E0	8.9E-1
Annotation Cluster 95		Enrichment Score: 2.52	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Ribonucleoprotein	RT	<div><div></div><div></div></div>	84	1.2E-9	1.9E0	1.1E-8	8.6E-9
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosolic small ribosomal subunit	RT	<div><div></div><div></div></div>	18	6.7E-4	2.4E0	8.1E-3	7.3E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	ribosome	RT	<div><div></div><div></div></div>	41	3.2E-3	1.6E0	3.2E-2	2.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	SRP-dependent cotranslational protein targeting to membrane	RT	<div><div></div><div></div></div>	27	5.9E-3	1.7E0	1.1E-1	1.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	translational initiation	RT	<div><div></div><div></div></div>	36	6.4E-3	1.6E0	1.2E-1	1.1E-1
<input type="checkbox"/>	KEGG_PATHWAY	Ribosome	RT	<div><div></div><div></div></div>	39	6.7E-3	1.5E0	1.3E-2	6.7E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	RT	<div><div></div><div></div></div>	32	7.3E-3	1.6E0	1.3E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	rRNA processing	RT	<div><div></div><div></div></div>	51	8.8E-3	1.4E0	1.5E-1	1.4E-1
<input type="checkbox"/>	UP_KEYWORDS	Ribosomal protein	RT	<div><div></div><div></div></div>	40	1.0E-2	1.5E0	4.8E-2	3.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	viral transcription	RT	<div><div></div><div></div></div>	29	1.8E-2	1.5E0	2.4E-1	2.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	translation	RT	<div><div></div><div></div></div>	48	2.6E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	structural constituent of ribosome	RT	<div><div></div><div></div></div>	42	2.7E-1	1.1E0	1.0E0	9.1E-1
Annotation Cluster 96		Enrichment Score: 2.51	<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	response to endoplasmic reticulum stress	RT	<div><div></div><div></div></div>	30	5.5E-6	2.4E0	2.8E-4	2.7E-4

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Thioredoxin 1	RT	<div><div></div><div></div></div>	9	7.3E-6	6.1E0	3.1E-4	3.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Thioredoxin 2	RT	<div><div></div><div></div></div>	9	7.3E-6	6.1E0	3.1E-4	3.0E-4
<input type="checkbox"/>	INTERPRO	Thioredoxin, conserved site	RT	<div><div></div><div></div></div>	12	9.0E-6	4.4E0	1.8E-4	1.6E-4
<input type="checkbox"/>	INTERPRO	Thioredoxin domain	RT	<div><div></div><div></div></div>	19	2.4E-5	2.9E0	4.4E-4	4.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Contributes to redox potential value	RT	<div><div></div><div></div></div>	6	1.1E-3	5.8E0	3.0E-2	2.9E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein disulfide isomerase activity	RT	<div><div></div><div></div></div>	11	1.6E-3	3.0E0	1.7E-2	1.6E-2
<input type="checkbox"/>	INTERPRO	Disulphide isomerase	RT	<div><div></div><div></div></div>	5	2.9E-3	6.2E0	3.4E-2	3.1E-2
<input type="checkbox"/>	UP_KEYWORDS	Redox-active center	RT	<div><div></div><div></div></div>	16	3.2E-3	2.2E0	1.7E-2	1.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell redox homeostasis	RT	<div><div></div><div></div></div>	24	3.3E-3	1.8E0	6.9E-2	6.6E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	cell	RT	<div><div></div><div></div></div>	26	1.1E-2	1.7E0	8.8E-2	7.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Lowers pKa of C-terminal Cys of first active site	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Lowers pKa of C-terminal Cys of second active site	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	Protein disulphide isomerase	RT	<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	RT	<div><div></div><div></div></div>	4	2.5E-2	5.4E0	4.6E-1	4.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Prevents secretion from ER	RT	<div><div></div><div></div></div>	13	1.8E-1	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	disulfide oxidoreductase activity	RT	<div><div></div><div></div></div>	3	2.6E-1	3.0E0	9.9E-1	9.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	isomerase activity	RT	<div><div></div><div></div></div>	6	2.7E-1	1.7E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Thioredoxin-like fold	RT	<div><div></div><div></div></div>	24	3.5E-1	1.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	endoplasmic reticulum lumen	RT	<div><div></div><div></div></div>	16	1.0E0	5.3E-1	1.0E0	1.0E0
Annotation Cluster 97		Enrichment Score: 2.48	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT	<div><div></div><div></div></div>	29	1.0E-6	2.6E0	2.4E-5	2.2E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	ATP-dependent RNA helicase activity	RT	<div><div></div><div></div></div>	27	6.9E-6	2.5E0	1.5E-4	1.4E-4
<input type="checkbox"/>	INTERPRO	RNA helicase, ATP-dependent, DEAD-box, conserved site	RT	<div><div></div><div></div></div>	10	2.2E-2	2.3E0	1.6E-1	1.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	RNA secondary structure unwinding	RT	<div><div></div><div></div></div>	14	2.6E-2	1.9E0	3.1E-1	2.9E-1
<input type="checkbox"/>	INTERPRO	RNA helicase, DEAD-box type, Q motif	RT	<div><div></div><div></div></div>	11	6.4E-2	1.8E0	3.9E-1	3.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Q motif	RT	<div><div></div><div></div></div>	10	1.2E-1	1.7E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:DEAD box	RT	<div><div></div><div></div></div>	9	1.5E-1	1.7E0	1.0E0	9.7E-1
Annotation Cluster 98		Enrichment Score: 2.34	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	E2F1 Destruction Pathway	RT	<div><div></div><div></div></div>	9	2.5E-3	2.8E0	1.3E-2	9.9E-3
<input type="checkbox"/>	BIOCARTA	Cyclin E Destruction Pathway	RT	<div><div></div><div></div></div>	8	6.3E-3	2.8E0	2.6E-2	1.9E-2
<input type="checkbox"/>	BIOCARTA	Regulation of p27 Phosphorylation during Cell Cycle Progression	RT	<div><div></div><div></div></div>	10	6.3E-3	2.4E0	2.6E-2	1.9E-2
Annotation Cluster 99		Enrichment Score: 2.32	<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	Nucleosome core	RT	<div><div></div><div></div></div>	30	1.4E-5	2.3E0	8.7E-5	7.0E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	chromatin silencing	RT	<div><div></div><div></div></div>	15	1.4E-2	2.0E0	2.0E-1	1.9E-1
<input type="checkbox"/>	INTERPRO	Histone H2A	RT	<div><div></div><div></div></div>	10	1.7E-2	2.4E0	1.3E-1	1.2E-1
<input type="checkbox"/>	SMART	H2A	RT	<div><div></div><div></div></div>	10	1.7E-1	1.6E0	7.0E-1	6.2E-1
Annotation Cluster 100		Enrichment Score: 2.27	<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	neuropeptide binding	RT	<div><div></div><div></div></div>	14	1.9E-6	4.2E0	4.7E-5	4.3E-5
<input type="checkbox"/>	INTERPRO	Somatostatin receptor family	RT	<div><div></div><div></div></div>	5	2.9E-3	6.2E0	3.4E-2	3.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular response to glucocorticoid stimulus	RT	<div><div></div><div></div></div>	10	3.1E-3	3.0E0	6.6E-2	6.3E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	somatostatin receptor activity	RT	<div><div></div><div></div></div>	5	3.4E-3	6.0E0	3.4E-2	3.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	somatostatin signaling pathway	RT	<div><div></div><div></div></div>	5	3.5E-3	5.9E0	7.1E-2	6.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	cerebellum development	RT	<div><div></div><div></div></div>	6	7.7E-1	9.6E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	response to starvation	RT	<div><div></div><div></div></div>	5	8.6E-1	8.5E-1	1.0E0	9.6E-1
Annotation Cluster 101		Enrichment Score: 2.24	<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:SH2	RT	<div><div></div><div></div></div>	30	7.8E-5	2.1E0	2.8E-3	2.7E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH3	RT	<div><div></div><div></div></div>	45	1.8E-4	1.8E0	6.0E-3	5.8E-3

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	SH3 domain	RT		47	4.2E-3	1.5E0	2.2E-2	1.7E-2
<input type="checkbox"/>	SMART	SH2	RT		36	2.2E-2	1.4E0	1.6E-1	1.4E-1
<input type="checkbox"/>	INTERPRO	Src homology-3 domain	RT		47	3.1E-2	1.3E0	2.3E-1	2.1E-1
<input type="checkbox"/>	SMART	SH3	RT		46	8.5E-1	9.0E-1	1.0E0	8.9E-1
Annotation Cluster 102		Enrichment Score: 2.23	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	error-prone translesion synthesis	RT		14	8.7E-7	4.4E0	5.7E-5	5.4E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA gap filling	RT		15	5.3E-6	3.7E0	2.7E-4	2.6E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	single-stranded DNA-dependent ATPase activity	RT		7	2.5E-3	4.2E0	2.6E-2	2.4E-2
<input type="checkbox"/>	KEGG_PATHWAY	Mismatch repair	RT		11	6.1E-3	2.5E0	1.2E-2	6.1E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	DNA replication factor C complex	RT		5	7.0E-3	5.3E0	6.0E-2	5.3E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA clamp loader activity	RT		5	3.1E-2	3.7E0	2.0E-1	1.8E-1
<input type="checkbox"/>	INTERPRO	DNA polymerase III, clamp loader complex, gamma/delta/delta subunit, C-terminal	RT		4	5.7E-2	4.1E0	3.8E-1	3.5E-1
<input type="checkbox"/>	INTERPRO	Replication factor C, C-terminal domain	RT		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of DNA-directed DNA polymerase activity	RT		4	9.9E-2	3.4E0	7.0E-1	6.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	Ctf18 RFC-like complex	RT		4	1.2E-1	3.2E0	5.3E-1	4.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA strand elongation involved in DNA replication	RT		4	4.8E-1	1.6E0	1.0E0	9.6E-1
Annotation Cluster 103		Enrichment Score: 2.21	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	DDT domain superfamily	RT		5	2.9E-3	6.2E0	3.4E-2	3.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DDT	RT		5	5.4E-3	5.7E0	1.3E-1	1.3E-1
<input type="checkbox"/>	SMART	DDT	RT		5	1.5E-2	4.0E0	1.1E-1	1.0E-1
Annotation Cluster 104		Enrichment Score: 2.19	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	SANT/Myb domain	RT		19	5.3E-5	2.7E0	9.2E-4	8.5E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	transcription factor activity, RNA polymerase II transcription factor recruiting	RT		7	4.5E-4	5.2E0	6.3E-3	5.8E-3
<input type="checkbox"/>	SMART	SANT	RT		19	1.0E-2	1.8E0	8.3E-2	7.4E-2
<input type="checkbox"/>	INTERPRO	SANT domain	RT		9	4.7E-2	2.1E0	3.2E-1	3.0E-1
<input type="checkbox"/>	INTERPRO	Homeodomain-like	RT		21	1.0E0	3.9E-1	1.0E0	1.0E0
Annotation Cluster 105		Enrichment Score: 2.18	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Cullin, N-terminal	RT		8	2.1E-4	5.0E0	3.3E-3	3.0E-3
<input type="checkbox"/>	INTERPRO	Cullin homology	RT		7	9.4E-4	4.8E0	1.2E-2	1.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in NEDD8)	RT		6	1.1E-3	5.8E0	3.0E-2	2.9E-2
<input type="checkbox"/>	INTERPRO	Cullin protein, neddylation domain	RT		6	4.0E-3	4.6E0	4.3E-2	4.0E-2
<input type="checkbox"/>	SMART	CULLIN	RT		6	1.2E-2	3.5E0	9.7E-2	8.6E-2
<input type="checkbox"/>	INTERPRO	Cullin, conserved site	RT		5	1.6E-2	4.4E0	1.2E-1	1.1E-1
<input type="checkbox"/>	SMART	SM00884	RT		6	2.6E-2	3.0E0	1.9E-1	1.6E-1
<input type="checkbox"/>	INTERPRO	Cullin repeat-like-containing domain	RT		6	3.2E-2	3.1E0	2.3E-1	2.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	cullin-RING ubiquitin ligase complex	RT		4	1.6E-1	2.8E0	6.7E-1	6.0E-1
Annotation Cluster 106		Enrichment Score: 2.12	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of axonogenesis	RT		12	5.7E-4	3.1E0	1.6E-2	1.5E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	Roundabout binding	RT		7	1.2E-3	4.6E0	1.4E-2	1.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	Roundabout signaling pathway	RT		6	3.8E-2	3.0E0	3.9E-1	3.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	axon extension involved in axon guidance	RT		5	1.3E-1	2.5E0	8.3E-1	7.9E-1
Annotation Cluster 107		Enrichment Score: 2.12	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	adenylate cyclase-inhibiting G-protein coupled glutamate receptor signaling pathway	RT		6	2.1E-3	5.1E0	4.8E-2	4.5E-2
<input type="checkbox"/>	INTERPRO	Extracellular ligand-binding receptor	RT		14	2.9E-3	2.4E0	3.4E-2	3.1E-2
<input type="checkbox"/>	INTERPRO	GPCR, family 3	RT		8	3.4E-3	3.5E0	3.8E-2	3.5E-2
<input type="checkbox"/>	INTERPRO	GPCR, family 3, conserved site	RT		8	3.4E-3	3.5E0	3.8E-2	3.5E-2
<input type="checkbox"/>	INTERPRO	GPCR, family 3, metabotropic glutamate receptor	RT		6	4.0E-3	4.6E0	4.3E-2	4.0E-2

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of synaptic transmission, glutamatergic	RT		10	9.3E-3	2.6E0	1.5E-1	1.5E-1
<input type="checkbox"/>	INTERPRO	GPCR, family 3, nine cysteines domain	RT		7	1.1E-2	3.3E0	1.0E-1	9.5E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	group III metabotropic glutamate receptor activity	RT		4	1.6E-2	6.0E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	GPCR, family 3, C-terminal	RT		9	1.7E-2	2.5E0	1.4E-1	1.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	glutamate receptor activity	RT		6	2.5E-2	3.3E0	1.7E-1	1.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	presynaptic membrane	RT		17	2.8E-2	1.7E0	2.0E-1	1.7E-1
Annotation Cluster 108		Enrichment Score: 2.08	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	lysine-acetylated histone binding	RT		10	1.2E-3	3.3E0	1.4E-2	1.3E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Bromo 1	RT		6	2.2E-2	3.4E0	4.2E-1	4.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Bromo 2	RT		6	2.2E-2	3.4E0	4.2E-1	4.0E-1
Annotation Cluster 109		Enrichment Score: 2.08	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	RNA-binding	RT		147	1.3E-7	1.5E0	9.8E-7	7.8E-7
<input type="checkbox"/>	INTERPRO	RNA recognition motif domain	RT		54	2.6E-3	1.5E0	3.2E-2	2.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:RRM	RT		32	6.7E-3	1.6E0	1.6E-1	1.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	nucleotide binding	RT		77	7.5E-3	1.3E0	6.9E-2	6.2E-2
<input type="checkbox"/>	INTERPRO	Nucleotide-binding, alpha-beta plait	RT		55	3.6E-2	1.3E0	2.5E-1	2.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:RRM 1	RT		26	6.4E-2	1.4E0	9.6E-1	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:RRM 2	RT		26	6.4E-2	1.4E0	9.6E-1	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:RRM 3	RT		14	1.0E-1	1.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	RRM	RT		51	6.8E-1	9.7E-1	1.0E0	8.9E-1
Annotation Cluster 110		Enrichment Score: 2.07	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein K6-linked ubiquitination	RT		7	4.7E-4	5.2E0	1.3E-2	1.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein K29-linked ubiquitination	RT		4	3.7E-2	4.7E0	3.8E-1	3.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein K27-linked ubiquitination	RT		4	3.7E-2	4.7E0	3.8E-1	3.7E-1
Annotation Cluster 111		Enrichment Score: 2.05	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	MyD88-dependent toll-like receptor signaling pathway	RT		23	2.7E-10	4.1E0	3.5E-8	3.3E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of cytokine secretion	RT		10	4.4E-6	5.4E0	2.4E-4	2.3E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 22	RT		10	4.5E-6	5.7E0	2.0E-4	2.0E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	toll-like receptor signaling pathway	RT		15	3.3E-5	3.3E0	1.3E-3	1.2E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LRR 24	RT		6	1.1E-3	5.8E0	3.0E-2	2.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	I-kappaB phosphorylation	RT		8	1.4E-3	3.9E0	3.3E-2	3.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:TIR	RT		10	6.9E-3	2.7E0	1.6E-1	1.5E-1
<input type="checkbox"/>	INTERPRO	Toll-like receptor	RT		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of chemokine production	RT		8	1.6E-2	2.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	toll-like receptor, 1/2/4/6/10 types [Parent=PIRSF800008]	RT		4	1.6E-2	6.0E0	2.5E-1	2.5E-1
<input type="checkbox"/>	INTERPRO	Toll/interleukin-1 receptor homology (TIR) domain	RT		10	1.7E-2	2.4E0	1.3E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interferon-alpha biosynthetic process	RT		4	1.7E-2	5.9E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interferon-beta biosynthetic process	RT		5	1.8E-2	4.2E0	2.4E-1	2.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of toll-like receptor signaling pathway	RT		4	3.7E-2	4.7E0	3.8E-1	3.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of NF-kappaB import into nucleus	RT		8	5.1E-2	2.3E0	4.8E-1	4.6E-1
<input type="checkbox"/>	SMART	TIR	RT		10	5.3E-2	1.9E0	2.9E-1	2.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interleukin-8 production	RT		9	5.9E-2	2.1E0	5.3E-1	5.0E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	endolysosome membrane	RT		5	1.1E-1	2.6E0	5.0E-1	4.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	microglial cell activation	RT		5	1.3E-1	2.5E0	8.3E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interferon-gamma biosynthetic process	RT		5	1.3E-1	2.5E0	8.3E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interleukin-8 biosynthetic process	RT		4	1.4E-1	3.0E0	8.3E-1	7.9E-1

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interleukin-6 production	RT		11	2.2E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	lipopeptide binding	RT		3	4.0E-1	2.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	phagocytic vesicle membrane	RT		7	9.2E-1	7.5E-1	1.0E0	9.2E-1
<input type="checkbox"/>	BIOCARTA	Dendritic cells in regulating TH1 and TH2 Development	RT		5	9.5E-1	7.1E-1	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	transmembrane signaling receptor activity	RT		15	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 112		Enrichment Score: 2.05	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	sister chromatid cohesion	RT		33	2.8E-4	1.9E0	8.3E-3	8.0E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	kinetochore	RT		25	1.2E-3	2.0E0	1.3E-2	1.2E-2
<input type="checkbox"/>	UP_KEYWORDS	Centromere	RT		32	7.4E-3	1.6E0	3.6E-2	2.9E-2
<input type="checkbox"/>	UP_KEYWORDS	Kinetochore	RT		20	1.2E-1	1.4E0	4.4E-1	3.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	condensed chromosome kinetochore	RT		18	2.0E-1	1.3E0	8.0E-1	7.2E-1
Annotation Cluster 113		Enrichment Score: 2.03	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	muscle filament sliding	RT		19	1.3E-5	3.0E0	5.8E-4	5.5E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	cardiac muscle contraction	RT		13	6.6E-2	1.7E0	5.6E-1	5.3E-1
<input type="checkbox"/>	KEGG_PATHWAY	Cardiac muscle contraction	RT		8	9.9E-1	5.6E-1	1.0E0	9.9E-1
Annotation Cluster 114		Enrichment Score: 2.01	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	CXCR3 chemokine receptor binding	RT		5	3.4E-3	6.0E0	3.4E-2	3.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	T cell chemotaxis	RT		6	4.9E-3	4.4E0	9.2E-2	8.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of leukocyte chemotaxis	RT		9	5.8E-3	3.0E0	1.1E-1	1.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of cAMP metabolic process	RT		5	9.1E-3	4.9E0	1.5E-1	1.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of release of sequestered calcium ion into cytosol	RT		10	2.8E-2	2.2E0	3.3E-1	3.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of cAMP-mediated signaling	RT		6	3.8E-2	3.0E0	3.9E-1	3.7E-1
Annotation Cluster 115		Enrichment Score: 1.96	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	transcription factor activity, RNA polymerase II transcription factor recruiting	RT		7	4.5E-4	5.2E0	6.3E-3	5.8E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HTH myb-type 1	RT		5	2.0E-3	6.8E0	5.3E-2	5.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HTH myb-type 2	RT		5	2.0E-3	6.8E0	5.3E-2	5.1E-2
<input type="checkbox"/>	INTERPRO	Myb-like domain	RT		6	4.0E-3	4.6E0	4.3E-2	4.0E-2
<input type="checkbox"/>	INTERPRO	Myb domain	RT		6	7.7E-3	4.1E0	7.5E-2	7.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HTH myb-type 3	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Myb-like 1	RT		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Myb-like 2	RT		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	INTERPRO	C-myb, C-terminal	RT		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	RT		7	1.7E-1	1.8E0	1.0E0	9.7E-1
Annotation Cluster 116		Enrichment Score: 1.95	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 14	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 15	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 2	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 3	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 4	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 5	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 6	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 7	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 8	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 9	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 1	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 2	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 3	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 4	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 1	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 10	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 11	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 12	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DAZ-like 13	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
Annotation Cluster 117		Enrichment Score: 1.94	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Ala/Asp-rich (DA-box)	RT		6	2.6E-3	5.1E0	6.6E-2	6.3E-2
<input type="checkbox"/>	INTERPRO	Structural maintenance of chromosomes protein	RT		5	2.9E-3	6.2E0	3.4E-2	3.1E-2
<input type="checkbox"/>	PIR_SUPERFAMILY	structural maintenance of chromosomes protein	RT		5	3.2E-3	6.0E0	1.9E-1	1.9E-1
<input type="checkbox"/>	INTERPRO	SMCs flexible hinge	RT		5	7.7E-3	5.2E0	7.5E-2	7.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Flexible hinge	RT		5	1.1E-2	4.9E0	2.3E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	RecF/RecN/SMC	RT		5	1.6E-2	4.4E0	1.2E-1	1.1E-1
<input type="checkbox"/>	SMART	SM00968	RT		5	3.6E-2	3.4E0	2.4E-1	2.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	meiotic cohesin complex	RT		3	2.4E-1	3.2E0	9.1E-1	8.1E-1
Annotation Cluster 118		Enrichment Score: 1.94	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FBA	RT		5	5.4E-3	5.7E0	1.3E-1	1.3E-1
<input type="checkbox"/>	INTERPRO	F-box associated (FBA) domain	RT		5	7.7E-3	5.2E0	7.5E-2	7.0E-2
<input type="checkbox"/>	SMART	SM01198	RT		5	3.6E-2	3.4E0	2.4E-1	2.1E-1
Annotation Cluster 119		Enrichment Score: 1.88	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:C2 tensin-type	RT		6	5.1E-3	4.5E0	1.3E-1	1.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Phosphatase tensin-type	RT		6	9.0E-3	4.1E0	2.1E-1	2.0E-1
<input type="checkbox"/>	INTERPRO	Tensin phosphatase, C2 domain	RT		6	1.3E-2	3.7E0	1.2E-1	1.1E-1
<input type="checkbox"/>	SMART	SM01326	RT		6	4.7E-2	2.7E0	2.8E-1	2.4E-1
Annotation Cluster 120		Enrichment Score: 1.76	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Phototransduction	RT		15	1.2E-4	2.9E0	3.0E-4	1.3E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	photoreceptor disc membrane	RT		9	5.5E-3	3.0E0	5.0E-2	4.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of rhodopsin mediated signaling pathway	RT		11	1.7E-2	2.2E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	rhodopsin mediated signaling pathway	RT		4	3.3E-1	2.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Vision	RT		19	4.1E-1	1.1E0	1.0E0	8.0E-1
Annotation Cluster 121		Enrichment Score: 1.7	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of interferon-gamma-mediated signaling pathway	RT		10	4.1E-5	4.6E0	1.6E-3	1.5E-3
<input type="checkbox"/>	BBID	48.mice minus JAKs and STATs	RT		8	8.1E-2	1.9E0	9.9E-1	9.9E-1
<input type="checkbox"/>	BBID	75.Stats activators of Apoptosis	RT		4	1.6E-1	2.6E0	9.9E-1	9.9E-1
<input type="checkbox"/>	BIOCARTA	IFN gamma signaling pathway	RT		4	2.9E-1	2.1E0	5.3E-1	4.0E-1
Annotation Cluster 122		Enrichment Score: 1.7	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HSA	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	Helicase/SANT-associated, DNA binding	RT		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	SMART	HSA	RT		4	4.9E-2	4.0E0	2.8E-1	2.4E-1
Annotation Cluster 123		Enrichment Score: 1.69	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	cadherin binding involved in cell-cell adhesion	RT		65	1.1E-2	1.3E0	9.1E-2	8.3E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	cell-cell adherens junction	RT		67	1.4E-2	1.3E0	1.1E-1	9.5E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell-cell adhesion	RT		57	5.8E-2	1.2E0	5.3E-1	5.0E-1
Annotation Cluster 124		Enrichment Score: 1.68	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Zinc finger, C6HC-type	RT		8	5.5E-3	3.3E0	5.8E-2	5.3E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:IBR-type	RT		7	6.8E-3	3.7E0	1.6E-1	1.5E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitin conjugating enzyme binding	RT	<div><div></div><div></div></div>	12	9.1E-3	2.3E0	7.9E-2	7.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:RING-type 2	RT	<div><div></div><div></div></div>	6	2.2E-2	3.4E0	4.2E-1	4.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:RING-type 1; atypical	RT	<div><div></div><div></div></div>	4	1.0E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	IBR	RT	<div><div></div><div></div></div>	7	1.1E-1	2.0E0	5.3E-1	4.7E-1
Annotation Cluster 125		Enrichment Score: 1.67	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	POLO box duplicated domain	RT	<div><div></div><div></div></div>	5	2.9E-3	6.2E0	3.4E-2	3.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:POLO box 1	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:POLO box 2	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
Annotation Cluster 126		Enrichment Score: 1.66	<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	receptor signaling protein tyrosine kinase activity	RT	<div><div></div><div></div></div>	9	2.0E-5	5.4E0	3.5E-4	3.2E-4
<input type="checkbox"/>	INTERPRO	EGF receptor, L domain	RT	<div><div></div><div></div></div>	6	1.7E-3	5.3E0	2.1E-2	2.0E-2
<input type="checkbox"/>	INTERPRO	Furin-like cysteine-rich domain	RT	<div><div></div><div></div></div>	6	1.7E-3	5.3E0	2.1E-2	2.0E-2
<input type="checkbox"/>	INTERPRO	Furin-like repeat	RT	<div><div></div><div></div></div>	9	4.3E-3	3.1E0	4.7E-2	4.4E-2
<input type="checkbox"/>	SMART	FU	RT	<div><div></div><div></div></div>	9	5.4E-2	2.0E0	2.9E-1	2.6E-1
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, insulin-like receptor	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	insulin receptor	RT	<div><div></div><div></div></div>	3	7.3E-2	6.0E0	6.0E-1	6.0E-1
<input type="checkbox"/>	INTERPRO	Tyrosine protein kinase, EGF/ERB/XmrK receptor	RT	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.2E-1	5.8E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	tyrosine-protein kinase, EGF receptor type	RT	<div><div></div><div></div></div>	3	1.3E-1	4.5E0	9.1E-1	9.1E-1
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, receptor class II, conserved site	RT	<div><div></div><div></div></div>	3	5.5E-1	1.7E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Fibronectin type-III 3	RT	<div><div></div><div></div></div>	6	1.0E0	4.9E-1	1.0E0	1.0E0
Annotation Cluster 127		Enrichment Score: 1.64	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Sphingosine 1-phosphate receptor	RT	<div><div></div><div></div></div>	5	2.9E-3	6.2E0	3.4E-2	3.1E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	sphingosine-1-phosphate receptor activity	RT	<div><div></div><div></div></div>	5	3.1E-2	3.7E0	2.0E-1	1.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	sphingosine-1-phosphate signaling pathway	RT	<div><div></div><div></div></div>	5	1.3E-1	2.5E0	8.3E-1	7.9E-1
Annotation Cluster 128		Enrichment Score: 1.64	<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	MLL5-L complex	RT	<div><div></div><div></div></div>	6	3.5E-3	4.8E0	3.5E-2	3.1E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	PTW/PP1 phosphatase complex	RT	<div><div></div><div></div></div>	5	1.4E-2	4.5E0	1.1E-1	9.5E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	entrainment of circadian clock by photoperiod	RT	<div><div></div><div></div></div>	6	2.4E-1	1.8E0	1.0E0	9.6E-1
Annotation Cluster 129		Enrichment Score: 1.62	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	cdc25 and chk1 Regulatory Pathway in response to DNA damage	RT	<div><div></div><div></div></div>	8	6.3E-3	2.8E0	2.6E-2	1.9E-2
<input type="checkbox"/>	BIOCARTA	Sonic Hedgehog (SHH) Receptor Ptc1 Regulates cell cycle	RT	<div><div></div><div></div></div>	8	3.0E-2	2.3E0	9.0E-2	6.7E-2
<input type="checkbox"/>	INTERPRO	M-phase inducer phosphatase	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
Annotation Cluster 130		Enrichment Score: 1.62	<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:TEA	RT	<div><div></div><div></div></div>	4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	Transcriptional enhancer factor	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	TEA/ATTS	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E









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	SM00838	RT	<div><div></div><div></div></div>	5	1.5E-2	4.0E0	1.1E-1	1.0E-1
<input type="checkbox"/>	INTERPRO	Ribosomal protein S5 domain 2-type fold	RT	<div><div></div><div></div></div>	14	1.8E-2	2.0E0	1.4E-1	1.3E-1
<input type="checkbox"/>	INTERPRO	Ribosomal protein S5 domain 2-type fold, subgroup	RT	<div><div></div><div></div></div>	9	3.0E-2	2.3E0	2.2E-1	2.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	translation elongation factor activity	RT	<div><div></div><div></div></div>	11	4.7E-2	1.9E0	2.9E-1	2.6E-1
<input type="checkbox"/>	SMART	SM00889	RT	<div><div></div><div></div></div>	4	4.9E-2	4.0E0	2.8E-1	2.4E-1
<input type="checkbox"/>	INTERPRO	Translation elongation factor EFTu/EF1A, C-terminal	RT	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	translational elongation	RT	<div><div></div><div></div></div>	6	1.7E-1	2.0E0	9.8E-1	9.4E-1
<input type="checkbox"/>	INTERPRO	Translation elongation factor EF1A/initiation factor IF2gamma, C-terminal	RT	<div><div></div><div></div></div>	4	2.6E-1	2.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_KEYWORDS	Protein biosynthesis	RT	<div><div></div><div></div></div>	23	5.5E-1	1.0E0	1.0E0	8.0E-1
Annotation Cluster 132		Enrichment Score: 1.6	<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	SWI/SNF complex	RT	<div><div></div><div></div></div>	8	4.7E-3	3.4E0	4.5E-2	4.0E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	npBAF complex	RT	<div><div></div><div></div></div>	6	2.9E-2	3.2E0	2.0E-1	1.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleosome disassembly	RT	<div><div></div><div></div></div>	7	5.3E-2	2.4E0	4.9E-1	4.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	nBAF complex	RT	<div><div></div><div></div></div>	6	5.6E-2	2.7E0	3.2E-1	2.9E-1
Annotation Cluster 133		Enrichment Score: 1.58	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Regulation of cell cycle progression by Plk3	RT	<div><div></div><div></div></div>	8	1.9E-3	3.1E0	1.1E-2	8.6E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	replicative senescence	RT	<div><div></div><div></div></div>	6	3.8E-2	3.0E0	3.9E-1	3.7E-1
<input type="checkbox"/>	BIOCARTA	Role of BRCA1, BRCA2 and ATR in Cancer Susceptibility	RT	<div><div></div><div></div></div>	10	2.5E-1	1.4E0	4.7E-1	3.5E-1
Annotation Cluster 134		Enrichment Score: 1.57	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	p53 Signaling Pathway	RT	<div><div></div><div></div></div>	13	1.2E-3	2.4E0	8.0E-3	6.0E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	cyclin-dependent protein kinase holoenzyme complex	RT	<div><div></div><div></div></div>	6	7.3E-2	2.5E0	3.9E-1	3.4E-1
<input type="checkbox"/>	BBID	4.cyclins & p27 cell cycle	RT	<div><div></div><div></div></div>	5	7.6E-2	2.6E0	9.9E-1	9.9E-1
<input type="checkbox"/>	BBID	94.E2F transcriptional activity cell cycle	RT	<div><div></div><div></div></div>	6	8.2E-2	2.2E0	9.9E-1	9.9E-1
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"/>	UP_KEYWORDS	Protein kinase inhibitor	RT	<div><div></div><div></div></div>	7	1.0E-2	3.4E0	4.8E-2	3.8E-2
<input type="checkbox"/>	INTERPRO	Pseudokinase tribbles family/serine-threonine-protein kinase 40	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	mitogen-activated protein kinase kinase binding	RT	<div><div></div><div></div></div>	7	3.8E-2	2.6E0	2.4E-1	2.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of MAP kinase activity	RT	<div><div></div><div></div></div>	5	5.0E-2	3.3E0	4.7E-1	4.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitin-protein transferase regulator activity	RT	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.6E-1
Annotation Cluster 136		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	histone methyltransferase activity (H3-K36 specific)	RT	<div><div></div><div></div></div>	5	8.8E-3	5.0E0	7.8E-2	7.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:AWS	RT	<div><div></div><div></div></div>	4	2.5E-2	5.4E0	4.6E-1	4.4E-1
<input type="checkbox"/>	INTERPRO	AWS	RT	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.3E-1	2.1E-1
<input type="checkbox"/>	SMART	AWS	RT	<div><div></div><div></div></div>	4	1.0E-1	3.2E0	5.1E-1	4.5E-1
Annotation Cluster 137		Enrichment Score: 1.52	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Zinc finger, PHD-finger	RT	<div><div></div><div></div></div>	24	2.6E-3	1.9E0	3.2E-2	3.0E-2
<input type="checkbox"/>	INTERPRO	Zinc finger, PHD-type	RT	<div><div></div><div></div></div>	25	6.3E-3	1.7E0	6.6E-2	6.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type	RT	<div><div></div><div></div></div>	15	1.6E-2	2.0E0	3.1E-1	3.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type 2	RT	<div><div></div><div></div></div>	10	2.4E-2	2.3E0	4.6E-1	4.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type 1	RT	<div><div></div><div></div></div>	10	4.4E-2	2.1E0	7.8E-1	7.5E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, FYVE/PHD-type	RT	<div><div></div><div></div></div>	31	6.4E-2	1.4E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, PHD-type, conserved site	RT	<div><div></div><div></div></div>	16	1.1E-1	1.5E0	5.9E-1	5.5E-1
<input type="checkbox"/>	SMART	PHD	RT	<div><div></div><div></div></div>	25	3.5E-1	1.1E0	1.0E0	8.9E-1
Annotation Cluster 138		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	four-way junction DNA binding	RT	<div><div></div><div></div></div>	9	7.0E-4	3.8E0	9.1E-3	8.3E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitotic recombination	RT	<div><div></div><div></div></div>	8	2.6E-3	3.6E0	5.7E-2	5.4E-2
















































Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	chromosome organization involved in meiotic cell cycle	RT	<div><div></div><div></div></div>	4	1.7E-2	5.9E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	reciprocal meiotic recombination	RT	<div><div></div><div></div></div>	11	2.1E-2	2.2E0	2.6E-1	2.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	recombinase activity	RT	<div><div></div><div></div></div>	5	3.1E-2	3.7E0	2.0E-1	1.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA recombinase assembly	RT	<div><div></div><div></div></div>	4	3.7E-2	4.7E0	3.8E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	DNA recombination and repair protein, RecA-like	RT	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	3.8E-1	3.5E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	DNA repair and recombination protein, Rad51 type	RT	<div><div></div><div></div></div>	4	6.1E-2	4.0E0	6.0E-1	6.0E-1
<input type="checkbox"/>	INTERPRO	DNA repair Rad51/transcription factor NusA, alpha-helical	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	DNA recombination/repair protein RecA/RadB, ATP-binding domain	RT	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.4E-1
<input type="checkbox"/>	INTERPRO	DNA recombination and repair protein Rad51, C-terminal	RT	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	strand invasion	RT	<div><div></div><div></div></div>	4	9.9E-2	3.4E0	7.0E-1	6.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	endodeoxyribonuclease activity	RT	<div><div></div><div></div></div>	7	1.5E-1	1.9E0	6.6E-1	6.0E-1
Annotation Cluster 139		Enrichment Score: 1.49	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Ubiquitin subgroup	RT	<div><div></div><div></div></div>	10	2.8E-5	4.8E0	5.0E-4	4.6E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA duplex unwinding	RT	<div><div></div><div></div></div>	12	3.5E-4	3.2E0	1.0E-2	1.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of necrotic cell death	RT	<div><div></div><div></div></div>	8	1.4E-3	3.9E0	3.3E-2	3.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of transcription from RNA polymerase II promoter in response to hypoxia	RT	<div><div></div><div></div></div>	12	4.0E-3	2.5E0	8.0E-2	7.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA damage recognition	RT	<div><div></div><div></div></div>	10	9.3E-3	2.6E0	1.5E-1	1.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of epidermal growth factor receptor signaling pathway	RT	<div><div></div><div></div></div>	10	1.3E-2	2.5E0	1.9E-1	1.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	MyD88-independent toll-like receptor signaling pathway	RT	<div><div></div><div></div></div>	7	1.3E-2	3.2E0	2.0E-1	1.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:Activating enzyme	RT	<div><div></div><div></div></div>	5	2.0E-2	4.3E0	3.9E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Ubiquitin conserved site	RT	<div><div></div><div></div></div>	6	2.1E-2	3.4E0	1.6E-1	1.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)	RT	<div><div></div><div></div></div>	7	3.8E-2	2.6E0	6.8E-1	6.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of type I interferon production	RT	<div><div></div><div></div></div>	6	5.4E-2	2.7E0	4.9E-1	4.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of type I interferon production	RT	<div><div></div><div></div></div>	10	5.4E-2	2.0E0	4.9E-1	4.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	viral life cycle	RT	<div><div></div><div></div></div>	10	6.5E-2	1.9E0	5.5E-1	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of epidermal growth factor receptor signaling pathway	RT	<div><div></div><div></div></div>	11	7.0E-2	1.8E0	5.8E-1	5.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:40S ribosomal protein S27a	RT	<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)	RT	<div><div></div><div></div></div>	4	7.0E-2	3.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Essential for function	RT	<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	RT	<div><div></div><div></div></div>	4	7.0E-2	3.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	virion assembly	RT	<div><div></div><div></div></div>	5	1.3E-1	2.5E0	8.3E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	glycogen biosynthetic process	RT	<div><div></div><div></div></div>	8	1.4E-1	1.8E0	8.3E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	interstrand cross-link repair	RT	<div><div></div><div></div></div>	10	4.5E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	intracellular transport of virus	RT	<div><div></div><div></div></div>	10	5.0E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	endocytic vesicle membrane	RT	<div><div></div><div></div></div>	9	8.4E-1	8.7E-1	1.0E0	8.9E-1

















































Annotation Cluster 1		Enrichment Score: ?	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Dynammin	RT	<div><div></div></div>	6	1.3E-1	2.2E0	6.2E-1	5.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitochondrial fission	RT	<div><div></div></div>	5	4.0E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	membrane fusion	RT	<div><div></div></div>	6	8.9E-1	8.1E-1	1.0E0	9.6E-1
Annotation Cluster 141		Enrichment Score: 1.48	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein kinase C activity	RT	<div><div></div></div>	10	1.9E-4	4.0E0	2.9E-3	2.6E-3
<input type="checkbox"/>	INTERPRO	Diacylglycerol/phorbol-ester binding	RT	<div><div></div></div>	11	3.7E-3	2.7E0	4.1E-2	3.8E-2
<input type="checkbox"/>	INTERPRO	Protein kinase C, delta/epsilon/eta/theta types	RT	<div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	protein kinase C, delta/epsilon/eta/theta types	RT	<div><div></div></div>	4	1.6E-2	6.0E0	2.5E-1	2.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 1	RT	<div><div></div></div>	8	3.3E-2	2.5E0	6.0E-1	5.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 2	RT	<div><div></div></div>	8	3.3E-2	2.5E0	6.0E-1	5.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium-independent protein kinase C activity	RT	<div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	Protein kinase C-like, phorbol ester/diacylglycerol binding	RT	<div><div></div></div>	15	1.7E-1	1.4E0	8.1E-1	7.5E-1
<input type="checkbox"/>	SMART	C1	RT	<div><div></div></div>	15	7.7E-1	9.3E-1	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type	RT	<div><div></div></div>	5	9.1E-1	7.6E-1	1.0E0	9.7E-1
Annotation Cluster 142		Enrichment Score: 1.46	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Signal Dependent Regulation of Myogenesis by Corepressor MITR	RT	<div><div></div></div>	9	6.9E-4	3.1E0	5.2E-3	3.9E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MADS-box	RT	<div><div></div></div>	5	5.4E-3	5.7E0	1.3E-1	1.3E-1
<input type="checkbox"/>	INTERPRO	Transcription factor, MADS-box	RT	<div><div></div></div>	5	7.7E-3	5.2E0	7.5E-2	7.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:Mef2-type	RT	<div><div></div></div>	4	2.5E-2	5.4E0	4.6E-1	4.4E-1
<input type="checkbox"/>	SMART	MADS	RT	<div><div></div></div>	5	3.6E-2	3.4E0	2.4E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Beta domain	RT	<div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	INTERPRO	Holliday junction regulator protein family C-terminal	RT	<div><div></div></div>	3	1.2E-1	4.6E0	6.2E-1	5.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Lys-rich (basic)	RT	<div><div></div></div>	3	3.9E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Cleavage	RT	<div><div></div></div>	8	9.1E-1	7.8E-1	1.0E0	9.7E-1
Annotation Cluster 143		Enrichment Score: 1.42	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	ROC GTPase	RT	<div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Roc	RT	<div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	INTERPRO	Mitochondrial Rho-like	RT	<div><div></div></div>	5	6.3E-2	3.1E0	3.9E-1	3.6E-1
Annotation Cluster 144		Enrichment Score: 1.41	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitotic cell cycle	RT	<div><div></div></div>	16	1.9E-3	2.3E0	4.4E-2	4.2E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	receptor signaling protein serine/threonine kinase activity	RT	<div><div></div></div>	16	2.4E-2	1.8E0	1.7E-1	1.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CRIB	RT	<div><div></div></div>	7	4.9E-2	2.5E0	8.4E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:GTPase-binding	RT	<div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Autoregulatory region	RT	<div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	INTERPRO	PAK-box/P21-Rho-binding	RT	<div><div></div></div>	7	9.0E-2	2.2E0	4.8E-1	4.4E-1
<input type="checkbox"/>	SMART	PBD	RT	<div><div></div></div>	7	1.8E-1	1.8E0	7.3E-1	6.5E-1
Annotation Cluster 145		Enrichment Score: 1.4	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Arg/Ser-rich (RS domain)	RT	<div><div></div></div>	9	2.4E-3	3.4E0	6.1E-2	5.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of mRNA splicing, via spliceosome	RT	<div><div></div></div>	9	1.7E-2	2.5E0	2.2E-1	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Gly-rich (hinge region)	RT	<div><div></div></div>	4	7.0E-2	3.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	mRNA splice site selection	RT	<div><div></div></div>	6	1.5E-1	2.1E0	8.5E-1	8.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	RS domain binding	RT	<div><div></div></div>	3	2.6E-1	3.0E0	9.9E-1	9.0E-1
Annotation Cluster 146		Enrichment Score: 1.39	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Leucine-rich repeat-containing protein 8, N-terminal	RT	<div><div></div></div>	5	2.9E-3	6.2E0	3.4E-2	3.1E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	volume-sensitive anion channel activity	RT	<div><div></div></div>	4	1.6E-2	6.0E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of anion transport	RT	<div><div></div></div>	5	7.2E-2	3.0E0	5.8E-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"/>	GOTERM_BP_DIRECT	anion transmembrane transport	RT	<div><div></div><div></div></div>	5	7.7E-1	9.9E-1	1.0E0	9.6E-1
Annotation Cluster 147		Enrichment Score: 1.37	<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	GMP metabolic process	RT	<div><div></div><div></div></div>	10	2.1E-4	3.9E0	6.6E-3	6.3E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	ionotropic glutamate receptor binding	RT	<div><div></div><div></div></div>	11	1.0E-3	3.1E0	1.2E-2	1.1E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	guanylate kinase activity	RT	<div><div></div><div></div></div>	8	1.3E-3	4.0E0	1.5E-2	1.4E-2
<input type="checkbox"/>	INTERPRO	Guanylate kinase, conserved site	RT	<div><div></div><div></div></div>	9	1.7E-3	3.5E0	2.1E-2	2.0E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	ionotropic glutamate receptor complex	RT	<div><div></div><div></div></div>	6	3.5E-3	4.8E0	3.5E-2	3.1E-2
<input type="checkbox"/>	INTERPRO	Guanylate kinase	RT	<div><div></div><div></div></div>	10	4.9E-3	2.8E0	5.3E-2	4.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	GDP metabolic process	RT	<div><div></div><div></div></div>	7	4.9E-3	3.8E0	9.2E-2	8.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Guanylate kinase-like	RT	<div><div></div><div></div></div>	10	5.1E-3	2.8E0	1.3E-1	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	establishment or maintenance of epithelial cell apical/basal polarity	RT	<div><div></div><div></div></div>	7	1.3E-2	3.2E0	2.0E-1	1.9E-1
<input type="checkbox"/>	INTERPRO	PDZ-associated domain of NMDA receptors	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Membrane-associated guanylate kinase (MAGUK), PEST domain, N-terminal	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Membrane-associated guanylate kinase (MAGUK) scaffold protein	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Guanylate kinase/L-type calcium channel	RT	<div><div></div><div></div></div>	10	1.7E-2	2.4E0	1.3E-1	1.2E-1
<input type="checkbox"/>	SMART	SM01277	RT	<div><div></div><div></div></div>	4	4.9E-2	4.0E0	2.8E-1	2.4E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	membrane-associated guanylate kinase (MAGUK) scaffold protein	RT	<div><div></div><div></div></div>	3	7.3E-2	6.0E0	6.0E-1	6.0E-1
<input type="checkbox"/>	BIOCARTA	Synaptic Proteins at the Synaptic Junction	RT	<div><div></div><div></div></div>	10	8.5E-2	1.7E0	2.1E-1	1.6E-1
<input type="checkbox"/>	SMART	GuKc	RT	<div><div></div><div></div></div>	10	1.4E-1	1.6E0	6.6E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	L27	RT	<div><div></div><div></div></div>	5	1.8E-1	2.2E0	8.6E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	receptor localization to synapse	RT	<div><div></div><div></div></div>	4	1.8E-1	2.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	INTERPRO	Variant SH3	RT	<div><div></div><div></div></div>	13	2.7E-1	1.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:L27 1	RT	<div><div></div><div></div></div>	3	2.7E-1	2.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:L27 2	RT	<div><div></div><div></div></div>	3	2.7E-1	2.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	receptor clustering	RT	<div><div></div><div></div></div>	5	4.4E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PDZ 3	RT	<div><div></div><div></div></div>	6	4.6E-1	1.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	L27, C-terminal	RT	<div><div></div><div></div></div>	3	5.0E-1	1.9E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	L27	RT	<div><div></div><div></div></div>	4	6.0E-1	1.3E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PDZ 1	RT	<div><div></div><div></div></div>	6	7.6E-1	9.7E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PDZ 2	RT	<div><div></div><div></div></div>	6	7.6E-1	9.7E-1	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	ligand-gated ion channel activity	RT	<div><div></div><div></div></div>	4	9.5E-1	6.6E-1	1.0E0	9.5E-1
Annotation Cluster 148		Enrichment Score: 1.37	<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	MAP kinase kinase activity	RT	<div><div></div><div></div></div>	8	1.3E-3	4.0E0	1.5E-2	1.4E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Cleavage; by anthrax lethal factor	RT	<div><div></div><div></div></div>	3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	proteolysis in other organism	RT	<div><div></div><div></div></div>	3	2.7E-1	3.0E0	1.0E0	9.6E-1
Annotation Cluster 149		Enrichment Score: 1.35	<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	fibroblast growth factor-activated receptor activity	RT	<div><div></div><div></div></div>	5	3.4E-3	6.0E0	3.4E-2	3.1E-2
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, fibroblast growth factor receptor	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	fibroblast growth factor receptor	RT	<div><div></div><div></div></div>	4	1.6E-2	6.0E0	2.5E-1	2.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of phospholipase activity	RT	<div><div></div><div></div></div>	4	1.4E-1	3.0E0	8.3E-1	7.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	fibroblast growth factor binding	RT	<div><div></div><div></div></div>	7	1.7E-1	1.8E0	7.4E-1	6.8E-1
<input type="checkbox"/>	UP_KEYWORDS	Craniosynostosis	RT	<div><div></div><div></div></div>	5	4.0E-1	1.6E0	1.0E0	8.0E-1
Annotation Cluster 150		Enrichment Score: 1.32	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	U box domain	RT	<div><div></div><div></div></div>	6	1.3E-2	3.7E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitin-ubiquitin ligase activity	RT	<div><div></div><div></div></div>	6	5.2E-2	2.8E0	3.1E-1	2.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:U-box	RT	<div><div></div><div></div></div>	4	7.0E-2	3.9E0	1.0E0	9.7E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	SMART	Ubox	RT	<div><div></div></div>	5	1.1E-1	2.5E0	5.3E-1	4.7E-1
Annotation Cluster 151		Enrichment Score: 1.31	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	BTB/Kelch-associated	RT	<div><div></div></div>	19	7.5E-3	1.9E0	7.5E-2	7.0E-2
<input type="checkbox"/>	INTERPRO	Kelch-like protein, gigaxonin	RT	<div><div></div></div>	14	1.2E-2	2.1E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	Cul3-RING ubiquitin ligase complex	RT	<div><div></div></div>	19	1.4E-2	1.8E0	1.1E-1	9.5E-2
<input type="checkbox"/>	PIR_SUPERFAMILY	kelch-like protein, gigaxonin type	RT	<div><div></div></div>	14	1.5E-2	2.0E0	2.5E-1	2.5E-1
<input type="checkbox"/>	INTERPRO	Kelch repeat type 1	RT	<div><div></div></div>	18	2.3E-2	1.7E0	1.7E-1	1.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 5	RT	<div><div></div></div>	17	2.7E-2	1.8E0	4.9E-1	4.8E-1
<input type="checkbox"/>	UP_KEYWORDS	Kelch repeat	RT	<div><div></div></div>	18	2.7E-2	1.7E0	1.2E-1	9.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 4	RT	<div><div></div></div>	17	4.4E-2	1.7E0	7.8E-1	7.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 1	RT	<div><div></div></div>	17	5.0E-2	1.6E0	8.5E-1	8.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 2	RT	<div><div></div></div>	17	5.0E-2	1.6E0	8.5E-1	8.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 3	RT	<div><div></div></div>	17	5.0E-2	1.6E0	8.5E-1	8.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Kelch 6	RT	<div><div></div></div>	13	7.1E-2	1.7E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BACK	RT	<div><div></div></div>	8	1.4E-1	1.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Galactose oxidase, beta-propeller	RT	<div><div></div></div>	8	1.8E-1	1.7E0	8.5E-1	7.8E-1
<input type="checkbox"/>	INTERPRO	Kelch-type beta propeller	RT	<div><div></div></div>	12	2.3E-1	1.4E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	Kelch	RT	<div><div></div></div>	18	2.5E-1	1.3E0	9.6E-1	8.5E-1
<input type="checkbox"/>	SMART	SM00875	RT	<div><div></div></div>	18	3.0E-1	1.2E0	1.0E0	8.9E-1
Annotation Cluster 152		Enrichment Score: 1.28	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	MOZ/SAS-like protein	RT	<div><div></div></div>	5	2.9E-3	6.2E0	3.4E-2	3.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C2HC-type	RT	<div><div></div></div>	5	2.0E-2	4.3E0	3.9E-1	3.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone acetylation	RT	<div><div></div></div>	12	2.0E-2	2.1E0	2.5E-1	2.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone acetyltransferase activity	RT	<div><div></div></div>	15	2.2E-2	1.9E0	1.6E-1	1.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	acetyltransferase activity	RT	<div><div></div></div>	6	5.2E-2	2.8E0	3.1E-1	2.8E-1
<input type="checkbox"/>	INTERPRO	Acyl-CoA N-acyltransferase	RT	<div><div></div></div>	7	7.7E-1	9.4E-1	1.0E0	9.2E-1
<input type="checkbox"/>	UP_KEYWORDS	Acyltransferase	RT	<div><div></div></div>	14	1.0E0	5.6E-1	1.0E0	1.0E0
Annotation Cluster 153		Enrichment Score: 1.28	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BBID	26.cyclin-CDK complexes	RT	<div><div></div></div>	12	6.0E-3	2.1E0	3.3E-1	3.3E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	cyclin-dependent protein serine/threonine kinase inhibitor activity	RT	<div><div></div></div>	5	9.7E-2	2.7E0	4.8E-1	4.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of phosphorylation	RT	<div><div></div></div>	7	1.1E-1	2.1E0	7.4E-1	7.1E-1
<input type="checkbox"/>	BBID	1.RBphosphoE2F	RT	<div><div></div></div>	9	1.2E-1	1.7E0	9.9E-1	9.9E-1
Annotation Cluster 154		Enrichment Score: 1.25	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	galanin receptor activity	RT	<div><div></div></div>	4	1.6E-2	6.0E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Galanin receptor family	RT	<div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	peptide hormone binding	RT	<div><div></div></div>	8	1.5E-1	1.8E0	6.7E-1	6.0E-1
Annotation Cluster 155		Enrichment Score: 1.25	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	OMIM_DISEASE	Schimmelpenning-Feuerstein-Mims syndrome, somatic mosaic	RT	<div><div></div></div>	3	4.0E-2	8.3E0	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Hypervariable region	RT	<div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	BBID	65.Integrin affinity modulation	RT	<div><div></div></div>	5	7.6E-2	2.6E0	9.9E-1	9.9E-1
Annotation Cluster 156		Enrichment Score: 1.25	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H3-K27 methylation	RT	<div><div></div></div>	4	1.7E-2	5.9E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K27 specific)	RT	<div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein-lysine N-methyltransferase activity	RT	<div><div></div></div>	6	1.4E-1	2.1E0	6.3E-1	5.7E-1
Annotation Cluster 157		Enrichment Score: 1.25	<div><div>G</div></div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Heat shock factor (HSF)-type, DNA-binding	RT	<div><div></div></div>	5	2.7E-2	3.9E0	2.0E-1	1.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Hydrophobic repeat HR-A/B	RT	<div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-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	region of interest:Hydrophobic repeat HR-C	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	SMART	HSF	RT	<div><div></div><div></div></div>	5	1.1E-1	2.5E0	5.3E-1	4.7E-1
Annotation Cluster 158		Enrichment Score: 1.22	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:GATA-type 1	RT	<div><div></div><div></div></div>	6	3.6E-4	6.8E0	1.1E-2	1.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:GATA-type 2	RT	<div><div></div><div></div></div>	6	3.6E-4	6.8E0	1.1E-2	1.1E-2
<input type="checkbox"/>	INTERPRO	Zinc finger, GATA-type	RT	<div><div></div><div></div></div>	7	2.4E-2	2.9E0	1.8E-1	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	anatomical structure formation involved in morphogenesis	RT	<div><div></div><div></div></div>	6	2.6E-2	3.2E0	3.0E-1	2.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	enhancer sequence-specific DNA binding	RT	<div><div></div><div></div></div>	8	3.8E-2	2.4E0	2.4E-1	2.1E-1
<input type="checkbox"/>	SMART	ZnF_GATA	RT	<div><div></div><div></div></div>	7	5.2E-2	2.4E0	2.9E-1	2.5E-1
<input type="checkbox"/>	INTERPRO	GATA-type transcription activator, N-terminal	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	intestinal epithelial cell differentiation	RT	<div><div></div><div></div></div>	4	9.9E-2	3.4E0	7.0E-1	6.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	tissue development	RT	<div><div></div><div></div></div>	4	4.8E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, NHR/GATA-type	RT	<div><div></div><div></div></div>	10	6.1E-1	1.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell fate commitment	RT	<div><div></div><div></div></div>	8	6.8E-1	1.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell development	RT	<div><div></div><div></div></div>	7	6.9E-1	1.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular response to BMP stimulus	RT	<div><div></div><div></div></div>	4	9.0E-1	7.9E-1	1.0E0	9.6E-1
Annotation Cluster 159		Enrichment Score: 1.22	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_MF_DIRECT	nucleosomal DNA binding	RT	<div><div></div><div></div></div>	17	2.3E-3	2.2E0	2.5E-2	2.3E-2
<input type="checkbox"/>	INTERPRO	Histone H3	RT	<div><div></div><div></div></div>	6	1.8E-1	2.0E0	8.6E-1	8.0E-1
<input type="checkbox"/>	SMART	H3	RT	<div><div></div><div></div></div>	6	5.2E-1	1.3E0	1.0E0	8.9E-1
Annotation Cluster 160		Enrichment Score: 1.22	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_KEYWORDS	Innate immunity	RT	<div><div></div><div></div></div>	55	4.3E-3	1.4E0	2.2E-2	1.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	innate immune response	RT	<div><div></div><div></div></div>	83	1.2E-1	1.1E0	8.2E-1	7.9E-1
<input type="checkbox"/>	UP_KEYWORDS	Immunity	RT	<div><div></div><div></div></div>	76	4.1E-1	1.0E0	1.0E0	8.0E-1
Annotation Cluster 161		Enrichment Score: 1.21	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 3	RT	<div><div></div><div></div></div>	5	2.0E-2	4.3E0	3.9E-1	3.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 4	RT	<div><div></div><div></div></div>	4	2.5E-2	5.4E0	4.6E-1	4.4E-1
<input type="checkbox"/>	INTERPRO	WW domain	RT	<div><div></div><div></div></div>	15	3.8E-2	1.8E0	2.7E-1	2.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 1	RT	<div><div></div><div></div></div>	9	5.3E-2	2.1E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 2	RT	<div><div></div><div></div></div>	9	5.3E-2	2.1E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW	RT	<div><div></div><div></div></div>	6	2.1E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	WW	RT	<div><div></div><div></div></div>	15	3.2E-1	1.2E0	1.0E0	8.9E-1
Annotation Cluster 162		Enrichment Score: 1.2	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	INTERPRO	2'-5'-oligoadenylate synthetase 1, domain 2/C-terminal	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	2'-5'-oligoadenylate synthase	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	2-5-oligoadenylate synthetase, conserved site	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	2'-5'-oligoadenylate synthetase activity	RT	<div><div></div><div></div></div>	4	1.6E-2	6.0E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	2-5-oligoadenylate synthetase, N-terminal	RT	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.3E-1	2.1E-1
<input type="checkbox"/>	INTERPRO	Nucleotidyl transferase domain	RT	<div><div></div><div></div></div>	4	2.1E-1	2.5E0	9.7E-1	9.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	nucleotidyltransferase activity	RT	<div><div></div><div></div></div>	5	6.8E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	transferase activity	RT	<div><div></div><div></div></div>	11	9.7E-1	6.8E-1	1.0E0	9.7E-1
Annotation Cluster 163		Enrichment Score: 1.2	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Rho-like	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BTB 1	RT	<div><div></div><div></div></div>	5	6.5E-2	3.1E0	9.7E-1	9.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BTB 2	RT	<div><div></div><div></div></div>	5	6.5E-2	3.1E0	9.7E-1	9.3E-1
Annotation Cluster 164		Enrichment Score: 1.18	<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"/>	GOTERM_BP_DIRECT	regulation of Golgi inheritance	RT		4	1.7E-2	5.9E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	face development	RT		8	2.2E-2	2.6E0	2.7E-1	2.6E-1
<input type="checkbox"/>	BIOCARTA	Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway	RT		9	2.7E-2	2.2E0	8.2E-2	6.2E-2
<input type="checkbox"/>	BIOCARTA	Roles of ?-arrestin-dependent Recruitment of Src Kinases in GPCR Signaling	RT		12	2.7E-2	1.9E0	8.3E-2	6.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of stress-activated MAPK cascade	RT		5	3.2E-2	3.7E0	3.5E-1	3.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of early endosome to late endosome transport	RT		5	3.2E-2	3.7E0	3.5E-1	3.4E-1
<input type="checkbox"/>	BIOCARTA	Pelp1 Modulation of Estrogen Receptor Activity	RT		6	3.8E-2	2.7E0	1.0E-1	7.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	Bergmann glial cell differentiation	RT		5	5.0E-2	3.3E0	4.7E-1	4.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	trachea formation	RT		4	6.4E-2	3.9E0	5.5E-1	5.3E-1
<input type="checkbox"/>	BIOCARTA	Sprouty regulation of tyrosine kinase signals	RT		10	8.5E-2	1.7E0	2.1E-1	1.6E-1
<input type="checkbox"/>	BIOCARTA	Regulation of Splicing through Sam68	RT		5	1.5E-1	2.2E0	3.2E-1	2.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	ERK1 and ERK2 cascade	RT		7	2.1E-1	1.7E0	1.0E0	9.6E-1
<input type="checkbox"/>	BIOCARTA	Role of ?-arrestins in the activation and targeting of MAP kinases	RT		8	2.2E-1	1.6E0	4.4E-1	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	thyroid gland development	RT		7	2.4E-1	1.7E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	lung morphogenesis	RT		4	3.8E-1	1.8E0	1.0E0	9.6E-1
Annotation Cluster 165		Enrichment Score: 1.18	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, receptor class III, conserved site	RT		8	1.9E-5	6.2E0	3.5E-4	3.3E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of phospholipase C activity	RT		8	1.0E-4	5.3E0	3.6E-3	3.4E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	vascular endothelial growth factor-activated receptor activity	RT		5	1.8E-2	4.3E0	1.3E-1	1.2E-1
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, CSF-1/PDGF receptor	RT		4	3.2E-2	5.0E0	2.3E-1	2.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	tyrosine-protein kinase, CSF-1/PDGF receptor type	RT		4	3.5E-2	4.8E0	4.6E-1	4.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	vascular endothelial growth factor signaling pathway	RT		4	6.4E-2	3.9E0	5.5E-1	5.3E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	vascular endothelial growth factor binding	RT		3	2.0E-1	3.6E0	8.0E-1	7.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 7	RT		5	4.1E-1	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	growth factor binding	RT		6	4.8E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 5	RT		9	5.7E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 3	RT		17	7.9E-1	9.0E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 6	RT		5	8.1E-1	9.2E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 4	RT		9	8.9E-1	8.1E-1	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Immunoglobulin	RT		10	9.3E-1	7.6E-1	1.0E0	9.3E-1
Annotation Cluster 166		Enrichment Score: 1.18	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	The IGF-1 Receptor and Longevity	RT		10	2.3E-2	2.1E0	7.5E-2	5.6E-2
<input type="checkbox"/>	BIOCARTA	Role of nicotinic acetylcholine receptors in the regulation of apoptosis	RT		9	1.0E-1	1.8E0	2.4E-1	1.8E-1
<input type="checkbox"/>	BIOCARTA	Phospholipase C Signaling Pathway	RT		6	1.2E-1	2.1E0	2.8E-1	2.1E-1
Annotation Cluster 167		Enrichment Score: 1.17	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:ZZ-type	RT		7	2.9E-2	2.8E0	5.3E-1	5.1E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, ZZ-type	RT		7	5.7E-2	2.4E0	3.8E-1	3.5E-1
<input type="checkbox"/>	SMART	ZnF_ZZ	RT		7	1.8E-1	1.8E0	7.3E-1	6.5E-1
Annotation Cluster 168		Enrichment Score: 1.17	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	HR1 rho-binding repeat	RT		5	2.7E-2	3.9E0	2.0E-1	1.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:REM 1	RT		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:REM 2	RT		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:REM 3	RT		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	SMART	Hr1	RT		5	6.8E-2	2.9E0	3.6E-1	3.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	epithelial cell migration	RT		3	2.7E-1	3.0E0	1.0E0	9.6E-1
Annotation Cluster 169		Enrichment Score: 1.17	G		Count	P_Value	Fold Change	Benjamini	FDR















































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptidyl-lysine monomethylation	RT		5	3.2E-2	3.7E0	3.5E-1	3.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptidyl-lysine dimethylation	RT		4	3.7E-2	4.7E0	3.8E-1	3.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:S-adenosyl-L-methionine binding	RT		9	1.3E-1	1.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein-lysine N-methyltransferase activity	RT		6	1.4E-1	2.1E0	6.3E-1	5.7E-1
Annotation Cluster 170		Enrichment Score: 1.16	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote	RT		16	2.7E-3	2.3E0	3.3E-2	3.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:UBA	RT		13	1.0E-2	2.2E0	2.3E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	Heat shock chaperonin-binding	RT		6	1.3E-2	3.7E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	polyubiquitin binding	RT		9	2.8E-2	2.3E0	1.9E-1	1.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of proteasomal ubiquitin-dependent protein catabolic process	RT		6	3.8E-2	3.0E0	3.9E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Ubiquilin	RT		4	5.7E-2	4.1E0	3.8E-1	3.5E-1
<input type="checkbox"/>	SMART	STI1	RT		6	7.5E-2	2.4E0	3.9E-1	3.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:UBA 1	RT		3	2.7E-1	2.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:UBA 2	RT		3	2.7E-1	2.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	UBA	RT		10	2.8E-1	1.4E0	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	UBA-like	RT		12	3.5E-1	1.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	autophagosome	RT		6	9.8E-1	6.0E-1	1.0E0	9.8E-1
Annotation Cluster 171		Enrichment Score: 1.16	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	NFkB activation by Nontypeable Hemophilus influenzae	RT		17	4.7E-4	2.2E0	3.8E-3	2.8E-3
<input type="checkbox"/>	BIOCARTA	The 4-1BB-dependent immune response	RT		13	2.5E-3	2.3E0	1.3E-2	9.9E-3
<input type="checkbox"/>	BIOCARTA	Signal transduction through IL1R	RT		18	1.5E-2	1.7E0	5.4E-2	4.0E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	I-kappaB/NF-kappaB complex	RT		4	3.0E-2	5.1E0	2.0E-1	1.8E-1
<input type="checkbox"/>	BIOCARTA	Activation of PKC through G protein coupled receptor	RT		6	3.8E-2	2.7E0	1.0E-1	7.9E-2
<input type="checkbox"/>	BIOCARTA	Acetylation and Deacetylation of RelA in The Nucleus	RT		10	3.8E-2	1.9E0	1.0E-1	7.9E-2
<input type="checkbox"/>	BIOCARTA	NF-kB Signaling Pathway	RT		12	8.2E-2	1.6E0	2.1E-1	1.5E-1
<input type="checkbox"/>	BBID	77.IkBα Kinase JNK MEKK1	RT		6	8.2E-2	2.2E0	9.9E-1	9.9E-1
<input type="checkbox"/>	BIOCARTA	CD40L Signaling Pathway	RT		8	1.7E-1	1.7E0	3.6E-1	2.7E-1
<input type="checkbox"/>	BIOCARTA	Double Stranded RNA Induced Gene Expression	RT		6	1.9E-1	1.9E0	3.8E-1	2.8E-1
<input type="checkbox"/>	BIOCARTA	TNF/Stress Related Signaling	RT		10	4.1E-1	1.2E0	6.8E-1	5.1E-1
<input type="checkbox"/>	BBID	90.IB and-cat-Arm processing of Ci	RT		4	4.3E-1	1.7E0	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	Erythropoietin mediated neuroprotection through NF-kB	RT		6	4.8E-1	1.3E0	8.0E-1	6.0E-1
<input type="checkbox"/>	BIOCARTA	TNFR2 Signaling Pathway	RT		7	5.4E-1	1.2E0	8.6E-1	6.4E-1
<input type="checkbox"/>	BIOCARTA	TACI and BCMA stimulation of B cell immune responses.	RT		6	5.5E-1	1.2E0	8.7E-1	6.5E-1
Annotation Cluster 172		Enrichment Score: 1.16	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	UBA/THIF-type NAD/FAD binding fold	RT		6	1.3E-2	3.7E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitin activating enzyme activity	RT		4	3.6E-2	4.8E0	2.3E-1	2.0E-1
<input type="checkbox"/>	INTERPRO	Ubiquitin-activating enzyme, E1	RT		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	Ubiquitin-activating enzyme e1, C-terminal	RT		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	small protein activating enzyme activity	RT		4	9.7E-2	3.4E0	4.8E-1	4.4E-1
<input type="checkbox"/>	INTERPRO	Ubiquitin/SUMO-activating enzyme E1	RT		3	1.2E-1	4.6E0	6.2E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	Ubiquitin-activating enzyme	RT		3	1.2E-1	4.6E0	6.2E-1	5.8E-1
<input type="checkbox"/>	SMART	SM00985	RT		3	1.5E-1	4.0E0	6.6E-1	5.8E-1
Annotation Cluster 173		Enrichment Score: 1.13	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of glucose import in response to insulin stimulus	RT		6	5.4E-2	2.7E0	4.9E-1	4.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2 1	RT		5	8.6E-2	2.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2 2	RT		5	8.6E-2	2.8E0	1.0E0	9.7E-1
Annotation Cluster 174		Enrichment Score: 1.13	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:IQ 5	RT	<div><div></div><div></div></div>	6	1.5E-2	3.7E0	2.9E-1	2.8E-1
<input type="checkbox"/>	INTERPRO	Dilute	RT	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Dilute	RT	<div><div></div><div></div></div>	4	1.0E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	SM01132	RT	<div><div></div><div></div></div>	4	2.4E-1	2.3E0	9.2E-1	8.2E-1
Annotation Cluster 175		Enrichment Score: 1.12	<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:BRO1	RT	<div><div></div><div></div></div>	4	4.5E-2	4.5E0	7.8E-1	7.5E-1
<input type="checkbox"/>	INTERPRO	BRO1 domain	RT	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	3.8E-1	3.5E-1
<input type="checkbox"/>	SMART	SM01041	RT	<div><div></div><div></div></div>	4	1.7E-1	2.7E0	6.8E-1	6.0E-1
Annotation Cluster 176		Enrichment Score: 1.11	<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:SWIRM	RT	<div><div></div><div></div></div>	4	4.5E-2	4.5E0	7.8E-1	7.5E-1
<input type="checkbox"/>	INTERPRO	SANT domain	RT	<div><div></div><div></div></div>	9	4.7E-2	2.1E0	3.2E-1	3.0E-1
<input type="checkbox"/>	INTERPRO	SWIRM domain	RT	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	3.8E-1	3.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SANT	RT	<div><div></div><div></div></div>	5	3.0E-1	1.8E0	1.0E0	9.7E-1
Annotation Cluster 177		Enrichment Score: 1.11	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	dendritic spine development	RT	<div><div></div><div></div></div>	7	1.3E-2	3.2E0	2.0E-1	1.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	axon guidance receptor activity	RT	<div><div></div><div></div></div>	4	9.7E-2	3.4E0	4.8E-1	4.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	central nervous system projection neuron axonogenesis	RT	<div><div></div><div></div></div>	4	1.4E-1	3.0E0	8.3E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	retinal ganglion cell axon guidance	RT	<div><div></div><div></div></div>	6	2.1E-1	1.9E0	1.0E0	9.6E-1
Annotation Cluster 178		Enrichment Score: 1.1	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:C2	RT	<div><div></div><div></div></div>	22	6.6E-3	1.8E0	1.5E-1	1.5E-1
<input type="checkbox"/>	INTERPRO	C2 calcium-dependent membrane targeting	RT	<div><div></div><div></div></div>	35	7.5E-2	1.3E0	4.1E-1	3.8E-1
<input type="checkbox"/>	SMART	C2	RT	<div><div></div><div></div></div>	19	1.0E0	6.0E-1	1.0E0	1.0E0
Annotation Cluster 179		Enrichment Score: 1.1	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:TFIIB-type	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	INTERPRO	Transcription factor TFIIB	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, TFIIB-type	RT	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.2E-1	5.8E-1
Annotation Cluster 180		Enrichment Score: 1.09	<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:Nop	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	INTERPRO	Nop domain	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	NOSIC	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	SMART	SM00931	RT	<div><div></div><div></div></div>	3	1.5E-1	4.0E0	6.6E-1	5.8E-1
Annotation Cluster 181		Enrichment Score: 1.07	<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	calmodulin-dependent protein kinase activity	RT	<div><div></div><div></div></div>	9	2.1E-2	2.4E0	1.5E-1	1.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Autoinhibitory domain	RT	<div><div></div><div></div></div>	4	4.5E-2	4.5E0	7.8E-1	7.5E-1
<input type="checkbox"/>	BIOCARTA	Ca+ +/- Calmodulin-dependent Protein Kinase Activation	RT	<div><div></div><div></div></div>	5	6.4E-1	1.2E0	9.7E-1	7.3E-1
Annotation Cluster 182		Enrichment Score: 1.06	<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	actomyosin	RT	<div><div></div><div></div></div>	7	5.9E-3	3.7E0	5.3E-2	4.7E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	myosin II filament	RT	<div><div></div><div></div></div>	3	6.6E-2	6.4E0	3.5E-1	3.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	myosin II complex	RT	<div><div></div><div></div></div>	4	8.3E-2	3.6E0	4.1E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	actomyosin structure organization	RT	<div><div></div><div></div></div>	7	3.0E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Cell shape	RT	<div><div></div><div></div></div>	5	5.0E-1	1.4E0	1.0E0	8.0E-1
Annotation Cluster 183		Enrichment Score: 1.06	<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	sensory perception	RT	<div><div></div><div></div></div>	6	5.4E-2	2.7E0	4.9E-1	4.7E-1
<input type="checkbox"/>	UP_KEYWORDS	Opioid peptide	RT	<div><div></div><div></div></div>	3	5.7E-2	6.9E0	2.4E-1	1.9E-1
<input type="checkbox"/>	INTERPRO	Opioid neuropeptide precursor	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	neuropeptide hormone activity	RT	<div><div></div><div></div></div>	9	1.2E-1	1.8E0	5.7E-1	5.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	opioid peptide activity	RT	<div><div></div><div></div></div>	3	1.3E-1	4.5E0	6.0E-1	5.5E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	opioid receptor binding	RT	<div><div></div><div></div></div>	3	1.3E-1	4.5E0	6.0E-1	5.5E-1
Annotation Cluster 184		Enrichment Score: 1.06	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	proteasome core complex, alpha-subunit complex	RT	<div><div></div><div></div></div>	5	2.5E-2	4.0E0	1.8E-1	1.6E-1
<input type="checkbox"/>	INTERPRO	Proteasome, alpha-subunit, N-terminal domain	RT	<div><div></div><div></div></div>	5	2.7E-2	3.9E0	2.0E-1	1.9E-1
<input type="checkbox"/>	INTERPRO	Proteasome A-type subunit	RT	<div><div></div><div></div></div>	5	2.7E-2	3.9E0	2.0E-1	1.9E-1
<input type="checkbox"/>	UP_KEYWORDS	Threonine protease	RT	<div><div></div><div></div></div>	7	6.0E-2	2.4E0	2.4E-1	2.0E-1
<input type="checkbox"/>	INTERPRO	Proteasome, subunit alpha/beta	RT	<div><div></div><div></div></div>	7	7.2E-2	2.3E0	4.0E-1	3.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	proteasome core complex	RT	<div><div></div><div></div></div>	7	9.9E-2	2.1E0	4.8E-1	4.2E-1
<input type="checkbox"/>	SMART	SM00948	RT	<div><div></div><div></div></div>	5	1.1E-1	2.5E0	5.3E-1	4.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	threonine-type endopeptidase activity	RT	<div><div></div><div></div></div>	7	1.3E-1	2.0E0	6.0E-1	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	proteolysis involved in cellular protein catabolic process	RT	<div><div></div><div></div></div>	10	4.2E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Proteasome, beta-type subunit, conserved site	RT	<div><div></div><div></div></div>	3	6.0E-1	1.5E0	1.0E0	9.2E-1
Annotation Cluster 185		Enrichment Score: 1.05	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:A.T hook 3	RT	<div><div></div><div></div></div>	5	4.7E-2	3.4E0	8.0E-1	7.7E-1
<input type="checkbox"/>	INTERPRO	AT hook, DNA-binding motif	RT	<div><div></div><div></div></div>	4	5.7E-2	4.1E0	3.8E-1	3.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:A.T hook 1	RT	<div><div></div><div></div></div>	5	1.1E-1	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:A.T hook 2	RT	<div><div></div><div></div></div>	5	1.1E-1	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	AT_hook	RT	<div><div></div><div></div></div>	4	1.7E-1	2.7E0	6.8E-1	6.0E-1
Annotation Cluster 186		Enrichment Score: 1.05	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Mitogen-activated protein (MAP) kinase, JNK	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	JUN kinase activity	RT	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	JUN phosphorylation	RT	<div><div></div><div></div></div>	3	1.3E-1	4.4E0	8.3E-1	7.9E-1
Annotation Cluster 187		Enrichment Score: 1.05	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of leukocyte apoptotic process	RT	<div><div></div><div></div></div>	5	9.1E-3	4.9E0	1.5E-1	1.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	establishment of T cell polarity	RT	<div><div></div><div></div></div>	4	6.4E-2	3.9E0	5.5E-1	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of cell motility	RT	<div><div></div><div></div></div>	6	7.2E-2	2.5E0	5.8E-1	5.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of dendritic cell antigen processing and presentation	RT	<div><div></div><div></div></div>	3	3.4E-1	2.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	response to prostaglandin E	RT	<div><div></div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	9.6E-1
Annotation Cluster 188		Enrichment Score: 1.04	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	JAK-STAT cascade involved in growth hormone signaling pathway	RT	<div><div></div><div></div></div>	9	1.4E-3	3.6E0	3.3E-2	3.2E-2
<input type="checkbox"/>	BIOCARTA	Stat3 Signaling Pathway	RT	<div><div></div><div></div></div>	8	1.9E-3	3.1E0	1.1E-2	8.6E-3
<input type="checkbox"/>	INTERPRO	Tyrosine-protein kinase, non-receptor Jak/Tyk2	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	tyrosine-protein kinase, Jak/Tyk2 type	RT	<div><div></div><div></div></div>	4	1.6E-2	6.0E0	2.5E-1	2.5E-1
<input type="checkbox"/>	BIOCARTA	IL22 Soluble Receptor Signaling Pathway	RT	<div><div></div><div></div></div>	9	2.7E-2	2.2E0	8.2E-2	6.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2; atypical	RT	<div><div></div><div></div></div>	4	4.5E-2	4.5E0	7.8E-1	7.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MyTH4 1	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MyTH4 2	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	BBID	48.mice minus JAKs and STATs	RT	<div><div></div><div></div></div>	8	8.1E-2	1.9E0	9.9E-1	9.9E-1
<input type="checkbox"/>	INTERPRO	MyTH4 domain	RT	<div><div></div><div></div></div>	4	1.7E-1	2.8E0	8.1E-1	7.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	growth hormone receptor binding	RT	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	8.0E-1	7.2E-1
<input type="checkbox"/>	SMART	MyTH4	RT	<div><div></div><div></div></div>	4	3.9E-1	1.8E0	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	FERM domain	RT	<div><div></div><div></div></div>	10	4.4E-1	1.2E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Band 4.1 domain	RT	<div><div></div><div></div></div>	10	4.4E-1	1.2E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	FERM central domain	RT	<div><div></div><div></div></div>	9	5.9E-1	1.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FERM	RT	<div><div></div><div></div></div>	8	5.9E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	B41	RT	<div><div></div><div></div></div>	10	9.1E-1	7.9E-1	1.0E0	9.1E-1















































Annotation Cluster 1		Enrichment Score: ?	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	FERM/acyl-CoA-binding protein, 3-helical bundle	RT	<div></div>	4	9.9E-1	5.0E-1	1.0E0	9.9E-1
Annotation Cluster 189		Enrichment Score: 1.04	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Proprotein convertase, P	RT	<div></div>	6	1.7E-3	5.3E0	2.1E-2	2.0E-2
<input type="checkbox"/>	INTERPRO	Peptidase S8, subtilisin, Asp-active site	RT	<div></div>	5	7.7E-3	5.2E0	7.5E-2	7.0E-2
<input type="checkbox"/>	INTERPRO	Peptidase S8, subtilisin, Ser-active site	RT	<div></div>	6	7.7E-3	4.1E0	7.5E-2	7.0E-2
<input type="checkbox"/>	INTERPRO	Peptidase S8, subtilisin, His-active site	RT	<div></div>	6	7.7E-3	4.1E0	7.5E-2	7.0E-2
<input type="checkbox"/>	INTERPRO	Peptidase S8, subtilisin-related	RT	<div></div>	6	1.3E-2	3.7E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Peptidase S8/S53 domain	RT	<div></div>	6	2.1E-2	3.4E0	1.6E-1	1.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptide biosynthetic process	RT	<div></div>	4	3.7E-2	4.7E0	3.8E-1	3.7E-1
<input type="checkbox"/>	INTERPRO	Proteinase inhibitor, propeptide	RT	<div></div>	6	1.3E-1	2.2E0	6.2E-1	5.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptide hormone processing	RT	<div></div>	5	2.8E-1	1.9E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein processing	RT	<div></div>	10	8.8E-1	8.2E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	signal peptide processing	RT	<div></div>	3	9.4E-1	7.1E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Zymogen	RT	<div></div>	17	1.0E0	5.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Serine protease	RT	<div></div>	9	1.0E0	4.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Charge relay system	RT	<div></div>	8	1.0E0	2.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	serine-type endopeptidase activity	RT	<div></div>	12	1.0E0	2.8E-1	1.0E0	1.0E0
Annotation Cluster 190		Enrichment Score: 1.03	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Natriuretic peptide receptor	RT	<div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	natriuretic peptide receptor activity	RT	<div></div>	3	7.5E-2	6.0E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	hormone binding	RT	<div></div>	5	9.7E-2	2.7E0	4.8E-1	4.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	peptide hormone binding	RT	<div></div>	8	1.5E-1	1.8E0	6.7E-1	6.0E-1
Annotation Cluster 191		Enrichment Score: 1.02	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	SANT domain	RT	<div></div>	9	4.7E-2	2.1E0	3.2E-1	3.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SANT 1	RT	<div></div>	4	1.3E-1	3.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SANT 2	RT	<div></div>	4	1.3E-1	3.0E0	1.0E0	9.7E-1
Annotation Cluster 192		Enrichment Score: 1.01	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	mRNA cleavage	RT	<div></div>	7	8.4E-3	3.5E0	1.4E-1	1.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	mRNA polyadenylation	RT	<div></div>	10	3.6E-2	2.1E0	3.8E-1	3.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	mRNA cleavage and polyadenylation specificity factor complex	RT	<div></div>	5	1.7E-1	2.3E0	7.0E-1	6.3E-1
<input type="checkbox"/>	BIOCARTA	Polyadenylation of mRNA	RT	<div></div>	6	1.9E-1	1.9E0	3.8E-1	2.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	tRNA splicing, via endonucleolytic cleavage and ligation	RT	<div></div>	5	2.4E-1	2.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	pre-mRNA cleavage required for polyadenylation	RT	<div></div>	3	4.0E-1	2.2E0	1.0E0	9.6E-1
Annotation Cluster 193		Enrichment Score: 0.99	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	natural killer cell differentiation	RT	<div></div>	6	3.8E-2	3.0E0	3.9E-1	3.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of lymphocyte activation	RT	<div></div>	3	7.6E-2	5.9E0	5.8E-1	5.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	apoptotic cell clearance	RT	<div></div>	6	9.4E-2	2.4E0	6.9E-1	6.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	vagina development	RT	<div></div>	4	1.8E-1	2.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	secretion by cell	RT	<div></div>	4	2.3E-1	2.4E0	1.0E0	9.6E-1
Annotation Cluster 194		Enrichment Score: 0.98	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	sulfate assimilation	RT	<div></div>	6	4.9E-3	4.4E0	9.2E-2	8.8E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor	RT	<div></div>	5	3.1E-2	3.7E0	2.0E-1	1.8E-1
<input type="checkbox"/>	INTERPRO	Thioredoxin	RT	<div></div>	4	3.2E-2	5.0E0	2.3E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	glycerol ether metabolic process	RT	<div></div>	4	3.7E-2	4.7E0	3.8E-1	3.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein-disulfide reductase activity	RT	<div></div>	3	2.6E-1	3.0E0	9.9E-1	9.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	thioredoxin-disulfide reductase activity	RT	<div></div>	3	5.2E-1	1.8E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein disulfide oxidoreductase activity	RT	<div></div>	5	5.9E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular oxidant detoxification	RT	<div></div>	5	1.0E0	4.2E-1	1.0E0	1.0E0

















































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 195		Enrichment Score: 0.98	<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	adenylate cyclase-inhibiting dopamine receptor signaling pathway	RT	<div><div></div><div></div></div>	5	3.5E-3	5.9E0	7.1E-2	6.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	dopamine metabolic process	RT	<div><div></div><div></div></div>	6	2.6E-2	3.2E0	3.0E-1	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	behavioral response to cocaine	RT	<div><div></div><div></div></div>	6	7.2E-2	2.5E0	5.8E-1	5.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	dopamine neurotransmitter receptor activity, coupled via Gi/Go	RT	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	response to histamine	RT	<div><div></div><div></div></div>	3	7.6E-2	5.9E0	5.8E-1	5.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of protein secretion	RT	<div><div></div><div></div></div>	5	1.6E-1	2.3E0	9.3E-1	8.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	synaptic transmission, dopaminergic	RT	<div><div></div><div></div></div>	5	1.6E-1	2.3E0	9.3E-1	8.9E-1
<input type="checkbox"/>	INTERPRO	Dopamine receptor family	RT	<div><div></div><div></div></div>	3	1.9E-1	3.7E0	8.7E-1	8.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	dopamine neurotransmitter receptor activity	RT	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	8.0E-1	7.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	response to amphetamine	RT	<div><div></div><div></div></div>	8	2.6E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	arachidonic acid secretion	RT	<div><div></div><div></div></div>	6	3.8E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	dopamine binding	RT	<div><div></div><div></div></div>	3	5.2E-1	1.8E0	1.0E0	9.1E-1
Annotation Cluster 196		Enrichment Score: 0.96	<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	chromatin silencing complex	RT	<div><div></div><div></div></div>	5	4.0E-2	3.5E0	2.5E-1	2.3E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	rDNA heterochromatin	RT	<div><div></div><div></div></div>	3	1.2E-1	4.8E0	5.3E-1	4.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	chromatin silencing at rDNA	RT	<div><div></div><div></div></div>	9	2.8E-1	1.4E0	1.0E0	9.6E-1
Annotation Cluster 197		Enrichment Score: 0.96	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	INTERPRO	Mitogen-activated protein (MAP) kinase kinase kinase, 9/10/11	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	mitogen-activated protein kinase kinase kinase, types 9/10/11	RT	<div><div></div><div></div></div>	3	7.3E-2	6.0E0	6.0E-1	6.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	JUN kinase kinase kinase activity	RT	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Leucine-zipper 1	RT	<div><div></div><div></div></div>	4	1.3E-1	3.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Leucine-zipper 2	RT	<div><div></div><div></div></div>	4	1.3E-1	3.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	activation of JNKK activity	RT	<div><div></div><div></div></div>	3	2.7E-1	3.0E0	1.0E0	9.6E-1
Annotation Cluster 198		Enrichment Score: 0.95	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Lysophosphatidic acid receptor	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	BIOCARTA	Rho-Selective Guanine Exchange Factor AKAP13 Mediates Stress Fiber Formation	RT	<div><div></div><div></div></div>	7	1.0E-1	2.0E0	2.4E-1	1.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	lysophosphatidic acid receptor activity	RT	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	8.0E-1	7.2E-1
Annotation Cluster 199		Enrichment Score: 0.95	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	chemokine receptor binding	RT	<div><div></div><div></div></div>	5	3.1E-2	3.7E0	2.0E-1	1.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of T cell migration	RT	<div><div></div><div></div></div>	5	7.2E-2	3.0E0	5.8E-1	5.6E-1
<input type="checkbox"/>	BBID	109.Chemokine families	RT	<div><div></div><div></div></div>	11	6.4E-1	1.0E0	1.0E0	1.0E0
Annotation Cluster 200		Enrichment Score: 0.94	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Domain A	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Domain B	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	INTERPRO	Retinoblastoma-associated protein, B-box	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	Retinoblastoma-associated protein, A-box	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	Rb C-terminal	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	Domain of unknown function DUF3452, retinoblastoma-associated	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	SMART	SM01367	RT	<div><div></div><div></div></div>	3	1.5E-1	4.0E0	6.6E-1	5.8E-1
<input type="checkbox"/>	SMART	SM01368	RT	<div><div></div><div></div></div>	3	1.5E-1	4.0E0	6.6E-1	5.8E-1
<input type="checkbox"/>	SMART	SM01369	RT	<div><div></div><div></div></div>	3	1.5E-1	4.0E0	6.6E-1	5.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of lipid kinase activity	RT	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Spacer	RT	<div><div></div><div></div></div>	4	7.1E-1	1.1E0	1.0E0	9.7E-1
Annotation Cluster 201		Enrichment Score: 0.94	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of norepinephrine secretion	RT	<div><div></div><div></div></div>	5	1.8E-2	4.2E0	2.4E-1	2.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of smooth muscle contraction	RT	<div><div></div><div></div></div>	7	4.0E-2	2.6E0	4.0E-1	3.8E-1

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Implicated in ligand binding	RT		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	activation of protein kinase B activity	RT		9	5.9E-2	2.1E0	5.3E-1	5.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	alpha2-adrenergic receptor activity	RT		3	7.5E-2	6.0E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	epidermal growth factor-activated receptor transactivation by G-protein coupled receptor signaling pathway	RT		3	1.3E-1	4.4E0	8.3E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of epinephrine secretion	RT		3	1.3E-1	4.4E0	8.3E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	activation of MAPK activity by adrenergic receptor signaling pathway	RT		3	1.3E-1	4.4E0	8.3E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of vasoconstriction	RT		6	2.4E-1	1.8E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	epinephrine binding	RT		3	2.6E-1	3.0E0	9.9E-1	9.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	adenylate cyclase-activating adrenergic receptor signaling pathway	RT		5	4.0E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Adrenergic receptor	RT		3	4.4E-1	2.1E0	1.0E0	9.2E-1
Annotation Cluster 202		Enrichment Score: 0.94	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	ESC/E(Z) complex	RT		8	7.3E-3	3.2E0	6.2E-2	5.5E-2
<input type="checkbox"/>	BIOCARTA	The PRC2 Complex Sets Long-term Gene Silencing Through Modification of Histone Tails	RT		7	3.4E-1	1.5E0	6.0E-1	4.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of gene expression, epigenetic	RT		9	6.2E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 203		Enrichment Score: 0.91	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of chemokine production	RT		8	1.6E-2	2.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interleukin-12 production	RT		10	1.7E-2	2.4E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of NF-kappaB import into nucleus	RT		8	5.1E-2	2.3E0	4.8E-1	4.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of nitric-oxide synthase biosynthetic process	RT		6	5.4E-2	2.7E0	4.9E-1	4.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interferon-beta production	RT		9	7.2E-2	2.0E0	5.8E-1	5.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of tumor necrosis factor production	RT		13	8.7E-2	1.6E0	6.5E-1	6.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interleukin-6 production	RT		11	2.2E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interferon-alpha production	RT		4	3.3E-1	2.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	lipopolysaccharide binding	RT		5	5.2E-1	1.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of interleukin-10 production	RT		5	5.6E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	BIOCARTA	Dendritic cells in regulating TH1 and TH2 Development	RT		5	9.5E-1	7.1E-1	1.0E0	9.5E-1
Annotation Cluster 204		Enrichment Score: 0.91	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA binding, bending	RT		8	2.1E-2	2.7E0	1.5E-1	1.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA topological change	RT		4	1.8E-1	2.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	BIOCARTA	Apoptotic DNA fragmentation and tissue homeostasis	RT		5	4.9E-1	1.4E0	8.0E-1	6.0E-1
Annotation Cluster 205		Enrichment Score: 0.9	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Dual specificity phosphatase	RT		11	2.0E-2	2.2E0	1.5E-1	1.4E-1
<input type="checkbox"/>	INTERPRO	M-phase inducer phosphatase	RT		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Rhodanese	RT		7	7.6E-2	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	dual specificity protein phosphatase (MAP kinase phosphatase)	RT		4	9.5E-2	3.4E0	7.4E-1	7.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	inactivation of MAPK activity	RT		8	1.1E-1	1.9E0	7.9E-1	7.5E-1
<input type="checkbox"/>	BIOCARTA	Regulation of MAP Kinase Pathways Through Dual Specificity Phosphatases	RT		6	1.2E-1	2.1E0	2.8E-1	2.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	MAP kinase tyrosine/serine/threonine phosphatase activity	RT		5	1.6E-1	2.3E0	6.9E-1	6.3E-1
<input type="checkbox"/>	INTERPRO	Rhodanese-like domain	RT		7	1.8E-1	1.8E0	8.6E-1	7.9E-1
<input type="checkbox"/>	INTERPRO	Mitogen-activated protein (MAP) kinase phosphatase	RT		4	2.1E-1	2.5E0	9.7E-1	9.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	endoderm formation	RT		4	3.3E-1	2.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	RHOD	RT		7	4.2E-1	1.3E0	1.0E0	8.9E-1
Annotation Cluster 206		Enrichment Score: 0.9	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	Rap protein signal transduction	RT		6	1.6E-2	3.6E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	microvillus assembly	RT		6	1.5E-1	2.1E0	8.5E-1	8.2E-1


















































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	recycling_endosome membrane	RT		6	8.4E-1	8.7E-1	1.0E0	8.9E-1
Annotation Cluster 207		Enrichment Score: 0.89	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K4 specific)	RT		9	5.5E-3	3.0E0	5.2E-2	4.7E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:PHD-type 3	RT		5	4.7E-2	3.4E0	8.0E-1	7.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:S-adenosyl-L-methionine binding	RT		9	1.3E-1	1.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	FY-rich, N-terminal	RT		3	1.9E-1	3.7E0	8.7E-1	8.1E-1
<input type="checkbox"/>	INTERPRO	FY-rich, C-terminal	RT		3	1.9E-1	3.7E0	8.7E-1	8.1E-1
<input type="checkbox"/>	SMART	FYRN	RT		3	3.6E-1	2.4E0	1.0E0	8.9E-1
<input type="checkbox"/>	SMART	FYRC	RT		3	3.6E-1	2.4E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:S-adenosyl-L-methionine	RT		9	4.8E-1	1.2E0	1.0E0	9.7E-1
Annotation Cluster 208		Enrichment Score: 0.88	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	postsynaptic membrane	RT		47	1.2E-2	1.4E0	9.6E-2	8.5E-2
<input type="checkbox"/>	UP_KEYWORDS	Postsynaptic cell membrane	RT		38	1.6E-2	1.5E0	7.5E-2	6.0E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	postsynaptic density	RT		38	6.6E-2	1.3E0	3.5E-1	3.1E-1
<input type="checkbox"/>	UP_KEYWORDS	Synapse	RT		53	5.2E-1	1.0E0	1.0E0	8.0E-1
<input type="checkbox"/>	UP_KEYWORDS	Cell junction	RT		91	8.4E-1	9.3E-1	1.0E0	8.4E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	cell junction	RT		64	9.0E-1	8.9E-1	1.0E0	9.0E-1
Annotation Cluster 209		Enrichment Score: 0.88	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	phospholipase C-activating G-protein coupled acetylcholine receptor signaling pathway	RT		5	3.2E-2	3.7E0	3.5E-1	3.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	G-protein coupled acetylcholine receptor activity	RT		4	9.7E-2	3.4E0	4.8E-1	4.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	adenylate cyclase-inhibiting G-protein coupled acetylcholine receptor signaling pathway	RT		4	9.9E-2	3.4E0	7.0E-1	6.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	synaptic transmission, cholinergic	RT		4	9.6E-1	6.4E-1	1.0E0	9.6E-1
Annotation Cluster 210		Enrichment Score: 0.88	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	endoplasmic reticulum chaperone complex	RT		5	8.0E-2	2.9E0	4.1E-1	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein folding in endoplasmic reticulum	RT		5	1.6E-1	2.3E0	9.3E-1	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Prevents secretion from ER	RT		13	1.8E-1	1.5E0	1.0E0	9.7E-1
Annotation Cluster 211		Enrichment Score: 0.87	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of glycolytic process	RT		7	2.0E-2	3.0E0	2.5E-1	2.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	fatty acid homeostasis	RT		5	1.6E-1	2.3E0	9.3E-1	8.9E-1
<input type="checkbox"/>	KEGG_PATHWAY	Regulation of autophagy	RT		5	7.3E-1	1.1E0	1.0E0	7.3E-1
Annotation Cluster 212		Enrichment Score: 0.87	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway	RT		13	8.7E-3	2.0E0	3.4E-2	2.6E-2
<input type="checkbox"/>	BIOCARTA	Regulation of eIF4e and p70 S6 Kinase	RT		14	1.9E-2	1.8E0	6.6E-2	5.0E-2
<input type="checkbox"/>	BIOCARTA	mTOR Signaling Pathway	RT		13	9.1E-2	1.6E0	2.2E-1	1.7E-1
<input type="checkbox"/>	BBID	106.Glycogen synthase-synthesis	RT		6	1.5E-1	1.9E0	9.9E-1	9.9E-1
<input type="checkbox"/>	BBID	2.Cytokine Receptors	RT		5	1.6E-1	2.1E0	9.9E-1	9.9E-1
<input type="checkbox"/>	BBID	104.Insulin signaling	RT		10	1.6E-1	1.5E0	9.9E-1	9.9E-1
<input type="checkbox"/>	BBID	105.Signaling glucose uptake	RT		6	3.3E-1	1.5E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	108.Regulating glucose transport	RT		6	3.3E-1	1.5E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	107.mRNA translation-protein synthesis	RT		7	4.7E-1	1.3E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	37.Akt-PKB Effector of P13K in Vivo	RT		4	6.6E-1	1.3E0	1.0E0	1.0E0
Annotation Cluster 213		Enrichment Score: 0.87	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	5-Hydroxytryptamine receptor family	RT		6	7.7E-3	4.1E0	7.5E-2	7.0E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	serotonin binding	RT		6	1.6E-2	3.6E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	adenylate cyclase-inhibiting serotonin receptor signaling pathway	RT		3	7.6E-2	5.9E0	5.8E-1	5.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	vasoconstriction	RT		5	3.2E-1	1.7E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	serotonin receptor signaling pathway	RT		4	3.8E-1	1.8E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	neurotransmitter receptor activity	RT		6	4.5E-1	1.4E0	1.0E0	9.1E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of behavior	RT	<div><div></div><div></div></div>	3	4.6E-1	2.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	G-protein coupled serotonin receptor activity	RT	<div><div></div><div></div></div>	6	5.1E-1	1.3E0	1.0E0	9.1E-1
Annotation Cluster 214		Enrichment Score: 0.86	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of protein metabolic process	RT	<div><div></div><div></div></div>	5	3.2E-2	3.7E0	3.5E-1	3.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular response to laminar fluid shear stress	RT	<div><div></div><div></div></div>	4	1.4E-1	3.0E0	8.3E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of response to cytokine stimulus	RT	<div><div></div><div></div></div>	3	2.0E-1	3.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of heterotypic cell-cell adhesion	RT	<div><div></div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	9.6E-1
Annotation Cluster 215		Enrichment Score: 0.86	<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:KEN	RT	<div><div></div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	INTERPRO	KEN domain	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	PUB domain	RT	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	PUG	RT	<div><div></div><div></div></div>	3	3.6E-1	2.4E0	1.0E0	8.9E-1
Annotation Cluster 216		Enrichment Score: 0.84	<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:DOC	RT	<div><div></div><div></div></div>	4	1.0E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Anaphase-promoting complex, subunit 10/DOC domain	RT	<div><div></div><div></div></div>	4	1.2E-1	3.1E0	6.2E-1	5.8E-1
<input type="checkbox"/>	SMART	SM01337	RT	<div><div></div><div></div></div>	4	2.4E-1	2.3E0	9.2E-1	8.2E-1
Annotation Cluster 217		Enrichment Score: 0.82	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Pseudouridine synthase, RsuA/RluB/C/D/E/F	RT	<div><div></div><div></div></div>	4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	tRNA pseudouridine synthesis	RT	<div><div></div><div></div></div>	4	6.4E-2	3.9E0	5.5E-1	5.3E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	deaminase activity	RT	<div><div></div><div></div></div>	4	1.4E-1	3.0E0	6.1E-1	5.5E-1
<input type="checkbox"/>	INTERPRO	Pseudouridine synthase, catalytic domain	RT	<div><div></div><div></div></div>	4	3.5E-1	1.9E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	pseudouridine synthase activity	RT	<div><div></div><div></div></div>	4	3.7E-1	1.8E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	pseudouridine synthesis	RT	<div><div></div><div></div></div>	3	6.7E-1	1.4E0	1.0E0	9.6E-1
Annotation Cluster 218		Enrichment Score: 0.82	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of the force of heart contraction	RT	<div><div></div><div></div></div>	8	3.0E-2	2.5E0	3.4E-1	3.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	ventricular cardiac muscle tissue morphogenesis	RT	<div><div></div><div></div></div>	8	1.1E-1	1.9E0	7.9E-1	7.5E-1
<input type="checkbox"/>	KEGG_PATHWAY	Cardiac muscle contraction	RT	<div><div></div><div></div></div>	8	9.9E-1	5.6E-1	1.0E0	9.9E-1
Annotation Cluster 219		Enrichment Score: 0.82	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	IL22 Soluble Receptor Signaling Pathway	RT	<div><div></div><div></div></div>	9	2.7E-2	2.2E0	8.2E-2	6.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	JAK-STAT cascade	RT	<div><div></div><div></div></div>	11	3.3E-2	2.0E0	3.7E-1	3.5E-1
<input type="checkbox"/>	BBID	48.mice minus JAKs and STATs	RT	<div><div></div><div></div></div>	8	8.1E-2	1.9E0	9.9E-1	9.9E-1
<input type="checkbox"/>	INTERPRO	STAT transcription factor, DNA-binding	RT	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.4E-1
<input type="checkbox"/>	INTERPRO	STAT transcription factor, coiled coil	RT	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.4E-1
<input type="checkbox"/>	INTERPRO	STAT transcription factor, core	RT	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.4E-1
<input type="checkbox"/>	INTERPRO	STAT transcription factor, DNA-binding, subdomain	RT	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.4E-1
<input type="checkbox"/>	INTERPRO	STAT transcription factor, protein interaction	RT	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.4E-1
<input type="checkbox"/>	INTERPRO	STAT transcription factor, all-alpha	RT	<div><div></div><div></div></div>	4	8.8E-2	3.5E0	4.7E-1	4.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	CCR5 chemokine receptor binding	RT	<div><div></div><div></div></div>	4	1.4E-1	3.0E0	6.1E-1	5.5E-1
<input type="checkbox"/>	SMART	SM00964	RT	<div><div></div><div></div></div>	4	2.4E-1	2.3E0	9.2E-1	8.2E-1
<input type="checkbox"/>	INTERPRO	p53-like transcription factor, DNA-binding	RT	<div><div></div><div></div></div>	10	2.7E-1	1.4E0	1.0E0	9.2E-1
<input type="checkbox"/>	BBID	12.IL-6 type cytok-signal-transduct	RT	<div><div></div><div></div></div>	9	3.9E-1	1.3E0	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	IL-10 Anti-inflammatory Signaling Pathway	RT	<div><div></div><div></div></div>	6	4.1E-1	1.4E0	6.8E-1	5.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of type I interferon-mediated signaling pathway	RT	<div><div></div><div></div></div>	6	4.5E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	BBID	11.IL-6 gp130-Jak-STAT	RT	<div><div></div><div></div></div>	3	6.4E-1	1.5E0	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	IFN alpha signaling pathway	RT	<div><div></div><div></div></div>	3	8.4E-1	1.0E0	1.0E0	8.4E-1
Annotation Cluster 220		Enrichment Score: 0.82	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of NFAT protein import into nucleus	RT	<div><div></div><div></div></div>	5	7.2E-2	3.0E0	5.8E-1	5.6E-1




















































Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	calcineurin complex	RT		3	1.2E-1	4.8E0	5.3E-1	4.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	calcineurin-NFAT signaling cascade	RT		3	4.0E-1	2.2E0	1.0E0	9.6E-1
Annotation Cluster 221		Enrichment Score: 0.82	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Hedgehog signaling pathway	RT		11	2.2E-2	2.1E0	3.9E-2	2.2E-2
<input type="checkbox"/>	BIOCARTA	Sonic Hedgehog (Shh) Pathway	RT		10	3.8E-2	1.9E0	1.0E-1	7.9E-2
<input type="checkbox"/>	BIOCARTA	ChREBP regulation by carbohydrates and cAMP	RT		12	4.1E-2	1.8E0	1.1E-1	8.3E-2
<input type="checkbox"/>	BIOCARTA	Regulation of ck1/cdk5 by type 1 glutamate receptors	RT		10	5.9E-2	1.8E0	1.5E-1	1.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	ciliary base	RT		8	1.2E-1	1.9E0	5.3E-1	4.7E-1
<input type="checkbox"/>	BIOCARTA	Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor	RT		11	1.3E-1	1.6E0	2.9E-1	2.2E-1
<input type="checkbox"/>	BIOCARTA	Transcription Regulation by Methyltransferase of CARM1	RT		7	1.5E-1	1.8E0	3.2E-1	2.4E-1
<input type="checkbox"/>	BIOCARTA	Attenuation of GPCR Signaling	RT		7	2.1E-1	1.7E0	4.2E-1	3.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	cAMP-dependent protein kinase complex	RT		3	3.0E-1	2.7E0	9.4E-1	8.3E-1
<input type="checkbox"/>	BIOCARTA	Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway	RT		6	3.3E-1	1.6E0	5.9E-1	4.4E-1
<input type="checkbox"/>	BIOCARTA	Phospholipase C-epsilon pathway	RT		6	3.3E-1	1.6E0	5.9E-1	4.4E-1
<input type="checkbox"/>	BIOCARTA	Stathmin and breast cancer resistance to antimicrotubule agents	RT		10	4.1E-1	1.2E0	6.8E-1	5.1E-1
<input type="checkbox"/>	UP_KEYWORDS	cAMP	RT		7	4.3E-1	1.3E0	1.0E0	8.0E-1
<input type="checkbox"/>	BIOCARTA	GATA3 participate in activating the Th2 cytokine genes expression	RT		6	6.2E-1	1.2E0	9.5E-1	7.2E-1
Annotation Cluster 222		Enrichment Score: 0.82	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	cyclin-dependent protein serine/threonine kinase regulator activity	RT		6	9.1E-2	2.4E0	4.7E-1	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of cyclin-dependent protein serine/threonine kinase activity	RT		8	9.6E-2	2.0E0	7.0E-1	6.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of phosphorylation of RNA polymerase II C-terminal domain	RT		3	4.0E-1	2.2E0	1.0E0	9.6E-1
Annotation Cluster 223		Enrichment Score: 0.8	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 9	RT		4	2.5E-2	5.4E0	4.6E-1	4.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 8	RT		4	4.5E-2	4.5E0	7.8E-1	7.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 7	RT		4	7.0E-2	3.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 6	RT		4	1.3E-1	3.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	RNA-processing protein, HAT helix	RT		4	2.1E-1	2.5E0	9.7E-1	9.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 5	RT		4	2.1E-1	2.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 4	RT		4	2.5E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 1	RT		4	3.0E-1	2.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 2	RT		4	3.0E-1	2.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HAT 3	RT		4	3.0E-1	2.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	HAT	RT		4	4.7E-1	1.6E0	1.0E0	8.9E-1
Annotation Cluster 224		Enrichment Score: 0.8	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A1	RT		3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A2	RT		3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A3	RT		3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Putative uncharacterized protein C21orf81	RT		3	1.6E-1	4.1E0	1.0E0	9.7E-1
Annotation Cluster 225		Enrichment Score: 0.8	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Phosphoserine intermediate	RT		6	9.0E-3	4.1E0	2.1E-1	2.0E-1
<input type="checkbox"/>	INTERPRO	Alkaline phosphatase	RT		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Alkaline phosphatase, active site	RT		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	SMART	alkPPc	RT		4	4.9E-2	4.0E0	2.8E-1	2.4E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	alkaline phosphatase activity	RT		4	6.3E-2	4.0E0	3.6E-1	3.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	lipid moiety-binding region:GPI-anchor amidated aspartate	RT		3	2.2E-1	3.4E0	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"/>	KEGG_PATHWAY	Folate biosynthesis	RT	<div></div>	5	2.7E-1	1.9E0	4.2E-1	2.7E-1
<input type="checkbox"/>	INTERPRO	Alkaline phosphatase-like, alpha/beta/alpha	RT	<div></div>	4	9.0E-1	8.0E-1	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Alkaline-phosphatase-like, core domain	RT	<div></div>	4	9.1E-1	7.7E-1	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	lipid moiety-binding region:GPI-anchor amidated serine	RT	<div></div>	4	9.9E-1	5.0E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_KEYWORDS	GPI-anchor	RT	<div></div>	8	1.0E0	4.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	anchored component of membrane	RT	<div></div>	6	1.0E0	3.4E-1	1.0E0	1.0E0
Annotation Cluster 226		Enrichment Score: 0.78	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	TATA-box binding protein	RT	<div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	Beta2-adaptin/TBP, C-terminal domain	RT	<div></div>	3	2.5E-1	3.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA-templated transcription, initiation	RT	<div></div>	9	2.5E-1	1.5E0	1.0E0	9.6E-1
Annotation Cluster 227		Enrichment Score: 0.78	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	type I interferon signaling pathway	RT	<div></div>	16	1.1E-1	1.5E0	7.6E-1	7.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of viral genome replication	RT	<div></div>	11	1.2E-1	1.6E0	8.3E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	defense response to virus	RT	<div></div>	33	2.2E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Antiviral defense	RT	<div></div>	21	2.4E-1	1.2E0	7.6E-1	6.1E-1
Annotation Cluster 228		Enrichment Score: 0.76	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA binding, bending	RT	<div></div>	8	2.1E-2	2.7E0	1.5E-1	1.4E-1
<input type="checkbox"/>	INTERPRO	HMG box A DNA-binding domain, conserved site	RT	<div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	High mobility group (HMG) box domain	RT	<div></div>	14	1.2E-1	1.5E0	6.2E-1	5.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA geometric change	RT	<div></div>	3	1.3E-1	4.4E0	8.3E-1	7.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:HMG box 1	RT	<div></div>	5	2.7E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:HMG box 2	RT	<div></div>	5	2.7E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:HMG box	RT	<div></div>	7	6.4E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	HMG	RT	<div></div>	13	7.1E-1	9.7E-1	1.0E0	8.9E-1
Annotation Cluster 229		Enrichment Score: 0.76	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	PIR_SUPERFAMILY	heat shock protein, HSP90/HTPG types	RT	<div></div>	4	1.6E-2	6.0E0	2.5E-1	2.5E-1
<input type="checkbox"/>	INTERPRO	Heat shock protein Hsp90, conserved site	RT	<div></div>	3	1.2E-1	4.6E0	6.2E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	Heat shock protein Hsp90, N-terminal	RT	<div></div>	4	1.7E-1	2.8E0	8.1E-1	7.4E-1
<input type="checkbox"/>	INTERPRO	Heat shock protein Hsp90	RT	<div></div>	4	2.6E-1	2.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	HATPase_c	RT	<div></div>	4	5.4E-1	1.5E0	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	Histidine kinase-like ATPase, ATP-binding domain	RT	<div></div>	6	6.3E-1	1.1E0	1.0E0	9.2E-1
Annotation Cluster 230		Enrichment Score: 0.75	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PDZ	RT	<div></div>	25	3.8E-2	1.5E0	6.8E-1	6.5E-1
<input type="checkbox"/>	INTERPRO	PDZ domain	RT	<div></div>	31	1.6E-1	1.2E0	7.9E-1	7.3E-1
<input type="checkbox"/>	SMART	PDZ	RT	<div></div>	31	9.2E-1	8.4E-1	1.0E0	9.2E-1
Annotation Cluster 231		Enrichment Score: 0.75	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Nitric Oxide Signaling Pathway	RT	<div></div>	11	1.3E-1	1.6E0	2.9E-1	2.2E-1
<input type="checkbox"/>	BIOCARTA	Role of MEF2D in T-cell Apoptosis	RT	<div></div>	9	1.9E-1	1.6E0	3.8E-1	2.8E-1
<input type="checkbox"/>	BIOCARTA	Effects of calcineurin in Keratinocyte Differentiation	RT	<div></div>	9	2.4E-1	1.5E0	4.5E-1	3.4E-1
Annotation Cluster 232		Enrichment Score: 0.74	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	beta-catenin destruction complex	RT	<div></div>	6	5.6E-2	2.7E0	3.2E-1	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	beta-catenin destruction complex assembly	RT	<div></div>	3	2.0E-1	3.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	beta-catenin destruction complex disassembly	RT	<div></div>	5	5.2E-1	1.3E0	1.0E0	9.6E-1
Annotation Cluster 233		Enrichment Score: 0.74	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Carbamoyl-phosphate synthetase large subunit-like, ATP-binding domain	RT	<div></div>	4	8.8E-2	3.5E0	4.7E-1	4.4E-1
<input type="checkbox"/>	INTERPRO	ATP-grasp fold, subdomain 2	RT	<div></div>	7	9.0E-2	2.2E0	4.8E-1	4.4E-1
<input type="checkbox"/>	INTERPRO	ATP-grasp fold	RT	<div></div>	5	1.4E-1	2.4E0	7.1E-1	6.6E-1

















































Annotation Cluster 1		Enrichment Score: ?	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Pre-ATP-grasp domain	RT	<div><div></div></div>	5	1.8E-1	2.2E0	8.6E-1	7.9E-1
<input type="checkbox"/>	INTERPRO	ATP-grasp fold, subdomain 1	RT	<div><div></div></div>	5	2.1E-1	2.1E0	9.8E-1	9.1E-1
<input type="checkbox"/>	INTERPRO	Rudiment single hybrid motif	RT	<div><div></div></div>	3	2.5E-1	3.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:ATP-grasp	RT	<div><div></div></div>	3	5.9E-1	1.6E0	1.0E0	9.7E-1
Annotation Cluster 234		Enrichment Score: 0.74	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	TRAF-like	RT	<div><div></div></div>	8	9.5E-2	2.0E0	5.1E-1	4.7E-1
<input type="checkbox"/>	INTERPRO	SIAH-type domain	RT	<div><div></div></div>	5	1.1E-1	2.6E0	6.0E-1	5.6E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, TRAF-type	RT	<div><div></div></div>	4	3.0E-1	2.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:TRAF-type	RT	<div><div></div></div>	3	3.3E-1	2.6E0	1.0E0	9.7E-1
Annotation Cluster 235		Enrichment Score: 0.73	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Pancreatic hormone-like, conserved site	RT	<div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	neuropeptide hormone activity	RT	<div><div></div></div>	9	1.2E-1	1.8E0	5.7E-1	5.2E-1
<input type="checkbox"/>	INTERPRO	Pancreatic hormone-like	RT	<div><div></div></div>	3	1.2E-1	4.6E0	6.2E-1	5.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of appetite	RT	<div><div></div></div>	4	2.3E-1	2.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	PAH	RT	<div><div></div></div>	3	2.6E-1	3.0E0	9.6E-1	8.5E-1
<input type="checkbox"/>	UP_KEYWORDS	Amidation	RT	<div><div></div></div>	7	6.6E-1	1.1E0	1.0E0	8.0E-1
Annotation Cluster 236		Enrichment Score: 0.73	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Small Leucine-rich Proteoglycan (SLRP) molecules	RT	<div><div></div></div>	6	1.5E-2	3.1E0	5.4E-2	4.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	keratan sulfate catabolic process	RT	<div><div></div></div>	6	3.8E-2	3.0E0	3.9E-1	3.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...) (keratan sulfate)	RT	<div><div></div></div>	3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_KEYWORDS	Proteoglycan	RT	<div><div></div></div>	11	1.7E-1	1.5E0	5.6E-1	4.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	keratan sulfate biosynthetic process	RT	<div><div></div></div>	6	5.2E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	lysosomal lumen	RT	<div><div></div></div>	13	7.0E-1	9.7E-1	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	Golgi lumen	RT	<div><div></div></div>	14	7.6E-1	9.3E-1	1.0E0	8.9E-1
<input type="checkbox"/>	UP_KEYWORDS	Extracellular matrix	RT	<div><div></div></div>	19	1.0E0	5.1E-1	1.0E0	1.0E0
Annotation Cluster 237		Enrichment Score: 0.73	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 7	RT	<div><div></div></div>	4	1.0E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Regulator of chromosome condensation, RCC1	RT	<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	RT	<div><div></div></div>	6	1.1E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 4	RT	<div><div></div></div>	6	1.3E-1	2.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 1	RT	<div><div></div></div>	6	1.6E-1	2.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 2	RT	<div><div></div></div>	6	1.6E-1	2.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 3	RT	<div><div></div></div>	6	1.6E-1	2.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II	RT	<div><div></div></div>	6	2.8E-1	1.7E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:RCC1 6	RT	<div><div></div></div>	4	3.0E-1	2.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	COG_ONTOLOGY	Cell division and chromosome partitioning/ Cytoskeleton	RT	<div><div></div></div>	5	1.0E0	5.1E-1	1.0E0	1.0E0
Annotation Cluster 238		Enrichment Score: 0.73	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Magnesium	RT	<div><div></div></div>	30	3.1E-3	1.7E0	7.8E-2	7.5E-2
<input type="checkbox"/>	INTERPRO	P-type ATPase, transmembrane domain	RT	<div><div></div></div>	8	8.4E-3	3.1E0	8.1E-2	7.5E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular sodium ion homeostasis	RT	<div><div></div></div>	9	8.5E-3	2.8E0	1.4E-1	1.4E-1
<input type="checkbox"/>	INTERPRO	Cation-transporting P-type ATPase, C-terminal	RT	<div><div></div></div>	8	1.2E-2	2.9E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Cation-transporting P-type ATPase, N-terminal	RT	<div><div></div></div>	8	1.7E-2	2.8E0	1.4E-1	1.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium-transporting ATPase activity	RT	<div><div></div></div>	5	4.9E-2	3.3E0	2.9E-1	2.7E-1
<input type="checkbox"/>	INTERPRO	P-type ATPase, A domain	RT	<div><div></div></div>	11	5.4E-2	1.9E0	3.7E-1	3.4E-1
<input type="checkbox"/>	INTERPRO	Cation-transporting P-type ATPase	RT	<div><div></div></div>	11	5.4E-2	1.9E0	3.7E-1	3.4E-1
<input type="checkbox"/>	INTERPRO	P-type ATPase, phosphorylation site	RT	<div><div></div></div>	11	5.4E-2	1.9E0	3.7E-1	3.4E-1
<input type="checkbox"/>	INTERPRO	P-type ATPase, cytoplasmic domain N	RT	<div><div></div></div>	11	5.4E-2	1.9E0	3.7E-1	3.4E-1

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:4-aspartylphosphate intermediate	RT		11	5.9E-2	1.9E0	8.9E-1	8.6E-1
<input type="checkbox"/>	INTERPRO	Calcium-transporting P-type ATPase, subfamily IIA, SERCA-type	RT		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	SMART	SM00831	RT		8	7.5E-2	2.0E0	3.9E-1	3.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 2; via carbonyl oxygen	RT		10	1.1E-1	1.7E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Sodium/potassium-transporting P-type ATPase, subfamily IIC	RT		3	2.5E-1	3.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	sarcoplasmic reticulum membrane	RT		8	2.8E-1	1.5E0	9.2E-1	8.2E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	sarcoplasmic reticulum	RT		8	2.8E-1	1.5E0	9.2E-1	8.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 2	RT		11	3.2E-1	1.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	platelet dense tubular network membrane	RT		3	4.3E-1	2.1E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	sodium:potassium-exchanging ATPase activity	RT		3	5.2E-1	1.8E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	sodium ion export from cell	RT		3	5.2E-1	1.8E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Sarcoplasmic reticulum	RT		7	5.4E-1	1.2E0	1.0E0	8.0E-1
<input type="checkbox"/>	INTERPRO	HAD-like domain	RT		14	5.5E-1	1.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular potassium ion homeostasis	RT		3	6.3E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	establishment or maintenance of transmembrane electrochemical gradient	RT		3	6.7E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of cardiac conduction	RT		9	7.5E-1	9.5E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	potassium ion import	RT		3	9.6E-1	6.3E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	ATP hydrolysis coupled proton transport	RT		3	9.8E-1	5.6E-1	1.0E0	9.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	calcium ion transmembrane transport	RT		12	9.9E-1	6.0E-1	1.0E0	9.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	ion transmembrane transport	RT		24	9.9E-1	6.8E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_KEYWORDS	Potassium transport	RT		7	1.0E0	4.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Potassium	RT		8	1.0E0	4.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Calcium transport	RT		5	1.0E0	3.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain:Lumenal	RT		17	1.0E0	2.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Ion transport	RT		24	1.0E0	2.6E-1	1.0E0	1.0E0
Annotation Cluster 239		Enrichment Score: 0.72	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	3'-UTR-mediated mRNA stabilization	RT		7	5.3E-2	2.4E0	4.9E-1	4.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	translation activator activity	RT		4	1.8E-1	2.7E0	7.6E-1	6.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	mRNA 3'-UTR binding	RT		8	7.3E-1	9.7E-1	1.0E0	9.1E-1
Annotation Cluster 240		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	6.0E-1	5.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 2	RT		8	3.3E-2	2.5E0	6.0E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	Protein kinase C, alpha/beta/gamma types	RT		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	protein kinase C, alpha/beta/gamma types	RT		3	7.3E-2	6.0E0	6.0E-1	6.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium-dependent protein kinase C activity	RT		3	1.3E-1	4.5E0	6.0E-1	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of glial cell apoptotic process	RT		3	3.4E-1	2.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 1	RT		9	3.9E-1	1.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	African trypanosomiasis	RT		8	4.4E-1	1.3E0	6.6E-1	4.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Calcium 3; via carbonyl oxygen	RT		4	6.1E-1	1.3E0	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		4	8.7E-1	8.5E-1	1.0E0	9.7E-1
Annotation Cluster 241		Enrichment Score: 0.69	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Formyl peptide receptor family	RT		5	4.3E-2	3.4E0	3.0E-1	2.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	N-formyl peptide receptor activity	RT		3	1.3E-1	4.5E0	6.0E-1	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	complement receptor mediated signaling pathway	RT		4	2.3E-1	2.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	complement receptor activity	RT		3	2.6E-1	3.0E0	9.9E-1	9.0E-1
<input type="checkbox"/>	KEGG_PATHWAY	Staphylococcus aureus infection	RT		7	9.6E-1	6.8E-1	1.0E0	9.6E-1
Annotation Cluster 242		Enrichment Score: 0.69	G		Count	P_Value	Fold Change	Benjamini	FDR

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div>G</div></div>	<div><div></div><div>RT</div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Btk-type	RT	<div><div></div><div>RT</div></div>		4	1.3E-1	3.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, Btk motif	RT	<div><div></div><div>RT</div></div>		4	1.7E-1	2.8E0	8.1E-1	7.4E-1
<input type="checkbox"/>	SMART	BTK	RT	<div><div></div><div>RT</div></div>		4	3.9E-1	1.8E0	1.0E0	8.9E-1
Annotation Cluster 243		Enrichment Score: 0.69	<div><div></div><div>G</div></div>	<div><div></div><div>RT</div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	peptide YY receptor activity	RT	<div><div></div><div>RT</div></div>		3	7.5E-2	6.0E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	Neuropeptide Y receptor family	RT	<div><div></div><div>RT</div></div>		4	2.6E-1	2.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	neuropeptide Y receptor activity	RT	<div><div></div><div>RT</div></div>		3	4.6E-1	2.0E0	1.0E0	9.1E-1
Annotation Cluster 244		Enrichment Score: 0.67	<div><div></div><div>G</div></div>	<div><div></div><div>RT</div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:I-domain	RT	<div><div></div><div>RT</div></div>		3	1.1E-1	5.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	XPG conserved site	RT	<div><div></div><div>RT</div></div>		3	1.2E-1	4.6E0	6.2E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	XPG/Rad2 endonuclease	RT	<div><div></div><div>RT</div></div>		3	1.9E-1	3.7E0	8.7E-1	8.1E-1
<input type="checkbox"/>	INTERPRO	5'-3' exonuclease, C-terminal domain	RT	<div><div></div><div>RT</div></div>		3	1.9E-1	3.7E0	8.7E-1	8.1E-1
<input type="checkbox"/>	INTERPRO	XPG-I domain	RT	<div><div></div><div>RT</div></div>		3	1.9E-1	3.7E0	8.7E-1	8.1E-1
<input type="checkbox"/>	INTERPRO	Helix-hairpin-helix motif, class 2	RT	<div><div></div><div>RT</div></div>		3	1.9E-1	3.7E0	8.7E-1	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:N-domain	RT	<div><div></div><div>RT</div></div>		3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	XPG N-terminal	RT	<div><div></div><div>RT</div></div>		3	2.5E-1	3.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	HhH2	RT	<div><div></div><div>RT</div></div>		3	3.6E-1	2.4E0	1.0E0	8.9E-1
<input type="checkbox"/>	SMART	XPGI	RT	<div><div></div><div>RT</div></div>		3	3.6E-1	2.4E0	1.0E0	8.9E-1
<input type="checkbox"/>	SMART	XPGN	RT	<div><div></div><div>RT</div></div>		3	3.6E-1	2.4E0	1.0E0	8.9E-1
Annotation Cluster 245		Enrichment Score: 0.67	<div><div></div><div>G</div></div>	<div><div></div><div>RT</div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Aspartic peptidase, DDI1-type	RT	<div><div></div><div>RT</div></div>		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	aspartic-type endopeptidase activity	RT	<div><div></div><div>RT</div></div>		10	8.8E-2	1.8E0	4.6E-1	4.2E-1
<input type="checkbox"/>	INTERPRO	Aspartic peptidase	RT	<div><div></div><div>RT</div></div>		8	1.3E-1	1.8E0	6.5E-1	6.1E-1
<input type="checkbox"/>	INTERPRO	Peptidase A1	RT	<div><div></div><div>RT</div></div>		4	2.1E-1	2.5E0	9.7E-1	9.0E-1
<input type="checkbox"/>	INTERPRO	Propeptide, peptidase A1	RT	<div><div></div><div>RT</div></div>		3	3.2E-1	2.7E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_KEYWORDS	Aspartyl protease	RT	<div><div></div><div>RT</div></div>		4	6.1E-1	1.3E0	1.0E0	8.0E-1
<input type="checkbox"/>	INTERPRO	Peptidase aspartic, active site	RT	<div><div></div><div>RT</div></div>		4	6.8E-1	1.2E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	propeptide:Activation peptide	RT	<div><div></div><div>RT</div></div>		4	1.0E0	3.6E-1	1.0E0	1.0E0
Annotation Cluster 246		Enrichment Score: 0.64	<div><div></div><div>G</div></div>	<div><div></div><div>RT</div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PDZ	RT	<div><div></div><div>RT</div></div>		25	3.8E-2	1.5E0	6.8E-1	6.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:LD motif 1	RT	<div><div></div><div>RT</div></div>		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:LD motif 2	RT	<div><div></div><div>RT</div></div>		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:LD motif 3	RT	<div><div></div><div>RT</div></div>		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding	RT	<div><div></div><div>RT</div></div>		5	3.0E-1	1.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding 3	RT	<div><div></div><div>RT</div></div>		6	3.0E-1	1.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_KEYWORDS	LIM domain	RT	<div><div></div><div>RT</div></div>		13	3.5E-1	1.2E0	1.0E0	8.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding 4	RT	<div><div></div><div>RT</div></div>		3	5.0E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, LIM-type	RT	<div><div></div><div>RT</div></div>		13	5.0E-1	1.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding 1	RT	<div><div></div><div>RT</div></div>		8	6.2E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:LIM zinc-binding 2	RT	<div><div></div><div>RT</div></div>		8	6.2E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	LIM	RT	<div><div></div><div>RT</div></div>		13	9.6E-1	7.3E-1	1.0E0	9.6E-1
Annotation Cluster 247		Enrichment Score: 0.63	<div><div></div><div>G</div></div>	<div><div></div><div>RT</div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Enolase, C-terminal	RT	<div><div></div><div>RT</div></div>		4	3.2E-2	5.0E0	2.3E-1	2.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	phosphopyruvate hydratase complex	RT	<div><div></div><div>RT</div></div>		4	5.4E-2	4.2E0	3.2E-1	2.8E-1
<input type="checkbox"/>	INTERPRO	Enolase	RT	<div><div></div><div>RT</div></div>		4	5.7E-2	4.1E0	3.8E-1	3.5E-1
<input type="checkbox"/>	INTERPRO	Enolase, N-terminal	RT	<div><div></div><div>RT</div></div>		4	5.7E-2	4.1E0	3.8E-1	3.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	phosphopyruvate hydratase activity	RT	<div><div></div><div>RT</div></div>		4	6.3E-2	4.0E0	3.6E-1	3.3E-1

Annotation Cluster 1		Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Enolase, conserved site	RT		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Glycolysis	RT		9	7.1E-2	2.0E0	2.8E-1	2.2E-1
<input type="checkbox"/>	SMART	SM01192	RT		4	1.0E-1	3.2E0	5.1E-1	4.5E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	enolase	RT		3	1.3E-1	4.5E0	9.1E-1	9.1E-1
<input type="checkbox"/>	SMART	SM01193	RT		4	1.7E-1	2.7E0	6.8E-1	6.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	canonical glycolysis	RT		7	2.7E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	glycolytic process	RT		8	3.5E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	BIOCARTA	Glycolysis Pathway	RT		3	8.8E-1	9.4E-1	1.0E0	8.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	gluconeogenesis	RT		6	8.9E-1	8.1E-1	1.0E0	9.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Biosynthesis of amino acids	RT		9	9.8E-1	6.6E-1	1.0E0	9.8E-1
<input type="checkbox"/>	KEGG_PATHWAY	Glycolysis / Gluconeogenesis	RT		8	9.8E-1	6.3E-1	1.0E0	9.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Substrate binding	RT		10	1.0E0	5.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Carbon metabolism	RT		11	1.0E0	5.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Biosynthesis of antibiotics	RT		17	1.0E0	4.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:Substrate	RT		16	1.0E0	3.6E-1	1.0E0	1.0E0
Annotation Cluster 248		Enrichment Score: 0.63			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Dorso-ventral axis formation	RT		12	7.3E-3	2.3E0	1.4E-2	7.3E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LNR 3	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	INTERPRO	Notch, NODP domain	RT		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	INTERPRO	Notch, NOD domain	RT		4	1.5E-2	6.2E0	1.2E-1	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LNR 1	RT		4	2.5E-2	5.4E0	4.6E-1	4.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LNR 2	RT		4	2.5E-2	5.4E0	4.6E-1	4.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 28	RT		4	2.5E-2	5.4E0	4.6E-1	4.4E-1
<input type="checkbox"/>	SMART	SM01338	RT		4	4.9E-2	4.0E0	2.8E-1	2.4E-1
<input type="checkbox"/>	SMART	SM01339	RT		4	4.9E-2	4.0E0	2.8E-1	2.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 29	RT		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 33	RT		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 34	RT		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	INTERPRO	Domain of unknown function DUF3454, notch	RT		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	Notch domain	RT		4	8.8E-2	3.5E0	4.7E-1	4.4E-1
<input type="checkbox"/>	SMART	SM01334	RT		3	1.5E-1	4.0E0	6.6E-1	5.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 20	RT		3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 24	RT		3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 26	RT		3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 27	RT		3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 13; calcium-binding	RT		4	2.1E-1	2.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 17; calcium-binding	RT		3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 21; calcium-binding	RT		3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 22	RT		3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 23; calcium-binding	RT		3	2.2E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	NL	RT		4	2.4E-1	2.3E0	9.2E-1	8.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 14; calcium-binding	RT		4	2.5E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 15; calcium-binding	RT		4	2.5E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	Notch signaling pathway	RT		12	3.0E-1	1.3E0	4.6E-1	3.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 19	RT		3	3.3E-1	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 11; calcium-binding	RT		4	3.4E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 12; calcium-binding	RT		4	3.8E-1	1.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_KEYWORDS	Notch signaling pathway	RT		9	4.7E-1	1.2E0	1.0E0	8.0E-1





Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 8; calcium-binding	RT		5	4.8E-1	1.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 16; calcium-binding	RT		3	5.0E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 9; calcium-binding	RT		3	7.0E-1	1.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 9	RT		4	7.1E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 10	RT		3	7.4E-1	1.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 6	RT		6	7.9E-1	9.3E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 7; calcium-binding	RT		4	8.0E-1	9.7E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 3	RT		9	8.9E-1	8.1E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 7	RT		3	9.3E-1	7.3E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 4	RT		6	9.5E-1	6.9E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 5	RT		4	9.6E-1	6.5E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 5; calcium-binding	RT		3	9.8E-1	5.4E-1	1.0E0	9.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 2	RT		8	9.8E-1	6.1E-1	1.0E0	9.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 1	RT		9	1.0E0	5.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	EGF-like calcium-binding, conserved site	RT		7	1.0E0	4.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	EGF-type aspartate/asparagine hydroxylation site	RT		7	1.0E0	4.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	EGF-like calcium-binding	RT		7	1.0E0	3.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	EGF-like, conserved site	RT		10	1.0E0	3.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	EGF-like domain	RT		10	1.0E0	2.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Epidermal growth factor-like domain	RT		11	1.0E0	3.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	EGF_CA	RT		7	1.0E0	2.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	EGF	RT		11	1.0E0	2.4E-1	1.0E0	1.0E0
Annotation Cluster 249		Enrichment Score: 0.62	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Glycogen metabolism	RT		8	7.3E-2	2.1E0	2.8E-1	2.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	glycogen metabolic process	RT		8	2.1E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Carbohydrate metabolism	RT		10	9.4E-1	7.3E-1	1.0E0	9.4E-1
Annotation Cluster 250		Enrichment Score: 0.61	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of establishment of endothelial barrier	RT		4	9.9E-2	3.4E0	7.0E-1	6.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of bicellular tight junction assembly	RT		3	1.3E-1	4.4E0	8.3E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of myosin-light-chain-phosphatase activity	RT		3	2.0E-1	3.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cortical actin cytoskeleton organization	RT		6	3.8E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	establishment of protein localization to plasma membrane	RT		6	8.6E-1	8.5E-1	1.0E0	9.6E-1
Annotation Cluster 251		Enrichment Score: 0.61	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Actin-related protein 3 (Arp3)	RT		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	Arp2/3 protein complex	RT		4	2.9E-1	2.1E0	9.2E-1	8.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	Arp2/3 complex-mediated actin nucleation	RT		4	7.4E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 252		Enrichment Score: 0.61	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Rotamase	RT		10	9.1E-2	1.8E0	3.5E-1	2.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein peptidyl-prolyl isomerization	RT		12	9.7E-2	1.7E0	7.0E-1	6.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PPIase cyclophilin-type	RT		7	1.3E-1	2.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	peptidyl-prolyl cis-trans isomerase activity	RT		12	1.4E-1	1.6E0	6.1E-1	5.5E-1
<input type="checkbox"/>	UP_KEYWORDS	Isomerase	RT		23	1.7E-1	1.3E0	5.6E-1	4.5E-1
<input type="checkbox"/>	INTERPRO	Cyclophilin-like peptidyl-prolyl cis-trans isomerase domain	RT		7	1.8E-1	1.8E0	8.6E-1	7.9E-1
<input type="checkbox"/>	INTERPRO	Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site	RT		6	2.4E-1	1.8E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Cyclophilin-type peptidyl-prolyl cis-trans isomerase	RT		6	3.1E-1	1.6E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	cyclosporin A binding	RT		3	3.3E-1	2.6E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type	RT		5	4.1E-1	1.5E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	chaperone-mediated protein folding	RT		8	4.4E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	FK506 binding	RT		5	4.4E-1	1.5E0	1.0E0	9.1E-1

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain	RT		4	5.7E-1	1.4E0	1.0E0	9.2E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	peptidyl-prolyl cis-trans isomerase	RT		3	6.2E-1	1.5E0	1.0E0	1.0E0
Annotation Cluster 253		Enrichment Score: 0.61	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Circadian rhythm	RT		13	8.3E-3	2.2E0	1.6E-2	8.3E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	AMP-activated protein kinase activity	RT		5	1.8E-2	4.3E0	1.3E-1	1.2E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleotide-activated protein kinase complex	RT		6	1.9E-2	3.5E0	1.4E-1	1.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CBS 3	RT		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CBS 4	RT		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	carnitine shuttle	RT		4	1.8E-1	2.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	BIOCARTA	Reversal of Insulin Resistance by Leptin	RT		6	2.6E-1	1.7E0	4.8E-1	3.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Fatty acid biosynthesis	RT		9	4.9E-1	1.2E0	1.0E0	8.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	fatty acid biosynthetic process	RT		9	6.7E-1	1.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CBS 1	RT		3	7.7E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CBS 2	RT		3	7.7E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_KEYWORDS	CBS domain	RT		3	8.1E-1	1.0E0	1.0E0	8.1E-1
<input type="checkbox"/>	INTERPRO	Cystathionine beta-synthase, core	RT		3	8.6E-1	9.3E-1	1.0E0	9.2E-1
<input type="checkbox"/>	UP_KEYWORDS	Fatty acid metabolism	RT		15	8.8E-1	8.3E-1	1.0E0	8.8E-1
<input type="checkbox"/>	SMART	CBS	RT		3	9.0E-1	8.7E-1	1.0E0	9.0E-1
<input type="checkbox"/>	UP_KEYWORDS	Lipid biosynthesis	RT		10	1.0E0	4.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Lipid metabolism	RT		21	1.0E0	3.3E-1	1.0E0	1.0E0
Annotation Cluster 254		Enrichment Score: 0.6	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	uCalpain and friends in Cell spread	RT		9	1.4E-1	1.7E0	3.1E-1	2.3E-1
<input type="checkbox"/>	BIOCARTA	Cell to Cell Adhesion Signaling	RT		7	2.7E-1	1.6E0	5.0E-1	3.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	signal complex assembly	RT		3	4.0E-1	2.2E0	1.0E0	9.6E-1
Annotation Cluster 255		Enrichment Score: 0.6	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of transporter activity	RT		4	9.9E-2	3.4E0	7.0E-1	6.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	chloride channel regulator activity	RT		4	2.3E-1	2.4E0	8.9E-1	8.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of sodium ion transport	RT		5	4.0E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	sodium channel regulator activity	RT		7	4.5E-1	1.3E0	1.0E0	9.1E-1
Annotation Cluster 256		Enrichment Score: 0.58	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	BRCT domain	RT		8	1.5E-1	1.8E0	7.5E-1	7.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BRCT 2	RT		4	2.5E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:BRCT 1	RT		4	2.5E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	BRCT	RT		6	4.7E-1	1.3E0	1.0E0	8.9E-1
Annotation Cluster 257		Enrichment Score: 0.58	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	GKAP/Homer scaffold activity	RT		3	1.3E-1	4.5E0	6.0E-1	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	vocalization behavior	RT		5	2.0E-1	2.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	adult behavior	RT		7	2.7E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of excitatory postsynaptic potential	RT		4	6.8E-1	1.2E0	1.0E0	9.6E-1
Annotation Cluster 258		Enrichment Score: 0.58	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:DXDXT motif	RT		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:N-LIP	RT		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:C-LIP	RT		3	5.8E-2	6.8E0	8.8E-1	8.5E-1
<input type="checkbox"/>	INTERPRO	Lipin, N-terminal	RT		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	INTERPRO	LNS2, Lipin/Ned1/Smp2	RT		3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:LXXIL motif	RT		3	1.1E-1	5.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	LNS2	RT		3	4.6E-1	2.0E0	1.0E0	8.9E-1


















































Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	fatty acid catabolic process	RT	<div><div></div><div></div></div>	3	4.6E-1	2.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	phosphatidate phosphatase activity	RT	<div><div></div><div></div></div>	3	5.7E-1	1.6E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	phosphatidylethanolamine biosynthetic process	RT	<div><div></div><div></div></div>	3	7.5E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	phosphatidylcholine biosynthetic process	RT	<div><div></div><div></div></div>	3	9.4E-1	7.1E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	triglyceride biosynthetic process	RT	<div><div></div><div></div></div>	3	9.5E-1	6.8E-1	1.0E0	9.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Glycerolipid metabolism	RT	<div><div></div><div></div></div>	3	1.0E0	2.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Glycerophospholipid metabolism	RT	<div><div></div><div></div></div>	6	1.0E0	3.3E-1	1.0E0	1.0E0
Annotation Cluster 259		Enrichment Score: 0.58	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of anoikis	RT	<div><div></div><div></div></div>	8	1.6E-2	2.8E0	2.2E-1	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of intrinsic apoptotic signaling pathway	RT	<div><div></div><div></div></div>	8	6.4E-2	2.2E0	5.5E-1	5.3E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	BH3 domain binding	RT	<div><div></div><div></div></div>	3	1.3E-1	4.5E0	6.0E-1	5.5E-1
<input type="checkbox"/>	INTERPRO	Apoptosis regulator, Bcl-2, BH1 motif, conserved site	RT	<div><div></div><div></div></div>	3	3.8E-1	2.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Apoptosis regulator, Bcl-2, BH2 motif, conserved site	RT	<div><div></div><div></div></div>	3	3.8E-1	2.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Apoptosis regulator, Bcl-2, BH3 motif, conserved site	RT	<div><div></div><div></div></div>	3	3.8E-1	2.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:BH1	RT	<div><div></div><div></div></div>	3	5.0E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Blc2 family	RT	<div><div></div><div></div></div>	3	5.5E-1	1.7E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Bcl2-like	RT	<div><div></div><div></div></div>	3	5.5E-1	1.7E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:BH2	RT	<div><div></div><div></div></div>	3	5.9E-1	1.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:BH3	RT	<div><div></div><div></div></div>	3	7.4E-1	1.2E0	1.0E0	9.7E-1
Annotation Cluster 260		Enrichment Score: 0.57	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase II transcription factor activity, TBP-class protein binding, involved in preinitiation complex assembly	RT	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	transcription factor TFIID complex	RT	<div><div></div><div></div></div>	9	2.0E-1	1.6E0	7.9E-1	7.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	transcription factor activity, RNA polymerase II core promoter sequence-specific binding involved in preinitiation complex assembly	RT	<div><div></div><div></div></div>	3	4.6E-1	2.0E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	RNA polymerase II transcriptional preinitiation complex assembly	RT	<div><div></div><div></div></div>	3	7.5E-1	1.2E0	1.0E0	9.6E-1
Annotation Cluster 261		Enrichment Score: 0.57	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	I-kappaB/NF-kappaB complex	RT	<div><div></div><div></div></div>	4	3.0E-2	5.1E0	2.0E-1	1.8E-1
<input type="checkbox"/>	INTERPRO	NF-kappa-B/Rel/Dorsal	RT	<div><div></div><div></div></div>	4	3.2E-2	5.0E0	2.3E-1	2.1E-1
<input type="checkbox"/>	INTERPRO	Rel homology domain	RT	<div><div></div><div></div></div>	4	2.1E-1	2.5E0	9.7E-1	9.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:RHD	RT	<div><div></div><div></div></div>	3	3.9E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Cell surface receptor IPT/TIG	RT	<div><div></div><div></div></div>	6	5.8E-1	1.2E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	transcriptional activator activity, RNA polymerase II distal enhancer sequence-specific binding	RT	<div><div></div><div></div></div>	5	6.2E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	SMART	IPT	RT	<div><div></div><div></div></div>	5	9.3E-1	7.5E-1	1.0E0	9.3E-1
<input type="checkbox"/>	INTERPRO	Immunoglobulin E-set	RT	<div><div></div><div></div></div>	11	9.8E-1	6.4E-1	1.0E0	9.8E-1
Annotation Cluster 262		Enrichment Score: 0.55	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	UP_KEYWORDS	Nucleotidyltransferase	RT	<div><div></div><div></div></div>	17	1.0E-1	1.5E0	3.8E-1	3.1E-1
<input type="checkbox"/>	INTERPRO	DNA-directed DNA polymerase, family B, exonuclease domain	RT	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.2E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	DNA-directed DNA polymerase, family B, multifunctional domain	RT	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.2E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	DNA-directed DNA polymerase, family B	RT	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.2E-1	5.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	3'-5' exonuclease activity	RT	<div><div></div><div></div></div>	6	2.0E-1	1.9E0	8.0E-1	7.3E-1
<input type="checkbox"/>	SMART	POLBc	RT	<div><div></div><div></div></div>	3	2.6E-1	3.0E0	9.6E-1	8.5E-1
<input type="checkbox"/>	UP_KEYWORDS	DNA-directed DNA polymerase	RT	<div><div></div><div></div></div>	6	2.7E-1	1.7E0	8.2E-1	6.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-directed DNA polymerase activity	RT	<div><div></div><div></div></div>	7	3.6E-1	1.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_KEYWORDS	4Fe-4S	RT	<div><div></div><div></div></div>	7	4.6E-1	1.3E0	1.0E0	8.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	4 iron, 4 sulfur cluster binding	RT	<div><div></div><div></div></div>	7	7.3E-1	1.0E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_KEYWORDS	Iron-sulfur	RT	<div><div></div><div></div></div>	7	8.9E-1	8.0E-1	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	Ribonuclease H-like domain	RT	<div><div></div><div></div></div>	8	9.7E-1	6.6E-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 263		Enrichment Score: 0.51	<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	male meiosis	RT	<div><div></div><div></div></div>	8	6.4E-2	2.2E0	5.5E-1	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA methylation involved in gamete generation	RT	<div><div></div><div></div></div>	4	6.1E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	piRNA metabolic process	RT	<div><div></div><div></div></div>	3	7.5E-1	1.2E0	1.0E0	9.6E-1
Annotation Cluster 264		Enrichment Score: 0.5	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Zinc finger, RanBP2-type	RT	<div><div></div><div></div></div>	7	2.1E-1	1.7E0	9.6E-1	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:RanBP2-type	RT	<div><div></div><div></div></div>	5	2.7E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	ZnF_RBZ	RT	<div><div></div><div></div></div>	6	5.7E-1	1.2E0	1.0E0	8.9E-1
Annotation Cluster 265		Enrichment Score: 0.5	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Bernard Soulier syndrome	RT	<div><div></div><div></div></div>	3	5.7E-2	6.9E0	2.4E-1	1.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	blood coagulation, intrinsic pathway	RT	<div><div></div><div></div></div>	6	1.7E-1	2.0E0	9.8E-1	9.4E-1
<input type="checkbox"/>	UP_KEYWORDS	Blood coagulation	RT	<div><div></div><div></div></div>	8	5.6E-1	1.1E0	1.0E0	8.0E-1
<input type="checkbox"/>	UP_KEYWORDS	Hemostasis	RT	<div><div></div><div></div></div>	8	5.6E-1	1.1E0	1.0E0	8.0E-1
<input type="checkbox"/>	KEGG_PATHWAY	ECM-receptor interaction	RT	<div><div></div><div></div></div>	7	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 266		Enrichment Score: 0.5	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Zinc finger, TFIIS-type	RT	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:TFIIS-type	RT	<div><div></div><div></div></div>	3	2.7E-1	2.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	ZnF_C2C2	RT	<div><div></div><div></div></div>	3	4.6E-1	2.0E0	1.0E0	8.9E-1
Annotation Cluster 267		Enrichment Score: 0.5	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Brix domain	RT	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Brix	RT	<div><div></div><div></div></div>	3	2.7E-1	2.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	SM00879	RT	<div><div></div><div></div></div>	3	4.6E-1	2.0E0	1.0E0	8.9E-1
Annotation Cluster 268		Enrichment Score: 0.49	<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:Glutamine amidotransferase type-1	RT	<div><div></div><div></div></div>	3	1.6E-1	4.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Glutamine amidotransferase	RT	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	glutamine metabolic process	RT	<div><div></div><div></div></div>	3	8.7E-1	8.9E-1	1.0E0	9.6E-1
Annotation Cluster 269		Enrichment Score: 0.48	<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	cellular response to interleukin-1	RT	<div><div></div><div></div></div>	17	1.3E-1	1.4E0	8.3E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular response to interferon-gamma	RT	<div><div></div><div></div></div>	14	1.5E-1	1.5E0	9.0E-1	8.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	monocyte chemotaxis	RT	<div><div></div><div></div></div>	10	2.7E-1	1.4E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	lymphocyte chemotaxis	RT	<div><div></div><div></div></div>	6	5.2E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	CC chemokine, conserved site	RT	<div><div></div><div></div></div>	5	5.6E-1	1.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	CCR chemokine receptor binding	RT	<div><div></div><div></div></div>	4	7.7E-1	1.0E0	1.0E0	9.1E-1
Annotation Cluster 270		Enrichment Score: 0.48	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Insulin, conserved site	RT	<div><div></div><div></div></div>	4	1.7E-1	2.8E0	8.1E-1	7.4E-1
<input type="checkbox"/>	INTERPRO	Insulin-like	RT	<div><div></div><div></div></div>	4	2.1E-1	2.5E0	9.7E-1	9.0E-1
<input type="checkbox"/>	INTERPRO	Insulin family	RT	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	IIGF	RT	<div><div></div><div></div></div>	4	4.7E-1	1.6E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	hormone activity	RT	<div><div></div><div></div></div>	12	9.3E-1	7.6E-1	1.0E0	9.3E-1
Annotation Cluster 271		Enrichment Score: 0.48	<div><div></div><div></div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	embryonic skeletal limb joint morphogenesis	RT	<div><div></div><div></div></div>	3	7.6E-2	5.9E0	5.8E-1	5.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	embryonic hindlimb morphogenesis	RT	<div><div></div><div></div></div>	6	5.2E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	embryonic forelimb morphogenesis	RT	<div><div></div><div></div></div>	4	9.2E-1	7.4E-1	1.0E0	9.6E-1
Annotation Cluster 272		Enrichment Score: 0.48	<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:G-patch	RT	<div><div></div><div></div></div>	7	1.1E-1	2.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	G-patch domain	RT	<div><div></div><div></div></div>	7	4.1E-1	1.4E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	G_patch	RT	<div><div></div><div></div></div>	7	8.2E-1	9.1E-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
Annotation Cluster 273		Enrichment Score: 0.47	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of binding	RT	<div><div></div><div></div></div>	4	1.7E-2	5.9E0	2.2E-1	2.1E-1
<input type="checkbox"/>	BIOCARTA	TGF beta signaling pathway	RT	<div><div></div><div></div></div>	11	4.9E-2	1.8E0	1.3E-1	9.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	SMAD protein complex assembly	RT	<div><div></div><div></div></div>	4	1.4E-1	3.0E0	8.3E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of epithelial to mesenchymal transition	RT	<div><div></div><div></div></div>	9	1.8E-1	1.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	endoderm development	RT	<div><div></div><div></div></div>	6	2.7E-1	1.7E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MH2	RT	<div><div></div><div></div></div>	3	3.3E-1	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MH1	RT	<div><div></div><div></div></div>	3	3.3E-1	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	SMAD protein complex	RT	<div><div></div><div></div></div>	3	3.7E-1	2.4E0	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	MAD homology, MH1	RT	<div><div></div><div></div></div>	3	3.8E-1	2.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	SMAD domain, Dwarfin-type	RT	<div><div></div><div></div></div>	3	3.8E-1	2.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Dwarfin	RT	<div><div></div><div></div></div>	3	3.8E-1	2.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of transforming growth factor beta receptor signaling pathway	RT	<div><div></div><div></div></div>	5	4.4E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	MAD homology 1, Dwarfin-type	RT	<div><div></div><div></div></div>	3	6.0E-1	1.5E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	DWB	RT	<div><div></div><div></div></div>	3	6.3E-1	1.5E0	1.0E0	8.9E-1
<input type="checkbox"/>	INTERPRO	SMAD domain-like	RT	<div><div></div><div></div></div>	3	7.6E-1	1.2E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	DWA	RT	<div><div></div><div></div></div>	3	8.4E-1	1.0E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	transforming growth factor beta receptor binding	RT	<div><div></div><div></div></div>	6	8.5E-1	8.5E-1	1.0E0	9.1E-1
<input type="checkbox"/>	BIOCARTA	Role of Tob in T-cell activation	RT	<div><div></div><div></div></div>	5	9.0E-1	8.2E-1	1.0E0	9.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	SMAD protein signal transduction	RT	<div><div></div><div></div></div>	7	9.6E-1	6.7E-1	1.0E0	9.6E-1
Annotation Cluster 274		Enrichment Score: 0.46	<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:CXXCXGXX motif	RT	<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	RT	<div><div></div><div></div></div>	3	1.1E-1	5.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Chaperone DnaJ	RT	<div><div></div><div></div></div>	3	1.2E-1	4.6E0	6.2E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	Heat shock protein DnaJ, cysteine-rich domain	RT	<div><div></div><div></div></div>	3	1.9E-1	3.7E0	8.7E-1	8.1E-1
<input type="checkbox"/>	INTERPRO	HSP40/DnaJ peptide-binding	RT	<div><div></div><div></div></div>	3	4.4E-1	2.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Chaperone DnaJ, C-terminal	RT	<div><div></div><div></div></div>	3	4.4E-1	2.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:J	RT	<div><div></div><div></div></div>	8	6.6E-1	1.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	DnaJ domain	RT	<div><div></div><div></div></div>	7	8.5E-1	8.5E-1	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	DnaJ domain, conserved site	RT	<div><div></div><div></div></div>	3	9.5E-1	6.9E-1	1.0E0	9.5E-1
<input type="checkbox"/>	SMART	DnaJ	RT	<div><div></div><div></div></div>	7	9.9E-1	5.9E-1	1.0E0	9.9E-1
Annotation Cluster 275		Enrichment Score: 0.44	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:B box-type 2	RT	<div><div></div><div></div></div>	5	2.0E-1	2.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:B box-type 1	RT	<div><div></div><div></div></div>	4	2.5E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	B-box, C-terminal	RT	<div><div></div><div></div></div>	4	4.4E-1	1.7E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	BBC	RT	<div><div></div><div></div></div>	4	7.6E-1	1.1E0	1.0E0	8.9E-1
Annotation Cluster 276		Enrichment Score: 0.44	<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	zinc finger region:UBR-type	RT	<div><div></div><div></div></div>	3	2.7E-1	2.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, N-recognin	RT	<div><div></div><div></div></div>	3	3.2E-1	2.7E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	ZnF UBR1	RT	<div><div></div><div></div></div>	3	5.5E-1	1.7E0	1.0E0	8.9E-1
Annotation Cluster 277		Enrichment Score: 0.43	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamin	FDR
<input type="checkbox"/>	INTERPRO	Proteasome component (PCI) domain	RT	<div><div></div><div></div></div>	5	2.9E-1	1.8E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PCI	RT	<div><div></div><div></div></div>	5	3.0E-1	1.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	PINT	RT	<div><div></div><div></div></div>	5	5.9E-1	1.3E0	1.0E0	8.9E-1
Annotation Cluster 278		Enrichment Score: 0.43	<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	short sequence motif:LXXLL motif 5	RT	<div><div></div><div></div></div>	3	2.7E-1	2.9E0	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	short sequence motif:LXXLL motif 1	RT	<div><div></div><div></div></div>	5	3.7E-1	1.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 2	RT	<div><div></div><div></div></div>	5	3.7E-1	1.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 4	RT	<div><div></div><div></div></div>	3	3.9E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 3	RT	<div><div></div><div></div></div>	3	5.0E-1	1.9E0	1.0E0	9.7E-1
Annotation Cluster 279		Enrichment Score: 0.42	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	KEGG_PATHWAY	Neuroactive ligand-receptor interaction	RT	<div><div></div><div></div></div>	78	1.8E-4	1.5E0	4.2E-4	1.9E-4
<input type="checkbox"/>	UP_KEYWORDS	Transducer	RT	<div><div></div><div></div></div>	166	8.1E-4	1.3E0	4.7E-3	3.7E-3
<input type="checkbox"/>	SMART	SM01381	RT	<div><div></div><div></div></div>	43	7.3E-3	1.4E0	6.5E-2	5.7E-2
<input type="checkbox"/>	UP_KEYWORDS	G-protein coupled receptor	RT	<div><div></div><div></div></div>	137	1.0E-1	1.1E0	3.7E-1	3.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	G-protein coupled receptor signaling pathway	RT	<div><div></div><div></div></div>	157	3.7E-1	1.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Receptor	RT	<div><div></div><div></div></div>	229	8.2E-1	9.5E-1	1.0E0	8.2E-1
<input type="checkbox"/>	INTERPRO	GPCR, rhodopsin-like, 7TM	RT	<div><div></div><div></div></div>	104	9.5E-1	8.8E-1	1.0E0	9.5E-1
<input type="checkbox"/>	UP_KEYWORDS	Cell membrane	RT	<div><div></div><div></div></div>	433	9.6E-1	9.4E-1	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	G protein-coupled receptor, rhodopsin-like	RT	<div><div></div><div></div></div>	101	9.6E-1	8.7E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	plasma membrane	RT	<div><div></div><div></div></div>	593	1.0E0	9.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	integral component of plasma membrane	RT	<div><div></div><div></div></div>	182	1.0E0	8.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	G-protein coupled receptor activity	RT	<div><div></div><div></div></div>	81	1.0E0	6.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT	<div><div></div><div></div></div>	291	1.0E0	5.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain:Extracellular	RT	<div><div></div><div></div></div>	266	1.0E0	6.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	transmembrane region	RT	<div><div></div><div></div></div>	341	1.0E0	4.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT	<div><div></div><div></div></div>	330	1.0E0	5.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	disulfide bond	RT	<div><div></div><div></div></div>	257	1.0E0	6.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Signal	RT	<div><div></div><div></div></div>	310	1.0E0	5.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	integral component of membrane	RT	<div><div></div><div></div></div>	362	1.0E0	4.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Disulfide bond	RT	<div><div></div><div></div></div>	314	1.0E0	6.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Transmembrane	RT	<div><div></div><div></div></div>	418	1.0E0	5.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Transmembrane helix	RT	<div><div></div><div></div></div>	415	1.0E0	5.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Membrane	RT	<div><div></div><div></div></div>	722	1.0E0	6.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Glycoprotein	RT	<div><div></div><div></div></div>	386	1.0E0	5.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	signal peptide	RT	<div><div></div><div></div></div>	264	1.0E0	5.4E-1	1.0E0	1.0E0
Annotation Cluster 280		Enrichment Score: 0.42	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	glial cell apoptotic process	RT	<div><div></div><div></div></div>	4	3.7E-2	4.7E0	3.8E-1	3.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	execution phase of apoptosis	RT	<div><div></div><div></div></div>	6	1.2E-1	2.2E0	7.9E-1	7.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c	RT	<div><div></div><div></div></div>	4	1.8E-1	2.6E0	1.0E0	9.5E-1
<input type="checkbox"/>	BIOCARTA	D4-GDI Signaling Pathway	RT	<div><div></div><div></div></div>	7	2.1E-1	1.7E0	4.2E-1	3.1E-1
<input type="checkbox"/>	BBID	86.Apoptosis Nematode& Vert	RT	<div><div></div><div></div></div>	6	2.4E-1	1.7E0	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	response to cobalt ion	RT	<div><div></div><div></div></div>	3	2.7E-1	3.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	death receptor binding	RT	<div><div></div><div></div></div>	5	2.7E-1	1.9E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	death-inducing signaling complex	RT	<div><div></div><div></div></div>	3	3.0E-1	2.7E0	9.4E-1	8.3E-1
<input type="checkbox"/>	INTERPRO	Peptidase C14, caspase precursor p45, core	RT	<div><div></div><div></div></div>	4	4.0E-1	1.8E0	1.0E0	9.2E-1
<input type="checkbox"/>	BIOCARTA	Role of Mitochondria in Apoptotic Signaling	RT	<div><div></div><div></div></div>	9	4.1E-1	1.3E0	6.8E-1	5.1E-1
<input type="checkbox"/>	BIOCARTA	Stress Induction of HSP Regulation	RT	<div><div></div><div></div></div>	7	4.1E-1	1.4E0	6.8E-1	5.1E-1
<input type="checkbox"/>	INTERPRO	Peptidase C14, ICE, catalytic subunit p20	RT	<div><div></div><div></div></div>	4	4.4E-1	1.7E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Peptidase C14, ICE, catalytic subunit p20, active site	RT	<div><div></div><div></div></div>	3	5.0E-1	1.9E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Peptidase C14, caspase non-catalytic subunit p10	RT	<div><div></div><div></div></div>	3	6.0E-1	1.5E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	CASC	RT	<div><div></div><div></div></div>	4	6.6E-1	1.2E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	cysteine-type endopeptidase activity involved in apoptotic process	RT	<div><div></div><div></div></div>	3	6.7E-1	1.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	BIOCARTA	Caspase Cascade in Apoptosis	RT	<div><div></div><div></div></div>	8	6.9E-1	1.0E0	1.0E0	7.5E-1
<input type="checkbox"/>	BBID	150.caspase and NFkB activation	RT	<div><div></div><div></div></div>	6	8.5E-1	9.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	BBID	72.IAP interaction with cell death pathways	RT	<div><div></div><div></div></div>	5	9.0E-1	8.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	cysteine-type endopeptidase activity	RT	<div><div></div><div></div></div>	8	9.0E-1	7.8E-1	1.0E0	9.1E-1
<input type="checkbox"/>	BBID	46.P13K PTEN	RT	<div><div></div><div></div></div>	3	9.8E-1	6.4E-1	1.0E0	1.0E0
Annotation Cluster 281		Enrichment Score: 0.42	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR	
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of guanylate cyclase activity	RT	<div><div></div><div></div></div>	7	4.9E-3	3.8E0	9.2E-2	8.8E-2
























































Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Nitric oxide synthase, oxygenase domain	RT	<div><div></div><div></div></div>	3	7.0E-2	6.2E0	3.9E-1	3.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	nitric-oxide synthase activity	RT	<div><div></div><div></div></div>	3	7.5E-2	6.0E0	3.9E-1	3.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Flavodoxin-like	RT	<div><div></div><div></div></div>	4	1.0E-1	3.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Flavodoxin/nitric oxide synthase	RT	<div><div></div><div></div></div>	4	1.2E-1	3.1E0	6.2E-1	5.8E-1
<input type="checkbox"/>	INTERPRO	Flavodoxin	RT	<div><div></div><div></div></div>	4	1.2E-1	3.1E0	6.2E-1	5.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	tetrahydrobiopterin binding	RT	<div><div></div><div></div></div>	3	1.3E-1	4.5E0	6.0E-1	5.5E-1
<input type="checkbox"/>	INTERPRO	FAD-binding, type 1	RT	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	NADPH-cytochrome p450 reductase, FAD-binding, alpha-helical domain-3	RT	<div><div></div><div></div></div>	3	2.5E-1	3.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:FMN	RT	<div><div></div><div></div></div>	4	3.0E-1	2.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Oxidoreductase FAD/NAD(P)-binding	RT	<div><div></div><div></div></div>	4	3.0E-1	2.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	arginine binding	RT	<div><div></div><div></div></div>	3	3.3E-1	2.6E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	NADP binding	RT	<div><div></div><div></div></div>	8	3.7E-1	1.4E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	nitric oxide biosynthetic process	RT	<div><div></div><div></div></div>	4	3.8E-1	1.8E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	arginine catabolic process	RT	<div><div></div><div></div></div>	3	4.0E-1	2.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Flavoprotein pyridine nucleotide cytochrome reductase	RT	<div><div></div><div></div></div>	3	4.4E-1	2.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	FMN binding	RT	<div><div></div><div></div></div>	4	4.7E-1	1.6E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FAD-binding FR-type	RT	<div><div></div><div></div></div>	4	5.4E-1	1.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	Arginine biosynthesis	RT	<div><div></div><div></div></div>	5	5.4E-1	1.3E0	8.0E-1	5.4E-1
<input type="checkbox"/>	UP_KEYWORDS	FMN	RT	<div><div></div><div></div></div>	4	6.1E-1	1.3E0	1.0E0	8.0E-1
<input type="checkbox"/>	INTERPRO	Ferredoxin reductase-type FAD-binding domain	RT	<div><div></div><div></div></div>	4	6.1E-1	1.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Riboflavin synthase-like beta-barrel	RT	<div><div></div><div></div></div>	4	6.1E-1	1.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:NADP	RT	<div><div></div><div></div></div>	8	9.3E-1	7.4E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:FAD	RT	<div><div></div><div></div></div>	6	9.6E-1	6.6E-1	1.0E0	9.7E-1
<input type="checkbox"/>	COG_ONTOLOGY	Inorganic ion transport and metabolism	RT	<div><div></div><div></div></div>	6	9.9E-1	5.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	heme binding	RT	<div><div></div><div></div></div>	14	9.9E-1	6.1E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	RT	<div><div></div><div></div></div>	7	1.0E0	4.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Arginine and proline metabolism	RT	<div><div></div><div></div></div>	4	1.0E0	4.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	flavin adenine dinucleotide binding	RT	<div><div></div><div></div></div>	4	1.0E0	3.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Heme	RT	<div><div></div><div></div></div>	8	1.0E0	4.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	FAD	RT	<div><div></div><div></div></div>	5	1.0E0	3.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Flavoprotein	RT	<div><div></div><div></div></div>	5	1.0E0	2.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	NADP	RT	<div><div></div><div></div></div>	9	1.0E0	3.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Oxidoreductase	RT	<div><div></div><div></div></div>	24	1.0E0	2.8E-1	1.0E0	1.0E0
Annotation Cluster 282		Enrichment Score: 0.4	<div><div></div><div></div></div>		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	TRAF-like	RT	<div><div></div><div></div></div>	8	9.5E-2	2.0E0	5.1E-1	4.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MATH	RT	<div><div></div><div></div></div>	3	5.4E-1	1.7E0	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 8	RT		10	5.3E-1	1.1E0	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
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 9	RT		7	6.4E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 12	RT		4	6.5E-1	1.2E0	1.0E0	9.7E-1
Annotation Cluster 285		Enrichment Score: 0.36	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	cysteine-type endopeptidase inhibitor activity involved in apoptotic process	RT		6	3.4E-1	1.6E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Baculoviral inhibition of apoptosis protein repeat	RT		3	3.8E-1	2.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	inhibition of cysteine-type endopeptidase activity involved in apoptotic process	RT		3	4.6E-1	2.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	BIR	RT		3	6.3E-1	1.5E0	1.0E0	8.9E-1
Annotation Cluster 286		Enrichment Score: 0.35	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 1; degenerate	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Interaction with KCND2	RT		4	1.1E-2	6.8E0	2.3E-1	2.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of potassium ion transmembrane transport	RT		4	4.8E-1	1.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cardiac conduction	RT		5	9.6E-1	6.6E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	voltage-gated ion channel activity	RT		3	9.8E-1	5.6E-1	1.0E0	9.8E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	voltage-gated potassium channel complex	RT		8	9.9E-1	5.8E-1	1.0E0	9.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	potassium channel activity	RT		3	9.9E-1	4.8E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_KEYWORDS	Potassium channel	RT		4	1.0E0	3.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Potassium transport	RT		7	1.0E0	4.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Potassium	RT		8	1.0E0	4.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	potassium ion transmembrane transport	RT		6	1.0E0	2.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Voltage-gated channel	RT		4	1.0E0	1.8E-1	1.0E0	1.0E0
Annotation Cluster 287		Enrichment Score: 0.34	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 10	RT		5	1.7E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 9	RT		5	1.7E-1	2.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 7	RT		6	2.7E-1	1.7E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 8	RT		5	3.0E-1	1.8E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 6	RT		6	4.6E-1	1.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 11	RT		3	5.0E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 5	RT		6	6.0E-1	1.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	HEAT, type 2	RT		4	6.1E-1	1.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 1	RT		8	7.7E-1	9.4E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 2	RT		8	7.7E-1	9.4E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 4	RT		6	7.8E-1	9.5E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 3	RT		6	8.8E-1	8.2E-1	1.0E0	9.7E-1
Annotation Cluster 288		Enrichment Score: 0.33	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein ADP-ribosylation	RT		7	1.3E-1	2.0E0	8.3E-1	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of telomere maintenance via telomere lengthening	RT		3	2.0E-1	3.6E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	NAD+ ADP-ribosyltransferase activity	RT		7	3.2E-1	1.5E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PARP catalytic	RT		3	7.4E-1	1.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Poly(ADP-ribose)_polymerase,_catalytic domain	RT		3	7.9E-1	1.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_KEYWORDS	NAD	RT		10	1.0E0	3.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Glycosyltransferase	RT		4	1.0E0	1.2E-1	1.0E0	1.0E0
Annotation Cluster 289		Enrichment Score: 0.32	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Filamin/ABP280 repeat-like	RT		4	3.0E-1	2.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Filamin/ABP280 repeat	RT		3	5.0E-1	1.9E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	IG_FLMN	RT		3	7.5E-1	1.2E0	1.0E0	8.9E-1
Annotation Cluster 290		Enrichment Score: 0.31	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1-2	RT		8	2.0E-1	1.7E0	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:1-1	RT		8	2.2E-1	1.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:2-1	RT		6	5.2E-1	1.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:2-2	RT		6	5.7E-1	1.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:2-3	RT		3	7.9E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1-4	RT		3	7.9E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1-3	RT		3	8.1E-1	1.0E0	1.0E0	9.7E-1
Annotation Cluster 291		Enrichment Score: 0.31	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CID	RT		3	3.3E-1	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	CID domain	RT		3	3.8E-1	2.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	ENTH/VHS	RT		3	9.5E-1	6.9E-1	1.0E0	9.5E-1
Annotation Cluster 292		Enrichment Score: 0.3	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	renin-angiotensin regulation of aldosterone production	RT		3	1.3E-1	4.4E0	8.3E-1	7.9E-1
<input type="checkbox"/>	KEGG_PATHWAY	Renin-angiotensin system	RT		3	9.5E-1	6.9E-1	1.0E0	9.5E-1
<input type="checkbox"/>	BIOCARTA	Angiotensin-converting enzyme 2 regulates heart function	RT		3	9.5E-1	7.2E-1	1.0E0	9.5E-1
Annotation Cluster 293		Enrichment Score: 0.28	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	box C/D snoRNP complex	RT		3	2.4E-1	3.2E0	9.1E-1	8.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	snoRNA binding	RT		4	7.1E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	small-subunit processome	RT		5	8.2E-1	9.1E-1	1.0E0	8.9E-1
Annotation Cluster 294		Enrichment Score: 0.28	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	NuA4 histone acetyltransferase complex	RT		5	3.1E-1	1.8E0	9.5E-1	8.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H4 acetylation	RT		6	6.2E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H2A acetylation	RT		3	7.5E-1	1.2E0	1.0E0	9.6E-1
Annotation Cluster 295		Enrichment Score: 0.28	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Immunoglobulin I-set	RT		37	2.7E-3	1.6E0	3.3E-2	3.0E-2
<input type="checkbox"/>	INTERPRO	Immunoglobulin subtype 2	RT		42	4.8E-1	1.0E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 3	RT		17	7.9E-1	9.0E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 1	RT		23	9.5E-1	7.8E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C2-type 2	RT		23	9.6E-1	7.7E-1	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	IGc2	RT		42	1.0E0	6.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Immunoglobulin domain	RT		48	1.0E0	6.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Immunoglobulin subtype	RT		46	1.0E0	5.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Immunoglobulin-like fold	RT		85	1.0E0	5.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	IG	RT		46	1.0E0	3.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Immunoglobulin-like domain	RT		50	1.0E0	4.0E-1	1.0E0	1.0E0
Annotation Cluster 296		Enrichment Score: 0.26	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	Role of Mitochondria in Apoptotic Signaling	RT		9	4.1E-1	1.3E0	6.8E-1	5.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CARD	RT		6	4.3E-1	1.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Caspase Recruitment	RT		6	5.1E-1	1.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	BIOCARTA	Caspase Cascade in Apoptosis	RT		8	6.9E-1	1.0E0	1.0E0	7.5E-1
<input type="checkbox"/>	SMART	CARD	RT		3	8.4E-1	1.0E0	1.0E0	8.9E-1
Annotation Cluster 297		Enrichment Score: 0.26	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	RNA catabolic process	RT		6	2.7E-1	1.7E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	RNA phosphodiester bond hydrolysis, exonucleolytic	RT		5	7.2E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	3'-5'-exoribonuclease activity	RT		3	8.7E-1	9.0E-1	1.0E0	9.1E-1
Annotation Cluster 298		Enrichment Score: 0.24	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Exportin-1/Importin-beta-like	RT		3	2.5E-1	3.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	Ran GTPase binding	RT		6	5.8E-1	1.2E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Importin-beta, N-terminal	RT		3	7.9E-1	1.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	SM00913	RT		3	9.3E-1	7.6E-1	1.0E0	9.3E-1

















Annotation Cluster 1		Enrichment Score: ?	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 299		Enrichment Score: 0.24	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of vascular endothelial growth factor production	<div><div>RT</div><div></div></div>	8	1.6E-1	1.8E0	9.2E-1	8.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of complement activation	<div><div>RT</div><div></div></div>	5	7.7E-1	9.9E-1	1.0E0	9.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Staphylococcus aureus infection	<div><div>RT</div><div></div></div>	7	9.6E-1	6.8E-1	1.0E0	9.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Complement and coagulation cascades	<div><div>RT</div><div></div></div>	8	9.9E-1	6.1E-1	1.0E0	9.9E-1
Annotation Cluster 300		Enrichment Score: 0.23	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MBD	<div><div>RT</div><div></div></div>	3	5.0E-1	1.9E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	DNA-binding, integrase-type	<div><div>RT</div><div></div></div>	3	5.5E-1	1.7E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Methyl-CpG DNA binding	<div><div>RT</div><div></div></div>	3	5.5E-1	1.7E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	MBD	<div><div>RT</div><div></div></div>	3	8.0E-1	1.1E0	1.0E0	8.9E-1
Annotation Cluster 301		Enrichment Score: 0.23	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	histone acetyltransferase complex	<div><div>RT</div><div></div></div>	6	2.9E-1	1.7E0	9.2E-1	8.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H4-K16 acetylation	<div><div>RT</div><div></div></div>	4	6.8E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H4-K5 acetylation	<div><div>RT</div><div></div></div>	3	7.8E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	histone H4-K8 acetylation	<div><div>RT</div><div></div></div>	3	7.8E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 302		Enrichment Score: 0.23	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Importin subunit alpha	<div><div>RT</div><div></div></div>	3	3.2E-1	2.7E0	1.0E0	9.2E-1
<input type="checkbox"/>	PIR_SUPERFAMILY	importin subunit alpha	<div><div>RT</div><div></div></div>	3	3.3E-1	2.6E0	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:IBB	<div><div>RT</div><div></div></div>	3	3.3E-1	2.6E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	NLS-bearing protein import into nucleus	<div><div>RT</div><div></div></div>	6	3.5E-1	1.5E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 8	<div><div>RT</div><div></div></div>	5	4.1E-1	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Importin-alpha, importin-beta-binding domain	<div><div>RT</div><div></div></div>	3	4.4E-1	2.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 7	<div><div>RT</div><div></div></div>	5	4.8E-1	1.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 6	<div><div>RT</div><div></div></div>	5	5.4E-1	1.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 5	<div><div>RT</div><div></div></div>	5	6.3E-1	1.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 4	<div><div>RT</div><div></div></div>	5	6.9E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	nuclear localization sequence binding	<div><div>RT</div><div></div></div>	5	7.1E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 9	<div><div>RT</div><div></div></div>	3	7.7E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 3	<div><div>RT</div><div></div></div>	5	8.0E-1	9.5E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 2	<div><div>RT</div><div></div></div>	5	8.1E-1	9.2E-1	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Armadillo	<div><div>RT</div><div></div></div>	5	9.3E-1	7.2E-1	1.0E0	9.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 1	<div><div>RT</div><div></div></div>	3	9.5E-1	6.6E-1	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	ARM	<div><div>RT</div><div></div></div>	5	9.9E-1	5.2E-1	1.0E0	9.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein transporter activity	<div><div>RT</div><div></div></div>	5	1.0E0	4.1E-1	1.0E0	1.0E0
Annotation Cluster 303		Enrichment Score: 0.22	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	K Homology domain	<div><div>RT</div><div></div></div>	8	4.2E-1	1.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KH	<div><div>RT</div><div></div></div>	4	4.2E-1	1.7E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	K Homology domain, type 1	<div><div>RT</div><div></div></div>	8	5.8E-1	1.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KH 3	<div><div>RT</div><div></div></div>	3	6.7E-1	1.4E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KH 1	<div><div>RT</div><div></div></div>	4	7.1E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KH 2	<div><div>RT</div><div></div></div>	4	7.1E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	KH	<div><div>RT</div><div></div></div>	8	8.6E-1	8.5E-1	1.0E0	8.9E-1
Annotation Cluster 304		Enrichment Score: 0.21	<div><div>G</div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	SMAD/FHA domain	<div><div>RT</div><div></div></div>	10	4.9E-1	1.2E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Forkhead-associated (FHA) domain	<div><div>RT</div><div></div></div>	7	5.6E-1	1.2E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FHA	<div><div>RT</div><div></div></div>	6	6.0E-1	1.2E0	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	FHA	<div><div>RT</div><div></div></div>	5	8.6E-1	8.8E-1	1.0E0	8.9E-1

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 305		Enrichment Score: 0.21	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Cyclic nucleotide-binding, conserved site	RT		5	2.5E-1	1.9E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Cyclic nucleotide-binding domain	RT		7	5.1E-1	1.2E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Cyclic nucleotide-binding-like	RT		7	5.9E-1	1.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_KEYWORDS	cAMP-binding	RT		3	7.3E-1	1.2E0	1.0E0	8.0E-1
<input type="checkbox"/>	INTERPRO	RmlC-like jelly roll fold	RT		7	7.9E-1	9.2E-1	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	cNMP	RT		7	8.2E-1	9.1E-1	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	cAMP binding	RT		3	9.3E-1	7.5E-1	1.0E0	9.3E-1
Annotation Cluster 306		Enrichment Score: 0.21	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BIOCARTA	TACI and BCMA stimulation of B cell immune responses.	RT		6	5.5E-1	1.2E0	8.7E-1	6.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	membrane protein intracellular domain proteolysis	RT		4	6.1E-1	1.3E0	1.0E0	9.6E-1
<input type="checkbox"/>	BIOCARTA	Bone Remodelling	RT		5	7.0E-1	1.1E0	1.0E0	7.5E-1
Annotation Cluster 307		Enrichment Score: 0.2	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Histone H2A type 1-D	RT		3	6.3E-1	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Histone H3.1	RT		3	6.3E-1	1.5E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:Histone H3.2	RT		3	6.3E-1	1.5E0	1.0E0	9.7E-1
Annotation Cluster 308		Enrichment Score: 0.17	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	eukaryotic 43S preinitiation complex	RT		4	4.3E-1	1.7E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of translational initiation	RT		7	5.8E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Initiation factor	RT		9	6.2E-1	1.1E0	1.0E0	8.0E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	eukaryotic 48S preinitiation complex	RT		3	7.1E-1	1.3E0	1.0E0	8.9E-1
<input type="checkbox"/>	BIOCARTA	Internal Ribosome entry pathway	RT		3	7.1E-1	1.3E0	1.0E0	7.5E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	translation initiation factor activity	RT		10	7.1E-1	9.8E-1	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	formation of translation preinitiation complex	RT		4	7.7E-1	1.0E0	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	eukaryotic translation initiation factor 3 complex	RT		3	7.7E-1	1.1E0	1.0E0	8.9E-1
<input type="checkbox"/>	BIOCARTA	Eukaryotic protein translation	RT		5	8.1E-1	9.7E-1	1.0E0	8.1E-1
Annotation Cluster 309		Enrichment Score: 0.16	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:OPR	RT		3	5.4E-1	1.7E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Phox/Bem1p	RT		3	6.9E-1	1.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	PB1	RT		3	9.0E-1	8.7E-1	1.0E0	9.0E-1
Annotation Cluster 310		Enrichment Score: 0.15	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Patatin/Phospholipase A2-related	RT		3	4.4E-1	2.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	Acyl transferase/acyl hydrolase/lysophospholipase	RT		3	8.1E-1	1.0E0	1.0E0	9.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	Glycerophospholipid metabolism	RT		6	1.0E0	3.3E-1	1.0E0	1.0E0
Annotation Cluster 311		Enrichment Score: 0.12	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	nuclear pore	RT		13	4.6E-1	1.1E0	1.0E0	8.9E-1
<input type="checkbox"/>	UP_KEYWORDS	mRNA transport	RT		14	7.9E-1	9.1E-1	1.0E0	8.0E-1
<input type="checkbox"/>	UP_KEYWORDS	Nuclear pore complex	RT		6	8.7E-1	8.2E-1	1.0E0	8.7E-1
<input type="checkbox"/>	UP_KEYWORDS	Translocation	RT		6	1.0E0	4.9E-1	1.0E0	1.0E0
Annotation Cluster 312		Enrichment Score: 0.11	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Phospholipid-transporting P-type ATPase, subfamily IV	RT		3	6.9E-1	1.3E0	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	phospholipid-translocating ATPase activity	RT		3	7.1E-1	1.3E0	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	phospholipid translocation	RT		4	7.4E-1	1.1E0	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Lipid transport	RT		3	1.0E0	2.1E-1	1.0E0	1.0E0
Annotation Cluster 313		Enrichment Score: 0.11	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	cAMP response element binding	RT		4	3.7E-1	1.8E0	1.0E0	9.1E-1
<input type="checkbox"/>	INTERPRO	Basic-leucine zipper domain	RT		4	1.0E0	4.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	BRLZ	RT		4	1.0E0	3.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:Basic motif	RT		7	1.0E0	2.9E-1	1.0E0	1.0E0

Annotation Cluster 1		Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 314		Enrichment Score: 0.1	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	BBID	18.Cytokine_astocytes	RT		9	2.4E-1	1.4E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	20.Cytokine_oligodendrocytes	RT		3	5.0E-1	1.9E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	21.Cytokine_neurons	RT		3	5.0E-1	1.9E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	19.Cytokine_microglia	RT		5	6.7E-1	1.2E0	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	Cells and Molecules involved in local acute inflammatory response	RT		6	6.8E-1	1.1E0	1.0E0	7.5E-1
<input type="checkbox"/>	KEGG_PATHWAY	Malaria	RT		9	7.4E-1	9.7E-1	1.0E0	7.4E-1
<input type="checkbox"/>	BBID	111.Stress_influences_immunity	RT		3	7.5E-1	1.3E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	112.StressandCRHinfluence	RT		3	7.5E-1	1.3E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	22.Cytokine-chemokine_CNS	RT		5	7.5E-1	1.1E0	1.0E0	1.0E0
<input type="checkbox"/>	BBID	56.Macrophage_regulation_of_CD4+T_cells	RT		4	8.1E-1	1.0E0	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	Adhesion and Diapedesis of Granulocytes	RT		4	9.0E-1	8.3E-1	1.0E0	9.0E-1
<input type="checkbox"/>	BBID	80.T_cell_Activation	RT		8	9.1E-1	8.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	BBID	58.(CD40L)_immunosurveillance	RT		5	9.2E-1	8.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	BIOCARTA	Cytokine Network	RT		5	9.5E-1	7.1E-1	1.0E0	9.5E-1
<input type="checkbox"/>	KEGG_PATHWAY	Graft-versus-host disease	RT		4	9.6E-1	6.4E-1	1.0E0	9.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Type I diabetes mellitus	RT		5	9.7E-1	6.3E-1	1.0E0	9.7E-1
<input type="checkbox"/>	BIOCARTA	Regulation of hematopoiesis by cytokines	RT		3	9.8E-1	6.2E-1	1.0E0	9.8E-1
<input type="checkbox"/>	BIOCARTA	Cytokines and Inflammatory Response	RT		6	9.8E-1	6.5E-1	1.0E0	9.8E-1
<input type="checkbox"/>	INTERPRO	Four-helical cytokine_core	RT		4	9.9E-1	4.9E-1	1.0E0	9.9E-1
<input type="checkbox"/>	INTERPRO	Four-helical cytokine-like_core	RT		4	1.0E0	4.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	KEGG_PATHWAY	Allograft rejection	RT		3	1.0E0	4.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	BBID	97.Immune_injury_MS-lesions_MS_antigen	RT		3	1.0E0	4.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	cytokine activity	RT		11	1.0E0	3.7E-1	1.0E0	1.0E0
Annotation Cluster 315		Enrichment Score: 0.1	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	proximal/distal pattern formation	RT		5	6.0E-1	1.2E0	1.0E0	9.6E-1
<input type="checkbox"/>	KEGG_PATHWAY	Basal cell carcinoma	RT		8	9.1E-1	7.8E-1	1.0E0	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	odontogenesis of dentin-containing tooth	RT		7	9.2E-1	7.5E-1	1.0E0	9.6E-1
Annotation Cluster 316		Enrichment Score: 0.1	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Zinc finger_B-box	RT		15	4.5E-1	1.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:B30.2/SPRY	RT		15	5.7E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:B box-type	RT		10	6.8E-1	1.0E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	B30.2/SPRY domain	RT		15	7.4E-1	9.4E-1	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	SP1a/Ryanodine receptor SPRY	RT		14	7.7E-1	9.2E-1	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	SPRY-associated	RT		6	9.2E-1	7.4E-1	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	BBOX	RT		14	9.5E-1	7.6E-1	1.0E0	9.5E-1
<input type="checkbox"/>	INTERPRO	Butyrophylin-like	RT		8	9.6E-1	6.9E-1	1.0E0	9.6E-1
<input type="checkbox"/>	SMART	SPRY	RT		14	1.0E0	6.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	PRY	RT		6	1.0E0	4.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Concanavalin A-like lectin/glucanase_subgroup	RT		18	1.0E0	4.8E-1	1.0E0	1.0E0
Annotation Cluster 317		Enrichment Score: 0.09	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:CCHC-type	RT		5	5.4E-1	1.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Zinc finger_CCHC-type	RT		4	9.7E-1	6.2E-1	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	ZnF_C2HC	RT		3	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 318		Enrichment Score: 0.09	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CS	RT		3	7.0E-1	1.3E0	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	CS-like domain	RT		3	7.9E-1	1.1E0	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	HSP20-like chaperone	RT		3	9.5E-1	6.6E-1	1.0E0	9.5E-1
Annotation Cluster 319		Enrichment Score: 0.09	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	peptidase activity	RT		16	5.5E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_KEYWORDS	Zymogen	RT		17	1.0E0	5.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Protease	RT		45	1.0E0	5.7E-1	1.0E0	1.0E0
Annotation Cluster 320		Enrichment Score: 0.08	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	innate immune response in mucosa	RT		5	6.3E-1	1.2E0	1.0E0	9.6E-1

Annotation Cluster 1		Enrichment Score: ?	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	antibacterial humoral response	RT	<div><div></div><div></div></div>	7	7.8E-1	9.4E-1	1.0E0	9.6E-1
<input type="checkbox"/>	UP_KEYWORDS	Antibiotic	RT	<div><div></div><div></div></div>	7	1.0E0	5.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Antimicrobial	RT	<div><div></div><div></div></div>	7	1.0E0	4.4E-1	1.0E0	1.0E0
Annotation Cluster 321		Enrichment Score: 0.06	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Steroid-binding	RT	<div><div></div><div></div></div>	4	4.2E-1	1.7E0	1.0E0	8.0E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	steroid binding	RT	<div><div></div><div></div></div>	5	6.8E-1	1.1E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:Nuclear receptor	RT	<div><div></div><div></div></div>	3	9.9E-1	4.5E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:NR C4-type	RT	<div><div></div><div></div></div>	3	9.9E-1	4.5E-1	1.0E0	9.9E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, nuclear hormone receptor-type	RT	<div><div></div><div></div></div>	3	1.0E0	4.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Steroid hormone receptor	RT	<div><div></div><div></div></div>	3	1.0E0	4.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Nuclear hormone receptor, ligand-binding, core	RT	<div><div></div><div></div></div>	3	1.0E0	3.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	steroid hormone receptor activity	RT	<div><div></div><div></div></div>	3	1.0E0	3.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	ZnF_C4	RT	<div><div></div><div></div></div>	3	1.0E0	2.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	HOLI	RT	<div><div></div><div></div></div>	3	1.0E0	2.5E-1	1.0E0	1.0E0
Annotation Cluster 322		Enrichment Score: 0.05	<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:Ig-like 3	RT	<div><div></div><div></div></div>	3	7.9E-1	1.1E0	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like 1	RT	<div><div></div><div></div></div>	3	9.4E-1	7.0E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like 2	RT	<div><div></div><div></div></div>	3	9.4E-1	7.0E-1	1.0E0	9.7E-1
Annotation Cluster 323		Enrichment Score: 0.04	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_MF_DIRECT	histone demethylase activity	RT	<div><div></div><div></div></div>	4	7.7E-1	1.0E0	1.0E0	9.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:JmjC	RT	<div><div></div><div></div></div>	4	8.7E-1	8.5E-1	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	JmjC domain	RT	<div><div></div><div></div></div>	4	9.2E-1	7.5E-1	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	JmjC	RT	<div><div></div><div></div></div>	4	9.9E-1	5.6E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_KEYWORDS	Dioxygenase	RT	<div><div></div><div></div></div>	5	1.0E0	4.1E-1	1.0E0	1.0E0
Annotation Cluster 324		Enrichment Score: 0.04	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	3'5'-cyclic nucleotide phosphodiesterase	RT	<div><div></div><div></div></div>	3	8.4E-1	9.8E-1	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	3'5'-cyclic nucleotide phosphodiesterase, conserved site	RT	<div><div></div><div></div></div>	3	8.7E-1	8.9E-1	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	3'5'-cyclic nucleotide phosphodiesterase, catalytic domain	RT	<div><div></div><div></div></div>	3	8.9E-1	8.5E-1	1.0E0	9.2E-1
<input type="checkbox"/>	INTERPRO	HD/PDEase domain	RT	<div><div></div><div></div></div>	3	9.1E-1	8.1E-1	1.0E0	9.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 1	RT	<div><div></div><div></div></div>	3	9.3E-1	7.3E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 2	RT	<div><div></div><div></div></div>	3	9.3E-1	7.3E-1	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	HDc	RT	<div><div></div><div></div></div>	3	9.9E-1	5.3E-1	1.0E0	9.9E-1
Annotation Cluster 325		Enrichment Score: 0.04	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	mitochondrial small ribosomal subunit	RT	<div><div></div><div></div></div>	4	7.8E-1	1.0E0	1.0E0	8.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitochondrial translational elongation	RT	<div><div></div><div></div></div>	12	8.7E-1	8.4E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitochondrial translation	RT	<div><div></div><div></div></div>	4	9.6E-1	6.6E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitochondrial translational termination	RT	<div><div></div><div></div></div>	10	9.7E-1	6.9E-1	1.0E0	9.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	mitochondrial large ribosomal subunit	RT	<div><div></div><div></div></div>	4	9.9E-1	5.3E-1	1.0E0	9.9E-1
Annotation Cluster 326		Enrichment Score: 0.04	<div><div></div><div>G</div></div>	<div><div></div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C3H1-type 1	RT	<div><div></div><div></div></div>	4	8.5E-1	8.8E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C3H1-type 2	RT	<div><div></div><div></div></div>	4	8.5E-1	8.8E-1	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, CCCH-type	RT	<div><div></div><div></div></div>	6	9.7E-1	6.3E-1	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	ZnF_C3H1	RT	<div><div></div><div></div></div>	6	1.0E0	4.9E-1	1.0E0	1.0E0
Annotation Cluster 327		Enrichment Score: 0.03	<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:SAP	RT	<div><div></div><div></div></div>	3	8.9E-1	8.5E-1	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	SAP domain	RT	<div><div></div><div></div></div>	3	9.2E-1	7.7E-1	1.0E0	9.2E-1
<input type="checkbox"/>	SMART	SAP	RT	<div><div></div><div></div></div>	3	9.9E-1	5.3E-1	1.0E0	9.9E-1
Annotation Cluster 328		Enrichment Score: 0.02	<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:LisH	RT	<div><div></div><div></div></div>	3	9.3E-1	7.3E-1	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	LisH dimerisation motif	RT	<div><div></div><div></div></div>	3	9.5E-1	6.6E-1	1.0E0	9.5E-1

Annotation Cluster 1		Enrichment Score: ?	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	SMART	LisH	RT	<div><div></div></div>	3	9.9E-1	5.3E-1	1.0E0	9.9E-1
Annotation Cluster 329		Enrichment Score: 0.02	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Cilium biogenesis/degradation	RT	<div><div></div></div>	17	9.3E-1	7.9E-1	1.0E0	9.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cilium morphogenesis	RT	<div><div></div></div>	17	9.6E-1	7.4E-1	1.0E0	9.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cilium assembly	RT	<div><div></div></div>	13	9.9E-1	6.2E-1	1.0E0	9.9E-1
Annotation Cluster 330		Enrichment Score: 0.02	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Host cell receptor for virus entry	RT	<div><div></div></div>	7	9.2E-1	7.5E-1	1.0E0	9.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	virus receptor activity	RT	<div><div></div></div>	7	9.8E-1	6.0E-1	1.0E0	9.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	viral entry into host cell	RT	<div><div></div></div>	8	9.9E-1	5.9E-1	1.0E0	9.9E-1
Annotation Cluster 331		Enrichment Score: 0.01	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:FYVE-type	RT	<div><div></div></div>	4	9.4E-1	7.0E-1	1.0E0	9.7E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, FYVE-type	RT	<div><div></div></div>	3	9.6E-1	6.4E-1	1.0E0	9.6E-1
<input type="checkbox"/>	INTERPRO	Zinc finger, FYVE-related	RT	<div><div></div></div>	3	9.8E-1	5.5E-1	1.0E0	9.8E-1
<input type="checkbox"/>	SMART	FYVE	RT	<div><div></div></div>	3	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 332		Enrichment Score: 0.01	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Ras-association	RT	<div><div></div></div>	4	9.7E-1	6.2E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ras-associating	RT	<div><div></div></div>	3	9.7E-1	6.0E-1	1.0E0	9.7E-1
<input type="checkbox"/>	SMART	RA	RT	<div><div></div></div>	3	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 333		Enrichment Score: 0	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:22	RT	<div><div></div></div>	4	9.5E-1	6.6E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:21	RT	<div><div></div></div>	4	9.6E-1	6.3E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:24	RT	<div><div></div></div>	3	9.7E-1	6.0E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:20	RT	<div><div></div></div>	4	9.7E-1	5.9E-1	1.0E0	9.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:19	RT	<div><div></div></div>	4	9.8E-1	5.7E-1	1.0E0	9.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:18	RT	<div><div></div></div>	4	9.8E-1	5.6E-1	1.0E0	9.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:2	RT	<div><div></div></div>	27	9.9E-1	7.1E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:17	RT	<div><div></div></div>	4	9.9E-1	4.9E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:9	RT	<div><div></div></div>	9	9.9E-1	5.7E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:10	RT	<div><div></div></div>	8	9.9E-1	5.6E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:1	RT	<div><div></div></div>	26	9.9E-1	6.9E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:11	RT	<div><div></div></div>	7	9.9E-1	5.4E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:6	RT	<div><div></div></div>	13	9.9E-1	6.0E-1	1.0E0	9.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:16	RT	<div><div></div></div>	4	1.0E0	4.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:8	RT	<div><div></div></div>	10	1.0E0	5.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:15	RT	<div><div></div></div>	5	1.0E0	4.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:3	RT	<div><div></div></div>	21	1.0E0	6.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:12	RT	<div><div></div></div>	6	1.0E0	4.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:5	RT	<div><div></div></div>	13	1.0E0	5.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:14	RT	<div><div></div></div>	5	1.0E0	4.3E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:7	RT	<div><div></div></div>	10	1.0E0	5.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:4	RT	<div><div></div></div>	16	1.0E0	5.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:13	RT	<div><div></div></div>	5	1.0E0	4.1E-1	1.0E0	1.0E0
Annotation Cluster 334		Enrichment Score: 0	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Rho-GAP	RT	<div><div></div></div>	4	1.0E0	4.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Rho GTPase-activating protein domain	RT	<div><div></div></div>	4	1.0E0	3.7E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Rho GTPase activation protein	RT	<div><div></div></div>	6	1.0E0	4.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	RhoGAP	RT	<div><div></div></div>	4	1.0E0	2.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	GTPase activation	RT	<div><div></div></div>	7	1.0E0	2.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	GTPase activator activity	RT	<div><div></div></div>	14	1.0E0	3.0E-1	1.0E0	1.0E0
Annotation Cluster 335		Enrichment Score: 0	<div>G</div>	<div><div></div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:DH	RT	<div><div></div></div>	4	1.0E0	4.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of Rho protein signal transduction	RT	<div><div></div></div>	6	1.0E0	4.4E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Dbl homology (DH) domain	RT	<div><div></div></div>	4	1.0E0	3.5E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	Rho guanyl-nucleotide exchange factor activity	RT	<div><div></div></div>	4	1.0E0	3.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	guanyl-nucleotide exchange factor activity	RT	<div><div></div></div>	6	1.0E0	3.0E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	RhoGEF	RT	<div><div></div></div>	4	1.0E0	2.4E-1	1.0E0	1.0E0

Annotation Cluster 1		Enrichment Score: ?	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Guanine-nucleotide releasing factor	RT	<div></div>	5	1.0E0	2.3E-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	domain:PH	RT	<div></div>	21	1.0E0	5.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Pleckstrin homology domain	RT	<div></div>	20	1.0E0	4.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Pleckstrin homology-like domain	RT	<div></div>	36	1.0E0	5.2E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	PH	RT	<div></div>	19	1.0E0	2.9E-1	1.0E0	1.0E0
Annotation Cluster 337		Enrichment Score: 0	<div>G</div>	<div></div>	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	mitochondrial matrix	RT	<div></div>	25	1.0E0	4.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	transit peptide:Mitochondrion	RT	<div></div>	29	1.0E0	4.1E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_KEYWORDS	Transit peptide	RT	<div></div>	31	1.0E0	4.0E-1	1.0E0	1.0E0
Annotation Cluster 338		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	RT	<div></div>	7	1.0E0	2.9E-1	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Helix-loop-helix motif	RT	<div></div>	3	1.0E0	1.8E-1	1.0E0	1.0E0
<input type="checkbox"/>	INTERPRO	Myc-type, basic helix-loop-helix (bHLH) domain	RT	<div></div>	3	1.0E0	1.6E-1	1.0E0	1.0E0
<input type="checkbox"/>	SMART	HLH	RT	<div></div>	3	1.0E0	1.1E-1	1.0E0	1.0E0

3181 terms

 were not clustered.