

Laboratory of Human Retrovirology and Immunoinformatics (LHRI)

Help and Manual

## BIC INFORMATION DOTABASE

## **Functional Annotation Clustering**

**Current Gene List: List\_1** 

**Current Background: Homo sapiens** 

2998 DAVID IDs

**■ Options** Classification Stringency Medium ✓

Rerun using options | Create Sublist

## 336 Cluster(s) Download File

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

Annot	tation Cluster 1	Enrichment Score: ?	G	<b>™</b>	Count	P_Value	Fold Change	Benjamini	i FDR
Annot	tation Cluster 2	Enrichment Score: 80.34	G	To the second second	Count	P_Value	Fold Change	Benjamini	i FDR
	UP_KEYWORDS	Nucleotide-binding	<u>RT</u>		769	1.5E- 209	3.0E0	1.1E-207	8.5E- 208
	UP_KEYWORDS	ATP-binding	<u>RT</u>		619	9.8E- 174	3.1E0	5.2E-172	4.0E- 172
	GOTERM_MF_DIRECT	ATP binding	<u>RT</u>		640	5.1E- 139	2.6E0	1.6E-136	1 55
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	<u>RT</u>	_	447	2.8E- 123	3.1E0	1.0E-120	1.0E
	UP_SEQ_FEATURE	domain:Protein kinase	RT	=	249	8.4E-	3.5E0	2.6E-81	2.5E
	INTERPRO	Protein kinase-like domain	RT	=	275	84 2.0E-	3.2E0	9.2E-80	81 8.4E
	INTERPRO	Protein kinase, catalytic domain	RT	=	259	82 8.9E-	3.3E0	3.4E-78	80 3.1E
	UP_SEQ_FEATURE			<u> </u>		81 4.2E-			78 1.2E
	INTERPRO	binding site:ATP	<u>RT</u>	_	264	77 3.0E-		1.2E-74	74 7.9E
	UP_KEYWORDS	<u>Protein kinase, ATP binding site</u>	<u>RT</u>	_	214	72 1.7E-	3.5E0	8.6E-70	70 4.5E
		<u>Kinase</u>	<u>RT</u>	-	301	70	2.8E0	5.8E-69	69
	UP_KEYWORDS	<u>Serine/threonine-protein kinase</u>	<u>RT</u>	=	187	2.7E- 55	3.3E0	6.8E-54	5.3E
	UP_SEQ_FEATURE	active site:Proton acceptor	<u>RT</u>	=	255	2.2E- 51	2.6E0	3.2E-49	3.0E 49
	GOTERM_MF_DIRECT	protein kinase activity	<u>RT</u>	=	180	1.4E- 48	3.0E0	2.3E-46	2.1E 46
	GOTERM_MF_DIRECT	protein serine/threonine kinase activity	<u>RT</u>	=	180	6.1E- 45	2.9E0	7.9E-43	7.0E- 43
	GOTERM_BP_DIRECT	protein phosphorylation	<u>RT</u>	=	201	5.6E- 43	2.6E0	4.1E-40	3.9E
	UP_KEYWORDS	<u>Transferase</u>	<u>RT</u>	_	454	4.7E- 42	1.8E0	9.7E-41	7.5E- 41
	INTERPRO	Serine/threonine-protein kinase, active site	<u>RT</u>	=	150	1.1E- 39	3.0E0	1.9E-37	1.7E
	SMART	<u>S. TKc</u>	<u>RT</u>	=	171	5.7E-	1.9E0	3.0E-20	2.7E
	tation Cluster 3	Enrichment Score: 59.99	G		Count	22 P_Value	Fold	Benjamini	20 FDR
	UP_SEQ_FEATURE	repeat:ANK 4	RT	=	133	2.9E-	Change 5.3E0	8.0E-74	7.7E
	UP_SEQ_FEATURE			_	117	76 1.1E-	5.6E0	2.7E-69	74 2.6E
	UP_KEYWORDS	repeat:ANK 5	<u>RT</u>	-		71 2.2E-			69 5.5E
	UP_SEQ_FEATURE	ANK repeat	<u>RT</u>	-	164	70 1.0E-	4.3E0	7.0E-69	69 2.3E
		repeat:ANK 3	<u>RT</u>	=	141	67	4.6E0	2.3E-65	65
	INTERPRO	Ankyrin repeat-containing domain	<u>RT</u>	=	165	1.7E- 64	3.9E0	3.4E-62	3.1E- 62
	INTERPRO	Ankyrin repeat	<u>RT</u>	=	161	3.5E- 64	3.9E0	6.6E-62	6.1E-
	UP_SEQ_FEATURE	repeat:ANK 2	<u>RT</u>	=	148	9.4E- 61	4.1E0	1.7E-58	1.7E- 58
	UP_SEQ_FEATURE	repeat:ANK 1	<u>RT</u>	=	147	4.0E- 60	4.1E0	7.2E-58	6.9E
	UP_SEQ_FEATURE	repeat:ANK 6	<u>RT</u>	<b>=</b>	85	7.5E- 55	5.8E0	1.2E-52	1.1E
	SMART	<u>ANK</u>	<u>RT</u>	=	159	9.3E- 40	2.6E0	1.1E-37	9.7E
	UP_SEQ_FEATURE	repeat:ANK 7	<u>RT</u>	•	56	1.0E-	6.1E0	1.3E-35	1.3E
Annot	tation Cluster 4	Enrichment Score: 41.28	G		Count	37 P_Value	Fold	Benjamini	35 FDR
	GOTERM_BP_DIRECT	rRNA processing	<u>RT</u>	=	150	1.7E-	Change 4.2E0	3.3E-63	3.2E
	UP_KEYWORDS	Ribonucleoprotein	RT		169	66 8.4E-	3.9E0	2.3E-63	63 1.8E
	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process,				65 1.1E-			63 1.6E
	GOTERM_BP_DIRECT	nonsense-mediated decay  SRP-dependent cotranslational protein	<u>RT</u>	-	99	55 7.7E-	4.9E0	1.6E-52	52 8.6E
		targeting to membrane	<u>RT</u>	•	81	48	5.1E0	9.1E-45	45
	GOTERM_BP_DIRECT	<u>translational initiation</u>	<u>RT</u>	=	100	7.7E- 47	4.3E0	7.6E-44	7.2E
	KEGG_PATHWAY	Ribosome	<u>RT</u>	=	101	5.0E- 44	3.9E0	6.2E-42	2.8E 42
	UP_KEYWORDS	<u>Ribosomal protein</u>	<u>RT</u>	=	104	4.5E- 39	3.9E0	9.0E-38	7.0E- 38
	GOTERM_BP_DIRECT	viral transcription	<u>RT</u>	•	81	1.8E- 37	4.3E0	1.2E-34	1.1E- 34
	GOTERM_CC_DIRECT	cytosolic large ribosomal subunit	<u>RT</u>	±	59	8.4E- 37	5.5E0	1.1E-34	9.3E
	GOTERM_CC_DIRECT	<u>ribosome</u>	<u>RT</u>	=	97	1.3E- 35	3.7E0	1.4E-33	1.3E
	GOTERM_MF_DIRECT	structural constituent of ribosome	<u>RT</u>	=	107	3.5E- 27	2.9E0	3.2E-25	2.9E
	GOTERM_BP_DIRECT	translation	RT		116	8.8E-	2.7E0	3.7E-24	25 3.5E
	GOTERM_CC_DIRECT	cytosolic small ribosomal subunit		-	35	27 1.9E-		1.2E-15	24 1.0E
		Cytosone Smail Hoosomal Subumit	<u>RT</u>	•	33	17		1.26-15	15
	tation Cluster 5	Enrichment Score: 36.85	G	i 🚾	Count	P_Value	Fold	Benjamini	

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

Annota	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamini	FDR
	SMART	SCAN	<u>RT</u>	ī	53	5.7E- 25	3.7E0	4.4E-23	3.9E- 23
Annota	ation Cluster 8	Enrichment Score: 25.16	G	<b>17</b> 8	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	mRNA splicing, via spliceosome	<u>RT</u>	=	132	3.9E- 46	3.5E0	3.3E-43	3.1E- 43
	KEGG_PATHWAY	<u>Spliceosome</u>	<u>RT</u>	<b>=</b>	88	3.7E- 32	3.5E0	2.2E-30	1.0E- 30
	UP_KEYWORDS	<u>Spliceosome</u>	<u>RT</u>	=	77	4.5E- 32	4.2E0	7.1E-31	5.5E- 31
	GOTERM_CC_DIRECT	catalytic step 2 spliceosome	<u>RT</u>	•	60	9.7E- 26	4.1E0	9.6E-24	8.3E- 24
	UP_KEYWORDS	mRNA splicing	<u>RT</u>	=	105	4.3E- 24	2.8E0	6.2E-23	4.8E- 23
	UP_KEYWORDS	mRNA processing	<u>RT</u>	<b>=</b>	121	4.5E- 23	2.5E0	6.2E-22	4.8E- 22
	GOTERM_CC_DIRECT	<u>spliceosomal complex</u>	<u>RT</u>		52	6.1E- 18	3.5E0	4.1E-16	3.6E- 16
	GOTERM_BP_DIRECT	RNA splicing	<u>RT</u>		52	7.0E-6	1.9E0	3.1E-4	3.0E- 4
Annota	ation Cluster 9	Enrichment Score: 21.2	G	17	Count	P_Value	Fold Change	Benjamini	1
	UP_KEYWORDS	<u>Helicase</u>	<u>RT</u>	=	94	2.3E- 43	4.5E0	5.2E-42	4.0E- 42
	INTERPRO	Helicase, superfamily 1/2, ATP-binding	<u>RT</u>	=	77	2.2E-	4.3E0	3.1E-33	2.8E-
	INTERPRO	domain  Helicase, C-terminal	<u>RT</u>	-	76	35 3.5E-	4.4E0	4.7E-33	33 4.3E-
	UP_SEQ_FEATURE	domain:Helicase C-terminal	RT		73	35 1.0E-	4.6E0	1.1E-32	33 1.1E-
	UP_SEQ_FEATURE	domain:Helicase ATP-binding	RT		74	34 2.0E-	4.4E0	2.2E-31	32 2.1E-
	GOTERM_MF_DIRECT	helicase activity	RT		57	33 5.5E-	4.0E0	4.1E-22	31 3.7E-
	SMART	DEXDc	RT		76	24 1.2E-		7.6E-21	22 6.8E-
	SMART	HELICC	RT.	-	75	1.4E-	2.9E0	7.9E-21	21 7.1E-
	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-	RT	-	46	22 5.9E-	4.1E0	5.4E-18	21 4.9E-
	GOTERM_MF_DIRECT	terminal				20 7.2E-			18 3.5E-
	UP_SEQ_FEATURE	ATP-dependent RNA helicase activity	RT	•	43	18 3.0E-	3.9E0	4.0E-16	16 2.4E-
	INTERPRO	short sequence motif:DEAH box	<u>RT</u>	•	32	17 1.5E-	5.1E0	2.5E-15	15 8.3E-
	GOTERM_BP_DIRECT	SNF2-related	<u>RT</u>	•	26	14 5.0E-	5.0E0	9.1E-13	13 6.0E-
	INTERPRO	RNA secondary structure unwinding	<u>RT</u>	•	29	12 3.6E-	3.9E0	6.3E-10	10 1.4E-
	UP_SEQ_FEATURE	RNA helicase, DEAD-box type, Q motif	<u>RT</u>	•	25	11 4.3E-	4.2E0	1.5E-9	9 2.5E-
	UP_SEQ_FEATURE	short sequence motif:Q motif	<u>RT</u>	•	24	10	4.1E0	2.6E-8	8
		short sequence motif:DEAD box	<u>RT</u>	i	22	1.7E-9	4.2E0	1.0E-7	9.8E- 8
	INTERPRO	RNA helicase, ATP-dependent, DEAD-box, conserved site	<u>RT</u>	i	19	5.6E-9	4.4E0	1.8E-7	1.7E- 7
Annota	ation Cluster 10	Enrichment Score: 19.83	G	To the second se	Count	P_Value	Fold Change	Benjamini	<u> </u>
	UP_KEYWORDS	<u>Cell cycle</u>	<u>RT</u>	=	216	6.2E- 34	2.3E0	1.0E-32	8.1E- 33
	UP_KEYWORDS	<u>Cell division</u>	<u>RT</u>	=	132	5.3E- 22	2.3E0	7.0E-21	5.4E- 21
	GOTERM_BP_DIRECT	cell division	<u>RT</u>	=	124	3.3E- 17	2.1E0	6.9E-15	6.6E- 15
	UP_KEYWORDS	<u>Mitosis</u>	<u>RT</u>	=	92	2.4E- 16	2.4E0	2.7E-15	2.1E- 15
	GOTERM_BP_DIRECT	mitotic nuclear division	<u>RT</u>	=	90	2.8E- 13	2.2E0	4.1E-11	3.9E- 11
Annota	ation Cluster 11	Enrichment Score: 19.26	G	<b>17</b>	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	<u>RT</u>	•	60	8.0E- 38	5.8E0	1.1E-35	1.0E- 35
	INTERPRO	<u>Ubiquitin-conjugating enzyme, active site</u>	<u>RT</u>	i e	26	3.1E- 19	6.2E0	2.6E-17	2.4E- 17
	INTERPRO	<u>Ubiquitin-conjugating enzyme, E2</u>	<u>RT</u>	i	34	5.7E- 19	5.0E0	4.6E-17	4.2E- 17
	GOTERM_MF_DIRECT	ubiquitin conjugating enzyme activity	<u>RT</u>	•	26	4.2E- 16	5.3E0	2.1E-14	1.9E- 14
	INTERPRO	Ubiquitin-conjugating enzyme/RWD-like	<u>RT</u>	i .	37	7.1E- 16	4.1E0	4.9E-14	4.5E- 14
	GOTERM_BP_DIRECT	protein K48-linked ubiquitination	<u>RT</u>	i .	30	6.5E- 12	3.8E0	7.9E-10	7.6E- 10
Annota	ation Cluster 12	Enrichment Score: 18.73	G	177	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	<u>RT</u>	=	60	8.0E- 38	5.8E0	1.1E-35	1.0E- 35
	UP_SEQ_FEATURE	domain:HECT	<u>RT</u>	i contraction	24	2.9E- 15	5.8E0	2.2E-13	2.2E- 13
	INTERPRO	<u>HECT</u>	<u>RT</u>	1	24	2.4E- 14	5.3E0	1.4E-12	1.3E- 12
	SMART	<u>HECTc</u>	<u>RT</u>	•	24	2.2E- 10	3.5E0	7.1E-9	6.4E- 9

Annot	tation Cluster 1	Enrichment Score: ?	G	. <mark>B</mark> e	Count	P_Value	Fold Change	Benjamin	ni FDF
Annot	tation Cluster 13	Enrichment Score: 18	G	- 100 miles	Count	P_Value	Fold Change	Benjamin	ni FDF
	UP_KEYWORDS	<u>Tyrosine-protein kinase</u>	<u>RT</u>	=	81	3.5E- 42	5.0E0	7.6E-41	5.9 41
	INTERPRO	Serine-threonine/tyrosine-protein kinase	<u>RT</u>	_	95	8.1E-	4.2E0	1.4E-39	1.3
_ 	INTERPRO	catalytic domain  Tyrosine-protein kinase, catalytic domain	RT		68	42 2.3E-	5.0E0	3.5E-35	3.2
_ _	INTERPRO			_		37 2.5E-			35 2.7
_	SMART	<u>Tyrosine-protein kinase, active site</u>	RT	•	69	33 5.1E-	4.5E0	3.0E-31	31 4.3
		<u>TyrKc</u>	<u>RT</u>	•	68	26	3.3E0	4.8E-24	24
	GOTERM_MF_DIRECT	<u>protein tyrosine kinase activity</u>	RT	•	76	2.2E- 25	3.4E0	1.9E-23	1.7 23
	GOTERM_BP_DIRECT	protein autophosphorylation	<u>RT</u>	•	88	1.5E- 24	3.0E0	5.8E-22	5.5 22
	GOTERM_BP_DIRECT	peptidyl-tyrosine phosphorylation	<u>RT</u>	•	79	1.9E- 22	3.1E0	7.1E-20	6.7 20
	GOTERM_MF_DIRECT	non-membrane spanning protein tyrosine kinase activity	<u>RT</u>	1	34	2.1E- 16	4.4E0	1.1E-14	9.4 15
	GOTERM_BP_DIRECT	peptidyl-tyrosine autophosphorylation	<u>RT</u>	1	31	7.6E- 16	4.6E0	1.5E-13	1.4 13
	GOTERM_MF_DIRECT	transmembrane receptor protein tyrosine	<u>RT</u>	•	25	1.9E-	3.9E0	6.0E-9	5.4
	GOTERM_CC_DIRECT	kinase activity extrinsic component of cytoplasmic side of	RT		34	10 2.4E-	3.2E0	9.6E-9	9 8.4
_ _	GOTERM_BP_DIRECT	<u>plasma membrane</u> <u>transmembrane receptor protein tyrosine</u>				10			9 1.8
	UP_KEYWORDS	kinase signaling pathway	<u>RT</u>	•	42	2.2E-9	2.6E0	1.9E-7	7 3.9
		SH2 domain	<u>RT</u>	•	37	7.2E-7	2.4E0	5.0E-6	6
	INTERPRO	SH2 domain	<u>RT</u>	•	39	3.6E-6	2.1E0	7.7E-5	7.1 5
	UP_SEQ_FEATURE	domain:SH2	<u>RT</u>	¥	31	2.9E-5	2.2E0	1.0E-3	1.0 3
	SMART	SH2	<u>RT</u>	1	36	1.9E-2	1.4E0	1.5E-1	1.3 1
	GOTERM_MF_DIRECT	receptor binding	<u>RT</u>		47	9.8E-1	7.9E-1	1.0E0	9.8
Annot	tation Cluster 14	Enrichment Score: 17.62	G	177	Count	P_Value	Fold Change	Benjamin	i FDI
	UP_KEYWORDS	GTP-binding	RT	=	149	3.1E-	3.0E0	5.9E-37	4.5
_ _	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	RT	_	137	38 8.1E-	3.0E0	1.0E-33	37 9.6
	GOTERM_MF_DIRECT			<u>-</u>		36 1.5E-			34 1.5
_	GOTERM_MF_DIRECT	GTP binding	<u>RT</u>	-	159	30	2.5E0	1.6E-28	28
		GTPase activity	<u>RT</u>	=	111	2.0E- 27	2.8E0	2.0E-25	1.8 25
	INTERPRO	Small GTP-binding protein domain	<u>RT</u>	•	78	5.4E- 20	2.9E0	5.1E-18	4.7 18
	INTERPRO	Small GTPase superfamily, Ras type	<u>RT</u>	1	33	1.7E- 19	5.2E0	1.5E-17	1.4 17
	INTERPRO	Small GTPase superfamily	<u>RT</u>	±	62	8.3E- 15	2.8E0	5.2E-13	4.8 13
	GOTERM_BP_DIRECT	small GTPase mediated signal transduction	<u>RT</u>	<b>=</b>	85	2.6E- 11	2.0E0	3.0E-9	2.9
	UP_SEQ_FEATURE	short sequence motif:Effector region	<u>RT</u>		41	7.7E-	2.8E0	4.6E-8	4.5
_ 	UP_KEYWORDS	Prenylation	RT	-	49	10 2.0E-6	2.0E0	1.3E-5	8 1.0
	UP_SEQ_FEATURE	lipid moiety-binding region:S-geranylgeranyl							5 8.0
	UP_SEQ_FEATURE	cysteine	<u>RT</u>	•	28	3.2E-3		8.3E-2	2
	OF_SEQ_FEATORE	propeptide:Removed in mature form	<u>RT</u>	i .	51	4.6E-3		1.2E-1	1.1 1
						P_Value	Fold Change	Benjamin	
nnot	tation Cluster 15	Enrichment Score: 17.43	G		Count				1.7
nnot	tation Cluster 15  UP_SEQ_FEATURE	Enrichment Score: 17.43  zinc finger region:C2H2-type 19	RT	=	Count 50	1.5E- 35	6.3E0	1.8E-33	
nnot						1.5E- 35 2.2E- 21	6.3E0 6.1E0	1.8E-33 2.1E-19	33 2.0
nnot	UP_SEQ_FEATURE	zinc finger region:C2H2-type 19	<u>RT</u>	=	50	35 2.2E-			33 2.0 19 8.1 15
innot	UP_SEQ_FEATURE UP_SEQ_FEATURE	zinc finger region:C2H2-type 19 zinc finger region:C2H2-type 20	RT RT	•	50 32	35 2.2E- 21 1.0E- 16 6.2E-	6.1E0	2.1E-19	33 2.0 19 8.1 15 4.7
nnot	UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE	zinc finger region:C2H2-type 19 zinc finger region:C2H2-type 20 zinc finger region:C2H2-type 21 zinc finger region:C2H2-type 22	RT RT RT RT		50 32 24 23	35 2.2E- 21 1.0E- 16 6.2E- 16 1.9E-	6.1E0 6.3E0 6.3E0	2.1E-19 8.4E-15 4.9E-14	33 2.0 19 8.1 15 4.7 14
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE	zinc finger region:C2H2-type 19 zinc finger region:C2H2-type 20 zinc finger region:C2H2-type 21 zinc finger region:C2H2-type 22 zinc finger region:C2H2-type 23	RT RT RT RT RT		50 32 24 23 15	35 2.2E- 21 1.0E- 16 6.2E- 16 1.9E- 10	6.1E0 6.3E0 6.3E0 6.4E0	2.1E-19 8.4E-15 4.9E-14 1.2E-8	33 2.0 19 8.1 15
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE	zinc finger region:C2H2-type 19 zinc finger region:C2H2-type 20 zinc finger region:C2H2-type 21 zinc finger region:C2H2-type 22 zinc finger region:C2H2-type 23 zinc finger region:C2H2-type 24	RT RT RT RT RT RT		50 32 24 23 15	35 2.2E- 21 1.0E- 16 6.2E- 16 1.9E- 10 6.7E-9	6.1E0 6.3E0 6.3E0 6.4E0 6.3E0	2.1E-19 8.4E-15 4.9E-14 1.2E-8 3.7E-7	33 2.0 19 8.1 15 4.7 14 1.1 8 3.6 7
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE	zinc finger region:C2H2-type 19 zinc finger region:C2H2-type 20 zinc finger region:C2H2-type 21 zinc finger region:C2H2-type 22 zinc finger region:C2H2-type 23 zinc finger region:C2H2-type 24 Enrichment Score: 15.74	RT RT RT RT RT RT		50 32 24 23 15 13	35 2.2E- 21 1.0E- 16 6.2E- 16 1.9E- 10 6.7E-9	6.1E0 6.3E0 6.3E0 6.4E0 6.3E0 Fold Change	2.1E-19 8.4E-15 4.9E-14 1.2E-8 3.7E-7 Benjamin	33 2.0 19 8.1 15 4.7 14 1.1 8 3.6 7
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE	zinc finger region:C2H2-type 19 zinc finger region:C2H2-type 20 zinc finger region:C2H2-type 21 zinc finger region:C2H2-type 22 zinc finger region:C2H2-type 23 zinc finger region:C2H2-type 24	RT RT RT RT RT RT		50 32 24 23 15	35 2.2E- 21 1.0E- 16 6.2E- 16 1.9E- 10 6.7E-9 P_Value 7.7E- 22	6.1E0 6.3E0 6.3E0 6.4E0 6.3E0	2.1E-19 8.4E-15 4.9E-14 1.2E-8 3.7E-7	33 2.C 19 8.11 15 4.7 14 1.11 8 3.6 7 7.6 21
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE	zinc finger region:C2H2-type 19 zinc finger region:C2H2-type 20 zinc finger region:C2H2-type 21 zinc finger region:C2H2-type 22 zinc finger region:C2H2-type 23 zinc finger region:C2H2-type 24 Enrichment Score: 15.74	RT RT RT RT RT RT		50 32 24 23 15 13	35 2.2E- 21 1.0E- 16 6.2E- 16 1.9E- 10 6.7E-9 P_Value 7.7E-	6.1E0 6.3E0 6.3E0 6.4E0 6.3E0 Fold Change	2.1E-19 8.4E-15 4.9E-14 1.2E-8 3.7E-7 Benjamin	333 2.0 19 8.1 15 4.7 14 1.1 8 3.6 7 7.6 21 1.3
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE	zinc finger region:C2H2-type 19 zinc finger region:C2H2-type 20 zinc finger region:C2H2-type 21 zinc finger region:C2H2-type 22 zinc finger region:C2H2-type 23 zinc finger region:C2H2-type 24 Enrichment Score: 15.74 Protein phosphatase	RT RT RT RT RT RT RT RT RT		50 32 24 23 15 13 Count	35 2.2E- 21 1.0E- 16 6.2E- 16 1.9E- 10 6.7E-9 P_Value 7.7E- 22 8.5E-	6.1E0 6.3E0 6.3E0 6.4E0 6.3E0 Fold Change 3.5E0	2.1E-19 8.4E-15 4.9E-14 1.2E-8 3.7E-7 Benjamin 9.8E-21	33 2.0 19 8.1 15 4.7 14 1.1 8 3.6 7 7.6 21 1.3 3.5 11 3.5 21 3.5
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  tation Cluster 16  UP_KEYWORDS  GOTERM_BP_DIRECT	zinc finger region:C2H2-type 19 zinc finger region:C2H2-type 20 zinc finger region:C2H2-type 21 zinc finger region:C2H2-type 22 zinc finger region:C2H2-type 23 zinc finger region:C2H2-type 24 Enrichment Score: 15.74  Protein phosphatase protein dephosphorylation	RT RT RT RT RT RT RT RT RT		50 32 24 23 15 13 Count 67 58	35 2.2E- 21 1.0E- 16 6.2E- 16 1.9E- 10 6.7E-9 P_Value 7.7E- 22 8.5E- 14 9.2E-	6.1E0 6.3E0 6.3E0 6.4E0 6.3E0 Fold Change 3.5E0 2.7E0 3.7E0	2.1E-19 8.4E-15 4.9E-14 1.2E-8 3.7E-7 Benjamin 9.8E-21 1.3E-11 3.9E-12	33 2.0 19 8.1 15 4.7 14 1.1 8 3.6 7 7.6 21 1.3 11 3.5 12
) ) ) ) ) )	UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  tation Cluster 16  UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT	zinc finger region:C2H2-type 19 zinc finger region:C2H2-type 20 zinc finger region:C2H2-type 21 zinc finger region:C2H2-type 22 zinc finger region:C2H2-type 23 zinc finger region:C2H2-type 24 Enrichment Score: 15.74 Protein phosphatase protein dephosphorylation protein serine/threonine phosphatase activity	RT RT RT RT RT RT RT RT RT		50 32 24 23 15 13 Count 67 58 36	35 2.2E- 21 1.0E- 16 6.2E- 16 1.9E- 10 6.7E-9 P_Value 7.7E- 22 8.5E- 14 9.2E- 14	6.1E0 6.3E0 6.3E0 6.4E0 6.3E0 Fold Change 3.5E0 2.7E0 3.7E0 Fold	2.1E-19 8.4E-15 4.9E-14 1.2E-8 3.7E-7 Benjamin 9.8E-21 1.3E-11 3.9E-12	33 2.C 19 8.1 15 4.7 14 1.1 8 3.6 7 7.6 21 1.3 11 3.5 11

Annot	tation Cluster 1	Enrichment Score: ?	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	<u>DNA repair</u>	RT		81	9.3E- 11	2.0E0	1.0E-8	9.5E- 9
Annot	tation Cluster 18	Enrichment Score: 15.12	G	178	Count	P_Value	Fold Change	Benjamini	Ť
	UP_SEQ_FEATURE	domain:BTB	<u>RT</u>	-	71	3.2E- 22	3.4E0	3.1E-20	3.0E- 20
	INTERPRO	BTB/POZ-like	<u>RT</u>		77	4.5E-	2.7E0	3.4E-15	3.1E-
	INTERPRO	BTB/POZ fold	RT	=	79	17 1.2E-	2.6E0	8.5E-15	15 7.8E-
	SMART	BTB	RT		75	16 1.9E-7		4.0E-6	15 3.6E-
Annot	tation Cluster 19	Enrichment Score: 13.83	G	-	Count	P_Value	Fold	Benjamini	6 FDR
	GOTERM_BP_DIRECT	protein K11-linked ubiquitination	RT		27	1.6E-	Change 5.9E0	4.3E-17	4.1E-
	GOTERM_CC_DIRECT	anaphase-promoting complex	RT	1	20	19 2.4E-	5.5E0	1.1E-10	17 9.8E-
	GOTERM_BP_DIRECT	regulation of ubiquitin-protein ligase activity	RT	1	20	12 8.6E-	5.2E0	1.0E-9	11 9.8E-
Annot	tation Cluster 20	involved in mitotic cell cycle  Enrichment Score: 13.04	G		Count	12 P_Value	Fold	Benjamini	10 EDP
Alliot	INTERPRO	Actin-related protein	RT	:	30	1.1E-	Change	8.5E-17	7.7E-
	SMART			_		18 2.4E-			17 7.7E-
	INTERPRO	ACTIN	<u>RT</u>		30	14 4.2E-	3.7E0	8.5E-13	13 1.9E-
	INTERPRO	Actin/actin-like conserved site	<u>RT</u>		19	12 6.3E-	5.6E0	2.1E-10	10 2.0E-
		Actin, conserved site	RT	i	16	10	Fold	2.2E-8	8
Annot	tation Cluster 21  GOTERM_BP_DIRECT	Enrichment Score: 11.05  proteasome-mediated ubiquitin-dependent	G	<b></b>	Count	P_Value	Change	Benjamini	
		protein catabolic process	<u>RT</u>	=	105	1.1E- 29	3.1E0	5.3E-27	5.0E- 27
	GOTERM_BP_DIRECT	anaphase-promoting complex-dependent catabolic process	<u>RT</u>	•	53	3.2E- 22	4.0E0	1.0E-19	9.9E- 20
	GOTERM_BP_DIRECT	positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	<u>RT</u>	E	50	1.9E- 20	3.9E0	6.0E-18	5.7E- 18
	GOTERM_BP_DIRECT	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	<u>RT</u>		47	2.1E- 19	3.9E0	5.4E-17	5.1E-
	GOTERM_BP_DIRECT	stimulatory C-type lectin receptor signaling	RT	=	57	1.1E-	3.2E0	2.5E-15	17 2.4E-
	GOTERM_BP_DIRECT	<u>pathway</u> <u>T cell receptor signaling pathway</u>	RT	-	64	17 1.4E-	2.6E0	2.0E-11	15 1.9E-
	GOTERM_BP_DIRECT	NIK/NF-kappaB signaling	RT		38	13 5.4E-	3.4E0	7.4E-11	11 7.0E-
	GOTERM_BP_DIRECT	regulation of ubiquitin-protein ligase activity	RT	-	20	13 8.6E-	5.2E0	1.0E-9	11 9.8E-
	GOTERM_BP_DIRECT	involved in mitotic cell cycle		-		12 2.1E-			10 2.4E-
	GOTERM_BP_DIRECT	Fc-epsilon receptor signaling pathway  positive regulation of canonical Wnt signaling	<u>RT</u>	_	68	11 4.0E-	2.3E0	2.5E-9	9 3.8E-
	GOTERM_BP_DIRECT	pathway	<u>RT</u>	•	50	10	2.5E0	4.0E-8	8 1.8E-
	GOTERM_CC_DIRECT	regulation of mRNA stability	<u>RT</u>	•	44	2.1E-9		1.9E-7	7 2.0E-
		proteasome complex	<u>RT</u>	•	28	7.6E-8	3.0E0	2.2E-6	6
	UP_KEYWORDS	<u>Proteasome</u>	<u>RT</u>	i	25	7.9E-8	3.2E0	6.1E-7	4.7E- 7
	GOTERM_BP_DIRECT	negative regulation of canonical Wnt signaling pathway	<u>RT</u>	•	53	1.7E-6	1.9E0	9.0E-5	8.6E- 5
	GOTERM_BP_DIRECT	Wnt signaling pathway, planar cell polarity pathway	<u>RT</u>	•	34	8.4E-6	2.2E0	3.6E-4	3.4E- 4
	GOTERM_BP_DIRECT	regulation of cellular amino acid metabolic process	<u>RT</u>	i e	23	9.3E-6	2.7E0	3.9E-4	3.7E- 4
	KEGG_PATHWAY	<u>Proteasome</u>	<u>RT</u>	i e	21	5.9E-5	2.5E0	1.5E-4	7.0E- 5
	GOTERM_BP_DIRECT	antigen processing and presentation of exogenous peptide antigen via MHC class I,	<u>RT</u>	1	21	2.7E-3	2.0E0	5.3E-2	5.0E- 2
	GOTERM_BP_DIRECT	TAP-dependent tumor necrosis factor-mediated signaling	<u>RT</u>		32	6.3E-3	1.6E0	1.0E-1	1.0E-
Annot	tation Cluster 22	pathway  Enrichment Score: 11.02	G	-		P_Value		Benjamini	1 FDR
	KEGG_PATHWAY	T cell receptor signaling pathway	RT	E	64	2.9E- 22	•	6.4E-21	2.9E-
	KEGG_PATHWAY	Prostate cancer	RT		59	4.8E-	3.5E0	9.2E-21	21 4.2E-
	KEGG_PATHWAY					22 8.7E-			21 5.4E-
	- KEGG_PATHWAY	Pancreatic cancer	<u>RT</u>	-	43	16 1.6E-		1.2E-14	15 8.5E-
	KEGG_PATHWAY	Acute myeloid leukemia	<u>RT</u>		38	14 2.4E-		1.9E-13	14 1.2E-
	KEGG_PATHWAY	Chronic myeloid leukemia	<u>RT</u>	•	44	14		2.7E-13	13
		Endometrial cancer	<u>RT</u>	•	36	3.5E- 14		3.3E-13	1.5E- 13
	KEGG_PATHWAY	ErbB signaling pathway	<u>RT</u>	•	49	5.3E- 14		4.8E-13	2.2E- 13
	KEGG_PATHWAY	Glioma	<u>RT</u>	•	40	3.2E- 13	3.2E0	2.8E-12	1.3E- 12
	KEGG_PATHWAY	<u>VEGF signaling pathway</u>	<u>RT</u>	i	38	8.2E- 13	3.3E0	6.7E-12	3.1E- 12

nnota	ation Cluster 1	Enrichment Score: ?	G	· <mark>**</mark>	Count	P_Value	Fold Change	Benjamin	i FDR
	KEGG_PATHWAY	Prolactin signaling pathway	RT	1	41	2.8E-	3.0E0	2.1E-11	9.8
_ 	KEGG_PATHWAY	B cell receptor signaling pathway	RT	-	40	12 4.6E-	3.0E0	3.4E-11	12 1.5E
	KEGG_PATHWAY					12 2.3E-			11 7.1E
	_	Renal cell carcinoma	<u>RT</u>	•	38	11	3.0E0	1.5E-10	11
	KEGG_PATHWAY	Non-small cell lung cancer	<u>RT</u>	•	34	4.4E- 11	3.2E0	2.8E-10	1.3E 10
	KEGG_PATHWAY	<u>Fc epsilon RI signaling pathway</u>	<u>RT</u>	1	38	7.4E- 11	2.9E0	4.6E-10	2.1E 10
	KEGG_PATHWAY	<u>Melanoma</u>	<u>RT</u>	i .	37	1.8E-9	2.7E0	9.2E-9	4.2E 9
	KEGG_PATHWAY	Sphingolipid signaling pathway	<u>RT</u>	±	52	2.5E-9	2.3E0	1.1E-8	5.2E
	KEGG_PATHWAY	<u>Bladder cancer</u>	<u>RT</u>	•	25	2.5E-8	3.2E0	1.0E-7	4.6E
7	KEGG_PATHWAY	Osteoclast differentiation	<u>RT</u>		53	2.9E-8	2.1E0	1.1E-7	5.18
_ 	KEGG_PATHWAY	Central carbon metabolism in cancer	RT	_	32	9.6E-8	2.6E0	3.6E-7	8 1.6E
	KEGG_PATHWAY			-					7 4.8
		Choline metabolism in cancer	<u>RT</u>	•	40	3.5E-6	2.1E0	1.1E-5	6
	KEGG_PATHWAY	Thyroid cancer	<u>RT</u>	•	16	8.0E-5	2.9E0	2.0E-4	9.1E 5
	KEGG_PATHWAY	Natural killer cell mediated cytotoxicity	<u>RT</u>	i	38	1.8E-3	1.6E0	3.8E-3	1.8E 3
nnota	ation Cluster 23	Enrichment Score: 10.73	G	<b></b>	Count	P_Value	Fold Change	Benjamin	i FDF
	UP_SEQ_FEATURE	lipid moiety-binding region:N-myristoyl glycine	<u>RT</u>	Ē	56	3.6E- 17	3.3E0	3.0E-15	2.9E 15
	UP_KEYWORDS	<u>Myristate</u>	<u>RT</u>	•	72	2.6E- 14	2.5E0	2.6E-13	2.01
	UP_KEYWORDS	<u>Lipoprotein</u>	<u>RT</u>	=	151		1.2E0	3.1E-2	2.4
nnot	ation Cluster 24	Enrichment Score: 10.49	G		Count	P_Value	Fold	Baniamin	2 i FDF
)	INTERPRO			-	24	3.5E-	Change 5.0E0	2.0E-11	1.9
_	UP_SEQ_FEATURE	<u>Protein kinase, C-terminal</u>	<u>RT</u>	•		13 1.6E-			11 1.18
J		domain:AGC-kinase C-terminal	<u>RT</u>	•	32	12	3.9E0	1.1E-10	10
	INTERPRO	AGC-kinase, C-terminal	<u>RT</u>	•	32	2.0E- 11	3.5E0	8.8E-10	8.18 10
	SMART	S TK X	<u>RT</u>	•	31	9.4E-8	2.5E0	2.2E-6	1.9I 6
nnota	ation Cluster 25	Enrichment Score: 9.8	G	in the second se	Count	P_Value	Fold Change	Benjamin	i FDF
	GOTERM_BP_DIRECT	negative regulation of protein kinase activity	<u>RT</u>	8	53	4.8E- 16	3.2E0	9.4E-14	8.9E
	GOTERM_MF_DIRECT	<u>protein kinase inhibitor activity</u>	<u>RT</u>	•	32	3.8E- 12	3.7E0	1.4E-10	1.3E
	GOTERM_BP_DIRECT	negative regulation of JAK-STAT cascade	RT		25	9.8E-	3.7E0	9.5E-8	9.08
- ገ	GOTERM_BP_DIRECT	cytokine-mediated signaling pathway	RT	_	39	10 3.6E-4	1.8E0	9.7E-3	8 9.2E
	ofice Chartes 20			-			Fold		3
nnota	ation Cluster 26  GOTERM_CC_DIRECT	Enrichment Score: 9.57	G	-	Count	P_Value	Change		5.7E
J		SCF ubiquitin ligase complex	<u>RT</u>	•	31	12	3.9E0	6.5E-11	11
	UP_SEQ_FEATURE	domain:F-box	<u>RT</u>	•	37	2.6E- 12	3.5E0	1.8E-10	1.8E 10
	INTERPRO	F-box domain, cyclin-like	<u>RT</u>	i .	38	1.4E- 11	3.2E0	6.4E-10	5.8E 10
	GOTERM_BP_DIRECT	SCF-dependent proteasomal ubiquitin- dependent protein catabolic process	<u>RT</u>	i .	18	7.2E-9	4.4E0	6.0E-7	5.7E 7
	SMART	<u>FBOX</u>	<u>RT</u>	1	24	4.5E-6	2.5E0	7.0E-5	6.3E
nnota	ation Cluster 27	Enrichment Score: 8.89	G	<b>17</b>	Count	P_Value	Fold Change	Benjamin	
	UP_SEQ_FEATURE	domain:EF-hand 3	RT		58	5.3E-	4.1E0	5.5E-22	5.3
7	UP_SEQ_FEATURE	domain:EF-hand 4	RT	-	36	24 2.6E-	4.0E0	2.0E-12	22 1.9E
7	UP_SEQ_FEATURE					14 7.7E-			12 5.5
J	UP_SEQ_FEATURE	domain:EF-hand 2	<u>RT</u>	•	69	14 9.4E-		5.7E-12	12 6.3
	SCEQ_I EATONE	domain:EF-hand 1	<u>RT</u>	•	65	12	2.4E0	6.5E-10	10
J	LID CEO FEATURE	calcium-binding region:3	<u>RT</u>	1	25	2.4E- 11	4.4E0	1.6E-9	1.6E 9
)	UP_SEQ_FEATURE					1.5E-	2.6E0	9.9E-9	9.6l 9
	UP_SEQ_FEATURE  UP_SEQ_FEATURE	calcium-binding region:1	<u>RT</u>	<b>=</b>	49	10			
			RT RT	- -	49 45	10 1.1E-9		6.4E-8	6.2l
	UP_SEQ_FEATURE	calcium-binding region:1				10	2.6E0	6.4E-8 3.6E-7	8 3.3I
	UP_SEQ_FEATURE UP_SEQ_FEATURE	calcium-binding region:1  calcium-binding region:2 <u>EF-hand domain</u>	RT RT	= =	45 72	10 1.1E-9 1.1E-8	2.6E0 2.0E0	3.6E-7	8 3.3l 7 4.4l
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO	calcium-binding region:1  calcium-binding region:2  EF-hand domain  EF-Hand 1, calcium-binding site	RT RT RT	- -	45 72 60	1.1E-9 1.1E-8 1.5E-8	2.6E0 2.0E0 2.1E0	3.6E-7 4.8E-7	3.3I 7 4.4I 7
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO	calcium-binding region:1  calcium-binding region:2  EF-hand domain  EF-Hand 1, calcium-binding site  EF-hand-like domain	RT RT RT RT	: : :	45 72 60 82	1.1E-9 1.1E-8 1.5E-8 3.6E-8	2.6E0 2.0E0 2.1E0 1.8E0	3.6E-7 4.8E-7 1.0E-6	8 3.31 7 4.41 7 9.51 7
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO	calcium-binding region:1  calcium-binding region:2  EF-hand domain  EF-Hand 1, calcium-binding site	RT RT RT	- -	45 72 60	1.1E-9 1.1E-8 1.5E-8	2.6E0 2.0E0 2.1E0 1.8E0	3.6E-7 4.8E-7	8 3.31 7 4.41 7 9.51

Annot	tation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_MF_DIRECT	<u>calcium ion binding</u>	<u>RT</u>	=	101	9.8E-1	8.4E-1	1.0E0	9.8E 1
	UP_KEYWORDS	<u>Calcium</u>	<u>RT</u>	=	95	1.0E0	7.4E-1	:	1.0E
Annot	tation Cluster 28	Enrichment Score: 8.81	G	-	Count	P_Value	Fold Change	Benjamini	
	UP_KEYWORDS	<u>Viral nucleoprotein</u>	<u>RT</u>	•	21	1.7E- 11	5.1E0	1.5E-10	1.2E 10
	GOTERM_CC_DIRECT	<u>viral nucleocapsid</u>	<u>RT</u>	•	21	6.9E- 11	4.8E0	2.9E-9	2.6E 9
	UP_KEYWORDS	<u>Virion</u>	<u>RT</u>	1	21	3.2E-6	3.1E0	2.0E-5	1.6E 5
Annot	tation Cluster 29	Enrichment Score: 8.51	G	170	Count	P_Value	Fold Change	Benjamini	FDR
	UP_KEYWORDS	<u>Myosin</u>	<u>RT</u>		44	1.5E- 28	5.9E0	2.3E-27	1.8E 27
	INTERPRO	Myosin head, motor domain	<u>RT</u>	•	34	3.4E- 20	5.3E0	3.3E-18	3.0E 18
	GOTERM_CC_DIRECT	<u>myosin complex</u>	<u>RT</u>		38	6.1E- 20	4.8E0	4.9E-18	4.3E 18
	UP_SEQ_FEATURE	domain:Myosin head-like	<u>RT</u>		31	3.0E-	5.7E0	2.7E-17	2.6E
_ 	UP_KEYWORDS	Motor protein	RT		63	19 1.8E-	3.2E0	2.1E-17	17 1.6E
	SMART			-		18 1.7E-			17 5.9E
	GOTERM_MF_DIRECT	MYSc	<u>RT</u>		34	14 2.8E-	3.5E0	6.5E-13	13 9.6E
	UP_KEYWORDS	motor activity	<u>RT</u>	•	37	12	3.3E0	1.1E-10	11
		Muscle protein	<u>RT</u>	•	33	7.2E- 12	3.7E0	6.8E-11	5.3E 11
	INTERPRO	IQ motif, EF-hand binding site	<u>RT</u>	=	42	1.2E- 11	3.0E0	6.0E-10	5.5E 10
	GOTERM_MF_DIRECT	microfilament motor activity	<u>RT</u>	•	18	4.2E- 11	5.4E0	1.5E-9	1.3E 9
	UP_SEQ_FEATURE	region of interest:Actin-binding	<u>RT</u>	•	21	5.3E- 11	4.9E0	3.6E-9	3.4E 9
	INTERPRO	Myosin, N-terminal, SH3-like	<u>RT</u>	i	15	1.0E- 10	6.2E0	4.1E-9	3.8E 9
	INTERPRO	Myosin-like IQ motif-containing domain	<u>RT</u>	•	17	1.2E- 10	5.5E0	4.8E-9	4.4E 9
	GOTERM_CC_DIRECT	muscle myosin complex	<u>RT</u>	•	15	4.8E- 10	6.0E0	1.7E-8	1.5E
	UP_SEQ_FEATURE	domain:IQ	<u>RT</u>		28	2.7E-8	3.1E0	1.5E-6	1.4E
_ 	INTERPRO	Myosin tail	RT		15	4.1E-8		1.1E-6	6 1.0E
_ _	UP_KEYWORDS								6 4.5E
	GOTERM_CC_DIRECT	<u>Calmodulin-binding</u>	<u>RT</u>		49	7.4E-8		5.8E-7	7 5.6E
	SMART	<u>myosin filament</u>	<u>RT</u>	•	12	2.9E-6		6.4E-5	5 2.3E
		<u>IQ</u>	<u>RT</u>	•	28	1.8E-5	2.2E0	2.5E-4	4
	UP_SEQ_FEATURE	domain:IQ 1	<u>RT</u>	i	16	2.3E-5	3.3E0	8.4E-4	8.1E 4
	UP_SEQ_FEATURE	domain:IQ 2	<u>RT</u>	•	16	2.3E-5	3.3E0	8.4E-4	8.1E 4
	UP_KEYWORDS	Thick filament	<u>RT</u>	i	11	3.1E-5	4.4E0	1.8E-4	1.4E 4
	GOTERM_MF_DIRECT	<u>calmodulin binding</u>	<u>RT</u>	=	54	6.6E-5	1.7E0	9.9E-4	8.8E 4
	UP_SEQ_FEATURE	domain:IQ 3	<u>RT</u>	i	12	9.8E-5	3.7E0	3.2E-3	3.1E 3
	GOTERM_BP_DIRECT	actin filament-based movement	<u>RT</u>	4	11	1.1E-4	3.8E0	3.5E-3	3.3E
	UP_SEQ_FEATURE	domain:IQ 4	<u>RT</u>	•	9	5.2E-4	4.1E0	1.5E-2	1.5E
	UP_KEYWORDS	Actin-binding	<u>RT</u>		60	1.1E-3	1.5E0	5.5E-3	4.3E
	KEGG_PATHWAY	<u>Tight junction</u>	<u>RT</u>		28	5.0E-3	1.7E0	1.0E-2	5.0E
	UP_SEQ_FEATURE	domain:IQ 5	RT		6	1.4E-2		2.9E-1	3 2.8E
	GOTERM_BP_DIRECT						1.6E0		1 2.2E
	GOTERM_MF_DIRECT	muscle contraction	<u>RT</u>	_	28				1 2.2E
	UP_SEQ_FEATURE	actin binding	<u>RT</u>		59	4.1E-2		2.5E-1	1 9.7E
	0014_1 EATONE	domain:IQ 6	<u>RT</u>	i	3	3.3E-1	Fold	1.0E0	1
Annot	tation Cluster 30	Enrichment Score: 8.4	G	-	Count	P_Value	Change		
	UP_SEQ_FEATURE	short sequence motif:DEAH box	<u>RT</u>	•	32	3.0E- 17	5.1E0	2.5E-15	2.4E 15
	INTERPRO	Domain of unknown function DUF1605	<u>RT</u>	i	15	3.3E-9	5.5E0	1.1E-7	1.0E 7
	INTERPRO	Helicase-associated domain	<u>RT</u>	•	15	1.3E-8	5.2E0	4.0E-7	3.7E 7
	INTERPRO	<u>DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site</u>	<u>RT</u>	i	16	6.9E-8	4.5E0	1.8E-6	1.7E
	SMART	SM00847	<u>RT</u>	•	15	3.0E-6	3.4E0	4.9E-5	4.4E 5
	GOTERM_MF_DIRECT	ATP-dependent helicase activity	<u>RT</u>		16	1.6E-5	3.3E0	2.9E-4	2.6E
						P_Value			4 FDR

An	nnotation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	repeat:ANK 6	<u>RT</u>	=	85	7.5E- 55		1.2E-52	1.1E- 52
	UP_SEQ_FEATURE	repeat:ANK 7	<u>RT</u>	•	56	1.0E- 37	6.1E0	1.3E-35	1.3E- 35
	UP_SEQ_FEATURE	repeat:ANK 8	<u>RT</u>		41	1.3E- 27	6.1E0	1.4E-25	1.4E- 25
	UP_SEQ_FEATURE	repeat:ANK 9	<u>RT</u>	i e	36	9.9E- 24	6.0E0	1.0E-21	9.7E- 22
	UP_SEQ_FEATURE	repeat:ANK 10	<u>RT</u>	i e	26	1.7E- 17	6.1E0	1.4E-15	1.4E- 15
	UP_SEQ_FEATURE	repeat:ANK 11	<u>RT</u>		23	6.2E- 16	6.3E0	4.9E-14	4.7E-
	UP_SEQ_FEATURE	repeat:ANK 12	<u>RT</u>	i de la companya de	16	1.6E- 10	6.1E0	1.0E-8	9.9E- 9
	UP_SEQ_FEATURE	repeat:ANK 13	<u>RT</u>	1	13		5.9E0	1.5E-6	1.5E-
	UP_SEQ_FEATURE	repeat:ANK 14	<u>RT</u>	1	13	2.9E-8		1.5E-6	6 1.5E-
	UP_SEQ_FEATURE	repeat:ANK 15	RT		13	2.9E-8		1.5E-6	6 1.5E-
	UP_SEQ_FEATURE	repeat:ANK 16	RT		11	8.5E-7		4.1E-5	6 3.9E-
	UP_SEQ_FEATURE	repeat: ANK 17	RT		10	4.5E-6		1.9E-4	5 1.9E-
	UP_SEQ_FEATURE	repeat:ANK 18	RT		10	4.5E-6		1.9E-4	4 1.9E-
	UP_SEQ_FEATURE	repeat:ANK 19	RT		10	4.5E-6		1.9E-4	4 1.9E-
	UP_SEQ_FEATURE								4 8.2E-
	UP_SEQ_FEATURE	repeat:ANK 20	RT	•	9	2.3E-5		8.4E-4	4 8.2E-
	UP_SEQ_FEATURE	repeat:ANK 21	<u>RT</u>	•	9	2.3E-5		8.4E-4	4 3.6E-
	UP_SEQ_FEATURE	repeat:ANK 22	<u>RT</u>	•	8	1.2E-4		3.7E-3	3 3.6E-
	UP_SEQ_FEATURE	repeat:ANK 23	<u>RT</u>		8	1.2E-4		3.7E-3	3 6.4E-
	INTERPRO	repeat:ANK 24	<u>RT</u>		6	2.6E-3		6.6E-2	6.2E-
	UP_SEQ_FEATURE	Death domain	<u>RT</u>	i	13	6.6E-3	2.3E0	6.8E-2	2
		domain:Death	<u>RT</u>	i	12	9.3E-3	2.3E0	2.2E-1	2.1E- 1
	UP_SEQ_FEATURE	repeat:ANK 25	<u>RT</u>	i	5	1.1E-2	4.9E0	2.3E-1	2.2E- 1
	UP_SEQ_FEATURE	repeat:ANK 26	<u>RT</u>	i	3	5.8E-2	6.8E0	9.1E-1	8.8E- 1
	UP_SEQ_FEATURE	repeat:ANK 27	<u>RT</u>	i	3	5.8E-2	6.8E0	9.1E-1	8.8E- 1
	INTERPRO	Death-like domain	<u>RT</u>	i	21	1.1E-1	1.4E0	6.0E-1	5.4E- 1
	GOTERM_BP_DIRECT	protein targeting to plasma membrane	<u>RT</u>	i	8	1.3E-1	1.8E0	8.1E-1	7.7E- 1
	GOTERM_MF_DIRECT	spectrin binding	<u>RT</u>	i	7	2.6E-1	1.6E0	9.5E-1	8.4E- 1
	INTERPRO	<u>ZU5</u>	<u>RT</u>	1	4	3.0E-1	2.1E0	9.8E-1	8.9E- 1
	UP_SEQ_FEATURE	domain:ZU5	<u>RT</u>	i .	3	3.9E-1	2.3E0	1.0E0	9.7E- 1
	SMART	<u>DEATH</u>	<u>RT</u>	i	8	5.1E-1	1.2E0	1.0E0	9.0E- 1
	SMART	<u>ZU5</u>	<u>RT</u>	i	3	6.9E-1	1.4E0	1.0E0	9.0E- 1
	GOTERM_MF_DIRECT	cytoskeletal adaptor activity	<u>RT</u>	i	3	7.8E-1	1.1E0	1.0E0	8.9E- 1
An	nnotation Cluster 32	Enrichment Score: 7.81	G	To the second se	Count	P_Value	Fold Change	Benjamini	FDR
	KEGG_PATHWAY	Chronic myeloid leukemia	<u>RT</u>	¥	44	2.4E- 14	3.2E0	2.7E-13	1.2E- 13
	BIOCARTA	<u>Influence of Ras and Rho proteins on G1 to S</u> <u>Transition</u>	<u>RT</u>	i	21	9.1E-6	2.4E0	2.9E-4	2.0E- 4
	KEGG_PATHWAY	Small cell lung cancer	<u>RT</u>	i .	34	1.7E-5	2.1E0	4.8E-5	2.2E- 5
An	nnotation Cluster 33	Enrichment Score: 7.68	G	To the second se	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:SET	<u>RT</u>	•	35	5.8E- 18	4.9E0	5.1E-16	4.9E- 16
	INTERPRO	SET domain	<u>RT</u>	i .	36	6.9E- 17	4.4E0	5.0E-15	4.6E- 15
	GOTERM_MF_DIRECT	histone-lysine N-methyltransferase activity	<u>RT</u>	i e	27	5.2E- 12	4.1E0	1.9E-10	1.7E- 10
	UP_SEQ_FEATURE	domain:Post-SET	<u>RT</u>	i .	15	1.9E- 10	6.4E0	1.2E-8	1.1E- 8
	SMART	<u>SET</u>	<u>RT</u>	£	29	2.3E- 10	3.1E0	7.1E-9	6.4E- 9
	INTERPRO	Post-SET domain	<u>RT</u>	1	14	1.7E-8	5.4E0	5.0E-7	4.6E- 7
	UP_KEYWORDS	S-adenosyl-L-methionine	<u>RT</u>	•	49	5.8E-6	1.9E0	3.6E-5	2.8E- 5
	UP_KEYWORDS	<u>Methyltransferase</u>	<u>RT</u>	•	50	5.1E-5	1.8E0	2.9E-4	2.3E- 4
	SMART	<u>PostSET</u>	<u>RT</u>	i	11	1.0E-4	3.5E0	1.3E-3	1.1E- 3
									3

Annota	ation Cluster 1	Enrichment Score: ?	G	<b></b>	Count	P_Value	Fold	Benjamin	i FDR
	KEGG_PATHWAY	Lysine degradation	RT	i	21		Change	1.9E-3	8.8E
	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K4	RT		10		3.3E0	1.2E-2	4 1.1E
	GOTERM_MF_DIRECT	specific) methyltransferase activity	RT		21		1.3E0	6.3E-1	2 5.6E
Annot	ation Cluster 34	Enrichment Score: 7.44	G		1	P_Value	Fold	Baniamin	1 i EDR
Allilota	INTERPRO	Bromodomain, conserved site		i	21	1.1E-	Change 5.0E0	5.6E-10	5.1E
	UP_KEYWORDS		<u>RT</u>			11 2.0E-			10 1.4E
	INTERPRO	<u>Bromodomain</u>	<u>RT</u>	•	25	11		1.9E-10	10 9.5E
	UP_SEQ_FEATURE	<u>Bromodomain</u>	<u>RT</u>	•	25	3.0E-9	3.6E0	1.0E-7	8
		domain:Bromo	<u>RT</u>	i	17	4.5E-7	4.0E0	2.2E-5	2.1E 5
	SMART	<u>BROMO</u>	<u>RT</u>	•	25	6.1E-6	2.4E0	9.1E-5	8.1E 5
	GOTERM_MF_DIRECT	lysine-acetylated histone binding	<u>RT</u>	i	10	1.2E-3	3.3E0	1.2E-2	1.1E 2
Annota	ation Cluster 35	Enrichment Score: 7.23	G	N .	Count	P_Value	Fold Change	Benjamin	
	GOTERM_BP_DIRECT	termination of RNA polymerase II transcription	<u>RT</u>	•	40	2.7E- 15	3.7E0	4.8E-13	4.6E 13
	GOTERM_BP_DIRECT	mRNA 3'-end processing	<u>RT</u>	i e	32	1.0E- 12	3.8E0	1.3E-10	1.3E 10
	GOTERM_BP_DIRECT	RNA export from nucleus	<u>RT</u>	1	26	7.0E-7	2.8E0	4.4E-5	4.2E 5
	GOTERM_BP_DIRECT	mRNA export from nucleus	<u>RT</u>	i	35	2.3E-5	2.1E0	8.7E-4	8.2E 4
	KEGG_PATHWAY	mRNA surveillance pathway	<u>RT</u>	1	35	3.3E-5	2.0E0	8.9E-5	4.1E 5
	UP_KEYWORDS	mRNA transport	<u>RT</u>	1	24	3.0E-2	1.6E0	1.2E-1	9.0E 2
Annota	ation Cluster 36	Enrichment Score: 7.04	G	To the second se	Count	P_Value	Fold Change	Benjamin	
	UP_SEQ_FEATURE	domain:SOCS box	<u>RT</u>	i	25	1.1E- 11		7.4E-10	7.2E 10
	INTERPRO	SOCS protein, C-terminal	<u>RT</u>		25	1.8E- 10	4.0E0	7.3E-9	6.6E
	SMART	SM00969	<u>RT</u>		25	9.5E-7	2.6E0	1.7E-5	1.5E
	SMART	<u>SOCS</u>	RT	1	10		2.0E0	2.4E-1	5 2.1E
Annota	ation Cluster 37	Enrichment Score: 7.01	G	-	Count	P_Value	Fold	Ponjamin	1 i FDR
	INTERPRO	Tubulin/FtsZ, C-terminal	RT		20	3.8E-	Change 5.4E0	2.0E-10	1.8E
	INTERPRO	Tubulin, C-terminal	RT		20	12 3.8E-	5.4E0	2.0E-10	10 1.8E
	INTERPRO	Tubulin, conserved site	RT		20	12 3.8E-	5.4E0	2.0E-10	10 1.8E
	INTERPRO			1	20	12 1.6E-	5.2E0	7.2E-10	10 6.6E
	INTERPRO	Tubulin	<u>RT</u>			11 2.0E-			10 8.1E
	INTERPRO	Tubulin/FtsZ, 2-layer sandwich domain	<u>RT</u>	•	19	11 5.5E-	5.4E0	8.8E-10	10 2.1E
	SMART	Tubulin/FtsZ, GTPase domain	<u>RT</u>	•	20	11	5.0E0	2.3E-9	9 5.7E
		<u>SM00865</u>	<u>RT</u>	i	19	2.5E-8	3.5E0	6.4E-7	7
	SMART	<u>SM00864</u>	<u>RT</u>	i	20	2.7E-8	3.4E0	6.5E-7	5.9E 7
	KEGG_PATHWAY	Pathogenic Escherichia coli infection	<u>RT</u>	1	26	1.3E-6	2.7E0	4.1E-6	1.9E 6
	INTERPRO	Beta tubulin	<u>RT</u>	i e	9	3.5E-6	6.2E0	7.6E-5	7.0E 5
	INTERPRO	Beta tubulin, autoregulation binding site	<u>RT</u>	1	9	3.5E-6	6.2E0	7.6E-5	7.0E 5
	GOTERM_BP_DIRECT	microtubule-based process	<u>RT</u>	i .	19	4.7E-6	3.1E0	2.3E-4	2.2E 4
	GOTERM_MF_DIRECT	structural constituent of cytoskeleton	<u>RT</u>	i contraction	37	3.0E-5	2.0E0	4.9E-4	4.4E 4
	INTERPRO	Alpha tubulin	<u>RT</u>	1	7	3.9E-3	3.9E0	4.1E-2	3.8E
	UP_KEYWORDS	<u>Microtubule</u>	<u>RT</u>	•	55	1.8E-2	1.3E0	7.3E-2	5.7E 2
	KEGG_PATHWAY	<u>Phagosome</u>	<u>RT</u>		27	7.4E-1	9.4E-1	1.0E0	7.4E
Annota	ation Cluster 38	Enrichment Score: 6.93	G	-	1	P_Value	Fold	Baniamin	1 ni FDR
	GOTERM_MF_DIRECT		RT	i	36	9.2E-	Change 3.7E0	3.9E-12	3.5E
	INTERPRO	Protein phosphatase 2C (PP2C)-like	RT	1	17	14 5.1E-	5.3E0	2.0E-8	12 1.8E
	UP_SEQ_FEATURE	metal ion-binding site: Manganese 1; via	RT	_	13	10 1 1F-0	6.8E0		8 6.2E
	INTERPRO	carbonyl oxygen						6.4E-8	8 1.5E
		Protein phosphatase 2C  Protein phosphatase 2C,	<u>RT</u>		14		5.1E0	1.6E-6	6 2.6E
	INTERPRO	and the state of t	-		4 4	1 1 5 7	6.2E0	2.8E-6	
	INTERPRO  GOTERM_BP_DIRECT	manganese/magnesium aspartate binding site  peptidyl-threonine dephosphorylation	RT RT	:	11			1.2E-5	6 1.1E

Annot	ation Cluster 1	Enrichment Score: ?	G	·	Count	P_Value	Fold	Benjamini	i FDR
	SMART	PP2Cc	RT	i	17	2.8E-7	Change	5.4E-6	4.9E-
	UP_SEQ_FEATURE	metal ion-binding site:Manganese 1	RT	•	15	6.3E-6	3.8E0	2.7E-4	6 2.6E-
	UP_SEQ_FEATURE	metal ion-binding site:Manganese 2	RT		15	6.3E-6		2.7E-4	4 2.6E-
	UP_SEQ_FEATURE	domain:PP2C-like	RT		10	1.3E-5		4.8E-4	4 4.7E-
	GOTERM_MF_DIRECT	cation binding	RT		7	8.1E-3		6.8E-2	4 6.0E-
Annot	ation Cluster 39	Enrichment Score: 6.83	G	•	Count	P_Value	Fold	Benjamini	2 EDP
Annot	UP_KEYWORDS	Protein phosphatase	RT		67	7.7E-	Change 3.5E0	9.8E-21	7.6E-
	INTERPRO	<u>Dual specificity phosphatase, catalytic domain</u>			31	22 6.1E-	4.5E0	4.1E-13	21 3.7E-
	INTERPRO	Dual specificity phosphatase, subgroup,				15 7.6E-			13 4.5E-
	INTERPRO	catalytic domain	<u>RT</u>	•	28	15 1.2E-	4.8E0	4.9E-13	13 5.9E-
	GOTERM_MF_DIRECT	<u>Dual specificity phosphatase</u> <u>protein tyrosine/serine/threonine</u>	<u>RT</u>	•	24	12 8.3E-	4.8E0	6.5E-11	11 2.4E-
	UP_SEQ_FEATURE	phosphatase activity	<u>RT</u>	•	25	11 9.1E-	4.0E0	2.7E-9	9
		domain:Tyrosine-protein phosphatase	<u>RT</u>	•	32	11	3.5E0	6.1E-9	5.9E- 9
	SMART	<u>DSPc</u>	<u>RT</u>	•	28	2.5E- 10	3.2E0	7.1E-9	6.4E- 9
	INTERPRO	Protein-tyrosine/Dual specificity phosphatase	<u>RT</u>	•	35	4.0E-8	2.6E0	1.1E-6	1.0E- 6
	UP_SEQ_FEATURE	domain:Rhodanese	<u>RT</u>	i	15	8.7E-8	4.9E0	4.5E-6	4.4E- 6
	UP_SEQ_FEATURE	active site:Phosphocysteine intermediate	<u>RT</u>	i .	33	2.1E-7	2.6E0	1.0E-5	1.0E- 5
	GOTERM_MF_DIRECT	protein tyrosine phosphatase activity	<u>RT</u>	¥	39	2.9E-7	2.3E0	6.8E-6	6.1E- 6
	INTERPRO	<u>Mitogen-activated protein (MAP) kinase</u> <u>phosphatase</u>	<u>RT</u>	i	10	6.2E-7	6.2E0	1.5E-5	1.4E- 5
	GOTERM_BP_DIRECT	peptidyl-tyrosine dephosphorylation	<u>RT</u>	i e	38	7.7E-7	2.3E0	4.8E-5	4.6E- 5
	GOTERM_MF_DIRECT	MAP kinase tyrosine/serine/threonine phosphatase activity	<u>RT</u>	1	11	3.0E-6	5.0E0	6.2E-5	5.5E- 5
	INTERPRO	Rhodanese-like domain	<u>RT</u>	i	15	3.1E-6	3.9E0	6.8E-5	6.2E-
	INTERPRO	Protein-tyrosine phosphatase, active site	<u>RT</u>	i de la companya de	29	9.6E-6	2.4E0	1.8E-4	1.7E-
	GOTERM_BP_DIRECT	inactivation of MAPK activity	<u>RT</u>	1	15	1.0E-5	3.6E0	4.0E-4	3.8E-
	SMART	RHOD	<u>RT</u>	•	15	5.2E-5	2.9E0	6.9E-4	4 6.2E-
	PIR_SUPERFAMILY	dual specificity protein phosphatase (MAP	RT		7	2.4E-4	5.3E0	1.5E-2	4 1.5E-
	BIOCARTA	<u>kinase phosphatase)</u> <u>Regulation of MAP Kinase Pathways Through</u>	RT		9	7.5E-4		6.2E-3	2 4.2E-
	GOTERM_MF_DIRECT	<u>Dual Specificity Phosphatases</u> <u>phosphatase activity</u>	RT	_	16	1.3E-3		1.4E-2	3 1.2E-
	INTERPRO			:					2 7.9E-
	GOTERM_MF_DIRECT	Protein-tyrosine phosphatase, catalytic  protein tyrosine/threonine phosphatase	<u>RT</u>		19	9.0E-3		8.7E-2	2 3.4E-
	GOTERM_BP_DIRECT	activity	<u>RT</u>		3	7.5E-2		3.9E-1	1 7.7E-
	SMART	endoderm formation	<u>RT</u>	•	5	1.3E-1		8.1E-1	1 8.7E-
		PTPc motif	<u>RT</u>	i	19	2.7E-1	Fold	9.7E-1	1
Annot	ation Cluster 40  GOTERM_MF_DIRECT	Enrichment Score: 6.19	G	_	Count	P_Value	Change	Benjamin	6.5E-
	UP_KEYWORDS	<u>ligase activity</u>	<u>RT</u>	•	104	1.4E- 17 5.7E-	2.3E0	7.3E-16	16 4.5E-
	_	<u>Ligase</u>	<u>RT</u>	•	108	5./E- 15	2.1E0	5.8E-14	14
	UP_SEQ_FEATURE	zinc finger region:RING-type	<u>RT</u>	•	59	1.7E-5	1.7E0	6.5E-4	6.3E- 4
	INTERPRO	Zinc finger, RING-type	<u>RT</u>	•	72	2.5E-4	1.5E0	3.5E-3	3.2E- 3
	INTERPRO	Zinc finger, RING/FYVE/PHD-type	<u>RT</u>	•	99	1.1E-3	1.4E0	1.4E-2	1.3E- 2
	INTERPRO	Zinc finger, RING-type, conserved site	<u>RT</u>	i .	34	1.4E-1	1.2E0	6.6E-1	6.0E- 1
	SMART	RING	<u>RT</u>	i .	54	8.6E-1	9.0E-1	1.0E0	9.0E- 1
Annot	ation Cluster 41	Enrichment Score: 6.18	G	<b>™</b>	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_BP_DIRECT	<u>transcription-coupled nucleotide-excision</u> <u>repair</u>	<u>RT</u>	•	41	3.1E- 13	3.3E0	4.4E-11	4.2E- 11
	GOTERM_BP_DIRECT	DNA damage response, detection of DNA damage	<u>RT</u>	i	22	2.2E-8	3.6E0	1.8E-6	1.7E- 6
	GOTERM_BP_DIRECT	nucleotide-excision repair, preincision complex assembly	<u>RT</u>	i .	19	6.0E-8	3.9E0	4.5E-6	4.3E- 6
	GOTERM_BP_DIRECT	telomere maintenance via recombination	<u>RT</u>	1	20	7.1E-8	3.7E0	5.2E-6	5.0E-
	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision, 5'-to lesion	<u>RT</u>	i	21	2.7E-7	3.4E0	1.8E-5	1.8E-
	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision	<u>RT</u>	i	21	4.8E-7	3.3E0	3.2E-5	3.0E- 5
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Annota	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold	Benjamini	i FDR
	GOTERM_BP_DIRECT	translesion synthesis	RT	i	19	4.7E-6	Change	2.3E-4	2.2E-
	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA gap filling	<u>RT</u>	•	15	5.2E-6	3.7E0	2.5E-4	4 2.3E-
	GOTERM_BP_DIRECT	error-free translesion synthesis	RT	•	13	8.0E-6		3.5E-4	4 3.3E-
	GOTERM_BP_DIRECT	error-prone translesion synthesis	RT		13	8.0E-6		3.5E-4	4 3.3E-
	KEGG_PATHWAY	Nucleotide excision repair	RT		23	1.4E-5		4.0E-5	4 1.8E-
	KEGG_PATHWAY			•					5 1.3E-
	KEGG_PATHWAY	DNA replication	RT		18	1.2E-4		2.9E-4	4 4.1E-
		Mismatch repair	<u>RT</u>	i e	13	3.8E-4	:	8.9E-4	4
Annota	ation Cluster 42 INTERPRO	Enrichment Score: 5.63	G	-			Change		4.7E-
	UP_SEQ_FEATURE	WD40 repeat, conserved site	<u>RT</u>	- -	57		2.1E0	5.2E-7	7 1.4E-
	INTERPRO	repeat:WD 7	<u>RT</u>	•	50	2.6E-8		1.5E-6	6 9.7E-
	UP_SEQ_FEATURE	G-protein beta WD-40 repeat	<u>RT</u>	•	38	3.8E-8		1.1E-6	7 2.2E-
	UP_SEQ_FEATURE	repeat:WD 5	<u>RT</u>	•	68	4.4E-8	2.0E0	2.3E-6	6 8.8E-
		repeat:WD 4	<u>RT</u>	•	70	1.8E-7	1.9E0	9.1E-6	6
	UP_SEQ_FEATURE	repeat:WD 6	<u>RT</u>	•	57	3.7E-7	2.0E0	1.8E-5	1.8E- 5
	UP_KEYWORDS	WD repeat	<u>RT</u>	=	73	7.1E-7	1.8E0	5.0E-6	3.9E- 6
	UP_SEQ_FEATURE	repeat:WD 3	<u>RT</u>	=	71	7.2E-7	1.8E0	3.5E-5	3.4E- 5
	UP_SEQ_FEATURE	repeat:WD 1	<u>RT</u>	Ē.	71	2.6E-6	1.7E0	1.2E-4	1.2E- 4
	UP_SEQ_FEATURE	repeat:WD 2	<u>RT</u>	Ē	71	2.6E-6	1.7E0	1.2E-4	1.2E- 4
	INTERPRO	WD40-repeat-containing domain	<u>RT</u>	■	78	2.9E-5	1.6E0	5.0E-4	4.6E- 4
	INTERPRO	WD40 repeat	<u>RT</u>	Ē	69	6.3E-5	1.6E0	1.1E-3	9.6E- 4
	INTERPRO	WD40/YVTN repeat-like-containing domain	<u>RT</u>	<b>■</b>	76	1.1E-3	1.4E0	1.3E-2	1.2E- 2
	SMART	<u>WD40</u>	<u>RT</u>	=	69	3.8E-1	1.1E0	1.0E0	9.0E- 1
Annota	ation Cluster 43	Enrichment Score: 5.46	G	To the second se	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_BP_DIRECT	positive regulation of telomere maintenance via telomerase	<u>RT</u>	i .	22	1.0E-9	4.1E0	9.9E-8	9.4E- 8
	GOTERM_BP_DIRECT	positive regulation of telomerase activity	<u>RT</u>	i .	16	1.8E-5	3.3E0	6.8E-4	6.5E- 4
	GOTERM_BP_DIRECT	positive regulation of telomere capping	<u>RT</u>	i .	9	2.3E-3	3.3E0	4.6E-2	4.4E- 2
Annota	ation Cluster 44	Enrichment Score: 5.36	G	To the second se	Count	P_Value	Fold Change	Benjamin	
	GOTERM_BP_DIRECT	gene expression	<u>RT</u>	i .	33	2.1E- 14	4.1E0	3.4E-12	3.3E- 12
	GOTERM_CC_DIRECT	DNA-directed RNA polymerase II, core complex	<u>RT</u>	i	14	1.4E-7	4.9E0	3.8E-6	3.3E- 6
	GOTERM_BP_DIRECT	7-methylguanosine mRNA capping	<u>RT</u>	•	20	1.4E-7	3.6E0	9.9E-6	9.4E- 6
	UP_KEYWORDS	DNA-directed RNA polymerase	<u>RT</u>		20	4.3E-7	3.5E0	3.2E-6	2.5E-
	GOTERM_BP_DIRECT	positive regulation of viral transcription	RT		18	4.6E-7	3.7E0	3.0E-5	6 2.9E-
	KEGG_PATHWAY	RNA polymerase	RT		20	5.3E-7		1.8E-6	5 8.3E-
								1.8E-5	7 1.6E-
	GOTERM_MF_DIRECT	RNA polymerase I activity	RT		11	8.2E-7	J.JEU		5
	GOTERM_MF_DIRECT  GOTERM_BP_DIRECT	transcription elongation from RNA polymerase	<u>RT</u> RT	•				5.1F-5	4.9E-
		transcription elongation from RNA polymerase I promoter transcription initiation from RNA polymerase I	<u>RT</u>		18	8.9E-7	3.6E0	5.1E-5 5.1E-5	4.9E- 5 4.9E-
	GOTERM_BP_DIRECT	transcription elongation from RNA polymerase I promoter transcription initiation from RNA polymerase I promoter	RT RT	i i	18 19	8.9E-7 9.1E-7	3.6E0 3.4E0	5.1E-5	4.9E- 5
	GOTERM_BP_DIRECT	transcription elongation from RNA polymerase I promoter transcription initiation from RNA polymerase I promoter  Pyrimidine metabolism	RT RT RT		18 19 41	8.9E-7 9.1E-7 1.2E-6	3.6E0 3.4E0 2.1E0	5.1E-5 4.1E-6	4.9E- 5 4.9E- 5
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  KEGG_PATHWAY  GOTERM_CC_DIRECT	transcription elongation from RNA polymerase I promoter transcription initiation from RNA polymerase I promoter  Pyrimidine metabolism  DNA-directed RNA polymerase I complex	RT RT RT RT		18 19 41 11	8.9E-7 9.1E-7 1.2E-6 1.6E-6	3.6E0 3.4E0 2.1E0 5.4E0	5.1E-5 4.1E-6 3.8E-5	4.9E-5 4.9E-5 1.9E-6 3.4E-5
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  KEGG_PATHWAY  GOTERM_CC_DIRECT  GOTERM_BP_DIRECT	transcription elongation from RNA polymerase I promoter transcription initiation from RNA polymerase I promoter Pyrimidine metabolism  DNA-directed RNA polymerase I complex termination of RNA polymerase I transcription	RT RT RT RT RT		18 19 41 11 18	8.9E-7 9.1E-7 1.2E-6 1.6E-6 1.7E-6	3.6E0 3.4E0 2.1E0 5.4E0 3.4E0	5.1E-5 4.1E-6 3.8E-5 9.0E-5	4.9E-5 4.9E-5 1.9E-6 3.4E-5 8.6E-5
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  KEGG_PATHWAY  GOTERM_CC_DIRECT  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT	transcription elongation from RNA polymerase I promoter transcription initiation from RNA polymerase I promoter  Pyrimidine metabolism  DNA-directed RNA polymerase I complex termination of RNA polymerase I transcription  DNA-directed RNA polymerase activity	RT RT RT RT RT RT		18 19 41 11 18 20	8.9E-7 9.1E-7 1.2E-6 1.6E-6 1.7E-6 2.4E-6	3.6E0 3.4E0 2.1E0 5.4E0 3.4E0 3.1E0	5.1E-5 4.1E-6 3.8E-5 9.0E-5 5.0E-5	4.9E-5 4.9E-5 1.9E-6 3.4E-5 8.6E-5 4.5E-5
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  KEGG_PATHWAY  GOTERM_CC_DIRECT  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT  GOTERM_BP_DIRECT	transcription elongation from RNA polymerase I promoter transcription initiation from RNA polymerase I promoter  Pyrimidine metabolism  DNA-directed RNA polymerase I complex termination of RNA polymerase I transcription  DNA-directed RNA polymerase activity transcription elongation from RNA polymerase II promoter	RT RT RT RT RT RT RT		18 19 41 11 18 20 32	8.9E-7 9.1E-7 1.2E-6 1.6E-6 1.7E-6 2.4E-6 1.4E-5	3.6E0 3.4E0 2.1E0 5.4E0 3.4E0 3.1E0 2.2E0	5.1E-5 4.1E-6 3.8E-5 9.0E-5 5.0E-5 5.5E-4	4.9E-5 5 4.9E-5 1.9E-6 3.4E-5 8.6E-5 4.5E-5 5.3E-4
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  KEGG_PATHWAY  GOTERM_CC_DIRECT  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT	transcription elongation from RNA polymerase I promoter transcription initiation from RNA polymerase I promoter  Pyrimidine metabolism  DNA-directed RNA polymerase I complex termination of RNA polymerase I transcription  DNA-directed RNA polymerase activity transcription elongation from RNA polymerase II promoter  RNA polymerase II activity	RT RT RT RT RT RT		18 19 41 11 18 20	8.9E-7 9.1E-7 1.2E-6 1.6E-6 1.7E-6 2.4E-6	3.6E0 3.4E0 2.1E0 5.4E0 3.4E0 3.1E0 2.2E0	5.1E-5 4.1E-6 3.8E-5 9.0E-5 5.0E-5	4.9E-5 4.9E-5 1.9E-6 3.4E-5 8.6E-5 4.5E-5 5.3E-4
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  KEGG_PATHWAY  GOTERM_CC_DIRECT  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT	transcription elongation from RNA polymerase I promoter transcription initiation from RNA polymerase I promoter  Pyrimidine metabolism  DNA-directed RNA polymerase I complex termination of RNA polymerase I transcription  DNA-directed RNA polymerase activity transcription elongation from RNA polymerase II promoter  RNA polymerase II activity positive regulation of gene expression, epigenetic	RT RT RT RT RT RT RT		18 19 41 11 18 20 32	8.9E-7 9.1E-7 1.2E-6 1.6E-6 1.7E-6 2.4E-6 1.4E-5	3.6E0 3.4E0 2.1E0 5.4E0 3.4E0 3.1E0 2.2E0 5.4E0	5.1E-5 4.1E-6 3.8E-5 9.0E-5 5.0E-5 5.5E-4	4.9E-5 4.9E-5 1.9E-6 3.4E-5 8.6E-5 4.5E-5 5.3E-4 1.1E-3
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  KEGG_PATHWAY  GOTERM_CC_DIRECT  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT	transcription elongation from RNA polymerase I promoter transcription initiation from RNA polymerase I promoter  Pyrimidine metabolism  DNA-directed RNA polymerase I complex termination of RNA polymerase I transcription  DNA-directed RNA polymerase activity transcription elongation from RNA polymerase II promoter  RNA polymerase II activity positive regulation of gene expression, epigenetic snRNA transcription from RNA polymerase II promoter	RT		18 19 41 11 18 20 32 9	8.9E-7 9.1E-7 1.2E-6 1.6E-6 1.7E-6 2.4E-6 1.4E-5 2.0E-5	3.6E0 3.4E0 2.1E0 5.4E0 3.4E0 2.2E0 5.4E0 2.4E0	5.1E-5 4.1E-6 3.8E-5 9.0E-5 5.0E-5 5.5E-4 3.4E-4	4.9E-5 4.9E-5 1.9E-6 3.4E-5 8.6E-5 4.5E-5 5.3E-4 3.0E-4 1.1E-3 1.8E-2
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  KEGG_PATHWAY  GOTERM_CC_DIRECT  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT	transcription elongation from RNA polymerase I promoter transcription initiation from RNA polymerase I promoter  Pyrimidine metabolism  DNA-directed RNA polymerase I complex termination of RNA polymerase I transcription  DNA-directed RNA polymerase activity transcription elongation from RNA polymerase II promoter  RNA polymerase II activity positive regulation of gene expression, epigenetic snRNA transcription from RNA polymerase II	RT		18 19 41 11 18 20 32 9 25	8.9E-7 9.1E-7 1.2E-6 1.6E-6 1.7E-6 2.4E-6 1.4E-5 2.0E-5 3.3E-5	3.6E0 3.4E0 2.1E0 5.4E0 3.4E0 2.2E0 5.4E0 2.4E0 2.0E0	5.1E-5 4.1E-6 3.8E-5 9.0E-5 5.0E-5 5.5E-4 3.4E-4 1.2E-3	4.9E-5 4.9E-5 1.9E-6 3.4E-5 8.6E-5 4.5E-5 5.3E-4 1.1E-3 1.8E-

mota	ation Cluster 1	Enrichment Score: ?	G	<b>17</b>	Count	P_Value	Fold Change	Benjamin	ii FDI
	GOTERM_CC_DIRECT	DNA-directed RNA polymerase III complex	<u>RT</u>	i i	8	2.1E-2	2.7E0	1.4E-1	1.2 1
	GOTERM_MF_DIRECT	RNA polymerase III activity	<u>RT</u>	1	8	2.1E-2	2.7E0	1.4E-1	1.3
nota	ation Cluster 45	Enrichment Score: 5.36	G	178	Count	P_Value	Fold Change	Benjamin	
	UP_KEYWORDS	<u>Cyclin</u>	RT		22	2.0E-8	3.8E0	1.6E-7	1.2
	INTERPRO	<u>Cyclin-like</u>	RT		24	3.4E-8	3.4F0	9.8E-7	7 9.0
	SMART								7 4.6
	INTERPRO	CYCLIN	<u>RT</u>	_	23	3.2E-6		5.1E-5	5 8.9
	INTERPRO	<u>Cyclin, N-terminal</u>	<u>RT</u>	•	18	4.7E-6	3.3E0	9.7E-5	5
		Cyclin, C-terminal domain	<u>RT</u>	•	11	1.5E-4	3.8E0	2.1E-3	3
	SMART	SM01332	<u>RT</u>	i	11	4.6E-3		4.3E-2	3.8 2
ota	ation Cluster 46	Enrichment Score: 5.31	G	To the second	Count	P_Value	Fold Change	Benjamin	
	KEGG_PATHWAY	Toll-like receptor signaling pathway	<u>RT</u>	•	46	2.3E-8	2.3E0	9.4E-8	4.3 8
	KEGG_PATHWAY	NOD-like receptor signaling pathway	<u>RT</u>	4	27	2.9E-6	2.5E0	8.8E-6	4.0 6
	KEGG_PATHWAY	<u>Leishmaniasis</u>	<u>RT</u>	4	29	5.3E-5	2.1E0	1.4E-4	6. <sub>4</sub> 5
	KEGG_PATHWAY	<u>Pertussis</u>	<u>RT</u>		29	1.6E-4	2.0E0	3.9E-4	1.8
ota	ation Cluster 47	Enrichment Score: 5.24	G	<b>15</b> 8	Count	P_Value	Fold Change	Benjamin	
	INTERPRO	ATPase, AAA-type, conserved site	<u>RT</u>		19	5.6E-9	4.4E0	1.8E-7	1.7
	INTERPRO	ATPase, AAA-type, core	RT		24	1.0E-6	2.9E0	2.5E-5	2.
	INTERPRO			_					5 9.9
	SMART	AAA+ ATPase domain	<u>RT</u>	-	44	5.3E-6		1.1E-4	5 2.:
		<u>AAA</u>	<u>RT</u>	i	44	3.5E-2	Fold	2.4E-1	1
ota	ation Cluster 48  INTERPRO	Enrichment Score: 4.97	G	<u> </u>	Count	P_Value	Change	Benjamin	
		<u>Tetratricopeptide repeat-containing domain</u>	<u>RT</u>	•	50	4.0E-9	2.3E0	1.3E-7	1.2 7
	UP_KEYWORDS	TPR repeat	<u>RT</u>	•	55	4.6E-9	2.3E0	3.9E-8	3.0 8
	INTERPRO	Tetratricopeptide repeat	<u>RT</u>		49	6.2E-8	2.2E0	1.6E-6	1 6
	INTERPRO	Tetratricopeptide-like helical	<u>RT</u>	=	65	6.2E-7	1.8E0	1.5E-5	1.4 5
	UP_SEQ_FEATURE	repeat:TPR 1	<u>RT</u>	4	49	1.2E-6	2.0E0	5.4E-5	5.2 5
	UP_SEQ_FEATURE	repeat:TPR 2	<u>RT</u>		49	1.2E-6	2.0E0	5.4E-5	5.2 5
	UP_SEQ_FEATURE	repeat:TPR 3	<u>RT</u>	4	45	3.0E-6	2.0E0	1.3E-4	1.3
	UP_SEQ_FEATURE	repeat:TPR 5	<u>RT</u>		28	8.8E-6	2.4E0	3.5E-4	3.4
	UP_SEQ_FEATURE	repeat:TPR 6	RT		26	1.0E-5		3.9E-4	4 3.8
	UP_SEQ_FEATURE			•					4 2.:
	UP_SEQ_FEATURE	repeat:TPR 4	<u>RT</u>	•	31	6.7E-5		2.2E-3	3.0
		repeat:TPR 7	<u>RT</u>	•	22	9.4E-5	2.5E0	3.1E-3	3
	UP_SEQ_FEATURE	repeat:TPR 8	<u>RT</u>	•	18	5.0E-4	2.5E0	1.5E-2	1.4 2
	SMART	<u>TPR</u>	<u>RT</u>	•	49	1.2E-3	1.5E0	1.3E-2	1.7
	UP_SEQ_FEATURE	repeat:TPR 9	<u>RT</u>		10	3.6E-2	2.1E0	6.6E-1	6.4 1
	UP_SEQ_FEATURE	repeat:TPR 10	<u>RT</u>	1	7	9.2E-2	2.2E0	1.0E0	9.1 1
ota	ation Cluster 49	Enrichment Score: 4.92	G	<b>-13</b>	Count	P_Value	Fold Change	Benjamin	ni FC
	UP_SEQ_FEATURE	short sequence motif:TXY	<u>RT</u>	1	11	2.3E-7	6.2E0	1.1E-5	1.: 5
	GOTERM_MF_DIRECT	MAP kinase activity	<u>RT</u>		12	6.4E-7	5.1E0	1.4E-5	1.3
	INTERPRO	Mitogen-activated protein (MAP) kinase,	<u>RT</u>	4	10	1.0E-5	5.2E0	1.9E-4	1.7
	INTERPRO	conserved site  Mitogen-activated protein (MAP) kinase, p38	RT		4	1.5E-2		1.2E-1	1.:
not	ation Cluster 50	Enrichment Score: 4.85	G	· ·	Count		Fold Change		1 ni FC
rota	KEGG_PATHWAY	Purine metabolism			68	-		•	4.9
	KEGG_PATHWAY		<u>RT</u>				2.0E0		9
	KEGG_PATHWAY	Pyrimidine metabolism  Motabolic pathways	RT DT		41		2.1E0		6
nota	ration Cluster 51	Metabolic pathways  Enrichment Score: 4.84	RT G		92 Count	1.0E0 P_Value	3.9E-1	B	1.0 ni FC
	KEGG_PATHWAY	Gap junction	RT	-	60	5.6E-	Onlange	1.5E-21	7.0
				_		23	3.020	21	22 4.1

Annot	ation Cluster 1	Enrichment Score: ?	G	· <mark>F</mark>	Count	P_Value	Fold Change	Benjamini	FDR
	KEGG_PATHWAY	Oxytocin signaling pathway	<u>RT</u>	•	70	3.3E- 14	2.4E0	3.3E-13	1.5E- 13
	GOTERM_MF_DIRECT	adenylate cyclase activity	<u>RT</u>	1	19	1.7E- 13	6.0E0	6.9E-12	6.1E- 12
	INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase	<u>RT</u>		18	4.0E-	5.9E0	2.1E-10	1.9E-
	INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase,	RT	_	17	12 2.2E-	5.9E0	9.7E-10	10 8.9E-
	KEGG_PATHWAY	conserved site		-		11 2.1E-			10 5.6E-
	SMART	GnRH signaling pathway	<u>RT</u>	•	45	10		1.2E-9	10 3.6E-
	KEGG_PATHWAY	<u>CYCc</u>	<u>RT</u>	•	17	1.5E-8	3.9E0	4.0E-7	7 5.1E-
	_	Vascular smooth muscle contraction	<u>RT</u>	•	49	2.9E-8	2.2E0	1.1E-7	8
	KEGG_PATHWAY	<u>Melanogenesis</u>	<u>RT</u>	•	43	9.6E-8	2.2E0	3.6E-7	1.6E- 7
	KEGG_PATHWAY	Chemokine signaling pathway	<u>RT</u>	•	66	1.8E-7	1.9E0	6.7E-7	3.1E- 7
	UP_KEYWORDS	cAMP biosynthesis	<u>RT</u>	i	10	2.5E-7	6.9E0	1.9E-6	1.5E- 6
	KEGG_PATHWAY	<u>Inflammatory mediator regulation of TRP</u> <u>channels</u>	<u>RT</u>	•	41	4.8E-7	2.2E0	1.7E-6	7.7E- 7
	KEGG_PATHWAY	Regulation of lipolysis in adipocytes	<u>RT</u>	1	28	7.2E-7	2.6E0	2.4E-6	1.1E- 6
	GOTERM_BP_DIRECT	cyclic nucleotide biosynthetic process	<u>RT</u>	1	11	8.7E-7	5.4E0	5.1E-5	4.9E- 5
	GOTERM_BP_DIRECT	activation of protein kinase A activity	<u>RT</u>	1	13	3.5E-6	4.3E0	1.8E-4	1.7E-
	UP_SEQ_FEATURE	metal ion-binding site:Magnesium 2; via	RT		10	4.5E-6	5.7E0	1.9E-4	1.9E-
	UP_SEQ_FEATURE	carbonyl oxygen metal ion-binding site: Magnesium 1	RT		19		3.2E0	2.7E-4	4 2.6E-
	KEGG_PATHWAY	Circadian entrainment	RT		37		2.0E0	3.9E-5	4 1.8E-
	GOTERM_MF_DIRECT								5 2.3E-
	KEGG_PATHWAY	phosphorus-oxygen lyase activity	RT		10		5.0E0	2.6E-4	4 2.4E-
	UP_SEQ_FEATURE	<u>Cholinergic synapse</u>	<u>RT</u>	•	41	1.9E-5	1.9E0	5.2E-5	5 7.0E-
		metal ion-binding site:Magnesium 2	<u>RT</u>	•	18	1.9E-5	3.1E0	7.3E-4	4
	GOTERM_BP_DIRECT	cAMP biosynthetic process	<u>RT</u>	i	11	1.1E-4	3.8E0	3.5E-3	3.3E- 3
	KEGG_PATHWAY	Gastric acid secretion	<u>RT</u>	•	28	2.5E-4	2.0E0	6.0E-4	2.7E- 4
	GOTERM_BP_DIRECT	renal water homeostasis	<u>RT</u>	1	15	3.3E-4	2.8E0	8.9E-3	8.4E- 3
	GOTERM_BP_DIRECT	cellular response to glucagon stimulus	<u>RT</u>	1	17	4.3E-4	2.5E0	1.1E-2	1.1E- 2
	GOTERM_BP_DIRECT	cellular response to forskolin	<u>RT</u>	1	7	4.7E-4	5.2E0	1.2E-2	1.2E- 2
	INTERPRO	Adenylate cyclase-like	<u>RT</u>	1	6	5.7E-4	6.2E0	7.2E-3	6.6E- 3
	KEGG_PATHWAY	Endocrine and other factor-regulated calcium reabsorption	<u>RT</u>	i .	19	9.2E-4	2.2E0	2.0E-3	9.2E- 4
	KEGG_PATHWAY	Thyroid hormone synthesis	<u>RT</u>	4	25	1.9E-3	1.9E0	3.9E-3	1.9E-
	KEGG_PATHWAY	Salivary secretion	RT		28	4.2E-3	1.7E0	8.6E-3	3 4.2E-
	KEGG_PATHWAY	Retrograde endocannabinoid signaling	RT		31			1.3E-2	3 6.5E-
	KEGG_PATHWAY	Glutamatergic synapse	RT	- <u></u>	34			1.3E-2	3 6.9E-
	GOTERM_BP_DIRECT	adenylate cyclase-inhibiting G-protein coupled							3 1.2E-
	KEGG_PATHWAY	receptor signaling pathway	<u>KI</u>	•	16			1.3E-1	1 1.4E-
	UP_KEYWORDS	Aldosterone synthesis and secretion	<u>RT</u>	•	25			2.7E-2	2 7.8E-
	GOTERM_BP_DIRECT	<u>Lyase</u>	<u>RT</u>	•	32			1.0E-1	2
		activation of adenylate cyclase activity	<u>RT</u>	•	13	2.8E-2	1.9E0	3.3E-1	3.1E- 1
	KEGG_PATHWAY	Ovarian steroidogenesis	<u>RT</u>	•	16	3.6E-2	1.7E0	6.3E-2	3.6E- 2
	GOTERM_BP_DIRECT	cAMP-mediated signaling	<u>RT</u>	1	12	4.5E-2	1.9E0	4.3E-1	4.1E- 1
	KEGG_PATHWAY	GABAergic synapse	<u>RT</u>	•	24	4.6E-2	1.5E0	8.0E-2	4.6E- 2
	KEGG_PATHWAY	Pancreatic secretion	<u>RT</u>	i .	25	6.8E-2	1.4E0	1.2E-1	6.8E- 2
	KEGG_PATHWAY	Insulin secretion	<u>RT</u>	4	23	7.6E-2	1.4E0	1.3E-1	7.6E- 2
	KEGG_PATHWAY	Dilated cardiomyopathy	<u>RT</u>	1	22	1.1E-1	1.4E0	1.8E-1	1.1E-
	GOTERM_BP_DIRECT	adenylate cyclase-activating G-protein	<u>RT</u>	1	13	1.2E-1	1.5E0	8.1E-1	7.7E-
	KEGG_PATHWAY	coupled receptor signaling pathway  Morphine addiction	RT		23			2.2E-1	1.4E-
	KEGG_PATHWAY	Bile secretion	RT		17			3.7E-1	1 2.3E-
	KEGG_PATHWAY								1 2.8E-
	KEGG_PATHWAY	Serotonergic synapse	<u>RT</u>	•	25		1.2E0	4.4E-1	1 3.2E-
		<u>Calcium signaling pathway</u>	<u>RT</u>	i	38	3.2E-1	1.1E0	5.0E-1	1

Annota	ation Cluster 1	Enrichment Score: ?	G	. ■	Count	P_Value	Fold Change	Benjamini	i FDR
	KEGG_PATHWAY	<u>Taste transduction</u>	<u>RT</u>	i	6	9.5E-1	7.0E-1	1.0E0	9.5E- 1
Annota	ation Cluster 52	Enrichment Score: 4.8	G	<b>™</b>	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_MF_DIRECT	cadherin binding involved in cell-cell adhesion	<u>RT</u>	=	79	7.9E-6	1.6E0	1.5E-4	1.4E- 4
	GOTERM_CC_DIRECT	cell-cell adherens junction	<u>RT</u>	<b>=</b>	81	1.5E-5	1.6E0	2.7E-4	2.4E- 4
	GOTERM_BP_DIRECT	cell-cell adhesion	<u>RT</u>	E	73	3.3E-5	1.6E0	1.2E-3	1.1E- 3
Annota	ation Cluster 53	Enrichment Score: 4.8	G	<b>™</b>	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:PI3K/PI4K	<u>RT</u>	i	15	3.6E-9	5.7E0	2.0E-7	2.0E- 7
	INTERPRO	Phosphatidylinositol 3/4-kinase, conserved site	<u>RT</u>	i .	14	1.7E-8	5.4E0	5.0E-7	4.6E- 7
	INTERPRO	Phosphatidylinositol 3-/4-kinase, catalytic domain	<u>RT</u>	i .	15	4.1E-8	4.9E0	1.1E-6	1.0E- 6
	SMART	<u>PI3Kc</u>	<u>RT</u>	i .	15	8.6E-7	3.6E0	1.6E-5	1.4E- 5
	UP_SEQ_FEATURE	domain:FAT	<u>RT</u>	i e	6	3.6E-4	6.8E0	1.1E-2	1.0E- 2
	UP_SEQ_FEATURE	domain:FATC	<u>RT</u>	i	6	3.6E-4	6.8E0	1.1E-2	1.0E- 2
	INTERPRO	PIK-related kinase	<u>RT</u>		6	5.7E-4	6.2E0	7.2E-3	6.6E-
	INTERPRO	PIK-related kinase, FATC	<u>RT</u>		6	5.7E-4	6.2E0	7.2E-3	6.6E-
	INTERPRO	PIK-related kinase, FAT	RT		5	2.9E-3		3.2E-2	3 2.9E-
	SMART	SM01343	RT		6			4.0E-2	2 3.6E-
Annota	ation Cluster 54	Enrichment Score: 4.77	G	- -	Count	P_Value	Fold	Benjamini	2 FDR
	GOTERM_BP_DIRECT	global genome nucleotide-excision repair	RT		21		Change 3.9E0		7.2E-
	GOTERM_BP_DIRECT	nucleotide-excision repair, preincision	RT		19	6.0E-8		4.5E-6	7 4.3E-
	GOTERM_BP_DIRECT	complex assembly nucleotide-excision repair, DNA incision, 5'-to	RT		21	2.7E-7		1.8E-5	6 1.8E-
	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision	RT	-	21	4.8E-7		3.2E-5	5 3.0E-
	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA duplex	RT		14			3.9E-4	5 3.7E-
	KEGG_PATHWAY	<u>unwinding</u>		-					4 1.8E-
	GOTERM_BP_DIRECT	Nucleotide excision repair  nucleotide-excision repair, DNA damage	<u>RT</u>		23	1.4E-5		4.0E-5	5 1.4E-
	GOTERM_BP_DIRECT	recognition nucleotide-excision repair, preincision	<u>RT</u>		12			1.4E-2	2 2.4E-
	GOTERM_BP_DIRECT	complex stabilization nucleotide-excision repair, DNA incision, 3'-to	<u>RT</u>	•	11	1.1E-3		2.5E-2	2 4.7E-
	GOTERM_BP_DIRECT	lesion	<u>RT</u>	•	11	2.5E-3		5.0E-2	7.8E-
	OOTEKIII_BF_BIKEOT	nucleotide-excision repair	<u>RT</u>	i	11	1.4E-1	Fold	8.2E-1	1
Annota	ation Cluster 55  GOTERM_BP_DIRECT	Enrichment Score: 4.63	G		Count	P_Value	Change	Benjamini	3.1E-
		DNA synthesis involved in DNA repair	<u>RT</u>	i	20	5.0E-7	3.4E0	3.2E-5	5
	GOTERM_BP_DIRECT	strand displacement	<u>RT</u>	i	15	1.8E-5	3.4E0	7.1E-4	6.8E- 4
	GOTERM_BP_DIRECT	DNA double-strand break processing	<u>RT</u>	•	11	2.4E-5	4.3E0	9.0E-4	8.5E- 4
	KEGG_PATHWAY	Homologous recombination	<u>RT</u>	i	14			2.9E-3	1.4E- 3
Annota	ntion Cluster 56	Enrichment Score: 4.49	G		Count	P_Value	Fold Change	Benjamini	
	INTERPRO	Heat shock protein 70, conserved site	<u>RT</u>	•	12	1.4E-6	5.0E0	3.1E-5	2.9E- 5
	INTERPRO	Heat shock protein 70 family	<u>RT</u>	i	12	1.4E-6	5.0E0	3.1E-5	2.9E- 5
	GOTERM_BP_DIRECT	response to unfolded protein	<u>RT</u>	î .	14	1.8E-2		2.3E-1	2.2E- 1
Annota	ntion Cluster 57	Enrichment Score: 4.44	G	M .	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 23	<u>RT</u>	i	15	1.9E- 10	6.4E0	1.2E-8	1.1E- 8
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 24	<u>RT</u>	i	13	6.7E-9	6.3E0	3.7E-7	3.6E- 7
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 26	<u>RT</u>	i	8	4.0E-5	6.1E0	1.4E-3	1.4E- 3
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 27	<u>RT</u>	i	7	2.1E-4	6.0E0	6.6E-3	6.4E- 3
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 25	<u>RT</u>	i e	7	2.1E-4	6.0E0	6.6E-3	6.4E- 3
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 28	<u>RT</u>	i .	6	3.6E-4	6.8E0	1.1E-2	1.0E- 2
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 29	<u>RT</u>	i	6	1.1E-3	5.8E0	3.1E-2	3.0E- 2
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 30	<u>RT</u>	i .	6	1.1E-3	5.8E0	3.1E-2	3.0E- 2
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 21; degenerate	<u>RT</u>	i e	3	1.1E-1	5.1E0	1.0E0	9.7E- 1

Annot	tation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
Annot	tation Cluster 58	Enrichment Score: 4.33	G	To the second se	Count	P_Value	Fold	Benjamini	FDR
	GOTERM_CC_DIRECT	<u>precatalytic spliceosome</u>	<u>RT</u>	i	17	6.6E-8		2.0E-6	1.8E- 6
	GOTERM_CC_DIRECT	U4/U6 x U5 tri-snRNP complex	<u>RT</u>	i .	16	1.2E-7	4.4E0	3.4E-6	3.0E- 6
	INTERPRO	Ribonucleoprotein LSM domain	<u>RT</u>	1	15	2.9E-7	4.4E0	7.2E-6	6.6E-
	GOTERM_CC_DIRECT	<u>U5 snRNP</u>	<u>RT</u>	1	13	6.4E-7	4.9E0	1.7E-5	1.5E- 5
	GOTERM_CC_DIRECT	U12-type spliceosomal complex	<u>RT</u>	1	16	1.2E-6	3.9E0	2.8E-5	2.4E- 5
	GOTERM_CC_DIRECT	<u>U4 snRNP</u>	<u>RT</u>	i	10	2.4E-6	5.8E0	5.4E-5	4.7E- 5
	INTERPRO	Like-Sm (LSM) domain	<u>RT</u>	i	15	3.1E-6	3.9E0	6.8E-5	6.2E- 5
	BIOCARTA	<u>Spliceosomal Assembly</u>	<u>RT</u>	i	14	3.8E-6	3.1E0	2.4E-4	1.6E-
	GOTERM_CC_DIRECT	U2 snRNP	<u>RT</u>	i .	13	8.1E-6	4.1E0	1.6E-4	1.4E-
	SMART	<u>Sm</u>	<u>RT</u>	i e	15	5.2E-5	2.9E0	6.9E-4	6.2E-
	GOTERM_CC_DIRECT	small nuclear ribonucleoprotein complex	<u>RT</u>	i de la companya de	11	6.1E-5	4.1E0	9.4E-4	8.2E- 4
	GOTERM_CC_DIRECT	<u>methylosome</u>	<u>RT</u>	1	9	1.0E-4	4.8E0	1.4E-3	1.2E- 3
	GOTERM_MF_DIRECT	<u>U1 snRNP binding</u>	<u>RT</u>	1	7	1.3E-4	6.0E0	1.8E-3	1.6E-
	GOTERM_BP_DIRECT	histone mRNA metabolic process	RT		9	1.7E-4		5.0E-3	3 4.7E-
	GOTERM_CC_DIRECT	U1 snRNP	RT		11	2.1E-4	3.7E0	2.6E-3	3 2.3E-
	GOTERM_CC_DIRECT	spliceosomal tri-snRNP complex	RT		5	2.7E-3	6.4E0	2.4E-2	3 2.1E-
	GOTERM_BP_DIRECT	nuclear import	RT		9	5.7E-3	3.0E0	9.5E-2	9.0E-
	GOTERM_CC_DIRECT	pICln-Sm protein complex	RT		5	7.0E-3		5.2E-2	2 4.6E-
	GOTERM_CC_DIRECT	SMN-Sm protein complex	RT		8	1.1E-2		7.6E-2	2 6.7E-
	GOTERM_BP_DIRECT	spliceosomal snRNP assembly	RT		11	1.3E-2		1.8E-1	2 1.7E-
	GOTERM_CC_DIRECT	U7 snRNP	RT		5	1.4E-2		9.8E-2	1 8.6E-
Annot	tation Cluster 59	Enrichment Score: 4.3	G	·	Count	P_Value	Fold	Benjamini	2 FDR
	GOTERM_MF_DIRECT	adenylate cyclase activity	<u>RT</u>	i	19	1.7E- 13	6.0E0	6.9E-12	6.1E- 12
	INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase	<u>RT</u>	i .	18	4.0E- 12	5.9E0	2.1E-10	1.9E- 10
	INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase, conserved site	<u>RT</u>	i de la companya de	17	2.2E- 11	5.9E0	9.7E-10	8.9E- 10
	SMART	<u>CYCc</u>	<u>RT</u>	i de la companya de	17	1.5E-8	3.9E0	4.0E-7	3.6E- 7
	UP_SEQ_FEATURE	domain:Guanylate cyclase	<u>RT</u>	1	8	1.0E-5	6.8E0	3.9E-4	3.8E-
	UP_KEYWORDS	cGMP biosynthesis	<u>RT</u>	i de la companya de	8	3.8E-5	6.1E0	2.2E-4	1.7E-
	GOTERM_CC_DIRECT	guanylate cyclase complex, soluble	<u>RT</u>	1	8	6.3E-5	5.7E0	9.4E-4	8.2E-
	GOTERM_MF_DIRECT	guanylate cyclase activity	<u>RT</u>		8	9.7E-5	5.3E0	1.4E-3	1.2E- 3
	INTERPRO	Haem NO binding associated	<u>RT</u>	1	6	1.7E-3	5.3E0	2.0E-2	1.8E-
	GOTERM_BP_DIRECT	cGMP biosynthetic process	RT		8	1.1E-2		1.5E-1	2 1.5E-
	GOTERM_BP_DIRECT	receptor guanylyl cyclase signaling pathway	<u>RT</u>	1	6	1.6E-2		2.2E-1	1 2.1E-
	INTERPRO	Heme-NO binding	RT		3	1.2E-1		6.1E-1	1 5.6E-
	GOTERM_BP_DIRECT	positive regulation of cGMP biosynthetic	RT	1	3	4.0E-1		1.0E0	9.5E-
	INTERPRO	NO signalling/Golgi transport ligand-binding	RT	1	3	4.4E-1		1.0E0	9.1E-
	BIOCARTA	domain  Ion Channels and Their Functional Role in	RT		7	6.2E-1		9.3E-1	1 6.3E-
	INTERPRO	Vascular Endothelium  Extracellular ligand-binding receptor	RT		5		8.6E-1		9.1E-
Annot	tation Cluster 60	Enrichment Score: 4.28	G		Count		Fold Change		1 FDR
	KEGG_PATHWAY	<u>Alcoholism</u>	<u>RT</u>	=	68	3.0E-9		1.4E-8	6.2E-
	INTERPRO	Histone core	RT		30	1.9E-7		4.8E-6	9 4.4E-
	UP_KEYWORDS	Nucleosome core	RT		31	4.5E-6		2.8E-5	6 2.2E-
	GOTERM_CC_DIRECT	nucleosome	RT		33	9.1E-6		1.8E-4	5 1.5E-
	GOTERM_CC_DIRECT	nuclear nucleosome	RT	-	18	2.0E-4		2.5E-3	4 2.2E-
	INTERPRO	Histone-fold	RT		34	2.8E-4		3.9E-3	3 3.5E-
				_					3

Annot	ation Cluster 1	Enrichment Score: ?	G	<b>15</b>	Count	P_Value	Fold Change	Benjamii	ni FDR
	INTERPRO	Histone H2B	<u>RT</u>	i	12	6.0E-4	3.1E0	7.5E-3	6.9E- 3
	GOTERM_BP_DIRECT	nucleosome assembly	<u>RT</u>	•	34	2.0E-3	1.7E0	4.0E-2	3.8E- 2
	KEGG_PATHWAY	Systemic lupus erythematosus	<u>RT</u>		39	5.7E-3	1.5E0	1.1E-2	5.7E-
ገ ገ	SMART	H2B	RT		12	1.8E-2	2 0F0	1.4E-1	3 1.3E-
ppot	ation Cluster 61	Enrichment Score: 4.07		·		1	Fold	1	1
nnot	KEGG_PATHWAY		G		Count	P_Value	Change	-	2.1E-
_	KEGG_PATHWAY	Adrenergic signaling in cardiomyocytes	<u>RT</u>		51		1.9E0	4.5E-6	6 7.6E-
	_	<u>Dopaminergic synapse</u>	<u>RT</u>	•	44	6.4E-5	1.8E0	1.7E-4	5
	KEGG_PATHWAY	Retrograde endocannabinoid signaling	<u>RT</u>	ī	31	6.5E-3		1.3E-2	6.5E- 3
nnot	ation Cluster 62	Enrichment Score: 4.04	G		Count	P_Value	Fold Change	Benjamiı	
	GOTERM_MF_DIRECT	G-protein beta/gamma-subunit complex binding	<u>RT</u>	i	16	1.5E-8	4.8E0	4.2E-7	3.8E- 7
	INTERPRO	G protein alpha subunit, helical insertion	<u>RT</u>	i	14	1.7E-8	5.4E0	5.0E-7	4.6E- 7
	INTERPRO	Guanine nucleotide binding protein (G- protein), alpha subunit	<u>RT</u>	1	14	1.7E-8	5.4E0	5.0E-7	4.6E- 7
	SMART	<u>SM00275</u>	<u>RT</u>	i	14	2.9E-6	3.6E0	4.9E-5	4.4E- 5
	INTERPRO	<u>G-protein alpha subunit, group I</u>	<u>RT</u>		8	1.9E-5	6.2E0	3.4E-4	3.1E- 4
	GOTERM_MF_DIRECT	guanyl nucleotide binding	<u>RT</u>		8	9.7E-5	5.3E0	1.4E-3	1.2E-
)	GOTERM_CC_DIRECT	heterotrimeric G-protein complex	RT		12	9.6E-3		7.0E-2	3 6.1E
ر ا	GOTERM_BP_DIRECT	adenylate cyclase-modulating G-protein		_					2 2.0E
_	GOTERM_MF_DIRECT	coupled receptor signaling pathway	<u>RT</u>	•	13	1.5E-2		2.1E-1	1 1.0E-
J		G-protein coupled serotonin receptor binding	<u>RT</u>	•	4	1.6E-2	6.0E0	1.1E-1	1
	GOTERM_MF_DIRECT	<u>G-protein coupled receptor binding</u>	<u>RT</u>	i	15		1.6E0	3.7E-1	3.3E- 1
nnot	UP_KEYWORDS ration Cluster 63	Transducer Enrichment Score: 3.94	RT G	-	29 Count	1.0E0 P_Value	Fold	1.0E0  Benjamii	1.0E(
	GOTERM_MF_DIRECT			_		-	Change	,	1.6E-
J	INTERPRO	<u>DNA helicase activity</u> Mini-chromosome maintenance, DNA-	<u>RT</u>	•	17	7.0E-8	4.2E0	1.8E-6	6 7.0E-
J		dependent ATPase	<u>RT</u>	•	9	3.5E-6	6.2E0	7.6E-5	5
	UP_SEQ_FEATURE	domain:MCM	<u>RT</u>	•	8	1.0E-5	6.8E0	3.9E-4	3.8E- 4
	SMART	<u>MCM</u>	<u>RT</u>	i	9	9.1E-5	4.1E0	1.1E-3	1.0E- 3
	INTERPRO	Mini-chromosome maintenance, conserved site	<u>RT</u>	i	6	5.7E-4	6.2E0	7.2E-3	6.6E- 3
	GOTERM_CC_DIRECT	MCM complex	<u>RT</u>	i	7	8.2E-4	4.9E0	8.2E-3	7.1E- 3
	GOTERM_BP_DIRECT	DNA replication initiation	<u>RT</u>		14	1.2E-3	2.6E0	2.8E-2	2.7E- 2
	GOTERM_BP_DIRECT	DNA unwinding involved in DNA replication	<u>RT</u>	1	7	2.6E-3	4.2E0	5.1E-2	4.8E-
- -	BIOCARTA	CDK Regulation of DNA Replication	RT		12	1.1E-2	2 1F0	4.7E-2	2 3.2E-
	ation Cluster 64	Enrichment Score: 3.91		•		P_Value	Fold		2
nnot	GOTERM_BP_DIRECT		G		Count		Change	•	4.7E-
	GOTERM_BP_DIRECT	<u>phosphatidylinositol-mediated signaling</u> <u>phosphatidylinositol-3-phosphate biosynthetic</u>	<u>RT</u>	•	42		2.3E0	4.9E-6	6 1.9E
		process	<u>RT</u>	i	21	6.1E-5	2.5E0	2.0E-3	3
	GOTERM_MF_DIRECT	1-phosphatidylinositol-3-kinase activity	<u>RT</u>	i	19	8.9E-5	2.6E0	1.3E-3	1.2E- 3
	GOTERM_MF_DIRECT	<u>phosphatidylinositol-4,5-bisphosphate 3-kinase activity</u>	<u>RT</u>	•	23	2.8E-4	2.2E0	3.6E-3	3.2E- 3
	GOTERM_BP_DIRECT	<u>regulation of phosphatidylinositol 3-kinase</u> <u>signaling</u>	<u>RT</u>	•	27	2.9E-4	2.1E0	8.1E-3	7.7E- 3
	GOTERM_BP_DIRECT	phosphatidylinositol phosphorylation	<u>RT</u>	•	30	5.8E-4	1.9E0	1.5E-2	1.4E- 2
	GOTERM_MF_DIRECT	Ras guanyl-nucleotide exchange factor activity	<u>RT</u>		29	2.3E-2	1.5E0	1.5E-1	1.4E-
nnot	ation Cluster 65	Enrichment Score: 3.9	G	To the second	Count	P_Value	Fold	Benjamii	-
)	BIOCARTA	Cell Cycle	RT		22		Change	2.9E-5	2.0E-
)	BIOCARTA	RB Tumor Suppressor/Checkpoint Signaling in							5 1.3E-
J	BIOCARTA	response to DNA damage	<u>KI</u>	•	12	1.5E-4		2.0E-3	3 9.5E-
J		Regulation of cell cycle progression by Plk3	<u>RT</u>	i	8	2.1E-3	3.1E0	1.4E-2	3
	BIOCARTA	cdc25 and chk1 Regulatory Pathway in response to DNA damage	<u>RT</u>	ī	8	6.8E-3		3.3E-2	2.2E- 2
	ation Cluster 66	Enrichment Score: 3.89	G	<b>100</b>	Count	P_Value	Fold Change	Benjamii	ni FDR
nnot		positive regulation of telomere maintenance		-	22	1.0E-9	4.1E0	9.9E-8	9.4E
nnot	GOTERM_BP_DIRECT	<u>via telomerase</u>	<u>RT</u>	i .		1102 3		3132 0	8
nnot	GOTERM_BP_DIRECT		RT RT		12	2.2E-6		1.1E-4	8 1.1E

	ation Cluster 1	Enrichment Score: ?	G	100	Count	P_Value	Fold	Benjamini	FDR
	INTERPRO	GroEL-like apical domain	RT		12	3.7E-6	Onlange	7.9E-5	7.2E
	INTERPRO	GroEL-like equatorial domain	RT		11	1.6E-5		2.9E-4	5 2.7E
	GOTERM_BP_DIRECT	positive regulation of protein localization to	RT	_	8	2.6E-5		9.6E-4	4 9.1E
	GOTERM_CC_DIRECT	Cajal body							4 8.2E
	GOTERM_CC_DIRECT	zona pellucida receptor complex	<u>RT</u>		8	6.3E-5		9.4E-4	4 8.2E
	INTERPRO	<u>chaperonin-containing T-complex</u>	<u>RT</u>	•	8	6.3E-5	5.7E0	9.4E-4	4
		Chaperonin TCP-1, conserved site	<u>RT</u>	•	8	7.5E-5	5.5E0	1.2E-3	1.1E
	GOTERM_BP_DIRECT	positive regulation of establishment of protein localization to telomere	<u>RT</u>	i	8	1.0E-4	5.3E0	3.2E-3	3.0E
	INTERPRO	<u>Chaperone tailless complex polypeptide 1</u> (TCP-1)	<u>RT</u>	1	9	1.2E-4	4.6E0	1.8E-3	1.7E
	INTERPRO	TCP-1-like chaperonin intermediate domain	<u>RT</u>	i	9	1.2E-4	4.6E0	1.8E-3	1.7E
	GOTERM_BP_DIRECT	toxin transport	<u>RT</u>	i .	11	6.9E-2	1.8E0	5.7E-1	5.4E- 1
	GOTERM_BP_DIRECT	scaRNA localization to Cajal body	<u>RT</u>	i	3	1.3E-1	4.4E0	8.1E-1	7.7E
	GOTERM_BP_DIRECT	binding of sperm to zona pellucida	<u>RT</u>	i	9	2.3E-1	1.5E0	1.0E0	9.5E
	GOTERM_MF_DIRECT	protein binding involved in protein folding	<u>RT</u>	i .	4	4.2E-1	1.7E0	1.0E0	8.9E
Annota	ation Cluster 67	Enrichment Score: 3.88	G	■ The state of th	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_MF_DIRECT	phosphoprotein phosphatase activity	<u>RT</u>	i .	27	5.5E- 10	3.6E0	1.7E-8	1.5E- 8
	INTERPRO	Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-	<u>RT</u>		12	1.1E-7	5.7E0	2.8E-6	2.5E
	SMART	<u>tetraphosphatase</u>							6 1.1E
	INTERPRO	<u>PP2Ac</u>	<u>RT</u>	•	12	8.8E-6	3.8E0	1.3E-4	4
		Metallophosphoesterase domain	<u>RT</u>	i	13	7.2E-4	2.9E0	9.0E-3	8.2E
	UP_SEQ_FEATURE	metal ion-binding site:Manganese	<u>RT</u>	•	11	2.1E-2	2.2E0	4.1E-1	4.0E
	UP_SEQ_FEATURE	metal ion-binding site:Iron	<u>RT</u>	i	12	9.5E-2	1.7E0	1.0E0	9.7E
	UP_SEQ_FEATURE	active site:Proton donor	<u>RT</u>	i	23	9.5E-1	7.8E-1	1.0E0	9.7E
Annota	ation Cluster 68	Enrichment Score: 3.83	G	<b>100</b>	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	<u>Tyrosine-protein kinase, receptor class V,</u> <u>conserved site</u>	<u>RT</u>	i	14	5.8E- 10	6.2E0	2.1E-8	1.9E
	INTERPRO	Ephrin receptor ligand binding domain	<u>RT</u>	i	14	5.8E- 10	6.2E0	2.1E-8	1.9E
	INTERPRO	Tyrosine-protein kinase, ephrin receptor	<u>RT</u>	i	14	5.8E- 10	6.2E0	2.1E-8	1.9E
	PIR_SUPERFAMILY	<u>tyrosine-protein kinase, ephrin receptor type</u>	<u>RT</u>	i .	14	3.2E-9	5.3E0	6.2E-7	6.1E
	SMART	EPH Ibd	<u>RT</u>	1	14	1.2E-7	4.1E0	2.7E-6	2.4E
	GOTERM_MF_DIRECT	ephrin receptor activity	<u>RT</u>	i	11		6.0E0	3.9E-6	3.5E
	INTERPRO	Tyrosine-protein kinase ephrin type A/B	рт			1.6E-7			
		recenter-like	<u>RT</u>	i .	15	1.6E-7 5.9E-6	3.7E0	1.2E-4	1.1E
	GOTERM_BP_DIRECT	receptor-like ephrin receptor signaling pathway				5.9E-6			4 1.3E
	GOTERM_BP_DIRECT INTERPRO	ephrin receptor signaling pathway	<u>RT</u>	•	15	5.9E-6 3.9E-5	2.1E0	1.4E-3	1.3E-3 7.5E-
		ephrin receptor signaling pathway  Galactose-binding domain-like	RT RT	: :	15 31 29	5.9E-6 3.9E-5 4.8E-5	2.1E0 2.2E0	1.4E-3 8.2E-4	1.3E-3 7.5E-4 2.9E-
	INTERPRO	ephrin receptor signaling pathway  Galactose-binding domain-like  domain:SAM	RT RT RT	: :	15 31 29 27	5.9E-6 3.9E-5 4.8E-5 9.1E-5	2.1E0 2.2E0 2.2E0	1.4E-3 8.2E-4 3.0E-3	4 1.3E 3 7.5E 4 2.9E 3 1.5E
	INTERPRO  UP_SEQ_FEATURE	ephrin receptor signaling pathway  Galactose-binding domain-like  domain:SAM  Sterile alpha motif domain	RT RT RT RT	: : :	15 31 29 27 31	5.9E-6 3.9E-5 4.8E-5 9.1E-5 1.1E-4	2.1E0 2.2E0 2.2E0 2.0E0	1.4E-3 8.2E-4 3.0E-3 1.7E-3	1.3E-3 7.5E-4 2.9E-3 1.5E-3
	INTERPRO  UP_SEQ_FEATURE  INTERPRO	ephrin receptor signaling pathway  Galactose-binding domain-like  domain:SAM  Sterile alpha motif domain  Sterile alpha motif/pointed domain	RT RT RT RT RT		15 31 29 27 31 35	5.9E-6 3.9E-5 4.8E-5 9.1E-5 1.1E-4 3.0E-4	2.1E0 2.2E0 2.2E0 2.0E0 1.9E0	1.4E-3 8.2E-4 3.0E-3 1.7E-3 4.2E-3	1.3E-3 7.5E-4 2.9E-3 1.5E-3 3.8E-3
	INTERPRO  UP_SEQ_FEATURE  INTERPRO  INTERPRO  SMART	ephrin receptor signaling pathway  Galactose-binding domain-like  domain:SAM  Sterile alpha motif domain  Sterile alpha motif/pointed domain  SM01411	RT RT RT RT RT RT	: : :	15 31 29 27 31 35	5.9E-6 3.9E-5 4.8E-5 9.1E-5 1.1E-4 3.0E-4 7.3E-4	2.1E0 2.2E0 2.2E0 2.0E0 1.9E0 2.4E0	1.4E-3 8.2E-4 3.0E-3 1.7E-3 4.2E-3 8.2E-3	1.3E-3 7.5E-4 2.9E-3 1.5E-3 3.8E-3 7.4E-3
	INTERPRO  UP_SEQ_FEATURE  INTERPRO  INTERPRO  SMART  GOTERM_MF_DIRECT	ephrin receptor signaling pathway  Galactose-binding domain-like  domain:SAM  Sterile alpha motif domain  Sterile alpha motif/pointed domain  SM01411  transmembrane-ephrin receptor activity	RT RT RT RT RT RT RT RT		15 31 29 27 31 35 15	5.9E-6 3.9E-5 4.8E-5 9.1E-5 1.1E-4 3.0E-4 7.3E-4 9.1E-3	2.1E0 2.2E0 2.2E0 2.0E0 1.9E0 2.4E0 4.0E0	1.4E-3 8.2E-4 3.0E-3 1.7E-3 4.2E-3 8.2E-3 7.2E-2	1.3E-3 7.5E-4 2.9E-3 1.5E-3 3.8E-3 7.4E-3 6.4E-2
	INTERPRO  UP_SEQ_FEATURE  INTERPRO  INTERPRO  SMART  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT	ephrin receptor signaling pathway  Galactose-binding domain-like  domain:SAM  Sterile alpha motif domain  Sterile alpha motif/pointed domain  SM01411	RT RT RT RT RT RT		15 31 29 27 31 35 15 6	5.9E-6 3.9E-5 4.8E-5 9.1E-5 1.1E-4 3.0E-4 7.3E-4 9.1E-3 1.8E-2	2.1E0 2.2E0 2.2E0 2.0E0 1.9E0 2.4E0 4.0E0 4.3E0	1.4E-3 8.2E-4 3.0E-3 1.7E-3 4.2E-3 8.2E-3 7.2E-2 1.2E-1	1.3E <sub>3</sub> 7.5E <sub>4</sub> 2.9E <sub>3</sub> 1.5E <sub>3</sub> 3.8E <sub>3</sub> 7.4E <sub>3</sub> 6.4E <sub>2</sub> 1.1E <sub>1</sub>
	INTERPRO  UP_SEQ_FEATURE  INTERPRO  INTERPRO  SMART  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  SMART	ephrin receptor signaling pathway  Galactose-binding domain-like  domain:SAM  Sterile alpha motif domain  Sterile alpha motif/pointed domain  SM01411  transmembrane-ephrin receptor activity	RT RT RT RT RT RT RT RT		15 31 29 27 31 35 15	5.9E-6 3.9E-5 4.8E-5 9.1E-5 1.1E-4 3.0E-4 7.3E-4 9.1E-3	2.1E0 2.2E0 2.2E0 2.0E0 1.9E0 2.4E0 4.0E0 4.3E0	1.4E-3 8.2E-4 3.0E-3 1.7E-3 4.2E-3 8.2E-3 7.2E-2	4 1.3E-3 7.5E-4 2.9E-3 1.5E-3 3.8E-3 7.4E-3 6.4E-2 1.1E-1
	INTERPRO  UP_SEQ_FEATURE  INTERPRO  INTERPRO  SMART  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  SMART  UP_SEQ_FEATURE	ephrin receptor signaling pathway  Galactose-binding domain-like  domain:SAM  Sterile alpha motif domain  Sterile alpha motif/pointed domain  SM01411  transmembrane-ephrin receptor activity  GPI-linked ephrin receptor activity	RT		15 31 29 27 31 35 15 6	5.9E-6 3.9E-5 4.8E-5 9.1E-5 1.1E-4 3.0E-4 7.3E-4 9.1E-3 1.8E-2	2.1E0 2.2E0 2.2E0 2.0E0 1.9E0 2.4E0 4.0E0 4.3E0 1.4E0	1.4E-3 8.2E-4 3.0E-3 1.7E-3 4.2E-3 8.2E-3 7.2E-2 1.2E-1	4 1.3E-3 7.5E-4 2.9E-3 1.5E-3 3.8E-3 6.4E-2 1.1E-1 2.6E-1 8.8E-1
	INTERPRO  UP_SEQ_FEATURE  INTERPRO  INTERPRO  SMART  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  SMART  UP_SEQ_FEATURE  UP_SEQ_FEATURE	ephrin receptor signaling pathway  Galactose-binding domain-like  domain:SAM  Sterile alpha motif domain  Sterile alpha motif/pointed domain  SM01411  transmembrane-ephrin receptor activity  GPI-linked ephrin receptor activity  SAM	RT		15 31 29 27 31 35 15 6 5	5.9E-6 3.9E-5 4.8E-5 9.1E-5 1.1E-4 3.0E-4 7.3E-4 9.1E-3 1.8E-2 4.9E-2	2.1E0 2.2E0 2.2E0 2.0E0 1.9E0 2.4E0 4.0E0 4.3E0 1.4E0	1.4E-3 8.2E-4 3.0E-3 1.7E-3 4.2E-3 8.2E-3 7.2E-2 1.2E-1 2.9E-1	4 1.3E-3 7.5E-4 2.9E-3 1.5E-3 3.8E-3 7.4E-2 1.1E-1 2.6E-1 9.7E-1
	INTERPRO  UP_SEQ_FEATURE  INTERPRO  INTERPRO  SMART  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  SMART  UP_SEQ_FEATURE	ephrin receptor signaling pathway  Galactose-binding domain-like  domain:SAM  Sterile alpha motif domain  Sterile alpha motif/pointed domain  SM01411  transmembrane-ephrin receptor activity  GPI-linked ephrin receptor activity  SAM  short sequence motif:PDZ-binding	RT		15 31 29 27 31 35 15 6 5 29	5.9E-6 3.9E-5 4.8E-5 9.1E-5 1.1E-4 3.0E-4 7.3E-4 9.1E-3 1.8E-2 4.9E-2 5.2E-2	2.1E0 2.2E0 2.2E0 2.0E0 1.9E0 2.4E0 4.0E0 4.3E0 1.4E0 1.6E0 1.3E0	1.4E-3 8.2E-4 3.0E-3 1.7E-3 4.2E-3 8.2E-3 7.2E-2 1.2E-1 2.9E-1 9.1E-1	4 1.3E-3 7.5E-4 2.9E-3 1.5E-3 3.8E-3 6.4E-2 1.1E-1 2.6E-1 1 8.8E-1
	INTERPRO  UP_SEQ_FEATURE  INTERPRO  INTERPRO  SMART  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  SMART  UP_SEQ_FEATURE  UP_SEQ_FEATURE	ephrin receptor signaling pathway  Galactose-binding domain-like  domain:SAM  Sterile alpha motif domain  Sterile alpha motif/pointed domain  SM01411  transmembrane-ephrin receptor activity  GPI-linked ephrin receptor activity  SAM  short sequence motif:PDZ-binding  compositionally biased region:Cys-rich	RT		15 31 29 27 31 35 15 6 5 29 18 30	5.9E-6 3.9E-5 4.8E-5 9.1E-5 1.1E-4 3.0E-4 7.3E-4 9.1E-3 1.8E-2 4.9E-2 5.2E-2 1.2E-1	2.1E0 2.2E0 2.2E0 2.0E0 1.9E0 2.4E0 4.0E0 4.3E0 1.4E0 1.6E0 1.3E0 1.2E0	1.4E-3 8.2E-4 3.0E-3 1.7E-3 4.2E-3 8.2E-3 7.2E-2 1.2E-1 2.9E-1 9.1E-1 1.0E0	4 1.3E 3 7.5E 4 2.9E 3 1.5E 3 3.8E 3 7.4E 2 1.1E 1 2.6E 1 8.8E 1 9.7E 1
	INTERPRO  UP_SEQ_FEATURE  INTERPRO  INTERPRO  SMART  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  SMART  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE	ephrin receptor signaling pathway  Galactose-binding domain-like  domain:SAM  Sterile alpha motif domain  Sterile alpha motif/pointed domain  SM01411  transmembrane-ephrin receptor activity  GPI-linked ephrin receptor activity  SAM  short sequence motif:PDZ-binding  compositionally biased region:Cys-rich  domain:Fibronectin type-III 2	RT		15 31 29 27 31 35 15 6 5 29 18 30 24	5.9E-6 3.9E-5 4.8E-5 9.1E-5 1.1E-4 3.0E-4 7.3E-4 9.1E-3 1.8E-2 4.9E-2 5.2E-2 1.2E-1 2.3E-1	2.1E0 2.2E0 2.2E0 2.0E0 1.9E0 2.4E0 4.0E0 4.3E0 1.4E0 1.6E0 1.3E0 1.2E0 1.2E0	1.4E-3 8.2E-4 3.0E-3 1.7E-3 4.2E-3 8.2E-3 7.2E-2 1.2E-1 2.9E-1 9.1E-1 1.0E0 1.0E0	4 1.3E-3 7.5E-4 2.9E-3 1.5E-3 3.8E-3 7.4E-3 6.4E-2 1.1E-1 2.6E-1 1 8.8E-1 9.7E-1 1 9.7E-1
	INTERPRO  UP_SEQ_FEATURE  INTERPRO  INTERPRO  SMART  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  SMART  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE	ephrin receptor signaling pathway  Galactose-binding domain-like  domain:SAM  Sterile alpha motif domain  Sterile alpha motif/pointed domain  SM01411  transmembrane-ephrin receptor activity  GPI-linked ephrin receptor activity  SAM  short sequence motif:PDZ-binding  compositionally biased region:Cys-rich  domain:Fibronectin type-III 2  domain:Fibronectin type-III 1  Fibronectin, type III  Insulin-like growth factor binding protein, N-	RT R		15 31 29 27 31 35 15 6 5 29 18 30 24 24	5.9E-6 3.9E-5 4.8E-5 9.1E-5 1.1E-4 3.0E-4 7.3E-4 9.1E-3 1.8E-2 4.9E-2 5.2E-2 1.2E-1 2.3E-1 2.4E-1	2.1E0 2.2E0 2.2E0 2.0E0 1.9E0 2.4E0 4.0E0 4.3E0 1.4E0 1.6E0 1.3E0 1.2E0 1.1E0	1.4E-3 8.2E-4 3.0E-3 1.7E-3 4.2E-3 8.2E-3 7.2E-2 1.2E-1 2.9E-1 9.1E-1 1.0E0 1.0E0 1.0E0	4 1.3E-3 7.5E-4 2.9E-3 1.5E-3 3.8E-3 7.4E-2 1.1E-1 2.6E-1 1 8.8E-1 9.7E-1 1 9.7E-1 1 8.8E-1
	INTERPRO  UP_SEQ_FEATURE  INTERPRO  INTERPRO  SMART  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  SMART  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO	ephrin receptor signaling pathway  Galactose-binding domain-like  domain:SAM  Sterile alpha motif domain  Sterile alpha motif/pointed domain  SM01411  transmembrane-ephrin receptor activity  GPI-linked ephrin receptor activity  SAM  short sequence motif:PDZ-binding  compositionally biased region:Cys-rich  domain:Fibronectin type-III 2  domain:Fibronectin type-III 1  Fibronectin, type III	RT R		15 31 29 27 31 35 15 6 5 29 18 30 24 24 38	5.9E-6 3.9E-5 4.8E-5 9.1E-5 1.1E-4 3.0E-4 7.3E-4 9.1E-3 1.8E-2 4.9E-2 5.2E-2 1.2E-1 2.3E-1 2.4E-1 2.7E-1 3.1E-1	2.1E0 2.2E0 2.2E0 2.0E0 1.9E0 2.4E0 4.0E0 4.3E0 1.4E0 1.6E0 1.3E0 1.2E0 1.1E0	1.4E-3 8.2E-4 3.0E-3 1.7E-3 4.2E-3 8.2E-3 7.2E-2 1.2E-1 2.9E-1 9.1E-1 1.0E0 1.0E0 1.0E0 9.6E-1 9.9E-1	4 1.3E <sub>3</sub> 7.5E <sub>4</sub> 2.9E <sub>3</sub> 1.5E <sub>3</sub> 3.8E <sub>3</sub> 7.4E <sub>2</sub> 1.1E <sub>1</sub> 2.6E <sub>1</sub> 1 9.7E <sub>1</sub> 1 9.7E <sub>1</sub> 1 9.7E <sub>1</sub> 1 9.7E <sub>1</sub> 1

not	ation Cluster 1	Enrichment Score: ?	G	<b>17</b>	Count	P_Value	Fold Change	Benjamiı	ni F
	BIOCARTA	<u>Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation</u>	<u>RT</u>	1	18	4.7E-5	2.4E0	9.2E-4	6 4
	BIOCARTA	Regulation of BAD phosphorylation	<u>RT</u>	i .	19	1.1E-4	2.3E0	1.6E-3	1
	BIOCARTA	<u>Transcription factor CREB and its extracellular signals</u>	<u>RT</u>		18	9.7E-4	2.1E0	7.8E-3	5
ot	ation Cluster 70	Enrichment Score: 3.59	G	<b>15</b>	Count	P_Value	Fold	Benjamiı	
	GOTERM_BP_DIRECT	nucleotide-binding oligomerization domain	<u>RT</u>	i	15	1.0E-5	3.6E0	4.0E-4	3
	GOTERM_BP_DIRECT	containing signaling pathway  I-kappaB kinase/NF-kappaB signaling	RT		23	1.8E-4	2.3E0	5.3E-3	5
	GOTERM_BP_DIRECT	TRIF-dependent toll-like receptor signaling	RT	_	13	1.1E-3		2.5E-2	2
	GOTERM_BP_DIRECT	pathway regulation of tumor necrosis factor-mediated							2
		signaling pathway	<u>RT</u>		13	1	2.6E0 Fold	4.5E-2	2
ot	ation Cluster 71  GOTERM_BP_DIRECT	Enrichment Score: 3.49	G		Count	P_Value	Change	•	ni F
		protein peptidyl-prolyl isomerization	<u>RT</u>	•	21	5.8E-6	2.9E0	2.7E-4	4
	UP_KEYWORDS	<u>Rotamase</u>	<u>RT</u>	•	18	7.6E-6	3.3E0	4.6E-5	3
	GOTERM_MF_DIRECT	peptidyl-prolyl cis-trans isomerase activity	<u>RT</u>	i	21	1.9E-5	2.7E0	3.3E-4	4
	UP_KEYWORDS	<u>Isomerase</u>	<u>RT</u>	1	35	1.0E-4	2.0E0	5.4E-4	4
	INTERPRO	<u>Cyclophilin-type peptidyl-prolyl cis-trans</u> isomerase, conserved site	<u>RT</u>	i .	12	1.4E-4	3.5E0	2.0E-3	1
	INTERPRO	Cyclophilin-like peptidyl-prolyl cis-trans isomerase domain	<u>RT</u>	1	12	6.0E-4	3.1E0	7.5E-3	6
	UP_SEQ_FEATURE	domain:PPIase cyclophilin-type	<u>RT</u>	1	11	1.2E-3	3.1E0	3.4E-2	3
	INTERPRO	Cyclophilin-type peptidyl-prolyl cis-trans	RT		11	1.8E-3	3.0E0	2.0E-2	1
	GOTERM_MF_DIRECT	<u>isomerase</u> <u>cyclosporin A binding</u>	RT	-	6		5.1E0	2.0E-2	1
	UP_KEYWORDS	<del></del>		•					3
	PIR_SUPERFAMILY	<u>Cyclosporin</u>	<u>RT</u>		5		4.9E0	4.6E-2	3
	FIR_SOFERFAMILI	peptidyl-prolyl cis-trans isomerase	<u>RT</u>	i	7	1.4E-2	3.1E0	3.6E-1	1
ot	ation Cluster 72	Enrichment Score: 3.33	G	<u> </u>	Count	P_Value	Fold Change	Benjamiı	_L
	GOTERM_MF_DIRECT	nucleotide binding	<u>RT</u>	=	96	4.2E-7	1.6E0	9.7E-6	6
	INTERPRO	RNA recognition motif domain	<u>RT</u>	•	63	1.0E-5	1.7E0	1.9E-4	1
	INTERPRO	Nucleotide-binding, alpha-beta plait	<u>RT</u>	•	67	1.3E-4	1.6E0	1.9E-3	1
	UP_SEQ_FEATURE	domain:RRM	<u>RT</u>	4	36	4.3E-4	1.8E0	1.3E-2	1 2
	UP_SEQ_FEATURE	domain:RRM 1	<u>RT</u>		32	1.9E-3	1.7E0	5.2E-2	5
	UP_SEQ_FEATURE	domain:RRM 2	<u>RT</u>	4	32	1.9E-3	1.7E0	5.2E-2	5
	UP_SEQ_FEATURE	domain:RRM 3	<u>RT</u>		16	2.8E-2	1.8E0	5.3E-1	5
	SMART	RRM	RT		62		1.2E0	4.6E-1	1
		_				1	Fold	1	1
ot	ation Cluster 73  GOTERM_BP_DIRECT	Enrichment Score: 3.27	G	-	Count	P_Value	Change		nı ı
	GOTERM_MF_DIRECT	ATP-dependent chromatin remodeling  RNA polymerase II distal enhancer sequence-	<u>RT</u>	•	13	1.1E-4	3.4E0	3.5E-3	3
		specific DNA binding	<u>RT</u>	•	23	6.0E-4	2.1E0	7.0E-3	3
	GOTERM_MF_DIRECT	<u>nucleosomal DNA binding</u>	<u>RT</u>	i	17	2.3E-3		2.3E-2	2
ot	ation Cluster 74	Enrichment Score: 3.17	G	<b>170</b>	Count	P_Value	Fold Change	Benjamii	
	GOTERM_CC_DIRECT	nuclear proteasome complex	<u>RT</u>	i	8	1.6E-5	6.4E0	2.9E-4	2
	GOTERM_CC_DIRECT	<u>proteasome regulatory particle, base</u> <u>subcomplex</u>	<u>RT</u>	1	9	1.0E-4	4.8E0	1.4E-3	1
	GOTERM_CC_DIRECT	cytosolic proteasome complex	<u>RT</u>	i .	8	1.8E-4	5.1E0	2.4E-3	2
	GOTERM_CC_DIRECT	proteasome accessory complex	<u>RT</u>		10	4.2E-4	3.7E0	4.6E-3	4
	INTERPRO	26S proteasome subunit P45	<u>RT</u>		6	5.7E-4	6.2E0	7.2E-3	6
	GOTERM_BP_DIRECT	protein catabolic process	RT		17		2.5E0	1.5E-2	1
	GOTERM_MF_DIRECT	proteasome-activating ATPase activity	RT	-	6		6.0E0	7.6E-3	2
	GOTERM_MF_DIRECT	· · · · · · · · · · · · · · · · · · ·							3
	GOTERM_BP_DIRECT	TBP-class protein binding	<u>RT</u>	•	11		3.1E0	1.1E-2	3
		positive regulation of RNA polymerase II transcriptional preinitiation complex assembly	<u>RT</u>	i	7	1.2E-3	4.6E0	2.8E-2	2
	GOTERM_BP_DIRECT	<u>positive regulation of proteasomal protein</u> <u>catabolic process</u>	<u>RT</u>	i	8	1.1E-2	3.0E0	1.5E-1	1
	GOTERM_BP_DIRECT	ER-associated ubiquitin-dependent protein catabolic process	<u>RT</u>	1	17	3.7E-2	1.7E0	3.8E-1	3
	ation Cluster 75		G	170		P_Value	Fold	Benjamii	

	tation Cluster 1	Enrichment Score: ?	G	· 🚾	Count	P_Value	Fold Change	Benjamin	i FDR
	UP_SEQ_FEATURE	domain:PI3K/PI4K	<u>RT</u>	i	15	3.6E-9		2.0E-7	2.0E
	INTERPRO	Phosphatidylinositol 3/4-kinase, conserved	<u>RT</u>		14	1.7E-8	5.4E0	5.0E-7	4.6E
	INTERPRO	<u>site</u> <u>Phosphatidylinositol 3-/4-kinase, catalytic</u>	RT		15	4.1E-8	4 9F0	1.1E-6	7 1.0E
	SMART	domain		_	15	8.6E-7		1.6E-5	6 1.4E
	INTERPRO	PI3Kc  Phosphoinositide 3-kinase, accessory (PIK)	<u>RT</u>						5 2.5E
	INTERPRO	domain  Phosphatidylinositol 3-kinase C2 (PI3K C2)	<u>RT</u>	•	9	1.5E-5	5.6E0	2.8E-4	4 3.1E
		<u>domain</u>	<u>RT</u>	•	8	1.9E-5	6.2E0	3.4E-4	4
	GOTERM_BP_DIRECT	<u>phosphatidylinositol-3-phosphate biosynthetic</u> <u>process</u>	RT	•	21	6.1E-5	2.5E0	2.0E-3	1.9E 3
	GOTERM_MF_DIRECT	1-phosphatidylinositol-3-kinase activity	<u>RT</u>	i	19	8.9E-5	2.6E0	1.3E-3	1.2E 3
	SMART	<u>PI3Ka</u>	<u>RT</u>	1	9	9.1E-5	4.1E0	1.1E-3	1.0E 3
	INTERPRO	Phosphatidylinositol 3-kinase Ras-binding (PI3K RBD) domain	<u>RT</u>	i .	7	1.1E-4	6.2E0	1.6E-3	1.5E 3
	INTERPRO	Phosphatidylinositol Kinase	<u>RT</u>	1	9	1.2E-4	4.6E0	1.8E-3	1.7E 3
	GOTERM_MF_DIRECT	1-phosphatidylinositol-4-phosphate 3-kinase	<u>RT</u>		7	1.3E-4	6.0E0	1.8E-3	1.6E
	SMART	<u>activity</u> <u>PI3K_C2</u>	RT		8	3.3E-4		3.9E-3	3 3.5E
_ _	GOTERM_CC_DIRECT			-					3 4.2E
	GOTERM_MF_DIRECT	phosphatidylinositol 3-kinase complex	RT		9	4.5E-4		4.9E-3	3 2.8E
	SMART	phosphatidylinositol 3-kinase activity	<u>RT</u>	•	5	3.4E-3	6.0E0	3.2E-2	2
		PI3K rbd	<u>RT</u>	i	6	4.2E-3	4.1E0	4.0E-2	3.6E 2
	INTERPRO	<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	1.1E 1
	GOTERM_BP_DIRECT	phosphatidylinositol biosynthetic process	<u>RT</u>	1	16	5.4E-2	1.6E0	4.8E-1	4.6E 1
	SMART	<u>PI3K_p85B</u>	<u>RT</u>	i .	3	1.5E-1	4.1E0	6.5E-1	5.8E
	KEGG_PATHWAY	Phosphatidylinositol signaling system	<u>RT</u>	1	18	7.1E-1	9.6E-1	1.0E0	7.1E
	KEGG_PATHWAY	<u>Inositol phosphate metabolism</u>	<u>RT</u>		13	7.3E-1	9.6E-1	1.0E0	7.3E
_ 	UP_SEQ_FEATURE	domain:PX	RT		4	9.8F-1	5.7E-1	1.0F0	1 9.8E
_ _	INTERPRO			-	5				1 9.8E
	GOTERM_MF_DIRECT	Phox homologous domain  phosphatidylinositol binding	RT RT		7	1.0E0	5.6E-1 4.9E-1		1 1.0E
	SMART	<u>PX</u>	RT	i	4	1.0E0	3.6E-1		1.0E
Annot	tation Cluster 76	Enrichment Score: 3.17	G		Count	P_Value	Fold Change	Benjamin	
	GOTERM_BP_DIRECT	protein K6-linked ubiquitination	<u>RT</u>	1	8	2.6E-5	5.9E0	9.6E-4	9.1E 4
	GOTERM_BP_DIRECT						5.9E0	6.5E-2	6.2E 2
		protein K29-linked ubiquitination	<u>RT</u>	i	5	3.5E-3			
	GOTERM_BP_DIRECT	protein K29-linked ubiquitination  protein K27-linked ubiquitination	RT RT	1	5 5	3.5E-3 3.5E-3		6.5E-2	6.2E 2
Annot	GOTERM_BP_DIRECT			_			5.9E0	Danie wie	1
Annot		protein K27-linked ubiquitination	<u>RT</u>	i	5	3.5E-3 P_Value	5.9E0 Fold	Danie wie	2
Annot	tation Cluster 77	protein K27-linked ubiquitination  Enrichment Score: 3.13	RT G	i ***	5 Count	3.5E-3 P_Value	5.9E0 Fold Change	Benjamin	2 i FDR 2.0E 4
Annot	tation Cluster 77 BIOCARTA	protein K27-linked ubiquitination  Enrichment Score: 3.13  Inhibition of Cellular Proliferation by Gleevec  EGF Signaling Pathway	RT G RT RT		5 Count 19 21	3.5E-3  P_Value  7.1E-6  9.1E-6	5.9E0  Fold Change 2.5E0 2.4E0	<b>Benjamin</b> 2.9E-4 2.9E-4	2 i FDR 2.0E 4 2.0E 4
Annot	tation Cluster 77  BIOCARTA  BIOCARTA	protein K27-linked ubiquitination  Enrichment Score: 3.13  Inhibition of Cellular Proliferation by Gleevec  EGF Signaling Pathway  PDGF Signaling Pathway	RT G RT RT RT		5 Count 19 21 21	3.5E-3  P_Value  7.1E-6  9.1E-6  2.2E-5	5.9E0 Fold Change 2.5E0 2.4E0 2.3E0	2.9E-4 2.9E-4 5.9E-4	2 .0E 4 .0E 4
Annot	BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA	protein K27-linked ubiquitination  Enrichment Score: 3.13  Inhibition of Cellular Proliferation by Gleevec  EGF Signaling Pathway  PDGF Signaling Pathway  IL-2 Receptor Beta Chain in T cell Activation	RT G RT RT RT RT		5 Count 19 21 21 26	3.5E-3  P_Value  7.1E-6  9.1E-6  2.2E-5  3.8E-5	5.9E0  Fold Change 2.5E0 2.4E0 2.3E0 2.1E0	2.9E-4 2.9E-4 5.9E-4 9.2E-4	2 2.0E 4 2.0E 4 4.0E 4 6.2E
Annot	BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA	protein K27-linked ubiquitination  Enrichment Score: 3.13  Inhibition of Cellular Proliferation by Gleevec  EGF Signaling Pathway  PDGF Signaling Pathway  IL-2 Receptor Beta Chain in T cell Activation  IGF-1 Signaling Pathway	RT G RT RT RT RT RT		5 Count 19 21 21 26 17	3.5E-3  P_Value  7.1E-6  9.1E-6  2.2E-5  3.8E-5  4.3E-5	5.9E0  Fold Change 2.5E0 2.4E0 2.3E0 2.1E0 2.5E0	2.9E-4 2.9E-4 5.9E-4 9.2E-4	2.0E 4.0E 4.0E 4.0E 4.0E 4.0E 4.0E 4.0E
Annot	BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA	protein K27-linked ubiquitination  Enrichment Score: 3.13  Inhibition of Cellular Proliferation by Gleevec  EGF Signaling Pathway  PDGF Signaling Pathway  IL-2 Receptor Beta Chain in T cell Activation	RT G RT RT RT RT		5 Count 19 21 21 26	3.5E-3  P_Value  7.1E-6  9.1E-6  2.2E-5  3.8E-5	5.9E0  Fold Change 2.5E0 2.4E0 2.3E0 2.1E0 2.5E0	2.9E-4 2.9E-4 5.9E-4 9.2E-4	2.0E 4 2.0E 4 4.0E 4 6.2E 4 6.2E 4
Annot	BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA	protein K27-linked ubiquitination  Enrichment Score: 3.13  Inhibition of Cellular Proliferation by Gleevec  EGF Signaling Pathway  PDGF Signaling Pathway  IL-2 Receptor Beta Chain in T cell Activation  IGF-1 Signaling Pathway	RT G RT RT RT RT RT		5 Count 19 21 21 26 17	3.5E-3  P_Value  7.1E-6  9.1E-6  2.2E-5  3.8E-5  4.3E-5	5.9E0  Fold Change 2.5E0 2.4E0 2.3E0 2.1E0 2.5E0 2.3E0	2.9E-4 2.9E-4 5.9E-4 9.2E-4	2.0E 4 2.0E 4 4.0E 4 6.2E 4 6.2E 4
Annot	BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA	protein K27-linked ubiquitination  Enrichment Score: 3.13  Inhibition of Cellular Proliferation by Gleevec  EGF Signaling Pathway  PDGF Signaling Pathway  IL-2 Receptor Beta Chain in T cell Activation  IGF-1 Signaling Pathway  Growth Hormone Signaling Pathway	RT  RT  RT  RT  RT  RT  RT		5 Count  19 21 21 26 17 20	3.5E-3  P_Value  7.1E-6  9.1E-6  2.2E-5  3.8E-5  4.3E-5  5.1E-5  1.1E-4	5.9E0  Fold Change 2.5E0 2.4E0 2.3E0 2.1E0 2.5E0 2.3E0	2.9E-4 2.9E-4 5.9E-4 9.2E-4 9.2E-4 1.6E-3	2.0E 4 2.0E 4 4.0E 4 6.2E 4 6.2E 4 1.1E 3
Annot	BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA	Enrichment Score: 3.13  Inhibition of Cellular Proliferation by Gleevec  EGF Signaling Pathway  PDGF Signaling Pathway  IL-2 Receptor Beta Chain in T cell Activation  IGF-1 Signaling Pathway  Growth Hormone Signaling Pathway  IL 2 signaling pathway	RT  RT  RT  RT  RT  RT  RT  RT  RT		5 Count 19 21 21 26 17 20 17	3.5E-3  P_Value  7.1E-6  9.1E-6  2.2E-5  3.8E-5  4.3E-5  5.1E-5  1.1E-4  1.1E-4	5.9E0  Fold Change 2.5E0 2.4E0 2.3E0 2.1E0 2.5E0 2.3E0 2.4E0	2.9E-4 2.9E-4 5.9E-4 9.2E-4 9.2E-4 1.6E-3 1.6E-3	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
	BIOCARTA	protein K27-linked ubiquitination  Enrichment Score: 3.13  Inhibition of Cellular Proliferation by Gleevec  EGF Signaling Pathway  PDGF Signaling Pathway  IL-2 Receptor Beta Chain in T cell Activation  IGF-1 Signaling Pathway  Growth Hormone Signaling Pathway  IL 2 signaling pathway  TPO Signaling Pathway  Angiotensin II mediated activation of JNK	RT  RT  RT  RT  RT  RT  RT  RT  RT  RT		5 Count  19 21 21 26 17 20 17 18	3.5E-3  P_Value  7.1E-6  9.1E-6  2.2E-5  3.8E-5  4.3E-5  5.1E-5  1.1E-4  1.1E-4	5.9E0  Fold Change 2.5E0 2.4E0 2.3E0 2.1E0 2.3E0 2.4E0 2.3E0 2.1E0 2.1E0	2.9E-4 2.9E-4 5.9E-4 9.2E-4 9.2E-4 1.6E-3 1.6E-3	2.0E 4 2.0E 4 4.0E 4 6.2E 4 1.1E 3 1.6E 3
	BIOCARTA	protein K27-linked ubiquitination  Enrichment Score: 3.13  Inhibition of Cellular Proliferation by Gleevec  EGF Signaling Pathway  PDGF Signaling Pathway  IL-2 Receptor Beta Chain in T cell Activation  IGF-1 Signaling Pathway  Growth Hormone Signaling Pathway  IL 2 signaling pathway  TPO Signaling Pathway  Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling	RT  RT  RT  RT  RT  RT  RT  RT  RT  RT		5 Count  19 21 21 26 17 20 17 18 22	3.5E-3  P_Value  7.1E-6  9.1E-6  2.2E-5  3.8E-5  4.3E-5  5.1E-5  1.1E-4  1.1E-4  1.9E-4	5.9E0  Fold Change 2.5E0 2.4E0 2.3E0 2.1E0 2.3E0 2.4E0 2.3E0 2.1E0 2.3E0 2.1E0	2.9E-4 2.9E-4 5.9E-4 9.2E-4 9.2E-4 1.6E-3 1.6E-3 2.4E-3	2 2 2 2 4 2 2 0 6 4 4 6 2 6 4 6 6 2 6 4 1 1 1 6 6 3 1 1 8 6 3 1 1 8 6 3 1 1 8 6 3 1 1 8 6 3 1 1 8 6 3 1 1 8 6 3 1 1 8 6 3 1 1 8 6 3 1 1 8 6 3 1 1 8 6 3 1 1 8 6 3 1 1 8 6 3 1 1 8 6 3 1 1 8 6 6 3 1 1 8 6 6 3 1 1 8 6 6 3 1 1 8 6 6 3 1 1 8 6 6 3 1 1 8 6 6 3 1 1 8 6 6 3 1 1 8 6 6 3 1 1 8 6 6 3 1 1 8 6 6 3 1 1 8 6 6 3 1 1 8 6 6 3 1 1 8 6 6 3 1 1 8 6 6 3 1 1 8 6 6 3 1 1 8 6 6 3 1 1 8 6 6 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	BIOCARTA	Enrichment Score: 3.13  Inhibition of Cellular Proliferation by Gleevec  EGF Signaling Pathway  PDGF Signaling Pathway  IL-2 Receptor Beta Chain in T cell Activation  IGF-1 Signaling Pathway  Growth Hormone Signaling Pathway  IL 2 signaling pathway  TPO Signaling Pathway  Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling  Insulin Signaling Pathway  IL 6 signaling pathway  Signaling of Hepatocyte Growth Factor	RT  RT  RT  RT  RT  RT  RT  RT  RT  RT		5 Count  19 21 21 26 17 20 17 18 22 16 16	3.5E-3  P_Value  7.1E-6  9.1E-6  2.2E-5  3.8E-5  4.3E-5  1.1E-4  1.1E-4  1.9E-4  2.6E-4  2.6E-4	5.9E0  Fold Change 2.5E0 2.4E0 2.3E0 2.1E0 2.3E0 2.4E0 2.3E0 2.1E0 2.3E0 2.1E0 2.3E0	2.9E-4 2.9E-4 5.9E-4 9.2E-4 9.2E-4 1.6E-3 1.6E-3 2.4E-3 2.7E-3	2 2 2 3 4 2 2 0 6 4 4 6 2 6 4 6 2 6 4 1 1 1 6 3 1 1 6 6 3 1 1 8 6 3 1 1 8 6 3 2 1 1 8 6 3 2 1 1 8 6 3 2 1 1 8 6 3 2 1 1 8 6 3 3 2 1 1 8 6 3 3 2 1 1 8 6 3 3 2 1 1 8 6 3 3 2 1 1 8 6 3 3 2 1 1 8 6 3 3 2 1 1 8 6 3 3 2 1 1 8 6 3 3 2 1 1 8 6 3 3 2 1 1 8 6 3 3 3 2 1 1 8 6 3 3 3 2 1 1 8 6 3 3 3 3 2 1 1 8 6 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
Annot	BIOCARTA	Enrichment Score: 3.13  Inhibition of Cellular Proliferation by Gleevec  EGF Signaling Pathway  PDGF Signaling Pathway  IL-2 Receptor Beta Chain in T cell Activation  IGF-1 Signaling Pathway  Growth Hormone Signaling Pathway  IL 2 signaling pathway  TPO Signaling Pathway  Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling  Insulin Signaling Pathway  IL 6 signaling pathway  Signaling of Hepatocyte Growth Factor Receptor	RT  RT  RT  RT  RT  RT  RT  RT  RT  RT		5 Count  19 21 21 26 17 20 17 18 22 16 16 16 23	3.5E-3  P_Value  7.1E-6  9.1E-6  2.2E-5  3.8E-5  4.3E-5  1.1E-4  1.1E-4  1.9E-4  2.6E-4  2.6E-4  3.2E-4	5.9E0  Fold Change 2.5E0 2.4E0 2.3E0 2.1E0 2.3E0 2.4E0 2.3E0 2.3E0 2.1E0 2.3E0 2.1E0 2.3E0 2.3E0	2.9E-4 2.9E-4 9.2E-4 9.2E-4 1.6E-3 1.6E-3 2.4E-3 2.7E-3 3.1E-3	2 2 2 3 4 2 2 0 6 4 4 6 2 6 4 6 2 6 4 1 1 1 6 3 1 1 6 6 3 1 1 8 6
	BIOCARTA	Enrichment Score: 3.13  Inhibition of Cellular Proliferation by Gleevec  EGF Signaling Pathway  PDGF Signaling Pathway  IL-2 Receptor Beta Chain in T cell Activation  IGF-1 Signaling Pathway  Growth Hormone Signaling Pathway  IL 2 signaling pathway  TPO Signaling Pathway  Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling  Insulin Signaling Pathway  IL 6 signaling pathway  Signaling of Hepatocyte Growth Factor Receptor  Role of ERBB2 in Signal Transduction and Oncology	RT  RT  RT  RT  RT  RT  RT  RT  RT  RT		5 Count  19 21 21 26 17 20 17 18 22 16 16 23 16	3.5E-3  P_Value  7.1E-6  9.1E-6  2.2E-5  3.8E-5  4.3E-5  1.1E-4  1.1E-4  1.9E-4  2.6E-4  2.6E-4  3.2E-4  1.2E-3	5.9E0  Fold Change 2.5E0 2.4E0 2.3E0 2.1E0 2.3E0 2.4E0 2.3E0 2.3E0 2.1E0 2.3E0 2.1E0 2.3E0 2.1E0 2.3E0 2.1E0	2.9E-4 2.9E-4 9.2E-4 9.2E-4 1.6E-3 1.6E-3 2.7E-3 2.7E-3 3.1E-3 9.0E-3	2 2 2 4 2 2 0 6 4 4 6 2 6 4 6 2 6 4 6 3 1 . 1 6 6 3 1 . 8 6 3 1 . 8 6 3 2 . 1 6 3 3 6 . 1 6 3 3 6 . 1 6 6 3 3 6 . 1 6 6 3 3 6 . 1 6 6 3 3 6 . 1 6 6 3 3 6 . 1 6 6 3 3 6 . 1 6 6 3 3 6 . 1 6 6 3 3 6 . 1 6 6 3 3 6 . 1 6 6 3 3 6 . 1 6 6 3 3 6 . 1 6 6 3 3 6 . 1 6 6 3 3 6 . 1 6 6 3 3 6 . 1 6 6 3 3 6 . 1 6 6 3 3 6 . 1 6 6 3 6 3 6 . 1 6 6 3 3 6 . 1 6 6 3 6 3 6 . 1 6 6 3 6 3 6 . 1 6 6 3 6 6 . 1 6 6 3 6 3 6 . 1 6 6 3 6 6 . 1 6 6 3 6 6 . 1 6 6 3 6 6 . 1 6 6 3 6 6 . 1 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
	BIOCARTA	Enrichment Score: 3.13  Inhibition of Cellular Proliferation by Gleevec  EGF Signaling Pathway  PDGF Signaling Pathway  IL-2 Receptor Beta Chain in T cell Activation  IGF-1 Signaling Pathway  Growth Hormone Signaling Pathway  IL 2 signaling pathway  TPO Signaling Pathway  Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling  Insulin Signaling Pathway  IL 6 signaling pathway  Signaling of Hepatocyte Growth Factor Receptor  Role of ERBB2 in Signal Transduction and	RT  RT  RT  RT  RT  RT  RT  RT  RT  RT		5 Count  19 21 21 26 17 20 17 18 22 16 16 16 23	3.5E-3  P_Value  7.1E-6  9.1E-6  2.2E-5  3.8E-5  4.3E-5  1.1E-4  1.1E-4  1.9E-4  2.6E-4  2.6E-4  3.2E-4	5.9E0  Fold Change 2.5E0 2.4E0 2.3E0 2.1E0 2.3E0 2.4E0 2.3E0 2.3E0 2.1E0 2.3E0 2.1E0 2.3E0 2.1E0 2.3E0 2.1E0	2.9E-4 2.9E-4 9.2E-4 9.2E-4 1.6E-3 1.6E-3 2.4E-3 2.7E-3 3.1E-3	2 2 2 3 4 2 2 0 6 4 4 6 2 6 4 6 2 6 4 6 3 1 1 6 6 3 1 8 6 3 1 8 6 3 6 1 6 3 6 7 6 7
	BIOCARTA	Enrichment Score: 3.13  Inhibition of Cellular Proliferation by Gleevec  EGF Signaling Pathway  PDGF Signaling Pathway  IL-2 Receptor Beta Chain in T cell Activation  IGF-1 Signaling Pathway  Growth Hormone Signaling Pathway  IL 2 signaling pathway  TPO Signaling Pathway  Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling  Insulin Signaling Pathway  IL 6 signaling pathway  Signaling of Hepatocyte Growth Factor Receptor  Role of ERBB2 in Signal Transduction and Oncology	RT  RT  RT  RT  RT  RT  RT  RT  RT  RT		5 Count  19 21 21 26 17 20 17 18 22 16 16 23 16	3.5E-3  P_Value  7.1E-6  9.1E-6  2.2E-5  3.8E-5  4.3E-5  1.1E-4  1.1E-4  1.9E-4  2.6E-4  2.6E-4  3.2E-4  1.2E-3	5.9E0  Fold Change 2.5E0 2.4E0 2.3E0 2.1E0 2.3E0 2.4E0 2.3E0 2.3E0 2.1E0 2.3E0 2.1E0 2.3E0 2.3E0 2.3E0 2.3E0	2.9E-4 2.9E-4 9.2E-4 9.2E-4 1.6E-3 1.6E-3 2.7E-3 2.7E-3 3.1E-3 9.0E-3	2 2 2 3 4 2 2 0 6 4 4 6 2 6 4 6 2 6 4 6 3 1 1 6 6 3 1 8 6 3 1 8 6 3 6 1 6 3 6 7 6 7
	BIOCARTA	Enrichment Score: 3.13  Inhibition of Cellular Proliferation by Gleevec  EGF Signaling Pathway  PDGF Signaling Pathway  IL-2 Receptor Beta Chain in T cell Activation  IGF-1 Signaling Pathway  Growth Hormone Signaling Pathway  IL 2 signaling pathway  TPO Signaling Pathway  Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling  Insulin Signaling Pathway  IL 6 signaling pathway  Signaling of Hepatocyte Growth Factor Receptor  Role of ERBB2 in Signal Transduction and Oncology  EPO Signaling Pathway	RT  RT  RT  RT  RT  RT  RT  RT  RT  RT		5 Count  19 21 21 26 17 20 17 18 22 16 16 23 16 14	3.5E-3  P_Value  7.1E-6  9.1E-6  2.2E-5  3.8E-5  4.3E-5  1.1E-4  1.1E-4  1.9E-4  2.6E-4  2.6E-4  3.2E-4  1.2E-3  1.3E-3	5.9E0  Fold Change 2.5E0 2.4E0 2.3E0 2.1E0 2.3E0 2.4E0 2.3E0 2.3E0 2.1E0 2.3E0 2.1E0 2.3E0 2.3E0 2.3E0 2.0E0 2.1E0	2.9E-4 2.9E-4 9.2E-4 9.2E-4 1.6E-3 1.6E-3 2.7E-3 2.7E-3 3.1E-3 9.0E-3 9.8E-3	2 2 2 4 2 2 0 6 4 4 6 2 6 4 6 2 6 4 6 3 1 . 1 6 6 3 1 . 8 6 3 1 . 8 6 3 2 . 1 6 3 6 . 7 6 3 8 . 5 6

Ammata	otion Charton 4	Furrishment Seems 2	<u>~</u>	<b>199</b>	Count	D. Value	Fold	Danismisi.	FDD
	BIOCARTA	Enrichment Score: ?	G	-	Count	P_Value	Change		1.6E
	BIOCARTA	Fc Epsilon Receptor I Signaling in Mast Cells	<u>RT</u>	•	22	4.1E-3		2.3E-2	2 1.7E
		T Cell Receptor Signaling Pathway	<u>RT</u>	•	24	4.4E-3	1.7E0	2.4E-2	2
	BIOCARTA	<u>IL 3 signaling pathway</u>	<u>RT</u>	i	11	6.5E-3	2.3E0	3.2E-2	2.2E 2
	BIOCARTA	Nerve growth factor pathway (NGF)	<u>RT</u>	i	13	9.7E-3	2.0E0	4.2E-2	2.9E 2
	BIOCARTA	Integrin Signaling Pathway	<u>RT</u>	i e	20	1.2E-2	1.7E0	5.0E-2	3.4E 2
	BIOCARTA	fMLP induced chemokine gene expression in HMC-1 cells	<u>RT</u>	i .	19	2.7E-2	1.6E0	9.1E-2	6.1E 2
	BIOCARTA	Sprouty regulation of tyrosine kinase signals	<u>RT</u>	i .	11	3.5E-2	1.9E0	1.0E-1	7.0E 2
	BIOCARTA	Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia	<u>RT</u>	i .	11	2.2E-1	1.4E0	4.5E-1	3.1E
Annota	ition Cluster 78	Enrichment Score: 3.11	G	· · ·	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	compositionally biased region:Arg/Ser-rich (RS domain)	<u>RT</u>	i	12	7.8E-6	4.5E0	3.1E-4	3.0E 4
	UP_SEQ_FEATURE	compositionally biased region:Gly-rich (hinge	<u>RT</u>	1	6	1.1E-3	5.8E0	3.1E-2	3.0E
	GOTERM_BP_DIRECT	region) mRNA splice site selection	RT		7	5.3E-2		4.8E-1	2 4.5E
Annota	ition Cluster 79	Enrichment Score: 3.07	G	-	Count	1	Fold	Ronjamini	1 EDP
	GOTERM_MF_DIRECT			_	22	P_Value	Change	3.3E-6	2.9E
	GOTERM_BP_DIRECT	histone deacetylase activity	<u>RT</u>	•		1.3E-7	3.4E0		6 2.2E
	UP_SEQ_FEATURE	histone deacetylation	<u>RT</u>	•	22			2.4E-4	4 2.9E
		region of interest:Histone deacetylase	<u>RT</u>	•	9	7.3E-6	6.1E0	3.0E-4	4
	INTERPRO	Histone deacetylase domain	<u>RT</u>		10	1.0E-5	5.2E0	1.9E-4	1.7E 4
	GOTERM_MF_DIRECT	NAD-dependent histone deacetylase activity (H3-K14 specific)	<u>RT</u>	i	10	1.4E-5	5.0E0	2.6E-4	2.3E 4
	GOTERM_MF_DIRECT	protein deacetylase activity	<u>RT</u>	•	9	2.0E-5	5.4E0	3.4E-4	3.0E 4
	GOTERM_BP_DIRECT	histone H3 deacetylation	<u>RT</u>	i .	13	3.4E-5	3.7E0	1.2E-3	1.1E 3
	INTERPRO	Histone deacetylase superfamily	<u>RT</u>	i .	10	6.7E-5	4.4E0	1.1E-3	1.0E
	GOTERM_BP_DIRECT	protein deacetylation	<u>RT</u>	i .	8	2.9E-4	4.7E0	8.0E-3	7.6E
	GOTERM_CC_DIRECT	histone deacetylase complex	<u>RT</u>	i e	15	6.7E-4	2.6E0	7.0E-3	6.2E
	GOTERM_BP_DIRECT	regulation of gene expression, epigenetic	<u>RT</u>		8	4.4E-3	3.4E0	7.7E-2	7.3E
	GOTERM_BP_DIRECT	histone H4 deacetylation	<u>RT</u>		6	9.4E-3	4.0E0	1.4E-1	2 1.3E
	GOTERM_BP_DIRECT	peptidyl-lysine deacetylation	RT		5	1.8E-2		2.3E-1	1 2.2E
	INTERPRO				4				1 2.2E
	GOTERM_BP_DIRECT	Histone deacetylase class II, eukaryotic	<u>RT</u>			3.2E-2		2.4E-1	1 3.7E
	PIR_SUPERFAMILY	negative regulation of myotube differentiation			7	4.0E-2		3.9E-1	1 6.1E
		Chromatin structure and dynamics /	<u>RT</u>	i	4	4.8E-2	4.3E0	6.2E-1	1
	COG_ONTOLOGY	Chromatin structure and dynamics / Secondary metabolites biosynthesis, transport, and catabolism	<u>RT</u>	i .	7	4.8E-2	2.2E0	5.0E-1	5.0E 1
	INTERPRO	Histone deacetylase	<u>RT</u>	i e	3	1.2E-1	4.6E0	6.1E-1	5.6E
	INTERPRO	Histone deacetylase, glutamine rich N-	RT		3	1.2E-1	4.6E0	6.1E-1	5.6E
	PIR_SUPERFAMILY	terminal domain  histone deacetylase class I, eukaryotic type	RT		3	1.6E-1		1.0E0	1 9.9E
Annota	ition Cluster 80	Enrichment Score: 3.07	G	· 	Count	P_Value	Fold	Barrianiai	1 FDR
	UP_SEQ_FEATURE	domain:Pre-SET	RT	i	7	6.1E-5	Change 6.8E0	2.1E-3	2.0E
	INTERPRO	Pre-SET domain	RT.		7	1.1E-4		1.6E-3	3 1.5E
	KEGG_PATHWAY								3 8.8E
	SMART	Lysine degradation	<u>RT</u>		21		2.1E0		4 1.2E
		PreSET	<u>RT</u>	i	7	1.2E-3	4.1E0	1.3E-2	2
	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K9 specific)	<u>RT</u>	i	5	3.4E-3	6.0E0	3.2E-2	2.8E 2
	GOTERM_BP_DIRECT	histone H3-K9 methylation	<u>RT</u>	i	4	1.7E-2		2.2E-1	2.1E 1
Annota		Enrichment Score: 3.06	G	<b>™</b>	Count	P_Value	Fold Change	Benjamini	<u> </u>
	ition Cluster 81			_		1.9E-			1.1E
	up_SEQ_FEATURE	domain:Post-SET	<u>RT</u>	i	15	10	6.4E0	1.2E-8	8
		domain:Post-SET  Post-SET domain	<u>RT</u> <u>RT</u>		15			1.2E-8 5.0E-7	
	UP_SEQ_FEATURE					10	5.4E0		4.6E 7
	UP_SEQ_FEATURE INTERPRO	Post-SET domain	<u>RT</u>	•	14	10 1.7E-8	5.4E0 3.5E0	5.0E-7	4.6E 7 1.1E 3
	UP_SEQ_FEATURE INTERPRO SMART	Post-SET domain  PostSET	RT RT	i i	14 11	10 1.7E-8 1.0E-4 3.1E-4	5.4E0 3.5E0	5.0E-7 1.3E-3 3.5E-3	4.6E 7 1.1E 3 3.1E

	ation Cluster 1	Enrichment Score: ?	G	<b>17</b>	Count	P_Value	Fold	Benjamin	i ENP
	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K4					Change		1.1E-
	UP_SEQ_FEATURE	specific)	<u>RT</u>	•	10	1.2E-3		1.2E-2	2 1.9E-
		zinc finger region:PHD-type 2	<u>RT</u>	•	11	8.2E-3	2.5E0	2.0E-1	1
	UP_SEQ_FEATURE	zinc finger region:PHD-type 3	<u>RT</u>	i	6	9.0E-3	4.1E0	2.1E-1	2.0E- 1
	UP_SEQ_FEATURE	zinc finger region:PHD-type 1	<u>RT</u>	1	11	1.7E-2	2.3E0	3.4E-1	3.3E- 1
	INTERPRO	<u>FY-rich, N-terminal</u>	<u>RT</u>	i	4	3.2E-2	5.0E0	2.4E-1	2.2E- 1
	INTERPRO	<u>FY-rich, C-terminal</u>	<u>RT</u>	i .	4	3.2E-2	5.0E0	2.4E-1	2.2E- 1
	SMART	<u>FYRN</u>	<u>RT</u>	i .	4	9.8E-2	3.3E0	4.9E-1	4.4E- 1
	SMART	<u>FYRC</u>	<u>RT</u>	i	4	9.8E-2	3.3E0	4.9E-1	4.4E-
	GOTERM_CC_DIRECT	MLL3/4 complex	<u>RT</u>	1	4	1.6E-1	2.8E0	6.4E-1	5.6E-
Annota	ation Cluster 82	Enrichment Score: 3.01	G	17	Count	P_Value	Fold	Benjamin	1 i FDR
	GOTERM_CC_DIRECT	proteasome regulatory particle, base	RT	ī	9	1.0E-4	Change 4.8E0	1.4E-3	1.2E-
	GOTERM_BP_DIRECT	subcomplex antigen processing and presentation of							3 5.0E-
		<u>exogenous peptide antigen via MHC class I,</u> <u>TAP-dependent</u>	<u>RT</u>	•	21	2.7E-3	2.0E0	5.3E-2	2
	GOTERM_CC_DIRECT	proteasome regulatory particle	<u>RT</u>	i .	7	3.4E-3	4.0E0	2.9E-2	2.5E- 2
Annota	ation Cluster 83	Enrichment Score: 3	G	17	Count	P_Value	Fold Change	Benjamin	i FDR
	UP_SEQ_FEATURE	region of interest:S-adenosyl-L-methionine binding	<u>RT</u>	1	16	5.3E-5	-	1.9E-3	1.8E- 3
	INTERPRO	Bacterial Fmu (Sun)/eukaryotic nucleolar NOL1/Nop2p	<u>RT</u>	i	7	9.4E-4	4.8E0	1.1E-2	1.0E- 2
	INTERPRO	RNA (C5-cytosine) methyltransferase	<u>RT</u>		6	4.0E-3	4.6E0	4.2E-2	3.8E-
	UP_SEQ_FEATURE	binding site:S-adenosyl-L-methionine	RT		16	5.2E-3		1.3E-1	2 1.3E-
Annota	ation Cluster 94		G	-		1	Fold	Panjamin	1 EDB
	ation Cluster 84  INTERPRO	Enrichment Score: 2.99			Count	P_Value	Change		1.1E-
	INTERPRO	<u>Translation protein SH3-like domain</u>	<u>RT</u>	1	11	6.3E-6		1.2E-4	4 1.1E-
		<u>KOW</u>	<u>RT</u>	•	8	7.5E-5	5.5E0	1.2E-3	3
	SMART	KOW	<u>RT</u>	i	5	3.5E-2	3.4E0	2.4E-1	2.1E- 1
	INTERPRO	Ribosomal protein L24/L26, conserved site	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E- 1
Annota	ation Cluster 85	Enrichment Score: 2.86	G	<b>17</b>	Count	P_Value	Fold Change	Benjamin	i FDR
	UP_KEYWORDS	Nucleosome core	<u>RT</u>	1	31	4.5E-6	2.4E0	2.8E-5	2.2E- 5
	GOTERM_BP_DIRECT	<u>chromatin silencing</u>	<u>RT</u>	i	17	1.9E-3	2.2E0	4.0E-2	3.8E- 2
	INTERPRO	Histone H2A	<u>RT</u>	i	11		2 6E0	5.3E-2	4.9E-
					11	5.1E-3	2.000		
	SMART	<u>H2A</u>	<u>RT</u>	i de la companya de	11	5.1E-3 8.1E-2		4.5E-1	2 4.0E-
	SMART ation Cluster 86	H2A Enrichment Score: 2.86	<u>RT</u>			8.1E-2	1.7E0	4.5E-1	2 4.0E- 1
Annota				<b>17</b>	11		1.7E0 Fold Change	4.5E-1	2 4.0E- 1 i <b>FDR</b> 2.5E-
Annota	ation Cluster 86	Enrichment Score: 2.86  protein peptidyl-prolyl isomerization	G RT	i	Count	8.1E-2 P_Value 5.8E-6	1.7E0 Fold Change 2.9E0	4.5E-1  Benjamin  2.7E-4	2 4.0E- 1 i FDR 2.5E- 4 3.6E-
Annota	ation Cluster 86  GOTERM_BP_DIRECT	Enrichment Score: 2.86  protein peptidyl-prolyl isomerization  Rotamase	G RT RT	i i	11 Count 21 18	8.1E-2  P_Value  5.8E-6  7.6E-6	1.7E0 Fold Change 2.9E0 3.3E0	4.5E-1  Benjamin  2.7E-4  4.6E-5	2 4.0E- 1 <b>FDR</b> 2.5E- 4
Annota	ation Cluster 86  GOTERM_BP_DIRECT  UP_KEYWORDS  GOTERM_MF_DIRECT	Enrichment Score: 2.86  protein_peptidyl-prolyl isomerization  Rotamase  peptidyl-prolyl cis-trans isomerase activity	G RT RT RT		11 Count 21 18 21	8.1E-2  P_Value  5.8E-6  7.6E-6  1.9E-5	1.7E0 Fold Change 2.9E0 3.3E0 2.7E0	4.5E-1  Benjamin  2.7E-4  4.6E-5  3.3E-4	2 4.0E-1 1 FDR 2.5E-4 3.6E-5 2.9E-4
Annota	ation Cluster 86  GOTERM_BP_DIRECT  UP_KEYWORDS  GOTERM_MF_DIRECT  UP_KEYWORDS	Enrichment Score: 2.86  protein peptidyl-prolyl isomerization  Rotamase  peptidyl-prolyl cis-trans isomerase activity  Isomerase	G RT RT RT RT	i i	11 Count 21 18	8.1E-2  P_Value  5.8E-6  7.6E-6	1.7E0 Fold Change 2.9E0 3.3E0 2.7E0	4.5E-1  Benjamin  2.7E-4  4.6E-5  3.3E-4  5.4E-4	2 4.0E-1 1 FDR 2.5E-4 3.6E-5 2.9E-4 4.2E-4
Annota	ation Cluster 86  GOTERM_BP_DIRECT  UP_KEYWORDS  GOTERM_MF_DIRECT  UP_KEYWORDS  INTERPRO	Enrichment Score: 2.86  protein_peptidyl-prolyl isomerization  Rotamase  peptidyl-prolyl cis-trans isomerase activity	G RT RT RT RT		11 Count 21 18 21	8.1E-2  P_Value  5.8E-6  7.6E-6  1.9E-5	1.7E0 Fold Change 2.9E0 3.3E0 2.7E0 2.0E0	4.5E-1  Benjamin  2.7E-4  4.6E-5  3.3E-4	2 4.0E-1 1 FDR 2.5E-4 3.6E-5 2.9E-4 4.2E-4 2.2E-1
Annota	ation Cluster 86  GOTERM_BP_DIRECT  UP_KEYWORDS  GOTERM_MF_DIRECT  UP_KEYWORDS  INTERPRO  GOTERM_BP_DIRECT	Enrichment Score: 2.86  protein peptidyl-prolyl isomerization  Rotamase  peptidyl-prolyl cis-trans isomerase activity  Isomerase	G RT RT RT RT		11 Count 21 18 21 35	8.1E-2  P_Value  5.8E-6  7.6E-6  1.9E-5  1.0E-4	1.7E0 Fold Change 2.9E0 3.3E0 2.7E0 2.0E0 2.5E0	4.5E-1  Benjamin  2.7E-4  4.6E-5  3.3E-4  5.4E-4	2 4.0E-1 1 FDR 2.5E-4 3.6E-5 2.9E-4 4.2E-4 2.2E-1 3.6E-1
Annota	ation Cluster 86  GOTERM_BP_DIRECT  UP_KEYWORDS  GOTERM_MF_DIRECT  UP_KEYWORDS  INTERPRO  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT	Enrichment Score: 2.86  protein peptidyl-prolyl isomerization  Rotamase  peptidyl-prolyl cis-trans isomerase activity  Isomerase  Peptidyl-prolyl cis-trans isomerase, FKBP-type	RT RT RT RT RT		11  Count  21  18  21  35  8	8.1E-2  P_Value  5.8E-6  7.6E-6  1.9E-5  1.0E-4  3.2E-2	1.7E0 Fold Change 2.9E0 3.3E0 2.7E0 2.0E0 2.5E0 1.9E0	4.5E-1  Benjamin  2.7E-4  4.6E-5  3.3E-4  5.4E-4  2.4E-1	2 4.0E-1 1 FDR 2.5E-4 3.6E-5 2.9E-4 4.2E-4 2.2E-1 3.6E-1
Annota	ation Cluster 86  GOTERM_BP_DIRECT  UP_KEYWORDS  GOTERM_MF_DIRECT  UP_KEYWORDS  INTERPRO  GOTERM_BP_DIRECT	Enrichment Score: 2.86  protein peptidyl-prolyl isomerization  Rotamase  peptidyl-prolyl cis-trans isomerase activity  Isomerase  Peptidyl-prolyl cis-trans isomerase, FKBP-type chaperone-mediated protein folding	RT RT RT RT RT RT		11  Count  21  18  21  35  8  12	8.1E-2  P_Value  5.8E-6  7.6E-6  1.9E-5  1.0E-4  3.2E-2  3.7E-2	1.7E0 Fold Change 2.9E0 3.3E0 2.7E0 2.0E0 2.5E0 1.9E0 2.4E0	4.5E-1  Benjamin  2.7E-4  4.6E-5  3.3E-4  5.4E-4  2.4E-1  3.8E-1	2 4.0E-1 1 FDR 2.5E-4 3.6E-5 2.9E-4 4.2E-4 2.2E-1 3.6E-1
Annota	ation Cluster 86  GOTERM_BP_DIRECT  UP_KEYWORDS  GOTERM_MF_DIRECT  UP_KEYWORDS  INTERPRO  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT	Enrichment Score: 2.86  protein peptidyl-prolyl isomerization  Rotamase  peptidyl-prolyl cis-trans isomerase activity  Isomerase  Peptidyl-prolyl cis-trans isomerase, FKBP-type  chaperone-mediated protein folding  FK506 binding  Peptidyl-prolyl cis-trans isomerase, FKBP-	RT RT RT RT RT RT RT RT		11  Count  21  18  21  35  8  12  8	8.1E-2  P_Value  5.8E-6  7.6E-6  1.9E-5  1.0E-4  3.2E-2  3.7E-2  3.8E-2	1.7E0 Fold Change 2.9E0 3.3E0 2.7E0 2.0E0 2.5E0 1.9E0 2.4E0 2.4E0	4.5E-1  Benjamin  2.7E-4  4.6E-5  3.3E-4  5.4E-4  2.4E-1  3.8E-1  2.3E-1	2 4.0E-1 1 FDR 2.5E-4 3.6E-5 2.9E-4 4.2E-4 2.2E-1 3.6E-1 2.1E-1
Annota	ation Cluster 86  GOTERM_BP_DIRECT  UP_KEYWORDS  GOTERM_MF_DIRECT  UP_KEYWORDS  INTERPRO  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT  INTERPRO	Enrichment Score: 2.86  protein peptidyl-prolyl isomerization  Rotamase  peptidyl-prolyl cis-trans isomerase activity  Isomerase  Peptidyl-prolyl cis-trans isomerase, FKBP-type chaperone-mediated protein folding  FK506 binding  Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain	RI R		11  Count  21  18  21  35  8  12  8  7	8.1E-2  P_Value  5.8E-6  7.6E-6  1.9E-5  1.0E-4  3.2E-2  3.7E-2  3.8E-2  5.7E-2	1.7E0 Fold Change 2.9E0 3.3E0 2.7E0 2.0E0 2.5E0 1.9E0 2.4E0 2.4E0 2.8E0 Fold	4.5E-1  Benjamin  2.7E-4  4.6E-5  3.3E-4  5.4E-4  2.4E-1  3.8E-1  2.3E-1  1.0E0	2 4.0E-1 1 FDR 2.5E-4 3.6E-5 2.9E-4 4.2E-4 2.2E-1 3.6E-1 2.1E-1 3.6E-1
Annota	ation Cluster 86  GOTERM_BP_DIRECT  UP_KEYWORDS  GOTERM_MF_DIRECT  UP_KEYWORDS  INTERPRO  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT  INTERPRO  UP_SEQ_FEATURE	Enrichment Score: 2.86  protein peptidyl-prolyl isomerization  Rotamase  peptidyl-prolyl cis-trans isomerase activity  Isomerase  Peptidyl-prolyl cis-trans isomerase, FKBP-type  chaperone-mediated protein folding  FK506 binding  Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain  domain:PPIase FKBP-type  Enrichment Score: 2.77  compositionally biased region:Ala/Asp-rich	RI R		11  Count  21  18  21  35  8  12  8  7  5	8.1E-2  P_Value  5.8E-6  7.6E-6  1.9E-5  1.0E-4  3.2E-2  3.7E-2  3.8E-2  5.7E-2  8.6E-2	1.7E0 Fold Change 2.9E0 3.3E0 2.7E0 2.0E0 2.5E0 1.9E0 2.4E0 2.4E0 2.8E0 Fold Change	4.5E-1  Benjamin  2.7E-4  4.6E-5  3.3E-4  5.4E-4  2.4E-1  3.8E-1  2.3E-1  1.0E0	2 4.0E-1 1 FDR 2.5E-4 3.6E-5 2.9E-4 4.2E-4 2.2E-1 3.6E-1 2.1E-1 3.6E-1 9.7E-1 1 FDR 3.8E-
Annota	ation Cluster 86  GOTERM_BP_DIRECT  UP_KEYWORDS  GOTERM_MF_DIRECT  UP_KEYWORDS  INTERPRO  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT  INTERPRO  UP_SEQ_FEATURE  ation Cluster 87	Enrichment Score: 2.86  protein peptidyl-prolyl isomerization  Rotamase  peptidyl-prolyl cis-trans isomerase activity  Isomerase  Peptidyl-prolyl cis-trans isomerase, FKBP-type chaperone-mediated protein folding  FK506 binding  Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain domain:PPIase FKBP-type  Enrichment Score: 2.77	RT R		11  Count  21  18  21  35  8  12  8  7  5  Count	8.1E-2  P_Value  5.8E-6  7.6E-6  1.9E-5  1.0E-4  3.2E-2  3.7E-2  3.8E-2  5.7E-2  8.6E-2  P_Value	1.7E0 Fold Change 2.9E0 3.3E0 2.7E0 2.0E0 2.5E0 1.9E0 2.4E0 2.4E0 2.8E0 Fold Change 6.8E0	4.5E-1  Benjamin  2.7E-4  4.6E-5  3.3E-4  5.4E-4  2.4E-1  3.8E-1  2.3E-1  3.9E-1  1.0E0  Benjamin	2 4.0E-1 1 FDR 2.5E-4 3.6E-5 2.9E-4 4.2E-1 3.6E-1 2.1E-1 3.6E-1 5 7 FDR 3.8E-4 2.0E-1
Annota	ation Cluster 86  GOTERM_BP_DIRECT  UP_KEYWORDS  GOTERM_MF_DIRECT  UP_KEYWORDS  INTERPRO  GOTERM_BP_DIRECT  INTERPRO  UP_SEQ_FEATURE  ation Cluster 87  UP_SEQ_FEATURE	Enrichment Score: 2.86  protein peptidyl-prolyl isomerization  Rotamase  peptidyl-prolyl cis-trans isomerase activity  Isomerase  Peptidyl-prolyl cis-trans isomerase, FKBP-type  chaperone-mediated protein folding  FK506 binding  Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain  domain:PPIase FKBP-type  Enrichment Score: 2.77  compositionally biased region:Ala/Asp-rich (DA-box)  region of interest:Flexible hinge	RI R		11  Count  21  18  21  35  8  12  8  7  Count  8  7	8.1E-2  P_Value  5.8E-6  7.6E-6  1.9E-5  1.0E-4  3.2E-2  3.7E-2  3.8E-2  5.7E-2  8.6E-2  P_Value  1.0E-5  6.1E-5	1.7E0 Fold Change 2.9E0 3.3E0 2.7E0 2.0E0 2.5E0 1.9E0 2.4E0 2.4E0 2.8E0 Fold Change 6.8E0 6.8E0	4.5E-1  Benjamin  2.7E-4  4.6E-5  3.3E-4  5.4E-4  2.4E-1  3.8E-1  2.3E-1  1.0E0  Benjamin  3.9E-4  2.1E-3	2 4.0E-1 1 FDR 2.5E-4 3.6E-5 2.9E-4 4.2E-4 2.2E-1 3.6E-1 2.1E-1 3.6E-1 2.7E-1 1 9.7E-1 1 FDR 3.8E-4 2.0E-3 1.5E-1
Annota	ation Cluster 86  GOTERM_BP_DIRECT  UP_KEYWORDS  GOTERM_MF_DIRECT  UP_KEYWORDS  INTERPRO  GOTERM_BP_DIRECT  INTERPRO  UP_SEQ_FEATURE  ation Cluster 87  UP_SEQ_FEATURE  UP_SEQ_FEATURE	Enrichment Score: 2.86  protein peptidyl-prolyl isomerization  Rotamase  peptidyl-prolyl cis-trans isomerase activity  Isomerase  Peptidyl-prolyl cis-trans isomerase, FKBP-type chaperone-mediated protein folding  FK506 binding  Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain domain:PPIase FKBP-type  Enrichment Score: 2.77  compositionally biased region:Ala/Asp-rich (DA-box)  region of interest:Flexible hinge  RecF/RecN/SMC	RI R		11  Count  21  18  21  35  8  12  8  7  Count  8  7	8.1E-2  P_Value  5.8E-6  7.6E-6  1.9E-5  1.0E-4  3.2E-2  3.7E-2  3.8E-2  5.7E-2  8.6E-2  P_Value  1.0E-5  6.1E-5  1.1E-4	1.7E0 Fold Change 2.9E0 3.3E0 2.7E0 2.0E0 2.5E0 1.9E0 2.4E0 2.4E0 2.8E0 Fold Change 6.8E0 6.8E0 6.2E0	4.5E-1  Benjamin  2.7E-4  4.6E-5  3.3E-4  5.4E-4  2.4E-1  3.8E-1  2.3E-1  1.0E0  Benjamin  3.9E-4  2.1E-3  1.6E-3	2 4.0E-1 1 FDR 2.5E-4 3.6E-5 2.9E-4 4.2E-4 2.2E-1 3.6E-1 9.7E-1 1 FDR 3.8E-4 2.0E-3 3.1.5E-3
Annota	ation Cluster 86  GOTERM_BP_DIRECT  UP_KEYWORDS  GOTERM_MF_DIRECT  UP_KEYWORDS  INTERPRO  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT  INTERPRO  UP_SEQ_FEATURE  ation Cluster 87  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  INTERPRO  INTERPRO	Enrichment Score: 2.86  protein peptidyl-prolyl isomerization  Rotamase  peptidyl-prolyl cis-trans isomerase activity  Isomerase  Peptidyl-prolyl cis-trans isomerase, FKBP-type chaperone-mediated protein folding  FK506 binding  Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain domain:PPIase FKBP-type  Enrichment Score: 2.77  compositionally biased region:Ala/Asp-rich (DA-box)  region of interest:Flexible hinge  RecF/RecN/SMC  Structural maintenance of chromosomes protein	RI R		11  Count  21  18  21  35  8  12  8  7  Count  8  7  5	8.1E-2  P_Value  5.8E-6  7.6E-6  1.9E-5  1.0E-4  3.2E-2  3.7E-2  3.8E-2  5.7E-2  8.6E-2  P_Value  1.0E-5  6.1E-5  1.1E-4  2.9E-3	1.7E0 Fold Change 2.9E0 3.3E0 2.7E0 2.0E0 2.5E0 1.9E0 2.4E0 2.4E0 2.8E0 Fold Change 6.8E0 6.8E0 6.2E0 6.2E0	4.5E-1  Benjamin  2.7E-4  4.6E-5  3.3E-4  5.4E-4  2.4E-1  3.8E-1  2.3E-1  1.0E0  Benjamin  3.9E-4  2.1E-3  1.6E-3  3.2E-2	2 4.0E-1 1 FDR 2.5E-4 3.6E-5 2.9E-4 2.2E-1 3.6E-1 2.1E-1 3.6E-1 9.7E-1 1 FDR 3.8E-4 2.0E-3 1.5E-3 2.9E-2
Annota	Action Cluster 86  GOTERM_BP_DIRECT  UP_KEYWORDS  GOTERM_MF_DIRECT  UP_KEYWORDS  INTERPRO  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT  INTERPRO  UP_SEQ_FEATURE  Action Cluster 87  UP_SEQ_FEATURE  INTERPRO  PIR_SUPERFAMILY	Enrichment Score: 2.86  protein peptidyl-prolyl isomerization  Rotamase  peptidyl-prolyl cis-trans isomerase activity  Isomerase  Peptidyl-prolyl cis-trans isomerase, FKBP-type chaperone-mediated protein folding  FK506 binding  Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain domain:PPIase FKBP-type  Enrichment Score: 2.77  compositionally biased region:Ala/Asp-rich (DA-box)  region of interest:Flexible hinge  RecF/RecN/SMC  Structural maintenance of chromosomes	RI R		11  Count  21  18  21  35  8  12  8  7  Count  8  7	8.1E-2  P_Value  5.8E-6  7.6E-6  1.9E-5  1.0E-4  3.2E-2  3.7E-2  3.8E-2  5.7E-2  8.6E-2  P_Value  1.0E-5  6.1E-5  1.1E-4	1.7E0 Fold Change 2.9E0 3.3E0 2.7E0 2.0E0 2.5E0 1.9E0 2.4E0 2.4E0 2.8E0 Fold Change 6.8E0 6.8E0 6.2E0 6.2E0	4.5E-1  Benjamin  2.7E-4  4.6E-5  3.3E-4  5.4E-4  2.4E-1  3.8E-1  2.3E-1  1.0E0  Benjamin  3.9E-4  2.1E-3  1.6E-3	2 4.0E-1 1 FDR 2.5E-4 3.6E-5 2.9E-4 4.2E-1 3.6E-1 2.1E-1 3.6E-1 1 9.7E-1 1 FDR 3.8E-4 2.0E-3 1.5E-3 2.9E-2
Annota	ation Cluster 86  GOTERM_BP_DIRECT  UP_KEYWORDS  GOTERM_MF_DIRECT  UP_KEYWORDS  INTERPRO  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT  INTERPRO  UP_SEQ_FEATURE  ation Cluster 87  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  INTERPRO  INTERPRO	Enrichment Score: 2.86  protein peptidyl-prolyl isomerization  Rotamase  peptidyl-prolyl cis-trans isomerase activity  Isomerase  Peptidyl-prolyl cis-trans isomerase, FKBP-type  chaperone-mediated protein folding  FK506 binding  Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain  domain:PPIase FKBP-type  Enrichment Score: 2.77  compositionally biased region:Ala/Asp-rich (DA-box)  region of interest:Flexible hinge  RecF/RecN/SMC  Structural maintenance of chromosomes protein  structural maintenance of chromosomes	RI R		11  Count  21  18  21  35  8  12  8  7  Count  8  7  5	8.1E-2  P_Value  5.8E-6  7.6E-6  1.9E-5  1.0E-4  3.2E-2  3.7E-2  3.8E-2  5.7E-2  8.6E-2  P_Value  1.0E-5  6.1E-5  1.1E-4  2.9E-3	1.7E0 Fold Change 2.9E0 3.3E0 2.7E0 2.0E0 2.5E0 1.9E0 2.4E0 2.4E0 2.8E0 Fold Change 6.8E0 6.8E0 6.2E0 6.2E0 5.3E0	4.5E-1  Benjamin  2.7E-4  4.6E-5  3.3E-4  5.4E-4  2.4E-1  3.8E-1  2.3E-1  1.0E0  Benjamin  3.9E-4  2.1E-3  1.6E-3  3.2E-2	2 4.0E-1 1 FDR 2.5E-4 3.6E-5 2.9E-1 3.6E-1 2.1E-1 3.6E-1 9.7E-1 1 FDR 3.8E-4 2.0E-3 1.5E-3 2.9E-2

Annota	ation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_CC_DIRECT	meiotic cohesin complex	<u>RT</u>	i	3	2.4E-1		8.4E-1	7.4E
Annota	ation Cluster 88	Enrichment Score: 2.76	G	<b>15</b>	Count	P_Value	Fold Change	Benjamin	
	UP_SEQ_FEATURE	domain:Chromo 2	RT		8	4.0E-5	Onlange	1.4E-3	1.4E 3
	INTERPRO	Chromo domain-like	<u>RT</u>		15	2.0E-4	2.9E0	2.9E-3	2.7E
	INTERPRO	Chromo domain/shadow	RT		15	3.0E-4		4.1E-3	3 3.8E
_ 	UP_SEQ_FEATURE	domain:Chromo 1	RT	_	8	1.1E-3		3.1E-2	3 3.0E
 	INTERPRO								2 4.9E
	SMART	Chromo domain	<u>RT</u>		11	5.1E-3		5.3E-2	2 1.3E
	INTERPRO	<u>CHROMO</u>	RT		15	1.8E-2		1.4E-1	1 8.7E
		Chromo domain, conserved site	<u>RT</u>	i	6	2.1E-1	Fold	9.5E-1	1
Annota	ation Cluster 89  GOTERM_CC_DIRECT	Enrichment Score: 2.72	G		Count	P_Value	Change		
		<u>U6 snRNP</u>	<u>RT</u>	1	7	9.1E-5	6.4E0	1.3E-3	1.1E 3
	GOTERM_BP_DIRECT	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation- dependent decay	<u>RT</u>	i	12	5.4E-3	2.5E0	9.3E-2	8.8E 2
	GOTERM_CC_DIRECT	Lsm1-7-Pat1 complex	<u>RT</u>	1	4	1.4E-2	6.4E0	9.7E-2	8.5E
Annota	ation Cluster 90	Enrichment Score: 2.71	G		Count	:	Fold Change	Benjamin	2 i FDR
	UP_SEQ_FEATURE	domain:Chromo 2	RT	i	8	- 4.0E-5		1.4E-3	1.4E
	INTERPRO	BRK domain	RT		6	5.7E-4		7.2E-3	3 6.6E
_	UP_SEQ_FEATURE			-					3 3.0E
	SMART	domain:Chromo 1	<u>RT</u>		8	1.1E-3		3.1E-2	2 3.6E
	GOTERM_MF_DIRECT	<u>BRK</u>	<u>RT</u>	•	6	4.2E-3	4.1E0	4.0E-2	2
	GOTERM_MF_DIRECT	hydrolase activity, acting on acid anhydrides	<u>RT</u>	i	3	2.7E-1		9.5E-1	8.4E 1
Annota	ation Cluster 91	Enrichment Score: 2.67	G		Count	P_Value	Fold Change	Benjamin	
	UP_KEYWORDS	Protein biosynthesis	<u>RT</u>	•	43	2.1E-5	1.9E0	1.2E-4	9.6E 5
	GOTERM_BP_DIRECT	regulation of translational initiation	<u>RT</u>	•	17	9.9E-5	2.8E0	3.2E-3	3.0E 3
	UP_KEYWORDS	Initiation factor	<u>RT</u>	i	21	1.2E-4	2.5E0	6.4E-4	4.9E 4
	GOTERM_BP_DIRECT	IRES-dependent viral translational initiation	<u>RT</u>	i	7	1.4E-4	5.9E0	4.2E-3	4.0E 3
	GOTERM_MF_DIRECT	translation initiation factor activity	<u>RT</u>	\$	23	2.2E-4	2.2E0	2.8E-3	2.5E 3
	GOTERM_CC_DIRECT	eukaryotic translation initiation factor 3 complex	<u>RT</u>	•	10	4.2E-4	3.7E0	4.6E-3	4.0E
	GOTERM_CC_DIRECT	eukaryotic 43S preinitiation complex	<u>RT</u>		9	8.4E-4	3.8E0	8.2E-3	7.18
_	GOTERM_CC_DIRECT	eukaryotic 48S preinitiation complex	RT		9	8.4E-4	3.8E0	8.2E-3	3 7.18
_ 	GOTERM_CC_DIRECT	eukaryotic translation initiation factor 3	RT	-	6	1.5E-3		1.4E-2	3 1.2
_ _	GOTERM_BP_DIRECT	complex, eIF3m							2 1.3E
	INTERPRO	formation of translation preinitiation complex	<u>RT</u>		10	9.2E-3		1.4E-1	1 5.6
	UP_SEQ_FEATURE	Proteasome component (PCI) domain	<u>RT</u>	•	6	1.3E-1	2.2E0	6.1E-1	1
		domain:PCI	<u>RT</u>	i	6	1.3E-1	2.2E0	1.0E0	9.7E
	GOTERM_BP_DIRECT	viral translational termination-reinitiation	<u>RT</u>	i	3	2.0E-1	3.6E0	1.0E0	9.5E 1
	SMART	<u>PINT</u>	<u>RT</u>	i	6	3.5E-1	1.5E0	1.0E0	9.0E 1
Annota	ation Cluster 92	Enrichment Score: 2.66	G	PR .	Count	P_Value	Fold Change	Benjamin	i FDF
	INTERPRO	Thioredoxin domain	<u>RT</u>	i	21	1.1E-6	3.2E0	2.7E-5	2.4I 5
	GOTERM_BP_DIRECT	response to endoplasmic reticulum stress	<u>RT</u>	•	30	5.4E-6	2.4E0	2.5E-4	2.4E 4
	UP_SEQ_FEATURE	domain:Thioredoxin 1	<u>RT</u>	1	9	7.3E-6	6.1E0	3.0E-4	2.9E 4
	UP_SEQ_FEATURE	domain:Thioredoxin 2	<u>RT</u>	i	9	7.3E-6	6.1E0	3.0E-4	2.9E
	INTERPRO	Thioredoxin, conserved site	<u>RT</u>		12	9.0E-6	4.4E0	1.7E-4	1.6E
7	GOTERM_BP_DIRECT	cell redox homeostasis	RT		27	2.3E-4		6.5E-3	4 6.2E
	UP_KEYWORDS	Redox-active center	RT	•	18	3.5E-4		1.8E-3	3 1.4E
	UP_SEQ_FEATURE								3 3.0
	GOTERM_MF_DIRECT	site:Contributes to redox potential value	<u>RT</u>	•	6	1.1E-3		3.1E-2	2
	OOTERWI_WIF_DIRECT	<u>protein disulfide isomerase activity</u>	<u>RT</u>	•	11	1.6E-3	3.0E0	1.6E-2	2
	LID OF S						2.750	4.75.0	4.5
	UP_SEQ_FEATURE INTERPRO	domain:Thioredoxin	<u>RT</u>	•	13	1.7E-3	2.7EU	4.7E-2	2

UP_SEQ_FEATURE Sectionway pick of C-terminal Cys of second git NYTERPRO Protein disabilishis isomerase RI  UP_SEQ_FEATURE domain_Thioredoxin_3	4 4 4 7 27 13 20 3 19	1.1E-2 1.5E-2 2.5E-2 1.3E-1	6.8E0 6.8E0 6.2E0 5.5E0 2.0E0	2.3E-1 2.3E-1 1.2E-1 4.8E-1 5.8E-1	2.2E- 1 2.2E- 1 1.1E- 1
UP_SEQ_FEATURE active site	4 4 7 227 13 20 3	1.5E-2 2.5E-2 1.3E-1 1.4E-1	6.2E0 5.5E0 2.0E0	1.2E-1 4.8E-1	1 1.1E-
INTERPRO	4 7 27 13 20 3	2.5E-2 1.3E-1 1.4E-1	5.5E0 2.0E0	4.8E-1	
GOTERM MF_DIRECT    Somersse_activity   RT	7 27 13 20 3	1.3E-1 1.4E-1	2.0E0		1
GOTERM_MF_DIRECT  INTERPRO  Thiorestoxin-like fold  IV_SEQ_FEATURE  short sequence motif-Prevents secretion from RI  GOTERM_CC_DIRECT  cell  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  UI_snRNP_binding  RI  GOTERM_CC_DIRECT  Commitment complex  RI  GOTERM_CC_DIRECT  DISSRP_binding  RI  GOTERM_CC_DIRECT  DISSRP_binding  RI  GOTERM_CC_DIRECT  DISSRP_binding  RI  FINAL COMMITMENT SCORES 2.64  GOTERM_CC_DIRECT  DISSRP_binding  RI  WP_SEQ_FEATURE  INTERPRO  Str_bomology_3 domain  RI  NITERPRO  14-3-3 grotein. Sonserved site  RI  INTERPRO  14-3-3 grotein.  SITERPRO  14-3-3 grotein  RI  SMART  14-3-3 grotein  SITERPRO  14-3-3 grotein  RI  SMART  14-3-3 grotein  SITERPRO  14-3-3 grotein  RI  GOTERM_BP_DIRECT  COTERM_BP_DIRECT  COTERM_BP_D	7 27 13 20 3	1.3E-1 1.4E-1	2.0E0		4.7E-
INTERPRO  Thioredoxin-like fold  UP_SEQ_FEATURE short sequence motif-Prevents secretion from RI ER  GOTERM_CC_DIRECT sell  GOTERM_MF_DIRECT disulfide oxidoreductase activity RI is additional content of the content of	27 13 20 3	1.4E-1		J.UL-I	1 5.2E-
UP_SEQ_FEATURE GOTERM_OC_DIRECT Cell GOTERM_MF_DIRECT GISHING evidence ductase activity GOTERM_OC_DIRECT GISHING evidence ductase activity GOTERM_OC_DIRECT GOTERM_OC_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_OC_DIRECT GOTERM_OC_DIRECT GOTERM_OC_DIRECT GOTERM_CC_DIRECT GOTERM_CC_DIRECT GOTERM_CC_DIRECT GOTERM_OC_DIRECT GOT	13 20 3		1.520	6.8E-1	1 6.2E-
GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  GOTERM_CC_DIRECT  endoalsamic reticulum lumen  RT in annotation cliuster 93  GOTERM_MF_DIRECT  GOTERM_CC_DIRECT  Commitment complex  RT in annotation cliuster 94  LI_SERNP_binding  RT in annotation cliuster 94  LI_SERNP_CC_DIRECT  COMMITMENT SCORE_264  LI_SERNP_CC_DIRECT  COTERM_SP_DIRECT  COTERM_SP	20 3 19	1.0L-1	1 5EO	1.0E0	1 9.7E-
GOTERM_MF_DIRECT  GOTERM_CC_DIRECT  Annotation Cluster 93  Enrichment Score: 2.66  GOTERM_CC_DIRECT  GOTERM_CC_DIRECT  GOTERM_CC_DIRECT  GOTERM_CC_DIRECT  GOTERM_CC_DIRECT  LUSEQ_FEATURE  GOTERM_CC_DIRECT  LUSEQ_FEATURE  GOTERM_CC_DIRECT  LUSEQ_FEATURE  LUSEQ_FEATURE  LUSEQ_FEATURE  LUKEYWORDS  SH3 domain  RI LUKEYWORDS  INTERPRO  14-3-3 protein, conserved site  RI LUKEYWORDS  INTERPRO  14-3-3 protein, conserved site  RI LUKEYWORDS  RI LUSEQ_FEATURE  SITE LOTER S	3 19	2 25 1			1 6.9E-
GOTERM_CC_DIRECT  Annotation Cluster 93  Enrichment Score; 2.66  GOTERM_MF_DIRECT  U1 snRNP binding  RT  GOTERM_CC_DIRECT  GOTERM_CC_DIRECT  GOTERM_CC_DIRECT  Drespliceosome  RT  Annotation Cluster 94  Enrichment Score; 2.64  GOTERM_CC_DIRECT  Drespliceosome  RT  Annotation Cluster 94  Enrichment Score; 2.64  GOTERM_CC_DIRECT  Drespliceosome  RT  Annotation Cluster 94  Enrichment Score; 2.64  GOTERM_CC_DIRECT  Drespliceosome  RT  Annotation Cluster 95  Enrichment Score; 2.69  INTERPRO  I4-3-3 protein, conserved site  RT  INTERPRO  I4-3-3 protein  INTERPRO  I4-3-3 protein  INTERPRO  I4-3-3 protein  INTERPRO  I4-3-3 protein  Site: Interaction with phosphoserine on interacting protein interacting protein interacting protein interacting protein interacting protein interacting protein insertion into nitochondrial membrane involved in aboutclet, signaling, pathway  GOTERM_BP_DIRECT  Trotein targeting  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  Trotein targeting  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  Trotein targeting  GOTERM_BP_DIRE	19		1.3E0	7.9E-1	1 8.4E-
Annotation Cluster 93 Enrichment Score; 2.66 GOTERM_MF_DIRECT UI_snRNP binding RI GOTERM_CC_DIRECT commitment complex RI GOTERM_CC_DIRECT prespliceosome RI  Annotation Cluster 94 Enrichment Score; 2.64 GOTERM_CC_DIRECT  Prespliceosome RI  UP_SEQ_FEATURE domain:SH3 RI UP_KEYWORDS SH3 domain RI SH3 RI SH3 RI SH3 RI Annotation Cluster 95 Enrichment Score; 2.69 GOTERM_CC_DIRECT  INTERPRO 14-3-3 protein, conserved site RI INTERPRO 14-3-3 protein, conserved site RI INTERPRO 14-3-3 protein INTERPRO 14-3-3 protein RI SH3 RI GOTERM_BP_DIRECT  positive regulation of protein insertion into nitochondrial membrane involved in anotatic, signaling, pathway membrane organization RI GOTERM_BP_DIRECT  HTP biosynthetic process  RI GOTERM_BP_DIRECT  HTP biosynthetic		2./E-1 1.0E0	3.0E0 6.3E-1	9.5E-1 1.0E0	1 1.0E0
GOTERM_CC_DIRECT commitment complex RT   GOTERM_CC_DIRECT prespliceosome RT   GOTERM_CC_DIRECT prespliceosome RT   DIVERTIFICATION   DIVER		P_Value	Fold	Ronjamini	
GOTERM_CC_DIRECT  prespliceosome  RI  Annotation Cluster 94  Enrichment Score: 2.64  UP_SEQ_FEATURE  domain:SH3  RI  UP_KEYWORDS  SH3 domain  RI  INTERPRO  Src homology-3 domain  RI  SMART  SH3  RI  Annotation Cluster 95  Enrichment Score: 2.69  INTERPRO  14-3-3 protein, conserved site  RI  INTERPRO  14-3-3 domain  RI  INTERPRO  14-3-3 protein  RI  UP_SEQ_FEATURE  Site:Interaction with phosphoserine on interacting protein  PIR_SUPERFAMILY  14-3-3 protein  RI  SMART  14-3-3  GOTERM_BP_DIRECT  positive regulation of protein insertion into milderhondrial membrane involved in spentives (singling) pathway  GOTERM_BP_DIRECT  protein targeting  RI  GOTERM_BP_DIRECT  protein targeting  RI  Annotation Cluster 96  Enrichment Score: 2.52  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  active site:Pros-phosphohistidine intermediate  not containing small molecule intercrometrics  RI  INTERPRO  Nucleoside diphosphate kinase	7	1.3E-4		1.8E-3	1.6E-
Annotation Cluster 94 Enrichment Score: 2.64  UP_SEQ_FEATURE domain: SH3 RI  UP_KEYWORDS SH3 domain RI  INTERPRO Src homology-3 domain RI  SMART SH3 RI  Annotation Cluster 95 Enrichment Score: 2.59  INTERPRO 14-3-3 protein RI  INTERPRO 14-3-3 protein RI  UP_SEQ_FEATURE site: Interaction with phosphoserine on interacting protein interacting protein RI  SMART 14-3-3 protein RI  GOTERM_BP_DIRECT positive regulation of protein insertion into mitochnodrial membrane involved in anontotic signaling nathway.  GOTERM_BP_DIRECT protein targeting RI  GOTERM_BP_DIRECT protein targeting RI  GOTERM_BP_DIRECT protein targeting RI  GOTERM_BP_DIRECT cytoplasmic vesicle membrane RI  Annotation Cluster 96 Enrichment Score: 2.52  GOTERM_BP_DIRECT UTP biosynthetic process RI  GOTERM_BP_DIRECT Thiosynthetic process RI  GOTERM_BP_DIRECT Thiosynthetic process RI  UP_SEQ_FEATURE active site: Pros-phosphohistidine intermediate riverwission Nucleoside diphosphate kinase RI  INTERPRO Nucleoside diphosphate kinase RI  INTERPRO Nucleoside diphosphate kinase RI  INTERPRO Nucleoside diphosphate kinase	5	1.5E-3	5.4E0	1.4E-2	1.2E-
Annotation Cluster 94  Enrichment Score: 2.64  UP_SEQ_FEATURE  domain: SH3  UP_KEYWORDS  SH3 domain  RI  INTERPRO Src homology-3 domain  RI  SMART  SH3  RI  Annotation Cluster 95  Enrichment Score: 2.59  INTERPRO  14-3-3 protein, conserved site RI  INTERPRO  14-3-3 domain  RI  INTERPRO  14-3-3 protein, conserved site RI  INTERPRO  14-3-3 protein  INTERPRO  14-3-3 protein  RI  UP_SEQ_FEATURE Site: Interaction with phosphoserine on interacting protein  PIR_SUPERFAMILY  14-3-3 protein  RI  SMART  14-3-3 protein  RI  GOTERM_BP_DIRECT  mositive regulation of protein insertion into mitochondrial membrane involved in apontotic signaling, pathway.  GOTERM_BP_DIRECT  membrane organization  RI  GOTERM_BP_DIRECT  protein targeting  RI  GOTERM_CC_DIRECT  cytoplasmic vesicle membrane  RI  Annotation Cluster 96  Enrichment Score: 2.52  GOTERM_BP_DIRECT  UTP_biosynthetic process  RI  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  active site: Pros-phosphohistidine intermediate  Intermediate  RI  INTERPRO  Nucleoside diphosphate kinase	4	5.4E-2	4.2E0	2.9E-1	2 2.5E-
UP_KEYWORDS  SH3.domain  INTERPRO  Src homology-3 domain  RI  SMART  SH3  Annotation Cluster 95  Enrichment Score: 2.59  INTERPRO  14-3-3 protein, conserved site  RI  INTERPRO  14-3-3 domain  RI  INTERPRO  14-3-3 domain  RI  INTERPRO  14-3-3 protein  Site: Interaction with phosphoserine on interacting protein interacting protein  PIR_SUPERFAMILY  14-3-3 protein  RI  SMART  14-3-3 protein  RI  SMART  14-3-3 protein  RI  GOTERM_BP_DIRECT  positive regulation of protein insertion into mitochondrial membrane involved in apportotic signaling, pathway.  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  protein targetting  GOTERM_CC_DIRECT  Cytoplasmic vesicle membrane  RI  Annotation Cluster 96  Enrichment Score: 2.52  GOTERM_BP_DIRECT  UTP_biosynthetic process  RI  GOTERM_BP_DIRECT  UTP_biosynthetic process  RI  GOTERM_BP_DIRECT  nucleoside diphosphate kinase  RI  INTERPRO  Nucleoside diphosphate kinase  RI  INTERPRO  Nucleoside diphosphate kinase  RI  INTERPRO  Nucleoside diphosphate kinase		P_Value	Fold		1 i FDR
UP_KEYWORDS   SH3 domain   RT	48	1	Change	7.1E-4	6.9E-
INTERPRO  Sinch homology-3 domain  SMART  SH3  RT  Annotation Cluster 95  Enrichment Score: 2.59  INTERPRO  14-3-3 protein, conserved site  RT  INTERPRO  14-3-3 domain  RT  INTERPRO  14-3-3 protein  UP_SEQ_FEATURE  Site: Interaction with phosphoserine on interacting protein  PIR_SUPERFAMILY  14-3-3 protein  RT  SMART  14-3-3 protein  RT  GOTERM_BP_DIRECT  positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling, pathway  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  protein targetting  RT  GOTERM_BP_DIRECT  CVtoplasmic vesicle membrane  RT  Annotation Cluster 96  Enrichment Score: 2.52  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  CTP biosynthetic process  RT  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  active site: Pros-phosphohistidine intermediate  uP_SEQ_FEATURE  active site: Pros-phosphohistidine intermediate  interconversion  Nucleoside diphosphate kinase  RT  INTERPRO  Nucleoside diphosphate kinase  RT  INTERPRO  Nucleoside diphosphate kinase	51		1.6E0	2.2E-3	4 1.7E-
Annotation Cluster 95 Enrichment Score: 2.59  INTERPRO 14-3-3 protein, conserved site RT INTERPRO 14-3-3 domain RT INTERPRO 14-3-3 protein INTERPRO 14-3-3 protein RT INTERPRO RT					3 5.0E-
Annotation Cluster 95	51		1.5E0		2 9.0E-
INTERPRO  14-3-3 protein, conserved site  RT  INTERPRO  14-3-3 domain  RT  UP_SEQ_FEATURE  site: Interaction with phosphoserine on interacting protein  PIR_SUPERFAMILY  14-3-3 protein  RT  SMART  14-3-3 protein  RT  SMART  4-3-3 protein  RT  GOTERM_BP_DIRECT  positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway  GOTERM_BP_DIRECT  protein targeting  RT  GOTERM_CC_DIRECT  protein targeting  RT  GOTERM_CC_DIRECT  Cytoplasmic vesicle membrane  RT  Annotation Cluster 96  Enrichment Score: 2.52  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  active site: Pros-phosphohistidine intermediate  INTERPRO  Nucleoside diphosphate kinase  RT  RT  RT  RT  RT  RT  RT  RT  RT  R	50	1	9.9E-1		1
INTERPRO  14-3-3 protein, conserved site  INTERPRO  14-3-3 domain  RT  UP_SEQ_FEATURE  site:Interaction with phosphoserine on interacting protein  PIR_SUPERFAMILY  14-3-3 protein  RT  SMART  14-3-3 protein  RT  GOTERM_BP_DIRECT  positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway  GOTERM_BP_DIRECT  membrane organization  RT  GOTERM_BP_DIRECT  protein targeting  RT  GOTERM_CC_DIRECT  cytoplasmic vesicle membrane  Annotation Clustor 96  Enrichment Score: 2.52  GOTERM_BP_DIRECT  UTP biosynthetic process  RT  UP_SEQ_FEATURE  active site:Pros-phosphohistidine intermediate  INTERPRO  Nucleoside diphosphate kinase  RT  RT  RT  RT  RT  RT  RT  RT  RT  R		P_Value	Change		
INTERPRO  14-3-3 domain  RT  UP_SEQ_FEATURE  site:Interaction with phosphoserine on interacting protein  PIR_SUPERFAMILY  14-3-3 protein  RI  SMART  14-3-3 protein  RI  GOTERM_BP_DIRECT  positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway  GOTERM_BP_DIRECT  membrane organization  RI  GOTERM_BP_DIRECT  protein targeting  RI  GOTERM_CC_DIRECT  cytoplasmic vesicle membrane  RI  Annotation Cluster 96  Enrichment Score: 2.52  GOTERM_BP_DIRECT  UTP biosynthetic process  RI  UP_SEQ_FEATURE  active site: Pros-phosphohistidine intermediate  nucleobase-containing small molecule interconversion  Nucleoside diphosphate kinase  RI  RI  RI  RI  RI  RI  RI  RI  RI  R	7	1.1E-4	6.2E0	1.6E-3	1.5E- 3
UP_SEQ_FEATURE  site:Interaction with phosphoserine on interacting protein  PIR_SUPERFAMILY  14-3-3 protein  RT  SMART  14 3 3  GOTERM_BP_DIRECT  positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway  GOTERM_BP_DIRECT  membrane organization  RT  GOTERM_BP_DIRECT  protein targeting  RT  GOTERM_CC_DIRECT  cytoplasmic vesicle membrane  RT  Annotation Cluster 96  Enrichment Score: 2.52  GOTERM_BP_DIRECT  UTP biosynthetic process  RT  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  active site: Pros-phosphohistidine intermediate  GOTERM_BP_DIRECT  nucleobase-containing small molecule interconversion  Nucleoside diphosphate kinase  RT  RT  RT  RT  RT  RT  RT  RT  RT  R	7	1.1E-4	6.2E0	1.6E-3	1.5E- 3
interacting protein  PIR_SUPERFAMILY  14-3-3 protein  RT  GOTERM_BP_DIRECT  positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway  GOTERM_BP_DIRECT  membrane organization  RT  GOTERM_BP_DIRECT  protein targeting  RT  GOTERM_CC_DIRECT  cytoplasmic vesicle membrane  RT  Annotation Cluster 96  Enrichment Score: 2.52  GOTERM_BP_DIRECT  UTP biosynthetic process  RT  GOTERM_BP_DIRECT  UTP biosynthetic process  RT  GOTERM_BP_DIRECT  CTP biosynthetic process  RT  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  active site: Pros-phosphohistidine intermediate  RT  INTERPRO  Nucleoside diphosphate kinase  RT  RT  RT  RT  RT  RT  RT  RT  RT  R	7	1.1E-4	6.2E0	1.6E-3	1.5E- 3
SMART  14 3 3  GOTERM_BP_DIRECT  positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway.  GOTERM_BP_DIRECT  membrane organization  RT  GOTERM_BP_DIRECT  protein targeting  RT  GOTERM_CC_DIRECT  cytoplasmic vesicle membrane  RT  Annotation Cluster 96  Enrichment Score: 2.52  GOTERM_BP_DIRECT  UTP biosynthetic process  RT  GOTERM_BP_DIRECT  Nucleobase-containing small molecule interconversion  Nucleoside diphosphate kinase  RT  GOTERM_BP_DIRECT  Nucleoside diphosphate kinase  RT  GOTERM_BP_DIRECT  Nucleoside diphosphate kinase	7	2.1E-4	6.0E0	6.6E-3	6.4E- 3
GOTERM_BP_DIRECT  positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway  GOTERM_BP_DIRECT  membrane organization  RT  GOTERM_BP_DIRECT  protein targeting  RT  GOTERM_CC_DIRECT  cytoplasmic vesicle membrane  RT  Annotation Cluster 96  Enrichment Score: 2.52  GOTERM_BP_DIRECT  UTP biosynthetic process  RT  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  active site: Pros-phosphohistidine intermediate intermediate  GOTERM_BP_DIRECT  nucleobase-containing small molecule interconversion  Nucleoside diphosphate kinase  RT  GOTERM_RT  GOTERM_BP_DIRECT  Nucleoside diphosphate kinase  RT  GOTERM_RT  GOTERM_BP_DIRECT  Nucleoside diphosphate kinase  RT  GOTERM_BP_DIRECT  Nucleoside diphosphate kinase  RT  GOTERM_BP_DIRECT  Nucleoside diphosphate kinase	7	2.4E-4	5.3E0	1.5E-2	1.5E- 2
mitochondrial membrane involved in apoptotic signaling pathway.  GOTERM_BP_DIRECT  membrane organization  RT  GOTERM_BP_DIRECT  protein targeting  RT  GOTERM_CC_DIRECT  cytoplasmic vesicle membrane  RT  Annotation Cluster 96  Enrichment Score: 2.52  GOTERM_BP_DIRECT  UTP biosynthetic process  RT  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  active site: Pros-phosphohistidine intermediate  GOTERM_BP_DIRECT  nucleobase-containing small molecule interconversion  Nucleoside diphosphate kinase  RT  GOTERM_BP_DIRECT  Nucleoside diphosphate kinase	7	1.2E-3	4.1E0	1.3E-2	1.2E- 2
GOTERM_BP_DIRECT  protein targeting  GOTERM_CC_DIRECT  cytoplasmic vesicle membrane  RT  Annotation Cluster 96  Enrichment Score: 2.52  GOTERM_BP_DIRECT  UTP biosynthetic process  RT  GOTERM_BP_DIRECT  CTP biosynthetic process  RT  UP_SEQ_FEATURE  active site: Pros-phosphohistidine intermediate intermediate  GOTERM_BP_DIRECT  nucleobase-containing small molecule interconversion  Nucleoside diphosphate kinase  RT  GOTERM_BP_DIRECT  Nucleoside diphosphate kinase  RT  GOTERM_BP_DIRECT  Nucleoside diphosphate kinase	13	2.2E-3	2.6E0	4.5E-2	4.3E- 2
GOTERM_CC_DIRECT  cytoplasmic vesicle membrane  RT  Annotation Cluster 96  Enrichment Score: 2.52  GOTERM_BP_DIRECT  UTP biosynthetic process  RT  GOTERM_BP_DIRECT  CTP biosynthetic process  RT  UP_SEQ_FEATURE  active site:Pros-phosphohistidine intermediate  GOTERM_BP_DIRECT  nucleobase-containing small molecule interconversion  Nucleoside diphosphate kinase  RT  RT  RT  RT  RT  RT  RT  RT  RT  R	3	2.9E-1	1.5E0	1.0E0	9.5E- 1
Annotation Cluster 96 Enrichment Score: 2.52 G TO STATE OF THE PROOF O	e	3.3E-1	1.4E0	1.0E0	9.5E- 1
GOTERM_BP_DIRECT  CTP biosynthetic process  RT  UP_SEQ_FEATURE  active site:Pros-phosphohistidine intermediate  GOTERM_BP_DIRECT  nucleobase-containing small molecule interconversion  INTERPRO  Nucleoside diphosphate kinase  RT  SO  RT  S	17	8.6E-1	8.6E-1	1.0E0	8.7E- 1
GOTERM_BP_DIRECT  UP_SEQ_FEATURE  active site:Pros-phosphohistidine intermediate  GOTERM_BP_DIRECT  nucleobase-containing small molecule interconversion  Nucleoside diphosphate kinase  RT  ST  ST  ST  ST  ST  ST  ST  ST  ST	Count	P_Value	e Fold Change	Benjamini	i FDR
UP_SEQ_FEATURE active site:Pros-phosphohistidine intermediate  GOTERM_BP_DIRECT nucleobase-containing small molecule interconversion  INTERPRO Nucleoside diphosphate kinase  RT   RT   RT   RT   RT   RT   RT   RT	9	1.7E-4		5.0E-3	4.7E-
intermediate  GOTERM_BP_DIRECT  nucleobase-containing small molecule interconversion  INTERPRO  Nucleoside diphosphate kinase  RT  SE	€	1.7E-4	4.4E0	5.0E-3	4.7E- 3
GOTERM_BP_DIRECT  nucleobase-containing small molecule interconversion  INTERPRO  Nucleoside diphosphate kinase  RT  State of the content of	7	2.1E-4	6.0E0	6.6E-3	6.4E- 3
INTERPRO  Nucleoside diphosphate kinase  RT  8	13		3.1E0	8.4E-3	8.0E- 3
	3	5.1E-4	4.5E0	6.8E-3	6.3E-
GOTERM_MF_DIRECT  nucleoside diphosphate kinase activity  RT	11			7.1E-3	3 6.3E-
GOTERM BP DIRECT	10		3.3E0	2.8E-2	3 2.6E-
GOTERM BP DIRECT					2 4.8E-
SMART	3		3.6E0	5.0E-2	2 5.5E-
NTERPRO	3		3.0E0	6.1E-2	2 1.2E-
GOTERM RP DIRECT			4.4E0	1.3E-1	1
	5	5.0E-2	3.3E0	4.6E-1	4.4E- 1
	5	7.2E-2	2.5E0	5.7E-1	5.4E- 1
GOTERM_BP_DIRECT  purine nucleotide metabolic process  RT		7.2E-2	3.0E0	5.7E-1	5.4E- 1
UP_KEYWORDS  Nucleotide metabolism  RT   8	5	1.0E-1	2.0E0	3.4E-1	2.6E- 1
Annotation Cluster 97 Enrichment Score: 2.52	5		Fold	Benjamini	i FDR

Annota	ation Cluster 1	Enrichment Score: ?	G	<b></b>	Count	P_Value	Fold Change	Benjamini	i FDR
	INTERPRO	Translation elongation factor EFTu/EF1A, domain 2	<u>RT</u>	i	11	1.6E-5		2.9E-4	2.7E- 4
	INTERPRO	Translation elongation/initiation factor/Ribosomal, beta-barrel	<u>RT</u>		16	1.7E-5	3.3E0	3.1E-4	2.8E-
	INTERPRO	Elongation factor, GTP-binding domain	<u>RT</u>	•	12	7.6E-5	3.7E0	1.2E-3	4 1.1E-
	INTERPRO	Ribosomal protein S5 domain 2-type fold,	RT		12	6.0E-4	3.1F0	7.5E-3	3 6.9E-
	UP_KEYWORDS	subgroup  Elongation factor	RT		12	2.3E-3		1.1E-2	3 8.6E-
	INTERPRO	Translation elongation factor EFG, V domain	RT	-	5	7.7E-3		7.5E-2	3 6.9E-
	INTERPRO								2 6.9E-
	SMART	Elongation factor G, III-V domain	<u>RT</u>		5	7.7E-3		7.5E-2	2 1.1E-
	INTERPRO	SM00838  Translation elongation factor EFG/EF2,	<u>RT</u>		5	1.4E-2		1.2E-1	1 1.1E-
	INTERPRO	domain IV  Translation elongation factor EFTu/EF1A, C-	<u>RT</u>		4	1.5E-2		1.2E-1	1 1.2E-
	INTERPRO	terminal	<u>RT</u>	•	5	1.6E-2	4.4E0	1.3E-1	1
		<u>Translation elongation factor EF1A/initiation</u> <u>factor IF2gamma, C-terminal</u>	<u>RT</u>	i	6	2.1E-2	3.4E0	1.7E-1	1.6E- 1
	GOTERM_BP_DIRECT	<u>translational elongation</u>	<u>RT</u>	•	8	2.2E-2	2.6E0	2.7E-1	2.5E- 1
	GOTERM_MF_DIRECT	translation elongation factor activity	<u>RT</u>	i	11	4.7E-2	1.9E0	2.8E-1	2.5E- 1
	SMART	SM00889	<u>RT</u>	i	4	4.8E-2	4.1E0	2.8E-1	2.6E- 1
Annota	ation Cluster 98	Enrichment Score: 2.44	G	<b>™</b>	Count	P_Value	Fold Change	Benjamini	i FDR
	GOTERM_BP_DIRECT	positive regulation of type I interferon production	<u>RT</u>	ī.	23	9.3E-6	2.7E0	3.9E-4	3.7E- 4
	GOTERM_BP_DIRECT	transcription from RNA polymerase III promoter	<u>RT</u>	i	14	1.7E-3	2.5E0	3.7E-2	3.5E- 2
	GOTERM_CC_DIRECT	DNA-directed RNA polymerase III complex	<u>RT</u>	i .	8	2.1E-2	2.7E0	1.4E-1	1.2E- 1
	GOTERM_MF_DIRECT	RNA polymerase III activity	<u>RT</u>	i .	8	2.1E-2	2.7E0	1.4E-1	1.3E-
	KEGG_PATHWAY	Cytosolic DNA-sensing pathway	<u>RT</u>	i	18	9.0E-2	1.5E0	1.5E-1	9.0E-
Annota	ation Cluster 99	Enrichment Score: 2.43	G	· ·	Count	P_Value	Fold Change	Benjamini	FDR
	KEGG_PATHWAY	<u>Shigellosis</u>	<u>RT</u>	i	26	1.6E-4	Onlange	3.8E-4	1.7E-
	KEGG_PATHWAY	Epithelial cell signaling in Helicobacter pylori	RT		23	5.2E-3	1.8E0	1.0E-2	4 5.2E-
	KEGG_PATHWAY	infection  RIG-I-like receptor signaling pathway	RT		20	6.3E-2		1.1E-1	3 6.3E-
Annota	ation Cluster 100	Enrichment Score: 2.41	G	<u>-</u>	Count	P_Value	Fold	Benjamini	2 FDR
	GOTERM_MF_DIRECT	four-way junction DNA binding	RT .	-	10	9.2E-5	Change	1.3E-3	1.2E-
	GOTERM_CC_DIRECT	replication fork	RT		10	4.2E-4		4.6E-3	3 4.0E-
	GOTERM_MF_DIRECT			_	7	4.5E-4		5.5E-3	3 4.9E-
	INTERPRO	<u>recombinase activity</u> <u>DNA recombination and repair protein, RecA-</u>	<u>RT</u>						3 6.6E-
	GOTERM_BP_DIRECT	<u>like</u>	<u>RT</u>	-	6	5.7E-4		7.2E-3	3 1.4E-
	PIR_SUPERFAMILY	reciprocal meiotic recombination  DNA repair and recombination protein, Rad51	<u>RT</u>		14	6.0E-4		1.5E-2	2 5.4E-
		type	<u>RT</u>	i	6	1.1E-3		5.4E-2	2
	KEGG_PATHWAY	Homologous recombination	<u>RT</u>	i	14	1.4E-3		2.9E-3	1.4E- 3
	INTERPRO	DNA recombination and repair protein Rad51, C-terminal	<u>RT</u>	i e	6	1.7E-3	5.3E0	2.0E-2	1.8E- 2
	INTERPRO	DNA recombination/repair protein RecA/RadB, ATP-binding domain	<u>RT</u>	i	6	1.7E-3	5.3E0	2.0E-2	1.8E- 2
	GOTERM_BP_DIRECT	strand invasion	<u>RT</u>	i	6	2.1E-3	5.1E0	4.3E-2	4.1E- 2
	GOTERM_BP_DIRECT	mitotic recombination	<u>RT</u>	i e	8	2.6E-3	3.6E0	5.0E-2	4.8E- 2
	GOTERM_MF_DIRECT	endodeoxyribonuclease activity	<u>RT</u>	1	10	6.3E-3	2.7E0	5.5E-2	4.9E- 2
	GOTERM_BP_DIRECT	chromosome organization involved in meiotic cell cycle	<u>RT</u>	i	4	1.7E-2	5.9E0	2.2E-1	2.1E- 1
	GOTERM_CC_DIRECT	Rad51B-Rad51C-Rad51D-XRCC2 complex	<u>RT</u>	i contraction	4	3.0E-2	5.1E0	1.9E-1	1.6E- 1
	GOTERM_BP_DIRECT	response to ionizing radiation	<u>RT</u>	i .	14	5.8E-2	1.7E0	5.1E-1	4.9E-
	INTERPRO	DNA repair Rad51/transcription factor NusA, alpha-helical	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E-
	GOTERM_BP_DIRECT	meiotic DNA recombinase assembly	<u>RT</u>		3	1.3E-1	4.4E0	8.1E-1	7.7E-
_	GOTERM_BP_DIRECT	DNA recombinase assembly	RT		3	2.0E-1		1.0E0	1 9.5E-
						P_Value	Fold	Benjamini	1 FDR
Annet	ation Cluster 101	Enrichment Score: 2.4							
Annota	ation Cluster 101	Pihosomal protein S1 PNA-hinding domain	G PT	- Total			Change		1.0E-
Annota		Ribosomal protein S1, RNA-binding domain  RNA-binding domain, S1	RT RT	i i	7	9.4E-4 9.4E-4	4.8E0	1.1E-2 1.1E-2	1.0E- 2 1.0E-

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

Annot	ation Cluster 1	Enrichment Score: ?	G	<b>™</b>	Count	P_Value	Fold Change	Benjamini	i FDR
	SMART	<u>PDZ</u>	<u>RT</u>	E	33	8.3E-1	9.0E-1	1.0E0	9.0E- 1
	GOTERM_MF_DIRECT	ligand-gated ion channel activity	<u>RT</u>	i	4	9.5E-1	6.6E-1	1.0E0	9.5E- 1
Annot	ation Cluster 105	Enrichment Score: 2.21	G	170	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	DDT domain superfamily	<u>RT</u>	i	5	2.9E-3	6.2E0	3.2E-2	2.9E- 2
	UP_SEQ_FEATURE	domain:DDT	<u>RT</u>	i	5	5.4E-3	5.7E0	1.3E-1	1.3E- 1
	SMART	<u>DDT</u>	<u>RT</u>	i	5	1.4E-2	4.1E0	1.2E-1	1.1E- 1
Annot	tation Cluster 106	Enrichment Score: 2.19	G	170	Count	P_Value	Fold Change	Benjamini	i FDR
	INTERPRO	<u>Cullin, N-terminal</u>	<u>RT</u>	i	8	2.1E-4	5.0E0	3.1E-3	2.8E
	INTERPRO	<u>Cullin homology</u>	<u>RT</u>	i	7	9.4E-4	4.8E0	1.1E-2	1.0E- 2
	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in NEDD8)	<u>RT</u>	i	6	1.1E-3	5.8E0	3.1E-2	3.0E 2
	INTERPRO	Cullin protein, neddylation domain	<u>RT</u>	i .	6	4.0E-3	4.6E0	4.2E-2	3.8E 2
	SMART	CULLIN	<u>RT</u>	i	6	1.2E-2	3.5E0	1.0E-1	9.0E 2
	INTERPRO	<u>Cullin, conserved site</u>	<u>RT</u>	i .	5	1.6E-2	4.4E0	1.3E-1	1.2E 1
	SMART	<u>SM00884</u>	<u>RT</u>	i .	6	2.5E-2	3.1E0	1.9E-1	1.7E 1
	INTERPRO	Cullin repeat-like-containing domain	<u>RT</u>	i	6	3.2E-2	3.1E0	2.4E-1	2.2E
	GOTERM_CC_DIRECT	cullin-RING ubiquitin ligase complex	<u>RT</u>	i	4	1.6E-1	2.8E0	6.4E-1	5.6E
Annot	ation Cluster 107	Enrichment Score: 2.16	G	170	Count	P_Value	Fold Change	Benjamini	
	GOTERM_MF_DIRECT	guanyl nucleotide binding	<u>RT</u>		8	9.7E-5	<u> </u>	1.4E-3	1.2E 3
	INTERPRO	G-protein alpha subunit, group Q	RT		4			1.2E-1	1.1E
	GOTERM_BP_DIRECT	phospholipase C-activating dopamine	RT		4		2.4E0	1.0E0	1 9.5E
Annot	tation Cluster 108	receptor signaling pathway  Enrichment Score: 2.1	G	·	Count	P_Value	Fold	Roniomini	1 i FDR
	UP_KEYWORDS	rRNA-binding	RT		15	8.6E-7	Change 4.3E0	5.9E-6	4.6E
_ 	INTERPRO	KOW	RT		8	7.5E-5		1.2E-3	6 1.1E
_ _	INTERPRO	RNA-binding S4 domain	RT		5	7.7E-3		7.5E-2	3 6.9E
	UP_SEQ_FEATURE								2 3.8E
	SMART	domain:S4 RNA-binding	<u>RT</u>		5		4.3E0	3.9E-1	1 2.6E
	INTERPRO	<u>S4</u>	<u>RT</u>	1	4		4.1E0	2.8E-1	1 3.6E
	INTERPRO	<u>Ribosomal protein S4e</u>	<u>RT</u>	1	3	7.0E-2		3.9E-1	3.6E
		Ribosomal protein S4e, N-terminal	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	1
	INTERPRO	Ribosomal protein S4e, central region	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E
	INTERPRO	Ribosomal protein S4e, N-terminal, conserved site	<u>RT</u>	1	3	7.0E-2	6.2E0	3.9E-1	3.6E 1
	PIR_SUPERFAMILY	ribosomal protein S4a/S4e	<u>RT</u>	i	3	9.1E-2	•	7.7E-1	7.6E 1
Annot	tation Cluster 109	Enrichment Score: 2.09	G	<b>17</b>	Count	P_Value	Fold Change	Benjamini	
	KEGG_PATHWAY	<u>Phototransduction</u>	<u>RT</u>	i	14	5.9E-4	2.7E0	1.3E-3	6.1E 4
	GOTERM_CC_DIRECT	photoreceptor disc membrane	<u>RT</u>	i e	8	2.1E-2	2.7E0	1.4E-1	1.2E 1
	GOTERM_BP_DIRECT	<u>regulation of rhodopsin mediated signaling</u> <u>pathway</u>	<u>RT</u>	1	10	4.4E-2	2.0E0	4.2E-1	4.0E 1
Annot	tation Cluster 110	Enrichment Score: 2.02	G	TW Commonwealth	Count	P_Value	Fold Change	Benjamini	i FDR
	BIOCARTA	Cadmium induces DNA synthesis and proliferation in macrophages	<u>RT</u>	i	14	2.3E-4	2.5E0	2.6E-3	1.8E 3
	BIOCARTA	Links between Pyk2 and Map Kinases	<u>RT</u>	i .	18	1.7E-3	2.0E0	1.3E-2	8.5E
	BIOCARTA	CXCR4 Signaling Pathway	<u>RT</u>	i .	16	2.2E-3	2.1E0	1.4E-2	9.5E
	BIOCARTA	CCR3 signaling in Eosinophils	<u>RT</u>	i	13	3.8E-2	1.7E0	1.1E-1	7.4E 2
	BIOCARTA	Aspirin Blocks Signaling Pathway Involved in Platelet Activation	<u>RT</u>	i .	11	1.0E-1	1.6E0	2.6E-1	1.7E
	BIOCARTA	Erk and PI-3 Kinase Are Necessary for	<u>RT</u>	1	11	2.2E-1	1.4E0	4.5E-1	3.1E
Annot	tation Cluster 111	Collagen Binding in Corneal Epithelia  Enrichment Score: 1.97	G	-	Count	P_Value		Baniamini	1 i FDR
	INTERPRO	SANT/Myb domain	RT	1	18		Change 2.6E0	2.9E-3	2.6
	GOTERM_MF_DIRECT	transcription factor activity, RNA polymerase	RT		7		5.2E0	5.5E-3	3 4.9E
	INTERPRO	II transcription factor recruiting  Myb domain	RT		6			7.5E-2	3 6.9E
		Pryb domain	IXI	1	J	7.7E-3	7.150	7.JL-Z	2

Annota	ation Cluster 1	Enrichment Score: ?	G	<b>™</b>	Count	P_Value	Fold Change	Benjamini	FDR
	SMART	SANT	<u>RT</u>	i	18	2.1E-2	•	1.6E-1	1.4E 1
	INTERPRO	SANT domain	<u>RT</u>	1	8	1.1E-1	1.9E0	5.9E-1	5.4E
	INTERPRO	<u>Homeodomain-like</u>	<u>RT</u>	1	22	1.0E0	4.1E-1	1.0E0	1.0E
Annota	ation Cluster 112	Enrichment Score: 1.96	G	<b>15</b>	Count	P_Value	Fold Change	Benjamini	
	GOTERM_MF_DIRECT	transcription factor activity, RNA polymerase II transcription factor recruiting	<u>RT</u>	i	7	4.5E-4	5.2E0	5.5E-3	4.9E 3
	UP_SEQ_FEATURE	domain:HTH myb-type 1	<u>RT</u>	i	5	2.0E-3	6.8E0	5.4E-2	5.2E 2
	UP_SEQ_FEATURE	domain:HTH myb-type 2	<u>RT</u>	i .	5	2.0E-3	6.8E0	5.4E-2	5.2E 2
	INTERPRO	Myb-like domain	<u>RT</u>	i .	6	4.0E-3	4.6E0	4.2E-2	3.8E 2
	INTERPRO	Myb domain	<u>RT</u>	1	6	7.7E-3	4.1E0	7.5E-2	6.9I
	UP_SEQ_FEATURE	domain:HTH myb-type 3	<u>RT</u>	1	4	1.1E-2	6.8E0	2.3E-1	2.2
	UP_SEQ_FEATURE	domain:Myb-like 1	<u>RT</u>	i de	3	5.8E-2	6.8E0	9.1E-1	8.81
	UP_SEQ_FEATURE	domain:Myb-like 2	<u>RT</u>	1	3	5.8E-2	6.8E0	9.1E-1	8.8
	INTERPRO	C-myb, C-terminal	RT		3	7.0E-2	6.2E0	3.9E-1	3.6
_ _	UP_SEQ_FEATURE	DNA-binding region:H-T-H motif	RT		7	1.7E-1		1.0E0	1 9.7l
Annote	ation Cluster 113	Enrichment Score: 1.95	G	· ·	Count		Fold		1 EDE
	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 1	RT	i	4	P_Value	•	2.3E-1	2.2
 	UP_SEQ_FEATURE								1 2.2
	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 2	<u>RT</u>		4	1.1E-2		2.3E-1	1 2.2
	UP_SEQ_FEATURE	domain:DAZ-like 1	<u>RT</u>	1	4		6.8E0		1 2.2
_	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 3	<u>RT</u>	•	4	1.1E-2	6.8E0	2.3E-1	1
		domain:DAZ-like 10	<u>RT</u>	i	4	1.1E-2	6.8E0	2.3E-1	2.2
	UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 4	<u>RT</u>	•	4	1.1E-2	6.8E0	2.3E-1	2.2
	UP_SEQ_FEATURE	domain:DAZ-like 11	<u>RT</u>	1	4	1.1E-2	6.8E0	2.3E-1	2.2
	UP_SEQ_FEATURE	domain:DAZ-like 12	<u>RT</u>	i	4	1.1E-2	6.8E0	2.3E-1	2.2 1
	UP_SEQ_FEATURE	domain:DAZ-like 13	<u>RT</u>	1	4	1.1E-2	6.8E0	2.3E-1	2.2 1
	UP_SEQ_FEATURE	domain:DAZ-like 14	<u>RT</u>	i	4	1.1E-2	6.8E0	2.3E-1	2.2
	UP_SEQ_FEATURE	domain:DAZ-like 15	<u>RT</u>	i .	4	1.1E-2	6.8E0	2.3E-1	2.2
	UP_SEQ_FEATURE	domain:DAZ-like 2	<u>RT</u>	1	4	1.1E-2	6.8E0	2.3E-1	2.2
	UP_SEQ_FEATURE	domain:DAZ-like 3	<u>RT</u>	1	4	1.1E-2	6.8E0	2.3E-1	2.2l
	UP_SEQ_FEATURE	domain:DAZ-like 4	<u>RT</u>	1	4	1.1E-2	6.8E0	2.3E-1	2.21
	UP_SEQ_FEATURE	domain:DAZ-like 5	<u>RT</u>	4	4	1.1E-2	6.8E0	2.3E-1	2.2
	UP_SEQ_FEATURE	domain:DAZ-like 6	<u>RT</u>		4	1.1E-2	6.8E0	2.3E-1	2.2
_ 	UP_SEQ_FEATURE	domain:DAZ-like 7	RT		4	1.1E-2		2.3E-1	1 2.2
_ _	UP_SEQ_FEATURE	domain:DAZ-like 8	RT		4	1.1E-2	6.8E0	2.3E-1	1 2.2
_ 	UP_SEQ_FEATURE	domain:DAZ-like 9	RT	-	4	1.1E-2		2.3E-1	1 2.2l
Annot	ation Cluster 114		G			1	Fold	Daniamini	1
Annota	GOTERM_BP_DIRECT	Enrichment Score: 1.95  regulation of interferon-gamma-mediated	RT	i	Count 10	P_Value 4.0E-5	Change 4.6E0	1.4E-3	1.3
	BBID	<u>signaling pathway</u>		•					3 9.8I
	BIOCARTA	75.Stats activators of Apoptosis	<u>RT</u>	1	4		2.9E0		1 3.8
		<u>IFN gamma signaling pathway</u>	<u>RT</u>	i	4	3.0E-1	Fold	5.5E-1	1
Annota	ation Cluster 115  UP_SEQ_FEATURE	Enrichment Score: 1.95	G		Count	P_Value	Change		
		domain:FBA	<u>RT</u>	i	5	5.4E-3		1.3E-1	1.3
	INTERPRO	<u>F-box associated (FBA) domain</u>	<u>RT</u>	•	5	7.7E-3	5.2E0	7.5E-2	6.91
	SMART	SM01198	<u>RT</u>	i	5	3.5E-2		2.4E-1	2.11
Annota	ation Cluster 116	Enrichment Score: 1.93	G	<b>100</b>	Count	P_Value	Fold Change	Benjamini	
	GOTERM_BP_DIRECT	MyD88-dependent toll-like receptor signaling pathway	<u>RT</u>	•	22	2.4E-9	4.0E0	2.1E-7	2.0I 7
	GOTERM_BP_DIRECT	regulation of cytokine secretion	<u>RT</u>	i .	10	4.3E-6	5.4E0	2.1E-4	2.0
	UP_SEQ_FEATURE	repeat:LRR 22	<u>RT</u>	•	10	4.5E-6	5.7E0	1.9E-4	1.9 4

	ition Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamin	i FDR
	UP_SEQ_FEATURE	repeat:LRR 24	<u>RT</u>	i	6	1.1E-3	Change	3.1E-2	3.0E-
	GOTERM_BP_DIRECT	I-kappaB phosphorylation	RT		8	1.4E-3		3.0E-2	2 2.9E-
	GOTERM_BP_DIRECT	positive regulation of chemokine production	RT		9	3.7E-3		6.8E-2	2 6.5E-
	UP_SEQ_FEATURE	domain:TIR	RT	1	10	6.9E-3		1.6E-1	2 1.6E-
	GOTERM_BP_DIRECT	positive regulation of interleukin-8 production		-	11	7.1E-3		1.2E-1	1 1.1E-
	INTERPRO								1 1.1E-
	GOTERM_BP_DIRECT	Toll-like receptor  positive regulation of NF-kappaB import into	<u>RT</u>	-	4	1.5E-2		1.2E-1	1 2.1E-
	INTERPRO	nucleus  Toll/interleukin-1 receptor homology (TIR)	<u>RT</u>		9	1.7E-2		2.2E-1	1
	GOTERM_BP_DIRECT	<u>domain</u>	<u>RT</u>	•	10	1.7E-2	2.4E0	1.4E-1	1
		biosynthetic process	<u>RT</u>	1	4	1.7E-2	5.9E0	2.2E-1	1
	GOTERM_BP_DIRECT	biosynthetic process	<u>RT</u>	i	5	1.8E-2	4.2E0	2.3E-1	1
	PIR_SUPERFAMILY	[Parent=PIRSF800008]	<u>RT</u>	i	4	2.2E-2	5.3E0	3.6E-1	3.5E- 1
	GOTERM_BP_DIRECT	positive regulation of interferon-beta production	<u>RT</u>	i	10	2.8E-2	2.2E0	3.3E-1	3.1E- 1
	GOTERM_BP_DIRECT								
	GOTERM_BP_DIRECT	Since   Sinc							
	GOTERM_BP_DIRECT	Diosynthetic process   Care   Care							
	GOTERM_BP_DIRECT	toll-like receptor, 1/2/4/6/10 types   RT							
	SMART		<u>RT</u>	1	10	5.0E-2	1.9E0	2.9E-1	2.6E- 1
	GOTERM_CC_DIRECT	endolysosome membrane	<u>RT</u>	i	5	1.1E-1	2.6E0	4.9E-1	4.3E-
	GOTERM_BP_DIRECT	positive regulation of interleukin-6 production	<u>RT</u>	i	12	1.2E-1	1.6E0	8.1E-1	7.7E-
	GOTERM_BP_DIRECT		<u>RT</u>	1	5	1.3E-1	2.5E0	8.1E-1	7.7E-
	GOTERM_BP_DIRECT	positive regulation of tumor necrosis factor	RT		11	2.6E-1	1.4E0	1.0E0	9.5E-
	UP_KEYWORDS	<u>production</u> <u>Inflammatory response</u>	10   1.7E-2   2.4E0   1.4E-1   1   1   1.4E-2   1.4E-1   1   1   1   1.4E-2   1.4E-1   1   1   1.4E-2   1.4E-1   1   1   1.4E-2   1.4E-1   1   1.4E-2   1.4E-1   1   1.4E-2   1.4E-2						
	GOTERM_MF_DIRECT			-					1 8.9E-
	GOTERM_BP_DIRECT								1 9.5E-
	GOTERM_BP_DIRECT	cellular response to lipoteichoic acid			3	4.6E-1		1.0E0	1 9.5E-
	GOTERM_CC_DIRECT		<u>RT</u>	-					1 8.7E-
	GOTERM_MF_DIRECT	phagocytic vesicle membrane transmembrane signaling receptor activity	RT RT		8 16	1.0E0	8.6E-1 4.5E-1		1 1.0E0
	ition Cluster 117	Enrichment Score: 1.9	G	TT	Count	P_Value	Fold	Ponjamin	
	GOTERM_BP_DIRECT	regulation of axonogenesis	<u>RT</u>	ī	12	5.7E-4		1.4E-2	1.4E- 2
	GOTERM_MF_DIRECT	Roundabout binding	<u>RT</u>	i	6	9.1E-3	4.0E0	7.2E-2	6.4E-
	GOTERM_BP_DIRECT	Roundabout signaling pathway	<u>RT</u>	1	6	3.8E-2	3.0E0	3.8E-1	3.6E-
	GOTERM_BP_DIRECT	axon extension involved in axon guidance	<u>RT</u>		5	1.3E-1	2.5E0	8.1E-1	7.7E-
Annota	ition Cluster 118	Enrichment Score: 1.89	G	- 	Count	P_Value	Fold	Benjamin	1 FDR
	UP_SEQ_FEATURE	domain:C2 tensin-type	RT	i	6	5.1E-3	Change	1.3E-1	1.2E-
	UP_SEQ_FEATURE	domain:Phosphatase tensin-type	RT		6	9.0E-3		2.1E-1	1 2.0E-
	INTERPRO	Tensin phosphatase, C2 domain	RT.		6	1.3E-2		1.2E-1	1 1.1E-
	SMART								1 2.6E-
		SM01326 Envishment Search 1.96	<u>RT</u>	1	6 Count	:	2.7E0 Fold	:	1
	tion Cluster 119  GOTERM_BP_DIRECT	Enrichment Score: 1.86	G	-		P_Value	Change		5.7E-
	GOTERM BP DIRECT	protein refolding	<u>RT</u>		10	2.0E-4		6.0E-3	3 2.2E-
	KEGG_PATHWAY	response to unfolded protein	<u>RT</u>	•	14	1.8E-2		2.3E-1	1
		Antigen processing and presentation	<u>RT</u>	i	14	7.2E-1	Fold		7.2E- 1
	GOTERM ME DIRECT	Enrichment Score: 1.85	G	- T	Count	P_Value	Change	Benjamin	
	GOTERM_MF_DIRECT	receptor signaling protein tyrosine kinase activity	<u>RT</u>	•	9	2.0E-5	5.4E0	3.4E-4	3.0E- 4
	GOTERM_MF_DIRECT	insulin receptor substrate binding	<u>RT</u>	i	9	6.3E-5	4.9E0	9.6E-4	8.5E- 4
	INTERPRO	EGF receptor, L domain	<u>RT</u>	1	6	1.7E-3	5.3E0	2.0E-2	1.8E- 2
	INTERPRO	Furin-like cysteine-rich domain	<u>RT</u>	i	6	1.7E-3	5.3E0	2.0E-2	1.8E- 2

Annota	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamini	FDR
	SMART	<u>FU</u>	RT	1	9	5.1E-2		2.9E-1	2.6E-
	INTERPRO	Tyrosine-protein kinase, insulin-like receptor	RT		3	7.0E-2	6.2F0	3 9F-1	1 3.6E-
	PIR_SUPERFAMILY		RT	-	3	9.1E-2			1 7.6E-
	INTERPRO	insulin receptor  Tyrosine protein kinase, EGF/ERB/XmrK							1 5.6E-
	PIR_SUPERFAMILY	receptor	<u>RT</u>	•	3	1.2E-1	4.6E0	6.1E-1	1 9.9E-
		tyrosine-protein kinase, EGF receptor type	<u>RT</u>	i	3	1.6E-1	4.0E0	1.0E0	1
	INTERPRO	<u>Tyrosine-protein kinase, receptor class II,</u> <u>conserved site</u>	<u>RT</u>	•	3	5.5E-1	1.7E0	1.0E0	9.1E- 1
Appote	UP_SEQ_FEATURE ation Cluster 121	domain:Fibronectin type-III 3  Enrichment Score: 1.85	RT G	<u>.</u>	6 Count	1.0E0	Fold		1.0E0
Allilota	GOTERM_BP_DIRECT			_		P_Value	Change		7.2E-
	GOTERM_CC_DIRECT	sister chromatid cohesion	<u>RT</u>	•	33	2.7E-4			3 2.1E-
	UP_KEYWORDS	<u>kinetochore</u>	<u>RT</u>	•	24	2.7E-3	1.9E0	2.4E-2	2
	_	<u>Centromere</u>	<u>RT</u>	•	32	7.4E-3	1.6E0	3.3E-2	2.6E- 2
	UP_KEYWORDS	<u>Kinetochore</u>	<u>RT</u>	i .	18	2.7E-1	1.2E0	7.8E-1	6.1E- 1
	GOTERM_CC_DIRECT	condensed chromosome kinetochore	<u>RT</u>	1	16	3.9E-1	1.2E0	1.0E0	8.7E- 1
Annota	ation Cluster 122	Enrichment Score: 1.84		PR .	Count	P_Value	Fold Change	Benjamini	FDR
	KEGG_PATHWAY	<u>Apoptosis</u>	<u>RT</u>	i	26	8.5E-5	2.2E0	2.2E0 3.9E-1 3.3E0 7.7E-1 3.6E0 6.1E-1 3.0E0 1.0E0 3.9E-1 1.0E0 3.9E-1 1.0E0 3.9E-1 1.0E0 3.3E-2 3.6E0 3.3E-2 3.2E0 7.8E-1 3.2E0 1.0E0 3.3E-1 3.2E0 2.1E-4 3.3E0 2.3E-1 3.2E0 6.4E-1 3.2E0 6.4E-1 3.2E0 7.6E-1	9.7E- 5
	BIOCARTA	HIV-I Nef	<u>RT</u>	•	26	9.4E-2	1.3E0	2.3E-1	1.6E-
	BIOCARTA	Induction of apoptosis through DR3 and	<u>RT</u>	1	13	3.7E-1	1.2E0	6.4E-1	4.3E-
Annota	ation Cluster 123	DR4/5 Death Receptors  Enrichment Score: 1.79	G						FDR
	BIOCARTA	p53 Signaling Pathway	RT	i i	13				6.7E-
	GOTERM_CC_DIRECT	cyclin-dependent protein kinase holoenzyme	RT	Ţ.	7				3 1.2E-
	BBID	complex				2.1E-2			1 7.6E-
	BBID	4.cyclins & p27 cell cycle	<u>RT</u>	•	5	4.9E-2	2.9E0	7.6E-1	1
	ВЫЛ	94.E2F transcriptional activity cell cycle	<u>RT</u>	i	6	4.9E-2		7.6E-1	7.6E- 1
Annota	ation Cluster 124	Enrichment Score: 1.78	G	<b>13</b>	Count	P_Value	Fold Change	Benjamini	
	BIOCARTA	Regulation of cell cycle progression by Plk3	<u>RT</u>	•	8	2.1E-3	3.1E0	1.4E-2	9.5E- 3
	GOTERM_BP_DIRECT	replicative senescence	<u>RT</u>	i .	7	8.4E-3	3.5E0	1.3E-1	1.2E- 1
	BIOCARTA	Role of BRCA1, BRCA2 and ATR in Cancer Susceptibility	<u>RT</u>	1	10	2.6E-1	1.4E0	5.1E-1	3.4E- 1
Annota	ation Cluster 125	Enrichment Score: 1.7	G	<b>178</b>	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:HSA	<u>RT</u>	i	4	1.1E-2	6.8E0	2.3E-1	2.2E-
	INTERPRO	Helicase/SANT-associated, DNA binding	<u>RT</u>	1	4	1.5E-2	6.2E0	1.2E-1	1.1E-
	SMART	<u>HSA</u>	RT		4	4.8E-2	4.1E0	2.8E-1	2.6E-
Annota	ation Cluster 126	Enrichment Score: 1.67	G	·	Count	P_Value	Fold	Benjamini	1 FDR
	INTERPRO	POLO box duplicated domain	RT	-	5		Change 6.2E0	3.2E-2	2.9E-
	UP_SEQ_FEATURE			•					2 8.8E-
	UP_SEQ_FEATURE	domain:POLO box 1	<u>RT</u>	•	3		6.8E0	9.1E-1	1 8.8E-
	or _ora_i exione	domain:POLO box 2	RT		3	5.8E-2		9.1E-1	1
		domain.FOLO BOX 2	KI				: Eald		Con .
Annota	ation Cluster 127	Enrichment Score: 1.66	G		Count	P_Value	Fold Change	Benjamini	
Annota	INTERPRO						Fold Change 2.6E0	Benjamini	1.0E- 4
Annota		Enrichment Score: 1.66	G	- -	Count		Change 2.6E0		1.0E-
Annota	INTERPRO	Enrichment Score: 1.66 <u>Ubiquitin</u>	G RT	- -	Count 25	5.7E-6 2.8E-5	Change 2.6E0	1.1E-4 4.9E-4	1.0E- 4
Annota	INTERPRO INTERPRO	Enrichment Score: 1.66  Ubiquitin  Ubiquitin subgroup  UBQ  cross-link:Glycyl lysine isopeptide (Gly-Lys)	RT RT	- -	25 10	5.7E-6 2.8E-5 4.6E-4	2.6E0 4.8E0	1.1E-4 4.9E-4 5.3E-3	1.0E- 4 4.4E- 4 4.8E-
Annota	INTERPRO INTERPRO SMART	Ubiquitin Ubiquitin subgroup UBQ	RT RT RT	- -	25 10 22	5.7E-6 2.8E-5 4.6E-4	2.6E0 4.8E0 2.1E0 3.4E0	1.1E-4 4.9E-4 5.3E-3	1.0E-4 4.4E-4 4.8E-3 5.9E-2 1.2E-
Annota	INTERPRO INTERPRO SMART UP_SEQ_FEATURE	Enrichment Score: 1.66  Ubiquitin  Ubiquitin subgroup  UBQ  cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)	G RT RT RT RT	- -	25 10 22 9	5.7E-6 2.8E-5 4.6E-4 2.3E-3	2.6E0 4.8E0 2.1E0 3.4E0 3.5E0	1.1E-4 4.9E-4 5.3E-3 6.1E-2	1.0E- 4 4.4E- 4 4.8E- 3 5.9E- 2 1.2E- 1
Annota	INTERPRO INTERPRO SMART UP_SEQ_FEATURE GOTERM_BP_DIRECT	Ubiquitin  Ubiquitin subgroup  UBQ  cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)  regulation of necrotic cell death  regulation of type I interferon production	RT RT RT RT RT	- -	25 10 22 9 7	5.7E-6 2.8E-5 4.6E-4 2.3E-3 8.4E-3 1.3E-2	2.6E0 4.8E0 2.1E0 3.4E0 3.5E0 3.2E0	1.1E-4 4.9E-4 5.3E-3 6.1E-2 1.3E-1 1.9E-1	1.0E-4 4.4E-4 4.8E-3 5.9E-2 1.2E-1 1.8E-1 3.8E-
Annota	INTERPRO INTERPRO SMART  UP_SEQ_FEATURE GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  UP_SEQ_FEATURE	Ubiquitin  Ubiquitin subgroup  UBQ  cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)  regulation of necrotic cell death  regulation of type I interferon production  binding site:Activating enzyme	RT RT RT RT RT RT RT	- -	25 10 22 9 7 7 5	5.7E-6 2.8E-5 4.6E-4 2.3E-3 8.4E-3 1.3E-2 2.0E-2	2.6E0 4.8E0 2.1E0 3.4E0 3.5E0 3.2E0 4.3E0	1.1E-4 4.9E-4 5.3E-3 6.1E-2 1.3E-1 1.9E-1 3.9E-1	1.0E-4 4.4E-4 4.8E-3 5.9E-2 1.2E-1 1.8E-1 3.8E-1
Annota	INTERPRO INTERPRO SMART  UP_SEQ_FEATURE GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  GOTERM_BP_DIRECT	Ubiquitin  Ubiquitin subgroup  UBQ  cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)  regulation of necrotic cell death  regulation of type I interferon production  binding site:Activating enzyme  negative regulation of type I interferon production	RT RT RT RT RT RT RT RT	- -	25 10 22 9 7 7 5 11	5.7E-6 2.8E-5 4.6E-4 2.3E-3 8.4E-3 1.3E-2 2.0E-2 2.1E-2	2.6E0 4.8E0 2.1E0 3.4E0 3.5E0 3.2E0 4.3E0 2.2E0	1.1E-4 4.9E-4 5.3E-3 6.1E-2 1.3E-1 1.9E-1	1.0E-4 4.4E-4 4.8E-3 5.9E-2 1.2E-1 1.8E-1 3.8E-1 2.5E-1
Annota	INTERPRO INTERPRO SMART  UP_SEQ_FEATURE GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  GOTERM_BP_DIRECT  INTERPRO	Ubiquitin  Ubiquitin subgroup  UBQ  cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)  regulation of necrotic cell death  regulation of type I interferon production  binding site:Activating enzyme  negative regulation of type I interferon production  Ubiquitin conserved site	RT RT RT RT RT RT RT	- -	25 10 22 9 7 7 5	5.7E-6 2.8E-5 4.6E-4 2.3E-3 8.4E-3 1.3E-2 2.0E-2	2.6E0 4.8E0 2.1E0 3.4E0 3.5E0 3.2E0 4.3E0 2.2E0	1.1E-4 4.9E-4 5.3E-3 6.1E-2 1.3E-1 1.9E-1 3.9E-1	1.0E-4 4.4E-4 4.8E-3 5.9E-2 1.2E-1 1.8E-1 2.5E-1 1.6E-1
Annota	INTERPRO INTERPRO SMART  UP_SEQ_FEATURE GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  GOTERM_BP_DIRECT  INTERPRO  GOTERM_BP_DIRECT	Ubiquitin  Ubiquitin subgroup  UBQ  cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)  regulation of necrotic cell death  regulation of type I interferon production  binding site:Activating enzyme  negative regulation of type I interferon production  Ubiquitin conserved site  negative regulation of epidermal growth factor receptor signaling pathway.	RT	- -	25 10 22 9 7 7 5 11	5.7E-6 2.8E-5 4.6E-4 2.3E-3 8.4E-3 1.3E-2 2.0E-2 2.1E-2	2.6E0 4.8E0 2.1E0 3.4E0 3.5E0 4.3E0 4.3E0 2.2E0 3.4E0	1.1E-4 4.9E-4 5.3E-3 6.1E-2 1.3E-1 1.9E-1 3.9E-1 2.6E-1	1.0E-4 4.4E-4 4.8E-3 5.9E-2 1.2E-1 1.8E-1 2.5E-1 1.6E-
Annota  O O O O O O O O O O O O O O O O O O	INTERPRO INTERPRO SMART  UP_SEQ_FEATURE GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  GOTERM_BP_DIRECT  INTERPRO	Ubiquitin  Ubiquitin subgroup  UBQ  cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)  regulation of necrotic cell death  regulation of type I interferon production  binding site:Activating enzyme  negative regulation of type I interferon production  Ubiquitin conserved site  negative regulation of epidermal growth	RT	- -	Count  25  10  22  9  7  7  5  11  6	5.7E-6 2.8E-5 4.6E-4 2.3E-3 8.4E-3 1.3E-2 2.0E-2 2.1E-2	Change 2.6E0 4.8E0 2.1E0 3.4E0 3.5E0 4.3E0 4.3E0 2.2E0 3.4E0 2.0E0	1.1E-4 4.9E-4 5.3E-3 6.1E-2 1.3E-1 1.9E-1 3.9E-1 2.6E-1 1.7E-1	1.0E-4 4.4E-4 4.8E-3 5.9E-2 1.2E-1 1.8E-1 2.5E-1 1.6E-1

Annot	ation Cluster 1	Enrichment Score: ?	G	100	Count	P_Value	Fold Change	Benjamin	i FDR
	UP_SEQ_FEATURE	site:Essential for function	<u>RT</u>	i	4	7.0E-2		1.0E0	9.7E
	UP_SEQ_FEATURE	chain:Ubiquitin	<u>RT</u>	4	4	7.0E-2	3.9E0	1.0E0	9.7E
_ _	UP_SEQ_FEATURE	compositionally biased region:Lys-rich (highly		-					1 9.7E
_		basic)	<u>RT</u>		4	7.0E-2	3.9E0	1.0E0	1 9.7E
	UP_SEQ_FEATURE	chain:40S ribosomal protein S27a	<u>RT</u>		4	7.0E-2	3.9E0	1.0E0	1
	GOTERM_BP_DIRECT	<u>virion assembly</u>	<u>RT</u>	i	5	1.3E-1	2.5E0	8.1E-1	7.7E 1
	GOTERM_BP_DIRECT	glycogen biosynthetic process	<u>RT</u>	i	8	1.3E-1	1.8E0	8.1E-1	7.7E 1
	GOTERM_BP_DIRECT	<u>viral life cycle</u>	<u>RT</u>		9	1.4E-1	1.7E0	8.1E-1	7.7E
٦	GOTERM_BP_DIRECT	intracellular transport of virus	<u>RT</u>		10	5.0E-1	1.2E0	1.0E0	9.5E
ے ا	GOTERM_CC_DIRECT			_					1 9.1E
ر ا	GOTERM_BP_DIRECT	endocytic vesicle membrane endosomal transport	RT RT		8 5	1.0E0	7.7E-1 4.5E-1		1 1.0E
nnot	ation Cluster 128	Enrichment Score: 1.66	G	178	Count	P_Value	Fold	Roniamin	
7	UP_KEYWORDS		RT	_	20	5.3E-5	Change	3.0E-4	2.3E
_	GOTERM_MF_DIRECT	<u>Exonuclease</u>		•					4 6.3E
J		<u>3'-5'-exoribonuclease activity</u>	<u>RT</u>	•	11	6.2E-4	3.3E0	7.1E-3	3
	GOTERM_BP_DIRECT	rRNA catabolic process	<u>RT</u>	•	8	6.7E-4	4.3E0	1.6E-2	1.6E 2
	GOTERM_BP_DIRECT	RNA phosphodiester bond hydrolysis, exonucleolytic	<u>RT</u>	•	12	4.0E-3	2.5E0	7.2E-2	6.9E 2
	UP_KEYWORDS	<u>Nuclease</u>	<u>RT</u>	8	31	9.7E-3	1.6E0	4.3E-2	3.3E 2
	INTERPRO	Ribonuclease II/R, conserved site	<u>RT</u>	1	4	1.5E-2	6.2E0	1.2E-1	1.1E
)	GOTERM_CC_DIRECT	nuclear exosome (RNase complex)	RT		7		3.0E0		1 1.2E
)	UP_KEYWORDS			•					1 9.0E
J	_	<u>Exosome</u>	<u>RT</u>	•	6	3.0E-2	3.2E0	1.2E-1	2
	GOTERM_CC_DIRECT	<u>cytoplasmic exosome (RNase complex)</u>	<u>RT</u>	1	6	4.1E-2	2.9E0	2.4E-1	2.1E 1
)	GOTERM_BP_DIRECT	nuclear mRNA surveillance	<u>RT</u>	1	5	5.0E-2	3.3E0	4.6E-1	4.4E 1
)	INTERPRO	Exoribonuclease, phosphorolytic domain 1	<u>RT</u>	1	4	8.8E-2	3.5E0	4.7E-1	4.3E
)	GOTERM_CC_DIRECT	exosome (RNase complex)	<u>RT</u>	4	6	9.3E-2	2.4E0	4.5E-1	3.9
ر ا	INTERPRO	Exoribonuclease, phosphorolytic domain 2		-	4	1.2E-1		6.1E-1	1 5.6E
J	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process,	<u>RT</u>		4				1 9.4E
J		exonucleolytic, 3'-5'	<u>RT</u>	•	4	1.8E-1	2.6E0	9.9E-1	1
	GOTERM_MF_DIRECT	exoribonuclease activity	<u>RT</u>	1	5	2.0E-1	2.1E0	7.6E-1	6.7E 1
	INTERPRO	PNPase/RNase PH domain	<u>RT</u>	1	3	2.5E-1	3.1E0	9.6E-1	8.8E 1
	GOTERM_BP_DIRECT	<u>U4 snRNA 3'-end processing</u>	<u>RT</u>	1	3	4.0E-1	2.2E0	1.0E0	9.5E
nnot	ation Cluster 129	Enrichment Score: 1.66	G	<b>- 19</b>	Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	Glutamine amidotransferase	RT		6	5.7E-4		7.2E-3	6.6E
- -	UP_SEQ_FEATURE	domain:Glutamine amidotransferase type-1	RT		5	2.0E-3		5.4E-2	3 5.2E
J	UP_KEYWORDS		_	•					2 1.9E
J	_	<u>Pyrimidine biosynthesis</u>	<u>RT</u>	•	4	6.8E-2	3.9E0	2.4E-1	1
	UP_SEQ_FEATURE	active site:For GATase activity	<u>RT</u>	1	4	1.0E-1	3.4E0	1.0E0	9.7E 1
	GOTERM_BP_DIRECT	glutamine metabolic process	<u>RT</u>	1	7	1.1E-1	2.1E0	7.2E-1	6.9E 1
	UP_KEYWORDS	Glutamine amidotransferase	<u>RT</u>	1	4	1.3E-1	3.1E0	4.3E-1	3.3E
nnot	ation Cluster 130	Enrichment Score: 1.65	G	170	Count	P_Value	Fold	Benjamin	i FDR
<b>1</b>	UP_KEYWORDS	Protein kinase inhibitor	RT	-	7			4.3E-2	3.3E
)	GOTERM_MF_DIRECT	mitogen-activated protein kinase kinase							2 7.0E
J		binding	<u>RT</u>	•	8	1.0E-2		7.9E-2	2
)	INTERPRO	Pseudokinase tribbles family/serine- threonine-protein kinase 40	<u>RT</u>	i	4	1.5E-2	6.2E0	1.2E-1	1.1E 1
	GOTERM_BP_DIRECT	regulation of MAP kinase activity	<u>RT</u>	i	5	5.0E-2	3.3E0	4.6E-1	4.4E 1
	GOTERM_MF_DIRECT	<u>ubiquitin-protein transferase regulator activity</u>	<u>RT</u>	1	3	7.5E-2	6.0E0	3.9E-1	3.4E 1
nnot	ation Cluster 131	Enrichment Score: 1.65	G	<b>178</b>	Count	P_Value	Fold Change	Benjamin	i FDR
)	KEGG_PATHWAY	Hedgehog signaling pathway	RT	-	12	7.7E-3	Change	1.4E-2	7.78
	BIOCARTA			_					3 3.5E
J		Sonic Hedgehog (Shh) Pathway	<u>RT</u>	•	11	1.2E-2		5.1E-2	2
	GOTERM CC DIRECT				8	1 2E 1	1 OEO	5.0E-1	4.4
	GOTERM_CC_DIRECT	<u>ciliary base</u>	<u>RT</u>	i	0	1.2E-1		J.UL-1	1
nnot	GOTERM_CC_DIRECT ation Cluster 132	ciliary base Enrichment Score: 1.64	RT G	i i	Count	P_Value	Fold	Ponjamin	i FDR

Annota	ation Cluster 1	Enrichment Score: ?	G	·	Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	Zinc finger, PHD-type	RT		26	3.0E-3	Change	3.3E-2	3.0E-
	UP_SEQ_FEATURE	zinc finger region:PHD-type 2	<u>RT</u>		11	8.2E-3	2.5E0	2.0E-1	2 1.9E-
	UP_SEQ_FEATURE	zinc finger region:PHD-type 1	RT		11	1.7E-2		3.4E-1	1 3.3E-
	UP_SEQ_FEATURE	zinc finger region:PHD-type	RT		14	3.4E-2		6.3E-1	1 6.1E-
	INTERPRO	Zinc finger, FYVE/PHD-type	RT	_	32	4.1E-2		3.0E-1	1 2.8E-
	INTERPRO								1 7.8E-
	SMART	Zinc finger, PHD-type, conserved site	<u>RT</u>		15	1.8E-1		8.6E-1	1 8.4E-
	allian Objection 100	PHD	<u>RT</u>		26	2.5E-1	Fold	9.4E-1	1
Annota	ation Cluster 133  BIOCARTA	Enrichment Score: 1.59  E2F1 Destruction Pathway	G RT	<u> </u>	Count 8	P_Value 1.6E-2	Change	Benjamin 6.2E-2	4.2E-
	BIOCARTA	Regulation of p27 Phosphorylation during Cell		_					2 6.1E-
	BIOCARTA	Cycle Progression	<u>RT</u>		9		2.1E0	9.1E-2	2 7.3E-
		Cyclin E Destruction Pathway	RT	i	7	3.6E-2	-	1.1E-1	2
Annota	ation Cluster 134  INTERPRO	Enrichment Score: 1.55	G	-	Count	P_Value	Change	•	5.7E-
	INTERPRO	P-type ATPase, transmembrane domain  Cation-transporting P-type ATPase, C-	<u>RT</u>		11	3.7E-5		6.3E-4	4 1.1E-
	INTERPRO	<u>terminal</u>	<u>RT</u>	•	11	7.6E-5		1.2E-3	3
	INTERPRO	Cation-transporting P-type ATPase, N- terminal	<u>RT</u>	i	11	1.5E-4	3.8E0	2.1E-3	2.0E- 3
		P-type ATPase, cytoplasmic domain N	<u>RT</u>	i	16	2.3E-4	2.8E0	3.3E-3	3.0E- 3
	INTERPRO	<u>P-type ATPase, A domain</u>	<u>RT</u>	•	16	2.3E-4	2.8E0	3.3E-3	3.0E- 3
	INTERPRO	Cation-transporting P-type ATPase	<u>RT</u>	1	16	2.3E-4	2.8E0	3.3E-3	3.0E- 3
	INTERPRO	P-type ATPase, phosphorylation site	<u>RT</u>	i	16	2.3E-4	2.8E0	3.3E-3	3.0E- 3
	UP_SEQ_FEATURE	active site:4-aspartylphosphate intermediate	<u>RT</u>	i	16	3.2E-4	2.7E0	9.9E-3	9.5E- 3
	GOTERM_BP_DIRECT	cellular sodium ion homeostasis	<u>RT</u>	i .	11	3.8E-4	3.4E0	1.0E-2	9.6E- 3
	INTERPRO	Sodium/potassium-transporting P-type ATPase, subfamily IIC	<u>RT</u>	1	6	5.7E-4	6.2E0	7.2E-3	6.6E- 3
	UP_SEQ_FEATURE	metal ion-binding site:Magnesium	<u>RT</u>	i .	32	7.0E-4	1.8E0	2.0E-2	2.0E- 2
	SMART	SM00831	<u>RT</u>	i .	11	1.4E-3	2.8E0	1.4E-2	1.3E- 2
	GOTERM_BP_DIRECT	establishment or maintenance of transmembrane electrochemical gradient	<u>RT</u>	i .	8	2.6E-3	3.6E0	5.0E-2	4.8E- 2
	GOTERM_MF_DIRECT	sodium: potassium-exchanging ATPase activity	<u>RT</u>	1	6	1.6E-2	3.6E0	1.1E-1	1.0E- 1
	GOTERM_BP_DIRECT	sodium ion export from cell	<u>RT</u>	i	6	1.6E-2	3.6E0	2.2E-1	2.1E- 1
	GOTERM_MF_DIRECT	steroid hormone binding	<u>RT</u>	i	4	3.6E-2	4.8E0	2.2E-1	2.0E-
	GOTERM_BP_DIRECT	cellular potassium ion homeostasis	<u>RT</u>	i .	6	3.8E-2	3.0E0	3.8E-1	3.6E-
	UP_SEQ_FEATURE	region of interest:Interaction with phosphoinositide-3 kinase	<u>RT</u>	1	3	5.8E-2	6.8E0	9.1E-1	8.8E-
	GOTERM_BP_DIRECT		<u>RT</u>		5	7.2E-2	3.0E0	5.7E-1	5.4E-
	GOTERM_BP_DIRECT	response to glycoside	RT		3	7.6E-2	5.9E0	5.7E-1	5.4E-
	UP_KEYWORDS	Sodium/potassium transport	RT		4	9.8E-2		3.3E-1	1 2.5E-
	GOTERM_BP_DIRECT	regulation of cardiac conduction	RT		13	2.3E-1		1.0E0	1 9.5E-
	GOTERM_CC_DIRECT	sodium: potassium-exchanging ATPase	RT		4	2.4E-1		8.4E-1	1 7.4E-
	KEGG_PATHWAY	complex  Carbohydrate digestion and absorption	RT		11	2.4E-1 2.7E-1		4.3E-1	1 2.7E-
	GOTERM_BP_DIRECT						1.4E0		1 9.5E-
	INTERPRO	ATP hydrolysis coupled proton transport	<u>RT</u>	•	8				1 9.1E-
	GOTERM_BP_DIRECT	HAD-like domain  cell communication by electrical coupling	RT DT		16		1.2E0		1 9.5E-
	GOTERM_BP_DIRECT	involved in cardiac conduction	<u>RT</u>		4		1.8E0		1 9.5E-
	KEGG_PATHWAY	potassium ion import	<u>RT</u>		6		1.3E0		1 8.4E-
	GOTERM_BP_DIRECT	Proximal tubule bicarbonate reclamation	<u>RT</u>	i	4		9.1E-1		9.5E-
		ion transmembrane transport	<u>RT</u>	•	30		8.5E-1		1
	KEGG_PATHWAY	<u>Cardiac muscle contraction</u>	<u>RT</u>	i	11	9.3E-1	7.7E-1	1.0E0	9.3E- 1
	UP_KEYWORDS	<u>Potassium</u>	<u>RT</u>	•	12	9.9E-1	6.4E-1	1.0E0	9.9E- 1
	UP_KEYWORDS	Potassium transport	<u>RT</u>	•	10	9.9E-1	5.9E-1	1.0E0	9.9E- 1
	KEGG_PATHWAY	Mineral absorption	<u>RT</u>	i	4	9.9E-1	4.8E-1	1.0E0	9.9E- 1

nnot	tation Cluster 1	Enrichment Score: ?	G	<b>17</b>	Count	P_Value	Fold Change	Benjamin	ıi FDI
) 	UP_KEYWORDS KEGG_PATHWAY	Sodium transport  Protein digestion and absorption	RT RT		4 4	1.0E0 1.0E0	2.3E-1 2.4E-1		1.0
	UP_KEYWORDS	Sodium	RT		4	1.0E0	2.4E-1 2.2E-1		1.0
	UP_SEQ_FEATURE	topological domain:Lumenal	<u>RT</u>	1	22	1.0E0	3.3E-1		1.0
	UP_KEYWORDS	Ion transport	RT	-	32	1.0E0	3.4E-1 Fold	1	1.0
nnot	dation Cluster 135  GOTERM_MF_DIRECT	Enrichment Score: 1.54  histone methyltransferase activity (H3-K36	G	-	Count	P_Value	Change		6.4
		specific)	<u>RT</u>	i	5	8.9E-3	5.0E0	7.2E-2	2
	UP_SEQ_FEATURE	domain:AWS	<u>RT</u>	i	4	2.5E-2	5.5E0	4.8E-1	4.7 1
	INTERPRO	AWS	<u>RT</u>	i .	4	3.2E-2	5.0E0	2.4E-1	2.2 1
	SMART	<u>AWS</u>	<u>RT</u>	1	4	9.8E-2	3.3E0	4.9E-1	4.4 1
nnot	tation Cluster 136	Enrichment Score: 1.51	G	<b>1</b>	Count	P_Value	Fold Change	Benjamin	
7	GOTERM_MF_DIRECT	single-stranded DNA-dependent ATPase	RT		7		4.2E0	2.4E-2	2.1
ے ا	GOTERM_CC_DIRECT	activity		•					2 4.6
_		DNA replication factor C complex	<u>RT</u>	•	5	7.0E-3	5.3E0	5.2E-2	2
	GOTERM_MF_DIRECT	DNA clamp loader activity	<u>RT</u>	i	5	3.1E-2	3.7E0	2.0E-1	1.8 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	3.9E-1	3.6 1
	INTERPRO	Replication factor C, C-terminal domain	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6 1
	GOTERM_BP_DIRECT	positive regulation of DNA-directed DNA	<u>RT</u>	i	4	9.8E-2	3.4E0	6.8E-1	6.5
1	GOTERM_CC_DIRECT	polymerase activity  Ctf18 RFC-like complex	<u>RT</u>	1	4	1 2F-1	3.2E0	5.0E-1	1 4.
	tation Objector 407			·		1	Fold	1	1
nnot	tation Cluster 137  GOTERM_BP_DIRECT	Enrichment Score: 1.5	G		Count	P_Value	Change	_	2.8
J		positive regulation of translational initiation	<u>RT</u>	•	9	1.4E-3	3.6E0	3.0E-2	2
	GOTERM_MF_DIRECT	translation activator activity	<u>RT</u>	1	5	4.9E-2	3.3E0	2.9E-1	2.6 1
	GOTERM_BP_DIRECT	3'-UTR-mediated mRNA stabilization	<u>RT</u>	i e	7	5.3E-2	2.4E0	4.8E-1	4.5 1
	GOTERM_MF_DIRECT	mRNA 3'-UTR binding	<u>RT</u>	i	11	3.0E-1	1.3E0	9.5E-1	8.
nnot	tation Cluster 138	Enrichment Score: 1.49	G	17	Count	P_Value	Fold	Benjamin	ni FC
)	INTERPRO	Dynamin, GTPase domain	RT		6		Change 5.3E0	2.0E-2	1.8
)	INTERPRO								2 6.9
J		<u>Dynamin, GTPase region, conserved site</u>	<u>RT</u>	•	5	7.7E-3	5.2E0	7.5E-2	2
	INTERPRO	<u>Dynamin central domain</u>	<u>RT</u>	1	5	7.7E-3	5.2E0	7.5E-2	6.9 2
	UP_SEQ_FEATURE	domain:GED	<u>RT</u>	i contraction	5	1.1E-2	4.9E0	2.3E-1	2.2 1
)	SMART	DYNc	<u>RT</u>	1	6	1.2E-2	3.5E0	1.0E-1	9. 2
)	INTERPRO	Dynamin GTPase effector	<u>RT</u>		5	1.6E-2	4.4E0	1.3E-1	1.
<b>,</b>	SMART								1 2.
	INTERPRO	<u>GED</u>	<u>RT</u>	•	5		3.4E0	2.4E-1	1
)		GTPase effector domain, GED	<u>RT</u>	i	5	4.3E-2	3.4E0	3.1E-1	2. 1
)	GOTERM_BP_DIRECT	<u>dynamin polymerization involved in</u> <u>mitochondrial fission</u>	<u>RT</u>	i	4	9.8E-2	3.4E0	6.8E-1	6. 1
)	INTERPRO	<u>Dynamin</u>	<u>RT</u>	i	6	1.3E-1	2.2E0	6.1E-1	5. 1
)	GOTERM_BP_DIRECT	mitochondrial fission	<u>RT</u>	i	5	4.0E-1	1.6E0	1.0E0	9. 1
1	GOTERM_BP_DIRECT	membrane fusion	<u>RT</u>	1	6	8.9F-1	8.1E-1	1.0E0	9.
, anot	tation Cluster 139	Enrichment Score: 1.47	G		Count	P_Value	Fold		1
iiiot	BBID			- V					1.
J		26.cyclin-CDK complexes	<u>RT</u>	•	12	1.9E-3	2.3E0	1.0E-1	1
)	BBID	1.RBphosphoE2F	<u>RT</u>	1	9	6.4E-2	1.9E0	8.2E-1	8. 1
)	GOTERM_MF_DIRECT	<u>cyclin-dependent protein serine/threonine</u> <u>kinase inhibitor activity</u>	<u>RT</u>	1	5	9.7E-2	2.7E0	4.6E-1	4. 1
)	GOTERM_BP_DIRECT	negative regulation of phosphorylation	<u>RT</u>	1	7	1.1E-1	2.1E0	7.2E-1	6.9 1
inot	tation Cluster 140	Enrichment Score: 1.47	G	<b>**</b>	Count	P_Value	Fold	Benjamin	ni FC
	GOTERM_BP_DIRECT	mitotic cell cycle	<u>RT</u>	:	16		Change 2.3E0	4.0E-2	3.
)	GOTERM_MF_DIRECT	receptor signaling protein serine/threonine							2 7.
J		kinase activity	<u>RT</u>	i	17	1.1E-2	1.9E0	8.3E-2	2
	UP_SEQ_FEATURE	domain:CRIB	<u>RT</u>	T.	7	4.9E-2	2.5E0	8.6E-1	8. 1
	UP_SEQ_FEATURE	region of interest:Autoregulatory region	<u>RT</u>	1	3	5.8E-2	6.8E0	9.1E-1	8. 1
)									_
)	UP_SEQ_FEATURE	region of interest:GTPase-binding	<u>RT</u>	i .	3	5.8E-2	6.8E0	9.1E-1	8. 1

Annota	ation Cluster 1	Enrichment Score: ?	G	·	Count	P_Value	Fold Change	Benjamini	FDR
	SMART	<u>PBD</u>	<u>RT</u>	i	7	1.8E-1	•	7.1E-1	6.4E- 1
Annota	ation Cluster 141	Enrichment Score: 1.42	G	<b>1</b>	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	ROC GTPase	<u>RT</u>	i	4	1.5E-2	-	1.2E-1	1.1E- 1
	UP_SEQ_FEATURE	domain:Roc	<u>RT</u>	i .	3	5.8E-2	6.8E0	9.1E-1	8.8E-
	INTERPRO	Mitochondrial Rho-like	<u>RT</u>	1	5	6.3E-2	3.1E0	3.9E-1	3.6E- 1
Annota	ation Cluster 142	Enrichment Score: 1.42	G	<b>1</b>	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process	<u>RT</u>	i .	8	2.6E-3	3.6E0	5.0E-2	4.8E- 2
	GOTERM_BP_DIRECT	nuclear mRNA surveillance	<u>RT</u>	i .	5	5.0E-2	3.3E0	4.6E-1	4.4E- 1
	GOTERM_BP_DIRECT	histone mRNA catabolic process	<u>RT</u>	i	4	4.3E-1	1.7E0	1.0E0	9.5E- 1
Annota	ation Cluster 143	Enrichment Score: 1.42	G	<b>™</b>	Count	P_Value	Fold Change	Benjamini	1
	UP_SEQ_FEATURE	DNA-binding region:A.T hook 3	<u>RT</u>	i	6	9.0E-3		2.1E-1	2.0E- 1
	UP_SEQ_FEATURE	DNA-binding region:A.T hook 1	<u>RT</u>	i	6	3.1E-2	3.1E0	5.8E-1	5.6E-
	UP_SEQ_FEATURE	DNA-binding region:A.T hook 2	<u>RT</u>	i	6	3.1E-2	3.1E0	5.8E-1	5.6E-
	INTERPRO	AT hook, DNA-binding motif	<u>RT</u>	i	4	5.7E-2	4.1E0	3.9E-1	3.6E-
	SMART	AT hook	<u>RT</u>	i	4	1.6E-1	2.7E0	6.6E-1	1 5.9E-
Annota	ation Cluster 144	Enrichment Score: 1.39	G		Count	P_Value	Fold	Benjamini	FDR
	INTERPRO	Leucine-rich repeat-containing protein 8, N-	<u>RT</u>	i	5	2.9E-3	6.2E0	3.2E-2	2.9E- 2
	GOTERM_MF_DIRECT	terminal volume-sensitive anion channel activity	RT		4	1.6E-2	6.0E0	1.1E-1	1.0E-
	GOTERM_BP_DIRECT	regulation of anion transport	RT		5	7.2E-2		5.7E-1	1 5.4E-
	GOTERM_BP_DIRECT	anion transmembrane transport	RT		5		9.9E-1		1 9.5E-
Annot	ation Cluster 145	Enrichment Score: 1.39	G	•	Count	P_Value	Fold	Benjamini	1 FDR
	GOTERM_CC_DIRECT	MLL5-L complex	RT	:	6	3.5E-3	Onlange	2.9E-2	2.6E-
	GOTERM_CC_DIRECT	PTW/PP1 phosphatase complex				8.3E-2		4.0E-1	2 3.5E-
	GOTERM_BP_DIRECT		<u>RT</u>		4				1 9.5E-
Annat		entrainment of circadian clock by photoperiod			6	2.4E-1	Fold	1.0E0	1
Annota	ation Cluster 146  GOTERM_MF_DIRECT	Enrichment Score: 1.38	G	- Total	Count 10	P_Value	Change	Benjamini 2.6E-3	2.3E-
	INTERPRO	protein kinase C activity	<u>RT</u>	_		2.0E-4			3 3.6E-
	INTERPRO	<u>Diacylglycerol/phorbol-ester binding</u> <u>Protein kinase C, delta/epsilon/eta/theta</u>	<u>RT</u>		11	3.7E-3		4.0E-2	2 1.1E-
	PIR_SUPERFAMILY	types  protein kinase C, delta/epsilon/eta/theta	<u>RT</u>		4	1.5E-2		1.2E-1	1 3.5E-
	UP_SEQ_FEATURE	<u>types</u>	<u>RT</u>	•	4	2.2E-2	5.3E0	3.6E-1	1 5.9E-
		zinc finger region:Phorbol-ester/DAG-type 1	<u>RT</u>	•	8	3.3E-2	2.5E0	6.1E-1	1
	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 2	<u>RT</u>	•	8	3.3E-2	2.5E0	6.1E-1	5.9E- 1
	GOTERM_MF_DIRECT	calcium-independent protein kinase C activity	RT	1	3	7.5E-2	6.0E0	3.9E-1	3.4E- 1
	INTERPRO	Protein kinase C-like, phorbol ester/diacylglycerol binding	<u>RT</u>	•	15	1.7E-1	1.4E0	8.0E-1	7.3E- 1
	GOTERM_BP_DIRECT	negative regulation of glial cell apoptotic process	<u>RT</u>	i	3	3.4E-1	2.5E0	1.0E0	9.5E- 1
	SMART	<u>C1</u>	<u>RT</u>	i .	15	7.5E-1	9.4E-1	1.0E0	9.0E- 1
	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type	<u>RT</u>	i	5		7.6E-1	1.0E0	9.7E- 1
Annota	ation Cluster 147	Enrichment Score: 1.35	G	<b>™</b>	Count	P_Value	Fold Change	Benjamini	
	GOTERM_BP_DIRECT	vagina development	<u>RT</u>	i .	6	9.4E-3	4.0E0	1.4E-1	1.3E- 1
	GOTERM_BP_DIRECT	apoptotic cell clearance	<u>RT</u>	1	7	2.9E-2	2.8E0	3.3E-1	3.1E- 1
	GOTERM_BP_DIRECT	natural killer cell differentiation	<u>RT</u>	i	6	3.8E-2	3.0E0	3.8E-1	3.6E- 1
	GOTERM_BP_DIRECT	negative regulation of lymphocyte activation	<u>RT</u>	i .	3	7.6E-2	5.9E0	5.7E-1	5.4E- 1
	GOTERM_BP_DIRECT	secretion by cell	<u>RT</u>	i .	4	2.3E-1	2.4E0	1.0E0	9.5E- 1
Annota	ation Cluster 148	Enrichment Score: 1.34	G	TN .	Count	P_Value	Fold Change	Benjamini	1
	INTERPRO	HRDC domain	<u>RT</u>	i	4	1.5E-2		1.2E-1	1.1E- 1
	INTERPRO	HRDC-like	<u>RT</u>	i	4	3.2E-2	5.0E0	2.4E-1	2.2E- 1
	UP_SEQ_FEATURE	domain:HRDC	<u>RT</u>	i .	3	5.8E-2	6.8E0	9.1E-1	8.8E-
			_						1

Annota	ation Cluster 1	Enrichment Score: ?	G	<b></b>	Count	P_Value	Fold Change	Benjamini	FDR
	SMART	HRDC	<u>RT</u>	i	3	1.5E-1	4.1E0	6.5E-1	5.8E- 1
Annota	ation Cluster 149	Enrichment Score: 1.33	G	To the second se	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_MF_DIRECT	fibroblast growth factor-activated receptor activity	<u>RT</u>	i	5	3.4E-3	•	3.2E-2	2.8E- 2
	INTERPRO	<u>Tyrosine-protein kinase, fibroblast growth</u>	<u>RT</u>	i .	4	1.5E-2	6.2E0	1.2E-1	1.1E- 1
	PIR_SUPERFAMILY	fibroblast growth factor receptor	RT		4	2.2E-2	5.3E0	3.6E-1	3.5E-
	GOTERM_BP_DIRECT	positive regulation of phospholipase activity	RT		4	1.4E-1	3.0F0	8.1E-1	1 7.7E-
	GOTERM_MF_DIRECT	fibroblast growth factor binding	RT		7	1.8E-1		7.2E-1	1 6.4E-
	UP_KEYWORDS								1 7.8E-
Annat	otion Chapter 450	Craniosynostosis  Fraichment Score 1 22	RT	•	5	4.0E-1	Fold	1.0E0	1
Annota	ation Cluster 150  GOTERM_BP_DIRECT	Enrichment Score: 1.33	G		Count	P_Value	Change		1.2E-
	GOTERM_BP_DIRECT	regulation of the force of heart contraction	<u>RT</u>	•	9	8.4E-3		1.3E-1	1 1.8E-
	KEGG_PATHWAY	cardiac muscle contraction	<u>RT</u>	•	15	1.3E-2		1.9E-1	1
	REGG_FAINWAI	Cardiac muscle contraction	<u>RT</u>	i	11	9.3E-1	7.7E-1	1.0E0	9.3E- 1
Annota	ation Cluster 151	Enrichment Score: 1.31	G	N .	Count	P_Value	Fold Change	Benjamini	
	GOTERM_BP_DIRECT	positive regulation of guanylate cyclase activity	<u>RT</u>	i	7	4.9E-3	3.8E0	8.4E-2	8.0E- 2
	GOTERM_MF_DIRECT	<u>calcium sensitive guanylate cyclase activator</u> <u>activity</u>	<u>RT</u>	i	4	3.6E-2	4.8E0	2.2E-1	2.0E- 1
	GOTERM_BP_DIRECT	phototransduction	<u>RT</u>	i	5	6.9E-1	1.1E0	1.0E0	9.5E- 1
Annota	ation Cluster 152	Enrichment Score: 1.3	G	<b>™</b>	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_MF_DIRECT	ubiquitin-ubiquitin ligase activity	<u>RT</u>	i	7	1.3E-2	3.2E0	9.7E-2	8.6E- 2
	INTERPRO	<u>U box domain</u>	<u>RT</u>	i .	5	6.3E-2	3.1E0	3.9E-1	3.6E- 1
	UP_SEQ_FEATURE	domain:U-box	<u>RT</u>	i	4	7.0E-2	3.9E0	1.0E0	9.7E- 1
	SMART	<u>Ubox</u>	<u>RT</u>	i	5	1.1E-1	2.5E0	5.2E-1	4.7E-
Annota	ation Cluster 153	Enrichment Score: 1.3	G	T.	Count	P_Value	Fold	Benjamini	Ť
	OMIM_DISEASE	Schimmelpenning-Feuerstein-Mims	RT	1	3	4.3E-2		1.0E0	1.0E0
	BBID	syndrome, somatic mosaic  65.Integrin affinity modulation	RT		5	4.9E-2	2.9E0	7.6E-1	7.6E-
	UP_SEQ_FEATURE	region of interest:Hypervariable region	RT		3	5.8E-2		9.1E-1	1 8.8E-
Annote	ation Cluster 154	Enrichment Score: 1.3	G	•	Count	P_Value	Fold	Benjamini	1 EDR
	UP_SEQ_FEATURE	region of interest:I-domain	RT	i	4	1.1E-2	Change	2.3E-1	2.2E-
	INTERPRO								1 2.2E-
	INTERPRO	Helix-hairpin-helix motif, class 2	<u>RT</u>		4	3.2E-2		2.4E-1	1 2.2E-
	INTERPRO	XPG/Rad2 endonuclease	<u>RT</u>	1	4	3.2E-2		2.4E-1	1 2.2E-
	INTERPRO	XPG-I domain	<u>RT</u>	•	4	3.2E-2	5.0E0	2.4E-1	1
		5'-3' exonuclease, C-terminal domain	<u>RT</u>	i	4	3.2E-2	5.0E0	2.4E-1	2.2E- 1
	UP_SEQ_FEATURE	region of interest:N-domain	<u>RT</u>	i .	4	4.5E-2	4.5E0	8.0E-1	7.7E- 1
	INTERPRO	XPG N-terminal	<u>RT</u>	i	4	5.7E-2	4.1E0	3.9E-1	3.6E- 1
	GOTERM_MF_DIRECT	nuclease activity	<u>RT</u>	i e	8	7.7E-2	2.1E0	3.9E-1	3.5E- 1
	SMART	HhH2	<u>RT</u>	1	4	9.8E-2	3.3E0	4.9E-1	4.4E- 1
	SMART	<u>XPGI</u>	<u>RT</u>	i	4	9.8E-2	3.3E0	4.9E-1	4.4E- 1
	SMART	<u>XPGN</u>	<u>RT</u>	i	4	9.8E-2	3.3E0	4.9E-1	4.4E- 1
	INTERPRO	XPG conserved site	<u>RT</u>	1	3	1.2E-1	4.6E0	6.1E-1	5.6E- 1
Annota	ation Cluster 155	Enrichment Score: 1.28	G	To the second se	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	histone H2A monoubiquitination	<u>RT</u>	i	7	8.4E-3		1.3E-1	1.2E-
	GOTERM_BP_DIRECT	UV-damage excision repair	<u>RT</u>	i .	5	9.9E-2	2.7E0	6.8E-1	6.5E-
	GOTERM_CC_DIRECT	Cul4B-RING E3 ubiquitin ligase complex	RT		3	1.8E-1	3.8E0	6.8E-1	1 5.9E-
Annot	ation Cluster 156	Enrichment Score: 1.27	G	•	Count	P_Value	Fold	Benjamini	1 FDR
	BIOCARTA	NFkB activation by Nontypeable Hemophilus	RT	i	18	1.1E-4	Change	1.6E-3	1.1E-
	BIOCARTA	<u>influenzae</u>							3 3.4E-
	BIOCARTA	The 4-1BB-dependent immune response	<u>RT</u>	•	14	5.8E-4		5.0E-3	3 4.2E-
		Signal transduction through IL1R	<u>RT</u>	•	18	1.7E-2	1.7E0	6.2E-2	2

	tation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamir	ni FDR
	BIOCARTA	Toll-Like Receptor Pathway	<u>RT</u>	-	20	1.7E-2	•	6.2E-2	4.2E
	GOTERM_CC_DIRECT	I-kappaB/NF-kappaB complex	RT		4	3.0E-2	5.1F0	1.9E-1	2 1.6E
	BIOCARTA	Activation of PKC through G protein coupled	RT		6	4.0E-2		1.1E-1	1 7.7E
	BBID	receptor		-					2 7.6E
	KEGG_PATHWAY	77.IkBa Kinase JNK MEKK1	<u>RT</u>		6	4.9E-2		7.6E-1	1 6.3E
	BIOCARTA	RIG-I-like receptor signaling pathway	<u>RT</u>	•	20	6.3E-2	1.5E0	1.1E-1	2
		Double Stranded RNA Induced Gene Expression	<u>RT</u>	i	7	6.7E-2	2.2E0	1.7E-1	1.2E 1
	BIOCARTA	Acetylation and Deacetylation of RelA in The Nucleus	<u>RT</u>	•	9	1.1E-1	1.7E0	2.6E-1	1.8E 1
	BIOCARTA	NF-kB Signaling Pathway	<u>RT</u>	•	11	1.8E-1	1.5E0	3.8E-1	2.6E 1
	BIOCARTA	CD40L Signaling Pathway	<u>RT</u>	•	8	1.8E-1	1.6E0	3.8E-1	2.6E 1
	BIOCARTA	Erythropoietin mediated neuroprotection through NF-kB	<u>RT</u>	4	7	2.8E-1	1.5E0	5.4E-1	3.6E 1
	BBID	90.IB and-cat-Arm processing of Ci	<u>RT</u>	4	4	3.4E-1	1.9E0	1.0E0	1.0E
	BIOCARTA	TNF/Stress Related Signaling	<u>RT</u>	•	10	4.2E-1	1.2E0	6.6E-1	4.5E 1
	BIOCARTA	TNFR2 Signaling Pathway	<u>RT</u>	4	7	5.5E-1	1.2E0	8.4E-1	5.7E 1
	BIOCARTA	TACI and BCMA stimulation of B cell immune responses.	<u>RT</u>	1	5	7.7E-1	1.0E0	1.0E0	7.7E 1
Anno	tation Cluster 157	Enrichment Score: 1.27	G	· ·	Count	P_Value	Fold Change	Benjamir	ni FDR
	INTERPRO	<u>Ubiquitin-associated/translation elongation</u> factor EF1B, N-terminal, eukaryote	<u>RT</u>	ī	16	2.7E-3		3.0E-2	2.8E
	UP_SEQ_FEATURE	domain:UBA	RT		13	1.0E-2	2.2E0	2.3E-1	2.2E
	INTERPRO	Heat shock chaperonin-binding	RT			1.3E-2			1 1.1E
_	GOTERM_MF_DIRECT			•					1 1.6E
	GOTERM_BP_DIRECT	polyubiquitin binding regulation of proteasomal ubiquitin-	<u>RT</u>	1	9	2.8E-2		1.9E-1	1 3.6E
		dependent protein catabolic process	<u>RT</u>	•	6	3.8E-2	3.0E0	3.8E-1	1
	INTERPRO	<u>Ubiquilin</u>	<u>RT</u>	•	4	5.7E-2	4.1E0	3.9E-1	3.6E 1
	SMART	STI1	<u>RT</u>	i	6	7.2E-2	2.4E0	4.0E-1	3.6E 1
	SMART	<u>UBA</u>	<u>RT</u>	•	10	2.7E-1	1.4E0	9.7E-1	8.7E 1
	UP_SEQ_FEATURE	domain:UBA 1	<u>RT</u>	1	3	2.7E-1	2.9E0	1.0E0	9.7E 1
	UP_SEQ_FEATURE	domain:UBA 2	<u>RT</u>	4	3	2.7E-1	2.9E0	1.0E0	9.7E
			121		J				
	INTERPRO	<u>UBA-like</u>	RT		12	3.5E-1	1.3E0	1.0E0	
Annot	INTERPRO tation Cluster 158	UBA-like Enrichment Score: 1.26	<u>RT</u>			3.5E-1 P_Value	Fold	Ponjamir	1
Annot		Enrichment Score: 1.26	RT G	i 178	12	P_Value	Fold Change	Benjamir	1 ni FDR 2.1E
Annot	tation Cluster 158	Enrichment Score: 1.26  UBA/THIF-type NAD/FAD binding fold	RT G		12 <b>Count</b>	P_Value 2.0E-3	Fold Change 4.3E0	Benjamir 2.3E-2	1 FDR 2.1E 2
Annot	tation Cluster 158	Enrichment Score: 1.26  UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity	RT G RT RT		12 <b>Count</b> 7	P_Value 2.0E-3 3.6E-2	Fold Change 4.3E0 4.8E0	2.3E-2 2.2E-1	1 FDR 2.1E 2 2.0E 1
Annot	INTERPRO  GOTERM_MF_DIRECT  INTERPRO	Enrichment Score: 1.26  UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1	RT G RT RT RT		7 4 3	P_Value 2.0E-3 3.6E-2 7.0E-2	Fold Change 4.3E0 4.8E0 6.2E0	2.3E-2 2.2E-1 3.9E-1	1 FDR 2.1E 2 2.0E 1 3.6E 1
Annot	INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO	Enrichment Score: 1.26  UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity	RT G RT RT		12 <b>Count</b> 7	P_Value 2.0E-3 3.6E-2	Fold Change 4.3E0 4.8E0 6.2E0	2.3E-2 2.2E-1	1 FDR 2.1E 2 2.0E 1 3.6E 1 3.6E 1
Annot	INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  GOTERM_MF_DIRECT	Enrichment Score: 1.26  UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1	RT G RT RT RT		7 4 3	P_Value 2.0E-3 3.6E-2 7.0E-2	Fold Change 4.3E0 4.8E0 6.2E0 6.2E0	2.3E-2 2.2E-1 3.9E-1	1 FDR 2.1E 2.0E 1 3.6E 1 4.1E 1
Annot	INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO	Enrichment Score: 1.26  UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1  Ubiquitin-activating enzyme e1, C-terminal	RT G RT RT RT RT		7 4 3 3	P_Value 2.0E-3 3.6E-2 7.0E-2 7.0E-2	Fold Change 4.3E0 4.8E0 6.2E0 6.2E0 3.4E0	2.3E-2 2.2E-1 3.9E-1 3.9E-1	1 FDR 2.1E 2 2.0E 1 3.6E 1 4.1E 1
Annot	INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  GOTERM_MF_DIRECT	UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1  Ubiquitin-activating enzyme e1, C-terminal  small protein activating enzyme activity	RT G RT RT RT RT RT		7 4 3 3 4	P_Value 2.0E-3 3.6E-2 7.0E-2 7.0E-2 9.7E-2	Fold Change 4.3E0 4.8E0 6.2E0 6.2E0 3.4E0 4.6E0	2.3E-2 2.2E-1 3.9E-1 3.9E-1 4.6E-1	1
Annot	INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  GOTERM_MF_DIRECT  INTERPRO	Enrichment Score: 1.26  UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1  Ubiquitin-activating enzyme e1, C-terminal  small protein activating enzyme activity  Ubiquitin/SUMO-activating enzyme E1	RT  G  RT  RT  RT  RT  RT  RT  RT		7 4 3 3 4 3	P_Value 2.0E-3 3.6E-2 7.0E-2 7.0E-2 9.7E-2 1.2E-1	Fold Change 4.3E0 4.8E0 6.2E0 6.2E0 3.4E0 4.6E0 4.6E0	2.3E-2 2.2E-1 3.9E-1 3.9E-1 4.6E-1 6.1E-1	1 FDR 2.1E 2 2.0E 1 3.6E 1 4.1E 1 5.6E 1 5.6E
	INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  INTERPRO  INTERPRO	Enrichment Score: 1.26  UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1  Ubiquitin-activating enzyme e1, C-terminal  small protein activating enzyme activity  Ubiquitin/SUMO-activating enzyme E1  Ubiquitin-activating enzyme	RT  G  RT  RT  RT  RT  RT  RT  RT  RT		7 4 3 3 4 3 3	P_Value 2.0E-3 3.6E-2 7.0E-2 7.0E-2 9.7E-2 1.2E-1 1.2E-1	Fold Change 4.3E0 4.8E0 6.2E0 3.4E0 4.6E0 4.1E0 Fold	2.3E-2 2.2E-1 3.9E-1 3.9E-1 4.6E-1 6.1E-1 6.5E-1	1 FDR 2.1E 2.0E 1 3.6E 1 4.1E 1 5.6E 1 5.6E 1 1
Annot	INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  INTERPRO  INTERPRO  SMART	UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1  Ubiquitin-activating enzyme e1, C-terminal  small protein activating enzyme activity  Ubiquitin/SUMO-activating enzyme E1  Ubiquitin-activating enzyme  SM00985	RT G RT RT RT RT RT RT RT RT		12  Count  7  4  3  3  4  3  3  3	P_Value 2.0E-3 3.6E-2 7.0E-2 9.7E-2 1.2E-1 1.5E-1 P_Value	Fold Change 4.3E0 4.8E0 6.2E0 6.2E0 3.4E0 4.6E0 4.1E0 Fold Change	2.3E-2 2.2E-1 3.9E-1 3.9E-1 4.6E-1 6.1E-1 6.5E-1	1
Annot	INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  INTERPRO  INTERPRO  SMART  station Cluster 159	Enrichment Score: 1.26  UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1  Ubiquitin-activating enzyme e1, C-terminal  small protein activating enzyme activity  Ubiquitin/SUMO-activating enzyme E1  Ubiquitin-activating enzyme  SM00985  Enrichment Score: 1.26  peptidyl-lysine monomethylation	RT G RT		12  Count  7  4  3  3  4  3  3  Count	P_Value 2.0E-3 3.6E-2 7.0E-2 9.7E-2 1.2E-1 1.5E-1 P_Value 3.2E-2	Fold Change 4.3E0 4.8E0 6.2E0 6.2E0 3.4E0 4.6E0 4.1E0 Fold Change	2.3E-2 2.2E-1 3.9E-1 3.9E-1 4.6E-1 6.1E-1 6.5E-1 Benjamir 3.5E-1	1 FDR 2.1E 2 2.0E 1 3.6E 1 4.1E 1 5.6E 1 5.6E 1 5.8E 1 1
Annot	INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  INTERPRO  INTERPRO  SMART  tation Cluster 159  GOTERM_BP_DIRECT	Enrichment Score: 1.26  UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1  Ubiquitin-activating enzyme e1, C-terminal  small protein activating enzyme activity  Ubiquitin/SUMO-activating enzyme E1  Ubiquitin-activating enzyme  SM00985  Enrichment Score: 1.26  peptidyl-lysine monomethylation  peptidyl-lysine dimethylation	RT G RT		12  Count  7  4  3  3  4  3  3  Count  5  4	P_Value 2.0E-3 3.6E-2 7.0E-2 7.0E-2 9.7E-2 1.2E-1 1.5E-1 P_Value 3.2E-2 3.7E-2	Fold Change 4.3E0 4.8E0 6.2E0 6.2E0 3.4E0 4.6E0 4.6E0 4.1E0 Fold Change 3.7E0 4.7E0	2.3E-2 2.2E-1 3.9E-1 3.9E-1 4.6E-1 6.1E-1 6.5E-1 Benjamir 3.5E-1 3.8E-1	2.1E 2.0E 1 3.6E 1 3.6E 1 5.6E 1 5.6E 1 5.8E 1 3.3E 1 3.3E
Annot	INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  INTERPRO  SMART  STATION Cluster 159  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT	UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1  Ubiquitin-activating enzyme e1, C-terminal  small protein activating enzyme activity  Ubiquitin/SUMO-activating enzyme E1  Ubiquitin-activating enzyme  SM00985  Enrichment Score: 1.26  peptidyl-lysine monomethylation  peptidyl-lysine dimethylation  protein-lysine N-methyltransferase activity	RT  G  RT  RT  RT  RT  RT  RT  RT  RT  R		12  Count  7  4  3  3  4  3  Count  5  4  6	P_Value 2.0E-3 3.6E-2 7.0E-2 7.0E-2 9.7E-2 1.2E-1 1.5E-1 P_Value 3.2E-2 3.7E-2 1.4E-1	Fold Change 4.3E0 4.8E0 6.2E0 3.4E0 4.6E0 4.1E0 Fold Change 3.7E0 4.7E0 2.1E0 Fold	2.3E-2 2.2E-1 3.9E-1 3.9E-1 4.6E-1 6.1E-1 6.5E-1 Benjamir 3.5E-1 3.8E-1 6.0E-1	1 FDR 2.1E 2.0E 1 3.6E 1 4.1E 1 5.6E 1 5.8E 1 3.3E 1 3.6E 1 5.3E 1 5.3E
Annot	INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  INTERPRO  SMART  Station Cluster 159  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT	UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1  Ubiquitin-activating enzyme e1, C-terminal  small protein activating enzyme activity  Ubiquitin/SUMO-activating enzyme E1  Ubiquitin-activating enzyme  SM00985  Enrichment Score: 1.26  peptidyl-lysine monomethylation  protein-lysine N-methyltransferase activity  Enrichment Score: 1.26	RT G RT G RT RT		12  Count  7  4  3  3  4  3  Count  5  4  6  Count	P_Value 2.0E-3 3.6E-2 7.0E-2 7.0E-2 9.7E-2 1.2E-1 1.5E-1 P_Value 3.2E-2 3.7E-2 1.4E-1 P_Value	Fold Change 4.3E0 4.8E0 6.2E0 6.2E0 3.4E0 4.6E0 4.6E0 4.1E0 Fold Change 3.7E0 4.7E0 2.1E0 Fold Change	2.3E-2 2.2E-1 3.9E-1 3.9E-1 4.6E-1 6.1E-1 6.5E-1 Benjamir 3.5E-1 3.8E-1 6.0E-1 Benjamir	1 FDR 2.1E 2.0E 1 3.6E 1 4.1E 5.6E 1 5.8E 1 3.3E 1 3.6E 1 5.3E 1 5.3E 1 5.3E 1 5.3E
Annot	INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  INTERPRO  SMART  STATEMATE TO STATEM	UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1  Ubiquitin-activating enzyme e1, C-terminal  small protein activating enzyme activity  Ubiquitin/SUMO-activating enzyme E1  Ubiquitin-activating enzyme  SM00985  Enrichment Score: 1.26  peptidyl-lysine monomethylation  protein-lysine N-methyltransferase activity  Enrichment Score: 1.26  Pwp2p-containing subcomplex of 90S  preribosome	RT  G  RT  RT  RT  RT  RT  RT  RT  RT  R		12  Count  7  4  3  3  4  3  3  Count  Count  5  4  6  Count	P_Value  2.0E-3  3.6E-2  7.0E-2  9.7E-2  1.2E-1  1.5E-1  P_Value  3.2E-2  3.7E-2  1.4E-1  P_Value  1.5E-3	Fold Change 4.3E0 4.8E0 6.2E0 6.2E0 4.6E0 4.6E0 4.1E0 Fold Change 3.7E0 4.7E0 2.1E0 Fold Change 5.4E0	2.3E-2 2.2E-1 3.9E-1 3.9E-1 4.6E-1 6.1E-1 6.5E-1 Benjamir 3.5E-1 3.8E-1 6.0E-1 Benjamir 1.4E-2	1
Annot	INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  INTERPRO  SMART  Station Cluster 159  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT  STATION Cluster 160  GOTERM_CC_DIRECT  UP_SEQ_FEATURE	Enrichment Score: 1.26  UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1  Ubiquitin-activating enzyme e1, C-terminal  small protein activating enzyme activity  Ubiquitin/SUMO-activating enzyme E1  Ubiquitin-activating enzyme  SM00985  Enrichment Score: 1.26  peptidyl-lysine monomethylation  peptidyl-lysine dimethylation  protein-lysine N-methyltransferase activity  Enrichment Score: 1.26  Pwp2p-containing subcomplex of 90S  preribosome  repeat:WD 8	RT G RT G RT RT		12  Count  7  4  3  3  4  3  Count  5  4  6  Count	P_Value 2.0E-3 3.6E-2 7.0E-2 7.0E-2 9.7E-2 1.2E-1 1.5E-1 P_Value 3.2E-2 3.7E-2 1.4E-1 P_Value	Fold Change 4.3E0 4.8E0 6.2E0 6.2E0 4.6E0 4.6E0 4.1E0 Fold Change 3.7E0 4.7E0 2.1E0 Fold Change 5.4E0	2.3E-2 2.2E-1 3.9E-1 3.9E-1 4.6E-1 6.1E-1 6.5E-1 Benjamir 3.5E-1 3.8E-1 6.0E-1 Benjamir	1 FDR 2.1E 2.0E 1 3.6E 1 3.6E 1 5.6E 1 5.6E 1 5.8E 1 3.6E 1 7 FDR 3.3E 1 3.6E 1 4.1E 5.4E 1 5.6E 1 5.6E 1 7 FDR 3.4E 1 7 FDR 4.6E 1 7 FDR
Annot	INTERPRO  GOTERM_MF_DIRECT INTERPRO INTERPRO GOTERM_MF_DIRECT INTERPRO INTERPRO INTERPRO INTERPRO SMART  STATEMAN STATEM	UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1  Ubiquitin-activating enzyme e1, C-terminal  small protein activating enzyme activity  Ubiquitin/SUMO-activating enzyme E1  Ubiquitin-activating enzyme  SM00985  Enrichment Score: 1.26  peptidyl-lysine monomethylation  protein-lysine N-methyltransferase activity  Enrichment Score: 1.26  Pwp2p-containing subcomplex of 90S  preribosome	RT  G  RT  RT  RT  RT  RT  RT  RT  RT  R		12  Count  7  4  3  3  4  3  3  Count  Count  5  4  6  Count	P_Value  2.0E-3  3.6E-2  7.0E-2  9.7E-2  1.2E-1  1.5E-1  P_Value  3.2E-2  3.7E-2  1.4E-1  P_Value  1.5E-3	Fold Change 4.3E0 4.8E0 6.2E0 3.4E0 4.6E0 4.1E0 Fold Change 3.7E0 4.7E0 2.1E0 Fold Change 5.4E0 1.8E0	2.3E-2 2.2E-1 3.9E-1 3.9E-1 4.6E-1 6.1E-1 6.5E-1 Benjamir 3.5E-1 3.8E-1 6.0E-1 Benjamir 1.4E-2	1 FDR 2.1E 2.0E 1 3.6E 1 3.6E 1 5.6E 1 5.8E 1 5.8E 1 1 FDR 3.3E 1 1.2E 2 4.6E 1 2.5E
Annot	INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  INTERPRO  SMART  Station Cluster 159  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT  STATION Cluster 160  GOTERM_CC_DIRECT  UP_SEQ_FEATURE	Enrichment Score: 1.26  UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1  Ubiquitin-activating enzyme e1, C-terminal  small protein activating enzyme activity  Ubiquitin/SUMO-activating enzyme E1.  Ubiquitin-activating enzyme  SM00985  Enrichment Score: 1.26  peptidyl-lysine monomethylation  peptidyl-lysine dimethylation  protein-lysine N-methyltransferase activity  Enrichment Score: 1.26  Pwp2p-containing subcomplex of 90S  preribosome  repeat:WD 8  Quinonprotein alcohol dehydrogenase-like	RI G RI		12  Count  7  4  3  3  4  3  Count  5  4  6  Count  6  16	P_Value  2.0E-3  3.6E-2  7.0E-2  9.7E-2  1.2E-1  1.5E-1  P_Value  3.2E-2  1.4E-1  P_Value  1.5E-3  2.4E-2  3.7E-2	Fold Change 4.3E0 4.8E0 6.2E0 3.4E0 4.6E0 4.1E0 Fold Change 3.7E0 4.7E0 2.1E0 Fold Change 5.4E0 1.8E0	2.3E-2 2.2E-1 3.9E-1 3.9E-1 4.6E-1 6.1E-1 6.1E-1 6.5E-1 Benjamir 3.5E-1 3.8E-1 6.0E-1 Benjamir 1.4E-2 4.8E-1	1 FDR 2.1E 2 2.0E 1 3.6E 1 3.6E 1 5.6E 1 5.8E 1 5.8E 1 1 FDR 3.3E 1 3.6E 1 1 1 FDR 1.2E 2 4.6E 1 1 2.5E
Annot	INTERPRO  GOTERM_MF_DIRECT INTERPRO INTERPRO GOTERM_MF_DIRECT INTERPRO INTERPRO INTERPRO INTERPRO SMART  STATEMAN STATEM	Enrichment Score: 1.26  UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1  Ubiquitin-activating enzyme e1, C-terminal  small protein activating enzyme activity  Ubiquitin/SUMO-activating enzyme E1  Ubiquitin-activating enzyme  SM00985  Enrichment Score: 1.26  peptidyl-lysine monomethylation  peptidyl-lysine dimethylation  protein-lysine N-methyltransferase activity  Enrichment Score: 1.26  Pwp2p-containing subcomplex of 90S  preribosome  repeat: WD 8  Quinonprotein alcohol dehydrogenase-like superfamily	RI G RI		12  Count  7  4  3  3  4  3  Count  5  4  6  Count  6  16  14	P_Value  2.0E-3  3.6E-2  7.0E-2  9.7E-2  1.2E-1  1.5E-1  P_Value  3.2E-2  3.7E-2  1.4E-1  P_Value  1.5E-3  2.4E-2  3.7E-2  4.9E-2	Fold Change 4.3E0 4.8E0 6.2E0 3.4E0 4.6E0 4.1E0 Fold Change 3.7E0 4.7E0 2.1E0 Fold Change 5.4E0 1.8E0 1.8E0	2.3E-2 2.2E-1 3.9E-1 3.9E-1 4.6E-1 6.1E-1 6.1E-1 6.5E-1  Benjamir 3.5E-1 3.8E-1 6.0E-1  Benjamir 1.4E-2 4.8E-1 2.7E-1 8.6E-1	1 FDR 2.1E 2 2.0E 1 3.6E 1 3.6E 1 5.6E 1 5.8E 1 5.8E 1 1 FDR 3.3E 1 1 3.6E 1 2 4.6E 1 1 8.4E
Annot	INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  GOTERM_MF_DIRECT  INTERPRO  INTERPRO  INTERPRO  SMART  STATEMATE  INTERPRO  UP_SEQ_FEATURE  INTERPRO  UP_SEQ_FEATURE	Enrichment Score: 1.26  UBA/THIF-type NAD/FAD binding fold  ubiquitin activating enzyme activity  Ubiquitin-activating enzyme, E1  Ubiquitin-activating enzyme e1, C-terminal  small protein activating enzyme activity  Ubiquitin/SUMO-activating enzyme E1  Ubiquitin-activating enzyme  SM00985  Enrichment Score: 1.26  peptidyl-lysine monomethylation  peptidyl-lysine dimethylation  protein-lysine N-methyltransferase activity  Enrichment Score: 1.26  Pwp2p-containing subcomplex of 90S  preribosome  repeat: WD 8  Quinonprotein alcohol dehydrogenase-like superfamily, repeat: WD 9	RI G RI		12  Count  7  4  3  3  4  3  Count  Count  5  4  6  Count  6  16  14  12	P_Value  2.0E-3  3.6E-2  7.0E-2  9.7E-2  1.2E-1  1.5E-1  P_Value  3.2E-2  3.7E-2  1.4E-1  P_Value  1.5E-3  2.4E-2  3.7E-2  4.9E-2	Fold Change 4.3E0 6.2E0 6.2E0 4.6E0 4.6E0 4.1E0 Fold Change 3.7E0 4.7E0 2.1E0 Fold Change 5.4E0 1.8E0 1.8E0 1.9E0 2.0E0	2.3E-2 2.2E-1 3.9E-1 3.9E-1 4.6E-1 6.1E-1 6.1E-1 6.5E-1  Benjamir 3.5E-1 3.8E-1 6.0E-1  Benjamir 1.4E-2 4.8E-1 2.7E-1 8.6E-1	1 FDR 2.1E 2.0E 1 3.6E 1 3.6E 1 5.6E 1 5.6E 1 5.8E 1 5.8E 1 1 FDR 3.3E 1 2.5E 1 4.6E 1 9.4E

Annot	tation Cluster 1	Enrichment Score: ?	G	T.	Count	P_Value	Fold Change	Benjamin	i FDR
	UP_SEQ_FEATURE	repeat:WD 12	<u>RT</u>	i	6	2.1E-1		1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:WD 14	<u>RT</u>	1	3	6.3E-1	1.5E0	1.0E0	9.7E- 1
Annot	tation Cluster 161	Enrichment Score: 1.26	G	17	Count	P_Value	Fold Change	Benjamin	
	GOTERM_BP_DIRECT	Bergmann glial cell differentiation	RT	1	7	1.2E-3		2.8E-2	2.6E-
	GOTERM_BP_DIRECT	regulation of Golgi inheritance	RT	1	4	1.7E-2	5.9E0	2.2E-1	2 2.1E-
	BIOCARTA	Phosphorylation of MEK1 by cdk5/p35 down	RT		9	2.9E-2		9.1E-2	1 6.1E-
	GOTERM_BP_DIRECT	regulates the MAP kinase pathway regulation of stress-activated MAPK cascade	RT		5	3.2E-2		3.5E-1	2 3.3E-
	GOTERM_BP_DIRECT	regulation of early endosome to late	RT	-	5	3.2E-2		3.5E-1	1 3.3E-
	BIOCARTA	endosome transport		-					1 7.0E-
	BIOCARTA	Sprouty regulation of tyrosine kinase signals  Pelp1 Modulation of Estrogen Receptor	<u>RT</u>		11	3.5E-2		1.0E-1	2 7.7E-
	GOTERM_BP_DIRECT	Activity	<u>RT</u>	1	6	4.0E-2		1.1E-1	2 5.1E-
	BIOCARTA	trachea formation	<u>RT</u>	•	4	6.4E-2	4.0E0	5.3E-1	1
		Roles of ?-arrestin-dependent Recruitment of Src Kinases in GPCR Signaling	<u>RT</u>	•	11	7.6E-2	1.7E0	2.0E-1	1.3E- 1
	BIOCARTA	Aspirin Blocks Signaling Pathway Involved in Platelet Activation	<u>RT</u>	•	11	1.0E-1	1.6E0	2.6E-1	1.7E- 1
	GOTERM_BP_DIRECT	thyroid gland development	<u>RT</u>	•	8	1.1E-1	1.9E0	7.7E-1	7.3E- 1
	BIOCARTA	Regulation of Splicing through Sam68	<u>RT</u>	i .	5	1.6E-1	2.2E0	3.5E-1	2.4E- 1
	GOTERM_BP_DIRECT	ERK1 and ERK2 cascade	<u>RT</u>	i .	7	2.1E-1	1.7E0	1.0E0	9.5E- 1
	BIOCARTA	Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia	<u>RT</u>	i contraction	11	2.2E-1	1.4E0	4.5E-1	3.1E- 1
	BIOCARTA	Role of ?-arrestins in the activation and targeting of MAP kinases	<u>RT</u>	1	7	4.2E-1	1.3E0	6.6E-1	4.5E- 1
Annot	tation Cluster 162	Enrichment Score: 1.25	G	To the second se	Count	P_Value	Fold Change	Benjamin	
	INTERPRO	Heat shock factor (HSF)-type, DNA-binding	<u>RT</u>	i e	5	2.7E-2		2.1E-1	2.0E-
	UP_SEQ_FEATURE	region of interest:Hydrophobic repeat HR-A/B	RT	1	3	5.8E-2	6.8E0	9.1E-1	8.8E-
	UP_SEQ_FEATURE	region of interest:Hydrophobic repeat HR-C	RT	1	3	5.8E-2	6.8E0	9.1E-1	8.8E-
	SMART	HSF	RT		5	1.1E-1		5.2E-1	1 4.7E-
Annot	tation Cluster 163	Enrichment Score: 1.25	G	· ·		P_Value	Fold	Benjamin	i FDR
	GOTERM_BP_DIRECT	histone H3-K27 methylation	RT		4	1.7E-2	Onlange	2.2E-1	2.1E-
	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K27	RT		3	7.5E-2		3.9E-1	1 3.4E-
	GOTERM_MF_DIRECT	<u>specific)</u> <u>protein-lysine N-methyltransferase activity</u>		•	3			6.0E-1	1 5.3E-
Amari					6	1.4E-1	Fold		1
Annot	tation Objects and Cd		<u>RT</u>	-	6	P_Value	Change		. FDD
	tation Cluster 164  GOTERM_CC_DIRECT	Enrichment Score: 1.24	G	• •	Count	4.0E-2	2.550	Benjamin	
	GOTERM_CC_DIRECT	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex	G RT	• • •	Count 5			2.3E-1	2.0E- 1
	GOTERM_CC_DIRECT BIOCARTA	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation	G RT RT	- - - - -	Count 5	4.1E-2	1.9E0	2.3E-1 1.1E-1	2.0E- 1 7.8E- 2
	GOTERM_CC_DIRECT BIOCARTA GOTERM_BP_DIRECT	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation  nuclear-transcribed mRNA poly(A) tail shortening	G RT	: :	Count 5	4.1E-2 4.4E-2	1.9E0	2.3E-1	2.0E- 1 7.8E- 2 4.0E- 1
	GOTERM_CC_DIRECT BIOCARTA	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation  nuclear-transcribed mRNA poly(A) tail	G RT RT RT RT	i i i	Count 5	4.4E-2 1.6E-1	1.9E0 2.0E0 2.2E0	2.3E-1 1.1E-1 4.2E-1 3.5E-1	2.0E- 1 7.8E- 2 4.0E- 1 2.4E- 1
Annota	GOTERM_CC_DIRECT  BIOCARTA  GOTERM_BP_DIRECT  BIOCARTA  tation Cluster 165	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation  nuclear-transcribed mRNA poly(A) tail shortening	G RT RT RT	: :	<b>Count</b> 5 10 10	4.4E-2	1.9E0 2.0E0 2.2E0	2.3E-1 1.1E-1 4.2E-1	2.0E-1 7.8E-2 4.0E-1 2.4E-1
Annota	GOTERM_CC_DIRECT  BIOCARTA  GOTERM_BP_DIRECT  BIOCARTA  tation Cluster 165  GOTERM_CC_DIRECT	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation  nuclear-transcribed mRNA poly(A) tail shortening  Internal Ribosome entry pathway  Enrichment Score: 1.24  nucleotide-activated protein kinase complex	G RT RT RT RT	i i i	Count 5 10 10 5	4.4E-2 1.6E-1	1.9E0 2.0E0 2.2E0 Fold Change	2.3E-1 1.1E-1 4.2E-1 3.5E-1	2.0E-1 7.8E-2 4.0E-1 2.4E-1 1 FDR 1.1E-1
Annota	GOTERM_CC_DIRECT  BIOCARTA  GOTERM_BP_DIRECT  BIOCARTA  tation Cluster 165  GOTERM_CC_DIRECT  GOTERM_MF_DIRECT	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation  nuclear-transcribed mRNA poly(A) tail shortening.  Internal Ribosome entry pathway  Enrichment Score: 1.24  nucleotide-activated protein kinase complex cAMP-dependent protein kinase regulator activity.	RT RT RT RT G	i i i	Count  5  10  10  5  Count	4.4E-2 1.6E-1 P_Value	1.9E0 2.0E0 2.2E0 Fold Change 3.5E0	2.3E-1 1.1E-1 4.2E-1 3.5E-1 Benjamin	2.0E-1 7.8E-2 4.0E-1 2.4E-1 1 FDR 1.1E-1 4.1E-1
Annot	GOTERM_CC_DIRECT  BIOCARTA  GOTERM_BP_DIRECT  BIOCARTA  tation Cluster 165  GOTERM_CC_DIRECT	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation  nuclear-transcribed mRNA poly(A) tail shortening  Internal Ribosome entry pathway  Enrichment Score: 1.24  nucleotide-activated protein kinase complex cAMP-dependent protein kinase regulator	G RT RT RT RT RT RT RT G RT	i i i	Count 5 10 10 5 Count 6 4 11	4.4E-2 1.6E-1 P_Value 1.9E-2 9.7E-2 1.0E-1	1.9E0 2.0E0 2.2E0 Fold Change 3.5E0 3.4E0 1.6E0	2.3E-1 1.1E-1 4.2E-1 3.5E-1 Benjamin 1.3E-1 4.6E-1 2.6E-1	2.0E-1 7.8E-2 4.0E-1 2.4E-1 1 FDR 1.1E-1 4.1E-1 1.7E-1
	GOTERM_CC_DIRECT  BIOCARTA  GOTERM_BP_DIRECT  BIOCARTA  tation Cluster 165  GOTERM_CC_DIRECT  GOTERM_MF_DIRECT	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation  nuclear-transcribed mRNA poly(A) tail shortening  Internal Ribosome entry pathway  Enrichment Score: 1.24  nucleotide-activated protein kinase complex cAMP-dependent protein kinase regulator activity ChREBP regulation by carbohydrates and	RT RT RT RT RT RT RT RT RT		Count 5 10 10 5 Count 6 4 11	4.4E-2 1.6E-1 P_Value 1.9E-2 9.7E-2 1.0E-1	1.9E0 2.0E0 2.2E0 Fold Change 3.5E0 3.4E0 1.6E0	2.3E-1 1.1E-1 4.2E-1 3.5E-1 Benjamin 1.3E-1 4.6E-1	2.0E-1 7.8E-2 4.0E-1 2.4E-1 1 FDR 1.1E-1 4.1E-1 1.7E-1
	GOTERM_CC_DIRECT  BIOCARTA  GOTERM_BP_DIRECT  BIOCARTA  tation Cluster 165  GOTERM_CC_DIRECT  GOTERM_MF_DIRECT  BIOCARTA	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation  nuclear-transcribed mRNA poly(A) tail shortening  Internal Ribosome entry pathway  Enrichment Score: 1.24  nucleotide-activated protein kinase complex cAMP-dependent protein kinase regulator activity ChREBP regulation by carbohydrates and cAMP	RT RT RT RT RT RT RT RT RT		Count 5 10 10 5 Count 6 4 11	4.4E-2 1.6E-1 P_Value 1.9E-2 9.7E-2 1.0E-1	1.9E0 2.0E0 2.2E0 Fold Change 3.5E0 3.4E0 1.6E0 Fold Change	2.3E-1 1.1E-1 4.2E-1 3.5E-1 Benjamin 1.3E-1 4.6E-1 2.6E-1	2.0E-1 7.8E-2 4.0E-1 2.4E-1 1 FDR 1.1E-1 4.1E-1 1.7E-1
	GOTERM_CC_DIRECT  BIOCARTA  GOTERM_BP_DIRECT  BIOCARTA  tation Cluster 165  GOTERM_CC_DIRECT  GOTERM_MF_DIRECT  BIOCARTA  tation Cluster 166	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation  nuclear-transcribed mRNA poly(A) tail shortening  Internal Ribosome entry pathway  Enrichment Score: 1.24  nucleotide-activated protein kinase complex cAMP-dependent protein kinase regulator activity ChREBP regulation by carbohydrates and cAMP  Enrichment Score: 1.22	RI R		Count 5 10 10 5 Count 6 4 11 Count	4.4E-2 1.6E-1 P_Value 1.9E-2 9.7E-2 1.0E-1 P_Value	1.9E0 2.0E0 2.2E0 Fold Change 3.5E0 3.4E0 1.6E0 Fold Change 2.2E0	2.3E-1 1.1E-1 4.2E-1 3.5E-1 Benjamin 1.3E-1 4.6E-1 2.6E-1 Benjamin	2.0E-1 7.8E-2 4.0E-1 2.4E-1 1 FDR 1.1E-1 1.7E-1 1 FDR 2.0E-
	GOTERM_CC_DIRECT  BIOCARTA  GOTERM_BP_DIRECT  BIOCARTA  tation Cluster 165  GOTERM_CC_DIRECT  GOTERM_MF_DIRECT  BIOCARTA  tation Cluster 166  GOTERM_MF_DIRECT	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation  nuclear-transcribed mRNA poly(A) tail shortening  Internal Ribosome entry pathway  Enrichment Score: 1.24  nucleotide-activated protein kinase complex  cAMP-dependent protein kinase regulator activity  ChREBP regulation by carbohydrates and cAMP  Enrichment Score: 1.22  nucleosomal DNA binding	RT R		Count 5 10 10 5 Count 6 4 11 Count	4.4E-2 1.6E-1 P_Value 1.9E-2 9.7E-2 1.0E-1 P_Value 2.3E-3	1.9E0 2.0E0 2.2E0 Fold Change 3.5E0 3.4E0 1.6E0 Fold Change 2.2E0 2.0E0	2.3E-1 1.1E-1 4.2E-1 3.5E-1 Benjamin 1.3E-1 4.6E-1 2.6E-1 Benjamin 2.3E-2	2.0E-1 7.8E-2 4.0E-1 2.4E-1 1 FDR 1.1E-1 1.7E-1 1 FDR 2.0E-2
Annota	GOTERM_CC_DIRECT  BIOCARTA  GOTERM_BP_DIRECT  BIOCARTA  tation Cluster 165  GOTERM_CC_DIRECT  GOTERM_MF_DIRECT  BIOCARTA  tation Cluster 166  GOTERM_MF_DIRECT  INTERPRO	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation  nuclear-transcribed mRNA poly(A) tail shortening  Internal Ribosome entry pathway  Enrichment Score: 1.24  nucleotide-activated protein kinase complex  cAMP-dependent protein kinase regulator activity  ChREBP regulation by carbohydrates and cAMP  Enrichment Score: 1.22  nucleosomal DNA binding  Histone H3	RT		Count 5 10 10 5 Count 6 4 11 Count 17 6 6	4.4E-2 1.6E-1 P_Value 1.9E-2 9.7E-2 1.0E-1 P_Value 2.3E-3 1.8E-1	1.9E0 2.0E0 2.2E0 Fold Change 3.5E0 3.4E0 1.6E0 Fold Change 2.2E0 2.0E0 1.3E0	2.3E-1 1.1E-1 4.2E-1 3.5E-1  Benjamin 1.3E-1 4.6E-1 2.6E-1  Benjamin 2.3E-2 8.5E-1	2.0E-1 7.8E-2 4.0E-1 2.4E-1 1.1E-1 1.7E-1 1.7E-1 1.7E-1 9.0E-1
Annota	GOTERM_CC_DIRECT  BIOCARTA  GOTERM_BP_DIRECT  BIOCARTA  tation Cluster 165  GOTERM_CC_DIRECT  GOTERM_MF_DIRECT  BIOCARTA  tation Cluster 166  GOTERM_MF_DIRECT  INTERPRO  SMART	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation  nuclear-transcribed mRNA poly(A) tail shortening  Internal Ribosome entry pathway  Enrichment Score: 1.24  nucleotide-activated protein kinase complex cAMP-dependent protein kinase regulator activity ChREBP regulation by carbohydrates and cAMP  Enrichment Score: 1.22  nucleosomal DNA binding  Histone H3  H3	RT R		Count 5 10 10 5 Count 6 4 11 Count 17 6 6	4.4E-2 1.6E-1 P_Value 1.9E-2 9.7E-2 1.0E-1 P_Value 2.3E-3 1.8E-1 5.1E-1	1.9E0 2.0E0 2.2E0 Fold Change 3.5E0 3.4E0 1.6E0 Fold Change 2.2E0 2.0E0 1.3E0 Fold Change	2.3E-1 1.1E-1 4.2E-1 3.5E-1 Benjamin 1.3E-1 4.6E-1 2.6E-1 Benjamin 2.3E-2 8.5E-1 1.0E0	2.0E-1 7.8E-2 4.0E-1 2.4E-1 1 FDR 1.1E-1 1.7E-1 1.7E-1 1 FDR 2.0E-2 7.7E-1 9.0E-1 9.0E- 1
Annota	GOTERM_CC_DIRECT  BIOCARTA  GOTERM_BP_DIRECT  BIOCARTA  tation Cluster 165  GOTERM_MF_DIRECT  BIOCARTA  tation Cluster 166  GOTERM_MF_DIRECT  INTERPRO  SMART  tation Cluster 167	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation  nuclear-transcribed mRNA poly(A) tail shortening  Internal Ribosome entry pathway  Enrichment Score: 1.24  nucleotide-activated protein kinase complex  cAMP-dependent protein kinase regulator activity  ChREBP regulation by carbohydrates and cAMP  Enrichment Score: 1.22  nucleosomal DNA binding  Histone H3  H3  Enrichment Score: 1.21	RI R		Count 5 10 10 5 Count 6 4 11 Count 17 6 6 Count	4.4E-2 1.6E-1 P_Value 1.9E-2 9.7E-2 1.0E-1 P_Value 2.3E-3 1.8E-1 5.1E-1 P_Value	1.9E0 2.0E0 2.2E0 Fold Change 3.5E0 3.4E0 1.6E0 Fold Change 2.2E0 2.0E0 1.3E0 Fold Change 3.8E0	2.3E-1 1.1E-1 4.2E-1 3.5E-1 Benjamin 1.3E-1 4.6E-1 2.6E-1 Benjamin 2.3E-2 8.5E-1 1.0E0 Benjamin	2.0E-1 7.8E-2 4.0E-1 2.4E-1 1 FDR 1.1E-1 1.7E-1 1.7E-1 1 FDR 2.0E-2 7.7E-1 9.0E-1 1 FDR 9.0E-2 1.3E-
Annota	GOTERM_CC_DIRECT  BIOCARTA  GOTERM_BP_DIRECT  BIOCARTA  tation Cluster 165  GOTERM_CC_DIRECT  GOTERM_MF_DIRECT  BIOCARTA  tation Cluster 166  GOTERM_MF_DIRECT  INTERPRO  SMART  tation Cluster 167  UP_KEYWORDS	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation  nuclear-transcribed mRNA poly(A) tail shortening  Internal Ribosome entry pathway  Enrichment Score: 1.24  nucleotide-activated protein kinase complex  cAMP-dependent protein kinase regulator activity  ChREBP regulation by carbohydrates and cAMP  Enrichment Score: 1.22  nucleosomal DNA binding  Histone H3  H3  Enrichment Score: 1.21  Xeroderma pigmentosum  Cockayne syndrome	RT R		Count 5 10 10 5 Count 6 4 11 Count 17 6 6 Count 5	4.4E-2 1.6E-1 P_Value 1.9E-2 9.7E-2 1.0E-1 P_Value 2.3E-3 1.8E-1 5.1E-1 P_Value 3.1E-2 4.4E-2	1.9E0 2.0E0 2.2E0 Fold Change 3.5E0 3.4E0 1.6E0 Fold Change 2.2E0 2.0E0 1.3E0 Fold Change 3.8E0 4.6E0	2.3E-1 1.1E-1 4.2E-1 3.5E-1 Benjamin 1.3E-1 4.6E-1 2.6E-1 Benjamin 2.3E-2 8.5E-1 1.0E0 Benjamin 1.2E-1 1.6E-1	2.0E-1 7.8E-2 4.0E-1 2.4E-1 1 FDR 1.1E-1 1.7E-1 1.7E-1 1 FDR 2.0E-2 7.7E-1 9.0E-1 1 FDR 9.0E-1 1.3E-1 3.5E-1
Annota	GOTERM_CC_DIRECT  BIOCARTA  GOTERM_BP_DIRECT  BIOCARTA  tation Cluster 165  GOTERM_CC_DIRECT  GOTERM_MF_DIRECT  BIOCARTA  tation Cluster 166  GOTERM_MF_DIRECT  INTERPRO  SMART  tation Cluster 167  UP_KEYWORDS  UP_KEYWORDS	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation  nuclear-transcribed mRNA poly(A) tail shortening.  Internal Ribosome entry pathway  Enrichment Score: 1.24  nucleotide-activated protein kinase complex cAMP-dependent protein kinase regulator activity. ChREBP regulation by carbohydrates and cAMP  Enrichment Score: 1.22  nucleosomal DNA binding.  Histone H3  H3  Enrichment Score: 1.21  Xeroderma pigmentosum  Cockayne syndrome holo TFIIH complex	RI R		Count 5 10 10 5 Count 6 4 11 Count 17 6 6 Count 5 4 5	4.4E-2 1.6E-1 P_Value 1.9E-2 9.7E-2 1.0E-1 P_Value 2.3E-3 1.8E-1 5.1E-1 P_Value 3.1E-2 4.4E-2 8.0E-2	1.9E0 2.0E0 2.2E0 Fold Change 3.5E0 3.4E0 1.6E0 Fold Change 2.2E0 2.0E0 1.3E0 Fold Change 3.8E0 4.6E0 2.9E0	2.3E-1 1.1E-1 4.2E-1 3.5E-1 Benjamin 1.3E-1 4.6E-1 2.6E-1 Benjamin 2.3E-2 8.5E-1 1.0E0 Benjamin 1.2E-1 1.6E-1 4.0E-1	2.0E-1 7.8E-2 4.0E-1 2.4E-1 1.1E-1 1.7E-1 1.
Annota	GOTERM_CC_DIRECT  BIOCARTA  GOTERM_BP_DIRECT  BIOCARTA  tation Cluster 165  GOTERM_MF_DIRECT  BIOCARTA  tation Cluster 166  GOTERM_MF_DIRECT  INTERPRO  SMART  tation Cluster 167  UP_KEYWORDS  UP_KEYWORDS  GOTERM_CC_DIRECT	Enrichment Score: 1.24  eukaryotic translation initiation factor 4F complex  Eukaryotic protein translation  nuclear-transcribed mRNA poly(A) tail shortening  Internal Ribosome entry pathway  Enrichment Score: 1.24  nucleotide-activated protein kinase complex  cAMP-dependent protein kinase regulator activity  ChREBP regulation by carbohydrates and cAMP  Enrichment Score: 1.22  nucleosomal DNA binding  Histone H3  H3  Enrichment Score: 1.21  Xeroderma pigmentosum  Cockayne syndrome	RT R		Count 5 10 10 5 Count 6 4 11 Count 17 6 6 Count 5 4 5 5	4.4E-2 1.6E-1 P_Value 1.9E-2 9.7E-2 1.0E-1 P_Value 2.3E-3 1.8E-1 5.1E-1 P_Value 3.1E-2 4.4E-2	1.9E0 2.0E0 2.2E0 Fold Change 3.5E0 3.4E0 1.6E0 Fold Change 2.2E0 2.0E0 1.3E0 Fold Change 3.8E0 4.6E0 2.9E0 2.5E0	2.3E-1 1.1E-1 4.2E-1 3.5E-1 Benjamin 1.3E-1 4.6E-1 2.6E-1 Benjamin 2.3E-2 8.5E-1 1.0E0 Benjamin 1.2E-1 1.6E-1	2.0E-1 7.8E-2 4.0E-1 2.4E-1 1

	ation Cluster 1	Enrichment Score: ?	G	- 100 miles	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_BP_DIRECT	extrinsic apoptotic signaling pathway in absence of ligand	<u>RT</u>	ī	15	6.9E-4	·	1.7E-2	1.6E-
	GOTERM_BP_DIRECT	regulation of mitochondrial membrane	RT	1	6	1.6E-2	3.6E0	2.2E-1	2.1E-
	GOTERM_MF_DIRECT	permeability  BH3 domain binding	RT		4	1.6E-2		1.1E-1	1 1.0E-
	INTERPRO	Apoptosis regulator, Bcl-2, BH1 motif,		-					1 2.0E-
	INTERPRO	conserved site  Apoptosis regulator, Bcl-2, BH2 motif,	<u>RT</u>		5	2.7E-2		2.1E-1	1 2.0E-
		conserved site	<u>RT</u>	•	5	2.7E-2	3.9E0	2.1E-1	1
	INTERPRO	<u>Apoptosis regulator, Bcl-2, BH3 motif,</u> <u>conserved site</u>	<u>RT</u>	•	5	2.7E-2	3.9E0	2.1E-1	2.0E- 1
	GOTERM_BP_DIRECT	regulation of protein heterodimerization activity	<u>RT</u>	i	5	3.2E-2	3.7E0	3.5E-1	3.3E- 1
	GOTERM_BP_DIRECT	regulation of mitochondrial membrane potential	<u>RT</u>	1	10	3.5E-2	2.1E0	3.8E-1	3.6E- 1
	GOTERM_BP_DIRECT	negative regulation of anoikis	<u>RT</u>	i	7	5.3E-2	2.4E0	4.8E-1	4.5E- 1
	UP_SEQ_FEATURE	short sequence motif:BH1	<u>RT</u>	1	5	6.5E-2	3.1E0	1.0E0	9.6E-
	GOTERM_CC_DIRECT	Bcl-2 family protein complex	<u>RT</u>	1	3	6.6E-2	6.4E0	3.5E-1	3.0E-
	GOTERM_BP_DIRECT	release of cytochrome c from mitochondria	<u>RT</u>		8	7.9E-2	2.1E0	5.9E-1	5.6E-
	INTERPRO	Bcl2-like	RT		5	8.7E-2		4.7E-1	1 4.3E-
	INTERPRO			-					1 4.3E-
	BBID	Blc2 family  152.altered synaptic signalling-	<u>RT</u>		5	8.7E-2		4.7E-1	1 9.7E-
		neurodegenerative disorders	<u>RT</u>	•	5	1.1E-1	2.4E0	9.7E-1	1
	UP_SEQ_FEATURE	short sequence motif:BH2	<u>RT</u>	1	5	1.1E-1	2.6E0	1.0E0	9.7E- 1
	BIOCARTA	Role of Mitochondria in Apoptotic Signaling	<u>RT</u>	ī	11	1.4E-1	1.5E0	3.1E-1	2.1E- 1
	UP_SEQ_FEATURE	short sequence motif:BH3	<u>RT</u>	1	5	2.3E-1	2.0E0	1.0E0	9.7E- 1
	GOTERM_BP_DIRECT	endoplasmic reticulum calcium ion homeostasis	<u>RT</u>	i .	5	2.4E-1	2.0E0	1.0E0	9.5E- 1
	GOTERM_BP_DIRECT	regulation of protein homodimerization activity	<u>RT</u>	i	3	3.4E-1	2.5E0	1.0E0	9.5E-
	BBID	127.Mito-stress	<u>RT</u>	i	4	3.4E-1	1.9E0	1.0E0	1.0E0
	GOTERM_CC_DIRECT	pore complex	<u>RT</u>	1	3	4.3E-1	2.1E0	1.0E0	8.7E- 1
Annota	ation Cluster 169	Enrichment Score: 1.2	G	<b>158</b>	Count	P_Value	Fold Change	Benjamin	i FDR
	UP_SEQ_FEATURE	region of interest:Rho-like	<u>RT</u>	i	3	5.8E-2	6.8E0	9.1E-1	8.8E- 1
	UP_SEQ_FEATURE	domain:BTB 2	<u>RT</u>	1	5	6.5E-2	3.1E0	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	domain:BTB 1	<u>RT</u>	i	5	6.5E-2	3.1E0	1.0E0	9.6E-
Annota	ation Cluster 170	Enrichment Score: 1.2	G	PR	Count	P_Value	Fold Change	Benjamin	i FDR
	KEGG_PATHWAY	Non-homologous end-joining		-	0	F 25 2		1.1E-2	5.3E-
$\neg$			<u>RT</u>		8	5.3E-3	J.ZLU	1.16-2	2
	GOTERM_CC_DIRECT	nonhomologous end joining complex	RT RT		8	1.2E-1		5.0E-1	3 4.4E-
	GOTERM_CC_DIRECT  GOTERM_BP_DIRECT	nonhomologous end joining complex	<u>RT</u>		4	1.2E-1	3.2E0	5.0E-1	
		establishment of integrated proviral latency	RT RT		4	1.2E-1 1.4E-1	3.2E0 3.0E0	5.0E-1 8.1E-1	4.4E- 1
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT	establishment of integrated proviral latency regulation of smooth muscle cell proliferation	RT RT RT		4 4 4	1.2E-1 1.4E-1 1.8E-1	3.2E0 3.0E0 2.6E0	5.0E-1 8.1E-1 9.9E-1	4.4E- 1 7.7E- 1 9.4E- 1
Annota	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 171	establishment of integrated proviral latency regulation of smooth muscle cell proliferation Enrichment Score: 1.19	RT RT RT G		4 4 4 Count	1.2E-1 1.4E-1 1.8E-1 P_Value	3.2E0 3.0E0 2.6E0 Fold Change	5.0E-1 8.1E-1 9.9E-1 Benjamin	4.4E- 1 7.7E- 1 9.4E- 1
Annota	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 171  UP_SEQ_FEATURE	establishment of integrated proviral latency regulation of smooth muscle cell proliferation	RT RT RT		4 4 4	1.2E-1 1.4E-1 1.8E-1	3.2E0 3.0E0 2.6E0 Fold Change	5.0E-1 8.1E-1 9.9E-1	4.4E-1 7.7E-1 9.4E-1 1 FDR 5.9E-2
Annota	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 171  UP_SEQ_FEATURE  GOTERM_MF_DIRECT	establishment of integrated proviral latency regulation of smooth muscle cell proliferation  Enrichment Score: 1.19 cross-link:Glycyl lysine isopeptide (Gly-Lys)	RT RT RT G	- -	4 4 4 Count	1.2E-1 1.4E-1 1.8E-1 P_Value	3.2E0 3.0E0 2.6E0 Fold Change 3.4E0	5.0E-1 8.1E-1 9.9E-1 Benjamin	4.4E-1 7.7E-1 9.4E-1 1 FDR 5.9E-2 5.2E-1
Annota	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 171  UP_SEQ_FEATURE	establishment of integrated proviral latency regulation of smooth muscle cell proliferation  Enrichment Score: 1.19  cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)	RT RT RT RT	- -	4 4 4 Count	1.2E-1 1.4E-1 1.8E-1 P_Value 2.3E-3	3.2E0 3.0E0 2.6E0 Fold Change 3.4E0 3.0E0	5.0E-1 8.1E-1 9.9E-1 Benjamin 6.1E-2	4.4E-1 7.7E-1 9.4E-1 1 FDR 5.9E-2 5.2E-
Annota	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 171  UP_SEQ_FEATURE  GOTERM_MF_DIRECT	establishment of integrated proviral latency regulation of smooth muscle cell proliferation  Enrichment Score: 1.19  cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins) protein tag	RT RT RT RT RT RT	- -	4 4 4 Count 9	1.2E-1 1.4E-1 1.8E-1 P_Value 2.3E-3 1.4E-1	3.2E0 3.0E0 2.6E0 Fold Change 3.4E0 3.0E0 3.7E0	5.0E-1 8.1E-1 9.9E-1 Benjamin 6.1E-2 5.8E-1	4.4E-1 7.7E-1 9.4E-1 1 FDR 5.9E-2 5.2E-1 7.8E-
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 171  UP_SEQ_FEATURE  GOTERM_MF_DIRECT  INTERPRO	establishment of integrated proviral latency regulation of smooth muscle cell proliferation  Enrichment Score: 1.19  cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins) protein tag  Small ubiquitin-related modifier, SUMO	RT RT RT G RT RT RT	- -	4 4 4 Count 9 4 3 4	1.2E-1 1.4E-1 1.8E-1 P_Value 2.3E-3 1.4E-1 1.9E-1 3.0E-1	3.2E0 3.0E0 2.6E0 Fold Change 3.4E0 3.0E0 3.7E0 2.1E0	5.0E-1 8.1E-1 9.9E-1 Benjamin 6.1E-2 5.8E-1 8.6E-1	4.4E-1 7.7E-1 9.4E-1 1 FDR 5.9E-2 5.2E-1 7.8E-1 3.8E-1
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 171  UP_SEQ_FEATURE  GOTERM_MF_DIRECT  INTERPRO  BIOCARTA	establishment of integrated proviral latency regulation of smooth muscle cell proliferation  Enrichment Score: 1.19  cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins) protein tag  Small ubiquitin-related modifier, SUMO  Basic Mechanisms of SUMOylation	RT RT RT G RT RT RT RT		4 4 4 Count 9 4 3 4	1.2E-1 1.4E-1 1.8E-1 P_Value 2.3E-3 1.4E-1 1.9E-1 3.0E-1 P_Value	3.2E0 3.0E0 2.6E0 Fold Change 3.4E0 3.0E0 3.7E0 2.1E0	5.0E-1 8.1E-1 9.9E-1 Benjamin 6.1E-2 5.8E-1 8.6E-1 5.5E-1 Benjamin	4.4E-1 7.7E-1 9.4E-1 1 FDR 5.9E-2 5.2E-1 7.8E-1 3.8E-1
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 171  UP_SEQ_FEATURE  GOTERM_MF_DIRECT  INTERPRO  BIOCARTA  ation Cluster 172	establishment of integrated proviral latency regulation of smooth muscle cell proliferation  Enrichment Score: 1.19  cross-link: Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins) protein tag  Small ubiquitin-related modifier, SUMO  Basic Mechanisms of SUMOylation  Enrichment Score: 1.19  Tyrosine-protein kinase, receptor class III,	RT RT RT RT RT RT RT RT		4 4 4 Count 9 4 3 4 Count	1.2E-1 1.4E-1 1.8E-1 P_Value 2.3E-3 1.4E-1 1.9E-1 3.0E-1 P_Value	3.2E0 3.0E0 2.6E0 Fold Change 3.4E0 3.0E0 2.1E0 Fold Change 6.2E0	5.0E-1 8.1E-1 9.9E-1 Benjamin 6.1E-2 5.8E-1 8.6E-1 5.5E-1 Benjamin	4.4E-1 7.7E-1 9.4E-1 1
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 171  UP_SEQ_FEATURE  GOTERM_MF_DIRECT  INTERPRO  BIOCARTA  ation Cluster 172  INTERPRO	establishment of integrated proviral latency regulation of smooth muscle cell proliferation  Enrichment Score: 1.19  cross-link: Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins) protein tag  Small ubiquitin-related modifier, SUMO  Basic Mechanisms of SUMOylation  Enrichment Score: 1.19  Tyrosine-protein kinase, receptor class III, conserved site positive regulation of phospholipase C activity vascular endothelial growth factor-activated	RT RT RT RT RT RT RT RT RT		4 4 4 Count 9 4 3 4 Count 8	1.2E-1 1.4E-1 1.8E-1 P_Value 2.3E-3 1.4E-1 1.9E-1 3.0E-1 P_Value 1.9E-5 1.0E-4	3.2E0 3.0E0 2.6E0 Fold Change 3.4E0 3.0E0 2.1E0 Fold Change 6.2E0 5.3E0	5.0E-1 8.1E-1 9.9E-1 Benjamin 6.1E-2 5.8E-1 8.6E-1 5.5E-1 Benjamin 3.4E-4 3.2E-3	4.4E-1 7.7E-1 9.4E-1 1 5.9E-2 5.2E-1 7.8E-1 3.8E-1 1 ii FDR 3.1E-4
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 171  UP_SEQ_FEATURE  GOTERM_MF_DIRECT  INTERPRO  BIOCARTA  ation Cluster 172  INTERPRO  GOTERM_BP_DIRECT	establishment of integrated proviral latency regulation of smooth muscle cell proliferation  Enrichment Score: 1.19  cross-link: Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins) protein tag  Small ubiquitin-related modifier, SUMO  Basic Mechanisms of SUMOylation  Enrichment Score: 1.19  Tyrosine-protein kinase, receptor class III, conserved site positive regulation of phospholipase C activity vascular endothelial growth factor-activated receptor activity	RT		4 4 4 7 Count 9 4 3 4 Count 8 8 8 5	1.2E-1 1.4E-1 1.8E-1  P_Value 2.3E-3 1.4E-1 1.9E-1 3.0E-1  P_Value 1.9E-5 1.0E-4 1.8E-2	3.2E0 3.0E0 2.6E0 Fold Change 3.4E0 3.0E0 2.1E0 Fold Change 6.2E0 5.3E0 4.3E0	5.0E-1 8.1E-1 9.9E-1  Benjamin 6.1E-2 5.8E-1 8.6E-1 5.5E-1  Benjamin 3.4E-4 3.2E-3 1.2E-1	4.4E-1 7.7E-1 9.4E-1 1 5.9E-2 5.2E-1 7.8E-1 3.8E-1 3.1E-4 3.0E-3
	GOTERM_BP_DIRECT  ation Cluster 171  UP_SEQ_FEATURE  GOTERM_MF_DIRECT  INTERPRO  BIOCARTA  ation Cluster 172  INTERPRO  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT  INTERPRO	establishment of integrated proviral latency regulation of smooth muscle cell proliferation  Enrichment Score: 1.19  cross-link: Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins) protein tag  Small ubiquitin-related modifier, SUMO  Basic Mechanisms of SUMOylation  Enrichment Score: 1.19  Tyrosine-protein kinase, receptor class III, conserved site positive regulation of phospholipase C activity vascular endothelial growth factor-activated receptor activity  Tyrosine-protein kinase, CSF-1/PDGF receptor	RT R		4 4 4 7 Count 9 4 3 4 Count 8 8 8 5 4	1.2E-1 1.4E-1 1.8E-1 P_Value 2.3E-3 1.4E-1 1.9E-1 3.0E-1 P_Value 1.9E-5 1.0E-4 1.8E-2 3.2E-2	3.2E0 3.0E0 2.6E0 Fold Change 3.4E0 3.0E0 2.1E0 Fold Change 6.2E0 5.3E0 4.3E0 5.0E0	5.0E-1 8.1E-1 9.9E-1  Benjamin 6.1E-2 5.8E-1 8.6E-1 5.5E-1  Benjamin 3.4E-4 3.2E-3 1.2E-1 2.4E-1	4.4E-1 7.7E-1 9.4E-1 1 5.9E-2 5.2E-1 7.8E-1 3.8E-1 3.1E-4 3.0E-3 1.1E-1 2.2E-1
	GOTERM_BP_DIRECT  ation Cluster 171  UP_SEQ_FEATURE  GOTERM_MF_DIRECT  INTERPRO  BIOCARTA  ation Cluster 172  INTERPRO  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  INTERPRO  PIR_SUPERFAMILY	establishment of integrated proviral latency regulation of smooth muscle cell proliferation  Enrichment Score: 1.19  cross-link: Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins) protein tag  Small ubiquitin-related modifier, SUMO  Basic Mechanisms of SUMOylation  Enrichment Score: 1.19  Tyrosine-protein kinase, receptor class III, conserved site positive regulation of phospholipase C activity, vascular endothelial growth factor-activated receptor activity  Tyrosine-protein kinase, CSF-1/PDGF receptor tyrosine-protein kinase, CSF-1/PDGF receptor type	RT R		4 4 4 7 Count 9 4 3 4 Count 8 8 8 5	1.2E-1 1.4E-1 1.8E-1 P_Value 2.3E-3 1.4E-1 1.9E-1 3.0E-1 P_Value 1.9E-5 1.0E-4 1.8E-2 3.2E-2 4.8E-2	3.2E0 3.0E0 2.6E0 Fold Change 3.4E0 3.0E0 2.1E0 Fold Change 6.2E0 5.3E0 4.3E0 5.0E0 4.3E0	5.0E-1 8.1E-1 9.9E-1 Benjamin 6.1E-2 5.8E-1 8.6E-1 5.5E-1 Benjamin 3.4E-4 3.2E-3 1.2E-1 2.4E-1 6.2E-1	4.4E-1 7.7E-1 9.4E-1 9.4E-1 7.8E-1 3.8E-1 3.1E-1 3.0E-3 1.1E-1 6.1E-1
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 171  UP_SEQ_FEATURE  GOTERM_MF_DIRECT  INTERPRO  BIOCARTA  ation Cluster 172  INTERPRO  GOTERM_BP_DIRECT  INTERPRO  GOTERM_MF_DIRECT  INTERPRO  PIR_SUPERFAMILY  GOTERM_BP_DIRECT	establishment of integrated proviral latency regulation of smooth muscle cell proliferation  Enrichment Score: 1.19  cross-link: Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins) protein tag  Small ubiquitin-related modifier, SUMO  Basic Mechanisms of SUMOylation  Enrichment Score: 1.19  Tyrosine-protein kinase, receptor class III, conserved site positive regulation of phospholipase C activity vascular endothelial growth factor-activated receptor activity  Tyrosine-protein kinase, CSF-1/PDGF receptor tyrosine-protein kinase, CSF-1/PDGF receptor	RT R		4 4 4 7 Count 9 4 3 4 Count 8 8 8 5 4	1.2E-1 1.4E-1 1.8E-1 P_Value 2.3E-3 1.4E-1 1.9E-1 3.0E-1 P_Value 1.9E-5 1.0E-4 1.8E-2 3.2E-2 4.8E-2	3.2E0 3.0E0 2.6E0 Fold Change 3.4E0 3.0E0 2.1E0 Fold Change 6.2E0 5.3E0 4.3E0 5.0E0	5.0E-1 8.1E-1 9.9E-1 Benjamin 6.1E-2 5.8E-1 8.6E-1 5.5E-1 Benjamin 3.4E-4 3.2E-3 1.2E-1 2.4E-1 6.2E-1	4.4E-1 7.7E-1 9.4E-1 1 9.4E-1 1 5.9E-2 5.2E-1 7.8E-1 3.8E-1 3.1E-1 3.1E-1 6.1E-1 5.1E-1
	GOTERM_BP_DIRECT  ation Cluster 171  UP_SEQ_FEATURE  GOTERM_MF_DIRECT  INTERPRO  BIOCARTA  ation Cluster 172  INTERPRO  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  INTERPRO  PIR_SUPERFAMILY	establishment of integrated proviral latency regulation of smooth muscle cell proliferation  Enrichment Score: 1.19  cross-link: Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins) protein tag  Small ubiquitin-related modifier, SUMO  Basic Mechanisms of SUMOylation  Enrichment Score: 1.19  Tyrosine-protein kinase, receptor class III, conserved site positive regulation of phospholipase C activity vascular endothelial growth factor-activated receptor activity  Tyrosine-protein kinase, CSF-1/PDGF receptor tyrosine-protein kinase, CSF-1/PDGF receptor type vascular endothelial growth factor signaling	RT R		4 4 4 4 Count 9 4 3 4 Count 8 8 5 4 4	1.2E-1 1.4E-1 1.8E-1 P_Value 2.3E-3 1.4E-1 1.9E-1 3.0E-1 P_Value 1.9E-5 1.0E-4 1.8E-2 3.2E-2 4.8E-2	3.2E0 3.0E0 2.6E0 Fold Change 3.4E0 3.0E0 2.1E0 Fold Change 6.2E0 5.3E0 4.3E0 4.3E0 4.0E0	5.0E-1 8.1E-1 9.9E-1 Benjamin 6.1E-2 5.8E-1 8.6E-1 5.5E-1 Benjamin 3.4E-4 3.2E-3 1.2E-1 2.4E-1 6.2E-1	4.4E-1 7.7E-1 9.4E-1 9.4E-1 7.8E-1 3.8E-1 3.1E-1 3.0E-3 1.1E-1 6.1E-1
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 171  UP_SEQ_FEATURE  GOTERM_MF_DIRECT  INTERPRO  BIOCARTA  ation Cluster 172  INTERPRO  GOTERM_BP_DIRECT  INTERPRO  GOTERM_MF_DIRECT  INTERPRO  PIR_SUPERFAMILY  GOTERM_BP_DIRECT	establishment of integrated proviral latency regulation of smooth muscle cell proliferation  Enrichment Score: 1.19  cross-link: Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins) protein tag  Small ubiquitin-related modifier, SUMO  Basic Mechanisms of SUMOylation  Enrichment Score: 1.19  Tyrosine-protein kinase, receptor class III, conserved site  positive regulation of phospholipase C activity vascular endothelial growth factor-activated receptor activity  Tyrosine-protein kinase, CSF-1/PDGF receptor tyrosine-protein kinase, CSF-1/PDGF receptor type vascular endothelial growth factor signaling pathway	RT R		4 4 4 7 Count 9 4 3 4 Count 8 8 5 4 4 4	1.2E-1 1.4E-1 1.8E-1  P_Value 2.3E-3 1.4E-1 1.9E-1 3.0E-1  P_Value 1.9E-5 1.0E-4 1.8E-2 3.2E-2 4.8E-2 6.4E-2 2.0E-1	3.2E0 3.0E0 2.6E0 Fold Change 3.4E0 3.0E0 2.1E0 Fold Change 6.2E0 5.3E0 4.3E0 4.3E0 4.0E0	5.0E-1 8.1E-1 9.9E-1 Benjamin 6.1E-2 5.8E-1 8.6E-1 5.5E-1 Benjamin 3.4E-4 3.2E-3 1.2E-1 2.4E-1 6.2E-1 5.3E-1 7.6E-1	4.4E-1 7.7E-1 9.4E-1 1 9.4E-1 1 5.9E-2 5.2E-1 7.8E-1 3.8E-1 3.1E-1 3.1E-1 6.1E-1 5.1E-1
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 171  UP_SEQ_FEATURE  GOTERM_MF_DIRECT  INTERPRO  BIOCARTA  ation Cluster 172  INTERPRO  GOTERM_BP_DIRECT  INTERPRO  PIR_SUPERFAMILY  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT	establishment of integrated proviral latency regulation of smooth muscle cell proliferation  Enrichment Score: 1.19  cross-link: Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins) protein tag  Small ubiquitin-related modifier, SUMO  Basic Mechanisms of SUMOylation  Enrichment Score: 1.19  Tyrosine-protein kinase, receptor class III, conserved site positive regulation of phospholipase C activity vascular endothelial growth factor-activated receptor activity.  Tyrosine-protein kinase, CSF-1/PDGF receptor tyrosine-protein kinase, CSF-1/PDGF receptor type vascular endothelial growth factor signaling pathway vascular endothelial growth factor binding	RT R		4 4 4 7 Count 9 4 3 4 Count 8 8 8 5 4 4 4 4 3	1.2E-1 1.4E-1 1.8E-1  P_Value 2.3E-3 1.4E-1 1.9E-1 3.0E-1  P_Value 1.9E-5 1.0E-4 1.8E-2 3.2E-2 4.8E-2 6.4E-2 2.0E-1	3.2E0 3.0E0 2.6E0 Fold Change 3.4E0 3.7E0 2.1E0 Fold Change 6.2E0 5.3E0 4.3E0 4.3E0 4.0E0 3.6E0 1.5E0	5.0E-1 8.1E-1 9.9E-1 Benjamin 6.1E-2 5.8E-1 8.6E-1 5.5E-1 Benjamin 3.4E-4 3.2E-3 1.2E-1 2.4E-1 6.2E-1 5.3E-1 7.6E-1	4.4E-1 7.7E-1 9.4E-1 1 9.4E-1 7.8E-1 3.8E-1 3.1E-1 3.0E-3 1.1E-1 6.1E-1 6.1E-1 6.7E-1
	GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 171  UP_SEQ_FEATURE  GOTERM_MF_DIRECT  INTERPRO  BIOCARTA  ation Cluster 172  INTERPRO  GOTERM_BP_DIRECT  INTERPRO  PIR_SUPERFAMILY  GOTERM_BP_DIRECT  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  GOTERM_MF_DIRECT	establishment of integrated proviral latency regulation of smooth muscle cell proliferation  Enrichment Score: 1.19  cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins) protein tag  Small ubiquitin-related modifier, SUMO  Basic Mechanisms of SUMOylation  Enrichment Score: 1.19  Tyrosine-protein kinase, receptor class III, conserved site positive regulation of phospholipase C activity vascular endothelial growth factor-activated receptor activity.  Tyrosine-protein kinase, CSF-1/PDGF receptor type vascular endothelial growth factor signaling pathway vascular endothelial growth factor binding	RT R		4 4 4 4 Count 9 4 3 4 Count 8 8 8 5 4 4 4 4 3 7	1.2E-1 1.4E-1 1.8E-1  P_Value 2.3E-3 1.4E-1 1.9E-1 3.0E-1  P_Value 1.9E-5 1.0E-4 1.8E-2 3.2E-2 4.8E-2 6.4E-2 2.0E-1 2.9E-1 4.1E-1	3.2E0 3.0E0 2.6E0 Fold Change 3.4E0 3.7E0 2.1E0 Fold Change 6.2E0 5.3E0 4.3E0 4.3E0 4.0E0 3.6E0 1.5E0	5.0E-1 8.1E-1 9.9E-1  Benjamin 6.1E-2 5.8E-1 8.6E-1 5.5E-1  Benjamin 3.4E-4 3.2E-3 1.2E-1 2.4E-1 6.2E-1 5.3E-1 7.6E-1 9.5E-1 1.0E0	4.4E-1 7.7E-1 9.4E-1 9.4E-1 7.8E-1 3.8E-1 3.1E-1 3.0E-3 1.1E-1 6.1E-1 6.7E-1 8.5E-1

Annota	ation Cluster 1	Enrichment Score: ?	G	- Total	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:Ig-like C2-type 3	<u>RT</u>	i	17	7.9E-1	9.0E-1		9.7E- 1
	UP_SEQ_FEATURE	domain:Ig-like C2-type 6	<u>RT</u>	i	5	8.1E-1	9.2E-1	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	domain:Ig-like C2-type 4	<u>RT</u>		9	8.9E-1	8.1E-1	1.0E0	9.7E-
	INTERPRO	<u>Immunoglobulin</u>	<u>RT</u>		10	9.3E-1	7.6E-1	1.0E0	1 9.3E-
Annota	ation Cluster 173	Enrichment Score: 1.18	G	<b>178</b>	Count	P_Value	Fold	Benjamini	1 FDR
	UP_SEQ_FEATURE	zinc finger region:ZZ-type	<u>RT</u>	1	7	2.9E-2		5.5E-1	5.3E-
	INTERPRO	Zinc finger, ZZ-type	RT		7	5.7E-2	2.4E0	3.9E-1	1 3.6E-
	SMART	<u>ZnF_ZZ</u>	RT		7	1.8E-1		7.1E-1	1 6.4E-
Annota	ation Cluster 174	Enrichment Score: 1.17	G	- -	Count	P_Value	Fold	Biii	1 FDR
	UP_KEYWORDS	<u>Threonine protease</u>	RT .		8	1.9E-2	Change	7.7E-2	6.0E-
	INTERPRO	Proteasome, subunit alpha/beta	RT		8	2.4E-2		1.9E-1	2 1.7E-
	GOTERM_CC_DIRECT	proteasome core complex, alpha-subunit	RT		5	2.5E-2		1.6E-1	1 1.4E-
	INTERPRO	complex  Proteasome A-type subunit	RT		5	2.7E-2		2.1E-1	1 2.0E-
	INTERPRO	Proteasome, alpha-subunit, N-terminal							1 2.0E-
	GOTERM_CC_DIRECT	domain	<u>RT</u>		5	2.7E-2		2.1E-1	1 1.9E-
	GOTERM_MF_DIRECT	proteasome core complex	<u>RT</u>		8	3.6E-2		2.2E-1	1 2.6E-
	SMART	threonine-type endopeptidase activity	<u>RT</u>		8	4.9E-2		2.9E-1	1 4.7E-
	INTERPRO	SM00948  Proteasome, beta-type subunit, conserved	<u>RT</u>		5	1.1E-1		5.2E-1	4.7E- 1 8.9E-
		site	<u>RT</u>	i	4	3.0E-1	2.1E0	9.8E-1	1
	INTERPRO	Proteasome B-type subunit	<u>RT</u>	i	3	5.5E-1	1.7E0	1.0E0	9.1E- 1
	GOTERM_BP_DIRECT	proteolysis involved in cellular protein catabolic process	<u>RT</u>	î	9	5.7E-1		1.0E0	9.5E- 1
Annota	ation Cluster 175	Enrichment Score: 1.16	G	<b>100</b>	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	Ribosomal protein L1, 2-layer alpha/beta- sandwich	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E- 1
	INTERPRO	Ribosomal protein L1, 3-layer alpha/beta- sandwich	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E- 1
	INTERPRO	Ribosomal protein L1, superfamily	<u>RT</u>	i	3	7.0E-2		3.9E-1	3.6E- 1
Annota	ntion Cluster 176	Enrichment Score: 1.16	G	<b>™</b>	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	Pseudouridine synthase, RsuA/RluB/C/D/E/F	<u>RT</u>	i	4	1.5E-2	6.2E0	1.2E-1	1.1E- 1
	INTERPRO	Pseudouridine synthase, catalytic domain	<u>RT</u>	i .	6	4.5E-2	2.9E0	3.2E-1	3.0E- 1
	GOTERM_MF_DIRECT	pseudouridine synthase activity	<u>RT</u>	i .	6	5.2E-2	2.8E0	3.0E-1	2.7E- 1
	GOTERM_BP_DIRECT	tRNA pseudouridine synthesis	<u>RT</u>	i	4	6.4E-2	4.0E0	5.3E-1	5.1E- 1
	GOTERM_MF_DIRECT	deaminase activity	<u>RT</u>	i .	4	1.4E-1	3.0E0	5.8E-1	5.2E- 1
	GOTERM_BP_DIRECT	<u>pseudouridine synthesis</u>	<u>RT</u>	1	4	3.8E-1	1.8E0	1.0E0	9.5E- 1
Annota	ation Cluster 177	Enrichment Score: 1.15	G	<b>100</b>	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	DNA-directed RNA polymerase, subunit 2, domain 6	<u>RT</u>	i	3	7.0E-2	<u> </u>	3.9E-1	3.6E- 1
	INTERPRO	RNA polymerase, beta subunit, conserved site	<u>RT</u>	1	3	7.0E-2	6.2E0	3.9E-1	3.6E-
	INTERPRO	DNA-directed RNA polymerase, subunit 2	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E-
	INTERPRO	RNA polymerase Rpb2, OB-fold	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E-
	INTERPRO	RNA polymerase Rpb2, domain 7	<u>RT</u>	i e	3	7.0E-2	6.2E0	3.9E-1	3.6E-
	INTERPRO	RNA polymerase Rpb2, domain 2	<u>RT</u>		3	7.0E-2		3.9E-1	3.6E-
	INTERPRO	RNA polymerase, beta subunit, protrusion	RT		3	7.0E-2		3.9E-1	1 3.6E-
	INTERPRO	RNA polymerase Rpb2, domain 3	RT		3	7.0E-2		3.9E-1	1 3.6E-
	GOTERM_MF_DIRECT	ribonucleoside binding	RT		3	7.5E-2		3.9E-1	1 3.4E-
Annot	ation Cluster 178	Enrichment Score: 1.13	G	· -	:	:	:	:	1 FDR
	UP_SEQ_FEATURE	domain:IQ 5	RT	i	6	P_Value 1.4E-2		2.9E-1	2.8E-
				•		,	217 20	,,_ 1	1
	INTERPRO	Dilute	RT	E	4	8 8F-2	3 5E0	4 7F-1	4.3E-
		<u>Dilute</u>	<u>RT</u>	i	4	8.8E-2		4.7E-1	1
	INTERPRO	Dilute  domain:Dilute  SM01132	<u>RT</u> <u>RT</u> <u>RT</u>	i i i	4 4	8.8E-2 1.0E-1 2.3E-1	3.4E0	4.7E-1 1.0E0 9.0E-1	

nota	ation Cluster 1	Enrichment Score: ?	G	<b>100</b>	Count	P_Value	Citalige	Benjamini	FDF
nota	ation Cluster 179	Enrichment Score: 1.13	G	<b>100</b>	Count	P_Value	Fold Change	Benjamini	FDF
)	UP_SEQ_FEATURE	zinc finger region:GATA-type 1	<u>RT</u>	1	6	3.6E-4	6.8E0	1.1E-2	1.0
)	UP_SEQ_FEATURE	zinc finger region:GATA-type 2	<u>RT</u>	i .	6	3.6E-4	6.8E0	1.1E-2	1.0
)	INTERPRO	GATA-type transcription activator, N-terminal	<u>RT</u>	1	3	7.0E-2	6.2E0	3.9E-1	3.6 1
)	INTERPRO	Zinc finger, GATA-type	<u>RT</u>	1	6	8.0E-2	2.5E0	4.4E-1	4.1 1
)	GOTERM_BP_DIRECT	intestinal epithelial cell differentiation	<u>RT</u>		4	9.8E-2	3.4E0	6.8E-1	6.5
)	GOTERM_BP_DIRECT	anatomical structure formation involved in	RT		5	9.9E-2		6.8E-1	1 6.5
	GOTERM_MF_DIRECT	morphogenesis enhancer sequence-specific DNA binding	RT		7	1.0E-1		4.9E-1	1 4.4
	SMART								1 5.8
	INTERPRO	ZnF GATA	<u>RT</u>		6	1.5E-1		6.5E-1	1 9.1
	GOTERM_BP_DIRECT	Zinc finger, NHR/GATA-type	<u>RT</u>	•	11	4.6E-1	1.2E0	1.0E0	1
		<u>cell fate commitment</u>	<u>RT</u>	i	7	8.1E-1	9.0E-1	1.0E0	9.5
	GOTERM_BP_DIRECT	<u>cell development</u>	<u>RT</u>	i	6	8.3E-1	8.9E-1	1.0E0	9.! 1
	GOTERM_BP_DIRECT	cellular response to BMP stimulus	<u>RT</u>	i	4	9.0E-1	7.9E-1	1.0E0	9.5 1
nota	ation Cluster 180	Enrichment Score: 1.13	G	<b>10</b>	Count	P_Value	Fold Change	Benjamini	FC
	UP_SEQ_FEATURE	region of interest:Bridging helix	<u>RT</u>	i .	3	5.8E-2	6.8E0	9.1E-1	8.1
	INTERPRO	RNA polymerase, N-terminal	<u>RT</u>	1	3	7.0E-2	6.2E0	3.9E-1	3.
	INTERPRO	RNA polymerase, alpha subunit	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.
	INTERPRO	RNA polymerase Rpb1, domain 3	<u>RT</u>		3	7.0E-2	6.2E0	3.9E-1	3.
	INTERPRO	RNA polymerase Rpb1, domain 1	RT		3	7.0E-2	6.2E0	3.9E-1	3.
	INTERPRO	RNA polymerase Rpb1, domain 5	RT		3	7.0E-2		3.9E-1	1 3.
	INTERPRO								1 3.
	SMART	RNA polymerase Rpb1, domain 4	<u>RT</u>		3	7.0E-2		3.9E-1	1 5.
		RPOLA N	<u>RT</u>	i	3	1.5E-1	Fold	6.5E-1	1
nota	ation Cluster 181	Enrichment Score: 1.12	G		Count	P_Value	Change	Benjamini	_
	INTERPRO	2-5-oligoadenylate synthetase, conserved site	<u>RT</u>	•	4	1.5E-2	6.2E0	1.2E-1	1.
	INTERPRO	2'-5'-oligoadenylate synthase	<u>RT</u>	1	4	1.5E-2	6.2E0	1.2E-1	1.
	INTERPRO	<u>2'-5'-oligoadenylate synthetase 1, domain</u> <u>2/C-terminal</u>	<u>RT</u>	1	4	1.5E-2	6.2E0	1.2E-1	1. 1
	GOTERM_MF_DIRECT	2'-5'-oligoadenylate synthetase activity	<u>RT</u>	i	4	1.6E-2	6.0E0	1.1E-1	1. 1
	INTERPRO	2-5-oligoadenylate synthetase, N-terminal	<u>RT</u>	1	4	3.2E-2	5.0E0	2.4E-1	2. 1
	INTERPRO	Nucleotidyl transferase domain	<u>RT</u>	1	4	2.1E-1	2.5E0	9.5E-1	8.
	GOTERM_MF_DIRECT	nucleotidyltransferase activity	<u>RT</u>		7	2.9E-1	1.5E0	9.5E-1	8.
	GOTERM_BP_DIRECT	interferon-gamma-mediated signaling	RT		11	7.8F-1	9.2E-1	1.0F0	9.
	GOTERM_MF_DIRECT	<u>pathway</u> <u>transferase activity</u>	RT		12		7.5E-1		1 9.
	attan Olyatan 100					1		<u> </u>	1
nota	ation Cluster 182	Enrichment Score: 1.12	G	-	Count	P_Value	Change	Benjamini	1.
	INTERPRO	Proprotein convertase, P	<u>RT</u>	•	6	1.7E-3		2.0E-2	2 6.
	INTERPRO	<u>Peptidase S8, subtilisin, Asp-active site</u>	<u>RT</u>	i	5	7.7E-3		7.5E-2	2
		Peptidase S8, subtilisin, His-active site	<u>RT</u>		6	7.7E-3	4.1E0	7.5E-2	6.
	INTERPRO	Peptidase S8, subtilisin, Ser-active site	<u>RT</u>	i	6	7.7E-3	4.1E0	7.5E-2	6. 2
	INTERPRO	Peptidase S8, subtilisin-related	<u>RT</u>	•	6	1.3E-2	3.7E0	1.2E-1	1. 1
	INTERPRO	Peptidase S8/S53 domain	<u>RT</u>	i .	6	2.1E-2	3.4E0	1.7E-1	1. 1
	GOTERM_BP_DIRECT	peptide biosynthetic process	<u>RT</u>	1	4	3.7E-2	4.7E0	3.8E-1	3. 1
	INTERPRO	Proteinase inhibitor, propeptide	<u>RT</u>	1	6	1.3E-1	2.2E0	6.1E-1	5.
	GOTERM_BP_DIRECT	peptide hormone processing	<u>RT</u>		5	2.8E-1	1.9E0	1.0E0	9.
	GOTERM_BP_DIRECT	protein processing	RT		12		9.9E-1		1 9.
	UP_KEYWORDS	<u>Zymogen</u>	RT		17	1.0E0	5.5E-1		1 1.
	UP_KEYWORDS	<u>Serine protease</u>	<u>RT</u>	1	9	1.0E0	4.4E-1	1.0E0	1.
	UP_SEQ_FEATURE GOTERM_MF_DIRECT	active site:Charge relay system <u>serine-type endopeptidase activity</u>	RT RT		8 10	1.0E0 1.0E0	2.7E-1 2.3E-1		1.0
	ation Cluster 183	Enrichment Score: 1.11	G			P_Value	:	Benjamini	

Annot	tation Cluster 1	Enrichment Score: ?	G	<b></b>	Count	P_Value	Fold Change	Benjamini	i FDR
	INTERPRO	Zinc finger, C6HC-type	<u>RT</u>	i	7	2.4E-2	2.9E0	1.9E-1	1.7E- 1
	UP_SEQ_FEATURE	zinc finger region:IBR-type	<u>RT</u>	i .	6	3.1E-2	3.1E0	5.8E-1	5.6E- 1
	UP_SEQ_FEATURE	zinc finger region:RING-type 2	<u>RT</u>	1	5	8.6E-2	2.8E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	zinc finger region:RING-type 1; atypical	<u>RT</u>	1	4	1.0E-1	3.4E0	1.0E0	9.7E- 1
	GOTERM_MF_DIRECT	ubiquitin conjugating enzyme binding	<u>RT</u>	i	9	1.3E-1	1.7E0	5.8E-1	5.2E-
	SMART	<u>IBR</u>	<u>RT</u>	i de la companya de l	6	2.4E-1	1.7E0	9.3E-1	8.4E-
Annot	tation Cluster 184	Enrichment Score: 1.11	G	7	Count	P_Value	Fold Change	Benjamini	1
	GOTERM_BP_DIRECT	mRNA cleavage	<u>RT</u>		6	3.8E-2		3.8E-1	3.6E-
	BIOCARTA	Polyadenylation of mRNA	<u>RT</u>	1	7	6.7E-2	2.2E0	1.7E-1	1.2E-
	GOTERM_BP_DIRECT	mRNA polyadenylation	RT		9	8.6E-2	1.9E0	6.3E-1	1 6.0E-
	GOTERM_CC_DIRECT	mRNA cleavage and polyadenylation	RT	1	5	1.7E-1		6.6E-1	1 5.8E-
Annot	tation Cluster 185	specificity factor complex  Enrichment Score: 1.11	G		Count	P_Value	Fold	Danismini	1 i FDR
	GOTERM_MF_DIRECT	MAP kinase kinase activity	RT RT		7	8.1E-3	Change	6.8E-2	6.0E-
	UP_SEQ_FEATURE	site:Cleavage; by anthrax lethal factor	RT	_	3	2.2E-1		1.0E0	2 9.7E-
	GOTERM_BP_DIRECT								1 9.5E-
		proteolysis in other organism	RT	i	3	2.7E-1	Fold	1.0E0	1
Annot	tation Cluster 186  GOTERM_BP_DIRECT	Enrichment Score: 1.11	G	-	Count	P_Value	Change		1.8E-
	GOTERM MF DIRECT	dendritic spine development	<u>RT</u>		7	1.3E-2		1.9E-1	1 4.1E-
	GOTERM_BP_DIRECT	axon guidance receptor activity	<u>RT</u>	•	4	9.7E-2	3.4E0		1 7.7E-
		central nervous system projection neuron axonogenesis	<u>RT</u>	•	4	1.4E-1	3.0E0	8.1E-1	1
	GOTERM_BP_DIRECT	retinal ganglion cell axon guidance	<u>RT</u>	i	6	2.1E-1		1.0E0	9.5E- 1
Annot	tation Cluster 187	Enrichment Score: 1.1	G	<u>~</u>	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	zinc finger region:TFIIB-type	<u>RT</u>	1	3	5.8E-2	6.8E0	9.1E-1	8.8E- 1
	INTERPRO	Transcription factor TFIIB	<u>RT</u>	1	3	7.0E-2	6.2E0	3.9E-1	3.6E- 1
	INTERPRO	Zinc finger, TFIIB-type	<u>RT</u>	i	3	1.2E-1		6.1E-1	5.6E- 1
Annot	tation Cluster 188	Enrichment Score: 1.1	G	<b>™</b>	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	Kelch-like protein, gigaxonin	<u>RT</u>	i	14	1.2E-2	2.1E0	1.2E-1	1.1E- 1
	INTERPRO	BTB/Kelch-associated	<u>RT</u>	1	18	1.7E-2	1.8E0	1.4E-1	1.2E- 1
	GOTERM_CC_DIRECT	Cul3-RING ubiquitin ligase complex	<u>RT</u>	i e	18	2.8E-2	1.7E0	1.7E-1	1.5E- 1
	PIR_SUPERFAMILY	kelch-like protein, gigaxonin type	<u>RT</u>	i	14	3.7E-2	1.8E0	5.4E-1	5.4E- 1
	INTERPRO	Kelch repeat type 1	<u>RT</u>	i contraction	17	4.5E-2	1.6E0	3.2E-1	2.9E- 1
	UP_KEYWORDS	Kelch repeat	<u>RT</u>	1	17	5.2E-2	1.6E0	1.9E-1	1.5E- 1
	UP_SEQ_FEATURE	repeat:Kelch 5	<u>RT</u>	i	16	5.3E-2	1.7E0	9.1E-1	8.8E-
	UP_SEQ_FEATURE	repeat:Kelch 4	<u>RT</u>	i de la companya de	16	8.1E-2	1.6E0	1.0E0	9.7E-
	UP_SEQ_FEATURE	repeat:Kelch 1	<u>RT</u>	1	16	8.9E-2	1.5E0	1.0E0	9.7E-
	UP_SEQ_FEATURE	repeat:Kelch 2	RT	1	16	8.9E-2		1.0E0	9.7E-
	UP_SEQ_FEATURE	repeat:Kelch 3	RT		16	8.9E-2		1.0E0	9.7E-
	UP_SEQ_FEATURE	repeat:Kelch 6	RT		12		1.6E0		1 9.7E-
	UP_SEQ_FEATURE	domain:BACK	RT		8		1.8E0		1 9.7E-
	INTERPRO						1.7E0		1 7.6E-
	SMART	Galactose oxidase, beta-propeller	<u>RT</u>		17				1 9.0E-
	INTERPRO	<u>Kelch</u>	<u>RT</u>		17	3.4E-1		1.0E0	9.1E-
	SMART	Kelch-type beta propeller	<u>RT</u>	i	11	3.5E-1		1.0E0	9.0E-
		<u>SM00875</u>	RT	i	17	4.0E-1	Fold	1.0E0	1
Annot	tation Cluster 189  UP_SEQ_FEATURE	Enrichment Score: 1.09	G	-		P_Value	Change		
	JI _OE W_I EATONE	domain:Nop	<u>RT</u>	•	3	5.8E-2		9.1E-1	8.8E- 1
	INTERDRO								3.6E-
	INTERPRO	Nop domain	<u>RT</u>	1	3	7.0E-2	6.2E0	3.9E-1	1 3.6E-

nota	ation Cluster 1	Enrichment Score: ?	G	i 🚾	Count	P_Value	Fold	Benjamir	ni Fl
	SMART	<u>SM00931</u>	RT	i	3	1.5E-1	Change	6.5E-1	5. 1
nota	ation Cluster 190	Enrichment Score: 1.08	G	178	Count	P_Value	Fold	Benjamir	-
	GOTERM_BP_DIRECT	rRNA methylation	RT		7		Change 2.8E0	3.3E-1	3.
	INTERPRO	Ribosomal RNA adenine methylase	RT		3	7.0E-2		3.9E-1	1 3.
	INTERPRO	<u>transferase</u> <u>Ribosomal RNA adenine methylase</u>	RT		3	7.0E-2		3.9E-1	1 3.
	SMART	transferase, N-terminal							1 5.
	GOTERM_MF_DIRECT	rADc  rRNA (adenine-N6,N6-)-dimethyltransferase	<u>RT</u>		3	1.5E-1		6.5E-1	1 6.
		<u>activity</u>	<u>RT</u>	i	3	1	Fold	7.6E-1	1
ıota	ation Cluster 191  GOTERM_CC_DIRECT	Enrichment Score: 1.07	G	- Tennes	Count	P_Value	Change	Benjamir	ni F
	GOTERM_CC_DIRECT	SWI/SNF complex	<u>RT</u>		7	2.1E-2		1.4E-1	1
	GOTERM_BP_DIRECT	npBAF complex	<u>RT</u>		5	1.1E-1		4.9E-1	1
		nucleosome disassembly	<u>RT</u>	•	6	1.4E-1	2.1E0	8.4E-1	1
	GOTERM_CC_DIRECT	nBAF complex	<u>RT</u>	i	5	1.7E-1	2.3E0	6.6E-1	5 1
nota	ation Cluster 192	Enrichment Score: 1.06	G	<u>~</u>	Count	P_Value	Fold Change	Benjamir	
	GOTERM_CC_DIRECT	actomyosin	<u>RT</u>	1	7	5.9E-3	3.7E0	4.5E-2	4 2
	GOTERM_CC_DIRECT	myosin II filament	<u>RT</u>	i	3	6.6E-2	6.4E0	3.5E-1	3 1
	GOTERM_CC_DIRECT	myosin II complex	<u>RT</u>	i .	4	8.3E-2	3.6E0	4.0E-1	3 1
	GOTERM_BP_DIRECT	actomyosin structure organization	<u>RT</u>	i .	7	3.0E-1	1.5E0	1.0E0	9
	UP_KEYWORDS	<u>Cell shape</u>	<u>RT</u>	i .	5	5.0E-1	1.4E0	1.0E0	7 1
ota	ation Cluster 193	Enrichment Score: 1.06	G	<b>**</b>	Count	P_Value	Fold Change	Benjamir	ni F
	UP_SEQ_FEATURE	domain:WW 4	<u>RT</u>	1	5	2.0E-3	6.8E0	5.4E-2	5 2
	UP_SEQ_FEATURE	domain:WW 3	<u>RT</u>	i e	6	2.6E-3	5.1E0	6.6E-2	6
	INTERPRO	WW domain	<u>RT</u>		15	3.8E-2	1.8E0	2.8E-1	2
	UP_SEQ_FEATURE	domain:WW 2	<u>RT</u>		9	5.2E-2	2.1E0	9.1E-1	8
	UP_SEQ_FEATURE	domain:WW 1	RT		9	5.2E-2	2.1E0	9.1E-1	8
	GOTERM_BP_DIRECT	regulation of potassium ion transmembrane	RT		4	6.4E-2		5.3E-1	1 5
	UP_SEQ_FEATURE	transporter activity domain:WW	RT		6	2.1E-1		1.0E0	1 9
	SMART			-					1 9
	GOTERM_BP_DIRECT	<u>ww</u>	<u>RT</u>		15	3.0E-1		1.0E0	1
	SMART	regulation of membrane potential  C2	RT RT		8 18	9.8E-1 1.0E0	6.3E-1 5.8E-1		1
	GOTERM_BP_DIRECT	regulation of ion transmembrane transport	RT	<u> </u>	3	1.0E0	1.6E-1		1
ota	ation Cluster 194	Enrichment Score: 1.05	G	<b>™</b>	Count	P_Value	Fold Change	Benjamir	ni F
	GOTERM_CC_DIRECT	beta-catenin destruction complex	<u>RT</u>	1	6	5.6E-2	2.7E0	3.0E-1	2 1
	GOTERM_BP_DIRECT	beta-catenin destruction complex disassembly	<u>RT</u>	i .	8	6.4E-2	2.2E0	5.3E-1	5 1
	GOTERM_BP_DIRECT	beta-catenin destruction complex assembly	<u>RT</u>	i .	3	2.0E-1	3.6E0	1.0E0	9
nota	ation Cluster 195	Enrichment Score: 1.04	G	<b>**</b>	Count	P_Value	Fold Change	Benjamir	ni F
	GOTERM_BP_DIRECT	activation of JNKK activity	<u>RT</u>	1	4	6.4E-2		5.3E-1	5
	INTERPRO	Mitogen-activated protein (MAP) kinase kinase, 9/10/11	<u>RT</u>	i .	3	7.0E-2	6.2E0	3.9E-1	3
	GOTERM_MF_DIRECT	JUN kinase kinase kinase activity	<u>RT</u>	1	3	7.5E-2	6.0E0	3.9E-1	3
	PIR_SUPERFAMILY	mitogen-activated protein kinase kinase	<u>RT</u>	1	3	9.1E-2	5.3E0	7.7E-1	7
	UP_SEQ_FEATURE	kinase, types 9/10/11 domain:Leucine-zipper 1	RT		4	1.3E-1		1.0E0	1 9
	UP_SEQ_FEATURE	domain:Leucine-zipper 2	RT		4	1.3E-1		1.0E0	1 9
104	ation Cluster 196	Enrichment Score: 1.04		•	<u> </u>	1	Fold	Daniamir	1
TULE	GOTERM_BP_DIRECT		G DT		Count	P_Value	Change		nı F 1
	INTERPRO	histone acetylation	<u>RT</u>		13	7.3E-3		1.2E-1	1
	GOTERM_MF_DIRECT	MOZ/SAS-like protein	<u>RT</u>	i	4	3.2E-2		2.4E-1	1
		histone acetyltransferase activity	<u>RT</u>	•	14	4.8E-2	1.7E0	2.9E-1	1
	GOTERM_MF_DIRECT	acetyltransferase activity	<u>RT</u>	i	6	5.2E-2	2.8E0	3.0E-1	2 1
	UP_SEQ_FEATURE	zinc finger region:C2HC-type	<u>RT</u>	i e	4	1.0E-1	3.4E0	1.0E0	9

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

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

Annot	ation Cluster 1	Enrichment Score: ?	G	·	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:CH 2	<u>RT</u>	i	6	3.6E-1	Change	1.0E0	9.7E- 1
	GOTERM_CC_DIRECT	<u>filopodium membrane</u>	<u>RT</u>		4	5.1E-1	1.5E0	1.0E0	8.7E-
	SMART	SPEC	RT		8	5.9E-1	1.1E0	1.0E0	1 9.0E-
	INTERPRO	Calponin homology domain	RT		12	7.0E-1	9.8E-1	1.0E0	1 9.1E-
	UP_SEQ_FEATURE	domain:CH	RT		6	7.6E-1	9.7E-1	1.0E0	1 9.7E-
	SMART	<u>CH</u>	RT		12		7.4E-1		1 9.5E-
Annot	ation Cluster 203	Enrichment Score: 0.96	G	<u>-</u>	Count	P_Value	Fold	Benjamini	1 FDR
	GOTERM_CC_DIRECT	chromatin silencing complex	RT		5	4.0E-2	Change	2.3E-1	2.0E-
	GOTERM_CC_DIRECT	rDNA heterochromatin	RT		3	1.2E-1		5.0E-1	1 4.4E-
	GOTERM_BP_DIRECT	chromatin silencing at rDNA	RT		9	2.8E-1		1.0E0	1 9.5E-
Annot	ation Cluster 204	Enrichment Score: 0.95	G	<u>.</u>	Count	P_Value	Fold	Benjamini	1 EDP
Allilot	GOTERM_BP_DIRECT	positive regulation of cyclin-dependent	RT	i	9	3.8E-2	Change	3.8E-1	3.6E-
	GOTERM_MF_DIRECT	protein serine/threonine kinase activity  cyclin-dependent protein serine/threonine		_					1 4.1E-
	GOTERM_BP_DIRECT	kinase regulator activity positive regulation of phosphorylation of RNA	<u>RT</u>		6	9.1E-2		4.6E-1	1 9.5E-
		polymerase II C-terminal domain	RT		3	4.0E-1	Fold	1.0E0	1
Annot	ation Cluster 205  UP_SEQ_FEATURE	Enrichment Score: 0.95	G	-	Count	P_Value	Change	Benjamini	FDR 7.7E-
	INTERPRO	domain:SWIRM	<u>RT</u>		4	4.5E-2		8.0E-1	1 3.6E-
	INTERPRO	SWIRM domain	<u>RT</u>		4	5.7E-2		3.9E-1	1 5.4E-
	UP_SEQ_FEATURE	SANT domain	<u>RT</u>	•	8		1.9E0		9.7E-
	OF_SEQ_FEATORE	domain:SANT	<u>RT</u>	i	4	5.4E-1	Fold	1.0E0	1
Annot	ation Cluster 206  UP_SEQ_FEATURE	Enrichment Score: 0.95	G		Count	P_Value	Fold Change	Benjamini	<b>FDR</b> 9.7E-
		zinc finger region:UBR-type	<u>RT</u>	i	4	7.0E-2	3.9E0	1.0E0	1
	INTERPRO	Zinc finger, N-recognin	<u>RT</u>	i	4	8.8E-2	3.5E0	4.7E-1	4.3E- 1
	SMART	ZnF UBR1	<u>RT</u>	•	4	2.3E-1	2 3F0	9.0E-1	8.1E- 1
			<u> </u>			!			1
Annot	ation Cluster 207	Enrichment Score: 0.95	G	• • • • • • • • • • • • • • • • • • •	Count	P_Value	Fold Change	Benjamini	FDR
Annot	UP_SEQ_FEATURE					1	Fold Change		FDR 8.8E- 1
Annot	UP_SEQ_FEATURE UP_SEQ_FEATURE	Enrichment Score: 0.95 region of interest:Domain A region of interest:Domain B	G		Count	P_Value	Fold Change 6.8E0	Benjamini	FDR 8.8E- 1 8.8E- 1
Annot	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO	Enrichment Score: 0.95 region of interest:Domain A	G RT		Count 3	P_Value 5.8E-2	Fold Change 6.8E0 6.8E0	Benjamini 9.1E-1	8.8E-1 8.8E-1 3.6E-1
Annot	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO	region of interest: Domain A region of interest: Domain B Domain of unknown function DUF3452,	G RT RT		Count 3	P_Value 5.8E-2 5.8E-2	Fold Change 6.8E0 6.8E0 6.2E0	<b>Benjamini</b> 9.1E-1 9.1E-1	8.8E-1 8.8E-1 3.6E-1
Annot	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO	region of interest: Domain A region of interest: Domain B Domain of unknown function DUF3452, retinoblastoma-associated	G RT RT RT		3 3 3	P_Value 5.8E-2 5.8E-2 7.0E-2	Fold Change 6.8E0 6.8E0 6.2E0 6.2E0	9.1E-1 9.1E-1 3.9E-1	8.8E-1 8.8E-1 3.6E-1 3.6E-1
Annot	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  INTERPRO	region of interest: Domain A region of interest: Domain B  Domain of unknown function DUF3452, retinoblastoma-associated  Retinoblastoma-associated protein, B-box	G RT RT RT RT		Count  3  3  3	P_Value 5.8E-2 5.8E-2 7.0E-2 7.0E-2	Fold Change 6.8E0 6.8E0 6.2E0 6.2E0 6.2E0	9.1E-1 9.1E-1 3.9E-1 3.9E-1	8.8E-1 8.8E-1 3.6E-1 3.6E-1 3.6E-1
Annot	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO	region of interest:Domain A region of interest:Domain B  Domain of unknown function DUF3452, retinoblastoma-associated  Retinoblastoma-associated protein, B-box  Retinoblastoma-associated protein, A-box	RT RT RT RT RT		Count  3  3  3  3	5.8E-2 5.8E-2 7.0E-2 7.0E-2 7.0E-2	Fold Change 6.8E0 6.8E0 6.2E0 6.2E0 6.2E0 6.2E0	9.1E-1 9.1E-1 3.9E-1 3.9E-1 3.9E-1	8.8E-1 8.8E-1 3.6E-1 3.6E-1 3.6E-1 3.6E-1
Annot	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  INTERPRO	region of interest:Domain A region of interest:Domain B  Domain of unknown function DUF3452, retinoblastoma-associated  Retinoblastoma-associated protein, B-box  Retinoblastoma-associated protein, A-box	RT RT RT RT RT RT		Count  3  3  3  3  3	P_Value 5.8E-2 5.8E-2 7.0E-2 7.0E-2 7.0E-2	Fold Change 6.8E0 6.8E0 6.2E0 6.2E0 6.2E0 4.1E0	9.1E-1 9.1E-1 3.9E-1 3.9E-1 3.9E-1 3.9E-1	FDR 8.8E-1 8.8E-1 3.6E-1 3.6E-1 3.6E-1 5.8E-
Annot	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  INTERPRO  SMART	region of interest: Domain A region of interest: Domain B  Domain of unknown function DUF3452, retinoblastoma-associated  Retinoblastoma-associated protein, B-box  Retinoblastoma-associated protein, A-box  Rb C-terminal  SM01367	RI RI RI RI RI RI RI RI RI		Count  3  3  3  3  3  3	P_Value 5.8E-2 5.8E-2 7.0E-2 7.0E-2 7.0E-2 1.5E-1	Fold Change 6.8E0 6.8E0 6.2E0 6.2E0 6.2E0 4.1E0 4.1E0	9.1E-1 9.1E-1 3.9E-1 3.9E-1 3.9E-1 6.5E-1	8.8E-1 8.8E-1 3.6E-1 3.6E-1 3.6E-1 5.8E-1
Annot	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  INTERPRO  SMART  SMART	region of interest:Domain A region of interest:Domain B  Domain of unknown function DUF3452, retinoblastoma-associated  Retinoblastoma-associated protein, B-box  Retinoblastoma-associated protein, A-box  Rb C-terminal  SM01367  SM01368	RI R		Count  3  3  3  3  3  3  3	P_Value 5.8E-2 5.8E-2 7.0E-2 7.0E-2 7.0E-2 1.5E-1 1.5E-1	Fold Change 6.8E0 6.8E0 6.2E0 6.2E0 6.2E0 4.1E0 4.1E0 4.1E0	9.1E-1 9.1E-1 3.9E-1 3.9E-1 3.9E-1 6.5E-1 6.5E-1	8.8E-1 8.8E-1 3.6E-1 3.6E-1 3.6E-1 5.8E-1 5.8E-1
Annot	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  SMART  SMART  SMART	region of interest:Domain A region of interest:Domain B  Domain of unknown function DUF3452, retinoblastoma-associated  Retinoblastoma-associated protein, B-box  Retinoblastoma-associated protein, A-box  Rb C-terminal  SM01367  SM01368  SM01369	RT		Count  3  3  3  3  3  3  3  3	P_Value 5.8E-2 5.8E-2 7.0E-2 7.0E-2 7.0E-2 1.5E-1 1.5E-1	Fold Change 6.8E0 6.8E0 6.2E0 6.2E0 6.2E0 4.1E0 4.1E0 4.1E0 3.6E0	9.1E-1 9.1E-1 3.9E-1 3.9E-1 3.9E-1 6.5E-1 6.5E-1	8.8E-1 8.8E-1 3.6E-1 3.6E-1 3.6E-1 5.8E-1 5.8E-1 9.5E-
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  SMART  SMART  SMART  GOTERM_BP_DIRECT	region of interest: Domain A region of interest: Domain B  Domain of unknown function DUF3452, retinoblastoma-associated Retinoblastoma-associated protein, B-box  Retinoblastoma-associated protein, A-box  Rb C-terminal  SM01367  SM01368  SM01369 regulation of lipid kinase activity	RI R		Count  3  3  3  3  3  3  4	P_Value  5.8E-2  7.0E-2  7.0E-2  7.0E-2  1.5E-1  1.5E-1  2.0E-1	Fold Change 6.8E0 6.8E0 6.2E0 6.2E0 6.2E0 4.1E0 4.1E0 4.1E0 3.6E0 1.1E0	9.1E-1 9.1E-1 3.9E-1 3.9E-1 3.9E-1 6.5E-1 6.5E-1 1.0E0	FDR  8.8E-1  8.8E-1  3.6E-1  3.6E-1  3.6E-1  5.8E-1  5.8E-1  9.5E-1  9.7E-1
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  SMART  SMART  SMART  GOTERM_BP_DIRECT  UP_SEQ_FEATURE	region of interest:Domain A region of interest:Domain B  Domain of unknown function DUF3452, retinoblastoma-associated Retinoblastoma-associated protein, B-box  Retinoblastoma-associated protein, A-box  Rb C-terminal  SM01367  SM01368  SM01369  regulation of lipid kinase activity region of interest:Spacer	RI R		Count  3  3  3  3  3  3  4	P_Value  5.8E-2  7.0E-2  7.0E-2  7.0E-2  1.5E-1  1.5E-1  2.0E-1  7.1E-1	Fold Change 6.8E0 6.8E0 6.2E0 6.2E0 6.2E0 4.1E0 4.1E0 4.1E0 3.6E0 1.1E0	9.1E-1 9.1E-1 3.9E-1 3.9E-1 3.9E-1 6.5E-1 6.5E-1 1.0E0 1.0E0 Benjamini	FDR  8.8E-1  8.8E-1  3.6E-1  3.6E-1  3.6E-1  5.8E-1  5.8E-1  9.5E-1  9.7E-1
Annot	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  SMART  SMART  SMART  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  ation Cluster 208	region of interest:Domain A region of interest:Domain B  Domain of unknown function DUF3452, retinoblastoma-associated  Retinoblastoma-associated protein, B-box  Retinoblastoma-associated protein, A-box  Rb C-terminal  SM01367  SM01368  SM01369  regulation of lipid kinase activity  region of interest:Spacer  Enrichment Score: 0.93	RI R		Count  3 3 3 3 3 3 3 4 Count	P_Value  5.8E-2  7.0E-2  7.0E-2  7.0E-2  1.5E-1  1.5E-1  2.0E-1  7.1E-1	Fold Change 6.8E0 6.8E0 6.2E0 6.2E0 6.2E0 4.1E0 4.1E0 3.6E0 1.1E0 Fold Change 3.0E0	9.1E-1 9.1E-1 3.9E-1 3.9E-1 3.9E-1 6.5E-1 6.5E-1 1.0E0 1.0E0 Benjamini	FDR  8.8E- 1  8.8E- 1  3.6E- 1  3.6E- 1  5.8E- 1  5.8E- 1  9.5E- 1  9.7E- 1  FDR  5.4E-
Annot	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  SMART  SMART  SMART  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  ation Cluster 208  GOTERM_BP_DIRECT	region of interest: Domain A region of interest: Domain B  Domain of unknown function DUF3452, retinoblastoma-associated Retinoblastoma-associated protein, B-box  Retinoblastoma-associated protein, A-box  Rb C-terminal  SM01367  SM01368  SM01369  regulation of lipid kinase activity region of interest: Spacer  Enrichment Score: 0.93  lung-associated mesenchyme development mesenchymal cell proliferation involved in	RI R		Count  3  3  3  3  3  3  4  Count  5	P_Value  5.8E-2  7.0E-2  7.0E-2  7.0E-2  1.5E-1  1.5E-1  2.0E-1  7.1E-1  P_Value  7.2E-2	Fold Change 6.8E0 6.8E0 6.2E0 6.2E0 6.2E0 4.1E0 4.1E0 3.6E0 1.1E0 Fold Change 3.0E0 5.9E0	9.1E-1 9.1E-1 3.9E-1 3.9E-1 3.9E-1 6.5E-1 6.5E-1 1.0E0 1.0E0 Benjamini 5.7E-1	8.8E-1 8.8E-1 3.6E-1 3.6E-1 3.6E-1 5.8E-1 5.8E-1 9.5E-1 9.7E-1 FDR 5.4E-1 5.4E-
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  SMART  SMART  SMART  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  ation Cluster 208  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT	region of interest: Domain A region of interest: Domain B  Domain of unknown function DUF3452, retinoblastoma-associated Retinoblastoma-associated protein, B-box  Retinoblastoma-associated protein, A-box  Rb C-terminal  SM01367  SM01368  SM01369  regulation of lipid kinase activity  region of interest: Spacer  Enrichment Score: 0.93  lung-associated mesenchyme development mesenchymal cell proliferation involved in lung development	RI R		Count  3  3  3  3  3  3  4  Count  5  3  7	P_Value  5.8E-2  7.0E-2  7.0E-2  7.0E-2  1.5E-1  1.5E-1  2.0E-1  7.1E-1  P_Value  7.2E-2  7.6E-2	Fold Change 6.8E0 6.8E0 6.2E0 6.2E0 6.2E0 4.1E0 4.1E0 4.1E0 3.6E0 1.1E0 Fold Change 3.0E0 5.9E0 1.5E0	9.1E-1 9.1E-1 3.9E-1 3.9E-1 3.9E-1 6.5E-1 6.5E-1 1.0E0 1.0E0 Benjamini 5.7E-1 5.7E-1	FDR  8.8E- 1  8.8E- 1  3.6E- 1  3.6E- 1  5.8E- 1  5.8E- 1  9.5E- 1  5.4E- 1  9.5E- 1  9.5E- 1
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  SMART  SMART  SMART  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  ation Cluster 208  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT	region of interest: Domain A region of interest: Domain B  Domain of unknown function DUF3452, retinoblastoma-associated Retinoblastoma-associated protein, B-box  Retinoblastoma-associated protein, A-box  Rb C-terminal  SM01367  SM01368  SM01369  regulation of lipid kinase activity  region of interest: Spacer  Enrichment Score: 0.93  lung-associated mesenchyme development mesenchymal cell proliferation involved in lung development hair follicle morphogenesis	RI R		Count  3  3  3  3  3  3  4  Count  5  3  7	P_Value  5.8E-2  7.0E-2  7.0E-2  7.0E-2  1.5E-1  1.5E-1  2.0E-1  7.1E-1  P_Value  7.2E-2  7.6E-2  3.0E-1	Fold Change 6.8E0 6.8E0 6.2E0 6.2E0 6.2E0 4.1E0 4.1E0 3.6E0 1.1E0 Fold Change 3.0E0 5.9E0 1.5E0 Fold Change	9.1E-1 9.1E-1 3.9E-1 3.9E-1 3.9E-1 6.5E-1 6.5E-1 1.0E0 1.0E0 Benjamini 5.7E-1 1.0E0	FDR  8.8E- 1  8.8E- 1  3.6E- 1  3.6E- 1  5.8E- 1  5.8E- 1  9.5E- 1  5.4E- 1  9.5E- 1  9.5E- 1
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  SMART  SMART  SMART  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  ation Cluster 208  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  Ation Cluster 209	region of interest:Domain A region of interest:Domain B  Domain of unknown function DUF3452, retinoblastoma-associated Retinoblastoma-associated protein, B-box  Retinoblastoma-associated protein, A-box  Rb C-terminal  SM01367  SM01368  SM01369  regulation of lipid kinase activity  region of interest:Spacer  Enrichment Score: 0.93  lung-associated mesenchyme development mesenchymal cell proliferation involved in lung development hair follicle morphogenesis  Enrichment Score: 0.92 regulation of actin polymerization or	RI R		Count  3 3 3 3 3 3 3 4 Count 5 3 7 Count	P_Value  5.8E-2  7.0E-2  7.0E-2  7.0E-2  1.5E-1  1.5E-1  2.0E-1  7.1E-1  P_Value  7.2E-2  3.0E-1  P_Value	Fold Change 6.8E0 6.2E0 6.2E0 6.2E0 4.1E0 4.1E0 3.6E0 1.1E0 Fold Change 3.0E0 5.9E0 1.5E0 Fold Change 3.4E0	Benjamini 9.1E-1 9.1E-1 3.9E-1 3.9E-1 3.9E-1 6.5E-1 6.5E-1 1.0E0 1.0E0 Benjamini 5.7E-1 1.0E0 Benjamini	FDR  8.8E- 1  8.8E- 1  3.6E- 1  3.6E- 1  5.8E- 1  5.8E- 1  9.5E- 1  FDR  5.4E- 1  9.5E- 1  5.4E- 1  9.5E- 1
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  SMART  SMART  SMART  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  ation Cluster 208  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 209  GOTERM_BP_DIRECT	region of interest:Domain A region of interest:Domain B Domain of unknown function DUF3452, retinoblastoma-associated Retinoblastoma-associated protein, B-box Retinoblastoma-associated protein, A-box Rb C-terminal SM01367 SM01368 SM01369 regulation of lipid kinase activity region of interest:Spacer Enrichment Score: 0.93 lung-associated mesenchyme development mesenchymal cell proliferation involved in lung development hair follicle morphogenesis Enrichment Score: 0.92 regulation of actin polymerization or depolymerization	RI R		Count  3 3 3 3 3 3 3 4 Count 5 3 7 Count 4	P_Value  5.8E-2  7.0E-2  7.0E-2  7.0E-2  1.5E-1  1.5E-1  2.0E-1  7.1E-1  P_Value  7.2E-2  7.6E-2  3.0E-1  P_Value  9.8E-2	Fold Change 6.8E0 6.2E0 6.2E0 6.2E0 4.1E0 4.1E0 4.1E0 3.6E0 1.1E0 Fold Change 3.0E0 5.9E0 1.5E0 Fold Change 3.4E0 4.6E0	9.1E-1 9.1E-1 3.9E-1 3.9E-1 3.9E-1 6.5E-1 6.5E-1 1.0E0 1.0E0 Benjamini 5.7E-1 1.0E0 Benjamini 6.8E-1	FDR  8.8E- 1  8.8E- 1  3.6E- 1  3.6E- 1  3.6E- 1  5.8E- 1  5.8E- 1  9.5E- 1  FDR  5.4E- 1  9.5E- 1  5.4E- 1  5.4E- 1  5.4E- 1  5.5.6E-
Annot	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  SMART  SMART  SMART  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  ation Cluster 208  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 209  GOTERM_BP_DIRECT  INTERPRO	region of interest:Domain A region of interest:Domain B  Domain of unknown function DUF3452, retinoblastoma-associated Retinoblastoma-associated protein, B-box  Retinoblastoma-associated protein, A-box  Rb C-terminal  SM01367  SM01368  SM01369  regulation of lipid kinase activity region of interest:Spacer  Enrichment Score: 0.93  lung-associated mesenchyme development mesenchymal cell proliferation involved in lung development hair follicle morphogenesis  Enrichment Score: 0.92  regulation of actin polymerization or depolymerization  DEK, C-terminal	RI R		Count  3  3  3  3  3  3  4  Count  5  3  7  Count  4  3  4	P_Value  5.8E-2  7.0E-2  7.0E-2  7.0E-2  1.5E-1  1.5E-1  2.0E-1  7.1E-1  P_Value  7.2E-2  3.0E-1  P_Value  9.8E-2  1.2E-1	Fold Change 6.8E0 6.8E0 6.2E0 6.2E0 6.2E0 4.1E0 4.1E0 4.1E0 3.6E0 1.1E0 Fold Change 3.0E0 5.9E0 1.5E0 Fold Change 3.4E0 4.6E0 3.0E0	9.1E-1 9.1E-1 3.9E-1 3.9E-1 3.9E-1 6.5E-1 6.5E-1 1.0E0 1.0E0 Benjamini 5.7E-1 1.0E0 Benjamini 6.8E-1 6.8E-1	FDR  8.8E- 1  8.8E- 1  3.6E- 1  3.6E- 1  3.6E- 1  5.8E- 1  5.8E- 1  9.5E- 1  9.7E- 1  FDR  6.5E- 1  5.6E- 1  7.7E- 1
Annot	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  INTERPRO  SMART  SMART  SMART  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  ation Cluster 208  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 209  GOTERM_BP_DIRECT  INTERPRO  GOTERM_BP_DIRECT  INTERPRO  GOTERM_BP_DIRECT	region of interest:Domain A region of interest:Domain B  Domain of unknown function DUF3452, retinoblastoma-associated Retinoblastoma-associated protein, B-box  Retinoblastoma-associated protein, A-box  Rb C-terminal  SM01367  SM01368  SM01369  regulation of lipid kinase activity  region of interest:Spacer  Enrichment Score: 0.93  lung-associated mesenchyme development mesenchymal cell proliferation involved in lung development hair follicle morphogenesis  Enrichment Score: 0.92  regulation of actin polymerization or depolymerization  DEK, C-terminal  regulation of lamellipodium assembly	RI R		Count  3  3  3  3  3  3  4  Count  5  3  7  Count  4  3  4	P_Value  5.8E-2  7.0E-2  7.0E-2  7.0E-2  1.5E-1  1.5E-1  2.0E-1  7.1E-1  P_Value  7.2E-2  3.0E-1  P_Value  9.8E-2  1.4E-1	Fold Change 6.8E0 6.2E0 6.2E0 6.2E0 6.2E0 4.1E0 4.1E0 4.1E0 3.6E0 1.1E0 Fold Change 3.0E0 5.9E0 1.5E0 Fold Change 3.4E0 4.6E0 3.0E0 Fold Change	Benjamini 9.1E-1 9.1E-1 3.9E-1 3.9E-1 3.9E-1 6.5E-1 6.5E-1 1.0E0 1.0E0 Benjamini 5.7E-1 1.0E0 Benjamini 6.8E-1 1.0E0 8-1 6.8E-1 6.1E-1 8.1E-1	FDR  8.8E- 1  8.8E- 1  3.6E- 1  3.6E- 1  3.6E- 1  5.8E- 1  5.8E- 1  9.5E- 1  9.7E- 1  FDR  6.5E- 1  5.6E- 1  7.7E- 1
Annot	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  INTERPRO  INTERPRO  INTERPRO  SMART  SMART  SMART  GOTERM_BP_DIRECT  UP_SEQ_FEATURE  ation Cluster 208  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  ation Cluster 209  GOTERM_BP_DIRECT  INTERPRO  GOTERM_BP_DIRECT  INTERPRO  GOTERM_BP_DIRECT  INTERPRO  GOTERM_BP_DIRECT	region of interest:Domain A region of interest:Domain B  Domain of unknown function DUF3452, retinoblastoma-associated Retinoblastoma-associated protein, B-box  Retinoblastoma-associated protein, A-box  Rb C-terminal  SM01367  SM01368  SM01369 regulation of lipid kinase activity. region of interest:Spacer  Enrichment Score: 0.93  lung-associated mesenchyme development mesenchymal cell proliferation involved in lung development hair follicle morphogenesis  Enrichment Score: 0.92 regulation of actin polymerization or depolymerization  DEK, C-terminal regulation of lamellipodium assembly.  Enrichment Score: 0.92	RI R		Count  3 3 3 3 3 3 3 4 Count  5 3 7 Count 4 3 4 Count	P_Value  5.8E-2  7.0E-2  7.0E-2  7.0E-2  1.5E-1  1.5E-1  2.0E-1  7.1E-1  P_Value  7.2E-2  3.0E-1  P_Value  9.8E-2  1.4E-1  1.4E-1  P_Value  4.0E-2	Fold Change 6.8E0 6.2E0 6.2E0 6.2E0 6.2E0 4.1E0 4.1E0 4.1E0 3.6E0 1.1E0 Fold Change 3.0E0 5.9E0 1.5E0 Fold Change 3.4E0 4.6E0 3.0E0 Fold Change	Benjamini 9.1E-1 9.1E-1 3.9E-1 3.9E-1 3.9E-1 6.5E-1 6.5E-1 1.0E0 Benjamini 5.7E-1 1.0E0 Benjamini 6.8E-1 6.1E-1 8.1E-1 Benjamini 2.3E-1	FDR  8.8E- 1  8.8E- 1  3.6E- 1  3.6E- 1  3.6E- 1  5.8E- 1  5.8E- 1  9.5E- 1  9.7E- 1  FDR  6.5E- 1  5.6E- 1  7.7E- 1  FDR

Annota	ation Cluster 1	Enrichment Score: ?	G	<b>■</b>	Count	P_Value	Fold Change	Benjamini	i FDR
	GOTERM_BP_DIRECT	histone H2A acetylation	<u>RT</u>	i	5	2.4E-1		1.0E0	9.5E- 1
	GOTERM_BP_DIRECT	histone H4 acetylation	<u>RT</u>	i	7	4.3E-1	1.3E0	1.0E0	9.5E- 1
Annota	ation Cluster 211	Enrichment Score: 0.91	G	To the second se	Count	P_Value	Fold Change	Benjamini	1
	INTERPRO	RNA-processing protein, HAT helix	<u>RT</u>	i	6	1.3E-2		1.2E-1	1.1E- 1
	SMART	<u>HAT</u>	<u>RT</u>	i	6	7.2E-2	2.4E0	4.0E-1	3.6E-
	UP_SEQ_FEATURE	repeat:HAT 4	<u>RT</u>	i	5	8.6E-2	2.8E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:HAT 1	<u>RT</u>	i	5	1.1E-1	2.6E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:HAT 2	<u>RT</u>	i	5	1.1E-1	2.6E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:HAT 3	<u>RT</u>	i	5	1.1E-1	2.6E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:HAT 9	<u>RT</u>	i	3	1.6E-1	4.1E0	1.0E0	9.7E-
	UP_SEQ_FEATURE	repeat:HAT 5	<u>RT</u>	1	4	2.1E-1	2.5E0	1.0E0	9.7E-
	UP_SEQ_FEATURE	repeat:HAT 8	<u>RT</u>		3	2.2E-1	3.4E0	1.0E0	1 9.7E-
	UP_SEQ_FEATURE	repeat:HAT 7	<u>RT</u>		3	2.7E-1	2.9E0	1.0E0	9.7E-
	UP_SEQ_FEATURE	repeat:HAT 6	RT		3	3.9E-1		1.0E0	1 9.7E-
Annota	ation Cluster 212	Enrichment Score: 0.9	G	- 	1	P_Value	Fold	Benjamini	1 i FDR
	GOTERM_BP_DIRECT	Rap protein signal transduction	<u>RT</u>	i	6	1.6E-2	Change	2.2E-1	2.1E-
	GOTERM_BP_DIRECT	microvillus assembly	<u>RT</u>		6	1.4E-1		8.4E-1	8.0E-
	GOTERM_CC_DIRECT	recycling endosome membrane	RT		6		8.7E-1		1 8.7E-
Annota	ation Cluster 213	Enrichment Score: 0.9	G	·		P_Value	Fold	Benjamini	1 i FDR
	INTERPRO	SANT domain	RT		8	1.1E-1	Change	5.9E-1	5.4E-
	UP_SEQ_FEATURE	domain:SANT 1	RT		4	1.3E-1		1.0E0	1 9.7E-
	UP_SEQ_FEATURE	domain:SANT 2	RT		4	1.3E-1		1.0E0	1 9.7E-
Annota	ation Cluster 214	Enrichment Score: 0.9	G	·	Count	P_Value	Fold	Benjamini	1 i FDR
	INTERPRO	Brix domain	RT .		4	5.7E-2	Change	3.9E-1	3.6E-
	UP_SEQ_FEATURE	domain:Brix	RT		4	7.0E-2		1.0E0	1 9.7E-
	SMART	SM00879	RT		4	1.6E-1		6.6E-1	1 5.9E-
	INTERPRO	Anticodon-binding	RT		4	4.0E-1		1.0E0	1 9.1E-
Annot	ation Cluster 215	Enrichment Score: 0.88	G		Count	P_Value	Fold	Benjamini	1 EDR
	GOTERM_CC_DIRECT	endoplasmic reticulum chaperone complex	RT	i	5	8.0E-2	Change	4.0E-1	3.5E-
	GOTERM_BP_DIRECT	protein folding in endoplasmic reticulum	RT		5	1.6E-1		9.2E-1	1 8.7E-
	UP_SEQ_FEATURE	short sequence motif:Prevents secretion from	RT		13	1.8E-1		1.0E0	1 9.7E-
Appot	ation Cluster 216	Enrichment Score: 0.86		•		1	Fold	Benjamini	1 EDB
Amilota	GOTERM_BP_DIRECT	positive regulation of protein metabolic	G RT	-	Count 5	P_Value 3.2E-2	Change	3.5E-1	3.3E-
	GOTERM_BP_DIRECT	process  cellular response to laminar fluid shear stress			4	1.4E-1		8.1E-1	1 7.7E-
	GOTERM_BP_DIRECT	negative regulation of response to cytokine	<u>RT</u>						1 9.5E-
	GOTERM_BP_DIRECT	stimulus  negative regulation of heterotypic cell-cell	<u>RT</u>		3	2.0E-1		1.0E0	1 9.5E-
Anne		<u>adhesion</u>	<u>RT</u>	-	3 Count	4.0E-1 P_Value		1.0E0	1
Annota	ation Cluster 217  UP_SEQ_FEATURE	Enrichment Score: 0.86	•	<u></u>		•	•		8.8E-
	INTERPRO	domain:KEN	<u>RT</u>		3			9.1E-1	1 3.6E-
	INTERPRO	KEN domain	<u>RT</u>		3	7.0E-2		3.9E-1	1 8.8E-
	SMART	PUB domain	<u>RT</u>	•	3	2.5E-1		9.6E-1	1 9.0E-
		<u>PUG</u>	RT	i	3	3.6E-1	Fold	1.0E0	1
Annota	ation Cluster 218  UP_SEQ_FEATURE	Enrichment Score: 0.85	G	-	Count	P_Value	Change	Benjamini	i <b>FDR</b> 9.7E-
	INTERPRO	domain:DOC  Anaphase-promoting complex, subunit	<u>RT</u>	i	4	1.0E-1		1.0E0	9.7E- 1 5.6E-
	SMART	10/DOC domain	<u>RT</u>	i	4	1.2E-1		6.1E-1	1
		<u>SM01337</u>	<u>RT</u>	i	4	2.3E-1	Fold	9.0E-1	8.1E- 1
Annota	ation Cluster 219	Enrichment Score: 0.84	G	i 🚾	Count	P_Value	Fold Change	Benjamini	i FDR

Annot	ation Cluster 1	Enrichment Score: ?	G	<b>100</b>	Count	P_Value	Fold Change	Benjamin	i FDR
$\neg$	UP_KEYWORDS	<u>Glycolysis</u>	RT	1	11	1.0E-2	•	4.3E-2	3.3E-
	INTERPRO			_					2 2.2E-
	GOTERM_CC_DIRECT	Enolase, C-terminal	<u>RT</u>		4	3.2E-2		2.4E-1	1 2.5E-
	INTERPRO	phosphopyruvate hydratase complex	<u>RT</u>	•	4	5.4E-2	4.2E0	2.9E-1	1
		<u>Enolase</u>	<u>RT</u>	i	4	5.7E-2	4.1E0	3.9E-1	3.6E-
	INTERPRO	Enolase, N-terminal	<u>RT</u>	1	4	5.7E-2	4.1E0	3.9E-1	3.6E- 1
	GOTERM_BP_DIRECT	canonical glycolysis	<u>RT</u>	i	9	5.9E-2	2.1E0	5.1E-1	4.9E
	GOTERM_MF_DIRECT	phosphopyruvate hydratase activity	<u>RT</u>	1	4	6.3E-2	4.0E0	3.5E-1	3.1E- 1
	INTERPRO	Enolase, conserved site	<u>RT</u>	i	3	7.0E-2	6.2E0	3.9E-1	3.6E- 1
	SMART	SM01192	<u>RT</u>	1	4	9.8E-2	3.3E0	4.9E-1	4.4E-
	GOTERM_BP_DIRECT	glycolytic process	<u>RT</u>		10	1.1E-1	1.7E0	7.2E-1	6.9E
	PIR_SUPERFAMILY	<u>enolase</u>	<u>RT</u>	1	3	1.6E-1	4.0E0	1.0E0	9.9E
	SMART	<u>———</u> SM01193	RT	1	4	1.6E-1		6.6E-1	1 5.9E
	BIOCARTA			-	5	4.1E-1			1 4.5E
	GOTERM_BP_DIRECT	Glycolysis Pathway	<u>RT</u>					6.6E-1	1 9.5E
	KEGG_PATHWAY	gluconeogenesis	<u>RT</u>	•	8	6.3E-1		1.0E0	1 8.4E
		Biosynthesis of amino acids	<u>RT</u>	•	12	8.4E-1	8.7E-1	1.0E0	1
	KEGG_PATHWAY	Glycolysis / Gluconeogenesis	<u>RT</u>	•	11	8.5E-1	8.6E-1	1.0E0	8.5E- 1
	KEGG_PATHWAY	<u>Carbon metabolism</u>	<u>RT</u>	•	15	9.8E-1	6.9E-1	1.0E0	9.8E
	UP_SEQ_FEATURE	binding site:Substrate	<u>RT</u>	i	21	1.0E0	4.8E-1 Fold		1.0E
Annot	ation Cluster 220  INTERPRO	Enrichment Score: 0.83	G		Count	P_Value	Change		6.9E
		Histone H2B	<u>RT</u>	•	12	6.0E-4	3.1E0	7.5E-3	3
	SMART	<u>H2B</u>	<u>RT</u>	•	12	1.8E-2	2.0E0	1.4E-1	1.3E
	GOTERM_BP_DIRECT	innate immune response in mucosa	<u>RT</u>	i	7	2.4E-1	1.7E0	1.0E0	9.5E 1
	GOTERM_BP_DIRECT	antibacterial humoral response	<u>RT</u>	1	7	7.7E-1	9.4E-1	1.0E0	9.5E 1
	GOTERM_BP_DIRECT	defense response to Gram-positive bacterium	<u>RT</u>	i .	13	7.9E-1	9.1E-1	1.0E0	9.5E 1
	UP_KEYWORDS	Antibiotic	<u>RT</u>	1	4	1.0E0	2.9E-1		1.0E
Annot	UP_KEYWORDS ation Cluster 221	Antimicrobial  Enrichment Score: 0.83	RT G	- -	4 Count	1.0E0 P_Value	2.5E-1 Fold	Bonjamin	1.0E
	UP_SEQ_FEATURE					-	Change		8.8E
	UP_SEQ_FEATURE	repeat:REM 1	<u>RT</u>	1	3	5.8E-2		9.1E-1	1 8.8E
		repeat:REM 2	<u>RT</u>	•	3	5.8E-2	6.8E0	9.1E-1	1
	UP_SEQ_FEATURE	repeat:REM 3	<u>RT</u>	i	3	5.8E-2	6.8E0	9.1E-1	8.8E
	GOTERM_BP_DIRECT	epithelial cell migration	<u>RT</u>	i	3	2.7E-1	3.0E0	1.0E0	9.5E
	INTERPRO	HR1 rho-binding repeat	<u>RT</u>	1	3	3.8E-1	2.3E0	1.0E0	9.1E
	SMART	Hr1	<u>RT</u>	i .	3	5.4E-1	1.7E0	1.0E0	9.0E 1
Annot	ation Cluster 222	Enrichment Score: 0.82	G	<b>15</b>	Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	JAB1/Mov34/MPN/PAD-1	<u>RT</u>	i	7	6.7E-3	3.6E0	6.8E-2	6.3E 2
	UP_SEQ_FEATURE	domain:MPN	<u>RT</u>		6	2.2E-2	3.4E0	4.3E-1	4.2E
7	SMART	JAB MPN	RT		7	3.1E-2		2.3E-1	1 2.0E
	UP_SEQ_FEATURE			-	4		3.9E0		1 9.7E
	INTERPRO	short sequence motif:JAMM motif	<u>RT</u>						1 5.6E
	GOTERM_MF_DIRECT	Rpn11/EIF3F C-terminal domain  thiol-dependent ubiquitin-specific protease	<u>RT</u>		3	1.2E-1		6.1E-1	1
		thiol-dependent ubiquitin-specific protease activity	<u>RT</u>	i	5	1.0E0	3.7E-1		1.0E
	GOTERM_MF_DIRECT UP_SEQ_FEATURE	<pre>metallopeptidase activity metal ion-binding site:Zinc; catalytic</pre>	RT RT		5 4	1.0E0 1.0E0	3.7E-1 2.1E-1		1.0E 1.0E
	UP_KEYWORDS	<u>Metalloprotease</u>	RT	i	4	1.0E0	1.8E-1		1.0E
nnot	ation Cluster 223	Enrichment Score: 0.82	G	<b>™</b>	Count	P_Value	Fold Change	Benjamin	
	GOTERM_BP_DIRECT	<u>positive regulation of cell adhesion mediated</u> <u>by integrin</u>	<u>RT</u>	•	6	5.3E-2	2.7E0	4.8E-1	4.5E 1
	UP_SEQ_FEATURE	domain:SH2 1	<u>RT</u>	i .	4	2.5E-1	2.3E0	1.0E0	9.7E 1
	UP_SEQ_FEATURE	domain:SH2 2	<u>RT</u>	1	4	2.5E-1	2.3E0	1.0E0	9.7E
		331131113112		•					_
nnot	ation Cluster 224	Enrichment Score: 0.81	G	- -	Count	P_Value	Fold Change	Benjamin	FDR

	tation Cluster 1	Enrichment Score: ?	G	- No.	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	Adenylate kinase	<u>RT</u>	1	4	1.7E-1	2.8E0	7.9E-1	7.2E 1
	GOTERM_MF_DIRECT	adenylate kinase activity	<u>RT</u>	i	4	1.8E-1	2.7E0	7.3E-1	6.5E
nnot	tation Cluster 225	Enrichment Score: 0.8	G	<b>10</b>	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	chain:Putative uncharacterized protein C21orf81	RT	i	3	1.6E-1	•	1.0E0	9.7E
<b>1</b>	UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing	<u>RT</u>		3	1.6E-1	4.1E0	1.0E0	9.7E
) 1	UP_SEQ_FEATURE	protein 20A1 chain:Ankyrin repeat domain-containing		-					1 9.7E
J	UP_SEQ_FEATURE	protein 20A2 chain:Ankyrin repeat domain-containing	<u>RT</u>		3	1.6E-1		1.0E0	1 9.7E
J	or_org_rearone	protein 20A3	<u>RT</u>	i	3	1.6E-1	•	1.0E0	1
nnot	tation Cluster 226	Enrichment Score: 0.79	G		Count	P_Value	Fold Change	Benjamini	FDF
	GOTERM_BP_DIRECT	<u>isotype switching</u>	<u>RT</u>	i	7	2.9E-2	2.8E0	3.3E-1	3.1
	OMIM_DISEASE	Mismatch repair cancer syndrome	<u>RT</u>	1	3	7.9E-2	6.0E0	1.0E0	1.0
	GOTERM_MF_DIRECT	g <u>uanine/thymine mispair binding</u>	RT	i	3	1.3E-1	4.5E0	5.8E-1	5.2 1
	GOTERM_BP_DIRECT	somatic hypermutation of immunoglobulin genes	<u>RT</u>	i	5	2.8E-1	1.9E0	1.0E0	9.5 1
	UP_KEYWORDS	Hereditary nonpolyposis colorectal cancer	<u>RT</u>	i	3	3.9E-1	2.3E0	1.0E0	7.8 1
	GOTERM_MF_DIRECT	mismatched DNA binding	<u>RT</u>	i .	3	5.7E-1	1.6E0	1.0E0	8.9 1
nnot	tation Cluster 227	Enrichment Score: 0.79	G	<b>15</b>	Count	P_Value	Fold	Benjamini	
	INTERPRO	TATA-box binding protein	<u>RT</u>		3	7.0E-2	Change 6.2E0	3.9E-1	3.6
J	INTERPRO			•					1 8.8
J		Beta2-adaptin/TBP, C-terminal domain	<u>RT</u>	•	3	2.5E-1	3.1E0	9.6E-1	1
	GOTERM_BP_DIRECT	DNA-templated transcription, initiation	<u>RT</u>	i	9	2.5E-1		1.0E0	9.5
nnot	tation Cluster 228	Enrichment Score: 0.76	G	<b>100</b>	Count	P_Value	Fold Change	Benjamini	FD
	BBID	104.Insulin signaling	<u>RT</u>	i .	10	8.4E-2	1.7E0	8.2E-1	8.2 1
)	BBID	108.Regulating glucose transport	<u>RT</u>	1	7	8.4E-2	2.0E0	8.2E-1	8.2
	BBID	105.Signaling glucose uptake	<u>RT</u>	1	6	2.3E-1	1.7E0	1.0E0	1.0
)	BBID BBID	106.Glycogen synthase-synthesis	RT	•	5	2.8E-1		1.0E0	1.0
anot	tation Cluster 229	107.mRNA translation-protein synthesis Enrichment Score: 0.76	RT G		7 Count	3.4E-1 P_Value	Fold	1.0E0 Benjamini	1.0
							Change		
)	GOTERM_BP_DIRECT	type I interferon signaling pathway	RT		16	1 1F-1	•	7 4F-1	7.1
		type I interferon signaling pathway	RT	1	16	1.1E-1	1.5E0	7.4E-1	1
)	UP_KEYWORDS	type I interferon signaling pathway  Antiviral defense	RT RT	i	16 22	1.1E-1 1.7E-1	1.5E0	7.4E-1 5.3E-1	1 4.1 1
)	UP_KEYWORDS  GOTERM_BP_DIRECT	Antiviral defense  defense response to virus					1.5E0 1.3E0		1 4.1 1
)	UP_KEYWORDS	Antiviral defense	<u>RT</u>		22	1.7E-1	1.5E0 1.3E0 1.2E0	5.3E-1	1 4.1 1 9.5 1
	UP_KEYWORDS  GOTERM_BP_DIRECT	Antiviral defense  defense response to virus  negative regulation of viral genome	RT RT	i i	22 33 10	1.7E-1 2.2E-1	1.5E0 1.3E0 1.2E0 1.5E0	5.3E-1 1.0E0	1 4.: 1 9.! 1 9.! 1
	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT	Antiviral defense  defense response to virus  negative regulation of viral genome replication	RT RT RT	i i	22 33 10	1.7E-1 2.2E-1 2.2E-1	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change	5.3E-1 1.0E0 1.0E0	1 4.: 1 9.! 1 9.! 1 5.!
	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types	RT RT RT G RT		22 33 10 Count	1.7E-1 2.2E-1 2.2E-1 P_Value	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1	1 41 91 1 91 55
	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230  PIR_SUPERFAMILY	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site	RT RT RT G RT RT		22 33 10 Count 4 3	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0 4.6E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1	1 4. 1 9. 1 9. 1 1 5. 1
	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230  PIR_SUPERFAMILY  INTERPRO  INTERPRO	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site  Heat shock protein Hsp90, N-terminal	RT RT RT G RT RT RT		22 33 10 Count 4 3	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1 1.7E-1	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0 4.6E0 2.8E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1 7.9E-1	1 4.: 1 9.! 1 3.! 1 5.0 1
	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230  PIR_SUPERFAMILY  INTERPRO  INTERPRO  INTERPRO	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site  Heat shock protein Hsp90, N-terminal  Heat shock protein Hsp90	RT RT RT G RT RT		22 33 10 Count 4 3	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0 4.6E0 2.8E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1	1 4.: 1 9.! 1 9.! 1 1 5.6 1 7.: 1 8.8
	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230  PIR_SUPERFAMILY  INTERPRO  INTERPRO  INTERPRO  INTERPRO	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site  Heat shock protein Hsp90, N-terminal	RT RT RT G RT RT RT		22 33 10 Count 4 3	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1 1.7E-1	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0 4.6E0 2.8E0 2.3E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1 7.9E-1	1 4.:1 9.:1 1 9.:1 1 5.:1 1 8.:1
	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230  PIR_SUPERFAMILY  INTERPRO  INTERPRO  INTERPRO	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site  Heat shock protein Hsp90, N-terminal  Heat shock protein Hsp90  Histidine kinase-like ATPase, ATP-binding	RT RT RT G RT RT RT		22 33 10 Count 4 3 4	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1 1.7E-1 2.6E-1	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0 4.6E0 2.8E0 2.3E0 1.3E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1 7.9E-1 9.6E-1	1 4 1 9 1 3 1 5 1 8.8 1
inot	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230  PIR_SUPERFAMILY  INTERPRO  INTERPRO  INTERPRO  INTERPRO	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site  Heat shock protein Hsp90, N-terminal  Heat shock protein Hsp90  Histidine kinase-like ATPase, ATP-binding domain	RT RT RT G RT RT RT RT		22 33 10 Count 4 3 4 7 4	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1 1.7E-1 2.6E-1 4.5E-1	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0 4.6E0 2.8E0 2.3E0 1.3E0 1.5E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1 7.9E-1 9.6E-1 1.0E0	1 4 1 9 1 3 1 5 1 8 1 9 1
) ) ) ) ) ) ) ) ) ) ) ) )	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230  PIR_SUPERFAMILY  INTERPRO  INTERPRO  INTERPRO  INTERPRO  SMART	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site  Heat shock protein Hsp90, N-terminal  Heat shock protein Hsp90  Histidine kinase-like ATPase, ATP-binding domain  HATPase c	RT RT RT RT RT RT RT RT		22 33 10 Count 4 3 4 7 4	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1 1.7E-1 2.6E-1 4.5E-1 5.3E-1	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0 4.6E0 2.8E0 2.3E0 1.3E0 1.5E0 Fold Change	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1 7.9E-1 9.6E-1 1.0E0 1.0E0	1 4.1 9.5 1 9.5 1 5.6 1 7.2 1 8.8 1 9.1 1
) ) ) ) ) ) ) ) ) ) ) ) )	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230  PIR_SUPERFAMILY  INTERPRO  INTERPRO  INTERPRO  INTERPRO  SMART  tation Cluster 231	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site  Heat shock protein Hsp90, N-terminal  Heat shock protein Hsp90  Histidine kinase-like ATPase, ATP-binding domain  HATPase c  Enrichment Score: 0.76  repeat:RCC1 7  Regulator of chromosome condensation,	RI R		22 33 10 Count 4 3 4 4 7 4 Count	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1 1.7E-1 2.6E-1 4.5E-1 5.3E-1 P_Value	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0 4.6E0 2.8E0 2.3E0 1.3E0 1.5E0 Fold Change 3.4E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1 7.9E-1 9.6E-1 1.0E0 1.0E0 Benjamini	1 4.1 1 9.5 1 9.5 1 7.2 1 8.8 1 9.1 1 9.7 1 1 9.5 1
) ) ) ) ) ) )	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230  PIR_SUPERFAMILY  INTERPRO  INTERPRO  INTERPRO  SMART  tation Cluster 231  UP_SEQ_FEATURE	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site  Heat shock protein Hsp90, N-terminal  Heat shock protein Hsp90  Histidine kinase-like ATPase, ATP-binding domain  HATPase c  Enrichment Score: 0.76  repeat:RCC1 7  Regulator of chromosome condensation, RCC1	RI R		22 33 10 Count 4 3 4 7 4 Count 4 7	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1 1.7E-1 2.6E-1 4.5E-1 5.3E-1 P_Value 1.0E-1 1.1E-1	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0 4.6E0 2.8E0 2.3E0 1.3E0 1.5E0 Fold Change 3.4E0 2.1E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1 7.9E-1 9.6E-1 1.0E0 Benjamini 1.0E0 5.8E-1	1 4.1 1 9.5 1 9.5 1 7.2 1 8.8 1 9.1 1 9.5 1 1 9.5 1
inot	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230  PIR_SUPERFAMILY  INTERPRO  INTERPRO  INTERPRO  SMART  tation Cluster 231  UP_SEQ_FEATURE  INTERPRO  UP_SEQ_FEATURE	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site  Heat shock protein Hsp90, N-terminal  Heat shock protein Hsp90  Histidine kinase-like ATPase, ATP-binding domain  HATPase c  Enrichment Score: 0.76  repeat:RCC1 7  Regulator of chromosome condensation, RCC1  repeat:RCC1 5	RI R		22 33 10 Count 4 3 4 7 4 Count 4 7	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1 1.7E-1 2.6E-1 4.5E-1 5.3E-1 P_Value 1.0E-1 1.1E-1 1.1E-1	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0 4.6E0 2.8E0 2.3E0 1.5E0 Fold Change 3.4E0 2.1E0 2.3E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1 7.9E-1 9.6E-1 1.0E0 Benjamini 1.0E0 5.8E-1 1.0E0	1 4.1 9.5 1 9.5 1 5.6 1 7.2 1 8.8 1 9.1 1 9.5 1 9.5 1
) ) ) ) ) ) )	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230  PIR_SUPERFAMILY  INTERPRO  INTERPRO  INTERPRO  SMART  tation Cluster 231  UP_SEQ_FEATURE  INTERPRO  UP_SEQ_FEATURE  INTERPRO	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site  Heat shock protein Hsp90, N-terminal  Heat shock protein Hsp90  Histidine kinase-like ATPase, ATP-binding domain  HATPase c  Enrichment Score: 0.76  repeat:RCC1 7  Regulator of chromosome condensation, RCC1	RI R		22 33 10 Count 4 3 4 7 4 Count 4 7	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1 1.7E-1 2.6E-1 4.5E-1 5.3E-1 P_Value 1.0E-1 1.1E-1	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0 4.6E0 2.8E0 2.3E0 1.5E0 Fold Change 3.4E0 2.1E0 2.3E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1 7.9E-1 9.6E-1 1.0E0 Benjamini 1.0E0 5.8E-1	1 4.1 1 9.5 1 9.5 1 7.2 1 8.8 1 9.1 1 9.7 1 9.7 1 5.8 1 9.5 1
) ) ) ) ) ) ) ) ) ) ) ) )	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230  PIR_SUPERFAMILY  INTERPRO  INTERPRO  INTERPRO  SMART  tation Cluster 231  UP_SEQ_FEATURE  INTERPRO  UP_SEQ_FEATURE  INTERPRO  UP_SEQ_FEATURE	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site  Heat shock protein Hsp90, N-terminal  Heat shock protein Hsp90  Histidine kinase-like ATPase, ATP-binding domain  HATPase c  Enrichment Score: 0.76  repeat:RCC1 7  Regulator of chromosome condensation, RCC1  repeat:RCC1 5  Regulator of chromosome condensation	RI R		22 33 10 Count 4 3 4 7 4 Count 4 7 6 7	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1 1.7E-1 2.6E-1 4.5E-1 5.3E-1 P_Value 1.0E-1 1.1E-1 1.1E-1	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0 4.6E0 2.8E0 1.3E0 1.5E0 Fold Change 3.4E0 2.1E0 2.3E0 2.3E0 2.3E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1 7.9E-1 9.6E-1 1.0E0 Benjamini 1.0E0 5.8E-1 1.0E0	1 4.1 1 9.5 1 9.5 1 7.2 1 8.8 1 9.1 1 9.7 1 1 1 9.7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
) ) ) ) ) ) ) ) ) ) ) ) )	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230  PIR_SUPERFAMILY  INTERPRO  INTERPRO  INTERPRO  SMART  tation Cluster 231  UP_SEQ_FEATURE  INTERPRO  UP_SEQ_FEATURE  INTERPRO	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site  Heat shock protein Hsp90, N-terminal  Heat shock protein Hsp90  Histidine kinase-like ATPase, ATP-binding domain  HATPase c  Enrichment Score: 0.76  repeat:RCC1 7  Regulator of chromosome condensation, RCC1  repeat:RCC1 5  Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II	RI R		22 33 10 Count 4 3 4 7 4 Count 4 7 6 7 6	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1 1.7E-1 2.6E-1 4.5E-1 5.3E-1 P_Value 1.0E-1 1.1E-1 1.1E-1 1.3E-1	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0 4.6E0 2.8E0 1.3E0 1.5E0 Fold Change 3.4E0 2.1E0 2.3E0 2.2E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1 7.9E-1 9.6E-1 1.0E0 Benjamini 1.0E0 5.8E-1 1.0E0 6.3E-1	1 4.1 1 9.5 1 9.5 1 7.2 1 8.8 1 9.1 1 9.7 1 1 9.5 1 1 9.5 1 1 9.5 1 1 9.5 1 1 9.5 1 1 9.5 1 1 9.5 1 1 1 9.5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
) ) ) ) ) ) ) ) ) ) ) ) )	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230  PIR_SUPERFAMILY  INTERPRO  INTERPRO  INTERPRO  SMART  tation Cluster 231  UP_SEQ_FEATURE  INTERPRO  UP_SEQ_FEATURE  INTERPRO  UP_SEQ_FEATURE	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site  Heat shock protein Hsp90, N-terminal  Heat shock protein Hsp90  Histidine kinase-like ATPase, ATP-binding domain  HATPase c  Enrichment Score: 0.76  repeat:RCC1 7  Regulator of chromosome condensation, RCC1  repeat:RCC1 5  Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II  repeat:RCC1 4	RI R		22 33 10 Count 4 3 4 7 4 Count 4 7 6 7 6 6 6	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1 1.7E-1 2.6E-1 4.5E-1 5.3E-1 P_Value 1.0E-1 1.1E-1 1.1E-1 1.3E-1 1.3E-1	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0 4.6E0 2.8E0 2.3E0 1.5E0 Fold Change 3.4E0 2.1E0 2.3E0 2.2E0 2.0E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1 7.9E-1 9.6E-1 1.0E0 Benjamini 1.0E0 5.8E-1 1.0E0 6.3E-1 1.0E0	1 4 1 9 1 3 1 5 1 9 1 1 9 1 1 9 1 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 1 1 9 1 1 9 1 1 1 1
) ) ) ) ) ) ) ) ) ) ) ) )	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230  PIR_SUPERFAMILY  INTERPRO  INTERPRO  INTERPRO  INTERPRO  SMART  tation Cluster 231  UP_SEQ_FEATURE  INTERPRO  UP_SEQ_FEATURE  INTERPRO  UP_SEQ_FEATURE  INTERPRO  UP_SEQ_FEATURE  UP_SEQ_FEATURE	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site  Heat shock protein Hsp90, N-terminal  Heat shock protein Hsp90  Histidine kinase-like ATPase, ATP-binding domain  HATPase c  Enrichment Score: 0.76  repeat:RCC1 7  Regulator of chromosome condensation, RCC1  repeat:RCC1 5  Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II  repeat:RCC1 4  repeat:RCC1 1	RI R		22 33 10 Count 4 3 4 4 7 4 Count 4 7 6 7 6 6 6 6	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1 1.7E-1 2.6E-1 4.5E-1 5.3E-1 P_Value 1.0E-1 1.1E-1 1.1E-1 1.3E-1 1.3E-1 1.6E-1 1.6E-1	1.5E0 1.3E0 1.2E0 1.5E0 1.5E0 Fold Change 5.3E0 4.6E0 2.8E0 1.3E0 1.5E0 Fold Change 3.4E0 2.1E0 2.3E0 2.2E0 2.0E0 2.0E0 2.0E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1 7.9E-1 9.6E-1 1.0E0 Benjamini 1.0E0 5.8E-1 1.0E0 6.3E-1 1.0E0 1.0E0 1.0E0	1 4 1 9 1 5 1 9 1 1 9 1 1 9 1 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 1 1 1
) ) ) ) ) ) ) ) ) ) ) )	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  tation Cluster 230  PIR_SUPERFAMILY  INTERPRO  INTERPRO  INTERPRO  INTERPRO  SMART  tation Cluster 231  UP_SEQ_FEATURE  INTERPRO  UP_SEQ_FEATURE  INTERPRO  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site  Heat shock protein Hsp90, N-terminal  Heat shock protein Hsp90  Histidine kinase-like ATPase, ATP-binding domain  HATPase c  Enrichment Score: 0.76  repeat: RCC1 7  Regulator of chromosome condensation, RCC1  repeat: RCC1 5  Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II  repeat: RCC1 4  repeat: RCC1 2  repeat: RCC1 2	RI R		22 33 10 Count 4 3 4 7 4 Count 4 7 6 7 6 6 6 6 6	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1 1.7E-1 2.6E-1 4.5E-1 5.3E-1 P_Value 1.0E-1 1.1E-1 1.1E-1 1.3E-1 1.3E-1 1.6E-1 1.6E-1 1.6E-1	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0 4.6E0 2.8E0 2.3E0 1.5E0 Fold Change 3.4E0 2.1E0 2.1E0 2.3E0 2.0E0 2.0E0 2.0E0 2.0E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1 7.9E-1 9.6E-1 1.0E0 Benjamini 1.0E0 5.8E-1 1.0E0 6.3E-1 1.0E0 1.0E0 1.0E0 1.0E0	1 4.1 9.1 1 9.1 1 5.1 1 9.1 1 1 1
inot	UP_KEYWORDS  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  Tation Cluster 230  PIR_SUPERFAMILY  INTERPRO  INTERPRO  INTERPRO  INTERPRO  SMART  Tation Cluster 231  UP_SEQ_FEATURE  INTERPRO  UP_SEQ_FEATURE  INTERPRO  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE  UP_SEQ_FEATURE	Antiviral defense  defense response to virus  negative regulation of viral genome replication  Enrichment Score: 0.76  heat shock protein, HSP90/HTPG types  Heat shock protein Hsp90, conserved site  Heat shock protein Hsp90, N-terminal  Heat shock protein Hsp90  Histidine kinase-like ATPase, ATP-binding domain  HATPase c  Enrichment Score: 0.76  repeat:RCC1 7  Regulator of chromosome condensation, RCC1  repeat:RCC1 5  Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II  repeat:RCC1 4  repeat:RCC1 1	RI R		22 33 10 Count 4 3 4 4 7 4 Count 4 7 6 7 6 6 6 6	1.7E-1 2.2E-1 2.2E-1 P_Value 2.2E-2 1.2E-1 1.7E-1 2.6E-1 4.5E-1 5.3E-1 P_Value 1.0E-1 1.1E-1 1.1E-1 1.3E-1 1.3E-1 1.6E-1 1.6E-1	1.5E0 1.3E0 1.2E0 1.5E0 Fold Change 5.3E0 4.6E0 2.8E0 2.3E0 1.5E0 Fold Change 3.4E0 2.1E0 2.1E0 2.3E0 2.0E0 2.0E0 2.0E0 2.0E0	5.3E-1 1.0E0 1.0E0 Benjamini 3.6E-1 6.1E-1 7.9E-1 9.6E-1 1.0E0 Benjamini 1.0E0 5.8E-1 1.0E0 6.3E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	1 4 1 9 1 5 1 9 1 1 9 1 1 9 1 1 9 1 1 1 1

Annota	ation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold	Benjamini	FDR
	UP_SEQ_FEATURE	domain:PUA	RT		3	1.6E-1	Change	1.0E0	9.7E-
	INTERPRO	PUA-like domain	RT		6	1.8E-1		8.5E-1	1 7.7E-
	INTERPRO	Pseudouridine synthase/archaeosine	RT		3	1.9E-1		8.6E-1	1 7.8E-
Appot	ation Cluster 233	transglycosylase Enrichment Score: 0.76	G	· 	Count	P_Value	Fold	Benjamini	1 FDR
Annot	UP_KEYWORDS						Change		7.4E-
	GOTERM_BP_DIRECT	Innate immunity	<u>RT</u>	•	51	2.4E-2		9.5E-2	2 9.5E-
	UP_KEYWORDS	innate immune response	<u>RT</u>	•	78	3.0E-1		1.0E0	1 7.8E-
	or_kerwokbo	<u>Immunity</u>	<u>RT</u>	-	69	7.5E-1	9.5E-1 Fold		1
Annota	ation Cluster 234  INTERPRO	Enrichment Score: 0.75	G		Count	P_Value	Change	Benjamini	
		Protein-tyrosine phosphatase, catalytic	<u>RT</u>	i	19	9.0E-3	1.9E0	8.7E-2	7.9E- 2
	GOTERM_MF_DIRECT	non-membrane spanning protein tyrosine phosphatase activity	<u>RT</u>	•	4	1.4E-1	3.0E0	5.8E-1	5.2E- 1
	SMART	PTPc motif	<u>RT</u>	i	19	2.7E-1	1.2E0	9.7E-1	8.7E- 1
	INTERPRO	<u>Protein-tyrosine phosphatase, receptor/non-receptor type</u>	<u>RT</u>	i	7	5.9E-1	1.1E0	1.0E0	9.1E- 1
	SMART	PTPc	<u>RT</u>	i .	7	9.2E-1	7.7E-1	1.0E0	9.2E- 1
Annota	ation Cluster 235	Enrichment Score: 0.74	G	<b>17</b>	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	<u>Carbamoyl-phosphate synthetase large</u> <u>subunit-like, ATP-binding domain</u>	<u>RT</u>	i	4	8.8E-2	3.5E0	4.7E-1	4.3E- 1
	INTERPRO	ATP-grasp fold, subdomain 2	<u>RT</u>	i	7	9.0E-2	2.2E0	4.8E-1	4.3E- 1
	INTERPRO	ATP-grasp fold	<u>RT</u>	i e	5	1.4E-1	2.4E0	7.0E-1	6.4E-
	INTERPRO	<u>Pre-ATP-grasp domain</u>	<u>RT</u>	•	5	1.8E-1	2.2E0	8.4E-1	7.7E-
	INTERPRO	ATP-grasp fold, subdomain 1	RT		5	2.1E-1		9.6E-1	1 8.8E-
	INTERPRO	Rudiment single hybrid motif	RT		3	2.5E-1		9.6E-1	1 8.8E-
	UP_SEQ_FEATURE								1 9.7E-
		domain:ATP-grasp	<u>RT</u>	1	3	5.9E-1	Fold	1.0E0	1
Annota	ation Cluster 236  UP_KEYWORDS	Enrichment Score: 0.74	G	-	Count	P_Value	Change	Benjamini	2.0E-
	GOTERM_CC_DIRECT	<u>Glycogen metabolism</u>	<u>RT</u>	•	8			2.5E-1	1 3.5E-
		PTW/PP1 phosphatase complex	<u>RT</u>	i	4	8.3E-2	3.6E0	4.0E-1	1
	GOTERM_BP_DIRECT	glycogen metabolic process	<u>RT</u>	i	8	2.1E-1	1.6E0	1.0E0	9.5E- 1
	UP_KEYWORDS	Carbohydrate metabolism	<u>RT</u>	i	11	8.9E-1	8.0E-1	1.0E0	8.9E- 1
Annota	ation Cluster 237	Enrichment Score: 0.73	G	<b>100</b>	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	DNA topological change	<u>RT</u>	i	5	5.0E-2	3.3E0	4.6E-1	4.4E- 1
	GOTERM_MF_DIRECT	DNA binding, bending	<u>RT</u>	i .	6	1.7E-1	2.0E0	7.1E-1	6.3E- 1
	BIOCARTA	Apoptotic DNA fragmentation and tissue homeostasis	<u>RT</u>	i	4	7.5E-1	1.1E0	1.0E0	7.5E- 1
Annota	ation Cluster 238	Enrichment Score: 0.71	G	<b>™</b>	Count	P_Value	Fold Change	Benjamini	FDR
	BIOCARTA	AKAP95 role in mitosis and chromosome dynamics	<u>RT</u>	i	8	5.7E-2	2.1E0	1.5E-1	1.0E- 1
	BIOCARTA	Protein Kinase A at the Centrosome	<u>RT</u>	i	8	1.8E-1	1.6E0	3.8E-1	2.6E-
	BIOCARTA	Rho-Selective Guanine Exchange Factor AKAP13 Mediates Stress Fiber Formation	<u>RT</u>		4	7.5E-1	1.1E0	1.0E0	7.5E- 1
Annota		Enrichment Score: 0.7	G	N .	Count	P_Value	Fold	Benjamini	
	ation Cluster 239					: -	Change		
	ation Cluster 239  UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 1	RT	i .	8	3.3E-2	2.5E0	6.1E-1	5.9E-
		zinc finger region:Phorbol-ester/DAG-type 1		i .	8				1 5.9E-
	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 1 zinc finger region:Phorbol-ester/DAG-type 2	<u>RT</u>		8	3.3E-2	2.5E0	6.1E-1	1 5.9E- 1
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO	zinc finger region:Phorbol-ester/DAG-type 1 zinc finger region:Phorbol-ester/DAG-type 2 Protein kinase C, alpha/beta/gamma types	RT RT	i i	8	3.3E-2 7.0E-2	2.5E0 6.2E0	6.1E-1 3.9E-1	1 5.9E- 1 3.6E- 1
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  PIR_SUPERFAMILY	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 RT RT		8 3 3	3.3E-2 7.0E-2 9.1E-2	2.5E0 6.2E0 5.3E0	6.1E-1 3.9E-1 7.7E-1	1 5.9E- 1 3.6E- 1 7.6E- 1
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  PIR_SUPERFAMILY  GOTERM_MF_DIRECT	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 RT RT RT	i i	8 3 3 3	3.3E-2 7.0E-2 9.1E-2 1.3E-1	2.5E0 6.2E0 5.3E0 4.5E0	6.1E-1 3.9E-1 7.7E-1 5.8E-1	1 5.9E- 1 3.6E- 1 7.6E- 1 5.2E- 1
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  PIR_SUPERFAMILY  GOTERM_MF_DIRECT  UP_SEQ_FEATURE	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 RT RT RT		8 3 3	3.3E-2 7.0E-2 9.1E-2	2.5E0 6.2E0 5.3E0 4.5E0	6.1E-1 3.9E-1 7.7E-1	1 5.9E- 1 3.6E- 1 7.6E- 1 5.2E- 1 9.7E- 1
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  PIR_SUPERFAMILY  GOTERM_MF_DIRECT  UP_SEQ_FEATURE  KEGG_PATHWAY	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 metal ion-binding site:Calcium 2; via carbonyl	RT RT RT RT		8 3 3 3	3.3E-2 7.0E-2 9.1E-2 1.3E-1 2.0E-1	2.5E0 6.2E0 5.3E0 4.5E0	6.1E-1 3.9E-1 7.7E-1 5.8E-1 1.0E0	1 5.9E- 1 3.6E- 1 7.6E- 1 5.2E- 1 9.7E- 1 2.9E- 1
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  PIR_SUPERFAMILY  GOTERM_MF_DIRECT  UP_SEQ_FEATURE	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 metal ion-binding site:Calcium 2; via carbonyl oxygen African trypanosomiasis metal ion-binding site:Calcium 1	RT RT RT RT RT RT RT RT RT		8 3 3 9	3.3E-2 7.0E-2 9.1E-2 1.3E-1 2.0E-1	2.5E0 6.2E0 5.3E0 4.5E0 1.6E0 1.4E0	6.1E-1 3.9E-1 7.7E-1 5.8E-1 1.0E0	1 5.9E- 1 3.6E- 1 7.6E- 1 5.2E- 1 9.7E- 1 2.9E-
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  PIR_SUPERFAMILY  GOTERM_MF_DIRECT  UP_SEQ_FEATURE  KEGG_PATHWAY	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 metal ion-binding site:Calcium 2; via carbonyl oxygen African trypanosomiasis	RT RT RT RT RT RT RT RT RT		8 3 3 3 9	3.3E-2 7.0E-2 9.1E-2 1.3E-1 2.0E-1 2.9E-1 5.5E-1	2.5E0 6.2E0 5.3E0 4.5E0 1.6E0 1.4E0	6.1E-1 3.9E-1 7.7E-1 5.8E-1 1.0E0 4.5E-1 1.0E0	1 5.9E- 1 3.6E- 1 7.6E- 1 5.2E- 1 9.7E- 1 9.7E-
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  PIR_SUPERFAMILY  GOTERM_MF_DIRECT  UP_SEQ_FEATURE  KEGG_PATHWAY  UP_SEQ_FEATURE	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 metal ion-binding site:Calcium 2; via carbonyl oxygen  African trypanosomiasis metal ion-binding site:Calcium 1 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 3 3 3 9 9	3.3E-2 7.0E-2 9.1E-2 1.3E-1 2.0E-1 2.9E-1 5.5E-1 8.4E-1	2.5E0 6.2E0 5.3E0 4.5E0 1.6E0 1.4E0 1.2E0	6.1E-1 3.9E-1 7.7E-1 5.8E-1 1.0E0 4.5E-1 1.0E0 1.0E0	1 5.9E- 1 3.6E- 1 7.6E- 1 5.2E- 1 9.7E- 1 9.7E- 1
	UP_SEQ_FEATURE  UP_SEQ_FEATURE  INTERPRO  PIR_SUPERFAMILY  GOTERM_MF_DIRECT  UP_SEQ_FEATURE  KEGG_PATHWAY  UP_SEQ_FEATURE  UP_SEQ_FEATURE	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 metal ion-binding site:Calcium 2; via carbonyl oxygen  African trypanosomiasis metal ion-binding site:Calcium 1 metal ion-binding site:Calcium 3; via carbonyl oxygen	RT RT RT RT RT RT RT RT RT		8 3 3 3 9 9 8 3	3.3E-2 7.0E-2 9.1E-2 1.3E-1 2.0E-1 2.9E-1 5.5E-1 8.4E-1 8.7E-1	2.5E0 6.2E0 5.3E0 4.5E0 1.6E0 1.4E0 1.2E0 9.7E-1	6.1E-1 3.9E-1 7.7E-1 5.8E-1 1.0E0 4.5E-1 1.0E0 1.0E0 1.0E0	1 5.9E-1 3.6E-1 7.6E-1 5.2E-1 9.7E-1 2.9E-1 9.7E-1 9.7E-1

nnota	ation Cluster 1	Enrichment Score: ?	G	- <del>- 1</del>	Count	P_Value	Fold Change	Benjamini	i FD
nnota	ation Cluster 240	Enrichment Score: 0.69	G	<b>100</b>	Count	P_Value	Fold Change	Benjamini	i FD
	UP_SEQ_FEATURE	zinc finger region:Btk-type	<u>RT</u>	i	4	1.3E-1	3.0E0	1.0E0	9.7 1
	INTERPRO	Zinc finger, Btk motif	<u>RT</u>	1	4	1.7E-1	2.8E0	7.9E-1	7.2 1
	SMART	<u>BTK</u>	<u>RT</u>	1	4	3.9E-1	1.8E0	1.0E0	9.0
nnota	ation Cluster 241	Enrichment Score: 0.69	G	<b>178</b>	Count	P_Value	Fold Change	Benjamini	
	BIOCARTA	Repression of Pain Sensation by the	RT	7	10	1.4E-2	Change	5.5E-2	3.7
) ]	BIOCARTA	<u>Transcriptional Regulator DREAM</u> <u>Transcription Regulation by Methyltransferase</u>	RT		8	5.7E-2		1.5E-1	2 1.0
ך ר	GOTERM_CC_DIRECT	of CARM1  ciliary base	RT	_	8	1.2E-1		5.0E-1	1 4.
) 1	BIOCARTA	Regulation of ck1/cdk5 by type 1 glutamate							1 2.
J	BIOCARTA	<u>receptors</u>	<u>RT</u>		9	1.5E-1		3.3E-1	1 3.
J	BIOCARTA	mCalpain and friends in Cell motility  Activation of Csk by cAMP-dependent Protein	<u>RT</u>	•	10	2.6E-1	1.4E0	5.1E-1	1
)	BIOGRAM	Kinase Inhibits Signaling through the T Cell Receptor	<u>RT</u>	•	10	2.6E-1	1.4E0	5.1E-1	3. 1
)	UP_KEYWORDS	<u>cAMP</u>	<u>RT</u>	4	8	2.6E-1	1.5E0	7.7E-1	6. 1
)	GOTERM_CC_DIRECT	cAMP-dependent protein kinase complex	<u>RT</u>	1	3	3.0E-1	2.7E0	8.7E-1	7. 1
1	BIOCARTA	Cystic fibrosis transmembrane conductance	рт		6	2 45 1	1 550	6 OF 1	4.
J	DIGG. 1774	regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway	<u>RT</u>	•	6	3.4E-1	1.500	6.0E-1	1
	BIOCARTA	Phospholipase C-epsilon pathway	<u>RT</u>	i	6	3.4E-1	1.5E0	6.0E-1	4. 1
	BIOCARTA	Attenuation of GPCR Signaling	<u>RT</u>	i	6	4.2E-1	1.4E0	6.6E-1	4.
	BIOCARTA	GATA3 participate in activating the Th2 cytokine genes expression	<u>RT</u>	4	7	4.2E-1	1.3E0	6.6E-1	4.
	BIOCARTA	Stathmin and breast cancer resistance to antimicrotubule agents	<u>RT</u>	i	8	7.5E-1	9.9E-1	1.0E0	7 1
nota	ation Cluster 242	Enrichment Score: 0.68	G	<u>~</u>	Count	P_Value	Fold Change	Benjamini	i F
	GOTERM_BP_DIRECT	positive regulation of transporter activity	<u>RT</u>	i	4	9.8E-2	3.4E0	6.8E-1	6
	GOTERM_MF_DIRECT	calcium channel regulator activity	<u>RT</u>	•	8	1.5E-1	1.8E0	6.4E-1	5 1
	GOTERM_MF_DIRECT	<u>chloride channel regulator activity</u>	<u>RT</u>	4	4	2.3E-1	2.4E0	8.5E-1	7
	GOTERM_MF_DIRECT	sodium channel regulator activity	<u>RT</u>	•	8	2.8E-1	1.5E0	9.5E-1	8
	GOTERM_BP_DIRECT	positive regulation of sodium ion transport	RT		5	4.0E-1		1.0E0	1 9
nota	ation Cluster 243	Enrichment Score: 0.68	G	· ·	Count	P_Value	Fold	Benjamini	1 F
1010	GOTERM_BP_DIRECT	ventral midline development	RT	-	3	7.6E-2	Change	5.7E-1	5
	GOTERM_BP_DIRECT	smoothened signaling pathway involved in	<u>KI</u>	•	3	7.02 2	3.720	5.72 1	1
			<u>RT</u>	•	3	1.3E-1	4.4E0	8.1E-1	7 1
	GOTERM_BP_DIRECT	smoothened signaling pathway	<u>RT</u>	•	9	9.1E-1	7.7E-1	1.0E0	9 1
nota	ation Cluster 244	Enrichment Score: 0.68	G	<b>178</b>	Count	P_Value	Fold Change	Benjamini	i F
	INTERPRO	DIX domain	<u>RT</u>	1	4	5.7E-2	4.1E0	3.9E-1	3
	GOTERM_BP_DIRECT	beta-catenin destruction complex disassembly	<u>RT</u>	•	8	6.4E-2	2.2E0	5.3E-1	5
	INTERPRO	<u>Dishevelled C-terminal</u>	<u>RT</u>	4	3	7.0E-2	6.2E0	3.9E-1	3
	INTERPRO	<u>Dishevelled family</u>	RT		3	7.0E-2	6.2E0	3.9E-1	3
	INTERPRO	Dishevelled protein domain	RT		3	7.0E-2		3.9E-1	1 3
	UP_SEQ_FEATURE	domain:DIX	RT		4	7.0E-2		1.0E0	1 9
	INTERPRO			•					1 5
	SMART	<u>Dishevelled-related_protein</u>	<u>RT</u>	1	3	1.2E-1		6.1E-1	1 5
	GOTERM_BP_DIRECT	<u>DAX</u>	<u>RT</u>		4	1.6E-1		6.6E-1	1
		cochlea morphogenesis	<u>RT</u>	1	6	3.1E-1		1.0E0	9
	GOTERM_BP_DIRECT	<u>planar cell polarity pathway involved in neural</u> <u>tube closure</u>	<u>RT</u>	i	4	3.3E-1	2.0E0	1.0E0	9
	KEGG_PATHWAY	Basal cell carcinoma	<u>RT</u>	i	12	4.6E-1	1.2E0	6.9E-1	4 1
	GOTERM_MF_DIRECT	Rac GTPase binding	<u>RT</u>	i	8	5.2E-1	1.2E0	1.0E0	8 1
	UP_SEQ_FEATURE	domain:DEP	<u>RT</u>	i	4	5.4E-1	1.4E0	1.0E0	9 1
	INTERPRO	DEP domain	<u>RT</u>	i	4	7.4E-1	1.1E0	1.0E0	9
									9
	SMART	<u>DEP</u>	<u>RT</u>	1	4	9.3E-1	7.4E-1	1.0E0	1

Annot	ation Cluster 1	Enrichment Score: ?	G	<b>15</b>	Count	P_Value	Fold Change	Benjamini	FDR
Annot	ation Cluster 245	Enrichment Score: 0.66	G	<b>100</b>	Count	P_Value	Fold Change	Benjamini	FDR
	UP_KEYWORDS	Purine biosynthesis	<u>RT</u>	1	5	1.1E-1	2.6E0	3.6E-1	2.8E
	GOTERM_BP_DIRECT	purine nucleobase biosynthetic process	<u>RT</u>	i	3	2.0E-1	3.6E0	1.0E0	9.5E
	GOTERM_BP_DIRECT	<u>'de novo' IMP biosynthetic process</u>	<u>RT</u>		3	2.7E-1	3.0E0	1.0E0	9.5E
_ 	GOTERM_BP_DIRECT	purine ribonucleoside monophosphate	RT	1	4	3.8E-1		1.0E0	1 9.5E
	ation Objective 040	biosynthetic process				1	Fold	1	1
Annot	ation Cluster 246  GOTERM_BP_DIRECT	Enrichment Score: 0.66  positive regulation of interleukin-12	G	- <b>15</b>	Count	P_Value	Change	Benjamini	4.3E
		<u>production</u>	<u>RT</u>	•	9	4.7E-2	2.1E0	4.5E-1	1
	GOTERM_BP_DIRECT	positive regulation of nitric-oxide synthase biosynthetic process	<u>RT</u>		5	1.6E-1	2.3E0	9.2E-1	8.7E 1
	GOTERM_BP_DIRECT	positive regulation of interleukin-10 production	RT	1	7	1.8E-1	1.8E0	9.9E-1	9.4E 1
	GOTERM_MF_DIRECT	<u>lipopolysaccharide binding</u>	<u>RT</u>	1	6	3.0E-1	1.6E0	9.5E-1	8.5l
	GOTERM_BP_DIRECT	positive regulation of interferon-alpha production	<u>RT</u>	1	4	3.3E-1	2.0E0	1.0E0	9.5I 1
	BIOCARTA	Dendritic cells in regulating TH1 and TH2 Development	<u>RT</u>		7	7.7E-1	9.8E-1	1.0E0	7.7I
Annot	ation Cluster 247	Enrichment Score: 0.65	G	178	Count	P_Value	Fold Change	Benjamini	
	GOTERM_CC_DIRECT	calcineurin complex	RT	-	3	1.2E-1	4.8E0	5.0E-1	4.4
_ 	GOTERM_BP_DIRECT	positive regulation of NFAT protein import		-		2.3E-1		1.0E0	1 9.5
	GOTERM_BP_DIRECT	into nucleus	<u>RT</u>	1	4				1 9.5
		calcineurin-NFAT signaling cascade	<u>RT</u>		3	4.0E-1	:	1.0E0	1
	ation Cluster 248	Enrichment Score: 0.63	G		Count	P_Value	Fold Change	Benjamini	
		lung-associated mesenchyme development	RT	1	5	7.2E-2	3.0E0	5.7E-1	5.4 1
	GOTERM_BP_DIRECT	<u>branching involved in salivary gland</u> <u>morphogenesis</u>	<u>RT</u>	1	4	2.8E-1	2.2E0	1.0E0	9.5 1
	GOTERM_BP_DIRECT	midbrain development	<u>RT</u>	1	6	6.2E-1	1.1E0	1.0E0	9.5 1
nnot	ation Cluster 249	Enrichment Score: 0.63	G	<b>100</b>	Count	P_Value	Fold Change	Benjamini	FD
	KEGG_PATHWAY	Circadian rhythm	<u>RT</u>		13	8.7E-3	•	1.6E-2	8.7
- ገ	GOTERM_MF_DIRECT	AMP-activated protein kinase activity	RT	1	5	1.8E-2		1.2E-1	3 1.1
ے ا	GOTERM_CC_DIRECT			_					1 1.1
	UP_SEQ_FEATURE	nucleotide-activated protein kinase complex	<u>RT</u>	1	6	1.9E-2		1.3E-1	1 8.8
J		domain:CBS 3	<u>RT</u>	1	3	5.8E-2	6.8E0	9.1E-1	1
	UP_SEQ_FEATURE	domain:CBS 4	<u>RT</u>		3	5.8E-2	6.8E0	9.1E-1	8.8 1
	BIOCARTA	Reversal of Insulin Resistance by Leptin	<u>RT</u>	1	7	1.1E-1	2.0E0	2.6E-1	1.8
	GOTERM_BP_DIRECT	carnitine shuttle	<u>RT</u>	i .	4	1.8E-1	2.6E0	9.9E-1	9.4 1
	UP_KEYWORDS	Fatty acid biosynthesis	<u>RT</u>	•	10	3.4E-1	1.3E0	9.5E-1	7.4 1
	GOTERM_BP_DIRECT	<u>fatty acid biosynthetic process</u>	RT		9	6.7E-1	1.0E0	1.0E0	9.5
_ 	UP_SEQ_FEATURE	domain:CBS 1	RT	1	3	7.6E-1	1 1F0	1.0E0	1 9.7
ے ا	UP_SEQ_FEATURE								1 9.7
	UP_KEYWORDS	domain:CBS 2	<u>RT</u>	1	3	7.6E-1		1.0E0	1 8.1
		CBS domain	<u>RT</u>	i	3	8.1E-1	1.0E0	1.0E0	1
	INTERPRO	Cystathionine beta-synthase, core	<u>RT</u>	i	3	8.6E-1	9.3E-1	1.0E0	9.1 1
	SMART	<u>CBS</u>	<u>RT</u>	1	3	8.9E-1	8.7E-1	1.0E0	9.0 1
	UP_KEYWORDS	Fatty acid metabolism	<u>RT</u>	•	12	9.8E-1	6.6E-1	1.0E0	9.8 1
	UP_KEYWORDS	<u>Lipid biosynthesis</u>	<u>RT</u>	•	11	1.0E0	4.8E-1		1.0
	UP_KEYWORDS	<u>Lipid metabolism</u>	<u>RT</u>		18	1.0E0	2.9E-1 Fold		1.0
nnot	ation Cluster 250  KEGG_PATHWAY	Enrichment Score: 0.63	G	<b></b>		P_Value	Change		
		<u>Dorso-ventral axis formation</u>	<u>RT</u>	i	12	7.7E-3	2.3E0	1.4E-2	7.7
	UP_SEQ_FEATURE	repeat:LNR 3	<u>RT</u>	i	4	1.1E-2	6.8E0	2.3E-1	2.2 1
	INTERPRO	Notch, NOD domain	<u>RT</u>	i	4	1.5E-2	6.2E0	1.2E-1	1.1 1
	INTERPRO	Notch, NODP domain	<u>RT</u>	i	4	1.5E-2	6.2E0	1.2E-1	1.1
	UP_SEQ_FEATURE	domain:EGF-like 28	<u>RT</u>	1	4	2.5E-2	5.5E0	4.8E-1	4.7
	UP_SEQ_FEATURE	repeat:LNR 1	RT		4	2.5E-2		4.8E-1	1 4.7
7	UP_SEQ_FEATURE								1 4.7
	SMART	repeat:LNR 2	<u>RT</u>	i	4	2.5E-2	5.5E0	4.8E-1	1
	SWARI	SM01338	<u>RT</u>	i i	4		4.1E0	2.8E-1	2.6

Aı	nota	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamini	FDR
	)	SMART	SM01339	<u>RT</u>	i	4	4.8E-2	4.1E0	2.8E-1	2.6E-
	)	UP_SEQ_FEATURE	domain:EGF-like 29	<u>RT</u>	1	3	5.8E-2	6.8E0	9.1E-1	8.8E-
	)	UP_SEQ_FEATURE	domain:EGF-like 33	<u>RT</u>		3	5.8E-2	6.8F0	9.1E-1	1 8.8E-
	ì	UP_SEQ_FEATURE	domain:EGF-like 34	RT		3	5.8E-2		9.1E-1	1 8.8E-
_	)	INTERPRO			_					1 3.6E-
	J	INTERPRO	Domain of unknown function DUF3454, notch			3	7.0E-2		3.9E-1	1 4.3E-
	J	SMART	Notch domain	<u>RT</u>	i	4	8.8E-2	3.5E0	4.7E-1	1
	)		<u>SM01334</u>	<u>RT</u>	i	3	1.5E-1	4.1E0	6.5E-1	5.8E- 1
	)	UP_SEQ_FEATURE	domain:EGF-like 20	<u>RT</u>	i	3	1.6E-1	4.1E0	1.0E0	9.7E- 1
	)	UP_SEQ_FEATURE	domain:EGF-like 24	<u>RT</u>	i	3	1.6E-1	4.1E0	1.0E0	9.7E- 1
	)	UP_SEQ_FEATURE	domain:EGF-like 26	<u>RT</u>	i .	3	1.6E-1	4.1E0	1.0E0	9.7E- 1
	)	UP_SEQ_FEATURE	domain:EGF-like 27	<u>RT</u>	i .	3	1.6E-1	4.1E0	1.0E0	9.7E- 1
	)	UP_SEQ_FEATURE	domain:EGF-like 13; calcium-binding	<u>RT</u>	i .	4	2.1E-1	2.5E0	1.0E0	9.7E- 1
	)	UP_SEQ_FEATURE	domain:EGF-like 17; calcium-binding	<u>RT</u>	i	3	2.2E-1	3.4E0	1.0E0	9.7E-
	)	UP_SEQ_FEATURE	domain:EGF-like 21; calcium-binding	<u>RT</u>	i de la companya de	3	2.2E-1	3.4E0	1.0E0	9.7E-
	)	UP_SEQ_FEATURE	domain:EGF-like 22	<u>RT</u>		3	2.2E-1	3.4E0	1.0E0	1 9.7E-
	<b>,</b>	UP_SEQ_FEATURE	domain:EGF-like 23; calcium-binding	RT		3	2.2E-1		1.0E0	1 9.7E-
_	)	SMART				4	2.3E-1		9.0E-1	1 8.1E-
	J	UP_SEQ_FEATURE	NL	<u>RT</u>						1 9.7E-
	J	UP_SEQ_FEATURE	domain:EGF-like 14; calcium-binding	<u>RT</u>		4	2.5E-1		1.0E0	1 9.7E-
	J		domain:EGF-like 15; calcium-binding	<u>RT</u>	1	4	2.5E-1	2.3E0	1.0E0	1
	)	UP_SEQ_FEATURE	domain:EGF-like 19	<u>RT</u>	i	3	3.3E-1	2.6E0	1.0E0	9.7E- 1
	)	UP_SEQ_FEATURE	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>	1	9	4.7E-1	1.2E0	1.0E0	7.8E- 1
	)	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>	i .	3	5.0E-1	1.9E0	1.0E0	9.7E-
	)	UP_SEQ_FEATURE	domain:EGF-like 9; calcium-binding	<u>RT</u>	i	3	7.0E-1	1.3E0	1.0E0	9.7E-
	)	UP_SEQ_FEATURE	domain:EGF-like 9	<u>RT</u>	i de la companya de	4	7.1E-1	1.1E0	1.0E0	9.7E-
	)	UP_SEQ_FEATURE	domain:EGF-like 10	<u>RT</u>		3	7.4E-1	1.2E0	1.0E0	9.7E-
	)	UP_SEQ_FEATURE	domain:EGF-like 6	RT		6	7.9E-1	9.3E-1	1.0E0	1 9.7E-
	) ]	UP_SEQ_FEATURE	domain:EGF-like 7; calcium-binding	RT		4		9.7E-1		1 9.7E-
_	)	UP_SEQ_FEATURE	domain:EGF-like 3							1 9.7E-
_	J	UP_SEQ_FEATURE		<u>RT</u>		9		8.1E-1		1 9.7E-
	J	UP_SEQ_FEATURE	domain:EGF-like 7	<u>RT</u>	•	3		7.3E-1		1 9.7E-
	J	UP_SEQ_FEATURE	domain:EGF-like 4	<u>RT</u>	•	6		6.9E-1		9.7E-
	J		domain:EGF-like 5	<u>RT</u>	i	4	9.6E-1	6.5E-1	1.0E0	1
	)	UP_SEQ_FEATURE	domain:EGF-like 5; calcium-binding	<u>RT</u>	i	3	9.8E-1	5.4E-1	1.0E0	9.8E- 1
	)	UP_SEQ_FEATURE	domain:EGF-like 2	<u>RT</u>	•	8		6.1E-1		9.8E- 1
	) )	UP_SEQ_FEATURE INTERPRO	domain:EGF-like 1 <u>EGF-like calcium-binding, conserved site</u>	RT RT		9 7	1.0E0 1.0E0	5.1E-1 4.3E-1		1.0E0 1.0E0
	)	INTERPRO	EGF-type aspartate/asparagine hydroxylation site	RT	1	7	1.0E0	4.1E-1		1.0E0
	)	INTERPRO	EGF-like calcium-binding	<u>RT</u>	1	7	1.0E0	3.4E-1		1.0E0
	) )	INTERPRO INTERPRO	EGF-like, conserved site  Epidermal growth factor-like domain	RT RT		10 12	1.0E0 1.0E0	3.1E-1 3.2E-1		1.0E0 1.0E0
	)	UP_KEYWORDS	EGF-like domain	<u>RT</u>	1	10	1.0E0	2.9E-1	1.0E0	1.0E0
	)	SMART SMART	EGF CA	RT RT		7 11	1.0E0 1.0E0	2.2E-1 2.4E-1		1.0E0 1.0E0
Aı	nota	ation Cluster 251	Enrichment Score: 0.63	G	<b>100</b>	Count	P_Value	Fold	Roniamini	
	)	BIOCARTA	Small Leucine-rich Proteoglycan (SLRP) molecules	<u>RT</u>	i	6	1.5E-2	3.1E0	5.9E-2	4.0E- 2
	)	GOTERM_BP_DIRECT	keratan sulfate catabolic process	<u>RT</u>	i	6	3.8E-2	3.0E0	3.8E-1	3.6E-
	)	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc) (keratan sulfate)	<u>RT</u>	i	3	5.8E-2	6.8E0	9.1E-1	8.8E- 1
			(Noracum Sanate)							

Annot	tation Cluster 1	Enrichment Score: ?	G	<b>™</b>	Count	P_Value	Fold Change	Benjamini	FDR
	UP_KEYWORDS	<u>Proteoglycan</u>	<u>RT</u>	1	10	2.8E-1	1.4E0	8.0E-1	6.2E- 1
	GOTERM_BP_DIRECT	keratan sulfate biosynthetic process	<u>RT</u>	1	6	5.2E-1	1.3E0	1.0E0	9.5E-
	GOTERM_CC_DIRECT	<u>lysosomal lumen</u>	<u>RT</u>		13	7.0F-1	9.7E-1	1.0F0	1 8.7E-
	GOTERM_CC_DIRECT						9.3E-1		1 8.7E-
	UP_KEYWORDS	<u>Golgi lumen</u>	<u>RT</u>		14				1 8.8E-
	_	Sulfation	<u>RT</u>	1	6		8.1E-1		1
Annot	UP_KEYWORDS tation Cluster 252	Extracellular matrix  Enrichment Score: 0.61	RT G	i N	18 Count	1.0E0 P_Value	4.8E-1 Fold	1.0E0 Benjamini	1.0E0
	INTERPRO			1			Onlange		3.6E-
	GOTERM_CC_DIRECT	Actin-related protein 3 (Arp3)	<u>RT</u>	-	3	7.0E-2		3.9E-1	1 7.4E-
		Arp2/3 protein complex	<u>RT</u>	•	4	2.9E-1	2.1E0	8.4E-1	1
	GOTERM_BP_DIRECT	Arp2/3 complex-mediated actin nucleation	<u>RT</u>	i	4	7.4E-1		1.0E0	9.5E- 1
Annot	tation Cluster 253	Enrichment Score: 0.6	G	<b>17</b>	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	Natriuretic peptide receptor	<u>RT</u>	1	3	7.0E-2	6.2E0	3.9E-1	3.6E- 1
	GOTERM_MF_DIRECT	natriuretic peptide receptor activity	<u>RT</u>	1	3	7.5E-2	6.0E0	3.9E-1	3.4E- 1
	GOTERM_MF_DIRECT	hormone binding	<u>RT</u>	1	4	2.8E-1	2.2E0	9.5E-1	8.5E-
	GOTERM_MF_DIRECT	peptide hormone binding	RT	1	4	8 5F-1	8.8E-1	1 OFO	1 8.9E-
	INTERPRO								1 9.1E-
		Extracellular ligand-binding receptor	RT	i	5	1	8.6E-1 Fold	1	1
Annot	tation Cluster 254	Enrichment Score: 0.59	G		Count	P_Value	Change	Benjamini	
	GOTERM_MF_DIRECT	GKAP/Homer scaffold activity	<u>RT</u>	i	3	1.3E-1	4.5E0	5.8E-1	5.2E- 1
	GOTERM_BP_DIRECT	vocalization behavior	<u>RT</u>	i	5	2.0E-1	2.1E0	1.0E0	9.5E- 1
	GOTERM_BP_DIRECT	adult behavior	<u>RT</u>	i	5	6.6E-1	1.1E0	1.0E0	9.5E- 1
Annot	tation Cluster 255	Enrichment Score: 0.58	G	<b>15</b>	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	SIAH-type domain	<u>RT</u>	i	5	1.1E-1		6.0E-1	5.4E-
	INTERPRO	TRAF-like	<u>RT</u>	1	7	2.1E-1	1.7F0	9.4E-1	8.6E-
	UP_SEQ_FEATURE			_					1 9.7E-
	INTERPRO	zinc finger region:TRAF-type	<u>RT</u>	•	3	3.3E-1		1.0E0	1 9.1E-
	INTERINO	Zinc finger, TRAF-type	<u>RT</u>	i	3	6.0E-1		1.0E0	1
Annot	tation Cluster 256	Enrichment Score: 0.57	G		Count	P_Value	Fold Change	Benjamini	
	BIOCARTA	Nitric Oxide Signaling Pathway	<u>RT</u>	1	11	1.4E-1	1.5E0	3.1E-1	2.1E- 1
	BIOCARTA	Effects of calcineurin in Keratinocyte Differentiation	<u>RT</u>	1	9	2.5E-1	1.5E0	4.9E-1	3.4E- 1
	BIOCARTA	Role of MEF2D in T-cell Apoptosis	<u>RT</u>	i .	7	5.5E-1	1.2E0	8.4E-1	5.7E- 1
Annot	tation Cluster 257	Enrichment Score: 0.57	G	<b>17</b> 8	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	repeat:CXXCXGXG motif	RT		3	1.1E-1	<u> </u>	1.0E0	9.7E-
	UP_SEQ_FEATURE	zinc finger region:CR-type	<u>RT</u>	1	3	1.1E-1	5 1F0	1.0E0	1 9.7E-
	INTERPRO								1 5.6E-
	INTERPRO	<u>Chaperone DnaJ</u>	<u>RT</u>	i	3	1.2E-1	4.6E0	6.1E-1	1
		<u>Chaperone DnaJ, C-terminal</u>	<u>RT</u>	i	4	1.7E-1	2.8E0	7.9E-1	7.2E- 1
	INTERPRO	HSP40/DnaJ peptide-binding	<u>RT</u>	i .	4	1.7E-1	2.8E0	7.9E-1	7.2E- 1
	INTERPRO	Heat shock protein Dnal, cysteine-rich domain	<u>RT</u>	1	3	1.9E-1	3.7E0	8.6E-1	7.8E- 1
	INTERPRO	DnaJ domain, conserved site	<u>RT</u>	1	5	6.5E-1	1.1E0	1.0E0	9.1E- 1
	UP_SEQ_FEATURE	domain:J	<u>RT</u>		8	6.6E-1	1.0E0	1.0E0	9.7E-
	INTERPRO	<u>DnaJ domain</u>	RT		8		9.7E-1		1 9.1E-
	SMART								1 9.7E-
		<u>DnaJ</u>	RT	i	8	1	6.8E-1 Fold		1
Annot	tation Cluster 258  GOTERM_BP_DIRECT	Enrichment Score: 0.56	G	-	Count	P_Value	Change	:	1
		embryonic skeletal limb joint morphogenesis	<u>RT</u>	•	3	7.6E-2	5.9E0	5.7E-1	5.4E- 1
	GOTERM_BP_DIRECT	embryonic hindlimb morphogenesis	<u>RT</u>	i	7	3.3E-1	1.5E0	1.0E0	9.5E- 1
	GOTERM_BP_DIRECT	embryonic forelimb morphogenesis	<u>RT</u>	i	5	8.1E-1	9.3E-1	1.0E0	9.5E- 1
	tation Cluster 259	Enrichment Score: 0.56	G	· ·	Count	P_Value	Fold Change	Benjamini	FDR
Annot							- IIII		1.0E-
Annot	GOTERM_MF_DIRECT	R-SMAD binding	<u>RT</u>	1	9	1.6E-2	2.6E0	1.1E-1	1
Annot	GOTERM_MF_DIRECT  GOTERM_BP_DIRECT	R-SMAD binding regulation of binding	RT RT	1	9	1.6E-2 1.7E-2		1.1E-1 2.2E-1	1 2.1E-

OUTEMAND DRIECT   SIMO DATAIN SOCIALISMONNO   RET	Δ	nnota	ition Cluster 1	Enrichment Score: ?	G	<b>100</b>	Count	P_Value	Fold	Benjamini	FDR
BOOLEAN   Male a conserve attended   El	_					-			Change		3.3E-
GOTIEN, MP_CREET   CONTEN, MP_	_	ر ا	BIOCARTA			-					1 9.8E-
COTENN_P_DIRECT	_	J	GOTERM CC DIRECT								2 4.4E-
COTIENT APPLICATIONS   CONTINUE AND AUTOMOTIVE AND AUTOMOTIVE AND AUTOMOTIVE AUTOMOTIV		J									
UP_SEG_PEATURE		_			<u>RT</u>						1
OFFINE   STATE		J		mesenchymal transition	<u>RT</u>	•	8	3.2E-1	1.4E0	1.0E0	1
INTERPRO				domain:MH1	<u>RT</u>	i	3	3.3E-1	2.6E0	1.0E0	1
INTERPRO				domain:MH2	<u>RT</u>	i	3	3.3E-1	2.6E0	1.0E0	_
MITERPRO   AMA Increases, MIS   3   361-1   230   100   93			INTERPRO	SMAD domain, Dwarfin-type	<u>RT</u>	i	3	3.8E-1	2.3E0	1.0E0	9.1E- 1
GOTERNA MP_DRECT   SEASON FROM SEASON SEAS			INTERPRO	<u>Dwarfin</u>	<u>RT</u>	i	3	3.8E-1	2.3E0	1.0E0	9.1E- 1
OCTERA_MP_DRECT   No.   Interpretation   No.     No.     No.     No.     No.     No.     No.     No.   No.     No.   N			INTERPRO	MAD homology, MH1	<u>RT</u>	i .	3	3.8E-1	2.3E0	1.0E0	9.1E- 1
INTERPRO   MAD International			GOTERM_BP_DIRECT		<u>RT</u>	i	5	4.4E-1	1.5E0	1.0E0	9.5E- 1
MITERPRO			GOTERM_MF_DIRECT		<u>RT</u>	i .	3	4.6E-1	2.0E0	1.0E0	8.9E- 1
MAD Domoslov   Doverfrintyce			INTERPRO		<u>RT</u>	i	4	4.9E-1	1.5E0	1.0E0	9.1E-
MART   DAYS   REST			INTERPRO	MAD homology 1, Dwarfin-type	<u>RT</u>	i e	3	6.0E-1	1.5E0	1.0E0	9.1E-
GOTERM_MF_DIRECT   Indicate the precedent   RT			SMART		RT	1	3	6.2E-1	1.5E0	1.0E0	9.0E-
BIDCARTA   Sole of Tob in T-roll activation   RT			GOTERM_MF_DIRECT	transforming growth factor beta receptor							8.9E-
SMART   DWA		7	BIOCARTA								7.9E-
OCTEM_BP_DIRECT   SAAD protein spend transduction   RT	_	ر ا	SMART								1 9.0E-
NTERPRO   SAMAD/THA domain   Sove 0.56   Count   P. Allino   P.	_	J	GOTERM BP DIRECT								1 9.5E-
Amotation Cluster 250		_									1
GOTERM_COURTECT   L'Asposabl/Ni-L'Asposabl Comblex   RI							1		Fold	1	1
NTERPRO	A	nnota					Count		Change		
NTERPRO		]		<u>I-kappaB/NF-kappaB complex</u>	<u>RT</u>	1	4	3.0E-2	5.1E0	1.9E-1	1
NTERPRO   OS3-like transcription factor, DNA-binding   RI		J		NF-kappa-B/Rel/Dorsal	<u>RT</u>	i	4	3.2E-2	5.0E0	2.4E-1	1
UP_SEQ_FEATURE   domain:RHD   RI				Rel homology domain	<u>RT</u>	i	4	2.1E-1	2.5E0	9.5E-1	_
INTERPRO   Cell surface receptor IPT/TIG   RT			INTERPRO	p53-like transcription factor, DNA-binding	<u>RT</u>	i	10	2.7E-1	1.4E0	9.6E-1	8.8E- 1
GOTERM_MF_DIRECT   Count   P_Value   Fold   Count   P_Value   Co			UP_SEQ_FEATURE	domain:RHD	<u>RT</u>	i	3	3.9E-1	2.3E0	1.0E0	9.7E- 1
Dolumerase II distal enhancer sequence: ST   1   1   1   1   1   1   1   1   1			INTERPRO	Cell surface receptor IPT/TIG	<u>RT</u>	i .	6	5.8E-1	1.2E0	1.0E0	9.1E- 1
SMART   IPT   RT			GOTERM_MF_DIRECT		<u>RT</u>	i	4	8.1E-1	9.5E-1	1.0E0	8.9E-
Interpro   Immunoglobulin E-set   RT		٦	SMART		DT	_	_	0.25.1	7.65.1	1.050	9.3E-
Annotation Cluster 261		J	INTERPRO			_					
INTERPRO   BRCT domain   RT					_			•	Fold		1
UP_SEQ_FEATURE   domain:BRCT 1	A					- -			Change		
UP_SEQ_FEATURE   domain:BRCT 2   RT											1
SMART   BRCT   RT					<u>RT</u>	1	4	2.5E-1	2.3E0	1.0E0	1
UP_SEQ_FEATURE   domain:BRCT   RT				domain:BRCT 2	RT	1	4	2.5E-1	2.3E0	1.0E0	_
Annotation Cluster 262				BRCT	<u>RT</u>	i	7	2.7E-1	1.6E0	9.7E-1	_
GOTERM_MF_DIRECT   3'-5' exonuclease activity   RT			UP_SEQ_FEATURE	domain:BRCT	RT	i	3	6.3E-1		1.0E0	9.7E- 1
INTERPRO   DNA-directed DNA polymerase, family B, exonuclease admin   RT	A	nnota		Enrichment Score: 0.55	G	N. Comments	Count	P_Value	Fold Change	Benjamini	
NTERPRO   DNA-directed DNA polymerase, family B, multifunctional domain   MT   M   MT   MTERPRO   DNA-directed DNA polymerase, family B   RT   MTERPRO   DNA-directed DNA polymerase, family B   RT   MTERPRO   DNA-directed DNA polymerase, family B   RT   MTERPRO   MTERPRO   MTERPRO   DNA-directed DNA polymerase, family B   RT   MTERPRO   MTERPO   MTERPRO   MTERPRO					<u>RT</u>	i	7	8.4E-2	2.2E0	4.3E-1	3.8E- 1
INTERPRO   DNA-directed DNA polymerase, family B   RT			INTERPRO		<u>RT</u>	i	3	1.2E-1	4.6E0	6.1E-1	5.6E- 1
SMART   POLBC   RT			INTERPRO		<u>RT</u>	i	3	1.2E-1	4.6E0	6.1E-1	5.6E- 1
SMART			INTERPRO		<u>RT</u>	i e	3	1.2E-1	4.6E0	6.1E-1	5.6E- 1
UP_KEYWORDS   4Fe-4S   RT			SMART	POLBC	<u>RT</u>	i	3	2.5E-1	3.1E0	9.4E-1	8.4E-
UP_KEYWORDS         DNA-directed DNA polymerase         RT         5         4.7E-1         1.4E0         1.0E0         7.8E           GOTERM_MF_DIRECT         DNA-directed DNA polymerase activity         RT         6         5.5E-1         1.2E0         1.0E0         8.9E           GOTERM_MF_DIRECT         4 iron 4 sulfur cluster binding         RT         7         7.3E-1         9.9E-1         1.0E0         8.9E			UP_KEYWORDS	<u>4Fe-4S</u>	<u>RT</u>	i	7	4.6E-1	1.3E0	1.0E0	7.8E-
GOTERM_MF_DIRECT  DNA-directed DNA polymerase activity  RT  6 5.5E-1 1.2E0 1.0E0 8.9E 1  GOTERM_MF_DIRECT  4 iron 4 sulfur cluster binding  RT  7 7.3E-1 9.9E-1 1.0E0 8.9E			UP_KEYWORDS	DNA-directed DNA polymerase	RT	i e	5	4.7E-1	1.4E0	1.0E0	7.8E-
GOTERM_MF_DIRECT  4 iron 4 sulfur cluster binding  RT  7 7 3F-1 9 9F-1 1 0F0 8.96			GOTERM_MF_DIRECT								8.9E-
	_	) ]	GOTERM_MF_DIRECT								8.9E-
				1 Holl, 4 Salial Guster Dillallig	<u>KI</u>	•		7.JL-1	J.JL-1	1.ULU	

M. J. P. M. SCANSERS   ST.   1.00	Annota	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold	Benjamini	FDR
Revision Guide #35   Certament Revision 15   G.   Certament Revision 15					_			Change		
MP_SEQ_FEATURE	Annota	ation Cluster 263					1	Fold		
MP_SEG_FEATURE								Change		
P. BOLZ, FEATURE		UP_SEQ_FEATURE			_					1 9.7E-
DP_SEG_FENTURE		UP_SEQ_FEATURE			_					_
UP_SEC_PEATURE		UP_SEQ_FEATURE								_
P. BEG, FEATURE		UP SEQ FEATURE	approximate repeats							1
PUBSEC_FEATURE										1
P.S.E., PEATURE		Part   Part								
Monototic Cluster 24d	UP_SEQ_FEATURE   repeat:1-2   RT   9   1.15-1			1						
OCTEM, NP_DIRECT   RESOURCE CONTRACT PAGES   NT						:	:	:	:	1
INTERPRO	Annota				_			Change	•	
Interpro					•	11				1
OCTERN_MP_DIRECT   therecome souther catalogic process   MT				<u>RT</u>	1	3	1.9E-1	3.7E0	8.6E-1	1
UP_SEQ_FEATURE   active flact/cyteine sufferior acid (-SOH)   RT			<u>Peroxiredoxin, C-terminal</u>	<u>RT</u>	i	3	1.9E-1	3.7E0	8.6E-1	1
UF_REVWORDS   Antionalant   NT				<u>RT</u>	i e	3	2.0E-1	3.6E0	7.6E-1	1
UP_SEYWORDS   Percoddate   NT				<u>RT</u>	i	3	2.2E-1	3.4E0	1.0E0	1
GOTERM_MF_DIRECT   antibolidant activity   RT			Antioxidant	<u>RT</u>	i e	4	3.3E-1	2.0E0	9.3E-1	1
GOTERM_BP_DIRECT   Nutroeness RT			<u>Peroxidase</u>	<u>RT</u>	i	5	5.0E-1	1.4E0	1.0E0	
Amotation Cluster 255		GOTERM_MF_DIRECT	antioxidant activity	<u>RT</u>	i	4	6.8E-1	1.2E0	1.0E0	
P. SEG_FEATURE   domain: MADS-box   RT		GOTERM_BP_DIRECT	hydrogen peroxide catabolic process	<u>RT</u>	i .	4	6.8E-1	1.2E0	1.0E0	
INTERPRO   Transcription factor, MADS-box   NT	Annota	ation Cluster 265	Enrichment Score: 0.54	G	M .	Count	P_Value	Fold Change	Benjamini	FDR
MADS		UP_SEQ_FEATURE	domain:MADS-box	<u>RT</u>	i	3	2.2E-1	3.4E0	1.0E0	9.7E- 1
Amotation Cluster 266		INTERPRO	Transcription factor, MADS-box	<u>RT</u>	i .	3	2.5E-1	3.1E0	9.6E-1	
Part   Annotation Cluster 265   Enrichment Score; 0.53   Bar   A 2, 1E-1   2, 5E0   1, 0E0   1   1     INTERPRO   Methyl-CGC DNA binding   RT   A 2, 6E-1   2, 3E0   9, 6E-1   8, 8E-1     INTERPRO   DNA-binding, integrasse-type   RT   A 2, 6E-1   2, 3E0   9, 6E-1   8, 8E-1     INTERPRO   DNA-binding, integrasse-type   RT   A 2, 6E-1   2, 3E0   9, 6E-1   8, 8E-1     SMART   MBD   RT   A 5, 3E-1   1, 5E0   1, 0E0   9, 0E-1     SMART   MBD   RT   A 5, 3E-1   1, 5E0   1, 0E0   9, 0E-1     SMART   MBD   RT   A 5, 3E-1   1, 5E0   1, 0E0   9, 0E-1     SMART   MBD   RT   A 5, 3E-1   1, 5E0   1, 0E0   9, 0E-1     SOTERM_MF_DIRECT   RNA polymerase II transcription factor activity. 1BP-class gracinal binding, involved in perilitation complex assembly   RT   A 5, 3E-1   1, 0E0   1, 0E0   9, 5E-1     SOTERM_BP_DIRECT   Rational Score; 0.52   G		SMART	MADS	<u>RT</u>	i	3	4.5E-1	2.0E0	1.0E0	
INTERPRO   Methyl-CpG DNA binding   RI	Annota	ation Cluster 266	Enrichment Score: 0.53	G	<b>178</b>	Count	P_Value		Benjamini	FDR
NTERPRO   DNA-binding_integrase_tyze   RI		UP_SEQ_FEATURE	domain:MBD	<u>RT</u>	i	4	2.1E-1	2.5E0	1.0E0	
SMART   MBD   RT		INTERPRO	Methyl-CpG DNA binding	<u>RT</u>	i	4	2.6E-1	2.3E0	9.6E-1	
Annotation Cluster 267 Enrichment Score: 0.53 GOTERM_MF_DIRECT GOTERM_MF_DIRECT  RNA polymerase II transcription factor activity. TBP-class protein binding, involved in RI GOTERM_MF_DIRECT  RNA polymerase II transcription factor activity. RNA polymerase II transcription in RI I		INTERPRO	<u>DNA-binding, integrase-type</u>	<u>RT</u>	i contract of	4	2.6E-1	2.3E0	9.6E-1	
### COTERM_MF_DIRECT   RNA polymerase II transcription factor activity. TBP-class protein binding, involved in RT		SMART	MBD	<u>RT</u>	i .	4	5.3E-1	1.5E0	1.0E0	
Count   P_Value   Foldange   RT	Annota	ation Cluster 267	Enrichment Score: 0.53	G	To the second se	Count	P_Value		Benjamini	FDR
GOTERM_MF_DIRECT   transcription factor activity, RNA polymerase   Il core promoter sequence-specific binding   Involved in preinitiation complex assembly   RT		GOTERM_MF_DIRECT		<u>RT</u>	i	3	7.5E-2	6.0E0	3.9E-1	
		GOTERM MF DIRECT	preinitiation complex assembly							
Annotation Cluster 268			II core promoter sequence-specific binding	<u>RT</u>		3	4.6E-1	2.0E0	1.0E0	
GOTERM_BP_DIRECT  mitochondrial translational elongation  RT		GOTERM_BP_DIRECT		<u>RT</u>	i e	3	7.5E-1	1.2E0	1.0E0	
GOTERM_CC_DIRECT   mitochondrial translational etoniquotin   RT	Annota	ation Cluster 268	Enrichment Score: 0.52	G	<b>™</b>	Count	P_Value		Benjamini	FDR
GOTERM_BP_DIRECT mitochondrial translational termination RT		GOTERM_BP_DIRECT	mitochondrial translational elongation	<u>RT</u>	i	19	1.8E-1	1.3E0	9.9E-1	9.4E- 1
GOTERM_BP_DIRECT  mitochondrial translation  RT  7 5.8E-1 1.2E0 1.0E0 9.5E-1  Annotation Cluster 269  Enrichment Score: 0.52  GOTERM_BP_DIRECT  activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  glial cell apoptotic process  RT  GOTERM_BP_DIRECT  BIOCARTA  D4-GDI Signaling Pathway  RT  BIOCARTA  Role of Mitochondria in Apoptotic Signaling  RT  ROLE  ROLE  RT  ROL		GOTERM_CC_DIRECT	mitochondrial large ribosomal subunit	<u>RT</u>	i	11	2.1E-1	1.5E0	7.8E-1	
Annotation Cluster 269 Enrichment Score: 0.52		GOTERM_BP_DIRECT	mitochondrial translational termination	<u>RT</u>	i	17	3.8E-1	1.2E0	1.0E0	
GOTERM_BP_DIRECT  activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c  GOTERM_BP_DIRECT  glial cell apoptotic process  RT  GOTERM_BP_DIRECT  glial cell apoptotic process  RT  BIOCARTA  D4-GDI Signaling Pathway  RT  BIOCARTA  Role of Mitochondria in Apoptotic Signaling  RT  INTERPRO  Peptidase C14, ICE, catalytic subunit p20, active site  GOTERM_BP_DIRECT  RT  Active site  RT  Active Site  Change  A.0E0  1.4E-1  1.3E-  1.5E-  1.5		GOTERM_BP_DIRECT	mitochondrial translation	<u>RT</u>	i contraction	7	5.8E-1	1.2E0	1.0E0	
GOTERM_BP_DIRECT  activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c  GOTERM_BP_DIRECT  glial cell apoptotic process  RT  BIOCARTA  D4-GDI Signaling Pathway  RT  BIOCARTA  Role of Mitochondria in Apoptotic Signaling  RT  INTERPRO  Peptidase C14, ICE, catalytic subunit p20, active site  GOTERM_BP_DIRECT  RT  Active site  RT  BT  BT  BOCARTA  B 9.4E-3 4.0E0 1.4E-1 1.3E-1 1.3E	Annota	ation Cluster 269	Enrichment Score: 0.52	G	178	Count	P_Value		Benjamini	
GOTERM_BP_DIRECT   glial cell apoptotic process   RT		GOTERM_BP_DIRECT	activity involved in apoptotic process by	<u>RT</u>	i	6	9.4E-3		1.4E-1	
BIOCARTA   D4-GDI Signaling Pathway   RT		GOTERM_BP_DIRECT	cytochrome c			4	3 75 2	4.750	3 QE 1	-
BIOCARTA  Role of Mitochondria in Apoptotic Signaling  RT  11 1.4E-1 1.5E0 3.1E-1 2.1E- 1 1  INTERPRO  Peptidase C14, ICE, catalytic subunit p20, active site  GOTERM_BP_DIRECT  RET  3 2.7E-1 3.0E0 1.0E0 9.5E-1										1
INTERPRO   Peptidase C14, ICE, catalytic subunit p20, active site										1
GOTERM_BP_DIRECT  response to cobalt ion  7 2.1E 1 2.5E0 9.5E 1  9.5E-  3 2.7E-1 3.0E0 1.0E0 9.5E-					_					1
TESTIONS IN CONSULTION			active site							1
			response to cobalt ion	RT	1	3	2.7E-1	3.0E0	1.0E0	

	ation Cluster 1	Enrichment Score: ?	G	<b>15</b>	Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	Peptidase C14, caspase non-catalytic subunit p10	<u>RT</u>	i	4	3.0E-1	2.1E0	9.8E-1	8.9E 1
	BBID	127.Mito-stress	<u>RT</u>	i e	4	3.4E-1	1.9E0	1.0E0	1.0E
	BIOCARTA	Induction of apoptosis through DR3 and DR4/5 Death Receptors	<u>RT</u>	•	13	3.7E-1	1.2E0	6.4E-1	4.3E 1
	BBID	86.Apoptosis Nematode& Vert	<u>RT</u>	•	5	3.7E-1	1.6E0	1.0E0	1.0E
	GOTERM_MF_DIRECT	<u>cysteine-type endopeptidase activity involved</u> <u>in apoptotic process</u>	<u>RT</u>	i	4	3.8E-1	1.8E0	1.0E0	8.9E 1
	INTERPRO	Peptidase C14, caspase precursor p45, core	<u>RT</u>	1	4	4.0E-1	1.8E0	1.0E0	9.1E 1
	BIOCARTA	Stress Induction of HSP Regulation	RT	4	7	4.2E-1	1.3E0	6.6E-1	4.5E
_ 	INTERPRO	Peptidase C14, ICE, catalytic subunit p20	RT		4	4.4E-1	1 7E0	1.0E0	1 9.1E
	BIOCARTA								1 5.6E
		<u>Caspase Cascade in Apoptosis</u>	<u>RT</u>	•	9	5.4E-1		8.3E-1	1
	BBID SMART	72.IAP interaction with cell death pathways		•	6	6.3E-1		1.0E0	1.0E 9.0E
		CASc	<u>RT</u>	•	4	6.5E-1		1.0E0	1
	BBID BBID	150.caspase and NFKB activation 46.P13K PTEN	<u>RT</u> RT		6 4	7.5E-1 8.4E-1	1.0E0 9.7E-1	1.0E0 1.0E0	1.0E 1.0E
	GOTERM_MF_DIRECT	cysteine-type endopeptidase activity	RT		8		7.8E-1		9.0E
	UP_KEYWORDS	Thiol protease	RT		8	1.0E0	3.6E-1	1.0E0	1 1.0E
Annota	ation Cluster 270	Enrichment Score: 0.5	G	<b>178</b>	Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	Zinc finger, TFIIS-type	RT		3	2.5E-1		9.6E-1	8.8E
_	UP_SEQ_FEATURE			-					1 9.7E
		zinc finger region:TFIIS-type	<u>RT</u>	•	3	2.7E-1	2.9E0	1.0E0	1
	SMART	ZnF C2C2	<u>RT</u>	i	3	4.5E-1		1.0E0	9.0E 1
nnota	ation Cluster 271	Enrichment Score: 0.46		<b>100</b>	Count	P_Value	Fold Change	Benjamin	i FDR
	BBID	68.Mitogen signaling in growth control	<u>RT</u>		4	3.4E-1		1.0E0	1.0E
	BBID BBID	2.Cytokine Receptors	RT DT		4	3.4E-1 3.5E-1		1.0E0	1.0E
nnota	ation Cluster 272	54.T-cell anergy  Enrichment Score: 0.46	RT G		8 Count	P_Value	Fold	1.0E0  Benjamin	1.0E
	UP_SEQ_FEATURE	domain:KH	RT	i	6	7.3E-2	Change	1.0E0	9.76
_	INTERPRO			_					1 6.5E
		K Homology domain	<u>RT</u>	•	10	1.5E-1	1.6E0	7.1E-1	1
	INTERPRO	K Homology domain, type 1	<u>RT</u>	•	10	2.7E-1	1.4E0	9.6E-1	8.8E 1
	SMART	<u>кн</u>	<u>RT</u>	•	10	6.1E-1	1.1E0	1.0E0	9.0E 1
	UP_SEQ_FEATURE	domain:KH 3	RT		3	6.7E-1	1.4E0	1.0E0	9.7E
$\neg$	UP_SEQ_FEATURE	domain:KH 2	<u>RT</u>		4	7.1E-1	1 1EO	1.0E0	1 9.7E
_	UP_SEQ_FEATURE	domain. Ni 2	<u>KI</u>	•	4				1 9.7E
	OF_OEQ_FEATORE	domain:KH 1	<u>RT</u>	i i	4	7.1E-1	1.1E0	1.0E0	1
Annota							:	:	
	ation Cluster 273	Enrichment Score: 0.45	G	<b>15</b>	Count	P_Value	Fold Change	Benjamin	i FDR
	ation Cluster 273  GOTERM_BP_DIRECT	positive regulation of guanylate cyclase	G RT	i i	Count	P_Value	Fold Change 3.8E0	Benjamin 8.4E-2	8.0
		positive regulation of guanylate cyclase activity	<u>RT</u>	i	7	4.9E-3	Change 3.8E0	8.4E-2	8.0E 2 3.6E
	GOTERM_BP_DIRECT INTERPRO	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain	RT RT	-	7	4.9E-3 7.0E-2	3.8E0 6.2E0	8.4E-2 3.9E-1	8.0E 2 3.6E
	GOTERM_BP_DIRECT INTERPRO GOTERM_MF_DIRECT	positive regulation of guanylate cyclase activity	<u>RT</u>	i	7	4.9E-3	3.8E0 6.2E0	8.4E-2	8.0E 2 3.6E 1 3.4E
	GOTERM_BP_DIRECT INTERPRO	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain	RT RT	i	7	4.9E-3 7.0E-2	3.8E0 6.2E0 6.0E0	8.4E-2 3.9E-1	8.0E 2 3.6E 1 3.4E
	GOTERM_BP_DIRECT INTERPRO GOTERM_MF_DIRECT	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain  nitric-oxide synthase activity	RT RT RT	i i i	7 3 3	4.9E-3 7.0E-2 7.5E-2	3.8E0 6.2E0 6.0E0 2.2E0	8.4E-2 3.9E-1 3.9E-1	8.0E 2 3.6E 1 3.4E 1 6.0E
	GOTERM_BP_DIRECT INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain  nitric-oxide synthase activity  nitric oxide mediated signal transduction	RT RT RT RT		7 3 3 7	4.9E-3 7.0E-2 7.5E-2 8.6E-2	3.8E0 6.2E0 6.0E0 2.2E0 3.4E0	8.4E-2 3.9E-1 3.9E-1 6.3E-1	8.0E 2 3.6E 1 3.4E 1 6.0E 1 9.7E 1
	GOTERM_BP_DIRECT INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain  nitric-oxide synthase activity  nitric oxide mediated signal transduction  domain:Flavodoxin-like  Flavodoxin/nitric oxide synthase	RT RT RT RT RT		7 3 3 7 4 4	4.9E-3 7.0E-2 7.5E-2 8.6E-2 1.0E-1 1.2E-1	3.8E0 6.2E0 6.0E0 2.2E0 3.4E0 3.1E0	8.4E-2 3.9E-1 3.9E-1 6.3E-1 1.0E0 6.1E-1	8.0E 2 3.6E 1 3.4E 1 6.0E 1 9.7E 1 5.6E
	GOTERM_BP_DIRECT INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO INTERPRO	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain  nitric-oxide synthase activity  nitric oxide mediated signal transduction  domain:Flavodoxin-like  Flavodoxin/nitric oxide synthase  Flavodoxin	RT RT RT RT RT		7 3 3 7 4	4.9E-3 7.0E-2 7.5E-2 8.6E-2 1.0E-1 1.2E-1	3.8E0 6.2E0 6.0E0 2.2E0 3.4E0 3.1E0 3.1E0	8.4E-2 3.9E-1 3.9E-1 6.3E-1 1.0E0 6.1E-1 6.1E-1	8.0E 2 3.6E 1 3.4E 1 6.0E 1 9.7E 1 5.6E 1
	GOTERM_BP_DIRECT INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO INTERPRO GOTERM_MF_DIRECT	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain  nitric-oxide synthase activity  nitric oxide mediated signal transduction  domain:Flavodoxin-like  Flavodoxin/nitric oxide synthase	RT RT RT RT RT		7 3 3 7 4 4	4.9E-3 7.0E-2 7.5E-2 8.6E-2 1.0E-1 1.2E-1	3.8E0 6.2E0 6.0E0 2.2E0 3.4E0 3.1E0 3.1E0	8.4E-2 3.9E-1 3.9E-1 6.3E-1 1.0E0 6.1E-1	8.0E 2 3.6E 1 3.4E 1 6.0E 1 5.6E 1 5.6E 1
	GOTERM_BP_DIRECT INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO INTERPRO	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain  nitric-oxide synthase activity  nitric oxide mediated signal transduction  domain:Flavodoxin-like  Flavodoxin/nitric oxide synthase  Flavodoxin	RT RT RT RT RT RT RT RT		7 3 3 7 4 4	4.9E-3 7.0E-2 7.5E-2 8.6E-2 1.0E-1 1.2E-1	3.8E0 6.2E0 6.0E0 2.2E0 3.4E0 3.1E0 4.5E0	8.4E-2 3.9E-1 3.9E-1 6.3E-1 1.0E0 6.1E-1 6.1E-1	8.0E 2 3.6E 1 3.4E 1 6.0E 1 5.6E 1 5.6E 1
	GOTERM_BP_DIRECT INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO INTERPRO GOTERM_MF_DIRECT	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain  nitric-oxide synthase activity  nitric oxide mediated signal transduction  domain:Flavodoxin-like  Flavodoxin/nitric oxide synthase  Flavodoxin  tetrahydrobiopterin binding	RT RT RT RT RT RT RT RT		7 3 3 7 4 4 4 4	4.9E-3 7.0E-2 7.5E-2 8.6E-2 1.0E-1 1.2E-1 1.2E-1	3.8E0 6.2E0 6.0E0 2.2E0 3.4E0 3.1E0 4.5E0 1.6E0	8.4E-2 3.9E-1 3.9E-1 6.3E-1 1.0E0 6.1E-1 6.1E-1 5.8E-1	8.0E 2 3.6E 1 3.4E 1 6.0E 1 5.6E 1 5.6E 1 9.5E
	GOTERM_BP_DIRECT INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO INTERPRO GOTERM_MF_DIRECT GOTERM_MF_DIRECT	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain  nitric-oxide synthase activity  nitric oxide mediated signal transduction  domain:Flavodoxin-like  Flavodoxin/nitric oxide synthase  Flavodoxin  tetrahydrobiopterin binding  positive regulation of vasodilation  NADP binding  NADPH-cytochrome p450 reductase, FAD-	RT		7 3 3 7 4 4 4 3 8	4.9E-3 7.0E-2 7.5E-2 8.6E-2 1.0E-1 1.2E-1 1.3E-1 2.1E-1 2.2E-1	3.8E0 6.2E0 6.0E0 2.2E0 3.4E0 3.1E0 4.5E0 1.6E0 1.5E0	8.4E-2 3.9E-1 3.9E-1 6.3E-1 1.0E0 6.1E-1 5.8E-1 1.0E0 8.4E-1	8.0E 2 3.6E 1 3.4E 1 6.0E 1 5.6E 1 5.6E 1 7.5E 1 8.8E
	GOTERM_BP_DIRECT INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT INTERPRO	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain  nitric-oxide synthase activity  nitric oxide mediated signal transduction  domain:Flavodoxin-like  Flavodoxin/nitric oxide synthase  Flavodoxin  tetrahydrobiopterin binding  positive regulation of vasodilation  NADP binding  NADPH-cytochrome p450 reductase, FAD-binding, alpha-helical domain-3	RT		7 3 3 7 4 4 4 3 8 9	4.9E-3 7.0E-2 7.5E-2 8.6E-2 1.0E-1 1.2E-1 1.3E-1 2.1E-1 2.2E-1 2.5E-1	3.8E0 6.2E0 6.0E0 2.2E0 3.4E0 3.1E0 4.5E0 1.6E0 1.5E0 3.1E0	8.4E-2 3.9E-1 3.9E-1 6.3E-1 1.0E0 6.1E-1 5.8E-1 1.0E0 8.4E-1 9.6E-1	8.0E 2 3.6E 1 3.4E 1 6.0E 1 5.6E 1 5.6E 1 7.5E 1 8.8E 1
	GOTERM_BP_DIRECT INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT INTERPRO INTERPRO	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain  nitric-oxide synthase activity  nitric oxide mediated signal transduction  domain:Flavodoxin-like  Flavodoxin/nitric oxide synthase  Flavodoxin  tetrahydrobiopterin binding  positive regulation of vasodilation  NADP binding  NADPH-cytochrome p450 reductase, FAD-	RT		7 3 3 7 4 4 4 3 8	4.9E-3 7.0E-2 7.5E-2 8.6E-2 1.0E-1 1.2E-1 1.3E-1 2.1E-1 2.2E-1	3.8E0 6.2E0 6.0E0 2.2E0 3.4E0 3.1E0 4.5E0 1.6E0 1.5E0 3.1E0	8.4E-2 3.9E-1 3.9E-1 6.3E-1 1.0E0 6.1E-1 5.8E-1 1.0E0 8.4E-1	8.0E 2 3.6E 1 3.4E 1 6.0E 1 5.6E 1 5.6E 1 7.5E 1 8.8E 1
	GOTERM_BP_DIRECT INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT INTERPRO	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain  nitric-oxide synthase activity  nitric oxide mediated signal transduction  domain:Flavodoxin-like  Flavodoxin/nitric oxide synthase  Flavodoxin  tetrahydrobiopterin binding  positive regulation of vasodilation  NADP binding  NADPH-cytochrome p450 reductase, FAD-binding, alpha-helical domain-3	RT		7 3 3 7 4 4 4 3 8 9	4.9E-3 7.0E-2 7.5E-2 8.6E-2 1.0E-1 1.2E-1 1.3E-1 2.1E-1 2.2E-1 2.5E-1	3.8E0 6.2E0 6.0E0 2.2E0 3.4E0 3.1E0 4.5E0 1.6E0 1.5E0 3.1E0 3.1E0	8.4E-2 3.9E-1 3.9E-1 6.3E-1 1.0E0 6.1E-1 5.8E-1 1.0E0 8.4E-1 9.6E-1	8.06 2 3.66 1 3.46 1 6.06 1 5.66 1 5.66 1 7.56 1 8.86 1
	GOTERM_BP_DIRECT INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT INTERPRO INTERPRO	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain  nitric-oxide synthase activity  nitric oxide mediated signal transduction  domain:Flavodoxin-like  Flavodoxin/nitric oxide synthase  Flavodoxin  tetrahydrobiopterin binding  positive regulation of vasodilation  NADP binding  NADPH-cytochrome p450 reductase, FAD-binding, alpha-helical domain-3  FAD-binding, type 1	RT		7 3 3 7 4 4 4 3 8 9	4.9E-3 7.0E-2 7.5E-2 8.6E-2 1.0E-1 1.2E-1 1.3E-1 2.1E-1 2.2E-1 2.5E-1	3.8E0 6.2E0 6.0E0 2.2E0 3.4E0 3.1E0 4.5E0 1.6E0 1.5E0 3.1E0 2.1E0	8.4E-2 3.9E-1 3.9E-1 6.3E-1 1.0E0 6.1E-1 5.8E-1 1.0E0 8.4E-1 9.6E-1	8.06 2 3.66 1 3.46 1 6.06 1 5.66 1 5.26 1 7.56 1 7.56 1 8.86 1 8.86 1 9.77 1 8.86 1
	GOTERM_BP_DIRECT INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT INTERPRO INTERPRO INTERPRO UP_SEQ_FEATURE	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain  nitric-oxide synthase activity  nitric oxide mediated signal transduction  domain:Flavodoxin-like  Flavodoxin/nitric oxide synthase  Flavodoxin  tetrahydrobiopterin binding  positive regulation of vasodilation  NADP binding  NADPH-cytochrome p450 reductase, FAD-binding, alpha-helical domain-3  FAD-binding, type 1  nucleotide phosphate-binding region:FMN  Oxidoreductase FAD/NAD(P)-binding	RT R		7 3 3 7 4 4 4 3 8 9 3 3 4 4 4	4.9E-3 7.0E-2 7.5E-2 8.6E-2 1.0E-1 1.2E-1 1.3E-1 2.1E-1 2.5E-1 2.5E-1 3.0E-1 3.0E-1	3.8E0 6.2E0 6.0E0 2.2E0 3.4E0 3.1E0 4.5E0 1.6E0 1.5E0 3.1E0 2.1E0 2.1E0	8.4E-2 3.9E-1 3.9E-1 6.3E-1 1.0E0 6.1E-1 5.8E-1 1.0E0 8.4E-1 9.6E-1 1.0E0 9.8E-1	8.0E 2 3.6E 1 3.4E 1 6.0E 1 5.6E 1 5.6E 1 7.5E 1 8.8E 1 8.8E 1 9.7E 1 8.9E
	GOTERM_BP_DIRECT INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO INTERPRO GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO INTERPRO UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE INTERPRO GOTERM_MF_DIRECT	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain  nitric-oxide synthase activity  nitric oxide mediated signal transduction  domain:Flavodoxin-like  Flavodoxin/nitric oxide synthase  Flavodoxin  tetrahydrobiopterin binding  positive regulation of vasodilation  NADP binding  NADPH-cytochrome p450 reductase, FAD-binding, alpha-helical domain-3  FAD-binding, type 1  nucleotide phosphate-binding region:FMN  Oxidoreductase FAD/NAD(P)-binding  arginine binding	RT R		7 3 3 7 4 4 4 3 8 9 3 3 3	4.9E-3 7.0E-2 7.5E-2 8.6E-2 1.0E-1 1.2E-1 1.3E-1 2.1E-1 2.5E-1 2.5E-1 3.0E-1 3.0E-1 3.3E-1	3.8E0 6.2E0 6.0E0 2.2E0 3.4E0 3.1E0 4.5E0 1.6E0 1.5E0 3.1E0 2.1E0 2.1E0 2.6E0	8.4E-2 3.9E-1 3.9E-1 6.3E-1 1.0E0 6.1E-1 5.8E-1 1.0E0 8.4E-1 9.6E-1 1.0E0 9.8E-1 1.0E0	8.06 2 3.66 1 3.46 1 6.06 1 5.66 1 5.66 1 7.56 1 8.86 1 8.86 1 8.86 1 8.86 1 8.86 1 8.86 1
	GOTERM_BP_DIRECT INTERPRO  GOTERM_MF_DIRECT  GOTERM_BP_DIRECT  UP_SEQ_FEATURE INTERPRO INTERPRO GOTERM_MF_DIRECT  GOTERM_MF_DIRECT  INTERPRO INTERPRO UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE INTERPRO GOTERM_MF_DIRECT INTERPRO UP_SEQ_FEATURE INTERPRO GOTERM_MF_DIRECT GOTERM_MF_DIRECT	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain  nitric-oxide synthase activity  nitric oxide mediated signal transduction  domain:Flavodoxin-like  Flavodoxin/nitric oxide synthase  Flavodoxin  tetrahydrobiopterin binding  positive regulation of vasodilation  NADP binding  NADPH-cytochrome p450 reductase, FAD-binding, alpha-helical domain-3  FAD-binding, type 1  nucleotide phosphate-binding region:FMN  Oxidoreductase FAD/NAD(P)-binding	RT R		7 3 3 7 4 4 4 3 8 9 3 3 4 4 4	4.9E-3 7.0E-2 7.5E-2 8.6E-2 1.0E-1 1.2E-1 1.3E-1 2.1E-1 2.5E-1 2.5E-1 3.0E-1 3.0E-1	3.8E0 6.2E0 6.0E0 2.2E0 3.4E0 3.1E0 4.5E0 1.6E0 1.5E0 3.1E0 2.1E0 2.1E0 2.6E0	8.4E-2 3.9E-1 3.9E-1 6.3E-1 1.0E0 6.1E-1 5.8E-1 1.0E0 8.4E-1 9.6E-1 1.0E0 9.8E-1	8.06 2 3.66 1 3.46 1 6.06 1 5.66 1 5.66 1 7.56 1 8.86 1 8.86 1 9.76 1 8.86 1 8.96 1 9.76 1
	GOTERM_BP_DIRECT INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT UP_SEQ_FEATURE INTERPRO INTERPRO GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO INTERPRO UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE INTERPRO GOTERM_MF_DIRECT	positive regulation of guanylate cyclase activity  Nitric oxide synthase, oxygenase domain  nitric-oxide synthase activity  nitric oxide mediated signal transduction  domain:Flavodoxin-like  Flavodoxin/nitric oxide synthase  Flavodoxin  tetrahydrobiopterin binding  positive regulation of vasodilation  NADP binding  NADPH-cytochrome p450 reductase, FAD-binding, alpha-helical domain-3  FAD-binding, type 1  nucleotide phosphate-binding region:FMN  Oxidoreductase FAD/NAD(P)-binding  arginine binding	RT R		7 3 3 7 4 4 4 3 8 9 3 3 4 4 4 3	4.9E-3 7.0E-2 7.5E-2 8.6E-2 1.0E-1 1.2E-1 1.3E-1 2.1E-1 2.5E-1 2.5E-1 3.0E-1 3.0E-1 3.3E-1	3.8E0 6.2E0 6.0E0 2.2E0 3.4E0 3.1E0 4.5E0 1.6E0 1.5E0 3.1E0 2.1E0 2.1E0 2.6E0 1.8E0	8.4E-2 3.9E-1 3.9E-1 6.3E-1 1.0E0 6.1E-1 5.8E-1 1.0E0 8.4E-1 9.6E-1 1.0E0 9.8E-1 1.0E0	8.06 2 3.66 1 3.46 1 6.06 1 5.66 1 5.66 1 7.56 1 8.86 1 8.86 1 8.86 1 8.86 1 8.86 1 8.86 1 8.86 1 1 8.86 1 1 8.86 1 1 8.86 1 1 8.86 1 1 8.86 1 1 8.86 1 8 1 8 1 8 1 8 1 8 1 8 1 8 1 8 1 8 1

An	nnotation Cluster 1	Enrichment Score: ?	G	<u> </u>	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_MF_DIRECT	FMN binding	<u>RT</u>	i	4	4.7E-1	1.6E0	1.0E0	8.9E- 1
	UP_SEQ_FEATURE	domain:FAD-binding FR-type	<u>RT</u>	i	4	5.4E-1	1.4E0	1.0E0	9.7E-
	KEGG_PATHWAY	Arginine biosynthesis	<u>RT</u>	1	5	5.5E-1	1.3E0	8.1E-1	5.5E-
	UP_KEYWORDS	<u>FMN</u>	<u>RT</u>	•	4	6.1E-1	1.3E0	1.0E0	7.8E-
	INTERPRO	Ferredoxin reductase-type FAD-binding	RT		4	6.1E-1		1.0E0	1 9.1E-
	INTERPRO	domain  Riboflavin synthase-like beta-barrel	RT		4	6.1E-1		1.0E0	1 9.1E-
	GOTERM_BP_DIRECT								1 9.5E-
	UP_SEQ_FEATURE	negative regulation of blood pressure	<u>RT</u>		4		7.9E-1		1 9.7E-
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:FAD	<u>RT</u>		7		7.7E-1		1 9.7E-
	) – –	nucleotide phosphate-binding region:NADP	<u>RT</u>	•	8	9.3E-1	7.4E-1	1.0E0	1
	UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	<u>RT</u>	i	8		5.5E-1		9.9E- 1
		Inorganic ion transport and metabolism flavin adenine dinucleotide binding	RT RT		6 5	1.0E0 1.0E0	5.6E-1 4.7E-1		1.0E0 1.0E0
	GOTERM_MF_DIRECT	heme binding	<u>RT</u>	1	13	1.0E0	5.7E-1		1.0E0
	KEGG_PATHWAY UP_KEYWORDS	Arginine and proline metabolism  Heme	RT RT		4 9	1.0E0 1.0E0	4.2E-1 4.7E-1		1.0E0 1.0E0
	UP_KEYWORDS	FAD	RT	i	6	1.0E0	3.7E-1		1.0E0
	UP_KEYWORDS UP_KEYWORDS	Flavoprotein	RT DT		6	1.0E0	3.4E-1		1.0E0
An	nnotation Cluster 274	NADP Enrichment Score: 0.45	RT G		10 Count	1.0E0 P_Value	3.7E-1 Fold	Benjamini	1.0E0
	GOTERM_CC_DIRECT			-			Change		3.5E-
	GOTERM_CC_DIRECT	RISC complex	<u>RT</u>		5	8.0E-2		4.0E-1	1 7.6E-
	,	RISC-loading complex	<u>RT</u>	•	3	3.0E-1	2.7E0	8.7E-1	1
	GOTERM_BP_DIRECT	miRNA loading onto RISC involved in gene silencing by miRNA	<u>RT</u>	i	3	3.4E-1	2.5E0	1.0E0	9.5E- 1
	GOTERM_BP_DIRECT	<u>pre-miRNA processing</u>	<u>RT</u>	i	4	3.8E-1	1.8E0	1.0E0	9.5E- 1
	GOTERM_BP_DIRECT	<u>production of miRNAs involved in gene</u> <u>silencing by miRNA</u>	<u>RT</u>	i	3	4.0E-1	2.2E0	1.0E0	9.5E- 1
	UP_SEQ_FEATURE	domain:PAZ	<u>RT</u>	i .	3	4.4E-1	2.0E0	1.0E0	9.7E- 1
	INTERPRO	Argonaute/Dicer protein, PAZ	<u>RT</u>	i	3	5.0E-1	1.9E0	1.0E0	9.1E- 1
	BIOCARTA	<u>Dicer Pathway</u>	<u>RT</u>	i	3	5.2E-1	1.9E0	8.1E-1	5.5E- 1
	SMART	SM00949	<u>RT</u>	i	3	6.9E-1	1.4E0	1.0E0	9.0E- 1
An	nnotation Cluster 275	Enrichment Score: 0.43	G	To the second se	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	social behavior	<u>RT</u>	i .	12	1.7E-1	1.5E0	9.7E-1	9.3E- 1
	GOTERM_BP_DIRECT	positive regulation of excitatory postsynaptic potential	<u>RT</u>	i	5	4.4E-1	1.5E0	1.0E0	9.5E- 1
	GOTERM_BP_DIRECT	adult behavior	<u>RT</u>	i	5	6.6E-1	1.1E0	1.0E0	9.5E- 1
An	nnotation Cluster 276	Enrichment Score: 0.43	G	<b>*</b>	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	MIF4G-like, type 3	<u>RT</u>	i	4	2.1E-1		9.5E-1	8.7E- 1
	UP_SEQ_FEATURE	domain:MIF4G	<u>RT</u>	•	3	4.4E-1	2.0E0	1.0E0	9.7E-
	INTERPRO	MIF4-like, type 1/2/3	RT		4	4.4E-1	1.7E0	1.0E0	9.1E-
	SMART	MIF4G	RT		4	4.6E-1		1.0E0	1 9.0E-
An	nnotation Cluster 277	Enrichment Score: 0.43	G	•	Count	P_Value	Fold	Benjamini	1 EDB
All	GOTERM_MF_DIRECT	cysteine-type endopeptidase inhibitor activity		-			Change		6.4E-
	INTERPRO	involved in apoptotic process	<u>RT</u>	•	7	1.8E-1	1.8E0	7.2E-1	1 9.1E-
		Baculoviral inhibition of apoptosis protein repeat	<u>RT</u>	i	3	3.8E-1	2.3E0	1.0E0	1
	GOTERM_BP_DIRECT	inhibition of cysteine-type endopeptidase activity involved in apoptotic process	<u>RT</u>	i	3	4.6E-1	2.0E0	1.0E0	9.5E- 1
	SMART	BIR	<u>RT</u>	i	3	6.2E-1	1.5E0	1.0E0	9.0E- 1
An	nnotation Cluster 278	Enrichment Score: 0.43	G	<b>17</b>	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 5	<u>RT</u>	i	3	2.7E-1		1.0E0	9.7E- 1
	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 1	<u>RT</u>	1	5	3.7E-1	1.6E0	1.0E0	9.7E-
	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 2	<u>RT</u>	i	5	3.7E-1	1.6E0	1.0E0	9.7E-
	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 4	RT	1	3	3.9E-1	2.3E0	1.0E0	9.7E-
	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 3	RT		3	5.0E-1		1.0E0	1 9.7E-
An	nnotation Cluster 279	Enrichment Score: 0.42	G	•		P_Value	Fold	Daniamini.	1 FDR
				•			Change		

	GOTERM_MF_DIRECT	calcium-transporting ATPase activity					Change		
	NTERPRO		<u>RT</u>	i	5	4.9E-2	3.3E0	2.9E-1	2.6E-
		<u>Calcium-transporting P-type ATPase,</u>	RT		3	7.0E-2		3.9E-1	1 3.6E-
	UP_SEQ_FEATURE	<pre>subfamily IIA, SERCA-type metal ion-binding site:Calcium 2; via carbonyl</pre>							1 9.7E-
	GOTERM_CC_DIRECT	oxygen	<u>RT</u>	•	9	2.0E-1		1.0E0	1 7.4E-
		sarcoplasmic reticulum	<u>RT</u>		8	2.8E-1		8.4E-1	1
	GOTERM_CC_DIRECT	sarcoplasmic reticulum membrane	<u>RT</u>	•	8	2.8E-1	1.5E0	8.4E-1	7.4E- 1
	GOTERM_CC_DIRECT	<u>platelet dense tubular network membrane</u>	<u>RT</u>	i	3	4.3E-1	2.1E0	1.0E0	8.7E- 1
	UP_SEQ_FEATURE	metal ion-binding site:Calcium 2	<u>RT</u>	i .	10	4.6E-1	1.2E0	1.0E0	9.7E- 1
_ \	UP_KEYWORDS	Sarcoplasmic reticulum	<u>RT</u>	i	7	5.4E-1	1.2E0	1.0E0	7.8E- 1
_ ·	UP_SEQ_FEATURE	metal ion-binding site:Calcium 1	<u>RT</u>	i .	8	5.5E-1	1.2E0	1.0E0	9.7E- 1
_ ·	GOTERM_BP_DIRECT	cellular calcium ion homeostasis	<u>RT</u>	•	11	9.6E-1	7.0E-1	1.0E0	9.6E-
	GOTERM_BP_DIRECT	calcium ion transport	<u>RT</u>	1	7	9.9E-1	5.5E-1	1.0E0	9.9E-
	GOTERM_BP_DIRECT	calcium ion transmembrane transport	RT	•	10	1.0E0	5.0E-1		1 1.0E0
\	UP_KEYWORDS	<u>Calcium transport</u>	<u>RT</u>	i	5	1.0E0	3.5E-1 Fold	1.0E0	1.0E0
	ion Cluster 280	Enrichment Score: 0.39	G		Count	P_Value	Change	Benjamini	
	UP_KEYWORDS	Postsynaptic cell membrane	<u>RT</u>	•	34	8.8E-2	1.3E0	3.0E-1	2.3E- 1
	GOTERM_CC_DIRECT	<u>postsynaptic membrane</u>	<u>RT</u>	•	39	2.0E-1	1.2E0	7.6E-1	6.6E- 1
	GOTERM_CC_DIRECT	postsynaptic density	<u>RT</u>	Ē	33	3.0E-1	1.1E0	8.6E-1	7.5E- 1
	UP_KEYWORDS	<u>Synapse</u>	<u>RT</u>	i e	47	8.4E-1	9.0E-1	1.0E0	8.4E- 1
	GOTERM_CC_DIRECT	cell junction	<u>RT</u>	•	58	9.8E-1	8.0E-1	1.0E0	9.8E-
_ ·	UP_KEYWORDS	<u>Cell junction</u>	<u>RT</u>	•	81	9.8E-1	8.2E-1	1.0E0	9.8E-
Annotati	ion Cluster 281	Enrichment Score: 0.39	G		Count	P_Value	Fold	Benjamini	1 FDR
	NTERPRO	Sirtuin family, catalytic core small domain	RT		3	2.5E-1	Change	9.6E-1	8.8E-
	UP_SEQ_FEATURE								1 9.7E-
	INTERPRO	domain:Deacetylase sirtuin-type	<u>RT</u>		3	2.7E-1		1.0E0	1 9.1E-
	NTERPRO	<u>Sirtuin family</u>	<u>RT</u>	•	3	3.2E-1	2.7E0	1.0E0	1
		<u>Sirtuin family, catalytic core domain</u>	<u>RT</u>	i	3	3.2E-1	2.7E0	1.0E0	9.1E- 1
	GOTERM_MF_DIRECT	NAD+ binding	<u>RT</u>	i	3	6.7E-1	1.4E0	1.0E0	8.9E- 1
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:NAD	<u>RT</u>	i	7	9.8E-1	6.0E-1	1.0E0	9.8E- 1
Annotati	ion Cluster 282	Enrichment Score: 0.39	G	Marie Control of the	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	protein ADP-ribosylation	<u>RT</u>	i	7	1.3E-1	2.0E0	8.1E-1	7.7E- 1
	GOTERM_BP_DIRECT	negative regulation of telomere maintenance via telomere lengthening	<u>RT</u>	i .	3	2.0E-1	3.6E0	1.0E0	9.5E- 1
	GOTERM_MF_DIRECT	NAD+ ADP-ribosyltransferase activity	<u>RT</u>	i e	7	3.2E-1	1.5E0	1.0E0	8.9E-
	UP_SEQ_FEATURE	domain:PARP catalytic	<u>RT</u>	1	3	7.4E-1	1.2E0	1.0E0	9.7E-
	NTERPRO	Poly(ADP-ribose) polymerase, catalytic	RT		3	7.9E-1		1.0E0	1 9.1E-
	UP_KEYWORDS	domain Glycosyltransferase	RT		5	1.0E0	1.5E-1		1 1.0E0
Annotati	ion Cluster 283	Enrichment Score: 0.37	G	F8	Count	P_Value	Fold Change	Benjamini	FDR
	UP_KEYWORDS	Bernard Soulier syndrome	<u>RT</u>	1	3	5.7E-2		2.1E-1	1.6E- 1
_ (	GOTERM_BP_DIRECT	blood coagulation, intrinsic pathway	<u>RT</u>	i	5	3.6E-1	1.6E0	1.0E0	9.5E- 1
n t	UP_KEYWORDS	Blood coagulation	RT		6	8.5E-1	8.6E-1	1.0E0	8.5E-
	UP_KEYWORDS	Hemostasis	RT		6		8.6E-1		1 8.5E-
	KEGG_PATHWAY	ECM-receptor interaction	RT		6	1.0E0	3.6E-1		1 1.0E0
	ion Cluster 284	Enrichment Score: 0.36	G	T		P_Value		Benjamini	
	UP_SEQ_FEATURE	repeat:HEAT 9	<u>RT</u>	1	5	1.7E-1		1.0E0	9.7E-
- L	UP_SEQ_FEATURE	repeat:HEAT 10	RT		5	1.7E-1		1.0E0	9.7E-
	UP_SEQ_FEATURE								1 9.7E-
	UP_SEQ_FEATURE	repeat:HEAT 7	<u>RT</u>	i	6	2.7E-1		1.0E0	1 9.7E-
		repeat:HEAT 8	<u>RT</u>	i	5	3.0E-1		1.0E0	1
	INTERPRO	HEAT, type 2	<u>RT</u>	i	5	3.7E-1	1.6E0	1.0E0	9.1E- 1
	UP_SEQ_FEATURE	repeat:HEAT 6	<u>RT</u>	i	6	4.6E-1	1.4E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:HEAT 11	<u>RT</u>	i de la companya de	3	5.0E-1	1.9E0	1.0E0	9.7E- 1

Annot	ation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold	Benjamini	FDR
	UP_SEQ_FEATURE	repeat:HEAT 5	RT		6	6.0E-1	Change	1.0E0	9.7E-
	UP_SEQ_FEATURE	repeat:HEAT 1	RT		8		9.4E-1		1 9.7E-
	UP_SEQ_FEATURE			•					1 9.7E-
	UP_SEQ_FEATURE	repeat:HEAT 2	<u>RT</u>		8		9.4E-1		1 9.7E-
	UP_SEQ_FEATURE	repeat:HEAT 4	<u>RT</u>		6		9.5E-1		1 9.7E-
	OI_OEQ_IENIONE	repeat:HEAT 3	<u>RT</u>	i	6	1	8.2E-1		1
Annot	ation Cluster 285  UP_SEQ_FEATURE	Enrichment Score: 0.36	G		Count	P_Value	Change	•	
		region of interest:Interaction with KCND2	<u>RT</u>	i	4	1.1E-2	6.8E0	2.3E-1	2.2E- 1
	UP_SEQ_FEATURE	domain:EF-hand 1; degenerate	<u>RT</u>	i	4	1.1E-2	6.8E0	2.3E-1	2.2E- 1
	GOTERM_BP_DIRECT	regulation of potassium ion transmembrane transport	<u>RT</u>	i	4	4.8E-1	1.6E0	1.0E0	9.5E- 1
	GOTERM_BP_DIRECT	cardiac conduction	<u>RT</u>	i	5	9.6E-1	6.6E-1	1.0E0	9.6E- 1
	GOTERM_MF_DIRECT	voltage-gated ion channel activity	<u>RT</u>	i .	3	9.8E-1	5.6E-1	1.0E0	9.8E- 1
	UP_KEYWORDS	<u>Potassium</u>	<u>RT</u>	i .	12	9.9E-1	6.4E-1	1.0E0	9.9E- 1
	GOTERM_CC_DIRECT	voltage-gated potassium channel complex	<u>RT</u>	i .	8	9.9E-1	5.8E-1	1.0E0	9.9E- 1
	GOTERM_MF_DIRECT	potassium channel activity	<u>RT</u>	i .	3	9.9E-1	4.8E-1	1.0E0	9.9E- 1
	UP_KEYWORDS	Potassium transport	<u>RT</u>	i .	10	9.9E-1	5.9E-1	1.0E0	9.9E-
	UP_KEYWORDS	Potassium channel	<u>RT</u>		4	1.0E0	3.7E-1		1.0E0
	GOTERM_BP_DIRECT UP_KEYWORDS	<u>potassium ion transmembrane transport</u> <u>Voltage-gated channel</u>	RT RT		5 4	1.0E0 1.0E0	2.5E-1 1.8E-1		1.0E0 1.0E0
Annot	ation Cluster 286	Enrichment Score: 0.32	G	<b>**</b>	Count	P_Value		Danismini	
	INTERPRO	RWD domain	<u>RT</u>	i	4	3.0E-1	•	9.8E-1	8.9E- 1
	UP_SEQ_FEATURE	domain:RWD	<u>RT</u>	i	3	5.0E-1	1.9E0	1.0E0	9.7E-
	SMART	<u>RWD</u>	<u>RT</u>	i	3	7.4E-1	1.2E0	1.0E0	9.0E-
Annot	ation Cluster 287	Enrichment Score: 0.28	G	·	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	Exportin-1/Importin-beta-like	RT	i	3	2.5E-1		9.6E-1	8.8E-
	INTERPRO	<u>Importin-beta, N-terminal</u>	<u>RT</u>	:	4	5.3E-1	1.5E0	1.0E0	9.1E-
	GOTERM_MF_DIRECT	Ran GTPase binding	RT		6	5.8E-1		1.0E0	1 8.9E-
	UP_SEQ_FEATURE	domain:Importin N-terminal	RT		3	6.3E-1		1.0E0	1 9.7E-
	SMART								1 9.0E-
		SM00913	<u>RT</u>		4	7.9E-1	Fold	1.0E0	1
Annot	ation Cluster 288  UP_SEQ_FEATURE	Enrichment Score: 0.27	G	-	Count	P_Value	Change	Benjamini	9.7E-
	UP_SEQ_FEATURE	short sequence motif:"KMSKS" region	<u>RT</u>	1	5	2.0E-1		1.0E0	1 9.7E-
	GOTERM_MF_DIRECT	short sequence motif:"HIGH" region	<u>RT</u>	i	5	2.7E-1	1.9E0	1.0E0	1 8.7E-
		aminoacyl-tRNA ligase activity	<u>RT</u>	i	5	3.2E-1	1.8E0	9.8E-1	1
	INTERPRO	Aminoacyl-tRNA synthetase, class I, conserved site	<u>RT</u>	i	4	4.4E-1	1.7E0	1.0E0	9.1E- 1
	INTERPRO	Glutathione S-transferase, C-terminal	<u>RT</u>	i	5	5.2E-1	1.3E0	1.0E0	9.1E- 1
	INTERPRO	Rossmann-like alpha/beta/alpha sandwich fold	<u>RT</u>	i	8	5.3E-1	1.2E0	1.0E0	9.1E- 1
	INTERPRO	<u>Aminoacyl-tRNA synthetase, class 1a,</u> <u>anticodon-binding</u>	<u>RT</u>	i	3	6.4E-1	1.4E0	1.0E0	9.1E- 1
	UP_KEYWORDS	Aminoacyl-tRNA synthetase	<u>RT</u>	i	6	6.7E-1	1.1E0	1.0E0	7.8E- 1
	GOTERM_BP_DIRECT	tRNA aminoacylation for protein translation	<u>RT</u>	i .	7	6.9E-1	1.0E0	1.0E0	9.5E- 1
	INTERPRO	Glutathione S-transferase, C-terminal-like	<u>RT</u>	i .	5	9.2E-1	7.6E-1	1.0E0	9.2E- 1
	UP_SEQ_FEATURE	domain:GST C-terminal	<u>RT</u>	i .	4	9.2E-1	7.4E-1	1.0E0	9.7E-
	KEGG_PATHWAY	Aminoacyl-tRNA biosynthesis	<u>RT</u>	i	6	1.0E0	4.8E-1	1.0E0	1.0E0
Annot	ration Cluster 289	Enrichment Score: 0.25	G	<b>**</b>	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	domain:CARD	<u>RT</u>	i	6	4.2E-1	1.4E0	1.0E0	9.7E- 1
	INTERPRO	<u>Caspase Recruitment</u>	<u>RT</u>	i	6	5.1E-1	1.3E0	1.0E0	9.1E- 1
	BIOCARTA	Caspase Cascade in Apoptosis	<u>RT</u>	i	9	5.4E-1	1.2E0	8.3E-1	5.6E- 1
	SMART	CARD	<u>RT</u>	i	3	8.3E-1	1.0E0	1.0E0	9.0E- 1
Annot		CARD Enrichment Score: 0.25	RT G	i 📆		8.3E-1 P_Value	Fold	Daniamini	1
Annot	SMART					1	Fold Change	Daniamini	1

	tation Cluster 1	Enrichment Score: ?	G	- <del></del>	Count	P_Value	Fold Change	Benjamin	ni FD
	INTERPRO	Immunoglobulin subtype 2	<u>RT</u>	-	41	5.5E-1	1.0E0	1.0E0	9.1
<b>-</b>	UP_SEQ_FEATURE	damain Ia lila C2 tura 2	D.T.	_	17	7.05.1	0.05.1	1.050	9.7
J		domain:Ig-like C2-type 3	<u>RT</u>	•	17	7.9E-1	9.0E-1	1.0E0	1
	UP_SEQ_FEATURE	domain:Ig-like C2-type 1	<u>RT</u>	•	23	9.5E-1	7.8E-1	1.0E0	9.7 1
	UP_SEQ_FEATURE	domain:Ig-like C2-type 2	RT	4	23	9.6E-1	7.7E-1	1.0E0	9.7
	SMART	IGc2	RT		41	1.0E0	6.7E-1	1.0E0	1.0
	UP_KEYWORDS	<u>Immunoglobulin domain</u>	RT		47	1.0E0	5.9E-1		1.0
	INTERPRO	<u>Immunoglobulin subtype</u>	<u>RT</u>	•	45	1.0E0	5.6E-1	1.0E0	1.0
	INTERPRO	Immunoglobulin-like fold	<u>RT</u>	•	82	1.0E0	5.3E-1		1.0
ا ا	SMART INTERPRO	<u>IG</u> <u>Immunoglobulin-like domain</u>	RT RT		45 49	1.0E0 1.0E0	3.7E-1 3.9E-1		1.0
nnot	tation Cluster 291	Enrichment Score: 0.23	G		Count	P_Value	Fold	Ronjamin	
	UP_KEYWORDS						Change		5.3
J	_	<u>Vision</u>	<u>RT</u>	•	21	2.3E-1	1.3E0	6.8E-1	1
	GOTERM_BP_DIRECT	visual perception	<u>RT</u>	1	29	8.9E-1	8.6E-1	1.0E0	9.5 1
	UP_KEYWORDS	Sensory transduction	<u>RT</u>	1	23	1.0E0	2.6E-1	1.0E0	1.0
not	tation Cluster 292	Enrichment Score: 0.23		<b>100</b>	Count	P_Value	Fold Change	Benjamin	ni FD
)	UP_SEQ_FEATURE	region of interest:Heparin-binding	RT	4	5	3.4E-1		1.0E0	9.7
,	COTERM PR DIRECT	region of interest. Trepariti binding	KI	•	J	J.4L 1	1.720	1.020	1
	GOTERM_BP_DIRECT	organ induction	<u>RT</u>	1	3	6.3E-1	1.5E0	1.0E0	9.! 1
	UP_KEYWORDS	<u>Heparin-binding</u>	<u>RT</u>	1	8	9.8E-1	6.2E-1	1.0E0	9.8 1
not	tation Cluster 202	Enrichment Score: 0.23	G	<b>178</b>	Count	D. Volue	Fold	Panjamir	
not	tation Cluster 293	Enrichment Score: 0.23	U	<u> </u>	Count	P_Value	Change	Benjamin	_
	GOTERM_MF_DIRECT	<u>protein-hormone receptor activity</u>	<u>RT</u>	i	3	7.5E-2	6.0E0	3.9E-1	3. 1
	INTERPRO	GPCR, rhodopsin-like, 7TM	<u>RT</u>	1	7	1.0E0	5.9E-2	1.0E0	1.
	GOTERM_MF_DIRECT	G-protein coupled receptor activity	<u>RT</u>		10	1.0E0	8.4E-2		1.
	INTERPRO UP_KEYWORDS	<u>G protein-coupled receptor, rhodopsin-like</u> <u>G-protein coupled receptor</u>	RT RT		7 11	1.0E0 1.0E0	6.0E-2 9.0E-2		1.
not	tation Cluster 294	Enrichment Score: 0.22	G		Count		Fold	Benjamin	
not	INTERPRO	Enrichment Score. 0.22	U	<u> </u>	Count	P_Value	Change	Бепјаппп	
	INTERPRO	Cyclic nucleotide-binding, conserved site	<u>RT</u>	i	5	2.5E-1	1.9E0	9.6E-1	8. 1
	INTERPRO	Cyclic nucleotide-binding domain	<u>RT</u>	1	7	5.1E-1	1.2E0	1.0E0	9. 1
	INTERPRO	Codia condentida bindia a liba		-	7	F 0F 1	1 150	1.050	9.
		Cyclic nucleotide-binding-like	<u>RT</u>	•	7	5.9E-1	1.1E0	1.0E0	1
	UP_KEYWORDS	<u>cAMP-binding</u>	<u>RT</u>	1	3	7.3E-1	1.2E0	1.0E0	7. 1
	INTERPRO	RmlC-like jelly roll fold	<u>RT</u>	4	7	7.9E-1	9.2E-1	1.0E0	9.
	GOTERM_MF_DIRECT								1 8.
	0012KM_M _DIKE01	<u>cAMP binding</u>	<u>RT</u>	1	4	7.9E-1	9.9E-1	1.0E0	1
	SMART	<u>cNMP</u>	<u>RT</u>	1	7	8.1E-1	9.2E-1	1.0E0	9. 1
		Enrichment Score: 0.22	G	<b>178</b>	Count	P_Value	Fold	Benjamin	
not	tation Cluster 295						Change		9.
not				_	_	4.0=.4		1.0E0	
not	UP_SEQ_FEATURE	domain:SAP	<u>RT</u>	i	5	4.8E-1	1.4E0		1
not		domain:SAP  SAP domain	RT RT	i i	5	4.8E-1 5.6E-1		1.0E0	9. 1
not	UP_SEQ_FEATURE	SAP domain	<u>RT</u>	1	5	5.6E-1	1.3E0	1.0E0	1
	UP_SEQ_FEATURE INTERPRO SMART	SAP domain SAP	RT RT	i i	5 5	5.6E-1 8.5E-1	1.3E0 8.9E-1	1.0E0 1.0E0	1 9. 1
	UP_SEQ_FEATURE INTERPRO	SAP domain	<u>RT</u>	1	5	5.6E-1	1.3E0 8.9E-1	1.0E0 1.0E0	1 9. 1
	UP_SEQ_FEATURE INTERPRO SMART	SAP domain  SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic	RT RT	i i	5 5	5.6E-1 8.5E-1	1.3E0 8.9E-1 Fold Change	1.0E0 1.0E0	1 9. 1 1i Fl
	UP_SEQ_FEATURE INTERPRO SMART tation Cluster 296	SAP domain  SAP  Enrichment Score: 0.21	RT RT G	i i	5 5 <b>Count</b> 6	5.6E-1 8.5E-1 P_Value 1.6E-2	1.3E0 8.9E-1 Fold Change 3.6E0	1.0E0 1.0E0 Benjamin 2.2E-1	1 9. 1 <b>FI</b> 2.
	UP_SEQ_FEATURE INTERPRO SMART  tation Cluster 296 GOTERM_BP_DIRECT GOTERM_BP_DIRECT	SAP domain  SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process	RT RT G	i i	5 5 Count	5.6E-1 8.5E-1 P_Value	1.3E0 8.9E-1 Fold Change 3.6E0	1.0E0 1.0E0 Benjamin	1 9. 1 <b>FI</b> 2. 1 5.
	UP_SEQ_FEATURE  INTERPRO  SMART  tation Cluster 296  GOTERM_BP_DIRECT	SAP domain  SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process positive regulation of calcidiol 1-	RT RT G	i i	5 5 <b>Count</b> 6	5.6E-1 8.5E-1 P_Value 1.6E-2	1.3E0 8.9E-1 Fold Change 3.6E0 5.9E0	1.0E0 1.0E0 Benjamin 2.2E-1	9. 1 1 2. 1 5.
	UP_SEQ_FEATURE INTERPRO SMART  tation Cluster 296 GOTERM_BP_DIRECT GOTERM_BP_DIRECT	SAP domain  SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process positive regulation of calcidiol 1- monooxygenase activity	RT RT G RT RT	i i	5 5 Count 6 3	5.6E-1 8.5E-1 P_Value 1.6E-2 7.6E-2	1.3E0 8.9E-1 Fold Change 3.6E0 5.9E0 1.9E0	1.0E0 1.0E0 Benjamin 2.2E-1 5.7E-1	1 9. 1 2. 1 5. 1 9.
	UP_SEQ_FEATURE INTERPRO SMART  tation Cluster 296 GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT BBID BBID	SAP domain  SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process positive regulation of calcidiol 1-monooxygenase activity  defense response to protozoan  111.Stress influences immunity 112.StressandCRHinfluence	RT RT RT RT RT RT	i i	5 5 <b>Count</b> 6 3 6	5.6E-1 8.5E-1 P_Value 1.6E-2 7.6E-2 2.1E-1	1.3E0 8.9E-1 Fold Change 3.6E0 5.9E0 1.9E0	1.0E0 1.0E0 Benjamin 2.2E-1 5.7E-1 1.0E0	1 9. 1 FI FI 2. 1 5. 1 9. 1 1. 1.
	UP_SEQ_FEATURE INTERPRO SMART  tation Cluster 296 GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT BBID	SAP domain  SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process positive regulation of calcidiol 1-monooxygenase activity defense response to protozoan  111.Stress influences immunity	RT RT RT RT RT RT	i i	5 5 Count 6 3 6 4	5.6E-1 8.5E-1 P_Value 1.6E-2 7.6E-2 2.1E-1 3.4E-1	1.3E0 8.9E-1 Fold Change 3.6E0 5.9E0 1.9E0 1.9E0 1.9E0	1.0E0 1.0E0 Benjamin 2.2E-1 5.7E-1 1.0E0 1.0E0	1 9. 1 FI FI 2. 1 5. 1 9. 1 1. 1.
	UP_SEQ_FEATURE INTERPRO SMART  tation Cluster 296 GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT BBID BBID BBID GOTERM_BP_DIRECT BBID	SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process positive regulation of calcidiol 1-monooxygenase activity  defense response to protozoan  111.Stress influences immunity 112.StressandCRHinfluence positive regulation of isotype switching to IgG isotypes 20.Cytokine oligodendrocytes	RT	i i	5 5 Count 6 3 6 4 4	5.6E-1 8.5E-1 P_Value 1.6E-2 7.6E-2 2.1E-1 3.4E-1 4.0E-1 4.2E-1	1.3E0 8.9E-1 Fold Change 3.6E0 5.9E0 1.9E0 1.9E0 1.9E0 2.2E0	1.0E0 1.0E0  Benjamin 2.2E-1 5.7E-1 1.0E0 1.0E0 1.0E0	1 9. 1 FI FI 1. 1. 9. 1
	UP_SEQ_FEATURE INTERPRO SMART  tation Cluster 296 GOTERM_BP_DIRECT GOTERM_BP_DIRECT BBID BBID GOTERM_BP_DIRECT BBID BBID BBID BBID BBID BBID BBID	SAP domain  SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process positive regulation of calcidiol 1-monooxygenase activity defense response to protozoan  111.Stress influences immunity 112.StressandCRHinfluence positive regulation of isotype switching to IgG isotypes	RT	i i	5 5 Count 6 3 6 4 4 4 3	5.6E-1 8.5E-1 P_Value 1.6E-2 7.6E-2 2.1E-1 3.4E-1 3.4E-1 4.0E-1	1.3E0 8.9E-1 Fold Change 3.6E0 5.9E0 1.9E0 1.9E0 1.9E0 2.2E0	1.0E0 1.0E0  Benjamin 2.2E-1 5.7E-1 1.0E0 1.0E0 1.0E0 1.0E0	1 9. 1 FI FI 2. 1 5. 1 9. 1 1. 1. 1. 1.
	UP_SEQ_FEATURE INTERPRO SMART  tation Cluster 296 GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT BBID BBID BBID GOTERM_BP_DIRECT BBID	SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process positive regulation of calcidiol 1-monooxygenase activity  defense response to protozoan  111.Stress influences immunity 112.StressandCRHinfluence positive regulation of isotype switching to IgG isotypes 20.Cytokine oligodendrocytes	RT	i i	5 5 Count 6 3 6 4 4 3 3	5.6E-1 8.5E-1 P_Value 1.6E-2 7.6E-2 2.1E-1 3.4E-1 4.0E-1 4.2E-1	1.3E0 8.9E-1 Fold Change 3.6E0 5.9E0 1.9E0 1.9E0 2.2E0 2.2E0 2.2E0	1.0E0 1.0E0  Benjamin 2.2E-1 5.7E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	1 9. 1 5. 1 9. 1 1. 1. 1. 1. 1.
	UP_SEQ_FEATURE INTERPRO SMART  tation Cluster 296 GOTERM_BP_DIRECT GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  BBID BBID GOTERM_BP_DIRECT  BBID BBID KEGG_PATHWAY  BBID	SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process positive regulation of calcidiol 1- monooxygenase activity  defense response to protozoan  111.Stress influences immunity 112.StressandCRHinfluence positive regulation of isotype switching to IgG isotypes 20.Cytokine oligodendrocytes 21.Cytokine neurons  Malaria  56.Macrophage regulation of CD4+T cells	RT	i i	5 5 Count 6 3 6 4 4 4 3 3 3 3	5.6E-1 8.5E-1 P_Value 1.6E-2 7.6E-2 2.1E-1 3.4E-1 4.0E-1 4.2E-1 4.2E-1	1.3E0 8.9E-1 Fold Change 3.6E0 5.9E0 1.9E0 1.9E0 2.2E0 2.2E0 2.2E0 1.2E0	1.0E0 1.0E0  Benjamin 2.2E-1 5.7E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	1 9. 1 1 5. 1 1. 1. 4. 1 1.
	UP_SEQ_FEATURE INTERPRO SMART  tation Cluster 296 GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT BBID BBID GOTERM_BP_DIRECT BBID BBID KEGG_PATHWAY	SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process positive regulation of calcidiol 1- monooxygenase activity defense response to protozoan  111.Stress influences immunity 112.StressandCRHinfluence positive regulation of isotype switching to IgG isotypes 20.Cytokine oligodendrocytes 21.Cytokine neurons  Malaria  56.Macrophage regulation of CD4+T cells positive regulation of membrane protein	RT R	i i	5 5 Count 6 3 6 4 4 4 3 3 3 3 3	5.6E-1 8.5E-1 P_Value 1.6E-2 7.6E-2 2.1E-1 3.4E-1 4.0E-1 4.2E-1 4.7E-1	1.3E0 8.9E-1 Fold Change 3.6E0 5.9E0 1.9E0 1.9E0 2.2E0 2.2E0 2.2E0 1.2E0 1.4E0	1.0E0 1.0E0  Benjamin 2.2E-1 5.7E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 7.0E-1	1 9. 1 1 5. 1 1. 9. 1 1. 4. 1 1. 9.
	UP_SEQ_FEATURE INTERPRO SMART  tation Cluster 296 GOTERM_BP_DIRECT GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  BBID BBID GOTERM_BP_DIRECT  BBID BBID KEGG_PATHWAY  BBID	SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process positive regulation of calcidiol 1- monooxygenase activity  defense response to protozoan  111.Stress influences immunity 112.StressandCRHinfluence positive regulation of isotype switching to IgG isotypes 20.Cytokine oligodendrocytes 21.Cytokine neurons  Malaria  56.Macrophage regulation of CD4+T cells positive regulation of membrane protein ectodomain proteolysis	RT R	i i	5 5 Count 6 3 6 4 4 3 3 3 11 5	5.6E-1 8.5E-1 P_Value 1.6E-2 7.6E-2 2.1E-1 3.4E-1 4.0E-1 4.2E-1 4.7E-1 4.7E-1	1.3E0 8.9E-1 Fold Change 3.6E0 5.9E0 1.9E0 1.9E0 2.2E0 2.2E0 2.2E0 1.4E0 1.6E0	1.0E0 1.0E0  Benjamin 2.2E-1 5.7E-1 1.0E0 1.0E0 1.0E0 1.0E0 7.0E-1 1.0E0	1 9. 1 5. 1 1. 1. 1. 4. 1 1. 9. 1
	UP_SEQ_FEATURE INTERPRO SMART  tation Cluster 296 GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT BBID BBID GOTERM_BP_DIRECT BBID BBID KEGG_PATHWAY BBID GOTERM_BP_DIRECT	SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process positive regulation of calcidiol 1- monooxygenase activity defense response to protozoan  111.Stress influences immunity 112.StressandCRHinfluence positive regulation of isotype switching to IgG isotypes 20.Cytokine oligodendrocytes 21.Cytokine neurons  Malaria  56.Macrophage regulation of CD4+T cells positive regulation of membrane protein	RT R	i i	5 5 Count 6 3 6 4 4 3 3 3 11 5 4	5.6E-1 8.5E-1 P_Value 1.6E-2 7.6E-2 2.1E-1 3.4E-1 4.0E-1 4.2E-1 4.7E-1 4.7E-1 4.8E-1	1.3E0 8.9E-1 Fold Change 3.6E0 5.9E0 1.9E0 1.9E0 2.2E0 2.2E0 2.2E0 1.4E0 1.6E0 1.3E0	1.0E0 1.0E0  Benjamin 2.2E-1 5.7E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 7.0E-1 1.0E0 1.0E0	1 9. 1 5. 1 9. 1 1. 4. 1 1. 9. 1 1. 1.
	UP_SEQ_FEATURE INTERPRO SMART  tation Cluster 296 GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT BBID BBID GOTERM_BP_DIRECT BBID BBID GOTERM_BP_DIRECT BBID BBID GOTERM_BP_DIRECT BBID BBID BBID BBID BBID BBID BBID BBI	SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process positive regulation of calcidiol 1- monooxygenase activity defense response to protozoan  111.Stress influences immunity 112.StressandCRHinfluence positive regulation of isotype switching to IgG isotypes 20.Cytokine oligodendrocytes 21.Cytokine neurons  Malaria  56.Macrophage regulation of CD4+T cells positive regulation of membrane protein ectodomain proteolysis 18.Cytokine astocytes	RT R	i i	5 5 Count 6 3 6 4 4 3 3 3 3 11 5 4 7	5.6E-1 8.5E-1 P_Value 1.6E-2 7.6E-2 2.1E-1 3.4E-1 4.0E-1 4.2E-1 4.7E-1 4.7E-1 4.8E-1 4.9E-1	1.3E0 8.9E-1 Fold Change 3.6E0 5.9E0 1.9E0 1.9E0 2.2E0 2.2E0 2.2E0 1.4E0 1.6E0 1.3E0 1.3E0	1.0E0 1.0E0 2.2E-1 5.7E-1 1.0E0	1 9. 1 1. 5. 1 1. 4. 1 1. 9. 1 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.
	UP_SEQ_FEATURE INTERPRO SMART  tation Cluster 296 GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT BBID BBID GOTERM_BP_DIRECT  BBID BBID GOTERM_BP_DIRECT  BBID BBID BBID BBID BBID BBID BBID BB	SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process positive regulation of calcidiol 1- monooxygenase activity defense response to protozoan  111.Stress influences immunity 112.StressandCRHinfluence positive regulation of isotype switching to IgG isotypes 20.Cytokine oligodendrocytes 21.Cytokine neurons  Malaria  56.Macrophage regulation of CD4+T cells positive regulation of membrane protein ectodomain proteolysis 18.Cytokine astocytes 19.Cytokine microglia 22.Cytokine-chemokine CNS 80.T cell Activation	RT R	i i	5 5 Count 6 3 6 4 4 3 3 3 11 5 4 7 5 5 9	5.6E-1 8.5E-1 P_Value 1.6E-2 7.6E-2 2.1E-1 3.4E-1 4.0E-1 4.2E-1 4.7E-1 4.7E-1 4.8E-1 4.9E-1 5.6E-1 6.4E-1 6.7E-1	1.3E0 8.9E-1 Fold Change 3.6E0 5.9E0 1.9E0 1.9E0 2.2E0 2.2E0 2.2E0 1.4E0 1.6E0 1.3E0 1.3E0 1.2E0 1.0E0	1.0E0 1.0E0 2.2E-1 5.7E-1 1.0E0	1 9 1 1 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	UP_SEQ_FEATURE INTERPRO SMART  tation Cluster 296 GOTERM_BP_DIRECT GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  BBID BBID GOTERM_BP_DIRECT  BBID BBID BBID BBID BBID BBID BBID BB	SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process positive regulation of calcidiol 1- monooxygenase activity  defense response to protozoan  111.Stress influences immunity 112.StressandCRHinfluence positive regulation of isotype switching to IgG isotypes 20.Cytokine oligodendrocytes 21.Cytokine neurons  Malaria  56.Macrophage regulation of CD4+T cells positive regulation of membrane protein ectodomain proteolysis 18.Cytokine astocytes 19.Cytokine microglia 22.Cytokine-chemokine CNS 80.T cell Activation 58.(CD40L) immnosurveillance	RT R	i i	5 5 Count 6 3 6 4 4 3 3 3 11 5 4 7 5 5 9 6	5.6E-1 8.5E-1 1.6E-2 7.6E-2 2.1E-1 3.4E-1 4.0E-1 4.2E-1 4.7E-1 4.7E-1 4.8E-1 4.9E-1 5.6E-1 6.4E-1 6.7E-1	1.3E0 8.9E-1 Fold Change 3.6E0 5.9E0 1.9E0 1.9E0 2.2E0 2.2E0 2.2E0 1.4E0 1.6E0 1.3E0 1.3E0 1.2E0 1.0E0 1.1E0	1.0E0 1.0E0 2.2E-1 5.7E-1 1.0E0	1 9. 1 1. 5. 1 1. 4. 1 1. 1. 1. 1. 1. 1. 1.
	UP_SEQ_FEATURE INTERPRO SMART  tation Cluster 296 GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT BBID BBID GOTERM_BP_DIRECT  BBID BBID GOTERM_BP_DIRECT  BBID BBID BBID BBID BBID BBID BBID BB	Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process positive regulation of calcidiol 1-monooxygenase activity defense response to protozoan  111.Stress influences immunity 112.StressandCRHinfluence positive regulation of isotype switching to IgG isotypes 20.Cytokine oligodendrocytes 21.Cytokine neurons  Malaria  56.Macrophage regulation of CD4+T cells positive regulation of membrane protein ectodomain proteolysis 18.Cytokine astocytes 19.Cytokine microglia 22.Cytokine-chemokine CNS 80.T cell Activation 58.(CD40L) immnosurveillance 113.Th1andTh2cells	RT R	i i	5 5 Count 6 3 6 4 4 3 3 3 11 5 4 7 5 5 9 6 3	5.6E-1 8.5E-1 P_Value 1.6E-2 7.6E-2 2.1E-1 3.4E-1 4.0E-1 4.2E-1 4.7E-1 4.7E-1 4.8E-1 4.9E-1 5.6E-1 6.4E-1 6.7E-1 6.9E-1 7.6E-1	1.3E0 8.9E-1 Fold Change 3.6E0 5.9E0 1.9E0 1.9E0 2.2E0 2.2E0 2.2E0 1.4E0 1.6E0 1.3E0 1.2E0 1.0E0 1.1E0 1.2E0	1.0E0 1.0E0 2.2E-1 5.7E-1 1.0E0	1 9. 1 5. 1 9. 1 1. 1. 1. 1. 1. 1. 1. 1. 1.
	UP_SEQ_FEATURE INTERPRO SMART  tation Cluster 296 GOTERM_BP_DIRECT GOTERM_BP_DIRECT  GOTERM_BP_DIRECT  BBID BBID GOTERM_BP_DIRECT  BBID BBID BBID BBID BBID BBID BBID BB	SAP  Enrichment Score: 0.21  positive regulation of chemokine biosynthetic process positive regulation of calcidiol 1- monooxygenase activity  defense response to protozoan  111.Stress influences immunity 112.StressandCRHinfluence positive regulation of isotype switching to IgG isotypes 20.Cytokine oligodendrocytes 21.Cytokine neurons  Malaria  56.Macrophage regulation of CD4+T cells positive regulation of membrane protein ectodomain proteolysis 18.Cytokine astocytes 19.Cytokine microglia 22.Cytokine-chemokine CNS 80.T cell Activation 58.(CD40L) immnosurveillance	RT R	i i	5 5 Count 6 3 6 4 4 3 3 3 11 5 4 7 5 5 9 6	5.6E-1 8.5E-1 1.6E-2 7.6E-2 2.1E-1 3.4E-1 4.0E-1 4.2E-1 4.7E-1 4.7E-1 4.8E-1 4.9E-1 5.6E-1 6.4E-1 6.7E-1	1.3E0 8.9E-1 Fold Change 3.6E0 5.9E0 1.9E0 1.9E0 2.2E0 2.2E0 2.2E0 1.4E0 1.6E0 1.3E0 1.2E0 1.0E0 1.1E0 1.2E0 1.2E0	1.0E0 1.0E0 2.2E-1 5.7E-1 1.0E0	1 9. 1 1. 5. 1 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.

nnot	ation Cluster 1	Enrichment Score: ?	G	<b>100</b>	Count	P_Value	Fold Change	Benjamini	i FDF
	BIOCARTA	Role of Tob in T-cell activation	<u>RT</u>	i .	6	7.9E-1	9.7E-1	1.0E0	7.9I
	BBID	88.Alternatively Activated APC	<u>RT</u>	1	4	7.9E-1	1.1E0	1.0E0	1.0
	KEGG_PATHWAY	Rheumatoid arthritis	<u>RT</u>	i .	15	8.2E-1	8.9E-1	1.0E0	8.2I 1
	KEGG_PATHWAY	Intestinal immune network for IgA production	<u>RT</u>	i	8	8.2E-1	8.9E-1	1.0E0	8.2I
	INTERPRO	Four-helical cytokine, core	<u>RT</u>		7	8.5E-1	8.5E-1	1.0E0	9.1
_ 	BIOCARTA	Cytokines and Inflammatory Response	RT		8	8 8F-1	8.5E-1	1 0F0	1 8.8
ے ا	INTERPRO			-					1 9.1
	BIOCARTA	Four-helical cytokine-like, core	<u>RT</u>		7		8.0E-1		1 8.91
		Cytokine Network	<u>RT</u>	•	6		8.4E-1		1
_ 	BBID KEGG_PATHWAY	15.T-cell polarization-chemokine receptors	<u>RT</u>		5		8.5E-1		1.0 9.0
_		Graft-versus-host disease	<u>RT</u>	•	5	9.0E-1	7.9E-1	1.0E0	1
	KEGG_PATHWAY	Type I diabetes mellitus	<u>RT</u>	i	6	9.3E-1	7.5E-1	1.0E0	9.3 1
	BIOCARTA	<u>Selective expression of chemokine receptors</u> <u>during T-cell polarization</u>	<u>RT</u>	i	7	9.3E-1	7.7E-1	1.0E0	9.3 1
	KEGG_PATHWAY	Allograft rejection	<u>RT</u>	1	5	9.4E-1	7.1E-1	1.0E0	9.4 1
	GOTERM_BP_DIRECT	regulation of insulin secretion	<u>RT</u>	1	8	9.5E-1	7.1E-1	1.0E0	9.5
	BBID	97.Immune injury MS-lesions MS antigen	RT	1	4	9.5E-1	7.2E-1	1.0E0	1 1.0
	BBID	5.B7 CD40 B-cell activa	<u>RT</u>	1	3	9.6E-1	7.2E-1	1.0E0	1.0
	BIOCARTA	Antigen Dependent B Cell Activation	<u>RT</u>	i	3	9.6E-1	7.1E-1	1.0E0	9.6 1
	BIOCARTA	Adhesion and Diapedesis of Granulocytes	<u>RT</u>	1	3	9.8E-1	6.2E-1	1.0E0	9.8 1
	BIOCARTA	Th1/Th2 Differentiation	<u>RT</u>		4	9.8E-1	6.2E-1	1.0E0	9.8
- ا	BIOCARTA	Cells and Molecules involved in local acute		-	2	0.05.1	E 4E 1	1.050	9.9
J	KECC DATHWAY	inflammatory response	RT DT		3		5.4E-1		1
) ]	KEGG_PATHWAY GOTERM_MF_DIRECT	<u>Autoimmune thyroid disease</u> <a href="mailto:cytokine activity">cytokine activity</a>	RT RT		3 13	1.0E0 1.0E0	3.0E-1 4.4E-1		1.0
	UP_KEYWORDS	<u>Cytokine</u>	<u>RT</u>	1	11	1.0E0	4.0E-1	1.0E0	1.0
)	KEGG_PATHWAY	Cytokine-cytokine receptor interaction	<u>RT</u>		15	1.0E0	3.2E-1 Fold		1.0
nnot	ation Cluster 297  UP_SEQ_FEATURE	Enrichment Score: 0.2	G	- The state of the	Count	P_Value	Change	Benjamini	9.7
_	UP_SEQ_FEATURE	chain:Histone H2A type 1-D	<u>RT</u>	i	3	6.3E-1	1.5E0	1.0E0	1 9.7
)		chain:Histone H3.1	<u>RT</u>	•	3	6.3E-1	1.5E0	1.0E0	1
)	UP_SEQ_FEATURE	chain:Histone H3.2	<u>RT</u>	i	3	6.3E-1	1.5E0	1.0E0	9.7 1
nnot	ation Cluster 298	Enrichment Score: 0.19		<b>- 13</b>	Count	P_Value	Fold Change	Benjamini	i FD
)	UP_SEQ_FEATURE	zinc finger region:RanBP2-type	<u>RT</u>	1	4	5.0E-1	1.5E0	1.0E0	9.7 1
)	INTERPRO	Zinc finger, RanBP2-type	<u>RT</u>	1	5	5.9E-1	1.2E0	1.0E0	9.1 1
1	SMART	ZnF RBZ	<u>RT</u>	•	4	9.0F-1	8.2E-1	1.0F0	9.0
,					<u> </u>		Fold		1
nnot	ation Cluster 299	Enrichment Score: 0.19	G	N .	Count	P_Value	Change	Benjamini	
)	BIOCARTA	Role of PI3K subunit p85 in regulation of Actin Organization and Cell Migration	<u>RT</u>	•	7	4.2E-1	1.3E0	6.6E-1	4.5 1
	BIOCARTA	How does salmonella hijack a cell	<u>RT</u>	1	5	6.5E-1	1.2E0	9.7E-1	6.6 1
)	BIOCARTA	Y branching of actin filaments	<u>RT</u>	1	4	9.8E-1	5.9E-1	1.0E0	9.8 1
nnot	ation Cluster 300	Enrichment Score: 0.18	G	<b>178</b>	Count	P_Value	Fold Change	Benjamini	i FD
	UP_SEQ_FEATURE	binding site:NAD; via carbonyl oxygen	RT		3	2.2E-1	<u> </u>	1.0E0	9.7
, 1	GOTERM_MF_DIRECT			-					1 9.0
J	UP SEQ FEATURE	NAD binding	<u>RT</u>	•	5		7.8E-1		1
J		binding site:NAD	<u>RT</u>	i	5	9.7E-1	6.3E-1	1.0E0	9.7 1
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:NAD	<u>RT</u>	i	7	9.8E-1	6.0E-1	1.0E0	9.8 1
nnot	ation Cluster 301	Enrichment Score: 0.18	G	<b>100</b>	Count	P_Value	Fold Change	Benjamini	i FD
)	GOTERM_BP_DIRECT	ATP hydrolysis coupled proton transport	<u>RT</u>	1	8	2.9E-1	1.5E0	1.0E0	9.5
)	UP_KEYWORDS	Hydrogen ion transport	<u>RT</u>	•	4	9.8F-1	5.6E-1	1,0F0	9.8
)	KEGG_PATHWAY	Oxidative phosphorylation	RT		6	1.0E0	2.4E-1		1
nnot	ation Cluster 302	Enrichment Score: 0.18	G	·	Count	P_Value	Fold	Doniemini	
	INTERPRO	PWWP		1	5	4.8E-1	Change	1.0E0	9.1
	SMART		<u>RT</u>						1 9.0
	Silizate	<u>PWWP</u>	<u>RT</u>	i	5	7.6E-1	1.0E0	1.0E0	1
)									
)	UP_SEQ_FEATURE	domain:PWWP	<u>RT</u>	i	3	7.9E-1	1.1E0	1.0E0	9.7

Annota	ation Cluster 1	Enrichment Score: ?	G	<b></b>	Count	P_Value	Fold	Benjamini	FDR
	INTERPRO	Importin subunit alpha	RT	i	3	3.2E-1	Citalige	1.0E0	9.1E-
	UP_SEQ_FEATURE	domain:IBB	RT		3	3.3E-1		1.0E0	1 9.7E-
	PIR_SUPERFAMILY		RT			3.9E-1		1.0E0	1 9.9E-
	INTERPRO	importin subunit alpha			3				1 9.1E-
	UP_SEQ_FEATURE	Importin-alpha, importin-beta-binding domain			3	4.4E-1		1.0E0	1 9.7E-
		repeat:ARM 8	<u>RT</u>	i	4	6.5E-1	1.2E0	1.0E0	1
	UP_SEQ_FEATURE	repeat:ARM 7	<u>RT</u>	i	4	7.1E-1	1.1E0	1.0E0	9.7E- 1
	GOTERM_MF_DIRECT	nuclear localization sequence binding	<u>RT</u>	•	5	7.1E-1	1.1E0	1.0E0	8.9E- 1
	UP_SEQ_FEATURE	repeat:ARM 6	<u>RT</u>	i	4	7.6E-1	1.0E0	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:ARM 9	<u>RT</u>	i .	3	7.6E-1	1.1E0	1.0E0	9.7E- 1
	GOTERM_BP_DIRECT	NLS-bearing protein import into nucleus	<u>RT</u>	i .	4	7.7E-1	1.0E0	1.0E0	9.5E- 1
	UP_SEQ_FEATURE	repeat:ARM 5	<u>RT</u>	i .	4	8.2E-1	9.4E-1	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:ARM 4	<u>RT</u>	i	4	8.5E-1	8.8E-1	1.0E0	9.7E-
	UP_SEQ_FEATURE	repeat:ARM 3	<u>RT</u>	i e	4	9.1E-1	7.6E-1	1.0E0	9.7E-
	UP_SEQ_FEATURE	repeat:ARM 2	<u>RT</u>		4	9.2E-1	7.4E-1	1.0E0	9.7E-
	INTERPRO	Armadillo	RT		4		5.8E-1		1 9.8E-
	GOTERM_MF_DIRECT	protein transporter activity	RT		6	1.0E0	5.0E-1		1 1.0E0
	SMART	<u>ARM</u>	<u>RT</u>	i	4	1.0E0	4.2E-1	1.0E0	1.0E0
Annota	ation Cluster 304	Enrichment Score: 0.16	G	N .	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	domain:OPR	<u>RT</u>	i	3	5.4E-1	1.7E0	1.0E0	9.7E- 1
	INTERPRO	Phox/Bem1p	<u>RT</u>	i	3	6.9E-1	1.3E0	1.0E0	9.1E- 1
	SMART	<u>PB1</u>	<u>RT</u>	i	3	8.9E-1	8.7E-1	1.0E0	9.0E- 1
Annota	ation Cluster 305	Enrichment Score: 0.15		<b>™</b>	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	Patatin/Phospholipase A2-related	<u>RT</u>	i	3	4.4E-1	2.1E0	1.0E0	9.1E- 1
	INTERPRO	Acyl transferase/acyl hydrolase/lysophospholipase	<u>RT</u>	i .	3	8.1E-1	1.0E0	1.0E0	9.1E- 1
	KEGG_PATHWAY	Glycerophospholipid metabolism	<u>RT</u>	i	3	1.0E0	1.7E-1	1.0E0	1.0E0
Annota	ation Cluster 306	Enrichment Score: 0.12	G	·	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	3'5'-cyclic nucleotide phosphodiesterase	<u>RT</u>	i	4	6.1E-1	1.3E0	1.0E0	9.1E- 1
	INTERPRO	<u>3'5'-cyclic nucleotide phosphodiesterase,</u> <u>conserved site</u>	<u>RT</u>	i .	4	6.8E-1	1.2E0	1.0E0	9.1E- 1
	INTERPRO	3'5'-cyclic nucleotide phosphodiesterase, catalytic domain	<u>RT</u>	i .	4	7.1E-1	1.1E0	1.0E0	9.1E- 1
	INTERPRO	HD/PDEase domain	<u>RT</u>	i .	4	7.4E-1	1.1E0	1.0E0	9.1E- 1
	GOTERM_MF_DIRECT	3',5'-cyclic-nucleotide phosphodiesterase activity	<u>RT</u>	i	4	7.7E-1	1.0E0	1.0E0	8.9E-
	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 1	<u>RT</u>	i	4	8.0E-1	9.7E-1	1.0E0	9.7E-
	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 2	RT		4	8.0E-1	9.7E-1	1.0E0	9.7E-
	SMART	HDc	RT		4	9.5E-1	7.1E-1	1.0E0	1 9.5E-
Annota	ation Cluster 307	Enrichment Score: 0.12	G	·	Count	P_Value	Fold	Benjamini	1 EDR
	KEGG_PATHWAY	One carbon pool by folate	RT	:	5	5.5E-1	Change	8.1E-1	5.5E-
	UP_KEYWORDS								1 7.8E-
	GOTERM_BP_DIRECT	One-carbon metabolism	<u>RT</u>		3	7.3E-1		1.0E0	1 9.5E-
	GOTERM_BP_DIRECT	folic acid metabolic process	<u>RT</u>		3		9.9E-1		9.7E-
		one-carbon metabolic process	<u>RT</u>	i	3	:	5.9E-1 Fold		1
Annota	INTERPRO	Enrichment Score: 0.11	G				Change	Benjamini	
	INTERPRO	<u>Phospholipid-transporting P-type ATPase,</u> <u>subfamily IV</u>	<u>RT</u>	•	3	6.9E-1	1.3E0	1.0E0	9.1E- 1
	GOTERM_MF_DIRECT	phospholipid-translocating ATPase activity	<u>RT</u>	i	3	7.1E-1	1.3E0	1.0E0	8.9E- 1
	GOTERM_BP_DIRECT	phospholipid translocation	<u>RT</u>	i	4	7.4E-1	1.1E0	1.0E0	9.5E- 1
	UP_KEYWORDS	<u>Lipid transport</u>	<u>RT</u>	i	4	1.0E0	2.9E-1 Fold		1.0E0
Annota	ation Cluster 309  INTERPRO	Enrichment Score: 0.11	G	-	Count	P_Value	Change	Benjamini	FDR 9.1E-
	GOTERM_MF_DIRECT	Peptidase A1	<u>RT</u>	i	3	5.0E-1		1.0E0	1
		aspartic-type endopeptidase activity	<u>RT</u>	i	5	8.3E-1	9.0E-1	1.0E0	8.9E- 1
	UP_KEYWORDS	Aspartyl protease	<u>RT</u>	i	3	8.3E-1	9.8E-1	1.0E0	8.3E- 1

	tion Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamir	ni Fl
	INTERPRO	Peptidase aspartic, active site	<u>RT</u>	i	3	8.7E-1	8.9E-1	1.0E0	9. 1
	INTERPRO	<u>Aspartic peptidase</u>	<u>RT</u>	1	3	9.5E-1	6.9E-1	1.0E0	9. 1
ota	tion Cluster 310	Enrichment Score: 0.11	G	To the second	Count	P_Value	Fold Change	Benjamir	-
	GOTERM_MF_DIRECT	cAMP response element binding	<u>RT</u>		4		Change	1.0E0	8
	INTERPRO	Basic-leucine zipper domain	RT	_	5		5.7E-1		1 9
	SMART	BRLZ	RT		5	1.0E0	4.0E-1		1 1
	UP_SEQ_FEATURE	DNA-binding region:Basic motif	RT	i	9	1.0E0	3.8E-1		1
nota	tion Cluster 311	Enrichment Score: 0.11	G	<b>13</b>	Count	P_Value	Fold Change	Benjamir	ni F
	UP_SEQ_FEATURE	domain:B30.2/SPRY	<u>RT</u>	1	16	4.6E-1	1.1E0	1.0E0	9
	INTERPRO	Zinc finger, B-box	<u>RT</u>	1	14	5.7E-1	1.1E0	1.0E0	9
	INTERPRO	B30.2/SPRY domain	<u>RT</u>		16	6.5E-1	1.0E0	1.0E0	ç
	INTERPRO	SPIa/RYanodine receptor SPRY	RT		15		9.9E-1		1 9
	UP_SEQ_FEATURE								1 9
	INTERPRO	zinc finger region:B box-type	<u>RT</u>	•	10			1.0E0	1
		<u>SPRY-associated</u>	RT	i	6	9.2E-1	7.4E-1	1.0E0	1
	INTERPRO	Butyrophylin-like	<u>RT</u>	1	8	9.6E-1	6.9E-1	1.0E0	1
	SMART	BBOX	<u>RT</u>	1	13	9.7E-1	7.2E-1	1.0E0	9 1
	SMART	<u>SPRY</u>	<u>RT</u>	i	15	9.9E-1	6.7E-1	1.0E0	9
	SMART	PRY	<u>RT</u>	i .	6	1.0E0	5.0E-1	1.0E0	1
	INTERPRO	<u>Concanavalin A-like lectin/glucanase,</u> <u>subgroup</u>	<u>RT</u>	i	19	1.0E0	5.1E-1	1.0E0	1
iota	tion Cluster 312	Enrichment Score: 0.1		<b>13</b>	Count	P_Value	Fold Change	Benjamir	ni F
	GOTERM_CC_DIRECT	<u>nuclear pore</u>	<u>RT</u>	i .	12	5.9E-1	1.1E0	1.0E0	1
	UP_KEYWORDS	Nuclear pore complex	<u>RT</u>	1	6	8.7E-1	8.2E-1	1.0E0	8
	UP_KEYWORDS	<u>Translocation</u>	<u>RT</u>		8	9.7E-1	6.5E-1	1.0E0	ç
ota	tion Cluster 313	Enrichment Score: 0.1	G	To the second	Count	P_Value	Fold	Benjamir	1 ni F
	INTERPRO	High mobility group (HMG) box domain	<u>RT</u>	1	10	<u> </u>	Change	1.0E0	9
	UP_SEQ_FEATURE			_					1 9
	SMART	DNA-binding region:HMG box	<u>RT</u>		5		7.7E-1		1
	OWAKI	<u>HMG</u>	<u>RT</u>	i	9	9.7E-1	6.8E-1	1.0E0	1
ota	tion Cluster 314	Enrichment Score: 0.09	G	<b>1</b>	Count	P_Value	Fold Change	Benjamir	
	UP_SEQ_FEATURE	domain:CS	<u>RT</u>	i	3	7.0E-1	1.3E0	1.0E0	9
	INTERPRO	CS-like domain	<u>RT</u>	i	3	7.9E-1	1.1E0	1.0E0	9 1
	INTERPRO	HSP20-like chaperone	<u>RT</u>	1	3	9.5E-1	6.6E-1	1.0E0	<u>9</u>
ota	tion Cluster 315	Enrichment Score: 0.08	G	No.	Count	P_Value	Fold Change	Benjamir	ni F
	UP_SEQ_FEATURE	DNA-binding region:HMG box 1	<u>RT</u>		3	7.6E-1	1.1E0	1.0E0	Ç
	UP_SEQ_FEATURE	DNA-binding region:HMG box 2	RT		3		1.1E0	1.0E0	9
	SMART								1 9
		HMG	<u>RT</u>	i	9	1	6.8E-1		1
ota	tion Cluster 316 UP_KEYWORDS	Enrichment Score: 0.07	G		Count	P_Value	Change	•	_
		<u>Steroid-binding</u>	<u>RT</u>	•	4	4.2E-1	1.7E0	1.0E0	1
	INTERPRO	Zinc finger, NHR/GATA-type	<u>RT</u>	i	11	4.6E-1	1.2E0	1.0E0	1
	UP_SEQ_FEATURE	region of interest:Modulating	<u>RT</u>	i	3	6.3E-1	1.5E0	1.0E0	9
	GOTERM_MF_DIRECT	steroid binding	<u>RT</u>	i .	4	8.5E-1	8.8E-1	1.0E0	8
	UP_SEQ_FEATURE	zinc finger region:NR C4-type	<u>RT</u>	1	5	9.1E-1	7.6E-1	1.0E0	9
	UP_SEQ_FEATURE	DNA-binding region:Nuclear receptor	<u>RT</u>		5	9.1E-1	7.6E-1	1.0E0	9
	UP_SEQ_FEATURE	region of interest:Hinge	RT		3		7.3E-1		1 9
	UP_SEQ_FEATURE			-					1
		region of interest:Ligand-binding	<u>RT</u>	•	3	9.5E-1	6.8E-1	1.0E0	1
	INTERPRO	Zinc finger, nuclear hormone receptor-type	<u>RT</u>	1	5	9.5E-1	6.7E-1	1.0E0	1
		RNA polymerase II transcription factor							9
	GOTERM_MF_DIRECT	activity, ligand-activated sequence-specific  DNA binding	<u>RT</u>	1	4	9.5E-1	6.6E-1	1.0E0	1

Annot	tation Cluster 1	Enrichment Score: ?	G	- <b>15</b>	Count	P_Value	Fold Change	Benjamiı	ni FDR
	INTERPRO	Nuclear hormone receptor, ligand-binding,	<u>RT</u>	i	5		6.5E-1		9.6E
	GOTERM_MF_DIRECT	core steroid hormone receptor activity	<u>RT</u>	4	5	0 0F-1	5.3E-1	1 0E0	1 9.9E
	GOTERM_BP_DIRECT	steroid hormone mediated signaling pathway	RT		4	1.0E0	4.2E-1		1 1.0E
	SMART	ZnF_C4	RT		5	1.0E0 1.0E0	4.2E-1 4.4E-1		1.0E
	SMART	<u>HOLI</u>	<u>RT</u>	i	5	1.0E0	4.2E-1		1.0E
Annot	tation Cluster 317	Enrichment Score: 0.07	G	i i i i i i i i i i i i i i i i i i i	Count	P_Value	Fold Change	Benjami	ni FDR
	GOTERM_MF_DIRECT	histone demethylase activity	<u>RT</u>	1	5	5.5E-1	1.3E0	1.0E0	8.9E
_	UP_SEQ_FEATURE			-	4	0 7E 1	0 FE 1	1 050	1 9.7E
		domain:JmjC	<u>RT</u>	•	4	8.7E-1	8.5E-1	1.000	1
	INTERPRO	<u>JmjC domain</u>	<u>RT</u>	i	4	9.2E-1	7.5E-1	1.0E0	9.2E
	SMART	<u>JmjC</u>	<u>RT</u>	1	4	9.8E-1	5.6E-1	1.0E0	9.8E 1
	UP_KEYWORDS	<u>Dioxygenase</u>	<u>RT</u>	1	6	1.0E0	5.0E-1	1.0E0	1.0E
Annot	tation Cluster 318	Enrichment Score: 0.06	G	<b></b>	Count	P_Value	Fold Change	Benjamiı	ni FDR
7	GOTERM_MF_DIRECT	peptidase activity	RT	1	15	6.6E-1			8.9E
_ 	UP_KEYWORDS	Zymogen	RT		17	1.0E0	5.5E-1		1 1.0E
	UP_KEYWORDS	<u>Protease</u>	RT		39	1.0E0	4.9E-1		1.0E
Annot	tation Cluster 319	Enrichment Score: 0.05		i 🚾	Count	P_Value	Fold Change	Benjamiı	ni FDR
	UP_SEQ_FEATURE	DNA-binding region:Fork-head	RT	1	7	7.6E-1	9.5E-1		9.7E
	INTERPRO			-					1 9.1E
		<u>Transcription factor, fork head</u>	<u>RT</u>	•	7	8.2E-1	8.9E-1	1.0E0	1
	INTERPRO	<u>Transcription factor, fork head, conserved site</u>	<u>RT</u>	i	3	9.8E-1	5.5E-1	1.0E0	9.8E 1
	SMART	<u>FH</u>	<u>RT</u>	1	7	9.9E-1	5.8E-1	1.0E0	9.9E
Annot	tation Cluster 320	Enrichment Score: 0.04	G	170	Count	P_Value	Fold	Benjamii	ni FDR
	UP_SEQ_FEATURE						Change		9.7E
		domain:LIM zinc-binding	<u>RT</u>	•	3	7.9E-1	1.1E0	1.0E0	1
	UP_SEQ_FEATURE	domain:LIM zinc-binding 3	<u>RT</u>	1	3	9.0E-1	8.2E-1	1.0E0	9.7E 1
	UP_KEYWORDS	<u>LIM domain</u>	<u>RT</u>	1	8	9.2E-1	7.6E-1	1.0E0	9.2E 1
$\neg$	UP_SEQ_FEATURE	domain:LIM zinc-binding 1	рт	-	5	0 FE 1	6.8E-1	1 050	9.7E
	UP_SEQ_FEATURE	domain.Lim zinc-binding 1	<u>RT</u>	•	3	9.31-1	0.6L-1	1.000	1
	UP_SEQ_FEATURE	domain:LIM zinc-binding 2	<u>RT</u>	1	5	9.5E-1	6.8E-1	1.0E0	9.7E 1
	INTERPRO	Zinc finger, LIM-type	<u>RT</u>	1	8	9.6E-1	6.9E-1	1.0E0	9.6E 1
	SMART	<u>LIM</u>	<u>RT</u>	i i	8	1.0E0	4.5E-1	1.0E0	1.0E
Annot	tation Cluster 321	Enrichment Score: 0.03		i 🚾	Count	P_Value	Fold Change	Benjamiı	ni FDR
	INTERPRO	Heparin-binding growth factor/Fibroblast	<u>RT</u>	1	3	8.9E-1	8.5E-1	1.0E0	9.1E
	INTERPRO	growth factor	рт		4	0.25.1	7 55 1	1.050	1 9.2E
	CMART	<u>Cytokine, IL-1-like</u>	<u>RT</u>		4	9.26-1	7.5E-1	1.000	1
	SMART	<u>FGF</u>	<u>RT</u>	i	3	9.8E-1	5.6E-1	1.0E0	9.8E 1
Annot	tation Cluster 322	Enrichment Score: 0.02		- 100 m	Count	P_Value	Fold Change	Benjamiı	ni FDR
	UP_SEQ_FEATURE	domain:LisH	<u>RT</u>	1	3	9.3E-1	7.3E-1	1.0E0	9.7E
_	INTERPRO	Light discouranties month		-	2	0.55.1	C CE 1	1.050	1 9.5E
	OMART	<u>LisH dimerisation motif</u>	<u>RT</u>	•	3	9.5E-1	6.6E-1	1.0E0	1
	SMART	<u>LisH</u>	<u>RT</u>	i	3	9.9E-1	5.3E-1	1.0E0	9.9E 1
Annot	tation Cluster 323	Enrichment Score: 0.01	G	- 100 m	Count	P_Value	Fold Change	Benjami	ni FDR
	UP_KEYWORDS	Growth factor	<u>RT</u>	1	15	9.2E-1	7.9E-1	•	9.2E
_	GOTERM_MF_DIRECT				10				1 9.8E
		growth factor activity	<u>RT</u>		19		7.0E-1		1
	GOTERM_MF_DIRECT	cytokine activity	<u>RT</u>		13	1.0E0	4.4E-1 Fold		1.0E
Annot	tation Cluster 324	Enrichment Score: 0.01	G		Count	P_Value	Change	Benjamii	
	UP_SEQ_FEATURE	zinc finger region:FYVE-type	<u>RT</u>	i	4	9.4E-1	7.0E-1	1.0E0	9.7E 1
	INTERPRO	Zinc finger, FYVE-type	<u>RT</u>	i	3	9.6E-1	6.4E-1	1.0E0	9.6E 1
	INTERPRO	Zinc finger, FYVE-related	<u>RT</u>	1	3	9.8E-1	5.5E-1	1.0E0	9.8E
	SMART	<u>FYVE</u>	RT		3	1.0E0	4.2E-1		1 1.0E
Annot	tation Cluster 325	Enrichment Score: 0.01	G		Count	P_Value	Fold	Banjami	
	UP_SEQ_FEATURE						Change		9.7E
		zinc finger region:C3H1-type 1	<u>RT</u>	i	3	9.5E-1	6.6E-1	1.0E0	1
	UP_SEQ_FEATURE	zinc finger region:C3H1-type 2	<u>RT</u>	i	3	9.5E-1	6.6E-1	1.0E0	9.7E 1
	INTERPRO	Zinc finger, CCCH-type	<u>RT</u>	1	5	9.9E-1	5.3E-1	1.0E0	9.9E 1
	SMART	ZnF_C3H1	<u>RT</u>	i	5	1.0E0	4.2E-1	1.0E0	1.0E
		Enrichment Score: 0.01	G	<b>173</b>	Count	P_Value	Fold		ni FDR

Annota	ation Cluster 1	Enrichment Score: ?	G	<b></b>	Count	P_Value	Fold Change	Benjamini	FDR
	UP_KEYWORDS	Host cell receptor for virus entry	RT		6		6.4E-1	1 0F0	9.7E-
	GOTERM_BP_DIRECT								1 9.7E-
		<u>viral entry into host cell</u>	<u>RT</u>	i	9	9.7E-1	6.7E-1	1.0E0	1
	GOTERM_MF_DIRECT	virus receptor activity	<u>RT</u>	i	6	9.9E-1	5.1E-1	1.0E0	9.9E- 1
Annota	ation Cluster 327	Enrichment Score: 0.01	G		Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	Ras-association	<u>RT</u>	i	4	9.7E-1	6.2E-1	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	domain:Ras-associating	<u>RT</u>		3	9 7F-1	6.0E-1	1 0F0	9.7E-
	SMART	RA	RT		3	1.0E0	4.2E-1		1 1.0E0
Annota	ation Cluster 328	Enrichment Score: 0.01	G			P_Value	Fold	Benjamini	
	UP_SEQ_FEATURE		<u>RT</u>	i	4		Change 6.6E-1		9.7E-
	UP_SEQ_FEATURE	repeat:22			4				1 9.7E-
		repeat:21	<u>RT</u>	i	4	9.6E-1	6.3E-1	1.0E0	1
	UP_SEQ_FEATURE	repeat:1	<u>RT</u>	i .	29	9.7E-1	7.7E-1	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:24	<u>RT</u>	i	3	9.7E-1	6.0E-1	1.0E0	9.7E- 1
	UP_SEQ_FEATURE	repeat:20	<u>RT</u>	i e	4	9.7F-1	5.9E-1	1.0F0	9.7E-
	UP_SEQ_FEATURE								1 9.7E-
		repeat:2	<u>RT</u>	i	29	9./E-1	7.6E-1	1.0E0	1
	UP_SEQ_FEATURE	repeat:19	<u>RT</u>	i	4	9.8E-1	5.7E-1	1.0E0	9.8E- 1
	UP_SEQ_FEATURE	repeat:18	<u>RT</u>	i	4	9.8E-1	5.6E-1	1.0E0	9.8E- 1
	UP_SEQ_FEATURE	repeat:17	<u>RT</u>	i .	4	9.9E-1	4.9E-1	1.0E0	9.9E- 1
	UP_SEQ_FEATURE	repeat:11	<u>RT</u>		7	9 9F-1	5.4E-1	1.0F0	9.9E-
	UP_SEQ_FEATURE	repeat:16	RT		4	1.0E0	4.5E-1		1 1.0E0
	UP_SEQ_FEATURE	repeat:8	RT		10	1.0E0	5.5E-1		1.0E0
	UP_SEQ_FEATURE	repeat:3	<u>RT</u>	1	21	1.0E0	6.4E-1		1.0E0
	UP_SEQ_FEATURE UP_SEQ_FEATURE	repeat:15 repeat:12	RT RT		5 6	1.0E0 1.0E0	4.6E-1 4.8E-1		1.0E0 1.0E0
	UP_SEQ_FEATURE	repeat:9	RT	i e	8	1.0E0	5.1E-1		1.0E0
	UP_SEQ_FEATURE	repeat:6	<u>RT</u>	•	12	1.0E0	5.6E-1		1.0E0
	UP_SEQ_FEATURE UP_SEQ_FEATURE	repeat:10 repeat:14	RT RT		7 5	1.0E0 1.0E0	4.9E-1 4.3E-1		1.0E0 1.0E0
	UP_SEQ_FEATURE	repeat:7	RT	1	10	1.0E0	5.1E-1		1.0E0
	UP_SEQ_FEATURE UP_SEQ_FEATURE	repeat:4	RT DT		16 5	1.0E0	5.7E-1		1.0E0
	UP_SEQ_FEATURE	repeat:13 repeat:5	RT RT		11	1.0E0 1.0E0	4.1E-1 4.7E-1		1.0E0 1.0E0
Annota	ation Cluster 329	Enrichment Score: 0	G	To the second se	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	cilium morphogenesis	<u>RT</u>	i	15	9.9E-1	6.5E-1	1.0E0	9.9E-
	UP_KEYWORDS	Cilium biogenesis/degradation	<u>RT</u>	•	13	0 0E-1	6.0E-1	1 0E0	1 9.9E-
	GOTERM_BP_DIRECT	cilium assembly	RT		11	1.0E0	5.3E-1		1 1.0E0
Annota	ation Cluster 330	Enrichment Score: 0	G		Count	P_Value	Fold	Benjamini	
	GOTERM_CC_DIRECT						Change		9.9E-
		mitochondrial matrix	<u>RT</u>	1 1	38		7.4E-1		1
	UP_SEQ_FEATURE UP_KEYWORDS	transit peptide: Mitochondrion <u>Transit peptide</u>	RT RT		43 47	1.0E0 1.0E0	6.1E-1 6.0E-1		1.0E0 1.0E0
	UP_KEYWORDS	Mitochondrion	<u>RT</u>	=	116	1.0E0	7.1E-1	1.0E0	1.0E0
Annota	ation Cluster 331	Enrichment Score: 0	G	<b>™</b>	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:Rho-GAP	RT DT		4	1.0E0	4.0E-1		1.0E0
	INTERPRO INTERPRO	Rho GTPase-activating protein domain  Rho GTPase activation protein	RT RT		4 6	1.0E0 1.0E0	3.7E-1 4.1E-1		1.0E0 1.0E0
	SMART	RhoGAP	<u>RT</u>	1	4	1.0E0	2.5E-1	1.0E0	1.0E0
	UP_KEYWORDS GOTERM_MF_DIRECT	GTPase activation GTPase activator activity	RT RT		9 15	1.0E0 1.0E0	3.1E-1 3.2E-1		1.0E0 1.0E0
Annota	ation Cluster 332	Enrichment Score: 0	G		Count	P_Value	Fold	Benjamini	
	UP_SEQ_FEATURE	domain:DH	RT	i	4	1.0E0	Change 4.0E-1		1.0E0
	GOTERM_BP_DIRECT	regulation of Rho protein signal transduction	<u>RT</u>	1	6	1.0E0	4.4E-1	1.0E0	1.0E0
	INTERPRO GOTERM_MF_DIRECT	Dbl homology (DH) domain  Rho guanyl-nucleotide exchange factor	<u>RT</u>	1	4	1.0E0	3.5E-1		1.0E0
		<u>activity</u>	<u>RT</u>	1	4	1.0E0	3.1E-1		1.0E0
	GOTERM_MF_DIRECT SMART	guanyl-nucleotide exchange factor activity  RhoGEF	RT RT		6 4	1.0E0 1.0E0	3.0E-1 2.4E-1		1.0E0 1.0E0
	UP_KEYWORDS	Guanine-nucleotide releasing factor	RT		5	1.0E0 1.0E0	2.4E-1 2.3E-1		1.0E0
Annota	ation Cluster 333	Enrichment Score: 0	G	178	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:PH	<u>RT</u>	i	19	1.0E0	5.3E-1		1.0E0
	INTERPRO INTERPRO	Pleckstrin homology domain	RT PT		18 33	1.0E0	4.1E-1		1.0E0
	SMART	Pleckstrin homology-like domain PH	RT RT		33 17	1.0E0 1.0E0	4.8E-1 2.6E-1		1.0E0 1.0E0

Anno	tation Cluster 1	Enrichment Score: ?	G	- 100 m	Count	P_Value	Fold Change	Benjamini	FDR
Anno	tation Cluster 334	Enrichment Score: 0	G	<b>100</b>	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	DNA-binding region:Basic motif	<u>RT</u>	i	9	1.0E0	3.8E-1	1.0E0	1.0E0
	UP_SEQ_FEATURE	domain:Helix-loop-helix motif	<u>RT</u>	i	4	1.0E0	2.4E-1	1.0E0	1.0E0
	INTERPRO	<u>Myc-type, basic helix-loop-helix (bHLH)</u> <u>domain</u>	<u>RT</u>	1	4	1.0E0	2.1E-1	1.0E0	1.0E0
	SMART	<u>HLH</u>	<u>RT</u>	i	4	1.0E0	1.4E-1	1.0E0	1.0E0
Anno	tation Cluster 335	Enrichment Score: -0	G	<b></b>	Count	P_Value	Fold Change	Benjamini	FDR
	UP_KEYWORDS	Cell membrane	<u>RT</u>		311	1.0E0	6.7E-1	1.0E0	1.0E0
	UP_KEYWORDS	<u>Membrane</u>	<u>RT</u>		602	1.0E0	5.5E-1	1.0E0	1.0E0
	GOTERM_CC_DIRECT	<u>plasma membrane</u>	<u>RT</u>		445	1.0E0	6.9E-1	1.0E0	1.0E0
Anno	tation Cluster 336	Enrichment Score: -0	G	<b>177</b>	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	topological domain:Cytoplasmic	<u>RT</u>		171	1.0E0	3.4E-1	-	1.0E0
	UP_SEQ_FEATURE	topological domain:Extracellular	<u>RT</u>		142	1.0E0	3.5E-1	1.0E0	1.0E0
	UP_KEYWORDS	<u>Transmembrane</u>	<u>RT</u>		306	1.0E0	3.7E-1	1.0E0	1.0E0
	UP_SEQ_FEATURE	transmembrane region	<u>RT</u>	=	224	1.0E0	3.0E-1	1.0E0	1.0E0
	UP_KEYWORDS	Transmembrane helix	<u>RT</u>	_	305	1.0E0	3.7E-1	1.0E0	1.0E0
	UP_KEYWORDS	<u>Disulfide bond</u>	<u>RT</u>	=	196	1.0E0	3.9E-1	1.0E0	1.0E0
	UP_KEYWORDS	<u>Membrane</u>	<u>RT</u>		602	1.0E0	5.5E-1	1.0E0	1.0E0
	UP_KEYWORDS	<u>Signal</u>	<u>RT</u>		262	1.0E0	4.3E-1	1.0E0	1.0E0
	GOTERM_CC_DIRECT	integral component of plasma membrane	<u>RT</u>	=	98	1.0E0	4.4E-1	1.0E0	1.0E0
	UP_KEYWORDS	<u>Glycoprotein</u>	<u>RT</u>		267	1.0E0	4.0E-1	1.0E0	1.0E0
	UP_SEQ_FEATURE	disulfide bond	<u>RT</u>	=	153	1.0E0	3.6E-1	1.0E0	1.0E0
	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc)	<u>RT</u>	=	209	1.0E0	3.4E-1	1.0E0	1.0E0
	UP_KEYWORDS	Receptor	<u>RT</u>	=	108	1.0E0	4.5E-1	1.0E0	1.0E0
	UP_SEQ_FEATURE	signal peptide	<u>RT</u>	=	212	1.0E0	4.3E-1	1.0E0	1.0E0
	GOTERM_CC_DIRECT	integral component of membrane	<u>RT</u>		281	1.0E0	3.5E-1	1.0E0	1.0E0