



Functional Annotation Clustering

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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Help and Manual

338 (Cluster(s)						₩ D	ownload	<u>d File</u>
Anno	tation Cluster 1	Enrichment Score: ?	G	**	Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	Zinc finger, C2H2	<u>RT</u>		655	0.0E0	5.1E0	0.0E0	0.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	<u>RT</u>	_	483	0.0E0	5.9E0	0.0E0	0.0E0
	INTERPRO	Zinc finger, C2H2-like	<u>RT</u>		649	0.0E0	5.3E0	0.0E0	0.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	<u>RT</u>		536	0.0E0	5.9E0	0.0E0	0.0E0
	INTERPRO	Zinc finger C2H2-type/integrase DNA-binding domain	<u>RT</u>		634	0.0E0	5.5E0	0.0E0	0.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 3	<u>RT</u>		565	0.0E0	6.0E0	0.0E0	0.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 4	<u>RT</u>	_	527	0.0E0	6.1E0	0.0E0	0.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 5	<u>RT</u>		504	0.0E0	6.2E0	0.0E0	0.0E0
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 6	<u>RT</u>		461	0.0E0	6.3E0	0.0E0	0.0E0
	UP_SEQ_FEATURE UP_SEQ_FEATURE	zinc finger region:C2H2-type 7	<u>RT</u>		433	0.0E0 1.2E-	6.4E0	0.0E0	0.0E0 8.2E-
	OF_SEQ_FEATORE	zinc finger region:C2H2-type 8	<u>RT</u>	_	399	299	6.4E0	8.5E-297	297
	SMART	ZnF C2H2	<u>RT</u>		649	1.6E- 297	3.4E0	7.1E-295	6.3E- 295
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 9	<u>RT</u>	_	361	1.3E- 271	6.4E0	7.9E-269	7 75
	UP_KEYWORDS	<u>Zinc-finger</u>	<u>RT</u>		842	6.5E- 269	3.2E0	3.1E-266	2 55
	UP_KEYWORDS	<u>Nucleus</u>	<u>RT</u>		1582	2.4E- 267	2.1E0	5.6E-265	4 FE
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 10	<u>RT</u>	=	324	3.4E- 248	6.5E0	1.9E-245	1 05
	INTERPRO	Krueppel-associated box	<u>RT</u>	=	355	7.4E- 230	5.5E0	3.9E-227	3.6E- 227
	UP_KEYWORDS	Transcription	<u>RT</u>		941	4.0E- 227	2.7E0	6.3E-225	5.0E- 225
	UP_SEQ_FEATURE	domain:KRAB	<u>RT</u>	=	314	1.0E- 226	6.2E0	5.4E-224	5.2E- 224
	UP_KEYWORDS	<u>Transcription regulation</u>	<u>RT</u>		923	2.6E- 225	2.7E0	3.0E-223	2.4E- 223
	GOTERM_MF_DIRECT	nucleic acid binding	<u>RT</u>	_	585	2.1E- 216	3.5E0	2.7E-213	2.5E- 213
	UP_KEYWORDS	<u>DNA-binding</u>	<u>RT</u>	_	841	8.4E- 215	2.8E0	7.9E-213	6.3E- 213
	UP_KEYWORDS	<u>Zinc</u>	<u>RT</u>	_	904	1.6E- 209	2.6E0	1.3E-207	1.0E- 207
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 11	<u>RT</u>	=	280	1.7E- 206	6.3E0	8.1E-204	7.8E- 204
	UP_KEYWORDS	<u>Metal-binding</u>	<u>RT</u>		1168	1.4E- 201	2.2E0	9.3E-200	7.4E- 200
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 12	<u>RT</u>	=	242	2.1E- 182	6.4E0	9.1E-180	8.8E- 180
	GOTERM_MF_DIRECT	metal ion binding	<u>RT</u>		854	5.4E- 181	2.5E0	3.5E-178	3.2E- 178
	GOTERM_BP_DIRECT	transcription, DNA-templated	<u>RT</u>		819	7.1E- 175	2.5E0	4.2E-171	4.0E- 171
	SMART	KRAB	<u>RT</u>	=	350	6.0E- 168	3.6E0	1.3E-165	1.2E- 165
	GOTERM_BP_DIRECT	regulation of transcription, DNA-templated	<u>RT</u>	_	679	4.5E- 162	2.7E0	1.3E-158	1.3E- 158
	GOTERM_MF_DIRECT	DNA binding	<u>RT</u>	_	700	2.3E- 147	2.5E0	1.0E-144	9.1E- 145
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 13	<u>RT</u>	=	192	5.5E- 143	6.4E0	2.2E-140	2.2E- 140
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 14	<u>RT</u>	=	148	4.3E- 111	6.5E0	1.5E-108	1.5E- 108
	GOTERM_CC_DIRECT	intracellular	<u>RT</u>	=	533	2.6E- 110	2.5E0	1.1E-107	1.0E- 107
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 15	<u>RT</u>	=	125	3.6E- 92	6.4E0	1.1E-89	1.1E- 89
	GOTERM_MF_DIRECT	<u>transcription factor activity, sequence-specific</u> <u>DNA binding</u>	<u>RT</u>	=	403	6.1E- 81	2.5E0	1.6E-78	1.5E- 78
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 16	<u>RT</u>	=	96	1.3E- 69	6.3E0	3.0E-67	2.9E- 67
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 17	<u>RT</u>	=	76	1.9E- 54	6.3E0	2.8E-52	2.7E- 52
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 18	<u>RT</u>	Ē.	60	1.4E- 42	6.3E0	1.9E-40	1.8E- 40
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 19	<u>RT</u>	•	50	35	6.3E0	2.0E-33	1.9E- 33
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 20	<u>RT</u>	i e	32	2.2E- 21	6.1E0	2.2E-19	2.1E- 19

Annot	ation Cluster 1	Enrichment Score: ?	G	To the second se	Count	P_Value	Fold Change	Benjamini	FDR
Annot	ation Cluster 2	Enrichment Score: 87.1	G	· Marian Company	Count	P_Value	Fold Change	Benjamini	FDR
	UP_KEYWORDS	Nucleotide-binding	<u>RT</u>		730	2.7E- 181	2.8E0	1.6E-179	1.3E- 179
	UP_KEYWORDS	ATP-binding	<u>RT</u>	_	586	1.0E- 149	2.9E0	5.3E-148	4.2E- 148
	GOTERM_MF_DIRECT	ATP binding	<u>RT</u>	_	606	7.3E- 118	2.4E0	2.4E-115	2.2E- 115
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	<u>RT</u>	_	439	2.2E- 117	3.0E0	8.5E-115	8.2E- 115
	UP_SEQ_FEATURE	domain:Protein kinase	<u>RT</u>	_	273	9.7E- 105	3.9E0	3.2E-102	3.1E- 102
	INTERPRO	Protein kinase-like domain	<u>RT</u>	=	300	5.9E- 103	3.5E0	2.5E-100	2.3E- 100
	INTERPRO	Protein kinase, catalytic domain	<u>RT</u>	=	284	5.7E-	3.6E0	2.0E-99	1.9E-
	INTERPRO	Protein kinase, ATP binding site	RT	=	239	102 6.5E-	3.9E0	1.9E-92	99 1.8E-
	UP_SEQ_FEATURE	binding site:ATP	RT	=	278	95 8.0E-	3.4E0	2.4E-85	92 2.3E-
	UP_KEYWORDS	<u>Kinase</u>	RT	_	319	88 1.8E-	3.0E0	7.7E-81	85 6.1E-
	UP_KEYWORDS	Serine/threonine-protein kinase	RT	=	209	82 8.8E-	3.7E0	3.4E-71	81 2.8E-
	UP_SEQ_FEATURE	active site:Proton acceptor	RT	=	274	73 8.1E-	2.8E0	1.5E-60	71 1.5E-
	GOTERM_MF_DIRECT	protein kinase activity	RT	=	194	63 3.6E-	3.2E0	7.9E-57	60 7.2E-
	INTERPRO			_	174	59 5.4E-	3.5E0	9.5E-56	57 8.8E-
	GOTERM_MF_DIRECT	Serine/threonine-protein kinase, active site	RT	_		58 3.2E-			56 5.5E-
	GOTERM_BP_DIRECT	protein serine/threonine kinase activity	<u>RT</u>	_	197	57 7.6E-	3.1E0	6.1E-55	55 1.4E-
	UP_KEYWORDS	protein phosphorylation	<u>RT</u>	_	218	54 4.7E-	2.8E0	1.5E-50	50 9.3E-
	SMART	<u>Transferase</u>	<u>RT</u>	_	454	42 6.0E-	1.8E0	1.2E-40	41 4.7E-
		S TKc	RT		195	34	2.2E0 Fold	5.3E-32	32
Annot	ation Cluster 3 UP_SEQ_FEATURE	Enrichment Score: 59.63	G		Count	P_Value 6.4E-	Change	Benjamini	FDR 1.8E-
	UP_SEQ_FEATURE	repeat:ANK 4	RT	=	132	75 1.2E-	5.3E0	1.8E-72	72 2.8E-
	UP_KEYWORDS	repeat:ANK 5	RT	=	117	71 2.2E-	5.6E0	2.9E-69	69 6.4E-
	UP_SEQ_FEATURE	ANK repeat	<u>RT</u>	-	163	69	4.2E0	7.9E-68	68
		repeat:ANK 3	<u>RT</u>	=	141	1.1E- 67	4.6E0	2.3E-65	2.2E- 65
	INTERPRO	Ankyrin repeat	<u>RT</u>	=	161	3.5E- 64	3.9E0	7.4E-62	6.8E- 62
	INTERPRO	Ankyrin repeat-containing domain	<u>RT</u>	=	164	1.5E- 63	3.8E0	2.8E-61	2.6E- 61
	UP_SEQ_FEATURE	repeat:ANK 2	<u>RT</u>	=	148	1.0E- 60	4.1E0	1.8E-58	1.7E- 58
	UP_SEQ_FEATURE	repeat:ANK 1	<u>RT</u>	=	147	4.4E- 60	4.1E0	7.3E-58	7.0E- 58
	UP_SEQ_FEATURE	repeat:ANK 6	<u>RT</u>	=	85	7.9E- 55	5.8E0	1.2E-52	1.2E- 52
	SMART	ANK	<u>RT</u>	=	159	3.2E- 39	2.6E0	3.6E-37	3.2E- 37
	UP_SEQ_FEATURE	repeat:ANK 7	<u>RT</u>	=	56	1.1E- 37	6.1E0	1.4E-35	1.4E- 35
Annot	ation Cluster 4	Enrichment Score: 47.49	G	13	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	<u>Leucine-rich repeat, typical subtype</u>	<u>RT</u>	=	144	1.1E- 80	5.0E0	3.0E-78	2.8E- 78
	UP_SEQ_FEATURE	repeat:LRR 5	<u>RT</u>	=	154	6.3E- 72	4.5E0	1.6E-69	1.6E- 69
	UP_SEQ_FEATURE	repeat:LRR 4	<u>RT</u>	=	161	4.6E- 70	4.3E0	1.1E-67	1.0E- 67
	UP_SEQ_FEATURE	repeat:LRR 6	<u>RT</u>	=	143	5.0E- 69	4.7E0	1.1E-66	1.0E- 66
	UP_KEYWORDS	Leucine-rich repeat	<u>RT</u>	=	178	1.6E- 68	3.9E0	5.5E-67	4.4E- 67
	INTERPRO	Leucine-rich repeat	<u>RT</u>	=	168	4.2E- 68	4.0E0	9.9E-66	9.1E- 66
	UP_SEQ_FEATURE	repeat:LRR 7	<u>RT</u>	=	129	5.6E- 68	5.0E0	1.2E-65	1.1E- 65
	UP_SEQ_FEATURE	repeat:LRR 3	<u>RT</u>	=	171	2.5E- 64	3.9E0	4.9E-62	4.8E- 62
	UP_SEQ_FEATURE	repeat:LRR 1	<u>RT</u>	=	174	1.3E- 61	3.7E0	2.4E-59	2.3E- 59
	UP_SEQ_FEATURE	repeat:LRR 2	<u>RT</u>	=	174	2.4E- 61	3.7E0	4.3E-59	4.1E- 59
	UP_SEQ_FEATURE	repeat:LRR 8	<u>RT</u>	=	109	9.7E- 58	5.0E0	1.6E-55	1.5E- 55
	SMART	LRR TYP	RT	=	144	8.9E-	3.3E0	1.3E-53	1.2E-
	UP_SEQ_FEATURE	repeat:LRR 9	RT	=	98	56 2.0E-	5.0E0	2.9E-49	53 2.8E-
	UP_SEQ_FEATURE	repeat:LRR 10	RT		84	51 1.6E-	4.9E0	2.2E-41	49 2.1E-
						43			41

Anno	tation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	i FDR
	UP_SEQ_FEATURE	repeat:LRR 11	RT	-	73	9.4E- 38	Onlange	1.3E-35	1.2E- 35
	UP_SEQ_FEATURE	repeat:LRR 12	<u>RT</u>	=	66	9.0E-		1.1E-32	1.0E-
	UP_SEQ_FEATURE	repeat:LRR 13	RT		53	35 1.1E-		1.2E-24	32 1.1E-
	INTERPRO	Cysteine-rich flanking region, C-terminal	RT		58	26 1.2E-		1.2E-24	24 1.1E-
	UP_SEQ_FEATURE	repeat:LRR 14	RT		43	26 4.4E-	4.9E0	4.4E-20	24 4.2E-
	UP_SEQ_FEATURE	repeat:LRR 15		-	37	22 2.6E-	4.9E0	2.4E-17	20 2.3E-
	SMART		RT			19 2.7E-			17 1.2E-
	UP_SEQ_FEATURE	LRRCT	<u>RT</u>	-	58	17 2.4E-	2.8E0	1.3E-15	15 1.9E-
	UP_SEQ_FEATURE	repeat:LRR 16	<u>RT</u>	•	32	16 6.6E-	4.8E0	1.9E-14	14 4.8E-
		repeat:LRR 17	RT	i	28	16	5.3E0 Fold	5.0E-14	14
Anno	tation Cluster 5 UP_KEYWORDS	Enrichment Score: 47.28	G		Count	P_Value	Change	•	7.2E-
	GOTERM_MF_DIRECT	<u>Ubl conjugation pathway</u>	RT	=	274	62	2.8E0	8.9E-61	61
		<u>ubiquitin-protein transferase activity</u>	<u>RT</u>	=	174	3.0E- 51	3.2E0	4.9E-49	4.5E- 49
	KEGG_PATHWAY	<u>Ubiquitin mediated proteolysis</u>	RT	-	107	1.2E- 50	4.1E0	3.0E-48	1.3E- 48
	GOTERM_BP_DIRECT	protein ubiquitination	<u>RT</u>	=	148	6.7E- 28	2.4E0	4.9E-25	4.7E- 25
Anno	tation Cluster 6	Enrichment Score: 30.08	G	<u> </u>	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	domain:SCAN box	<u>RT</u>	•	53	2.4E- 35	6.0E0	3.0E-33	2.9E- 33
	INTERPRO	Transcription regulator SCAN	<u>RT</u>	•	54	7.8E- 35	5.6E0	9.6E-33	8.9E- 33
	INTERPRO	Retrovirus capsid, C-terminal	RT	=	54	2.8E- 28	4.8E0	3.3E-26	3.0E- 26
	SMART	SCAN	<u>RT</u>	=	53	9.0E- 25	3.6E0	5.7E-23	5.1E- 23
Anno	tation Cluster 7	Enrichment Score: 21.8	G	17	Count	P_Value	Fold Change	Benjamini	i FDR
	KEGG_PATHWAY	Pathways in cancer	<u>RT</u>	=	169	2.8E- 29	2.3E0	8.4E-28	3.7E- 28
	KEGG_PATHWAY	PI3K-Akt signaling pathway	<u>RT</u>	=	137	6.8E- 20	2.1E0	1.0E-18	4.6E- 19
	KEGG_PATHWAY	Ras signaling pathway	<u>RT</u>	=	100	2.1E- 18	2.3E0	2.6E-17	1.2E- 17
Anno	tation Cluster 8	Enrichment Score: 19.22	G	TT .	Count	P_Value	Fold Change	Benjamini	i FDR
	UP_KEYWORDS	Cell cycle	<u>RT</u>	=	218	6.5E- 35	2.3E0	1.4E-33	1.1E- 33
	UP_KEYWORDS	Cell division	<u>RT</u>	=	131	1.6E- 21	2.3E0	2.4E-20	1.9E- 20
	GOTERM_BP_DIRECT	cell division	<u>RT</u>	=	123	2.1E- 16	2.1E0	5.1E-14	4.9E- 14
	UP_KEYWORDS	<u>Mitosis</u>	<u>RT</u>	=	90	2.0E- 15	2.4E0	2.7E-14	2.2E- 14
	GOTERM_BP_DIRECT	mitotic nuclear division	<u>RT</u>	=	86	1.7E- 11	2.1E0	2.6E-9	2.5E-
Anno	tation Cluster 9	Enrichment Score: 18.67	G	To the second se	Count	P_Value	Fold Change	Benjamini	i FDR
	UP_KEYWORDS	<u>Tyrosine-protein kinase</u>	<u>RT</u>	=	84	8.7E- 46	5.1E0	2.3E-44	1.8E- 44
	INTERPRO	Serine-threonine/tyrosine-protein kinase catalytic domain	<u>RT</u>	=	98	5.4E- 45	4.3E0	8.7E-43	8.1E- 43
	INTERPRO	<u>Tyrosine-protein kinase, catalytic domain</u>	<u>RT</u>	=	69	1.2E- 38	5.0E0	1.6E-36	1.5E- 36
	INTERPRO	<u>Tyrosine-protein kinase, active site</u>	<u>RT</u>	=	71	1.3E- 35	4.6E0	1.7E-33	1.6E- 33
	SMART	<u>TyrKc</u>	<u>RT</u>	-	69	7.8E- 27	3.3E0	5.7E-25	5.1E- 25
	GOTERM_MF_DIRECT	protein tyrosine kinase activity	RT	-	76	2.1E-	3.4E0	2.1E-23	1.9E-
	GOTERM_BP_DIRECT	peptidyl-tyrosine phosphorylation	RT		79	25 2.1E-		1.1E-19	23 1.0E-
	GOTERM_MF_DIRECT	non-membrane spanning protein tyrosine	RT	-	36	22 1.0E-		7.1E-17	19 6.5E-
	GOTERM_BP_DIRECT	kinase activity peptidyl-tyrosine autophosphorylation	RT	-	33	18 2.9E-		9.9E-16	17 9.5E-
	GOTERM_CC_DIRECT	extrinsic component of cytoplasmic side of	RT	-	35	18 4.6E-	3.3E0	2.8E-9	16 2.5E-
	GOTERM_MF_DIRECT	plasma membrane transmembrane receptor protein tyrosine				11 1.8E-			9 6.5E-
	GOTERM_BP_DIRECT	kinase activity transmembrane receptor protein tyrosine	<u>RT</u>	-	25	10 5.8E-		7.1E-9	9 6.6E-
	UP_KEYWORDS	kinase signaling pathway	<u>RT</u>	-	43	10		6.9E-8	8 1.4E-
	INTERPRO	SH2 domain	<u>RT</u>		38			1.7E-6	6 6.8E-
	UP_SEQ_FEATURE	SH2 domain	<u>RT</u>		39			7.4E-5	5
	JI _OLG_I LATORE	domain:SH2	<u>RT</u>		30	7.8E-5	2.1E0	2.8E-3	2.7E- 3
	SMART								1.45
	SMART	SH2	<u>RT</u>		36	2.2E-2	1.4E0	1.6E-1	1.4E- 1

nnota	ation Cluster 1	Enrichment Score: ?	G	17	Count	P_Value	Fold	Benjamin	ni FD
	GOTERM_MF_DIRECT	receptor binding	RT	=	55	7.9E-1	Change		9.1
nnota	ation Cluster 10	Enrichment Score: 18.33	G	<u> </u>		P_Value	Fold	Ponjamin	1 ni FD
	UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	RT	-	58	5.5E-	Change 5.6E0	6.8E-33	6.5
ے ا	INTERPRO	Ubiquitin-conjugating enzyme, E2	RT	1	34	35 5.7E-	5.0E0	5.2E-17	33 4.8
ر ا	INTERPRO				25	19 2.0E-			17 1.5
J	GOTERM_MF_DIRECT	<u>Ubiquitin-conjugating enzyme, active site</u>	<u>RT</u>			17 4.1E-	6.0E0	1.6E-15	15 2.2
J	INTERPRO	ubiquitin conjugating enzyme activity	<u>RT</u>	•	26	16 6.1E-	5.4E0	2.5E-14	14 3.5
	GOTERM_BP_DIRECT	<u>Ubiquitin-conjugating enzyme/RWD-like</u>	<u>RT</u>	•	36	15	4.0E0	3.7E-13	13
	GOTERM_BP_DIRECT	protein K48-linked ubiquitination	<u>RT</u>	i	30	6.6E- 12	Fold	1.1E-9	1.0 9
nnota	cotten PR DIRECT	Enrichment Score: 17.69	G		Count	P_Value	Fold Change	Benjamin	
	GOTERM_BP_DIRECT	mRNA splicing, via spliceosome	RT	=	119	1.7E- 35	3.2E0	2.0E-32	1.9
	KEGG_PATHWAY	<u>Spliceosome</u>	<u>RT</u>	=	79	1.4E- 24	3.1E0	2.8E-23	1.3 23
	UP_KEYWORDS	<u>Spliceosome</u>	<u>RT</u>	=	67	2.8E- 23	3.6E0	4.4E-22	3.0 22
	GOTERM_CC_DIRECT	spliceosomal complex	<u>RT</u>	E	52	6.2E- 18	3.5E0	9.1E-16	8. 16
)	UP_KEYWORDS	mRNA processing	<u>RT</u>	=	105	4.3E- 15	2.2E0	5.8E-14	4. 14
)	UP_KEYWORDS	mRNA splicing	<u>RT</u>	=	88	1.1E- 14	2.3E0	1.4E-13	1. 13
)	GOTERM_CC_DIRECT	catalytic step 2 spliceosome	<u>RT</u>		46	9.5E- 14	3.2E0	9.2E-12	8.
)	GOTERM_BP_DIRECT	RNA splicing	<u>RT</u>		40		1.4E0	2.3E-1	2.
nnota	ition Cluster 12	Enrichment Score: 17.54	G		Count	P_Value	Fold	Reniemin	1 ni FC
	UP_KEYWORDS	GTP-binding	<u>RT</u>	=	143	2.5E-	Change 2.9E0	5.0E-33	4.
) 1	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	RT		132	34 1.7E-	2.9E0	2.0E-30	33 1.
)	GOTERM_MF_DIRECT					32 8.2E-			30 9.
J	GOTERM_MF_DIRECT	GTPase activity	RT	-	110	27 9.3E-	2.8E0	1.1E-24	25 9.
J	INTERPRO	GTP binding	<u>RT</u>	-	150	26 1.7E-	2.3E0	1.0E-23	2 ²
J		Small GTPase superfamily, Ras type	<u>RT</u>	•	33	19	5.2E0	1.7E-17	17
)	INTERPRO	Small GTP-binding protein domain	<u>RT</u>	=	77	2.4E- 19	2.9E0	2.3E-17	2. 17
)	INTERPRO	Small GTPase superfamily	<u>RT</u>	•	62	8.3E- 15	2.8E0	4.8E-13	4. 13
)	UP_KEYWORDS	Prenylation	<u>RT</u>	=	61	6.6E- 12	2.5E0	7.2E-11	5. 11
)	GOTERM_BP_DIRECT	small GTPase mediated signal transduction	<u>RT</u>	=	85	2.8E- 11	2.0E0	4.1E-9	3. 9
)	UP_SEQ_FEATURE	short sequence motif:Effector region	<u>RT</u>	•	41	7.9E- 10	2.8E0	4.8E-8	4. 8
)	UP_SEQ_FEATURE	propeptide:Removed in mature form	<u>RT</u>	=	66		1.9E0	1.3E-5	1. 5
)	UP_SEQ_FEATURE	lipid moiety-binding region:S-geranylgeranyl	<u>RT</u>		35	7.3E-6	2.2E0	3.1E-4	3.
ınota	ition Cluster 13	cysteine Enrichment Score: 17.43	G	17	Count	P_Value	Fold	Benjamin	4 ni Fl
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 19	RT	Ē.	50	1.5E-	Change 6.3E0	2.0E-33	1.
)]	UP_SEQ_FEATURE	zinc finger region:C2H2-type 20	RT		32	35 2.2E-	6.1E0	2.2E-19	33 2.
)	UP_SEQ_FEATURE	zinc finger region:C2H2-type 21	RT		24	21 1.0E-	6.3E0	8.6E-15	19 8.
J n	UP_SEQ_FEATURE					16 6.3E-			15 4.
J	UP_SEQ_FEATURE	zinc finger region:C2H2-type 22	<u>RT</u>	•	23	16 1.9E-	6.3E0	4.8E-14	14 1.
J	UP_SEQ_FEATURE	zinc finger region:C2H2-type 23	<u>RT</u>	•	15	10	6.4E0	1.2E-8	8
)		zinc finger region:C2H2-type 24	<u>RT</u>	i	13	6.7E-9	6.3E0	3.9E-7	3. 7
nnota	ition Cluster 14	Enrichment Score: 17.07	G	17	Count	P_Value	Change	-	
	UP_SEQ_FEATURE	repeat:LRR 8	<u>RT</u>	=	109	9.7E- 58	5.0E0	1.6E-55	1. 55
)	UP_SEQ_FEATURE	repeat:LRR 9	<u>RT</u>	=	98	2.0E- 51	5.0E0	2.9E-49	2. 49
)	UP_SEQ_FEATURE	repeat:LRR 10	<u>RT</u>	=	84	1.6E- 43	4.9E0	2.2E-41	2. 41
)	UP_SEQ_FEATURE	repeat:LRR 11	<u>RT</u>	=	73	9.4E- 38	4.9E0	1.3E-35	1. 35
)	UP_SEQ_FEATURE	repeat:LRR 12	<u>RT</u>	•	66	9.0E- 35	5.0E0	1.1E-32	1. 32
	UP_SEQ_FEATURE	repeat:LRR 13	<u>RT</u>	•	53	1.1E- 26	4.8E0	1.2E-24	1. 24
)									
)	UP_SEQ_FEATURE	repeat:LRR 14	<u>RT</u>		43	4.4E- 22	4.9E0	4.4E-20	4. 20

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

Annot	ation Cluster 1	Enrichment Score: ?	G	17	Count	P_Value	Fold Change	Benjamini	FDF
	COG_ONTOLOGY	<u>Signal transduction mechanisms /</u> <u>Cytoskeleton / Cell division and chromosome</u> <u>partitioning / General function prediction only</u>	<u>RT</u>	i e	33	1.8E-6	2.0E0	2.8E-5	2.8 5
)	GOTERM_MF_DIRECT	<u>calcium ion binding</u>	<u>RT</u>	=	117	6.8E-1	9.7E-1	1.0E0	9.1 1
)	UP_KEYWORDS	Calcium	<u>RT</u>	=	112	9.6E-1	8.8E-1	1.0E0	9.6 1
not	ation Cluster 20	Enrichment Score: 13.32	G	17	Count	P_Value	Fold Change	Benjamini	i FD
)	KEGG_PATHWAY	Oxytocin signaling pathway	<u>RT</u>	=	76	3.7E- 18	2.7E0	4.4E-17	2.0 17
	KEGG_PATHWAY	cGMP-PKG signaling pathway	<u>RT</u>	=	71	1.6E- 13	2.4E0	9.2E-13	4.1 13
	KEGG_PATHWAY	Vascular smooth muscle contraction	<u>RT</u>	•	53	1.9E- 10	2.4E0	8.0E-10	3.5 10
nnot	ation Cluster 21	Enrichment Score: 13.01	G	-	Count	P_Value	Fold Change	Benjamini	FD
)	INTERPRO	Actin-related protein	<u>RT</u>	1	30	1.1E- 18	5.5E0	9.5E-17	8.8 17
	SMART	<u>ACTIN</u>	<u>RT</u>	•	30	3.1E- 14	3.7E0	1.4E-12	1.2
	INTERPRO	Actin/actin-like conserved site	<u>RT</u>		19	4.2E- 12	5.6E0	1.9E-10	1.8
	INTERPRO	Actin, conserved site	<u>RT</u>	1	16	6.3E- 10	5.5E0	2.1E-8	1.9
nnot	ation Cluster 22	Enrichment Score: 12.97	G	178	Count	P_Value	Fold Change	Benjamini	
	KEGG_PATHWAY	Neurotrophin signaling pathway	<u>RT</u>	=	76	3.8E- 26	3.3E0	1.0E-24	4.5 25
	KEGG_PATHWAY	Prostate cancer	<u>RT</u>	•	62	4.5E- 25	3.7E0	9.9E-24	4.4 24
	KEGG_PATHWAY	Hepatitis B	RT		79	2.4E-	2.9E0	4.1E-20	1.8
-]	KEGG_PATHWAY	T cell receptor signaling pathway	RT		62	21 1.1E-	3.3E0	1.7E-19	20 7.6
ر ا	KEGG_PATHWAY	Pancreatic cancer	RT		47	20 8.8E-	3.8E0	1.2E-18	5.!
ך ר	KEGG_PATHWAY	ErbB signaling pathway	RT		54	20 4.1E-	3.3E0	4.7E-17	19 2.:
)]	KEGG_PATHWAY	Chronic myeloid leukemia	RT		47	18 4.7E-	3.4E0	4.4E-16	1.9
٦	KEGG_PATHWAY				44	17 7.4E-	3.6E0	6.6E-16	16 2.9
J	KEGG_PATHWAY	Glioma	<u>RT</u>			17 1.4E-			16 5.3
J	- KEGG_PATHWAY	Acute myeloid leukemia	<u>RT</u>	•	39	15 2.5E-	3.7E0	1.2E-14	15 8.3
J	KEGG_PATHWAY	Sphingolipid signaling pathway	<u>RT</u>	•	62	15 3.1E-	2.7E0	1.9E-14	15
	KEGG_PATHWAY	Endometrial cancer	<u>RT</u>	•	37	15 1.3E-	3.7E0	2.3E-14	14 3.9
	KEGG_PATHWAY	VEGF signaling pathway	<u>RT</u>	•	40	14	3.4E0	8.8E-14	14
		<u>Colorectal cancer</u>	<u>RT</u>	•	40	2.8E- 14	3.4E0	1.9E-13	8.3
	KEGG_PATHWAY	<u>Prolactin signaling pathway</u>	<u>RT</u>	•	43	6.3E- 14	3.2E0	4.0E-13	1.8
	KEGG_PATHWAY	Non-small cell lung cancer	<u>RT</u>	•	37	1.1E- 13	3.5E0	6.4E-13	2.9
	KEGG_PATHWAY	B cell receptor signaling pathway	<u>RT</u>	•	41	6.3E- 13	3.1E0	3.4E-12	1.5 12
	KEGG_PATHWAY	Renal cell carcinoma	<u>RT</u>	•	39	3.2E- 12	3.1E0	1.6E-11	6.9 12
	KEGG_PATHWAY	Fc epsilon RI signaling pathway	<u>RT</u>	•	39	1.1E- 11	3.0E0	5.1E-11	2.3
	KEGG_PATHWAY	Bladder cancer	<u>RT</u>	•	28	5.9E- 11	3.6E0	2.5E-10	1.1 10
	KEGG_PATHWAY	Hepatitis C	<u>RT</u>	•	58	1.5E- 10	2.3E0	6.3E-10	2.8 10
	KEGG_PATHWAY	Thyroid hormone signaling pathway	<u>RT</u>	•	52	3.2E- 10	2.4E0	1.3E-9	5.6 10
	KEGG_PATHWAY	<u>Insulin signaling pathway</u>	<u>RT</u>	=	58	8.3E- 10	2.2E0	3.2E-9	1.4 9
	KEGG_PATHWAY	<u>Melanoma</u>	<u>RT</u>	•	37		2.7E0	5.5E-9	2.4
	KEGG_PATHWAY	Central carbon metabolism in cancer	<u>RT</u>	•	33	1.9E-8	2.7E0	6.4E-8	2.8
	KEGG_PATHWAY	Choline metabolism in cancer	<u>RT</u>	•	41	1.0E-6	2.1E0	3.0E-6	1.3
	KEGG_PATHWAY	Fc gamma R-mediated phagocytosis	<u>RT</u>		32	8.4E-5	2.0E0	2.1E-4	9.3
)	KEGG_PATHWAY	Signaling pathways regulating pluripotency of	RT		45	2.6E-4		5.9E-4	2.6
)	KEGG_PATHWAY	stem cells Natural killer cell mediated cytotoxicity	RT	1	38	1.6E-3		3.3E-3	1.6
nnot	ation Cluster 23	Enrichment Score: 12.77	G	-		P_Value	Fold	Baniamini	3 i FD
	GOTERM_BP_DIRECT	protein K11-linked ubiquitination	RT	i	26	1.1E-	Onlange	3.3E-15	3.2
)	GOTERM_BP_DIRECT	regulation of ubiquitin-protein ligase activity	RT	1	20	17 8.8E-	5.2E0	1.3E-9	15 1.3
ر م	GOTERM_CC_DIRECT	involved in mitotic cell cycle		:	19	12 5.1E-	5.2E0 5.2E0	2.9E-9	9 2.6
		anaphase-promoting complex	<u>RT</u>	•	19	11	Fold	2.95-9	9

Annota	ation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:F-box	<u>RT</u>	1	43	2.4E- 17	4.0E0	2.0E-15	2.0E- 15
	INTERPRO	F-box domain, cyclin-like	<u>RT</u>	•	44	2.0E- 16	3.7E0	1.4E-14	1.3E- 14
	GOTERM_CC_DIRECT	SCF ubiquitin ligase complex	<u>RT</u>	:	31	1.3E- 12	3.9E0	9.3E-11	8.3E- 11
	GOTERM_BP_DIRECT	SCF-dependent proteasomal ubiquitin- dependent protein catabolic process	<u>RT</u>	i e	19	5.6E- 10	4.7E0	6.9E-8	6.6E- 8
	SMART	FBOX	<u>RT</u>		25		2.6E0	1.9E-5	1.7E- 5
Annota	ation Cluster 25	Enrichment Score: 11.88	G	T.	Count	P_Value	Fold Change	Benjamini	
	UP_KEYWORDS	<u>Helicase</u>	<u>RT</u>	=	67	1.1E- 19	3.2E0	1.5E-18	1.2E- 18
	UP_SEQ_FEATURE	domain:Helicase C-terminal	<u>RT</u>		53	1.2E-	3.3E0	9.6E-15	9.2E-
	INTERPRO	Helicase, superfamily 1/2, ATP-binding	<u>RT</u>	•	56	16 1.2E-	3.2E0	8.9E-15	15 8.2E-
	INTERPRO	domain Helicase, C-terminal	RT		55	16 2.3E-	3.2E0	1.6E-14	15 1.4E-
	UP_SEQ_FEATURE	domain:Helicase ATP-binding	RT		54	16 5.0E-	3.2E0	4.0E-14	14 3.9E-
	INTERPRO	SNF2-related	RT	-	25	16 2.5E-	4.8E0	1.4E-11	14 1.3E-
	UP_SEQ_FEATURE	short sequence motif:DEAH box	RT		28	13 6.8E-	4.4E0	4.7E-11	11 4.5E-
	GOTERM_MF_DIRECT			_		13 3.3E-			11 1.1E-
	SMART	helicase activity	RT DT	•	40 55	10	2.8E0	1.2E-8	8 4.8E-
	SMART	DEXDC	<u>RT</u>	-		1.7E-8		5.4E-7	7 5.9E-
	INTERPRO	HELICC DNA/RNA helicase, DEAD/DEAH box type, N-	<u>RT</u>	•	54	2.3E-8		6.6E-7	7 2.2E-
	GOTERM_MF_DIRECT	terminal	<u>RT</u>	•	29	1.0E-6	2.6E0	2.4E-5	5 1.4E-
	GOTEKW_WIP_DIRECT	ATP-dependent RNA helicase activity	<u>RT</u>	1	27	6.9E-6	2.5E0 Fold	1.5E-4	4
Annota	ation Cluster 26 KEGG_PATHWAY	Enrichment Score: 11.43	G		Count	P_Value 3.7E-	Change	Benjamini	2.0E-
	KEGG_PATHWAY	Oxytocin signaling pathway	<u>RT</u>		76	18	2.7E0	4.4E-17	17
		<u>Long-term potentiation</u>	<u>RT</u>	•	38	1.9E- 11	3.0E0	8.2E-11	3.7E- 11
	KEGG_PATHWAY	<u>Melanogenesis</u>	<u>RT</u>	i	41	7.7E-7	2.2E0	2.3E-6	1.0E- 6
Annota	ation Cluster 27 KEGG_PATHWAY	Enrichment Score: 11.29	G	N .	Count	P_Value	Change	Benjamini	
		<u>Chagas disease (American trypanosomiasis)</u>	<u>RT</u>	•	60	6.4E- 18	3.0E0	7.0E-17	3.1E- 17
	KEGG_PATHWAY	TNF signaling pathway	<u>RT</u>	•	54	6.6E- 13	2.7E0	3.5E-12	1.5E- 12
	KEGG_PATHWAY	Toll-like receptor signaling pathway	<u>RT</u>	•	53	1.8E- 12	2.6E0	8.8E-12	3.9E- 12
	KEGG_PATHWAY	Fc epsilon RI signaling pathway	<u>RT</u>	•	39	1.1E- 11	3.0E0	5.1E-11	2.3E- 11
	KEGG_PATHWAY	<u>Hepatitis C</u>	<u>RT</u>	•	58	1.5E- 10	2.3E0	6.3E-10	2.8E- 10
	KEGG_PATHWAY	Influenza A	<u>RT</u>	•	68	9.9E- 10	2.1E0	3.7E-9	1.6E- 9
	KEGG_PATHWAY	Osteoclast differentiation	<u>RT</u>	Ē	54	7.8E-9	2.2E0	2.6E-8	1.2E- 8
Annota	ation Cluster 28	Enrichment Score: 11.2	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_MF_DIRECT	protein serine/threonine phosphatase activity	<u>RT</u>	i	36	8.9E- 14	3.7E0	4.5E-12	4.1E- 12
	UP_KEYWORDS	<u>Protein phosphatase</u>	<u>RT</u>	•	53	3.1E- 12	2.7E0	3.6E-11	2.9E- 11
	GOTERM_BP_DIRECT	protein dephosphorylation	<u>RT</u>	E	51	9.1E- 10	2.4E0	1.0E-7	9.6E- 8
Annota	ation Cluster 29	Enrichment Score: 11.07	G	To the second se	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:AGC-kinase C-terminal	<u>RT</u>	•	33	2.2E- 13	4.0E0	1.5E-11	1.5E- 11
	INTERPRO	Protein kinase, C-terminal	<u>RT</u>	•	24	3.5E- 13	5.0E0	1.9E-11	1.7E- 11
	INTERPRO	AGC-kinase, C-terminal	<u>RT</u>	i .	33	2.9E- 12	3.7E0	1.5E-10	1.4E- 10
	SMART	<u>S TK X</u>	<u>RT</u>	i .	32	2.4E-8	2.6E0	6.6E-7	5.9E- 7
Annota	ation Cluster 30	Enrichment Score: 10	G	™	Count	P_Value	Fold Change	Benjamini	FDR
	KEGG_PATHWAY	Chronic myeloid leukemia	<u>RT</u>	i .	47	4.7E- 17	3.4E0	4.4E-16	1.9E- 16
	BIOCARTA	<u>Influence of Ras and Rho proteins on G1 to S</u> <u>Transition</u>	<u>RT</u>	1	23	1.3E-7	2.7E0	1.3E-5	9.8E- 6
	KEGG_PATHWAY	Small cell lung cancer	<u>RT</u>	•	38	1.6E-7	2.4E0	5.0E-7	2.2E- 7
Annota	ation Cluster 31	Enrichment Score: 9.5	G	·	Count	P_Value	Fold Change	Benjamini	
	KEGG_PATHWAY	<u>Cholinergic synapse</u>	<u>RT</u>	E	59	2.4E- 15	2.8E0	1.8E-14	8.2E- 15
	KEGG_PATHWAY	<u>Circadian entrainment</u>	<u>RT</u>	•	52	2.9E- 14	2.9E0	1.9E-13	8.3E- 14
						-1			

nnota	ation Cluster 1	Enrichment Score: ?	G	. Total	Count	P_Value	Fold Change	Benjamini	i FDR
	KEGG_PATHWAY	<u>Dopaminergic synapse</u>	<u>RT</u>	=	61	4.4E- 13	2.5E0	2.4E-12	1.1E 12
	GOTERM_BP_DIRECT	cellular response to glucagon stimulus	<u>RT</u>		26	1.3E- 10	3.9E0	1.7E-8	1.6E
	KEGG_PATHWAY	<u>Glutamatergic synapse</u>	<u>RT</u>	4	52	2.2E-	2.4E0	8.8E-10	3.9E
آ ا	KEGG_PATHWAY	Retrograde endocannabinoid signaling	RT		44	10 3.5E-8	2.3E0	1.1E-7	10 5.0E
) 1	KEGG_PATHWAY								8 2.2E
J	KEGG_PATHWAY	GABAergic synapse	<u>RT</u>	•	38	1.6E-7	2.4E0	5.0E-7	7 1.5E
J	_	Morphine addiction	<u>RT</u>	•	38	1.2E-6	2.2E0	3.5E-6	6
	KEGG_PATHWAY	<u>Serotonergic synapse</u>	<u>RT</u>	ī	42	6.2E-6	2.0E0	1.7E-5	7.4E 6
nnota	ation Cluster 32	Enrichment Score: 9.24	G	15	Count	P_Value	Fold Change	Benjamini	i FDR
	GOTERM_MF_DIRECT	bitter taste receptor activity	<u>RT</u>	i	24	2.7E- 16	5.7E0	1.7E-14	1.5E 14
	INTERPRO	Mammalian taste receptor	<u>RT</u>	•	24	8.5E- 16	5.7E0	5.6E-14	5.2E 14
	KEGG_PATHWAY	Taste transduction	<u>RT</u>	•	32	3.4E- 13	3.7E0	1.9E-12	8.6E
	UP_KEYWORDS	<u>Taste</u>	<u>RT</u>	•	24	2.9E- 12	4.8E0	3.4E-11	2.8E
)	GOTERM_BP_DIRECT	detection of chemical stimulus involved in	<u>RT</u>		26	1.3E-	3.9E0	1.7E-8	1.6E
- ገ	GOTERM_BP_DIRECT	sensory perception of bitter taste sensory perception of taste	RT	-	16	10 1.8E-5	3.3E0	7.6E-4	8 7.2E
J	GOTERM_MF_DIRECT			_					4 3.6E
J	UP_KEYWORDS	taste receptor activity Sensory transduction	RT RT	1	11 47	2.3E-5 1.0E0	4.4E0	3.9E-4 1.0E0	4 1.0E
nnota	ation Cluster 33	Enrichment Score: 9.21	G		Count	P_Value	1	Benjamini	
)	GOTERM_BP_DIRECT	proteasome-mediated ubiquitin-dependent	RT		101	8.1E-		5.3E-24	5.0E
)]	GOTERM_BP_DIRECT	<u>protein catabolic process</u> <u>anaphase-promoting complex-dependent</u>	RT	Ē.	50	27 2.3E-		9.5E-17	24 9.1E
J	GOTERM_BP_DIRECT	catabolic process positive regulation of ubiquitin-protein ligase	<u>KI</u>	•	30	19	3.720	9.JL-17	17
)		activity involved in regulation of mitotic cell cycle transition	<u>RT</u>	•	47	1.1E- 17	3.7E0	3.4E-15	3.2E 15
)	GOTERM_BP_DIRECT	stimulatory C-type lectin receptor signaling pathway	<u>RT</u>	=	56	6.4E- 17	3.2E0	1.7E-14	1.6E
)	GOTERM_BP_DIRECT	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	<u>RT</u>	•	44	1.3E- 16	3.7E0	3.2E-14	3.1E 14
)	GOTERM_BP_DIRECT	T cell receptor signaling pathway	RT	=	64	1.4E-	2.6E0	2.9E-11	2.88
ر ا	GOTERM_BP_DIRECT	NIK/NF-kappaB signaling	RT	4	37	13 3.4E-	3.3E0	6.1E-10	11 5.8E
J T	GOTERM_BP_DIRECT			<u>-</u>		12 7.2E-			10 1.1E
J	GOTERM_BP_DIRECT	Fc-epsilon receptor signaling pathway regulation of ubiquitin-protein ligase activity	<u>RT</u>	-	69	12 8.8E-	2.3E0	1.1E-9	9 1.3E
J		involved in mitotic cell cycle	<u>RT</u>	•	20	12	5.2E0	1.3E-9	9
	GOTERM_BP_DIRECT	positive regulation of canonical Wnt signaling pathway	<u>RT</u>	•	44	4.1E-7	2.2E0	3.0E-5	2.8E 5
	GOTERM_CC_DIRECT	proteasome complex	<u>RT</u>	•	26	1.4E-6	2.8E0	4.8E-5	4.3E 5
	UP_KEYWORDS	<u>Proteasome</u>	<u>RT</u>	•	23	1.7E-6	3.0E0	1.2E-5	9.4E 6
	GOTERM_BP_DIRECT	regulation of mRNA stability	<u>RT</u>	•	37	6.7E-6	2.1E0	3.3E-4	3.2E 4
	GOTERM_BP_DIRECT	regulation of cellular amino acid metabolic process	<u>RT</u>		21	1.2E-4	2.4E0	4.1E-3	3.9E
	GOTERM_BP_DIRECT	negative regulation of canonical Wnt signaling	<u>RT</u>	4	47	1.9E-4	1.7E0	6.3E-3	6.0E
)	GOTERM_CC_DIRECT	proteasome accessory complex	RT		10	4.2E-4		5.6E-3	3 5.0E
1	KEGG_PATHWAY			<u>-</u>	19		2.3E0		3 6.2E
)	GOTERM_BP_DIRECT	Proteasome Wnt signaling pathway, planar cell polarity	<u>RT</u>	•				1.3E-3	4 2.3E
J	GOTERM_BP_DIRECT	pathway antigen processing and presentation of	<u>RT</u>	•	29	9.2E-4	1.9E0	2.4E-2	2
	JOILINII DI LINEOT	exogenous peptide antigen via MHC class I, TAP-dependent	<u>RT</u>	i	19	1.4E-2	1.8E0	2.1E-1	2.0E 1
	GOTERM_BP_DIRECT	tumor necrosis factor-mediated signaling	<u>RT</u>		30	2.1E-2	1.5E0	2.6E-1	2.4E 1
nnota	ation Cluster 34	pathway Enrichment Score: 8.96	G	100	Count	P_Value	Fold	Benjamini	
	GOTERM_BP_DIRECT	negative regulation of protein kinase activity	RT	ī	49	3.3E-	Change 2.9E0	6.4E-11	6.1E
)	GOTERM_MF_DIRECT	·				13 2.6E-			11 9.8E
J	GOTERM_BP_DIRECT	protein kinase inhibitor activity	<u>RT</u>	•	31	11	3.6E0	1.1E-9	10
J		negative regulation of JAK-STAT cascade	<u>RT</u>	•	25	1.0E-9	3.7E0	1.1E-7	1.0E 7
	GOTERM_BP_DIRECT	cytokine-mediated signaling pathway	<u>RT</u>	ī	40	1.7E-4	1.8E0	5.7E-3	5.5E 3
nnota	ation Cluster 35	Enrichment Score: 8.93	G	15	Count	P_Value	Fold Change	Benjamini	i FDR
)	UP_KEYWORDS	Motor protein	<u>RT</u>	=	75	7.3E- 28	3.8E0	1.4E-26	1.1E 26
1	UP_KEYWORDS	<u>Myosin</u>	<u>RT</u>	•	43	4.2E- 27	5.8E0	7.3E-26	5.9E
J						-/			20

Annot	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_CC_DIRECT	myosin complex	<u>RT</u>	i	36	1.2E- 17	•	1.4E-15	1.3E- 15
	INTERPRO	Myosin head, motor domain	<u>RT</u>		32	1.4E-	5.0E0	1.1E-15	1.0E-
	GOTERM_MF_DIRECT	motor activity	RT		37	17 2.7E-		1.2E-10	15 1.1E-
	SMART	MYSc	RT		32	12 3.2E-		1.3E-10	10 1.1E-
	UP_KEYWORDS	Muscle protein	RT		33	12 7.2E-		7.7E-11	10 6.1E-
	INTERPRO	IQ motif, EF-hand binding site	RT	_	42	12 1.2E-	3.0E0	5.3E-10	11 4.9E-
	UP_KEYWORDS			-		11 2.7E-			10 2.2E-
	GOTERM_MF_DIRECT	<u>Calmodulin-binding</u>	<u>RT</u>		56	11 4.2E-	2.5E0	2.7E-10	10 1.5E-
	UP_SEQ_FEATURE	microfilament motor activity	<u>RT</u>		18	11 5.4E-		1.7E-9	9 3.4E-
	INTERPRO	region of interest:Actin-binding	<u>RT</u>		21	11 1.0E-	4.9E0	3.6E-9	9 3.5E-
	INTERPRO	Myosin, N-terminal, SH3-like	<u>RT</u>	•	15	1.0E 10 1.2E-	6.2E0	3.8E-9	9 4.2E-
	GOTERM_CC_DIRECT	Myosin-like IQ motif-containing domain	<u>RT</u>	i	17	10	5.5E0	4.5E-9	9
		muscle myosin complex	<u>RT</u>	•	15	4.9E- 10	6.0E0	2.4E-8	2.1E- 8
	UP_SEQ_FEATURE	domain:IQ	<u>RT</u>	•	28	2.7E-8	3.1E0	1.5E-6	1.5E- 6
	INTERPRO	Myosin tail	<u>RT</u>	•	15	4.1E-8	4.9E0	1.1E-6	1.0E- 6
	GOTERM_MF_DIRECT	calmodulin binding	<u>RT</u>	•	60	6.1E-7	1.9E0	1.6E-5	1.5E- 5
	GOTERM_CC_DIRECT	myosin filament	<u>RT</u>	i	12	2.9E-6	4.8E0	8.2E-5	7.3E- 5
	SMART	IQ	<u>RT</u>	1	29	6.1E-6	2.3E0	9.0E-5	8.0E- 5
	UP_KEYWORDS	Actin-binding	<u>RT</u>	•	67	1.8E-5	1.7E0	1.1E-4	9.2E- 5
	UP_KEYWORDS	Thick filament	<u>RT</u>	i .	11	3.1E-5	4.4E0	1.9E-4	1.5E- 4
	UP_SEQ_FEATURE	domain:IQ 3	<u>RT</u>	i .	12	9.8E-5	3.7E0	3.5E-3	3.4E- 3
	UP_SEQ_FEATURE	domain:IQ 1	<u>RT</u>	i contraction	15	1.1E-4	3.1E0	3.8E-3	3.7E- 3
	UP_SEQ_FEATURE	domain:IQ 2	<u>RT</u>	1	15	1.1E-4	3.1E0	3.8E-3	3.7E- 3
	GOTERM_BP_DIRECT	actin filament-based movement	<u>RT</u>	i .	11	1.1E-4	3.8E0	3.9E-3	3.7E- 3
	UP_SEQ_FEATURE	domain:IQ 4	<u>RT</u>	i de la companya de	9	5.2E-4	4.1E0	1.6E-2	1.5E- 2
	KEGG_PATHWAY	<u>Tight junction</u>	<u>RT</u>		29	2.2E-3	1.8E0	4.5E-3	2.2E- 3
	UP_SEQ_FEATURE	domain:IQ 5	<u>RT</u>	1	6	1.5E-2	3.7E0	2.9E-1	2.8E-
	GOTERM_BP_DIRECT	muscle contraction	<u>RT</u>		27	3.1E-2	1.5E0	3.5E-1	1 3.4E-
	UP_SEQ_FEATURE	domain:IQ 6	RT		3	3.3E-1		1.0E0	1 9.7E-
Annot	tation Cluster 36	Enrichment Score: 8.54	G	·	Count	P_Value	Fold	Benjamin	1 FDR
	UP_KEYWORDS	DNA damage	<u>RT</u>	=	98	1.4E-	Change 1.9E0	1.4E-9	1.1E-
	UP_KEYWORDS	DNA repair	RT		85	10 2.9E-	2.0E0	2.6E-9	9 2.1E-
	GOTERM_BP_DIRECT	DNA repair	RT		71	10 5.8E-7		4.0E-5	9 3.8E-
Annot	tation Cluster 37	Enrichment Score: 8.14	G	-	Count	P_Value	Fold	Benjamin	5 FDR
	UP_SEQ_FEATURE	repeat:ANK 6	RT	=	85	7.9E- 55	Change 5.8E0	1.2E-52	1.2E-
	UP_SEQ_FEATURE	repeat:ANK 7	RT	-	56	1.1E-	6.1E0	1.4E-35	52 1.4E-
	UP_SEQ_FEATURE	repeat:ANK 8	RT	-	41	37 1.4E-		1.4E-33	35 1.5E-
	UP_SEQ_FEATURE			:	36	27 1.0E- 23		1.0E-25 1.1E-21	25 1.0E-
	UP_SEQ_FEATURE	repeat:ANK 9	<u>RT</u>			23 1.7E-			21 1.4E-
	UP_SEQ_FEATURE	repeat:ANK 10	<u>RT</u>		26	17 6.3E-		1.5E-15	15 4.6E-
	UP_SEQ_FEATURE	repeat:ANK 11	<u>RT</u>		23	16 1.6E-		4.8E-14	14 1.0E-
	UP_SEQ_FEATURE	repeat:ANK 12	<u>RT</u>	•	16	10		1.0E-8	8 1.5E-
	UP_SEQ_FEATURE	repeat:ANK 13	<u>RT</u>	•	13	2.9E-8		1.6E-6	6
		repeat:ANK 14	<u>RT</u>	i	13	2.9E-8		1.6E-6	1.5E- 6
	UP_SEQ_FEATURE	repeat:ANK 15	<u>RT</u>	•	13	2.9E-8	5.9E0	1.6E-6	1.5E- 6
	UP_SEQ_FEATURE	repeat:ANK 16	<u>RT</u>	i	11	8.6E-7	5.8E0	4.4E-5	4.3E- 5
	UP_SEQ_FEATURE	repeat:ANK 17	<u>RT</u>	i	10	4.5E-6	5.7E0	2.0E-4	2.0E- 4
	UP_SEQ_FEATURE	repeat:ANK 18	<u>RT</u>	i	10	4.5E-6	5.7E0	2.0E-4	2.0E- 4

Anno	tation Cluster 1	Enrichment Score: ?	G	To the second se	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	repeat:ANK 19	<u>RT</u>	i	10	4.5E-6	5.7E0	2.0E-4	2.0E- 4
	UP_SEQ_FEATURE	repeat:ANK 20	<u>RT</u>	1	9	2.3E-5	5.6E0	9.0E-4	8.7E- 4
	UP_SEQ_FEATURE	repeat:ANK 21	<u>RT</u>	i .	9	2.3E-5	5.6E0	9.0E-4	8.7E- 4
	UP_SEQ_FEATURE	repeat:ANK 22	<u>RT</u>	i	8	1.2E-4	5.4E0	4.0E-3	3.9E- 3
	UP_SEQ_FEATURE	repeat:ANK 23	<u>RT</u>	i e	8	1.2E-4	5.4E0	4.0E-3	3.9E- 3
	UP_SEQ_FEATURE	repeat:ANK 24	<u>RT</u>	i .	6	2.6E-3	5.1E0	6.6E-2	6.3E-
	INTERPRO	Death domain	<u>RT</u>		13	6.6E-3	2.3E0	7.0E-2	2 6.4E-
	UP_SEQ_FEATURE	domain:Death	RT		12	9.3E-3	2.3E0	2.1E-1	2 2.1E-
	UP_SEQ_FEATURE	repeat:ANK 25	RT	1	5	1.1E-2		2.3E-1	1 2.2E-
	UP_SEQ_FEATURE	repeat:ANK 26	RT	1	3	5.8E-2		8.8E-1	1 8.5E-
	UP_SEQ_FEATURE	repeat:ANK 27	RT	1	3	5.8E-2		8.8E-1	1 8.5E-
	GOTERM_BP_DIRECT	protein targeting to plasma membrane	RT		9	5.9E-2		5.3E-1	1 5.0E-
	INTERPRO	Death-like domain	RT		22	7.1E-2		4.0E-1	1 3.7E-
	GOTERM_MF_DIRECT			1					1 5.5E-
	INTERPRO	spectrin binding	<u>RT</u>		8	1.3E-1		6.0E-1	1 9.2E-
	UP_SEQ_FEATURE	ZU5	<u>RT</u>		4	3.0E-1		1.0E0	1 9.7E-
	SMART	domain:ZU5	<u>RT</u>	i	3	3.9E-1		1.0E0	1 8.9E-
	SMART	<u>DEATH</u>	<u>RT</u>		8	5.2E-1		1.0E0	1 8.9E-
	GOTERM_MF_DIRECT	<u>ZU5</u>	<u>RT</u>		3	6.9E-1		1.0E0	9.1E-
		cytoskeletal adaptor activity	RT	i	3	7.8E-1	Eald	1.0E0	1
Anno	tation Cluster 38 UP_KEYWORDS	Enrichment Score: 7.86	G	-	Count	P_Value 2.2E-	Change	Benjamini	FDR 1.6E-
	GOTERM_CC_DIRECT	<u>Viral nucleoprotein</u>	RT	1	20	10 8.5E-	4.9E0	2.0E-9	9 3.5E-
	UP_KEYWORDS	<u>viral nucleocapsid</u>	RT	i	20	10	4.5E0	3.9E-8	8 7.0E-
		Virion	RT	i	20	1.4E-5	2.9E0 Fold	8.7E-5	5
Anno	tation Cluster 39 INTERPRO	Enrichment Score: 7.42	G	-	Count	P_Value 1.1E-	Change	Benjamini	FDR 4.6E-
	UP_KEYWORDS	Bromodomain, conserved site	<u>RT</u>	1	21	11 1.8E-	5.0E0	5.0E-10	10 1.4E-
	INTERPRO	<u>Bromodomain</u>	<u>RT</u>	•	24	10	4.2E0	1.7E-9	9
	III III III	<u>Bromodomain</u>	<u>RT</u>	•					8 7F-
	LID SEO FEATURE				25	3.0E-9	3.6E0	9.4E-8	8.7E- 8
	UP_SEQ_FEATURE	domain:Bromo	<u>RT</u>	i	18	3.0E-9 5.8E-8	3.6E0 4.2E0	9.4E-8 3.1E-6	8 3.0E- 6
	SMART	domain:Bromo BROMO	RT RT	: :					8 3.0E- 6 9.1E- 5
				i i	18	5.8E-8	4.2E0 2.4E0 3.3E0	3.1E-6	8 3.0E- 6 9.1E-
Anno	SMART GOTERM_MF_DIRECT tation Cluster 40	BROMO lysine-acetylated histone binding Enrichment Score: 7.38	RT RT G		18 25 10 Count	5.8E-8 7.2E-6 1.2E-3 P_Value	4.2E0 2.4E0 3.3E0 Fold Change	3.1E-6 1.0E-4 1.4E-2 Benjamini	8 3.0E- 6 9.1E- 5 1.3E- 2
Anno	SMART GOTERM_MF_DIRECT tation Cluster 40 INTERPRO	BROMO lysine-acetylated histone binding Enrichment Score: 7.38 Tubulin, C-terminal	RT RT G RT	i i	18 25 10 Count 20	5.8E-8 7.2E-6 1.2E-3 P_Value 3.8E- 12	4.2E0 2.4E0 3.3E0 Fold Change 5.4E0	3.1E-6 1.0E-4 1.4E-2 Benjamini 1.8E-10	8 3.0E-6 9.1E-5 1.3E-2 FDR 1.7E-10
Anno	SMART GOTERM_MF_DIRECT tation Cluster 40 INTERPRO INTERPRO	BROMO lysine-acetylated histone binding Enrichment Score: 7.38	RT RT G		18 25 10 Count 20 20	5.8E-8 7.2E-6 1.2E-3 P_Value 3.8E- 12 3.8E- 12	4.2E0 2.4E0 3.3E0 Fold Change 5.4E0 5.4E0	3.1E-6 1.0E-4 1.4E-2 Benjamini 1.8E-10 1.8E-10	8 3.0E-6 9.1E-5 1.3E-2 FDR 1.7E-10 1.7E-10
Anno	SMART GOTERM_MF_DIRECT tation Cluster 40 INTERPRO INTERPRO INTERPRO	BROMO lysine-acetylated histone binding Enrichment Score: 7.38 Tubulin, C-terminal	RT RT G RT		18 25 10 Count 20	5.8E-8 7.2E-6 1.2E-3 P_Value 3.8E- 12 3.8E- 12 3.8E- 12	4.2E0 2.4E0 3.3E0 Fold Change 5.4E0 5.4E0	3.1E-6 1.0E-4 1.4E-2 Benjamini 1.8E-10	8 3.0E-6 9.1E-5 1.3E-2 FDR 1.7E-10 1.7E-10
Anno	SMART GOTERM_MF_DIRECT tation Cluster 40 INTERPRO INTERPRO INTERPRO INTERPRO	BROMO lysine-acetylated histone binding Enrichment Score: 7.38 Tubulin, C-terminal Tubulin/FtsZ, C-terminal	RT RT G RT RT		18 25 10 Count 20 20	5.8E-8 7.2E-6 1.2E-3 P_Value 3.8E- 12 3.8E- 12 1.6E- 11	4.2E0 2.4E0 3.3E0 Fold Change 5.4E0 5.4E0 5.4E0	3.1E-6 1.0E-4 1.4E-2 Benjamini 1.8E-10 1.8E-10	8 3.0E-6 9.1E-5 1.3E-2 FDR 1.7E-10 1.7E-10 6.0E-10
Anno	SMART GOTERM_MF_DIRECT tation Cluster 40 INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO	BROMO lysine-acetylated histone binding Enrichment Score: 7.38 Tubulin, C-terminal Tubulin/FtsZ, C-terminal Tubulin, conserved site	RT RT G RT RT RT		18 25 10 Count 20 20 20	5.8E-8 7.2E-6 1.2E-3 P_Value 3.8E- 12 3.8E- 12 1.6E- 11 2.0E- 11	4.2E0 2.4E0 3.3E0 Fold Change 5.4E0 5.4E0 5.4E0 5.2E0	3.1E-6 1.0E-4 1.4E-2 Benjamini 1.8E-10 1.8E-10 1.8E-10	8 3.0E-6 9.1E-5 1.3E-2 FDR 1.7E-10 1.7E-10 6.0E-10 7.5E-10
Anno	SMART GOTERM_MF_DIRECT tation Cluster 40 INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO	BROMO lysine-acetylated histone binding Enrichment Score: 7.38 Tubulin, C-terminal Tubulin/FtsZ, C-terminal Tubulin, conserved site Tubulin	RT RT G RT RT RT RT		18 25 10 Count 20 20 20 20	5.8E-8 7.2E-6 1.2E-3 P_Value 3.8E- 12 3.8E- 12 1.6E- 11 2.0E-	4.2E0 2.4E0 3.3E0 Fold Change 5.4E0 5.4E0 5.4E0 5.2E0 5.4E0	3.1E-6 1.0E-4 1.4E-2 Benjamini 1.8E-10 1.8E-10 6.5E-10	8 3.0E-6 9.1E-5 1.3E-2 FDR 1.7E-10 1.7E-10 6.0E-10 7.5E-10 2.0E-9
Anno	SMART GOTERM_MF_DIRECT tation Cluster 40 INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO SMART	BROMO lysine-acetylated histone binding Enrichment Score: 7.38 Tubulin, C-terminal Tubulin/FtsZ, C-terminal Tubulin, conserved site Tubulin Tubulin Tubulin/FtsZ, 2-layer sandwich domain	RT RT RT RT RT RT RT RT		18 25 10 Count 20 20 20 20 19	5.8E-8 7.2E-6 1.2E-3 P_Value 3.8E- 12 3.8E- 12 1.6E- 11 2.0E- 11 5.5E-	4.2E0 2.4E0 3.3E0 Fold Change 5.4E0 5.4E0 5.2E0 5.4E0 5.0E0	3.1E-6 1.0E-4 1.4E-2 Benjamini 1.8E-10 1.8E-10 6.5E-10 8.1E-10	8 3.0E-6 9.1E-5 1.3E-2 FDR 1.7E-10 1.7E-10 6.0E-10 7.5E-10 2.0E-9 6.5E-7
Anno	SMART GOTERM_MF_DIRECT tation Cluster 40 INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO SMART SMART	BROMO lysine-acetylated histone binding Enrichment Score: 7.38 Tubulin, C-terminal Tubulin/FtsZ, C-terminal Tubulin, conserved site Tubulin Tubulin/FtsZ, 2-layer sandwich domain Tubulin/FtsZ, GTPase domain	RT RT RT RT RT RT RT RT		18 25 10 Count 20 20 20 19 20	5.8E-8 7.2E-6 1.2E-3 P_Value 3.8E- 12 3.8E- 12 1.6E- 11 2.0E- 11 5.5E- 11	4.2E0 2.4E0 3.3E0 Fold Change 5.4E0 5.4E0 5.4E0 5.4E0 5.2E0 5.4E0 5.0E0 3.5E0	3.1E-6 1.0E-4 1.4E-2 Benjamini 1.8E-10 1.8E-10 6.5E-10 8.1E-10 2.2E-9	8 3.0E-6 9.1E-5 1.3E-2 FDR 1.7E-10 1.7E-10 6.0E-10 7.5E-10 2.0E-9 6.5E-
Anno	SMART GOTERM_MF_DIRECT tation Cluster 40 INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO SMART	BROMO lysine-acetylated histone binding Enrichment Score: 7.38 Tubulin, C-terminal Tubulin/FtsZ, C-terminal Tubulin, conserved site Tubulin Tubulin/FtsZ, 2-layer sandwich domain Tubulin/FtsZ, GTPase domain SM00865	RT RT RT RT RT RT RT RT RT		18 25 10 Count 20 20 20 19 20 19	5.8E-8 7.2E-6 1.2E-3 P_Value 3.8E-12 3.8E-12 1.6E-11 2.0E-11 5.5E-11 2.9E-8	4.2E0 2.4E0 3.3E0 Fold Change 5.4E0 5.4E0 5.4E0 5.2E0 5.4E0 5.0E0 3.5E0 3.4E0	3.1E-6 1.0E-4 1.4E-2 Benjamini 1.8E-10 1.8E-10 6.5E-10 8.1E-10 2.2E-9 7.4E-7	8 3.0E-6 9.1E-5 1.3E-2 FDR 1.7E-10 1.7E-10 6.0E-10 7.5E-10 2.0E-9 6.5E-7 6.5E-
Anno	SMART GOTERM_MF_DIRECT tation Cluster 40 INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO SMART SMART	BROMO lysine-acetylated histone binding Enrichment Score: 7.38 Tubulin, C-terminal Tubulin/FtsZ, C-terminal Tubulin, conserved site Tubulin Tubulin/FtsZ, 2-layer sandwich domain Tubulin/FtsZ, GTPase domain SM00865 SM00864	RT		18 25 10 Count 20 20 20 19 20 19 20	5.8E-8 7.2E-6 1.2E-3 P_Value 3.8E-12 3.8E-12 1.6E-11 2.0E-11 5.5E-11 2.9E-8 3.2E-8	4.2E0 2.4E0 3.3E0 Fold Change 5.4E0 5.4E0 5.4E0 5.4E0 5.0E0 3.5E0 3.4E0 2.7E0	3.1E-6 1.0E-4 1.4E-2 Benjamini 1.8E-10 1.8E-10 6.5E-10 8.1E-10 2.2E-9 7.4E-7 7.4E-7	8 3.0E-6 9.1E-5 1.3E-2 FDR 1.7E-10 1.7E-10 6.0E-10 7.5E-10 2.0E-9 6.5E-7 1.4E-
Anno	SMART GOTERM_MF_DIRECT tation Cluster 40 INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO SMART SMART KEGG_PATHWAY	BROMO lysine-acetylated histone binding Enrichment Score: 7.38 Tubulin, C-terminal Tubulin/FtsZ, C-terminal Tubulin, conserved site Tubulin Tubulin/FtsZ, 2-layer sandwich domain Tubulin/FtsZ, GTPase domain SM00865 SM00864 Pathogenic Escherichia coli infection	RT		18 25 10 Count 20 20 20 19 20 19 20 26	5.8E-8 7.2E-6 1.2E-3 P_Value 3.8E- 12 3.8E- 12 1.6E- 11 2.0E- 11 5.5E- 11 2.9E-8 3.2E-8 1.1E-6	4.2E0 2.4E0 3.3E0 Fold Change 5.4E0 5.4E0 5.4E0 5.4E0 5.2E0 5.4E0 3.5E0 3.4E0 2.7E0 6.2E0	3.1E-6 1.0E-4 1.4E-2 Benjamini 1.8E-10 1.8E-10 6.5E-10 8.1E-10 2.2E-9 7.4E-7 7.4E-7 3.2E-6	8 3.0E-6 9.1E-5 1.3E-2 FDR 1.7E-10 1.7E-10 6.0E-10 7.5E-10 2.0E-9 6.5E-7 1.4E-6 6.7E-
Anno	SMART GOTERM_MF_DIRECT tation Cluster 40 INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO SMART SMART KEGG_PATHWAY INTERPRO	BROMO lysine-acetylated histone binding Enrichment Score: 7.38 Tubulin, C-terminal Tubulin/FtsZ, C-terminal Tubulin, conserved site Tubulin Tubulin/FtsZ, 2-layer sandwich domain Tubulin/FtsZ, GTPase domain SM00865 SM00864 Pathogenic Escherichia coli infection Beta tubulin, autoregulation binding site	RT		18 25 10 Count 20 20 20 19 20 19 20 19 20 19	5.8E-8 7.2E-6 1.2E-3 P_Value 3.8E-12 3.8E-12 1.6E-11 2.0E-11 5.5E-11 2.9E-8 3.2E-8 1.1E-6 3.5E-6	4.2E0 2.4E0 3.3E0 Fold Change 5.4E0 5.4E0 5.4E0 5.4E0 5.4E0 3.5E0 3.4E0 2.7E0 6.2E0 6.2E0	3.1E-6 1.0E-4 1.4E-2 Benjamini 1.8E-10 1.8E-10 6.5E-10 8.1E-10 2.2E-9 7.4E-7 7.4E-7 3.2E-6 7.3E-5	8 3.0E-6 9.1E-5 1.3E-2 FDR 1.7E-10 1.7E-10 1.7E-10 7.5E-10 2.0E-9 6.5E-7 6.5E-7 1.4E-6 6.7E-5 6.7E-5
Anno	SMART GOTERM_MF_DIRECT tation Cluster 40 INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO SMART SMART KEGG_PATHWAY INTERPRO INTERPRO INTERPRO	BROMO lysine-acetylated histone binding Enrichment Score: 7.38 Tubulin, C-terminal Tubulin/FtsZ, C-terminal Tubulin, conserved site Tubulin Tubulin/FtsZ, 2-layer sandwich domain Tubulin/FtsZ, GTPase domain SM00865 SM00864 Pathogenic Escherichia coli infection Beta tubulin, autoregulation binding site Beta tubulin	RT R		18 25 10 Count 20 20 20 19 20 19 20 19 20 19 20 19	5.8E-8 7.2E-6 1.2E-3 P_Value 3.8E- 12 3.8E- 12 1.6E- 11 2.0E- 11 5.5E- 11 2.9E-8 3.2E-8 1.1E-6 3.5E-6	4.2E0 2.4E0 3.3E0 Fold Change 5.4E0 5.4E0 5.4E0 5.4E0 5.4E0 3.5E0 3.4E0 2.7E0 6.2E0 6.2E0 3.1E0	3.1E-6 1.0E-4 1.4E-2 Benjamini 1.8E-10 1.8E-10 6.5E-10 8.1E-10 2.2E-9 7.4E-7 7.4E-7 3.2E-6 7.3E-5 7.3E-5	8 3.0E-6 9.1E-5 1.3E-2 FDR 1.7E-10 1.7E-10 1.7E-10 6.0E-10 7.5E-10 2.0E-9 6.5E-7 1.4E-6 6.7E-5 6.7E-5 2.5E-
Anno	SMART GOTERM_MF_DIRECT tation Cluster 40 INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO SMART SMART KEGG_PATHWAY INTERPRO INTERPRO INTERPRO INTERPRO GOTERM_BP_DIRECT	BROMO lysine-acetylated histone binding Enrichment Score: 7.38 Tubulin, C-terminal Tubulin/FtsZ, C-terminal Tubulin, conserved site Tubulin Tubulin/FtsZ, 2-layer sandwich domain Tubulin/FtsZ, GTPase domain SM00865 SM00864 Pathogenic Escherichia coli infection Beta tubulin, autoregulation binding site Beta tubulin microtubule-based process	RT R		18 25 10 Count 20 20 20 19 20 19 20 19 20 19 20 19	5.8E-8 7.2E-6 1.2E-3 P_Value 3.8E- 12 3.8E- 12 1.6E- 11 2.0E- 11 2.9E-8 3.2E-8 1.1E-6 3.5E-6 4.8E-6	4.2E0 2.4E0 3.3E0 Fold Change 5.4E0 5.4E0 5.4E0 5.4E0 5.4E0 3.5E0 3.4E0 2.7E0 6.2E0 6.2E0 3.1E0 2.1E0	3.1E-6 1.0E-4 1.4E-2 Benjamini 1.8E-10 1.8E-10 6.5E-10 8.1E-10 2.2E-9 7.4E-7 7.4E-7 3.2E-6 7.3E-5 7.3E-5 2.6E-4	8 3.0E-6 9.1E-5 1.3E-2 FDR 1.7E-10 1.7E-10 6.0E-10 7.5E-10 2.0E-9 6.5E-7 1.4E-6 6.7E-5 6.7E-5 2.5E-4 2.1E-
Anno	SMART GOTERM_MF_DIRECT tation Cluster 40 INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO SMART SMART KEGG_PATHWAY INTERPRO INTERPRO INTERPRO GOTERM_BP_DIRECT GOTERM_MF_DIRECT	BROMO lysine-acetylated histone binding Enrichment Score: 7.38 Tubulin, C-terminal Tubulin/FtsZ, C-terminal Tubulin, conserved site Tubulin Tubulin/FtsZ, 2-layer sandwich domain Tubulin/FtsZ, GTPase domain SM00865 SM00864 Pathogenic Escherichia coli infection Beta tubulin, autoregulation binding site Beta tubulin microtubule-based process structural constituent of cytoskeleton	RT R		18 25 10 Count 20 20 20 19 20 19 20 19 20 19 38	5.8E-8 7.2E-6 1.2E-3 P_Value 3.8E- 12 3.8E- 12 1.6E- 11 5.5E- 11 2.9E-8 3.2E-8 1.1E-6 3.5E-6 4.8E-6 1.1E-5 3.9E-3	4.2E0 2.4E0 3.3E0 Fold Change 5.4E0 5.4E0 5.4E0 5.4E0 5.4E0 3.5E0 3.4E0 2.7E0 6.2E0 6.2E0 3.1E0 2.1E0	3.1E-6 1.0E-4 1.4E-2 Benjamini 1.8E-10 1.8E-10 6.5E-10 8.1E-10 2.2E-9 7.4E-7 7.4E-7 3.2E-6 7.3E-5 7.3E-5 2.6E-4 2.3E-4 4.3E-2	8 3.0E-6 9.1E-5 1.3E-2 FDR 1.7E-10 1.7E-10 1.7E-10 6.0E-10 7.5E-10 2.0E-9 6.5E-7 6.5E-7 6.7E-5 6.7E-5 6.7E-5 4.0E-4

nota	ation Cluster 1	Enrichment Score: ?	G	. <mark>™</mark> 	Count	P_Value	Citalige	1	
nota	ation Cluster 41	Enrichment Score: 7.21	G	- 1	Count	P_Value	Fold Change	Benjamir	
	GOTERM_CC_DIRECT	heterotrimeric G-protein complex	<u>RT</u>	•	23	6.6E- 11	4.4E0	3.6E-9	3.2 9
	GOTERM_MF_DIRECT	G-protein beta/gamma-subunit complex binding	<u>RT</u>	1	17	9.0E- 10	5.1E0	3.2E-8	2.9 8
	UP_KEYWORDS	ADP-ribosylation	<u>RT</u>		30	2.2E-9	3.3E0	1.9E-8	1. 8
	INTERPRO	Guanine nucleotide binding protein (G-	<u>RT</u>		14	1.7E-8	5.4E0	4.8E-7	4.
	INTERPRO	protein), alpha subunit				1.7E-8	5.4E0		7 4.
	SMART	<u>G protein alpha subunit, helical insertion</u>	<u>RT</u>		14			4.8E-7	7 4.
		<u>SM00275</u>	<u>RT</u>	•	14	3.2E-6	3.5E0	5.0E-5	5
	INTERPRO	G-protein alpha subunit, group I	<u>RT</u>	•	8	1.9E-5	6.2E0	3.5E-4	3. 4
	GOTERM_MF_DIRECT	guanyl nucleotide binding	<u>RT</u>	1	8	9.6E-5	5.3E0	1.6E-3	1. 3
ota	ation Cluster 42	Enrichment Score: 7.01		™	Count	P_Value	Fold Change	Benjamir	ni Fl
	UP_SEQ_FEATURE	domain:SOCS box	<u>RT</u>	1	25	1.1E- 11	4.5E0	7.4E-10	7. 10
	INTERPRO	SOCS protein, C-terminal	RT	4	25	1.8E-	4.0E0	6.7E-9	6.
	SMART	SM00969	RT		25	10 1.1E-6	2.6E0	1.9E-5	9 1.
	SMART								5 2.
		<u>SOCS</u>	<u>RT</u>	i	10	1	2.0E0	2.5E-1	1
ota	ation Cluster 43	Enrichment Score: 6.92	G	- 1	Count	P_Value	Change	Benjamir	_
	GOTERM_MF_DIRECT	protein serine/threonine phosphatase activity	<u>RT</u>		36	8.9E- 14	3.7E0	4.5E-12	4. 12
	INTERPRO	Protein phosphatase 2C (PP2C)-like	<u>RT</u>	1	17	5.1E- 10	5.3E0	1.8E-8	1. 8
	UP_SEQ_FEATURE	metal ion-binding site:Manganese 1; via carbonyl oxygen	<u>RT</u>	1	13	1.1E-9	6.8E0	6.6E-8	6.
	INTERPRO	Protein phosphatase 2C	<u>RT</u>	•	14	6.1E-8	5.1E0	1.6E-6	1.
	INTERPRO	<u>Protein phosphatase 2C,</u>	<u>RT</u>		11	1.1E-7	6.2F0	2.8E-6	6 2.
	GOTERM_BP_DIRECT	manganese/magnesium aspartate binding site							6 1.
	SMART	peptidyl-threonine dephosphorylation	<u>RT</u>	i	11	1.7E-7		1.3E-5	5
		PP2Cc	<u>RT</u>	•	17	3.2E-7	3.4E0	6.1E-6	5. 6
	UP_SEQ_FEATURE	metal ion-binding site:Manganese 1	<u>RT</u>	i	15	6.3E-6	3.8E0	2.8E-4	2. 4
	UP_SEQ_FEATURE	metal ion-binding site:Manganese 2	<u>RT</u>	1	15	6.3E-6	3.8E0	2.8E-4	2. 4
	UP_SEQ_FEATURE	domain:PP2C-like	<u>RT</u>	1	10	1.3E-5	5.2E0	5.1E-4	4. 4
	GOTERM_MF_DIRECT	<u>cation binding</u>	<u>RT</u>		7	8.1E-3	3.5E0	7.3E-2	6.
ota	ation Cluster 44	Enrichment Score: 6.76	G		Count	P_Value	Fold	Benjamir	
	GOTERM_MF_DIRECT	ligase activity	RT		109	3.3E-	Change 2.4E0	2.6E-18	2
	UP_KEYWORDS					20 6.9E-			16
		<u>Ligase</u>	<u>RT</u>	=	103	13	2.0E0	8.4E-12	12
	UP_SEQ_FEATURE	zinc finger region:RING-type	<u>RT</u>		62	1.9E-6	1.8E0	9.4E-5	9. 5
	INTERPRO	Zinc finger, RING-type	<u>RT</u>	=	77	1.4E-5	1.6E0	2.6E-4	2. 4
	INTERPRO	Zinc finger, RING/FYVE/PHD-type	<u>RT</u>	=	104	1.3E-4	1.4E0	2.1E-3	1. 3
	INTERPRO	Zinc finger, RING-type, conserved site	<u>RT</u>	•	35	9.7E-2	1.3E0	5.2E-1	4.
	SMART	<u>RING</u>	<u>RT</u>		60	6.0E-1	9.9E-1	1.0E0	8.
ota	ation Cluster 45	Enrichment Score: 6.55	G				Fold	Ponjamir	1 ni F
ro (c	UP_SEQ_FEATURE			_		6.8E-	Change		4.
	INTERPRO	short sequence motif:DEAH box	<u>RT</u>	•	28	13	4.4E0	4.7E-11	1:
		Domain of unknown function DUF1605	<u>RT</u>	•	14	6.1E-8	5.1E0	1.6E-6	6
	INTERPRO	<u>DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site</u>	<u>RT</u>	•	16	6.9E-8	4.5E0	1.8E-6	1. 6
	INTERPRO	Helicase-associated domain	<u>RT</u>	•	14	1.9E-7	4.8E0	4.6E-6	4. 6
	INTERPRO	<u>DNA/RNA helicase, DEAD/DEAH box type, N-</u> terminal	<u>RT</u>		29	1.0E-6	2.6E0	2.4E-5	2. 5
	GOTERM_MF_DIRECT	ATP-dependent RNA helicase activity	<u>RT</u>	4	27	6.9E-6	2.5E0	1.5E-4	1.
	SMART		RT						4 3.
	GOTERM_MF_DIRECT	SM00847			14		3.1E0	3.9E-4	4
		ATP-dependent helicase activity	<u>RT</u>	i	14		2.9E0	5.4E-3	3
ota	ation Cluster 46	Enrichment Score: 6.49	G	- 10	Count	P_Value	Fold Change	Benjamir	
	INTERPRO	Peptidase C2, calpain, catalytic domain	<u>RT</u>	1	15	1.0E-	6.2E0	3.8E-9	3. 9
		reptidase ez, eaipani, edealytic domani		•		10			9

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

Annot	ation Cluster 1	Enrichment Score: ?	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	Phosphatidylinositol 3-/4-kinase, catalytic domain	<u>RT</u>	ī	16	2.5E-9		8.1E-8	7.5E- 8
	INTERPRO	Phosphatidylinositol 3/4-kinase, conserved site	<u>RT</u>	i	14	1.7E-8	5.4E0	4.8E-7	4.5E- 7
	SMART	PI3Kc	<u>RT</u>	i	15	9.7E-7	3.6E0	1.7E-5	1.5E- 5
	UP_SEQ_FEATURE	domain:FAT	<u>RT</u>	i	6	3.6E-4	6.8E0	1.1E-2	1.1E- 2
	UP_SEQ_FEATURE	domain:FATC	<u>RT</u>	i .	6	3.6E-4	6.8E0	1.1E-2	1.1E-
	INTERPRO	PIK-related kinase	<u>RT</u>	1	6	5.7E-4	6.2E0	7.8E-3	2 7.2E-
	INTERPRO	PIK-related kinase, FATC	RT	1	6	5.7E-4		7.8E-3	3 7.2E-
	INTERPRO	PIK-related kinase, FAT	RT	1	5	2.9E-3		3.4E-2	3 3.1E-
	SMART	SM01343	RT		6	4.4E-3		4.0E-2	2 3.6E-
Annot	ation Cluster 53	Enrichment Score: 4.93	G	- -	Count	P_Value		:	2 FDR
	UP_KEYWORDS	TPR repeat	<u>RT</u>	=	54	1.3E-8		1.1E-7	8.7E-
	INTERPRO	Tetratricopeptide repeat-containing domain	RT		48	3.7E-8		1.0E-6	9.6E-
	INTERPRO	Tetratricopeptide repeat	RT		48	1.7E-7		4.3E-6	7 4.0E-
	INTERPRO	Tetratricopeptide-like helical	RT		64	1.4E-6		3.0E-5	6 2.8E-
	UP_SEQ_FEATURE	repeat:TPR 5	RT	_	29	2.7E-6		1.3E-4	5 1.3E-
	UP_SEQ_FEATURE								4 1.3E-
	UP_SEQ_FEATURE	repeat:TPR 1	<u>RT</u>		48	2.9E-6		1.4E-4	4 1.3E-
	UP_SEQ_FEATURE	repeat:TPR 1	<u>RT</u>		48	2.9E-6		1.4E-4	4 1.4E-
	INTERPRO	repeat:TPR 6	<u>RT</u>		27	3.0E-6		1.4E-4	4 1.1E-
	UP_SEQ_FEATURE	Tetratricopeptide TPR-1	<u>RT</u>	1	16	5.7E-6		1.2E-4	4 3.0E-
	UP_SEQ_FEATURE	repeat:TPR 3	<u>RT</u>	•	44	7.5E-6		3.1E-4	9.5E-
	UP_SEQ_FEATURE	repeat:TPR 4	<u>RT</u>	•	32	2.6E-5		9.8E-4	4 1.1E-
	UP_SEQ_FEATURE	repeat:TPR 7	<u>RT</u>	•	23	2.9E-5	2.6E0	1.1E-3	3
		repeat:TPR 8	<u>RT</u>	i	19	1.5E-4	2.6E0	5.0E-3	4.9E- 3
	SMART	<u>TPR</u>	<u>RT</u>	•	48	2.7E-3	1.5E0	2.8E-2	2.4E- 2
	UP_SEQ_FEATURE	repeat:TPR 9	<u>RT</u>	•	11	1.3E-2	2.3E0	2.7E-1	2.6E- 1
	UP_SEQ_FEATURE	repeat:TPR 10	<u>RT</u>	i	7	9.2E-2		1.0E0	9.7E- 1
Annot	ation Cluster 54	Enrichment Score: 4.86	G		Count	P_value	Fold Change	Benjamini	
	KEGG_PATHWAY	Alcoholism	<u>RT</u>	=	83	3.4E- 17	2.5E0	3.4E-16	1.5E- 16
	INTERPRO	<u>Histone core</u>	<u>RT</u>	•	29	7.3E-7	2.6E0	1.7E-5	1.5E- 5
	UP_KEYWORDS	Nucleosome core	<u>RT</u>	1	30	1.4E-5	2.3E0	8.7E-5	7.0E- 5
	GOTERM_CC_DIRECT	nucleosome	<u>RT</u>	i	32	2.6E-5	2.2E0	5.3E-4	4.7E- 4
	GOTERM_CC_DIRECT	nuclear nucleosome	<u>RT</u>	i	18	2.0E-4	2.6E0	2.9E-3	2.6E- 3
	INTERPRO	Histone H2B	<u>RT</u>	i	12	6.0E-4	3.1E0	8.3E-3	7.6E- 3
	INTERPRO	<u>Histone-fold</u>	<u>RT</u>	i e	33	6.3E-4	1.8E0	8.5E-3	7.9E- 3
	KEGG_PATHWAY	Systemic lupus erythematosus	<u>RT</u>	•	41	1.5E-3	1.6E0	3.1E-3	1.5E- 3
	GOTERM_BP_DIRECT	nucleosome assembly	<u>RT</u>	i .	31	1.3E-2	1.5E0	2.0E-1	1.9E- 1
	SMART	H2B	<u>RT</u>	i	12	2.0E-2	2.0E0	1.4E-1	1.3E- 1
Annot	ation Cluster 55	Enrichment Score: 4.75	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:SET	<u>RT</u>	ī	31	9.4E- 14	4.3E0	6.9E-12	6.7E- 12
	INTERPRO	SET domain	<u>RT</u>	i .	32	6.4E- 13	3.9E0	3.4E-11	3.1E- 11
	GOTERM_MF_DIRECT	histone-lysine N-methyltransferase activity	<u>RT</u>	i contraction	24	3.1E-9	3.7E0	1.0E-7	9.1E- 8
	UP_SEQ_FEATURE	domain:Post-SET	<u>RT</u>	i .	14	5.2E-9	6.0E0	3.1E-7	3.0E- 7
	INTERPRO	Post-SET domain	<u>RT</u>	1	13	2.9E-7	5.0E0	6.9E-6	6.3E-
	SMART	<u>SET</u>	<u>RT</u>	i .	25	5.7E-7	2.7E0	1.1E-5	9.3E- 6
	SMART	<u>PostSET</u>	<u>RT</u>	i .	10	9.0E-4	3.1E0	9.7E-3	8.6E- 3
	GOTERM_CC_DIRECT	histone methyltransferase complex	<u>RT</u>	1	11	1.4E-3	3.0E0	1.6E-2	1.4E- 2
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Annot	tation Cluster 1	Enrichment Score: ?	G	TR CONTRACTOR	Count	P_Value	Fold	Benjamini	i FDR
	GOTERM_BP_DIRECT	histone H3-K4 methylation	RT	i	10	3.1E-3	Change	6.6E-2	6.3E-
	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K4	<u>RT</u>		9	5.5E-3	3.0E0	5.2E-2	2 4.7E-
	KEGG_PATHWAY	specific) Lysine degradation	RT		19	5.6E-3		1.1E-2	2 5.6E-
	UP_KEYWORDS	S-adenosyl-L-methionine	RT		36	2.8E-2		1.2E-1	3 9.8E-
	UP_KEYWORDS	Methyltransferase	RT		36	9.7E-2		3.7E-1	2 2.9E-
	GOTERM_CC_DIRECT	MLL3/4 complex		_	4	1.6E-1		6.7E-1	1 6.0E-
	GOTERM_MF_DIRECT		<u>RT</u>						1 9.1E-
		methyltransferase activity	<u>RT</u>		16	6.2E-1	Fold	1.0E0	1
Anno	tation Cluster 56 UP_KEYWORDS	Enrichment Score: 4.64 Cyclin	G RT	<u> </u>	Count 21	P_Value 1.2E-7	Change	Benjamin	7.6E-
	INTERPRO								7 4.3E-
	SMART	Cyclin-like	<u>RT</u>		23	1.9E-7		4.6E-6	6 2.1E-
	INTERPRO	CYCLIN	<u>RT</u>	•	22	1.7E-5		2.3E-4	4 4.0E-
	INTERPRO	<u>Cyclin, N-terminal</u>	<u>RT</u>	•	17	2.4E-5		4.3E-4	4 1.1E-
		Cyclin, C-terminal domain	<u>RT</u>	•	10	8.8E-4	3.4E0	1.2E-2	2
	SMART	<u>SM01332</u>	<u>RT</u>	i	10	1.8E-2	:	1.3E-1	1.2E- 1
Annot	tation Cluster 57	Enrichment Score: 4.62	G	-	Count	P_Value	Onlange	Benjamin	
	GOTERM_MF_DIRECT	adenylate cyclase activity	<u>RT</u>	i	19	1.6E- 13	6.0E0	7.9E-12	7.2E- 12
	INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase	<u>RT</u>	•	18	4.0E- 12	5.9E0	1.9E-10	1.7E- 10
	INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase, conserved site	<u>RT</u>	1	17	2.2E- 11	5.9E0	9.0E-10	8.3E- 10
	SMART	CYCc	<u>RT</u>	i	17	1.7E-8	3.8E0	5.4E-7	4.8E- 7
	UP_SEQ_FEATURE	domain:Guanylate cyclase	<u>RT</u>	i	8	1.0E-5	6.8E0	4.1E-4	4.0E- 4
	UP_KEYWORDS	cGMP biosynthesis	<u>RT</u>	i .	8	3.8E-5	6.1E0	2.3E-4	1.8E- 4
	GOTERM_CC_DIRECT	guanylate cyclase complex, soluble	<u>RT</u>	i .	8	6.4E-5	5.6E0	1.0E-3	9.1E- 4
	GOTERM_MF_DIRECT	guanylate cyclase activity	<u>RT</u>	i .	8	9.6E-5	5.3E0	1.6E-3	1.4E- 3
	INTERPRO	Haem NO binding associated	<u>RT</u>	i	6	1.7E-3	5.3E0	2.1E-2	2.0E- 2
	GOTERM_BP_DIRECT	cGMP biosynthetic process	<u>RT</u>	i contraction	8	1.1E-2	3.0E0	1.7E-1	1.6E- 1
	GOTERM_BP_DIRECT	receptor guanylyl cyclase signaling pathway	<u>RT</u>	i	6	1.6E-2	3.6E0	2.2E-1	2.1E- 1
	INTERPRO	Heme-NO binding	<u>RT</u>	i	3	1.2E-1	4.6E0	6.2E-1	5.8E-
	GOTERM_BP_DIRECT	positive regulation of cGMP biosynthetic process	<u>RT</u>	i	4	1.4E-1	3.0E0	8.3E-1	7.9E-
	BIOCARTA	Ion Channels and Their Functional Role in Vascular Endothelium	<u>RT</u>		8	4.1E-1	1.3E0	6.8E-1	5.1E- 1
	INTERPRO	NO signalling/Golgi transport ligand-binding	RT	1	3	4.4E-1	2.1E0	1.0E0	9.2E-
Annot	tation Cluster 58	domain Enrichment Score: 4.44	G	- -	Count	P_Value	Fold	Benjamin	1 i FDR
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 23	RT		15	1.9E-	6.4E0	1.2E-8	1.1E-
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 24	RT		13	10 6.7E-9	6.3E0	3.9E-7	8 3.8E-
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 26	RT	1	8	4.0E-5		1.5E-3	7 1.4E-
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 25	RT		7	2.1E-4		6.8E-3	3 6.6E-
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 27	RT	-	7	2.1E-4		6.8E-3	3 6.6E-
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 28	RT		6	3.6E-4		1.1E-2	3 1.1E-
	UP_SEQ_FEATURE								2 2.9E-
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 30	<u>RT</u>		6	1.1E-3		3.0E-2	2 2.9E-
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 29	<u>RT</u>		6	1.1E-3		3.0E-2	2 9.7E-
		zinc finger region:C2H2-type 21; degenerate	<u>RT</u>	i	3	1.1E-1	Fold	1.0E0	1
Annot	tation Cluster 59 GOTERM_BP_DIRECT	Enrichment Score: 4.44	G	-	Count	P_Value 2.9E-	Change	Benjamin	i FDR 3.5E-
	GOTERM_BP_DIRECT	chemokine-mediated signaling pathway	<u>RT</u>	•	36	10 8.2E-		3.7E-8	8.8E-
	GOTERM_BP_DIRECT	<u>chemotaxis</u>	<u>RT</u>	•	50	10	2.4E0	9.2E-8	8
		cell chemotaxis	<u>RT</u>	•	33	1.7E-9		1.8E-7	1.7E- 7
	UP_KEYWORDS	<u>Chemotaxis</u>	<u>RT</u>	•	38	9.0E-9	2.7E0	7.7E-8	6.1E- 8
	INTERPRO	CXC chemokine, conserved site	<u>RT</u>	i	12	1.1E-7	5.7E0	2.7E-6	2.5E- 6

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

Annota	ation Cluster 1	Enrichment Score: ?	G	17	Count	P_Value	Fold Change	Benjamini	i FDR
	BIOCARTA	Transcription factor CREB and its extracellular signals	<u>RT</u>	1	20	4.2E-5	2.3E0	5.7E-4	4.3E- 4
	BIOCARTA	Regulation of BAD phosphorylation	<u>RT</u>	i .	19	9.6E-5	2.3E0	1.0E-3	7.7E- 4
Annota	ation Cluster 62	Enrichment Score: 4.26	G	TN .	Count	P_Value	Fold Change	Benjamini	1
	INTERPRO	<u>Ubiquitin</u>	<u>RT</u>	i	26	1.5E-6		3.3E-5	3.0E- 5
	INTERPRO	<u>Ubiquitin subgroup</u>	<u>RT</u>		10	2.8E-5	4.8E0	5.0E-4	4.6E-
	UP_SEQ_FEATURE	domain:Ubiquitin-like	RT		17	4.1E-4	2.6E0	1.3E-2	4 1.2E-
	SMART	UBQ	RT		22	5.2E-4	2.1E0	5.9E-3	2 5.3E-
Annota	ation Cluster 63	Enrichment Score: 4.22	G	- 	Count	P_Value	Fold	Benjamini	3 i FDR
	GOTERM_BP_DIRECT	transcription-coupled nucleotide-excision	RT		35	5.3E-9	Change	5.1E-7	4.9E-
	GOTERM_BP_DIRECT	repair error-prone translesion synthesis	RT		14	8.7E-7		5.7E-5	7 5.4E-
	GOTERM_BP_DIRECT	nucleotide-excision repair, preincision	RT	- -	17	3.1E-6		1.8E-4	5 1.7E-
	GOTERM_BP_DIRECT	<u>complex assembly</u> <u>DNA damage response, detection of DNA</u>							4 2.5E-
	GOTERM_BP_DIRECT	<u>damage</u>	<u>RT</u>		19	4.8E-6		2.6E-4	4 2.5E-
	GOTERM_BP_DIRECT	translesion synthesis	<u>RT</u>		19	4.8E-6		2.6E-4	4 2.6E-
		nucleotide-excision repair, DNA gap filling	<u>RT</u>	•	15	5.3E-6		2.7E-4	4
	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision, 5'-to lesion	<u>RT</u>	•	19	7.9E-6	3.0E0	3.9E-4	3.7E- 4
	GOTERM_BP_DIRECT	error-free translesion synthesis	<u>RT</u>	•	13	8.1E-6	4.1E0	3.9E-4	3.8E-
	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision	<u>RT</u>	1	19	1.3E-5	3.0E0	5.8E-4	5.5E- 4
	GOTERM_BP_DIRECT	global genome nucleotide-excision repair	<u>RT</u>	i	17	1.6E-5	3.1E0	7.2E-4	6.9E- 4
	GOTERM_BP_DIRECT	telomere maintenance via recombination	<u>RT</u>	i	17	1.6E-5	3.1E0	7.2E-4	6.9E- 4
	KEGG_PATHWAY	DNA replication	<u>RT</u>	1	19	2.6E-5	2.8E0	6.6E-5	2.9E- 5
	KEGG_PATHWAY	Nucleotide excision repair	<u>RT</u>	i .	21	1.7E-4	2.3E0	4.0E-4	1.8E
	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA duplex unwinding	<u>RT</u>	i .	12	3.5E-4	3.2E0	1.0E-2	1.0E- 2
	KEGG_PATHWAY	Mismatch repair	<u>RT</u>	1	11	6.1E-3	2.5E0	1.2E-2	6.1E-
	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA damage recognition	<u>RT</u>	i .	10	9.3E-3	2.6E0	1.5E-1	1.5E-
	GOTERM_BP_DIRECT	nucleotide-excision repair, preincision complex stabilization	<u>RT</u>	i e	9	1.7E-2	2.5E0	2.2E-1	2.1E-
	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision, 3'-to	<u>RT</u>		9	2.9E-2	2.3E0	3.4E-1	3.2E
	UP_KEYWORDS	<u>lesion</u> <u>Xeroderma pigmentosum</u>	RT		3	3.9E-1		1.0E0	1 8.0E
Annota	ation Cluster 64	Enrichment Score: 3.96	G	- -	Count	P_Value	Fold	Benjamini	1 i FDR
	GOTERM_BP_DIRECT	termination of RNA polymerase II	RT		31	<u> </u>	Change 2.9E0	2.0E-6	1.9E
	GOTERM_BP_DIRECT	mRNA 3'-end_processing	RT	- -	24	1.5E-6		9.3E-5	6 8.9E
	GOTERM_BP_DIRECT								5 3.7E
	GOTERM_BP_DIRECT	RNA export from nucleus	<u>RT</u>		16	3.6E-2		3.8E-1	1 7.3E
		mRNA export from nucleus	RT		23	1.1E-1	Enlet	7.6E-1	1
Annota	ation Cluster 65 BIOCARTA	Enrichment Score: 3.95	G	-		P_Value	Change	Benjamini	9.8E
	BIOCARTA	Cell Cycle RB Tumor Suppressor/Checkpoint Signaling in	<u>RT</u>	•	22	9.5E-8		1.3E-5	9.8E
	BIOCARTA	response to DNA damage	<u>RT</u>	i	12	1.3E-4	2.9E0	1.3E-3	4
		Regulation of cell cycle progression by PIk3	<u>RT</u>	•	8	1.9E-3	3.1E0	1.1E-2	8.6E 3
	BIOCARTA	cdc25 and chk1 Regulatory Pathway in response to DNA damage	<u>RT</u>	i	8	6.3E-3		2.6E-2	1.9E- 2
Annota	ation Cluster 66	Enrichment Score: 3.91	G	17	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	<u>Tyrosine-protein kinase, receptor class V,</u> <u>conserved site</u>	<u>RT</u>	i	14	5.8E- 10	6.2E0	2.0E-8	1.8E- 8
	INTERPRO	Ephrin receptor ligand binding domain	<u>RT</u>	i e	14	5.8E- 10	6.2E0	2.0E-8	1.8E- 8
	INTERPRO	Tyrosine-protein kinase, ephrin receptor	<u>RT</u>	1	14	5.8E- 10	6.2E0	2.0E-8	1.8E- 8
	PIR_SUPERFAMILY	tyrosine-protein kinase, ephrin receptor type	<u>RT</u>	i	14	6.9E- 10	6.0E0	1.2E-7	1.2E
	SMART	EPH Ibd	<u>RT</u>	i contraction	14	1.4E-7	4.0E0	2.7E-6	2.4E 6
	GOTERM_MF_DIRECT	ephrin receptor activity	<u>RT</u>	i .	11	1.6E-7	6.0E0	4.5E-6	4.1E 6
	GOTERM_BP_DIRECT	ephrin receptor signaling pathway	<u>RT</u>	i e	34	1.6E-6	2.3E0	9.3E-5	8.9E 5
	INTERPRO	Tyrosine-protein kinase ephrin type A/B	<u>RT</u>	1	15	5.9E-6	3.7E0	1.2E-4	1.1E
		receptor-like							4

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

Anno	tation Cluster 1	Enrichment Score: ?	G	™	Count	P_Value	Fold Change	Benjamini	FDR
	BIOCARTA	T Cell Receptor Signaling Pathway	<u>RT</u>	i .	25	1.4E-3	1.8E0	9.1E-3	6.8E- 3
	BIOCARTA	fMLP induced chemokine gene expression in HMC-1 cells	<u>RT</u>	•	22	1.4E-3	1.9E0	9.1E-3	6.8E- 3
	BIOCARTA	Links between Pyk2 and Map Kinases	<u>RT</u>	i .	18	1.5E-3	2.0E0	9.3E-3	7.0E- 3
	BIOCARTA	Nerve growth factor pathway (NGF)	<u>RT</u>	i .	14	2.3E-3	2.2E0	1.3E-2	9.9E- 3
	BIOCARTA	BCR Signaling Pathway	<u>RT</u>	i .	20	3.1E-3	1.8E0	1.5E-2	1.1E- 2
	BIOCARTA	EPO Signaling Pathway	<u>RT</u>	•	13	4.9E-3	2.1E0	2.2E-2	1.7E- 2
	BIOCARTA	Erk and PI-3 Kinase Are Necessary for	<u>RT</u>		14	1.9E-2	1.8E0	6.6E-2	5.0E-
	BIOCARTA	Collagen Binding in Corneal Epithelia IL 3 signaling pathway	RT		10	2.3E-2	2.1E0	7.5E-2	2 5.6E-
	BIOCARTA	Trka Receptor Signaling Pathway	RT		9	4.5E-2		1.2E-1	2 9.0E-
	BIOCARTA	Sprouty regulation of tyrosine kinase signals	RT		10	8.5E-2		2.1E-1	2 1.6E-
Anno	tation Cluster 71	Enrichment Score: 3.53	G	-	Count	P_Value	Fold	Benjamini	1 FDR
	GOTERM_BP_DIRECT	ATP-dependent chromatin remodeling	RT	i	14			7.8E-4	7.5E-
	GOTERM_MF_DIRECT	RNA polymerase II distal enhancer sequence-	RT		23	5.9E-4		8.1E-3	4 7.4E-
	GOTERM_MF_DIRECT	specific DNA binding nucleosomal DNA binding	RT		17	2.3E-3		2.5E-2	3 2.3E-
Anno	tation Cluster 72	Enrichment Score: 3.52	G	<u>-</u>	Count	P_Value	Fold	Benjamini	2
	INTERPRO	Mini-chromosome maintenance, DNA-	RT	i	9	3.5E-6	Change	7.3E-5	6.7E-
	UP_SEQ_FEATURE	dependent ATPase domain:MCM	RT		8	1.0E-5		4.1E-4	5 4.0E-
	GOTERM_BP_DIRECT	DNA replication initiation	RT				3.0E0		4 2.7E-
	SMART	MCM	RT		9	9.7E-5		1.2E-3	3 1.0E-
	INTERPRO	Mini-chromosome maintenance, conserved							3 7.2E-
	GOTERM_CC_DIRECT	<u>site</u>	<u>RT</u>		6	5.7E-4		7.8E-3	3 8.8E-
	GOTERM_MF_DIRECT	MCM complex	<u>RT</u>		7	8.2E-4		9.8E-3	3 9.6E-
	BIOCARTA	DNA helicase activity	<u>RT</u>	•	12	8.4E-4		1.1E-2	3 9.9E-
	GOTERM_BP_DIRECT	CDK Regulation of DNA Replication	<u>RT</u>		13	2.5E-3		1.3E-2	3 5.4E-
	INTERPRO	DNA unwinding involved in DNA replication	<u>RT</u>	i	7	2.6E-3		5.7E-2	2 8.0E-
		Nucleic acid-binding, OB-fold	<u>RT</u>	i	22	8.9E-3		8.6E-2	2
Anno	tation Cluster 73 GOTERM_CC_DIRECT	Enrichment Score: 3.48	G RT	<u> </u>	Count 14	P_Value 9.2E-7	Change	Benjamini 3.5E-5	FDR 3.1E-
	GOTERM_CC_DIRECT	U2 snRNP							5 3.6E-
	GOTERM_CC_DIRECT	U4/U6 x U5 tri-snRNP complex	<u>RT</u>	•	15	1.1E-6		4.0E-5	5 6.1E-
	GOTERM_CC_DIRECT	U4 snRNP	<u>RT</u>	•	10	2.4E-6		6.9E-5	5 5.6E-
	BIOCARTA	U1 snRNP	<u>RT</u>	•	12	3.2E-5		6.3E-4	4 4.7E-
	GOTERM_CC_DIRECT	Spliceosomal Assembly	<u>RT</u>	•	13	4.8E-5		6.3E-4	4 9.1E-
	GOTERM_CC_DIRECT	small nuclear ribonucleoprotein complex	<u>RT</u>	•	11	6.1E-5		1.0E-3	9.1E-
	GOTERM_CC_DIRECT	<u>U5 snRNP</u>	<u>RT</u>		11	6.1E-5		1.0E-3	4 1.4E-
	GOTERM_MF_DIRECT	<u>methylosome</u>	<u>RT</u>		9	1.0E-4		1.5E-3	1.4E- 3 1.8E-
	INTERPRO	<u>U1 snRNP binding</u>	<u>RT</u>	i	7	1.3E-4		2.0E-3	3
		Ribonucleoprotein LSM domain	<u>RT</u>	i	12		3.5E0	2.1E-3	2.0E- 3
	GOTERM_CC_DIRECT	<u>U2-type prespliceosome</u>	<u>RT</u>	•	10	4.2E-4	3.7E0	5.6E-3	5.0E- 3
	INTERPRO	<u>Like-Sm (LSM) domain</u>	<u>RT</u>	•	12	6.0E-4	3.1E0	8.3E-3	7.6E- 3
	GOTERM_BP_DIRECT	spliceosomal snRNP assembly	<u>RT</u>	•	13	1.1E-3	2.8E0	2.8E-2	2.7E- 2
	GOTERM_CC_DIRECT	<u>U12-type spliceosomal complex</u>	<u>RT</u>	i e	12	1.1E-3	2.9E0	1.3E-2	1.1E- 2
				1	9	5.8E-3	2 050		1.0E-
	GOTERM_BP_DIRECT	nuclear import	<u>RT</u>	-	9	J.0L J	3.0L0	1.1E-1	1
		nuclear import Sm	RT RT	•	12	5.8E-3		1.1E-1 5.3E-2	4.7E- 2
	GOTERM_BP_DIRECT						2.3E0		4.7E-
	GOTERM_BP_DIRECT SMART	<u>Sm</u>	<u>RT</u>	i e	12	5.8E-3	2.3E0 5.3E0	5.3E-2	4.7E- 2 5.3E-
	GOTERM_BP_DIRECT SMART GOTERM_CC_DIRECT	Sm pICIn-Sm protein complex	RT RT	i i	12 5	5.8E-3 7.0E-3	2.3E0 5.3E0 3.5E0	5.3E-2 6.0E-2	4.7E- 2 5.3E- 2 1.4E-
	GOTERM_BP_DIRECT SMART GOTERM_CC_DIRECT GOTERM_BP_DIRECT	Sm pICIn-Sm protein complex histone mRNA metabolic process	RT RT RT	i i i	12 5 7	5.8E-3 7.0E-3 8.4E-3 1.1E-2	2.3E0 5.3E0 3.5E0	5.3E-2 6.0E-2 1.4E-1 8.7E-2	4.7E- 2 5.3E- 2 1.4E- 1 7.8E-

nnota	ation Cluster 1	Enrichment Score: ?	G	- 1	Count	P_Value	Fold Change	Benjamir	ni FD
	GOTERM_CC_DIRECT	spliceosomal tri-snRNP complex	<u>RT</u>	i	4	3.0E-2	5.1E0	2.0E-1	1.8 1
nnota	ation Cluster 74	Enrichment Score: 3.47	G	17	Count	P_Value	Fold Change	Benjamir	ni FD
)	UP_SEQ_FEATURE	domain:Post-SET	<u>RT</u>	1	14	5.2E-9	6.0E0	3.1E-7	3.0 7
)	UP_SEQ_FEATURE	domain:Pre-SET	<u>RT</u>	1	6	1.1E-3	5.8E0	3.0E-2	2.9
)	INTERPRO	Pre-SET domain	<u>RT</u>	1	6	1.7E-3	5.3E0	2.1E-2	2.0
)	SMART	<u>PreSET</u>	<u>RT</u>	1	6	1.2E-2	3.5E0	9.7E-2	8.6 2
)	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K9	<u>RT</u>	1	4	3.6E-2	4.8E0	2.3E-1	2.0
nnota	ation Cluster 75	specific) Enrichment Score: 3.34	G	-	Count	P_Value	Fold Change	Benjamir	-
	INTERPRO	Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase	<u>RT</u>	i .	12	1.1E-7	Change	2.7E-6	2. 6
)	GOTERM_MF_DIRECT	phosphoprotein phosphatase activity	<u>RT</u>	1	22	2.9E-6	2.9E0	6.8E-5	6. 5
)	SMART	PP2Ac	<u>RT</u>	1	12	9.7E-6	3.7E0	1.3E-4	1. 4
)	INTERPRO	Metallophosphoesterase domain	<u>RT</u>	1	13	7.2E-4	2.9E0	9.7E-3	9.
)	UP_SEQ_FEATURE	metal ion-binding site:Manganese	<u>RT</u>	4	11	2.1E-2	2.2E0	4.0E-1	3.
	UP_SEQ_FEATURE	metal ion-binding site:Iron	RT		12	9.5E-2	1.7E0	1.0E0	1 9.
)]	UP_SEQ_FEATURE	active site:Proton donor	RT		20		6.8E-1		1 9.
anot	ation Cluster 76	Enrichment Score: 3.28	G		Count		Fold	Barriage	1
	UP_SEQ_FEATURE	domain:PI3K/PI4K			16	1.6E-	Change 6.1E0	1.0E-8	1.
	INTERPRO	Phosphatidylinositol 3-/4-kinase, catalytic	<u>RT</u>	-		10			8 7.
	INTERPRO	domain Phosphatidylinositol 3/4-kinase, conserved	<u>RT</u>	•	16	2.5E-9	5.2E0	8.1E-8	8
	SMART	site	<u>RT</u>	•	14	1.7E-8	5.4E0	4.8E-7	7
		<u>PI3Kc</u>	<u>RT</u>	•	15	9.7E-7	3.6E0	1.7E-5	1. 5
	GOTERM_CC_DIRECT	phosphatidylinositol 3-kinase complex	<u>RT</u>	•	11	5.0E-6	5.0E0	1.2E-4	1. 4
	INTERPRO	<u>Phosphoinositide 3-kinase, accessory (PIK)</u> <u>domain</u>	<u>RT</u>	i	9	1.5E-5	5.6E0	2.8E-4	2. 4
	INTERPRO	<u>Phosphatidylinositol 3-kinase C2 (PI3K C2)</u> <u>domain</u>	<u>RT</u>	i e	8	1.9E-5	6.2E0	3.5E-4	3. 4
	GOTERM_BP_DIRECT	<u>phosphatidylinositol-3-phosphate biosynthetic</u> <u>process</u>	<u>RT</u>	1	21	6.2E-5	2.5E0	2.3E-3	2. 3
	GOTERM_MF_DIRECT	1-phosphatidylinositol-3-kinase activity	<u>RT</u>	1	19	8.7E-5	2.6E0	1.5E-3	1. 3
)	SMART	<u>PI3Ka</u>	<u>RT</u>	1	9	9.7E-5	4.0E0	1.2E-3	1.
)	INTERPRO	Phosphatidylinositol 3-kinase Ras-binding (PI3K RBD) domain	<u>RT</u>	1	7	1.1E-4	6.2E0	1.7E-3	1.
)	INTERPRO	Phosphatidylinositol Kinase	<u>RT</u>	4	9	1.2E-4	4.6E0	1.9E-3	1.
)	GOTERM_MF_DIRECT	1-phosphatidylinositol-4-phosphate 3-kinase	RT		7	1.3E-4		2.0E-3	3 1.
, 1	SMART	activity PI3K C2	RT		8		4.0E0	4.1E-3	3 3.
)	GOTERM_MF_DIRECT								3 3.
J	SMART	phosphatidylinositol 3-kinase activity	<u>RT</u>		5	3.4E-3		3.4E-2	2 3.
J	GOTERM_BP_DIRECT	PI3K_rbd	<u>RT</u>		6		4.0E0	4.0E-2	2
]	INTERPRO	phosphatidylinositol biosynthetic process	<u>RT</u>	•	19	5.7E-3	1.9E0	1.1E-1	1
		<u>Phosphatidylinositol 3-kinase adaptor-binding</u> (<u>PI3K ABD</u>) <u>domain</u>	<u>RT</u>	i	4	1.5E-2	6.2E0	1.2E-1	1.
	SMART	<u>PI3K_p85B</u>	<u>RT</u>	i	3	1.5E-1	4.0E0	6.6E-1	5. 1
	KEGG_PATHWAY	Phosphatidylinositol signaling system	<u>RT</u>	i	21	4.0E-1	1.1E0	6.1E-1	4. 1
	KEGG_PATHWAY	<u>Carbohydrate digestion and absorption</u>	<u>RT</u>	i	10	4.0E-1	1.3E0	6.1E-1	4. 1
	KEGG_PATHWAY	Inositol phosphate metabolism	<u>RT</u>	i	13	7.2E-1	9.6E-1	1.0E0	7. 1
	UP_SEQ_FEATURE	domain:PX	<u>RT</u>	i .	4	9.8E-1	5.7E-1	1.0E0	9. 1
	INTERPRO	Phox homologous domain	<u>RT</u>	i	5	9.8E-1	5.6E-1	1.0E0	9. 1
	GOTERM_MF_DIRECT	phosphatidylinositol binding	<u>RT</u>	1	8	9.9E-1	5.6E-1	1.0E0	9. 1
	SMART	<u>PX</u>	<u>RT</u>	i	4	1.0E0	3.6E-1	1.0E0	1.
nota	ation Cluster 77	Enrichment Score: 3.24	G	100	Count	P_Value	Fold Change	Benjamir	ıi FI
)	GOTERM_BP_DIRECT	positive regulation of telomere maintenance via telomerase	<u>RT</u>	i	22	1.1E-9	4.1E0	1.1E-7	1. 7
	GOTERM_BP_DIRECT	positive regulation of protein localization to Cajal body	<u>RT</u>	i	8	2.6E-5	5.9E0	1.1E-3	1. 3
	GOTERM_CC_DIRECT	chaperonin-containing T-complex	<u>RT</u>	1	8	C 4F F	5.6E0	1.0E-3	9.

Annota	ation Cluster 1	Enrichment Score: ?	G	™	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_CC_DIRECT	zona pellucida receptor complex	RT	i	8		Change	1.0E-3	9.1E-
	INTERPRO	Chaperonin TCP-1, conserved site	RT		8	7.5E-5		1.3E-3	4 1.2E-
	INTERPRO	TCP-1-like chaperonin intermediate domain	RT		9	1.2E-4		1.9E-3	3 1.8E-
	INTERPRO	Chaperone tailless complex polypeptide 1	RT		9			1.9E-3	3 1.8E-
	INTERPRO	(TCP-1) Chaperonin Cpn60/TCP-1	RT	_	10	2.8E-4		4.2E-3	3 3.9E-
	INTERPRO	GroEL-like apical domain	RT		10	2.8E-4		4.2E-3	3 3.9E-
	INTERPRO								3 1.2E-
	GOTERM_BP_DIRECT	GroEL-like equatorial domain positive regulation of establishment of protein	<u>RT</u>		9	1.0E-3		1.3E-2	2 2.9E-
	GOTERM_BP_DIRECT	localization to telomere positive regulation of telomerase RNA	<u>RT</u>		7	1.2E-3		3.0E-2	2 1.2E-
	GOTERM_BP_DIRECT	localization to Cajal body	<u>RT</u>	•	8	7.1E-3		1.3E-1	1.2E 1 7.9E-
	GOTERM_BP_DIRECT	scaRNA localization to Cajal body	<u>RT</u>		3	1.3E-1	4.4E0	8.3E-1	1
		toxin transport	<u>RT</u>	•	10	1.4E-1	1.6E0	8.4E-1	8.0E- 1
	GOTERM_BP_DIRECT	binding of sperm to zona pellucida	<u>RT</u>		9	2.3E-1	1.5E0	1.0E0	9.6E- 1
	GOTERM_MF_DIRECT	protein binding involved in protein folding	<u>RT</u>	i	4	4.2E-1	•	1.0E0	9.1E- 1
Annota	ation Cluster 78	Enrichment Score: 3.2	G	100	Count	P_Value	Fold Change	Benjamin	
	BIOCARTA	CXCR4 Signaling Pathway	<u>RT</u>	i	19	1.7E-5	2.5E0	3.3E-4	2.5E- 4
	BIOCARTA	CCR3 signaling in Eosinophils	<u>RT</u>	i	16	1.0E-3	2.2E0	7.2E-3	5.4E- 3
	BIOCARTA	Aspirin Blocks Signaling Pathway Involved in Platelet Activation	<u>RT</u>	i	13	1.5E-2		5.4E-2	4.0E- 2
Annota	ation Cluster 79	Enrichment Score: 3.1	G	<u>™</u>	Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	Heat shock protein 70, conserved site	<u>RT</u>	i e	12	1.4E-6	5.0E0	3.0E-5	2.8E- 5
	INTERPRO	Heat shock protein 70 family	<u>RT</u>	i e	12	1.4E-6	5.0E0	3.0E-5	2.8E- 5
	GOTERM_BP_DIRECT	protein refolding	<u>RT</u>	i	8	7.1E-3	3.2E0	1.3E-1	1.2E- 1
	GOTERM_BP_DIRECT	response to unfolded protein	<u>RT</u>	i e	13	4.1E-2	1.8E0	4.0E-1	3.9E- 1
	KEGG_PATHWAY	Antigen processing and presentation	<u>RT</u>	i e	15	6.0E-1	1.0E0	8.7E-1	6.0E- 1
Annota	ation Cluster 80	Enrichment Score: 3.09	G	15	Count	P_Value	Fold Change	Benjamin	i FDR
Annota	ation Cluster 80	Enrichment Score: 3.09 phosphatidylinositol-mediated signaling	G RT	™	Count 40	P_Value 6.4E-7	Change	Benjamin 4.4E-5	4.2E- 5
Annota						<u> </u>	Change 2.2E0		4.2E-
Annota	GOTERM_BP_DIRECT	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic	<u>RT</u>	<u> </u>	40	6.4E-7	2.2E0 2.5E0	4.4E-5	4.2E- 5 2.2E-
Annota	GOTERM_BP_DIRECT GOTERM_BP_DIRECT	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process	RT RT	: :	40	6.4E-7 6.2E-5	2.2E0 2.5E0 2.6E0	4.4E-5 2.3E-3	4.2E- 5 2.2E- 3 1.3E-
Annota	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3-	RT RT RT	: :	40 21 19	6.4E-7 6.2E-5 8.7E-5 5.9E-4	2.2E0 2.5E0 2.6E0 1.9E0	4.4E-5 2.3E-3 1.5E-3	4.2E- 5 2.2E- 3 1.3E- 3 1.6E- 2
Annota	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3-kinase activity regulation of phosphatidylinositol 3-kinase	RT RT RT RT		40 21 19 30	6.4E-7 6.2E-5 8.7E-5 5.9E-4	2.2E0 2.5E0 2.6E0 1.9E0 2.1E0	4.4E-5 2.3E-3 1.5E-3 1.6E-2	4.2E- 5 2.2E- 3 1.3E- 3 1.6E- 2 8.9E- 3
Annota	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3-kinase activity	RT RT RT RT RT		40 21 19 30 22	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4	2.2E0 2.5E0 2.6E0 1.9E0 2.1E0 1.9E0	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3	4.2E- 5 2.2E- 3 1.3E- 3 1.6E- 2 8.9E- 3
Annota	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3-kinase activity regulation of phosphatidylinositol 3-kinase signaling phosphatidylinositol biosynthetic process Ras guanyl-nucleotide exchange factor	RT RT RT RT RT RT		40 21 19 30 22 25	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4 1.8E-3	2.2E0 2.5E0 2.6E0 1.9E0 2.1E0 1.9E0 1.9E0	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3 4.1E-2	4.2E-5 5 2.2E-3 1.3E-3 1.6E-2 8.9E-3 3.9E-2 1.0E-1
Annota	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3- kinase activity regulation of phosphatidylinositol 3-kinase signaling phosphatidylinositol biosynthetic process Ras guanyl-nucleotide exchange factor activity	RT RT RT RT RT RT RT RT		40 21 19 30 22 25	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4 1.8E-3 5.7E-3 1.3E-2	2.2E0 2.5E0 2.6E0 1.9E0 2.1E0 1.9E0 1.9E0	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3 4.1E-2 1.1E-1	4.2E-5 5 2.2E-3 1.3E-3 1.6E-2 8.9E-3 3.9E-2 1.0E-1 9.9E-2 7.2E-
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3-kinase activity regulation of phosphatidylinositol 3-kinase signaling phosphatidylinositol biosynthetic process Ras guanyl-nucleotide exchange factor	RT RT RT RT RT RT RT RT RT		40 21 19 30 22 25 19	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4 1.8E-3 5.7E-3 1.3E-2 7.2E-1	2.2E0 2.5E0 2.6E0 1.9E0 1.9E0 1.9E0 1.6E0 9.6E-1	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3 4.1E-2 1.1E-1 1.1E-1 1.0E0	4.2E-5 5 2.2E-3 1.3E-3 1.6E-2 8.9E-3 3.9E-2 1.0E-1 9.9E-2 7.2E-1
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT KEGG_PATHWAY	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3- kinase activity regulation of phosphatidylinositol 3-kinase signaling phosphatidylinositol biosynthetic process Ras guanyl-nucleotide exchange factor activity Inositol phosphate metabolism	RT RT RT RT RT RT RT RT		40 21 19 30 22 25 19 30	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4 1.8E-3 5.7E-3 1.3E-2	2.2E0 2.5E0 2.6E0 1.9E0 1.9E0 1.9E0 1.6E0 9.6E-1	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3 4.1E-2 1.1E-1	4.2E-5 5 2.2E-3 1.3E-3 1.6E-2 8.9E-3 3.9E-2 1.0E-1 9.9E-2 7.2E-1 1 FDR
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT KEGG_PATHWAY	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3- kinase activity regulation of phosphatidylinositol 3-kinase signaling phosphatidylinositol biosynthetic process Ras guanyl-nucleotide exchange factor activity Inositol phosphate metabolism Enrichment Score: 3.05	RT		40 21 19 30 22 25 19 30 13	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4 1.8E-3 5.7E-3 1.3E-2 7.2E-1 P_Value	2.2E0 2.5E0 2.6E0 1.9E0 1.9E0 1.9E0 1.6E0 9.6E-1	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3 4.1E-2 1.1E-1 1.0E0 Benjamin	4.2E-5 5 2.2E-3 1.3E-3 1.6E-2 8.9E-3 3.9E-2 1.0E-1 9.9E-2 7.2E-1 i FDR 3.5E-6 2.5E-
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT KEGG_PATHWAY ation Cluster 81 GOTERM_MF_DIRECT	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3- kinase activity regulation of phosphatidylinositol 3-kinase signaling phosphatidylinositol biosynthetic process Ras guanyl-nucleotide exchange factor activity Inositol phosphate metabolism Enrichment Score: 3.05 histone deacetylase activity histone deacetylation	RT R		40 21 19 30 22 25 19 30 13 Count 22	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4 1.8E-3 5.7E-3 1.3E-2 7.2E-1 P_Value 1.3E-7 5.1E-6	Change 2.2E0 2.5E0 2.6E0 1.9E0 1.9E0 1.9E0 1.6E0 9.6E-1 Fold Change 3.4E0 2.8E0	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3 4.1E-2 1.1E-1 1.0E0 Benjamin 3.8E-6 2.7E-4	4.2E-5 2.2E-3 1.3E-3 1.6E-2 8.9E-3 3.9E-2 1.0E-1 9.9E-2 7.2E-1 i FDR 3.5E-6 2.5E-4 3.0E-
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT KEGG_PATHWAY ation Cluster 81 GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3- kinase activity regulation of phosphatidylinositol 3-kinase signaling phosphatidylinositol biosynthetic process Ras guanyl-nucleotide exchange factor activity Inositol phosphate metabolism Enrichment Score: 3.05 histone deacetylase activity histone deacetylation region of interest:Histone deacetylase	RT R		40 21 19 30 22 25 19 30 13 Count 22 22	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4 1.8E-3 5.7E-3 1.3E-2 7.2E-1 P_Value 1.3E-7 5.1E-6 7.3E-6	Change 2.2E0 2.5E0 2.6E0 1.9E0 1.9E0 1.9E0 1.6E0 9.6E-1 Fold Change 3.4E0 2.8E0 6.1E0	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3 4.1E-2 1.1E-1 1.0E0 Benjamin 3.8E-6 2.7E-4 3.1E-4	4.2E-5 2.2E-3 1.3E-3 1.6E-2 8.9E-3 3.9E-2 1.0E-1 9.9E-2 7.2E-1 i FDR 3.5E-6 2.5E-4 3.0E-4 1.8E-
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT KEGG_PATHWAY Ation Cluster 81 GOTERM_MF_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3- kinase activity regulation of phosphatidylinositol 3-kinase signaling phosphatidylinositol biosynthetic process Ras guanyl-nucleotide exchange factor activity Inositol phosphate metabolism Enrichment Score: 3.05 histone deacetylase activity histone deacetylation region of interest:Histone deacetylase Histone deacetylase domain NAD-dependent histone deacetylase activity	RT R		40 21 19 30 22 25 19 30 13 Count 22 22 9 10	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4 1.8E-3 5.7E-3 1.3E-2 7.2E-1 P_Value 1.3E-7 5.1E-6 7.3E-6 1.0E-5	Change 2.2E0 2.5E0 2.6E0 1.9E0 1.9E0 1.9E0 1.6E0 9.6E-1 Fold Change 3.4E0 2.8E0 6.1E0 5.2E0	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3 4.1E-2 1.1E-1 1.0E0 Benjamin 3.8E-6 2.7E-4 3.1E-4 2.0E-4	4.2E-5 2.2E-3 1.3E-3 1.6E-2 8.9E-3 3.9E-2 1.0E-1 9.9E-2 7.2E-1 i FDR 3.5E-6 2.5E-4 3.0E-4
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT KEGG_PATHWAY Ation Cluster 81 GOTERM_MF_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3- kinase activity regulation of phosphatidylinositol 3-kinase signaling phosphatidylinositol biosynthetic process Ras guanyl-nucleotide exchange factor activity. Inositol phosphate metabolism Enrichment Score: 3.05 histone deacetylase activity histone deacetylase activity Histone deacetylase domain NAD-dependent histone deacetylase activity (H3-K14 specific)	RT R		40 21 19 30 22 25 19 30 13 Count 22 22 9 10 10	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4 1.8E-3 5.7E-3 1.3E-2 7.2E-1 P_Value 1.3E-7 5.1E-6 7.3E-6 1.0E-5 1.4E-5	Change 2.2E0 2.5E0 2.6E0 1.9E0 1.9E0 1.9E0 1.6E0 9.6E-1 Fold Change 3.4E0 2.8E0 6.1E0 5.2E0 5.0E0	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3 4.1E-2 1.1E-1 1.0E0 Benjamin 3.8E-6 2.7E-4 2.0E-4 2.7E-4	4.2E-5 5 2.2E-3 1.3E-3 1.6E-2 8.9E-3 3.9E-2 1.0E-1 9.9E-2 7.2E-1 1 FDR 3.5E-6 2.5E-4 3.0E-4 1.8E-4
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT KEGG_PATHWAY Ation Cluster 81 GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3- kinase activity regulation of phosphatidylinositol 3-kinase signaling phosphatidylinositol biosynthetic process Ras guanyl-nucleotide exchange factor activity Inositol phosphate metabolism Enrichment Score: 3.05 histone deacetylase activity histone deacetylation region of interest: Histone deacetylase Histone deacetylase domain NAD-dependent histone deacetylase activity (H3-K14 specific) protein deacetylase activity	RT R		40 21 19 30 22 25 19 30 13 Count 22 22 9 10 10 9	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4 1.8E-3 5.7E-3 1.3E-2 7.2E-1 P_Value 1.3E-7 5.1E-6 7.3E-6 1.0E-5 1.4E-5 2.0E-5	Change 2.2E0 2.5E0 2.6E0 1.9E0 1.9E0 1.9E0 1.6E0 9.6E-1 Fold Change 3.4E0 2.8E0 6.1E0 5.2E0 5.0E0 5.4E0	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3 4.1E-2 1.1E-1 1.0E0 Benjamin 3.8E-6 2.7E-4 3.1E-4 2.0E-4 2.7E-4 3.5E-4	4.2E-5 2.2E-3 1.3E-3 1.6E-2 8.9E-3 3.9E-2 1.0E-1 9.9E-2 7.2E-1 i FDR 3.5E-6 2.5E-4 3.0E-4 1.8E-4 3.2E-4
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT KEGG_PATHWAY Ation Cluster 81 GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3- kinase activity regulation of phosphatidylinositol 3-kinase signaling phosphatidylinositol biosynthetic process Ras guanyl-nucleotide exchange factor activity Inositol phosphate metabolism Enrichment Score: 3.05 histone deacetylase activity histone deacetylase domain NAD-dependent histone deacetylase activity (H3-K14 specific) protein deacetylase activity histone H3 deacetylation	RT		40 21 19 30 22 25 19 30 13 Count 22 22 9 10 10 9 13	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4 1.8E-3 5.7E-3 1.3E-2 7.2E-1 P_Value 1.3E-7 5.1E-6 7.3E-6 1.0E-5 1.4E-5 2.0E-5 3.4E-5	Change 2.2E0 2.5E0 2.6E0 1.9E0 1.9E0 1.9E0 1.6E0 9.6E-1 Fold Change 3.4E0 2.8E0 6.1E0 5.2E0 5.0E0 5.4E0 3.7E0	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3 4.1E-2 1.1E-1 1.0E0 Benjamin 3.8E-6 2.7E-4 3.1E-4 2.0E-4 2.7E-4 3.5E-4 1.3E-3	4.2E-5 5 2.2E-3 1.3E-3 1.6E-2 8.9E-3 3.9E-2 1.0E-1 9.9E-2 7.2E-1 1 5 FDR 3.5E-6 2.5E-4 3.0E-4 1.8E-4 2.5E-4 1.3E-3
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT KEGG_PATHWAY Ation Cluster 81 GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3- kinase activity regulation of phosphatidylinositol 3-kinase signaling phosphatidylinositol biosynthetic process Ras guanyl-nucleotide exchange factor activity Inositol phosphate metabolism Enrichment Score: 3.05 histone deacetylase activity histone deacetylase domain NAD-dependent histone deacetylase activity (H3-K14 specific) protein deacetylase activity histone H3 deacetylation Histone deacetylase superfamily	RT R		40 21 19 30 22 25 19 30 13 Count 22 22 9 10 10 10 9 13 10	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4 1.8E-3 5.7E-3 1.3E-2 7.2E-1 P_Value 1.3E-7 5.1E-6 7.3E-6 1.0E-5 1.4E-5 2.0E-5 3.4E-5 6.7E-5	Change 2.2E0 2.5E0 2.6E0 1.9E0 1.9E0 1.9E0 1.6E0 9.6E-1 Fold Change 3.4E0 2.8E0 6.1E0 5.2E0 5.0E0 5.4E0 3.7E0 4.4E0	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3 4.1E-2 1.1E-1 1.0E0 Benjamin 3.8E-6 2.7E-4 3.1E-4 2.0E-4 2.7E-4 1.3E-3 1.2E-3	4.2E-5 2.2E-3 1.3E-3 1.6E-2 8.9E-3 3.9E-2 1.0E-1 9.9E-2 7.2E-1 i FDR 3.5E-6 2.5E-4 3.0E-4 1.8E-4 2.5E-4 1.3E-3 1.1E-3
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT KEGG_PATHWAY INTO Cluster 81 GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO GOTERM_MF_DIRECT INTERPRO GOTERM_BP_DIRECT INTERPRO GOTERM_BP_DIRECT INTERPRO GOTERM_BP_DIRECT	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3- kinase activity, regulation of phosphatidylinositol 3-kinase signaling, phosphatidylinositol biosynthetic process Ras guanyl-nucleotide exchange factor activity, Inositol phosphate metabolism Enrichment Score: 3.05 histone deacetylase activity histone deacetylation region of interest: Histone deacetylase Histone deacetylase domain NAD-dependent histone deacetylase activity, (H3-K14 specific) protein deacetylase activity histone H3 deacetylation Histone deacetylase superfamily, protein deacetylation	RT		40 21 19 30 22 25 19 30 13 Count 22 22 9 10 10 9 13 10 8	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4 1.8E-3 5.7E-3 1.3E-2 7.2E-1 P_Value 1.3E-7 5.1E-6 7.3E-6 1.0E-5 1.4E-5 2.0E-5 3.4E-5 6.7E-5 2.9E-4	Change 2.2E0 2.5E0 2.6E0 1.9E0 1.9E0 1.9E0 1.6E0 9.6E-1 Fold Change 3.4E0 2.8E0 6.1E0 5.2E0 5.0E0 5.4E0 4.4E0 4.7E0	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3 4.1E-2 1.1E-1 1.0E0 Benjamin 3.8E-6 2.7E-4 3.1E-4 2.0E-4 2.7E-4 3.5E-4 1.3E-3 1.2E-3 8.7E-3	4.2E-5 2.2E-3 1.3E-3 1.6E-2 8.9E-3 3.9E-2 1.0E-1 9.9E-2 7.2E-1 1
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT KEGG_PATHWAY ACTION Cluster 81 GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT INTERPRO GOTERM_BP_DIRECT INTERPRO GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3- kinase activity regulation of phosphatidylinositol 3-kinase signaling phosphatidylinositol biosynthetic process Ras guanyl-nucleotide exchange factor activity Inositol phosphate metabolism Enrichment Score: 3.05 histone deacetylase activity histone deacetylase domain NAD-dependent histone deacetylase activity (H3-K14 specific) protein deacetylase activity histone H3 deacetylation Histone deacetylase superfamily	RT R		40 21 19 30 22 25 19 30 13 Count 22 22 9 10 10 10 9 13 10	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4 1.8E-3 5.7E-3 1.3E-2 7.2E-1 P_Value 1.3E-7 5.1E-6 7.3E-6 1.0E-5 1.4E-5 2.0E-5 3.4E-5 6.7E-5	Change 2.2E0 2.5E0 2.6E0 1.9E0 1.9E0 1.9E0 1.6E0 9.6E-1 Fold Change 3.4E0 2.8E0 6.1E0 5.2E0 5.0E0 5.4E0 4.4E0 4.7E0	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3 4.1E-2 1.1E-1 1.0E0 Benjamin 3.8E-6 2.7E-4 3.1E-4 2.0E-4 2.7E-4 1.3E-3 1.2E-3	4.2E-5 2.2E-3 1.3E-3 1.6E-2 8.9E-3 3.9E-2 1.0E-1 9.9E-2 7.2E-1 1 FDR 3.5E-6 2.5E-4 3.0E-4 1.8E-4 2.5E-4 1.3E-3 1.1E-3 8.3E-3 7.3E-3
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT KEGG_PATHWAY ATTOM Cluster 81 GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT INTERPRO GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	phosphatidylinositol-mediated signaling phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3- kinase activity, regulation of phosphatidylinositol 3-kinase signaling, phosphatidylinositol biosynthetic process Ras guanyl-nucleotide exchange factor activity, Inositol phosphate metabolism Enrichment Score: 3.05 histone deacetylase activity histone deacetylation region of interest: Histone deacetylase Histone deacetylase domain NAD-dependent histone deacetylase activity, (H3-K14 specific) protein deacetylase activity histone H3 deacetylation Histone deacetylase superfamily, protein deacetylation	RT R		40 21 19 30 22 25 19 30 13 Count 22 22 9 10 10 9 13 10 8	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4 1.8E-3 5.7E-3 1.3E-2 7.2E-1 P_Value 1.3E-7 5.1E-6 7.3E-6 1.0E-5 1.4E-5 2.0E-5 3.4E-5 6.7E-5 2.9E-4	Change 2.2E0 2.5E0 2.6E0 1.9E0 1.9E0 1.9E0 1.6E0 9.6E-1 Fold Change 3.4E0 2.8E0 6.1E0 5.2E0 5.0E0 5.4E0 3.7E0 4.4E0 4.7E0 2.6E0	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3 4.1E-2 1.1E-1 1.0E0 Benjamin 3.8E-6 2.7E-4 3.1E-4 2.0E-4 2.7E-4 3.5E-4 1.3E-3 1.2E-3 8.7E-3	4.2E-5 5 2.2E-3 1.3E-3 1.6E-2 8.9E-3 3.9E-2 1.0E-1 9.9E-2 7.2E-1 1 FDR 3.5E-6 2.5E-4 3.0E-4 1.8E-4 1.8E-4 1.3E-3 1.1E-3 8.3E-3 7.3E-3 1.5E-1
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT KEGG_PATHWAY ACTION Cluster 81 GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT INTERPRO GOTERM_BP_DIRECT INTERPRO GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	phosphatidylinositol-mediated signaling. phosphatidylinositol-3-phosphate biosynthetic process 1-phosphatidylinositol-3-kinase activity. phosphatidylinositol phosphorylation phosphatidylinositol-4,5-bisphosphate 3-kinase activity. regulation of phosphatidylinositol 3-kinase signaling. phosphatidylinositol biosynthetic process Ras guanyl-nucleotide exchange factor activity. Inositol phosphate metabolism Enrichment Score: 3.05 histone deacetylase activity histone deacetylase activity histone deacetylase domain NAD-dependent histone deacetylase activity (H3-K14 specific). protein deacetylase activity histone H3 deacetylation Histone deacetylase superfamily. protein deacetylase superfamily. histone deacetylase complex	RT R		40 21 19 30 22 25 19 30 13 Count 22 22 9 10 10 9 13 10 8 15	6.4E-7 6.2E-5 8.7E-5 5.9E-4 7.7E-4 1.8E-3 5.7E-3 1.3E-2 7.2E-1 P_Value 1.3E-7 5.1E-6 7.3E-6 1.0E-5 1.4E-5 2.0E-5 3.4E-5 6.7E-5 2.9E-4 6.7E-4	Change 2.2E0 2.5E0 2.6E0 1.9E0 1.9E0 1.9E0 1.6E0 9.6E-1 Fold Change 3.4E0 2.8E0 6.1E0 5.2E0 5.0E0 5.4E0 3.7E0 4.4E0 4.7E0 2.6E0 3.9E0	4.4E-5 2.3E-3 1.5E-3 1.6E-2 9.8E-3 4.1E-2 1.1E-1 1.0E0 Benjamin 3.8E-6 2.7E-4 3.1E-4 2.0E-4 2.7E-4 3.5E-4 1.3E-3 1.2E-3 8.7E-3 8.1E-3	4.2E-5 5 2.2E-3 1.3E-3 1.6E-2 8.9E-3 3.9E-2 1.0E-1 9.9E-2 7.2E-1 1 FDR 3.5E-6 2.5E-4 3.0E-4 1.8E-4 1.8E-4 1.3E-3 1.1E-3 8.3E-3 1.5E-3

Annota	ition Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_BP_DIRECT	regulation of gene expression, epigenetic	<u>RT</u>	i	7	2.0E-2	•	2.5E-1	2.4E- 1
	INTERPRO	Histone deacetylase class II, eukaryotic	RT	•	4	3.2E-2	5.0E0	2.3E-1	2.1E-
	PIR_SUPERFAMILY	histone deacetylase class II, eukaryotic type	RT		4	3.5E-2	4.8E0	4.6E-1	1 4.6E-
	GOTERM_BP_DIRECT	negative regulation of myotube differentiation			7	4.0E-2		4.0E-1	1 3.8E-
_	COG_ONTOLOGY	Chromatin structure and dynamics /	<u>KI</u>		,	1.02 2	2.020	1.02 1	1 4.4E-
		<u>Secondary metabolites biosynthesis,</u> <u>transport, and catabolism</u>	<u>RT</u>	i	7	4.2E-2	2.3E0	4.4E-1	1
	INTERPRO	Histone deacetylase	<u>RT</u>	i	3	1.2E-1	4.6E0	6.2E-1	5.8E- 1
	INTERPRO	<u>Histone deacetylase, glutamine rich N-terminal domain</u>	<u>RT</u>	i	3	1.2E-1	4.6E0	6.2E-1	5.8E- 1
	PIR_SUPERFAMILY	histone deacetylase class I, eukaryotic type	<u>RT</u>	i	3	1.3E-1	4.5E0	9.1E-1	9.1E- 1
Annota	ition Cluster 82	Enrichment Score: 2.99	G	™	Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	<u>14-3-3 protein</u>	<u>RT</u>	i e	7	1.1E-4	6.2E0	1.7E-3	1.6E- 3
	INTERPRO	14-3-3 protein, conserved site	<u>RT</u>	i	7	1.1E-4	6.2E0	1.7E-3	1.6E- 3
	INTERPRO	<u>14-3-3 domain</u>	<u>RT</u>	i .	7	1.1E-4	6.2E0	1.7E-3	1.6E- 3
	PIR_SUPERFAMILY	<u>14-3-3 protein</u>	<u>RT</u>	i .	7	1.2E-4	6.0E0	1.0E-2	1.0E- 2
	UP_SEQ_FEATURE	site:Interaction with phosphoserine on interacting protein	<u>RT</u>	1	7	2.1E-4	6.0E0	6.8E-3	6.6E-
	GOTERM_BP_DIRECT	positive regulation of protein insertion into mitochondrial membrane involved in	RT		14	6.0E-4	2 8F0	1.6E-2	1.6E-
	SMART	apoptotic signaling pathway							2 1.2E-
	GOTERM BP DIRECT	<u>14 3 3</u>	<u>RT</u>		7	1.3E-3		1.3E-2	2
		<u>protein targeting</u>	<u>RT</u>	i	10	2.0E-1	1.5E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	membrane organization	<u>RT</u>	i	8	2.9E-1		1.0E0	9.6E- 1
Annota	ition Cluster 83	Enrichment Score: 2.96	G		Count	P_Value	Fold Change	Benjamin	
	UP_SEQ_FEATURE	domain:Actin-binding	<u>RT</u>	i	13	3.9E-6	4.4E0	1.8E-4	1.8E- 4
	UP_SEQ_FEATURE	repeat:Spectrin 4	<u>RT</u>	i	13	7.9E-6	4.2E0	3.3E-4	3.1E- 4
	INTERPRO	Actinin-type, actin-binding, conserved site	<u>RT</u>	i .	14	1.1E-5	3.8E0	2.1E-4	2.0E- 4
	UP_SEQ_FEATURE	repeat:Spectrin 3	<u>RT</u>	1	13	1.5E-5	4.0E0	5.9E-4	5.7E- 4
	UP_SEQ_FEATURE	domain:CH 1	<u>RT</u>	i	14	3.8E-5	3.5E0	1.4E-3	1.4E- 3
	UP_SEQ_FEATURE	domain:CH 2	<u>RT</u>	i	14	3.8E-5	3.5E0	1.4E-3	1.4E- 3
	UP_SEQ_FEATURE	repeat:Spectrin 1	<u>RT</u>	i .	13	1.3E-4	3.4E0	4.3E-3	4.2E- 3
	UP_SEQ_FEATURE	repeat:Spectrin 2	<u>RT</u>	1	13	1.3E-4	3.4E0	4.3E-3	4.2E- 3
	UP_SEQ_FEATURE	repeat:Spectrin 6	<u>RT</u>	i .	9	1.4E-4	4.7E0	4.6E-3	4.4E- 3
	UP_SEQ_FEATURE	repeat:Spectrin 7	<u>RT</u>	i	9	1.4E-4	4.7E0	4.6E-3	4.4E- 3
	UP_SEQ_FEATURE	repeat:Spectrin 8	<u>RT</u>	i e	9	1.4E-4	4.7E0	4.6E-3	4.4E- 3
	UP_SEQ_FEATURE	repeat:Spectrin 9	<u>RT</u>	•	9	1.4E-4	4.7E0	4.6E-3	4.4E- 3
	UP_SEQ_FEATURE	repeat:Spectrin 5	RT		9	2.8E-4		8.8E-3	8.5E-
	UP_SEQ_FEATURE	repeat:Spectrin 10	RT		8	5.9E-4		1.7E-2	3 1.6E-
	UP_SEQ_FEATURE	repeat:Spectrin 11	RT		8	5.9E-4		1.7E-2	2 1.6E-
	UP_SEQ_FEATURE	repeat:Spectrin 12	RT		8	5.9E-4		1.7E-2	2 1.6E-
	UP_SEQ_FEATURE	repeat:Spectrin 13	RT	_	8	5.9E-4		1.7E-2	2 1.6E-
	UP_SEQ_FEATURE	repeat:Spectrin 14				5.9E-4 5.9E-4			2 1.6E-
	UP_SEQ_FEATURE		<u>RT</u>		8			1.7E-2	2 1.6E-
	UP_SEQ_FEATURE	repeat:Spectrin 15	<u>RT</u>	•	8	5.9E-4		1.7E-2	2 1.6E-
	UP_SEQ_FEATURE	repeat:Spectrin 16	<u>RT</u>	•	8	5.9E-4		1.7E-2	1.6E-
	INTERPRO	repeat:Spectrin 17	<u>RT</u>	•	8	5.9E-4		1.7E-2	2
		<u>Spectrin repeat</u>	<u>RT</u>	i	12	9.2E-4		1.2E-2	1.1E- 2
	INTERPRO	Spectrin/alpha-actinin	<u>RT</u>	•	13	1.1E-3	2.8E0	1.4E-2	1.3E- 2
	UP_SEQ_FEATURE	repeat:Spectrin 19	<u>RT</u>	i	6	2.6E-3	5.1E0	6.6E-2	6.3E- 2
	UP_SEQ_FEATURE	repeat:Spectrin 20	<u>RT</u>	i	6	2.6E-3	5.1E0	6.6E-2	6.3E- 2
	UP_SEQ_FEATURE	repeat:Spectrin 18	<u>RT</u>	i	6	5.1E-3	4.5E0	1.3E-1	1.2E- 1

NTERPRO	9E0 2.3E-1 2.2E- 6E0 2.3E-1 2.1E- 8E0 2.4E-1 2.1E- 5E0 7.8E-1 7.5E- 8E0 6.7E-1 6.0E- 1 1.0E0 9.7E- 2E0 9.7E-1 8.6E- 8E0 1.0E0 9.6E-
NTERPRO Calconin homology domain NT 20 3.06-2	9E0 2.3E-1 2.2E- 6E0 2.3E-1 2.1E- 8E0 2.4E-1 7.5E- 8E0 7.8E-1 7.5E- 1 8E0 6.7E-1 6.0E- 1 1E0 1.0E0 9.7E- 2E0 9.7E-1 8.6E- 8E0 1.0E0 9.6E- 4E0 1.0E0 9.6E- Old 8.0E- Old Benjamini FDR 0E0 2.0E-3 1.8E- 2.2 6.21
SMART SPEC	2.1E- 1 8E0 2.4E-1 2.1E- 5E0 7.8E-1 7.5E- 8E0 6.7E-1 6.0E- 1 1E0 1.0E0 9.7E- 2E0 9.7E-1 8.6E- 8E0 1.0E0 9.6E- 1 4E0 1.0E0 9.6E- 1 0Id 8.0E- DId 9.6E- 1 0E0 2.0E-3 1.8E- 2E- 2E- 2E- 2E- 2E- 2E- 2E- 2E- 2E- 2
SMART	8E0 2.4E-1 2.1E-1 5E0 7.8E-1 7.5E-1 8E0 6.7E-1 6.0E-1 1E0 1.0E0 9.7E-1 2E0 9.7E-1 8.6E-1 8E0 1.0E0 9.6E-1 4E0 1.0E0 8.0E-1 0Id hange Benjamini FDR 0E0 2.0E-3 1.8E-3 4E0 1.7E-2 1.5E-2
UP_SEQ_FEATURE	5E0 7.8E-1 7.5E-1 8E0 6.7E-1 6.0E-1 1E0 1.0E0 9.7E-1 2E0 9.7E-1 8.6E-1 8E0 1.0E0 9.6E-1 4E0 1.0E0 8.0E- Old Benjamini FDR 0E0 2.0E-3 1.8E- 2 1.5E-
OOTERM_CC_DIRECT Spectrin S	8E0 6.7E-1 6.0E- 1E0 1.0E0 9.7E- 2E0 9.7E-1 8.6E- 8E0 1.0E0 9.6E- 4E0 1.0E0 8.0E- Did hange Benjamini FDR 0E0 2.0E-3 1.8E- 3 4E0 1.7E-2 1.5E-
UP_SEQ_FEATURE	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
SMART	2E0 9.7E-1 8.6E- 8E0 1.0E0 9.6E- 1 4E0 1.0E0 8.0E- 1 Old hange Benjamini FDR 0E0 2.0E-3 1.8E- 3 4E0 1.7E-2 1.5E-
GOTERN_BP_DIRECT actin filament capping RT	8E0 1.0E0 9.6E- 4E0 1.0E0 8.0E- 1 Old hange Benjamini FDR 0E0 2.0E-3 1.8E- 3 4E0 1.7E-2 1.5E-
UP_KEYWORDS	1.0E0 1 4E0 1.0E0 1 9.0E-1 10Id Benjamini FDR 0E0 2.0E-3 1.8E-3 4E0 1.7E-2 1.5E-2
Annotation Cluster 84	Did hange Benjamini FDR 0E0 2.0E-3 1.8E-3 4E0 1.7E-2 1.5E-2
GOTERM_MF_DIRECT GOTERM_MF_DIRECT U1 snRNP-binding	0E0 2.0E-3 1.8E- 3 1.5E- 2 1.5E-
GOTERM_CC_DIRECT	4E0 1.7E-2 1.5E-
GOTERM_CC_DIRECT presellicesome RI 5 7.0E-3 3 Annotation Gluster 85 Enrichment Score: 2.95 BIOCARTA Control of skeletal myoognesis by HDAC 8 salkium/calmodulin-dependent kinase (calk). BIOCARTA Signal Dependent Regulation of Myoognesis by HDAC 8 salkium/calmodulin-dependent kinase (calk). BIOCARTA Signal Dependent Regulation of Myoognesis by Corperpassor MIII 9 6.9E-4 3 by Corperpassor MIII 9 6.9E-4 3 by Corperpassor MIII 13 4.9E-2 1 13	2
Annotation Cluster 85	3E0 6.0E-2 2
BIOCARTA Control of skeletal myogenesis by HDAC 8 RT	old
BIOCARTA Signal Department Regulation of Myogenesis DV-Corepressor MITR BIOCARTA Regulation of PGC-1a RI 13 4.9E-2 1 Annotation Cluster 86 Enrichment Score: 2.9 Count P-Value UP_SEQ_FEATURE domain:Chromo 2 RI INTERPRO Chromo domain/shadow RI INTERPRO Chromo domain-like RI INTERPRO Chromo domain:Chromo 1 RI INTERPRO Chromo domain RI INTERPRO Chromo domain, conserved site RI INTERPRO Chemokine receptor family RI INTERPRO Chemokine receptor activity RI INTERPRO Chemokine receptor activity RI BBID RICHOMO RI INTERPRO Chemokine receptor activity RI	bld hange Benjamini FDR 4.3E-
BIOCARTA Regulation of PGC-1a RI 13 4.9E-2 13 4.9E-2 14 4.9E-2 15	3.05
Annotation Cluster 86	3.25-3
UP_SEQ_FEATURE domain:Chromo 2 RT	2
INTERPRO Chromo domain/shadow RT 16 7.1E-5 3 INTERPRO Chromo domain-like RT 15 2.0E-4 2 UP_SEQ_FEATURE domain:Chromo 1 RT 18 1.1E-3 2 INTERPRO Chromo domain RT 11 5.1E-3 2 INTERPRO Chromo domain RT 16 7.5E-3 2 SMART CHROMO RT 6 2.1E-1 1 Annotation Cluster 87 Enrichment Score: 2.74 6 7 7 8.2 7 INTERPRO Chemokine receptor family RT 13 2.9E-7 5 GOTERM_MF_DIRECT C-C chemokine receptor activity RT 10 1.4E-5 5 GOTERM_MF_DIRECT Chemokine receptor activity RT 11 1.1E-4 3 BBID 14.chemokine receptor-ligand RT 8 8 1.9E-2 2 BBID 15.T-cell polarization-chemokine receptors RT 10 5.7E-1	old hange Benjamini FDR
INTERPRO Chromo domain/snadow RI INTERPRO Chromo domain-like RI UP_SEQ_FEATURE domain:Chromo 1 RI INTERPRO Chromo domain RI INTERPRO Chromo domain, conserved site RI Annotation Cluster 87 Enrichment Score: 2.74 INTERPRO Chemokine receptor family RI GOTERM_MF_DIRECT C-C chemokine receptor activity RI BBID 14.chemokine receptor-ligand RI BBID 15.T-cell polarization-chemokine receptors RI BIOCARTA Selective expression of chemokine receptors RI Annotation Cluster 88 Enrichment Score: 2.74 Count RI INTERPRO RI INTERPRO Chemokine receptor-ligand RI BBID 15.T-cell polarization Chemokine receptors RI INTERPRO RI Count RI INTERPRO	3
UP_SEQ_FEATURE domain:Chromo 1 RT RT RT RT RT RT RT RT RT R	3
INTERPRO Chromo domain RT SMART CHROMO RT SMART CHROMO RT SMART Chromo domain, conserved site RT SMART Chromo domain Chromo Chromo domain RT SMART Chromo domain Chromo domain Chromo domain RT SMART Chromo domain Chromo domain Chromo domain Chromo domain Chromo domain Chromo domain RT SMART Chromo domain Count P_Value RT SMART Chromo domain Chromo	9E0 3.1E-3 2.9E-
SMART CHROMO RT 16 7.5E-3 2 INTERPRO Chromo domain, conserved site RT Annotation Cluster 87 Enrichment Score: 2.74 Count NTERPRO Chemokine receptor family RT GOTERM_MF_DIRECT C-C chemokine receptor activity RT GOTERM_MF_DIRECT Chemokine receptor activity RT BBID 14.chemokine receptor-ligand RT BBID 15.T-cell polarization-chemokine receptors during T-cell polarization Annotation Cluster 88 Enrichment Score: 2.74 Count P_Value 11 5.TE-3 2 Count P_Value RT	2E0 3.0E-2 2.9E-
INTERPRO Chromo domain, conserved site RT 6 2.1E-1 1 Annotation Cluster 87 Enrichment Score: 2.74 INTERPRO Chemokine receptor family GOTERM_MF_DIRECT C-C chemokine receptor activity RT GOTERM_MF_DIRECT Chemokine receptor activity RT BBID 14.chemokine receptor-ligand RT BBID 16.Chemokines-rec-T-cells RT BBID 15.T-cell polarization-chemokine receptors during T-cell polarization Annotation Cluster 88 Enrichment Score: 2.74 Count P_Value 6 9E- GOTERM_RP_DIRECT Chemokine receptors RT Count Count P_Value 6 9E- GOTERM_RP_DIRECT	6E0 5.5E-2 5.1E-
Annotation Cluster 87 Enrichment Score: 2.74	0E0 6.5E-2 5.8E-
INTERPRO Chemokine receptor family GOTERM_MF_DIRECT C-C chemokine receptor activity RT 10 1.4E-5 GOTERM_MF_DIRECT chemokine receptor activity RT 11 1.1E-4 BBID 14.chemokine receptor-ligand RT BBID 16.Chemokines-rec-T-cells RT BBID 15.T-cell polarization-chemokine receptors RT BIOCARTA Selective expression of chemokine receptors during T-cell polarization Annotation Cluster 88 Enrichment Score: 2.74 GOTERM_RP_DIRECT Count P_value 6 9F-	9E0 9.7E-1 9.0E-
GOTERM_MF_DIRECT C-C chemokine receptor activity RT 10 1.4E-5 GOTERM_MF_DIRECT chemokine receptor activity RT 11 1.1E-4 BBID 14.chemokine receptor-ligand RT 8 1.9E-2 BBID 16.Chemokines-rec-T-cells RT 7 8.3E-2 BBID 15.T-cell polarization-chemokine receptors BIOCARTA Selective expression of chemokine receptors during T-cell polarization Annotation Cluster 88 Enrichment Score: 2.74 Count P_Value GOTERM BP_DIRECT	old hange Benjamini FDR
GOTERM_MF_DIRECT chemokine receptor activity RT 11 1.1E-4 3 BBID 14.chemokine receptor-ligand RT 8 1.9E-2 2 BBID 16.Chemokines-rec-T-cells RT 7 8.3E-2 2 BBID 15.T-cell polarization-chemokine receptors RT 10 1.6E-1 1 BIOCARTA Selective expression of chemokine receptors during T-cell polarization Annotation Cluster 88 Enrichment Score: 2.74 GOTERM BP DIRECT	0E0 6.9E-6 6.3E-
BBID 14.chemokine receptor-ligand BBID 16.Chemokines-rec-T-cells RT 7 8.3E-2 BBID 15.T-cell polarization-chemokine receptors BIOCARTA Selective expression of chemokine receptors during T-cell polarization Annotation Cluster 88 Enrichment Score: 2.74 GOTERM BP DIRECT 6.95-	0E0 2.7E-4 2.5E-
BBID 16.Chemokine receptor-ligand RT 7 8.3E-2 2 BBID 15.T-cell polarization-chemokine receptors BIOCARTA Selective expression of chemokine receptors aduring T-cell polarization Annotation Cluster 88 Enrichment Score: 2.74 GOTERM RP DIRECT 10 5.7E-1 1	9E0 1.7E-3 1.5E-
BBID 15.T-cell polarization-chemokine receptors RT 10 1.6E-1 1 BIOCARTA Selective expression of chemokine receptors during T-cell polarization Annotation Cluster 88 Enrichment Score: 2.74 GOTERM RP DIRECT 7 8.3E-2 2 10 1.6E-1 1 10 5.7E-1 1	3E0 7.0E-1 7.0E-
BIOCARTA Selective expression of chemokine receptors during T-cell polarization Annotation Cluster 88 Enrichment Score: 2.74 GOTERM RP. DIRECT	0E0 9.9E-1 9.9E-
Annotation Cluster 88 Enrichment Score: 2.74 GOTERM RP. DIRECT	The second secon
Annotation Cluster 88 Enrichment Score: 2.74 G	5E0 9.9E-1 9.9E-
GOTERM BP DIRECT	9.9E-1 1
gene expression gene expression 28 0.91-3	1F0 8.8F-1 6.6E-
GOTERM_CC_DIRECT DNA-directed RNA polymerase II, core complex 12 1.6E-5 4	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
GOTERM_BP_DIRECT positive regulation of viral transcription RT 16 1.8E-5 3	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
GOTERM_MF_DIRECT RNA polymerase II activity RT 9 2.0E-5 5	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
GOTERM_BP_DIRECT transcription initiation from RNA polymerase I RT 15 4 9E-4 2	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
GOTERM_BP_DIRECT 7-methylguanosine mRNA capping RT 15 1.52 1.52 1.52 1.52 1.52 1.52 1.52	3E0 9.9E-1 1 1E0 8.8E-1 6.6E-1 DId hange Benjamini FDR 5E0 7.9E-8 7.6E-8 2E0 3.3E-4 2.9E-4 3E0 7.6E-4 7.2E-4 4E0 3.5E-4 3.2E-4 7F0 1.4E-2 1.3E-1
GOTERM_BP_DIRECT termination of RNA polymerase I transcription RT 14 8.8E-4 2	3E0 9.9E-1 1 1E0 8.8E-1 6.6E-1 3E0 Benjamini FDR 5E0 7.9E-8 7.6E-8 2E0 3.3E-4 2.9E-4 3E0 7.6E-4 7.2E-4 4E0 3.5E-4 3.2E-4 7E0 1.4E-2 1.3E-1 7E0 1.4E-2 1.3E-1
GOTERM MF DIRECT	3E0 9.9E-1 1 1E0 8.8E-1 6.6E-1 3E0 Benjamini FDR 5E0 7.9E-8 7.6E-8 2E0 3.3E-4 2.9E-4 3E0 7.6E-4 7.2E-4 4E0 3.5E-4 3.2E-4 7E0 1.4E-2 1.3E-2 7E0 1.4E-2 1.3E-2 7E0 2.3E-2 2.2E-7
— GOTERM RP DIPECT transcription elemention from DNA polymerace	3EO 9.9E-1 1 1EO 8.8E-1 6.6E-1 3EO Benjamini FDR 5EO 7.9E-8 7.6E-8 2EO 3.3E-4 2.9E-4 3EO 7.6E-4 7.2E-4 4EO 3.5E-4 3.2E-4 7EO 1.4E-2 1.3E-2 7EO 1.4E-2 2.2E-2 7EO 2.3E-2 2.2E-2 1.4E-2 1.4E-2
II promoter 27 1.5E-5 1	3EO 9.9E-1 1 1EO 8.8E-1 6.6E-1 3EO 7.9E-8 7.6E-1 3EO 7.6E-4 2.9E-1 4EO 3.3E-4 7.2E-1 4EO 3.5E-4 3.2E-1 7EO 1.4E-2 1.3E-1 7EO 1.4E-2 2.2E-1 7EO 2.3E-2 2.2E-1 0EO 1.5E-2 1.4E-2
GOTERM BP DIRECT transcription elongation from RNA polymerase =	3EO 9.9E-1 1 1EO 8.8E-1 6.6E-1 3EO 7.9E-8 7.6E-8 2EO 3.3E-4 2.9E-4 3EO 7.6E-4 7.2E-4 4EO 3.5E-4 3.2E-4 7EO 1.4E-2 1.3E-2 7EO 2.3E-2 2.2E-2 0EO 1.5E-2 1.4E-2 9EO 3.6E-2 3.5E-2 1.6E-2 1.6E-2
I promoter 13 2.2E-3 2	3E0 9.9E-1 1 1E0 8.8E-1 6.6E-1 3E0 Benjamini FDR 5E0 7.9E-8 7.6E-8 2E0 3.3E-4 2.9E-4 3E0 7.6E-4 7.2E-4 4E0 3.5E-4 3.2E-4 7E0 1.4E-2 1.3E-2 7E0 2.3E-2 2.2E-2 0E0 1.5E-2 1.4E-2 9E0 3.6E-2 3.5E-2 9E0 1.8E-2 1.6E-2 1.8E-2 1.6E-2

Annota	ation Cluster 1	Enrichment Score: ?	G	N Comment	Count	P_Value	Fold Change	Benjamini	FDR
	UP_KEYWORDS	DNA-directed RNA polymerase	<u>RT</u>	i	14	2.6E-3		1.4E-2	1.1E- 2
	GOTERM_BP_DIRECT	positive regulation of type I interferon	<u>RT</u>	i de la companya de	18	3.1E-3	2.1E0	6.7E-2	6.4E-
	KEGG_PATHWAY	production RNA polymerase	RT		14	3.7E-3	2.3E0	7.5E-3	3.7E-
	GOTERM_BP_DIRECT	positive regulation of gene expression,	RT		20	5.3E-3		9.9E-2	3 9.5E-
	GOTERM_MF_DIRECT	epigenetic DNA directed DNA polymerace activity	RT						2 5.7E-
	GOTERM_BP_DIRECT	<u>DNA-directed RNA polymerase activity</u> <u>transcription initiation from RNA polymerase</u>		-	14	6.8E-3		6.3E-2	2 1.2E-
	GOTERM_BP_DIRECT	II promoter transcription from RNA polymerase III	<u>RT</u>	•	39	6.8E-3		1.2E-1	1 2.1E-
	GOTERM_BP_DIRECT	promoter snRNA transcription from RNA polymerase II	<u>RT</u>		12	1.6E-2		2.2E-1	1
		promoter	<u>RT</u>	•	20	2.1E-2	1.7E0	2.6E-1	2.4E- 1
	KEGG_PATHWAY	<u>Pyrimidine metabolism</u>	<u>RT</u>	•	26	9.0E-2	1.4E0	1.5E-1	9.0E- 2
	GOTERM_CC_DIRECT	DNA-directed RNA polymerase III complex	<u>RT</u>	i	6	1.7E-1	2.0E0	7.0E-1	6.3E- 1
	GOTERM_BP_DIRECT	gene silencing by RNA	<u>RT</u>	i	24	1.7E-1	1.3E0	9.5E-1	9.1E- 1
	GOTERM_MF_DIRECT	RNA polymerase III activity	<u>RT</u>	i	6	1.7E-1	2.0E0	7.3E-1	6.6E- 1
	KEGG_PATHWAY	Cytosolic DNA-sensing pathway	<u>RT</u>	i .	16	2.2E-1	1.3E0	3.5E-1	2.2E- 1
Annota	ation Cluster 89	Enrichment Score: 2.74	G	™	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:Protein kinase 1	<u>RT</u>	i .	11	6.8E-6	5.0E0	2.9E-4	2.8E- 4
	UP_SEQ_FEATURE	domain:Protein kinase 2	<u>RT</u>	i .	11	6.8E-6	5.0E0	2.9E-4	2.8E- 4
	INTERPRO	<u>Tyrosine-protein kinase, non-receptor</u> <u>Jak/Tyk2</u>	<u>RT</u>	i e	4	1.5E-2	6.2E0	1.2E-1	1.1E-
	PIR_SUPERFAMILY	tyrosine-protein kinase, Jak/Tyk2 type	<u>RT</u>	i	4	1.6E-2	6.0E0	2.5E-1	2.5E-
	INTERPRO	Ribosomal protein S6 kinase II	<u>RT</u>	1	4	5.7E-2	4.1E0	3.8E-1	3.5E-
	PIR_SUPERFAMILY	ribosomal protein S6 kinase II	RT		4	6.1E-2	4.0E0	6.0E-1	6.0E-
Annota	ation Cluster 90	Enrichment Score: 2.71	G	- -	Count	P_Value	Fold	Benjamini	1 FDR
	UP_SEQ_FEATURE	domain:Chromo 2	RT	•	8	4.0E-5	Onlange	1.5E-3	1.4E-
	INTERPRO	BRK domain	RT		6	5.7E-4		7.8E-3	3 7.2E-
	UP_SEQ_FEATURE	domain:Chromo 1	RT		8	1.1E-3		3.0E-2	3 2.9E-
	SMART				6	4.4E-3		4.0E-2	2 3.6E-
	GOTERM_MF_DIRECT	BRK	<u>RT</u>						2 9.0E-
Appot	otion Cluster 04	hydrolase activity, acting on acid anhydrides	<u>RT</u>	1	3 Count	2.6E-1	Fold	9.9E-1	1
Annota	ation Cluster 91 GOTERM_CC_DIRECT	Enrichment Score: 2.7 proteasome regulatory particle, base	G	i i	Count	P_Value	Onlange	Benjamini	1.4E-
	GOTERM_BP_DIRECT	subcomplex	<u>RT</u>		9	1.0E-4		1.5E-3	3 5.5E-
	GOTERM_CC_DIRECT	protein catabolic process	<u>RT</u>		18	1.7E-4		5.7E-3	3 3.9E-
	GOTERM_CC_DIRECT	nuclear proteasome complex	<u>RT</u>	i	7	3.2E-4		4.4E-3	3 5.0E-
	INTERPRO	proteasome accessory complex	<u>RT</u>	i	10	4.2E-4		5.6E-3	3
		ATPase, AAA-type, conserved site	<u>RT</u>	•	13	4.8E-4	3.0E0	7.1E-3	6.5E- 3
	INTERPRO	26S proteasome subunit P45	<u>RT</u>	i	6	5.7E-4	6.2E0	7.8E-3	7.2E- 3
	GOTERM_MF_DIRECT	proteasome-activating ATPase activity	<u>RT</u>	i	6	6.8E-4	6.0E0	9.0E-3	8.2E- 3
	GOTERM_MF_DIRECT	TBP-class protein binding	<u>RT</u>	•	11	1.0E-3	3.1E0	1.2E-2	1.1E- 2
	GOTERM_BP_DIRECT	<u>positive regulation of RNA polymerase II</u> <u>transcriptional preinitiation complex assembly</u>	<u>RT</u>	i	7	1.2E-3	4.6E0	3.0E-2	2.9E- 2
	GOTERM_CC_DIRECT	cytosolic proteasome complex	<u>RT</u>	i	7	1.8E-3	4.4E0	1.9E-2	1.7E- 2
	INTERPRO	ATPase, AAA-type, core	<u>RT</u>	i .	17	5.1E-3	2.1E0	5.5E-2	5.1E- 2
	GOTERM_BP_DIRECT	positive regulation of proteasomal protein catabolic process	<u>RT</u>	i .	8	1.1E-2	3.0E0	1.7E-1	1.6E- 1
	GOTERM_BP_DIRECT	ER-associated ubiquitin-dependent protein catabolic process	<u>RT</u>	i	18	1.8E-2	1.8E0	2.4E-1	2.3E- 1
	INTERPRO	AAA+ ATPase domain	<u>RT</u>	•	31	4.2E-2	1.4E0	3.0E-1	2.8E-
	SMART	AAA	<u>RT</u>	•	31	7.9E-1	9.2E-1	1.0E0	8.9E-
Annota	ation Cluster 92	Enrichment Score: 2.64	G	N .	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	G-protein beta WD-40 repeat	<u>RT</u>	ī	33	1.2E-5	-	2.3E-4	2.1E- 4
	INTERPRO	WD40 repeat, conserved site	<u>RT</u>	•	47	1.1E-4	1.8E0	1.7E-3	1.6E- 3
	UP_SEQ_FEATURE	repeat:WD 7	RT		41	1.1E-4		3.8E-3	3.7E-
									3

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

nnota	ation Cluster 1	Enrichment Score: ?	G	13	Count	P_Value	Fold Change	Benjamir	ii FDR
	UP_SEQ_FEATURE	domain:Thioredoxin 1	<u>RT</u>	i	9	7.3E-6	6.1E0	3.1E-4	3.0E-
	UP_SEQ_FEATURE	domain:Thioredoxin 2	<u>RT</u>	i .	9	7.3E-6	6.1E0	3.1E-4	3.0E
	INTERPRO	Thioredoxin, conserved site	<u>RT</u>		12	9.0E-6	4.4E0	1.8E-4	1.6E
-]	INTERPRO	Thioredoxin domain	RT		19	2.4E-5	2.9F0	4.4E-4	4 4.0E
ך ה	UP_SEQ_FEATURE			-	6				4 2.9E
J	GOTERM_MF_DIRECT	site:Contributes to redox potential value	<u>RT</u>			1.1E-3		3.0E-2	2 1.6E
_	INTERPRO	protein disulfide isomerase activity	<u>RT</u>		11	1.6E-3		1.7E-2	2 3.1E
		<u>Disulphide isomerase</u>	<u>RT</u>	•	5	2.9E-3	6.2E0	3.4E-2	2
	UP_KEYWORDS	Redox-active center	<u>RT</u>	i	16	3.2E-3	2.2E0	1.7E-2	1.4E 2
	GOTERM_BP_DIRECT	cell redox homeostasis	<u>RT</u>	•	24	3.3E-3	1.8E0	6.9E-2	6.6E 2
	GOTERM_CC_DIRECT	<u>cell</u>	<u>RT</u>	i	26	1.1E-2	1.7E0	8.8E-2	7.8E 2
	UP_SEQ_FEATURE	site:Lowers pKa of C-terminal Cys of first active site	<u>RT</u>	i	4	1.1E-2	6.8E0	2.3E-1	2.2E 1
	UP_SEQ_FEATURE	site:Lowers pKa of C-terminal Cys of second active site	<u>RT</u>	i .	4	1.1E-2	6.8E0	2.3E-1	2.2E 1
	INTERPRO	Protein disulphide isomerase	<u>RT</u>	i	4	1.5E-2	6.2E0	1.2E-1	1.1E 1
	UP_SEQ_FEATURE	domain:Thioredoxin 3	<u>RT</u>	1	4	2.5E-2	5.4E0	4.6E-1	4.4E
	UP_SEQ_FEATURE	short sequence motif:Prevents secretion from	RT		13	1.8E-1		1.0E0	9.7E
)	GOTERM_MF_DIRECT	ER disulfide oxidoreductase activity	RT		3	2.6E-1		9.9E-1	1 9.0E
٦	GOTERM_MF_DIRECT			-					1 9.1E
	INTERPRO	isomerase activity	<u>RT</u>	1	6	2.7E-1		1.0E0	1 9.2E
J		Thioredoxin-like fold	<u>RT</u>	•	24	3.5E-1		1.0E0	1
nnota	GOTERM_CC_DIRECT ation Cluster 97	endoplasmic reticulum lumen Enrichment Score: 2.48	RT G		16 Count	1.0E0 P_Value	5.3E-1 Fold	Danismin	1.0E
<u> </u>	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-	RT	-	29		Change 2.6E0	2.4E-5	2.2E
) 1	GOTERM_MF_DIRECT	terminal ATP dependent PNA believes activity		_	27				5 1.4E
J	INTERPRO	ATP-dependent RNA helicase activity RNA helicase, ATP-dependent, DEAD-box,	<u>RT</u>			6.9E-6		1.5E-4	4 1.5E
J		conserved site	<u>RT</u>	•	10	2.2E-2	2.3E0	1.6E-1	1
)	GOTERM_BP_DIRECT	RNA secondary structure unwinding	<u>RT</u>	•	14	2.6E-2	1.9E0	3.1E-1	2.9E 1
)	INTERPRO	RNA helicase, DEAD-box type, Q motif	<u>RT</u>	i	11	6.4E-2	1.8E0	3.9E-1	3.6E 1
	UP_SEQ_FEATURE	short sequence motif:Q motif	<u>RT</u>	i	10	1.2E-1	1.7E0	1.0E0	9.7E 1
	UP_SEQ_FEATURE	short sequence motif:DEAD box	<u>RT</u>	i .	9	1.5E-1	1.7E0	1.0E0	9.7E 1
nnota	ation Cluster 98	Enrichment Score: 2.34	G	™	Count	P_Value	Fold Change	Benjamir	ii FDR
)	BIOCARTA	E2F1 Destruction Pathway	<u>RT</u>	i	9	2.5E-3	2.8E0	1.3E-2	9.9E 3
)	BIOCARTA	Cyclin E Destruction Pathway	<u>RT</u>	i .	8	6.3E-3	2.8E0	2.6E-2	1.9E 2
	BIOCARTA	Regulation of p27 Phosphorylation during Cell	<u>RT</u>		10	6.3E-3	2.4E0	2.6E-2	1.9E 2
nnota	ation Cluster 99	Cycle Progression Enrichment Score: 2.32	G	170	Count	P_Value	Fold	Benjamir	
)	UP_KEYWORDS	Nucleosome core	RT		30	1.4E-5	Change	8.7E-5	7.0E
<u> </u>	GOTERM_BP_DIRECT	chromatin silencing	RT		15	1.4E-2		2.0E-1	5 1.9E
) 1	INTERPRO			_					1 1.2E
J	SMART	Histone H2A	<u>RT</u>		10	1.7E-2		1.3E-1	1 6.2E
J		H2A	<u>RT</u>		10	1.7E-1		7.0E-1	1
nnota	ation Cluster 100	Enrichment Score: 2.27	G		Count	P_Value			
)	GOTERM_MF_DIRECT	neuropeptide binding	<u>RT</u>	i	14	1.9E-6	4.2E0	4.7E-5	4.3E 5
)	INTERPRO	Somatostatin receptor family	<u>RT</u>	i	5	2.9E-3	6.2E0	3.4E-2	3.1E 2
)	GOTERM_BP_DIRECT	cellular response to glucocorticoid stimulus	<u>RT</u>	i .	10	3.1E-3	3.0E0	6.6E-2	6.3E 2
)	GOTERM_MF_DIRECT	somatostatin receptor activity	<u>RT</u>	i	5	3.4E-3	6.0E0	3.4E-2	3.1E 2
)	GOTERM_BP_DIRECT	somatostatin signaling pathway	<u>RT</u>	i .	5	3.5E-3	5.9E0	7.1E-2	6.8E 2
)	GOTERM_BP_DIRECT	<u>cerebellum development</u>	<u>RT</u>	i	6	7.7E-1	9.6E-1	1.0E0	9.6E
	GOTERM_BP_DIRECT	response to starvation	<u>RT</u>	•	5	8.6E-1	8.5E-1	1.0E0	9.6E
	ation Cluster 101	Enrichment Score: 2.24	G	-	Count		Fold Change		1 i FDR
nnota	ation Cluster IV				471111	Talue	Change	THE PERSON NAMED IN COLUMN	
nnota	UP_SEQ_FEATURE	domain:SH2	RT .		30	7.8E-5	•	2.8E-3	2.7E 3

Annot	ation Cluster 1	Enrichment Score: ?	G	- - 10	Count	P_Value	Fold Change	Benjamin	ii FDR
	UP_KEYWORDS	SH3 domain	<u>RT</u>	4	47	4.2E-3		2.2E-2	1.7E- 2
	SMART	<u>SH2</u>	<u>RT</u>	•	36	2.2E-2	1.4E0	1.6E-1	1.4E
	INTERPRO	Src homology-3 domain	<u>RT</u>		47	3.1E-2	1.3E0	2.3E-1	2.1E
	SMART	<u>SH3</u>	RT		46	8.5E-1	9.0E-1	1.0E0	8.9E
Annota	ation Cluster 102	Enrichment Score: 2.23	G		Count	P_Value	Fold	Benjamin	1 ni FDR
	GOTERM_BP_DIRECT	error-prone translesion synthesis	RT	1	14	8.7E-7	Change	5.7E-5	5.4E
_ 	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA gap filling	RT		15	5.3E-6		2.7E-4	5 2.6E
→	GOTERM_MF_DIRECT	single-stranded DNA-dependent ATPase		_					4 2.4E
	KEGG_PATHWAY	<u>activity</u>	<u>RT</u>		7	2.5E-3		2.6E-2	2 6.1E
	GOTERM_CC_DIRECT	<u>Mismatch repair</u>	<u>RT</u>		11	6.1E-3		1.2E-2	3 5.3E
		DNA replication factor C complex	<u>RT</u>	•	5	7.0E-3	5.3E0	6.0E-2	2
	GOTERM_MF_DIRECT	<u>DNA clamp loader activity</u>	<u>RT</u>	i	5	3.1E-2	3.7E0	2.0E-1	1.8E 1
	INTERPRO	<u>DNA polymerase III, clamp loader complex,</u> gamma/delta/delta subunit, C-terminal	<u>RT</u>	i	4	5.7E-2	4.1E0	3.8E-1	3.5E 1
	INTERPRO	Replication factor C, C-terminal domain	<u>RT</u>	1	3	7.0E-2	6.2E0	3.9E-1	3.6E 1
	GOTERM_BP_DIRECT	positive regulation of DNA-directed DNA polymerase activity	<u>RT</u>	i	4	9.9E-2	3.4E0	7.0E-1	6.7E 1
	GOTERM_CC_DIRECT	Ctf18 RFC-like complex	<u>RT</u>	i	4	1.2E-1	3.2E0	5.3E-1	4.7E 1
	GOTERM_BP_DIRECT	<u>DNA strand elongation involved in DNA</u> <u>replication</u>	<u>RT</u>	1	4	4.8E-1	1.6E0	1.0E0	9.6E
Annot	ation Cluster 103	Enrichment Score: 2.21	G	178	Count	P_Value	Fold Change	Benjamin	1
	INTERPRO	DDT domain superfamily	<u>RT</u>	i	5	2.9E-3		3.4E-2	3.1E
	UP_SEQ_FEATURE	domain:DDT	RT		5	5.4E-3	5.7E0	1.3E-1	1.3E
_ 	SMART	DDT	RT		5	1.5E-2		1.1E-1	1 1.0E
nnot	ation Cluster 104	Enrichment Score: 2.19	G	•	Count	P_Value	Fold	Daniamia	1 Si EDB
	INTERPRO			i			Change		8.5E
	GOTERM_MF_DIRECT	SANT/Myb domain transcription factor activity, RNA polymerase	<u>RT</u>		19	5.3E-5		9.2E-4	4 5.8E
	SMART	II transcription factor recruiting	<u>RT</u>		7	4.5E-4		6.3E-3	3 7.4E
	INTERPRO	<u>SANT</u>	<u>RT</u>	•	19	1.0E-2	1.8E0	8.3E-2	2
		SANT domain	<u>RT</u>	i	9	4.7E-2		3.2E-1	3.0E
Annot	INTERPRO ation Cluster 105	Homeodomain-like Enrichment Score: 2.18	RT G	· •	21 Count	1.0E0 P_Value	3.9E-1 Fold	Danismin	1.0E
	INTERPRO	Cullin, N-terminal	RT	•	8	2.1E-4	Change	3.3E-3	3.0E
	INTERPRO			_					3 1.1E
	UP_SEQ_FEATURE	<u>Cullin homology</u> cross-link:Glycyl lysine isopeptide (Lys-Gly)	<u>RT</u>		7	9.4E-4		1.2E-2	2 2.9E
	INTERPRO	(interchain with G-Cter in NEDD8)	<u>RT</u>	•	6	1.1E-3	5.8E0	3.0E-2	2
		Cullin protein, neddylation domain	<u>RT</u>	i	6	4.0E-3	4.6E0	4.3E-2	4.0E 2
	SMART	CULLIN	<u>RT</u>	i	6	1.2E-2	3.5E0	9.7E-2	8.6E 2
	INTERPRO	Cullin, conserved site	<u>RT</u>	i	5	1.6E-2	4.4E0	1.2E-1	1.1E 1
	SMART	<u>SM00884</u>	<u>RT</u>	i	6	2.6E-2	3.0E0	1.9E-1	1.6E 1
	INTERPRO	Cullin repeat-like-containing domain	<u>RT</u>	i	6	3.2E-2	3.1E0	2.3E-1	2.1E 1
	GOTERM_CC_DIRECT	cullin-RING ubiquitin ligase complex	<u>RT</u>	1	4	1.6E-1	2.8E0	6.7E-1	6.0E 1
Annota	ation Cluster 106	Enrichment Score: 2.12	G	15	Count	P_Value	Fold Change	Benjamin	ii FDR
	GOTERM_BP_DIRECT	regulation of axonogenesis	<u>RT</u>	1	12	·		1.6E-2	1.5E
	GOTERM_MF_DIRECT	Roundabout binding	<u>RT</u>	1	7	1.2E-3	4.6E0	1.4E-2	1.3E
	GOTERM_BP_DIRECT	Roundabout signaling pathway	RT		6	3.8E-2		3.9E-1	3.7E
	GOTERM_BP_DIRECT	axon extension involved in axon guidance	RT		5		2.5E0		1 7.9E
nnot	ation Cluster 107	Enrichment Score: 2.12	G	•		P_Value			1 ni FDR
	GOTERM_BP_DIRECT	adenylate cyclase-inhibiting G-protein coupled		i	6	2.1E-3		4.8E-2	4.5E
	INTERPRO	glutamate receptor signaling pathway	<u>KI</u>						2 3.1E
	INTERPRO	Extracellular ligand-binding receptor	<u>RT</u>	i	14	2.9E-3		3.4E-2	2
		GPCR, family 3	<u>RT</u>	i	8	3.4E-3	3.5E0	3.8E-2	3.5E 2
	INTERPRO	GPCR, family 3, conserved site	<u>RT</u>	i .	8	3.4E-3	3.5E0	3.8E-2	3.5E 2
	INTERPRO	GPCR, family 3, metabotropic glutamate receptor	RT	1	6	4.0E-3	4.6E0	4.3E-2	4.0E 2

Annot	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold	Benjamin	i EDP
Annot	GOTERM_BP_DIRECT	regulation of synaptic transmission,		_			Change		1.5E-
	INTERPRO	glutamatergic	<u>RT</u>		10	9.3E-3		1.5E-1	1 9.5E-
		GPCR, family 3, nine cysteines domain	<u>RT</u>	•	7	1.1E-2	3.3E0	1.0E-1	2
	GOTERM_MF_DIRECT	group III metabotropic glutamate receptor activity	<u>RT</u>	i	4	1.6E-2	6.0E0	1.2E-1	1.1E- 1
	INTERPRO	GPCR, family 3, C-terminal	<u>RT</u>	i	9	1.7E-2	2.5E0	1.4E-1	1.2E- 1
	GOTERM_MF_DIRECT	glutamate receptor activity	<u>RT</u>	i .	6	2.5E-2	3.3E0	1.7E-1	1.5E- 1
	GOTERM_CC_DIRECT	<u>presynaptic membrane</u>	<u>RT</u>	i .	17	2.8E-2	1.7E0	2.0E-1	1.7E- 1
Annot	ation Cluster 108	Enrichment Score: 2.08	G	10	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_MF_DIRECT	lysine-acetylated histone binding	<u>RT</u>	i	10	1.2E-3	3.3E0	1.4E-2	1.3E- 2
	UP_SEQ_FEATURE	domain:Bromo 1	<u>RT</u>	i .	6	2.2E-2	3.4E0	4.2E-1	4.0E-
	UP_SEQ_FEATURE	domain:Bromo 2	<u>RT</u>		6	2.2E-2	3.4E0	4.2E-1	4.0E-
Annot	ation Cluster 109	Enrichment Score: 2.08	G		Count	:	Fold Change	:	i FDR
	UP_KEYWORDS	RNA-binding	RT	=	147	1.3E-7		9.8E-7	7.8E-
	INTERPRO			_					7 2.9E-
	UP_SEQ_FEATURE	RNA recognition motif domain	<u>RT</u>	•	54	2.6E-3		3.2E-2	2 1.5E-
		domain:RRM	<u>RT</u>	•	32	6.7E-3	1.6E0	1.6E-1	1
	GOTERM_MF_DIRECT	nucleotide binding	<u>RT</u>	•	77	7.5E-3	1.3E0	6.9E-2	6.2E- 2
	INTERPRO	Nucleotide-binding, alpha-beta plait	<u>RT</u>	•	55	3.6E-2	1.3E0	2.5E-1	2.3E- 1
	UP_SEQ_FEATURE	domain:RRM 1	<u>RT</u>	i contract	26	6.4E-2	1.4E0	9.6E-1	9.2E- 1
	UP_SEQ_FEATURE	domain:RRM 2	<u>RT</u>	i .	26	6.4E-2	1.4E0	9.6E-1	9.2E- 1
	UP_SEQ_FEATURE	domain:RRM 3	<u>RT</u>	1	14	1.0E-1	1.6E0	1.0E0	9.7E- 1
	SMART	<u>RRM</u>	<u>RT</u>		51	6.8E-1	9.7E-1	1.0E0	8.9E-
Annot	ation Cluster 110	Enrichment Score: 2.07	G	·	Count	P_Value	Fold Change	Benjamin	-
	GOTERM_BP_DIRECT	protein K6-linked ubiquitination	RT		7	4.7E-4	Change	1.3E-2	1.3E-
	GOTERM_BP_DIRECT	protein K29-linked ubiquitination	RT		4	3.7E-2		3.8E-1	2 3.7E-
	GOTERM_BP_DIRECT	protein K27-linked ubiquitination			4	3.7E-2		3.8E-1	1 3.7E-
Annot	ection Cluster 444		<u>RT</u>			1	Fold		1 EDB
Annot	ation Cluster 111 GOTERM_BP_DIRECT	Enrichment Score: 2.05 MyD88-dependent toll-like receptor signaling	G	-	Count	P_Value 2.7E-	Change	Benjamin	3.3E-
	GOTERM_BP_DIRECT	<u>pathway</u>	<u>RT</u>	•	23	10		3.5E-8	8 2.3E-
		regulation of cytokine secretion	<u>RT</u>	•	10	4.4E-6	5.4E0	2.4E-4	4
	UP_SEQ_FEATURE	repeat:LRR 22	<u>RT</u>	•	10	4.5E-6	5.7E0	2.0E-4	2.0E- 4
	GOTERM_BP_DIRECT	toll-like receptor signaling pathway	<u>RT</u>	i	15	3.3E-5	3.3E0	1.3E-3	1.2E- 3
	UP_SEQ_FEATURE	repeat:LRR 24	<u>RT</u>	i .	6	1.1E-3	5.8E0	3.0E-2	2.9E- 2
	GOTERM_BP_DIRECT	I-kappaB phosphorylation	<u>RT</u>	i	8	1.4E-3	3.9E0	3.3E-2	3.2E- 2
	UP_SEQ_FEATURE	domain:TIR	<u>RT</u>	i .	10	6.9E-3	2.7E0	1.6E-1	1.5E- 1
	INTERPRO	Toll-like receptor	<u>RT</u>	i	4	1.5E-2	6.2E0	1.2E-1	1.1E- 1
	GOTERM_BP_DIRECT	positive regulation of chemokine production	<u>RT</u>	1	8	1.6E-2	2.8E0	2.2E-1	2.1E-
	PIR_SUPERFAMILY	toll-like receptor, 1/2/4/6/10 types	RT		4		6.0E0	2.5E-1	1 2.5E-
	INTERPRO	[Parent=PIRSF800008] Toll/interleukin-1 receptor homology (TIR)	RT	-	10	1.7E-2		1.3E-1	1 1.2E-
	GOTERM_BP_DIRECT	domain positive regulation of interferon-alpha							1 2.1E-
	GOTERM_BP_DIRECT	biosynthetic process positive regulation of interferon-beta	<u>RT</u>		4	1.7E-2		2.2E-1	1 2.3E-
	GOTERM_BP_DIRECT	biosynthetic process	<u>RT</u>	1	5	1.8E-2		2.4E-1	1
		positive regulation of toll-like receptor signaling pathway	<u>RT</u>	i .	4	3.7E-2	4.7E0	3.8E-1	3.7E- 1
	GOTERM_BP_DIRECT	positive regulation of NF-kappaB import into nucleus	<u>RT</u>	i	8	5.1E-2	2.3E0	4.8E-1	4.6E- 1
		TIR	<u>RT</u>	i	10	5.3E-2	1.9E0	2.9E-1	2.5E- 1
	SMART	_							
	SMART GOTERM_BP_DIRECT	positive regulation of interleukin-8 production	<u>RT</u>	i	9	5.9E-2	2.1E0	5.3E-1	5.0E- 1
			RT RT	i i	9	5.9E-2 1.1E-1		5.3E-1 5.0E-1	
	GOTERM_BP_DIRECT	positive regulation of interleukin-8 production		i i i			2.6E0		1 4.4E- 1 7.9E-
	GOTERM_BP_DIRECT GOTERM_CC_DIRECT	positive regulation of interleukin-8 production endolysosome membrane microglial cell activation positive regulation of interferon-gamma	<u>RT</u>	i i i	5	1.1E-1	2.6E0 2.5E0	5.0E-1	1 4.4E- 1 7.9E- 1 7.9E-
	GOTERM_BP_DIRECT GOTERM_CC_DIRECT GOTERM_BP_DIRECT	positive regulation of interleukin-8 production endolysosome membrane microglial cell activation	RT RT	i i i	5	1.1E-1 1.3E-1	2.6E0 2.5E0 2.5E0	5.0E-1 8.3E-1	1 4.4E- 1 7.9E- 1

Annota	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_BP_DIRECT	positive regulation of interleukin-6 production	<u>RT</u>	1	11	2.2E-1	<u> </u>	1.0E0	9.6E- 1
	GOTERM_MF_DIRECT	<u>lipopeptide binding</u>	<u>RT</u>	i .	3	4.0E-1	2.2E0	1.0E0	9.1E- 1
	GOTERM_CC_DIRECT	phagocytic vesicle membrane	<u>RT</u>		7	9.2E-1	7.5E-1	1.0E0	9.2E-
	BIOCARTA	Dendritic cells in regulating TH1 and TH2	RT		5	9 5F-1	7.1E-1	1 0F0	1 9.5E-
	GOTERM_MF_DIRECT	<u>Development</u> <u>transmembrane signaling receptor activity</u>	RT		15	1.0E0	4.2E-1		1 1.0E(
Annota	ation Cluster 112	Enrichment Score: 2.05	G	-	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_BP_DIRECT	sister chromatid cohesion	<u>RT</u>	1	33	2.8E-4		8.3E-3	8.0E- 3
	GOTERM_CC_DIRECT	<u>kinetochore</u>	<u>RT</u>	•	25	1.2E-3	2.0E0	1.3E-2	1.2E- 2
	UP_KEYWORDS	<u>Centromere</u>	<u>RT</u>		32	7.4E-3	1.6E0	3.6E-2	2.9E- 2
	UP_KEYWORDS	<u>Kinetochore</u>	<u>RT</u>		20	1.2E-1	1.4E0	4.4E-1	3.5E-
	GOTERM_CC_DIRECT	condensed chromosome kinetochore	<u>RT</u>		18	2.0E-1	1.3E0	8.0E-1	7.2E-
Annota	ation Cluster 113	Enrichment Score: 2.03	G		Count	P_Value	Fold	Panjamin	1 i FDR
	GOTERM_BP_DIRECT	muscle filament sliding	RT		19	1.3E-5	Change 3.0E0	5.8E-4	5.5E-
	GOTERM_BP_DIRECT	cardiac muscle contraction	RT	-	13	6.6E-2		5.6E-1	4 5.3E-
	KEGG_PATHWAY								1 9.9E
		Cardiac muscle contraction	<u>RT</u>		8	1	5.6E-1 Fold	1	1
Annota	ation Cluster 114 GOTERM_MF_DIRECT	Enrichment Score: 2.01	G	- Telephone	Count	P_Value	Change		3.1E
	GOTERM_BP_DIRECT	CXCR3 chemokine receptor binding	<u>RT</u>		5	3.4E-3		3.4E-2	2 8.8E
		<u>T cell chemotaxis</u>	<u>RT</u>	•	6	4.9E-3	4.4E0	9.2E-2	2
	GOTERM_BP_DIRECT	positive regulation of leukocyte chemotaxis	<u>RT</u>	•	9	5.8E-3	3.0E0	1.1E-1	1.0E 1
	GOTERM_BP_DIRECT	positive regulation of cAMP metabolic process	<u>RT</u>	i	5	9.1E-3	4.9E0	1.5E-1	1.4E 1
	GOTERM_BP_DIRECT	positive regulation of release of sequestered calcium ion into cytosol	<u>RT</u>	1	10	2.8E-2	2.2E0	3.3E-1	3.1E 1
	GOTERM_BP_DIRECT	positive regulation of cAMP-mediated signaling	<u>RT</u>	1	6	3.8E-2	3.0E0	3.9E-1	3.7E 1
Annota	ation Cluster 115	Enrichment Score: 1.96	G	100	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_MF_DIRECT	transcription factor activity, RNA polymerase II transcription factor recruiting	<u>RT</u>	i .	7	4.5E-4	5.2E0	6.3E-3	5.8E 3
	UP_SEQ_FEATURE	domain:HTH myb-type 1	<u>RT</u>	1	5	2.0E-3	6.8E0	5.3E-2	5.1E 2
	UP_SEQ_FEATURE	domain:HTH myb-type 2	<u>RT</u>	i .	5	2.0E-3	6.8E0	5.3E-2	5.1E
	INTERPRO	Myb-like domain	<u>RT</u>		6	4.0E-3	4.6E0	4.3E-2	4.0E
	INTERPRO	Myb domain	<u>RT</u>		6	7.7E-3	4.1E0	7.5E-2	2 7.0E
_ _	UP_SEQ_FEATURE	domain:HTH myb-type 3	RT		4	1.1E-2		2.3E-1	2 2.2E
	UP_SEQ_FEATURE				3	5.8E-2		8.8E-1	1 8.5E
	UP_SEQ_FEATURE	domain:Myb-like 1	<u>RT</u>						1 8.5E
	INTERPRO	domain:Myb-like 2	<u>RT</u>		3	5.8E-2		8.8E-1	1 3.6E
		<u>C-myb, C-terminal</u>	<u>RT</u>	•	3	7.0E-2	6.2E0	3.9E-1	1
	UP_SEQ_FEATURE	DNA-binding region:H-T-H motif	<u>RT</u>	i	7	1.7E-1		1.0E0	9.7E 1
Annota	ation Cluster 116	Enrichment Score: 1.95	G	N .	Count	P_Value	Fold Change	Benjamin	
	UP_SEQ_FEATURE	domain:DAZ-like 14	<u>RT</u>	•	4	1.1E-2	6.8E0	2.3E-1	2.2E 1
	UP_SEQ_FEATURE	domain:DAZ-like 15	<u>RT</u>	i	4	1.1E-2	6.8E0	2.3E-1	2.2E 1
	UP_SEQ_FEATURE	domain:DAZ-like 2	<u>RT</u>	i	4	1.1E-2	6.8E0	2.3E-1	2.2E 1
	UP_SEQ_FEATURE	domain:DAZ-like 3	<u>RT</u>	1	4	1.1E-2	6.8E0	2.3E-1	2.2E 1
	UP_SEQ_FEATURE	domain:DAZ-like 4	<u>RT</u>	1	4	1.1E-2	6.8E0	2.3E-1	2.2E 1
	UP_SEQ_FEATURE	domain:DAZ-like 5	<u>RT</u>	1	4	1.1E-2	6.8E0	2.3E-1	2.2E 1
	UP_SEQ_FEATURE	domain:DAZ-like 6	<u>RT</u>	1	4	1.1E-2	6.8E0	2.3E-1	2.2E 1
	UP_SEQ_FEATURE	domain:DAZ-like 7	<u>RT</u>		4	1.1E-2	6.8E0	2.3E-1	2.2E
	UP_SEQ_FEATURE	domain:DAZ-like 8	RT	1	4	1.1E-2		2.3E-1	2.2E
	UP_SEQ_FEATURE	domain:DAZ-like 9	RT		4	1.1E-2		2.3E-1	1 2.2E
	UP_SEQ_FEATURE								1 2.2E
	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 1	<u>RT</u>	•	4	1.1E-2		2.3E-1	1 2.2E
		chain:Deleted in azoospermia protein 2	<u>RT</u>	i	4	1.1E-2	6.8E0	2.3E-1	1
	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 3	RT	i			6.8E0		2.2E

Annot	ation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	chain: Deleted in azoospermia protein 4	<u>RT</u>	i	4	1.1E-2	Change	2.3E-1	2.2E-
	UP_SEQ_FEATURE	domain:DAZ-like 1	<u>RT</u>	1	4	1.1E-2	6.8E0	2.3E-1	2.2E-
	UP_SEQ_FEATURE	domain:DAZ-like 10	<u>RT</u>		4	1.1E-2	6.8E0	2.3E-1	1 2.2E-
	UP_SEQ_FEATURE	domain:DAZ-like 11	RT		4	1.1E-2	6.8E0	2.3E-1	1 2.2E-
	UP_SEQ_FEATURE	domain:DAZ-like 12	RT		4	1.1E-2		2.3E-1	1 2.2E-
	UP_SEQ_FEATURE	domain:DAZ-like 13	RT		4	1.1E-2		2.3E-1	1 2.2E-
Annot	ation Cluster 117	Enrichment Score: 1.94	G	· 	:	:	:	:	1 FDR
	UP_SEQ_FEATURE	compositionally biased region:Ala/Asp-rich	RT		6	2.6E-3	Fold Change	6.6E-2	6.3E-
	INTERPRO	(DA-box) Structural maintenance of chromosomes	RT		5	2.9E-3		3.4E-2	2 3.1E-
	PIR_SUPERFAMILY	<u>structural maintenance of chromosomes</u>	RT		5	3.2E-3		1.9E-1	2 1.9E-
	INTERPRO	protein SMCs flevible bings						7.5E-2	1 7.0E-
	UP_SEQ_FEATURE	SMCs flexible hinge	<u>RT</u>		5	7.7E-3			2 2.2E-
	INTERPRO	region of interest:Flexible hinge	<u>RT</u>		5	1.1E-2		2.3E-1	1 1.1E-
	SMART	RecF/RecN/SMC	<u>RT</u>		5	1.6E-2		1.2E-1	1 2.1E-
	GOTERM_CC_DIRECT	<u>SM00968</u>	<u>RT</u>	•	5	3.6E-2		2.4E-1	1
	GOTEKM_CC_DIRECT	meiotic cohesin complex	<u>RT</u>	i	3	2.4E-1	•	9.1E-1	8.1E- 1
Annota	ation Cluster 118	Enrichment Score: 1.94	G		Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	domain:FBA	<u>RT</u>	i	5	5.4E-3	5.7E0	1.3E-1	1.3E- 1
	INTERPRO	F-box associated (FBA) domain	<u>RT</u>	i	5	7.7E-3	5.2E0	7.5E-2	7.0E- 2
	SMART	SM01198	<u>RT</u>	i	5	3.6E-2	•	2.4E-1	2.1E- 1
Annota	ation Cluster 119	Enrichment Score: 1.88	G	<mark>™</mark>	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	domain:C2 tensin-type	<u>RT</u>	i e	6	5.1E-3	4.5E0	1.3E-1	1.2E- 1
	UP_SEQ_FEATURE	domain:Phosphatase tensin-type	<u>RT</u>	i	6	9.0E-3	4.1E0	2.1E-1	2.0E- 1
	INTERPRO	<u>Tensin phosphatase, C2 domain</u>	<u>RT</u>	i	6	1.3E-2	3.7E0	1.2E-1	1.1E- 1
	SMART	SM01326	<u>RT</u>	i .	6	4.7E-2	2.7E0	2.8E-1	2.4E- 1
Annota	ation Cluster 120	Enrichment Score: 1.76	G	™	Count	P_Value	Fold Change	Benjamini	FDR
	KEGG_PATHWAY	<u>Phototransduction</u>	<u>RT</u>	i .	15	1.2E-4	2.9E0	3.0E-4	1.3E- 4
	GOTERM_CC_DIRECT	photoreceptor disc membrane	<u>RT</u>	i e	9	5.5E-3	3.0E0	5.0E-2	4.4E- 2
	GOTERM_BP_DIRECT	regulation of rhodopsin mediated signaling pathway	<u>RT</u>	i	11	1.7E-2	2.2E0	2.2E-1	2.1E- 1
	GOTERM_BP_DIRECT	rhodopsin mediated signaling pathway	<u>RT</u>	i .	4	3.3E-1	2.0E0	1.0E0	9.6E- 1
	UP_KEYWORDS	Vision	<u>RT</u>	i .	19	4.1E-1	1.1E0	1.0E0	8.0E- 1
Annot	ation Cluster 121	Enrichment Score: 1.7	G	The second secon	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	regulation of interferon-gamma-mediated signaling pathway	<u>RT</u>	i .	10	4.1E-5	<u> </u>	1.6E-3	1.5E- 3
	BBID	48.mice minus JAKs and STATs	<u>RT</u>	i e	8	8.1E-2	1.9E0	9.9E-1	9.9E- 1
	BBID	75.Stats activators of Apoptosis	<u>RT</u>	i	4	1.6E-1	2.6E0	9.9E-1	9.9E-
	BIOCARTA	<u>IFN gamma signaling pathway</u>	<u>RT</u>	i	4	2.9E-1	2.1E0	5.3E-1	4.0E-
Annot	ation Cluster 122	Enrichment Score: 1.7	G	To the second se	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	domain:HSA	<u>RT</u>	i	4		Change	2.3E-1	2.2E- 1
	INTERPRO	Helicase/SANT-associated, DNA binding	<u>RT</u>	i	4	1.5E-2		1.2E-1	1.1E- 1
	SMART	HSA	RT		4	4.9E-2		2.8E-1	2.4E-
Annot	ation Cluster 123	Enrichment Score: 1.69	G	<u>.</u>	•	:	Fold Change	:	1 FDR
	GOTERM_MF_DIRECT		RT	-	65	1.1E-2		9.1E-2	8.3E-
									2
	GOTERM_CC_DIRECT	cell-cell adherens junction	RT		67	1.4F-2	1.3F0	1.1E-1	9.5E-
	GOTERM_CC_DIRECT GOTERM_BP_DIRECT	cell-cell adherens junction	<u>RT</u> RT		67 57	1.4E-2 5.8F-2		1.1E-1 5.3E-1	9.5E- 2 5.0E-
Annote	GOTERM_BP_DIRECT	cell-cell adhesion	<u>RT</u>	=	57	5.8E-2	1.2E0	5.3E-1	2 5.0E- 1
Annota		cell-cell adhesion Enrichment Score: 1.68	RT G	=	57 Count	5.8E-2 P_Value	1.2E0 Fold Change	5.3E-1 Benjamini	2 5.0E- 1 FDR 5.3E-
Annota	GOTERM_BP_DIRECT ation Cluster 124	cell-cell adhesion	<u>RT</u>	=	57	5.8E-2 P_Value 5.5E-3	1.2E0 Fold Change	5.3E-1 Benjamini 5.8E-2	2 5.0E- 1 FDR

Annota	ation Cluster 1	Enrichment Score: ?	G	To the second	Count	P_Value	Fold Change	Benjamini	i FDR
	GOTERM_MF_DIRECT	ubiquitin conjugating enzyme binding	RT		12	9.1E-3	•	7.9E-2	7.2E
	UP_SEQ_FEATURE			-					2 4.0E
_	UP_SEQ_FEATURE	zinc finger region:RING-type 2	<u>RT</u>	•	6	2.2E-2	3.4E0	4.2E-1	1
		zinc finger region:RING-type 1; atypical	<u>RT</u>	i	4	1.0E-1	3.4E0	1.0E0	9.7E 1
	SMART	<u>IBR</u>	<u>RT</u>	i	7	1.1E-1	2.0E0	5.3E-1	4.7E 1
Annota	ation Cluster 125	Enrichment Score: 1.67	G	in the second second	Count	P_Value	Fold Change	Benjamini	i FDR
	INTERPRO	POLO box duplicated domain	<u>RT</u>	i	5	2.9E-3	6.2E0	3.4E-2	3.1E 2
	UP_SEQ_FEATURE	domain:POLO box 1	<u>RT</u>	1	3	5.8E-2	6.8E0	8.8E-1	8.5E
	UP_SEQ_FEATURE	domain:POLO box 2		-					1 8.5E
			<u>RT</u>	-	3	5.8E-2	E-14	8.8E-1	1
Annota	ation Cluster 126	Enrichment Score: 1.66	G	1	Count	P_Value	Change	Benjamini	
	GOTERM_MF_DIRECT	receptor signaling protein tyrosine kinase activity	<u>RT</u>	•	9	2.0E-5	5.4E0	3.5E-4	3.2E 4
	INTERPRO	EGF receptor, L domain	<u>RT</u>	i e	6	1.7E-3	5.3E0	2.1E-2	2.0E 2
	INTERPRO	Furin-like cysteine-rich domain	<u>RT</u>	i contract	6	1.7E-3	5.3E0	2.1E-2	2.0E 2
	INTERPRO	Furin-like repeat	<u>RT</u>	•	9	4.3E-3	3.1E0	4.7E-2	4.4E
\neg	SMART	<u>FU</u>	RT	-	9	5.4E-2	2 0E0	2.9E-1	2 2.6E
	INTERPRO								1 3.6E
		<u>Tyrosine-protein kinase, insulin-like receptor</u>	<u>RT</u>	•	3	7.0E-2	6.2E0	3.9E-1	1
	PIR_SUPERFAMILY	insulin receptor	<u>RT</u>	1	3	7.3E-2	6.0E0	6.0E-1	6.0E
	INTERPRO	<u>Tyrosine protein kinase, EGF/ERB/XmrK</u> <u>receptor</u>	<u>RT</u>	1	3	1.2E-1	4.6E0	6.2E-1	5.8E 1
	PIR_SUPERFAMILY	tyrosine-protein kinase, EGF receptor type	<u>RT</u>	1	3	1.3E-1	4.5E0	9.1E-1	9.1E
	INTERPRO	<u>Tyrosine-protein kinase, receptor class II,</u>	<u>RT</u>	4	3	5.5E-1	1.7E0	1.0E0	9.2E
	UP_SEQ_FEATURE	<pre>conserved site domain:Fibronectin type-III 3</pre>	RT		6	1.0E0	4.9E-1	1.0E0	1 1.0E
Annota	ation Cluster 127	Enrichment Score: 1.64	G	170	Count	P_Value	Fold Change	Benjamini	i FDR
	INTERPRO	Sphingosine 1-phosphate receptor	RT	1	5	2.9E-3	6.2E0	3.4E-2	3.1E
_ 	GOTERM_MF_DIRECT	sphingosine-1-phosphate receptor activity	RT		5	3.1E-2		2.0E-1	2 1.8E
_	GOTERM_BP_DIRECT								1 7.9E
		sphingosine-1-phosphate signaling pathway	<u>RT</u>	•	5	1.3E-1		8.3E-1	1
Annota	ation Cluster 128	Enrichment Score: 1.64	G		Count	P_Value	Fold Change	Benjamini	i FDR
	GOTERM_CC_DIRECT	MLL5-L complex	<u>RT</u>	i	6	3.5E-3	4.8E0	3.5E-2	3.1E 2
	GOTERM_CC_DIRECT	PTW/PP1 phosphatase complex	<u>RT</u>	i e	5	1.4E-2	4.5E0	1.1E-1	9.5E 2
	GOTERM_BP_DIRECT	entrainment of circadian clock by photoperiod	<u>RT</u>	1	6	2.4E-1	1.8E0	1.0E0	9.6E
Annota	ation Cluster 129	Enrichment Score: 1.62	G	**	Count	P_Value	Fold	Benjamini	1 FDR
	BIOCARTA	cdc25 and chk1 Regulatory Pathway in					Change		1.9E
	BIOCARTA	response to DNA damage	<u>RT</u>	•	8	6.3E-3	2.8E0	2.6E-2	2
		Sonic Hedgehog (SHH) Receptor Ptc1 Regulates cell cycle	<u>RT</u>	•	8	3.0E-2	2.3E0	9.0E-2	6.7E 2
	INTERPRO	<u>M-phase inducer phosphatase</u>	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E 1
Annota	ation Cluster 130	Enrichment Score: 1.62	G	To the second se	Count	P_Value	Fold Change	Benjamini	i FDR
	UP_SEQ_FEATURE	DNA-binding region:TEA	<u>RT</u>	1	4	1.1E-2	•	2.3E-1	2.2E 1
	INTERPRO	Transcriptional enhancer factor	RT		4	1.5E-2	6.2F0	1.2E-1	1.1E
	INTERPRO								1 1.1E
	PIR_SUPERFAMILY	TEA/ATTS	<u>RT</u>		4	1.5E-2		1.2E-1	1 2.5E
	_	transcriptional enhancer factor	<u>RT</u>	1	4	1.6E-2	6.0E0	2.5E-1	1
	SMART	<u>TEA</u>	<u>RT</u>	i	4	4.9E-2	4.0E0	2.8E-1	2.4E 1
	UP_SEQ_FEATURE	region of interest:Transcriptional activation	<u>RT</u>	i .	3	1.1E-1	5.1E0	1.0E0	9.7E 1
Annota	ation Cluster 131	Enrichment Score: 1.6	G	· ·	Count	P_Value	Fold Change	Benjamini	i FDR
	UP_KEYWORDS	Elongation factor	RT	Ŧ.	12	2.3E-3	Change	1.3E-2	1.0E
	INTERPRO	<u>Translation elongation/initiation</u>							2 5.1E
	INTERPRO	factor/Ribosomal, beta-barrel Translation elongation factor EFTu/EF1A,	<u>RT</u>		12	5.2E-3		5.6E-2	2 5.3E
		domain 2	<u>RT</u>	1	8	5.5E-3	3.3E0	5.8E-2	2
	INTERPRO	Elongation factor G, III-V domain	<u>RT</u>	1	5	7.7E-3	5.2E0	7.5E-2	7.0E 2
	INTERPRO	Translation elongation factor EFG, V domain	<u>RT</u>	1	5	7.7E-3	5.2E0	7.5E-2	7.0E 2
									8.2E
	INTERPRO	Elongation factor, GTP-hinding domain	RT		9	9.2F-3	2.8F0	8.8F-2	
	INTERPRO	Elongation factor, GTP-binding domain Translation elongation factor EFG/EF2,	RT RT	1	9	9.2E-3	2.8E0 6.2E0	8.8E-2	2 1.1E

INTERPRO	notation Clu	uster 1	Enrichment Score: ?	G	T .	Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	SMART	т	<u>SM00838</u>	<u>RT</u>	i .	5	1.5E-2	4.0E0	1.1E-1	1.0E- 1
SAME 1	INTERP	PRO	Ribosomal protein S5 domain 2-type fold	<u>RT</u>	i	14	1.8E-2	2.0E0	1.4E-1	1.3E- 1
GOTERAL M. DIRECT Introduction elabopation factor ETT AVEILLO. SIL	INTERP	PRO		<u>RT</u>	i e	9	3.0E-2	2.3E0	2.2E-1	2.0E-
NTERPRO Translation factor IFFLATED.C. 1	GOTER	RM_MF_DIRECT		<u>RT</u>	i	11	4.7E-2	1.9E0	2.9E-1	2.6E-
GOTERAL DE JORGET Consistent factor El Africia Consistent factor El Africa Consistent factor Con	SMART	т	<u>SM00889</u>	<u>RT</u>	i	4	4.9E-2	4.0E0	2.8E-1	2.4E-
GOTEM, SP, DIRECT Interfactional elementation factor Eff-Administration ST, Communication ST, Comm	INTERP	PRO		<u>RT</u>	1	4	8.8E-2	3.5E0	4.7E-1	4.4E-
MTERPRO Resolution absoration factor EFL-Africitation RT	GOTER	RM_BP_DIRECT		RT		6	1.7E-1	2.0E0	9.8E-1	9.4E-
OF NETWORPOOR Profession RT	INTERP	PRO	Translation elongation factor EF1A/initiation		-	4			1.0E0	1 9.2E-
## Count P. Vision Count Count	UP_KE	EYWORDS								1 8.0E-
OCTERN_CC_DIRECT	notation Clu	uster 132				1	1	Fold	Benjamini	1 FDR
GOTERM_BP_DRECT no.04ccome. disassembly. BI								Change	4.5E-2	4.0E-
GOTERM_BP_DIRECT mucleosome_disasembly RT	GOTER	RM_CC_DIRECT			•					2 1.8E-
GOTERM_OC_DIRECT REAL Complex RT	GOTER	RM_BP_DIRECT			-					1 4.7E-
Discretion Cluster 132										1 2.9E-
BIOCARTA Beoulation of cell cycle progression by Bids RT						1	1			1
SOTERM_BP_DIRECT Pepilocative senescence RT								Change	Benjamini	FDR 8.6E-
BIOCARTA Role of BRCAZ and ATR in Cancer Surceribility Count Public Count Pub									1.1E-2	3 3.7E-
Annotation Cluster 134					•				3.9E-1	1
BIOCARTA p.53 Eignedigendent protein kinase holdenzwine Count P. Value Count	БЮСАР	INTA		<u>RT</u>		10	2.5E-1		4.7E-1	3.5E- 1
GOTERM_CC_DIRECT			Enrichment Score: 1.57	G	<u> </u>	Count	P_Value		Benjamini	
BBID 4_cycling & p.27_cell_cycle RT				<u>RT</u>		13	1.2E-3	2.4E0	8.0E-3	6.0E- 3
BBID 94.E2F transcriptional activity cell cycle RT 1 6 8.26-2 2.26-0 95-6 Annotation Cluster 135 Enrichment Score: 1.54 6 7 1.06-2 3.460 4.86 UP_KEYWORDS Protein kinase inhibitor RT 1 7 1.06-2 3.460 4.86 INTERPRO Pseudokinase tribbles family/serine: threonine-protein kinase inhibitor RT 1 7 3.86-2 2.6620 1.26 GOTERM_MF_DIRECT mitocene-activated protein kinase kinase RT 1 7 3.86-2 2.660 2.46 GOTERM_MF_DIRECT regulation of MAP kinase activity RT 1 3 7.55-2 5.06-2 3.500 3.76 Annotation Cluster 136 Enrichment Score: 1.54 6 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RM_CC_DIRECT		<u>RT</u>	i	6	7.3E-2	2.5E0	3.9E-1	3.4E- 1
Annotation Cluster 135			4.cyclins & p27 cell cycle	<u>RT</u>	i	5	7.6E-2	2.6E0	9.9E-1	9.9E- 1
UP_KEYWORDS	BBID		94.E2F transcriptional activity cell cycle	<u>RT</u>	i	6	8.2E-2	2.2E0	9.9E-1	9.9E- 1
INTERPRO			Enrichment Score: 1.54	G	M .	Count	P_Value	Fold Change	Benjamini	
Count Coun	_		Protein kinase inhibitor	<u>RT</u>	i e	7	1.0E-2	3.4E0	4.8E-2	3.8E- 2
GOTERM_BP_DIRECT requisition of MAP kinase activity RT	INTERP	PRO		<u>RT</u>	i	4	1.5E-2	6.2E0	1.2E-1	1.1E- 1
Some	GOTER	RM_MF_DIRECT		<u>RT</u>	i e	7	3.8E-2	2.6E0	2.4E-1	2.2E- 1
Annotation Cluster 136	GOTER	RM_BP_DIRECT	regulation of MAP kinase activity	<u>RT</u>	i .	5	5.0E-2	3.3E0	4.7E-1	4.5E- 1
GOTERM_MF_DIRECT histone methyltransferase activity (H3-K36 RT	GOTER	RM_MF_DIRECT	ubiquitin-protein transferase regulator activity	<u>RT</u>	i	3	7.5E-2	6.0E0	3.9E-1	3.6E- 1
UP_SEQ_FEATURE domain:AWS RT	notation Clu	uster 136	Enrichment Score: 1.54	G	™	Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO AWS RT	GOTER	RM_MF_DIRECT		<u>RT</u>	i	5	8.8E-3	5.0E0	7.8E-2	7.1E- 2
SMART	UP_SEC	EQ_FEATURE	domain:AWS	<u>RT</u>	i e	4	2.5E-2	5.4E0	4.6E-1	4.4E- 1
ANNS ANNO ANNO ANNO ANNO ANNO ANNO ANNO ANNO	INTERP	PRO	AWS	<u>RT</u>	1	4	3.2E-2	5.0E0	2.3E-1	2.1E- 1
INTERPRO Zinc finger, PHD-type RT	SMART	т	AWS	<u>RT</u>	i	4	1.0E-1	3.2E0	5.1E-1	4.5E- 1
INTERPRO Zinc finger, PHD-finger RT	notation Clu	uster 137	Enrichment Score: 1.52	G	**	Count	P_Value		Benjamini	
UP_SEQ_FEATURE zinc finger region: PHD-type RT	INTERP	PRO	Zinc finger, PHD-finger	<u>RT</u>		24	2.6E-3		3.2E-2	3.0E- 2
UP_SEQ_FEATURE zinc finger region:PHD-type 2 RT 10 2.4E-2 2.3E0 4.6E UP_SEQ_FEATURE zinc finger region:PHD-type 1 RT 10 4.4E-2 2.1E0 7.8E INTERPRO Zinc finger, FYVE/PHD-type RT 31 6.4E-2 1.4E0 3.9E INTERPRO Zinc finger, PHD-type, conserved site RT 16 1.1E-1 1.5E0 5.9E SMART PHD RT 25 3.5E-1 1.1E0 1.0E Annotation Cluster 138 Enrichment Score: 1.51 G T Count P_Value Fold Change Benj GOTERM_MF_DIRECT four-way junction DNA binding RT 9 7.0E-4 3.8E0 9.1E CONTENT DR DIRECT STATE STATE PHD PLOSE P. Value Fold Change Benj P. Value Fold Change Benj P. Value Fold Change Fold Change Fold Change P. Value Fold Change P. Value	INTERP	PRO	Zinc finger, PHD-type	<u>RT</u>		25	6.3E-3	1.7E0	6.6E-2	6.1E- 2
UP_SEQ_FEATURE zinc finger region:PHD-type 2 RT 10 2.4E-2 2.3E0 4.6E UP_SEQ_FEATURE zinc finger region:PHD-type 1 RT 10 4.4E-2 2.1E0 7.8E INTERPRO Zinc finger, FYVE/PHD-type RT 31 6.4E-2 1.4E0 3.9E INTERPRO Zinc finger, PHD-type, conserved site RT 16 1.1E-1 1.5E0 5.9E SMART PHD RT 25 3.5E-1 1.1E0 1.0E Annotation Cluster 138 Enrichment Score: 1.51 Count P_Value Fold Change Benj GOTERM_MF_DIRECT four-way junction DNA binding RT 9 7.0E-4 3.8E0 9.1E	UP_SEC	EQ_FEATURE	zinc finger region:PHD-type	<u>RT</u>	i	15	1.6E-2	2.0E0	3.1E-1	3.0E-
UP_SEQ_FEATURE zinc finger region: PHD-type 1 RT 10 4.4E-2 2.1E0 7.8E INTERPRO Zinc finger, FYVE/PHD-type RT 31 6.4E-2 1.4E0 3.9E INTERPRO Zinc finger, PHD-type, conserved site RT 16 1.1E-1 1.5E0 5.9E SMART PHD RT 25 3.5E-1 1.1E0 1.0E Annotation Cluster 138 Enrichment Score: 1.51 G Count P_Value Fold Change Benj GOTERM_MF_DIRECT four-way junction DNA binding RT 9 7.0E-4 3.8E0 9.1E	UP_SEC	Q_FEATURE	zinc finger region:PHD-type 2			10			4.6E-1	4.4E-
INTERPRO Zinc finger, FYVE/PHD-type RT 31 6.4E-2 1.4E0 3.9E INTERPRO Zinc finger, PHD-type, conserved site RT 1 16 1.1E-1 1.5E0 5.9E SMART PHD RT 25 3.5E-1 1.1E0 1.0E Annotation Cluster 138 Enrichment Score: 1.51 G T Count P_Value Fold Change Benj GOTERM_MF_DIRECT four-way junction DNA binding RT 1 9 7.0E-4 3.8E0 9.1E	UP_SEC	EQ_FEATURE							7.8E-1	1 7.5E-
INTERPRO Zinc finger, PHD-type, conserved site RT SMART PHD RT Count P_Value Fold Change Benj GOTERM_MF_DIRECT four-way junction DNA binding RT COTERM_RP DIRECT	INTERP	PRO							3.9E-1	1 3.6E-
SMART PHD RT Count P_Value Fold Change Benj GOTERM_MF_DIRECT Four-way junction DNA binding RT SMART PHD RT Count P_Value Fold Change Benj RT OCTERM_RP_DIRECT FOUr-way junction DNA binding RT COTERM_RP_DIRECT	INTERP	PRO							5.9E-1	1 5.5E-
Annotation Cluster 138 Enrichment Score: 1.51	SMART	т								1 8.9E-
GOTERM_RP_DIRECT GOTERM_RP_DIRECT F_value Change Berry F_value Change Berry 9 7.0E-4 3.8E0 9.1E	notation Cl	ustor 138				:	:	:	:	1
COTEDM DD DIDECT								Change		8.3E-
mitotic recombination RI N 8 2 6F-3 3 6F0 5 7F										3 5.4E-
0 2.02 3.020 3.72			Initotic recombination	<u>K1</u>	•	d	2.0E-3	3.0EU	5.7E-2	2

Annota	ation Cluster 1	Enrichment Score: ?	G	·	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	chromosome organization involved in meiotic cell cycle	<u>RT</u>	i	4	1.7E-2		2.2E-1	2.1E-
	GOTERM_BP_DIRECT	reciprocal meiotic recombination	<u>RT</u>	1	11	2.1E-2	2.2E0	2.6E-1	2.5E-
	GOTERM_MF_DIRECT	recombinase activity	<u>RT</u>		5	3.1E-2	3.7E0	2.0E-1	1.8E-
	GOTERM_BP_DIRECT	DNA recombinase assembly	<u>RT</u>		4	3.7E-2	4.7E0	3.8E-1	1 3.7E-
	INTERPRO	DNA recombination and repair protein, RecA-	RT		4	5.7E-2	4.1E0	3.8E-1	3.5E-
	PIR_SUPERFAMILY	<u>like</u> <u>DNA repair and recombination protein, Rad51</u>	RT		4	6.1E-2		6.0E-1	1 6.0E-
	INTERPRO	<u>type</u> <u>DNA repair Rad51/transcription factor NusA,</u>	RT		3	7.0E-2		3.9E-1	1 3.6E-
	INTERPRO	<u>alpha-helical</u> <u>DNA recombination/repair protein RecA/RadB,</u>			4	8.8E-2		4.7E-1	1 4.4E-
	INTERPRO	ATP-binding domain DNA recombination and repair protein Rad51,	RT	-	4	8.8E-2		4.7E-1	1 4.4E-
	GOTERM_BP_DIRECT	C-terminal	RT		4	9.9E-2		7.0E-1	1 6.7E-
	GOTERM_MF_DIRECT	strand invasion							1 6.0E-
Annat		endodeoxyribonuclease activity	<u>RT</u>	•	7	1.5E-1	Fold	6.6E-1	1
Annota	ation Cluster 139 INTERPRO	Enrichment Score: 1.49	G	i	Count	P_Value	Change	Benjamini	4.6E-
	GOTERM_BP_DIRECT	<u>Ubiquitin subgroup</u> <u>nucleotide-excision repair, DNA duplex</u>	<u>RT</u>		10	2.8E-5		5.0E-4	4 1.0E-
	GOTERM_BP_DIRECT	<u>unwinding</u>	<u>RT</u>		12	3.5E-4		1.0E-2	2 3.2E-
	GOTERM_BP_DIRECT	regulation of necrotic cell death regulation of transcription from RNA	<u>RT</u>	•	8	1.4E-3	3.9E0	3.3E-2	2
		polymerase II promoter in response to hypoxia	<u>RT</u>	•	12	4.0E-3	2.5E0	8.0E-2	7.6E- 2
	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA damage recognition	<u>RT</u>	i contraction	10	9.3E-3	2.6E0	1.5E-1	1.5E- 1
	GOTERM_BP_DIRECT	positive regulation of epidermal growth factor receptor signaling pathway	<u>RT</u>	i .	10	1.3E-2	2.5E0	1.9E-1	1.8E- 1
	GOTERM_BP_DIRECT	MyD88-independent toll-like receptor signaling pathway	<u>RT</u>	1	7	1.3E-2	3.2E0	2.0E-1	1.9E- 1
	UP_SEQ_FEATURE	binding site:Activating enzyme	<u>RT</u>	i	5	2.0E-2	4.3E0	3.9E-1	3.7E-
	INTERPRO	<u>Ubiquitin conserved site</u>	<u>RT</u>	i	6	2.1E-2	3.4E0	1.6E-1	1.5E-
	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)	<u>RT</u>	i	7	3.8E-2	2.6E0	6.8E-1	6.6E-
	GOTERM_BP_DIRECT	regulation of type I interferon production	<u>RT</u>	1	6	5.4E-2	2.7E0	4.9E-1	4.7E-
	GOTERM_BP_DIRECT	negative regulation of type I interferon	<u>RT</u>		10	5.4E-2	2.0E0	4.9E-1	4.7E-
	GOTERM_BP_DIRECT	production viral life cycle	RT	•	10	6.5E-2	1.9E0	5.5E-1	1 5.3E-
	GOTERM_BP_DIRECT	negative regulation of epidermal growth	RT		11	7.0E-2	1.8E0	5.8E-1	1 5.6E-
	UP_SEQ_FEATURE	factor receptor signaling pathway chain:40S ribosomal protein S27a	RT		4	7.0E-2		1.0E0	1 9.7E-
	UP_SEQ_FEATURE	compositionally biased region:Lys-rich (highly	RT		4	7.0E-2		1.0E0	1 9.7E-
	UP_SEQ_FEATURE	basic) site:Essential for function	RT		4	7.0E-2		1.0E0	1 9.7E-
	UP_SEQ_FEATURE	chain: Ubiquitin	RT		4	7.0E-2		1.0E0	1 9.7E-
	GOTERM_BP_DIRECT	virion assembly	RT		5	1.3E-1		8.3E-1	1 7.9E-
	GOTERM_BP_DIRECT	glycogen biosynthetic process	RT		8	1.4E-1		8.3E-1	1 7.9E-
	GOTERM_BP_DIRECT	interstrand cross-link repair	RT		10	4.5E-1		1.0E0	1 9.6E-
	GOTERM_BP_DIRECT	intracellular transport of virus	RT		10	5.0E-1		1.0E0	1 9.6E-
	GOTERM_CC_DIRECT	endocytic vesicle membrane		_	9	8.4E-1			1 8.9E-
	GOTERM_BP_DIRECT	endosomal transport	RT RT		5	1.0E0			1 1.0E0
Annota	ation Cluster 140	Enrichment Score: 1.49	G	■ The state of th	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	<u>Dynamin, GTPase domain</u>	<u>RT</u>	i	6	1.7E-3		2.1E-2	2.0E- 2
	INTERPRO	<u>Dynamin central domain</u>	<u>RT</u>	1	5	7.7E-3	5.2E0	7.5E-2	7.0E- 2
	INTERPRO	<u>Dynamin, GTPase region, conserved site</u>	<u>RT</u>	1	5	7.7E-3	5.2E0	7.5E-2	7.0E- 2
	UP_SEQ_FEATURE	domain:GED	<u>RT</u>	i	5	1.1E-2	4.9E0	2.3E-1	2.2E-
	SMART	<u>DYNc</u>	<u>RT</u>	i	6	1.2E-2	3.5E0	9.7E-2	8.6E- 2
	INTERPRO	<u>Dynamin GTPase effector</u>	<u>RT</u>	i .	5	1.6E-2	4.4E0	1.2E-1	1.1E- 1
	SMART	<u>GED</u>	<u>RT</u>	i	5	3.6E-2	3.4E0	2.4E-1	2.1E-
	INTERPRO	GTPase effector domain, GED	<u>RT</u>		5	4.3E-2		3.0E-1	2.8E-
	GOTERM_BP_DIRECT	dynamin polymerization involved in	RT		4	9.9E-2		7.0E-1	1 6.7E-
		mitochondrial fission	_						1

Annota	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	<u>Dynamin</u>	<u>RT</u>	i	6	1.3E-1		6.2E-1	5.8E-
	GOTERM_BP_DIRECT	mitochondrial fission	<u>RT</u>	i	5	4.0E-1	1.6E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	membrane fusion	<u>RT</u>	i .	6	8.9E-1	8.1E-1	1.0E0	9.6E-
Annota	ation Cluster 141	Enrichment Score: 1.48	G	17	Count	P_Value	Fold	Benjamini	1
	GOTERM_MF_DIRECT	protein kinase C activity	<u>RT</u>	i	10	1.9E-4		2.9E-3	2.6E-
	INTERPRO	Diacylglycerol/phorbol-ester binding	RT		11	3.7E-3	2.7E0	4.1E-2	3.8E-
	INTERPRO	Protein kinase C, delta/epsilon/eta/theta	RT		4	1.5E-2		1.2E-1	2 1.1E-
	PIR_SUPERFAMILY	<u>types</u> <u>protein kinase C, delta/epsilon/eta/theta</u>	RT		4	1.6E-2		2.5E-1	1 2.5E-
	UP_SEQ_FEATURE	<u>types</u> zinc finger region: Phorbol-ester/DAG-type 1	RT	-	8	3.3E-2		6.0E-1	1 5.8E-
	UP_SEQ_FEATURE								1 5.8E-
	GOTERM_MF_DIRECT	zinc finger region:Phorbol-ester/DAG-type 2	<u>RT</u>		8	3.3E-2		6.0E-1	1 3.6E-
	INTERPRO	<u>calcium-independent protein kinase C activity</u> <u>Protein kinase C-like, phorbol</u>			3	7.5E-2		3.9E-1	1 7.5E-
	SMART	ester/diacylglycerol binding	<u>RT</u>		15	1.7E-1	1.4E0	8.1E-1	1 8.9E-
	UP_SEQ_FEATURE	<u>C1</u>	<u>RT</u>	•	15	7.7E-1	9.3E-1	1.0E0	1
	OF_SEQ_FEATORE	zinc finger region:Phorbol-ester/DAG-type	<u>RT</u>	i	5	9.1E-1	7.6E-1	1.0E0	9.7E- 1
Annota	ation Cluster 142	Enrichment Score: 1.46	G	17	Count	P_Value	Fold Change	Benjamini	
	BIOCARTA	Signal Dependent Regulation of Myogenesis by Corepressor MITR	<u>RT</u>	•	9	6.9E-4	3.1E0	5.2E-3	3.9E- 3
	UP_SEQ_FEATURE	domain:MADS-box	<u>RT</u>	i .	5	5.4E-3	5.7E0	1.3E-1	1.3E- 1
	INTERPRO	<u>Transcription factor, MADS-box</u>	<u>RT</u>	i	5	7.7E-3	5.2E0	7.5E-2	7.0E- 2
	UP_SEQ_FEATURE	DNA-binding region:Mef2-type	<u>RT</u>	i	4	2.5E-2	5.4E0	4.6E-1	4.4E- 1
	SMART	MADS	<u>RT</u>	i .	5	3.6E-2	3.4E0	2.4E-1	2.1E- 1
	UP_SEQ_FEATURE	region of interest:Beta domain	<u>RT</u>	i	3	5.8E-2	6.8E0	8.8E-1	8.5E- 1
	INTERPRO	Holliday junction regulator protein family C- terminal	<u>RT</u>	i	3	1.2E-1	4.6E0	6.2E-1	5.8E- 1
	UP_SEQ_FEATURE	compositionally biased region:Lys-rich (basic)	<u>RT</u>	1	3	3.9E-1	2.3E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	site:Cleavage	<u>RT</u>	1	8	9.1E-1	7.8E-1	1.0E0	9.7E-
Annota	ation Cluster 143	Enrichment Score: 1.42	G	15	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	ROC GTPase	<u>RT</u>	i	4	1.5E-2	6.2E0	1.2E-1	1.1E- 1
	UP_SEQ_FEATURE	domain:Roc	<u>RT</u>	i	3	5.8E-2	6.8E0	8.8E-1	8.5E- 1
	INTERPRO	Mitochondrial Rho-like	<u>RT</u>	i	5	6.3E-2	3.1E0	3.9E-1	3.6E-
Annota	ation Cluster 144	Enrichment Score: 1.41	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	mitotic cell cycle	<u>RT</u>	i	16	1.9E-3	<u> </u>	4.4E-2	4.2E-
	GOTERM_MF_DIRECT	receptor signaling protein serine/threonine							2
			<u>RT</u>		16	2.4E-2	1.8E0	1.7E-1	1.5E-
	UP_SEQ_FEATURE	kinase activity domain:CRIB	<u>RT</u> <u>RT</u>	i i	16 7	2.4E-2 4.9E-2		1.7E-1 8.4E-1	1.5E- 1 8.1E-
	UP_SEQ_FEATURE UP_SEQ_FEATURE	kinase activity		i			2.5E0		1
		kinase activity domain:CRIB region of interest:GTPase-binding	RT RT	i i	7	4.9E-2 5.8E-2	2.5E0 6.8E0	8.4E-1 8.8E-1	1 8.1E- 1
	UP_SEQ_FEATURE	kinase activity domain:CRIB region of interest:GTPase-binding region of interest:Autoregulatory region	RT RT RT	i i	7 3 3	4.9E-2 5.8E-2 5.8E-2	2.5E0 6.8E0 6.8E0	8.4E-1 8.8E-1 8.8E-1	1 8.1E- 1 8.5E- 1
	UP_SEQ_FEATURE UP_SEQ_FEATURE	kinase activity domain:CRIB region of interest:GTPase-binding region of interest:Autoregulatory region PAK-box/P21-Rho-binding	RT RT RT RT	i i i	7 3 3 7	4.9E-2 5.8E-2 5.8E-2 9.0E-2	2.5E0 6.8E0 6.8E0 2.2E0	8.4E-1 8.8E-1 8.8E-1 4.8E-1	1 8.1E- 1 8.5E- 1 8.5E- 1
Annet	UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO SMART	kinase activity domain:CRIB region of interest:GTPase-binding region of interest:Autoregulatory region PAK-box/P21-Rho-binding PBD	RT RT RT RT RT	i i i	7 3 3 7 7	4.9E-2 5.8E-2 5.8E-2 9.0E-2 1.8E-1	2.5E0 6.8E0 6.8E0 2.2E0 1.8E0	8.4E-1 8.8E-1 8.8E-1 4.8E-1 7.3E-1	1 8.1E-1 8.5E-1 8.5E-1 4.4E-1 6.5E-1
Annota	UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO	kinase activity domain:CRIB region of interest:GTPase-binding region of interest:Autoregulatory region PAK-box/P21-Rho-binding PBD Enrichment Score: 1.4 compositionally biased region:Arg/Ser-rich	RT RT RT RT RT G	i i i i	7 3 3 7 7	4.9E-2 5.8E-2 5.8E-2 9.0E-2 1.8E-1 P_Value	2.5E0 6.8E0 6.8E0 2.2E0 1.8E0 Fold Change	8.4E-1 8.8E-1 4.8E-1 7.3E-1 Benjamini	1 8.1E-1 8.5E-1 8.5E-1 4.4E-1 6.5E-1
Annota	UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO SMART ation Cluster 145	kinase activity domain:CRIB region of interest:GTPase-binding region of interest:Autoregulatory region PAK-box/P21-Rho-binding PBD Enrichment Score: 1.4	RT RT RT RT RT RT RT RT		7 3 3 7 7 Count	4.9E-2 5.8E-2 5.8E-2 9.0E-2 1.8E-1 P_Value 2.4E-3	2.5E0 6.8E0 6.8E0 2.2E0 1.8E0 Fold Change 3.4E0	8.4E-1 8.8E-1 4.8E-1 7.3E-1 Benjamini 6.1E-2	8.1E-1 8.5E-1 8.5E-1 4.4E-1 6.5E-1
Annota	UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO SMART ation Cluster 145 UP_SEQ_FEATURE GOTERM_BP_DIRECT	kinase activity domain:CRIB region of interest:GTPase-binding region of interest:Autoregulatory region PAK-box/P21-Rho-binding PBD Enrichment Score: 1.4 compositionally biased region:Arg/Ser-rich (RS domain) negative regulation of mRNA splicing, via spliceosome	RT		7 3 3 7 7 Count 9	4.9E-2 5.8E-2 5.8E-2 9.0E-2 1.8E-1 P_Value 2.4E-3 1.7E-2	2.5E0 6.8E0 6.8E0 2.2E0 1.8E0 Fold Change 3.4E0 2.5E0	8.4E-1 8.8E-1 4.8E-1 7.3E-1 Benjamini 6.1E-2 2.2E-1	8.1E-1 8.5E-1 8.5E-1 4.4E-1 6.5E-1 FDR 5.9E-2 2.1E-1
Annota	UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO SMART ation Cluster 145 UP_SEQ_FEATURE GOTERM_BP_DIRECT UP_SEQ_FEATURE	kinase activity domain:CRIB region of interest:GTPase-binding region of interest:Autoregulatory region PAK-box/P21-Rho-binding PBD Enrichment Score: 1.4 compositionally biased region:Arg/Ser-rich (RS domain) negative regulation of mRNA splicing, via spliceosome compositionally biased region:Gly-rich (hinge region)	RT		7 3 3 7 7 Count 9 9 4	4.9E-2 5.8E-2 9.0E-2 1.8E-1 P_Value 2.4E-3 1.7E-2 7.0E-2	2.5E0 6.8E0 6.8E0 2.2E0 1.8E0 Fold Change 3.4E0 2.5E0 3.9E0	8.4E-1 8.8E-1 4.8E-1 7.3E-1 Benjamini 6.1E-2 2.2E-1 1.0E0	1 8.1E-1 8.5E-1 8.5E-1 4.4E-1 6.5E-1 5.9E-2 2.1E-1 9.7E-1
Annota	UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO SMART ation Cluster 145 UP_SEQ_FEATURE GOTERM_BP_DIRECT UP_SEQ_FEATURE GOTERM_BP_DIRECT	kinase activity domain:CRIB region of interest:GTPase-binding region of interest:Autoregulatory region PAK-box/P21-Rho-binding PBD Enrichment Score: 1.4 compositionally biased region:Arg/Ser-rich (RS domain) negative regulation of mRNA splicing, via spliceosome compositionally biased region:Gly-rich (hinge region) mRNA splice site selection	RT		7 3 3 7 7 Count 9 9 4 6	4.9E-2 5.8E-2 5.8E-2 9.0E-2 1.8E-1 P_Value 2.4E-3 1.7E-2 7.0E-2 1.5E-1	2.5E0 6.8E0 6.8E0 2.2E0 1.8E0 Fold Change 3.4E0 2.5E0 3.9E0 2.1E0	8.4E-1 8.8E-1 4.8E-1 7.3E-1 Benjamini 6.1E-2 2.2E-1 1.0E0 8.5E-1	8.1E-1 8.5E-1 8.5E-1 4.4E-1 6.5E-1 5.9E-2 2.1E-1 9.7E-1 8.2E-1
Annota	UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO SMART ation Cluster 145 UP_SEQ_FEATURE GOTERM_BP_DIRECT UP_SEQ_FEATURE	kinase activity domain:CRIB region of interest:GTPase-binding region of interest:Autoregulatory region PAK-box/P21-Rho-binding PBD Enrichment Score: 1.4 compositionally biased region:Arg/Ser-rich (RS domain) negative regulation of mRNA splicing, via spliceosome compositionally biased region:Gly-rich (hinge region)	RT		7 3 3 7 7 Count 9 9 4 6 3	4.9E-2 5.8E-2 5.8E-2 9.0E-2 1.8E-1 P_Value 2.4E-3 1.7E-2 7.0E-2 1.5E-1 2.6E-1	2.5E0 6.8E0 6.8E0 2.2E0 1.8E0 Fold Change 3.4E0 2.5E0 3.9E0 2.1E0 3.0E0	8.4E-1 8.8E-1 4.8E-1 7.3E-1 Benjamini 6.1E-2 2.2E-1 1.0E0 8.5E-1 9.9E-1	1 8.1E-1 8.5E-1 8.5E-1 4.4E-1 6.5E-1 5.9E-2 2.1E-1 9.7E-1 8.2E-1
	UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO SMART ation Cluster 145 UP_SEQ_FEATURE GOTERM_BP_DIRECT UP_SEQ_FEATURE GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT ation Cluster 146	kinase activity domain:CRIB region of interest:GTPase-binding region of interest:Autoregulatory region PAK-box/P21-Rho-binding PBD Enrichment Score: 1.4 compositionally biased region:Arg/Ser-rich (RS domain) negative regulation of mRNA splicing, via spliceosome compositionally biased region:Gly-rich (hinge region) mRNA splice site selection RS domain binding Enrichment Score: 1.39	RT R		7 3 3 7 7 Count 9 9 4 6	4.9E-2 5.8E-2 9.0E-2 1.8E-1 P_Value 2.4E-3 1.7E-2 7.0E-2 1.5E-1 2.6E-1 P_Value	2.5E0 6.8E0 6.8E0 2.2E0 1.8E0 Fold Change 3.4E0 2.5E0 3.9E0 2.1E0 3.0E0 Fold Change	8.4E-1 8.8E-1 4.8E-1 7.3E-1 Benjamini 6.1E-2 2.2E-1 1.0E0 8.5E-1 9.9E-1 Benjamini	8.1E-1 8.5E-1 8.5E-1 4.4E-1 6.5E-1 5.9E-2 2.1E-1 9.7E-1 8.2E-1 9.0E-1
	UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO SMART ation Cluster 145 UP_SEQ_FEATURE GOTERM_BP_DIRECT UP_SEQ_FEATURE GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT ation Cluster 146 INTERPRO	kinase activity domain:CRIB region of interest:GTPase-binding region of interest:Autoregulatory region PAK-box/P21-Rho-binding PBD Enrichment Score: 1.4 compositionally biased region:Arg/Ser-rich (RS domain) negative regulation of mRNA splicing, via spliceosome compositionally biased region:Gly-rich (hinge region) mRNA splice site selection RS domain binding	RT		7 3 3 7 7 Count 9 9 4 6 3	4.9E-2 5.8E-2 5.8E-2 9.0E-2 1.8E-1 P_Value 2.4E-3 1.7E-2 7.0E-2 1.5E-1 2.6E-1	2.5E0 6.8E0 6.8E0 2.2E0 1.8E0 Fold Change 3.4E0 2.5E0 3.9E0 2.1E0 3.0E0 Fold Change	8.4E-1 8.8E-1 4.8E-1 7.3E-1 Benjamini 6.1E-2 2.2E-1 1.0E0 8.5E-1 9.9E-1	1 8.1E-1 8.5E-1 8.5E-1 4.4E-1 6.5E-1 5.9E-2 2.1E-1 9.7E-1 8.2E-1 9.0E-1
	UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO SMART ation Cluster 145 UP_SEQ_FEATURE GOTERM_BP_DIRECT UP_SEQ_FEATURE GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT ation Cluster 146	kinase activity domain:CRIB region of interest:GTPase-binding region of interest:Autoregulatory region PAK-box/P21-Rho-binding PBD Enrichment Score: 1.4 compositionally biased region:Arg/Ser-rich (RS domain) negative regulation of mRNA splicing, via spliceosome compositionally biased region:Gly-rich (hinge region) mRNA splice site selection RS domain binding Enrichment Score: 1.39 Leucine-rich repeat-containing protein 8, N-	RT R		7 3 3 7 7 Count 9 9 4 6 3 Count	4.9E-2 5.8E-2 9.0E-2 1.8E-1 P_Value 2.4E-3 1.7E-2 7.0E-2 1.5E-1 2.6E-1 P_Value	2.5E0 6.8E0 6.8E0 2.2E0 1.8E0 Fold Change 3.4E0 2.5E0 3.9E0 2.1E0 3.0E0 Fold Change 6.2E0	8.4E-1 8.8E-1 4.8E-1 7.3E-1 Benjamini 6.1E-2 2.2E-1 1.0E0 8.5E-1 9.9E-1 Benjamini	1 8.1E-1 8.5E-1 8.5E-1 4.4E-1 6.5E-1 5.9E-2 2.1E-1 9.7E-1 8.2E-1 9.0E-1 1 FDR

Annot	tation Cluster 1	Enrichment Score: ?	G	·	Count	P_Value	Fold Change	Benjamir	ni FDF
	GOTERM_BP_DIRECT	anion transmembrane transport	<u>RT</u>	i	5	7.7E-1	9.9E-1	•	9.6l
Annot	tation Cluster 147	Enrichment Score: 1.37	G	178	Count	P_Value	Fold Change	Benjamir	
	GOTERM_BP_DIRECT	GMP metabolic process	<u>RT</u>	ī	10	2.1E-4	3.9E0	6.6E-3	6.3
	GOTERM_MF_DIRECT	ionotropic glutamate receptor binding	<u>RT</u>		11	1.0E-3	3.1E0	1.2E-2	1.1
	GOTERM_MF_DIRECT	guanylate kinase activity	RT		8	1.3E-3	4.0E0	1.5E-2	1.4
_ 	INTERPRO	Guanylate kinase, conserved site	RT	-	9	1.7E-3		2.1E-2	2 2.0
_ _	GOTERM_CC_DIRECT	ionotropic glutamate receptor complex	RT	- -	6		4.8E0	3.5E-2	2 3.1
	INTERPRO								2 4.9
	GOTERM_BP_DIRECT	Guanylate kinase	<u>RT</u>	•	10	4.9E-3		5.3E-2	2 8.8
	UP_SEQ_FEATURE	GDP metabolic process	<u>RT</u>	i	7		3.8E0	9.2E-2	1.2
		domain:Guanylate kinase-like	<u>RT</u>	•	10	5.1E-3	2.8E0	1.3E-1	1
	GOTERM_BP_DIRECT	establishment or maintenance of epithelial cell apical/basal polarity	<u>RT</u>	i	7	1.3E-2	3.2E0	2.0E-1	1.9 1
	INTERPRO	PDZ-associated domain of NMDA receptors	<u>RT</u>	1	4	1.5E-2	6.2E0	1.2E-1	1.1
	INTERPRO	<u>Membrane-associated guanylate kinase</u> (MAGUK), PEST domain, N-terminal	<u>RT</u>	i	4	1.5E-2	6.2E0	1.2E-1	1.1 1
	INTERPRO	Membrane-associated guanylate kinase (MAGUK) scaffold protein	<u>RT</u>	1	4	1.5E-2	6.2E0	1.2E-1	1.1 1
	INTERPRO	Guanylate kinase/L-type calcium channel	<u>RT</u>	1	10	1.7E-2	2.4E0	1.3E-1	1.2 1
	SMART	<u>SM01277</u>	<u>RT</u>	1	4	4.9E-2	4.0E0	2.8E-1	2.4
	PIR_SUPERFAMILY	membrane-associated guanylate kinase (MAGUK) scaffold protein	<u>RT</u>	1	3	7.3E-2	6.0E0	6.0E-1	6.0
7	BIOCARTA	Synaptic Proteins at the Synaptic Junction	<u>RT</u>		10	8.5E-2	1.7E0	2.1E-1	1.6
ے ا	SMART	<u>GuKc</u>	RT	-	10	1.4E-1		6.6E-1	1 5.8
ے ا	INTERPRO			1				8.6E-1	1 7.9
J	GOTERM_BP_DIRECT	<u>L27</u>	<u>RT</u>		5	1.8E-1			1 9.5
J	INTERPRO	receptor localization to synapse	<u>RT</u>	•	4	1.8E-1		1.0E0	9.2
)		<u>Variant SH3</u>	<u>RT</u>	•	13	2.7E-1	1.3E0	1.0E0	1
	UP_SEQ_FEATURE	domain:L27 1	<u>RT</u>	1	3	2.7E-1	2.9E0	1.0E0	9.7
	UP_SEQ_FEATURE	domain:L27 2	<u>RT</u>	i	3	2.7E-1	2.9E0	1.0E0	9.7 1
	GOTERM_BP_DIRECT	receptor clustering	<u>RT</u>	1	5	4.4E-1	1.5E0	1.0E0	9.6 1
	UP_SEQ_FEATURE	domain:PDZ 3	<u>RT</u>	i	6	4.6E-1	1.4E0	1.0E0	9.7 1
	INTERPRO	L27, C-terminal	<u>RT</u>	1	3	5.0E-1	1.9E0	1.0E0	9.2 1
	SMART	<u>L27</u>	<u>RT</u>	i .	4	6.0E-1	1.3E0	1.0E0	8.9
	UP_SEQ_FEATURE	domain:PDZ 1	<u>RT</u>		6	7.6E-1	9.7E-1	1.0E0	9.7
- ገ	UP_SEQ_FEATURE	domain:PDZ 2	RT		6		9.7E-1		1 9.7
ے ا	GOTERM_MF_DIRECT	ligand-gated ion channel activity	RT		4		6.6E-1		1 9.5
	tation Charton 449					!	Fold	1	1
nnot	tation Cluster 148 GOTERM_MF_DIRECT	Enrichment Score: 1.37	G	-	Count	P_Value	Change	•	1.4
J	UP_SEQ_FEATURE	MAP kinase kinase activity	<u>RT</u>	•	8	1.3E-3		1.5E-2	2 9.7
	GOTERM_BP_DIRECT	site:Cleavage; by anthrax lethal factor	<u>RT</u>	i	3	2.2E-1		1.0E0	1
	GOTEKWI_BP_DIKECT	<u>proteolysis in other organism</u>	<u>RT</u>	i	3	2.7E-1	•	1.0E0	9.6 1
nnot	tation Cluster 149	Enrichment Score: 1.35	G	17	Count	P_Value	Fold Change	Benjamir	
	GOTERM_MF_DIRECT	fibroblast growth factor-activated receptor activity	<u>RT</u>	1	5	3.4E-3	6.0E0	3.4E-2	3.1
)	INTERPRO	<u>Tyrosine-protein kinase, fibroblast growth</u> <u>factor receptor</u>	<u>RT</u>	i	4	1.5E-2	6.2E0	1.2E-1	1.1
)	PIR_SUPERFAMILY	fibroblast growth factor receptor	<u>RT</u>	1	4	1.6E-2	6.0E0	2.5E-1	2.5 1
)	GOTERM_BP_DIRECT	positive regulation of phospholipase activity	<u>RT</u>	i	4	1.4E-1	3.0E0	8.3E-1	7.9 1
	GOTERM_MF_DIRECT	fibroblast growth factor binding	<u>RT</u>	1	7	1.7E-1	1.8E0	7.4E-1	6.8
	UP_KEYWORDS	<u>Craniosynostosis</u>	<u>RT</u>	i	5	4.0E-1	1.6E0	1.0E0	8.0
nnot	tation Cluster 150	Enrichment Score: 1.32	G	-	Count	P_Value	Fold		-
	INTERPRO	U box domain	<u>RT</u>		6	1.3E-2	Change	1.2E-1	1.1
)	GOTERM_MF_DIRECT	ubiquitin-ubiquitin ligase activity		<u>.</u>	6		2.8E0	3.1E-1	1 2.8
J		abiquium-ubiquium iigase activity	<u>RT</u>	•					1 9.7
	UP_SEQ_FEATURE	domain:U-box	RT	•	4		3.9E0	1.0E0	1.1

AIIIIOLO	ation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	i FDR
	SMART	<u>Ubox</u>	<u>RT</u>	i	5	1.1E-1	2.5E0	5.3E-1	4.7E
Annota	ation Cluster 151	Enrichment Score: 1.31	G	100	Count	P_Value	Fold Change	Benjamini	i FDR
	INTERPRO	BTB/Kelch-associated	<u>RT</u>	•	19	7.5E-3		7.5E-2	7.0E
	INTERPRO	Kelch-like protein, gigaxonin	<u>RT</u>		14	1.2E-2	2.1E0	1.2E-1	1.18
_ 	GOTERM_CC_DIRECT	Cul3-RING ubiquitin ligase complex	RT		19	1.4E-2	1.8E0	1.1E-1	1 9.5
ے ا	PIR_SUPERFAMILY	kelch-like protein, gigaxonin type	RT		14	1.5E-2		2.5E-1	2 2.5l
ا ا	INTERPRO								1 1.6
	UP_SEQ_FEATURE	Kelch repeat type 1	<u>RT</u>	•	18	2.3E-2		1.7E-1	1 4.8
	UP_KEYWORDS	repeat:Kelch 5	<u>RT</u>	1	17	2.7E-2		4.9E-1	1
	_	<u>Kelch repeat</u>	<u>RT</u>	•	18	2.7E-2	1.7E0	1.2E-1	9.8
	UP_SEQ_FEATURE	repeat:Kelch 4	<u>RT</u>	•	17	4.4E-2	1.7E0	7.8E-1	7.5 1
	UP_SEQ_FEATURE	repeat:Kelch 1	<u>RT</u>	•	17	5.0E-2	1.6E0	8.5E-1	8.2 1
	UP_SEQ_FEATURE	repeat:Kelch 2	<u>RT</u>	•	17	5.0E-2	1.6E0	8.5E-1	8.2 1
	UP_SEQ_FEATURE	repeat:Kelch 3	<u>RT</u>	•	17	5.0E-2	1.6E0	8.5E-1	8.2 1
	UP_SEQ_FEATURE	repeat:Kelch 6	<u>RT</u>	•	13	7.1E-2	1.7E0	1.0E0	9.7 1
	UP_SEQ_FEATURE	domain:BACK	<u>RT</u>	•	8	1.4E-1	1.8E0	1.0E0	9.7
	INTERPRO	Galactose oxidase, beta-propeller	<u>RT</u>		8	1.8E-1	1.7E0	8.5E-1	7.8
ے ا	INTERPRO	Kelch-type beta propeller	RT		12	2.3E-1		1.0E0	1 9.2
	SMART			-					1 8.5
	SMART	<u>Kelch</u>	<u>RT</u>	•	18	2.5E-1		9.6E-1	1 8.9
		<u>SM00875</u>	<u>RT</u>	-	18	3.0E-1	Fold	1.0E0	1
nnota	ation Cluster 152	Enrichment Score: 1.28	G		Count	P_Value	Change	Benjamini	
	INTERPRO	MOZ/SAS-like protein	<u>RT</u>	•	5	2.9E-3	6.2E0	3.4E-2	3.1
	UP_SEQ_FEATURE	zinc finger region:C2HC-type	<u>RT</u>	•	5	2.0E-2	4.3E0	3.9E-1	3.7 1
	GOTERM_BP_DIRECT	histone acetylation	<u>RT</u>	•	12	2.0E-2	2.1E0	2.5E-1	2.4 1
	GOTERM_MF_DIRECT	histone acetyltransferase activity	<u>RT</u>	•	15	2.2E-2	1.9E0	1.6E-1	1.4 1
	GOTERM_MF_DIRECT	acetyltransferase activity	<u>RT</u>	1	6	5.2E-2	2.8E0	3.1E-1	2.8 1
	INTERPRO	Acyl-CoA N-acyltransferase	<u>RT</u>	1	7	7.7E-1	9.4E-1	1.0E0	9.2 1
	UP_KEYWORDS	<u>Acyltransferase</u>	<u>RT</u>	ā.	14	1.0E0	5.6E-1	1.0E0	1.0
nnota	ation Cluster 153	Enrichment Score: 1.28	G	- 1	Count	P_Value	Fold Change	Benjamini	i FDI
	BBID	26.cyclin-CDK complexes	<u>RT</u>	•	12	6.0E-3	2.1E0	3.3E-1	3.3 1
	GOTERM_MF_DIRECT	cyclin-dependent protein serine/threonine kinase inhibitor activity	<u>RT</u>	i	5	9.7E-2	2.7E0	4.8E-1	4.4 1
	GOTERM_BP_DIRECT	negative regulation of phosphorylation	<u>RT</u>	4	7	1.1E-1	2.1E0	7.4E-1	7.1 1
	BBID	1.RBphosphoE2F	<u>RT</u>		9	1.2E-1	1.7E0	9.9E-1	9.9 1
nnota	ation Cluster 154	Enrichment Score: 1.25	G	170	Count	P_Value	Fold Change	Benjamini	
<u> </u>	GOTERM_MF_DIRECT	galanin receptor activity	RT	7	4	1.6E-2	Change	1.2E-1	1.1
- ገ	INTERPRO	Galanin receptor family	RT		3	7.0E-2		3.9E-1	1 3.6
ے ا	GOTERM_MF_DIRECT			_					1 6.0
		peptide hormone binding	RT	i	8	1.5E-1		6.7E-1	1
nnota	ation Cluster 155 OMIM_DISEASE	Enrichment Score: 1.25 Schimmelpenning-Feuerstein-Mims	G	-		•	•	Benjamini	
	_	syndrome, somatic mosaic	<u>RT</u>	i	3	4.0E-2	8.3E0	1.0E0	1.0
	UP_SEQ_FEATURE	region of interest:Hypervariable region	<u>RT</u>	i	3	5.8E-2	6.8E0	8.8E-1	8.5 1
	BBID	65.Integrin affinity modulation	<u>RT</u>	i	5	7.6E-2		9.9E-1	9.9 1
nnota	ation Cluster 156	Enrichment Score: 1.25	G	. ■	Count	P_Value	Fold Change	Benjamini	i FDI
	GOTERM_BP_DIRECT	histone H3-K27 methylation	<u>RT</u>	i	4	1.7E-2	5.9E0	2.2E-1	2.1 1
	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K27 specific)	<u>RT</u>	i	3	7.5E-2	6.0E0	3.9E-1	3.6 1
	GOTERM_MF_DIRECT	<u>protein-lysine N-methyltransferase activity</u>	<u>RT</u>	i	6	1.4E-1	2.1E0	6.3E-1	5.7 1
	ation Cluster 157	Enrichment Score: 1.25	G	1	Count	P_Value	Fold Change	Benjamini	
nnota	ation Gluster 137						- 2116111919		
nnota	INTERPRO	Heat shock factor (HSF)-type, DNA-binding	RT	Ŧ.	5	2.7E-2		2.0E-1	1.9 1

Annota	ation Cluster 1	Enrichment Score: ?	G	· Control of the cont	Count	P_Value	Fold Change	Benjamini	i FDR
	UP_SEQ_FEATURE	region of interest:Hydrophobic repeat HR-C	<u>RT</u>	i	3	5.8E-2	· · ·	8.8E-1	8.5E
	SMART	<u>HSF</u>	<u>RT</u>	i .	5	1.1E-1	2.5E0	5.3E-1	4.7E
Annota	ation Cluster 158	Enrichment Score: 1.22	G	170	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	zinc finger region:GATA-type 1	<u>RT</u>	i	6	3.6E-4	6.8E0	1.1E-2	1.1E 2
	UP_SEQ_FEATURE	zinc finger region:GATA-type 2	<u>RT</u>	i .	6	3.6E-4	6.8E0	1.1E-2	1.1E 2
	INTERPRO	Zinc finger, GATA-type	<u>RT</u>	i .	7	2.4E-2	2.9E0	1.8E-1	1.6E
	GOTERM_BP_DIRECT	anatomical structure formation involved in morphogenesis	<u>RT</u>	i .	6	2.6E-2	3.2E0	3.0E-1	2.9E
	GOTERM_MF_DIRECT	enhancer sequence-specific DNA binding	<u>RT</u>	1	8	3.8E-2	2.4E0	2.4E-1	2.1E
	SMART	ZnF GATA	<u>RT</u>	1	7	5.2E-2	2.4E0	2.9E-1	2.5E
	INTERPRO	GATA-type transcription activator, N-terminal	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E
	GOTERM_BP_DIRECT	intestinal epithelial cell differentiation	<u>RT</u>	i	4	9.9E-2	3.4E0	7.0E-1	6.7E
	GOTERM_BP_DIRECT	tissue development	<u>RT</u>	i	4	4.8E-1	1.6E0	1.0E0	9.6E
	INTERPRO	Zinc finger, NHR/GATA-type	<u>RT</u>	i de la companya de	10	6.1E-1	1.1E0	1.0E0	9.2E
	GOTERM_BP_DIRECT	cell fate commitment	<u>RT</u>	1	8	6.8E-1	1.0E0	1.0E0	9.6E
	GOTERM_BP_DIRECT	cell development	RT	1	7	6.9E-1	1.0E0	1.0E0	9.6E
	GOTERM_BP_DIRECT	cellular response to BMP stimulus	RT		4	9.0E-1	7.9E-1	1.0E0	1 9.6E
Annota	ation Cluster 159	Enrichment Score: 1.22	G	- 	Count	P_Value	Fold		1 FDR
	GOTERM_MF_DIRECT	nucleosomal DNA binding	<u>RT</u>		17		Change	2.5E-2	2.3E
	INTERPRO	Histone H3	RT		6	1.8E-1		8.6E-1	2 8.0E
_ 	SMART	H3	RT		6	5.2E-1		1.0E0	1 8.9E
Annote	ation Cluster 160	Enrichment Score: 1.22	G	•	Count	P_Value	Fold	Benjamini	1 EDF
	UP_KEYWORDS	Innate immunity	RT	-	55	4.3E-3	Change	2.2E-2	1.8
_	GOTERM_BP_DIRECT	innate immune response		_	83	1.2E-1		8.2E-1	2 7.9l
_	UP_KEYWORDS		<u>RT</u>	_					1 8.0
Aunot	ation Charten 464	Immunity	<u>RT</u>	-	76	4.1E-1	Fold	1.0E0	1
Annota	ation Cluster 161 UP_SEQ_FEATURE	Enrichment Score: 1.21	G	i		P_Value	Change	Benjamini 3.9E-1	3.7
	UP_SEQ_FEATURE	domain:WW 3	<u>RT</u>	_	5	2.0E-2			1 4.4I
	INTERPRO	domain:WW 4	<u>RT</u>		4	2.5E-2		4.6E-1	1 2.5I
	UP_SEQ_FEATURE	WW domain	<u>RT</u>	•	15	3.8E-2		2.7E-1	1 8.5
	UP_SEQ_FEATURE	domain:WW 1	<u>RT</u>	i	9	5.3E-2		8.8E-1	1 8.5
	UP_SEQ_FEATURE	domain:WW 2	<u>RT</u>	•	9	5.3E-2		8.8E-1	9.7
		domain:WW	<u>RT</u>	i	6	2.1E-1	1.9E0	1.0E0	1
	SMART	<u>ww</u>	<u>RT</u>	i	15	3.2E-1		1.0E0	8.9
Annota	ation Cluster 162 INTERPRO	Enrichment Score: 1.2	G	■ The state of th	Count	P_Value	Fold Change	Benjamini	
		<u>2'-5'-oligoadenylate synthetase 1, domain</u>	<u>RT</u>	and 💳 and a state of the state	4	1.5E-2	6.2E0	1.2E-1	1.1
		2/C-terminal	<u>KT</u>	•				1.2E-1	1.1 1
	INTERPRO		RT	i	4	1.5E-2	6.2E0		
	INTERPRO	2/C-terminal	<u>RT</u>	-		1.5E-2 1.5E-2		1.2E-1	1
	INTERPRO INTERPRO GOTERM_MF_DIRECT	2'-5'-oligoadenylate synthase	<u>RT</u>	•	4	1.5E-2			1 1.1 1
	INTERPRO INTERPRO GOTERM_MF_DIRECT INTERPRO	2/C-terminal 2'-5'-oligoadenylate synthase 2-5-oligoadenylate synthetase, conserved site	RT RT	i i	4	1.5E-2	6.2E0 6.0E0		1 1.1 1 2.1 1
	INTERPRO INTERPRO GOTERM_MF_DIRECT	2/C-terminal 2'-5'-oligoadenylate synthase 2-5-oligoadenylate synthetase, conserved site 2'-5'-oligoadenylate synthetase activity	RT RT RT	i i	4 4 4	1.5E-2 1.6E-2	6.2E0 6.0E0 5.0E0	1.2E-1	1 1.11 1 2.11 1
	INTERPRO INTERPRO GOTERM_MF_DIRECT INTERPRO	2'-5'-oligoadenylate synthase 2-5-oligoadenylate synthetase, conserved site 2'-5'-oligoadenylate synthetase activity 2-5-oligoadenylate synthetase, N-terminal	RT RT RT RT	i i i	4 4 4	1.5E-2 1.6E-2 3.2E-2	6.2E0 6.0E0 5.0E0 2.5E0	1.2E-1 2.3E-1	1 1.11 1 2.11 1 9.01
	INTERPRO INTERPRO GOTERM_MF_DIRECT INTERPRO INTERPRO	2'-5'-oligoadenylate synthase 2-5-oligoadenylate synthetase, conserved site 2'-5'-oligoadenylate synthetase activity 2-5-oligoadenylate synthetase, N-terminal Nucleotidyl transferase domain	RT RT RT RT RT	i i i	4 4 4 4	1.5E-2 1.6E-2 3.2E-2 2.1E-1 6.8E-1	6.2E0 6.0E0 5.0E0 2.5E0	1.2E-1 2.3E-1 9.7E-1 1.0E0	1 1.11 1 2.11 1 9.01 1 9.11
Annota	INTERPRO INTERPRO GOTERM_MF_DIRECT INTERPRO INTERPRO GOTERM_MF_DIRECT	2/C-terminal 2'-5'-oligoadenylate synthase 2-5-oligoadenylate synthetase, conserved site 2'-5'-oligoadenylate synthetase activity 2-5-oligoadenylate synthetase, N-terminal Nucleotidyl transferase domain nucleotidyltransferase activity	RT RT RT RT RT RT	i i i i	4 4 4 4 5 11	1.5E-2 1.6E-2 3.2E-2 2.1E-1 6.8E-1	6.2E0 6.0E0 5.0E0 2.5E0 1.1E0 6.8E-1	1.2E-1 2.3E-1 9.7E-1 1.0E0 1.0E0	1 1.11 1 2.11 1 9.01 1 9.71 1
Annota	INTERPRO INTERPRO GOTERM_MF_DIRECT INTERPRO INTERPRO GOTERM_MF_DIRECT GOTERM_MF_DIRECT	2/C-terminal 2'-5'-oligoadenylate synthase 2-5-oligoadenylate synthetase, conserved site 2'-5'-oligoadenylate synthetase activity 2-5-oligoadenylate synthetase, N-terminal Nucleotidyl transferase domain nucleotidyltransferase activity transferase activity	RT RT RT RT RT RT RT RT	i i i i	4 4 4 4 5 11	1.5E-2 1.6E-2 3.2E-2 2.1E-1 6.8E-1 9.7E-1	6.2E0 6.0E0 5.0E0 2.5E0 1.1E0 6.8E-1 Fold Change	1.2E-1 2.3E-1 9.7E-1 1.0E0 1.0E0	1 1.18 1 2.18 1 9.08 1 9.18 1 9.78
Annota	INTERPRO INTERPRO GOTERM_MF_DIRECT INTERPRO INTERPRO GOTERM_MF_DIRECT GOTERM_MF_DIRECT ation Cluster 163	2/C-terminal 2'-5'-oligoadenylate synthase 2-5-oligoadenylate synthetase, conserved site 2'-5'-oligoadenylate synthetase activity 2-5-oligoadenylate synthetase, N-terminal Nucleotidyl transferase domain nucleotidyltransferase activity transferase activity Enrichment Score: 1.2	RT RT RT RT RT RT RT		4 4 4 4 5 11 Count	1.5E-2 1.6E-2 3.2E-2 2.1E-1 6.8E-1 9.7E-1 P_Value	6.2E0 6.0E0 5.0E0 2.5E0 1.1E0 6.8E-1 Fold Change 6.8E0	1.2E-1 2.3E-1 9.7E-1 1.0E0 1.0E0 Benjamini	1 1.18 1 2.18 1 9.08 1 9.18 1 9.78 1
Annota	INTERPRO INTERPRO GOTERM_MF_DIRECT INTERPRO INTERPRO GOTERM_MF_DIRECT GOTERM_MF_DIRECT ation Cluster 163 UP_SEQ_FEATURE	2/C-terminal 2'-5'-oligoadenylate synthase 2-5-oligoadenylate synthetase, conserved site 2'-5'-oligoadenylate synthetase activity 2-5-oligoadenylate synthetase, N-terminal Nucleotidyl transferase domain nucleotidyltransferase activity transferase activity Enrichment Score: 1.2 region of interest:Rho-like	RT		4 4 4 4 5 11 Count	1.5E-2 1.6E-2 3.2E-2 2.1E-1 6.8E-1 9.7E-1 P_Value 5.8E-2	6.2E0 6.0E0 5.0E0 2.5E0 1.1E0 6.8E-1 Fold Change 6.8E0 3.1E0	1.2E-1 2.3E-1 9.7E-1 1.0E0 1.0E0 Benjamini 8.8E-1	1.1E 1 2.1E 1 9.0E 1 9.1E 1 9.7E 1 8.5E 1

Anno	tation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	regulation of Golgi inheritance	<u>RT</u>	i	4	1.7E-2		2.2E-1	2.1E-
	GOTERM_BP_DIRECT	face development	<u>RT</u>	i	8	2.2E-2	2.6E0	2.7E-1	2.6E-
	BIOCARTA	Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway	<u>RT</u>	i e	9	2.7E-2	2.2E0	8.2E-2	6.2E- 2
	BIOCARTA	Roles of ?-arrestin-dependent Recruitment of	<u>RT</u>		12	2.7E-2	1.9E0	8.3E-2	6.2E-
	GOTERM_BP_DIRECT	Src Kinases in GPCR Signaling regulation of stress-activated MAPK cascade	RT		5	3.2E-2		3.5E-1	2 3.4E-
	GOTERM_BP_DIRECT	regulation of early endosome to late	RT		5	3.2E-2		3.5E-1	1 3.4E-
	BIOCARTA	endosome transport Pelp1 Modulation of Estrogen Receptor	RT		6	3.8E-2		1.0E-1	1 7.9E-
	GOTERM_BP_DIRECT	Activity Bergmann glial cell differentiation	RT		5	5.0E-2		4.7E-1	2 4.5E-
	GOTERM_BP_DIRECT								1 5.3E-
	BIOCARTA	trachea formation	<u>RT</u>		4	6.4E-2		5.5E-1	1 1.6E-
	BIOCARTA	Sprouty regulation of tyrosine kinase signals	<u>RT</u>		10	8.5E-2		2.1E-1	1 2.4E-
	GOTERM_BP_DIRECT	Regulation of Splicing through Sam68	<u>RT</u>	1	5	1.5E-1		3.2E-1	1 9.6E-
	BIOCARTA	ERK1 and ERK2 cascade	<u>RT</u>	1	7	2.1E-1	1.7E0	1.0E0	1
		Role of ?-arrestins in the activation and targeting of MAP kinases	<u>RT</u>	i	8	2.2E-1	1.6E0	4.4E-1	3.3E- 1
	GOTERM_BP_DIRECT	thyroid gland development	<u>RT</u>	i	7	2.4E-1	1.7E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	lung morphogenesis	<u>RT</u>	i	4	3.8E-1	•	1.0E0	9.6E- 1
Anno	tation Cluster 165	Enrichment Score: 1.18	G	17	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	<u>Tyrosine-protein kinase, receptor class III,</u> <u>conserved site</u>	<u>RT</u>	i	8	1.9E-5	6.2E0	3.5E-4	3.3E- 4
	GOTERM_BP_DIRECT	positive regulation of phospholipase C activity	<u>RT</u>	i .	8	1.0E-4	5.3E0	3.6E-3	3.4E- 3
	GOTERM_MF_DIRECT	vascular endothelial growth factor-activated receptor activity	<u>RT</u>	i	5	1.8E-2	4.3E0	1.3E-1	1.2E- 1
	INTERPRO	Tyrosine-protein kinase, CSF-1/PDGF receptor	<u>RT</u>	i	4	3.2E-2	5.0E0	2.3E-1	2.1E- 1
	PIR_SUPERFAMILY	tyrosine-protein kinase, CSF-1/PDGF receptor type	<u>RT</u>	i .	4	3.5E-2	4.8E0	4.6E-1	4.6E-
	GOTERM_BP_DIRECT	vascular endothelial growth factor signaling pathway	<u>RT</u>	i	4	6.4E-2	3.9E0	5.5E-1	5.3E-
	GOTERM_MF_DIRECT	vascular endothelial growth factor binding	<u>RT</u>	i	3	2.0E-1	3.6E0	8.0E-1	7.2E-
	UP_SEQ_FEATURE	domain:Ig-like C2-type 7	<u>RT</u>	1	5	4.1E-1	1.5E0	1.0E0	9.7E-
	GOTERM_MF_DIRECT	growth factor binding	<u>RT</u>		6	4.8E-1	1.3E0	1.0E0	9.1E-
	UP_SEQ_FEATURE	domain:Ig-like C2-type 5	RT		9	5.7E-1	1.1E0	1.0E0	9.7E-
	UP_SEQ_FEATURE	domain:Ig-like C2-type 3	RT		17		9.0E-1		1 9.7E-
	UP_SEQ_FEATURE	domain:Ig-like C2-type 6	RT		5		9.2E-1		1 9.7E-
	UP_SEQ_FEATURE	domain:Ig-like C2-type 4	RT	_	9		8.1E-1		1 9.7E-
	INTERPRO								1 9.3E-
	tation Olerandon	<u>Immunoglobulin</u>	<u>RT</u>		10		7.6E-1 Fold		1
Anno	tation Cluster 166 BIOCARTA	Enrichment Score: 1.18	G	- The state of the	Count	P_Value	Change	Benjamini	5.6E-
	BIOCARTA	The IGF-1 Receptor and Longevity Role of nicotinic acetylcholine receptors in the	<u>RT</u>	•	10	2.3E-2		7.5E-2	2 1.8E-
	BIOCARTA	regulation of apoptosis	<u>RT</u>		9	1.0E-1		2.4E-1	1 2.1E-
		Phospholipase C Signaling Pathway	<u>RT</u>	i	6	1.2E-1	Fold	2.8E-1	1
Anno	tation Cluster 167 UP_SEQ_FEATURE	Enrichment Score: 1.17	G	-	Count	P_Value	Change	Benjamini	FDR 5.1E-
	INTERPRO	zinc finger region:ZZ-type	<u>RT</u>	1	7	2.9E-2	2.8E0	5.3E-1	1
		Zinc finger, ZZ-type	<u>RT</u>	i	7	5.7E-2	2.4E0	3.8E-1	3.5E- 1
	SMART	ZnF ZZ	<u>RT</u>	i	7	1.8E-1	Fold	7.3E-1	6.5E- 1
Anno	tation Cluster 168	Enrichment Score: 1.17	G	5	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	HR1 rho-binding repeat	<u>RT</u>	i	5	2.7E-2	3.9E0	2.0E-1	1.9E- 1
	UP_SEQ_FEATURE	repeat:REM 1	<u>RT</u>	i	3	5.8E-2	6.8E0	8.8E-1	8.5E- 1
	UP_SEQ_FEATURE	repeat:REM 2	<u>RT</u>	i .	3	5.8E-2	6.8E0	8.8E-1	8.5E- 1
	UP_SEQ_FEATURE	repeat:REM 3	<u>RT</u>	1	3	5.8E-2	6.8E0	8.8E-1	8.5E- 1
	SMART	Hr1	<u>RT</u>	i	5	6.8E-2	2.9E0	3.6E-1	3.2E- 1
	GOTERM_BP_DIRECT	epithelial cell migration	<u>RT</u>	i	3	2.7E-1	3.0E0	1.0E0	9.6E- 1
Anno	tation Cluster 169	Enrichment Score: 1.17	G	178	Count	P_Value	Fold Change	Benjamini	FDR
							· - - 0-	: _	

Annot	ation Cluster 1	Enrichment Score: ?	G	17	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_BP_DIRECT	peptidyl-lysine monomethylation	<u>RT</u>	i	5	3.2E-2	3.7E0	3.5E-1	3.4E 1
	GOTERM_BP_DIRECT	peptidyl-lysine dimethylation	<u>RT</u>	1	4	3.7E-2	4.7E0	3.8E-1	3.7E
	UP_SEQ_FEATURE	region of interest:S-adenosyl-L-methionine	<u>RT</u>		9	1.3E-1	1.8E0	1.0E0	9.7E
	GOTERM_MF_DIRECT	binding protein-lysine N-methyltransferase activity	RT		6	1.4E-1	2.1E0	6.3E-1	5.7E
Annot	ation Cluster 170	Enrichment Score: 1.16	G	-	Count	P_Value	Fold	Barriania	1 i FDR
	INTERPRO	Ubiquitin-associated/translation elongation	RT	i	16	2.7E-3	Citalige	3.3E-2	3.0E
	UP_SEQ_FEATURE	factor EF1B, N-terminal, eukaryote		- -					2 2.2E
	INTERPRO	domain:UBA	<u>RT</u>		13	1.0E-2		2.3E-1	1 1.1E
		<u>Heat shock chaperonin-binding</u>	<u>RT</u>	•	6	1.3E-2	3.7E0	1.2E-1	1
	GOTERM_MF_DIRECT	<u>polyubiquitin binding</u>	<u>RT</u>	•	9	2.8E-2	2.3E0	1.9E-1	1.7E 1
	GOTERM_BP_DIRECT	regulation of proteasomal ubiquitin- dependent protein catabolic process	<u>RT</u>	1	6	3.8E-2	3.0E0	3.9E-1	3.7E 1
	INTERPRO	<u>Ubiquilin</u>	<u>RT</u>	i	4	5.7E-2	4.1E0	3.8E-1	3.5E 1
	SMART	STI1	<u>RT</u>	i	6	7.5E-2	2.4E0	3.9E-1	3.4E 1
	UP_SEQ_FEATURE	domain:UBA 1	<u>RT</u>	1	3	2.7E-1	2.9E0	1.0E0	9.7E
	UP_SEQ_FEATURE	domain:UBA 2	<u>RT</u>	i	3	2.7E-1	2.9E0	1.0E0	9.7E
	SMART	<u>UBA</u>	<u>RT</u>		10	2.8E-1	1.4E0	1.0E0	8.9E
	INTERPRO	UBA-like	RT		12	3.5E-1		1.0E0	1 9.2E
_ 	GOTERM_CC_DIRECT			- -	6				1 9.8E
A 10.00		autophagosome	<u>RT</u>	1		1	6.0E-1	Baniamin	1
Annot	ation Cluster 171 BIOCARTA	Enrichment Score: 1.16 NFkB activation by Nontypeable Hemophilus	G		Count	P_Value	Change	•	2.8E
		influenzae	<u>RT</u>	•	17	4.7E-4	2.2E0	3.8E-3	3
	BIOCARTA	The 4-1BB-dependent immune response	<u>RT</u>	•	13	2.5E-3	2.3E0	1.3E-2	9.9E 3
	BIOCARTA	Signal transduction through IL1R	<u>RT</u>	•	18	1.5E-2	1.7E0	5.4E-2	4.0E 2
	GOTERM_CC_DIRECT	I-kappaB/NF-kappaB complex	<u>RT</u>	1	4	3.0E-2	5.1E0	2.0E-1	1.8E 1
	BIOCARTA	Activation of PKC through G protein coupled receptor	<u>RT</u>	i	6	3.8E-2	2.7E0	1.0E-1	7.9E 2
	BIOCARTA	Acetylation and Deacetylation of RelA in The Nucleus	<u>RT</u>	•	10	3.8E-2	1.9E0	1.0E-1	7.9E 2
	BIOCARTA	NF-kB Signaling Pathway	<u>RT</u>	•	12	8.2E-2	1.6E0	2.1E-1	1.5E
	BBID	77.IkBa Kinase JNK MEKK1	RT		6	8.2E-2	2.2E0	9.9E-1	9.9E
_ 	BIOCARTA	CD40L Signaling Pathway	RT		8	1.7E-1	1 7F0	3.6E-1	1 2.7E
_ _	BIOCARTA	Double Stranded RNA Induced Gene		-	6	1.9E-1		3.8E-1	1 2.8E
	BIOCARTA	Expression	<u>RT</u>						1 5.1E
	BBID	TNF/Stress Related Signaling 90.IB and-cat-Arm processing of Ci	RT RT	1	10 4	4.1E-1 4.3E-1		6.8E-1 1.0E0	1 1.0E
	BIOCARTA	Erythropoietin mediated neuroprotection	RT		6	4.8E-1		8.0E-1	6.0E
_ 	BIOCARTA	through NF-kB TNFR2 Signaling Pathway	RT		7	5.4E-1	1 2F0	8.6E-1	1 6.4E
	BIOCARTA	TACI and BCMA stimulation of B cell immune		-					1 6.5E
		responses.	RT		6	1	1.2E0	8.7E-1	1
Annot	ation Cluster 172 INTERPRO	Enrichment Score: 1.16	G	-	Count	P_Value	Change		1.1E
		UBA/THIF-type NAD/FAD binding fold	<u>RT</u>	•	6	1.3E-2		1.2E-1	1
	GOTERM_MF_DIRECT	ubiquitin activating enzyme activity	<u>RT</u>	•	4	3.6E-2	4.8E0	2.3E-1	2.0E 1
	INTERPRO	<u>Ubiquitin-activating enzyme, E1</u>	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E 1
	INTERPRO	<u>Ubiquitin-activating enzyme e1, C-terminal</u>	<u>RT</u>	1	3	7.0E-2	6.2E0	3.9E-1	3.6E 1
	GOTERM_MF_DIRECT	small protein activating enzyme activity	<u>RT</u>	1	4	9.7E-2	3.4E0	4.8E-1	4.4E 1
	INTERPRO	<u>Ubiquitin/SUMO-activating enzyme E1</u>	<u>RT</u>	1	3	1.2E-1	4.6E0	6.2E-1	5.8E 1
	INTERPRO	<u>Ubiquitin-activating enzyme</u>	<u>RT</u>	i	3	1.2E-1	4.6E0	6.2E-1	5.8E
	SMART	<u>SM00985</u>	<u>RT</u>	1	3	1.5E-1	4.0E0	6.6E-1	5.8E
Annot	ation Cluster 173	Enrichment Score: 1.13	G	· TS	Count	P_Value	Fold	Roniamin	1 i FDR
	GOTERM_BP_DIRECT	positive regulation of glucose import in		i	6		Change	4.9E-1	4.7E
	UP_SEQ_FEATURE	response to insulin stimulus	<u>RT</u>	_					1 9.7E
\neg		domain:SH2 1	<u>RT</u>	•	5	8.6E-2	2.8E0	1.0E0	1
	UP_SEQ_FEATURE	domain:SH2 2	<u>RT</u>	4	5		2.8E0	1.0E0	9.7E

Annot	tation Cluster 1	Enrichment Score: ?	G	·	Count	P. Volud	Fold	Benjamini	; EDB
Alliot	UP_SEQ_FEATURE	domain:IQ 5	RT RT	_	6	P_Value 1.5E-2	Change	2.9E-1	2.8E-
	INTERPRO								1 4.4E-
	UP_SEQ_FEATURE	<u>Dilute</u>	<u>RT</u>		4	8.8E-2		4.7E-1	1 9.7E-
	SMART	domain:Dilute	<u>RT</u>		4	1.0E-1		1.0E0	1 8.2E-
		SM01132	<u>RT</u>	1	4	2.4E-1	Fold	9.2E-1	1
Annot	tation Cluster 175 UP_SEQ_FEATURE	Enrichment Score: 1.12	G	-		P_Value	Change	•	i FDR 7.5E-
	INTERPRO	domain:BRO1	<u>RT</u>		4	4.5E-2	4.5E0	7.8E-1	1 3.5E-
	SMART	BRO1 domain	<u>RT</u>	•	4	5.7E-2	4.1E0	3.8E-1	1
	SWART	<u>SM01041</u>	<u>RT</u>	i	4	1.7E-1	Fold	6.8E-1	6.0E- 1
Annot	tation Cluster 176	Enrichment Score: 1.11	G	No.	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	domain:SWIRM	<u>RT</u>	i	4	4.5E-2	4.5E0	7.8E-1	7.5E- 1
	INTERPRO	SANT domain	<u>RT</u>	i	9	4.7E-2	2.1E0	3.2E-1	3.0E- 1
	INTERPRO	SWIRM domain	<u>RT</u>	i	4	5.7E-2	4.1E0	3.8E-1	3.5E- 1
	UP_SEQ_FEATURE	domain:SANT	<u>RT</u>	i	5	3.0E-1	,	1.0E0	9.7E- 1
Annot	tation Cluster 177	Enrichment Score: 1.11	G	10	Count	P_Value	Fold Change	Benjamini	
	GOTERM_BP_DIRECT	dendritic spine development	<u>RT</u>	i	7	1.3E-2	3.2E0	2.0E-1	1.9E- 1
	GOTERM_MF_DIRECT	axon guidance receptor activity	<u>RT</u>	i	4	9.7E-2	3.4E0	4.8E-1	4.4E- 1
	GOTERM_BP_DIRECT	central nervous system projection neuron axonogenesis	<u>RT</u>	i	4	1.4E-1	3.0E0	8.3E-1	7.9E- 1
	GOTERM_BP_DIRECT	retinal ganglion cell axon guidance	<u>RT</u>	i .	6	2.1E-1	1.9E0	1.0E0	9.6E- 1
Annot	tation Cluster 178	Enrichment Score: 1.1	G	™	Count	P_Value	Fold Change	Benjamini	i FDR
	UP_SEQ_FEATURE	domain:C2	<u>RT</u>	i .	22	6.6E-3	1.8E0	1.5E-1	1.5E- 1
	INTERPRO	C2 calcium-dependent membrane targeting	<u>RT</u>	i .	35	7.5E-2	1.3E0	4.1E-1	3.8E- 1
	SMART	<u>C2</u>	<u>RT</u>	i	19	1.0E0	6.0E-1		1.0E0
Annot	tation Cluster 179 UP_SEQ_FEATURE	Enrichment Score: 1.1	G	-	Count	P_Value	Change	·	i FDR 8.5E-
	INTERPRO	zinc finger region:TFIIB-type	<u>RT</u>	•	3	5.8E-2	6.8E0	8.8E-1	1
	INTERPRO	<u>Transcription factor TFIIB</u>	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E- 1
	INTERFRO	Zinc finger, TFIIB-type	<u>RT</u>	i	3	1.2E-1	4.6E0 Fold	6.2E-1	5.8E- 1
Annot	tation Cluster 180 UP_SEQ_FEATURE	Enrichment Score: 1.09	G	-	Count	P_Value	Change	•	i FDR 8.5E-
	INTERPRO	domain:Nop	<u>RT</u>	•	3	5.8E-2	6.8E0	8.8E-1	1
		Nop domain	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E- 1
	INTERPRO	NOSIC	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E-
	SMART	<u>SM00931</u>	<u>RT</u>	i	3	1.5E-1		6.6E-1	5.8E- 1
Annot	tation Cluster 181	Enrichment Score: 1.07	G	5	Count	P_Value	Fold Change	Benjamini	
	GOTERM_MF_DIRECT	calmodulin-dependent protein kinase activity	<u>RT</u>	•	9	2.1E-2	2.4E0	1.5E-1	1.4E- 1
	UP_SEQ_FEATURE	region of interest:Autoinhibitory domain	<u>RT</u>	i	4	4.5E-2	4.5E0	7.8E-1	7.5E- 1
	BIOCARTA	<u>Ca++/ Calmodulin-dependent Protein Kinase</u> <u>Activation</u>	<u>RT</u>	1	5	6.4E-1		9.7E-1	7.3E- 1
Annot	tation Cluster 182	Enrichment Score: 1.06	G	M .	Count	P_Value	Fold Change	Benjamini	
	GOTERM_CC_DIRECT	actomyosin	<u>RT</u>	i	7	5.9E-3	3.7E0	5.3E-2	4.7E- 2
	GOTERM_CC_DIRECT	myosin II filament	<u>RT</u>	i	3	6.6E-2	6.4E0	3.5E-1	3.1E- 1
	GOTERM_CC_DIRECT	myosin II complex	<u>RT</u>	i .	4	8.3E-2	3.6E0	4.1E-1	3.6E- 1
	GOTERM_BP_DIRECT	actomyosin structure organization	<u>RT</u>	1	7	3.0E-1	1.5E0	1.0E0	9.6E- 1
	UP_KEYWORDS	Cell shape	<u>RT</u>	i	5			1.0E0	8.0E- 1
Annot	tation Cluster 183	Enrichment Score: 1.06	G	10	Count	P_Value	Fold Change	Benjamini	i FDR
	GOTERM_BP_DIRECT	sensory perception	<u>RT</u>	i	6	5.4E-2	2.7E0	4.9E-1	4.7E- 1
	UP_KEYWORDS	Opioid peptide	<u>RT</u>	i	3	5.7E-2	6.9E0	2.4E-1	1.9E- 1
	INTERPRO	Opioid neuropeptide precursor	<u>RT</u>	i .	3	7.0E-2	6.2E0	3.9E-1	3.6E- 1
	GOTERM_MF_DIRECT	neuropeptide hormone activity	<u>RT</u>	i e	9	1.2E-1	1.8E0	5.7E-1	5.2E-
		Treat op op class Treatments a delitite)	101						
	GOTERM_MF_DIRECT	opioid peptide activity	RT		3	1.3E-1		6.0E-1	5.5E- 1

nota	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamir	ni F
	GOTERM_MF_DIRECT	opioid receptor binding	<u>RT</u>	1	3	1.3E-1	•	6.0E-1	5 1
ota	ation Cluster 184	Enrichment Score: 1.06	G	178	Count	P_Value	Fold Change	Benjamir	
	GOTERM_CC_DIRECT	proteasome core complex, alpha-subunit complex	<u>RT</u>	i	5	2.5E-2	4.0E0	1.8E-1	1
	INTERPRO	Proteasome, alpha-subunit, N-terminal	<u>RT</u>	1	5	2.7E-2	3.9E0	2.0E-1	1
	INTERPRO	domain Proteasome A-type subunit	RT		5	2.7E-2	3.9E0	2.0E-1	1
	UP_KEYWORDS	Threonine protease	RT		7		2.4E0	2.4E-1	1 2
	INTERPRO	Proteasome, subunit alpha/beta	RT		7		2.3E0	4.0E-1	1
	GOTERM_CC_DIRECT								1
	SMART	proteasome core complex	<u>RT</u>		7		2.1E0	4.8E-1	1
	GOTERM_MF_DIRECT	<u>SM00948</u>	<u>RT</u>	•	5		2.5E0	5.3E-1	1
		threonine-type endopeptidase activity	<u>RT</u>	•	7	1.3E-1	2.0E0	6.0E-1	1
	GOTERM_BP_DIRECT	proteolysis involved in cellular protein catabolic process	<u>RT</u>	•	10	4.2E-1	1.2E0	1.0E0	1
	INTERPRO	<u>Proteasome, beta-type subunit, conserved</u> <u>site</u>	<u>RT</u>	i	3	6.0E-1	1.5E0	1.0E0	9
ota	ation Cluster 185	Enrichment Score: 1.05	G	100	Count	P_Value	Fold Change	Benjamir	ni F
	UP_SEQ_FEATURE	DNA-binding region:A.T hook 3	<u>RT</u>	i	5	4.7E-2	3.4E0	8.0E-1	1
	INTERPRO	AT hook, DNA-binding motif	<u>RT</u>	1	4	5.7E-2	4.1E0	3.8E-1	3 1
	UP_SEQ_FEATURE	DNA-binding region:A.T hook 1	<u>RT</u>	1	5	1.1E-1	2.6E0	1.0E0	9 1
	UP_SEQ_FEATURE	DNA-binding region:A.T hook 2	<u>RT</u>	1	5	1.1E-1	2.6E0	1.0E0	<u>9</u> 1
	SMART	AT hook	<u>RT</u>	1	4	1.7E-1	2.7E0	6.8E-1	6
ota	ation Cluster 186	Enrichment Score: 1.05	G	To the second	Count	P_Value	Fold Change	Benjamir	ni I
	INTERPRO	Mitogen-activated protein (MAP) kinase, JNK	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3
	GOTERM_MF_DIRECT	JUN kinase activity	<u>RT</u>	1	3	7.5E-2	6.0E0	3.9E-1	3
	GOTERM_BP_DIRECT	JUN phosphorylation	<u>RT</u>		3	1.3E-1	4.4E0	8.3E-1	-
ota	ation Cluster 187	Enrichment Score: 1.05	G	PN .	Count	P_Value	Fold	Benjamir	ni l
	GOTERM_BP_DIRECT	negative regulation of leukocyte apoptotic	RT		5		Change 4.9E0	1.5E-1	
	GOTERM_BP_DIRECT	establishment of T cell polarity	RT		4		3.9E0	5.5E-1	5
	GOTERM_BP_DIRECT	positive regulation of cell motility	RT		6		2.5E0	5.8E-1	1
	GOTERM_BP_DIRECT	positive regulation of dendritic cell antigen			3		2.5E0	1.0E0	1 9
	GOTERM_BP_DIRECT	processing and presentation	<u>RT</u>						1
		response to prostaglandin E	RT		3	1	2.2E0 Fold	1.0E0	1
iota	ation Cluster 188 GOTERM_BP_DIRECT	JAK-STAT cascade involved in growth	G	- T	Count	P_Value	Change	•	ni F
	BIOCARTA	hormone signaling pathway	<u>RT</u>	•	9	1.4E-3	3.6E0	3.3E-2	2
		Stat3 Signaling Pathway	<u>RT</u>	•	8	1.9E-3	3.1E0	1.1E-2	3
	INTERPRO	<u>Tyrosine-protein kinase, non-receptor</u> <u>Jak/Tyk2</u>	<u>RT</u>	•	4	1.5E-2	6.2E0	1.2E-1	1
	PIR_SUPERFAMILY	tyrosine-protein kinase, Jak/Tyk2 type	<u>RT</u>	•	4	1.6E-2	6.0E0	2.5E-1	1
	BIOCARTA	IL22 Soluble Receptor Signaling Pathway	<u>RT</u>	•	9	2.7E-2	2.2E0	8.2E-2	2
	UP_SEQ_FEATURE	domain:SH2; atypical	<u>RT</u>	1	4	4.5E-2	4.5E0	7.8E-1	7
	UP_SEQ_FEATURE	domain:MyTH4 1	<u>RT</u>	i	3	5.8E-2	6.8E0	8.8E-1	1
	UP_SEQ_FEATURE	domain:MyTH4 2	<u>RT</u>	i	3	5.8E-2	6.8E0	8.8E-1	8
	BBID	48.mice minus JAKs and STATs	<u>RT</u>	•	8	8.1E-2	1.9E0	9.9E-1	9
	INTERPRO	MyTH4 domain	<u>RT</u>	i .	4	1.7E-1	2.8E0	8.1E-1	7
	GOTERM_MF_DIRECT	growth hormone receptor binding	<u>RT</u>	1	3	2.0E-1	3.6E0	8.0E-1	7
	SMART	MyTH4	RT		4		1.8E0	1.0E0	1
	INTERPRO	FERM domain	RT		10		1.2E0	1.0E0	1 9
	INTERPRO								1
	INTERPRO	Band 4.1 domain	<u>RT</u>		10		1.2E0	1.0E0	1
		FERM central domain	<u>RT</u>	•	9		1.1E0	1.0E0	1
	LID SEO FEATURE								2
	UP_SEQ_FEATURE SMART	domain:FERM	<u>RT</u>	•	8	5.9E-1	1.1E0	1.0E0	1

not	tation Cluster 1	Enrichment Score: ?	G	17 8	(Count	P_Value	Fold	Benjamini	i FC
	INTERPRO	FERM/acyl-CoA-binding_protein, 3-helical	RT	1	4			Change 5.0E-1		9.9
not	tation Cluster 189	bundle Enrichment Score: 1.04	G	- 		Count	P_Value	Fold	Benjamini	1 F
1000	INTERPRO	Proprotein convertase, P	RT RT	-	6		1.7E-3	Change	2.1E-2	2.0
	INTERPRO									2 7.0
	INTERPRO	Peptidase S8, subtilisin, Asp-active site	<u>RT</u>	•	5	5	7.7E-3	5.2E0	7.5E-2	2
		Peptidase S8, subtilisin, Ser-active site	<u>RT</u>	i	6	5	7.7E-3	4.1E0	7.5E-2	7.0 2
	INTERPRO	Peptidase S8, subtilisin, His-active site	<u>RT</u>	i	6	5	7.7E-3	4.1E0	7.5E-2	7.0 2
	INTERPRO	Peptidase S8, subtilisin-related	<u>RT</u>	i	ϵ	5	1.3E-2	3.7E0	1.2E-1	1. 1
	INTERPRO	Peptidase S8/S53 domain	<u>RT</u>	i	ϵ	5	2.1E-2	3.4E0	1.6E-1	1. 1
	GOTERM_BP_DIRECT	peptide biosynthetic process	<u>RT</u>	i	4	ļ	3.7E-2	4.7E0	3.8E-1	3.
	INTERPRO	Proteinase inhibitor, propeptide	<u>RT</u>	1	6	5	1.3E-1	2.2E0	6.2E-1	5.
	GOTERM_BP_DIRECT	peptide hormone processing	RT		5	;	2.8E-1	1 9F0	1.0E0	9.
	GOTERM_BP_DIRECT									1 9
	GOTERM_BP_DIRECT	protein processing	<u>RT</u>			.0		8.2E-1		1 9
		signal peptide processing	<u>RT</u>	1		3		7.1E-1		1
	UP_KEYWORDS UP_KEYWORDS	Zymogen Serine protease	RT RT		1 9	17)	1.0E0 1.0E0	5.5E-1 4.4E-1		1
	UP_SEQ_FEATURE	active site:Charge relay system	RT	1	8		1.0E0	2.7E-1		1
	GOTERM_MF_DIRECT	serine-type endopeptidase activity	<u>RT</u>	i		2	1.0E0	2.8E-1	1.0E0	1
ota	ation Cluster 190	Enrichment Score: 1.03	G		(Count	P_Value	Fold Change	Benjamini	i F
	INTERPRO	Natriuretic peptide receptor	<u>RT</u>	i	3	3	7.0E-2	6.2E0	3.9E-1	3
	GOTERM_MF_DIRECT	natriuretic peptide receptor activity	<u>RT</u>	i	3	3	7.5E-2	6.0E0	3.9E-1	3
	GOTERM_MF_DIRECT	hormone binding	<u>RT</u>	1	5	5	9.7E-2	2.7E0	4.8E-1	4
	GOTERM_MF_DIRECT	peptide hormone binding	RT		8	₹	1.5E-1		6.7E-1	1 6
							!	Fold		1
ota	INTERPRO	Enrichment Score: 1.02	G		(Count	P_Value	Change	Benjamini	Ł
		SANT domain	<u>RT</u>	i	ģ)	4.7E-2	2.1E0	3.2E-1	3 1
	UP_SEQ_FEATURE	domain:SANT 1	<u>RT</u>	•	4	ļ	1.3E-1	3.0E0	1.0E0	9
	UP_SEQ_FEATURE	domain:SANT 2	<u>RT</u>	i	4	ŀ	1.3E-1	3.0E0	1.0E0	9 1
ota	ation Cluster 192	Enrichment Score: 1.01		17	(Count	P_Value	Fold Change	Benjamini	i Fl
	GOTERM_BP_DIRECT	mRNA cleavage	<u>RT</u>	i	7	7	8.4E-3	3.5E0	1.4E-1	1 1
	GOTERM_BP_DIRECT	mRNA polyadenylation	<u>RT</u>	•	1	.0	3.6E-2	2.1E0	3.8E-1	3
	GOTERM_CC_DIRECT	mRNA cleavage and polyadenylation	<u>RT</u>		5	5	1.7E-1	2.3E0	7.0E-1	6
	BIOCARTA	specificity factor complex		- -						1 2
	GOTERM_BP_DIRECT	Polyadenylation of mRNA tRNA splicing, via endonucleolytic cleavage	<u>RT</u>		6		1.9E-1		3.8E-1	1 9
		and ligation	<u>RT</u>	•	5	5	2.4E-1	2.0E0	1.0E0	1
	GOTERM_BP_DIRECT	<u>pre-mRNA cleavage required for</u> polyadenylation	<u>RT</u>	i	3	3	4.0E-1	2.2E0	1.0E0	9 1
_	tation Cluster 193	Enrichment Score: 0.99	G	- Table 1	(Count	P_Value	Fold Change	Benjamini	i F
ota									3.9E-1	3
ota	GOTERM_BP_DIRECT	natural killer cell differentiation	<u>RT</u>	i	6	5	3.8E-2	3.0E0		
ota		natural killer cell differentiation		1	6				5.8E-1	
ota	GOTERM_BP_DIRECT	natural killer cell differentiation negative regulation of lymphocyte activation	<u>RT</u>	i	3	3	7.6E-2	5.9E0	5.8E-1	1
ot	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	natural killer cell differentiation negative regulation of lymphocyte activation apoptotic cell clearance	RT RT	i i	3	3	7.6E-2 9.4E-2	5.9E0 2.4E0	6.9E-1	1 6 1
iot	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	natural killer cell differentiation negative regulation of lymphocyte activation	<u>RT</u>	i i i	3	3	7.6E-2	5.9E0 2.4E0		1 6 1 9
ot	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	natural killer cell differentiation negative regulation of lymphocyte activation apoptotic cell clearance	RT RT	i i i i	3	3 5	7.6E-2 9.4E-2	5.9E0 2.4E0 2.6E0 2.4E0	6.9E-1	1 6 1 9
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	natural killer cell differentiation negative regulation of lymphocyte activation apoptotic cell clearance vagina development	RT RT RT	i	3 6 4	} ; !	7.6E-2 9.4E-2 1.8E-1	5.9E0 2.4E0 2.6E0 2.4E0	6.9E-1 1.0E0	1 6 1 9 1 9
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	natural killer cell differentiation negative regulation of lymphocyte activation apoptotic cell clearance vagina development secretion by cell	RT RT RT RT	i i i	3 6 4	S F Count	7.6E-2 9.4E-2 1.8E-1 2.3E-1	5.9E0 2.4E0 2.6E0 2.4E0 Fold Change	6.9E-1 1.0E0 1.0E0	1 6 1 9 1 9 1 F
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	natural killer cell differentiation negative regulation of lymphocyte activation apoptotic cell clearance vagina development secretion by cell Enrichment Score: 0.98 sulfate assimilation oxidoreductase activity, acting on a sulfur	RT RT RT RT	i i i	3	S S Count	7.6E-2 9.4E-2 1.8E-1 2.3E-1 P_Value	5.9E0 2.4E0 2.6E0 2.4E0 Fold Change 4.4E0	6.9E-1 1.0E0 1.0E0 Benjamini	1 6 1 9 1 9 1 F 8 2
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT tation Cluster 194 GOTERM_BP_DIRECT	natural killer cell differentiation negative regulation of lymphocyte activation apoptotic cell clearance vagina development secretion by cell Enrichment Score: 0.98 sulfate assimilation oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor	RT RT RT RT RT RT RT		3 6 4 4 6	Count	7.6E-2 9.4E-2 1.8E-1 2.3E-1 P_Value 4.9E-3 3.1E-2	5.9E0 2.4E0 2.6E0 2.4E0 Fold Change 4.4E0 3.7E0	6.9E-1 1.0E0 1.0E0 Benjamini 9.2E-2 2.0E-1	1 6 1 9 1 9 1 F 8 2 1 1 2
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT tation Cluster 194 GOTERM_BP_DIRECT GOTERM_BP_DIRECT INTERPRO	natural killer cell differentiation negative regulation of lymphocyte activation apoptotic cell clearance vagina development secretion by cell Enrichment Score: 0.98 sulfate assimilation oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor Thioredoxin	RT RT RT RT RT RT RT RT RT		3 6 4 4 6	Count	7.6E-2 9.4E-2 1.8E-1 2.3E-1 P_Value 4.9E-3 3.1E-2 3.2E-2	5.9E0 2.4E0 2.6E0 2.4E0 Fold Change 4.4E0 3.7E0 5.0E0	6.9E-1 1.0E0 1.0E0 Benjamini 9.2E-2 2.0E-1 2.3E-1	1 6 1 9 1 9 1 1 8 2 1 1 1
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT tation Cluster 194 GOTERM_BP_DIRECT GOTERM_MF_DIRECT INTERPRO GOTERM_BP_DIRECT	natural killer cell differentiation negative regulation of lymphocyte activation apoptotic cell clearance vagina development secretion by cell Enrichment Score: 0.98 sulfate assimilation oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor	RT RT RT RT RT RT RT		3 6 4 4 6	Count	7.6E-2 9.4E-2 1.8E-1 2.3E-1 P_Value 4.9E-3 3.1E-2	5.9E0 2.4E0 2.6E0 2.4E0 Fold Change 4.4E0 3.7E0 5.0E0	6.9E-1 1.0E0 1.0E0 Benjamini 9.2E-2 2.0E-1	1 6 1 9 1 1 1 1 2 1 3 1
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT Cation Cluster 194 GOTERM_BP_DIRECT INTERPRO GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	natural killer cell differentiation negative regulation of lymphocyte activation apoptotic cell clearance vagina development secretion by cell Enrichment Score: 0.98 sulfate assimilation oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor Thioredoxin	RT RT RT RT RT RT RT RT RT		3 6 4 4 6	Count	7.6E-2 9.4E-2 1.8E-1 2.3E-1 P_Value 4.9E-3 3.1E-2 3.2E-2	5.9E0 2.4E0 2.6E0 2.4E0 Fold Change 4.4E0 3.7E0 5.0E0 4.7E0	6.9E-1 1.0E0 1.0E0 Benjamini 9.2E-2 2.0E-1 2.3E-1	1 6 1 9 1 9 1 1 1 2 1 3 1 9 1
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT tation Cluster 194 GOTERM_BP_DIRECT GOTERM_MF_DIRECT INTERPRO GOTERM_BP_DIRECT	natural killer cell differentiation negative regulation of lymphocyte activation apoptotic cell clearance vagina development secretion by cell Enrichment Score: 0.98 sulfate assimilation oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor Thioredoxin glycerol ether metabolic process	RT		3 6 4 4 4 4 4	Count	7.6E-2 9.4E-2 1.8E-1 2.3E-1 P_Value 4.9E-3 3.1E-2 3.2E-2 3.7E-2	5.9E0 2.4E0 2.6E0 2.4E0 Fold Change 4.4E0 3.7E0 5.0E0 4.7E0 3.0E0	6.9E-1 1.0E0 1.0E0 Benjamini 9.2E-2 2.0E-1 2.3E-1 3.8E-1	1 6 1 9 1 9 1 1 1 2 1 3 1 9 1
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT Cation Cluster 194 GOTERM_BP_DIRECT INTERPRO GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	natural killer cell differentiation negative regulation of lymphocyte activation apoptotic cell clearance vagina development secretion by cell Enrichment Score: 0.98 sulfate assimilation oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor Thioredoxin glycerol ether metabolic process protein-disulfide reductase activity	RT		3 6 4 4 4 4 3 3	Count	7.6E-2 9.4E-2 1.8E-1 2.3E-1 P_Value 4.9E-3 3.1E-2 3.2E-2 3.7E-2 2.6E-1	5.9E0 2.4E0 2.6E0 2.4E0 Fold Change 4.4E0 3.7E0 5.0E0 4.7E0 3.0E0 1.8E0	6.9E-1 1.0E0 1.0E0 Benjamini 9.2E-2 2.0E-1 2.3E-1 3.8E-1 9.9E-1	6. 1 9. 1 9. 1 1 3. 1 9. 1 9.

Annot	ation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	i FDR
Annot	ation Cluster 195	Enrichment Score: 0.98	G	· ·	Count	P_Value	Fold	Roniamini	i FDR
	GOTERM_BP_DIRECT	adenylate cyclase-inhibiting dopamine	RT	i	5	3.5E-3		7.1E-2	6.8E- 2
	GOTERM_BP_DIRECT	receptor signaling pathway dopamine metabolic process	<u>RT</u>		6	2.6E-2	3.2E0	3.0E-1	2.9E-
	GOTERM_BP_DIRECT	behavioral response to cocaine	RT		6	7.2E-2	2.5E0	5.8E-1	1 5.6E-
	GOTERM_MF_DIRECT	dopamine neurotransmitter receptor activity,	RT		3	7.5E-2		3.9E-1	1 3.6E-
	GOTERM_BP_DIRECT	coupled via Gi/Go							1 5.6E-
	GOTERM_BP_DIRECT	response to histamine	<u>RT</u>	•	3	7.6E-2		5.8E-1	1 8.9E-
		negative regulation of protein secretion	<u>RT</u>	•	5	1.6E-1	2.3E0	9.3E-1	1
	GOTERM_BP_DIRECT	synaptic transmission, dopaminergic	<u>RT</u>	i	5	1.6E-1	2.3E0	9.3E-1	8.9E- 1
	INTERPRO	Dopamine receptor family	<u>RT</u>	i	3	1.9E-1	3.7E0	8.7E-1	8.1E- 1
	GOTERM_MF_DIRECT	dopamine neurotransmitter receptor activity	<u>RT</u>	i	3	2.0E-1	3.6E0	8.0E-1	7.2E- 1
	GOTERM_BP_DIRECT	response to amphetamine	<u>RT</u>	1	8	2.6E-1	1.5E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	arachidonic acid secretion	<u>RT</u>	i .	6	3.8E-1	1.5E0	1.0E0	9.6E- 1
	GOTERM_MF_DIRECT	dopamine binding	<u>RT</u>	1	3	5.2E-1	1.8E0	1.0E0	9.1E- 1
Annot	ation Cluster 196	Enrichment Score: 0.96	G	178	Count	P_Value	Fold Change	Benjamini	
	GOTERM_CC_DIRECT	chromatin silencing complex	RT	i	5	4.0E-2	<u> </u>	2.5E-1	2.3E-
	GOTERM_CC_DIRECT	rDNA heterochromatin	RT		3	1.2E-1	4.8E0	5.3E-1	1 4.7E-
	GOTERM_BP_DIRECT	chromatin silencing at rDNA	RT	- -	9	2.8E-1		1.0E0	1 9.6E-
Annat	antion Chapter 407			1		1	Fold	Bandanda	1
Annot	ation Cluster 197 INTERPRO	Enrichment Score: 0.96 Mitogen-activated protein (MAP) kinase	G	- 100	Count	P_Value	Onlange		3.6E-
	PIR_SUPERFAMILY	kinase kinase, 9/10/11 mitogen-activated protein kinase kinase	<u>RT</u>	•	3	7.0E-2		3.9E-1	1 6.0E-
	_	kinase, types 9/10/11	<u>RT</u>	•	3	7.3E-2	6.0E0	6.0E-1	1
	GOTERM_MF_DIRECT	JUN kinase kinase kinase activity	<u>RT</u>	i	3	7.5E-2	6.0E0	3.9E-1	3.6E- 1
	UP_SEQ_FEATURE	domain:Leucine-zipper 1	<u>RT</u>	i	4	1.3E-1	3.0E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	domain:Leucine-zipper 2	<u>RT</u>	1	4	1.3E-1	3.0E0	1.0E0	9.7E- 1
	GOTERM_BP_DIRECT	activation of JNKK activity	<u>RT</u>	i	3	2.7E-1	3.0E0	1.0E0	9.6E- 1
Annot	ation Cluster 198	Enrichment Score: 0.95	G	15	Count	P_Value	Fold Change	Benjamini	i FDR
	INTERPRO	<u>Lysophosphatidic acid receptor</u>	<u>RT</u>	1	3	7.0E-2	6.2E0	3.9E-1	3.6E- 1
	BIOCARTA	Rho-Selective Guanine Exchange Factor AKAP13 Mediates Stress Fiber Formation	<u>RT</u>	1	7	1.0E-1	2.0E0	2.4E-1	1.8E- 1
	GOTERM_MF_DIRECT	lysophosphatidic acid receptor activity	<u>RT</u>	1	3	2.0E-1	3.6E0	8.0E-1	7.2E-
Annot	ation Cluster 199	Enrichment Score: 0.95	G	178	Count	P_Value	Fold	Benjamini	i FDR
	GOTERM_MF_DIRECT	chemokine receptor binding	RT		5	3.1E-2	Change	2.0E-1	1.8E-
	GOTERM_BP_DIRECT	positive regulation of T cell migration	RT		5	7.2E-2		5.8E-1	1 5.6E-
	BBID	109.Chemokine families	RT		11	6.4E-1		1.0E0	1 1.0E0
Annot	ation Cluster 200	Enrichment Score: 0.94	G	100	Count	P_Value	Fold	Ponjamini	1
	UP_SEQ_FEATURE	region of interest:Domain A	<u>RT</u>	i	3	5.8E-2	•	8.8E-1	8.5E- 1
	UP_SEQ_FEATURE	region of interest:Domain B	<u>RT</u>	1	3	5.8E-2	6.8E0	8.8E-1	8.5E-
	INTERPRO	Retinoblastoma-associated protein, B-box	RT		3	7.0E-2		3.9E-1	1 3.6E-
	INTERPRO	Retinoblastoma-associated protein, A-box	RT		3	7.0E-2			1 3.6E-
	INTERPRO								1 3.6E-
	INTERPRO	Rb C-terminal Domain of unknown function DUF3452,	<u>RT</u>		3		6.2E0		1 3.6E-
	SMART	retinoblastoma-associated	<u>RT</u>		3		6.2E0		1 5.8E-
		<u>SM01367</u>	<u>RT</u>	i	3	1.5E-1	4.0E0	6.6E-1	1
	SMART	<u>SM01368</u>	<u>RT</u>	•	3	1.5E-1	4.0E0	6.6E-1	5.8E- 1
	SMART	<u>SM01369</u>	<u>RT</u>	i	3	1.5E-1	4.0E0	6.6E-1	5.8E- 1
	GOTERM_BP_DIRECT	regulation of lipid kinase activity	<u>RT</u>	1	3	2.0E-1	3.6E0	1.0E0	9.6E- 1
				_	4	7 1 5 1	1.150		9.7E-
	UP_SEQ_FEATURE	region of interest:Spacer	<u>RT</u>	i	4	/.1L-1	1.1E0	1.0E0	1
Annot		region of interest:Spacer Enrichment Score: 0.94	RT G	· ·	Count	P_Value			1
Annot	UP_SEQ_FEATURE	Enrichment Score: 0.94 negative regulation of norepinephrine					Fold Change		1
Annot	UP_SEQ_FEATURE	Enrichment Score: 0.94	G	7	Count	P_Value 1.8E-2	Fold Change	Benjamini 2.4E-1	i FDR 2.3E-

Annota	ation Cluster 1	Enrichment Score: ?	G	To the second se	Count	P_Value	Fold Change	Benjamini	ii FDR
	UP_SEQ_FEATURE	site:Implicated in ligand binding	<u>RT</u>	i	3	5.8E-2		8.8E-1	8.5E- 1
	GOTERM_BP_DIRECT	activation of protein kinase B activity	<u>RT</u>	i	9	5.9E-2	2.1E0	5.3E-1	5.0E- 1
	GOTERM_MF_DIRECT	alpha2-adrenergic receptor activity	<u>RT</u>	i	3	7.5E-2	6.0E0	3.9E-1	3.6E-
	GOTERM_BP_DIRECT	epidermal growth factor-activated receptor transactivation by G-protein coupled receptor	RT		3	1.3E-1	4.4E0	8.3E-1	7.9E-
	GOTERM_BP_DIRECT	<u>signaling pathway</u>	<u>Ki</u>						1 7.0F-
		negative regulation of epinephrine secretion	<u>RT</u>	i	3	1.3E-1	4.4E0	8.3E-1	7.9E- 1
	GOTERM_BP_DIRECT	activation of MAPK activity by adrenergic receptor signaling pathway	<u>RT</u>	i	3	1.3E-1	4.4E0	8.3E-1	7.9E- 1
	GOTERM_BP_DIRECT	regulation of vasoconstriction	<u>RT</u>	i	6	2.4E-1	1.8E0	1.0E0	9.6E- 1
	GOTERM_MF_DIRECT	epinephrine binding	<u>RT</u>	i	3	2.6E-1	3.0E0	9.9E-1	9.0E- 1
	GOTERM_BP_DIRECT	adenylate cyclase-activating adrenergic receptor signaling pathway	<u>RT</u>	i	5	4.0E-1	1.6E0	1.0E0	9.6E- 1
	INTERPRO	Adrenergic receptor	<u>RT</u>	i	3	4.4E-1	2.1E0	1.0E0	9.2E- 1
Annota	ation Cluster 202	Enrichment Score: 0.94	G	17	Count	P_Value	Fold Change	Benjamini	i FDR
	GOTERM_CC_DIRECT	ESC/E(Z) complex	<u>RT</u>	i	8	7.3E-3	3.2E0	6.2E-2	5.5E- 2
	BIOCARTA	<u>The PRC2 Complex Sets Long-term Gene</u> <u>Silencing Through Modification of Histone</u>	<u>RT</u>	i	7	3.4E-1	1.5E0	6.0E-1	4.5E- 1
	GOTERM_BP_DIRECT	<u>Tails</u> <u>negative regulation of gene expression,</u>	<u>RT</u>		9	6.2E-1	1 1F0	1.0E0	9.6E-
Annote	ation Cluster 203	epigenetic Enrichment Score: 0.91	G		Count	P_Value	Fold	Roniamini	1 EDR
Alliota	GOTERM_BP_DIRECT	positive regulation of chemokine production	RT	_	8	1.6E-2	Change	2.2E-1	2.1E-
	GOTERM_BP_DIRECT	positive regulation of interleukin-12							1 2.1E-
	GOTERM_BP_DIRECT	production positive regulation of NF-kappaB import into	<u>RT</u>	-	10	1.7E-2		2.2E-1	1 4.6E-
	GOTERM_BP_DIRECT	nucleus positive regulation of nitric-oxide synthase	<u>RT</u>		8	5.1E-2		4.8E-1	1 4.7E-
	GOTERM_BP_DIRECT	biosynthetic process positive regulation of interferon-beta	<u>RT</u>	1	6	5.4E-2		4.9E-1	1 5.6E-
		production	<u>RT</u>	•	9	7.2E-2	2.0E0	5.8E-1	1
	GOTERM_BP_DIRECT	positive regulation of tumor necrosis factor production	<u>RT</u>	i	13	8.7E-2	1.6E0	6.5E-1	6.2E- 1
	GOTERM_BP_DIRECT	positive regulation of interleukin-6 production	<u>RT</u>	•	11	2.2E-1	1.4E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	positive regulation of interferon-alpha production	<u>RT</u>	1	4	3.3E-1	2.0E0	1.0E0	9.6E- 1
	GOTERM_MF_DIRECT	<u>lipopolysaccharide binding</u>	<u>RT</u>	i	5	5.2E-1	1.4E0	1.0E0	9.1E- 1
	GOTERM_BP_DIRECT	positive regulation of interleukin-10 production	<u>RT</u>	i	5	5.6E-1	1.3E0	1.0E0	9.6E- 1
	BIOCARTA	<u>Dendritic cells in regulating TH1 and TH2</u> <u>Development</u>	<u>RT</u>	i .	5	9.5E-1	7.1E-1	1.0E0	9.5E- 1
Annota	ation Cluster 204	Enrichment Score: 0.91	G	5	Count	P_Value	Fold Change	Benjamini	ii FDR
	GOTERM_MF_DIRECT	<u>DNA binding, bending</u>	<u>RT</u>	1	8	2.1E-2	2.7E0	1.5E-1	1.4E- 1
	GOTERM_BP_DIRECT	DNA topological change	<u>RT</u>	i	4	1.8E-1	2.6E0	1.0E0	9.5E- 1
	BIOCARTA	Apoptotic DNA fragmentation and tissue homeostasis	<u>RT</u>	i	5	4.9E-1	1.4E0	8.0E-1	6.0E- 1
Annota	ation Cluster 205	Enrichment Score: 0.9	G	100	Count	P_Value	Fold Change	Benjamini	ii FDR
	INTERPRO	<u>Dual specificity phosphatase</u>	<u>RT</u>	i	11	2.0E-2	2.2E0	1.5E-1	1.4E- 1
	INTERPRO	M-phase inducer phosphatase	<u>RT</u>	i .	3	7.0E-2	6.2E0	3.9E-1	3.6E- 1
	UP_SEQ_FEATURE	domain:Rhodanese	<u>RT</u>	1	7	7.6E-2	2.3E0	1.0E0	9.7E- 1
	PIR_SUPERFAMILY	dual specificity protein phosphatase (MAP kinase phosphatase)	<u>RT</u>	1	4	9.5E-2	3.4E0	7.4E-1	7.4E- 1
	GOTERM_BP_DIRECT	inactivation of MAPK activity	<u>RT</u>	1	8	1.1E-1	1.9E0	7.9E-1	7.5E- 1
	BIOCARTA	Regulation of MAP Kinase Pathways Through Dual Specificity Phosphatases	<u>RT</u>	i	6	1.2E-1	2.1E0	2.8E-1	2.1E-
	GOTERM_MF_DIRECT	MAP kinase tyrosine/serine/threonine	<u>RT</u>	1	5	1.6E-1	2.3E0	6.9E-1	6.3E-
	INTERPRO	<u>phosphatase activity</u> <u>Rhodanese-like domain</u>	RT		7	1.8E-1		8.6E-1	1 7.9E-
	INTERPRO	Mitogen-activated protein (MAP) kinase	RT		4	2.1E-1		9.7E-1	1 9.0E-
	GOTERM_BP_DIRECT	phosphatase endoderm formation	RT	:	4	3.3E-1		1.0E0	1 9.6E-
	SMART	RHOD	RT		7	4.2E-1		1.0E0	1 8.9E-
Appet	ation Cluster 206	Enrichment Score: 0.9	_	•	1		Fold	Roniomini	1
Annota	GOTERM_BP_DIRECT		G RT	i	Count 6	P_Value 1.6E-2	Change	•	2.1E-
		Rap protein signal transduction	IXI	•	U	1.02-2	5.020	2.2E-1	1
	GOTERM_BP_DIRECT	microvillus assembly	<u>RT</u>	i	6	1.5E-1	2.150	8.5E-1	8.2E-

Annota	GOTERM_CC_DIRECT	recycling endosome membrane	<u>RT</u>	1	6	0.45.4	Change		2 -
					0	8.4E-1	8.7E-1	1.0E0	8.9E-
		Enrichment Score: 0.89	G	177	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K4	<u>RT</u>		9	5.5E-3	3.0E0	5.2E-2	4.7E-
	UP_SEQ_FEATURE	<pre>specific) zinc finger region:PHD-type 3</pre>	RT	4	5	4.7E-2	3.4F0	8.0E-1	2 7.7E-
	UP_SEQ_FEATURE	region of interest:S-adenosyl-L-methionine	RT		9	1.3E-1		1.0E0	1 9.7E-
	INTERPRO	binding		•					1 8.1E-
	INTERPRO	<u>FY-rich, N-terminal</u>	<u>RT</u>	•	3	1.9E-1	3.7E0	8.7E-1	1
		<u>FY-rich, C-terminal</u>	<u>RT</u>		3	1.9E-1	3.7E0	8.7E-1	8.1E-
	SMART	<u>FYRN</u>	<u>RT</u>	1	3	3.6E-1	2.4E0	1.0E0	8.9E- 1
	SMART	<u>FYRC</u>	<u>RT</u>	i	3	3.6E-1	2.4E0	1.0E0	8.9E
	UP_SEQ_FEATURE	binding site:S-adenosyl-L-methionine	<u>RT</u>	•	9	4.8E-1	1.2E0	1.0E0	9.7E
Annota	ation Cluster 208	Enrichment Score: 0.88	G	100	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_CC_DIRECT	postsynaptic membrane	<u>RT</u>	-	47	1.2E-2	1.4E0	9.6E-2	8.5E-
	UP_KEYWORDS	Postsynaptic cell membrane	<u>RT</u>	•	38	1.6E-2	1.5E0	7.5E-2	6.0E 2
	GOTERM_CC_DIRECT	<u>postsynaptic density</u>	<u>RT</u>		38	6.6E-2	1.3E0	3.5E-1	3.1E
_ 	UP_KEYWORDS	<u>Synapse</u>	RT		53	5.2E-1		1.0E0	1 8.0E
_	UP_KEYWORDS								1 8.4E
	GOTERM_CC_DIRECT	<u>Cell junction</u>	<u>RT</u>	-	91	8.4E-1	9.3E-1		1 9.0E
	OOTEKIM_OO_BIKEOT	<u>cell junction</u>	<u>RT</u>	-	64		8.9E-1		1
	ation Cluster 209	Enrichment Score: 0.88	G		Count	P_Value	Fold Change	Benjamin	
	GOTERM_BP_DIRECT	<u>phospholipase C-activating G-protein coupled</u> <u>acetylcholine receptor signaling pathway</u>	<u>RT</u>	1	5	3.2E-2	3.7E0	3.5E-1	3.4E 1
	GOTERM_MF_DIRECT	<u>G-protein coupled acetylcholine receptor</u> <u>activity</u>	<u>RT</u>	1	4	9.7E-2	3.4E0	4.8E-1	4.4E 1
	GOTERM_BP_DIRECT	adenylate cyclase-inhibiting G-protein coupled acetylcholine receptor signaling pathway	<u>RT</u>	1	4	9.9E-2	3.4E0	7.0E-1	6.7E 1
	GOTERM_BP_DIRECT	synaptic transmission, cholinergic	<u>RT</u>	1	4	9.6E-1	6.4E-1	1.0E0	9.6E
Annota	ation Cluster 210	Enrichment Score: 0.88	G	170	Count	P_Value	Fold Change	Benjamin	i FDR
7	GOTERM_CC_DIRECT	endoplasmic reticulum chaperone complex	RT	-	5	8.0E-2	Change	4.1E-1	3.6E
_ 	GOTERM_BP_DIRECT	protein folding in endoplasmic reticulum	RT	-	5	1.6E-1		9.3E-1	1 8.9E
	UP_SEQ_FEATURE	short sequence motif:Prevents secretion from							1 9.7E
		ER	<u>RT</u>	-	13	1.8E-1	Fold	1.0E0	1
	ation Cluster 211 GOTERM_BP_DIRECT	Enrichment Score: 0.87	G		Count	P_Value	Change	Benjamin	
		positive regulation of glycolytic process	<u>RT</u>		7	2.0E-2	3.0E0	2.5E-1	2.4E 1
	GOTERM_BP_DIRECT	fatty acid homeostasis	<u>RT</u>	1	5	1.6E-1	2.3E0	9.3E-1	8.9E 1
	KEGG_PATHWAY	Regulation of autophagy	<u>RT</u>	1	5	7.3E-1	1.1E0	1.0E0	7.3E 1
Annota	ation Cluster 212	Enrichment Score: 0.87	G	17	Count	P_Value	Fold Change	Benjamin	i FDR
	BIOCARTA	Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway	<u>RT</u>	1	13	8.7E-3	2.0E0	3.4E-2	2.6E 2
	BIOCARTA	Regulation of eIF4e and p70 S6 Kinase	<u>RT</u>	•	14	1.9E-2	1.8E0	6.6E-2	5.0E 2
	BIOCARTA	mTOR Signaling Pathway	RT		13	9.1E-2	1.6E0	2.2E-1	1.7E
_ 	BBID	106.Glycogen synthase-synthesis	RT	-	6	1.5E-1		9.9E-1	1 9.9E
_	BBID								1 9.9E
	BBID	2.Cytokine Receptors	<u>RT</u>		5	1.6E-1	2.1E0	9.9E-1	1 9.9E
		104.Insulin signaling	RT DT		10	1.6E-1		9.9E-1	1
	BBID BBID	105.Signaling glucose uptake 108.Regulating glucose transport	RT RT		6 6	3.3E-1 3.3E-1		1.0E0 1.0E0	1.0E 1.0E
	BBID	107.mRNA translation-protein synthesis	<u>RT</u>	1	7	4.7E-1		1.0E0	1.0E
npete	BBID ation Cluster 213	37.Akt-PKB Effector of P13K in Vivo Enrichment Score: 0.87	<u>RT</u>		4 Count	6.6E-1		1.0E0	1.0E
	INTERPRO		G		Count	·	Fold Change	•	7.0E
		5-Hydroxytryptamine receptor family	<u>RT</u>	i	6	7.7E-3		7.5E-2	2
	GOTERM_MF_DIRECT	serotonin binding	<u>RT</u>	1	6	1.6E-2	3.6E0	1.2E-1	1.1E 1
	GOTERM_BP_DIRECT	adenylate cyclase-inhibiting serotonin receptor signaling pathway	<u>RT</u>	1	3	7.6E-2	5.9E0	5.8E-1	5.6E 1
	GOTERM_BP_DIRECT	vasoconstriction	<u>RT</u>	i	5	3.2E-1	1.7E0	1.0E0	9.6E 1
	GOTERM_BP_DIRECT	serotonin receptor signaling pathway	<u>RT</u>	1	4	3.8E-1	1.8E0	1.0E0	9.6E
	GOTERM_MF_DIRECT	neurotransmitter receptor activity	RT	1	6	4.5E-1	1.4F0	1.0E0	9.1E
			141	•	0		_, , , L U		1

	tation Cluster 1	Enrichment Score: ?	G	· Control of the cont	Count	P_Value	Fold Change	Benjamin	i FD
	GOTERM_BP_DIRECT	regulation of behavior	<u>RT</u>	i	3	4.6E-1		1.0E0	9.6
	GOTERM_MF_DIRECT	G-protein coupled serotonin receptor activity	<u>RT</u>	i	6	5.1E-1	1.3E0	1.0E0	9.1
nnot	tation Cluster 214	Enrichment Score: 0.86	G	173	Count	P_Value	Fold Change	Benjamin	
	GOTERM_BP_DIRECT	positive regulation of protein metabolic	RT	1	5	3.2E-2	Change	3.5E-1	3.4
	GOTERM_BP_DIRECT	cellular response to laminar fluid shear stress	RT		4	1.4E-1	3.0E0	8.3E-1	7.9
ے ا	GOTERM_BP_DIRECT	negative regulation of response to cytokine	RT		3	2.0E-1		1.0E0	1 9.6
ے ا	GOTERM_BP_DIRECT	stimulus negative regulation of heterotypic cell-cell	RT	-	3	4.0E-1		1.0E0	1 9.6
	tation Chastan 245	adhesion		• •		:	Fold	1	1
nnot	tation Cluster 215 UP_SEQ_FEATURE	Enrichment Score: 0.86	G	i	Count	P_Value	Change		8.5
J	INTERPRO	domain:KEN	<u>RT</u>		3	5.8E-2		8.8E-1	1 3.
J	INTERPRO	KEN domain	<u>RT</u>		3	7.0E-2		3.9E-1	1 9.
J	SMART	PUB domain	<u>RT</u>	•	3	2.5E-1	3.1E0	1.0E0	1
	SWART	<u>PUG</u>	<u>RT</u>	i	3	3.6E-1		1.0E0	8. 1
not	tation Cluster 216	Enrichment Score: 0.84	G		Count	P_Value	Fold Change	Benjamin	
	UP_SEQ_FEATURE	domain:DOC	<u>RT</u>	i	4	1.0E-1	3.4E0	1.0E0	9. 1
	INTERPRO	Anaphase-promoting complex, subunit 10/DOC domain	<u>RT</u>	1	4	1.2E-1	3.1E0	6.2E-1	5. 1
	SMART	SM01337	<u>RT</u>	i	4	2.4E-1	2.3E0	9.2E-1	8. 1
not	tation Cluster 217	Enrichment Score: 0.82	G	178	Count	P_Value	Fold Change	Benjamin	i FI
	INTERPRO	Pseudouridine synthase, RsuA/RluB/C/D/E/F	<u>RT</u>	i .	4	1.5E-2	6.2E0	1.2E-1	1. 1
	GOTERM_BP_DIRECT	tRNA pseudouridine synthesis	<u>RT</u>	i e	4	6.4E-2	3.9E0	5.5E-1	5. 1
)	GOTERM_MF_DIRECT	deaminase activity	<u>RT</u>	i .	4	1.4E-1	3.0E0	6.1E-1	5. 1
	INTERPRO	Pseudouridine synthase, catalytic domain	<u>RT</u>	1	4	3.5E-1	1.9E0	1.0E0	9. 1
	GOTERM_MF_DIRECT	<u>pseudouridine synthase activity</u>	<u>RT</u>	i	4	3.7E-1	1.8E0	1.0E0	9.
)	GOTERM_BP_DIRECT	<u>pseudouridine synthesis</u>	<u>RT</u>	1	3	6.7E-1	1.4E0	1.0E0	9. 1
nnot	tation Cluster 218	Enrichment Score: 0.82	G	178	Count	P_Value	Fold Change	Benjamin	
)	GOTERM_BP_DIRECT	regulation of the force of heart contraction	RT	-	8	3.0E-2		3.4E-1	3.
)	GOTERM_BP_DIRECT	ventricular cardiac muscle tissue	RT		8	1.1E-1	1.9E0	7.9E-1	1 7.
í I	KEGG_PATHWAY	morphogenesis Cardiac muscle contraction	RT		8		5.6E-1		1 9.
not	tation Cluster 219	Enrichment Score: 0.82	G	- -		P_Value	Fold	Baniamin	1
mot		Enrichment Score: 0.02		C			: ~ .	Benjamin	" ["
)	BIOCARTA	II 22 Soluble Recentor Signaling Pathway	рт		Count		Change	0 25 2	6.
	BIOCARTA	IL22 Soluble Receptor Signaling Pathway	<u>RT</u>	1	9	2.7E-2	2.2E0	8.2E-2	2
)	BIOCARTA GOTERM_BP_DIRECT	JAK-STAT cascade	<u>RT</u>	•	9	2.7E-2 3.3E-2	2.2E0 2.0E0	3.7E-1	2 3. 1
)	BIOCARTA GOTERM_BP_DIRECT BBID			_	9	2.7E-2	2.2E0 2.0E0		2 3. 1 9.
)))	BIOCARTA GOTERM_BP_DIRECT BBID INTERPRO	JAK-STAT cascade 48.mice minus JAKs and STATs STAT transcription factor, DNA-binding	<u>RT</u>	•	9	2.7E-2 3.3E-2	2.2E0 2.0E0 1.9E0	3.7E-1	2 3. 1 9. 1 4. 1
	BIOCARTA GOTERM_BP_DIRECT BBID INTERPRO INTERPRO	JAK-STAT cascade 48.mice minus JAKs and STATs	RT RT		9 11 8	2.7E-2 3.3E-2 8.1E-2	2.2E0 2.0E0 1.9E0 3.5E0	3.7E-1 9.9E-1	2 3. 1 9. 1 4. 1
	BIOCARTA GOTERM_BP_DIRECT BBID INTERPRO INTERPRO INTERPRO	JAK-STAT cascade 48.mice minus JAKs and STATs STAT transcription factor, DNA-binding STAT transcription factor, coiled coil STAT transcription factor, core	RT RT RT		9 11 8 4	2.7E-2 3.3E-2 8.1E-2 8.8E-2	2.2E0 2.0E0 1.9E0 3.5E0 3.5E0	3.7E-1 9.9E-1 4.7E-1	2 3. 1 9. 1 4. 1 4. 1
	BIOCARTA GOTERM_BP_DIRECT BBID INTERPRO INTERPRO INTERPRO INTERPRO	JAK-STAT cascade 48.mice minus JAKs and STATs STAT transcription factor, DNA-binding STAT transcription factor, coiled coil	RT RT RT RT		9 11 8 4 4	2.7E-2 3.3E-2 8.1E-2 8.8E-2 8.8E-2	2.2E0 2.0E0 1.9E0 3.5E0 3.5E0 3.5E0	3.7E-1 9.9E-1 4.7E-1 4.7E-1	2 3. 1 9. 1 4. 1 4. 1
	BIOCARTA GOTERM_BP_DIRECT BBID INTERPRO INTERPRO INTERPRO	JAK-STAT cascade 48.mice minus JAKs and STATs STAT transcription factor, DNA-binding STAT transcription factor, coiled coil STAT transcription factor, core STAT transcription factor, DNA-binding,	RT RT RT RT		9 11 8 4 4	2.7E-2 3.3E-2 8.1E-2 8.8E-2 8.8E-2 8.8E-2	2.2E0 2.0E0 1.9E0 3.5E0 3.5E0 3.5E0 3.5E0	3.7E-1 9.9E-1 4.7E-1 4.7E-1 4.7E-1	2 3. 1 9. 1 4. 1 4. 1 4. 1
	BIOCARTA GOTERM_BP_DIRECT BBID INTERPRO INTERPRO INTERPRO INTERPRO	JAK-STAT cascade 48.mice minus JAKs and STATs STAT transcription factor, DNA-binding STAT transcription factor, coiled coil STAT transcription factor, core STAT transcription factor, DNA-binding, subdomain	RT RT RT RT RT RT		9 11 8 4 4 4	2.7E-2 3.3E-2 8.1E-2 8.8E-2 8.8E-2 8.8E-2 8.8E-2 8.8E-2	2.2E0 2.0E0 1.9E0 3.5E0 3.5E0 3.5E0 3.5E0	3.7E-1 9.9E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1	2 3. 1 9. 1 4. 1 4. 1 4. 1 4. 1
	BIOCARTA GOTERM_BP_DIRECT BBID INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO	JAK-STAT cascade 48.mice minus JAKs and STATs STAT transcription factor, DNA-binding STAT transcription factor, coiled coil STAT transcription factor, core STAT transcription factor, DNA-binding, subdomain STAT transcription factor, protein interaction	RT RT RT RT RT RT RT		9 11 8 4 4 4 4	2.7E-2 3.3E-2 8.1E-2 8.8E-2 8.8E-2 8.8E-2 8.8E-2 8.8E-2	2.2E0 2.0E0 1.9E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0	3.7E-1 9.9E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1	2 3. 1 9. 1 4. 1 4. 1 4. 1 4. 1 4. 1 4. 1
	BIOCARTA GOTERM_BP_DIRECT BBID INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO	JAK-STAT cascade 48.mice minus JAKs and STATs STAT transcription factor, DNA-binding STAT transcription factor, coiled coil STAT transcription factor, core STAT transcription factor, DNA-binding, subdomain STAT transcription factor, protein interaction STAT transcription factor, all-alpha	RT RT RT RT RT RT RT RT		9 11 8 4 4 4 4 4	2.7E-2 3.3E-2 8.1E-2 8.8E-2 8.8E-2 8.8E-2 8.8E-2 8.8E-2 8.8E-2	2.2E0 2.0E0 1.9E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0	3.7E-1 9.9E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1	2 3. 1 9. 1 4. 1 4. 1 4. 1 4. 1 5. 1
	BIOCARTA GOTERM_BP_DIRECT BBID INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT	JAK-STAT cascade 48.mice minus JAKs and STATs STAT transcription factor, DNA-binding STAT transcription factor, coiled coil STAT transcription factor, core STAT transcription factor, DNA-binding, subdomain STAT transcription factor, protein interaction STAT transcription factor, all-alpha CCR5 chemokine receptor binding	RT		9 11 8 4 4 4 4 4 4	2.7E-2 3.3E-2 8.1E-2 8.8E-2 8.8E-2 8.8E-2 8.8E-2 8.8E-2 1.4E-1	2.2E0 2.0E0 1.9E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 2.3E0	3.7E-1 9.9E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 6.1E-1	2 3. 1 9. 1 4. 1 4. 1 4. 1 4. 1 5. 1 8. 1 9.
	BIOCARTA GOTERM_BP_DIRECT BBID INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART	JAK-STAT cascade 48.mice minus JAKs and STATs STAT transcription factor, DNA-binding STAT transcription factor, coiled coil STAT transcription factor, core STAT transcription factor, DNA-binding, subdomain STAT transcription factor, protein interaction STAT transcription factor, all-alpha CCR5 chemokine receptor binding SM00964	RT		9 11 8 4 4 4 4 4 4	2.7E-2 3.3E-2 8.1E-2 8.8E-2 8.8E-2 8.8E-2 8.8E-2 1.4E-1 2.4E-1	2.2E0 2.0E0 1.9E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 1.4E0	3.7E-1 9.9E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 6.1E-1 9.2E-1	2 3. 1 9. 1 4. 1 4. 1 4. 1 4. 1 5. 1 8. 1
	BIOCARTA GOTERM_BP_DIRECT BBID INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART INTERPRO	JAK-STAT cascade 48.mice minus JAKs and STATs STAT transcription factor, DNA-binding STAT transcription factor, coiled coil STAT transcription factor, core STAT transcription factor, DNA-binding, subdomain STAT transcription factor, protein interaction STAT transcription factor, all-alpha CCR5 chemokine receptor binding SM00964 p53-like transcription factor, DNA-binding	RT		9 11 8 4 4 4 4 4 4 10	2.7E-2 3.3E-2 8.1E-2 8.8E-2 8.8E-2 8.8E-2 8.8E-2 1.4E-1 2.4E-1 2.7E-1	2.2E0 2.0E0 1.9E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 1.4E0 1.3E0	3.7E-1 9.9E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 6.1E-1 9.2E-1 1.0E0	2 3. 1 9. 1 4. 1 4. 1 4. 1 5. 1 8. 1 9. 1
	BIOCARTA GOTERM_BP_DIRECT BBID INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART INTERPRO BBID	JAK-STAT cascade 48.mice minus JAKs and STATs STAT transcription factor, DNA-binding STAT transcription factor, coiled coil STAT transcription factor, core STAT transcription factor, DNA-binding, subdomain STAT transcription factor, protein interaction STAT transcription factor, all-alpha CCR5 chemokine receptor binding SM00964 p53-like transcription factor, DNA-binding 12.IL-6 type cytok-signal-transduct	RT		9 111 8 4 4 4 4 4 10 9	2.7E-2 3.3E-2 8.1E-2 8.8E-2 8.8E-2 8.8E-2 8.8E-2 1.4E-1 2.4E-1 2.7E-1 3.9E-1	2.2E0 2.0E0 1.9E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 1.4E0 1.4E0 1.4E0	3.7E-1 9.9E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 9.2E-1 1.0E0 1.0E0	2 3. 1 9. 1 4. 1 4. 1 4. 1 4. 1 5. 1 8. 1 1 5.
	BIOCARTA GOTERM_BP_DIRECT BBID INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART INTERPRO BBID BIOCARTA GOTERM_BP_DIRECT BBID	JAK-STAT cascade 48.mice minus JAKs and STATs STAT transcription factor, DNA-binding STAT transcription factor, coiled coil STAT transcription factor, core STAT transcription factor, DNA-binding, subdomain STAT transcription factor, protein interaction STAT transcription factor, all-alpha CCR5 chemokine receptor binding SM00964 p53-like transcription factor, DNA-binding 12.IL-6 type cytok-signal-transduct IL-10 Anti-inflammatory Signaling Pathway regulation of type I interferon-mediated	RT		9 11 8 4 4 4 4 4 10 9 6	2.7E-2 3.3E-2 8.1E-2 8.8E-2 8.8E-2 8.8E-2 8.8E-2 1.4E-1 2.4E-1 2.7E-1 3.9E-1 4.1E-1	2.2E0 2.0E0 1.9E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 1.4E0 1.4E0 1.4E0	3.7E-1 9.9E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 6.1E-1 9.2E-1 1.0E0 1.0E0 6.8E-1	2 3. 1 9. 1 4. 1 4. 1 4. 1 5. 1 8. 1 9. 1 1. 5. 1 9. 1 1.
	BIOCARTA GOTERM_BP_DIRECT BBID INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART INTERPRO BBID BIOCARTA GOTERM_BP_DIRECT	JAK-STAT cascade 48.mice minus JAKs and STATs STAT transcription factor, DNA-binding STAT transcription factor, coiled coil STAT transcription factor, core STAT transcription factor, DNA-binding, subdomain STAT transcription factor, protein interaction STAT transcription factor, all-alpha CCR5 chemokine receptor binding SM00964 p53-like transcription factor, DNA-binding 12.IL-6 type cytok-signal-transduct IL-10 Anti-inflammatory Signaling Pathway regulation of type I interferon-mediated signaling pathway	RT R		9 111 8 4 4 4 4 4 10 9 6 6	2.7E-2 3.3E-2 8.1E-2 8.8E-2 8.8E-2 8.8E-2 8.8E-2 1.4E-1 2.4E-1 2.7E-1 3.9E-1 4.1E-1 4.5E-1	2.2E0 2.0E0 1.9E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 1.4E0 1.4E0 1.4E0 1.5E0 1.0E0	3.7E-1 9.9E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 6.1E-1 9.2E-1 1.0E0 1.0E0 6.8E-1 1.0E0	2 3. 1 9. 1 4. 1 4. 1 4. 1 5. 1 8. 1 9. 1 1. 5. 1 9. 1 1.
	BIOCARTA GOTERM_BP_DIRECT BBID INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART INTERPRO BBID BIOCARTA GOTERM_BP_DIRECT BBID	JAK-STAT cascade 48.mice minus JAKs and STATs STAT transcription factor, DNA-binding STAT transcription factor, coiled coil STAT transcription factor, core STAT transcription factor, DNA-binding, subdomain STAT transcription factor, protein interaction STAT transcription factor, all-alpha CCR5 chemokine receptor binding SM00964 p53-like transcription factor, DNA-binding 12.IL-6 type cytok-signal-transduct IL-10 Anti-inflammatory Signaling Pathway regulation of type I interferon-mediated signaling pathway 11.IL-6 gp130-Jak-STAT	RT R		9 111 8 4 4 4 4 4 10 9 6 6 3 3	2.7E-2 3.3E-2 8.1E-2 8.8E-2 8.8E-2 8.8E-2 8.8E-2 1.4E-1 2.4E-1 2.7E-1 3.9E-1 4.1E-1 4.5E-1 6.4E-1	2.2E0 2.0E0 1.9E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 3.5E0 1.4E0 1.4E0 1.4E0 1.5E0 1.0E0	3.7E-1 9.9E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 4.7E-1 6.1E-1 9.2E-1 1.0E0 1.0E0 6.8E-1 1.0E0 1.0E0 1.0E0	3. 1 9. 1 4. 1 4. 1 4. 1 5. 1 8. 1 9. 1 1. 8. 1 1. 8. 1

Annota	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_CC_DIRECT	<u>calcineurin complex</u>	<u>RT</u>	i	3	1.2E-1	•	5.3E-1	4.7E-
	GOTERM_BP_DIRECT	calcineurin-NFAT signaling cascade	<u>RT</u>	i	3	4.0E-1	2.2E0	1.0E0	9.6E-
Annota	ation Cluster 221	Enrichment Score: 0.82	G		Count	P_Value	Fold Change	Benjamin	
	KEGG_PATHWAY	Hedgehog signaling pathway	<u>RT</u>	1	11	2.2E-2	•	3.9E-2	2.2E- 2
	BIOCARTA	Sonic Hedgehog (Shh) Pathway	<u>RT</u>	1	10	3.8E-2	1.9E0	1.0E-1	7.9E- 2
	BIOCARTA	ChREBP regulation by carbohydrates and cAMP	<u>RT</u>	1	12	4.1E-2	1.8E0	1.1E-1	8.3E- 2
	BIOCARTA	Regulation of ck1/cdk5 by type 1 glutamate receptors	<u>RT</u>	1	10	5.9E-2	1.8E0	1.5E-1	1.1E-
	GOTERM_CC_DIRECT	ciliary base	<u>RT</u>	i	8	1.2E-1	1.9E0	5.3E-1	4.7E-
	BIOCARTA	Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor	<u>RT</u>	i e	11	1.3E-1	1.6E0	2.9E-1	2.2E- 1
	BIOCARTA	<u>Transcription Regulation by Methyltransferase</u> of CARM1	<u>RT</u>	i .	7	1.5E-1	1.8E0	3.2E-1	2.4E- 1
	BIOCARTA	Attenuation of GPCR Signaling	<u>RT</u>	i .	7	2.1E-1	1.7E0	4.2E-1	3.1E- 1
	GOTERM_CC_DIRECT	cAMP-dependent protein kinase complex	<u>RT</u>	1	3	3.0E-1	2.7E0	9.4E-1	8.3E- 1
	BIOCARTA	Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway	<u>RT</u>	i e	6	3.3E-1	1.6E0	5.9E-1	4.4E- 1
	BIOCARTA	Phospholipase C-epsilon pathway	<u>RT</u>	i	6	3.3E-1	1.6E0	5.9E-1	4.4E- 1
	BIOCARTA	Stathmin and breast cancer resistance to antimicrotubule agents	<u>RT</u>	i .	10	4.1E-1	1.2E0	6.8E-1	5.1E- 1
	UP_KEYWORDS	<u>camp</u>	<u>RT</u>	i .	7	4.3E-1	1.3E0	1.0E0	8.0E- 1
	BIOCARTA	GATA3 participate in activating the Th2 cytokine genes expression	<u>RT</u>	i .	6	6.2E-1	1.2E0	9.5E-1	7.2E- 1
Annota	ation Cluster 222	Enrichment Score: 0.82	G	N .	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_MF_DIRECT	cyclin-dependent protein serine/threonine kinase regulator activity	<u>RT</u>	i	6	9.1E-2	2.4E0	4.7E-1	4.3E- 1
	GOTERM_BP_DIRECT	positive regulation of cyclin-dependent protein serine/threonine kinase activity	<u>RT</u>	1	8	9.6E-2	2.0E0	7.0E-1	6.7E- 1
	GOTERM_BP_DIRECT	positive regulation of phosphorylation of RNA polymerase II C-terminal domain	<u>RT</u>	i .	3	4.0E-1	2.2E0	1.0E0	9.6E- 1
Annota	ation Cluster 223	Enrichment Score: 0.8	G	**	Count	P_Value	Fold Change	Benjamin	i FDR
	UP_SEQ_FEATURE	repeat:HAT 9	<u>RT</u>	i .	4	2.5E-2		4.6E-1	4.4E- 1
	UP_SEQ_FEATURE	repeat:HAT 8	<u>RT</u>	i .	4	4.5E-2	4.5E0	7.8E-1	7.5E- 1
	UP_SEQ_FEATURE	repeat:HAT 7	<u>RT</u>	i .	4	7.0E-2	3.9E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:HAT 6	<u>RT</u>	i .	4	1.3E-1	3.0E0	1.0E0	9.7E- 1
	INTERPRO	RNA-processing protein, HAT helix	<u>RT</u>	i	4	2.1E-1	2.5E0	9.7E-1	9.0E-
	UP_SEQ_FEATURE	repeat:HAT 5	<u>RT</u>	i	4	2.1E-1	2.5E0	1.0E0	9.7E-
	UP_SEQ_FEATURE	repeat:HAT 4	<u>RT</u>	i	4	2.5E-1	2.3E0	1.0E0	9.7E-
	UP_SEQ_FEATURE	repeat:HAT 1	<u>RT</u>	i	4	3.0E-1	2.1E0	1.0E0	9.7E-
	UP_SEQ_FEATURE	repeat:HAT 2	<u>RT</u>	i .	4	3.0E-1	2.1E0	1.0E0	9.7E-
	UP_SEQ_FEATURE	repeat:HAT 3	<u>RT</u>	i	4	3.0E-1	2.1E0	1.0E0	9.7E-
	SMART	<u>HAT</u>	<u>RT</u>	i e	4	4.7E-1	1.6E0	1.0E0	8.9E-
Annota	ation Cluster 224	Enrichment Score: 0.8	G	17	Count	P_Value	Fold Change	Benjamin	
	UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A1	<u>RT</u>	i	3	1.6E-1	•	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A2	<u>RT</u>	i	3	1.6E-1	4.1E0	1.0E0	9.7E-
	UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A3	<u>RT</u>	i	3	1.6E-1	4.1E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	chain:Putative uncharacterized protein C21orf81	<u>RT</u>	i	3	1.6E-1	4.1E0	1.0E0	9.7E-
Annota	ation Cluster 225	Enrichment Score: 0.8	G	100	Count	P_Value	Fold Change	Benjamin	
	UP_SEQ_FEATURE	active site:Phosphoserine intermediate	<u>RT</u>	i e	6	9.0E-3		2.1E-1	2.0E- 1
	INTERPRO	Alkaline phosphatase	<u>RT</u>	i	4	1.5E-2	6.2E0	1.2E-1	1.1E- 1
	INTERPRO	Alkaline phosphatase, active site	<u>RT</u>	i	4	1.5E-2	6.2E0	1.2E-1	1.1E- 1
	SMART	alkPPc	<u>RT</u>	i	4	4.9E-2	4.0E0	2.8E-1	2.4E-
	GOTERM_MF_DIRECT	alkaline phosphatase activity	RT	1	4	6.3E-2		3.6E-1	3.3E-
	UP_SEQ_FEATURE	lipid moiety-binding region:GPI-anchor	RT		3		3.4E0		1 9.7E-
		amidated aspartate							1

	4.2E-1 2. 1 1.0E0 9. 1 1.0E0 1. 2 Benjamini Fi 1 1.0E0 9. 1 1.0E0
NITERPRO Alkaline-nhotophatase-like, core domain RI	1 1.0E0 1 1 1.0E0 9. 1 1.0E0 1.
UP_SEQ_FEATURE	1 1.0E0 9. 1 1.0E0 1. 1 1.0E0 1. 1 1.0E0 1. 1 1.0E0 1. 2 Benjamini Fi 2 1.0E0 9. 1 1.0E0 9.
UP_KEYWORDS Interferon signaling pathway RI	1 1.0E0 9. 1 1.0E0 1. 1 1.0E0 1. 1 1.0E0 1. 2 Benjamini Fi 1 1.0E0 9. 1 1.0E0 9. 1 1.0E0 9. 1 1.0E0 7.6E-1 7. 1 1.0E0 7.6E-1 7. 1 1.0E0 9. 1 1.0E0 9.
UP_KEYWORDS GPI-anchor ST	1 1.0E0 1. 1 1.0E0 1. 1 1.0E0 1. ge Benjamini Fi 1 1.0E0 9. 1 1.0E0 9. 1 1.0E0 7.6E-1 7. 1 8.3E-1 7. 1 1.0E0 9.
GOTERM_CC_DIRECT anchored component of membrane RT	1 1.0E0 1. ge Benjamini Fi 1.0E0 9. 1.0E0 9. 1.0E0 1 ge Benjamini Fi 7.6E-1 7. 1.0E0 9. 1.0E0 9. 1.0E0 9.
NITERPRO	3.9E-1 3.1 1.0E0 9.1 1.0E0 9.1 1.0E0 7.6E-1 7.1 1.0E0 7.6E-1 7.1 1.0E0 9.1
INTERPRO	1.0E0 9. 1.0E0 9. 1.0E0 7.6E-1 7. 1.0E0 7.6E-1 7. 1.0E0 9.
GOTERM_BP_DIRECT DNA-templated transcription. Initiation RI 9 2.56-1 1.56 Annotation Cluster 227 Enrichment Score: 0.78 G	1.0E0 1 1.0E0 9. 1 Benjamini FI 7.6E-1 7. 1 8.3E-1 7. 1
Annotation Cluster 227 Enrichment Score: 0.75	ge Benjamini Fi 7.6E-1 7. 1 8.3E-1 7. 1 1.0F0 9.
GOTERM_BP_DIRECT Type Interferon signaling pathway RT	7.6E-1 7.1 7.0 9.1.0F0 9.1.0F0
GOTERM_BP_DIRECT negative regulation of viral genome RT	1 8.3E-1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
GOTERM_BP_DIRECT defense response to virus RT 33 2.2E-1 1.2E	1.0F0 9.
GOTERM_BP_DIRECT defense response to virus RT	1.0F0 9.
Annotation Cluster 228 Enrichment Score: 0.76 GOTERM_MF_DIRECT DNA binding, bending RT NTERPRO HMG box A DNA-binding domain, conserved site NINTERPRO High mobility group (HMG) box domain RT NOA-binding region: HMG box 1 RT NA-binding region: HMG box 2 RT NA-binding region: HMG box 3 RT NART NAMA NART NAMA NAMA NAMA NAMA NAMA NAMA NAMA NAM	1
Annotation Cluster 228	7.6E-1 6.
GOTERM_MF_DIRECT DNA binding, bending RT	Doniemini El
INTERPRO	ge
INTERPRO	1
GOTERM_BP_DIRECT DNA geometric change RT	1
UP_SEQ_FEATURE DNA-binding region:HMG box 1 RT	0.21-1
UP_SEQ_FEATURE DNA-binding region: HMG box 2 RT	1
UP_SEQ_FEATURE DNA-binding region:HMG box RT	1
SMART HMG RT 13 7.1E-1 9.7E Annotation Cluster 229 Enrichment Score: 0.76 PIR_SUPERFAMILY heat shock protein, HSP90/HTPG types INTERPRO Heat shock protein Hsp90, conserved site INTERPRO Heat shock protein Hsp90, N-terminal RT INTERPRO Heat shock protein Hsp90 RT INTERPRO Heat shock protein Hsp90 RT SMART HATPase c INTERPRO Histidine kinase-like ATPase, ATP-binding domain Annotation Cluster 230 Enrichment Score: 0.75 Count P_Value Fold Chair Fold Chair Count P_Value Fold Chair Fold Ch	1.0E0 9.
Annotation Cluster 229 Enrichment Score: 0.76 G	1.0E0 9.
PIR_SUPERFAMILY heat shock protein, HSP90/HTPG types INTERPRO Heat shock protein Hsp90, conserved site INTERPRO Heat shock protein Hsp90, N-terminal INTERPRO Heat shock protein Hsp90, N-terminal RT INTERPRO Heat shock protein Hsp90 RT SMART HATPase c INTERPRO Histidine kinase-like ATPase, ATP-binding domain Annotation Cluster 230 Enrichment Score: 0.75 Count P_Value Fold Char	1 1.0E0 8.
INTERPRO Heat shock protein Hsp90, conserved site INTERPRO Heat shock protein Hsp90, N-terminal INTERPRO Heat shock protein Hsp90 RT INTERPRO Histidine kinase-like ATPase, ATP-binding domain Annotation Cluster 230 Enrichment Score: 0.75 Count P_Value Fold Char	ge Benjamini Fl
INTERPRO Heat shock protein Hsp90, N-terminal NTERPRO Heat shock protein Hsp90 RT SMART HATPase c Histidine kinase-like ATPase, ATP-binding domain Annotation Cluster 230 Enrichment Score: 0.75 Heat shock protein Hsp90, N-terminal RT Annotation Cluster 230 RT Count P_Value Fold Char	2.5E-1 2.
INTERPRO Heat shock protein Hsp90, N-terminal RT 4 1.7E-1 2.8E INTERPRO Heat shock protein Hsp90 RT SMART HATPase c RT INTERPRO Histidine kinase-like ATPase, ATP-binding domain Annotation Cluster 230 Enrichment Score: 0.75 Count P_Value Fold Char	6.2E-1 5.
SMART HATPase c Histidine kinase-like ATPase, ATP-binding domain Annotation Cluster 230 Enrichment Score: 0.75 Heat snock protein Hsp90 RT 4 2.6E-1 2.3E 4 5.4E-1 1.5E 6 6.3E-1 1.1E	8.1E-1 7.
INTERPRO Histidine kinase-like ATPase, ATP-binding domain Annotation Cluster 230 Enrichment Score: 0.75 Histidine kinase-like ATPase, ATP-binding domain Count P_Value Fold Characterists Fig. 1.15 Count P_Value Fold Characterists Count P	1.0E0 9.
Annotation Cluster 230 Histidine kinase-like ATPase, ATP-binding domain Enrichment Score: 0.75 Enrichment Score: 0.75 G Count P_Value Character Character Count	1.0E0 8.
Annotation Cluster 230 Enrichment Score: 0.75 G T Count P_Value Char	1
UR OFO FEATURE	1 B 1 1 1 5
uolilaii.rb2 <u>Ki</u> 23 3.8L-2 1.3L	ge
INTERPRO DE LA CELLA DE	1
PDZ domain	7.9L-1 1
PDZ RT 31 9.2E-1 8.4E	1 1.000 1
Annotation Cluster 231 Enrichment Score: 0.75 G TO Count P_Value Character P_Value C	2
BIOCARTA Nitric Oxide Signaling Pathway RT 11 1.3E-1 1.6E	1
BIOCARTA Role of MEF2D in T-cell Apoptosis RT 9 1.9E-1 1.6E	1
BIOCARTA Effects of calcineurin in Keratinocyte Differentiation 9 2.4E-1 1.5E	4.5E-1 3.
Annotation Cluster 232 Enrichment Score: 0.74 G TO Count P_Value Character Count P_Value Character Count Character Character Character Count Character Charact	ge Benjamini Fl
GOTERM_CC_DIRECT beta-catenin destruction complex RT 6 5.6E-2 2.7E	3.2E-1 ² .
GOTERM_BP_DIRECT beta-catenin destruction complex assembly RT 3 2.0E-1 3.6E	1
GOTERM_BP_DIRECT beta-catenin destruction complex disassembly RT 5 5.2E-1 1.3E	1
Annotation Cluster 233 Enrichment Score: 0.74 G TO Count P_Value Chair	1.0E0 9.
INTERPRO Carbamoyl-phosphate synthetase large subunit-like, ATP-binding domain RT 4 8.8E-2 3.5E	1.0E0 9. 1.0E0 9. 1
	1.0E0 9. 1.0E0 9. 1.0E0 9. 1.0E0 4.7E-1 4.
INTERPRO ATP-grasp fold, subdomain 2 RT 7 9.0E-2 2.2E	1.0E0 9. 1.0E0 9. 1.0E0 1 Benjamini Fi 4.7E-1 4. 1.0E0 4.8E-1
INTERPRO ATP-grasp fold, subdomain 2 RT 7 9.0E-2 2.2E INTERPRO ATP-grasp fold RT 5 1.4E-1 2.4E	1.0E0 9. 1.0E0 9. 1.0E0 1 Benjamini FI 4.7E-1 4. 1 4.8E-1 1

Annota	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	<u>Pre-ATP-grasp domain</u>	<u>RT</u>	i	5	1.8E-1		8.6E-1	7.9E-
	INTERPRO	ATP-grasp fold, subdomain 1	RT		5	2.1E-1	2.1E0	9.8E-1	9.1E-
	INTERPRO	Rudiment single hybrid motif	RT	-	3	2.5E-1		1.0E0	1 9.2E-
	UP_SEQ_FEATURE		_	:	3	5.9E-1			1 9.7E-
		domain:ATP-grasp	<u>RT</u>			1	Fold	1.0E0	1
Annota	INTERPRO	Enrichment Score: 0.74	G	-	Count	P_Value	Change	•	4.7E-
	INTERPRO	TRAF-like	<u>RT</u>	•	8	9.5E-2	2.0E0	5.1E-1	1
		SIAH-type domain	RT	i	5	1.1E-1	2.6E0	6.0E-1	5.6E- 1
	INTERPRO	Zinc finger, TRAF-type	<u>RT</u>	i	4	3.0E-1	2.1E0	1.0E0	9.2E- 1
	UP_SEQ_FEATURE	zinc finger region:TRAF-type	<u>RT</u>	i	3	3.3E-1	2.6E0	1.0E0	9.7E- 1
Annota	ation Cluster 235	Enrichment Score: 0.73	G	178	Count	P_Value	Fold Change	Benjamin	FDR
	INTERPRO	Pancreatic hormone-like, conserved site	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E- 1
	GOTERM_MF_DIRECT	neuropeptide hormone activity	<u>RT</u>	i e	9	1.2E-1	1.8E0	5.7E-1	5.2E- 1
	INTERPRO	Pancreatic hormone-like	<u>RT</u>	1	3	1.2E-1	4.6E0	6.2E-1	5.8E- 1
	GOTERM_BP_DIRECT	regulation of appetite	<u>RT</u>	i e	4	2.3E-1	2.4E0	1.0E0	9.6E-
	SMART	<u>РАН</u>	<u>RT</u>	1	3	2.6E-1	3.0E0	9.6E-1	8.5E-
	UP_KEYWORDS	Amidation	RT		7	6.6E-1		1.0E0	1 8.0E-
Annot	ation Cluster 236	Enrichment Score: 0.73	G	· ·	Count	P_Value	Fold	Daniamin	I FDR
	BIOCARTA	Small Leucine-rich Proteoglycan (SLRP)	RT		6	1.5E-2	Change	5.4E-2	4.0E-
	GOTERM_BP_DIRECT	molecules							2 3.7E-
	UP_SEQ_FEATURE	keratan sulfate catabolic process glycosylation site:N-linked (GlcNAc)	<u>RT</u>		6	3.8E-2		3.9E-1	1 8.5E-
	UP_KEYWORDS	(keratan sulfate)	<u>RT</u>		3	5.8E-2	6.8E0	8.8E-1	1
		<u>Proteoglycan</u>	<u>RT</u>	•	11	1.7E-1	1.5E0	5.6E-1	4.5E- 1
	GOTERM_BP_DIRECT	keratan sulfate biosynthetic process	<u>RT</u>	i	6	5.2E-1	1.3E0	1.0E0	9.6E- 1
	GOTERM_CC_DIRECT	<u>lysosomal lumen</u>	<u>RT</u>	i e	13	7.0E-1	9.7E-1	1.0E0	8.9E- 1
	GOTERM_CC_DIRECT	<u>Golgi lumen</u>	<u>RT</u>	1	14	7.6E-1	9.3E-1	1.0E0	8.9E- 1
	UP_KEYWORDS	Extracellular matrix	<u>RT</u>		19	1.0E0	5.1E-1 Fold		1.0E0
Annota	ation Cluster 237 UP_SEQ_FEATURE	Enrichment Score: 0.73	G	- T	Count	P_Value	Change	:	9.7E-
	INTERPRO	repeat:RCC1 7 Regulator of chromosome condensation,	<u>RT</u>	1	4	1.0E-1		1.0E0	1 5.3E-
	UP_SEQ_FEATURE	RCC1	<u>RT</u>	•	7	1.1E-1	2.1E0	5.8E-1	1
		repeat:RCC1 5	RT	i	6	1.1E-1	2.3E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:RCC1 4	<u>RT</u>	i	6	1.3E-1	2.1E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:RCC1 1	<u>RT</u>	i contraction	6	1.6E-1	2.0E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:RCC1 2	<u>RT</u>	1	6	1.6E-1	2.0E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:RCC1 3	<u>RT</u>	i contraction	6	1.6E-1	2.0E0	1.0E0	9.7E- 1
	INTERPRO	Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II	<u>RT</u>	1	6	2.8E-1	1.7E0	1.0E0	9.2E- 1
	UP_SEQ_FEATURE	repeat:RCC1 6	<u>RT</u>	i	4	3.0E-1	2.1E0	1.0E0	9.7E-
	COG_ONTOLOGY	<u>Cell division and chromosome partitioning /</u> Cytoskeleton	<u>RT</u>	i de	5	1.0E0	5.1E-1	1.0E0	1.0E0
A 10 10 10 1			G	*	Count	P_Value	Fold	Benjamin	i FDR
Annota	ation Cluster 238	Enrichment Score: 0.73					Change		7.5E-
Annota	uP_SEQ_FEATURE	metal ion-binding site:Magnesium	RT		30	·	1.7E0	7.8E-2	7.52
Annota		metal ion-binding site:Magnesium		•	30	3.1E-3			2 7.5E-
Annota	UP_SEQ_FEATURE	metal ion-binding site:Magnesium P-type ATPase, transmembrane domain	<u>RT</u>	:	30 8	3.1E-3 8.4E-3	3.1E0	8.1E-2	2
Annota	UP_SEQ_FEATURE INTERPRO GOTERM_BP_DIRECT	metal ion-binding site:Magnesium P-type ATPase, transmembrane domain cellular sodium ion homeostasis	RT RT		30 8 9	3.1E-3 8.4E-3 8.5E-3	3.1E0 2.8E0	8.1E-2 1.4E-1	2 7.5E- 2 1.4E- 1
	UP_SEQ_FEATURE INTERPRO GOTERM_BP_DIRECT INTERPRO	metal ion-binding site:Magnesium P-type ATPase, transmembrane domain cellular sodium ion homeostasis Cation-transporting P-type ATPase, C-terminal	RT RT RT		30 8 9 8	3.1E-3 8.4E-3 8.5E-3 1.2E-2	3.1E0 2.8E0 2.9E0	8.1E-2 1.4E-1 1.2E-1	2 7.5E- 2 1.4E- 1 1.1E- 1
	UP_SEQ_FEATURE INTERPRO GOTERM_BP_DIRECT INTERPRO INTERPRO	metal ion-binding site:Magnesium P-type ATPase, transmembrane domain cellular sodium ion homeostasis Cation-transporting P-type ATPase, C-	RT RT		30 8 9	3.1E-3 8.4E-3 8.5E-3 1.2E-2 1.7E-2	3.1E0 2.8E0 2.9E0 2.8E0	8.1E-2 1.4E-1 1.2E-1 1.4E-1	2 7.5E- 2 1.4E- 1 1.1E- 1 1.2E-
	UP_SEQ_FEATURE INTERPRO GOTERM_BP_DIRECT INTERPRO INTERPRO GOTERM_MF_DIRECT	metal ion-binding site:Magnesium P-type ATPase, transmembrane domain cellular sodium ion homeostasis Cation-transporting P-type ATPase, C-terminal Cation-transporting P-type ATPase, N-	RT RT RT		30 8 9 8	3.1E-3 8.4E-3 8.5E-3 1.2E-2 1.7E-2	3.1E0 2.8E0 2.9E0	8.1E-2 1.4E-1 1.2E-1 1.4E-1	2 7.5E-2 1.4E-1 1.1E-1 1.2E-1 2.7E-1
	UP_SEQ_FEATURE INTERPRO GOTERM_BP_DIRECT INTERPRO INTERPRO GOTERM_MF_DIRECT INTERPRO	metal ion-binding site:Magnesium P-type ATPase, transmembrane domain cellular sodium ion homeostasis Cation-transporting P-type ATPase, C-terminal Cation-transporting P-type ATPase, N-terminal	RT RT RT RT		30 8 9 8	3.1E-3 8.4E-3 8.5E-3 1.2E-2 1.7E-2 4.9E-2	3.1E0 2.8E0 2.9E0 2.8E0	8.1E-2 1.4E-1 1.2E-1 1.4E-1 2.9E-1	2 7.5E- 2 1.4E- 1 1.1E- 1 1.2E- 1
	UP_SEQ_FEATURE INTERPRO GOTERM_BP_DIRECT INTERPRO INTERPRO GOTERM_MF_DIRECT	metal ion-binding site:Magnesium P-type ATPase, transmembrane domain cellular sodium ion homeostasis Cation-transporting P-type ATPase, C-terminal Cation-transporting P-type ATPase, N-terminal calcium-transporting ATPase activity	RT RT RT RT RT		30 8 9 8 8	3.1E-3 8.4E-3 8.5E-3 1.2E-2 1.7E-2 4.9E-2 5.4E-2	3.1E0 2.8E0 2.9E0 2.8E0 3.3E0	8.1E-2 1.4E-1 1.2E-1 1.4E-1 2.9E-1 3.7E-1	2 7.5E-2 1.4E-1 1.1E-1 1.2E-1 2.7E-1 3.4E-
	UP_SEQ_FEATURE INTERPRO GOTERM_BP_DIRECT INTERPRO INTERPRO GOTERM_MF_DIRECT INTERPRO	metal ion-binding site:Magnesium P-type ATPase, transmembrane domain cellular sodium ion homeostasis Cation-transporting P-type ATPase, C-terminal Cation-transporting P-type ATPase, N-terminal calcium-transporting ATPase activity P-type ATPase, A domain	RT RT RT RT RT RT		30 8 9 8 8 5	3.1E-3 8.4E-3 8.5E-3 1.2E-2 1.7E-2 4.9E-2 5.4E-2	3.1E0 2.8E0 2.9E0 2.8E0 3.3E0 1.9E0	8.1E-2 1.4E-1 1.2E-1 1.4E-1 2.9E-1 3.7E-1	2 7.5E- 2 1.4E- 1 1.1E- 1 1.2E- 1 2.7E- 1 3.4E- 1

	ation Cluster 1	Enrichment Score: ?	G	·	Count	P_Value	Fold Change	Benjamini	i FDR
	UP_SEQ_FEATURE	active site:4-aspartylphosphate intermediate	<u>RT</u>	i	11	5.9E-2	1.9E0	8.9E-1	8.6E-
	INTERPRO	<u>Calcium-transporting P-type ATPase,</u> <u>subfamily IIA, SERCA-type</u>	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E-
	SMART	SM00831	<u>RT</u>		8	7.5E-2	2.0E0	3.9E-1	3.4E-
	UP_SEQ_FEATURE	metal ion-binding site:Calcium 2; via carbonyl	RT		10	1.1E-1		1.0E0	1 9.7E-
	INTERPRO	oxygen Sodium/potassium-transporting P-type							1 9.2E-
	GOTERM_CC_DIRECT	ATPase, subfamily IIC	<u>RT</u>		3	2.5E-1		1.0E0	1 8.2E-
		sarcoplasmic reticulum membrane	<u>RT</u>	•	8	2.8E-1	1.5E0	9.2E-1	1
	GOTERM_CC_DIRECT	sarcoplasmic reticulum	<u>RT</u>	i	8	2.8E-1	1.5E0	9.2E-1	8.2E- 1
	UP_SEQ_FEATURE	metal ion-binding site:Calcium 2	<u>RT</u>	i	11	3.2E-1	1.3E0	1.0E0	9.7E- 1
	GOTERM_CC_DIRECT	platelet dense tubular network membrane	<u>RT</u>	i .	3	4.3E-1	2.1E0	1.0E0	8.9E- 1
	GOTERM_MF_DIRECT	sodium: potassium-exchanging ATPase activity	<u>RT</u>	i .	3	5.2E-1	1.8E0	1.0E0	9.1E- 1
	GOTERM_BP_DIRECT	sodium ion export from cell	<u>RT</u>	i	3	5.2E-1	1.8E0	1.0E0	9.6E-
	UP_KEYWORDS	Sarcoplasmic reticulum	<u>RT</u>		7	5.4E-1	1.2E0	1.0E0	8.0E-
	INTERPRO	HAD-like domain	RT	-	14	5.5E-1		1.0E0	1 9.2E-
	GOTERM_BP_DIRECT								1 9.6E-
		cellular potassium ion homeostasis	<u>RT</u>	•	3	6.3E-1	1.5E0	1.0E0	1
	GOTERM_BP_DIRECT	establishment or maintenance of transmembrane electrochemical gradient	<u>RT</u>	i	3	6.7E-1	1.4E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	regulation of cardiac conduction	<u>RT</u>	1	9	7.5E-1	9.5E-1	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	potassium ion import	<u>RT</u>	i .	3	9.6E-1	6.3E-1	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	ATP hydrolysis coupled proton transport	<u>RT</u>	i .	3	9.8E-1	5.6E-1	1.0E0	9.8E-
	GOTERM_BP_DIRECT	calcium ion transmembrane transport	<u>RT</u>	i e	12	9.9E-1	6.0E-1	1.0E0	9.9E-
	GOTERM_BP_DIRECT	ion transmembrane transport	<u>RT</u>		24	9.9E-1	6.8E-1	1.0E0	9.9E-
	UP_KEYWORDS	Potassium transport	RT	i	7	1.0E0	4.1E-1		1 1.0E(
	UP_KEYWORDS	<u>Potassium</u>	<u>RT</u>	1	8	1.0E0	4.3E-1		1.0E
	UP_KEYWORDS UP_SEQ_FEATURE	<u>Calcium transport</u> topological domain:Lumenal	RT RT		5 17	1.0E0 1.0E0	3.5E-1 2.6E-1		1.0E(
	UP_KEYWORDS	Ion transport	<u>RT</u>	i	24	1.0E0	2.6E-1		1.0E0
Annot	ation Cluster 239	Enrichment Score: 0.72	G	™	Count	P_Value	Fold Change	Benjamini	i FDR
	GOTERM_BP_DIRECT	3'-UTR-mediated mRNA stabilization	<u>RT</u>	i .	7	5.3E-2	2.4E0	4.9E-1	4.7E- 1
	GOTERM_MF_DIRECT	translation activator activity	<u>RT</u>		4	1.8E-1	2.7E0	7.6E-1	6.9E-
	GOTERM_MF_DIRECT GOTERM_MF_DIRECT	mRNA 3'-UTR binding	RT RT	i i	8		2.7E0 9.7E-1		1
Annota							9.7E-1 Fold		1 9.1E- 1
Annota	GOTERM_MF_DIRECT	mRNA 3'-UTR binding	RT G	- - -	8	7.3E-1	9.7E-1 Fold Change	1.0E0	1 9.1E- 1 FDR 5.8E-
Annota	GOTERM_MF_DIRECT ation Cluster 240	mRNA 3'-UTR binding Enrichment Score: 0.7 zinc finger region:Phorbol-ester/DAG-type 1	RT G RT	i 	8 Count	7.3E-1 P_Value 3.3E-2	9.7E-1 Fold Change 2.5E0	1.0E0 Benjamini 6.0E-1	9.1E- 1 FDR 5.8E- 1
Annota	GOTERM_MF_DIRECT ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE	mRNA 3'-UTR binding Enrichment Score: 0.7 zinc finger region:Phorbol-ester/DAG-type 1 zinc finger region:Phorbol-ester/DAG-type 2	RT G RT RT		8 Count 8	7.3E-1 P_Value 3.3E-2 3.3E-2	9.7E-1 Fold Change 2.5E0 2.5E0	1.0E0 Benjamini 6.0E-1 6.0E-1	9.1E 1 FDR 5.8E 1 5.8E
Annot	GOTERM_MF_DIRECT ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO	mRNA 3'-UTR binding Enrichment Score: 0.7 zinc finger region: Phorbol-ester/DAG-type 1 zinc finger region: Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types	RT G RT RT RT	i 	8 Count	7.3E-1 P_Value 3.3E-2 3.3E-2 7.0E-2	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0	1.0E0 Benjamini 6.0E-1 6.0E-1 3.9E-1	9.1E- 1 5.8E- 1 5.8E- 1 3.6E- 1
Annot	GOTERM_MF_DIRECT ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO PIR_SUPERFAMILY	mRNA 3'-UTR binding Enrichment Score: 0.7 zinc finger region:Phorbol-ester/DAG-type 1 zinc finger region:Phorbol-ester/DAG-type 2	RT G RT RT		8 Count 8	7.3E-1 P_Value 3.3E-2 3.3E-2	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0	1.0E0 Benjamini 6.0E-1 6.0E-1	9.1E-1 1 FDR 5.8E-1 5.8E-1 1 3.6E-1
Annot	GOTERM_MF_DIRECT ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO PIR_SUPERFAMILY GOTERM_MF_DIRECT	mRNA 3'-UTR binding Enrichment Score: 0.7 zinc finger region: Phorbol-ester/DAG-type 1 zinc finger region: Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types protein kinase C, alpha/beta/gamma types calcium-dependent protein kinase C activity	RT G RT RT RT		8 8 8 3	7.3E-1 P_Value 3.3E-2 3.3E-2 7.0E-2	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0 6.0E0	1.0E0 Benjamini 6.0E-1 6.0E-1 3.9E-1	9.1E-1 1 FDR 5.8E-1 3.6E-1 6.0E-1 5.5E-1
Annot	GOTERM_MF_DIRECT ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO PIR_SUPERFAMILY	mRNA 3'-UTR binding Enrichment Score: 0.7 zinc finger region: Phorbol-ester/DAG-type 1 zinc finger region: Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types protein kinase C, alpha/beta/gamma types	RT G RT RT RT RT		8 8 8 3 3	7.3E-1 P_Value 3.3E-2 3.3E-2 7.0E-2 7.3E-2	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0 6.0E0 4.5E0	1.0E0 Benjamini 6.0E-1 6.0E-1 3.9E-1 6.0E-1	9.1E- 1 5.8E- 1 3.6E- 1 6.0E- 1 5.5E- 1
Annot	GOTERM_MF_DIRECT ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO PIR_SUPERFAMILY GOTERM_MF_DIRECT	mRNA 3'-UTR binding Enrichment Score: 0.7 zinc finger region: Phorbol-ester/DAG-type 1 zinc finger region: Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types protein kinase C, alpha/beta/gamma types calcium-dependent protein kinase C activity negative regulation of glial cell apoptotic	RT RT RT RT RT RT		8	7.3E-1 P_Value 3.3E-2 3.3E-2 7.0E-2 7.3E-2 1.3E-1	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0 6.0E0 4.5E0 2.5E0	1.0E0 Benjamini 6.0E-1 6.0E-1 3.9E-1 6.0E-1 6.0E-1	9.1E-1 1 5.8E-1 3.6E-1 6.0E-1 9.6E-1
Annot	GOTERM_MF_DIRECT ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO PIR_SUPERFAMILY GOTERM_MF_DIRECT GOTERM_BP_DIRECT	mRNA 3'-UTR binding Enrichment Score: 0.7 zinc finger region:Phorbol-ester/DAG-type 1 zinc finger region:Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types protein kinase C, alpha/beta/gamma types calcium-dependent protein kinase C activity negative regulation of glial cell apoptotic process	RT RT RT RT RT RT RT		8 8 8 3 3 3	7.3E-1 P_Value 3.3E-2 3.3E-2 7.0E-2 7.3E-1 3.4E-1	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0 6.0E0 4.5E0 2.5E0 1.3E0	1.0E0 Benjamini 6.0E-1 6.0E-1 3.9E-1 6.0E-1 6.0E-1 1.0E0	9.1E-1 1 5.8E-1 5.8E-1 3.6E-1 6.0E-1 1 9.6E-1 1 9.7E-1
Annot	GOTERM_MF_DIRECT ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO PIR_SUPERFAMILY GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE	Enrichment Score: 0.7 zinc finger region: Phorbol-ester/DAG-type 1 zinc finger region: Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types protein kinase C, alpha/beta/gamma types calcium-dependent protein kinase C activity negative regulation of glial cell apoptotic process metal ion-binding site: Calcium 1 African trypanosomiasis metal ion-binding site: Calcium 3; via carbonyl	RT RT RT RT RT RT RT RT RT		8 8 8 3 3 3 9	7.3E-1 P_Value 3.3E-2 3.3E-2 7.0E-2 7.3E-1 3.4E-1 3.9E-1	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0 6.0E0 4.5E0 2.5E0 1.3E0 1.3E0	1.0E0 Benjamini 6.0E-1 6.0E-1 3.9E-1 6.0E-1 1.0E0 1.0E0	9.1E-1 5.8E-1 5.8E-1 3.6E-1 6.0E-1 9.6E-1 9.7E-1 4.4E-1
Annot	GOTERM_MF_DIRECT ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO PIR_SUPERFAMILY GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE KEGG_PATHWAY	mRNA 3'-UTR binding Enrichment Score: 0.7 zinc finger region:Phorbol-ester/DAG-type 1 zinc finger region:Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types protein kinase C, alpha/beta/gamma types calcium-dependent protein kinase C activity negative regulation of glial cell apoptotic process metal ion-binding site:Calcium 1 African trypanosomiasis metal ion-binding site:Calcium 3; via carbonyl oxygen metal ion-binding site:Calcium 1; via carbonyl	RT RT RT RT RT RT RT RT RT		8 8 8 3 3 3 9 8 4	7.3E-1 P_Value 3.3E-2 3.3E-2 7.0E-2 7.3E-1 3.4E-1 3.9E-1 4.4E-1 6.1E-1	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0 6.0E0 4.5E0 2.5E0 1.3E0 1.3E0 1.3E0	1.0E0 Benjamini 6.0E-1 6.0E-1 3.9E-1 6.0E-1 1.0E0 1.0E0 6.6E-1 1.0E0	1 9.1E-1 1 5.8E-1 3.6E-1 1 6.0E-1 1 9.6E-1 1 9.7E-1 1 9.7E-1
Annot	GOTERM_MF_DIRECT ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO PIR_SUPERFAMILY GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE KEGG_PATHWAY UP_SEQ_FEATURE	Enrichment Score: 0.7 zinc finger region:Phorbol-ester/DAG-type 1 zinc finger region:Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types protein kinase C, alpha/beta/gamma types calcium-dependent protein kinase C activity negative regulation of glial cell apoptotic process metal ion-binding site:Calcium 1 African trypanosomiasis metal ion-binding site:Calcium 1; via carbonyl oxygen metal ion-binding site:Calcium 1; via carbonyl oxygen	RT		8 8 8 3 3 3 9 8 4 4	7.3E-1 P_Value 3.3E-2 7.0E-2 7.3E-2 1.3E-1 3.4E-1 4.4E-1 6.1E-1 8.7E-1	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0 6.0E0 4.5E0 2.5E0 1.3E0 1.3E0 8.5E-1	1.0E0 Benjamini 6.0E-1 6.0E-1 3.9E-1 6.0E-1 1.0E0 1.0E0 6.6E-1 1.0E0 1.0E0	9.1E-1 1 5.8E-1 5.8E-1 3.6E-1 6.0E-1 5.5E-1 9.7E-1 4.4E-1
	GOTERM_MF_DIRECT ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO PIR_SUPERFAMILY GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE KEGG_PATHWAY UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE	Enrichment Score: 0.7 zinc finger region:Phorbol-ester/DAG-type 1 zinc finger region:Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types protein kinase C, alpha/beta/gamma types calcium-dependent protein kinase C activity negative regulation of glial cell apoptotic process metal ion-binding site:Calcium 1 African trypanosomiasis metal ion-binding site:Calcium 1; via carbonyl oxygen metal ion-binding site:Calcium 3	RT		8 8 8 8 3 3 3 9 8 4 4 4	7.3E-1 P_Value 3.3E-2 3.3E-2 7.0E-2 7.3E-1 3.4E-1 3.9E-1 4.4E-1 6.1E-1 8.7E-1 8.7E-1	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0 6.0E0 4.5E0 2.5E0 1.3E0 1.3E0 8.5E-1 8.5E-1	1.0E0 Benjamini 6.0E-1 6.0E-1 3.9E-1 6.0E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	1 9.1E-1 1 5.8E-1 3.6E-1 6.0E-1 9.6E-1 1 9.7E-1 1 9.7E-1 1
	ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO PIR_SUPERFAMILY GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE KEGG_PATHWAY UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 241	Enrichment Score: 0.7 zinc finger region:Phorbol-ester/DAG-type 1 zinc finger region:Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types protein kinase C, alpha/beta/gamma types calcium-dependent protein kinase C activity negative regulation of glial cell apoptotic process metal ion-binding site:Calcium 1 African trypanosomiasis metal ion-binding site:Calcium 1; via carbonyl oxygen metal ion-binding site:Calcium 3 Enrichment Score: 0.69	RT		8 Count 8 8 3 3 3 9 8 4 4 4 Count	7.3E-1 P_Value 3.3E-2 7.0E-2 7.3E-2 1.3E-1 3.4E-1 4.4E-1 6.1E-1 8.7E-1 8.7E-1 P_Value	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0 6.0E0 4.5E0 2.5E0 1.3E0 1.3E0 8.5E-1 8.5E-1 Fold Change	1.0E0 Benjamini 6.0E-1 6.0E-1 3.9E-1 6.0E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini	1 9.1E-1 1 5.8E-1 3.6E-1 6.0E-1 9.7E-1 9.7E-1 9.7E-1 1 9.7E-1 9.7E-1
	GOTERM_MF_DIRECT ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO PIR_SUPERFAMILY GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE KEGG_PATHWAY UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE Ation Cluster 241 INTERPRO	Enrichment Score: 0.7 zinc finger region:Phorbol-ester/DAG-type 1 zinc finger region:Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types protein kinase C, alpha/beta/gamma types calcium-dependent protein kinase C activity negative regulation of glial cell apoptotic process metal ion-binding site:Calcium 1 African trypanosomiasis metal ion-binding site:Calcium 1; via carbonyl oxygen metal ion-binding site:Calcium 3	RT		8 8 8 8 3 3 3 9 8 4 4 4	7.3E-1 P_Value 3.3E-2 3.3E-2 7.0E-2 7.3E-1 3.4E-1 3.9E-1 4.4E-1 6.1E-1 8.7E-1 8.7E-1	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0 6.0E0 4.5E0 2.5E0 1.3E0 1.3E0 8.5E-1 8.5E-1 Fold Change	1.0E0 Benjamini 6.0E-1 6.0E-1 3.9E-1 6.0E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	1 9.1E-1 1 5.8E-1 3.6E-1 1 6.0E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1
	ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO PIR_SUPERFAMILY GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE KEGG_PATHWAY UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 241	Enrichment Score: 0.7 zinc finger region:Phorbol-ester/DAG-type 1 zinc finger region:Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types protein kinase C, alpha/beta/gamma types calcium-dependent protein kinase C activity negative regulation of glial cell apoptotic process metal ion-binding site:Calcium 1 African trypanosomiasis metal ion-binding site:Calcium 1; via carbonyl oxygen metal ion-binding site:Calcium 3 Enrichment Score: 0.69	RT		8 Count 8 8 3 3 3 9 8 4 4 4 Count	7.3E-1 P_Value 3.3E-2 7.0E-2 7.3E-2 1.3E-1 3.4E-1 4.4E-1 6.1E-1 8.7E-1 8.7E-1 P_Value	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0 6.0E0 4.5E0 2.5E0 1.3E0 1.3E0 8.5E-1 8.5E-1 Fold Change 3.4E0	1.0E0 Benjamini 6.0E-1 6.0E-1 3.9E-1 6.0E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini	1 9.1E 1 5.8E 1 3.6E 1 6.0E 1 9.7E 1 9.7E 1 9.7E 1 9.7E 1 9.7E
	GOTERM_MF_DIRECT ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO PIR_SUPERFAMILY GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE KEGG_PATHWAY UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE Ation Cluster 241 INTERPRO	Enrichment Score: 0.7 zinc finger region:Phorbol-ester/DAG-type 1 zinc finger region:Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types protein kinase C, alpha/beta/gamma types calcium-dependent protein kinase C activity negative regulation of glial cell apoptotic process metal ion-binding site:Calcium 1 African trypanosomiasis metal ion-binding site:Calcium 1; via carbonyl oxygen metal ion-binding site:Calcium 3 Enrichment Score: 0.69 Formyl peptide receptor family	RT R		8 Count 8 8 3 3 3 9 8 4 4 4 Count 5	7.3E-1 P_Value 3.3E-2 7.0E-2 7.3E-2 1.3E-1 3.4E-1 4.4E-1 6.1E-1 8.7E-1 8.7E-1 P_Value 4.3E-2	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0 6.0E0 4.5E0 2.5E0 1.3E0 1.3E0 8.5E-1 8.5E-1 Fold Change 3.4E0 4.5E0	1.0E0 Benjamini 6.0E-1 6.0E-1 3.9E-1 6.0E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini 3.0E-1	1 9.1E-1 1 5.8E-1 3.6E-1 1 6.0E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1
	ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO PIR_SUPERFAMILY GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE KEGG_PATHWAY UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE Ation Cluster 241 INTERPRO GOTERM_MF_DIRECT	Enrichment Score: 0.7 zinc finger region:Phorbol-ester/DAG-type 1 zinc finger region:Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types protein kinase C, alpha/beta/gamma types calcium-dependent protein kinase C activity negative regulation of glial cell apoptotic process metal ion-binding site:Calcium 1 African trypanosomiasis metal ion-binding site:Calcium 3; via carbonyl oxygen metal ion-binding site:Calcium 1; via carbonyl oxygen metal ion-binding site:Calcium 3 Enrichment Score: 0.69 Formyl peptide receptor family N-formyl peptide receptor activity complement receptor mediated signaling	RT G RT		8 Count 8 8 3 3 3 9 8 4 4 4 Count 5 3	7.3E-1 P_Value 3.3E-2 7.0E-2 7.3E-2 1.3E-1 3.4E-1 4.4E-1 6.1E-1 8.7E-1 8.7E-1 P_Value 4.3E-2 1.3E-1	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0 6.0E0 4.5E0 2.5E0 1.3E0 1.3E0 1.3E0 8.5E-1 8.5E-1 Fold Change 3.4E0 4.5E0 2.4E0	1.0E0 Benjamini 6.0E-1 6.0E-1 3.9E-1 6.0E-1 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini 3.0E-1 6.0E-1	1 9.1E-1 1 5.8E-1 3.6E-1 1 9.6E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1
	GOTERM_MF_DIRECT ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO PIR_SUPERFAMILY GOTERM_MF_DIRECT UP_SEQ_FEATURE KEGG_PATHWAY UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE Ation Cluster 241 INTERPRO GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT	Enrichment Score: 0.7 zinc finger region:Phorbol-ester/DAG-type 1 zinc finger region:Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types protein kinase C, alpha/beta/gamma types calcium-dependent protein kinase C activity negative regulation of glial cell apoptotic process metal ion-binding site:Calcium 1 African trypanosomiasis metal ion-binding site:Calcium 3; via carbonyl oxygen metal ion-binding site:Calcium 3 Enrichment Score: 0.69 Formyl peptide receptor family N-formyl peptide receptor activity complement receptor mediated signaling pathway	RT G RT		8 Count 8 8 3 3 3 9 8 4 4 4 Count 5 3 4	7.3E-1 P_Value 3.3E-2 7.0E-2 7.3E-2 1.3E-1 3.4E-1 4.4E-1 6.1E-1 8.7E-1 8.7E-1 P_Value 4.3E-2 1.3E-1 2.3E-1 2.6E-1	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0 6.0E0 4.5E0 2.5E0 1.3E0 1.3E0 1.3E0 8.5E-1 8.5E-1 Fold Change 3.4E0 4.5E0 2.4E0	1.0E0 Benjamini 6.0E-1 6.0E-1 3.9E-1 6.0E-1 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini 3.0E-1 6.0E-1 1.0E0 9.9E-1	1 9.1E-1 5.8E-1 3.6E-1 6.0E-1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1
Annota	GOTERM_MF_DIRECT ation Cluster 240 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO PIR_SUPERFAMILY GOTERM_MF_DIRECT UP_SEQ_FEATURE KEGG_PATHWAY UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT	Enrichment Score: 0.7 zinc finger region:Phorbol-ester/DAG-type 1 zinc finger region:Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types protein kinase C, alpha/beta/gamma types calcium-dependent protein kinase C activity negative regulation of glial cell apoptotic process metal ion-binding site:Calcium 1 African trypanosomiasis metal ion-binding site:Calcium 3; via carbonyl oxygen metal ion-binding site:Calcium 1; via carbonyl oxygen metal ion-binding site:Calcium 3 Enrichment Score: 0.69 Formyl peptide receptor family N-formyl peptide receptor activity complement receptor mediated signaling pathway complement receptor activity	RI G RI		8 8 8 8 3 3 3 9 8 4 4 4 Count 5 3 4 3 7	7.3E-1 P_Value 3.3E-2 7.0E-2 7.3E-2 1.3E-1 3.4E-1 4.4E-1 6.1E-1 8.7E-1 8.7E-1 P_Value 4.3E-2 1.3E-1 2.3E-1 2.6E-1	9.7E-1 Fold Change 2.5E0 2.5E0 6.2E0 6.0E0 4.5E0 1.3E0 1.3E0 1.3E0 8.5E-1 8.5E-1 Fold Change 3.4E0 4.5E0 2.4E0 3.0E0 6.8E-1	1.0E0 Benjamini 6.0E-1 6.0E-1 6.0E-1 6.0E-1 1.0E0 1.0E0 1.0E0 Benjamini 3.0E-1 6.0E-1 1.0E0 9.9E-1 1.0E0	1 9.1E-1 5.8E-1 5.8E-1 1 3.6E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1 1 9.7E-1

	tation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamiı	ni FC
	UP_SEQ_FEATURE	zinc finger region:Btk-type	<u>RT</u>	i .	4	1.3E-1	3.0E0	1.0E0	9. 1
	INTERPRO	Zinc finger, Btk motif	<u>RT</u>	i	4	1.7E-1	2.8E0	8.1E-1	7. 1
)	SMART	<u>BTK</u>	<u>RT</u>	1	4	3.9E-1	1.8E0	1.0E0	8. 1
not	tation Cluster 243	Enrichment Score: 0.69	G		Count	P_Value	Fold Change	Benjamii	ni FC
	GOTERM_MF_DIRECT	peptide YY receptor activity	<u>RT</u>	1	3	7.5E-2	6.0E0	3.9E-1	3. 1
	INTERPRO	Neuropeptide Y receptor family	<u>RT</u>	i	4	2.6E-1	2.3E0	1.0E0	9. 1
	GOTERM_MF_DIRECT	neuropeptide Y receptor activity	<u>RT</u>	1	3	4.6E-1	2.0E0	1.0E0	9. 1
not	tation Cluster 244	Enrichment Score: 0.67	G	177	Count	P_Value	Fold Change	Benjamii	
	UP_SEQ_FEATURE	region of interest:I-domain	<u>RT</u>	i	3	1.1E-1		1.0E0	9. 1
	INTERPRO	XPG conserved site	<u>RT</u>		3	1.2E-1	4.6E0	6.2E-1	5. 1
	INTERPRO	XPG/Rad2 endonuclease	<u>RT</u>		3	1.9E-1	3.7E0	8.7E-1	8
	INTERPRO	5'-3' exonuclease, C-terminal domain	RT	1	3	1.9E-1	3.7E0	8.7E-1	8
	INTERPRO	XPG-I domain	RT	1	3	1.9E-1		8.7E-1	8
	INTERPRO	Helix-hairpin-helix motif, class 2	RT	1	3	1.9E-1		8.7E-1	1 8
	UP_SEQ_FEATURE	region of interest:N-domain	RT	1	3	2.2E-1		1.0E0	1 9
	INTERPRO	XPG N-terminal	RT	1	3	2.5E-1		1.0E0	1 9
	SMART			•					1
	SMART	HhH2	<u>RT</u>		3	3.6E-1		1.0E0	1 8
	SMART	<u>XPGI</u>	<u>RT</u>		3	3.6E-1		1.0E0	1 8
		<u>XPGN</u>	RT		3	3.6E-1	E-14	1.0E0	1
ota	tation Cluster 245 INTERPRO	Enrichment Score: 0.67	G	-	Count	P_Value	Change	_	ni F 1
	GOTERM_MF_DIRECT	Aspartic peptidase, DDI1-type	RT	i	4	1.5E-2		1.2E-1	1
		aspartic-type endopeptidase activity	<u>RT</u>	•	10	8.8E-2	1.8E0	4.6E-1	1
	INTERPRO	Aspartic peptidase	<u>RT</u>	•	8	1.3E-1	1.8E0	6.5E-1	6
	INTERPRO	Peptidase A1	<u>RT</u>	•	4	2.1E-1	2.5E0	9.7E-1	9
	INTERPRO	Propeptide, peptidase A1	<u>RT</u>	1	3	3.2E-1	2.7E0	1.0E0	9
	UP_KEYWORDS	Aspartyl protease	<u>RT</u>	i	4	6.1E-1	1.3E0	1.0E0	8
	INTERPRO	Peptidase aspartic, active site	<u>RT</u>	1	4	6.8E-1	1.2E0	1.0E0	9 1
	UP_SEQ_FEATURE	propeptide:Activation peptide	<u>RT</u>	•	1		3.6E-1	1.0E0	1
				_	4	1.0E0	Fold		
iota	tation Cluster 246 UP SEQ FEATURE	Enrichment Score: 0.64	G	13	Count	P_Value	Fold Change	_	
iot	UP_SEQ_FEATURE	domain:PDZ	G RT	**	Count 25	P_Value 3.8E-2	Fold Change 1.5E0	6.8E-1	6
iota	UP_SEQ_FEATURE UP_SEQ_FEATURE	domain:PDZ short sequence motif:LD motif 1	RT RT	i i	Count	P_Value 3.8E-2 5.8E-2	Fold Change 1.5E0 6.8E0	6.8E-1 8.8E-1	6 1 8 1
iota	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE	domain:PDZ	G RT	**	Count 25	P_Value 3.8E-2	Fold Change 1.5E0 6.8E0	6.8E-1	6 1 8 1 8
iota	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE	domain:PDZ short sequence motif:LD motif 1	RT RT	i i	25 3	P_Value 3.8E-2 5.8E-2	Fold Change 1.5E0 6.8E0 6.8E0	6.8E-1 8.8E-1	6 1 8 1 8 1 8
nota	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE	domain:PDZ short sequence motif:LD motif 1 short sequence motif:LD motif 2	G RT RT RT	i i	25 3 3	P_Value 3.8E-2 5.8E-2 5.8E-2	Fold Change 1.5E0 6.8E0 6.8E0 6.8E0	6.8E-1 8.8E-1 8.8E-1	6 1 8 1 8 1 8 1
iota	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE	domain:PDZ short sequence motif:LD motif 1 short sequence motif:LD motif 2 short sequence motif:LD motif 3	RT RT RT RT		25 3 3 3	P_Value 3.8E-2 5.8E-2 5.8E-2 5.8E-2	Fold Change 1.5E0 6.8E0 6.8E0 6.8E0 1.8E0	6.8E-1 8.8E-1 8.8E-1 8.8E-1	66 11 88 11 88 11 99 11
101	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE	domain:PDZ short sequence motif:LD motif 1 short sequence motif:LD motif 2 short sequence motif:LD motif 3 domain:LIM zinc-binding	RT RT RT RT RT		25 3 3 3 5	P_Value 3.8E-2 5.8E-2 5.8E-2 5.8E-2 3.0E-1	Fold Change 1.5E0 6.8E0 6.8E0 6.8E0 1.6E0	6.8E-1 8.8E-1 8.8E-1 1.0E0	6 1 8 1 8 1 8 1 9 1 9
101	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE	domain:PDZ short sequence motif:LD motif 1 short sequence motif:LD motif 2 short sequence motif:LD motif 3 domain:LIM zinc-binding domain:LIM zinc-binding 3	RT RT RT RT RT		25 3 3 5 6	P_Value 3.8E-2 5.8E-2 5.8E-2 3.0E-1 3.0E-1 3.5E-1	Fold Change 1.5E0 6.8E0 6.8E0 1.8E0 1.6E0 1.2E0	6.8E-1 8.8E-1 8.8E-1 1.0E0 1.0E0	6 6 1 8 1 8 1 1 8 1 1 9 1 1 8 1 1 9 1 1 8 1 1 9 1 1 9 1 1 9 1 1 1 1
TOTAL	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE	short sequence motif:LD motif 1 short sequence motif:LD motif 2 short sequence motif:LD motif 3 domain:LIM zinc-binding domain:LIM zinc-binding 3 LIM domain	RT RT RT RT RT RT RT		25 3 3 5 6 13	P_Value 3.8E-2 5.8E-2 5.8E-2 3.0E-1 3.0E-1 3.5E-1	Fold Change 1.5E0 6.8E0 6.8E0 1.8E0 1.6E0 1.9E0	6.8E-1 8.8E-1 8.8E-1 1.0E0 1.0E0	6 1 8 1 8 1 9 1 1 8 1 9 1 1 9 1 9
TOTAL	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE	short sequence motif:LD motif 1 short sequence motif:LD motif 2 short sequence motif:LD motif 3 domain:LIM zinc-binding domain:LIM zinc-binding 3 LIM domain domain:LIM zinc-binding 4	RT RT RT RT RT RT RT		25 3 3 5 6 13 3	P_Value 3.8E-2 5.8E-2 5.8E-2 3.0E-1 3.5E-1 5.0E-1	Fold Change 1.5E0 6.8E0 6.8E0 1.8E0 1.6E0 1.2E0 1.9E0 1.1E0	6.8E-1 8.8E-1 8.8E-1 1.0E0 1.0E0 1.0E0	6 1 8 1 8 1 8 1 9 1 8 1 9 1 1 8 1 9 1 9 1
TOTAL	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO	short sequence motif:LD motif 1 short sequence motif:LD motif 2 short sequence motif:LD motif 3 domain:LIM zinc-binding domain:LIM zinc-binding 3 LIM domain domain:LIM zinc-binding 4 Zinc finger, LIM-type	RI		25 3 3 3 5 6 13 3 13	P_Value 3.8E-2 5.8E-2 5.8E-2 3.0E-1 3.5E-1 5.0E-1 5.0E-1	Fold Change 1.5E0 6.8E0 6.8E0 1.8E0 1.6E0 1.2E0 1.9E0 1.1E0 1.1E0	6.8E-1 8.8E-1 8.8E-1 1.0E0 1.0E0 1.0E0 1.0E0	6 1 8 1 8 1 8 1 9 1 1 8 1 9 1 1 1 9 1 1 1 9 1 1 1 9 1 1 1 1 9 1
101	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE	short sequence motif:LD motif 1 short sequence motif:LD motif 2 short sequence motif:LD motif 3 domain:LIM zinc-binding domain:LIM zinc-binding 3 LIM domain domain:LIM zinc-binding 4 Zinc finger, LIM-type domain:LIM zinc-binding 1	RI		25 3 3 3 5 6 13 3 13	P_Value 3.8E-2 5.8E-2 5.8E-2 3.0E-1 3.5E-1 5.0E-1 6.2E-1 6.2E-1	Fold Change 1.5E0 6.8E0 6.8E0 1.8E0 1.6E0 1.2E0 1.9E0 1.1E0 1.1E0	6.8E-1 8.8E-1 8.8E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	6 1 8 1 8 1 9 1 1 9 1 9 1 9 1 9 1 9 1 9
	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE	short sequence motif:LD motif 1 short sequence motif:LD motif 2 short sequence motif:LD motif 3 domain:LIM zinc-binding domain:LIM zinc-binding 3 LIM domain domain:LIM zinc-binding 4 Zinc finger, LIM-type domain:LIM zinc-binding 1 domain:LIM zinc-binding 2	RI		Count 25 3 3 5 6 13 3 13 8	P_Value 3.8E-2 5.8E-2 5.8E-2 3.0E-1 3.0E-1 5.0E-1 6.2E-1 9.6E-1	Fold Change 1.5E0 6.8E0 6.8E0 1.8E0 1.6E0 1.2E0 1.9E0 1.1E0 1.1E0 7.3E-1	6.8E-1 8.8E-1 8.8E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	6 1 8 1 8 1 8 1 9 1 1 8 1 9 1 1 9 1 1 9 1 1 9 1 1
	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE SMART	short sequence motif:LD motif 1 short sequence motif:LD motif 2 short sequence motif:LD motif 3 domain:LIM zinc-binding domain:LIM zinc-binding 3 LIM domain domain:LIM zinc-binding 4 Zinc finger, LIM-type domain:LIM zinc-binding 1 domain:LIM zinc-binding 2 LIM	RI R		25 3 3 3 5 6 13 3 13 8 8 13	P_Value 3.8E-2 5.8E-2 5.8E-2 3.0E-1 3.5E-1 5.0E-1 6.2E-1 6.2E-1	Fold Change 1.5E0 6.8E0 6.8E0 1.8E0 1.6E0 1.2E0 1.1E0 1.1E0 7.3E-1 Fold Change	6.8E-1 8.8E-1 8.8E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	6 1 8 1 8 1 8 1 9 1 8 1 9 1 9 1 9 1 9 1 1
	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE SMART	short sequence motif:LD motif 1 short sequence motif:LD motif 2 short sequence motif:LD motif 3 domain:LIM zinc-binding domain:LIM zinc-binding 3 LIM domain domain:LIM zinc-binding 4 Zinc finger, LIM-type domain:LIM zinc-binding 1 domain:LIM zinc-binding 2 LIM Enrichment Score: 0.63	RI R		25 3 3 3 5 6 13 3 13 8 8 13 Count	P_Value 3.8E-2 5.8E-2 5.8E-2 3.0E-1 3.0E-1 5.0E-1 6.2E-1 9.6E-1 P_Value	Fold Change 1.5E0 6.8E0 6.8E0 1.8E0 1.6E0 1.2E0 1.1E0 1.1E0 1.1E0 7.3E-1 Fold Change 5.0E0	6.8E-1 8.8E-1 8.8E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 Benjamin	6 1 8 1 8 1 8 1 9 1 9 1 9 1 9 1 1 9 1 1 2 1 2
	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE SMART	short sequence motif:LD motif 1 short sequence motif:LD motif 2 short sequence motif:LD motif 3 domain:LIM zinc-binding domain:LIM zinc-binding 3 LIM domain domain:LIM zinc-binding 4 Zinc finger, LIM-type domain:LIM zinc-binding 1 domain:LIM zinc-binding 2 LIM Enrichment Score: 0.63 Enolase, C-terminal	RI R		Count 25 3 3 3 5 6 13 3 13 8 8 13 Count	P_Value 3.8E-2 5.8E-2 5.8E-2 3.0E-1 3.0E-1 5.0E-1 6.2E-1 9.6E-1 P_Value 3.2E-2	Fold Change 1.5E0 6.8E0 6.8E0 1.8E0 1.6E0 1.2E0 1.9E0 1.1E0 1.1E0 7.3E-1 Fold Change 5.0E0 4.2E0	6.8E-1 8.8E-1 8.8E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 2.3E-1	6 1 8 1 8 1 8 1 9 1 1 9 1 1 9 1 1 9 1 1 2 1 1 3
	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE OUP_SEQ_FEATURE SMART tation Cluster 247 INTERPRO GOTERM_CC_DIRECT	short sequence motif:LD motif 1 short sequence motif:LD motif 2 short sequence motif:LD motif 3 domain:LIM zinc-binding domain:LIM zinc-binding 3 LIM domain domain:LIM zinc-binding 4 Zinc finger, LIM-type domain:LIM zinc-binding 1 domain:LIM zinc-binding 2 LIM Enrichment Score: 0.63 Enolase, C-terminal phosphopyruvate hydratase complex	RI R		25 3 3 3 3 5 6 13 3 13 8 8 13 Count 4 4	P_Value 3.8E-2 5.8E-2 5.8E-2 3.0E-1 3.0E-1 5.0E-1 6.2E-1 9.6E-1 P_Value 3.2E-2 5.4E-2	Fold Change 1.5E0 6.8E0 6.8E0 1.8E0 1.6E0 1.2E0 1.1E0 1.1E0 7.3E-1 Fold Change 5.0E0 4.2E0 4.1E0	6.8E-1 8.8E-1 8.8E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 2.3E-1 3.2E-1	6 1 8 1 8 1 9 1 9 1 9 1 9 1 9 1

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

Anno	otation Cluster 1	Enrichment Score: ?	G	™	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:EGF-like 8; calcium-binding	<u>RT</u>	i	5	4.8E-1	1.4E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	domain:EGF-like 16; calcium-binding	<u>RT</u>		3	5.0E-1	1.9E0	1.0E0	9.7E-
	UP_SEQ_FEATURE	domain:EGF-like 9; calcium-binding	RT		3	7.0E-1		1.0E0	1 9.7E-
	UP_SEQ_FEATURE			-					1 9.7E-
	UP_SEQ_FEATURE	domain:EGF-like 9	<u>RT</u>	•	4	7.1E-1	1.1E0	1.0E0	1
		domain:EGF-like 10	<u>RT</u>	i	3	7.4E-1	1.2E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	domain:EGF-like 6	<u>RT</u>	i	6	7.9E-1	9.3E-1	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	domain:EGF-like 7; calcium-binding	<u>RT</u>	i	4	8.0E-1	9.7E-1	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	domain:EGF-like 3	<u>RT</u>	i .	9	8.9E-1	8.1E-1	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	domain:EGF-like 7	<u>RT</u>	i contraction	3	9.3E-1	7.3E-1	1.0E0	9.7E-
	UP_SEQ_FEATURE	domain:EGF-like 4	<u>RT</u>	i	6	9.5E-1	6.9E-1	1.0E0	9.7E-
	UP_SEQ_FEATURE	domain:EGF-like 5	<u>RT</u>		4	9.6E-1	6.5E-1	1.0E0	9.7E-
	UP_SEQ_FEATURE	domain:EGF-like 5; calcium-binding	RT		3		5.4E-1		1 9.8E-
	UP_SEQ_FEATURE			-					1 9.8E-
	UP_SEQ_FEATURE	domain:EGF-like 2 domain:EGF-like 1	RT RT		9	1.0E0	6.1E-1 5.1E-1		1 1.0E0
	INTERPRO	EGF-like calcium-binding, conserved site	RT	i e	7	1.0E0	4.3E-1		1.0E0
	INTERPRO	EGF-type aspartate/asparagine hydroxylation site	<u>RT</u>	i	7	1.0E0	4.1E-1	1.0E0	1.0E0
	INTERPRO	EGF-like calcium-binding	<u>RT</u>	1	7	1.0E0	3.4E-1	1.0E0	1.0E0
	INTERPRO UP_KEYWORDS	EGF-like, conserved site EGF-like domain	RT DT		10	1.0E0	3.1E-1		1.0E0
	INTERPRO	Epidermal growth factor-like domain	RT RT		10 11	1.0E0 1.0E0	2.9E-1 3.0E-1		1.0E0 1.0E0
	SMART	EGF CA	RT	i	7	1.0E0	2.2E-1		1.0E0
	SMART	<u>EGF</u>	<u>RT</u>	i	11	1.0E0	2.4E-1	1.0E0	1.0E0
Anno	otation Cluster 249	Enrichment Score: 0.62			Count	P_Value	Fold Change	Benjamini	FDR
	UP_KEYWORDS	<u>Glycogen metabolism</u>	<u>RT</u>	i	8	7.3E-2	2.1E0	2.8E-1	2.3E- 1
	GOTERM_BP_DIRECT	glycogen metabolic process	<u>RT</u>	i .	8	2.1E-1	1.6E0	1.0E0	9.6E-
	UP_KEYWORDS	Carbohydrate metabolism	<u>RT</u>	i	10	9.4E-1	7.3E-1	1.0E0	9.4E-
Anno	otation Cluster 250	Enrichment Score: 0.61	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	regulation of establishment of endothelial	<u>RT</u>	:	4	9.9E-2	<u> </u>	7.0E-1	6.7E-
	GOTERM_BP_DIRECT	<u>harrier</u> <u>negative regulation of bicellular tight junction</u>	RT		3	1.3E-1		8.3E-1	1 7.9E-
	GOTERM_BP_DIRECT	assembly negative regulation of myosin-light-chain-	RT		3	2.0E-1		1.0E0	1 9.6E-
	GOTERM_BP_DIRECT	phosphatase activity							1 9.6E-
	GOTERM_BP_DIRECT	cortical actin cytoskeleton organization establishment of protein localization to	<u>RT</u>		6	3.8E-1		1.0E0	1 9.6E-
		plasma membrane	<u>RT</u>		6	•	8.5E-1		1
Anno	otation Cluster 251	Enrichment Score: 0.61	G		Count	P_Value	Change	Benjamini	
	INTERPRO	Actin-related protein 3 (Arp3)	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E- 1
	GOTERM_CC_DIRECT	Arp2/3 protein complex	<u>RT</u>	i e	4	2.9E-1	2.1E0	9.2E-1	8.2E- 1
	GOTERM_BP_DIRECT	Arp2/3 complex-mediated actin nucleation	<u>RT</u>	i	4	7.4E-1	1.1E0	1.0E0	9.6E- 1
Anno	otation Cluster 252	Enrichment Score: 0.61	G	™	Count	P_Value	Fold Change	Benjamini	FDR
	UP_KEYWORDS	<u>Rotamase</u>	<u>RT</u>	1	10	9.1E-2	1.8E0	3.5E-1	2.8E-
	GOTERM_BP_DIRECT	protein peptidyl-prolyl isomerization	<u>RT</u>	i	12	9.7E-2	1.7E0	7.0E-1	6.7E-
	UP_SEQ_FEATURE	domain:PPIase cyclophilin-type	<u>RT</u>		7	1.3E-1	2.0E0	1.0E0	9.7E-
	GOTERM_MF_DIRECT	peptidyl-prolyl cis-trans isomerase activity	<u>RT</u>	•	12	1.4E-1	1.6E0	6.1E-1	5.5E-
	UP_KEYWORDS	<u>Isomerase</u>	RT		23		1.3E0		1 4.5E-
	INTERPRO	Cyclophilin-like peptidyl-prolyl cis-trans	RT		7	1.8E-1		8.6E-1	1 7.9E-
	INTERPRO	isomerase domain Cyclophilin-type peptidyl-prolyl cis-trans							1 9.2E-
	INTERPRO	isomerase, conserved site Cyclophilin-type peptidyl-prolyl cis-trans	<u>RT</u>		6	2.4E-1		1.0E0	9.2E-
		<u>isomerase</u>	<u>RT</u>	T.	6	3.1E-1		1.0E0	1
	GOTERM_MF_DIRECT	cyclosporin A binding	<u>RT</u>	1	3	3.3E-1	2.6E0	1.0E0	9.1E- 1
	INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type	<u>RT</u>	i	5	4.1E-1	1.5E0	1.0E0	9.2E- 1
	GOTERM_BP_DIRECT	<u>chaperone-mediated protein folding</u>	<u>RT</u>	i .	8	4.4E-1	1.3E0	1.0E0	9.6E- 1
	GOTERM_MF_DIRECT	FK506 binding	<u>RT</u>	i .	5	4.4E-1	1.5E0	1.0E0	9.1E- 1

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

Annota	ation Cluster 1	Enrichment Score: ?	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	fatty acid catabolic process	<u>RT</u>	i	3	4.6E-1		1.0E0	9.6E-
	GOTERM_MF_DIRECT			- -	3	5.7E-1		1.0E0	1 9.1E-
	GOTERM_BP_DIRECT	phosphatidate phosphatase activity	<u>RT</u>	1	3	5./E-1	1.650	1.000	1
		<u>phosphatidylethanolamine biosynthetic</u> <u>process</u>	<u>RT</u>	i	3	7.5E-1	1.2E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	phosphatidylcholine biosynthetic process	<u>RT</u>	1	3	9.4E-1	7.1E-1	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	triglyceride biosynthetic process	<u>RT</u>	1	3	9.5E-1	6.8E-1	1.0E0	9.6E- 1
	KEGG_PATHWAY	Glycerolipid metabolism	<u>RT</u>	1	3	1.0E0	2.7E-1	1.0E0	1.0E0
	KEGG_PATHWAY	<u>Glycerophospholipid metabolism</u>	<u>RT</u>	i	6	1.0E0	3.3E-1	1.0E0	1.0E0
Annota	ation Cluster 259	Enrichment Score: 0.58	G		Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	negative regulation of anoikis	<u>RT</u>	i e	8	1.6E-2	2.8E0	2.2E-1	2.1E- 1
	GOTERM_BP_DIRECT	negative regulation of intrinsic apoptotic signaling pathway	<u>RT</u>	i	8	6.4E-2	2.2E0	5.5E-1	5.3E- 1
	GOTERM_MF_DIRECT	BH3 domain binding	RT	1	3	1.3E-1	4 5F0	6.0E-1	5.5E-
	INTERPRO	Apoptosis regulator, Bcl-2, BH1 motif,							1 9.2E-
		conserved site	<u>RT</u>	*	3	3.8E-1	2.3E0	1.0E0	1
	INTERPRO	<u>Apoptosis regulator, Bcl-2, BH2 motif,</u> <u>conserved site</u>	<u>RT</u>	1	3	3.8E-1	2.3E0	1.0E0	9.2E- 1
	INTERPRO	Apoptosis regulator, Bcl-2, BH3 motif, conserved site	<u>RT</u>	i .	3	3.8E-1	2.3E0	1.0E0	9.2E- 1
	UP_SEQ_FEATURE	short sequence motif:BH1	<u>RT</u>	i	3	5.0E-1	1.9E0	1.0E0	9.7E-
	INTERPRO	Blc2 family	RT		3	5.5E-1	1 7F0	1.0E0	1 9.2E-
	INTERPRO								1 9.2E-
		Bcl2-like	<u>RT</u>	1	3	5.5E-1	1.7E0	1.0E0	1
	UP_SEQ_FEATURE	short sequence motif:BH2	<u>RT</u>	i	3	5.9E-1	1.6E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	short sequence motif:BH3	<u>RT</u>	i	3	7.4E-1	1.2E0	1.0E0	9.7E- 1
Annota	ation Cluster 260	Enrichment Score: 0.57	G	**	Count	P_Value	Fold	Benjamini	1
	GOTERM_MF_DIRECT	RNA polymerase II transcription factor					Change	,	
		activity, TBP-class protein binding, involved in preinitiation complex assembly	<u>RT</u>	i	3	7.5E-2	6.0E0	3.9E-1	3.6E- 1
	GOTERM_CC_DIRECT	transcription factor TFIID complex	RT	•	9	2.0E-1	1.6E0	7.9E-1	7.1E-
	GOTERM_MF_DIRECT	transcription factor activity, RNA polymerase							0.15
		II core promoter sequence-specific binding involved in preinitiation complex assembly	<u>RT</u>	i	3	4.6E-1	2.0E0	1.0E0	9.1E- 1
	GOTERM_BP_DIRECT	RNA polymerase II transcriptional preinitiation complex assembly	<u>RT</u>	1	3	7.5E-1	1.2E0	1.0E0	9.6E- 1
Annota	ation Cluster 261	Enrichment Score: 0.57	G	<u> </u>	Count	P_Value	Fold Change	Benjamini	
	GOTERM_CC_DIRECT	I-kappaB/NF-kappaB complex	RT	1	4	3.0E-2	Change	2.0E-1	1.8E-
	INTERPRO								1 2.1E-
		<u>NF-kappa-B/Rel/Dorsal</u>	<u>RT</u>	i	4	3.2E-2	5.0E0	2.3E-1	1
	INTERPRO	Rel homology domain	<u>RT</u>	i	4	2.1E-1	2.5E0	9.7E-1	9.0E- 1
	UP_SEQ_FEATURE	domain:RHD	<u>RT</u>	1	3	3.9E-1	2.3E0	1.0E0	9.7E- 1
	INTERPRO	Cell surface receptor IPT/TIG	<u>RT</u>	1	6	5.8E-1	1.2E0	1.0E0	9.2E-
	GOTERM_MF_DIRECT	transcriptional activator activity, RNA							1
		polymerase II distal enhancer sequence- specific binding	<u>RT</u>	1	5	6.2E-1	1.2E0	1.0E0	9.1E- 1
	SMART	IPT	<u>RT</u>	i e	5	9.3E-1	7.5E-1	1.0E0	9.3E-
	INTERPRO	Immunoglobulin E-set	RT		11		6.4E-1		1 9.8E-
						•	Fold		1
Annota	ation Cluster 262	Enrichment Score: 0.55	G		Count	P_Value	Change	Benjamini	FDR
		Emichinent Score. 0.33							2 4 -
	UP_KEYWORDS	<u>Nucleotidyltransferase</u>	RT	:	17	1.0E-1	1.5E0	3.8E-1	3.1E- 1
						1.0E-1 1.2E-1		3.8E-1 6.2E-1	
	UP_KEYWORDS	Nucleotidyltransferase DNA-directed DNA polymerase, family B, exonuclease domain DNA-directed DNA polymerase, family B,	<u>RT</u>		17	1.2E-1		6.2E-1	1 5.8E- 1 5.8E-
	UP_KEYWORDS INTERPRO	Nucleotidyltransferase DNA-directed DNA polymerase, family B, exonuclease domain DNA-directed DNA polymerase, family B, multifunctional domain	RT RT RT	i i	17 3 3	1.2E-1 1.2E-1	4.6E0 4.6E0	6.2E-1 6.2E-1	1 5.8E- 1
	UP_KEYWORDS INTERPRO INTERPRO INTERPRO	Nucleotidyltransferase DNA-directed DNA polymerase, family B, exonuclease domain DNA-directed DNA polymerase, family B, multifunctional domain DNA-directed DNA polymerase, family B	RT RT RT RT		17 3 3 3	1.2E-1 1.2E-1 1.2E-1	4.6E0 4.6E0 4.6E0	6.2E-1 6.2E-1 6.2E-1	1 5.8E- 1 5.8E- 1 5.8E- 1
	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT	Nucleotidyltransferase DNA-directed DNA polymerase, family B, exonuclease domain DNA-directed DNA polymerase, family B, multifunctional domain	RT RT RT	i i	17 3 3	1.2E-1 1.2E-1	4.6E0 4.6E0 4.6E0	6.2E-1 6.2E-1	1 5.8E- 1 5.8E- 1 5.8E- 1 7.3E- 1
	UP_KEYWORDS INTERPRO INTERPRO INTERPRO	Nucleotidyltransferase DNA-directed DNA polymerase, family B, exonuclease domain DNA-directed DNA polymerase, family B, multifunctional domain DNA-directed DNA polymerase, family B	RT RT RT RT	i i i	17 3 3 3	1.2E-1 1.2E-1 1.2E-1	4.6E0 4.6E0 4.6E0 1.9E0	6.2E-1 6.2E-1 6.2E-1	1 5.8E- 1 5.8E- 1 5.8E- 1 7.3E-
	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT	Nucleotidyltransferase DNA-directed DNA polymerase, family B, exonuclease domain DNA-directed DNA polymerase, family B, multifunctional domain DNA-directed DNA polymerase, family B 3'-5' exonuclease activity	RI RI RI RI RI	i i i	17 3 3 3 6	1.2E-1 1.2E-1 1.2E-1 2.0E-1	4.6E0 4.6E0 4.6E0 1.9E0 3.0E0	6.2E-1 6.2E-1 6.2E-1 8.0E-1	1 5.8E-1 5.8E-1 5.8E-1 7.3E-1 8.5E-1 6.6E-
	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART	Nucleotidyltransferase DNA-directed DNA polymerase, family B, exonuclease domain DNA-directed DNA polymerase, family B, multifunctional domain DNA-directed DNA polymerase, family B 3'-5' exonuclease activity POLBC DNA-directed DNA polymerase	RT RT RT RT RT RT RT RT RT		17 3 3 3 6 3	1.2E-1 1.2E-1 1.2E-1 2.0E-1 2.6E-1 2.7E-1	4.6E0 4.6E0 4.6E0 1.9E0 3.0E0 1.7E0	6.2E-1 6.2E-1 6.2E-1 8.0E-1 9.6E-1 8.2E-1	1 5.8E-1 5.8E-1 7.3E-1 8.5E-1 6.6E-1 9.1E-
	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_KEYWORDS GOTERM_MF_DIRECT	Nucleotidyltransferase DNA-directed DNA polymerase, family B, exonuclease domain DNA-directed DNA polymerase, family B, multifunctional domain DNA-directed DNA polymerase, family B 3'-5' exonuclease activity POLBC DNA-directed DNA polymerase DNA-directed DNA polymerase	RT	i i i	17 3 3 3 6 3 6 7	1.2E-1 1.2E-1 1.2E-1 2.0E-1 2.6E-1 2.7E-1 3.6E-1	4.6E0 4.6E0 4.6E0 1.9E0 3.0E0 1.7E0 1.4E0	6.2E-1 6.2E-1 6.2E-1 8.0E-1 9.6E-1 8.2E-1 1.0E0	1 5.8E-1 5.8E-1 7.3E-1 8.5E-1 6.6E-1 9.1E-1
	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_KEYWORDS GOTERM_MF_DIRECT UP_KEYWORDS	Nucleotidyltransferase DNA-directed DNA polymerase, family B, exonuclease domain DNA-directed DNA polymerase, family B, multifunctional domain DNA-directed DNA polymerase, family B 3'-5' exonuclease activity POLBC DNA-directed DNA polymerase	RT RT RT RT RT RT RT RT RT		17 3 3 3 6 3	1.2E-1 1.2E-1 1.2E-1 2.0E-1 2.6E-1 2.7E-1	4.6E0 4.6E0 4.6E0 1.9E0 3.0E0 1.7E0 1.4E0	6.2E-1 6.2E-1 6.2E-1 8.0E-1 9.6E-1 8.2E-1	1 5.8E-1 5.8E-1 7.3E-1 8.5E-1 6.6E-1 9.1E-1 8.0E-1
	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_KEYWORDS GOTERM_MF_DIRECT	Nucleotidyltransferase DNA-directed DNA polymerase, family B, exonuclease domain DNA-directed DNA polymerase, family B, multifunctional domain DNA-directed DNA polymerase, family B 3'-5' exonuclease activity POLBC DNA-directed DNA polymerase DNA-directed DNA polymerase	RT		17 3 3 3 6 3 6 7	1.2E-1 1.2E-1 1.2E-1 2.0E-1 2.6E-1 2.7E-1 3.6E-1	4.6E0 4.6E0 4.6E0 1.9E0 3.0E0 1.7E0 1.4E0 1.3E0	6.2E-1 6.2E-1 6.2E-1 8.0E-1 9.6E-1 8.2E-1 1.0E0	1 5.8E-1 5.8E-1 7.3E-1 8.5E-1 6.6E-1 9.1E-1 8.0E-
	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_KEYWORDS GOTERM_MF_DIRECT UP_KEYWORDS	Nucleotidyltransferase DNA-directed DNA polymerase, family B, exonuclease domain DNA-directed DNA polymerase, family B, multifunctional domain DNA-directed DNA polymerase, family B 3'-5' exonuclease activity POLBC DNA-directed DNA polymerase DNA-directed DNA polymerase DNA-directed DNA polymerase	RT		17 3 3 3 6 3 6 7 7	1.2E-1 1.2E-1 1.2E-1 2.0E-1 2.6E-1 2.7E-1 3.6E-1 4.6E-1 7.3E-1	4.6E0 4.6E0 4.6E0 1.9E0 3.0E0 1.7E0 1.4E0 1.3E0	6.2E-1 6.2E-1 6.2E-1 8.0E-1 9.6E-1 8.2E-1 1.0E0 1.0E0	1 5.8E-1 5.8E-1 7.3E-1 8.5E-1 6.6E-1 9.1E-1 8.0E-1
	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_KEYWORDS GOTERM_MF_DIRECT UP_KEYWORDS GOTERM_MF_DIRECT	Nucleotidyltransferase DNA-directed DNA polymerase, family B, exonuclease domain DNA-directed DNA polymerase, family B, multifunctional domain DNA-directed DNA polymerase, family B 3'-5' exonuclease activity POLBC DNA-directed DNA polymerase DNA-directed DNA polymerase DNA-directed DNA polymerase 4Fe-4S 4 iron, 4 sulfur cluster binding	RT		17 3 3 3 6 7 7	1.2E-1 1.2E-1 1.2E-1 2.0E-1 2.6E-1 2.7E-1 3.6E-1 4.6E-1 7.3E-1	4.6E0 4.6E0 4.6E0 1.9E0 3.0E0 1.7E0 1.4E0 1.3E0 1.0E0	6.2E-1 6.2E-1 6.2E-1 8.0E-1 9.6E-1 1.0E0 1.0E0 1.0E0	1 5.8E-1 5.8E-1 7.3E-1 8.5E-1 6.6E-1 9.1E-1 9.1E-1 1 8.9E-

nnot	tation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamin	i FD
nnot	tation Cluster 263	Enrichment Score: 0.51	G	100	Count	P_Value	Fold	Ponjamin	i FD
	GOTERM_BP_DIRECT	male meiosis	RT	i e	8	6.4E-2		5.5E-1	5.3
- ገ	GOTERM_BP_DIRECT	DNA methylation involved in gamete	RT	1	4	6.1E-1	1.3F0	1.0E0	9.6
ך ר	GOTERM_BP_DIRECT	generation piRNA metabolic process		-	3			1.0E0	1 9.6
			RT			7.5E-1	Fold	1	1
nnot	INTERPRO	Enrichment Score: 0.5	G	- <mark>- 18</mark> 	Count	P_Value	Change	=	8.9
_	UP_SEQ_FEATURE	Zinc finger, RanBP2-type	<u>RT</u>	•	7	2.1E-1	1.7E0	9.6E-1	1
		zinc finger region:RanBP2-type	<u>RT</u>	i	5	2.7E-1	1.9E0	1.0E0	9.7
	SMART	ZnF RBZ	<u>RT</u>	i	6	5.7E-1		1.0E0	8.9
nnot	tation Cluster 265	Enrichment Score: 0.5	G		Count	P_Value	Fold Change	Benjamin	
	UP_KEYWORDS	Bernard Soulier syndrome	<u>RT</u>	i	3	5.7E-2	6.9E0	2.4E-1	1.9
	GOTERM_BP_DIRECT	blood coagulation, intrinsic pathway	<u>RT</u>	1	6	1.7E-1	2.0E0	9.8E-1	9.4 1
	UP_KEYWORDS	Blood coagulation	<u>RT</u>	1	8	5.6E-1	1.1E0	1.0E0	8.0
	UP_KEYWORDS	<u>Hemostasis</u>	<u>RT</u>	1	8	5.6E-1	1.1E0	1.0E0	8. 1
	KEGG_PATHWAY	ECM-receptor interaction	<u>RT</u>	i	7	1.0E0	4.2E-1	1.0E0	1.0
not	tation Cluster 266	Enrichment Score: 0.5	G	5	Count	P_Value	Fold Change	Benjamin	i FC
)	INTERPRO	Zinc finger, TFIIS-type	<u>RT</u>	i .	3	2.5E-1	3.1E0	1.0E0	9. 1
)	UP_SEQ_FEATURE	zinc finger region:TFIIS-type	<u>RT</u>	i e	3	2.7E-1	2.9E0	1.0E0	9. 1
)	SMART	ZnF C2C2	<u>RT</u>	i	3	4.6E-1	2.0E0	1.0E0	8.
nnot	tation Cluster 267	Enrichment Score: 0.5	G	PR .	Count	P_Value	Fold Change	Benjamin	i F
)	INTERPRO	<u>Brix domain</u>	RT	7	3	2.5E-1	Change	1.0E0	9.
í 1	UP_SEQ_FEATURE	domain:Brix	RT	_	3	2.7E-1		1.0E0	1 9.
)	SMART								1 8.
J		<u>SM00879</u>	<u>RT</u>		3	4.6E-1	Fold	1.0E0	1
nnot	tation Cluster 268	Enrichment Score: 0.49	G		Count	P_Value	Change	Benjamin	_
)	UP_SEQ_FEATURE	domain:Glutamine amidotransferase type-1	<u>RT</u>	i	3	1.6E-1	4.1E0	1.0E0	9. 1
)	INTERPRO	Glutamine amidotransferase	<u>RT</u>	i	3	2.5E-1	3.1E0	1.0E0	9. 1
	GOTERM_BP_DIRECT	glutamine metabolic process	<u>RT</u>	1	3	8.7E-1	8.9E-1	1.0E0	9. 1
not	tation Cluster 269	Enrichment Score: 0.48	G	100	Count	P_Value	Fold Change	Benjamin	i FI
)	GOTERM_BP_DIRECT	cellular response to interleukin-1	<u>RT</u>	1	17	1.3E-1	1.4E0	8.3E-1	7. 1
)	GOTERM_BP_DIRECT	cellular response to interferon-gamma	<u>RT</u>	1	14	1.5E-1	1.5E0	9.0E-1	8. 1
)	GOTERM_BP_DIRECT	monocyte chemotaxis	<u>RT</u>	1	10	2.7E-1	1.4E0	1.0E0	9. 1
)	GOTERM_BP_DIRECT	<u>lymphocyte chemotaxis</u>	<u>RT</u>		6	5.2E-1	1.3E0	1.0E0	9.
)	INTERPRO	CC chemokine, conserved site	<u>RT</u>		5	5.6E-1	1.3F0	1.0E0	1 9.
) 1	GOTERM_MF_DIRECT	CCR chemokine receptor binding			4	7.7E-1		1.0E0	1 9.
			RT			1			1
nnot	tation Cluster 270 INTERPRO	Enrichment Score: 0.48	G	- <mark>- 18</mark> 	Count	P_Value	Change	·	7.
J		Insulin, conserved site	<u>RT</u>	•	4	1.7E-1		8.1E-1	1
J	INTERPRO	<u>Insulin-like</u>	<u>RT</u>	i	4	2.1E-1	2.5E0	9.7E-1	9.
)	INTERPRO	<u>Insulin family</u>	<u>RT</u>	i	3	2.5E-1	3.1E0	1.0E0	9. 1
)	SMART	<u>IIGF</u>	<u>RT</u>	i	4	4.7E-1	1.6E0	1.0E0	8. 1
)	GOTERM_MF_DIRECT	hormone activity	<u>RT</u>	1	12	9.3E-1	7.6E-1	1.0E0	9. 1
not	tation Cluster 271	Enrichment Score: 0.48	G	178	Count	P_Value	Fold Change	Benjamin	i Fl
	GOTERM_BP_DIRECT	embryonic skeletal limb joint morphogenesis	<u>RT</u>	i	3	7.6E-2		5.8E-1	5. 1
)	GOTERM_BP_DIRECT	embryonic hindlimb morphogenesis	<u>RT</u>	i	6	5.2E-1	1.3E0	1.0E0	9. 1
)	GOTERM_BP_DIRECT	embryonic forelimb morphogenesis	<u>RT</u>		4	9.2E-1	7.4E-1	1.0E0	9.
not	tation Cluster 272	Enrichment Score: 0.48	G	· ·	<u> </u>	:	Fold Change	:	1 i F
	UP_SEQ_FEATURE	domain:G-patch	<u>RT</u>	i	7			1.0E0	9.
)	INTERPRO			_					1 9.
	SMART	<u>G-patch domain</u>	<u>RT</u>	•	7	4.1E-1		1.0E0	1 8.
		<u>G_patch</u>	<u>RT</u>	_	7		9.1E-1		Ŏ.

Annota	ation Cluster 1	Enrichment Score: ?	G	· Control of the cont	Count	P_Value	Fold Change	Benjamini	FDR
Annota	ation Cluster 273	Enrichment Score: 0.47	G	MR CONTRACTOR	Count	P_Value	Eold	Benjamini	FDR
	GOTERM_BP_DIRECT	regulation of binding	<u>RT</u>	i	4	1.7E-2		2.2E-1	2.1E- 1
	BIOCARTA	TGF beta signaling pathway	<u>RT</u>	i	11	4.9E-2	1.8E0	1.3E-1	9.7E- 2
	GOTERM_BP_DIRECT	SMAD protein complex assembly	<u>RT</u>	i	4	1.4E-1	3.0E0	8.3E-1	7.9E-
	GOTERM_BP_DIRECT	positive regulation of epithelial to	<u>RT</u>		9	1.8E-1	1.6E0	1.0E0	9.5E-
	GOTERM_BP_DIRECT	mesenchymal transition endoderm development	RT		6	2.7E-1		1.0E0	1 9.6E-
	UP_SEQ_FEATURE	domain:MH2	RT		3	3.3E-1		1.0E0	1 9.7E-
	UP_SEQ_FEATURE	domain:MH1	RT	-	3	3.3E-1		1.0E0	1 9.7E-
	GOTERM_CC_DIRECT								1 8.9E-
	INTERPRO	SMAD protein complex	<u>RT</u>		3	3.7E-1		1.0E0	1 9.2E-
	INTERPRO	MAD homology, MH1	<u>RT</u>		3	3.8E-1		1.0E0	1 9.2E-
		SMAD domain, Dwarfin-type	<u>RT</u>	i	3	3.8E-1	2.3E0	1.0E0	1
	INTERPRO	<u>Dwarfin</u>	<u>RT</u>	i	3	3.8E-1	2.3E0	1.0E0	9.2E- 1
	GOTERM_BP_DIRECT	regulation of transforming growth factor beta receptor signaling pathway	<u>RT</u>	i	5	4.4E-1	1.5E0	1.0E0	9.6E- 1
	INTERPRO	MAD homology 1, Dwarfin-type	<u>RT</u>	i	3	6.0E-1	1.5E0	1.0E0	9.2E- 1
	SMART	DWB	<u>RT</u>	i	3	6.3E-1	1.5E0	1.0E0	8.9E- 1
	INTERPRO	SMAD domain-like	<u>RT</u>	i .	3	7.6E-1	1.2E0	1.0E0	9.2E- 1
	SMART	<u>DWA</u>	<u>RT</u>	i	3	8.4E-1	1.0E0	1.0E0	8.9E- 1
	GOTERM_MF_DIRECT	transforming growth factor beta receptor binding	<u>RT</u>	i	6	8.5E-1	8.5E-1	1.0E0	9.1E- 1
	BIOCARTA	Role of Tob in T-cell activation	<u>RT</u>		5	9.0E-1	8.2E-1	1.0E0	9.0E-
	GOTERM_BP_DIRECT	SMAD protein signal transduction	RT		7	9 6F-1	6.7E-1	1 0F0	1 9.6E-
Annota	ation Cluster 274	Enrichment Score: 0.46	G	·	Count	P_Value	Fold	Benjamini	1 FDR
	UP_SEQ_FEATURE	repeat:CXXCXGXG motif	RT .		3	1.1E-1	Onlange	1.0E0	9.7E-
	UP_SEQ_FEATURE	zinc finger region:CR-type	RT		3	1.1E-1		1.0E0	1 9.7E-
	INTERPRO								1 5.8E-
	INTERPRO	Chaperone DnaJ Heat shock protein DnaJ, cysteine-rich	<u>RT</u>		3	1.2E-1		6.2E-1	1 8.1E-
	INTERPRO	domain	<u>RT</u>	i	3	1.9E-1		8.7E-1	1
		<u>HSP40/DnaJ peptide-binding</u>	<u>RT</u>	i	3	4.4E-1	2.1E0	1.0E0	9.2E- 1
	INTERPRO	<u>Chaperone DnaJ, C-terminal</u>	<u>RT</u>	i	3	4.4E-1	2.1E0	1.0E0	9.2E- 1
	UP_SEQ_FEATURE	domain:J	<u>RT</u>	i	8	6.6E-1	1.0E0	1.0E0	9.7E- 1
	INTERPRO	<u>DnaJ domain</u>	<u>RT</u>	i	7	8.5E-1	8.5E-1	1.0E0	9.2E- 1
	INTERPRO	DnaJ domain, conserved site	<u>RT</u>	i	3	9.5E-1	6.9E-1	1.0E0	9.5E- 1
	SMART	<u>DnaJ</u>	<u>RT</u>	i	7	9.9E-1	5.9E-1	1.0E0	9.9E- 1
Annota	ation Cluster 275	Enrichment Score: 0.44	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	zinc finger region:B box-type 2	<u>RT</u>	i	5	2.0E-1	2.1E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	zinc finger region:B box-type 1	<u>RT</u>	i	4	2.5E-1	2.3E0	1.0E0	9.7E-
	INTERPRO	B-box, C-terminal	<u>RT</u>	i	4	4.4E-1	1.7E0	1.0E0	9.2E- 1
	SMART	BBC	<u>RT</u>	•	4	7.6E-1	1.1E0	1.0E0	8.9E-
Annota	ation Cluster 276	Enrichment Score: 0.44	G	·	:	P_Value	:	:	1 FDR
	UP_SEQ_FEATURE	zinc finger region:UBR-type	RT .	1	3	2.7E-1		1.0E0	9.7E-
	INTERPRO	Zinc finger, N-recognin	RT		3	3.2E-1		1.0E0	1 9.2E-
	SMART								1 8.9E-
		ZnF UBR1	<u>RT</u>	i	3	5.5E-1	Fold	1.0E0	1
Annota	ation Cluster 277 INTERPRO	Enrichment Score: 0.43	G	-	Count	P_Value	Change	Benjamini	FDR 9.2E-
	UP_SEQ_FEATURE	Proteasome component (PCI) domain	<u>RT</u>	i	5	2.9E-1		1.0E0	1
	OI_OLG ILAIUNE	domain:PCI	<u>RT</u>	i .	5	3.0E-1	1.8E0	1.0E0	9.7E- 1
									UNE
	SMART	<u>PINT</u>	<u>RT</u>	i	5	5.9E-1		1.0E0	8.9E- 1
Annota		PINT Enrichment Score: 0.43	RT G	i	5 Count	5.9E-1 P_Value	Fold	1.0E0 Benjamini	1

Annot	ation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 1	<u>RT</u>	1	5	3.7E-1		1.0E0	9.7E
\neg	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 2	<u>RT</u>		5	3.7E-1	1 6F0	1.0E0	9.7E
	UP_SEQ_FEATURE	·		•					1 9.7E
		short sequence motif:LXXLL motif 4	<u>RT</u>	•	3	3.9E-1	2.3E0	1.0E0	1
	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 3	<u>RT</u>	i	3	5.0E-1	1.9E0	1.0E0	9.7E 1
nnot	ation Cluster 279	Enrichment Score: 0.42	G		Count	P_Value	Fold Change	Benjamini	FDR
	KEGG_PATHWAY	Neuroactive ligand-receptor interaction	<u>RT</u>	=	78	1.8E-4	1.5E0	4.2E-4	1.9E 4
7	UP_KEYWORDS	<u>Transducer</u>	<u>RT</u>	=	166	8.1E-4	1.3E0	4.7E-3	3.78
ے م	SMART								3 5.7E
J	IID KEVIMODDS	<u>SM01381</u>	<u>RT</u>	•	43	7.3E-3	1.4E0	6.5E-2	2
	UP_KEYWORDS	G-protein coupled receptor	<u>RT</u>	=	137	1.0E-1	1.1E0	3.7E-1	3.0E 1
	GOTERM_BP_DIRECT	G-protein coupled receptor signaling pathway	<u>RT</u>	=	157	3.7E-1	1.0E0	1.0E0	9.6l
	UP_KEYWORDS	Receptor	<u>RT</u>	=	229	8.2E-1	9.5E-1	1.0E0	8.21
٦	INTERPRO	GPCR, rhodopsin-like, 7TM	<u>RT</u>	=	104	9.5F-1	8.8E-1	1.0F0	9.5
ے ا	UP_KEYWORDS			<u> </u>					1 9.6l
J	_	<u>Cell membrane</u>	<u>RT</u>	_	433	9.6E-1	9.4E-1	1.0E0	1
	INTERPRO	G protein-coupled receptor, rhodopsin-like	<u>RT</u>	<u> </u>	101	9.6E-1	8.7E-1	1.0E0	9.6l 1
	GOTERM_CC_DIRECT GOTERM_CC_DIRECT	plasma membrane	RT PT		593 182	1.0E0	9.1E-1		1.0
_]	GOTERM_MF_DIRECT	<u>integral component of plasma membrane</u> <u>G-protein coupled receptor activity</u>	RT RT	=	182 81	1.0E0 1.0E0	8.2E-1 6.8E-1		1.0
	UP_SEQ_FEATURE	topological domain:Cytoplasmic	<u>RT</u>		291	1.0E0	5.7E-1		1.0
) 7	UP_SEQ_FEATURE UP_SEQ_FEATURE	topological domain:Extracellular transmembrane region	RT RT		266 341	1.0E0 1.0E0	6.5E-1 4.6E-1		1.0
	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc)	RT		330	1.0E0	5.3E-1		1.0
	UP_SEQ_FEATURE	disulfide bond	<u>RT</u>		257	1.0E0	6.0E-1		1.0
	UP_KEYWORDS GOTERM_CC_DIRECT	Signal integral component of membrane	RT RT		310 362	1.0E0 1.0E0	5.1E-1 4.5E-1		1.0
	UP_KEYWORDS	Disulfide bond	RT		314	1.0E0	6.3E-1		1.0
	UP_KEYWORDS	<u>Transmembrane</u>	<u>RT</u>		418	1.0E0	5.1E-1		1.0
	UP_KEYWORDS UP_KEYWORDS	<u>Transmembrane helix</u> <u>Membrane</u>	RT RT		415 722	1.0E0 1.0E0	5.1E-1 6.6E-1		1.0
_									
	UP_KEYWORDS	Glycoprotein	RT		386	1.0E0	5.8E-1	1.0E0	1.0
	UP_SEQ_FEATURE	signal peptide	RT RT	=	386 264	1.0E0	5.4E-1	1.0E0	1.0
nnot	UP_SEQ_FEATURE		<u>RT</u>		386		5.4E-1	1.0E0	1.0E
] nnot	UP_SEQ_FEATURE tation Cluster 280 GOTERM_BP_DIRECT	signal peptide	RT RT	=	386 264	1.0E0	5.4E-1 Fold Change	1.0E0	1.06 FDF 3.76
nnot	UP_SEQ_FEATURE	signal peptide Enrichment Score: 0.42	RT RT G		386 264 Count	1.0E0 P_Value	5.4E-1 Fold Change 4.7E0	1.0E0 Benjamini	3.78
nnot	UP_SEQ_FEATURE tation Cluster 280 GOTERM_BP_DIRECT	signal peptide Enrichment Score: 0.42 glial cell apoptotic process	RT RT G		386 264 Count	1.0E0 P_Value 3.7E-2	5.4E-1 Fold Change 4.7E0 2.2E0	1.0E0 Benjamini 3.8E-1	1.0E FDR 3.7E 1 7.6E
nnot	UP_SEQ_FEATURE tation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by	RT RT G RT RT		386 264 Count 4	1.0E0 P_Value 3.7E-2 1.2E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0	1.0E0 Benjamini 3.8E-1 7.9E-1	1.0E FDR 3.7E 1 7.6E 1 9.5E 1
	UP_SEQ_FEATURE tation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c	RT RT G RT RT RT		386 264 Count 4 6	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0	1.08 FDF 3.78 1 7.68 1
	UP_SEQ_FEATURE tation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway	RT RT RT RT RT RT		386 264 Count 4 6 4	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1	1.00 FDF 3.70 1 7.60 1 9.50 1 1.00 9.60
	UP_SEQ_FEATURE tation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion	RT RT RT RT RT RT RT RT		386 264 Count 4 6 4 7 6 3	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.4E-1 2.7E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0	1.00 FDF 3.71 7.60 1 9.51 1 1.00 9.60 1 9.11
	UP_SEQ_FEATURE Ration Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion death receptor binding	RT RT RT RT RT RT RT RT		386 264 Count 4 6 4 7 6 3 5	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.4E-1 2.7E-1 2.7E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0 1.0E0	1.00 FDR 3.76 1 9.56 1 1.00 9.66 1 9.11
	UP_SEQ_FEATURE Tation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_COTERM_BP_DIRECT	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion	RT RT RT RT RT RT RT RT		386 264 Count 4 6 4 7 6 3	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.4E-1 2.7E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0	1.00 FDF 3.7/1 7.60 1 9.5/1 1.00 9.6/1 9.11 1.8.3/1
	UP_SEQ_FEATURE Ration Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion death receptor binding	RT RT RT RT RT RT RT RT		386 264 Count 4 6 4 7 6 3 5	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.4E-1 2.7E-1 2.7E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0 2.7E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0 1.0E0	1.00 FDF 3.7/1 7.60 1 9.5/1 1.00 9.6/1 9.11 1.8.3/1
	UP_SEQ_FEATURE Tation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_COTERM_BP_DIRECT	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion death receptor binding death-inducing signaling complex	RT RT RT RT RT RT RT RT RT		386 264 Count 4 6 4 7 6 3 5 3	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.4E-1 2.7E-1 3.0E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0 2.7E0 1.8E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0 1.0E0 9.4E-1	1.00 FDF 3.71 7.60 1 9.51 1 1.00 9.61 1 9.11 1 9.21 1
	UP_SEQ_FEATURE Ration Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT INTERPRO	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion death receptor binding death-inducing signaling complex Peptidase C14, caspase precursor p45, core	RT		386 264 Count 4 6 4 7 6 3 5 3 4	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.4E-1 2.7E-1 3.0E-1 4.0E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0 2.7E0 1.8E0 1.3E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0 9.4E-1 1.0E0	1.00 FDF 3.71 7.61 1 9.51 1 9.61 1 9.11 1 8.31 1 9.21 1 5.11 5.11
	UP_SEQ_FEATURE Station Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT INTERPRO BIOCARTA	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion death receptor binding death-inducing signaling complex Peptidase C14, caspase precursor p45, core Role of Mitochondria in Apoptotic Signaling Stress Induction of HSP Regulation	RT R		386 264 Count 4 6 4 7 6 3 5 3 4 9 7	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.7E-1 3.0E-1 4.0E-1 4.1E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0 2.7E0 1.8E0 1.3E0 1.4E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0 9.4E-1 1.0E0 6.8E-1 6.8E-1	1.00 FDR 3.7/1 7.66/1 9.5/1 1.00/9.6/1 9.11/1 8.3/1 9.2/1 5.11/1
	UP_SEQ_FEATURE ation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT INTERPRO BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA INTERPRO	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion death receptor binding death-inducing signaling complex Peptidase C14, caspase precursor p45, core Role of Mitochondria in Apoptotic Signaling Stress Induction of HSP Regulation Peptidase C14, ICE, catalytic subunit p20	RT R		386 264 Count 4 6 4 7 6 3 5 3 4 9 7 4	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.7E-1 3.0E-1 4.0E-1 4.1E-1 4.1E-1 4.4E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0 2.7E0 1.8E0 1.3E0 1.4E0 1.7E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0 9.4E-1 1.0E0 6.8E-1 6.8E-1 1.0E0	1.00 FDF 3.7/1 7.60/1 9.5/1 1.00/9.6/1 9.1/1 9.2/1 5.1/1 9.2/1
	UP_SEQ_FEATURE ation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO BIOCARTA BIOCARTA BIOCARTA BIOCARTA INTERPRO INTERPRO	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion death receptor binding death-inducing signaling complex Peptidase C14, caspase precursor p45, core Role of Mitochondria in Apoptotic Signaling Stress Induction of HSP Regulation Peptidase C14, ICE, catalytic subunit p20 Peptidase C14, ICE, catalytic subunit p20, active site	RT R		386 264 Count 4 6 4 7 6 3 5 3 4 9 7	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.7E-1 3.0E-1 4.0E-1 4.1E-1 4.1E-1 4.4E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0 2.7E0 1.8E0 1.3E0 1.4E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0 9.4E-1 1.0E0 6.8E-1 6.8E-1 1.0E0	1.00 FDF 3.71 7.61 1 9.51 1 9.61 1 9.21 1 9.21 1 9.21 1 9.21 1
	UP_SEQ_FEATURE ation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT INTERPRO BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA INTERPRO	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion death receptor binding death-inducing signaling complex Peptidase C14, caspase precursor p45, core Role of Mitochondria in Apoptotic Signaling Stress Induction of HSP Regulation Peptidase C14, ICE, catalytic subunit p20 Peptidase C14, ICE, catalytic subunit p20,	RT R		386 264 Count 4 6 4 7 6 3 5 3 4 9 7 4	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.7E-1 3.0E-1 4.0E-1 4.1E-1 4.1E-1 4.4E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0 1.8E0 1.3E0 1.4E0 1.7E0 1.9E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0 9.4E-1 1.0E0 6.8E-1 6.8E-1 1.0E0	1.00 FDF 3.71 7.61 1 9.51 1 9.61 1 9.21 1 9.21 1 9.21 1 9.21 1
	UP_SEQ_FEATURE ation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO BIOCARTA BIOCARTA BIOCARTA BIOCARTA INTERPRO INTERPRO	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion death receptor binding death-inducing signaling complex Peptidase C14, caspase precursor p45, core Role of Mitochondria in Apoptotic Signaling Stress Induction of HSP Regulation Peptidase C14, ICE, catalytic subunit p20 Peptidase C14, ICE, catalytic subunit p20, active site Peptidase C14, caspase non-catalytic subunit	RT R		386 264 Count 4 6 4 7 6 3 5 3 4 9 7 4 3	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.7E-1 2.7E-1 4.0E-1 4.1E-1 4.1E-1 4.4E-1 5.0E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0 1.8E0 1.3E0 1.4E0 1.7E0 1.9E0 1.5E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0 9.4E-1 1.0E0 6.8E-1 1.0E0 1.0E0	1.00 FDF 3.71 7.66 1 9.51 1 9.11 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1
	UP_SEQ_FEATURE ation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT INTERPRO BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA INTERPRO INTERPRO INTERPRO INTERPRO	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion death receptor binding death-inducing signaling complex Peptidase C14, caspase precursor p45, core Role of Mitochondria in Apoptotic Signaling Stress Induction of HSP Regulation Peptidase C14, ICE, catalytic subunit p20 Peptidase C14, ICE, catalytic subunit p20, active site Peptidase C14, caspase non-catalytic subunit p10 CASc cysteine-type endopeptidase activity involved	RT R		386 264 Count 4 6 4 7 6 3 5 3 4 9 7 4 3 3 3 4	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.7E-1 3.0E-1 4.0E-1 4.1E-1 4.4E-1 5.0E-1 6.0E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0 1.8E0 1.3E0 1.4E0 1.7E0 1.5E0 1.5E0 1.2E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0 9.4E-1 1.0E0 6.8E-1 1.0E0 1.0E0 1.0E0 1.0E0	1.00 FDF 3.71 7.60 1 9.51 1 9.61 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1
	UP_SEQ_FEATURE ation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA INTERPRO INTERPRO INTERPRO SMART GOTERM_MF_DIRECT	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion death receptor binding death-inducing signaling complex Peptidase C14, caspase precursor p45, core Role of Mitochondria in Apoptotic Signaling Stress Induction of HSP Regulation Peptidase C14, ICE, catalytic subunit p20 Peptidase C14, ICE, catalytic subunit p20, active site Peptidase C14, caspase non-catalytic subunit p10 CASc cysteine-type endopeptidase activity involved in apoptotic process	RT R		386 264 Count 4 6 4 7 6 3 5 3 4 9 7 4 3 3 4 3 4 3	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.4E-1 2.7E-1 3.0E-1 4.0E-1 4.1E-1 4.4E-1 5.0E-1 6.6E-1 6.7E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0 1.8E0 1.3E0 1.4E0 1.7E0 1.9E0 1.7E0 1.7E0 1.7E0 1.7E0 1.7E0 1.7E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0 9.4E-1 1.0E0 6.8E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	1.00 FDF 3.71 7.60 1 9.51 1 9.61 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1
	UP_SEQ_FEATURE ation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO BIOCARTA BIOCARTA BIOCARTA INTERPRO INTERPRO INTERPRO SMART GOTERM_MF_DIRECT BIOCARTA BIOCARTA INTERPRO INTERPRO INTERPRO INTERPRO SMART GOTERM_MF_DIRECT BIOCARTA	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion death receptor binding death-inducing signaling complex Peptidase C14, caspase precursor p45, core Role of Mitochondria in Apoptotic Signaling Stress Induction of HSP Regulation Peptidase C14, ICE, catalytic subunit p20 Peptidase C14, caspase non-catalytic subunit p10 CASc cysteine-type endopeptidase activity involved in apoptotic process Caspase Cascade in Apoptosis	RT R		386 264 Count 4 6 4 7 6 3 5 3 4 9 7 4 3 3 4 3 8	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.4E-1 2.7E-1 3.0E-1 4.0E-1 4.1E-1 4.1E-1 5.0E-1 6.0E-1 6.6E-1 6.7E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0 1.8E0 1.4E0 1.7E0 1.5E0 1.5E0 1.4E0 1.10E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0 9.4E-1 1.0E0 6.8E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	1.00 FDF 3.71 7.61 1.00 9.61 1.00 9.21 1.1 9.21 9.
	UP_SEQ_FEATURE ation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO BIOCARTA BIOCARTA INTERPRO INTERPRO INTERPRO SMART GOTERM_MF_DIRECT BIOCARTA BIOCARTA	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion death receptor binding death-inducing signaling complex Peptidase C14, caspase precursor p45, core Role of Mitochondria in Apoptotic Signaling Stress Induction of HSP Regulation Peptidase C14, ICE, catalytic subunit p20 Peptidase C14, ICE, catalytic subunit p20, active site Peptidase C14, caspase non-catalytic subunit p10 CASc cysteine-type endopeptidase activity involved in apoptotic process Caspase Cascade in Apoptosis 150.caspase and NFKB activation	RT R		386 264 Count 4 6 4 7 6 3 5 3 4 9 7 4 3 3 3 4 3 8 6	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.4E-1 2.7E-1 3.0E-1 4.0E-1 4.1E-1 4.1E-1 5.0E-1 6.0E-1 6.6E-1 6.7E-1 8.5E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0 1.3E0 1.4E0 1.7E0 1.5E0 1.5E0 1.4E0 1.1E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0 9.4E-1 1.0E0 6.8E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	1.00 FDF 3.71 7.60 1 9.51 1 9.11 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1 1 1 1 1 1 1 1 1 1 1 1 1
	UP_SEQ_FEATURE ation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO BIOCARTA BIOCARTA BIOCARTA INTERPRO INTERPRO INTERPRO SMART GOTERM_MF_DIRECT BIOCARTA BIOCARTA INTERPRO INTERPRO INTERPRO INTERPRO SMART GOTERM_MF_DIRECT BIOCARTA	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion death receptor binding death-inducing signaling complex Peptidase C14, caspase precursor p45, core Role of Mitochondria in Apoptotic Signaling Stress Induction of HSP Regulation Peptidase C14, ICE, catalytic subunit p20 Peptidase C14, ICE, catalytic subunit p20, active site Peptidase C14, caspase non-catalytic subunit p10 CASc cysteine-type endopeptidase activity involved in apoptotic process Caspase Cascade in Apoptosis 150.caspase and NFKB activation 72.IAP interaction with cell death pathways	RT R		386 264 Count 4 6 4 7 6 3 5 3 4 9 7 4 3 3 4 3 8	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.4E-1 2.7E-1 3.0E-1 4.0E-1 4.1E-1 4.4E-1 5.0E-1 6.6E-1 6.7E-1 6.9E-1 8.5E-1 9.0E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0 1.8E0 1.4E0 1.7E0 1.5E0 1.5E0 1.4E0 1.10E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0 9.4E-1 1.0E0 6.8E-1 1.0E0	1.0 FDF 3.7 1 9.5 1 1.0 9.6 1 9.1 1 9.2 1 9.3 1 9.3 1 9.4 1 9.5 1
	UP_SEQ_FEATURE ation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_CC_DIRECT INTERPRO BIOCARTA BIOCARTA INTERPRO INTERPRO INTERPRO SMART GOTERM_MF_DIRECT BIOCARTA BIOCARTA	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion death receptor binding death-inducing signaling complex Peptidase C14, caspase precursor p45, core Role of Mitochondria in Apoptotic Signaling Stress Induction of HSP Regulation Peptidase C14, ICE, catalytic subunit p20 Peptidase C14, ICE, catalytic subunit p20, active site Peptidase C14, caspase non-catalytic subunit p10 CASc cysteine-type endopeptidase activity involved in apoptotic process Caspase Cascade in Apoptosis 150.caspase and NFKB activation 72.IAP interaction with cell death pathways cysteine-type endopeptidase activity	RT R		386 264 Count 4 6 4 7 6 3 5 3 4 9 7 4 3 3 4 3 8 6 5 8	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.4E-1 2.7E-1 3.0E-1 4.0E-1 4.1E-1 4.1E-1 6.0E-1 6.0E-1 6.7E-1 6.9E-1 8.5E-1 9.0E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0 1.8E0 1.4E0 1.7E0 1.5E0 1.5E0 1.4E0 1.5E0 1.4E0 1.7E0 1.5E0 1.4E0 1.7E0 1.7E0 1.8E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0 9.4E-1 1.0E0 6.8E-1 1.0E0 1.0E0	1.00 FDF 3.71 7.60 1 9.51 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1 9.31 1 9.11 9.11
	UP_SEQ_FEATURE ation Cluster 280 GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT BIOCARTA BBID GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO BIOCARTA BIOCARTA INTERPRO INTERPRO INTERPRO SMART GOTERM_MF_DIRECT BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA INTERPRO INTERPRO SMART GOTERM_MF_DIRECT BIOCARTA BBID BOCARTA	signal peptide Enrichment Score: 0.42 glial cell apoptotic process execution phase of apoptosis activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c D4-GDI Signaling Pathway 86.Apoptosis Nematode& Vert response to cobalt ion death receptor binding death-inducing signaling complex Peptidase C14, caspase precursor p45, core Role of Mitochondria in Apoptotic Signaling Stress Induction of HSP Regulation Peptidase C14, ICE, catalytic subunit p20 Peptidase C14, ICE, catalytic subunit p20, active site Peptidase C14, caspase non-catalytic subunit p10 CASc cysteine-type endopeptidase activity involved in apoptotic process Caspase Cascade in Apoptosis 150.caspase and NFKB activation 72.IAP interaction with cell death pathways	RT R		386 264 Count 4 6 4 7 6 3 5 3 4 9 7 4 3 3 4 3 4 3 8 6 5 5	1.0E0 P_Value 3.7E-2 1.2E-1 1.8E-1 2.1E-1 2.4E-1 2.7E-1 3.0E-1 4.0E-1 4.1E-1 4.1E-1 6.0E-1 6.0E-1 6.7E-1 6.9E-1 8.5E-1 9.0E-1	5.4E-1 Fold Change 4.7E0 2.2E0 2.6E0 1.7E0 1.7E0 3.0E0 1.9E0 1.3E0 1.4E0 1.7E0 1.5E0 1.5E0 1.4E0 1.6E0 1.7E0 1.6E0	1.0E0 Benjamini 3.8E-1 7.9E-1 1.0E0 4.2E-1 1.0E0 1.0E0 9.4E-1 1.0E0 6.8E-1 1.0E0	1.00 FDF 3.71 7.61 1 9.51 1 9.61 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1 9.21 1 1 9.21 1 1 1 1 1 1 1 1 1 1 1 1 1

Annota	ation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	i FDR
	INTERPRO	Nitric oxide synthase, oxygenase domain	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E-
	GOTERM_MF_DIRECT	nitric-oxide synthase activity	<u>RT</u>	-	3	7.5E-2	6.0E0	3.9E-1	3.6E-
	UP_SEQ_FEATURE				3				1 9.7E-
		domain:Flavodoxin-like	<u>RT</u>	i	4	1.0E-1	3.4E0	1.0E0	1
	INTERPRO	Flavodoxin/nitric oxide synthase	<u>RT</u>	i e	4	1.2E-1	3.1E0	6.2E-1	5.8E- 1
	INTERPRO	<u>Flavodoxin</u>	<u>RT</u>	i .	4	1.2E-1	3.1E0	6.2E-1	5.8E-
	GOTERM_MF_DIRECT	<u>tetrahydrobiopterin binding</u>	<u>RT</u>	1	3	1.3E-1	4.5F0	6.0E-1	5.5E-
	INTERPRO			-					1 9.2E-
		FAD-binding, type 1	<u>RT</u>	1	3	2.5E-1	3.1E0	1.0E0	1
	INTERPRO	NADPH-cytochrome p450 reductase, FAD- binding, alpha-helical domain-3	<u>RT</u>	i	3	2.5E-1	3.1E0	1.0E0	9.2E- 1
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:FMN	<u>RT</u>	i contract of	4	3.0E-1	2.1E0	1.0E0	9.7E- 1
	INTERPRO	Oxidoreductase FAD/NAD(P)-binding	<u>RT</u>	i .	4	3.0E-1	2.1E0	1.0E0	9.2E- 1
	GOTERM_MF_DIRECT	arginine binding	<u>RT</u>	1	3	3.3E-1	2.6F0	1.0E0	9.1E-
	GOTERM_MF_DIRECT								1 9.1E-
		NADP binding	<u>RT</u>	i	8	3.7E-1	1.4E0	1.0E0	1
	GOTERM_BP_DIRECT	nitric oxide biosynthetic process	<u>RT</u>	i e	4	3.8E-1	1.8E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	arginine catabolic process	<u>RT</u>	i	3	4.0E-1	2.2E0	1.0E0	9.6E- 1
	INTERPRO	Flavoprotein pyridine nucleotide cytochrome reductase	<u>RT</u>	1	3	4.4E-1	2.1E0	1.0E0	9.2E- 1
	GOTERM_MF_DIRECT	FMN binding	RT	1	4	4.7E-1	1 6E0	1.0E0	9.1E-
	UP_SEQ_FEATURE			-					1 9.7E-
		domain:FAD-binding FR-type	<u>RT</u>	•	4	5.4E-1	1.4E0	1.0E0	1
	KEGG_PATHWAY	Arginine biosynthesis	<u>RT</u>	i	5	5.4E-1	1.3E0	8.0E-1	5.4E- 1
	UP_KEYWORDS	<u>FMN</u>	<u>RT</u>	i	4	6.1E-1	1.3E0	1.0E0	8.0E- 1
	INTERPRO	Ferredoxin reductase-type FAD-binding	<u>RT</u>	1	4	6.1E-1	1.3E0	1.0E0	9.2E-
	INTERPRO	domain Riboflavin synthase-like beta-barrel	RT		4	6.1E-1	1 350	1.0E0	1 9.2E-
	UP_SEQ_FEATURE			1	4	0.16-1	1.360	1.000	1 9.7E-
		nucleotide phosphate-binding region:NADP	<u>RT</u>	•	8	9.3E-1	7.4E-1	1.0E0	1
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:FAD	<u>RT</u>	i	6	9.6E-1	6.6E-1	1.0E0	9.7E- 1
	COG_ONTOLOGY	<u>Inorganic ion transport and metabolism</u>	<u>RT</u>	i	6	9.9E-1	5.7E-1	1.0E0	1.0E0
	GOTERM_MF_DIRECT	<u>heme binding</u>	<u>RT</u>	i	14	9.9E-1	6.1E-1	1.0E0	9.9E- 1
	UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	<u>RT</u>	i	7	1.0E0	4.8E-1	1.0E0	1.0E0
	KEGG_PATHWAY	Arginine and proline metabolism	<u>RT</u>	i contract of	4	1.0E0	4.2E-1	1.0E0	1.0E0
	GOTERM_MF_DIRECT UP_KEYWORDS	flavin adenine dinucleotide binding	RT RT		4 8	1.0E0 1.0E0	3.7E-1 4.2E-1		1.0E0 1.0E0
	UP_KEYWORDS	Heme FAD	RT			1.0E0	3.1E-1		1.0E0
	UP_KEYWORDS	<u>Flavoprotein</u>	<u>RT</u>	1	5	1.0E0	2.8E-1		1.0E0
	UP_KEYWORDS UP_KEYWORDS	NADP Oxidoreductase	RT RT		9 24	1.0E0 1.0E0	3.3E-1 2.8E-1		1.0E0 1.0E0
Annota	ation Cluster 282	Enrichment Score: 0.4	G		Count	P_Value	Fold	Benjamini	
	INTERPRO	<u>TRAF-like</u>	<u>RT</u>	1	8	9.5E-2	Change	5.1E-1	4.7E-
	UP_SEQ_FEATURE								1 9.7E-
		domain:MATH	<u>RT</u>	i	3	5.4E-1	1.7E0	1.0E0	1
	INTERPRO	<u>MATH</u>	<u>RT</u>	i	3	6.0E-1	1.5E0	1.0E0	9.2E- 1
	SMART	<u>MATH</u>	<u>RT</u>	i e	3	8.4E-1	1.0E0	1.0E0	8.9E- 1
Annota	ation Cluster 283	Enrichment Score: 0.39	G	- 13	Count	P_Value	Fold Change	Benjamini	1
	INTERPRO	Sirtuin family, catalytic core small domain	RT		3	2.5E-1	Change	1.0E0	9.2E-
	UP_SEQ_FEATURE								1 9.7E-
		domain:Deacetylase sirtuin-type	<u>RT</u>	•	3	2.7E-1	2.9E0	1.0E0	1
	INTERPRO	Sirtuin family, catalytic core domain	<u>RT</u>	i	3	3.2E-1	2.7E0	1.0E0	9.2E- 1
	INTERPRO	Sirtuin family	<u>RT</u>	i	3	3.2E-1	2.7E0	1.0E0	9.2E- 1
	GOTERM_MF_DIRECT	NAD+ binding	<u>RT</u>	i	3	6.7E-1	1.4E0	1.0E0	9.1E-
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:NAD	RT	i	5	1.0E0	4.3E-1		1 1.0E0
Annota	ation Cluster 284	Enrichment Score: 0.36	G	· ·		P_Value	Falst	Roniamini	
	INTERPRO	Quinonprotein alcohol dehydrogenase-like	<u>RT</u>	ī	11	2.4E-1		1.0E0	9.2E-
	UP_SEQ_FEATURE	superfamily							1 9.7E-
		repeat:WD 11	<u>RT</u>	1	7	2.7E-1		1.0E0	1
	UP_SEQ_FEATURE	repeat:WD 10	<u>RT</u>	i	7	3.0E-1	1.5E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE								9.7E-

UP_SEQ_FEATURE	3.4E-1 3.8E-1 4.6E-1 6.3E-1 P_Value 1.1E-2 1.1E-2 4.8E-1 9.6E-1	1.5E0 1.1E0 1.2E0 Fold Change 1.6E0 2.3E0 2.0E0 1.5E0 Fold Change 6.8E0	1.0E0 1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0 1.0E0	9.1E- 1 9.2E- 1 9.6E- 1 8.9E- 1
UP_SEQ_FEATURE	6.4E-1 6.5E-1 P_Value 3.4E-1 3.8E-1 4.6E-1 6.3E-1 P_Value 1.1E-2 4.8E-1 9.6E-1 9.8E-1	1.1E0 1.2E0 Fold Change 1.6E0 2.3E0 2.0E0 1.5E0 Fold Change 6.8E0	1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0 1.0E0	9.7E-1 9.7E-1 9.7E-1 9.7E-1 9.1E-1 9.2E-1 9.6E-1
UP_SEQ_FEATURE	6.4E-1 6.5E-1 P_Value 3.4E-1 3.8E-1 4.6E-1 6.3E-1 P_Value 1.1E-2 4.8E-1 9.6E-1 9.8E-1	1.1E0 1.2E0 Fold Change 1.6E0 2.3E0 2.0E0 1.5E0 Fold Change 6.8E0	1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0 1.0E0	9.7E-1 9.7E-1 1 FDR 9.1E-1 9.2E-1 9.6E-1
UP_SEQ_FEATURE	P_Value 3.4E-1 3.8E-1 4.6E-1 6.3E-1 P_Value 1.1E-2 1.1E-2 4.8E-1 9.6E-1	1.2E0 Fold Change 1.6E0 2.3E0 2.0E0 1.5E0 Fold Change 6.8E0	1.0E0 Benjamini 1.0E0 1.0E0 1.0E0 1.0E0	9.7E- 1 FDR 9.1E- 1 9.2E- 1 9.6E- 1 8.9E- 1
Annotation Cluster 235 Enrichment Score: 0.35 G Count OOTERM MF_DIRECT Inhibition of concidences annotation of count inhibition of count of count	P_Value 3.4E-1 3.8E-1 4.6E-1 6.3E-1 P_Value 1.1E-2 4.8E-1 9.6E-1 9.8E-1	Fold Change 1.6E0 2.3E0 2.0E0 1.5E0 Fold Change 6.8E0	Benjamini 1.0E0 1.0E0 1.0E0 1.0E0	9.1E-1 9.2E-1 9.6E-1
OSTERM_MF_DIRECT NTERPRO Baculoviral inhibition of apoptosis protein repair inhibition of cysteine-type endopsetidase inhibitor activity inhibition of cysteine-type endopsetidase activity involved in anoptosis protein repair activity involved involved in activity involved in activity involved in activity involved i	3.4E-1 3.8E-1 4.6E-1 6.3E-1 P_Value 1.1E-2 1.1E-2 4.8E-1 9.6E-1	Change 1.6E0 2.3E0 2.0E0 1.5E0 Fold Change 6.8E0	1.0E0 1.0E0 1.0E0 1.0E0	9.1E- 1 9.2E- 1 9.6E- 1 8.9E- 1
INTERPRO Bacalovaria Importation process GOTERM_BP_DIRECT Inhibition of expateine-type endoseptidase activity involved in apoptotic process SMART SIR RT 3 Annotation Cluster 286 Enrichment Score; 0.35 GOTERM_BP_DIRECT UP_SEQ_FEATURE region of interest: interaction with KCND2 GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE RT GOTERM_MF_DIRECT Dotassium channel activity RT	3.8E-1 4.6E-1 6.3E-1 P_Value 1.1E-2 1.1E-2 4.8E-1 9.6E-1	2.3E0 2.0E0 1.5E0 Fold Change 6.8E0	1.0E0 1.0E0 1.0E0	1 9.2E- 1 9.6E- 1 8.9E- 1
GOTERM_BP_DIRECT Inhibition of cysteine-type endopeotidase activity involved in apoptotic process RY 3 Annotation Cluster 286 Enrichment Score: 0.35 Annotation Cluster 286 Enrichment Score: 0.35 GW Count UP_SEQ_FEATURE UP_SEQ_FEATURE Tegion of interest: Interaction with KCND2 RY 4 GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT Toridac conduction RY 3 GOTERM_MF_DIRECT GOTERM_MF_DIRECT Toridac conduction RY 4 GOTERM_MF_DIRECT Toridac conduction GOTERM_MF_DIRECT Dotassium channel activity RY 3 GOTERM_MF_DIRECT Dotassium channel activity RY 3 GOTERM_MF_DIRECT Dotassium channel activity RY 3 GOTERM_MF_DIRECT Dotassium channel activity RY 4 UP_KEYWORDS Potassium channel activity RY 3 GOTERM_MF_DIRECT Dotassium channel activity RY 4 UP_KEYWORDS Potassium channel RY 4 ANDOTERM_MF_DIRECT Dotassium transport RY 4 UP_KEYWORDS Potassium transport RY 8 GOTERM_MF_DIRECT Dotassium transport RY 9 Potassium transport RY 9 RY 9 ANDOTERM_MF_DIRECT Dotassium transport RY 9 Potassium transport RY 9 Potassium transport RY 9 RY 9 Count Count UP_KEYWORDS Voltage_gated channel RY 9 Count UP_SEQ_FEATURE REPEA:HEAT 10 RY 1 DP_SEQ_FEATURE REPEA:HEAT 9 RY 1 COUNT RY 1 DP_SEQ_FEATURE REPEA:HEAT 9 RY 1 COUNT RY 1 DP_SEQ_FEATURE REPEA:HEAT 1 RY 1 DP_SEQ_FEATURE REPEA:HEAT 1 RY 1 R	4.6E-1 6.3E-1 P_Value 1.1E-2 1.1E-2 4.8E-1 9.6E-1 9.8E-1	2.0E0 1.5E0 Fold Change 6.8E0	1.0E0 1.0E0	1 9.6E- 1 8.9E- 1
Annotation Cluster 288 Enrichment Score: 0.35 G Count DIP_SEQ_FEATURE domain:EF-hand 12 degenerate RT	6.3E-1 P_Value 1.1E-2 1.1E-2 4.8E-1 9.6E-1 9.8E-1	1.5E0 Fold Change 6.8E0	1.0E0	1 8.9E- 1
Annotation Cluster 286	P_Value 1.1E-2 1.1E-2 4.8E-1 9.6E-1 9.8E-1	Fold Change 6.8E0	Daniamini	1
UP_SEQ_FEATURE domain:EF-hand 1; degenerate RT 4 UP_SEQ_FEATURE region of interest:Interaction with KCND2 RT 4 GOTERM_BP_DIRECT requisition of potassium ion transmembrane RT 4 GOTERM_BP_DIRECT dardiac conduction RT 5 GOTERM_MF_DIRECT voltage-gated ion channel activity RT 3 GOTERM_CC_DIRECT voltage-gated potassium channel complex RT 4 GOTERM_MF_DIRECT potassium channel activity RT 3 UP_KEYWORDS Potassium channel RT 4 UP_KEYWORDS Potassium channel RT 4 UP_KEYWORDS Potassium transport RT 7 UP_KEYWORDS Potassium transport RT 8 GOTERM_BP_DIRECT potassium ion transmembrane transport RT 8 GOTERM_BP_DIRECT potassium ion transmembrane transport RT 8 UP_KEYWORDS Voltage-gated channel RT 5 UP_KEYWORDS Voltage-gated channel RT 6 UP_SEQ_FEATURE repeat:HEAT 10 RT 5 UP_SEQ_FEATURE repeat:HEAT 9 RT 6 UP_SEQ_FEATURE repeat:HEAT 9 RT 6 UP_SEQ_FEATURE repeat:HEAT 6 RT 6 UP_SEQ_FEATURE repeat:HEAT 8 RT 6 UP_SEQ_FEATURE repeat:HEAT 11 RT 6 UP_SEQ_FEATURE repeat:HEAT 5 RT 6 UP_SEQ_FEATURE repeat:HEAT 5 RT 6 UP_SEQ_FEATURE repeat:HEAT 1 RT 6 UP_SEQ_FEATURE repeat:HEAT 2 RT 6 UP_SEQ_FEATURE repeat:HEAT 3 RT 6 UP_SEQ_FEATURE repeat:HEAT 1 RT 6 UP_SEQ_FEATURE repeat:HEAT 2 RT 6 UP_SEQ_FEATURE repeat:HEAT 3 RT 6 UP_SEQ_FEATURE repeat:HEAT 4 RT 6 UP_SEQ_FEATURE repeat:HEAT 5 RT 6 UP_SEQ_FEATURE repeat:HEAT 6 RT 6 UP_SEQ_FEATURE repeat:HEAT 1 RT 6 UP_SEQ_FEATURE repeat:HEAT 3 RT 6 UP_SEQ_FEATURE repeat:HEAT 4 RT 6 UP_SEQ_FEATURE repeat:HEAT 3 RT 6 UP_SEQ_FEATURE repeat:HEAT 4 RT 6 UP_SEQ_FEATURE repeat:HEAT 4 RT 6 UP_SEQ_FEATURE repe	1.1E-2 1.1E-2 4.8E-1 9.6E-1 9.8E-1	Change 6.8E0	Benjamini	FDR
UP_SEQ_FEATURE region of interest:Interaction with KCND2 RI	1.1E-2 4.8E-1 9.6E-1 9.8E-1	6.8E0		ALC: UNITED IN
GOTERM_BP_DIRECT	4.8E-1 9.6E-1 9.8E-1	6.8E0	2.3E-1	2.2E-
GOTERM_BP_DIRECT regulation of potassium ion transmembrane ransport	4.8E-1 9.6E-1 9.8E-1		2.3E-1	1 2.2E-
GOTERM_BP_DIRECT cardiac.conduction GOTERM_MF_DIRECT Voltage-gated ion channel activity GOTERM_MF_DIRECT voltage-gated potassium channel complex GOTERM_MF_DIRECT potassium channel activity RT GOTERM_MF_DIRECT potassium channel activity RT UP_KEYWORDS Potassium channel RT UP_KEYWORDS Potassium channel RT GOTERM_BP_DIRECT Potassium ion transmembrane transport RT GOTERM_BP_DIRECT Potassium ion transmembrane transport RT GOTERM_BP_DIRECT Potassium ion transmembrane transport RT Annotation Cluster 287 Enrichment Score: 0.34 GOTERM_BP_DIRECT POTASSIUM ion transmembrane transport RT Annotation Cluster 287 Enrichment Score: 0.34 GOTERM_BP_DIRECT POTASSIUM ion transmembrane transport RT Annotation Cluster 287 Enrichment Score: 0.34 GOTERM_BP_DIRECT POTASSIUM ion transmembrane transport RT Annotation Cluster 287 Enrichment Score: 0.34 GOTERM_BP_DIRECT POTASSIUM ion transmembrane transport RT Annotation Cluster 287 Enrichment Score: 0.34 GOTERM_BP_DIRECT POTASSIUM ion transmembrane transport RT Annotation Cluster 288 Enrichment Score: 0.34 GOTERM_BP_DIRECT SOUNT ANNotation Cluster 288 Enrichment Score: 0.33 GOTERM_BP_DIRECT SOUNT ANNOTATION STORE SCORE ANNOTATION STORE SCOR	9.6E-1 9.8E-1	1.6E0	1.0E0	1 9.6E-
GOTERM_MF_DIRECT yoltage-gated lon channel activity GOTERM_CC_DIRECT voltage-gated potassium channel complex RT	9.8E-1			1 9.6E-
GOTERM_CC_DIRECT Voltage-gated potassium channel complex RI				1
GOTERM_MF_DIRECT Dotassium channel activity RI UP_KEYWORDS Potassium channel RI UP_KEYWORDS Potassium in transport RI UP_KEYWORDS Potassium in transport RI GOTERM_BP_DIRECT Dotassium in transport RI RI 8 GOTERM_BP_DIRECT Dotassium in transport RI UP_KEYWORDS Potassium in transport RI 6 UP_KEYWORDS Voltage-gated channel RI Annotation Cluster 287 Enrichment Score: 0.34 Count UP_SEQ_FEATURE repeat:HEAT 10 RI UP_SEQ_FEATURE repeat:HEAT 9 RI UP_SEQ_FEATURE repeat:HEAT 7 RI UP_SEQ_FEATURE repeat:HEAT 8 RI UP_SEQ_FEATURE repeat:HEAT 6 RI UP_SEQ_FEATURE repeat:HEAT 6 RI UP_SEQ_FEATURE repeat:HEAT 11 RI UP_SEQ_FEATURE repeat:HEAT 5 RI UP_SEQ_FEATURE repeat:HEAT 1 RI UP_SEQ_FEATURE repeat:HEAT 1 RI UP_SEQ_FEATURE repeat:HEAT 1 RI UP_SEQ_FEATURE repeat:HEAT 2 RI UP_SEQ_FEATURE repeat:HEAT 2 RI UP_SEQ_FEATURE repeat:HEAT 2 RI OUP_SEQ_FEATURE repeat:HEAT 3 RI Annotation Cluster 288 Enrichment Score: 0.33 Count	9.9E-1	5.6E-1	1.0E0	9.8E- 1
UP_KEYWORDS Potassium channel RT 4 UP_KEYWORDS Potassium transport RT 7 UP_KEYWORDS Potassium in transmembrane transport RT 8 GOTERM_BP_DIRECT potassium in transmembrane transport RT 9 UP_KEYWORDS Voltage-gated channel RT 4 Annotation Cluster 287 Enrichment Score: 0.34 G		5.8E-1	1.0E0	9.9E- 1
UP_KEYWORDS	9.9E-1	4.8E-1	1.0E0	9.9E- 1
□ UP_KEYWORDS	1.0E0 1.0E0	3.7E-1 4.1E-1		1.0E0 1.0E0
□ UP_KEYWORDS Voltage-gated channel RT 4 Annotation Cluster 287 Enrichment Score: 0.34 © Count □ UP_SEQ_FEATURE repeat:HEAT 10 RT 5 □ UP_SEQ_FEATURE repeat:HEAT 9 RT 6 □ UP_SEQ_FEATURE repeat:HEAT 7 RT 6 □ UP_SEQ_FEATURE repeat:HEAT 8 RT 6 □ UP_SEQ_FEATURE repeat:HEAT 6 RT 6 □ UP_SEQ_FEATURE repeat:HEAT 11 RT 3 □ UP_SEQ_FEATURE repeat:HEAT 5 RT 6 □ UP_SEQ_FEATURE repeat:HEAT 1 RT 8 □ UP_SEQ_FEATURE repeat:HEAT 2 RT 8 □ UP_SEQ_FEATURE repeat:HEAT 4 RT 6 □ UP_SEQ_FEATURE repeat:HEAT 3 RT 6 □ UP_SEQ_FEATURE repeat:HEAT 3 RT 6	1.0E0 1.0E0	4.1E-1 4.3E-1		1.0E0
Annotation Cluster 287	1.0E0	2.9E-1		1.0E0
UP_SEQ_FEATURE repeat:HEAT 10 RT 5 UP_SEQ_FEATURE repeat:HEAT 9 RT 5 UP_SEQ_FEATURE repeat:HEAT 7 RT 6 UP_SEQ_FEATURE repeat:HEAT 8 RT 5 UP_SEQ_FEATURE repeat:HEAT 6 RT 6 UP_SEQ_FEATURE repeat:HEAT 11 RT 3 UP_SEQ_FEATURE repeat:HEAT 5 RT 6 INTERPRO HEAT, type 2 RT 4 UP_SEQ_FEATURE repeat:HEAT 1 RT 8 UP_SEQ_FEATURE repeat:HEAT 2 RT 8 UP_SEQ_FEATURE repeat:HEAT 3 RT 6	1.0E0 P_Value	1.8E-1 Fold	Ronjamini	1.0E0 FDR
□ UP_SEQ_FEATURE repeat:HEAT 9 RT 5 □ UP_SEQ_FEATURE repeat:HEAT 7 RT 6 □ UP_SEQ_FEATURE repeat:HEAT 8 RT i 5 □ UP_SEQ_FEATURE repeat:HEAT 6 RT i 6 □ UP_SEQ_FEATURE repeat:HEAT 11 RT i 3 □ UP_SEQ_FEATURE repeat:HEAT 5 RT i 6 □ UP_SEQ_FEATURE repeat:HEAT 1 RT i 8 □ UP_SEQ_FEATURE repeat:HEAT 2 RT i 8 □ UP_SEQ_FEATURE repeat:HEAT 4 RT i 6 □ UP_SEQ_FEATURE repeat:HEAT 3 RT i 6 Annotation Cluster 288 Enrichment Score: 0.33 Count	- 1.7E-1	Change	1.0E0	9.7E-
UP_SEQ_FEATURE repeat:HEAT 7 RT				1 9.7E-
UP_SEQ_FEATURE repeat:HEAT 8 RT	1.7E-1		1.0E0	1 9.7E-
UP_SEQ_FEATURE repeat:HEAT 6 UP_SEQ_FEATURE repeat:HEAT 11 UP_SEQ_FEATURE repeat:HEAT 5 INTERPRO HEAT, type 2 UP_SEQ_FEATURE repeat:HEAT 1 RT B UP_SEQ_FEATURE repeat:HEAT 1 RT B UP_SEQ_FEATURE repeat:HEAT 1 RT B UP_SEQ_FEATURE repeat:HEAT 2 RT B UP_SEQ_FEATURE repeat:HEAT 2 RT B UP_SEQ_FEATURE repeat:HEAT 3 Annotation Cluster 288 Enrichment Score: 0.33 Count	2.7E-1	1.7E0	1.0E0	1
UP_SEQ_FEATURE repeat:HEAT 11 UP_SEQ_FEATURE repeat:HEAT 5 INTERPRO HEAT, type 2 RT UP_SEQ_FEATURE repeat:HEAT 1 RT S UP_SEQ_FEATURE repeat:HEAT 1 RT S UP_SEQ_FEATURE repeat:HEAT 2 RT UP_SEQ_FEATURE repeat:HEAT 2 RT S Annotation Cluster 288 Enrichment Score: 0.33	3.0E-1	1.8E0	1.0E0	9.7E- 1
UP_SEQ_FEATURE repeat:HEAT 5 INTERPRO HEAT, type 2 UP_SEQ_FEATURE repeat:HEAT 1 UP_SEQ_FEATURE repeat:HEAT 2 UP_SEQ_FEATURE repeat:HEAT 2 UP_SEQ_FEATURE repeat:HEAT 4 UP_SEQ_FEATURE repeat:HEAT 3 Annotation Cluster 288 Enrichment Score: 0.33 Count	4.6E-1	1.4E0	1.0E0	9.7E- 1
INTERPRO HEAT, type 2 UP_SEQ_FEATURE repeat:HEAT 1 UP_SEQ_FEATURE repeat:HEAT 2 UP_SEQ_FEATURE repeat:HEAT 4 UP_SEQ_FEATURE repeat:HEAT 3 Annotation Cluster 288 Enrichment Score: 0.33	5.0E-1	1.9E0	1.0E0	9.7E- 1
UP_SEQ_FEATURE repeat:HEAT 1 RT 8 UP_SEQ_FEATURE repeat:HEAT 2 RT 6 UP_SEQ_FEATURE repeat:HEAT 4 RT 6 UP_SEQ_FEATURE repeat:HEAT 3 RT 6 Annotation Cluster 288 Enrichment Score: 0.33 Count	6.0E-1	1.2E0	1.0E0	9.7E- 1
UP_SEQ_FEATURE repeat:HEAT 1 RT	6.1E-1	1.3E0	1.0E0	9.2E-
UP_SEQ_FEATURE repeat:HEAT 2 RT	7.7F-1	9.4E-1	1.0F0	1 9.7E-
UP_SEQ_FEATURE repeat:HEAT 4 UP_SEQ_FEATURE repeat:HEAT 3 RT 6 Annotation Cluster 288 Enrichment Score: 0.33 COUTENM RD RIPECT				1 9.7E-
UP_SEQ_FEATURE repeat:HEAT 3 RT 6 Annotation Cluster 288 Enrichment Score: 0.33 GOVERNMED PURSON COULT BY DESCRIPTION OF THE ACT OF THE		9.4E-1		1 9.7E-
Annotation Cluster 288 Enrichment Score: 0.33 G 😽 Count		9.5E-1		1
COTEDM DD DIDECT		8.2E-1	1.0E0	9.7E- 1
GOTERM_BP_DIRECT protein ADP-ribosylation RT 7	P_Value	Fold Change	Benjamini	
	1.3E-1	2.0E0	8.3E-1	7.9E- 1
GOTERM_BP_DIRECT negative regulation of telomere maintenance via telomere lengthening RT 3	2.0E-1	3.6E0	1.0E0	9.6E- 1
COTEDM ME DIPECT	3.2E-1	1.5E0	1.0E0	9.1E- 1
UP_SEQ_FEATURE domain:PARP catalytic RT 3	7.4E-1	1.2E0	1.0E0	9.7E-
INTERPRO Poly(ADP-ribose) polymerase, catalytic RT 3	7.9E-1		1.0E0	1 9.2E-
<u>domain</u>	1.0E0	3.9E-1		1 1.0E0
UP_KEYWORDS Glycosyltransferase RT 4		1.2E-1		1.0E0
	P_Value	Fold Change	Benjamini	
INTERPRO Filamin/ABP280 repeat-like RT 4		2.1E0	1.0E0	9.2E- 1
INTERPRO Filamin/ABP280 repeat RT 3	3.0E-1	1.9E0	1.0E0	9.2E- 1
SMART IG FLMN RT 3	3.0E-1 5.0E-1	1.2E0	1.0E0	8.9E- 1
		Fold	Benjamini	
— IIP SEO FEATURE	5.0E-1 7.5E-1	. Спапge		
····	5.0E-1 7.5E-1 P_Value	1.7E0	1.0E0	9.7E- 1

Anno	tation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold	Benjamini	EDP
Allilo	UP_SEQ_FEATURE					-	Change		9.7E-
	UP_SEQ_FEATURE	repeat:1-1	<u>RT</u>		8	2.2E-1		1.0E0	1 9.7E-
	UP_SEQ_FEATURE	repeat:2-1	<u>RT</u>	•	6	5.2E-1	1.3E0	1.0E0	1
		repeat:2-2	<u>RT</u>	i	6	5.7E-1	1.2E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:2-3	<u>RT</u>	i	3	7.9E-1	1.1E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:1-4	<u>RT</u>	i	3	7.9E-1	1.1E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:1-3	<u>RT</u>	i .	3	8.1E-1	1.0E0	1.0E0	9.7E- 1
Anno	tation Cluster 291	Enrichment Score: 0.31		™	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:CID	<u>RT</u>	i	3	3.3E-1	2.6E0	1.0E0	9.7E- 1
	INTERPRO	CID domain	<u>RT</u>	i .	3	3.8E-1	2.3E0	1.0E0	9.2E- 1
	INTERPRO	ENTH/VHS	<u>RT</u>	i	3	9.5E-1	6.9E-1	1.0E0	9.5E-
Anno	tation Cluster 292	Enrichment Score: 0.3	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	renin-angiotensin regulation of aldosterone	<u>RT</u>	i	3	1.3E-1	•	8.3E-1	7.9E-
	KEGG_PATHWAY	<u>production</u> <u>Renin-angiotensin system</u>	<u>RT</u>	1	3	9.5F-1	6.9E-1	1.0F0	1 9.5E-
	BIOCARTA	Angiotensin-converting enzyme 2 regulates	RT		3		7.2E-1		1 9.5E-
Anno	tation Chapter 202	heart function		•		1		!	1
Anno	tation Cluster 293 GOTERM_CC_DIRECT	Enrichment Score: 0.28	G		Count	P_Value	Change	Benjamini	8.1E-
	GOTERM_MF_DIRECT	box C/D snoRNP complex	<u>RT</u>	i	3	2.4E-1		9.1E-1	1 9.1E-
	GOTERM CC DIRECT	snoRNA binding	<u>RT</u>	•	4	7.1E-1		1.0E0	1
	GOTERM_CC_DIRECT	small-subunit processome	<u>RT</u>	i	5	8.2E-1	9.1E-1	1.0E0	8.9E- 1
Anno	tation Cluster 294	Enrichment Score: 0.28	G	1	Count	P_Value	Fold Change	Benjamini	
	GOTERM_CC_DIRECT	NuA4 histone acetyltransferase complex	<u>RT</u>	i	5	3.1E-1	1.8E0	9.5E-1	8.4E- 1
	GOTERM_BP_DIRECT	histone H4 acetylation	<u>RT</u>	i .	6	6.2E-1	1.1E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	histone H2A acetylation	<u>RT</u>	i	3	7.5E-1	1.2E0	1.0E0	9.6E- 1
Anno	tation Cluster 295	Enrichment Score: 0.28	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	Immunoglobulin I-set	<u>RT</u>	i	37	2.7E-3	1.6E0	3.3E-2	3.0E- 2
	INTERPRO	Immunoglobulin subtype 2	<u>RT</u>	•	42	4.8E-1	1.0E0	1.0E0	9.2E-
	UP_SEQ_FEATURE	domain:Ig-like C2-type 3	<u>RT</u>	i de la companya de	17	7.9E-1	9.0E-1	1.0E0	9.7E-
	UP_SEQ_FEATURE	domain:Ig-like C2-type 1	<u>RT</u>		23	9.5E-1	7.8E-1	1.0E0	9.7E-
	UP_SEQ_FEATURE	domain:Ig-like C2-type 2	RT		23	9.6F-1	7.7E-1	1.0F0	1 9.7E-
	SMART	IGc2	RT		42	1.0E0	6.8E-1		1 1.0E0
	UP_KEYWORDS	Immunoglobulin domain	<u>RT</u>		48	1.0E0	6.0E-1		1.0E0
	INTERPRO INTERPRO	<u>Immunoglobulin subtype</u> <u>Immunoglobulin-like fold</u>	RT RT		46 85	1.0E0 1.0E0	5.7E-1 5.5E-1		1.0E0 1.0E0
	SMART INTERPRO	IG	RT		46	1.0E0	3.7E-1		1.0E0
Anno	tation Cluster 296	Immunoglobulin-like domain Enrichment Score: 0.26	RT G	•	50 Count	1.0E0 P_Value	4.0E-1	Benjamini	1.0E0
	BIOCARTA	Role of Mitochondria in Apoptotic Signaling	<u>RT</u>	i	9	4.1E-1	Change	6.8E-1	5.1E-
	UP_SEQ_FEATURE	domain:CARD	RT		6	4.3E-1		1.0E0	1 9.7E-
	INTERPRO	Caspase Recruitment	RT	-	6	5.1E-1		1.0E0	1 9.2E-
	BIOCARTA								1 7.5E-
	SMART	Caspase Cascade in Apoptosis	<u>RT</u>		8	6.9E-1		1.0E0	1 8.9E-
	SMAKI	<u>CARD</u>	<u>RT</u>	i	3	8.4E-1		1.0E0	1
Anno	tation Cluster 297	Enrichment Score: 0.26	G	-	Count	P_Value	Fold Change	Benjamini	
	GOTERM_BP_DIRECT	RNA catabolic process	<u>RT</u>	i	6	2.7E-1	1.7E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	RNA phosphodiester bond hydrolysis, exonucleolytic	<u>RT</u>	i	5	7.2E-1	1.1E0	1.0E0	9.6E- 1
	GOTERM_MF_DIRECT	3'-5'-exoribonuclease activity	<u>RT</u>	i .	3	8.7E-1	9.0E-1	1.0E0	9.1E- 1
Anno	tation Cluster 298	Enrichment Score: 0.24	G	178	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	Exportin-1/Importin-beta-like	<u>RT</u>	i	3	2.5E-1	3.1E0	1.0E0	9.2E- 1
	GOTERM_MF_DIRECT	Ran GTPase binding	<u>RT</u>	i .	6	5.8E-1	1.2E0	1.0E0	9.1E- 1
	INTERPRO	Importin-beta, N-terminal	<u>RT</u>	i	3	7.9E-1	1.1E0	1.0E0	9.2E- 1
	SMART	<u>SM00913</u>	<u>RT</u>	1	3	9.3E-1	7.6E-1	1.0E0	9.3E-
									1

ınota	ation Cluster 1	Enrichment Score: ?	G	108	Count	P_Value	Change	Benjamin	ni FD
nnota	ation Cluster 299	Enrichment Score: 0.24	G	-3	Count	P_Value	Fold Change	Benjamin	ıi FD
)	GOTERM_BP_DIRECT	<u>positive regulation of vascular endothelial</u> <u>growth factor production</u>	<u>RT</u>	1	8	1.6E-1	1.8E0	9.2E-1	8.8 1
	GOTERM_BP_DIRECT	regulation of complement activation	<u>RT</u>	1	5	7.7E-1	9.9E-1	1.0E0	9.6 1
)	KEGG_PATHWAY	Staphylococcus aureus infection	<u>RT</u>	1	7	9.6E-1	6.8E-1	1.0E0	9.6 1
)	KEGG_PATHWAY	Complement and coagulation cascades	<u>RT</u>	8	8	9.9E-1	6.1E-1	1.0E0	9.9 1
nnota	ation Cluster 300	Enrichment Score: 0.23	G	178	Count	P_Value	Fold Change	Benjamin	ni FC
)	UP_SEQ_FEATURE	domain:MBD	<u>RT</u>	1	3	5.0E-1	•	1.0E0	9. 1
)	INTERPRO	<u>DNA-binding, integrase-type</u>	<u>RT</u>	1	3	5.5E-1	1.7E0	1.0E0	9. 1
	INTERPRO	Methyl-CpG DNA binding	<u>RT</u>	4	3	5.5E-1	1.7E0	1.0E0	9.
)	SMART	MBD	RT		3	8.0E-1	1.1E0	1.0E0	8.
nnota	ation Cluster 301	Enrichment Score: 0.23	G	·	Count	P_Value	Fold	<u>.</u>	1 ni Fi
)	GOTERM_CC_DIRECT	histone acetyltransferase complex	RT	i	6	2.9E-1	Change	9.2E-1	8.
)	GOTERM_BP_DIRECT			_					1 9.
J	GOTERM_BP_DIRECT	histone H4-K16 acetylation	<u>RT</u>		4	6.8E-1		1.0E0	1 9.
J	GOTERM_BP_DIRECT	histone H4-K5 acetylation	<u>RT</u>	1	3	7.8E-1		1.0E0	1 9.
J	GOTEKIN_BI _BIKEOT	histone H4-K8 acetylation	<u>RT</u>	i	3	7.8E-1	1.1E0	1.0E0	1
inota	ation Cluster 302	Enrichment Score: 0.23	G		Count	P_Value	Change	Benjamin	
	INTERPRO	Importin subunit alpha	<u>RT</u>	•	3	3.2E-1		1.0E0	9.
	PIR_SUPERFAMILY UP_SEQ_FEATURE	importin subunit alpha domain:IBB	<u>RT</u>		3			1.0E0 1.0E0	1 9
	GOTERM_BP_DIRECT		<u>RT</u>	_					1 9
	UP_SEQ_FEATURE	NLS-bearing protein import into nucleus	<u>RT</u>	•	6			1.0E0	1
		repeat:ARM 8	<u>RT</u>	•	5	4.1E-1	1.5E0	1.0E0	1
	INTERPRO	Importin-alpha, importin-beta-binding domai	n RT	•	3	4.4E-1	2.1E0	1.0E0	9
	UP_SEQ_FEATURE	repeat:ARM 7	<u>RT</u>	1	5	4.8E-1	1.4E0	1.0E0	9
	UP_SEQ_FEATURE	repeat:ARM 6	<u>RT</u>	1	5	5.4E-1	1.3E0	1.0E0	9 1
	UP_SEQ_FEATURE	repeat:ARM 5	<u>RT</u>	1	5	6.3E-1	1.2E0	1.0E0	9
	UP_SEQ_FEATURE	repeat:ARM 4	<u>RT</u>	4	5	6.9E-1	1.1E0	1.0E0	9
	GOTERM_MF_DIRECT	nuclear localization sequence binding	<u>RT</u>		5	7.1E-1	1.1E0	1.0E0	9
	UP_SEQ_FEATURE	repeat:ARM 9	<u>RT</u>	4	3	7.7E-1	1.1E0	1.0E0	9
	UP_SEQ_FEATURE	repeat:ARM 3	RT	1	5	8.0F-1	9.5E-1	1.0E0	9
	UP_SEQ_FEATURE	repeat:ARM 2	RT		5		9.2E-1		1 9
	INTERPRO								1 9
	UP_SEQ_FEATURE	<u>Armadillo</u>	<u>RT</u>	i	5		7.2E-1		1
	SMART	repeat:ARM 1	<u>RT</u>	i	3		6.6E-1		1
		<u>ARM</u>	<u>RT</u>	•	5		5.2E-1		9
nota	GOTERM_MF_DIRECT ation Cluster 303	protein transporter activity Enrichment Score: 0.22	RT G	·	5 Count	1.0E0 P_Value	4.1E-1 Fold	Danie min	1 ni F
11010	INTERPRO	K Homology domain	<u>RT</u>	-	8	4.2E-1	Change	1.0E0	9
	UP_SEQ_FEATURE	domain:KH		_				1.0E0	1 9
	INTERPRO		<u>RT</u>		4				1
	UP_SEQ_FEATURE	K Homology domain, type 1	<u>RT</u>		8			1.0E0	1
		domain:KH 3	<u>RT</u>	1	3			1.0E0	1
	UP_SEQ_FEATURE	domain:KH 1	<u>RT</u>	i	4	7.1E-1	1.1E0	1.0E0	9
	UP_SEQ_FEATURE	domain:KH 2	<u>RT</u>	i	4	7.1E-1	1.1E0	1.0E0	9
	SMART	<u>KH</u>	<u>RT</u>	i	8		8.5E-1		8 1
nota	ation Cluster 304	Enrichment Score: 0.21	G	17 8	Count	P_Value	Fold Change	Benjamin	i F
	INTERPRO	SMAD/FHA domain	<u>RT</u>	i	10	4.9E-1	1.2E0	1.0E0	9
	INTERPRO	Forkhead-associated (FHA) domain	<u>RT</u>	i	7	5.6E-1	1.2E0	1.0E0	9
	UP_SEQ_FEATURE	domain:FHA	<u>RT</u>		6	6.0E-1	1.2E0	1.0E0	9

Annot	ation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
Annot	ation Cluster 305	Enrichment Score: 0.21	G	100	Count	P_Value	Fold	Benjamini	FDR
	INTERPRO	Cyclic nucleotide-binding, conserved site	<u>RT</u>	i	5	2.5E-1	Change	1.0E0	9.2E
_ 	INTERPRO			<u>-</u>					1 9.2E
_	INTERPRO	Cyclic nucleotide-binding domain	<u>RT</u>	•	7	5.1E-1	1.2EU	1.0E0	1
		<u>Cyclic nucleotide-binding-like</u>	<u>RT</u>	1	7	5.9E-1	1.1E0	1.0E0	9.2E
	UP_KEYWORDS	cAMP-binding	<u>RT</u>	i	3	7.3E-1	1.2E0	1.0E0	8.0E
	INTERPRO	RmIC-like jelly roll fold	<u>RT</u>	i	7	7.9E-1	9.2E-1	1.0E0	9.2E
	SMART	<u>cNMP</u>	<u>RT</u>	i .	7	8.2E-1	9.1E-1	1.0E0	8.9E
\neg	GOTERM_MF_DIRECT	cAMP binding	<u>RT</u>	1	3	9 3F-1	7.5E-1	1 0F0	9.3E
Annot	ation Cluster 206		G	-		1	Fold	Benjamini	1 EDB
Annot	ation Cluster 306 BIOCARTA	Enrichment Score: 0.21 TACI and BCMA stimulation of B cell immune		-	Count	P_Value	Change		6.5E
		<u>responses.</u>	<u>RT</u>	•	6	5.5E-1	1.2E0	8.7E-1	1
	GOTERM_BP_DIRECT	membrane protein intracellular domain proteolysis	<u>RT</u>	1	4	6.1E-1	1.3E0	1.0E0	9.6E 1
	BIOCARTA	Bone Remodelling	<u>RT</u>	1	5	7.0E-1	1.1E0	1.0E0	7.5E 1
nnot	ation Cluster 307	Enrichment Score: 0.2	G	15	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	chain:Histone H2A type 1-D	<u>RT</u>	i	3	6.3E-1	•	1.0E0	9.7E
_ 	UP_SEQ_FEATURE	chain:Histone H3.1	RT		3	6.3E-1	1 5F0	1.0E0	1 9.7E
	UP_SEQ_FEATURE								1 9.7E
		chain:Histone H3.2	<u>RT</u>	i	3	6.3E-1	:	1.0E0	1
nnot	ation Cluster 308	Enrichment Score: 0.17	G		Count	P_Value	Fold Change	Benjamini	
	GOTERM_CC_DIRECT	eukaryotic 43S preinitiation complex	<u>RT</u>	i	4	4.3E-1	1.7E0	1.0E0	8.9E 1
	GOTERM_BP_DIRECT	regulation of translational initiation	<u>RT</u>	1	7	5.8E-1	1.2E0	1.0E0	9.6E
	UP_KEYWORDS	Initiation factor	<u>RT</u>	1	9	6.2E-1	1.1E0	1.0E0	8.0
آ ا	GOTERM_CC_DIRECT	eukaryotic 48S preinitiation complex	RT		3	7.1E-1		1.0E0	1 8.9
)	BIOCARTA								1 7.5I
J		<u>Internal Ribosome entry pathway</u>	<u>RT</u>	•	3	7.1E-1	1.3E0	1.0E0	1
	GOTERM_MF_DIRECT	translation initiation factor activity	<u>RT</u>	•	10	7.1E-1	9.8E-1	1.0E0	9.1E 1
	GOTERM_BP_DIRECT	formation of translation preinitiation complex	<u>RT</u>	i	4	7.7E-1	1.0E0	1.0E0	9.6E 1
	GOTERM_CC_DIRECT	eukaryotic translation initiation factor 3 complex	<u>RT</u>	1	3	7.7E-1	1.1E0	1.0E0	8.9l
7	BIOCARTA	Eukaryotic protein translation	<u>RT</u>		5	8.1E-1	9.7E-1	1.0E0	8.1
nnot	ation Cluster 309	Enrichment Score: 0.16	G	- -	Count	P_Value	Fold	Benjamini	1 EDE
	UP_SEQ_FEATURE						Change		9.7
J		domain:OPR	<u>RT</u>	•	3	5.4E-1	1.7E0	1.0E0	1
	INTERPRO	Phox/Bem1p	<u>RT</u>	i .	3	6.9E-1	1.3E0	1.0E0	9.2I 1
	SMART	<u>PB1</u>	<u>RT</u>	i	3	9.0E-1	8.7E-1	1.0E0	9.0I 1
nnot	ation Cluster 310	Enrichment Score: 0.15	G	· ·	Count	P_Value	Fold Change	Benjamini	FDF
	INTERPRO	Patatin/Phospholipase A2-related	RT	i	3	4.4E-1	•	1.0E0	9.21
ے ا	INTERPRO	Acyl transferase/acyl	RT	_	3	8.1E-1		1.0E0	1 9.2I
ر ا	KEGG_PATHWAY	<u>hydrolase/lysophospholipase</u> <u>Glycerophospholipid metabolism</u>	RT		6	1.0E0	3.3E-1		1.0
nnot	ation Cluster 311	Enrichment Score: 0.12	G		Count	P_Value	Fold	Benjamini	
7	GOTERM_CC_DIRECT						Change		8.91
_	UP_KEYWORDS	<u>nuclear pore</u>	<u>RT</u>	•	13	4.6E-1		1.0E0	1
	_	mRNA transport	<u>RT</u>	i	14	7.9E-1	9.1E-1	1.0E0	8.0I 1
	UP_KEYWORDS	Nuclear pore complex	<u>RT</u>	i .	6	8.7E-1	8.2E-1	1.0E0	8.7E
	UP_KEYWORDS	<u>Translocation</u>	<u>RT</u>	i	6	1.0E0	4.9E-1	1.0E0	1.0
nnot	ation Cluster 312	Enrichment Score: 0.11	G		Count	P_Value	Fold Change	Benjamini	
	INTERPRO	<u>Phospholipid-transporting P-type ATPase,</u> <u>subfamily IV</u>	<u>RT</u>	1	3	6.9E-1	1.3E0	1.0E0	9.2l 1
	GOTERM_MF_DIRECT	phospholipid-translocating ATPase activity	<u>RT</u>	1	3	7.1E-1	1.3E0	1.0E0	9.1I 1
)	GOTERM_BP_DIRECT	phospholipid translocation	<u>RT</u>		4	7.4E-1	1.1F0	1.0E0	9.6
ر ا	UP_KEYWORDS	Lipid transport	RT		3	1.0E0	2.1E-1		1 1.0
nnot	ation Cluster 313	Enrichment Score: 0.11	G		Count	P_Value	Fold	Benjamini	
	GOTERM_MF_DIRECT	cAMP response element binding				3.7E-1	Change	1.0E0	9.1
	INTERPRO		RT PT		4		4.6E-1		1
	SMART	Basic-leucine zipper domain BRLZ	RT RT		4	1.0E0 1.0E0	4.6E-1 3.2E-1		1.0E
	UP_SEQ_FEATURE	DNA-binding region:Basic motif	RT	i e	7	1.0E0	2.9E-1		1.0E

Annot	tation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamini	FDR
Annot	tation Cluster 314	Enrichment Score: 0.1	G	· 🚾	Count	P_Value	Fold Change	Benjamini	FDR
	BBID	18.Cytokine astocytes	<u>RT</u>	i	9	2.4E-1		1.0E0	1.0E0
	BBID	20.Cytokine oligodendrocytes	<u>RT</u>	1	3	5.0E-1		1.0E0	1.0E0
	BBID BBID	21.Cytokine neurons 19.Cytokine microglia	RT RT		3 5	5.0E-1 6.7E-1		1.0E0 1.0E0	1.0E(
	BIOCARTA	Cells and Molecules involved in local acute	RT		6	6.8E-1		1.0E0	7.5E-
	VECC BATHIMAY	<u>inflammatory response</u>	<u>KI</u>	•	0	0.00-1	1.100	1.020	1
	KEGG_PATHWAY	<u>Malaria</u>	<u>RT</u>	i	9	7.4E-1	9.7E-1	1.0E0	7.4E- 1
	BBID	111.Stress influences immunity	<u>RT</u>	1	3	7.5E-1		1.0E0	1.0E
	BBID BBID	112.StressandCRHinfluence 22.Cytokine-chemokine CNS	RT DT		3 5	7.5E-1 7.5E-1		1.0E0 1.0E0	1.0E(
	BBID	56.Macrophage regulation of CD4+T cells	RT RT		4	8.1E-1		1.0E0	1.0E(
	BIOCARTA	Adhesion and Diapedesis of Granulocytes	RT	•	4		8.3E-1	1.0E0	9.0E
	BBID	80.T cell Activation	RT		8		8.2E-1		1 1.0E
	BBID	58.(CD40L) immnosurveillance	RT	1	5		8.0E-1		1.0E
	BIOCARTA	Cytokine Network	RT	1	5	9.5E-1	7.1E-1	1.0E0	9.5E
	KEGG_PATHWAY	Graft-versus-host disease	RT		4	0 6E-1	6.4E-1	1 050	1 9.6E
	KEGG_PATHWAY								1 9.7E-
		Type I diabetes mellitus	<u>RT</u>	•	5	9.7E-1	6.3E-1	1.0E0	1
	BIOCARTA	Regulation of hematopoiesis by cytokines	<u>RT</u>	i .	3	9.8E-1	6.2E-1	1.0E0	9.8E- 1
	BIOCARTA	Cytokines and Inflammatory Response	<u>RT</u>	1	6	9.8E-1	6.5E-1	1.0E0	9.8E-
	INTERPRO	Four-helical cytokine, core	<u>RT</u>		4	9.9F-1	4.9E-1	1,0F0	9.9E
	INTERPRO	Four-helical cytokine-like, core	RT		4	1.0E0	4.6E-1		1 1.0E
	KEGG_PATHWAY	Allograft rejection	RT		3		4.8E-1		1.0E
	BBID	97.Immune injury MS-lesions MS antigen	RT	1	3		4.8E-1		1.0E
	GOTERM_MF_DIRECT	<u>cytokine activity</u>	<u>RT</u>	i	11	1.0E0	3.7E-1	1.0E0	1.0E
Annot	ation Cluster 315	Enrichment Score: 0.1	G	<u>™</u>	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	proximal/distal pattern formation	<u>RT</u>	1	5	6.0E-1	1.2E0	1.0E0	9.6E
	KEGG_PATHWAY	Basal cell carcinoma	<u>RT</u>	•	8	9.1E-1	7.8E-1	1.0E0	9.1E
	GOTERM_BP_DIRECT								1 9.6E
		odontogenesis of dentin-containing tooth	<u>RT</u>		7	1	7.5E-1 Fold		1
Annot	tation Cluster 316	Enrichment Score: 0.1	G		Count	P_Value	Change	Benjamini	
	INTERPRO	Zinc finger, B-box	<u>RT</u>	i	15	4.5E-1	1.1E0	1.0E0	9.2E- 1
	UP_SEQ_FEATURE	domain:B30.2/SPRY	<u>RT</u>	1	15	5.7E-1	1.1E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	zinc finger region:B box-type	<u>RT</u>		10	6.8E-1	1 0F0	1.0E0	9.7E
_	INTERPRO	Zinc iniger region.b box-type	<u>KI</u>		10	0.0L-1	1.000	1.020	1
	INTERPRO	B30.2/SPRY domain	<u>RT</u>	i	15	7.4E-1	9.4E-1	1.0E0	9.2E
	INTERPRO	SPla/RYanodine receptor SPRY	<u>RT</u>	1	14	7.7E-1	9.2E-1	1.0E0	9.2E
	INTERPRO	SPRY-associated	<u>RT</u>	1	6	9 2F-1	7.4E-1	1 0F0	9.2E
	SMART	<u>51 KT #330cluted</u>			Ü	J.ZL 1	/TL I	1.020	1
	SWARI	BBOX	<u>RT</u>	•	14	9.5E-1	7.6E-1	1.0E0	9.5E- 1
	INTERPRO	Butyrophylin-like	<u>RT</u>	1	8	9.6E-1	6.9E-1	1.0E0	9.6E
	SMART	<u>SPRY</u>	<u>RT</u>	1	14	1.0E0	6.2E-1	1.0E0	1.0E
	SMART	PRY	RT	1	6	1.0E0	4.9E-1	1.0E0	1.0E
	INTERPRO	<u>Concanavalin A-like lectin/glucanase,</u> <u>subgroup</u>	<u>RT</u>	1	18	1.0E0	4.8E-1	1.0E0	1.0E
Annot	tation Cluster 317	Enrichment Score: 0.09	G	178	Count	P_Value	Fold	Benjamini	FDR
	UP_SEQ_FEATURE	zinc finger region:CCHC-type	<u>RT</u>	_	5		Change 1.3E0	1.0E0	9.7E
	INTERPRO								1
	INTERFRO	Zinc finger, CCHC-type	<u>RT</u>	i	4	9.7E-1	6.2E-1	1.0E0	9.7E- 1
	SMART	ZnF C2HC	<u>RT</u>	i	3	1.0E0	4.2E-1	1.0E0	1.0E
Annot	tation Cluster 318	Enrichment Score: 0.09	G	- National Control	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:CS	<u>RT</u>	i	3	7.0E-1	1.3E0	1.0E0	9.7E- 1
	INTERPRO	CS-like domain	<u>RT</u>	i e	3	7.9E-1	1.1E0	1.0E0	9.2E
	INTERPRO	HSP20-like chaperone			3		6.6E-1		1 9.5E
			RT	<u> </u>		1	Fold		1
	tation Cluster 319	Enrichment Score: 0.09	G	<u> </u>	Count	P_Value	Change	Benjamini	
Annot	COTEDU III DITE	peptidase activity	<u>RT</u>	1	16	5.5E-1	1.1E0	1.0E0	9.1E 1
Annot	GOTERM_MF_DIRECT	<u>peptidase activity</u>							1.0E
Annot	UP_KEYWORDS	Zymogen	<u>RT</u>	1	17	1.0E0	5.5E-1		
	UP_KEYWORDS UP_KEYWORDS	· · · · · · · · · · · · · · · · · · ·	<u>RT</u>	1	17 45	1.0E0	5.7E-1		
	UP_KEYWORDS	<u>Zymogen</u>					5.7E-1		1.0E0

Annot	ation Cluster 1	Enrichment Score: ?	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	antibacterial humoral response	<u>RT</u>	i	7	7.8E-1	9.4E-1		9.6E-
	UP_KEYWORDS	<u>Antibiotic</u>	<u>RT</u>	i	7	1.0E0	5.1E-1	1.0E0	1.0E
	UP_KEYWORDS	Antimicrobial	<u>RT</u>	i	7	1.0E0	4.4E-1 Fold	1	1.0E
Annota	ution Cluster 321 UP_KEYWORDS	Enrichment Score: 0.06	G		Count	P_Value	Change	Benjamini	8.0E-
	_	<u>Steroid-binding</u>	<u>RT</u>	•	4	4.2E-1	1.7E0	1.0E0	1
	GOTERM_MF_DIRECT	steroid binding	<u>RT</u>	i	5	6.8E-1	1.1E0	1.0E0	9.1E
	UP_SEQ_FEATURE	DNA-binding region:Nuclear receptor	<u>RT</u>	i .	3	9.9E-1	4.5E-1	1.0E0	9.9E
	UP_SEQ_FEATURE	zinc finger region:NR C4-type	<u>RT</u>	1	3	9.9E-1	4.5E-1	1.0E0	9.9E
	INTERPRO	Zinc finger, nuclear hormone receptor-type	<u>RT</u>	i	3	1.0E0	4.0E-1	1.0E0	1.0E
	INTERPRO INTERPRO	Steroid hormone receptor Nuclear hormone receptor, ligand-binding,	<u>RT</u>	1		1.0E0	4.0E-1		1.0E
		core	RT DT			1.0E0	3.9E-1		1.0E
	GOTERM_MF_DIRECT SMART	steroid hormone receptor activity ZnF C4	RT RT		3 3	1.0E0 1.0E0	3.2E-1 2.6E-1		1.0E
	SMART	HOLI	<u>RT</u>	i	3	1.0E0	2.5E-1	1.0E0	1.0E
Annot	ation Cluster 322	Enrichment Score: 0.05	G		Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	domain:Ig-like 3	<u>RT</u>	i	3	7.9E-1	1.1E0	1.0E0	9.7E 1
	UP_SEQ_FEATURE	domain:Ig-like 1	<u>RT</u>	1	3	9.4E-1	7.0E-1	1.0E0	9.7E 1
	UP_SEQ_FEATURE	domain:Ig-like 2	<u>RT</u>	1	3	9.4E-1	7.0E-1	1.0E0	9.7E
Annot	ation Cluster 323	Enrichment Score: 0.04	G		Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_MF_DIRECT	histone demethylase activity	<u>RT</u>	i	4	7.7E-1	Onlange	1.0E0	9.15
_ 	UP_SEQ_FEATURE	domain:JmjC	RT		4		8.5E-1		1 9.7E
 	INTERPRO			-					1 9.2E
	SMART	<u>JmjC domain</u>	<u>RT</u>		4		7.5E-1		1 9.9E
		<u>JmjC</u>	<u>RT</u>	•	4		5.6E-1		1
nnot	UP_KEYWORDS ration Cluster 324	<u>Dioxygenase</u> Enrichment Score: 0.04	RT G	· •	5 Count	1.0E0 P_Value	4.1E-1 Fold	Bonjamini	1.0E
	INTERPRO						Change		9.2
	INTERPRO	3'5'-cyclic nucleotide phosphodiesterase 3'5'-cyclic nucleotide phosphodiesterase,	<u>RT</u>	i	3		9.8E-1		1 9.2
		conserved site	<u>RT</u>	•	3	8.7E-1	8.9E-1	1.0E0	1
	INTERPRO	3'5'-cyclic nucleotide phosphodiesterase, catalytic domain	<u>RT</u>	1	3	8.9E-1	8.5E-1	1.0E0	9.2E 1
	INTERPRO	HD/PDEase domain	<u>RT</u>	i	3	9.1E-1	8.1E-1	1.0E0	9.2E 1
	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 1	<u>RT</u>	i	3	9.3E-1	7.3E-1	1.0E0	9.7E 1
	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 2	<u>RT</u>	i e	3	9.3E-1	7.3E-1	1.0E0	9.7E
	SMART	<u>HDc</u>	<u>RT</u>	1	3	9.9E-1	5.3E-1	1.0E0	9.9
Annot	ation Cluster 325	Enrichment Score: 0.04	G	- -	Count	P_Value	Fold	Baniamini	1 EDR
	GOTERM_CC_DIRECT	mitochondrial small ribosomal subunit		-	4	7.8E-1	Change	1.0E0	8.9
	GOTERM_BP_DIRECT		<u>RT</u>	1					1 9.6E
		mitochondrial translational elongation	<u>RT</u>	•	12	8.7E-1	8.4E-1	1.0E0	1
	GOTERM_BP_DIRECT	mitochondrial translation	<u>RT</u>	i	4	9.6E-1	6.6E-1	1.0E0	9.6E 1
	GOTERM_BP_DIRECT	mitochondrial translational termination	<u>RT</u>	•	10	9.7E-1	6.9E-1	1.0E0	9.7E 1
	GOTERM_CC_DIRECT	mitochondrial large ribosomal subunit	<u>RT</u>	i .	4	9.9E-1	5.3E-1	1.0E0	9.9E 1
Annot	ation Cluster 326	Enrichment Score: 0.04	G	To the second se	Count	P_Value	Fold Change	Benjamini	FDF
	UP_SEQ_FEATURE	zinc finger region:C3H1-type 1	<u>RT</u>	i	4	8.5E-1	8.8E-1		9.7E
	UP_SEQ_FEATURE	zinc finger region:C3H1-type 2	<u>RT</u>		4	8.5E-1	8.8E-1	1.0E0	9.7
	INTERPRO	Zinc finger, CCCH-type	RT		6		6.3E-1		1 9.7E
	SMART	ZnF_C3H1	RT		6	1.0E0	4.9E-1		1 1.0E
nnot	ation Cluster 327	Enrichment Score: 0.03	G			P_Value	Fold		
	UP_SEQ_FEATURE	domain:SAP	<u>RT</u>		3	8.9E-1	8.5E-1		9.7E
	INTERPRO	SAP domain	RT		3		7.7E-1		1 9.2
	SMART								1 9.9I
		SAP	RT	i	3		5.3E-1 Fold	1	1
Annota	ation Cluster 328	Enrichment Score: 0.02	G			P_Value	Change		
	UP_SEQ_FEATURE	domain:LisH	<u>RT</u>	1	3	9.3E-1	7.3E-1	1.0E0	9.7E
	INTERPRO								9.5E

nnota	ntion Cluster 1	Enrichment Score: ?	G	178	Count	P_Value	Fold Change	Benjamin	i FDF
	SMART	<u>LisH</u>	<u>RT</u>	i	3	9.9E-1	5.3E-1	1.0E0	9.9I
nnota	ntion Cluster 329	Enrichment Score: 0.02	G	· ·	Count	P_Value	Fold Change	Benjamin	i FDF
	UP_KEYWORDS	Cilium biogenesis/degradation	RT		17	9.3E-1	7.9E-1	-	9.31
ے ا	GOTERM_BP_DIRECT				17		7.4E-1		1 9.6l
	GOTERM_BP_DIRECT	cilium morphogenesis	<u>RT</u>	•	17				1 9.9
	OOTEKIII_BI _BIKEOT	<u>cilium assembly</u>	<u>RT</u>	1	13	9.9E-1	6.2E-1	1.0E0	1
nnota	ation Cluster 330	Enrichment Score: 0.02	G	- 1	Count	P_Value	Fold Change	Benjamin	i FDI
	UP_KEYWORDS	Host cell receptor for virus entry	<u>RT</u>	1	7	9.2E-1	7.5E-1	1.0E0	9.2 1
	GOTERM_MF_DIRECT	virus receptor activity	<u>RT</u>	1	7	9.8E-1	6.0E-1	1.0E0	9.8 1
	GOTERM_BP_DIRECT	viral entry into host cell	<u>RT</u>		8	9.9E-1	5.9E-1	1.0E0	9.9 1
nnota	ation Cluster 331	Enrichment Score: 0.01	G	170	Count	P_Value	Fold	Benjamin	
7	UP_SEQ_FEATURE			1	4		Change 7.0E-1		9.7
J	INTERPRO	zinc finger region:FYVE-type	<u>RT</u>						1 9.6
J		<u>Zinc finger, FYVE-type</u>	<u>RT</u>	•	3	9.6E-1	6.4E-1	1.0E0	1
	INTERPRO	Zinc finger, FYVE-related	<u>RT</u>	1	3	9.8E-1	5.5E-1	1.0E0	9.8 1
	SMART	<u>FYVE</u>	<u>RT</u>	i	3	1.0E0	4.2E-1 Fold		1.0
nnota	ntion Cluster 332	Enrichment Score: 0.01	G	178	Count	P_Value	Change	Benjamin	
)	INTERPRO	Ras-association	<u>RT</u>	•	4	9.7E-1	6.2E-1	1.0E0	9.7 1
	UP_SEQ_FEATURE	domain:Ras-associating	<u>RT</u>	1	3	9.7E-1	6.0E-1	1.0E0	9.7 1
	SMART	RA	<u>RT</u>	i	3	1.0E0	4.2E-1	1.0E0	1.0
nota	ation Cluster 333	Enrichment Score: 0	G		Count	P_Value	Fold Change	Benjamin	
)	UP_SEQ_FEATURE	repeat:22	<u>RT</u>	i	4	9.5E-1	6.6E-1	1.0E0	9.7 1
)	UP_SEQ_FEATURE	repeat:21	<u>RT</u>	1	4	9.6E-1	6.3E-1	1.0E0	9.7 1
	UP_SEQ_FEATURE	repeat:24	<u>RT</u>	1	3	9.7E-1	6.0E-1	1.0E0	9.7
	UP_SEQ_FEATURE	repeat:20	RT	1	4		5.9E-1		1 9.7
	UP_SEQ_FEATURE								1 9.8
		repeat:19	<u>RT</u>	•	4	9.8E-1	5.7E-1	1.0E0	1
)	UP_SEQ_FEATURE	repeat:18	<u>RT</u>	1	4	9.8E-1	5.6E-1	1.0E0	9.8 1
)	UP_SEQ_FEATURE	repeat:2	<u>RT</u>	•	27	9.9E-1	7.1E-1	1.0E0	9.9 1
	UP_SEQ_FEATURE	repeat:17	<u>RT</u>	1	4	9.9E-1	4.9E-1	1.0E0	9.9 1
)	UP_SEQ_FEATURE	repeat:9	<u>RT</u>		9	9.9E-1	5.7E-1	1.0E0	9.9
) 1	UP_SEQ_FEATURE								1 9.9
J		repeat:10	<u>RT</u>	1	8	9.9E-1	5.6E-1	1.0E0	1
)	UP_SEQ_FEATURE	repeat:1	<u>RT</u>	•	26	9.9E-1	6.9E-1	1.0E0	9.9
	UP_SEQ_FEATURE	repeat:11	<u>RT</u>	1	7	9.9E-1	5.4E-1	1.0E0	9.9 1
)	UP_SEQ_FEATURE	repeat:6	<u>RT</u>	4	13	9.9E-1	6.0E-1	1.0E0	9.9 1
)	UP_SEQ_FEATURE	repeat:16	<u>RT</u>	i	4	1.0E0	4.5E-1	1.0E0	1.0
))	UP_SEQ_FEATURE	repeat:8	<u>RT</u>		10	1.0E0	5.5E-1		1.0
)	UP_SEQ_FEATURE UP_SEQ_FEATURE	repeat:15 repeat:3	RT RT		5 21	1.0E0 1.0E0	4.6E-1 6.4E-1		1.0
	UP_SEQ_FEATURE	repeat:12	RT	1	6	1.0E0	4.7E-1	1.0E0	1.0
	UP_SEQ_FEATURE	repeat:5	<u>RT</u>	•	13	1.0E0	5.5E-1		1.0
	UP_SEQ_FEATURE UP_SEQ_FEATURE	repeat:14 repeat:7	RT RT		5 10	1.0E0 1.0E0	4.3E-1 5.1E-1		1.0
	UP_SEQ_FEATURE	repeat:4	RT		16	1.0E0	5.7E-1		1.0
	UP_SEQ_FEATURE	repeat:13	<u>RT</u>	i	5	1.0E0	4.1E-1	1.0E0	1.0
nota	ation Cluster 334	Enrichment Score: 0	G	- 18	Count	P_Value	Fold Change	Benjamin	i FC
	UP_SEQ_FEATURE	domain:Rho-GAP	<u>RT</u>	i	4	1.0E0	4.0E-1	1.0E0	1.0
	INTERPRO	Rho GTPase activation protein domain	RT DT		4	1.0E0	3.7E-1		1.0
	INTERPRO SMART	Rho GTPase activation protein RhoGAP	RT RT		6 4	1.0E0 1.0E0	4.1E-1 2.5E-1		1.0
	UP_KEYWORDS	GTPase activation	RT		7	1.0E0	2.4E-1		1.0
	GOTERM_MF_DIRECT	GTPase activator activity	<u>RT</u>	1	14	1.0E0	3.0E-1	1.0E0	1.0
nota	ation Cluster 335	Enrichment Score: 0	G	100	Count	P_Value	Fold Change	Benjamin	FC
	UP_SEQ_FEATURE	domain:DH	<u>RT</u>		4	1.0E0	4.0E-1	1.0E0	1.0
	GOTERM_BP_DIRECT	regulation of Rho protein signal transduction	RT DT		6	1.0E0	4.4E-1		1.0
	INTERPRO GOTERM_MF_DIRECT	<u>Dbl homology (DH) domain</u> <u>Rho guanyl-nucleotide exchange factor</u>	RT DT		4	1.0E0	3.5E-1		1.0
		<u>activity</u>	<u>RT</u>		4	1.0E0	3.1E-1		1.0
J	GOTERM_MF_DIRECT	<u>guanyl-nucleotide exchange factor activity</u> <u>RhoGEF</u>	RT RT		6 4	1.0E0 1.0E0	3.0E-1 2.4E-1		1.0

Annotation Cluster	1 Enri	ichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_KEYWO	ORDS Gua	nine-nucleotide releasing factor	<u>RT</u>	1	5	1.0E0	2.3E-1	1.0E0	1.0E0
Annotation Cluster	336 Enri	ichment Score: 0	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FI	EATURE dom	nain:PH	<u>RT</u>	1	21	1.0E0	5.8E-1	1.0E0	1.0E0
INTERPRO	<u>Plec</u>	kstrin homology domain	<u>RT</u>	i	20	1.0E0	4.6E-1	1.0E0	1.0E0
INTERPRO	<u>Plec</u>	kstrin homology-like domain	<u>RT</u>	i	36	1.0E0	5.2E-1	1.0E0	1.0E0
SMART	<u>PH</u>		<u>RT</u>	Ē	19	1.0E0	2.9E-1	1.0E0	1.0E0
Annotation Cluster	337 Enri	ichment Score: 0	G		Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_C	C_DIRECT mite	ochondrial matrix	<u>RT</u>	-	25	1.0E0	4.9E-1	1.0E0	1.0E0
UP_SEQ_FI	EATURE tran	nsit peptide:Mitochondrion	<u>RT</u>	1 m	29	1.0E0	4.1E-1	1.0E0	1.0E0
UP_KEYWO	DRDS <u>Tran</u>	nsit peptide	<u>RT</u>	Ē	31	1.0E0	4.0E-1	1.0E0	1.0E0
Annotation Cluster	338 Enri	ichment Score: 0	G	™	Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FI	EATURE DNA	A-binding region:Basic motif	<u>RT</u>	i .	7	1.0E0	2.9E-1	1.0E0	1.0E0
UP_SEQ_FI	EATURE dom	nain:Helix-loop-helix motif	<u>RT</u>	i e	3	1.0E0	1.8E-1	1.0E0	1.0E0
INTERPRO	<u>Myc</u> dom	<u>atype, basic helix-loop-helix (bHLH)</u>	<u>RT</u>	i e	3	1.0E0	1.6E-1	1.0E0	1.0E0
SMART	HLH	1	RT	i -	3	1.0E0	1.1E-1	1.0F0	1.0E0