

Laboratory of Human Retrovirology and Immunoinformatics (LHRI)

Functional Annotation Clustering

Current Gene List: List_1

Current Background: Homo sapiens

2998 DAVID IDs

■ Options Classification Stringency Medium ✓

Rerun using options | Create Sublist

341 Cluster(s)

March Download File

Help and Manual

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

Annot	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 21	<u>RT</u>	i	24	1.0E- 16	6.3E0	8.6E-15	8.3E- 15
	UP_SEQ_FEATURE	Continue Property Continue Continue							
	UP_SEQ_FEATURE	The proper proper part The							
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 24							
Annot	ation Cluster 2	Enrichment Score: 92.97	G	To the second se	Count	P_Value	Fold Change	Benjamini	
	UP_KEYWORDS	Nucleotide-binding	<u>RT</u>		786	2.0E-		1.9E-220	
	UP_KEYWORDS	ATP-binding	<u>RT</u>		640	7.5E-	3.2E0	4.0E-188	3.1E-
	GOTERM_MF_DIRECT	ATP binding	<u>RT</u>		661	8.9E-	2.6E0	3.8E-150	3.4E-
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	<u>RT</u>	_	472	3.3E-	3.2E0	1.3E-139	1.3E-
	UP_SEQ_FEATURE	domain:Protein kinase	<u>RT</u>	=	267	2.4E-	3.8E0	7.9E-97	7.6E-
	INTERPRO	Protein kinase-like domain	RT	=	294	7.9E-	3.4E0	3.6E-95	3.3E-
	INTERPRO	Protein kinase, catalytic domain		=	278	1.2E-	3.5E0	4.4E-94	4.0E-
	UP_SEQ_FEATURE			=		4.3E-	3.4E0	1.3E-88	1.3E-
	INTERPRO			=		2.9E-			8.8E-
	UP_KEYWORDS			_		3.0E-			9.3E-
	UP_KEYWORDS			_		8.6E-			2.1E-
	UP_SEQ_FEATURE			=		1.3E-			2.6E-
	GOTERM_MF_DIRECT			=		6.6E-			1.1E-
	GOTERM_MF_DIRECT			<u>-</u>		4.6E-			6.5E-
	GOTERM_BP_DIRECT			\equiv		8.3E-			8.0E-
	INTERPRO					1.6E-			
	UP_KEYWORDS					1.1E-			
		Transierase	14.1		403	47	1.520	2.76 40	46
	SMART	S TKc	RT	=	188	2.5E-	2.1F0	2.4F-28	
Annot					1	30	Fold		28
Annot	SMART ation Cluster 3 UP_SEQ_FEATURE	Enrichment Score: 57.69	G	17	Count	30 P_Value 1.2E-	Fold Change	Benjamini	28 FDR 3.2E-
Annot	ation Cluster 3	Enrichment Score: 57.69 repeat: ANK 4	G RT	=	Count	30 P_Value 1.2E- 73 7.0E-	Fold Change 5.2E0	Benjamini 3.3E-71	28 FDR 3.2E- 71 1.7E-
Annot	ation Cluster 3 UP_SEQ_FEATURE	Enrichment Score: 57.69 repeat:ANK 4 repeat:ANK 5	G RT RT		Count 131 115	30 P_Value 1.2E- 73 7.0E- 69 2.0E-	Fold Change 5.2E0 5.5E0	Benjamini 3.3E-71 1.8E-66	28 FDR 3.2E- 71 1.7E- 66 4.7E-
Annot	ation Cluster 3 UP_SEQ_FEATURE UP_SEQ_FEATURE	repeat:ANK 4 repeat:ANK 5 ANK repeat	RT RT RT		Count 131 115 161	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E-	Fold Change 5.2E0 5.5E0 4.2E0	Benjamini 3.3E-71 1.8E-66 6.1E-66	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-
Annot	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS	repeat: ANK 4 repeat: ANK 5 ANK repeat repeat: ANK 3	RT RT RT RT		Count 131 115 161 139	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E-	Fold Change 5.2E0 5.5E0 4.2E0 4.6E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-63 6.0E-
Annot	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE	repeat:ANK 4 repeat:ANK 5 ANK repeat repeat:ANK 3 Ankyrin repeat	RT RT RT RT RT		Count 131 115 161 139 159	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E-	Fold Change 5.2E0 5.5E0 4.2E0 4.6E0 3.9E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60	28 FDR 3.2E- 71 1.7E- 66 4.7E- 66 3.8E- 63 6.0E- 60 2.1E-
Annot	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO	repeat: ANK 4 repeat: ANK 5 ANK repeat repeat: ANK 3 Ankyrin repeat Ankyrin repeat-containing domain	RT RT RT RT RT RT		Count 131 115 161 139 159 162	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E- 61 7.5E-	Fold Change 5.2E0 5.5E0 4.2E0 4.6E0 3.9E0 3.8E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60 2.2E-59	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-63 6.0E-60 2.1E-59 1.4E-
Annot	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO	repeat: ANK 4 repeat: ANK 5 ANK repeat repeat: ANK 3 Ankyrin repeat Ankyrin repeat-containing domain repeat: ANK 2	RT RT RT RT RT RT RT		Count 131 115 161 139 159 162 146	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E- 61 7.5E- 59 3.2E-	Fold Change 5.2E0 5.5E0 4.2E0 4.6E0 3.9E0 3.8E0 4.1E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60 2.2E-59 1.4E-56	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-63 6.0E-60 2.1E-59 1.4E-56 5.5E-
Annot	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE	repeat:ANK 4 repeat:ANK 5 ANK repeat repeat:ANK 3 Ankyrin repeat Ankyrin repeat-containing domain repeat:ANK 2 repeat:ANK 1	RT RT RT RT RT RT RT RT		Count 131 115 161 139 159 162 146 145	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E- 61 7.5E- 59 3.2E- 58 6.8E-	Fold Change 5.2E0 5.5E0 4.2E0 4.6E0 3.9E0 3.8E0 4.1E0 4.0E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60 2.2E-59 1.4E-56 5.7E-56	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-63 6.0E-60 2.1E-59 1.4E-56 5.5E-56 1.0E-
Anno	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE	repeat:ANK 4 repeat:ANK 5 ANK repeat repeat:ANK 3 Ankyrin repeat Ankyrin repeat-containing domain repeat:ANK 2 repeat:ANK 1 repeat:ANK 6	RT		Count 131 115 161 139 159 162 146 145 83	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E- 61 7.5E- 59 3.2E- 58 6.8E- 52 4.9E-	Fold Change 5.2E0 5.5E0 4.2E0 4.6E0 3.9E0 3.8E0 4.1E0 4.0E0 5.7E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60 2.2E-59 1.4E-56 5.7E-56 1.1E-49	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-63 6.0E-60 2.1E-59 1.4E-56 5.5E-56 1.0E-49 5.2E-
Annot	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE	repeat: ANK 4 repeat: ANK 5 ANK repeat repeat: ANK 3 Ankyrin repeat Ankyrin repeat-containing domain repeat: ANK 2 repeat: ANK 1 repeat: ANK 6 ANK	RT		Count 131 115 161 139 159 162 146 145 83 157	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E- 61 7.5E- 59 3.2E- 58 6.8E- 52 4.9E- 38 3.8E-	Fold Change 5.2E0 5.5E0 4.2E0 4.6E0 3.9E0 3.8E0 4.1E0 4.0E0 5.7E0 2.6E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60 2.2E-59 1.4E-56 5.7E-56 1.1E-49 5.8E-36	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-63 6.0E-60 2.1E-59 1.4E-56 5.5E-56 1.0E-49 5.2E-36 4.8E-
	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART	repeat:ANK 4 repeat:ANK 5 ANK repeat repeat:ANK 3 Ankyrin repeat Ankyrin repeat-containing domain repeat:ANK 2 repeat:ANK 1 repeat:ANK 6 ANK repeat:ANK 7	RT		Count 131 115 161 139 159 162 146 145 83 157 55	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E- 61 7.5E- 59 3.2E- 58 6.8E- 52 4.9E- 38 3.8E- 36	Fold Change 5.2E0 5.5E0 4.2E0 4.6E0 3.9E0 4.1E0 4.0E0 5.7E0 2.6E0 5.9E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60 2.2E-59 1.4E-56 5.7E-56 1.1E-49 5.8E-36 5.0E-34	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-63 6.0E-60 2.1E-59 1.4E-56 5.5E-56 1.0E-49 5.2E-36 4.8E-34
	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE	repeat:ANK 4 repeat:ANK 5 ANK repeat repeat:ANK 3 Ankyrin repeat Ankyrin repeat-containing domain repeat:ANK 2 repeat:ANK 1 repeat:ANK 6 ANK repeat:ANK 7 Enrichment Score: 37.87	RT R		Count 131 115 161 139 159 162 146 145 83 157 55 Count	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E- 61 7.5E- 59 3.2E- 58 6.8E- 52 4.9E- 38 3.8E- 36 P_Value 3.1E-	Fold Change 5.2E0 5.5E0 4.2E0 4.6E0 3.9E0 4.1E0 4.0E0 5.7E0 2.6E0 5.9E0 Fold Change	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60 2.2E-59 1.4E-56 5.7E-56 1.1E-49 5.8E-36 5.0E-34 Benjamini	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-63 6.0E-60 2.1E-59 1.4E-56 5.5E-56 1.0E-49 5.2E-36 4.8E-34 FDR 5.9E-
	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_SEQ_FEATURE	repeat: ANK 4 repeat: ANK 5 ANK repeat repeat: ANK 3 Ankyrin repeat Ankyrin repeat-containing domain repeat: ANK 2 repeat: ANK 1 repeat: ANK 6 ANK repeat: ANK 7 Enrichment Score: 37.87	RT R		Count 131 115 161 139 159 162 146 145 83 157 55 Count 147	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E- 61 7.5E- 59 3.2E- 58 6.8E- 52 4.9E- 38 3.8E- 36 P_Value 3.1E- 63 7.0E-	Fold Change 5.2E0 5.5E0 4.2E0 4.6E0 3.9E0 4.1E0 4.0E0 5.7E0 2.6E0 5.9E0 Fold Change 4.1E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60 2.2E-59 1.4E-56 5.7E-56 1.1E-49 5.8E-36 5.0E-34 Benjamini 6.1E-60	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-63 6.0E-60 2.1E-59 1.4E-56 5.5E-56 1.0E-49 5.2E-36 4.8E-34 FDR 5.9E-60 1.5E-
	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_SEQ_FEATURE ation Cluster 4 GOTERM_BP_DIRECT	repeat:ANK 4 repeat:ANK 5 ANK repeat repeat:ANK 3 Ankyrin repeat Ankyrin repeat-containing domain repeat:ANK 2 repeat:ANK 1 repeat:ANK 6 ANK repeat:ANK 7 Enrichment Score: 37.87 rRNA processing Ribonucleoprotein nuclear-transcribed mRNA catabolic process,	RT R		Count 131 115 161 139 159 162 146 145 83 157 55 Count 147 160	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E- 61 7.5E- 59 3.2E- 58 6.8E- 52 4.9E- 38 3.8E- 36 P_Value 3.1E- 63 7.0E- 57 6.2E-	Fold Change 5.2E0 5.5E0 4.2E0 4.6E0 3.9E0 3.8E0 4.1E0 4.0E0 5.7E0 2.6E0 5.9E0 Fold Change 4.1E0 3.7E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60 2.2E-59 1.4E-56 5.7E-56 1.1E-49 5.8E-36 5.0E-34 Benjamini 6.1E-60 1.9E-55	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-63 6.0E-59 1.4E-56 5.5E-56 1.0E-49 5.2E-36 4.8E-34 FDR 5.9E-60 1.5E-55 7.1E-
	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_SEQ_FEATURE ation Cluster 4 GOTERM_BP_DIRECT UP_KEYWORDS	repeat:ANK 4 repeat:ANK 5 ANK repeat repeat:ANK 3 Ankyrin repeat Ankyrin repeat Ankyrin repeat-containing domain repeat:ANK 2 repeat:ANK 1 repeat:ANK 6 ANK repeat:ANK 7 Enrichment Score: 37.87 rRNA processing Ribonucleoprotein nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, SRP-dependent cotranslational protein	RT R		Count 131 115 161 139 159 162 146 145 83 157 55 Count 147 160 97	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E- 61 7.5E- 59 3.2E- 58 6.8E- 52 4.9E- 38 3.8E- 36 P_Value 3.1E- 63 7.0E- 57 6.2E- 53 2.3E-	Fold Change 5.2E0 5.5E0 4.2E0 4.6E0 3.9E0 3.8E0 4.1E0 4.0E0 5.7E0 2.6E0 5.9E0 Fold Change 4.1E0 3.7E0 4.8E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60 2.2E-59 1.4E-56 5.7E-56 1.1E-49 5.8E-36 5.0E-34 Benjamini 6.1E-60 1.9E-55 7.4E-50	28 FDR 3.2E- 71 1.7E- 66 4.7E- 66 3.8E- 63 6.0E- 60 2.1E- 59 1.4E- 56 5.5E- 56 1.0E- 49 5.2E- 36 4.8E- 34 FDR 5.9E- 60 1.5E- 55 7.1E- 50 1.9E-
	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_SEQ_FEATURE ation Cluster 4 GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_BP_DIRECT	repeat:ANK 4 repeat:ANK 5 ANK repeat repeat:ANK 3 Ankyrin repeat Ankyrin repeat-containing domain repeat:ANK 2 repeat:ANK 1 repeat:ANK 6 ANK repeat:ANK 7 Enrichment Score: 37.87 rRNA processing Ribonucleoprotein nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, SRP-dependent cotranslational protein targeting to membrane	RT R		Count 131 115 161 139 159 162 146 145 83 157 55 Count 147 160 97 80	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E- 61 7.5E- 59 3.2E- 58 6.8E- 52 4.9E- 38 3.8E- 36 P_Value 3.1E- 63 7.0E- 57 6.2E- 53 2.3E- 46 1.7E-	Fold Change 5.2E0 5.5E0 4.2E0 4.6E0 3.9E0 3.8E0 4.1E0 4.0E0 5.7E0 2.6E0 5.9E0 Fold Change 4.1E0 3.7E0 4.8E0 5.0E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60 2.2E-59 1.4E-56 5.7E-56 1.1E-49 5.8E-36 5.0E-34 Benjamini 6.1E-60 1.9E-55 7.4E-50 2.0E-43	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-63 6.0E-60 2.1E-59 1.4E-56 5.5E-56 1.0E-49 5.2E-36 4.8E-34 FDR 5.9E-60 1.5E-55 7.1E-50 1.9E-43 1.2E-
	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_SEQ_FEATURE ation Cluster 4 GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_BP_DIRECT GOTERM_BP_DIRECT	repeat:ANK 4 repeat:ANK 5 ANK repeat repeat:ANK 3 Ankyrin repeat Ankyrin repeat-containing domain repeat:ANK 2 repeat:ANK 1 repeat:ANK 6 ANK repeat:ANK 7 Enrichment Score: 37.87 rRNA processing Ribonucleoprotein nuclear-transcribed mRNA catabolic process, nonsense-mediated decay SRP-dependent cotranslational protein targeting to membrane translational initiation	RT R		Count 131 115 161 139 159 162 146 145 83 157 55 Count 147 160 97 80 97	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E- 61 7.5E- 59 3.2E- 58 6.8E- 52 4.9E- 38 3.8E- 36 P_Value 3.1E- 63 7.0E- 57 6.2E- 53 2.3E- 46 1.7E- 43 1.9E-	Fold Change 5.2E0 5.5E0 4.2E0 4.6E0 3.9E0 3.8E0 4.1E0 4.0E0 5.7E0 2.6E0 5.9E0 Fold Change 4.1E0 3.7E0 4.8E0 5.0E0 4.2E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60 2.2E-59 1.4E-56 5.7E-56 1.1E-49 5.8E-36 5.0E-34 Benjamini 6.1E-60 1.9E-55 7.4E-50 2.0E-43 1.3E-40	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-63 6.0E-60 2.1E-59 1.4E-56 5.5E-56 1.0E-49 5.2E-36 4.8E-34 FDR 5.99-60 1.5E-55 7.1E-50 1.9E-43 1.2E-40 1.1E-
	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_SEQ_FEATURE ation Cluster 4 GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	repeat:ANK 4 repeat:ANK 5 ANK repeat repeat:ANK 3 Ankyrin repeat Ankyrin repeat-containing domain repeat:ANK 2 repeat:ANK 1 repeat:ANK 6 ANK repeat:ANK 7 Enrichment Score: 37.87 rRNA processing Ribonucleoprotein nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, SRP-dependent cotranslational protein targeting to membrane translational initiation Ribosome	RT R		Count 131 115 161 139 159 162 146 145 83 157 55 Count 147 160 97 80 97 96	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E- 61 7.5E- 59 3.2E- 58 6.8E- 52 4.9E- 38 3.8E- 36 P_Value 3.1E- 63 7.0E- 57 6.2E- 53 2.3E- 46 1.7E- 43 1.9E- 38 2.0E-	Fold Change 5.2E0 5.5E0 4.2E0 4.6E0 3.9E0 3.8E0 4.1E0 4.0E0 5.7E0 2.6E0 5.9E0 Fold Change 4.1E0 4.8E0 5.0E0 4.2E0 3.7E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60 2.2E-59 1.4E-56 5.7E-56 1.1E-49 5.8E-36 5.0E-34 Benjamini 6.1E-60 1.9E-55 7.4E-50 2.0E-43 1.3E-40 2.4E-36	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-63 6.0E-60 2.1E-59 1.4E-56 5.5E-56 1.0E-49 5.2E-36 4.8E-34 FDR 5.9E-60 1.5E-55 7.1E-50 1.9E-43 1.2E-40 1.1E-36 1.3E-
	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_SEQ_FEATURE ation Cluster 4 GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_BP_DIRECT GOTERM_BP_DIRECT KEGG_PATHWAY	repeat:ANK 4 repeat:ANK 5 ANK repeat repeat:ANK 3 Ankyrin repeat Ankyrin repeat-containing domain repeat:ANK 2 repeat:ANK 1 repeat:ANK 6 ANK repeat:ANK 7 Enrichment Score: 37.87 rRNA processing Ribonucleoprotein nuclear-transcribed mRNA catabolic process, nonsense-mediated decay. SRP-dependent cotranslational protein targeting to membrane translational initiation Ribosome viral transcription	RT R		Count 131 115 161 139 159 162 146 145 83 157 55 Count 147 160 97 80 97 96 81	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E- 61 7.5E- 59 3.2E- 58 6.8E- 52 4.9E- 38 3.8E- 36 P_Value 3.1E- 63 7.0E- 57 6.2E- 53 2.3E- 46 1.7E- 43 1.9E- 38 2.0E- 37 2.5E-	Fold Change 5.2E0 5.5E0 4.2E0 4.6E0 3.9E0 3.8E0 4.1E0 4.0E0 5.7E0 2.6E0 5.9E0 Fold Change 4.1E0 3.7E0 4.8E0 5.0E0 4.2E0 3.7E0 4.3E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60 2.2E-59 1.4E-56 5.7E-56 1.1E-49 5.8E-36 5.0E-34 Benjamini 6.1E-60 1.9E-55 7.4E-50 2.0E-43 1.3E-40 2.4E-36 1.3E-34	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-63 6.0E-60 2.1E-59 1.4E-56 5.5E-56 1.0E-49 5.2E-36 4.8E-34 FDR 5.9E-60 1.5E-55 7.1E-50 1.9E-43 1.2E-40 1.1E-36 1.3E-34 2.8E-
	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_SEQ_FEATURE ation Cluster 4 GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_BP_DIRECT GOTERM_BP_DIRECT KEGG_PATHWAY GOTERM_BP_DIRECT	repeat:ANK 4 repeat:ANK 5 ANK repeat repeat:ANK 3 Ankyrin repeat Ankyrin repeat-containing domain repeat:ANK 2 repeat:ANK 1 repeat:ANK 6 ANK repeat:ANK 7 Enrichment Score: 37.87 rRNA processing Ribonucleoprotein nuclear-transcribed mRNA catabolic process, nonsense-mediated decay. SRP-dependent cotranslational protein targeting to membrane translational initiation Ribosome viral transcription	RT R		Count 131 115 161 139 159 162 146 145 83 157 55 Count 147 160 97 80 97 96 81	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E- 61 7.5E- 59 3.2E- 58 6.8E- 52 4.9E- 38 3.8E- 36 P_Value 3.1E- 63 7.0E- 57 6.2E- 53 2.3E- 46 1.7E- 43 1.9E- 38 2.0E- 37 2.5E- 35 5.8E-	Fold Change 5.2E0 4.2E0 4.6E0 3.9E0 3.8E0 4.1E0 4.0E0 5.7E0 2.6E0 5.9E0 Fold Change 4.1E0 3.7E0 4.8E0 5.0E0 4.2E0 3.7E0 4.3E0 5.4E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60 2.2E-59 1.4E-56 5.7E-56 1.1E-49 5.8E-36 5.0E-34 Benjamini 6.1E-60 1.9E-55 7.4E-50 2.0E-43 1.3E-40 2.4E-36 1.3E-34	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-63 6.0E-59 1.4E-56 5.5E-56 1.0E-49 5.2E-36 4.8E-34 FDR 5.9E-60 1.5E-55 7.1E-50 1.9E-43 1.1E-36 1.3E-34 2.8E-33 8.4E-
	UP_SEQ_FEATURE UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_SEQ_FEATURE ation Cluster 4 GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_BP_DIRECT GOTERM_BP_DIRECT KEGG_PATHWAY GOTERM_BP_DIRECT GOTERM_BP_DIRECT KEGG_PATHWAY GOTERM_BP_DIRECT GOTERM_BP_DIRECT	repeat:ANK 4 repeat:ANK 5 ANK repeat repeat:ANK 3 Ankyrin repeat Ankyrin repeat-containing domain repeat:ANK 2 repeat:ANK 1 repeat:ANK 6 ANK repeat:ANK 7 Enrichment Score: 37.87 rRNA processing Ribonucleoprotein nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, SRP-dependent cotranslational protein targeting to membrane translational initiation Ribosome viral transcription cytosolic large ribosomal subunit	RI R		Count 131 115 161 139 159 162 146 145 83 157 55 Count 147 160 97 80 97 96 81 58	30 P_Value 1.2E- 73 7.0E- 69 2.0E- 67 1.6E- 65 2.9E- 62 1.1E- 61 7.5E- 59 3.2E- 58 6.8E- 52 4.9E- 38 3.8E- 36 P_Value 3.1E- 63 7.0E- 57 6.2E- 53 2.3E- 46 1.7E- 43 1.9E- 38 2.0E- 37 2.5E- 35	Fold Change 5.2E0 4.2E0 4.6E0 3.9E0 3.8E0 4.1E0 4.0E0 5.7E0 2.6E0 5.9E0 Fold Change 4.1E0 4.1E0 3.7E0 4.8E0 5.0E0 4.2E0 3.7E0 4.3E0 5.4E0 5.4E0 3.6E0	Benjamini 3.3E-71 1.8E-66 6.1E-66 3.9E-63 6.6E-60 2.2E-59 1.4E-56 5.7E-56 1.1E-49 5.8E-36 5.0E-34 Benjamini 6.1E-60 1.9E-55 7.4E-50 2.0E-43 1.3E-40 2.4E-36 1.3E-34 3.2E-33	28 FDR 3.2E-71 1.7E-66 4.7E-66 3.8E-63 6.0E-59 1.4E-56 5.5E-56 1.0E-49 5.2E-36 4.8E-34 FDR 5.9E-60 1.5E-55 7.1E-50 1.9E-43 1.2E-40 1.1E-36 1.3E-34 2.8E-33

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

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

	tion Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	i FDF
Annota	ition Cluster 12	Enrichment Score: 16.09	G	**	Count	P_Value	Fold Change	Benjamini	i FDF
	UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	<u>RT</u>	=	55	4.7E- 31	5.3E0	5.6E-29	5.4E 29
	UP_SEQ_FEATURE	domain:HECT	<u>RT</u>	•	23	6.6E- 14	5.6E0	4.8E-12	4.7E 12
	INTERPRO	<u>HECT</u>	<u>RT</u>	•	23	4.8E- 13	5.1E0	3.0E-11	2.7E
	SMART	<u>HECTc</u>	<u>RT</u>	•	23	2.8E-9	3.3E0	7.9E-8	7.2E
Annota	ition Cluster 13	Enrichment Score: 15.77	G		Count	P_Value	Fold Change	Benjamini	
	UP_KEYWORDS	<u>Helicase</u>	<u>RT</u>		82	1.0E- 31	3.9E0	1.8E-30	1.4E 30
	INTERPRO	Helicase, superfamily 1/2, ATP-binding	<u>RT</u>		68	1.9E-	3.8E0	2.1E-24	2.0
_ 	INTERPRO	domain Helicase, C-terminal	RT		67	26 3.4E-	3.8E0	3.7E-24	3.4
_ _	UP_SEQ_FEATURE	domain:Helicase C-terminal	RT	-	64	26 8.9E-	4.0E0	9.6E-24	24 9.3
_ _	UP_SEQ_FEATURE	domain:Helicase ATP-binding	RT		65	26 6.9E-	3.9E0	7.3E-23	24 7.0
_ _	GOTERM_MF_DIRECT			-		25 1.3E-			23 7.7
	SMART	helicase activity	<u>RT</u>	-	50	17 1.2E-	3.5E0	8.6E-16	16 5.2
	SMART	<u>DEXDc</u>	<u>RT</u>	•	67	15	2.5E0	5.7E-14	14 6.4
		HELICC	<u>RT</u>	•	66	1.6E- 15	2.5E0	7.0E-14	14
	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N- terminal	<u>RT</u>	•	41	2.8E- 15	3.7E0	2.1E-13	1.9 13
	GOTERM_MF_DIRECT	ATP-dependent RNA helicase activity	<u>RT</u>	•	38	2.4E- 13	3.5E0	1.0E-11	8.9 12
	UP_SEQ_FEATURE	short sequence motif:DEAH box	<u>RT</u>	•	28	6.7E- 13	4.4E0	4.6E-11	4.4 11
	GOTERM_BP_DIRECT	RNA secondary structure unwinding	<u>RT</u>	•	26	2.2E-9	3.5E0	2.1E-7	2.0 7
	INTERPRO	RNA helicase, DEAD-box type, Q motif	<u>RT</u>	1	22	2.0E-8	3.7E0	6.2E-7	5.7 7
	UP_SEQ_FEATURE	short sequence motif:Q motif	<u>RT</u>		21	1.4E-7	3.6E0	7.2E-6	6.9
	UP_SEQ_FEATURE	short sequence motif:DEAD box	<u>RT</u>		19	6.0E-7	3.6E0	2.6E-5	2.5
٦	INTERPRO	RNA helicase, ATP-dependent, DEAD-box,	<u>RT</u>		16	3.1E-6	3.7E0	7.3E-5	6.7
nnota	ition Cluster 14	conserved site Enrichment Score: 15.47	G	- 	Count	P_Value	Fold	Benjamini	5 i FDI
	UP_KEYWORDS	Protein phosphatase	RT	=	66	4.5E-	Change 3.4E0	5.7E-20	4.4
_ _	GOTERM_BP_DIRECT	protein dephosphorylation	RT		58	21 9.1E-	2.7E0	1.4E-11	20 1.4
_ _	GOTERM_MF_DIRECT					14 9.5E-			11 3.9
		protein serine/threonine phosphatase activity	<u>RT</u>	i	36	14	3.7E0 Fold	4.4E-12	12
	ution Cluster 15 UP_SEQ_FEATURE	Enrichment Score: 15.15	G	- T	Count	P_Value 4.7E-	Change	Benjamini	i FD I 5.4
	INTERPRO	active site:Glycyl thioester intermediate	<u>RT</u>	•	55	31	5.3E0	5.6E-29	29
		<u>Ubiquitin-conjugating enzyme, active site</u>	<u>RT</u>	•	24	8.5E- 16	5.7E0	6.7E-14	6.2 14
	INTERPRO	<u>Ubiquitin-conjugating enzyme, E2</u>	<u>RT</u>	•	31	2.1E- 15	4.6E0	1.6E-13	1.5 13
	INTERPRO	<u>Ubiquitin-conjugating enzyme/RWD-like</u>	<u>RT</u>	•	33	2.9E- 12	3.7E0	1.6E-10	1.5 10
	GOTERM_MF_DIRECT	ubiquitin conjugating enzyme activity	<u>RT</u>	•	23	3.8E- 12	4.7E0	1.4E-10	1.3 10
	GOTERM_BP_DIRECT	protein K48-linked ubiquitination	<u>RT</u>	•	26	1.4E-8	3.3E0	1.2E-6	1.1 6
nnota	ition Cluster 16	Enrichment Score: 12.35	G	**	Count	P_Value	Fold Change	Benjamini	i FDI
	UP_KEYWORDS	DNA repair	<u>RT</u>	=	98	6.9E- 16	2.3E0	7.8E-15	6.0 15
	UP_KEYWORDS	<u>DNA damage</u>	<u>RT</u>	_	110	2.3E- 15	2.1E0	2.5E-14	1.9 14
	GOTERM_BP_DIRECT	<u>DNA repair</u>	<u>RT</u>	=	74	5.3E-8	1.9E0	4.1E-6	4.0
nnota	ition Cluster 17	Enrichment Score: 12.02	G		Count	P_Value	Fold	Benjamini	6 i FDI
	GOTERM_BP_DIRECT	proteasome-mediated ubiquitin-dependent	RT	=	99	1.9E-	Change 2.9E0	8.9E-23	8.6
7	GOTERM_BP_DIRECT	<u>protein catabolic process</u> <u>anaphase-promoting complex-dependent</u>	RT	_	54	25 3.5E-	4.0E0	1.4E-20	23 1.3
	GOTERM_BP_DIRECT	catabolic process positive regulation of ubiquitin-protein ligase	<u>KI</u>	•	34	23	-r.0L0	1.76-20	20
		activity involved in regulation of mitotic cell cycle transition	<u>RT</u>	•	52	2.3E- 22	4.1E0	7.5E-20	7.2 20
	GOTERM_BP_DIRECT	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	<u>RT</u>	=	48	2.4E- 20	4.0E0	6.5E-18	6.2 18
	GOTERM_BP_DIRECT	stimulatory C-type lectin receptor signaling pathway	<u>RT</u>	•	60	5.3E- 20	3.4E0	1.4E-17	1.3 17
	GOTERM_BP_DIRECT	<u>T cell receptor signaling pathway</u>	<u>RT</u>	=	68	5.6E-	2.7E0	1.1E-13	1.0
						16			13
	GOTERM_BP_DIRECT	NIK/NF-kappaB signaling	<u>RT</u>		41	1.6E- 15	3.7E0	2.9E-13	2.8 13

Annota	ition Cluster 1	Enrichment Score: ?	G	· R	Count	P_Value	Fold Change	Benjamini	i FDR
	GOTERM_BP_DIRECT	positive regulation of canonical Wnt signaling pathway	<u>RT</u>	i	53	8.5E- 12	2.6E0	1.1E-9	1.1E- 9
	GOTERM_BP_DIRECT	regulation of mRNA stability	<u>RT</u>	•	46	1.5E- 10	2.6E0	1.7E-8	1.7E- 8
	GOTERM_BP_DIRECT	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	<u>RT</u>	i de la companya de	18	2.5E-9	4.6E0	2.4E-7	2.3E- 7
	UP_KEYWORDS	Proteasome	<u>RT</u>		27	2.7E-9	3.5E0	2.4E-8	1.8E-
	GOTERM_CC_DIRECT	proteasome complex	RT		29	1.6E-8	3.1E0	5.0E-7	8 4.4E-
	GOTERM_BP_DIRECT	regulation of cellular amino acid metabolic	RT		26	1.2E-7	3.0E0	8.3E-6	7 8.0E-
	GOTERM_BP_DIRECT	<u>negative regulation of canonical Wnt signaling</u>	RT		55	2.9E-7	2.0E0	1.9E-5	6 1.8E-
	GOTERM_BP_DIRECT	<u>pathway</u> <u>Wnt signaling pathway, planar cell polarity</u>	RT		35	3.0E-6		1.5E-4	5 1.5E-
	KEGG_PATHWAY	<u>pathway</u> Proteasome	RT		23	4.1E-6		1.2E-5	4 5.8E-
	GOTERM_BP_DIRECT	antigen processing and presentation of		_					6 4.1E-
		exogenous peptide antigen via MHC class I, TAP-dependent	<u>RT</u>	•	24	1.4E-4	2.3E0	4.3E-3	3
	GOTERM_BP_DIRECT	tumor necrosis factor-mediated signaling pathway	RT	i	36	4.0E-4		1.0E-2	1.0E- 2
Annota	tion Cluster 18	Enrichment Score: 11.69	G	No.	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	Actin-related protein	<u>RT</u>	•	29	2.8E- 17	5.3E0	2.4E-15	2.2E- 15
	SMART	ACTIN	<u>RT</u>	•	29	4.9E- 13	3.6E0	1.8E-11	1.6E- 11
	INTERPRO	Actin/actin-like conserved site	<u>RT</u>	•	18	1.0E- 10	5.3E0	4.3E-9	3.9E- 9
	INTERPRO	Actin, conserved site	<u>RT</u>	i	15	1.3E-8	5.2E0	4.2E-7	3.9E- 7
Annota	tion Cluster 19	Enrichment Score: 11.41	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	protein K11-linked ubiquitination	<u>RT</u>	i	25	4.5E- 16	5.5E0	8.9E-14	8.6E- 14
	GOTERM_CC_DIRECT	anaphase-promoting complex	<u>RT</u>	i .	19	5.0E- 11	5.2E0	2.1E-9	1.9E- 9
	GOTERM_BP_DIRECT	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	<u>RT</u>	i .	18	2.5E-9	4.6E0	2.4E-7	2.3E- 7
Annota	tion Cluster 20	Enrichment Score: 11.35	G	™	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:EF-hand 3	<u>RT</u>	•	61	6.9E- 27	4.3E0	7.6E-25	7.3E- 25
	UP_SEQ_FEATURE	domain:EF-hand 2	<u>RT</u>	■	76	5.4E- 18	2.8E0	4.9E-16	4.7E- 16
	UP_SEQ_FEATURE	domain:EF-hand 4	<u>RT</u>	•	38	3.5E- 16	4.2E0	2.9E-14	2.8E- 14
	UP_SEQ_FEATURE	domain:EF-hand 1	<u>RT</u>	•	72	1.7E- 15	2.7E0	1.3E-13	1.3E- 13
	UP_SEQ_FEATURE	calcium-binding region:1	<u>RT</u>	E .	55	4.0E- 14	2.9E0	3.0E-12	2.9E- 12
	UP_SEQ_FEATURE	calcium-binding region:3	<u>RT</u>	i e	27	2.2E- 13	4.7E0	1.6E-11	1.5E- 11
	UP_SEQ_FEATURE	calcium-binding region:2	<u>RT</u>	¥	51	2.8E- 13	2.9E0	2.0E-11	1.9E- 11
	INTERPRO	EF-Hand 1, calcium-binding site	<u>RT</u>	£	67	9.0E- 12	2.3E0	4.5E-10	4.1E- 10
	INTERPRO	EF-hand domain	<u>RT</u>	=	79	1.4E- 11	2.1E0	6.7E-10	6.1E- 10
	INTERPRO	EF-hand-like domain	<u>RT</u>	=	90	3.9E- 11	2.0E0	1.7E-9	1.6E- 9
	SMART	<u>EFh</u>	<u>RT</u>	•	72	9.8E- 11	2.0E0	3.1E-9	2.8E-
	COG_ONTOLOGY	Signal transduction mechanisms / Cytoskeleton / Cell division and chromosome	<u>RT</u>		31		1.8E0	7.6E-4	7.6E-
	GOTERM_MF_DIRECT	partitioning / General function prediction only calcium ion binding	<u>RT</u>	=	110	8 9F-1	9.1E-1	1 0F0	8.9E-
	UP_KEYWORDS	<u>Calcium</u>	RT	=	107		8.4E-1		1 9.9E-
Annota	ition Cluster 21	Enrichment Score: 11.32	<u></u>	198		P_Value		Roniamini	1 i FDR
	UP_KEYWORDS	Motor protein	RT	-	84	3.8E- 36		7.7E-35	5.9E-
	UP_SEQ_FEATURE	domain: Kinesin-motor	RT	1	33	5.9E-	5.1E0	5.2E-16	35 5.0E-
	GOTERM_CC_DIRECT	kinesin complex	RT		37	18 1.8E-	4.4E0	1.2E-15	16 1.0E-
	INTERPRO	Kinesin, motor region, conserved site	RT		32	17 4.7E-	4.8E0	4.0E-15	15 3.6E-
	INTERPRO	Kinesin, motor domain	RT		33	17 2.9E-	4.5E0	2.4E-14	15 2.2E-
	GOTERM_MF_DIRECT	microtubule motor activity	RT		42	16 1.4E-	3.1E0	5.4E-11	14 4.8E-
	GOTERM_CC_DIRECT	microtubule	RT		96	12 3.1E-		1.4E-9	11 1.3E-
	SMART	<u>KISc</u>	RT	7	33	11 6.1E-		2.1E-9	9 1.9E-
	GOTERM_BP_DIRECT	microtubule-based movement	RT	:	38	11 1.4E-9		1.4E-7	9 1.3E-
		STATE		-				/	7

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

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

Annot	ation Cluster 1	Enrichment Score: ?	G	■	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	Personal Metal							
	UP_SEQ_FEATURE	PROPERTY NET							
	P. SEC_PEATURE	1.5E-6							
	UP_SEQ_FEATURE SMART UP_SEQ_FEATURE SMART UP_SEQ_FEATURE SMART UP_SEQ_FEATURE SMART UP_SEQ_FEATURE INTERPRO INTERPRO INTERPRO SMART tion Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO INTERPRO SMART tion Cluster 31 KEGG_PATHWAY	repeat:ANK 14	<u>RT</u>	1	13	2.9E-8	5.9E0	1.5E-6	
	UP_SEQ_FEATURE repeat:ANK 11 RI UP_SEQ_FEATURE repeat:ANK 12 RI UP_SEQ_FEATURE repeat:ANK 13 RI UP_SEQ_FEATURE repeat:ANK 14 RI UP_SEQ_FEATURE repeat:ANK 15 RI UP_SEQ_FEATURE repeat:ANK 16 RI UP_SEQ_FEATURE repeat:ANK 17 RI UP_SEQ_FEATURE repeat:ANK 18 RI UP_SEQ_FEATURE repeat:ANK 19 RI UP_SEQ_FEATURE repeat:ANK 20 RI UP_SEQ_FEATURE repeat:ANK 21 RI UP_SEQ_FEATURE repeat:ANK 22 RI UP_SEQ_FEATURE repeat:ANK 23 RI UP_SEQ_FEATURE repeat:ANK 25 RI UP_SEQ_FEATURE repeat:ANK 26 RI UP_SEQ_FEATURE repeat:ANK 27 RI GOTERM_BP_DIRECT protein tarceting to plasma membrane RI INTERPRO ZUS RI SMART DEATH RI UP_SEQ_FEATURE domain:ZUS RI	i	13	2.9E-8	5.9E0	1.5E-6	1.5E-		
	Page	3.6E-5	3.5E-						
	UP_SEQ_FEATURE	Property Property							
	UP_SEQ_FEATURE	SEG_FEATURE PROCESSION 12 ST.							
	PATE		1.7E-						
	UP_SEQ_FEATURE repeat:ANK 11 RI P_SEQ_FEATURE repeat:ANK 12 RI P_SEQ_FEATURE repeat:ANK 13 RI P_SEQ_FEATURE repeat:ANK 14 RI P_SEQ_FEATURE repeat:ANK 15 RI P_SEQ_FEATURE repeat:ANK 15 RI P_SEQ_FEATURE repeat:ANK 15 RI P_SEQ_FEATURE repeat:ANK 16 RI P_SEQ_FEATURE repeat:ANK 16 RI P_SEQ_FEATURE repeat:ANK 18 RI P_SEQ_FEATURE repeat:ANK 19 RI P_SEQ_FEATURE repeat:ANK 19 RI P_SEQ_FEATURE repeat:ANK 19 RI P_SEQ_FEATURE repeat:ANK 20 RI P_SEQ_FEATURE repeat:ANK 20 RI P_SEQ_FEATURE repeat:ANK 21 RI P_SEQ_FEATURE repeat:ANK 21 RI P_SEQ_FEATURE repeat:ANK 22 RI P_SEQ_FEATURE repeat:ANK 23 RI P_SEQ_FEATURE repeat:ANK 24 RI P_SEQ_FEATURE repeat:ANK 24 RI P_SEQ_FEATURE repeat:ANK 25 RI P_SEQ_FEATURE repeat:ANK 26 RI P_SEQ_FEATURE repeat:ANK 26 RI P_SEQ_FEATURE repeat:ANK 27 RI						7.6E-		
	UP SECFEATURE PROPRETABLE PRO		7.6E-						
	UP_SEQ_FEATURE		3.4E-						
	Page								
	UP_SEQ_FEATURE								_
									2
	P. P. C. P	1							
									1
				1					1
					9	5.9E-2	2.0E0	5.2E-1	1
		<u>ZU5</u>	<u>RT</u>		4	3.0E-1	2.1E0	1.0E0	1
		<u>DEATH</u>	<u>RT</u>	i	9	3.4E-1	1.4E0	1.0E0	1
		domain:ZU5	<u>RT</u>	1	3	3.9E-1	2.3E0	1.0E0	1
	SMART	<u>ZU5</u>	<u>RT</u>	i e	3	6.9E-1	1.4E0	1.0E0	
	GOTERM_MF_DIRECT	cytoskeletal adaptor activity	<u>RT</u>	i	3	7.8E-1		1.0E0	
Annot	ation Cluster 30					P_Value	Fold		1 FDR
Annot	ation Cluster 30 UP_SEQ_FEATURE	Enrichment Score: 8.33	G	17	Count	P_Value	Fold Change	Benjamini	1 FDR 1.5E-
Annot	ation Cluster 30 UP_SEQ_FEATURE INTERPRO	Enrichment Score: 8.33 domain:BTB	G RT	=	Count 58	P_Value 2.1E- 13	Fold Change 2.7E0	5.0E-14 1.0E-8 1.5E-6 1.5E-6 1.5E-6 1.5E-6 3.6E-5 1.8E-4 1.8E-4 1.8E-4 7.9E-4 7.9E-4 3.5E-3 3.5E-3 6.2E-2 2.2E-1 8.4E-1 5.2E-1 1.0E0	1 FDR 1.5E- 11 4.1E-
Annot	ation Cluster 30 UP_SEQ_FEATURE INTERPRO	Enrichment Score: 8.33 domain:BTB BTB/POZ-like	G RT RT		Count 58 63	P_Value 2.1E- 13 1.2E-9	Fold Change 2.7E0 2.2E0	Benjamini 1.5E-11 4.5E-8	1 FDR 1.5E- 11 4.1E- 8 6.1E-
Annot	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO	Enrichment Score: 8.33 domain:BTB BTB/POZ-like BTB/POZ fold	G RT RT RT		Count 58 63 65	P_Value 2.1E- 13 1.2E-9 1.9E-9	Fold Change 2.7E0 2.2E0 2.1E0	Benjamini 1.5E-11 4.5E-8 6.7E-8	1 FDR 1.5E- 11 4.1E- 8 6.1E- 8 1.1E-
	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART	Enrichment Score: 8.33 domain:BTB BTB/POZ-like BTB/POZ fold BTB	G RT RT RT RT		Count 58 63 65 63	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4	Fold Change 2.7E0 2.2E0 2.1E0 1.5E0 Fold	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2	1 FDR 1.5E- 11 4.1E- 8 6.1E- 8 1.1E- 2
	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31	Enrichment Score: 8.33 domain:BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8	G RT RT RT RT G		Count 58 63 65 63 Count	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E-	Fold Change 2.7E0 2.2E0 2.1E0 1.5E0 Fold Change	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini	1 FDR 1.5E- 11 4.1E- 8 6.1E- 8 1.1E- 2 FDR 1.1E-
	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31 KEGG_PATHWAY	Enrichment Score: 8.33 domain:BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8 Estrogen signaling pathway	G RT RT RT RT RT RT RT		Count 58 63 65 63 Count 58	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E- 17	Fold Change 2.7E0 2.2E0 2.1E0 1.5E0 Fold Change 3.0E0	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini 2.4E-16	1.5E- 11.4.1E- 8.6.1E- 8.1.1E- 2.FDR.1.1E- 16.7.4E-
	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31 KEGG_PATHWAY KEGG_PATHWAY	Enrichment Score: 8.33 domain:BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8 Estrogen signaling pathway Chemokine signaling pathway	RI R		Count 58 63 65 63 Count 58 68	2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E- 17 4.2E-8	Fold Change 2.7E0 2.2E0 2.1E0 1.5E0 Fold Change 3.0E0 1.9E0	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini 2.4E-16 1.6E-7	1.5E- 11 4.1E- 8 6.1E- 8 1.1E- 2 FDR 1.1E- 16 7.4E- 8 1.8E-
	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31 KEGG_PATHWAY KEGG_PATHWAY	Enrichment Score: 8.33 domain:BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8 Estrogen signaling pathway Chemokine signaling pathway Melanogenesis	RI		Count 58 63 65 63 Count 58 68 41	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E- 17 4.2E-8 1.1E-6	Fold Change 2.7E0 2.2E0 2.1E0 1.5E0 Fold Change 3.0E0 1.9E0 2.1E0	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini 2.4E-16 1.6E-7 3.8E-6	1.5E- 11.5E- 11.4.1E- 8.6.1E- 8.1.1E- 2.FDR.1.1E- 16.7.4E- 8.1.8E- 6.1.2E-
	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31 KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY	Enrichment Score: 8.33 domain:BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8 Estrogen signaling pathway Chemokine signaling pathway Melanogenesis Cholinergic synapse	RT		Count 58 63 65 63 Count 58 68 41 42	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E- 17 4.2E-8 1.1E-6 8.8E-6	Fold Change 2.7E0 2.2E0 2.1E0 1.5E0 Fold Change 3.0E0 1.9E0 2.1E0 2.0E0	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini 2.4E-16 1.6E-7 3.8E-6 2.5E-5	1.15E- 1.16- 8.1.1E- 2.FDR 1.1E- 1.6.7.4E- 8.1.8E- 6.1.2E- 5.1.7E-
Annot	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31 KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY	Enrichment Score: 8.33 domain:BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8 Estrogen signaling pathway Chemokine signaling pathway Melanogenesis Cholinergic synapse cAMP signaling pathway	RI R		Count 58 63 65 63 Count 58 68 41 42 64	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E- 17 4.2E-8 1.1E-6 8.8E-6 1.3E-5	Fold Change 2.7E0 2.2E0 2.1E0 1.5E0 Fold Change 3.0E0 1.9E0 2.1E0 2.0E0 1.7E0 Fold	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini 2.4E-16 1.6E-7 3.8E-6 2.5E-5 3.5E-5	1.5E- 11.5E- 11.4.1E- 8.6.1E- 8.1.1E- 2.FDR 1.1E- 16.7.4E- 8.1.8E- 6.1.2E- 5.1.7E- 5.
Annot	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31 KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY	Enrichment Score: 8.33 domain:BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8 Estrogen signaling pathway Chemokine signaling pathway Melanogenesis Cholinergic synapse cAMP signaling pathway Enrichment Score: 7.87	RI R		Count 58 63 65 63 Count 58 68 41 42 64 Count	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E- 17 4.2E-8 1.1E-6 8.8E-6 1.3E-5 P_Value 2.2E-	Fold Change 2.7E0 2.2E0 2.1E0 1.5E0 Fold Change 3.0E0 1.9E0 2.1E0 2.0E0 1.7E0 Fold Change	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini 2.4E-16 1.6E-7 3.8E-6 2.5E-5 3.5E-5 Benjamini	1.5E- 1.1E- 8.6.1E- 8.1.1E- 2. FDR 1.1E- 1.6 7.4E- 8.1.8E- 6.1.7E- 5.1.7E- 5.1.7E- 5.1.7E- 1.5E-
Annot	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31 KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY UP_KEYWORDS	Enrichment Score: 8.33 domain:BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8 Estrogen signaling pathway Chemokine signaling pathway Melanogenesis Cholinergic synapse cAMP signaling pathway Enrichment Score: 7.87 Viral nucleoprotein	RI R		Count 58 63 65 63 Count 58 41 42 64 Count 20	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E- 17 4.2E-8 1.1E-6 8.8E-6 1.3E-5 P_Value 2.2E- 10 8.5E-	Fold Change 2.7E0 2.2E0 2.1E0 1.5E0 Fold Change 3.0E0 1.9E0 2.1E0 2.0E0 1.7E0 Fold Change 4.9E0	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini 2.4E-16 1.6E-7 3.8E-6 2.5E-5 3.5E-5 Benjamini 2.0E-9	1.5E- 1.5E- 11 4.1E- 8 6.1E- 8 1.1E- 2 FDR 1.1E- 16 7.4E- 8 1.8E- 6 1.2E- 5 1.7E- 5 FDR 1.5E- 9 2.8E-
Annot	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31 KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY GUSTER 32 UP_KEYWORDS GOTERM_CC_DIRECT	Enrichment Score: 8.33 domain:BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8 Estrogen signaling pathway Chemokine signaling pathway Melanogenesis Cholinergic synapse cAMP signaling pathway Enrichment Score: 7.87 Viral nucleoprotein viral nucleocapsid	RI R		Count 58 63 65 63 Count 58 68 41 42 64 Count 20 20	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E- 17 4.2E-8 1.1E-6 8.8E-6 1.3E-5 P_Value 2.2E- 10 8.5E- 10	Fold Change 2.7E0 2.2E0 2.1E0 1.5E0 Fold Change 3.0E0 1.9E0 2.1E0 2.0E0 1.7E0 Fold Change 4.9E0 4.5E0	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini 2.4E-16 1.6E-7 3.8E-6 2.5E-5 3.5E-5 Benjamini 2.0E-9 3.1E-8	1.5E- 1.1E- 8.6.1E- 8.1.1E- 2.FDR 1.1E- 1.6 7.4E- 8.1.2E- 5.1.7E- 5.1.7E- 5.2 FDR 1.5E- 9.2.8E- 8.6.6E-
Annot	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31 KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY GUSTER 32 UP_KEYWORDS GOTERM_CC_DIRECT UP_KEYWORDS	Enrichment Score: 8.33 domain:BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8 Estrogen signaling pathway Chemokine signaling pathway Melanogenesis Cholinergic synapse cAMP signaling pathway Enrichment Score: 7.87 Viral nucleoprotein viral nucleocapsid Virion	RI R		Count 58 63 65 63 Count 58 68 41 42 64 Count 20 20 20	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E- 17 4.2E-8 1.1E-6 8.8E-6 1.3E-5 P_Value 2.2E- 10 8.5E- 10 1.4E-5	Fold Change 2.7E0 2.2E0 2.1E0 1.5E0 Fold Change 3.0E0 1.9E0 2.1E0 2.0E0 1.7E0 Fold Change 4.9E0 4.5E0 2.9E0 Fold	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini 2.4E-16 1.6E-7 3.8E-6 2.5E-5 3.5E-5 Benjamini 2.0E-9 3.1E-8 8.5E-5	1.5E-11 4.1E-8 6.1E-8 1.1E-2 FDR 1.1E-16 7.4E-8 1.8E-6 1.2E-5 1.7E-5 FDR 2.8E-8 6.6E-5
Annot	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31 KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY GOTERM_CC_DIRECT UP_KEYWORDS ation Cluster 33	Enrichment Score: 8.33 domain:BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8 Estrogen signaling pathway Chemokine signaling pathway Melanogenesis Cholinergic synapse cAMP signaling pathway Enrichment Score: 7.87 Viral nucleoprotein viral nucleocapsid Virion Enrichment Score: 7.86	RI R		Count 58 63 Count 58 68 41 42 64 Count 20 20 20 Count	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E- 17 4.2E-8 1.1E-6 8.8E-6 1.3E-5 P_Value 2.2E- 10 8.5E- 10 1.4E-5 P_Value 3.2E-	Fold Change 2.7E0 2.2E0 1.5E0 Fold Change 3.0E0 1.9E0 2.1E0 2.0E0 1.7E0 Fold Change 4.9E0 4.5E0 2.9E0 Fold Change	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini 2.4E-16 1.6E-7 3.8E-6 2.5E-5 3.5E-5 Benjamini 2.0E-9 3.1E-8 8.5E-5 Benjamini	1.5E-11 4.1E-8 6.1E-8 1.1E-2 FDR 1.1E-16 7.4E-8 1.8E-6 1.2E-5 1.7E-5 FDR 1.5E-9 2.8E-8 6.6E-5 FDR 1.4E-8
Annot	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31 KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY GUSTER 32 UP_KEYWORDS GOTERM_CC_DIRECT UP_KEYWORDS ation Cluster 33 KEGG_PATHWAY	Enrichment Score: 8.33 domain: BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8 Estrogen signaling pathway Chemokine signaling pathway Melanogenesis Cholinergic synapse cAMP signaling pathway Enrichment Score: 7.87 Viral nucleoprotein viral nucleocapsid Virion Enrichment Score: 7.86 Chronic myeloid leukemia	RI R		Count 58 63 65 63 Count 58 68 41 42 64 Count 20 20 Count 44	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E- 17 4.2E-8 1.1E-6 8.8E-6 1.3E-5 P_Value 2.2E- 10 8.5E- 10 1.4E-5 P_Value 3.2E- 14	Fold Change 2.7E0 2.2E0 2.1E0 1.5E0 Fold Change 3.0E0 1.9E0 2.1E0 2.0E0 1.7E0 Fold Change 4.9E0 4.5E0 2.9E0 Fold Change 3.2E0	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini 2.4E-16 1.6E-7 3.8E-6 2.5E-5 3.5E-5 Benjamini 2.0E-9 3.1E-8 8.5E-5 Benjamini 3.1E-13	1.15E-11 4.1E-8 6.1E-8 1.1E-2 FDR 1.1E-16 7.4E-8 1.8E-6 1.7E-5 1.7E-5 FDR 1.5E-9 2.8E-8 6.6E-5 FDR 1.4E-13 9.4E-13
Annot	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31 KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY GUSTER 32 UP_KEYWORDS GOTERM_CC_DIRECT UP_KEYWORDS ation Cluster 33 KEGG_PATHWAY KEGG_PATHWAY	Enrichment Score: 8.33 domain:BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8 Estrogen signaling pathway Chemokine signaling pathway Melanogenesis Cholinergic synapse cAMP signaling pathway Enrichment Score: 7.87 Viral nucleoprotein viral nucleocapsid Virion Enrichment Score: 7.86 Chronic myeloid leukemia Small cell lung cancer Influence of Ras and Rho proteins on G1 to S	RI R		Count 58 63 65 63 Count 58 68 41 42 64 Count 20 20 20 Count 44 35	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E- 17 4.2E-8 1.1E-6 8.8E-6 1.3E-5 P_Value 2.2E- 10 8.5E- 10 1.4E-5 P_Value 3.2E- 14 7.0E-6	Fold Change 2.7E0 2.2E0 2.1E0 1.5E0 Fold Change 3.0E0 1.9E0 2.1E0 2.0E0 1.7E0 Fold Change 4.9E0 4.5E0 2.9E0 Fold Change 3.2E0 2.1E0	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini 2.4E-16 1.6E-7 3.8E-6 2.5E-5 3.5E-5 Benjamini 2.0E-9 3.1E-8 8.5E-5 Benjamini 3.1E-13	1.5E-11 4.1E-8 6.1E-8 1.1E-2 FDR 1.1E-16 7.4E-8 1.2E-5 1.7E-5 1.7E-5 FDR 1.5E-9 2.8E-8 6.6E-5 1.4E-13 9.4E-6 4.0E-
Annot	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31 KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY Ation Cluster 32 UP_KEYWORDS GOTERM_CC_DIRECT UP_KEYWORDS ation Cluster 33 KEGG_PATHWAY KEGG_PATHWAY	Enrichment Score: 8.33 domain:BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8 Estrogen signaling pathway Chemokine signaling pathway Melanogenesis Cholinergic synapse cAMP signaling pathway Enrichment Score: 7.87 Viral nucleoprotein viral nucleocapsid Virion Enrichment Score: 7.86 Chronic myeloid leukemia Small cell lung cancer Influence of Ras and Rho proteins on G1 to S Transition	RI R		Count 58 63 Count 58 68 41 42 64 Count 20 20 20 Count 44 35 21	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E- 17 4.2E-8 1.1E-6 8.8E-6 1.3E-5 P_Value 2.2E- 10 8.5E- 10 1.4E-5 P_Value 3.2E- 14 7.0E-6 1.1E-5	Fold Change 2.7E0 2.2E0 2.1E0 1.5E0 Fold Change 3.0E0 1.9E0 2.1E0 2.0E0 1.7E0 Fold Change 4.9E0 4.5E0 2.9E0 Fold Change 3.2E0 2.1E0 2.4E0 Fold	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini 2.4E-16 1.6E-7 3.8E-6 2.5E-5 3.5E-5 Benjamini 2.0E-9 3.1E-8 8.5E-5 Benjamini 3.1E-13 2.0E-5 5.6E-4	1.5E-11 4.1E-8 6.1E-8 1.1E-2 FDR 1.1E-16 7.4E-8 1.8E-6 1.7E-5 1.7E-5 FDR 1.5E-9 2.8E-8 6.6E-5 FDR 1.4E-13 9.4E-6 4.0E-4
Annot	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31 KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY ATION Cluster 32 UP_KEYWORDS GOTERM_CC_DIRECT UP_KEYWORDS ation Cluster 33 KEGG_PATHWAY KEGG_PATHWAY BIOCARTA	Enrichment Score: 8.33 domain:BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8 Estrogen signaling pathway. Chemokine signaling pathway. Melanogenesis Cholinergic synapse cAMP signaling pathway. Enrichment Score: 7.87 Viral nucleoprotein viral nucleocapsid Virion Enrichment Score: 7.86 Chronic myeloid leukemia Small cell lung cancer Influence of Ras and Rho proteins on G1 to S Transition Enrichment Score: 7.48	RI R		Count 58 63 65 63 Count 58 68 41 42 64 Count 20 20 Count 44 35 21 Count	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E- 17 4.2E-8 1.1E-6 8.8E-6 1.3E-5 P_Value 2.2E- 10 8.5E- 10 1.4E-5 P_Value 3.2E- 14 7.0E-6 1.1E-5 P_Value 3.8E-	Fold Change 2.7E0 2.2E0 1.5E0 1.5E0 Fold Change 3.0E0 1.9E0 2.1E0 2.0E0 1.7E0 Fold Change 4.9E0 4.5E0 2.9E0 Fold Change 3.2E0 2.1E0 2.4E0 Fold Change	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini 2.4E-16 1.6E-7 3.8E-6 2.5E-5 3.5E-5 Benjamini 2.0E-9 3.1E-8 8.5E-5 Benjamini 3.1E-13 2.0E-5 5.6E-4 Benjamini	1.5E-11 4.1E-8 6.1E-8 1.1E-2 FDR 1.1E-16 7.4E-8 1.8E-6 1.2E-5 1.7E-5 FDR 1.5E-9 2.8E-8 6.6E-5 FDR 1.4E-13 9.4E-6 4.0E-4 FDR 1.8E-
Annot	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31 KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY Ation Cluster 32 UP_KEYWORDS GOTERM_CC_DIRECT UP_KEYWORDS ation Cluster 33 KEGG_PATHWAY KEGG_PATHWAY ATION CLUSTER 33 KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY BIOCARTA ation Cluster 34 INTERPRO	Enrichment Score: 8.33 domain: BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8 Estrogen signaling_pathway. Chemokine signaling_pathway. Melanogenesis Cholinergic synapse cAMP signaling_pathway. Enrichment Score: 7.87 Viral nucleoprotein viral nucleocapsid Virion Enrichment Score: 7.86 Chronic myeloid leukemia Small cell lung cancer Influence of Ras and Rho proteins on G1 to S Transition Enrichment Score: 7.48 Tubulin/FtsZ, C-terminal	RI R		Count 58 63 65 63 Count 58 68 41 42 64 Count 20 20 Count 44 35 21 Count 20	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E- 17 4.2E-8 1.1E-6 8.8E-6 1.3E-5 P_Value 2.2E- 10 8.5E- 10 1.4E-5 P_Value 3.2E- 14 7.0E-6 1.1E-5 P_Value 3.8E- 12 3.8E-	Fold Change 2.7E0 2.2E0 2.1E0 1.5E0 Fold Change 3.0E0 1.9E0 2.1E0 2.0E0 1.7E0 Fold Change 4.9E0 2.9E0 Fold Change 3.2E0 2.1E0 2.4E0 Fold Change 5.4E0	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini 2.4E-16 1.6E-7 3.8E-6 2.5E-5 3.5E-5 Benjamini 2.0E-9 3.1E-8 8.5E-5 Benjamini 3.1E-13 2.0E-5 5.6E-4 Benjamini 2.0E-10	1.5E-11 4.1E-8 6.1E-8 1.1E-2 FDR 1.1E-16 7.4E-8 1.8E-6 1.7E-5 1.7E-5 FDR 1.5E-9 2.8E-8 6.6E-5 1.4E-13 9.4E-6 4.0E-4 FDR 1.8E-10 1.8E-10 1.8E-10
Annot	ation Cluster 30 UP_SEQ_FEATURE INTERPRO INTERPRO SMART ation Cluster 31 KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY Ation Cluster 32 UP_KEYWORDS GOTERM_CC_DIRECT UP_KEYWORDS ation Cluster 33 KEGG_PATHWAY KEGG_PATHWAY ATION CLUSTER 33 KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY KEGG_PATHWAY BIOCARTA ation Cluster 34 INTERPRO	Enrichment Score: 8.33 domain: BTB BTB/POZ-like BTB/POZ fold BTB Enrichment Score: 8 Estrogen signaling_pathway. Chemokine signaling_pathway. Melanogenesis Cholinergic synapse cAMP signaling_pathway. Enrichment Score: 7.87 Viral nucleoprotein viral nucleocapsid Virion Enrichment Score: 7.86 Chronic myeloid leukemia Small cell lung cancer Influence of Ras and Rho proteins on G1 to S Transition Enrichment Score: 7.48 Tubulin/FtsZ, C-terminal	RI R		Count 58 63 65 63 Count 58 68 41 42 64 Count 20 20 Count 44 35 21 Count 20	P_Value 2.1E- 13 1.2E-9 1.9E-9 9.5E-4 P_Value 1.8E- 17 4.2E-8 1.1E-6 8.8E-6 1.3E-5 P_Value 2.2E- 10 8.5E- 10 1.4E-5 P_Value 3.2E- 14 7.0E-6 1.1E-5 P_Value 3.8E- 12 3.8E- 12	Fold Change 2.7E0 2.2E0 1.5E0 Fold Change 3.0E0 1.9E0 2.1E0 2.0E0 1.7E0 Fold Change 4.9E0 2.9E0 Fold Change 3.2E0 2.1E0 2.4E0 Fold Change 5.4E0 5.4E0 5.4E0	Benjamini 1.5E-11 4.5E-8 6.7E-8 1.2E-2 Benjamini 2.4E-16 1.6E-7 3.8E-6 2.5E-5 3.5E-5 Benjamini 2.0E-9 3.1E-8 8.5E-5 Benjamini 3.1E-13 2.0E-5 5.6E-4 Benjamini 2.0E-10	1.5E- 1.1E- 8.6.1E- 8.1.1E- 2.FDR 1.1E- 16.7.4E- 8.1.2E- 5.1.7E- 5. FDR 1.5E- 9.2.8E- 8.6.6E- 5. FDR 1.4E- 1.3 9.4E- 6.4.0E- 4.0E- 4.0E- 1.8E- 1.0 1.8E- 1.0

Annot	ation Cluster 1	Enrichment Score: ?	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	<u>Tubulin</u>	RT	i	20	1.6E-	Change	7.4E-10	6.8E-
	INTERPRO	Tubulin/FtsZ, 2-layer sandwich domain	RT	•	19	11 2.0E-	5.4E0	9.2E-10	10 8.4E-
	INTERPRO	Tubulin/FtsZ, GTPase domain	RT		20	11 5.5E-		2.4E-9	10 2.2E-
	SMART	SM00865	RT		19	11 2.6E-8		6.3E-7	9 5.7E-
	SMART				20	2.9E-8		6.5E-7	7 5.9E-
	KEGG_PATHWAY	SM00864	<u>RT</u>						7 5.7E-
	GOTERM_MF_DIRECT	Pathogenic Escherichia coli infection	<u>RT</u>	•	27	3.4E-7		1.2E-6	7 3.2E-
	INTERPRO	structural constituent of cytoskeleton	<u>RT</u>	•	40	1.6E-6		3.6E-5	5 7.3E-
	INTERPRO	Beta tubulin	<u>RT</u>	•	9	3.5E-6		8.0E-5	5
		Beta tubulin, autoregulation binding site	<u>RT</u>	•	9	3.5E-6	6.2E0	8.0E-5	7.3E- 5
	GOTERM_BP_DIRECT	microtubule-based process	<u>RT</u>	i	19	4.8E-6	3.1E0	2.4E-4	2.3E- 4
	INTERPRO	Alpha tubulin	<u>RT</u>	i	7	3.9E-3	3.9E0	4.3E-2	4.0E- 2
	KEGG_PATHWAY	<u>Phagosome</u>	<u>RT</u>	i	27	7.6E-1		1.0E0	7.6E- 1
Annot	tation Cluster 35	Enrichment Score: 6.92	G	5	Count	P_Value	Fold Change	Benjamini	
	GOTERM_MF_DIRECT	protein serine/threonine phosphatase activity	<u>RT</u>	•	36	9.5E- 14	3.7E0	4.4E-12	3.9E- 12
	INTERPRO	Protein phosphatase 2C (PP2C)-like	<u>RT</u>	•	17	5.1E- 10	5.3E0	2.1E-8	1.9E- 8
	UP_SEQ_FEATURE	metal ion-binding site:Manganese 1; via carbonyl oxygen	<u>RT</u>	i	13	1.1E-9	6.8E0	6.7E-8	6.4E- 8
	INTERPRO	Protein phosphatase 2C	<u>RT</u>	i	14	6.1E-8	5.1E0	1.8E-6	1.7E- 6
	INTERPRO	<u>Protein phosphatase 2C,</u> <u>manganese/magnesium aspartate binding site</u>	<u>RT</u>	i	11	1.1E-7	6.2E0	3.2E-6	3.0E- 6
	GOTERM_BP_DIRECT	peptidyl-threonine dephosphorylation	<u>RT</u>	i .	11	1.7E-7	5.9E0	1.2E-5	1.1E- 5
	SMART	PP2Cc	<u>RT</u>	i	17	3.0E-7	3.5E0	5.8E-6	5.3E- 6
	UP_SEQ_FEATURE	metal ion-binding site:Manganese 1	<u>RT</u>	i .	15	6.3E-6	3.8E0	2.4E-4	2.3E- 4
	UP_SEQ_FEATURE	metal ion-binding site:Manganese 2	<u>RT</u>	1	15	6.3E-6	3.8E0	2.4E-4	2.3E- 4
	UP_SEQ_FEATURE	domain:PP2C-like	<u>RT</u>	i de la companya de	10	1.3E-5	5.2E0	4.5E-4	4.3E-
							5.220		4
	GOTERM_MF_DIRECT	cation binding	<u>RT</u>	i	7	8.2E-3		6.9E-2	6.2E- 2
Annot	GOTERM_MF_DIRECT	cation binding Enrichment Score: 6.28	RT G	i N	7 Count	8.2E-3 P_Value	3.5E0		6.2E- 2
Annot							3.5E0 Fold	6.9E-2	6.2E- 2
Annot	tation Cluster 36	Enrichment Score: 6.28	G RT	17	Count	P_Value	3.5E0 Fold Change 3.4E0	6.9E-2 Benjamini	6.2E- 2 FDR 4.4E-
Annot	tation Cluster 36 UP_KEYWORDS	Enrichment Score: 6.28 Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup,	G RT	=	Count 66	P_Value 4.5E- 21 6.1E-	3.5E0 Fold Change 3.4E0	6.9E-2 Benjamini 5.7E-20	6.2E- 2 FDR 4.4E- 20 4.0E-
Annot	tation Cluster 36 UP_KEYWORDS INTERPRO	Enrichment Score: 6.28 Protein phosphatase Dual specificity phosphatase, catalytic domain	G RT RT		Count 66 31	4.5E- 21 6.1E- 15 7.6E- 15 1.2E-	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0	6.9E-2 Benjamini 5.7E-20 4.4E-13	6.2E- 2 FDR 4.4E- 20 4.0E- 13 4.8E- 13 6.4E-
Annot	unterpro	Enrichment Score: 6.28 Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine	RT RT RT		Count 66 31 28	4.5E- 21 6.1E- 15 7.6E- 15 1.2E- 12 8.5E-	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13	6.2E- 2 FDR 4.4E- 20 4.0E- 13 4.8E- 13 6.4E- 11 2.5E-
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO	Enrichment Score: 6.28 Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase	G RT RT RT RT		Count 66 31 28 24	4.5E- 21 6.1E- 15 7.6E- 15 1.2E- 12 8.5E- 11 2.7E-	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.8E0 4.0E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11	6.2E- 2 FDR 4.4E- 20 4.0E- 13 4.8E- 13 6.4E- 11 2.5E- 9 7.3E-
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT	Enrichment Score: 6.28 Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine phosphatase activity	RT RT RT RT RT		Count 66 31 28 24 25	4.5E- 21 6.1E- 15 7.6E- 15 1.2E- 12 8.5E- 11 2.7E- 10 5.1E-	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.0E0 3.2E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11 2.8E-9	6.2E- 2 FDR 4.4E- 20 4.0E- 13 4.8E- 13 6.4E- 11 2.5E- 9 7.3E- 9
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART	Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine phosphatase activity DSPc	G RT RT RT RT RT RT		Count 66 31 28 24 25 28	4.5E- 21 6.1E- 15 7.6E- 15 1.2E- 12 8.5E- 11 2.7E- 10	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.0E0 3.2E0 3.4E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11 2.8E-9 8.1E-9	6.2E-2 FDR 4.4E-20 4.0E-13 4.8E-13 6.4E-11 2.5E-9 7.3E-9 3.0E-8 4.3E-
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_SEQ_FEATURE	Enrichment Score: 6.28 Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine phosphatase activity DSPc domain:Tyrosine-protein phosphatase	RT RT RT RT RT RT RT RT		Count 66 31 28 24 25 28 31	4.5E- 21 6.1E- 15 7.6E- 15 1.2E- 12 8.5E- 11 2.7E- 10 5.1E- 10	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.0E0 3.2E0 3.4E0 4.9E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11 2.8E-9 8.1E-9 3.1E-8	6.2E-2 FDR 4.4E-20 4.0E-13 4.8E-13 6.4E-11 2.5E-9 7.3E-9 3.0E-8 4.3E-6 3.8E-
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_SEQ_FEATURE UP_SEQ_FEATURE	Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine phosphatase activity DSPc domain:Tyrosine-protein phosphatase domain:Rhodanese Protein-tyrosine/Dual specificity phosphatase Mitogen-activated protein (MAP) kinase	RI R		Count 66 31 28 24 25 28 31 15 34	4.5E-21 6.1E-15 7.6E-15 1.2E-12 8.5E-11 2.7E-10 5.1E-10 8.7E-8	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.0E0 3.2E0 3.4E0 4.9E0 2.6E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11 2.8E-9 8.1E-9 3.1E-8 4.4E-6 4.2E-6	6.2E-2 FDR 4.4E-20 4.0E-13 4.8E-13 6.4E-11 2.5E-9 7.3E-9 3.0E-8 4.3E-6 3.8E-6 1.6E-
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO	Enrichment Score: 6.28 Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine phosphatase activity DSPc domain:Tyrosine-protein phosphatase domain:Rhodanese Protein-tyrosine/Dual specificity phosphatase Mitogen-activated protein (MAP) kinase phosphatase	RI R		Count 66 31 28 24 25 28 31 15 34 10	4.5E-21 6.1E-15 7.6E-15 1.2E-12 8.5E-11 2.7E-10 5.1E-10 8.7E-8 1.5E-7 6.2E-7	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.0E0 3.2E0 3.4E0 4.9E0 2.6E0 6.2E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11 2.8E-9 8.1E-9 3.1E-8 4.4E-6 4.2E-6 1.7E-5	6.2E-2 FDR 4.4E-20 4.0E-13 4.8E-13 6.4E-11 2.5E-9 7.3E-9 3.0E-8 4.3E-6 1.6E-5 3.0E-
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO INTERPRO	Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine phosphatase activity DSPc domain:Tyrosine-protein phosphatase domain:Rhodanese Protein-tyrosine/Dual specificity phosphatase Mitogen-activated protein (MAP) kinase phosphatase active site:Phosphocysteine intermediate	RI R		Count 66 31 28 24 25 28 31 15 34 10 32	4.5E-21 6.1E-15 7.6E-15 1.2E-12 8.5E-11 2.7E-10 5.1E-10 8.7E-8 1.5E-7 6.2E-7	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.0E0 3.2E0 3.4E0 4.9E0 2.6E0 6.2E0 2.5E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11 2.8E-9 8.1E-9 3.1E-8 4.4E-6 4.2E-6 1.7E-5 3.1E-5	6.2E-2 FDR 4.4E-20 4.0E-13 4.8E-13 6.4E-11 2.5E-9 7.3E-9 3.0E-8 4.3E-6 3.8E-6 1.6E-5 3.0E-5
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO INTERPRO INTERPRO UP_SEQ_FEATURE	Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine phosphatase activity DSPc domain:Tyrosine-protein phosphatase domain:Rhodanese Protein-tyrosine/Dual specificity phosphatase Mitogen-activated protein (MAP) kinase phosphatase active site:Phosphocysteine intermediate protein tyrosine phosphatase activity	RI R		Count 66 31 28 24 25 28 31 15 34 10 32 38	4.5E-21 6.1E-15 7.6E-15 1.2E-12 8.5E-11 2.7E-10 5.1E-10 8.7E-8 1.5E-7 6.2E-7 7.2E-7	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.0E0 3.2E0 3.4E0 4.9E0 2.6E0 6.2E0 2.5E0 2.3E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11 2.8E-9 8.1E-9 3.1E-8 4.4E-6 4.2E-6 1.7E-5 3.1E-5 2.1E-5	6.2E-2 FDR 4.4E-20 4.0E-13 4.8E-13 6.4E-11 2.5E-9 7.3E-9 3.0E-8 4.3E-6 3.8E-6 1.6E-5 3.0E-5
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE GOTERM_MF_DIRECT	Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine phosphatase activity DSPc domain:Tyrosine-protein phosphatase domain:Rhodanese Protein-tyrosine/Dual specificity phosphatase Mitogen-activated protein (MAP) kinase phosphatase active site:Phosphocysteine intermediate	RI R		Count 66 31 28 24 25 28 31 15 34 10 32 38 37	4.5E-21 6.1E-15 7.6E-15 1.2E-12 8.5E-11 2.7E-10 5.1E-10 8.7E-8 1.5E-7 6.2E-7 7.2E-7 9.1E-7	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.0E0 3.2E0 3.4E0 4.9E0 2.6E0 6.2E0 2.5E0 2.3E0 2.2E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11 2.8E-9 8.1E-9 3.1E-8 4.4E-6 4.2E-6 1.7E-5 3.1E-5 2.1E-5 1.3E-4	6.2E-2 FDR 4.4E-20 4.0E-13 4.8E-13 6.4E-11 2.5E-9 7.3E-9 3.0E-8 4.3E-6 1.6E-5 3.0E-5 1.9E-5 1.2E-4
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE GOTERM_MF_DIRECT GOTERM_MF_DIRECT	Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine phosphatase activity DSPc domain:Tyrosine-protein phosphatase domain:Rhodanese Protein-tyrosine/Dual specificity phosphatase Mitogen-activated protein (MAP) kinase phosphatase active site:Phosphocysteine intermediate protein tyrosine phosphatase activity peptidyl-tyrosine dephosphorylation MAP kinase tyrosine/serine/threonine phosphatase activity	RI R		Count 66 31 28 24 25 28 31 15 34 10 32 38 37 11	4.5E-21 6.1E-15 7.6E-15 1.2E-12 8.5E-11 2.7E-10 5.1E-10 8.7E-8 1.5E-7 6.2E-7 7.2E-7 9.1E-7 2.4E-6 3.0E-6	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.8E0 4.0E0 3.2E0 3.4E0 4.9E0 2.6E0 6.2E0 2.5E0 2.3E0 2.2E0 5.0E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11 2.8E-9 8.1E-9 3.1E-8 4.4E-6 4.2E-6 1.7E-5 3.1E-5 2.1E-5 1.3E-4 6.2E-5	6.2E-2 FDR 4.4E-20 4.0E-13 4.8E-13 6.4E-11 2.5E-9 7.3E-9 3.0E-8 4.3E-6 3.8E-6 1.6E-5 3.0E-5 1.9E-5 1.2E-4 5.6E-5
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO	Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine phosphatase activity DSPc domain:Tyrosine-protein phosphatase domain:Rhodanese Protein-tyrosine/Dual specificity phosphatase Mitogen-activated protein (MAP) kinase phosphatase active site:Phosphocysteine intermediate protein tyrosine phosphatase activity peptidyl-tyrosine dephosphorylation MAP kinase tyrosine/serine/threonine phosphatase activity Rhodanese-like domain	RI R		Count 66 31 28 24 25 28 31 15 34 10 32 38 37 11 15	4.5E-21 6.1E-15 7.6E-15 1.2E-12 8.5E-11 2.7E-10 5.1E-10 8.7E-8 1.5E-7 6.2E-7 7.2E-7 9.1E-7 2.4E-6 3.0E-6	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.8E0 4.0E0 3.2E0 3.4E0 4.9E0 2.6E0 6.2E0 2.5E0 2.3E0 2.2E0 5.0E0 3.9E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11 2.8E-9 8.1E-9 3.1E-8 4.4E-6 4.2E-6 1.7E-5 3.1E-5 2.1E-5 1.3E-4 6.2E-5 7.2E-5	6.2E-2 FDR 4.4E-20 4.0E-13 4.8E-13 6.4E-11 2.5E-9 7.3E-9 3.0E-8 4.3E-6 1.6E-5 1.9E-5 1.2E-4 5.6E-5 6.6E-5
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO INTERPRO UP_SEQ_FEATURE	Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine phosphatase activity DSPc domain:Tyrosine-protein phosphatase domain:Rhodanese Protein-tyrosine/Dual specificity phosphatase Mitogen-activated protein (MAP) kinase phosphatase active site:Phosphocysteine intermediate protein tyrosine phosphatase activity peptidyl-tyrosine dephosphorylation MAP kinase tyrosine/serine/threonine phosphatase activity Rhodanese-like domain inactivation of MAPK activity	RI R		Count 66 31 28 24 25 28 31 15 34 10 32 38 37 11 15 15	4.5E-21 6.1E-15 7.6E-15 1.2E-12 8.5E-11 2.7E-10 5.1E-10 8.7E-8 1.5E-7 6.2E-7 7.2E-7 9.1E-7 2.4E-6 3.0E-6 1.0E-5	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.8E0 4.0E0 3.2E0 3.4E0 4.9E0 2.6E0 6.2E0 2.5E0 2.3E0 2.2E0 5.0E0 3.9E0 3.6E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11 2.8E-9 8.1E-9 3.1E-8 4.4E-6 4.2E-6 1.7E-5 3.1E-5 2.1E-5 1.3E-4 6.2E-5 7.2E-5 4.3E-4	6.2E-2 FDR 4.4E-20 4.0E-13 4.8E-13 6.4E-11 2.5E-9 7.3E-9 3.0E-8 4.3E-6 1.6E-5 3.0E-5 1.9E-5 1.2E-4 5.6E-5 4.1E-4
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_BP_DIRECT INTERPRO GOTERM_BP_DIRECT INTERPRO GOTERM_BP_DIRECT INTERPRO	Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine phosphatase activity DSPC domain:Tyrosine-protein phosphatase domain:Rhodanese Protein-tyrosine/Dual specificity phosphatase Mitogen-activated protein (MAP) kinase phosphatase active site:Phosphocysteine intermediate protein tyrosine phosphatase activity peptidyl-tyrosine dephosphorylation MAP kinase tyrosine/serine/threonine phosphatase activity Rhodanese-like domain inactivation of MAPK activity Protein-tyrosine phosphatase, active site	RI R		Count 66 31 28 24 25 28 31 15 34 10 32 38 37 11 15 15 28	4.5E-21 6.1E-15 7.6E-15 1.2E-12 8.5E-11 2.7E-10 5.1E-10 8.7E-8 1.5E-7 6.2E-7 7.2E-7 9.1E-7 2.4E-6 3.0E-6 1.0E-5 3.0E-5	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.8E0 4.0E0 3.2E0 3.4E0 4.9E0 2.6E0 6.2E0 2.5E0 2.3E0 2.2E0 5.0E0 3.9E0 3.6E0 2.3E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11 2.8E-9 8.1E-9 3.1E-8 4.4E-6 4.2E-6 1.7E-5 3.1E-5 2.1E-5 1.3E-4 6.2E-5 7.2E-5 4.3E-4 5.5E-4	6.2E-2 FDR 4.4E-20 4.0E-13 4.8E-13 6.4E-11 2.5E-9 7.3E-9 3.0E-8 4.3E-6 1.6E-5 3.0E-5 1.9E-5 1.2E-4 5.6E-5 6.6E-5 4.1E-4 5.0E-4
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO GOTERM_MF_DIRECT INTERPRO GOTERM_MF_DIRECT INTERPRO GOTERM_BP_DIRECT INTERPRO SMART	Enrichment Score: 6.28 Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine phosphatase activity DSPC domain:Tyrosine-protein phosphatase domain:Rhodanese Protein-tyrosine/Dual specificity phosphatase Mitogen-activated protein (MAP) kinase phosphatase active site:Phosphocysteine intermediate protein tyrosine phosphatase activity peptidyl-tyrosine dephosphorylation MAP kinase tyrosine/serine/threonine phosphatase activity. Rhodanese-like domain inactivation of MAPK activity Protein-tyrosine phosphatase, active site RHOD	RI R		Count 66 31 28 24 25 28 31 15 34 10 32 38 37 11 15 15	4.5E-21 6.1E-15 7.6E-15 1.2E-12 8.5E-11 2.7E-10 5.1E-10 8.7E-8 1.5E-7 6.2E-7 7.2E-7 9.1E-7 2.4E-6 3.0E-6 1.0E-5 3.0E-5	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.8E0 4.0E0 3.2E0 3.4E0 4.9E0 2.6E0 6.2E0 2.5E0 2.3E0 2.2E0 5.0E0 3.9E0 3.6E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11 2.8E-9 8.1E-9 3.1E-8 4.4E-6 4.2E-6 1.7E-5 3.1E-5 2.1E-5 1.3E-4 6.2E-5 7.2E-5 4.3E-4 5.5E-4	6.2E-2 FDR 4.4E-20 4.0E-13 4.8E-13 6.4E-11 2.5E-9 7.3E-9 3.0E-8 4.3E-6 1.6E-5 5.0E-4 5.6E-5 4.1E-4 5.0E-4 8.2E-4
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO GOTERM_BP_DIRECT INTERPRO GOTERM_BP_DIRECT INTERPRO SMART PIR_SUPERFAMILY	Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine phosphatase activity DSPc domain:Tyrosine-protein phosphatase domain:Rhodanese Protein-tyrosine/Dual specificity phosphatase Mitogen-activated protein (MAP) kinase phosphatase active site:Phosphocysteine intermediate protein tyrosine phosphatase activity peptidyl-tyrosine dephosphorylation MAP kinase tyrosine/serine/threonine phosphatase activity Rhodanese-like domain inactivation of MAPK activity Protein-tyrosine phosphatase, active site RHOD dual specificity protein phosphatase (MAP kinase phosphatase)	RI R		Count 66 31 28 24 25 28 31 15 34 10 32 38 37 11 15 15 28	4.5E-21 6.1E-15 7.6E-15 1.2E-12 8.5E-11 2.7E-10 5.1E-10 8.7E-8 1.5E-7 6.2E-7 7.2E-7 9.1E-7 2.4E-6 3.0E-6 1.0E-5 3.0E-5 5.5E-5	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.8E0 4.0E0 3.2E0 3.4E0 4.9E0 2.6E0 6.2E0 2.5E0 2.3E0 2.2E0 5.0E0 3.9E0 3.6E0 2.3E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11 2.8E-9 8.1E-9 3.1E-8 4.4E-6 4.2E-6 1.7E-5 3.1E-5 2.1E-5 1.3E-4 6.2E-5 7.2E-5 4.3E-4 5.5E-4	6.2E-2 FDR 4.4E-20 4.0E-13 4.8E-13 6.4E-11 2.5E-9 7.3E-9 3.0E-8 4.3E-6 1.6E-5 5.0E-5 1.9E-5 1.2E-4 5.6E-5 4.1E-4 5.0E-4 8.2E-4 1.4E-2
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE GOTERM_MF_DIRECT GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO GOTERM_MF_DIRECT INTERPRO GOTERM_BP_DIRECT INTERPRO SMART PIR_SUPERFAMILY BIOCARTA	Enrichment Score: 6.28 Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine phosphatase activity DSPc domain:Tyrosine-protein phosphatase domain:Rhodanese Protein-tyrosine/Dual specificity phosphatase Mitogen-activated protein (MAP) kinase phosphatase active site:Phosphocysteine intermediate protein tyrosine phosphatase activity peptidyl-tyrosine dephosphorylation MAP kinase tyrosine/serine/threonine phosphatase activity Rhodanese-like domain inactivation of MAPK activity Protein-tyrosine phosphatase, active site RHOD dual specificity protein phosphatase (MAP)	RI R		Count 66 31 28 24 25 28 31 15 34 10 32 38 37 11 15 15 15 15	4.5E-21 6.1E-15 7.6E-15 1.2E-12 8.5E-11 2.7E-10 5.1E-10 8.7E-8 1.5E-7 6.2E-7 7.2E-7 9.1E-7 2.4E-6 3.0E-6 1.0E-5 3.0E-5 5.5E-5	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.8E0 4.0E0 3.4E0 4.9E0 2.6E0 6.2E0 2.5E0 2.3E0 2.2E0 5.0E0 3.9E0 3.6E0 2.3E0 2.3E0 2.3E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11 2.8E-9 8.1E-9 3.1E-8 4.4E-6 4.2E-6 1.7E-5 3.1E-5 2.1E-5 1.3E-4 6.2E-5 7.2E-5 4.3E-4 9.0E-4 1.4E-2	6.2E-2 FDR 4.4E-20 4.0E-13 4.8E-13 6.4E-11 2.5E-9 7.3E-9 3.0E-8 4.3E-6 1.6E-5 3.0E-5 1.9E-5 1.2E-4 5.6E-5 4.1E-4 5.0E-4 8.2E-4 1.4E-2 6.0E-3
Annot	UP_KEYWORDS INTERPRO INTERPRO INTERPRO GOTERM_MF_DIRECT SMART UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO INTERPRO UP_SEQ_FEATURE GOTERM_MF_DIRECT GOTERM_MF_DIRECT INTERPRO GOTERM_BP_DIRECT INTERPRO GOTERM_BP_DIRECT INTERPRO SMART PIR_SUPERFAMILY	Protein phosphatase Dual specificity phosphatase, catalytic domain Dual specificity phosphatase, subgroup, catalytic domain Dual specificity phosphatase protein tyrosine/serine/threonine phosphatase activity DSPC domain:Tyrosine-protein phosphatase domain:Rhodanese Protein-tyrosine/Dual specificity phosphatase Mitogen-activated protein (MAP) kinase phosphatase active site:Phosphocysteine intermediate protein tyrosine phosphatase activity peptidyl-tyrosine dephosphorylation MAP kinase tyrosine/serine/threonine phosphatase activity Rhodanese-like domain inactivation of MAPK activity Protein-tyrosine phosphatase, active site RHOD dual specificity protein phosphatase (MAP kinase phosphatase) Regulation of MAP Kinase Pathways Through	RI R		Count 66 31 28 24 25 28 31 15 34 10 32 38 37 11 15 15 15 7	4.5E-21 6.1E-15 7.6E-15 1.2E-12 8.5E-11 2.7E-10 5.1E-10 8.7E-8 1.5E-7 6.2E-7 7.2E-7 9.1E-7 2.4E-6 3.0E-6 3.1E-6 1.0E-5 3.0E-5 5.5E-5 2.2E-4 8.3E-4	3.5E0 Fold Change 3.4E0 4.5E0 4.8E0 4.8E0 4.0E0 3.2E0 3.4E0 4.9E0 2.6E0 6.2E0 2.5E0 2.3E0 2.2E0 5.0E0 3.9E0 3.6E0 2.3E0 2.3E0 2.3E0 5.0E0 5.0E0 5.0E0	6.9E-2 Benjamini 5.7E-20 4.4E-13 5.3E-13 7.0E-11 2.8E-9 8.1E-9 3.1E-8 4.4E-6 4.2E-6 1.7E-5 3.1E-5 2.1E-5 1.3E-4 6.2E-5 7.2E-5 4.3E-4 9.0E-4 1.4E-2 8.4E-3	6.2E-2 FDR 4.4E-20 4.0E-13 4.8E-13 6.4E-11 2.5E-9 7.3E-9 3.0E-8 4.3E-6 3.8E-6 1.6E-5 5.0E-5 1.9E-5 4.1E-4 5.0E-4 8.2E-4 1.4E-2 6.0E-

Annot	ation Cluster 1	Enrichment Score: ?	G	17	Count	P_Value	Fold	Benjamin	i FDR
	GOTERM_MF_DIRECT	protein tyrosine/threonine phosphatase	RT	ī	3	7.5E-2		3.9E-1	3.4E-
	GOTERM_BP_DIRECT		RT		5	1.3E-1	2.5E0	8.2E-1	7.9E-
	SMART		RT	- -	18	3.8E-1	1.2E0	1.0E0	1 9.1E-
	INTERPRO	Protein-tyrosine phosphatase, receptor/non-		-					1 9.1E-
	SMART	March Marc	1 9.7E-						
Annot	ation Cluster 37					!	Fold		1 EDB
Annot	GOTERM_BP_DIRECT						Change	<u> </u>	1.3E-
	GOTERM_BP_DIRECT	repair				11			9 7.9E-
	GOTERM_BP_DIRECT								7 1.8E-
		<u>damage</u>							6 4.5E-
		complex assembly	<u>RT</u>		19	6.1E-8	3.9E0	4.7E-6	6
			<u>RT</u>	i	21	2.8E-7	3.4E0	1.8E-5	1.8E- 5
	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision	<u>RT</u>	1	21	4.9E-7	3.3E0	3.0E-5	2.9E- 5
	GOTERM_BP_DIRECT	error-prone translesion synthesis	<u>RT</u>	i	14	8.7E-7	4.4E0	4.9E-5	4.7E- 5
	KEGG_PATHWAY	Nucleotide excision repair	<u>RT</u>	E	24	4.0E-6	2.6E0	1.2E-5	5.7E- 6
	GOTERM_BP_DIRECT	nucleotide-excision repair, DNA gap filling	<u>RT</u>	i .	15	5.3E-6	3.7E0	2.5E-4	2.4E- 4
	GOTERM_BP_DIRECT	error-free translesion synthesis	<u>RT</u>	i	13	8.2E-6	4.1E0	3.6E-4	3.5E- 4
	GOTERM_BP_DIRECT	translesion synthesis	<u>RT</u>	1	18	2.3E-5	3.0E0	8.9E-4	8.5E- 4
	KEGG_PATHWAY	Mismatch repair	<u>RT</u>	i	13	4.1E-4	2.9E0	9.6E-4	4.5E-
	KEGG_PATHWAY	DNA replication	<u>RT</u>	1	17	4.8E-4	2.4E0	1.1E-3	5.3E- 4
Annot	ation Cluster 38	Enrichment Score: 6.12	G	178	Count	P_Value		Benjamin	
	GOTERM_MF_DIRECT	ATP-dependent RNA helicase activity			38	2.4E-	Change	•	8.9E- 12
	INTERPRO	Domain of unknown function DUF1605	RT		13		4.7E0	2.3E-5	2.1E-
	INTERPRO							5.2E-5	5 4.8E-
	INTERPRO	DNA/RNA helicase, ATP-dependent, DEAH-							5 1.1E-
	SMART								4 2.6E-
	GOTERM_MF_DIRECT								3 4.4E-
						!	Fold		3
Annot	ation Cluster 39 UP_SEQ_FEATURE						Change		7.1E-
	INTERPRO					15			13 4.7E-
		SET domain	<u>RT</u>		33		4.0E0		12
		<u>histone-lysine N-methyltransferase activity</u>	<u>RT</u>	i	24	3.2E-9	3.7E0	9.6E-8	8.6E- 8
	SMART	<u>SET</u>	<u>RT</u>	•	26	9.1E-8	2.8E0	2.0E-6	1.8E- 6
	UP_SEQ_FEATURE	domain:Post-SET	<u>RT</u>	i .	12	1.4E-6	5.1E0	6.0E-5	5.8E- 5
	INTERPRO	Post-SET domain	<u>RT</u>	i e	11	3.7E-5	4.3E0	6.6E-4	6.0E- 4
	UP_KEYWORDS	S-adenosyl-L-methionine	<u>RT</u>	=	46	6.3E-5	1.8E0	3.6E-4	2.8E- 4
	UP_KEYWORDS	<u>Methyltransferase</u>	<u>RT</u>	•	47	4.1E-4	1.7E0	2.2E-3	1.7E- 3
	SMART	<u>PostSET</u>	<u>RT</u>	i	9	5.0E-3	2.8E0	5.1E-2	4.6E- 2
	KEGG_PATHWAY	<u>Lysine degradation</u>	<u>RT</u>	i .	18	1.5E-2	1.8E0	2.8E-2	1.5E- 2
	GOTERM_MF_DIRECT	methyltransferase activity	<u>RT</u>	i	19	3.1E-1	1.2E0	1.0E0	8.9E-
Annot	ation Cluster 40	Enrichment Score: 5.45	G		Count	P_Value		Benjamin	
	GOTERM_BP_DIRECT	positive regulation of telomere maintenance			22		Change	<u>'</u>	1.0E-
	GOTERM_BP_DIRECT								7 6.7E-
	GOTERM_BP_DIRECT								4 4.5E-
Appet	ation Cluster 41					1	Fold	Ponjamin	2
7-MIIIOU	INTERPRO						Change	<u> </u>	1.8E-
		ATrase, AAA-L <u>ype, Conserved Site</u>	<u>KI</u>		19	5.0E-9	4.4EU	1.9E-/	7
	INTERPRO	ATD		_				0	/ 5E-
	INTERPRO	ATPase, AAA-type, core AAA+ ATPase domain	RT RT		24		2.9E0 2.0E0		2.5E- 5 1.0E-

nota	ation Cluster 1	Enrichment Score: ?	G	- 1	Count	P_Value	Fold Change	Benjami	ni F
	SMART	AAA	<u>RT</u>	¥	44	3.7E-2	1.3E0	2.7E-1	2 1
ota	ation Cluster 42	Enrichment Score: 5.05	G	15	Count	P_Value	Fold Change	Benjami	ni F
	UP_SEQ_FEATURE	domain:PI3K/PI4K	<u>RT</u>	i	16	1.6E- 10	6.1E0	1.0E-8	1 8
	INTERPRO	Phosphatidylinositol 3-/4-kinase, catalytic domain	<u>RT</u>	1	16	2.5E-9	5.2E0	9.0E-8	8
	INTERPRO	Phosphatidylinositol 3/4-kinase, conserved site	<u>RT</u>	1	14	1.7E-8	5.4E0	5.4E-7	5 7
	SMART	<u>PI3Kc</u>	<u>RT</u>		15	9.0E-7	3.6E0	1.7E-5	1 5
	UP_SEQ_FEATURE	domain:FAT	<u>RT</u>	1	6	3.6E-4	6.8E0	9.9E-3	9
	UP_SEQ_FEATURE	domain:FATC	<u>RT</u>		6	3.6E-4	6.8E0	9.9E-3	9
	INTERPRO	PIK-related kinase, FATC	RT		6		6.2E0	7.8E-3	3 7
	INTERPRO	PIK-related kinase	RT		6	5.7E-4		7.8E-3	3 7
	INTERPRO			_					3
	SMART	PIK-related kinase, FAT	<u>RT</u>		5	2.9E-3		3.3E-2	2
		SM01343	<u>RT</u>	i	6		4.1E0	4.5E-2	2
ota	ation Cluster 43 GOTERM_BP_DIRECT	Enrichment Score: 5.01	G		Count	P_Value	Change		
		nucleotide-binding oligomerization domain containing signaling pathway	<u>RT</u>	•	17	1.8E-7	4.0E0	1.2E-5	1 5
	GOTERM_BP_DIRECT	<u>I-kappaB kinase/NF-kappaB signaling</u>	<u>RT</u>	•	27	1.3E-6	2.7E0	7.3E-5	5
	GOTERM_BP_DIRECT	regulation of tumor necrosis factor-mediated signaling pathway	<u>RT</u>	•	15	1.4E-4	3.0E0	4.4E-3	3
	GOTERM_BP_DIRECT	TRIF-dependent toll-like receptor signaling pathway	<u>RT</u>	i	14	2.6E-4	3.0E0		7 3
ota	ation Cluster 44	Enrichment Score: 4.99	G	5	Count	P_Value	Fold Change	Benjami	ni F
	INTERPRO	WD40 repeat, conserved site	<u>RT</u>	=	55	1.2E-7	2.1E0	3.6E-6	3
	UP_SEQ_FEATURE	repeat:WD 5	<u>RT</u>	=	66	2.4E-7	1.9E0	1.1E-5	1 5
	UP_SEQ_FEATURE	repeat:WD 4	<u>RT</u>	=	69	3.9E-7	1.8E0	1.8E-5	1 5
	INTERPRO	G-protein beta WD-40 repeat	<u>RT</u>	•	36	4.3E-7	2.4E0	1.2E-5	1
	UP_SEQ_FEATURE	repeat:WD 7	<u>RT</u>		47	5.5E-7	2.1E0	2.4E-5	2
	UP_SEQ_FEATURE	repeat:WD 6	<u>RT</u>	•	55	2.1E-6	1.9E0	8.5E-5	8
	UP_KEYWORDS	WD repeat	RT		71		1.7E0	2.0E-5	1
	UP_SEQ_FEATURE	repeat:WD 3	RT	4	69		1.7E0	1.3E-4	5 1
	UP_SEQ_FEATURE								4 3
	UP_SEQ_FEATURE	repeat:WD 2	<u>RT</u>	•	69		1.7E0	3.7E-4	4
	INTERPRO	repeat:WD 1	<u>RT</u>	•	69		1.7E0	3.7E-4	1
		WD40-repeat-containing domain	<u>RT</u>	•	76	9.2E-5	1.5E0	1.6E-3	3
	INTERPRO	WD40 repeat	<u>RT</u>	•	67	2.0E-4	1.5E0	3.1E-3	3
	INTERPRO	WD40/YVTN repeat-like-containing domain	<u>RT</u>	=	74	2.7E-3	1.4E0	3.2E-2	2
	SMART	<u>WD40</u>	<u>RT</u>	=	67	5.1E-1	1.0E0	1.0E0	9 1
ota	ation Cluster 45	Enrichment Score: 4.92	G	<u>■</u>	Count	P_Value	Fold Change	Benjami	ni F
	UP_SEQ_FEATURE	short sequence motif:TXY	<u>RT</u>	i	11	2.3E-7	6.2E0	1.0E-5	1 5
	GOTERM_MF_DIRECT	MAP kinase activity	<u>RT</u>	1	12	6.4E-7	5.1E0	1.6E-5	1 5
	INTERPRO	<u>Mitogen-activated protein (MAP) kinase,</u> <u>conserved site</u>	<u>RT</u>	i .	10	1.0E-5	5.2E0	2.0E-4	1 4
	INTERPRO	Mitogen-activated protein (MAP) kinase, p38	<u>RT</u>	1	4	1.5E-2	6.2E0	1.3E-1	1
ota	ation Cluster 46	Enrichment Score: 4.88	G	13	Count	P_Value	Fold Change	Benjami	ni F
	GOTERM_MF_DIRECT	cadherin binding involved in cell-cell adhesion	<u>RT</u>	=	80	4.3E-6	1.6E0	8.7E-5	7
	GOTERM_CC_DIRECT	cell-cell adherens junction	<u>RT</u>	=	82	8.2E-6	1.6E0	1.5E-4	1
	GOTERM_BP_DIRECT	cell-cell adhesion	RT		72		1.6E0	2.1E-3	2
ota	ation Cluster 47	Enrichment Score: 4.87	G		Count			Daniomi	ni E
	INTERPRO	Actinin-type, actin-binding, conserved site	RT	i	18	1.2E-9		4.5E-8	4
	UP_SEQ_FEATURE								1
	UP_SEQ_FEATURE	domain:Actin-binding	<u>RT</u>	•	16		5.5E0	1.4E-7	7
		repeat:Spectrin 4	<u>RT</u>	•	16	6.9E-9	5.2E0	4.0E-7	7
	UP_SEQ_FEATURE	domain:CH 1	<u>RT</u>	•	18	1.3E-8	4.5E0	7.1E-7	6 7

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

nnot	tation Cluster 1	Enrichment Score: ?	G	- 10	Count	P_Value	Fold Change	Benjamini	i FDR
	GOTERM_BP_DIRECT	<u>nucleotide-excision repair, DNA incision, 3'-to lesion</u>	<u>RT</u>	i	11	2.5E-3	2.8E0	5.0E-2	4.8E 2
	GOTERM_BP_DIRECT	nucleotide-excision repair	<u>RT</u>	1	11	1.4E-1	1.6E0	8.3E-1	8.0E 1
nnot	ation Cluster 49	Enrichment Score: 4.66	G	15	Count	P_Value	Fold Change	Benjamini	i FDR
)	UP_KEYWORDS	Biological rhythms	<u>RT</u>		40	1.7E-6	2.2E0	1.2E-5	9.1E
	GOTERM_BP_DIRECT	<u>regulation of circadian rhythm</u>	<u>RT</u>	1	21	6.3E-5	2.5E0	2.1E-3	2.0E
7	GOTERM_BP_DIRECT	rhythmic process	RT		22	9.6E-5	2.4E0	3.1E-3	3.0E
nnot	ation Cluster 50	Enrichment Score: 4.65	G		Count	P_Value	Fold	B	3 FDR
))	GOTERM_BP_DIRECT			_	31	1.8E-	Change 3.8E0	2.6E-10	2.5
J	GOTERM_CC_DIRECT	gene expression DNA-directed RNA polymerase II, core	<u>RT</u>	•		12			10 3.3E
J	GOTERM_BP_DIRECT	complex	<u>RT</u>		14	1.4E-7		3.7E-6	6 9.7E
J		7-methylguanosine mRNA capping	<u>RT</u>	•	20	1.4E-7	3.6E0	1.0E-5	6
)	GOTERM_BP_DIRECT	positive regulation of viral transcription	<u>RT</u>	•	18	4.6E-7	3.7E0	2.9E-5	2.8E 5
	KEGG_PATHWAY	Pyrimidine metabolism	<u>RT</u>	•	41	1.5E-6	2.1E0	4.9E-6	2.3l 6
)	UP_KEYWORDS	<u>DNA-directed RNA polymerase</u>	<u>RT</u>	1	19	2.4E-6	3.3E0	1.6E-5	1.2l 5
)	KEGG_PATHWAY	RNA polymerase	<u>RT</u>	1	19	3.6E-6	3.1E0	1.1E-5	5.18 6
)	GOTERM_BP_DIRECT	transcription initiation from RNA polymerase I	<u>RT</u>	1	18	5.3E-6	3.2E0	2.5E-4	2.4I 4
	GOTERM_BP_DIRECT	transcription elongation from RNA polymerase I promoter	<u>RT</u>	1	17	5.6E-6	3.4E0	2.6E-4	2.5l
	GOTERM_BP_DIRECT	termination of RNA polymerase I transcription	<u>RT</u>	1	17	9.7E-6	3.2E0	4.2E-4	4.01
_]	GOTERM_MF_DIRECT	DNA-directed RNA polymerase activity	RT		19	1.2E-5	3.0E0	2.2E-4	2.01
ך ר	GOTERM_MF_DIRECT	RNA polymerase I activity	RT		10	1.4E-5		2.6E-4	4 2.3I
J 1	GOTERM_BP_DIRECT	transcription elongation from RNA polymerase		•					4 5.6l
J	GOTERM_MF_DIRECT	II promoter	<u>KI</u>	•	32	1.4E-5		5.8E-4	4 3.2I
		RNA polymerase II activity	<u>RT</u>	•	9	2.0E-5	5.4E0	3.5E-4	4
)	GOTERM_CC_DIRECT	DNA-directed RNA polymerase I complex	<u>RT</u>	•	10	2.3E-5	4.9E0	3.8E-4	3.3
)	GOTERM_BP_DIRECT	<u>positive regulation of type I interferon</u> <u>production</u>	<u>RT</u>	i	21	1.2E-4	2.4E0	3.7E-3	3.6 3
	GOTERM_BP_DIRECT	<u>transcription initiation from RNA polymerase</u> <u>II promoter</u>	<u>RT</u>	•	44	2.9E-4	1.7E0	8.0E-3	7.7 3
)	GOTERM_BP_DIRECT	snRNA transcription from RNA polymerase II promoter	<u>RT</u>	1	24	8.1E-4	2.0E0	1.9E-2	1.9l 2
)	GOTERM_BP_DIRECT	positive regulation of gene expression, epigenetic	<u>RT</u>	1	22	8.6E-4	2.1E0	2.0E-2	2.0E 2
)	GOTERM_BP_DIRECT	transcription from RNA polymerase III promoter	<u>RT</u>	1	14	1.8E-3	2.5E0	3.7E-2	3.5l 2
	GOTERM_BP_DIRECT	gene silencing by RNA	<u>RT</u>		31	4.7E-3	1.7E0	8.3E-2	8.0
)	GOTERM_CC_DIRECT	DNA-directed RNA polymerase III complex	<u>RT</u>		8	2.1E-2	2.7E0	1.3E-1	2
í 1	GOTERM_MF_DIRECT	RNA polymerase III activity	RT	<u>-</u>	8	2.1E-2		1.4E-1	1 1.2
)	KEGG_PATHWAY								1 5.4
J		Cytosolic DNA-sensing pathway	RT		19	5.4E-2	Fold	9.5E-2	2
nnot	tation Cluster 51 KEGG_PATHWAY	Enrichment Score: 4.63	G	-	Count	P_Value	Change	Benjamini	
)	_	<u>Purine metabolism</u>	<u>RT</u>	•	67	8.4E-9	2.0E0	3.4E-8	1.68
	KEGG_PATHWAY	<u>Pyrimidine metabolism</u>	<u>RT</u>	•	41	1.5E-6	2.1E0	4.9E-6	2.3E 6
not	KEGG_PATHWAY	Metabolic pathways Enrichment Score: 4.62	RT G	= 	98 Count	1.0E0 P_Value	Fold	1.0E0 Benjamini	1.0
11100	GOTERM_BP_DIRECT			_			Change	i e e	2.9
J	GOTERM_BP_DIRECT	DNA synthesis involved in DNA repair	<u>RT</u>		20			3.0E-5	5 7.0I
	KEGG_PATHWAY	strand displacement	<u>RT</u>	•	15	1.9E-5		7.3E-4	4 1.5
		Homologous recombination	<u>RT</u>	i	14	1.5E-3		3.2E-3	3
not	tation Cluster 53	Enrichment Score: 4.49	G	· ·	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	Heat shock protein 70 family	<u>RT</u>	1	12	1.4E-6	5.0E0	3.5E-5	3.2l 5
)	INTERPRO	Heat shock protein 70, conserved site	<u>RT</u>	i	12	1.4E-6	5.0E0	3.5E-5	3.2l 5
)	GOTERM_BP_DIRECT	response to unfolded protein	<u>RT</u>	1	14	1.8E-2	2.0E0	2.2E-1	2.18
not	tation Cluster 54	Enrichment Score: 4.46	G	178	Count	P_Value	Fold Change	Benjamini	i FDF
)	KEGG_PATHWAY	Gap junction	<u>RT</u>	•	60	8.4E- 23	3.5E0	1.9E-21	8.8I 22
)	GOTERM_MF_DIRECT	adenylate cyclase activity	<u>RT</u>		19	1.7E-	6.0E0	7.5E-12	6.71
	INTERPRO				18	13 4.0E-			12 1.9

Annota	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamin	ii FDR
	INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase, conserved site	<u>RT</u>	i	17	2.2E- 11		1.0E-9	9.4E- 10
	KEGG_PATHWAY	GnRH signaling pathway	<u>RT</u>		45	2.7E- 10	2.6E0	1.5E-9	7.0E- 10
	KEGG_PATHWAY	Vascular smooth muscle contraction	RT		53	3.2E-	2.4E0	1.7E-9	8.2E-
	SMART	CYCc	RT		17	10 1.6E-8	3.8E0	4.1E-7	10 3.8E-
	UP_KEYWORDS	<u>cAMP biosynthesis</u>	RT		10	2.5E-7		1.9E-6	7 1.5E-
	KEGG_PATHWAY	Inflammatory mediator regulation of TRP	RT		41	5.9E-7		2.1E-6	6 9.7E-
	KEGG_PATHWAY	<u>channels</u> <u>Regulation of lipolysis in adipocytes</u>	RT		28	8.5E-7		2.9E-6	7 1.4E-
	GOTERM_BP_DIRECT	cyclic nucleotide biosynthetic process	RT		11	8.8E-7		4.9E-5	6 4.7E-
	KEGG_PATHWAY			•					5 1.8E-
	KEGG_PATHWAY	<u>Melanogenesis</u>	<u>RT</u>	•	41	1.1E-6		3.8E-6	6 2.7E-
	GOTERM_BP_DIRECT	Adrenergic signaling in cardiomyocytes	<u>RT</u>	•	51	1.8E-6		5.8E-6	6 1.7E-
	UP_SEQ_FEATURE	activation of protein kinase A activity metal ion-binding site:Magnesium 2; via	<u>RT</u>	•	13	3.6E-6		1.8E-4	4 1.7E-
		carbonyl oxygen	<u>RT</u>	i	10	4.5E-6	5.7E0	1.8E-4	4
	KEGG_PATHWAY	<u>Cholinergic synapse</u>	<u>RT</u>	•	42	8.8E-6	2.0E0	2.5E-5	1.2E- 5
	KEGG_PATHWAY	Gastric acid secretion	<u>RT</u>	•	31	1.3E-5	2.2E0	3.5E-5	1.6E- 5
	GOTERM_MF_DIRECT	phosphorus-oxygen lyase activity	<u>RT</u>	i	10	1.4E-5	5.0E0	2.6E-4	2.3E- 4
	KEGG_PATHWAY	<u>Dopaminergic synapse</u>	<u>RT</u>	i e	46	1.5E-5	1.9E0	3.8E-5	1.8E- 5
	UP_SEQ_FEATURE	metal ion-binding site:Magnesium 1	<u>RT</u>	•	18	2.9E-5	3.0E0	9.6E-4	9.2E- 4
	KEGG_PATHWAY	<u>Circadian entrainment</u>	<u>RT</u>	•	36	4.2E-5	2.0E0	1.1E-4	5.0E- 5
	UP_SEQ_FEATURE	metal ion-binding site:Magnesium 2	<u>RT</u>	i	17	8.3E-5	2.9E0	2.6E-3	2.5E- 3
	GOTERM_BP_DIRECT	cAMP biosynthetic process	<u>RT</u>	i .	11	1.1E-4	3.8E0	3.5E-3	3.4E- 3
	GOTERM_BP_DIRECT	renal water homeostasis	<u>RT</u>	1	15	3.3E-4	2.8E0	9.0E-3	8.6E-
	GOTERM_BP_DIRECT	cellular response to glucagon stimulus	<u>RT</u>	i	17	4.4E-4	2.5E0	1.1E-2	1.1E- 2
	GOTERM_BP_DIRECT	cellular response to forskolin	<u>RT</u>	i	7	4.7E-4	5.2E0	1.2E-2	1.2E- 2
	INTERPRO	Adenylate cyclase-like	<u>RT</u>	i de la companya de	6	5.7E-4	6.2E0	7.8E-3	7.1E- 3
	KEGG_PATHWAY	Thyroid hormone synthesis	RT		25	2.1E-3	1.9E0	4.5E-3	2.1E-
	KEGG_PATHWAY	Endocrine and other factor-regulated calcium	RT		18	2.9E-3	2.1E0	6.1E-3	3 2.9E-
	KEGG_PATHWAY	reabsorption Aldosterone synthesis and secretion	RT		27	3.9E-3		8.2E-3	3 3.9E-
	KEGG_PATHWAY	Salivary secretion	RT	_	28	4.7E-3		9.7E-3	3 4.7E-
	KEGG_PATHWAY		RT	-	31	7.3E-3		1.5E-2	3 7.3E-
	KEGG_PATHWAY	Retrograde endocannabinoid signaling							3 7.7E-
	GOTERM_BP_DIRECT	Glutamatergic synapse adenylate cyclase-inhibiting G-protein coupled	<u>RT</u>		34	7.7E-3		1.5E-2	3 1.3E-
	KEGG_PATHWAY	receptor signaling pathway	<u>K1</u>	•	16	8.4E-3		1.3E-1	1 3.8E-
	GOTERM_BP_DIRECT	Ovarian steroidogenesis	<u>RT</u>		16	3.8E-2		6.8E-2	2 4.1E-
	KEGG_PATHWAY	<u>cAMP-mediated signaling</u>	<u>RT</u>	•	12	4.5E-2		4.3E-1	1
	_	GABAergic synapse	<u>RT</u>	•	24	4.9E-2	1.5E0	8.7E-2	4.9E- 2
	GOTERM_BP_DIRECT	activation of adenylate cyclase activity	<u>RT</u>	•	12	6.3E-2	1.8E0	5.5E-1	5.2E- 1
	KEGG_PATHWAY	Pancreatic secretion	<u>RT</u>	•	25	7.3E-2	1.4E0	1.3E-1	7.3E- 2
	KEGG_PATHWAY	Insulin secretion	<u>RT</u>	i	23	8.1E-2	1.4E0	1.4E-1	8.1E- 2
	KEGG_PATHWAY	<u>Calcium signaling pathway</u>	<u>RT</u>	i e	43	9.1E-2	1.2E0	1.5E-1	9.1E- 2
	KEGG_PATHWAY	<u>Dilated cardiomyopathy</u>	<u>RT</u>	i .	22	1.2E-1	1.4E0	1.9E-1	1.2E- 1
	GOTERM_BP_DIRECT	adenylate cyclase-activating G-protein coupled receptor signaling pathway	<u>RT</u>	i .	13	1.3E-1	1.5E0	8.2E-1	7.9E- 1
	KEGG_PATHWAY	Morphine addiction	<u>RT</u>	i .	23	1.4E-1	1.3E0	2.4E-1	1.4E- 1
	KEGG_PATHWAY	Bile secretion	<u>RT</u>	i .	17	2.4E-1	1.3E0	3.8E-1	2.4E- 1
	KEGG_PATHWAY	<u>Serotonergic synapse</u>	<u>RT</u>	1	25	3.0E-1	1.2E0	4.6E-1	3.0E- 1
	KEGG_PATHWAY	Taste transduction	<u>RT</u>	i	6	9.5E-1	6.9E-1	1.0E0	9.5E- 1
Annota	ation Cluster 55	Enrichment Score: 4.45	G	1	Count	P_Value	Fold Change	Benjamin	
	UP_KEYWORDS	ADP-ribosylation	RT	i	30		3.3E0		1.5E-
									8

Anno	tation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamir	i FDR
	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
	INTERPRO	Guanine nucleotide binding protein (G- protein), alpha subunit	<u>RT</u>	1	14	1.7E-8	5.4E0	5.4E-7	5.0E
	INTERPRO	G protein alpha subunit, helical insertion	<u>RT</u>		14	1.7E-8	5.4E0	5.4E-7	7 5.0E
	SMART	SM00275	RT		14		3.6E0	5.6E-5	7 5.0E
_	INTERPRO				8	1.9E-5			5 3.3E
	GOTERM_MF_DIRECT	G-protein alpha subunit, group I	<u>RT</u>	_				3.6E-4	4 1.3E
	GOTERM_CC_DIRECT	guanyl nucleotide binding	<u>RT</u>	•	8	9.8E-5		1.5E-3	3 6.2E
	GOTERM_BP_DIRECT	heterotrimeric G-protein complex	<u>RT</u>	•	12	9.6E-3	2.3E0	7.0E-2	2
		adenylate cyclase-modulating G-protein coupled receptor signaling pathway	<u>RT</u>	i	13	1.5E-2	2.1E0	2.0E-1	1.9E
	GOTERM_MF_DIRECT	<u>G-protein coupled serotonin receptor binding</u>	RT	i	4	1.6E-2	6.0E0	1.2E-1	1.0E 1
	GOTERM_MF_DIRECT	G-protein coupled receptor binding	<u>RT</u>	1	16	3.4E-2	1.7E0	2.1E-1	1.9E 1
hno	UP_KEYWORDS tation Cluster 56	Transducer Enrichment Score: 4.44	RT G		29	1.0E0	2.2E-1 Fold	Danismin	1.0E
	UP_SEQ_FEATURE			i v	Count	P_Value	Change		1.1E
_	UP_SEQ_FEATURE	zinc finger region:C2H2-type 23	<u>RT</u>		15	10		1.2E-8	8 3.8E
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 24	<u>RT</u>		13		6.3E0	4.0E-7	7 1.2E
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 26	<u>RT</u>	•	8	4.0E-5		1.3E-3	3
		zinc finger region:C2H2-type 25	<u>RT</u>	•	7	2.1E-4	6.0E0	6.2E-3	5.9E 3
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 27	<u>RT</u>	i	7	2.1E-4	6.0E0	6.2E-3	5.9E 3
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 28	<u>RT</u>	i	6	3.6E-4	6.8E0	9.9E-3	9.5E 3
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 30	<u>RT</u>	i	6	1.1E-3	5.8E0	2.9E-2	2.8E 2
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 29	<u>RT</u>	i	6	1.1E-3	5.8E0	2.9E-2	2.8E 2
	UP_SEQ_FEATURE	zinc finger region:C2H2-type 21; degenerate	<u>RT</u>	i	3	1.1E-1	5.1E0	1.0E0	9.6E 1
nno	tation Cluster 57	Enrichment Score: 4.34	G	100	Count	P_Value	Fold Change	Benjamir	i FDR
	UP_KEYWORDS	TPR repeat	<u>RT</u>	•	53	3.7E-8	2.2E0	2.9E-7	2.3E 7
	INTERPRO	Tetratricopeptide repeat-containing domain	<u>RT</u>	•	48	3.7E-8	2.3E0	1.2E-6	1.1E 6
	INTERPRO	Tetratricopeptide repeat	<u>RT</u>	•	47	4.8E-7	2.1E0	1.3E-5	1.2E 5
	INTERPRO	Tetratricopeptide-like helical	<u>RT</u>	=	62	6.2E-6	1.8E0	1.3E-4	1.2E 4
	UP_SEQ_FEATURE	repeat:TPR 1	<u>RT</u>	•	47	6.8E-6	2.0E0	2.6E-4	2.5E 4
	UP_SEQ_FEATURE	repeat:TPR 2	<u>RT</u>		47	6.8E-6	2.0E0	2.6E-4	2.5E
	UP_SEQ_FEATURE	repeat:TPR 3	<u>RT</u>	•	43	1.7E-5	2.0E0	6.2E-4	6.0E
	UP_SEQ_FEATURE	repeat:TPR 5	<u>RT</u>		27	2.8E-5	2.4E0	9.3E-4	9.0E
_	UP_SEQ_FEATURE	repeat:TPR 6	RT		25	3.3E-5	2.4E0	1.1E-3	4 1.0E
_ 	UP_SEQ_FEATURE	repeat:TPR 7	RT		21	2.9E-4		8.2E-3	3 7.9E
_ 	UP_SEQ_FEATURE	repeat:TPR 4	RT		29	4.1E-4		1.1E-2	3 1.1E
_ _	UP_SEQ_FEATURE	repeat:TPR 8	RT	-	17	1.5E-3		3.9E-2	2 3.7E
	SMART								2 4.1E
	UP_SEQ_FEATURE	<u>TPR</u>	<u>RT</u>		47	4.3E-3		4.5E-2	2 6.0E
	UP_SEQ_FEATURE	repeat:TPR 9	<u>RT</u>		10		2.1E0	6.2E-1	9.6E
		repeat:TPR 10	RT	i	7	9.2E-2	Fold	1.0E0	1
Anno	tation Cluster 58 UP_KEYWORDS	Enrichment Score: 4.19	G		Count		Change	•	i FDR 4.0E
	INTERPRO	Cyclin	<u>RT</u>		20	7.1E-7		5.2E-6	6 2.3E
	SMART	<u>Cyclin-like</u>	<u>RT</u>	•	22		3.1E0		5 9.6E
		CYCLIN	<u>RT</u>	i	21	6.7E-5		1.1E-3	4
	INTERPRO	<u>Cyclin, N-terminal</u>	<u>RT</u>	•	16	1.1E-4	2.9E0	1.7E-3	1.6E 3
	INTERPRO	Cyclin, C-terminal domain	<u>RT</u>	i	10	8.8E-4	3.4E0	1.2E-2	1.1E 2
	SMART	<u>SM01332</u>	<u>RT</u>	i	10	1.7E-2		1.5E-1	1.4E 1
\nno	tation Cluster 59	Enrichment Score: 4.18	G	™	Count	P_Value	Fold Change	Benjamir	
									1.0E
	UP_SEQ_FEATURE	DNA-binding region:Fork-head	<u>RT</u>		22	2.6E-6	3.0E0	1.1E-4	4

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

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

ШО	tation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamin	i FDF
	GOTERM_CC_DIRECT	SMN-Sm protein complex	<u>RT</u>	1	6	1.2E-1	2.2E0	4.9E-1	4.3E 1
nnot	tation Cluster 67	Enrichment Score: 3.79	G		Count	P_Value	Fold Change	Benjamin	i FDF
)	GOTERM_BP_DIRECT	regulation of cellular amino acid metabolic process	<u>RT</u>	-	26	1.2E-7	3.0E0	8.3E-6	8.0E
	GOTERM_CC_DIRECT	proteasome regulatory particle, base subcomplex	<u>RT</u>		11	4.4E-7	5.8E0	1.1E-5	9.9E
	GOTERM_CC_DIRECT	proteasome accessory complex	RT		12	7.0E-6	4.5E0	1.3E-4	1.1
<u> </u>	GOTERM_CC_DIRECT	nuclear proteasome complex	RT		8	1.6E-5	6.4F0	2.7E-4	4 2.4
)]	GOTERM_CC_DIRECT	proteasome regulatory particle	RT	_	9	3.9E-5		6.2E-4	4 5.5
J	GOTERM_BP_DIRECT	antigen processing and presentation of	<u>KI</u>	•	9	3.96-3	5.260	0.26-4	4
)		exogenous peptide antigen via MHC class I, TAP-dependent	<u>RT</u>	i	24	1.4E-4	2.3E0	4.3E-3	4.1 3
)	GOTERM_CC_DIRECT	cytosolic proteasome complex	<u>RT</u>	1	8	1.8E-4	5.1E0	2.2E-3	2.0 3
)	INTERPRO	26S proteasome subunit P45	<u>RT</u>	i	6	5.7E-4	6.2E0	7.8E-3	7.1 3
)	GOTERM_MF_DIRECT	proteasome-activating ATPase activity	<u>RT</u>	1	6	6.8E-4	6.0E0	7.8E-3	7.0 3
)	GOTERM_MF_DIRECT	TBP-class protein binding	<u>RT</u>	4	11	1.0E-3	3.1E0	1.1E-2	9.9
1	GOTERM_BP_DIRECT	positive regulation of RNA polymerase II	<u>RT</u>		7	1.2E-3	4.6E0	2.8E-2	3 2.7
	GOTERM_BP_DIRECT	<u>transcriptional preinitiation complex assembly</u> <u>protein catabolic process</u>	RT		16	1.9E-3		4.0E-2	2 3.8
	GOTERM_BP_DIRECT	positive regulation of proteasomal protein							2 1.5
J	GOTERM_BP_DIRECT	catabolic process ER-associated ubiquitin-dependent protein	<u>RT</u>		8	1.1E-2		1.5E-1	1 7.8
		catabolic process	<u>RT</u>	i	15	1.2E-1		8.2E-1	1
not	tation Cluster 68	Enrichment Score: 3.72	G		Count	P_Value	Change	Benjamin	
)	INTERPRO	<u>Tyrosine-protein kinase, receptor class V,</u> <u>conserved site</u>	<u>RT</u>	•	14	5.8E- 10	6.2E0	2.2E-8	2.0 8
)	INTERPRO	Ephrin receptor ligand binding domain	<u>RT</u>	•	14	5.8E- 10	6.2E0	2.2E-8	2.0 8
	INTERPRO	Tyrosine-protein kinase, ephrin receptor	<u>RT</u>		14	5.8E- 10	6.2E0	2.2E-8	2.0 8
	PIR_SUPERFAMILY	tyrosine-protein kinase, ephrin receptor type	<u>RT</u>		14	2.5E-9	5.4E0	4.9E-7	4.8 7
	SMART	EPH Ibd	<u>RT</u>	4	14	1.3E-7	4.1E0	2.6E-6	2.4 6
	GOTERM_MF_DIRECT	ephrin receptor activity	<u>RT</u>		11	1.6E-7	6.0E0	4.2E-6	3.7
	INTERPRO	Tyrosine-protein kinase ephrin type A/B	RT		15	5.9E-6	3.7E0	1.2E-4	1.1
)	GOTERM_BP_DIRECT	receptor-like ephrin receptor signaling pathway	RT		32	1.4E-5	2.2F0	5.8E-4	4 5.6
, 1	UP_SEQ_FEATURE	domain:SAM	RT	<u>-</u>	26	2.4E-4		7.0E-3	4 6.8
J	INTERPRO								3 3.6
J	INTERPRO	Sterile alpha motif domain	<u>RT</u>	•	30	2.7E-4	2.0E0	4.0E-3	3
)		Sterile alpha motif/pointed domain	<u>RT</u>	•	34	6.7E-4	1.8E0	9.0E-3	8.2
)	SMART	<u>SM01411</u>	<u>RT</u>	•	15	7.6E-4	2.4E0	1.0E-2	9.1 3
)	GOTERM_MF_DIRECT	transmembrane-ephrin receptor activity	<u>RT</u>	1	6	9.2E-3	4.0E0	7.5E-2	6.7 2
)	INTERPRO	Galactose-binding domain-like	<u>RT</u>	•	23	9.2E-3	1.7E0	9.2E-2	8. ² 2
)	GOTERM_MF_DIRECT	GPI-linked ephrin receptor activity	<u>RT</u>	1	5	1.8E-2	4.3E0	1.2E-1	1.1 1
)	UP_SEQ_FEATURE	short sequence motif:PDZ-binding	<u>RT</u>		19	2.8E-2	1.7E0	4.9E-1	4.8
)	SMART	<u>SAM</u>	<u>RT</u>	4	28	8.1E-2	1.3E0	4.7E-1	4.3
)	UP_SEQ_FEATURE	compositionally biased region:Cys-rich	RT		30	1.2E-1		1.0E0	1 9.6
, 1	UP_SEQ_FEATURE	domain:Fibronectin type-III 2		-	25	1.6E-1			1 9.6
)	UP_SEQ_FEATURE		<u>RT</u>	-					1 9.6
	INTERPRO	domain: Fibronectin type-III 1 Insulin-like growth factor binding protein, N-	<u>RT</u>	•	25		1.3E0		9.1
		<u>terminal</u>	<u>RT</u>	•	27	2.3E-1	1.2E0	1.0E0	1
	INTERPRO	<u>Fibronectin, type III</u>	<u>RT</u>	•	38	2.7E-1	1.1E0	1.0E0	9.1
	SMART	FN3	<u>RT</u>	i .	30	9.5E-1	8.1E-1		9.5 1
not	tation Cluster 69	Enrichment Score: 3.68	G		Count	P_Value	Fold Change	Benjamin	
)	BIOCARTA	<u>Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation</u>	<u>RT</u>	i	18	5.8E-5	2.4E0	1.4E-3	1.0 3
)	BIOCARTA	Regulation of BAD phosphorylation	<u>RT</u>	1	19	1.4E-4	2.2E0	2.4E-3	1.7 3
)	BIOCARTA	<u>Transcription factor CREB and its extracellular signals</u>	<u>RT</u>	1	18	1.1E-3	2.0E0	1.1E-2	7.7 3
nnot	tation Cluster 70	Enrichment Score: 3.67	G		Count	P_Value	Fold	Benjamin	i FD
							Change		

Annot	ation Cluster 1	Enrichment Score: ?	G	100	Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-	<u>RT</u>	1	12	1.1E-7	5.7E0	3.2E-6	2.9E
	SMART	tetraphosphatase PP2Ac	<u>RT</u>	1	12	9.2E-6	3.8E0	1.6E-4	1.4E
	INTERPRO	Metallophosphoesterase domain	<u>RT</u>	i	12	2.8E-3	2.7E0	3.3E-2	3.0E- 2
	UP_SEQ_FEATURE	metal ion-binding site:Manganese	<u>RT</u>	i	11	2.1E-2	2.2E0	3.9E-1	3.7E
	UP_SEQ_FEATURE	metal ion-binding site:Iron	<u>RT</u>	i e	12	9.5E-2	1.7E0	1.0E0	9.6E
	UP_SEQ_FEATURE	active site:Proton donor	<u>RT</u>	i	21	9.8E-1	7.2E-1	1.0E0	9.8E
Annot	ation Cluster 71	Enrichment Score: 3.67	G	15	Count	P_Value	Fold Change	Benjamin	
	UP_KEYWORDS	<u>Bromodomain</u>	<u>RT</u>	i	20	4.3E-7		3.3E-6	2.5E
	INTERPRO	Bromodomain, conserved site	<u>RT</u>	1	16	1.6E-6	3.8E0	4.0E-5	3.7E 5
	INTERPRO	<u>Bromodomain</u>	<u>RT</u>	1	20	1.3E-5	2.9E0	2.6E-4	2.3E 4
	UP_SEQ_FEATURE	domain:Bromo	<u>RT</u>	1	12	1.8E-3	2.8E0	4.5E-2	4.4E 2
	SMART	BROMO	<u>RT</u>	1	20	2.8E-3	1.9E0	3.1E-2	2.8E
	UP_SEQ_FEATURE	domain:Bromo 1	<u>RT</u>	1	7	4.1E-3	4.0E0	9.8E-2	9.4E 2
	UP_SEQ_FEATURE	domain:Bromo 2	<u>RT</u>	i e	7	4.1E-3	4.0E0	9.8E-2	9.4E 2
	GOTERM_MF_DIRECT	<u>lysine-acetylated histone binding</u>	<u>RT</u>	•	9	5.5E-3	3.0E0	4.9E-2	4.4E 2
Annot	ation Cluster 72	Enrichment Score: 3.41	G	- 19	Count	P_Value	Fold Change	Benjamin	
	GOTERM_CC_DIRECT	extrinsic component of cytoplasmic side of plasma membrane	<u>RT</u>	i .	33	1.2E-9	Change	4.3E-8	3.8E
	UP_SEQ_FEATURE	domain:SH2	<u>RT</u>		31	2.9E-5	2.2E0	9.6E-4	9.2E 4
	UP_SEQ_FEATURE	domain:SH3	<u>RT</u>	•	44	3.6E-4	1.7E0	1.0E-2	9.7
	UP_KEYWORDS	SH3 domain	RT		46	7.0E-3	1.5E0	3.3E-2	3 2.5E
_ _	INTERPRO	Src homology-3 domain	RT		46	4.5E-2		3.3E-1	3.0
	SMART	SH3	RT		45		8.9E-1		9.1
Annot	ation Cluster 73	Enrichment Score: 3.4	G		Count	P_Value	Fold	Bandamia	1 ii FDR
	GOTERM_MF_DIRECT	nucleotide binding	<u>RT</u>		97	2.3E-7	Change	5.7E-6	5.1E
	INTERPRO	RNA recognition motif domain	<u>RT</u>	•	64	5.1E-6	1.8E0	1.1E-4	1.0E
	UP_SEQ_FEATURE	domain:RRM	<u>RT</u>		39	3.8E-5	2.0E0	1.2E-3	1.2E
	INTERPRO	Nucleotide-binding, alpha-beta plait	<u>RT</u>	•	68	7.0E-5	1.6E0	1.2E-3	1.1E 3
	UP_SEQ_FEATURE	domain:RRM 1	<u>RT</u>	•	30	7.3E-3	1.6E0	1.6E-1	1.6
	UP_SEQ_FEATURE	domain:RRM 2	RT		30	7.3E-3		1.6E-1	1.6
	UP_SEQ_FEATURE	domain:RRM 3	RT					8.4E-1	1 8.1E
					15	5.6E-2	1./ []		1
	SMART	RRM	RT		15 63	5.6E-2		4 0F-1	3.61
Annota		RRM Enrichment Score: 3.24	<u>RT</u>	a	63	6.8E-2	1.2E0	4.0E-1	1
Annota	SMART ation Cluster 74 UP_SEQ_FEATURE	Enrichment Score: 3.24	G	= 175	63 Count	6.8E-2 P_Value 1.6E-	1.2E0 Fold Change	Benjamin	1 i FDF 1.0
Annota	ation Cluster 74		G RT	= ○ ○ ○ ○ ○ ○ ○ ○ ○ ○	63 Count 16	6.8E-2 P_Value 1.6E- 10	1.2E0 Fold Change	Benjamin	
Annot	ation Cluster 74 UP_SEQ_FEATURE	Enrichment Score: 3.24 domain:PI3K/PI4K Phosphatidylinositol 3-/4-kinase, catalytic domain Phosphatidylinositol 3/4-kinase, conserved	G RT RT	=	63 Count 16 16	6.8E-2 P_Value 1.6E- 10 2.5E-9	1.2E0 Fold Change 6.1E0 5.2E0	Benjamin 1.0E-8 9.0E-8	1 FDF 1.0E 8 8.2E 8 5.0E
Annot	ation Cluster 74 UP_SEQ_FEATURE INTERPRO	Enrichment Score: 3.24 domain:PI3K/PI4K Phosphatidylinositol 3-/4-kinase, catalytic domain Phosphatidylinositol 3/4-kinase, conserved site	G RT RT RT		63 Count 16 16 14	6.8E-2 P_Value 1.6E- 10 2.5E-9 1.7E-8	1.2E0 Fold Change 6.1E0 5.2E0 5.4E0	Benjamin 1.0E-8 9.0E-8 5.4E-7	1 FDF 1.0E 8 8.2E 8 5.0E 7
Annot	ation Cluster 74 UP_SEQ_FEATURE INTERPRO INTERPRO	Enrichment Score: 3.24 domain:PI3K/PI4K Phosphatidylinositol 3-/4-kinase, catalytic domain Phosphatidylinositol 3/4-kinase, conserved	RT RT RT RT		63 Count 16 16 14 15	6.8E-2 P_Value 1.6E- 10 2.5E-9 1.7E-8 9.0E-7	1.2E0 Fold Change 6.1E0 5.2E0 5.4E0 3.6E0	9.0E-8 5.4E-7 1.7E-5	1 FDF 1.06 8 8.26 8 5.06 7 1.66 5
Annot	ation Cluster 74 UP_SEQ_FEATURE INTERPRO INTERPRO SMART	Enrichment Score: 3.24 domain:PI3K/PI4K Phosphatidylinositol 3-/4-kinase, catalytic domain Phosphatidylinositol 3/4-kinase, conserved site PI3Kc	RT RT RT RT RT		63 Count 16 16 14 15 9	6.8E-2 P_Value 1.6E- 10 2.5E-9 1.7E-8 9.0E-7 1.5E-5	1.2E0 Fold Change 6.1E0 5.2E0 5.4E0 3.6E0 5.6E0	Benjamin 1.0E-8 9.0E-8 5.4E-7 1.7E-5 2.9E-4	1 FDF 1.01 8 8.21 8 5.01 7 1.61 5 2.71 4
Annot	ation Cluster 74 UP_SEQ_FEATURE INTERPRO INTERPRO SMART INTERPRO	Enrichment Score: 3.24 domain:PI3K/PI4K Phosphatidylinositol 3-/4-kinase, catalytic domain Phosphatidylinositol 3/4-kinase, conserved site PI3Kc Phosphoinositide 3-kinase, accessory (PIK) domain Phosphatidylinositol 3-kinase C2 (PI3K C2) domain	RT RT RT RT RT RT		63 Count 16 16 14 15 9 8	6.8E-2 P_Value 1.6E- 10 2.5E-9 1.7E-8 9.0E-7 1.5E-5 1.9E-5	1.2E0 Fold Change 6.1E0 5.2E0 5.4E0 3.6E0 5.6E0 6.2E0	1.0E-8 9.0E-8 5.4E-7 1.7E-5 2.9E-4 3.6E-4	1.0E 8 8.2E 8 5.0E 7 1.6E 5 2.7E 4 3.3E 4
Annot	ation Cluster 74 UP_SEQ_FEATURE INTERPRO INTERPRO SMART INTERPRO INTERPRO	Enrichment Score: 3.24 domain:PI3K/PI4K Phosphatidylinositol 3-/4-kinase, catalytic domain Phosphatidylinositol 3/4-kinase, conserved site PI3Kc Phosphoinositide 3-kinase, accessory (PIK) domain Phosphatidylinositol 3-kinase C2 (PI3K C2) domain PI3Ka	RT RT RT RT RT RT RT		63 Count 16 16 14 15 9 8 9	6.8E-2 P_Value 1.6E- 10 2.5E-9 1.7E-8 9.0E-7 1.5E-5 1.9E-5 9.4E-5	1.2E0 Fold Change 6.1E0 5.2E0 5.4E0 3.6E0 5.6E0 6.2E0 4.1E0	9.0E-8 5.4E-7 1.7E-5 2.9E-4 3.6E-4 1.4E-3	1.06 8 8.26 8 5.06 7 1.66 5 2.76 4 3.36 4 1.36
Annot	ation Cluster 74 UP_SEQ_FEATURE INTERPRO INTERPRO SMART INTERPRO SMART INTERPRO SMART INTERPRO	domain:PI3K/PI4K Phosphatidylinositol 3-/4-kinase, catalytic domain Phosphatidylinositol 3/4-kinase, conserved site PI3Kc Phosphoinositide 3-kinase, accessory (PIK) domain Phosphatidylinositol 3-kinase C2 (PI3K C2) domain PI3Ka Phosphatidylinositol 3-kinase Ras-binding (PI3K RBD) domain	RT RT RT RT RT RT RT RT		63 Count 16 16 14 15 9 8 9 7	6.8E-2 P_Value 1.6E- 10 2.5E-9 1.7E-8 9.0E-7 1.5E-5 1.9E-5 1.1E-4	1.2E0 Fold Change 6.1E0 5.2E0 5.4E0 3.6E0 6.2E0 4.1E0 6.2E0	9.0E-8 5.4E-7 1.7E-5 2.9E-4 3.6E-4 1.4E-3 1.7E-3	1 1.0E 8 8.2E 8 5.0E 7 1.6E 5 2.7E 4 1.3E 3 1.6E 3
Annot	ation Cluster 74 UP_SEQ_FEATURE INTERPRO INTERPRO SMART INTERPRO INTERPRO SMART INTERPRO INTERPRO INTERPRO	domain:PI3K/PI4K Phosphatidylinositol 3-/4-kinase, catalytic domain Phosphatidylinositol 3/4-kinase, conserved site PI3Kc Phosphoinositide 3-kinase, accessory (PIK) domain Phosphatidylinositol 3-kinase C2 (PI3K C2) domain PI3Ka Phosphatidylinositol 3-kinase Ras-binding (PI3K RBD) domain Phosphatidylinositol Kinase	RT		63 Count 16 16 14 15 9 8 9 7 9	6.8E-2 P_Value 1.6E- 10 2.5E-9 1.7E-8 9.0E-7 1.5E-5 1.9E-5 1.1E-4 1.2E-4	1.2E0 Fold Change 6.1E0 5.2E0 5.4E0 3.6E0 6.2E0 4.1E0 6.2E0 4.6E0	9.0E-8 9.0E-8 5.4E-7 1.7E-5 2.9E-4 3.6E-4 1.4E-3 1.7E-3	1 1.01 8 8.21 8 5.01 7 1.61 5 2.71 4 1.31 3 1.61 3 1.71 3
Annot	ation Cluster 74 UP_SEQ_FEATURE INTERPRO INTERPRO SMART INTERPRO SMART INTERPRO SMART INTERPRO SMART INTERPRO GOTERM_MF_DIRECT	Enrichment Score: 3.24 domain:PI3K/PI4K Phosphatidylinositol 3-/4-kinase, catalytic domain Phosphatidylinositol 3/4-kinase, conserved site PI3Kc Phosphoinositide 3-kinase, accessory (PIK) domain Phosphatidylinositol 3-kinase C2 (PI3K C2) domain PI3Ka Phosphatidylinositol 3-kinase Ras-binding (PI3K RBD) domain Phosphatidylinositol Kinase 1-phosphatidylinositol Kinase	RT		63 Count 16 16 14 15 9 8 9 7 9 7	6.8E-2 P_Value 1.6E- 10 2.5E-9 1.7E-8 9.0E-7 1.5E-5 1.9E-5 1.1E-4 1.2E-4 1.3E-4	1.2E0 Fold Change 6.1E0 5.2E0 5.4E0 3.6E0 6.2E0 4.1E0 6.2E0 4.6E0 6.0E0	1.0E-8 9.0E-8 5.4E-7 1.7E-5 2.9E-4 3.6E-4 1.4E-3 1.7E-3 1.9E-3	1 1.01 8 8.21 8 5.01 7 1.61 5 2.71 4 3.31 4 1.31 3 1.61 3 1.71 3 1.71 3
Annot	ation Cluster 74 UP_SEQ_FEATURE INTERPRO INTERPRO SMART INTERPRO INTERPRO SMART INTERPRO SMART INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT	domain:PI3K/PI4K Phosphatidylinositol 3-/4-kinase, catalytic domain Phosphatidylinositol 3/4-kinase, conserved site PI3Kc Phosphoinositide 3-kinase, accessory (PIK) domain Phosphatidylinositol 3-kinase C2 (PI3K C2) domain PI3Ka Phosphatidylinositol 3-kinase Ras-binding (PI3K RBD) domain Phosphatidylinositol Kinase 1-phosphatidylinositol Kinase 1-phosphatidylinositol-4-phosphate 3-kinase activity phosphatidylinositol-3-phosphate biosynthetic process	RT		63 Count 16 16 14 15 9 8 9 7 9 7 20	6.8E-2 P_Value 1.6E- 10 2.5E-9 1.7E-8 9.0E-7 1.5E-5 1.9E-5 1.1E-4 1.2E-4 1.3E-4 2.1E-4	1.2E0 Fold Change 6.1E0 5.2E0 5.4E0 3.6E0 6.2E0 4.1E0 6.2E0 4.6E0 6.0E0 2.4E0	1.0E-8 9.0E-8 5.4E-7 1.7E-5 2.9E-4 3.6E-4 1.4E-3 1.7E-3 1.9E-3 6.1E-3	1 1.01 8 8.21 8 5.01 7 1.61 5 2.71 4 1.31 3 1.61 3 1.71 3 5.91 3
Annot	ation Cluster 74 UP_SEQ_FEATURE INTERPRO INTERPRO SMART INTERPRO INTERPRO SMART INTERPRO SMART INTERPRO GOTERM_MF_DIRECT GOTERM_MF_DIRECT	domain:PI3K/PI4K Phosphatidylinositol 3-/4-kinase, catalytic domain Phosphatidylinositol 3/4-kinase, conserved site PI3Kc Phosphoinositide 3-kinase, accessory (PIK) domain Phosphatidylinositol 3-kinase C2 (PI3K C2) domain PI3Ka Phosphatidylinositol 3-kinase Ras-binding (PI3K RBD) domain Phosphatidylinositol Kinase 1-phosphatidylinositol-4-phosphate 3-kinase activity phosphatidylinositol-3-phosphate biosynthetic	RT		63 Count 16 16 14 15 9 8 9 7 9 7	6.8E-2 P_Value 1.6E- 10 2.5E-9 1.7E-8 9.0E-7 1.5E-5 1.9E-5 1.1E-4 1.2E-4 1.3E-4	1.2E0 Fold Change 6.1E0 5.2E0 5.4E0 3.6E0 6.2E0 4.1E0 6.2E0 4.6E0 6.0E0 2.4E0	1.0E-8 9.0E-8 5.4E-7 1.7E-5 2.9E-4 3.6E-4 1.4E-3 1.7E-3 1.9E-3	1 1.0E 8 8.2E 8 5.0E 7 1.6E 5 2.7E 4 1.3E 3 1.6E 3 1.7E 3 3.9E 3 3.9E 3 3.9E 3 3
Annot	ation Cluster 74 UP_SEQ_FEATURE INTERPRO INTERPRO SMART INTERPRO INTERPRO SMART INTERPRO SMART INTERPRO GOTERM_MF_DIRECT GOTERM_BP_DIRECT	domain:PI3K/PI4K Phosphatidylinositol 3-/4-kinase, catalytic domain Phosphatidylinositol 3/4-kinase, conserved site PI3Kc Phosphoinositide 3-kinase, accessory (PIK) domain Phosphatidylinositol 3-kinase C2 (PI3K C2) domain PI3Ka Phosphatidylinositol 3-kinase Ras-binding (PI3K RBD) domain Phosphatidylinositol Kinase 1-phosphatidylinositol Kinase 1-phosphatidylinositol-4-phosphate 3-kinase activity phosphatidylinositol-3-phosphate biosynthetic process	RT		63 Count 16 16 14 15 9 8 9 7 9 7 20	6.8E-2 P_Value 1.6E- 10 2.5E-9 1.7E-8 9.0E-7 1.5E-5 1.9E-5 1.1E-4 1.2E-4 1.3E-4 2.1E-4	1.2E0 Fold Change 6.1E0 5.2E0 5.4E0 3.6E0 6.2E0 4.1E0 6.2E0 4.6E0 6.0E0 2.4E0 2.5E0	1.0E-8 9.0E-8 5.4E-7 1.7E-5 2.9E-4 3.6E-4 1.4E-3 1.7E-3 1.9E-3 6.1E-3	1 1.0E 8 8.2E 8 5.0E 7 1.6E 5 2.7E 4 3.3E 4 1.3E 3 1.7E 3 1.7E 3 3 3.9E 3 3.9E

Anno	tation Cluster 1	Enrichment Score: ?	G	· · · ·	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_MF_DIRECT	phosphatidylinositol 3-kinase activity	<u>RT</u>	i	5	3.4E-3	•	3.2E-2	2.9E- 2
	SMART	PI3K rbd	<u>RT</u>	i .	6	4.3E-3	4.1E0	4.5E-2	4.1E- 2
	INTERPRO	Phosphatidylinositol 3-kinase adaptor-binding	<u>RT</u>	1	4	1.5E-2	6.2E0	1.3E-1	1.1E-
	GOTERM_BP_DIRECT	(PI3K ABD) domain phosphatidylinositol biosynthetic process	<u>RT</u>		17	2.8E-2	1.7E0	3.1E-1	1 3.0E-
	SMART	PI3K p85B	RT		3	1.5E-1		6.9E-1	1 6.2E-
	KEGG_PATHWAY	Inositol phosphate metabolism	RT		14	6.3E-1		9.0E-1	1 6.3E-
	KEGG_PATHWAY				19			9.0E-1	1 6.3E-
	UP_SEQ_FEATURE	Phosphatidylinositol signaling system	RT			6.3E-1			1 9.8E-
	INTERPRO	domain:PX	<u>RT</u>		4		5.7E-1		1 9.8E-
	GOTERM_MF_DIRECT	Phox homologous domain phosphatidylinositol binding	RT RT		5 7	9.8E-1 1.0E0	5.6E-1 4.9E-1		1 1.0E0
	SMART DIRECT	PX	RT	<u> </u>	4	1.0E0	3.6E-1		1.0E0 1.0E0
Anno	tation Cluster 75	Enrichment Score: 3.19	G	15	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_MF_DIRECT	receptor signaling protein tyrosine kinase activity	<u>RT</u>	i	10	8.8E-7	6.0E0	2.1E-5	1.8E- 5
	INTERPRO	EGF receptor, L domain	<u>RT</u>	i .	7	1.1E-4	6.2E0	1.7E-3	1.6E- 3
	INTERPRO	Furin-like cysteine-rich domain	<u>RT</u>	i	7	1.1E-4	6.2E0	1.7E-3	1.6E- 3
	INTERPRO	<u>Furin-like repeat</u>	<u>RT</u>	i .	10	8.8E-4	3.4E0	1.2E-2	1.1E- 2
	INTERPRO	Tyrosine protein kinase, EGF/ERB/XmrK receptor	<u>RT</u>	i	4	1.5E-2	6.2E0	1.3E-1	1.1E-
	SMART	<u>FU</u>	<u>RT</u>	i	10	1.7E-2	2.3E0	1.5E-1	1.4E-
	PIR_SUPERFAMILY	tyrosine-protein kinase, EGF receptor type	<u>RT</u>	i .	4	2.1E-2	5.4E0	2.9E-1	2.9E-
Anno	otation Cluster 76	Enrichment Score: 3.09	G	TN .	Count	P_Value	Fold Change	Benjamin	1
	GOTERM_MF_DIRECT	<u>ligase activity</u>	RT	Ē	88	2.8E-	1.9E0	8.7E-9	7.7E-
	UP_KEYWORDS	Ligase	RT	-	91	10 1.7E-8		1.4E-7	9 1.1E-
	UP_SEQ_FEATURE	zinc finger region:RING-type	RT	-	48	1.1E-2		2.2E-1	7 2.1E-
	INTERPRO			-	60	4.3E-2			1 2.9E-
	INTERPRO	Zinc finger, RING-type	<u>RT</u>					3.2E-1	1 7.7E-
	INTERPRO	Zinc finger, RING/FYVE/PHD-type	<u>RT</u>	-	82	1.7E-1		8.4E-1	1 9.1E-
	SMART	Zinc finger, RING-type, conserved site	<u>RT</u>	•	27	6.4E-1	9.9E-1	1.0E0	9.9E-
	SWART	RING	<u>RT</u>	i	46	<u> </u>	7.7E-1 Fold		1
Anno	otation Cluster 77 BIOCARTA	Enrichment Score: 3.08	G	No.	Count	P_Value	Change	Benjamin	4.0E-
		Cell Cycle	<u>RT</u>	i	20	1.0E-5	2.4E0	5.6E-4	4
	BIOCARTA	cdc25 and chk1 Regulatory Pathway in response to DNA damage	<u>RT</u>	•	8	7.3E-3	2.7E0	3.7E-2	2.6E- 2
	BIOCARTA	RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage	<u>RT</u>	i	10	7.6E-3		3.7E-2	2.6E- 2
Anno	tation Cluster 78	Enrichment Score: 3.04	G	™	Count	P_Value	Fold Change	Benjamin	
	GOTERM_MF_DIRECT	histone deacetylase activity	<u>RT</u>	i	22	1.4E-7	3.4E0	3.6E-6	3.2E- 6
	GOTERM_BP_DIRECT	histone deacetylation	<u>RT</u>	i .	22	5.1E-6	2.8E0	2.5E-4	2.4E- 4
	UP_SEQ_FEATURE	region of interest:Histone deacetylase	<u>RT</u>	i .	9	7.3E-6	6.1E0	2.7E-4	2.6E- 4
	INTERPRO	Histone deacetylase domain	<u>RT</u>	i .	10	1.0E-5	5.2E0	2.0E-4	1.8E- 4
	GOTERM_MF_DIRECT	NAD-dependent histone deacetylase activity (H3-K14 specific)	<u>RT</u>	1	10	1.4E-5	5.0E0	2.6E-4	2.3E- 4
	GOTERM_MF_DIRECT	protein deacetylase activity	<u>RT</u>	i .	9	2.0E-5	5.4E0	3.5E-4	3.2E- 4
	GOTERM_BP_DIRECT	histone H3 deacetylation	<u>RT</u>	i e	13	3.4E-5	3.7E0	1.2E-3	1.2E-
	INTERPRO	Histone deacetylase superfamily	RT		10	6.7E-5		1.2E-3	1.1E-
	GOTERM_BP_DIRECT	protein deacetylation	RT		8	2.9E-4		7.9E-3	3 7.6E-
	GOTERM_CC_DIRECT	histone deacetylase complex	RT		15	6.7E-4		7.1E-3	3 6.2E-
	GOTERM_BP_DIRECT					9.4E-3		1.4E-1	3 1.3E-
	GOTERM_BP_DIRECT	histone H4 deacetylation	<u>RT</u>		6				1 2.1E-
	GOTERM_BP_DIRECT	peptidyl-lysine deacetylation	<u>RT</u>		5	1.8E-2		2.2E-1	1 2.3E-
	INTERPRO	regulation of gene expression, epigenetic	<u>RT</u>	i	7	2.0E-2		2.4E-1	1
		<u>Histone deacetylase class II, eukaryotic</u>	<u>RT</u>	i	4	3.2E-2	5.0E0	2.4E-1	2.2E- 1
	GOTERM_BP_DIRECT	negative regulation of myotube differentiation	<u>RT</u>	i	7	4.0E-2	2.6E0	3.9E-1	3.8E- 1

Annot	tation Cluster 1	Enrichment Score: ?	G	- 1	Count	P_Value	Fold Change	Benjamin	i FDR
	PIR_SUPERFAMILY	histone deacetylase class II, eukaryotic type	<u>RT</u>	i	4	4.6E-2	4.4E0	5.6E-1	5.5E- 1
	COG_ONTOLOGY	<u>Chromatin structure and dynamics /</u> <u>Secondary metabolites biosynthesis,</u> <u>transport, and catabolism</u>	<u>RT</u>	1	7	4.7E-2	2.2E0	4.8E-1	4.8E-
	INTERPRO	Histone deacetylase, glutamine rich N- terminal domain	<u>RT</u>	i	3	1.2E-1	4.6E0	6.4E-1	5.8E-
	INTERPRO	Histone deacetylase	<u>RT</u>	1	3	1.2E-1	4.6E0	6.4E-1	5.8E-
	PIR_SUPERFAMILY	histone deacetylase class I, eukaryotic type	<u>RT</u>	1	3	1.6E-1		1.0E0	1.0E
Annot	tation Cluster 79	Enrichment Score: 2.99	G	- 1	Count	P_Value	Fold Change	Benjamin	i FDR
	BIOCARTA	IL-2 Receptor Beta Chain in T cell Activation	<u>RT</u>		28	2.7E-6	2.2E0	3.9E-4	2.8E- 4
	BIOCARTA	Inhibition of Cellular Proliferation by Gleevec	<u>RT</u>	1	19	8.8E-6	2.5E0	5.6E-4	4.0E- 4
	BIOCARTA	EGF Signaling Pathway	<u>RT</u>	4	21	1.1E-5	2.4E0	5.6E-4	4.0E 4
	BIOCARTA	PDGF Signaling Pathway	<u>RT</u>		21	2.8E-5	2.3E0	9.1E-4	6.5E 4
	BIOCARTA	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling	<u>RT</u>		23	5.9E-5	2.1E0	1.4E-3	1.0E
	BIOCARTA	Growth Hormone Signaling Pathway	<u>RT</u>		20	6.3E-5	2.3E0	1.4E-3	1.0E
_ 	BIOCARTA	IL 2 signaling pathway	RT		17	1.3E-4		2.4E-3	3 1.7E
_ _	BIOCARTA								3 1.7E
_ 	BIOCARTA	TPO Signaling Pathway	<u>RT</u>		18	1.4E-4		2.4E-3	3 2.9E
_	BIOCARTA	IGF-1 Signaling Pathway Role of ERBB2 in Signal Transduction and	<u>RT</u>	i	16	3.0E-4		4.1E-3	3
		Oncology	<u>RT</u>	i	16	1.3E-3	2.1E0	1.2E-2	8.8E 3
	BIOCARTA	<u>IL 6 signaling pathway</u>	<u>RT</u>	•	15	1.4E-3	2.2E0	1.2E-2	8.8E 3
	BIOCARTA	<u>Insulin Signaling Pathway</u>	<u>RT</u>	•	15	1.4E-3	2.2E0	1.2E-2	8.8E 3
	BIOCARTA	EPO Signaling Pathway	<u>RT</u>	1	14	1.5E-3	2.2E0	1.3E-2	8.9E 3
	BIOCARTA	Links between Pyk2 and Map Kinases	<u>RT</u>	4	18	2.0E-3	2.0E0	1.6E-2	1.2E 2
	BIOCARTA	Signaling of Hepatocyte Growth Factor Receptor	<u>RT</u>		21	3.7E-3	1.8E0	2.3E-2	1.6E
7	BIOCARTA	BCR Signaling Pathway	<u>RT</u>		20	4.3E-3	1.8E0	2.6E-2	1.88
- ገ	BIOCARTA	Fc Epsilon Receptor I Signaling in Mast Cells	RT		22	4.9E-3	1 7F0	2.9E-2	2 2.0E
ے ا	BIOCARTA	T Cell Receptor Signaling Pathway	RT		24	5.3E-3		3.0E-2	2 2.1E
ر ا	BIOCARTA			_					2 2.2E
	BIOCARTA	<u>Integrin Signaling Pathway</u>	<u>RT</u>	•	21	5.6E-3		3.1E-2	2 2.6E
	BIOCARTA	<u>IL 3 signaling pathway</u>	<u>RT</u>	•	11	7.2E-3	2.2E0	3.7E-2	2
		Bioactive Peptide Induced Signaling Pathway	<u>RT</u>	•	21	8.3E-3	1.7E0	3.9E-2	2.7E 2
	BIOCARTA	Nerve growth factor pathway (NGF)	<u>RT</u>	i .	13	1.1E-2	2.0E0	4.9E-2	3.5E 2
	BIOCARTA	fMLP induced chemokine gene expression in HMC-1 cells	<u>RT</u>	1	20	1.4E-2	1.6E0	5.9E-2	4.2E 2
	BIOCARTA	Erk1/Erk2 Mapk Signaling pathway	<u>RT</u>	1	17	1.5E-2	1.7E0	6.3E-2	4.5E 2
	BIOCARTA	Sprouty regulation of tyrosine kinase signals	<u>RT</u>	4	11	3.8E-2	1.9E0	1.2E-1	8.8E 2
	BIOCARTA	Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia	<u>RT</u>	4	12	1.3E-1	1.5E0	3.1E-1	2.2E
nnot	tation Cluster 80	Enrichment Score: 2.95	G	M	Count	P_Value	Fold Change	Benjamin	
	GOTERM_MF_DIRECT	<u>U1 snRNP binding</u>	RT	1	7	1.3E-4	Change	1.9E-3	1.7E
ے ا	GOTERM_CC_DIRECT	commitment complex	RT	-	6	1.5E-3		1.5E-2	3 1.3E
ے ا	GOTERM_CC_DIRECT								2 4.7E
		<u>prespliceosome</u>	RT		5	7.0E-3	Fold	5.3E-2	2
nnot	INTERPRO	Enrichment Score: 2.9	G		Count	P_Value	Change	-	1.6E
J		14-3-3 protein	<u>RT</u>	i	7	1.1E-4	6.2E0	1.7E-3	3
	INTERPRO	14-3-3 protein, conserved site	<u>RT</u>	•	7	1.1E-4	6.2E0	1.7E-3	1.6E 3
	INTERPRO	<u>14-3-3 domain</u>	<u>RT</u>	i	7	1.1E-4	6.2E0	1.7E-3	1.6E 3
	UP_SEQ_FEATURE	site:Interaction with phosphoserine on interacting protein	<u>RT</u>	i e	7	2.1E-4	6.0E0	6.2E-3	5.9E 3
	PIR_SUPERFAMILY	14-3-3 protein	<u>RT</u>	i	7	2.2E-4	5.4E0	1.4E-2	1.4E 2
	SMART	<u>14 3 3</u>	<u>RT</u>	i	7	1.2E-3	4.1E0	1.5E-2	1.3E
	GOTERM_BP_DIRECT	positive regulation of protein insertion into	DT		12	2.25.2	2.650	4 FF 2	4.3
		mitochondrial membrane involved in apoptotic signaling pathway	<u>RT</u>	•	13	2.3E-3	2.6E0	4.5E-2	2
	GOTERM_BP_DIRECT	<u>protein targeting</u>	<u>RT</u>	i	10	2.0E-1	1.5E0	1.0E0	9.6E 1
	GOTERM_BP_DIRECT	membrane organization	<u>RT</u>	1	8	2.9E-1	1.5E0	1.0E0	9.6E 1

Anno	tation Cluster 1	Enrichment Score: ?	G	To the second second	Count	P_Value	Fold Change	Benjamini	FDR
Anno	tation Cluster 82	Enrichment Score: 2.79	G	MR CONTRACTOR	Count	P_Value	Fold	Benjamini	FDR
	GOTERM_BP_DIRECT	MyD88-dependent toll-like receptor signaling pathway	<u>RT</u>	i	24	2.5E- 11		3.1E-9	2.9E-
	UP_SEQ_FEATURE	repeat:LRR 20	<u>RT</u>	i .	18	2.7E- 10	5.3E0	1.7E-8	1.6E-
	UP_SEQ_FEATURE	repeat:LRR 21	<u>RT</u>	1	14	5.9E-8	5.3E0	3.0E-6	2.9E-
	GOTERM_BP_DIRECT	regulation of cytokine secretion	RT		10	4.4E-6	5.4E0	2.2E-4	6 2.1E-
	UP_SEQ_FEATURE	repeat:LRR 22	RT		10	4.5E-6		1.8E-4	4 1.7E-
	GOTERM_BP_DIRECT	toll-like receptor signaling pathway	RT		16	5.6E-6		2.6E-4	4 2.5E-
	UP_SEQ_FEATURE	repeat:LRR 23	RT		8	1.2E-4		3.5E-3	4 3.4E-
	UP_SEQ_FEATURE	repeat:LRR 24	RT		6	1.1E-3		2.9E-2	3 2.8E-
	GOTERM_BP_DIRECT	I-kappaB phosphorylation	RT		8	1.4E-3		3.0E-2	2 2.9E-
	UP_SEQ_FEATURE	domain:TIR	RT		11			4.5E-2	2 4.4E-
	GOTERM_BP_DIRECT					1.8E-3			2 6.6E-
	INTERPRO	positive regulation of chemokine production Toll/interleukin-1 receptor homology (TIR)	<u>RT</u>		9	3.8E-3		6.9E-2	2 5.1E-
	UP_SEQ_FEATURE	domain	<u>RT</u>		11	5.1E-3		5.6E-2	2 1.2E-
	GOTERM_BP_DIRECT	repeat:LRR 25	<u>RT</u>		5	5.4E-3		1.2E-1	1 1.1E-
	INTERPRO	· · · · · · · · · · · · · · · · · · ·	<u>RT</u>	•	11	7.2E-3		1.2E-1	1
		Toll-like receptor	<u>RT</u>	i	4	1.5E-2	6.2E0	1.3E-1	1.1E- 1
	GOTERM_BP_DIRECT	positive regulation of NF-kappaB import into nucleus	<u>RT</u>	i	9	1.7E-2	2.5E0	2.1E-1	2.0E- 1
	GOTERM_BP_DIRECT	positive regulation of interferon-alpha biosynthetic process	<u>RT</u>	i	4	1.7E-2	5.9E0	2.1E-1	2.0E- 1
	SMART	TIR	<u>RT</u>	•	11	1.8E-2	2.1E0	1.6E-1	1.4E- 1
	GOTERM_BP_DIRECT	positive regulation of interferon-beta biosynthetic process	<u>RT</u>	1	5	1.8E-2	4.2E0	2.2E-1	2.1E- 1
	PIR_SUPERFAMILY	toll-like receptor, 1/2/4/6/10 types [Parent=PIRSF800008]	<u>RT</u>	i	4	2.1E-2	5.4E0	2.9E-1	2.9E- 1
	UP_SEQ_FEATURE	repeat:LRR 26	<u>RT</u>	i	4	2.5E-2	5.5E0	4.4E-1	4.3E- 1
	GOTERM_BP_DIRECT	positive regulation of toll-like receptor signaling pathway	<u>RT</u>	i .	4	3.7E-2	4.7E0	3.7E-1	3.6E- 1
	GOTERM_BP_DIRECT	positive regulation of interleukin-6 production	<u>RT</u>	i .	13	6.6E-2	1.7E0	5.6E-1	5.3E- 1
	UP_KEYWORDS	Inflammatory response	<u>RT</u>	i .	30	7.5E-2	1.4E0	2.6E-1	2.0E- 1
	UP_SEQ_FEATURE	repeat:LRR 27	<u>RT</u>	i .	3	1.1E-1	5.1E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	positive regulation of interferon-gamma biosynthetic process	<u>RT</u>	i .	5	1.3E-1	2.5E0	8.2E-1	7.9E- 1
	GOTERM_CC_DIRECT	endolysosome membrane	<u>RT</u>	1	4	2.9E-1	2.1E0	8.6E-1	7.5E- 1
	GOTERM_MF_DIRECT	lipopeptide binding	<u>RT</u>	i	3	4.0E-1	2.2E0	1.0E0	8.9E-
	GOTERM_CC_DIRECT	phagocytic vesicle membrane	<u>RT</u>	i	8	8.4E-1	8.6E-1	1.0E0	8.8E-
	GOTERM_MF_DIRECT	transmembrane signaling receptor activity	<u>RT</u>	i	17	1.0E0	4.7E-1	1.0E0	1.0E0
Anno	tation Cluster 83	Enrichment Score: 2.78	G	To the second se	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	compositionally biased region:Ala/Asp-rich (DA-box)	<u>RT</u>	•	8	1.0E-5	6.8E0	3.7E-4	3.5E- 4
	UP_SEQ_FEATURE	region of interest:Flexible hinge	<u>RT</u>	i	7	6.1E-5	6.8E0	1.9E-3	1.8E- 3
	INTERPRO	RecF/RecN/SMC	<u>RT</u>	i	7	1.1E-4	6.2E0	1.7E-3	1.6E- 3
	INTERPRO	Structural maintenance of chromosomes protein	<u>RT</u>	i	5	2.9E-3	6.2E0	3.3E-2	3.1E- 2
	PIR_SUPERFAMILY	structural maintenance of chromosomes protein	<u>RT</u>	i	5	4.7E-3	5.4E0	2.3E-1	2.3E- 1
	INTERPRO	SMCs flexible hinge	<u>RT</u>	i	5	7.7E-3	5.2E0	7.7E-2	7.1E- 2
	SMART	SM00968	<u>RT</u>	1	5	3.5E-2	3.4E0	2.6E-1	2.3E- 1
	GOTERM_CC_DIRECT	meiotic cohesin complex	<u>RT</u>	i	3	2.4E-1	3.2E0	8.3E-1	7.3E- 1
Anno	tation Cluster 84	Enrichment Score: 2.76	G	170	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	SNF2-related	<u>RT</u>	1	22	4.5E- 10	4.3E0	1.8E-8	1.7E- 8
	UP_SEQ_FEATURE	domain:Chromo 2	<u>RT</u>	i	8	4.0E-5	6.1E0	1.3E-3	1.2E- 3
	INTERPRO	Chromo domain-like	<u>RT</u>	i contraction	14	8.1E-4	2.7E0	1.1E-2	9.9E- 3
	UP_SEQ_FEATURE	domain:Chromo 1	<u>RT</u>	1	8	1.1E-3	4.2E0	2.9E-2	2.8E- 2
	INTERPRO	Chromo domain/shadow	<u>RT</u>	1	14	1.1E-3	2.6E0	1.4E-2	1.3E- 2

Annota	ation Cluster 1	Enrichment Score: ?	G	To the second second	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	BRK domain	<u>RT</u>	i	5	7.7E-3		7.7E-2	7.1E- 2
	INTERPRO	Chromo domain	<u>RT</u>	1	10	1.7E-2	2.4E0	1.4E-1	1.3E- 1
	SMART	<u>BRK</u>	<u>RT</u>	i	5	3.5E-2	3.4E0	2.6E-1	2.3E-
	SMART	<u>CHROMO</u>	<u>RT</u>	i	14	4.3E-2	1.7E0	3.0E-1	2.7E-
	GOTERM_MF_DIRECT	hydrolase activity, acting on acid anhydrides	<u>RT</u>	i .	3	2.7E-1	3.0E0	9.9E-1	8.8E-
	INTERPRO	Chromo domain, conserved site	<u>RT</u>		5	4.1E-1	1.5E0	1.0E0	9.1E-
Annota	ation Cluster 85	Enrichment Score: 2.74	G	T7	Count	P_Value	Fold Change	Benjamini	1 FDR
	GOTERM_BP_DIRECT	sister chromatid cohesion	RT		35	4.7E-5	Change	1.7E-3	1.6E-
	GOTERM_CC_DIRECT	<u>kinetochore</u>	RT		28	6.8E-5	2.2E0	9.2E-4	3 8.0E-
	UP_KEYWORDS	Centromere	RT		35	1.0E-3	1.8E0	5.3E-3	4 4.1E-
	UP_KEYWORDS	<u>Kinetochore</u>	RT		22	4.6E-2		1.7E-1	3 1.3E-
	GOTERM_CC_DIRECT	condensed chromosome kinetochore	RT		19	1.3E-1		5.3E-1	1 4.7E-
Annot	ation Cluster 86	Enrichment Score: 2.74	G	-	Count	P_Value	Fold	Benjamini	1 FDR
	UP_SEQ_FEATURE	region of interest:S-adenosyl-L-methionine	RT	i	15	2.3E-4	Change	6.6E-3	6.3E-
	INTERPRO	binding <u>Bacterial Fmu (Sun)/eukaryotic nucleolar</u>							3 1.1E-
	INTERPRO	NOL1/Nop2p	<u>RT</u>		7	9.4E-4		1.2E-2	2 4.0E-
	UP_SEQ_FEATURE	RNA (C5-cytosine) methyltransferase	<u>RT</u>		6	4.0E-3		4.4E-2	2 2.4E-
		binding site:S-adenosyl-L-methionine	RT	i	15	1.3E-2		2.5E-1	1
Annota	ation Cluster 87 UP_SEQ_FEATURE	Enrichment Score: 2.74	G	-			Fold Change	•	FDR 5.8E-
	INTERPRO	domain:Post-SET	<u>RT</u>		12	1.4E-6		6.0E-5	5 6.0E-
		Post-SET domain	<u>RT</u>	•	11	3.7E-5	4.3E0	6.6E-4	4
	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K36 specific)	<u>RT</u>	i	5	8.9E-3	5.0E0	7.3E-2	6.5E- 2
	UP_SEQ_FEATURE	domain:AWS	<u>RT</u>	i	4	2.5E-2	5.5E0	4.4E-1	4.3E- 1
	INTERPRO	<u>AWS</u>	<u>RT</u>	i	4	3.2E-2	5.0E0	2.4E-1	2.2E- 1
	SMART	<u>AWS</u>	<u>RT</u>	i	4	9.9E-2		5.3E-1	4.8E- 1
Annota	ation Cluster 88	Enrichment Score: 2.7	G	To the second se	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	domain:Protein kinase 1	<u>RT</u>	1	11	6.7E-6	5.0E0	2.6E-4	2.5E- 4
		domain:Protein kinase 2				6 75 6			
	UP_SEQ_FEATURE	domaini rotein kindse 2	<u>RT</u>	1	11	0.76-0	5.0E0	2.6E-4	2.5E- 4
	INTERPRO	Tyrosine-protein kinase, non-receptor Jak/Tyk2	RT RT	i i	11	1.5E-2		2.6E-4 1.3E-1	2.5E- 4 1.1E- 1
		Tyrosine-protein kinase, non-receptor					6.2E0		4
	INTERPRO	<u>Tyrosine-protein kinase, non-receptor</u> <u>Jak/Tyk2</u>	<u>RT</u>	i	4	1.5E-2	6.2E0 5.4E0	1.3E-1	4 1.1E- 1
	INTERPRO PIR_SUPERFAMILY	Tyrosine-protein kinase, non-receptor Jak/Tyk2 tyrosine-protein kinase, Jak/Tyk2 type	RT RT	i i	4	1.5E-2 2.1E-2	6.2E0 5.4E0 4.1E0	1.3E-1 2.9E-1	4 1.1E- 1 2.9E- 1
Annota	INTERPRO PIR_SUPERFAMILY INTERPRO	Tyrosine-protein kinase, non-receptor Jak/Tyk2 tyrosine-protein kinase, Jak/Tyk2 type Ribosomal protein S6 kinase II	RT RT RT	i i i	4 4 4	1.5E-2 2.1E-2 5.7E-2	6.2E0 5.4E0 4.1E0 3.6E0	1.3E-1 2.9E-1 4.0E-1	4 1.1E- 1 2.9E- 1 3.7E- 1 6.8E- 1
Annota	INTERPRO PIR_SUPERFAMILY INTERPRO PIR_SUPERFAMILY	Tyrosine-protein kinase, non-receptor Jak/Tyk2 tyrosine-protein kinase, Jak/Tyk2 type Ribosomal protein S6 kinase II ribosomal protein S6 kinase II	RT RT RT RT	i i i	4 4 4	1.5E-2 2.1E-2 5.7E-2 7.9E-2	6.2E0 5.4E0 4.1E0 3.6E0 Fold Change	1.3E-1 2.9E-1 4.0E-1 6.9E-1	4 1.1E- 1 2.9E- 1 3.7E- 1 6.8E- 1
Annota	INTERPRO PIR_SUPERFAMILY INTERPRO PIR_SUPERFAMILY ation Cluster 89	Tyrosine-protein kinase, non-receptor Jak/Tyk2 tyrosine-protein kinase, Jak/Tyk2 type Ribosomal protein S6 kinase II ribosomal protein S6 kinase II Enrichment Score: 2.63	RT RT RT RT	i i i	4 4 4 4 Count	1.5E-2 2.1E-2 5.7E-2 7.9E-2 P_Value	6.2E0 5.4E0 4.1E0 3.6E0 Fold Change 2.8E0	1.3E-1 2.9E-1 4.0E-1 6.9E-1 Benjamini	4 1.1E-1 2.9E-1 3.7E-1 6.8E-1 FDR 9.0E-
Annota	INTERPRO PIR_SUPERFAMILY INTERPRO PIR_SUPERFAMILY ation Cluster 89 GOTERM_BP_DIRECT	Tyrosine-protein kinase, non-receptor Jak/Tyk2 tyrosine-protein kinase, Jak/Tyk2 type Ribosomal protein S6 kinase II ribosomal protein S6 kinase II Enrichment Score: 2.63 protein peptidyl-prolyl isomerization	RT RT RT RT RT		4 4 4 Count 20	1.5E-2 2.1E-2 5.7E-2 7.9E-2 P_Value 2.5E-5	6.2E0 5.4E0 4.1E0 3.6E0 Fold Change 2.8E0 3.1E0	1.3E-1 2.9E-1 4.0E-1 6.9E-1 Benjamini 9.4E-4	4 1.1E-1 2.9E-1 3.7E-1 6.8E-1 FDR 9.0E-4 1.6E-
Annota	INTERPRO PIR_SUPERFAMILY INTERPRO PIR_SUPERFAMILY ation Cluster 89 GOTERM_BP_DIRECT UP_KEYWORDS	Tyrosine-protein kinase, non-receptor Jak/Tyk2 tyrosine-protein kinase, Jak/Tyk2 type Ribosomal protein S6 kinase II ribosomal protein S6 kinase II Enrichment Score: 2.63 protein peptidyl-prolyl isomerization Rotamase	RT RT RT RT RT RT RT		4 4 4 Count 20 17	1.5E-2 2.1E-2 5.7E-2 7.9E-2 P_Value 2.5E-5 3.6E-5	6.2E0 5.4E0 4.1E0 3.6E0 Fold Change 2.8E0 3.1E0 2.6E0	1.3E-1 2.9E-1 4.0E-1 6.9E-1 Benjamini 9.4E-4 2.1E-4	4 1.1E-1 2.9E-1 3.7E-1 6.8E-1 FDR 9.0E-4 1.6E-4 1.0E-
Annota	INTERPRO PIR_SUPERFAMILY INTERPRO PIR_SUPERFAMILY ation Cluster 89 GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_MF_DIRECT	Tyrosine-protein kinase, non-receptor Jak/Tyk2 tyrosine-protein kinase, Jak/Tyk2 type Ribosomal protein S6 kinase II ribosomal protein S6 kinase II Enrichment Score: 2.63 protein peptidyl-prolyl isomerization Rotamase peptidyl-prolyl cis-trans isomerase activity Cyclophilin-like peptidyl-prolyl cis-trans	RT RT RT RT RT RT RT		4 4 4 Count 20 17 20	1.5E-2 2.1E-2 5.7E-2 7.9E-2 P_Value 2.5E-5 3.6E-5 7.2E-5	6.2E0 5.4E0 4.1E0 3.6E0 Fold Change 2.8E0 3.1E0 2.6E0 2.8E0	1.3E-1 2.9E-1 4.0E-1 6.9E-1 Benjamini 9.4E-4 2.1E-4 1.2E-3	4 1.1E-1 2.9E-1 3.7E-1 6.8E-1 FDR 9.0E-4 1.6E-4 1.0E-3 2.8E-
Annota	INTERPRO PIR_SUPERFAMILY INTERPRO PIR_SUPERFAMILY ation Cluster 89 GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_MF_DIRECT INTERPRO	Tyrosine-protein kinase, non-receptor Jak/Tyk2 tyrosine-protein kinase, Jak/Tyk2 type Ribosomal protein S6 kinase II ribosomal protein S6 kinase II Enrichment Score: 2.63 protein peptidyl-prolyl isomerization Rotamase peptidyl-prolyl cis-trans isomerase activity Cyclophilin-like peptidyl-prolyl cis-trans isomerase domain Cyclophilin-type peptidyl-prolyl cis-trans	RT		4 4 4 Count 20 17 20 11	1.5E-2 2.1E-2 5.7E-2 7.9E-2 P_Value 2.5E-5 3.6E-5 7.2E-5 2.6E-3	6.2E0 5.4E0 4.1E0 3.6E0 Fold Change 2.8E0 3.1E0 2.6E0 2.8E0 3.0E0	1.3E-1 2.9E-1 4.0E-1 6.9E-1 Benjamini 9.4E-4 2.1E-4 1.2E-3 3.1E-2	4 1.1E-1 2.9E-1 3.7E-1 6.8E-1 FDR 9.0E-4 1.6E-4 1.0E-3 2.8E-2 3.5E-
Annota O O O O O O O O O O O O O	INTERPRO PIR_SUPERFAMILY INTERPRO PIR_SUPERFAMILY ation Cluster 89 GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_MF_DIRECT INTERPRO	Tyrosine-protein kinase, non-receptor Jak/Tyk2 tyrosine-protein kinase, Jak/Tyk2 type Ribosomal protein S6 kinase II ribosomal protein S6 kinase II Enrichment Score: 2.63 protein peptidyl-prolyl isomerization Rotamase peptidyl-prolyl cis-trans isomerase activity Cyclophilin-like peptidyl-prolyl cis-trans isomerase domain Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site domain:PPIase cyclophilin-type Cyclophilin-type peptidyl-prolyl cis-trans	RT RT RT RT RT RT RT RT		4 4 4 4 Count 20 17 20 11 10	1.5E-2 2.1E-2 5.7E-2 7.9E-2 P_Value 2.5E-5 3.6E-5 7.2E-5 2.6E-3 3.4E-3	6.2E0 5.4E0 4.1E0 3.6E0 Fold Change 2.8E0 3.1E0 2.6E0 2.8E0 3.0E0 2.8E0	1.3E-1 2.9E-1 4.0E-1 6.9E-1 Benjamini 9.4E-4 2.1E-4 1.2E-3 3.1E-2 3.8E-2	4 1.1E-1 2.9E-1 3.7E-1 6.8E-1 FDR 9.0E-4 1.6E-4 1.0E-3 2.8E-2 3.5E-2 1.1E-1 6.8E-
Annota	INTERPRO PIR_SUPERFAMILY INTERPRO PIR_SUPERFAMILY ation Cluster 89 GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_MF_DIRECT INTERPRO INTERPRO UP_SEQ_FEATURE	Tyrosine-protein kinase, non-receptor Jak/Tyk2 tyrosine-protein kinase, Jak/Tyk2 type Ribosomal protein S6 kinase II ribosomal protein S6 kinase II Enrichment Score: 2.63 protein peptidyl-prolyl isomerization Rotamase peptidyl-prolyl cis-trans isomerase activity Cyclophilin-like peptidyl-prolyl cis-trans isomerase domain Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site domain: PPIase cyclophilin-type	RT RT RT RT RT RT RT RT		4 4 4 4 Count 20 17 20 11 10 10	1.5E-2 2.1E-2 5.7E-2 7.9E-2 P_Value 2.5E-5 3.6E-5 7.2E-5 2.6E-3 3.4E-3 5.0E-3	6.2E0 5.4E0 4.1E0 3.6E0 Fold Change 2.8E0 3.1E0 2.6E0 2.8E0 3.0E0 2.8E0 2.7E0	1.3E-1 2.9E-1 4.0E-1 6.9E-1 Benjamini 9.4E-4 2.1E-4 1.2E-3 3.1E-2 3.8E-2 1.2E-1	4 1.1E-1 2.9E-1 3.7E-1 6.8E-1 FDR 9.0E-4 1.6E-4 1.0E-3 2.8E-2 3.5E-2 1.1E-1 6.8E-2 3.6E-
Annota	INTERPRO PIR_SUPERFAMILY INTERPRO PIR_SUPERFAMILY ation Cluster 89 GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_MF_DIRECT INTERPRO INTERPRO UP_SEQ_FEATURE INTERPRO	Tyrosine-protein kinase, non-receptor Jak/Tyk2 tyrosine-protein kinase, Jak/Tyk2 type Ribosomal protein S6 kinase II ribosomal protein S6 kinase II Enrichment Score: 2.63 protein peptidyl-prolyl isomerization Rotamase peptidyl-prolyl cis-trans isomerase activity Cyclophilin-like peptidyl-prolyl cis-trans isomerase domain Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site domain:PPIase cyclophilin-type Cyclophilin-type peptidyl-prolyl cis-trans isomerase.	RT RT RT RT RT RT RT RT RT		4 4 4 4 Count 20 17 20 11 10 10	1.5E-2 2.1E-2 5.7E-2 7.9E-2 P_Value 2.5E-5 3.6E-5 7.2E-5 2.6E-3 3.4E-3 5.0E-3 6.9E-3	6.2E0 5.4E0 4.1E0 3.6E0 Fold Change 2.8E0 3.1E0 2.6E0 2.8E0 3.0E0 2.8E0 4.9E0 4.9E0	1.3E-1 2.9E-1 4.0E-1 6.9E-1 Benjamini 9.4E-4 2.1E-4 1.2E-3 3.1E-2 3.8E-2 1.2E-1 7.4E-2	4 1.1E-1 2.9E-1 3.7E-1 6.8E-1 9.0E-4 1.0E-3 2.8E-2 3.5E-2 1.1E-1 6.8E-2 1.1E-1
Annota Annota O O O O O O O O O O O O O	INTERPRO PIR_SUPERFAMILY INTERPRO PIR_SUPERFAMILY ation Cluster 89 GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_MF_DIRECT INTERPRO INTERPRO UP_SEQ_FEATURE INTERPRO UP_KEYWORDS	Tyrosine-protein kinase, non-receptor Jak/Tyk2 tyrosine-protein kinase, Jak/Tyk2 type Ribosomal protein S6 kinase II ribosomal protein S6 kinase II Enrichment Score: 2.63 protein peptidyl-prolyl isomerization Rotamase peptidyl-prolyl cis-trans isomerase activity Cyclophilin-like peptidyl-prolyl cis-trans isomerase domain Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site domain:PPIase cyclophilin-type Cyclophilin-type peptidyl-prolyl cis-trans isomerase Cyclosporin	RT		4 4 4 4 20 17 20 11 10 10 5	1.5E-2 2.1E-2 5.7E-2 7.9E-2 P_Value 2.5E-5 3.6E-5 7.2E-5 2.6E-3 3.4E-3 5.0E-3 6.9E-3 1.1E-2	6.2E0 5.4E0 4.1E0 3.6E0 Fold Change 2.8E0 3.1E0 2.6E0 2.8E0 3.0E0 2.8E0 4.9E0 4.3E0	1.3E-1 2.9E-1 4.0E-1 6.9E-1 Benjamini 9.4E-4 2.1E-4 1.2E-3 3.1E-2 3.8E-2 1.2E-1 7.4E-2 4.6E-2	4 1.1E-1 2.9E-1 3.7E-1 6.8E-1 1.0E-3 2.8E-2 3.5E-2 1.1E-1 6.8E-2 1.1E-1 5.9E-
Annota	INTERPRO PIR_SUPERFAMILY INTERPRO PIR_SUPERFAMILY ation Cluster 89 GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_MF_DIRECT INTERPRO UP_SEQ_FEATURE INTERPRO UP_KEYWORDS GOTERM_MF_DIRECT	Tyrosine-protein kinase, non-receptor Jak/Tyk2 tyrosine-protein kinase, Jak/Tyk2 type Ribosomal protein S6 kinase II ribosomal protein S6 kinase II Enrichment Score: 2.63 protein peptidyl-prolyl isomerization Rotamase peptidyl-prolyl cis-trans isomerase activity Cyclophilin-like peptidyl-prolyl cis-trans isomerase domain Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site domain:PPIase cyclophilin-type Cyclophilin-type peptidyl-prolyl cis-trans isomerase Cyclosporin cyclosporin cyclosporin A binding peptidyl-prolyl cis-trans isomerase Peptidyl-prolyl cis-trans isomerase, FKBP-	RT R		4 4 4 4 7 Count 20 17 20 11 10 10 5 5 6	1.5E-2 2.1E-2 5.7E-2 7.9E-2 P_Value 2.5E-5 3.6E-5 7.2E-5 2.6E-3 3.4E-3 5.0E-3 6.9E-3 1.1E-2 1.8E-2 5.2E-2	6.2E0 5.4E0 4.1E0 3.6E0 Fold Change 2.8E0 3.1E0 2.6E0 2.8E0 3.0E0 2.7E0 4.9E0 4.3E0 2.7E0	1.3E-1 2.9E-1 4.0E-1 6.9E-1 Benjamini 9.4E-4 2.1E-4 1.2E-3 3.1E-2 3.8E-2 1.2E-1 7.4E-2 4.6E-2 1.2E-1 5.9E-1	4 1.1E-1 2.9E-1 3.7E-1 6.8E-1 FDR 9.0E-4 1.6E-4 1.0E-3 2.8E-2 3.5E-2 1.1E-1 6.8E-2 1.1E-1 5.9E-1 1
	INTERPRO PIR_SUPERFAMILY INTERPRO PIR_SUPERFAMILY ation Cluster 89 GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_MF_DIRECT INTERPRO UP_SEQ_FEATURE INTERPRO UP_KEYWORDS GOTERM_MF_DIRECT PIR_SUPERFAMILY	Tyrosine-protein kinase, non-receptor Jak/Tyk2 tyrosine-protein kinase, Jak/Tyk2 type Ribosomal protein S6 kinase II ribosomal protein S6 kinase II Enrichment Score: 2.63 protein peptidyl-prolyl isomerization Rotamase peptidyl-prolyl cis-trans isomerase activity Cyclophilin-like peptidyl-prolyl cis-trans isomerase domain Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site domain:PPIase cyclophilin-type Cyclophilin-type peptidyl-prolyl cis-trans isomerase Cyclosporin cyclosporin A binding peptidyl-prolyl cis-trans isomerase Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain	RT R		4 4 4 4 7 Count 20 17 20 11 10 10 5 5 6 7	1.5E-2 2.1E-2 5.7E-2 7.9E-2 P_Value 2.5E-5 3.6E-5 7.2E-5 2.6E-3 3.4E-3 5.0E-3 6.9E-3 1.1E-2 1.8E-2 5.2E-2 5.7E-2	6.2E0 5.4E0 4.1E0 3.6E0 Fold Change 2.8E0 3.1E0 2.6E0 2.8E0 3.0E0 2.8E0 4.9E0 4.3E0 2.7E0 4.3E0 2.7E0 4.3E0 2.7E0 Fold	1.3E-1 2.9E-1 4.0E-1 6.9E-1 Benjamini 9.4E-4 1.2E-3 3.1E-2 3.8E-2 1.2E-1 7.4E-2 4.6E-2 1.2E-1 5.9E-1 4.0E-1	4 1.1E-1 2.9E-1 3.7E-1 6.8E-1 9.0E-4 1.0E-3 2.8E-2 1.1E-1 6.8E-2 1.1E-1 5.9E-1 3.7E-1
	INTERPRO PIR_SUPERFAMILY INTERPRO PIR_SUPERFAMILY ation Cluster 89 GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_MF_DIRECT INTERPRO INTERPRO UP_SEQ_FEATURE INTERPRO UP_KEYWORDS GOTERM_MF_DIRECT PIR_SUPERFAMILY INTERPRO	Tyrosine-protein kinase, non-receptor Jak/Tyk2 tyrosine-protein kinase, Jak/Tyk2 type Ribosomal protein S6 kinase II ribosomal protein S6 kinase II Enrichment Score: 2.63 protein peptidyl-prolyl isomerization Rotamase peptidyl-prolyl cis-trans isomerase activity Cyclophilin-like peptidyl-prolyl cis-trans isomerase domain Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site domain:PPIase cyclophilin-type Cyclophilin-type peptidyl-prolyl cis-trans isomerase Cyclosporin cyclosporin A binding peptidyl-prolyl cis-trans isomerase Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain Enrichment Score: 2.61	RT R		4 4 4 4 7 Count 20 17 20 11 10 10 5 5 6 7 Count	1.5E-2 2.1E-2 5.7E-2 7.9E-2 P_Value 2.5E-5 3.6E-5 7.2E-5 2.6E-3 3.4E-3 5.0E-3 6.9E-3 1.1E-2 1.8E-2 5.2E-2 5.7E-2 P_Value	6.2E0 5.4E0 4.1E0 3.6E0 Fold Change 2.8E0 3.1E0 2.6E0 2.8E0 3.0E0 2.8E0 4.9E0 4.9E0 4.3E0 2.7E0 2.4E0 Fold Change	1.3E-1 2.9E-1 4.0E-1 6.9E-1 Benjamini 9.4E-4 2.1E-4 1.2E-3 3.1E-2 3.8E-2 1.2E-1 7.4E-2 4.6E-2 1.2E-1 5.9E-1 4.0E-1 Benjamini	4 1.1E-1 2.9E-1 3.7E-1 6.8E-1 9.0E-4 1.0E-3 2.8E-2 1.1E-1 6.8E-2 1.1E-1 5.9E-1 1 5.9E-1 9.0E-
	INTERPRO PIR_SUPERFAMILY INTERPRO PIR_SUPERFAMILY ation Cluster 89 GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_MF_DIRECT INTERPRO INTERPRO UP_SEQ_FEATURE INTERPRO UP_KEYWORDS GOTERM_MF_DIRECT PIR_SUPERFAMILY INTERPRO ation Cluster 90	Tyrosine-protein kinase, non-receptor Jak/Tyk2 tyrosine-protein kinase, Jak/Tyk2 type Ribosomal protein S6 kinase II ribosomal protein S6 kinase II Enrichment Score: 2.63 protein peptidyl-prolyl isomerization Rotamase peptidyl-prolyl cis-trans isomerase activity Cyclophilin-like peptidyl-prolyl cis-trans isomerase domain Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site domain:PPIase cyclophilin-type Cyclophilin-type peptidyl-prolyl cis-trans isomerase Cyclosporin cyclosporin A binding peptidyl-prolyl cis-trans isomerase Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain	RT R		4 4 4 4 7 Count 20 17 20 11 10 10 5 5 6 7	1.5E-2 2.1E-2 5.7E-2 7.9E-2 P_Value 2.5E-5 3.6E-5 7.2E-5 2.6E-3 3.4E-3 5.0E-3 6.9E-3 1.1E-2 1.8E-2 5.2E-2 5.7E-2	6.2E0 5.4E0 4.1E0 3.6E0 Fold Change 2.8E0 3.1E0 2.6E0 2.8E0 3.0E0 2.7E0 4.9E0 4.3E0 2.7E0 2.4E0 Fold Change 2.8E0	1.3E-1 2.9E-1 4.0E-1 6.9E-1 Benjamini 9.4E-4 1.2E-3 3.1E-2 3.8E-2 1.2E-1 7.4E-2 4.6E-2 1.2E-1 5.9E-1 4.0E-1	4 1.1E-1 2.9E-1 3.7E-1 6.8E-1 9.0E-4 1.0E-3 2.8E-2 1.1E-1 6.8E-2 1.1E-1 5.9E-1 1 3.7E-1

Annot	tation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold	Benjamini	FDR
	GOTERM_MF_DIRECT	peptidyl-prolyl cis-trans isomerase activity	RT	:	20	7.2E-5	Change	1.2E-3	1.0E-
	UP_KEYWORDS	Isomerase	RT		34	2.3E-4		1.3E-3	3 1.0E-
	INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type		=	8	3.2E-2		2.4E-1	3 2.2E-
	GOTERM_BP_DIRECT								1 3.6E-
	GOTERM_MF_DIRECT	chaperone-mediated protein folding	<u>RT</u>		12	3.7E-2		3.8E-1	1 2.0E-
	INTERPRO	FK506 binding Pentidyl probletic transiscemerace FKBB	<u>RT</u>		8	3.8E-2		2.3E-1	1 3.7E-
		<u>Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain</u>	<u>RT</u>	1	7	5.7E-2	2.4E0	4.0E-1	1
	UP_SEQ_FEATURE	domain:PPIase FKBP-type	<u>RT</u>	i	5	8.6E-2	:	1.0E0	9.6E- 1
Annot	tation Cluster 91	Enrichment Score: 2.56	G		Count	P_Value	Fold Change	Benjamini	
	GOTERM_CC_DIRECT	<u>U6 snRNP</u>	<u>RT</u>	1	7	9.1E-5	6.4E0	1.2E-3	1.0E- 3
	GOTERM_CC_DIRECT	<u>Lsm1-7-Pat1 complex</u>	<u>RT</u>	i	4	1.4E-2	6.4E0	9.3E-2	8.2E- 2
	GOTERM_BP_DIRECT	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay	<u>RT</u>	•	11	1.7E-2	2.2E0	2.1E-1	2.0E- 1
Annot	tation Cluster 92	Enrichment Score: 2.55	G	To the second se	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	compositionally biased region:Arg/Ser-rich (RS domain)	<u>RT</u>	1	11	6.4E-5	4.2E0	2.0E-3	1.9E- 3
	UP_SEQ_FEATURE	compositionally biased region:Gly-rich (hinge region)	<u>RT</u>	i e	6	1.1E-3	5.8E0	2.9E-2	2.8E- 2
	GOTERM_BP_DIRECT	negative regulation of mRNA splicing, via	<u>RT</u>		9	1.7E-2	2.5E0	2.1E-1	2.0E-
	GOTERM_BP_DIRECT	<u>mRNA splice site selection</u>	RT	1	7	5.3E-2	2.4E0	4.9E-1	1 4.7E-
Annot	tation Cluster 93	Enrichment Score: 2.47	G	- -	Count	P_Value	Fold	Benjamini	1 FDR
	GOTERM_BP_DIRECT	UTP biosynthetic process	RT		9	1.7E-4	Change	5.0E-3	4.8E-
	GOTERM_BP_DIRECT	CTP biosynthetic process	RT		9	1.7E-4		5.0E-3	3 4.8E-
	UP_SEQ_FEATURE	active site:Pros-phosphohistidine							3 5.9E-
	INTERPRO	intermediate	<u>RT</u>		7	2.1E-4		6.2E-3	3 6.7E-
	GOTERM_MF_DIRECT	Nucleoside diphosphate kinase	<u>RT</u>	•	8	5.1E-4		7.3E-3	3 6.5E-
		nucleoside diphosphate kinase activity	<u>RT</u>	•	11	6.3E-4	3.3E0	7.3E-3	3
	GOTERM_BP_DIRECT	nucleoside diphosphate phosphorylation	<u>RT</u>	•	10	1.2E-3	3.3E0	2.8E-2	2.7E- 2
	GOTERM_BP_DIRECT	nucleobase-containing small molecule interconversion	<u>RT</u>	1	12	1.4E-3	2.8E0	3.0E-2	2.9E- 2
	GOTERM_BP_DIRECT	GTP biosynthetic process	<u>RT</u>	i	8	2.6E-3	3.6E0	5.0E-2	4.8E- 2
	SMART	<u>NDK</u>	<u>RT</u>	1	8	6.8E-3	3.0E0	6.8E-2	6.1E- 2
	INTERPRO	Nucleoside diphosphate kinase, active site	<u>RT</u>	i .	5	1.6E-2	4.4E0	1.3E-1	1.2E- 1
	GOTERM_BP_DIRECT	<u>pyrimidine nucleotide metabolic process</u>	<u>RT</u>	i .	5	5.0E-2	3.3E0	4.7E-1	4.5E- 1
	GOTERM_BP_DIRECT	nucleoside triphosphate biosynthetic process	<u>RT</u>	1	6	7.2E-2	2.5E0	5.8E-1	5.5E- 1
	GOTERM_BP_DIRECT	purine nucleotide metabolic process	<u>RT</u>	i	5	7.3E-2	3.0E0	5.8E-1	5.5E-
	UP_KEYWORDS	Nucleotide metabolism	<u>RT</u>	1	8	1.0E-1	2.0E0	3.4E-1	2.6E-
Annot	tation Cluster 94	Enrichment Score: 2.41	G	17	Count	P_Value	Fold Change	Benjamini	Ť
	GOTERM_BP_DIRECT	protein K6-linked ubiquitination	RT	i	7	4.7E-4		1.2E-2	1.2E-
	GOTERM_BP_DIRECT	protein K29-linked ubiquitination	RT		5	3.5E-3		6.6E-2	2 6.3E-
	GOTERM_BP_DIRECT	protein K27-linked ubiquitination	RT		4	3.7E-2		3.7E-1	2 3.6E-
Appet	ration Cluster 95			• •		!	Fold	Roniamini	1
Annot	INTERPRO	Pilescomal protein S1 PNA binding domain	G			P_Value	Change		1.1E-
	INTERPRO	Ribosomal protein S1, RNA-binding domain	<u>RT</u>		7	9.4E-4		1.2E-2	2 1.1E-
	SMART	RNA-binding domain, S1	<u>RT</u>		7	9.4E-4		1.2E-2	7.9E-
		<u>SM00316</u>	<u>RT</u>	i	7	9.2E-3		8.7E-2	2
	UP_SEQ_FEATURE	domain:S1 motif	<u>RT</u>	i	5	3.1E-2		5.4E-1	5.2E- 1
Annot	cotten PR DIRECT	Enrichment Score: 2.31	G		Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-	<u>RT</u>	i .	9	5.0E-6	5.9E0	2.5E-4	2.4E- 4
	GOTERM_BP_DIRECT	maturation of 5.8S rRNA from tricistronic	D.T.		4	1 75 0	E 052	2.45.4	2.0E-
U		rrna transcript (SSU-rrna, 5.8S rrna, LSU-rrna)	RT	i	4	1.7E-2	5.9E0	2.1E-1	1
	UP_SEQ_FEATURE	region of interest:Sufficient for nucleolar localization	<u>RT</u>	i	3	5.8E-2	6.8E0	8.4E-1	8.1E- 1
	GOTERM_CC_DIRECT	PeBoW complex	<u>RT</u>	i .	3	1.2E-1	4.8E0	4.9E-1	4.3E- 1

nnot	ation Cluster 1	Enrichment Score: ?	G	To the second se	Count	P_Value	Fold Change	Benjamir	ni FC
not	ation Cluster 97	Enrichment Score: 2.31	G		Count	P_Value	Fold	Roniamir	ni FC
)	UP_KEYWORDS	<u>Exonuclease</u>	<u>RT</u>	1	18	6.0E-4	2.4E0	3.2E-3	2.4
)	GOTERM_MF_DIRECT	3'-5'-exoribonuclease activity	<u>RT</u>	i	11	6.3E-4	3.3E0	7.3E-3	6.5
)	GOTERM_BP_DIRECT	RNA phosphodiester bond hydrolysis,	<u>RT</u>		11	1.3E-2	2.3E0	1.8E-1	1.7
)	GOTERM_CC_DIRECT	exonucleolytic nuclear exosome (RNase complex)	<u>RT</u>	1	7	2.1E-2	3.0E0	1.3E-1	1.1
í l	UP_KEYWORDS	<u>Nuclease</u>	RT		29		1.5E0	1.1E-1	1 8.8
not	ation Cluster 98	Enrichment Score: 2.3	G	- 	Count	P_Value	Fold	Ponjamir	2 ni E l
	GOTERM_BP_DIRECT	regulation of axonogenesis		_	13	1.1E-4	Change	3.5E-3	3.4
J	GOTERM_MF_DIRECT		<u>RT</u>						3 1.
J	GOTERM_BP_DIRECT	Roundabout binding	<u>RT</u>		7	1.2E-3		1.3E-2	2 3.
J	GOTERM_BP_DIRECT	Roundabout signaling pathway	<u>RT</u>		6	3.8E-2	3.0E0	3.8E-1	1
	GOTERM_BP_DIRECT	axon extension involved in axon guidance	<u>RT</u>	i	5	1.3E-1	:	8.2E-1	7. 1
not	ation Cluster 99	Enrichment Score: 2.24	G	**	Count	P_Value	Fold Change	Benjamir	
	BIOCARTA	<u>Cadmium induces DNA synthesis and</u> <u>proliferation in macrophages</u>	<u>RT</u>	•	14	2.6E-4	2.5E0	4.0E-3	3
	BIOCARTA	Links between Pyk2 and Map Kinases	<u>RT</u>	i .	18	2.0E-3	2.0E0	1.6E-2	1 2
	BIOCARTA	CXCR4 Signaling Pathway	<u>RT</u>	i .	16	2.5E-3	2.0E0	1.8E-2	1 2
	BIOCARTA	CCR3 signaling in Eosinophils	<u>RT</u>	1	13	4.2E-2	1.7E0	1.3E-1	9
	BIOCARTA	Aspirin Blocks Signaling Pathway Involved in Platelet Activation	<u>RT</u>	i	11	1.1E-1	1.6E0	2.9E-1	2
nota	ation Cluster 100	Enrichment Score: 2.19	G	17	Count	P_Value	Fold Change	Benjamir	
	INTERPRO	Cullin, N-terminal	RT		8		5.0E0	3.3E-3	3
	INTERPRO	<u>Cullin homology</u>	RT	1	7	9.4E-4		1.2E-2	3 1
	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly)	RT	- -	6	1.1E-3		2.9E-2	2
	INTERPRO	(interchain with G-Cter in NEDD8)							2
	SMART	<u>Cullin protein, neddylation domain</u>	<u>RT</u>		6	4.0E-3		4.4E-2	2
		<u>CULLIN</u>	<u>RT</u>	1	6	1.2E-2	3.5E0	1.1E-1	2
	INTERPRO	<u>Cullin, conserved site</u>	<u>RT</u>	1	5	1.6E-2	4.4E0	1.3E-1	1
	SMART	<u>SM00884</u>	<u>RT</u>	i	6	2.5E-2	3.0E0	2.0E-1	1 1
	INTERPRO	Cullin repeat-like-containing domain	<u>RT</u>	1	6	3.2E-2	3.1E0	2.4E-1	2 1
	GOTERM_CC_DIRECT	cullin-RING ubiquitin ligase complex	<u>RT</u>	i .	4	1.6E-1	2.8E0	6.2E-1	5 1
not	ation Cluster 101	Enrichment Score: 2.16	G	17	Count	P_Value	Fold Change	Benjamir	ni F
	GOTERM_MF_DIRECT	guanyl nucleotide binding	<u>RT</u>	i	8	9.8E-5	5.3E0	1.5E-3	1
	INTERPRO	G-protein alpha subunit, group Q	<u>RT</u>	1	4	1.5E-2	6.2E0	1.3E-1	1
	GOTERM_BP_DIRECT	phospholipase C-activating dopamine	RT		4	2.3E-1	2.4E0	1.0E0	9
not:	ation Cluster 102	receptor signaling pathway Enrichment Score: 2.14	G		Count	P_Value	Fold	Banjamir	1 ni F
100	UP_SEQ_FEATURE	domain:Thioredoxin 1		•	9	7.3E-6	Change 6.1E0	2.7E-4	2
	UP_SEQ_FEATURE		<u>RT</u>	-					2
	GOTERM_BP_DIRECT	domain:Thioredoxin 2	<u>RT</u>		9	7.3E-6		2.7E-4	4
	INTERPRO	response to endoplasmic reticulum stress	<u>RT</u>	i	29	1.7E-5		6.8E-4	4
		Thioredoxin domain	<u>RT</u>	i	18	9.8E-5	2.7E0	1.7E-3	3
	INTERPRO	Thioredoxin, conserved site	<u>RT</u>	1	10	5.1E-4	3.6E0	7.3E-3	3
	INTERPRO	<u>Disulphide isomerase</u>	<u>RT</u>	i	5	2.9E-3	6.2E0	3.3E-2	2
	GOTERM_BP_DIRECT	cell redox homeostasis	<u>RT</u>	i .	24	3.3E-3	1.8E0	6.3E-2	6
	GOTERM_MF_DIRECT	protein disulfide isomerase activity	<u>RT</u>	i contract	10	6.4E-3	2.7E0	5.6E-2	5
	UP_KEYWORDS	Redox-active center	<u>RT</u>	i	15	8.4E-3	2.1E0	3.8E-2	2
	UP_SEQ_FEATURE	site:Contributes to redox potential value	<u>RT</u>	i .	5	1.1E-2	4.9E0	2.2E-1	2
	UP_SEQ_FEATURE	site:Lowers pKa of C-terminal Cys of first	RT		4	1.1E-2		2.2E-1	2
	UP_SEQ_FEATURE	active site site:Lowers pKa of C-terminal Cys of second							1 2
	INTERPRO	active site	<u>RT</u>	i	4	1.1E-2		2.2E-1	1
		Protein disulphide isomerase	<u>RT</u>	1	4	1.5E-2	6.2E0	1.3E-1	1
	UP_SEQ_FEATURE	domain:Thioredoxin 3	<u>RT</u>	i .	4	2 5F-2	5.5E0	4 4F-1	4

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

Anr	notation Cluster 1	Enrichment Score: ?	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	PIR_SUPERFAMILY	DNA repair and recombination protein, Rad51 type	<u>RT</u>	i	5	1.2E-2		2.9E-1	2.9E- 1
	INTERPRO	DNA recombination and repair protein Rad51, C-terminal	<u>RT</u>	i	5	1.6E-2	4.4E0	1.3E-1	1.2E-
	INTERPRO	DNA recombination (renair protein DecA/DadB	<u>RT</u>	i	5	1.6E-2	4.4E0	1.3E-1	1.2E-
	GOTERM_BP_DIRECT	chromosome organization involved in meiotic	<u>RT</u>	i .	4	1.7E-2	5.9E0	2.1E-1	2.0E-
	GOTERM_BP_DIRECT	cell cycle strand invasion	<u>RT</u>	1	5	1.8E-2	4.2E0	2.2E-1	2.1E-
	GOTERM_MF_DIRECT	endodeoxyribonuclease activity	RT		9	2.2E-2		1.4E-1	1.2E-
	GOTERM_BP_DIRECT	DNA recombinase assembly	RT		4	3.7E-2		3.7E-1	1 3.6E-
	INTERPRO	DNA repair Rad51/transcription factor NusA,	RT		3	7.0E-2		4.1E-1	1 3.7E-
	GOTERM_CC_DIRECT	alpha-helical Rad51B-Rad51C-Rad51D-XRCC2 complex	RT		3	1.8E-1		6.7E-1	1 5.9E-
Apr	notation Cluster 106	Enrichment Score: 1.92	G		1		·	<u>!</u>	1 EDP
	UP_SEQ_FEATURE	repeat:Spectrin 18	RT	•	8	P_Value 4.0E-5		1.3E-3	1.2E-
	UP_SEQ_FEATURE	repeat:Spectrin 20	RT		7	2.1E-4		6.2E-3	3 5.9E-
	UP_SEQ_FEATURE	repeat:Spectrin 19	RT		7	2.1E-4		6.2E-3	3 5.9E-
	UP_SEQ_FEATURE	repeat:Spectrin 21	RT	-	6	1.1E-3		2.9E-2	3 2.8E-
	UP_SEQ_FEATURE								2 1.2E-
	UP_SEQ_FEATURE	repeat:Spectrin 22	<u>RT</u>		5	5.4E-3		1.2E-1	1 4.3E-
	UP_SEQ_FEATURE	repeat:Spectrin 23	<u>RT</u>		4	2.5E-2		4.4E-1	1 8.1E-
	UP_SEQ_FEATURE	repeat:Spectrin 30	<u>RT</u>		3	5.8E-2		8.4E-1	1 8.1E-
	UP_SEQ_FEATURE	repeat:Spectrin 31	<u>RT</u>		3	5.8E-2		8.4E-1	1
		repeat:Spectrin 24	<u>RT</u>	i	3	1.1E-1	5.1E0	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	repeat:Spectrin 25	<u>RT</u>	i	3	1.1E-1	5.1E0	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	repeat:Spectrin 26	<u>RT</u>	i	3	1.1E-1	5.1E0	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	repeat:Spectrin 27	<u>RT</u>	i	3	1.1E-1	5.1E0	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	repeat:Spectrin 28	<u>RT</u>	i	3	1.1E-1	5.1E0	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	repeat:Spectrin 29	<u>RT</u>	i	3	1.1E-1		1.0E0	9.6E- 1
Anr	notation Cluster 107	Enrichment Score: 1.9	G	17	Count	P_Value	Fold Change	Benjamini	
	UP_KEYWORDS	<u>rRNA-binding</u>	<u>RT</u>	i	14	6.6E-6	4.0E0	4.3E-5	3.3E- 5
	INTERPRO	KOW	<u>RT</u>	i	7	9.4E-4	4.8E0	1.2E-2	1.1E- 2
	INTERDO	RNA-binding S4 domain	<u>RT</u>	i de la companya del companya de la companya del companya de la co	5			7.7E-2	7 4 5
	INTERPRO	KNA-billding 34 domain			3	7.7E-3	5.2E0	7.7L-Z	7.1E- 2
	UP_SEQ_FEATURE	domain:S4 RNA-binding	RT	1	5	7.7E-3 2.0E-2		3.7E-1	
				i i			4.3E0		2 3.6E-
	UP_SEQ_FEATURE	domain:S4 RNA-binding	<u>RT</u>		5	2.0E-2	4.3E0 4.1E0	3.7E-1	2 3.6E- 1 2.7E-
	UP_SEQ_FEATURE SMART	domain:S4 RNA-binding	RT RT	i	5	2.0E-2 4.9E-2	4.3E0 4.1E0 6.2E0	3.7E-1 3.0E-1	2 3.6E- 1 2.7E- 1 3.7E-
	UP_SEQ_FEATURE SMART INTERPRO	domain:S4 RNA-binding S4 Ribosomal protein S4e	RT RT RT	i i	5 4 3	2.0E-2 4.9E-2 7.0E-2	4.3E0 4.1E0 6.2E0 6.2E0	3.7E-1 3.0E-1 4.1E-1	2 3.6E- 1 2.7E- 1 3.7E- 1 3.7E-
	UP_SEQ_FEATURE SMART INTERPRO INTERPRO	domain:S4 RNA-binding S4 Ribosomal protein S4e Ribosomal protein S4e, N-terminal	RT RT RT RT	i i i	5 4 3 3	2.0E-2 4.9E-2 7.0E-2 7.0E-2	4.3E0 4.1E0 6.2E0 6.2E0 6.2E0	3.7E-1 3.0E-1 4.1E-1 4.1E-1	2 3.6E- 1 2.7E- 1 3.7E- 1 3.7E- 1 3.7E-
	UP_SEQ_FEATURE SMART INTERPRO INTERPRO INTERPRO	domain:S4 RNA-binding S4 Ribosomal protein S4e Ribosomal protein S4e, N-terminal Ribosomal protein S4e, central region Ribosomal protein S4e, N-terminal, conserved	RT RT RT RT RT	i i i	5 4 3 3	2.0E-2 4.9E-2 7.0E-2 7.0E-2 7.0E-2	4.3E0 4.1E0 6.2E0 6.2E0 6.2E0 6.2E0	3.7E-1 3.0E-1 4.1E-1 4.1E-1 4.1E-1	2 3.6E-1 1 2.7E-1 3.7E-1 3.7E-1 3.7E-1 3.7E-1
Anr	UP_SEQ_FEATURE SMART INTERPRO INTERPRO INTERPRO INTERPRO	domain:S4 RNA-binding S4 Ribosomal protein S4e Ribosomal protein S4e, N-terminal Ribosomal protein S4e, central region Ribosomal protein S4e, N-terminal, conserved site	RT RT RT RT RT RT	i i i	5 4 3 3 3	2.0E-2 4.9E-2 7.0E-2 7.0E-2 7.0E-2 7.0E-2	4.3E0 4.1E0 6.2E0 6.2E0 6.2E0 6.2E0 5.4E0	3.7E-1 3.0E-1 4.1E-1 4.1E-1 4.1E-1 6.9E-1	2 3.6E-1 1 2.7E-1 3.7E-1 3.7E-1 3.7E-1 6.8E-1
Anr	UP_SEQ_FEATURE SMART INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO PIR_SUPERFAMILY	domain:S4 RNA-binding S4 Ribosomal protein S4e Ribosomal protein S4e, N-terminal Ribosomal protein S4e, central region Ribosomal protein S4e, N-terminal, conserved site ribosomal protein S4a/S4e	RT RT RT RT RT RT RT	i i i i	5 4 3 3 3 3	2.0E-2 4.9E-2 7.0E-2 7.0E-2 7.0E-2 8.8E-2	4.3E0 4.1E0 6.2E0 6.2E0 6.2E0 5.4E0 Fold Change	3.7E-1 3.0E-1 4.1E-1 4.1E-1 4.1E-1 6.9E-1	2 3.6E-1 1 2.7E-1 3.7E-1 3.7E-1 3.7E-1 6.8E-1
Ann	UP_SEQ_FEATURE SMART INTERPRO INTERPRO INTERPRO INTERPRO PIR_SUPERFAMILY	domain:S4 RNA-binding S4 Ribosomal protein S4e Ribosomal protein S4e, N-terminal Ribosomal protein S4e, central region Ribosomal protein S4e, N-terminal, conserved site ribosomal protein S4a/S4e Enrichment Score: 1.89	RT RT RT RT RT RT RT G	i i i i	5 4 3 3 3 3 Count	2.0E-2 4.9E-2 7.0E-2 7.0E-2 7.0E-2 8.8E-2 P_Value	4.3E0 4.1E0 6.2E0 6.2E0 6.2E0 5.4E0 Fold Change 2.2E0	3.7E-1 3.0E-1 4.1E-1 4.1E-1 4.1E-1 6.9E-1 Benjamini	2 3.6E-1 1 2.7E-1 3.7E-1 3.7E-1 3.7E-1 6.8E-1 FDR 4.3E-3 2.9E-
Ann	UP_SEQ_FEATURE SMART INTERPRO INTERPRO INTERPRO INTERPRO PIR_SUPERFAMILY notation Cluster 108 UP_KEYWORDS	domain:S4 RNA-binding S4 Ribosomal protein S4e Ribosomal protein S4e, N-terminal Ribosomal protein S4e, central region Ribosomal protein S4e, N-terminal, conserved site ribosomal protein S4a/S4e Enrichment Score: 1.89 Initiation factor	RT	i i i i	5 4 3 3 3 3 Count	2.0E-2 4.9E-2 7.0E-2 7.0E-2 7.0E-2 8.8E-2 P_Value 1.1E-3	4.3E0 4.1E0 6.2E0 6.2E0 6.2E0 5.4E0 Fold Change 2.2E0 2.5E0	3.7E-1 3.0E-1 4.1E-1 4.1E-1 4.1E-1 6.9E-1 Benjamini 5.5E-3	2 3.6E-1 2.7E-1 3.7E-1 3.7E-1 3.7E-1 6.8E-1 FDR 4.3E-3 2.9E-2 1.5E-
Anir	UP_SEQ_FEATURE SMART INTERPRO INTERPRO INTERPRO INTERPRO PIR_SUPERFAMILY notation Cluster 108 UP_KEYWORDS GOTERM_BP_DIRECT	domain:S4 RNA-binding S4 Ribosomal protein S4e Ribosomal protein S4e, N-terminal Ribosomal protein S4e, central region Ribosomal protein S4e, N-terminal, conserved site ribosomal protein S4a/S4e Enrichment Score: 1.89 Initiation factor regulation of translational initiation	RT R		5 4 3 3 3 3 Count 19 15	2.0E-2 4.9E-2 7.0E-2 7.0E-2 7.0E-2 8.8E-2 P_Value 1.1E-3 1.4E-3	4.3E0 4.1E0 6.2E0 6.2E0 6.2E0 5.4E0 Fold Change 2.2E0 2.5E0 2.1E0	3.7E-1 3.0E-1 4.1E-1 4.1E-1 4.1E-1 6.9E-1 Benjamini 5.5E-3 3.0E-2	2 3.6E-1 1 2.7E-1 3.7E-1 3.7E-1 3.7E-1 6.8E-1 1 6.8E-1 1 5.7E-2 1.5E-2 7.1E-
Ann	UP_SEQ_FEATURE SMART INTERPRO INTERPRO INTERPRO INTERPRO PIR_SUPERFAMILY notation Cluster 108 UP_KEYWORDS GOTERM_BP_DIRECT GOTERM_MF_DIRECT	domain:S4 RNA-binding S4 Ribosomal protein S4e Ribosomal protein S4e, N-terminal Ribosomal protein S4e, central region Ribosomal protein S4e, N-terminal, conserved site ribosomal protein S4a/S4e Enrichment Score: 1.89 Initiation factor regulation of translational initiation translation initiation factor activity Protein biosynthesis eukaryotic translation initiation factor 3	RT R		5 4 3 3 3 3 Count 19 15 21	2.0E-2 4.9E-2 7.0E-2 7.0E-2 7.0E-2 8.8E-2 P_Value 1.1E-3 1.4E-3 1.6E-3	4.3E0 4.1E0 6.2E0 6.2E0 6.2E0 5.4E0 Fold Change 2.2E0 2.5E0 2.1E0 1.7E0	3.7E-1 3.0E-1 4.1E-1 4.1E-1 4.1E-1 6.9E-1 Benjamini 5.5E-3 3.0E-2 1.7E-2	2 3.6E-1 1 2.7E-1 3.7E-1 3.7E-1 3.7E-1 6.8E-1 4.3E-3 2.9E-2 7.1E-3 2.0E-
Anr	UP_SEQ_FEATURE SMART INTERPRO INTERPRO INTERPRO INTERPRO PIR_SUPERFAMILY notation Cluster 108 UP_KEYWORDS GOTERM_BP_DIRECT GOTERM_MF_DIRECT UP_KEYWORDS	domain:S4 RNA-binding S4 Ribosomal protein S4e Ribosomal protein S4e, N-terminal Ribosomal protein S4e, central region Ribosomal protein S4e, N-terminal, conserved site ribosomal protein S4a/S4e Enrichment Score: 1.89 Initiation factor regulation of translational initiation translation initiation factor activity Protein biosynthesis eukaryotic translation initiation factor 3 complex	RT		5 4 3 3 3 3 Count 19 15 21 37	2.0E-2 4.9E-2 7.0E-2 7.0E-2 7.0E-2 8.8E-2 P_Value 1.1E-3 1.4E-3 1.6E-3 1.8E-3	4.3E0 4.1E0 6.2E0 6.2E0 6.2E0 5.4E0 Fold Change 2.2E0 2.5E0 2.1E0 1.7E0 3.4E0	3.7E-1 3.0E-1 4.1E-1 4.1E-1 4.1E-1 6.9E-1 Benjamini 5.5E-3 3.0E-2 1.7E-2 9.1E-3	2 3.6E-1 1 2.7E-1 3.7E-1 3.7E-1 3.7E-1 6.8E-1 FDR 4.3E-3 2.9E-2 1.5E-2 7.1E-3 2.0E-2 3.5E-
Anir	UP_SEQ_FEATURE SMART INTERPRO INTERPRO INTERPRO INTERPRO PIR_SUPERFAMILY notation Cluster 108 UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_CC_DIRECT	domain:S4 RNA-binding S4 Ribosomal protein S4e Ribosomal protein S4e, N-terminal Ribosomal protein S4e, central region Ribosomal protein S4e, N-terminal, conserved site ribosomal protein S4a/S4e Enrichment Score: 1.89 Initiation factor regulation of translational initiation translation initiation factor activity Protein biosynthesis eukaryotic translation initiation complex eukaryotic 48S preinitiation complex eukaryotic translation initiation factor 3	RT		5 4 3 3 3 3 Count 19 15 21 37 9 8	2.0E-2 4.9E-2 7.0E-2 7.0E-2 7.0E-2 8.8E-2 P_Value 1.1E-3 1.4E-3 1.6E-3 1.8E-3 2.4E-3 4.7E-3	4.3E0 4.1E0 6.2E0 6.2E0 6.2E0 5.4E0 Fold Change 2.2E0 2.5E0 2.1E0 1.7E0 3.4E0 3.4E0	3.7E-1 3.0E-1 4.1E-1 4.1E-1 4.1E-1 6.9E-1 Benjamini 5.5E-3 3.0E-2 1.7E-2 9.1E-3 2.2E-2 4.0E-2	2 3.6E-1 2.7E-1 3.7E-1 3.7E-1 3.7E-1 6.8E-1 1 6.8E-1 1 5.7E-2 1.5E-2 2.0E-2 3.5E-2 8.2E-
Anir	UP_SEQ_FEATURE SMART INTERPRO INTERPRO INTERPRO INTERPRO PIR_SUPERFAMILY notation Cluster 108 UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_CC_DIRECT GOTERM_CC_DIRECT	domain:S4 RNA-binding S4 Ribosomal protein S4e Ribosomal protein S4e, N-terminal Ribosomal protein S4e, central region Ribosomal protein S4e, N-terminal, conserved site ribosomal protein S4a/S4e Enrichment Score: 1.89 Initiation factor regulation of translational initiation translation initiation factor activity Protein biosynthesis eukaryotic translation initiation complex eukaryotic translation initiation factor 3 complex, eIF3m	RT R		5 4 3 3 3 3 Count 19 15 21 37 9 8 5	2.0E-2 4.9E-2 7.0E-2 7.0E-2 7.0E-2 8.8E-2 P_Value 1.1E-3 1.4E-3 1.6E-3 1.8E-3 2.4E-3 4.7E-3 1.4E-2	4.3E0 4.1E0 6.2E0 6.2E0 6.2E0 5.4E0 Fold Change 2.2E0 2.5E0 2.1E0 1.7E0 3.4E0 4.5E0	3.7E-1 3.0E-1 4.1E-1 4.1E-1 4.1E-1 6.9E-1 Benjamini 5.5E-3 3.0E-2 1.7E-2 9.1E-3 2.2E-2 4.0E-2 9.4E-2	2 3.6E-1 2.7E-1 3.7E-1 3.7E-1 3.7E-1 6.8E-1 6.8E-1 1.5E-2 7.1E-3 2.0E-2 8.2E-2 1.0E-
Ani	UP_SEQ_FEATURE SMART INTERPRO INTERPRO INTERPRO INTERPRO PIR_SUPERFAMILY notation Cluster 108 UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_CC_DIRECT GOTERM_CC_DIRECT GOTERM_CC_DIRECT GOTERM_CC_DIRECT	domain:S4 RNA-binding S4 Ribosomal protein S4e Ribosomal protein S4e, N-terminal Ribosomal protein S4e, central region Ribosomal protein S4e, N-terminal, conserved site ribosomal protein S4a/S4e Enrichment Score: 1.89 Initiation factor regulation of translational initiation translation initiation factor activity Protein biosynthesis eukaryotic translation initiation complex eukaryotic translation initiation factor 3 complex eukaryotic translation initiation factor 3 complex, eIF3m translation initiation factor binding	RI R		5 4 3 3 3 3 Count 19 15 21 37 9 8 5	2.0E-2 4.9E-2 7.0E-2 7.0E-2 7.0E-2 8.8E-2 P_Value 1.1E-3 1.4E-3 1.6E-3 1.8E-3 2.4E-3 4.7E-3 1.4E-2 1.6E-2	4.3E0 4.1E0 6.2E0 6.2E0 6.2E0 5.4E0 Fold Change 2.2E0 2.5E0 2.1E0 1.7E0 3.4E0 3.4E0 4.5E0 2.6E0	3.7E-1 3.0E-1 4.1E-1 4.1E-1 4.1E-1 6.9E-1 Benjamini 5.5E-3 3.0E-2 1.7E-2 9.1E-3 2.2E-2 4.0E-2 9.4E-2 1.2E-1	2 3.6E-1 2.7E-1 3.7E-1 3.7E-1 3.7E-1 6.8E-1 1 6.8E-1 2.9E-2 7.1E-3 2.0E-2 3.5E-2 8.2E-2
Anr	UP_SEQ_FEATURE SMART INTERPRO INTERPRO INTERPRO INTERPRO PIR_SUPERFAMILY notation Cluster 108 UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS GOTERM_CC_DIRECT GOTERM_CC_DIRECT GOTERM_CC_DIRECT GOTERM_CC_DIRECT GOTERM_CC_DIRECT GOTERM_CC_DIRECT GOTERM_CC_DIRECT GOTERM_CC_DIRECT	domain:S4 RNA-binding S4 Ribosomal protein S4e Ribosomal protein S4e, N-terminal Ribosomal protein S4e, central region Ribosomal protein S4e, N-terminal, conserved site ribosomal protein S4a/S4e Enrichment Score: 1.89 Initiation factor regulation of translational initiation translation initiation factor activity Protein biosynthesis eukaryotic translation initiation factor 3 complex eukaryotic translation initiation factor 3 complex, eIF3m translation initiation factor binding eukaryotic 43S preinitiation complex	RT R		5 4 3 3 3 3 Count 19 15 21 37 9 8 5	2.0E-2 4.9E-2 7.0E-2 7.0E-2 7.0E-2 8.8E-2 P_Value 1.1E-3 1.4E-3 1.6E-3 1.8E-3 2.4E-3 4.7E-3 1.4E-2 1.6E-2 2.1E-2	4.3E0 4.1E0 6.2E0 6.2E0 6.2E0 5.4E0 Fold Change 2.2E0 2.5E0 2.1E0 1.7E0 3.4E0 3.4E0 4.5E0 2.6E0	3.7E-1 3.0E-1 4.1E-1 4.1E-1 4.1E-1 6.9E-1 Benjamini 5.5E-3 3.0E-2 1.7E-2 9.1E-3 2.2E-2 4.0E-2 9.4E-2 1.2E-1 1.3E-1	2 3.6E-1 2.7E-1 3.7E-1 3.7E-1 3.7E-1 6.8E-1 FDR 4.3E-3 2.9E-2 1.5E-2 7.1E-3 2.0E-2 3.5E-2 1.0E-1

Anno	tation Cluster 1	Enrichment Score: ?	G	<u>□3</u>	Count	P_Value	Fold Change	Benjamin	i FDR
	KEGG_PATHWAY	RNA transport	<u>RT</u>	=	42	7.7E-2	1.3E0	1.3E-1	7.7E- 2
	INTERPRO	Proteasome component (PCI) domain	<u>RT</u>	1	6	1.3E-1	2.2E0	6.4E-1	5.8E-
	UP_SEQ_FEATURE	domain:PCI	<u>RT</u>	4	6	1.3E-1	2.2E0	1.0E0	9.6E-
_	SMART	PINT	RT		6	3.6E-1	1.5E0	1.0E0	1 9.1E-
Annoi	tation Cluster 109	Enrichment Score: 1.89	G	- -	Count	P_Value	Fold	Panjamin	1 i FDR
	UP_SEQ_FEATURE			i		5.1E-3	Onlange	1.2E-1	1.1E-
	UP_SEQ_FEATURE	domain:C2 tensin-type	<u>RT</u>		6				1 1.9E-
	INTERPRO	domain:Phosphatase tensin-type	<u>RT</u>	1	6	9.0E-3		2.0E-1	1 1.1E-
		Tensin phosphatase, C2 domain	<u>RT</u>	i	6	1.3E-2	3.7E0	1.3E-1	1
	SMART	<u>SM01326</u>	<u>RT</u>	i	6	4.6E-2		3.0E-1	2.7E- 1
Annot	tation Cluster 110	Enrichment Score: 1.83	G	- 100	Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	Mini-chromosome maintenance, DNA- dependent ATPase	<u>RT</u>	i	7	9.4E-4	4.8E0	1.2E-2	1.1E- 2
	UP_SEQ_FEATURE	domain:MCM	<u>RT</u>	1	6	2.6E-3	5.1E0	6.2E-2	6.0E- 2
	SMART	<u>MCM</u>	<u>RT</u>	i	7	9.2E-3	3.2E0	8.7E-2	7.9E- 2
	GOTERM_CC_DIRECT	MCM complex	<u>RT</u>	1	5	4.0E-2	3.5E0	2.3E-1	2.0E-
	INTERPRO	Mini-chromosome maintenance, conserved	<u>RT</u>	4	4	5.7E-2	4.1E0	4.0E-1	3.7E
	BIOCARTA	site CDK Regulation of DNA Replication	RT		9	2.1E-1		4.4E-1	3.1E
nno	tation Cluster 111	Enrichment Score: 1.8	G	<u>-</u>	Count	P_Value	Fold	Bandanda	1 i FDR
	UP_SEQ_FEATURE	domain:Post-SET	RT	_	12	1.4E-6	Change	6.0E-5	5.8E-
_ _	INTERPRO			-					5 6.0E
_	SMART	Post-SET domain	<u>RT</u>		11	3.7E-5		6.6E-4	4 4.6E
		PostSET	<u>RT</u>	•	9	5.0E-3	2.8E0	5.1E-2	2
	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K4 specific)	<u>RT</u>	•	9	5.5E-3	3.0E0	4.9E-2	4.4E-
	GOTERM_CC_DIRECT	histone methyltransferase complex	<u>RT</u>	•	10	5.8E-3	2.8E0	4.8E-2	4.2E- 2
	GOTERM_BP_DIRECT	histone H3-K4 methylation	<u>RT</u>	•	9	1.2E-2	2.7E0	1.7E-1	1.6E- 1
	UP_SEQ_FEATURE	zinc finger region:PHD-type 3	<u>RT</u>	1	5	4.7E-2	3.4E0	7.7E-1	7.4E ⁻
	UP_SEQ_FEATURE	zinc finger region:PHD-type 2	<u>RT</u>	4	9	6.3E-2	2.0E0	9.0E-1	8.7E
	UP_SEQ_FEATURE	zinc finger region:PHD-type 1	<u>RT</u>	1	9	1.0E-1	1.9E0	1.0E0	9.6E
	INTERPRO	FY-rich, N-terminal	<u>RT</u>		3	1.9E-1	3.7E0	8.9E-1	8.1E
7	INTERPRO	<u>FY-rich, C-terminal</u>	<u>RT</u>		3	1.9E-1	3.7E0	8.9E-1	1 8.1E-
_ 	SMART	<u>FYRC</u>	RT		3	3.6E-1		1.0E0	1 9.1E
_ _	SMART								1 9.1E
	GOTERM_CC_DIRECT	<u>FYRN</u>	<u>RT</u>		3	3.6E-1		1.0E0	1 8.8E
	007EMM_00_BINE01	Set1C/COMPASS complex	<u>RT</u>	i	3	5.4E-1		1.0E0	1
nnot	tation Cluster 112	Enrichment Score: 1.79	G	- N	Count	P_Value	Fold Change	Benjamin	
	GOTERM_MF_DIRECT	transcription factor activity, RNA polymerase II transcription factor recruiting	<u>RT</u>	i	7	4.6E-4	5.2E0	5.6E-3	5.0E-
	UP_SEQ_FEATURE	domain:HTH myb-type 1	<u>RT</u>	i	5	2.0E-3	6.8E0	5.0E-2	4.8E- 2
	UP_SEQ_FEATURE	domain:HTH myb-type 2	<u>RT</u>	i	5	2.0E-3	6.8E0	5.0E-2	4.8E- 2
	INTERPRO	SANT/Myb domain	<u>RT</u>	i	16	2.1E-3	2.3E0	2.5E-2	2.3E- 2
	INTERPRO	Myb-like domain	<u>RT</u>	i	6	4.0E-3	4.6E0	4.4E-2	4.0E-
	INTERPRO	<u>Myb domain</u>	<u>RT</u>	1	6	7.7E-3	4.1E0	7.7E-2	7.1E
	UP_SEQ_FEATURE	domain:HTH myb-type 3	<u>RT</u>		4	1.1E-2	6.8E0	2.2E-1	2.1E
7	UP_SEQ_FEATURE	domain:Myb-like 1	RT		3		6.8E0		1 8.1E
	UP_SEQ_FEATURE			-	3				1 8.1E
	INTERPRO	domain:Myb-like 2	<u>RT</u>				6.8E0		1 3.7E
	SMART	<u>C-myb, C-terminal</u>	<u>RT</u>	1	3		6.2E0		1
		<u>SANT</u>	<u>RT</u>	i	16	8.5E-2	1.5E0	4.9E-1	4.4E
	UP_SEQ_FEATURE	DNA-binding region:H-T-H motif	<u>RT</u>	1	7	1.7E-1		1.0E0	9.6E- 1
	INTERPRO	Homeodomain-like	<u>RT</u>	-	19	_	3.5E-1 Fold		1.0E
annot	tation Cluster 113 KEGG_PATHWAY	Enrichment Score: 1.76	G		Count	P_Value	Change	Benjamin	T FDR

1100	ation Cluster 1	Enrichment Score: ?	G	To the second se	Count	P_Value	Fold	Benjamir	ıi Fr
	GOTERM_CC_DIRECT	photoreceptor disc membrane	RT RT	i	8	2.1E-2	Change	1.3E-1	1.
	GOTERM_BP_DIRECT	regulation of rhodopsin mediated signaling		_					1 6.
		pathway	<u>RT</u>	•	9	1.0E-1	Fold	7.1E-1	1
ota	ation Cluster 114 INTERPRO	Enrichment Score: 1.76	G	1	Count	P_Value	Change		
		Death domain	<u>RT</u>	i	14	2.1E-3	2.5E0	2.6E-2	2.
	UP_SEQ_FEATURE	domain:Death	<u>RT</u>	1	13	3.0E-3	2.5E0	7.2E-2	7. 2
	INTERPRO	Death-like domain	<u>RT</u>	1	23	4.2E-2	1.5E0	3.1E-1	2. 1
	SMART	<u>DEATH</u>	<u>RT</u>	i .	9	3.4E-1	1.4E0	1.0E0	9. 1
ota	ation Cluster 115	Enrichment Score: 1.73	G	To the second se	Count	P_Value	Fold Change	Benjamir	ni Fl
	INTERPRO	EGF receptor, L domain	<u>RT</u>	i	7	1.1E-4	6.2E0	1.7E-3	1.
	INTERPRO	Furin-like cysteine-rich domain	<u>RT</u>	i .	7	1.1E-4	6.2E0	1.7E-3	1.
	GOTERM_MF_DIRECT	insulin receptor substrate binding	RT		8	6.5E-4	4.3F0	7.5E-3	6.
	INTERPRO			-					3.
	PIR_SUPERFAMILY	Tyrosine-protein kinase, insulin-like receptor	<u>RT</u>		3	7.0E-2		4.1E-1	1 6.
	_	insulin receptor	<u>RT</u>	•	3	8.8E-2	5.4E0	6.9E-1	1
	INTERPRO	<u>Tyrosine-protein kinase, receptor class II,</u> <u>conserved site</u>	<u>RT</u>	i	3	5.5E-1	1.7E0	1.0E0	9. 1
	GOTERM_CC_DIRECT	receptor complex	<u>RT</u>	i	20	6.3E-1	1.0E0	1.0E0	8. 1
	UP_SEQ_FEATURE	domain:Fibronectin type-III 3	<u>RT</u>	i	6	1.0E0	4.9E-1 Fold	1	1.
ota	ation Cluster 116 GOTERM_BP_DIRECT	Enrichment Score: 1.69	G	No.	Count	P_Value	Change	•	_
		mRNA cleavage	<u>RT</u>	i	8	1.4E-3	3.9E0	3.0E-2	2.
	BIOCARTA	Polyadenylation of mRNA	<u>RT</u>	i	7	7.1E-2	2.1E0	2.0E-1	1.
	GOTERM_BP_DIRECT	mRNA polyadenylation	<u>RT</u>	i .	9	8.6E-2	1.9E0	6.4E-1	6. 1
ota	ation Cluster 117	Enrichment Score: 1.67	G	170	Count	P_Value	Fold Change	Benjamir	ni F
	BIOCARTA	Cyclins and Cell Cycle Regulation	<u>RT</u>	1	18	3.0E-4	2.2E0	4.1E-3	2. 3
	BBID	26.cyclin-CDK complexes	<u>RT</u>		11	1.6E-2	2.0E0	8.5E-1	8.
	BBID	1.RBphosphoE2F	<u>RT</u>	i	9	9.2E-2	1.7E0	1.0E0	1
	GOTERM_MF_DIRECT	cyclin-dependent protein serine/threonine kinase inhibitor activity	<u>RT</u>	i	5	9.7E-2	2.7E0	4.7E-1	4. 1
									_
	GOTERM_BP_DIRECT	negative regulation of phosphorylation	<u>RT</u>	i e	7	1.1E-1	2.1E0	7.3E-1	/. 1
ota	ation Cluster 118	negative regulation of phosphorylation Enrichment Score: 1.67	RT G	i T	7 Count	1.1E-1 P_Value	Fold	Ponjamir	1
ota						1	Fold	Ponjamir	1 ni Fi 3.
ota	ation Cluster 118	Enrichment Score: 1.67 POLO box duplicated domain	G RT	i i	Count	P_Value 2.9E-3	Fold Change 6.2E0	Benjamir 3.3E-2	1 Fi 3. 2 8.
nota	ation Cluster 118	Enrichment Score: 1.67 POLO box duplicated domain domain: POLO box 1	G RT RT	i i	Count 5	P_Value 2.9E-3 5.8E-2	Fold Change 6.2E0	3.3E-2 8.4E-1	1 3. 2 8. 1
	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE	Enrichment Score: 1.67 POLO box duplicated domain domain:POLO box 1 domain:POLO box 2	G RT RT RT	i i i	Count 5 3	P_Value 2.9E-3 5.8E-2 5.8E-2	Fold Change 6.2E0 6.8E0 6.8E0	3.3E-2 8.4E-1 8.4E-1	1 3. 2 8. 1 8.
	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119	Enrichment Score: 1.67 POLO box duplicated domain domain: POLO box 1 domain: POLO box 2 Enrichment Score: 1.66	G RT RT RT G	i i i	Count 5 3 Count	P_Value 2.9E-3 5.8E-2 5.8E-2 P_Value	Fold Change 6.2E0 6.8E0 Fold Change	3.3E-2 8.4E-1 8.4E-1	1 F 3. 2 8. 1 8. 1
	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119 INTERPRO	Enrichment Score: 1.67 POLO box duplicated domain domain:POLO box 1 domain:POLO box 2	G RT RT RT		Count 5 3	P_Value 2.9E-3 5.8E-2 5.8E-2	Fold Change 6.2E0 6.8E0 Fold Change	3.3E-2 8.4E-1 8.4E-1 Benjamir 7.8E-3	1 3. 2 8. 1 8. 1 7. 3
	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119 INTERPRO UP_SEQ_FEATURE	Enrichment Score: 1.67 POLO box duplicated domain domain: POLO box 1 domain: POLO box 2 Enrichment Score: 1.66	G RT RT RT G		Count 5 3 Count	P_Value 2.9E-3 5.8E-2 5.8E-2 P_Value	6.2E0 6.8E0 6.8E0 Fold Change	3.3E-2 8.4E-1 8.4E-1	1 3. 2 8. 1 8. 1 7. 3 4. 2
	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119 INTERPRO	Enrichment Score: 1.67 POLO box duplicated domain domain:POLO box 1 domain:POLO box 2 Enrichment Score: 1.66 Glutamine amidotransferase	RT RT RT G		5 3 Count 6	2.9E-3 5.8E-2 5.8E-2 P_Value 5.7E-4	Fold Change 6.2E0 6.8E0 6.2E0 6.8E0 6.8E0	3.3E-2 8.4E-1 8.4E-1 Benjamir 7.8E-3	1
	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119 INTERPRO UP_SEQ_FEATURE	Enrichment Score: 1.67 POLO box duplicated domain domain:POLO box 1 domain:POLO box 2 Enrichment Score: 1.66 Glutamine amidotransferase domain:Glutamine amidotransferase type-1	G RT RT RT G RT RT		Count 5 3 Count 6 5	P_Value 2.9E-3 5.8E-2 5.8E-2 P_Value 5.7E-4 2.0E-3	Fold Change 6.2E0 6.8E0 6.2E0 6.8E0 3.9E0	3.3E-2 8.4E-1 8.4E-1 Benjamir 7.8E-3 5.0E-2	1
	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119 INTERPRO UP_SEQ_FEATURE UP_KEYWORDS	Enrichment Score: 1.67 POLO box duplicated domain domain:POLO box 1 domain:POLO box 2 Enrichment Score: 1.66 Glutamine amidotransferase domain:Glutamine amidotransferase type-1 Pyrimidine biosynthesis	G RT RT RT G RT RT RT		Count 5 3 Count 6 5 4	P_Value 2.9E-3 5.8E-2 5.8E-2 P_Value 5.7E-4 2.0E-3 6.8E-2	Fold Change 6.2E0 6.8E0 6.2E0 6.8E0 3.9E0 3.4E0	3.3E-2 8.4E-1 8.4E-1 Benjamir 7.8E-3 5.0E-2 2.4E-1	1 3. 2 8. 1 8. 1 7. 3 4. 2 1. 1 9. 1
	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119 INTERPRO UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE	Enrichment Score: 1.67 POLO box duplicated domain domain:POLO box 1 domain:POLO box 2 Enrichment Score: 1.66 Glutamine amidotransferase domain:Glutamine amidotransferase type-1 Pyrimidine biosynthesis active site:For GATase activity	G RT RT RT G RT RT RT RT RT		Count 5 3 Count 6 5 4	P_Value 2.9E-3 5.8E-2 5.8E-2 P_Value 5.7E-4 2.0E-3 6.8E-2 1.0E-1	Fold Change 6.2E0 6.8E0 6.2E0 6.8E0 3.9E0 3.4E0 2.1E0	3.3E-2 8.4E-1 8.4E-1 8.4E-1 7.8E-3 5.0E-2 2.4E-1 1.0E0	1
ıot	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119 INTERPRO UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE GOTERM_BP_DIRECT	Enrichment Score: 1.67 POLO box duplicated domain domain:POLO box 1 domain:POLO box 2 Enrichment Score: 1.66 Glutamine amidotransferase domain:Glutamine amidotransferase type-1 Pyrimidine biosynthesis active site:For GATase activity glutamine metabolic process	G RT RT RT RT RT RT RT RT		Count 5 3 Count 6 5 4 7 4	P_Value 2.9E-3 5.8E-2 5.8E-2 P_Value 5.7E-4 2.0E-3 6.8E-2 1.0E-1 1.1E-1	Fold Change 6.2E0 6.8E0 6.2E0 6.8E0 3.9E0 3.4E0 2.1E0 3.1E0	3.3E-2 8.4E-1 8.4E-1 8.4E-1 7.8E-3 5.0E-2 2.4E-1 1.0E0 7.3E-1 4.2E-1	1
ıot	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119 INTERPRO UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE GOTERM_BP_DIRECT UP_KEYWORDS	Enrichment Score: 1.67 POLO box duplicated domain domain: POLO box 1 domain: POLO box 2 Enrichment Score: 1.66 Glutamine amidotransferase domain: Glutamine amidotransferase type-1 Pyrimidine biosynthesis active site: For GATase activity glutamine metabolic process Glutamine amidotransferase Enrichment Score: 1.65	G RT RT RT G RT RT RT RT RT RT RT G G		Count 5 3 Count 6 5 4 7 4	P_Value 2.9E-3 5.8E-2 5.8E-2 P_Value 5.7E-4 2.0E-3 6.8E-2 1.0E-1 1.1E-1 1.3E-1 P_Value	Fold Change 6.2E0 6.8E0 6.2E0 6.8E0 3.9E0 3.4E0 2.1E0 3.1E0 Fold Change	3.3E-2 8.4E-1 8.4E-1 8.4E-1 7.8E-3 5.0E-2 2.4E-1 1.0E0 7.3E-1 4.2E-1 Benjamir	1
ıot	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119 INTERPRO UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 120	Enrichment Score: 1.67 POLO box duplicated domain domain: POLO box 1 domain: POLO box 2 Enrichment Score: 1.66 Glutamine amidotransferase domain: Glutamine amidotransferase type-1 Pyrimidine biosynthesis active site: For GATase activity glutamine metabolic process Glutamine amidotransferase Enrichment Score: 1.65 Protein kinase inhibitor mitogen-activated protein kinase kinase	RI R		Count 5 3 Count 6 5 4 7 4 Count 7	P_Value 2.9E-3 5.8E-2 P_Value 5.7E-4 2.0E-3 6.8E-2 1.0E-1 1.1E-1 1.3E-1 P_Value 1.0E-2	Fold Change 6.2E0 6.8E0 6.2E0 6.8E0 3.9E0 3.4E0 2.1E0 3.1E0 Fold Change 3.4E0	3.3E-2 8.4E-1 8.4E-1 8.4E-1 7.8E-3 5.0E-2 2.4E-1 1.0E0 7.3E-1 4.2E-1 Benjamir 4.4E-2	1
ıot	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119 INTERPRO UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 120 UP_KEYWORDS GOTERM_MF_DIRECT	Enrichment Score: 1.67 POLO box duplicated domain domain:POLO box 1 domain:POLO box 2 Enrichment Score: 1.66 Glutamine amidotransferase domain:Glutamine amidotransferase type-1 Pyrimidine biosynthesis active site:For GATase activity glutamine metabolic process Glutamine amidotransferase Enrichment Score: 1.65 Protein kinase inhibitor mitogen-activated protein kinase kinase binding.	RI R		Count 5 3 3 Count 6 5 4 7 4 Count 7 8	P_Value 2.9E-3 5.8E-2 5.8E-2 P_Value 5.7E-4 2.0E-3 6.8E-2 1.0E-1 1.1E-1 1.3E-1 P_Value 1.0E-2 1.0E-2	Fold Change 6.2E0 6.8E0 6.2E0 6.8E0 3.9E0 3.4E0 2.1E0 3.4E0 3.4E0 3.0E0	3.3E-2 8.4E-1 8.4E-1 Benjamir 7.8E-3 5.0E-2 2.4E-1 1.0E0 7.3E-1 4.2E-1 Benjamir 4.4E-2 8.2E-2	1
ıot	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119 INTERPRO UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 120 UP_KEYWORDS GOTERM_MF_DIRECT INTERPRO	Enrichment Score: 1.67 POLO box duplicated domain domain: POLO box 1 domain: POLO box 2 Enrichment Score: 1.66 Glutamine amidotransferase domain: Glutamine amidotransferase type-1 Pyrimidine biosynthesis active site: For GATase activity glutamine metabolic process Glutamine amidotransferase Enrichment Score: 1.65 Protein kinase inhibitor mitogen-activated protein kinase kinase binding Pseudokinase tribbles family/serine-threonine-protein kinase 40	RI R		Count 5 3 Count 6 5 4 7 4 Count 7	P_Value 2.9E-3 5.8E-2 P_Value 5.7E-4 2.0E-3 6.8E-2 1.0E-1 1.1E-1 1.3E-1 P_Value 1.0E-2	Fold Change 6.2E0 6.8E0 6.2E0 6.8E0 3.9E0 3.4E0 2.1E0 3.4E0 3.4E0 3.0E0	3.3E-2 8.4E-1 8.4E-1 8.4E-1 7.8E-3 5.0E-2 2.4E-1 1.0E0 7.3E-1 4.2E-1 Benjamir 4.4E-2	1 Fi 3. 2 8. 1 8. 1 1 7. 3 4. 2 1. 1 3. 1 1 Fi 3. 2 7. 2 1. 1 1
ıot	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119 INTERPRO UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 120 UP_KEYWORDS GOTERM_MF_DIRECT INTERPRO GOTERM_BP_DIRECT	Enrichment Score: 1.67 POLO box duplicated domain domain: POLO box 1 domain: POLO box 2 Enrichment Score: 1.66 Glutamine amidotransferase domain: Glutamine amidotransferase type-1 Pyrimidine biosynthesis active site: For GATase activity glutamine metabolic process Glutamine amidotransferase Enrichment Score: 1.65 Protein kinase inhibitor mitogen-activated protein kinase kinase binding Pseudokinase tribbles family/serine-	RI R		Count 5 3 3 Count 6 5 4 7 4 Count 7 8	P_Value 2.9E-3 5.8E-2 5.8E-2 P_Value 5.7E-4 2.0E-3 6.8E-2 1.0E-1 1.1E-1 1.3E-1 P_Value 1.0E-2 1.0E-2	Fold Change 6.2E0 6.8E0 6.2E0 6.8E0 3.9E0 3.4E0 3.1E0 Fold Change 3.4E0 3.0E0 6.2E0	3.3E-2 8.4E-1 8.4E-1 Benjamir 7.8E-3 5.0E-2 2.4E-1 1.0E0 7.3E-1 4.2E-1 Benjamir 4.4E-2 8.2E-2	1
ıot	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119 INTERPRO UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 120 UP_KEYWORDS GOTERM_MF_DIRECT INTERPRO	Enrichment Score: 1.67 POLO box duplicated domain domain: POLO box 1 domain: POLO box 2 Enrichment Score: 1.66 Glutamine amidotransferase domain: Glutamine amidotransferase type-1 Pyrimidine biosynthesis active site: For GATase activity glutamine metabolic process Glutamine amidotransferase Enrichment Score: 1.65 Protein kinase inhibitor mitogen-activated protein kinase kinase binding Pseudokinase tribbles family/serine-threonine-protein kinase 40	RI R		Count 5 3 Count 6 5 4 7 4 Count 7 8 4	P_Value 2.9E-3 5.8E-2 5.8E-2 P_Value 5.7E-4 2.0E-3 6.8E-2 1.0E-1 1.1E-1 1.3E-1 P_Value 1.0E-2 1.0E-2 1.5E-2	Fold Change 6.2E0 6.8E0 6.2E0 6.8E0 3.9E0 3.4E0 2.1E0 3.1E0 Fold Change 3.4E0 3.0E0 6.2E0 3.3E0	3.3E-2 8.4E-1 8.4E-1 8.4E-1 7.8E-3 5.0E-2 2.4E-1 1.0E0 7.3E-1 4.2E-1 Benjamir 4.4E-2 8.2E-2 1.3E-1	1
not	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119 INTERPRO UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 120 UP_KEYWORDS GOTERM_MF_DIRECT INTERPRO GOTERM_BP_DIRECT	Enrichment Score: 1.67 POLO box duplicated domain domain: POLO box 1 domain: POLO box 2 Enrichment Score: 1.66 Glutamine amidotransferase domain: Glutamine amidotransferase type-1 Pyrimidine biosynthesis active site: For GATase activity glutamine metabolic process Glutamine amidotransferase Enrichment Score: 1.65 Protein kinase inhibitor mitogen-activated protein kinase kinase binding Pseudokinase tribbles family/serine-threonine-protein kinase 40 regulation of MAP kinase activity	RI R		Count 5 3 3 Count 6 5 4 4 7 4 Count 7 8 4 5 3	P_Value 2.9E-3 5.8E-2 5.8E-2 P_Value 5.7E-4 2.0E-3 6.8E-2 1.0E-1 1.1E-1 1.3E-1 P_Value 1.0E-2 1.0E-2 1.5E-2 5.0E-2	Fold Change 6.2E0 6.8E0 6.2E0 6.8E0 3.9E0 3.4E0 3.1E0 Fold Change 3.4E0 3.0E0 6.2E0 3.3E0 6.0E0	3.3E-2 8.4E-1 8.4E-1 8.4E-1 8.4E-1 1.0E0 7.3E-1 4.2E-1 8.2E-2 1.3E-1 4.7E-1 3.9E-1	1
not	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119 INTERPRO UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 120 UP_KEYWORDS GOTERM_MF_DIRECT INTERPRO GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	Enrichment Score: 1.67 POLO box duplicated domain domain: POLO box 1 domain: POLO box 2 Enrichment Score: 1.66 Glutamine amidotransferase domain: Glutamine amidotransferase type-1 Pyrimidine biosynthesis active site: For GATase activity glutamine metabolic process Glutamine amidotransferase Enrichment Score: 1.65 Protein kinase inhibitor mitogen-activated protein kinase kinase binding Pseudokinase tribbles family/serine-threonine-protein kinase 40 regulation of MAP kinase activity ubiquitin-protein transferase regulator activity	RI R		Count 5 3 3 Count 6 5 4 4 7 4 Count 7 8 4 5 3	P_Value 2.9E-3 5.8E-2 5.8E-2 P_Value 5.7E-4 2.0E-3 6.8E-2 1.0E-1 1.1E-1 1.3E-1 1.0E-2 1.0E-2 1.5E-2 5.0E-2 7.5E-2	Fold Change 6.2E0 6.8E0 3.9E0 3.4E0 3.1E0 Fold Change 3.4E0 3.0E0 6.2E0 3.3E0 6.2E0 5.0E0 Fold Change 5.0E0 Fold Change 6.2E0 5.0E0 Fold Change 6.0E0	3.3E-2 8.4E-1 8.4E-1 8.4E-1 8.4E-1 1.0E0 7.3E-1 4.2E-1 8.2E-2 1.3E-1 4.7E-1 3.9E-1	1 F 3. 2 8. 1 8. 1 9. 1 7. 1 3. 1 1 F 3. 2 7. 2 1. 1 4. 1 3. 1 F 5 1 F 6
nota	ation Cluster 118 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE ation Cluster 119 INTERPRO UP_SEQ_FEATURE UP_KEYWORDS UP_SEQ_FEATURE GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 120 UP_KEYWORDS GOTERM_MF_DIRECT INTERPRO GOTERM_BP_DIRECT ation Cluster 121	Enrichment Score: 1.67 POLO box duplicated domain domain: POLO box 1 domain: POLO box 2 Enrichment Score: 1.66 Glutamine amidotransferase domain: Glutamine amidotransferase type-1 Pyrimidine biosynthesis active site: For GATase activity glutamine metabolic process Glutamine amidotransferase Enrichment Score: 1.65 Protein kinase inhibitor mitogen-activated protein kinase kinase binding Pseudokinase tribbles family/serine-threonine-protein kinase 40 regulation of MAP kinase activity ubiquitin-protein transferase regulator activity Enrichment Score: 1.63	G RI		Count 5 3 3 Count 6 5 4 4 7 4 Count 7 8 4 5 3 Count	P_Value 2.9E-3 5.8E-2 5.8E-2 P_Value 5.7E-4 2.0E-3 6.8E-2 1.0E-1 1.1E-1 1.3E-1 P_Value 1.0E-2 1.0E-2 1.0E-2 7.5E-2 P_Value	Fold Change 6.2E0 6.8E0 3.9E0 3.4E0 3.1E0 Fold Change 3.4E0 3.0E0 6.2E0 6.2E0 6.2E0 6.2E0 7.0E0 7.0E0 Fold Change 4.9E0 4.9E0	3.3E-2 8.4E-1 8.4E-1 8.4E-1 7.8E-3 5.0E-2 2.4E-1 1.0E0 7.3E-1 4.2E-1 8.2E-2 1.3E-1 4.7E-1 3.9E-1 Benjamir	3. 2 8. 1 8. 1 7. 3 4. 2 1. 1 9. 1 7. 1 3. 1 7. 2 1. 1 4. 1 3. 1

inota	ation Cluster 1	Enrichment Score: ?	G	**	Count	P_Value	Fold Change	Benjamin	i FC
	GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K9 specific)	<u>RT</u>	i	4	3.6E-2	4.8E0	2.2E-1	1. 1
	SMART	<u>PreSET</u>	<u>RT</u>	i .	5	6.7E-2	2.9E0	4.0E-1	3. 1
nota	ation Cluster 122	Enrichment Score: 1.63	G	™	Count	P_Value	Fold Change	Benjamin	i FC
	KEGG_PATHWAY	<u>Shigellosis</u>	<u>RT</u>		29	5.9E-6	2.4E0	1.7E-5	8. 6
	BIOCARTA	The 4-1BB-dependent immune response	<u>RT</u>	i e	14	6.7E-4	2.4E0	7.4E-3	5. 3
	BIOCARTA	Toll-Like Receptor Pathway	<u>RT</u>		23	1.1E-3	1.8E0	1.1E-2	7. 3
	BIOCARTA	Signal transduction through IL1R	<u>RT</u>	1	20	2.7E-3	1.8E0	1.8E-2	1.
	KEGG_PATHWAY	Epithelial cell signaling in Helicobacter pylori	RT		23	5.7E-3	1.8E0	1.2E-2	2 5.
	BIOCARTA	infection NFkB activation by Nontypeable Hemophilus	RT		15	8.4E-3		3.9E-2	3 2.
	BIOCARTA	<u>influenzae</u> NF-kB Signaling Pathway	RT	_	14	1.6E-2		6.4E-2	2 4.
	BIOCARTA			-					2 7
	GOTERM_CC_DIRECT	CD40L Signaling Pathway	<u>RT</u>		10	2.7E-2		1.0E-1	2
	KEGG_PATHWAY	<u>I-kappaB/NF-kappaB complex</u>	<u>RT</u>		4	3.0E-2	5.1E0	1.8E-1	1
		RIG-I-like receptor signaling pathway	<u>RT</u>	•	21	3.8E-2	1.6E0	6.8E-2	2
	BIOCARTA	Activation of PKC through G protein coupled receptor	<u>RT</u>	i	6	4.2E-2		1.3E-1	9
	BBID BIOCARTA	77.IkBa Kinase JNK MEKK1 Acetylation and Deacetylation of RelA in The	RT RT		6 9	6.5E-2 1.2E-1		1.0E0 2.9E-1	1 2
	BIOCARTA	Nucleus Double Stranded RNA Induced Gene		•	6	2.0E-1			1 3
	BIOCARTA	<u>Expression</u>	<u>RT</u>	•				4.3E-1	1 3
	BIOCARTA	TNF/Stress Related Signaling Erythropoietin mediated neuroprotection	<u>RT</u>	•	11	2.8E-1		5.5E-1	1
	BIOCARTA	through NF-kB	<u>RT</u>		7	2.9E-1	1.5E0	5.7E-1	1
		TNFR2 Signaling Pathway	<u>RT</u>		8	3.7E-1		6.8E-1	1
	BBID BIOCARTA	90.IB and-cat-Arm processing of Ci TACI and BCMA stimulation of B cell immune	RT RT		4 6	3.8E-1 5.8E-1		1.0E0 9.0E-1	1 6
a o t o	ation Cluster 123	responses. Enrichment Score: 1.6	G	· **	Count	P_Value	Fold	Daniamin	1
IUla	BIOCARTA	Control of skeletal myogenesis by HDAC &					Change		2
	BIOCARTA	<u>calcium/calmodulin-dependent kinase (CaMK)</u> <u>Signal Dependent Regulation of Myogenesis</u>	<u>RT</u>	•	20	2.8E-4		4.0E-3	3 6
	UP_SEQ_FEATURE	by Corepressor MITR	<u>RT</u>	•	9	8.3E-4		8.4E-3	3
		domain:MADS-box	<u>RT</u>	•	5	5.4E-3	5.7E0	1.2E-1	1
	INTERPRO	<u>Transcription factor, MADS-box</u>	<u>RT</u>	1	5	7.7E-3	5.2E0	7.7E-2	7 2
	UP_SEQ_FEATURE	DNA-binding region:Mef2-type	<u>RT</u>	1	4	2.5E-2	5.5E0	4.4E-1	4
	SMART	MADS	<u>RT</u>	i	5	3.5E-2	3.4E0	2.6E-1	2 1
	UP_SEQ_FEATURE	region of interest:Beta domain	<u>RT</u>	i .	3	5.8E-2	6.8E0	8.4E-1	8
	INTERPRO	Holliday junction regulator protein family C- terminal	<u>RT</u>	i	3	1.2E-1	4.6E0	6.4E-1	5 1
	BIOCARTA	Regulation of PGC-1a	<u>RT</u>	1	12	1.3E-1	1.5E0	3.1E-1	2
	UP_SEQ_FEATURE	compositionally biased region:Lys-rich (basic)	<u>RT</u>	i e	3	3.9E-1	2.3E0	1.0E0	9
	UP_SEQ_FEATURE	site:Cleavage	<u>RT</u>	•	9	8.2E-1	8.8E-1	1.0E0	9
nota	ation Cluster 124	Enrichment Score: 1.6	G	178	Count	P_Value	Fold Change	Benjamin	
	UP_SEQ_FEATURE	DNA-binding region:TEA	RT		4	1.1E-2	Change	2.2E-1	2
	INTERPRO	TEA/ATTS	RT		4	1.5E-2		1.3E-1	1
	INTERPRO	Transcriptional enhancer factor	RT		4	1.5E-2		1.3E-1	1 1
		transcriptional enhancer factor		•					1 2
	PIR_SUPERFAMILY	transcriptional ennancer factor	<u>RT</u>	•	4	2.1E-2		2.9E-1	1 2
	_			-		4.0-	a 1 F 0	3.0E-1	1
	SMART	<u>TEA</u>	<u>RT</u>	i	4	4.9E-2			0
	SMART UP_SEQ_FEATURE	TEA region of interest:Transcriptional activation	<u>RT</u>	i	3	1.1E-1	5.1E0	1.0E0	1
nota	SMART UP_SEQ_FEATURE ation Cluster 125	<u>TEA</u>		i M	3	1.1E-1 P_Value	5.1E0 Fold Change	Panjamin	1 i F
nota	SMART UP_SEQ_FEATURE ation Cluster 125 UP_SEQ_FEATURE	TEA region of interest:Transcriptional activation	<u>RT</u>	i	3	1.1E-1	5.1E0 Fold Change	Panjamin	1 i F 7 4
nota	SMART UP_SEQ_FEATURE ation Cluster 125 UP_SEQ_FEATURE INTERPRO	TEA region of interest:Transcriptional activation Enrichment Score: 1.57	RT G	i M	3 Count	1.1E-1 P_Value	5.1E0 Fold Change 2.1E0	Benjamin	1 i F 7 4 6
nota	SMART UP_SEQ_FEATURE ation Cluster 125 UP_SEQ_FEATURE	TEA region of interest:Transcriptional activation Enrichment Score: 1.57 metal ion-binding site:Magnesium	RT G		Count	1.1E-1 P_Value 2.3E-5	5.1E0 Fold Change 2.1E0 4.3E0	Benjamin 7.9E-4	1 i F 7 4 6 4
nota	SMART UP_SEQ_FEATURE ation Cluster 125 UP_SEQ_FEATURE INTERPRO	region of interest:Transcriptional activation Enrichment Score: 1.57 metal ion-binding site:Magnesium P-type ATPase, transmembrane domain Cation-transporting P-type ATPase, C-	RT G RT RT		3 Count 36 11	1.1E-1 P_Value 2.3E-5 3.7E-5	5.1E0 Fold Change 2.1E0 4.3E0 4.0E0	Benjamin 7.9E-4 6.6E-4	7

Anno	otation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	<u>Cation-transporting P-type ATPase</u>	<u>RT</u>	i	16	2.3E-4	•	3.5E-3	3.2E- 3
	INTERPRO	P-type ATPase, phosphorylation site	<u>RT</u>		16	2.3E-4	2.8E0	3.5E-3	3.2E-
	INTERPRO	P-type ATPase, cytoplasmic domain N	RT	•	16	2.3E-4	2.8F0	3.5E-3	3 3.2E-
	UP_SEQ_FEATURE	active site:4-aspartylphosphate intermediate	RT		16		2.7E0	9.1E-3	3 8.7E-
	INTERPRO	Sodium/potassium-transporting P-type		-					3 7.1E-
	SMART	ATPase, subfamily IIC	<u>RT</u>		6	5.7E-4		7.8E-3	3 1.5E-
	GOTERM_BP_DIRECT	<u>SM00831</u>	<u>RT</u>		11	1.4E-3		1.7E-2	2 3.9E-
	GOTERM_BP_DIRECT	cellular sodium ion homeostasis establishment or maintenance of	<u>RT</u>	•	10	2.0E-3	3.1E0	4.1E-2	2 4.8E-
		transmembrane electrochemical gradient	<u>RT</u>	•	8	2.6E-3	3.6E0	5.0E-2	2
	GOTERM_MF_DIRECT	sodium:potassium-exchanging ATPase activity	<u>RT</u>	i	6	1.6E-2	3.6E0	1.2E-1	1.0E- 1
	GOTERM_BP_DIRECT	sodium ion export from cell	<u>RT</u>	i	6	1.6E-2	3.6E0	2.1E-1	2.0E- 1
	GOTERM_MF_DIRECT	steroid hormone binding	<u>RT</u>	i	4	3.6E-2	4.8E0	2.2E-1	1.9E- 1
	GOTERM_BP_DIRECT	cellular potassium ion homeostasis	<u>RT</u>	i .	6	3.8E-2	3.0E0	3.8E-1	3.6E- 1
	UP_SEQ_FEATURE	region of interest:Interaction with phosphoinositide-3 kinase	<u>RT</u>	i	3	5.8E-2	6.8E0	8.4E-1	8.1E- 1
	GOTERM_BP_DIRECT	cellular response to steroid hormone stimulus	<u>RT</u>	i	5	7.3E-2	3.0E0	5.8E-1	5.5E- 1
	GOTERM_BP_DIRECT	response to glycoside	<u>RT</u>	i .	3	7.6E-2	5.9E0	5.8E-1	5.5E- 1
	UP_KEYWORDS	Sodium/potassium transport	<u>RT</u>	i	4	9.8E-2	3.4E0	3.3E-1	2.5E- 1
	INTERPRO	HAD-like domain	<u>RT</u>	i	17	2.3E-1	1.3E0	1.0E0	9.1E- 1
	GOTERM_CC_DIRECT	sodium: potassium-exchanging ATPase	<u>RT</u>	i de la companya de l	4	2.4E-1	2.3E0	8.3E-1	7.3E-
	KEGG_PATHWAY	<u>complex</u> <u>Carbohydrate digestion and absorption</u>	<u>RT</u>	•	11	2.8E-1	1.4E0	4.4E-1	1 2.8E-
	GOTERM_BP_DIRECT	ATP hydrolysis coupled proton transport	RT		8	2.9E-1		1.0E0	1 9.6E-
	GOTERM_BP_DIRECT	regulation of cardiac conduction	RT		12	3.4E-1		1.0E0	1 9.6E-
	GOTERM_BP_DIRECT	cell communication by electrical coupling		-					1 9.6E-
	GOTERM_BP_DIRECT	involved in cardiac conduction	<u>RT</u>		4	3.8E-1		1.0E0	1 9.6E-
	KEGG_PATHWAY	potassium ion import	<u>RT</u>		6	5.2E-1		1.0E0	1 8.5E-
	GOTERM_BP_DIRECT	Proximal tubule bicarbonate reclamation	<u>RT</u>	•	4		9.0E-1		1 9.6E-
		ion transmembrane transport	<u>RT</u>	•	30	9.0E-1	8.5E-1	1.0E0	1
	KEGG_PATHWAY	Cardiac muscle contraction	<u>RT</u>	i	11	9.3E-1	7.6E-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>	i	10	9.9E-1	5.9E-1	1.0E0	9.9E- 1
	KEGG_PATHWAY	Mineral absorption	<u>RT</u>	i	4	9.9E-1	4.7E-1	1.0E0	9.9E- 1
	UP_KEYWORDS KEGG_PATHWAY	Sodium transport Protein digestion and absorption	RT RT		4	1.0E0 1.0E0	2.3E-1 2.4E-1		1.0E0 1.0E0
	UP_KEYWORDS	Sodium	<u>RT</u>		4	1.0E0	2.2E-1	1.0E0	1.0E0
	UP_SEQ_FEATURE UP_KEYWORDS	topological domain:Lumenal <u>Ion transport</u>	RT RT		22 31	1.0E0 1.0E0	3.3E-1 3.3E-1		1.0E0 1.0E0
Anno	otation Cluster 126	Enrichment Score: 1.51	G		Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_MF_DIRECT	single-stranded DNA-dependent ATPase activity	<u>RT</u>	i	7	2.5E-3		2.5E-2	2.2E- 2
	GOTERM_CC_DIRECT	DNA replication factor C complex	<u>RT</u>	i	5	7.0E-3	5.3E0	5.3E-2	4.7E-
	GOTERM_MF_DIRECT	DNA clamp loader activity	<u>RT</u>	i	5	3.1E-2	3.7E0	1.9E-1	1.7E-
	INTERPRO	DNA polymerase III, clamp loader complex, gamma/delta/delta subunit, C-terminal	<u>RT</u>	1	4	5.7E-2	4.1E0	4.0E-1	3.7E-
	INTERPRO	Replication factor C, C-terminal domain	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-
	GOTERM_BP_DIRECT	positive regulation of DNA-directed DNA	RT		4		3.4E0	6.9E-1	1 6.6E-
	GOTERM_CC_DIRECT	polymerase activity Ctf18 RFC-like complex	RT		4	1.2E-1		4.9E-1	1 4.3E-
Anne	otation Cluster 127	Enrichment Score: 1.49	G	•			Fold Change		i FDR
	UP_SEQ_FEATURE	domain:Bromo	RT		12			4.5E-2	4.4E-
	INTERPRO	DDT domain superfamily	RT		4			2.4E-1	2 2.2E-
	UP_SEQ_FEATURE	domain:DDT						7.4E-1	1 7.2E-
	SMART		<u>RT</u>		4				1 4.8E-
	UP_SEQ_FEATURE	DDT	RT DT		4		3.3E0		1 9.6E-
		zinc finger region:PHD-type	<u>RT</u>	i	12	1.3E-1	1.6E0	1.0E0	1

Annota	ation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamin	ni FDR
Annota	ation Cluster 128	Enrichment Score: 1.49	G		Count	P_Value	Fold	Roniamin	ii FDR
	GOTERM_CC_DIRECT	MLL5-L complex	<u>RT</u>	i	6	3.5E-3	4.8E0	3.1E-2	2.7E- 2
	GOTERM_CC_DIRECT	PTW/PP1 phosphatase complex	<u>RT</u>		5	1.4E-2	4.5E0	9.4E-2	8.2E
_ 	GOTERM_BP_DIRECT	entrainment of circadian clock by photoperiod			4	6.8E-1		1.0E0	9.6E
Annota	ation Cluster 129	Enrichment Score: 1.49	G	·	Count	P_Value	Fold	Benjamin	1 ni FDR
	INTERPRO	Dynamin, GTPase domain	RT	:	6	1.7E-3	Change	2.1E-2	1.9E
_ 	INTERPRO	Dynamin, GTPase region, conserved site	RT		5	7.7E-3		7.7E-2	2 7.1E
	INTERPRO	Dynamin central domain	RT	-	5	7.7E-3		7.7E-2	2 7.1E
	UP_SEQ_FEATURE								2 2.1E
_	SMART	domain:GED	<u>RT</u>		5	1.1E-2		2.2E-1	1 9.9E
	INTERPRO	<u>DYNc</u>	<u>RT</u>		6	1.2E-2		1.1E-1	2 1.2E
	SMART	<u>Dynamin GTPase effector</u>	<u>RT</u>		5	1.6E-2		1.3E-1	1 2.3E
		<u>GED</u>	<u>RT</u>	i	5	3.5E-2	3.4E0	2.6E-1	1
	INTERPRO	GTPase effector domain, GED	<u>RT</u>	i	5	4.3E-2	3.4E0	3.2E-1	2.9E 1
	GOTERM_BP_DIRECT	<u>dynamin polymerization involved in</u> <u>mitochondrial fission</u>	<u>RT</u>	i	4	9.9E-2	3.4E0	6.9E-1	6.6E 1
	INTERPRO	<u>Dynamin</u>	<u>RT</u>	i	6	1.3E-1	2.2E0	6.4E-1	5.8E 1
	GOTERM_BP_DIRECT	mitochondrial fission	<u>RT</u>	i .	5	4.0E-1	1.6E0	1.0E0	9.6E 1
	GOTERM_BP_DIRECT	membrane fusion	<u>RT</u>	i	6	8.9E-1	8.1E-1	1.0E0	9.6E 1
Annota	ation Cluster 130	Enrichment Score: 1.47	G	170	Count	P_Value	Fold Change	Benjamin	ii FDR
	GOTERM_MF_DIRECT	ubiquitin-ubiquitin ligase activity	<u>RT</u>	i	7	1.3E-2	3.2E0	9.9E-2	8.9E 2
	INTERPRO	U box domain	<u>RT</u>	i	6	1.3E-2	3.7E0	1.3E-1	1.1E
	UP_SEQ_FEATURE	domain:U-box	<u>RT</u>	i	4	7.0E-2	3.9E0	9.7E-1	9.3E
	SMART	<u>Ubox</u>	<u>RT</u>	i de la companya de	5	1.1E-1	2.5E0	5.6E-1	5.1E
Annota	ation Cluster 131	Enrichment Score: 1.47	G	T.	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_MF_DIRECT	RNA polymerase II transcription factor	RT		20	1.0E-4	Onlange	1.5E-3	1.4E
	UP_SEQ_FEATURE	binding zinc finger region:GATA-type 1	<u>RT</u>	•	6	3.6E-4	6.8E0	9.9E-3	3 9.5E
_ 	UP_SEQ_FEATURE	zinc finger region:GATA-type 2	RT		6	3.6E-4		9.9E-3	3 9.5E
_ _	INTERPRO	Zinc finger, GATA-type	RT		7	2.4E-2		1.9E-1	3 1.7E
	GOTERM_BP_DIRECT	anatomical structure formation involved in							1 2.8E
	GOTERM_MF_DIRECT	morphogenesis	<u>RT</u>		6	2.6E-2		2.9E-1	1 2.0E
	SMART	enhancer sequence-specific DNA binding	<u>RT</u>	•	8	3.8E-2		2.3E-1	1 2.8E
	INTERPRO	ZnF GATA	<u>RT</u>		7	5.1E-2		3.1E-1	1 3.7E
		GATA-type transcription activator, N-terminal	<u>RT</u>	i	3	7.0E-2	6.2E0	4.1E-1	1
	GOTERM_BP_DIRECT	intestinal epithelial cell differentiation	<u>RT</u>	i	4	9.9E-2	3.4E0	6.9E-1	6.6E
	INTERPRO	Zinc finger, NHR/GATA-type	<u>RT</u>	1	13	2.2E-1	1.4E0	1.0E0	9.1E 1
	GOTERM_BP_DIRECT	tissue development	<u>RT</u>	i	4	4.8E-1	1.6E0	1.0E0	9.6E 1
	GOTERM_BP_DIRECT	<u>cell development</u>	<u>RT</u>	i .	8	5.2E-1	1.2E0	1.0E0	9.6E 1
	GOTERM_BP_DIRECT	cell fate commitment	<u>RT</u>	1	9	5.2E-1	1.2E0	1.0E0	9.6E 1
	GOTERM_BP_DIRECT	cellular response to BMP stimulus	<u>RT</u>	i	3	9.7E-1	5.9E-1	1.0E0	9.7E 1
Annota	ation Cluster 132	Enrichment Score: 1.47	G	17	Count	P_Value	Fold Change	Benjamin	ii FDR
	GOTERM_MF_DIRECT	protein kinase C activity	<u>RT</u>	i	10	2.0E-4	4.0E0	2.8E-3	2.5E 3
	INTERPRO	<u>Diacylglycerol/phorbol-ester binding</u>	<u>RT</u>	1	11	3.7E-3	2.7E0	4.1E-2	3.8E 2
	INTERPRO	Protein kinase C, delta/epsilon/eta/theta	<u>RT</u>	i	4	1.5E-2	6.2E0	1.3E-1	1.1E
	PIR_SUPERFAMILY	<u>types</u> <u>protein kinase C, delta/epsilon/eta/theta</u> types	<u>RT</u>	i .	4	2.1E-2	5.4E0	2.9E-1	2.9E
	UP_SEQ_FEATURE	types zinc finger region:Phorbol-ester/DAG-type 1	RT		8	3.3E-2		5.7E-1	5.5E
	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 2	RT	:	8	3.3E-2		5.7E-1	1 5.58
	GOTERM_MF_DIRECT			_					1 3.4
\neg		calcium-independent protein kinase C activity	<u>KT</u>	•	3	7.5E-2	6.0E0	3.9E-1	1
	INTERPRO	Protein kinase C-like, phorbol	<u>RT</u>	i .	15		1.4E0		7.6E

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

ınota	ation Cluster 1	Enrichment Score: ?	G	17	Count	P_Value	Fold Change	Benjamin	ni FC
	INTERPRO	Mitochondrial Rho-like	RT	-	5	6.3E-2	Change	4.1E-1	3.7
nota	ation Cluster 140	Enrichment Score: 1.42	G	17	Count	P_Value	Fold	Benjamin	1 ni FD
	GOTERM_BP_DIRECT	positive regulation of translational initiation	RT	i	9		Change 3.6E0	3.0E-2	2.9
' I	GOTERM_MF_DIRECT	translation activator activity	RT		5	4.9E-2		2.8E-1	2.5
1	GOTERM_BP_DIRECT	3'-UTR-mediated mRNA stabilization	RT		7	5.3E-2		4.9E-1	1 4.7
1	GOTERM_MF_DIRECT			_					1 8.9
		mRNA 3'-UTR binding	RT	i	9	5.9E-1	Fold	1.0E0	1
inota	ation Cluster 141 GOTERM_BP_DIRECT	Enrichment Score: 1.42	G	-		P_Value	Change	_	11 FL 4.8
	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process	<u>RT</u>		8	2.6E-3		5.0E-2	2
		nuclear mRNA surveillance	<u>RT</u>	•	5	5.0E-2	3.3E0	4.7E-1	1
	GOTERM_BP_DIRECT	histone mRNA catabolic process	<u>RT</u>	i	4	4.3E-1		1.0E0	9. 1
nota	ation Cluster 142	Enrichment Score: 1.42	G	-	Count	P_Value	Fold Change	Benjamin	_
	UP_SEQ_FEATURE	DNA-binding region: A.T hook 3	<u>RT</u>	1	6	9.0E-3	4.1E0	2.0E-1	1. 1
	UP_SEQ_FEATURE	DNA-binding region:A.T hook 1	<u>RT</u>	i	6	3.1E-2	3.1E0	5.4E-1	5. 1
	UP_SEQ_FEATURE	DNA-binding region:A.T hook 2	<u>RT</u>	1	6	3.1E-2	3.1E0	5.4E-1	5. 1
	INTERPRO	AT hook, DNA-binding motif	<u>RT</u>	i .	4	5.7E-2	4.1E0	4.0E-1	3. 1
١	SMART	AT hook	<u>RT</u>	1	4	1.6E-1	2.7E0	7.0E-1	6. 1
nota	ation Cluster 143	Enrichment Score: 1.4	G	To the second se	Count	P_Value	Fold Change	Benjamin	ni Fl
	INTERPRO	RNA-processing protein, HAT helix	<u>RT</u>	i	6	1.3E-2	<u> </u>	1.3E-1	1. 1
	UP_SEQ_FEATURE	repeat:HAT 4	<u>RT</u>		6	2.2E-2	3.4E0	4.0E-1	3.
	UP_SEQ_FEATURE	repeat:HAT 9	RT		4	2.5E-2		4.4E-1	1 4.
	UP_SEQ_FEATURE	repeat:HAT 1	RT	-	6	3.1E-2		5.4E-1	1 5.
	UP_SEQ_FEATURE								1 5.
	UP_SEQ_FEATURE	repeat:HAT 2	<u>RT</u>		6	3.1E-2		5.4E-1	1 5.
		repeat:HAT 3	<u>RT</u>	•	6	3.1E-2	3.1E0	5.4E-1	1
	UP_SEQ_FEATURE	repeat:HAT 8	<u>RT</u>	•	4	4.5E-2	4.5E0	7.4E-1	7.
	UP_SEQ_FEATURE	repeat:HAT 5	<u>RT</u>	1	5	6.5E-2	3.1E0	9.2E-1	8.
	UP_SEQ_FEATURE	repeat:HAT 7	<u>RT</u>	1	4	7.0E-2	3.9E0	9.7E-1	9. 1
	SMART	HAT	<u>RT</u>	1	6	7.3E-2	2.4E0	4.3E-1	3. 1
	UP_SEQ_FEATURE	repeat:HAT 6	<u>RT</u>	1	4	1.3E-1	3.0E0	1.0E0	9. 1
nota	ation Cluster 144	Enrichment Score: 1.39	G	17	Count	P_Value	Fold Change	Benjamin	ni Fl
	INTERPRO	<u>Leucine-rich repeat-containing protein 8, N-</u> terminal	<u>RT</u>	i	5	2.9E-3	6.2E0	3.3E-2	3.
	GOTERM_MF_DIRECT	volume-sensitive anion channel activity	<u>RT</u>	1	4	1.6E-2	6.0E0	1.2E-1	1.
	GOTERM_BP_DIRECT	regulation of anion transport	<u>RT</u>	4	5	7.3E-2	3.0E0	5.8E-1	5.
	GOTERM_BP_DIRECT	anion transmembrane transport	RT		5	7.7E-1	9.9E-1	1.0E0	1 9.
nota	ation Cluster 145	Enrichment Score: 1.35	G	-	<u> </u>	P_Value	Fold		1 ni F
Hoto	GOTERM_MF_DIRECT	histone serine kinase activity	RT	i	5	3.4E-3		3.2E-2	2.
	GOTERM_CC_DIRECT								2 1.
	GOTERM_CC_DIRECT	<u>chromosome passenger complex</u> <u>condensed nuclear chromosome, centromeric</u>	<u>RT</u>		4	3.0E-2		1.8E-1	1
	GOTERM_CC_DIRECT	<u>region</u>	<u>RT</u>		4	2.0E-1		7.3E-1	1
	JOILMIN_GO_DIREGI	spindle pole centrosome	<u>RT</u>	i	4	2.0E-1	Fold	7.3E-1	6. 1
nota	ation Cluster 146	Enrichment Score: 1.35	G	<u> </u>	Count	P_Value	Fold Change	Benjamin	_
	GOTERM_CC_DIRECT	ESC/E(Z) complex	<u>RT</u>	1	9	1.5E-3	3.6E0	1.4E-2	1. 2
	BIOCARTA	The PRC2 Complex Sets Long-term Gene Silencing Through Modification of Histone	<u>RT</u>	•	8	1.9E-1	1.6E0	4.1E-1	2. 1
	GOTERM_BP_DIRECT	<u>Tails</u> <u>negative regulation of gene expression,</u>	<u>RT</u>		11	3.3E-1	1 3E0	1.0E0	9.
		<u>epigenetic</u>			•		Fold	Baniamin	1
nota	ation Cluster 147 INTERPRO	Enrichment Score: 1.34	G	-		P_Value	Change	<u> </u>	ni F 1.
	INTERPRO	HRDC domain	<u>RT</u>	i	4	1.5E-2		1.3E-1	1
		HRDC-like	<u>RT</u>	•	4	3.2E-2	5.0E0	2.4E-1	2.
	UP_SEQ_FEATURE	domain:HRDC	<u>RT</u>	1	3	5.8E-2	6.8E0	8.4E-1	8. 1

Annot	ation Cluster 1	Enrichment Score: ?	G	- 10	Count	P_Value	Fold Change	Benjamini	FDR
	SMART	HRDC	<u>RT</u>	i	3	1.5E-1	4.1E0	6.9E-1	6.2E- 1
nnot	ation Cluster 148	Enrichment Score: 1.33	G	15	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_MF_DIRECT	fibroblast growth factor-activated receptor	RT	1	5	3.4E-3	•	3.2E-2	2.9E
ے ا	INTERPRO	<u>activity</u> <u>Tyrosine-protein kinase, fibroblast growth</u>	RT	_	4	1.5E-2	6 2E0	1.3E-1	2 1.1E
	PIR_SUPERFAMILY	factor receptor							1 2.9E
	_	<u>fibroblast growth factor receptor</u>	<u>RT</u>	•	4	2.1E-2	5.4E0	2.9E-1	1
	GOTERM_BP_DIRECT	positive regulation of phospholipase activity	<u>RT</u>	i	4	1.4E-1	3.0E0	8.2E-1	7.9E 1
	GOTERM_MF_DIRECT	fibroblast growth factor binding	<u>RT</u>	i	7	1.8E-1	1.8E0	7.5E-1	6.7E 1
	UP_KEYWORDS	<u>Craniosynostosis</u>	<u>RT</u>	1	5	4.0E-1	1.6E0	1.0E0	7.8E
nnot	ation Cluster 149	Enrichment Score: 1.3	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	positive regulation of guanylate cyclase activity	<u>RT</u>	i	7	4.9E-3		8.5E-2	8.1E
	GOTERM_MF_DIRECT	calcium sensitive guanylate cyclase activator	RT		4	3.6E-2	4.8E0	2.2E-1	1.9E
_ _	GOTERM_BP_DIRECT	activity phototropoduction			5				1 9.6E
		<u>phototransduction</u>	RT			6.9E-1	Fold	1.0E0	1
nnot	ation Cluster 150	Enrichment Score: 1.3	G		Count	P_Value	Change	Benjamini	
	INTERPRO	<u>Ubiquitin subgroup</u>	<u>RT</u>	i	9	2.7E-4	4.3E0	4.0E-3	3.6E
	GOTERM_BP_DIRECT	regulation of necrotic cell death	<u>RT</u>	i	8	1.4E-3	3.9E0	3.0E-2	2.9E 2
	GOTERM_BP_DIRECT	regulation of type I interferon production	<u>RT</u>	i	7	1.3E-2	3.2E0	1.8E-1	1.7E 1
	GOTERM_BP_DIRECT	MyD88-independent toll-like receptor signaling pathway	<u>RT</u>	1	7	1.3E-2	3.2E0	1.8E-1	1.7E
	INTERPRO	<u>Ubiquitin conserved site</u>	<u>RT</u>	1	6	2.1E-2	3.4E0	1.7E-1	1.6E
_ 	GOTERM_BP_DIRECT	negative regulation of epidermal growth	RT		12	3.1E-2		3.4E-1	3.3E
	GOTERM_BP_DIRECT	factor receptor signaling pathway regulation of transcription from RNA	KI	•	12	J.1L 2	2.000	5.46 1	1
		polymerase II promoter in response to hypoxia	<u>RT</u>	1	10	3.6E-2	2.1E0	3.7E-1	3.6E 1
	GOTERM_BP_DIRECT	positive regulation of epidermal growth factor receptor signaling pathway	<u>RT</u>	1	9	3.8E-2	2.2E0	3.8E-1	3.6E
٦	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Gly-Lys)	<u>RT</u>		7	3.8E-2	2 6F0	6.4E-1	6.2E
ے ا	GOTERM_BP_DIRECT	(interchain with K-? in acceptor proteins) negative regulation of type I interferon							1 4.7E
_	GOTERM_BP_DIRECT	production	<u>RT</u>	•	10	5.4E-2	2.0E0	4.9E-1	1 5.3E
		<u>viral life cycle</u>	<u>RT</u>	•	10	6.5E-2	1.9E0	5.5E-1	1
	UP_SEQ_FEATURE	chain:40S ribosomal protein S27a	<u>RT</u>	1	4	7.0E-2	3.9E0	9.7E-1	9.3E 1
	UP_SEQ_FEATURE	site:Essential for function	<u>RT</u>	i	4	7.0E-2	3.9E0	9.7E-1	9.3E 1
	UP_SEQ_FEATURE	compositionally biased region:Lys-rich (highly basic)	RT	1	4	7.0E-2	3.9E0	9.7E-1	9.3E
	UP_SEQ_FEATURE	chain:Ubiquitin	<u>RT</u>	1	4	7.0E-2	3.9E0	9.7E-1	9.3E
_ 	UP_SEQ_FEATURE	binding site:Activating enzyme	RT		4	1.0E-1	3 4F0	1.0E0	9.6E
ے ا	GOTERM_BP_DIRECT								1 7.9E
		<u>virion assembly</u>	<u>RT</u>	•	5	1.3E-1	2.5E0	8.2E-1	1
	GOTERM_BP_DIRECT	glycogen biosynthetic process	<u>RT</u>	i	8	1.4E-1	1.8E0	8.2E-1	7.9E 1
	GOTERM_BP_DIRECT	interstrand cross-link repair	<u>RT</u>	i	12	1.9E-1	1.5E0	1.0E0	9.6E 1
	GOTERM_BP_DIRECT	intracellular transport of virus	<u>RT</u>	1	11	3.6E-1	1.3E0	1.0E0	9.6E 1
	GOTERM_CC_DIRECT	endocytic vesicle membrane	<u>RT</u>	1	8	9.1E-1	7.7E-1	1.0E0	9.1E
	GOTERM_BP_DIRECT	endosomal transport	<u>RT</u>	i	5	1.0E0	4.5E-1	1.0E0	1.0E
nnot	ation Cluster 151	Enrichment Score: 1.27	G	100	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	dendritic spine development	<u>RT</u>	i	7	1.3E-2	3.2E0	1.8E-1	1.7E 1
	GOTERM_BP_DIRECT	central nervous system projection neuron axonogenesis	<u>RT</u>	i	5	3.2E-2	3.7E0	3.4E-1	3.3E
	GOTERM_MF_DIRECT	axon guidance receptor activity	<u>RT</u>	i	4	9.7E-2	3.4E0	4.7E-1	4.2E
7	GOTERM_BP_DIRECT	retinal ganglion cell axon guidance	RT		6	2.1E-1		1.0E0	9.6E
naci	ation Cluster 452	Enrichment Score: 1.26		-		1			1
mnot	ation Cluster 152 OMIM_DISEASE	Schimmelpenning-Feuerstein-Mims	G		Count	P_Value	Change	Benjamini	
		syndrome, somatic mosaic	<u>RT</u>	•	3	4.5E-2	7.8E0	1.0E0	1.0E
	UP_SEQ_FEATURE	region of interest:Hypervariable region	<u>RT</u>	i	3	5.8E-2		8.4E-1	8.1E 1
	BBID	65.Integrin affinity modulation	<u>RT</u>	i	5	6.2E-2		1.0E0	1.0E
nnot	ation Cluster 153 UP_SEQ_FEATURE	Enrichment Score: 1.26	G	- 10	Count	P_Value	Change	Benjamini	
		region of interest:I-domain	<u>RT</u>	i	4	1.1E-2	6.8E0	2.2E-1	2.1E 1
	INTERPRO	5'-3' exonuclease, C-terminal domain	<u>RT</u>	•	4	3.2E-2	5.0E0	2.4E-1	2.2E

Annot	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	Helix-hairpin-helix motif, class 2	<u>RT</u>	i	4	3.2E-2		2.4E-1	2.2E- 1
	INTERPRO	XPG/Rad2 endonuclease	<u>RT</u>	i .	4	3.2E-2	5.0E0	2.4E-1	2.2E- 1
	INTERPRO	XPG-I 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	7.4E-1	7.2E-
	INTERPRO	XPG N-terminal	<u>RT</u>	i	4	5.7E-2	4.1E0	4.0E-1	3.7E-
	SMART	<u>HhH2</u>	<u>RT</u>	i e	4	9.9E-2	3.3E0	5.3E-1	4.8E-
	SMART	<u>XPGI</u>	<u>RT</u>		4	9.9E-2	3.3E0	5.3E-1	4.8E-
	SMART	<u>XPGN</u>	<u>RT</u>		4	9.9E-2	3.3E0	5.3E-1	4.8E-
	INTERPRO	XPG conserved site	RT		3	1.2E-1		6.4E-1	1 5.8E-
	GOTERM_MF_DIRECT	nuclease activity	RT		7	1.8E-1		7.5E-1	1 6.7E-
Anno	ation Cluster 154	Enrichment Score: 1.26	G	- -	Count	P_Value	Fold	Benjamini	1 FDR
	GOTERM_BP_DIRECT	peptidyl-lysine monomethylation	RT		5	3.2E-2	Change	3.4E-1	3.3E-
	GOTERM_BP_DIRECT	peptidyl-lysine dimethylation	RT		4	3.7E-2		3.7E-1	1 3.6E-
	GOTERM_MF_DIRECT	protein-lysine N-methyltransferase activity	RT		6	1.4E-1		6.1E-1	1 5.5E-
Appe	ation Cluster 155	Enrichment Score: 1.25	G	• F78	Count	P_Value	Fold	Benjamini	1
Allilo	GOTERM_BP_DIRECT	rRNA catabolic process	RT	ī	8	6.8E-4	Change	1.7E-2	1.6E-
	INTERPRO					1.5E-2			2 1.1E-
	GOTERM_CC_DIRECT	Ribonuclease II/R, conserved site	<u>RT</u>		4			1.3E-1	1 1.1E-
	UP_KEYWORDS	nuclear exosome (RNase complex)	<u>RT</u>		6		3.0E0		1 9.2E-
	GOTERM_CC_DIRECT	<u>Exosome</u>	<u>RT</u>		6	3.0E-2		1.2E-1	2 2.0E-
	GOTERM_BP_DIRECT	cytoplasmic exosome (RNase complex)	<u>RT</u>		6	4.1E-2		2.3E-1	1 4.5E-
	INTERPRO	nuclear mRNA surveillance	<u>RT</u>		5	5.0E-2		4.7E-1	1 4.5E-
	GOTERM_CC_DIRECT	Exoribonuclease, phosphorolytic domain 1	<u>RT</u>	•	4	8.8E-2		4.9E-1	1
		exosome (RNase complex)	<u>RT</u>	i	6	9.3E-2	2.4E0	4.3E-1	3.8E- 1
	INTERPRO	Exoribonuclease, phosphorolytic domain 2	<u>RT</u>	i	4	1.2E-1	3.1E0	6.4E-1	5.8E- 1
	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5'	<u>RT</u>	i	4	1.8E-1	2.6E0	1.0E0	9.6E- 1
	GOTERM_MF_DIRECT	exoribonuclease activity	<u>RT</u>	i	5	2.0E-1	2.1E0	7.8E-1	7.0E- 1
	INTERPRO	PNPase/RNase PH domain	<u>RT</u>	i	3	2.5E-1	3.1E0	1.0E0	9.1E- 1
	GOTERM_BP_DIRECT	<u>U4 snRNA 3'-end processing</u>	<u>RT</u>	i	3	4.0E-1	2.2E0	1.0E0	9.6E- 1
Annot	ation Cluster 156	Enrichment Score: 1.25	G	™	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	<u>Heat shock factor (HSF)-type, DNA-binding</u>	<u>RT</u>	i	5	2.7E-2	3.9E0	2.2E-1	2.0E- 1
	UP_SEQ_FEATURE	region of interest:Hydrophobic repeat HR-A/B	<u>RT</u>	i	3	5.8E-2	6.8E0	8.4E-1	8.1E- 1
	UP_SEQ_FEATURE	region of interest:Hydrophobic repeat HR-C	<u>RT</u>	1	3	5.8E-2	6.8E0	8.4E-1	8.1E- 1
	SMART	HSF	<u>RT</u>	i	5	1.1E-1	2.5E0	5.6E-1	5.1E- 1
Annot	ation Cluster 157	Enrichment Score: 1.25	G	15	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	<u>Guanylate kinase, conserved site</u>	<u>RT</u>	i .	9	1.7E-3	3.5E0	2.1E-2	1.9E- 2
	GOTERM_CC_DIRECT	ionotropic glutamate receptor complex	<u>RT</u>	1	6	3.5E-3	4.8E0	3.1E-2	2.7E- 2
	GOTERM_MF_DIRECT	ionotropic glutamate receptor binding	<u>RT</u>	i .	10	4.4E-3	2.8E0	4.1E-2	3.7E- 2
	INTERPRO	Guanylate kinase	<u>RT</u>	i e	10	4.9E-3	2.8E0	5.3E-2	4.9E- 2
	UP_SEQ_FEATURE	domain:Guanylate kinase-like	<u>RT</u>	i .	10	5.0E-3	2.8E0	1.2E-1	1.1E- 1
	GOTERM_BP_DIRECT	GMP metabolic process	<u>RT</u>	i e	8	7.1E-3	3.2E0	1.2E-1	1.1E- 1
	GOTERM_MF_DIRECT	guanylate kinase activity	<u>RT</u>	1	7	8.2E-3	3.5E0	6.9E-2	6.2E- 2
	GOTERM_BP_DIRECT	establishment or maintenance of epithelial cell apical/basal polarity	<u>RT</u>	i e	7	1.3E-2	3.2E0	1.8E-1	1.7E-
	INTERPRO	PDZ-associated domain of NMDA receptors	<u>RT</u>	i	4	1.5E-2	6.2E0	1.3E-1	1.1E-
	INTERPRO	Membrane-associated guanylate kinase (MAGUK), PEST domain, N-terminal	<u>RT</u>	i	4	1.5E-2	6.2E0	1.3E-1	1.1E-
	INTERPRO	Membrane-associated guanylate kinase	<u>RT</u>		4	1.5E-2	6.2E0	1.3E-1	1.1E-
	INTERPRO	(MAGUK) scaffold protein Guanylate kinase/L-type calcium channel	RT		10		2.4E0		1 1.3E-
									1

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

nnota	ation Cluster 1	Enrichment Score: ?	G	<u>■</u>	Count	P_Value	Fold Change	Benjamir	ni FD
)	KEGG_PATHWAY	<u>Apoptosis</u>	<u>RT</u>	i	28	9.7E-6	2.3E0	2.7E-5	1.2
)	GOTERM_BP_DIRECT	activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c	<u>RT</u>	i	6	9.4E-3	3.9E0	1.4E-1	1.3
	GOTERM_BP_DIRECT	glial cell apoptotic process	<u>RT</u>	1	4	3.7E-2	4.7E0	3.7E-1	3.6
	BIOCARTA	HIV-I Nef	<u>RT</u>		28	3.8E-2	1.4E0	1.2E-1	8.8
]	BIOCARTA	Role of Mitochondria in Apoptotic Signaling	<u>RT</u>		12	7.0E-2	1.7E0	2.0E-1	1.4
ر ا	BIOCARTA	D4-GDI Signaling Pathway	RT		8	9.5E-2	1 9F0	2.5E-1	1 1.8
)]	BIOCARTA	Induction of apoptosis through DR3 and	RT	1	15	1.6E-1		3.6E-1	1 2.6
)	BBID	DR4/5 Death Receptors 86.Apoptosis Nematode& Vert	RT		6	2.0E-1		1.0E0	1
)	BIOCARTA	Caspase Cascade in Apoptosis	<u>RT</u>	•	10	3.8E-1	1.3E0	7.0E-1	4. 1
)	BBID	127.Mito-stress	<u>RT</u>	1	4	3.8E-1	1.8E0	1.0E0	1.
)	BIOCARTA	Stress Induction of HSP Regulation	<u>RT</u>	i	6	6.4E-1	1.1E0	9.6E-1	6. 1
	BBID	46.P13K PTEN	<u>RT</u>	i	4		9.0E-1 Fold		1.
inota	ation Cluster 163	Enrichment Score: 1.22	G		Count	P_Value	Change	Benjamir	
	BIOCARTA	Signaling of Hepatocyte Growth Factor Receptor	<u>RT</u>	•	21	3.7E-3	1.8E0	2.3E-2	1. 2
	BIOCARTA	Role of MAL in Rho-Mediated Activation of SRF	<u>RT</u>	i	13	6.1E-3	2.1E0	3.3E-2	2. 2
	GOTERM_BP_DIRECT	Bergmann glial cell differentiation	<u>RT</u>	1	6	9.4E-3	3.9E0	1.4E-1	1. 1
	GOTERM_BP_DIRECT	regulation of Golgi inheritance	<u>RT</u>	1	4	1.7E-2	5.9E0	2.1E-1	2.
	BIOCARTA	Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway	<u>RT</u>		9	3.1E-2	2.1E0	1.1E-1	7
	GOTERM_BP_DIRECT	regulation of early endosome to late	<u>RT</u>		5	3.2E-2	3.7E0	3.4E-1	3
	BIOCARTA	endosome transport Sprouty regulation of tyrosine kinase signals	RT		11	3 8F-2	1.9E0	1.2E-1	1 8
	GOTERM_BP_DIRECT			•					2 5
	BIOCARTA	trachea formation Roles of ?-arrestin-dependent Recruitment of	<u>RT</u>		4		3.9E0	5.5E-1	1 1
		Src Kinases in GPCR Signaling	<u>RT</u>	•	11	8.2E-2	1.7E0	2.2E-1	1
	BIOCARTA	Aspirin Blocks Signaling Pathway Involved in Platelet Activation	<u>RT</u>	•	11	1.1E-1	1.6E0	2.9E-1	2 1
	GOTERM_BP_DIRECT	thyroid gland development	<u>RT</u>	i	8	1.2E-1	1.9E0	7.7E-1	7 1
	BIOCARTA	Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia	<u>RT</u>	1	12	1.3E-1	1.5E0	3.1E-1	2 1
	GOTERM_BP_DIRECT	regulation of stress-activated MAPK cascade	<u>RT</u>	1	4	1.4E-1	3.0E0	8.2E-1	7 1
	BIOCARTA	Regulation of Splicing through Sam68	<u>RT</u>	1	5	1.6E-1	2.2E0	3.7E-1	2
	GOTERM_BP_DIRECT	ERK1 and ERK2 cascade	<u>RT</u>	1	6	3.8E-1	1.5E0	1.0E0	9
	BIOCARTA	Pelp1 Modulation of Estrogen Receptor	<u>RT</u>		4	4.2E-1	1.7E0	7.3E-1	5
	BIOCARTA	Activity Role of ?-arrestins in the activation and	RT	-	7			7.3E-1	1 5
		targeting of MAP kinases				1			1
10ta	ation Cluster 164 UP_KEYWORDS	Enrichment Score: 1.21	G	-	Count	P_Value	Change	-	11 F 9
		<u>Xeroderma pigmentosum</u>	<u>RT</u>	•	5	3.1E-2	3.8E0	1.2E-1	2
	UP_KEYWORDS	<u>Cockayne syndrome</u>	<u>RT</u>	•	4	4.4E-2	4.6E0	1.6E-1	1
	GOTERM_CC_DIRECT	holo TFIIH complex	<u>RT</u>	i	5	8.0E-2	2.9E0	3.9E-1	3 1
	GOTERM_BP_DIRECT	UV protection	<u>RT</u>	1	5	1.3E-1	2.5E0	8.2E-1	7 1
ıota	ation Cluster 165	Enrichment Score: 1.2	G	<u>■</u> 8	Count	P_Value	Fold Change	Benjamir	ni F
	GOTERM_BP_DIRECT	positive regulation of chemokine production	<u>RT</u>	1	9	3.8E-3	3.1E0	6.9E-2	6
	GOTERM_BP_DIRECT	positive regulation of interferon-beta production	<u>RT</u>	i de	10	2.8E-2	2.2E0	3.2E-1	3
	GOTERM_BP_DIRECT	' 	<u>RT</u>		13	6.6E-2	1.7E0	5.6E-1	5
	GOTERM_BP_DIRECT	positive regulation of interleukin-12	RT		8	1.2E-1		7.7E-1	7
	GOTERM_BP_DIRECT	<u>production</u> positive regulation of tumor necrosis factor	RT		12	1.6E-1		9.1E-1	1 8
	GOTERM_BP_DIRECT	production							1
		cellular response to lipoteichoic acid	<u>RT</u>	i	3	4.6E-1	Fold	1.0E0	1
nota	ation Cluster 166	Enrichment Score: 1.2	G	· ·	Count	P_Value	Change	Benjamir	
	UP_SEQ_FEATURE	region of interest:Rho-like	<u>RT</u>	1	3	5.8E-2	6.8E0	8.4E-1	8
	UP_SEQ_FEATURE	domain:BTB 1	<u>RT</u>	•	5	6.5E-2	3.1E0	9.2E-1	8
	UP_SEQ_FEATURE	domain:BTB 2	<u>RT</u>	i .	5	6.5E-2	3.1E0	9.2E-1	8 1
				™		P_Value	Fold		ni F

Annot	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamini	FDR
	BIOCARTA	Regulation of cell cycle progression by Plk3	<u>RT</u>	i	7	1.8E-2		7.0E-2	5.0E- 2
	GOTERM_BP_DIRECT	replicative senescence	<u>RT</u>	i	6	3.8E-2	3.0E0	3.8E-1	3.6E-
	GOTERM_BP_DIRECT	DNA damage checkpoint	<u>RT</u>	i e	10	5.4E-2	2.0E0	4.9E-1	4.7E-
	BIOCARTA	Role of BRCA1, BRCA2 and ATR in Cancer Susceptibility	<u>RT</u>		9	4.4E-1	1.2E0	7.3E-1	5.2E-
Annot	ation Cluster 168	Enrichment Score: 1.18	G	T.	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:WW 4	<u>RT</u>	i	5	2.0E-3	•	5.0E-2	4.8E- 2
	UP_SEQ_FEATURE	domain:WW 3	<u>RT</u>	i	6	2.6E-3	5.1E0	6.2E-2	6.0E- 2
	INTERPRO	WW domain	<u>RT</u>	i e	16	1.8E-2	1.9E0	1.5E-1	1.3E-
	UP_SEQ_FEATURE	domain:WW 1	<u>RT</u>	i de la companya de	10	1.9E-2	2.3E0	3.7E-1	3.5E- 1
	UP_SEQ_FEATURE	domain:WW 2	<u>RT</u>		10	1.9E-2	2.3E0	3.7E-1	3.5E-
	GOTERM_BP_DIRECT	regulation of potassium ion transmembrane	<u>RT</u>	1	4	6.4E-2	3.9E0	5.5E-1	1 5.2E-
	SMART	transporter activity WW	RT		16	2.1E-1	1.3E0	8.6E-1	1 7.8E-
	UP_SEQ_FEATURE	domain:WW	RT		6	2.1E-1		1.0E0	1 9.6E-
	GOTERM_BP_DIRECT	regulation of membrane potential	RT		8		6.3E-1		1 9.8E-
	SMART	<u>C2</u>	RT	1	18	1.0E0	5.8E-1		1 1.0E0
	GOTERM_BP_DIRECT	regulation of ion transmembrane transport	<u>RT</u>	i	3	1.0E0	1.6E-1 Fold	1	1.0E0
Annot	ation Cluster 169 GOTERM_BP_DIRECT	Enrichment Score: 1.17	G	-	Count	P_Value	Change	Benjamini	FDR 2.0E-
	GOTERM_MF_DIRECT	histone H3-K27 methylation histone methyltransferase activity (H3-K27	<u>RT</u>		4	1.7E-2	5.9E0	2.1E-1	1 3.4E-
	GOTERM_BP_DIRECT	specific)	<u>RT</u>		3	7.5E-2		3.9E-1	1 7.4E-
	GOTERM_MF_DIRECT	DNA methylation	<u>RT</u>		8	1.2E-1	1.9E0	7.7E-1	1
	GOTERIM_WIF_DIRECT	protein-lysine N-methyltransferase activity	<u>RT</u>	i	6	1.4E-1	Fold	6.1E-1	5.5E- 1
Annot	INTERPRO	Enrichment Score: 1.16	G	-	Count	P_Value	Change	Benjamini	FDR 1.1E-
	GOTERM_MF_DIRECT	UBA/THIF-type NAD/FAD binding fold	<u>RT</u>		6	1.3E-2		1.3E-1	1.1L- 1 1.9E-
	INTERPRO	ubiquitin activating enzyme activity	<u>RT</u>	1	4	3.6E-2	4.8E0	2.2E-1	1
	INTERPRO	<u>Ubiquitin-activating enzyme e1, C-terminal</u>	<u>RT</u>	i	3	7.0E-2	6.2E0	4.1E-1	3.7E- 1
		<u>Ubiquitin-activating enzyme, E1</u>	<u>RT</u>	i	3	7.0E-2	6.2E0	4.1E-1	3.7E- 1
	GOTERM_MF_DIRECT	small protein activating enzyme activity	<u>RT</u>	i	4	9.7E-2	3.4E0	4.7E-1	4.2E- 1
	INTERPRO	<u>Ubiquitin-activating enzyme</u>	<u>RT</u>	i .	3	1.2E-1	4.6E0	6.4E-1	5.8E- 1
	INTERPRO	<u>Ubiquitin/SUMO-activating enzyme E1</u>	<u>RT</u>	i	3	1.2E-1	4.6E0	6.4E-1	5.8E- 1
	SMART	SM00985	<u>RT</u>	i	3	1.5E-1	9	6.9E-1	6.2E- 1
Annot	ation Cluster 171	Enrichment Score: 1.16	G	To the second se	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	4.1E-1	3.7E- 1
	INTERPRO	Ribosomal protein L1, 3-layer alpha/beta- sandwich	<u>RT</u>	i	3	7.0E-2	6.2E0	4.1E-1	3.7E- 1
	INTERPRO	Ribosomal protein L1, superfamily	<u>RT</u>	i	3	7.0E-2		4.1E-1	3.7E- 1
Annot	ration Cluster 172	Enrichment Score: 1.16	G	-	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	Pseudouridine synthase, RsuA/RluB/C/D/E/F	<u>RT</u>	1	4	1.5E-2	6.2E0	1.3E-1	1.1E- 1
	INTERPRO	Pseudouridine synthase, catalytic domain	<u>RT</u>	i	6	4.5E-2	2.9E0	3.3E-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	3.9E0	5.5E-1	5.2E- 1
	GOTERM_MF_DIRECT	deaminase activity	<u>RT</u>	i	4	1.4E-1	3.0E0	5.9E-1	5.3E- 1
	GOTERM_BP_DIRECT	<u>pseudouridine synthesis</u>	<u>RT</u>	i	4	3.8E-1		1.0E0	9.6E- 1
Annot	ation Cluster 173	Enrichment Score: 1.15	G	100	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	RNA polymerase Rpb2, domain 3	<u>RT</u>	i	3	7.0E-2	6.2E0	4.1E-1	3.7E- 1
	INTERPRO	DNA-directed RNA polymerase, subunit 2	<u>RT</u>	i	3	7.0E-2	6.2E0	4.1E-1	3.7E- 1
	INTERPRO	<u>DNA-directed RNA polymerase, subunit 2, domain 6</u>	<u>RT</u>	i	3	7.0E-2	6.2E0	4.1E-1	3.7E- 1
	INTERPRO	RNA polymerase, beta subunit, conserved site	<u>RT</u>	1	3	7.0E-2	6.2E0	4.1E-1	3.7E- 1
	INTERPRO	RNA polymerase Rpb2, OB-fold	<u>RT</u>	i	3	7.0E-2	6.2E0	4.1E-1	3.7E- 1

Annot	ation Cluster 1	Enrichment Score: ?	G	178	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	RNA polymerase Rpb2, domain 7	RT	1	3	7.0E-2	Change	4.1E-1	3.7E-
	INTERPRO	RNA polymerase Rpb2, domain 2	RT		3	7.0E-2		4.1E-1	1 3.7E-
	INTERPRO	RNA polymerase, beta subunit, protrusion	RT		3	7.0E-2		4.1E-1	1 3.7E-
	GOTERM_MF_DIRECT								1 3.4E-
		ribonucleoside binding	RT	1	3	7.5E-2	Fold	3.9E-1	1
Annot	up_SEQ_FEATURE	Enrichment Score: 1.14	G	-	Count	P_Value	Change	Benjamini	FDR 6.0E-
	INTERPRO	zinc finger region:C2HC-type	<u>RT</u>		6	2.6E-3		6.2E-2	2 3.1E-
		MOZ/SAS-like protein	<u>RT</u>	1	5	2.9E-3	6.2E0	3.3E-2	2
	GOTERM_BP_DIRECT	histone acetylation	<u>RT</u>	•	11	4.9E-2	1.9E0	4.7E-1	4.5E- 1
	GOTERM_MF_DIRECT	histone acetyltransferase activity	<u>RT</u>	1	13	9.5E-2	1.6E0	4.7E-1	4.2E- 1
	GOTERM_MF_DIRECT	acetyltransferase activity	<u>RT</u>	i	4	3.8E-1	1.8E0	1.0E0	8.9E- 1
	INTERPRO	Acyl-CoA N-acyltransferase	<u>RT</u>	i	7	7.7E-1	9.4E-1	1.0E0	9.1E- 1
	UP_KEYWORDS	<u>Acyltransferase</u>	<u>RT</u>	i e	12	1.0E0	4.8E-1 Fold	1	1.0E0
Anno	ation Cluster 175 GOTERM_BP_DIRECT	Enrichment Score: 1.13 extrinsic apoptotic signaling pathway in	G	-	Count	P_Value	Change	Benjamini	1.7E-
	GOTERM_MF_DIRECT	absence of ligand	<u>RT</u>	•	15	7.0E-4	2.6E0	1.7E-2	2
		BH3 domain binding	<u>RT</u>	i	4	1.6E-2	6.0E0	1.2E-1	1.0E- 1
	INTERPRO	Apoptosis regulator, Bcl-2, BH1 motif, conserved site	<u>RT</u>	i	5	2.7E-2	3.9E0	2.2E-1	2.0E- 1
	INTERPRO	<u>Apoptosis regulator, Bcl-2, BH2 motif,</u> <u>conserved site</u>	<u>RT</u>	1	5	2.7E-2	3.9E0	2.2E-1	2.0E- 1
	INTERPRO	<u>Apoptosis regulator, Bcl-2, BH3 motif,</u> <u>conserved site</u>	<u>RT</u>	i	5	2.7E-2	3.9E0	2.2E-1	2.0E- 1
	GOTERM_BP_DIRECT	regulation of protein heterodimerization activity	<u>RT</u>	i	5	3.2E-2	3.7E0	3.4E-1	3.3E- 1
	GOTERM_BP_DIRECT	regulation of mitochondrial membrane potential	<u>RT</u>	1	10	3.6E-2	2.1E0	3.7E-1	3.6E- 1
	GOTERM_BP_DIRECT	negative regulation of anoikis	<u>RT</u>	i	7	5.3E-2	2.4E0	4.9E-1	4.7E- 1
	UP_SEQ_FEATURE	short sequence motif:BH1	<u>RT</u>	i .	5	6.5E-2	3.1E0	9.2E-1	8.9E- 1
	GOTERM_CC_DIRECT	Bcl-2 family protein complex	<u>RT</u>	i .	3	6.6E-2	6.4E0	3.3E-1	2.9E-
	GOTERM_BP_DIRECT	regulation of mitochondrial membrane permeability	<u>RT</u>	i e	5	7.3E-2	3.0E0	5.8E-1	5.5E-
	GOTERM_BP_DIRECT	release of cytochrome c from mitochondria	<u>RT</u>		8	7.9E-2	2.1E0	6.0E-1	5.7E-
	INTERPRO	Blc2 family	RT		5	8.7E-2		4.9E-1	1 4.5E-
	INTERPRO	Bcl2-like	RT	-	5	8.7E-2		4.9E-1	1 4.5E-
	UP_SEQ_FEATURE								1 9.6E-
	UP_SEQ_FEATURE	short sequence motif:BH2	<u>RT</u>		5	1.1E-1		1.0E0	1 9.6E-
	GOTERM_BP_DIRECT	short sequence motif:BH3 endoplasmic reticulum calcium ion	<u>RT</u>	1	5	2.3E-1		1.0E0	1 9.6E-
	GOTERM_BP_DIRECT	homeostasis	<u>RT</u>	•	5	2.4E-1	2.0E0	1.0E0	1
		positive regulation of intrinsic apoptotic signaling pathway	<u>RT</u>	i	8	3.2E-1	1.4E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	regulation of protein homodimerization activity	<u>RT</u>	1	3	3.4E-1		1.0E0	9.6E- 1
	BBID BBID	127.Mito-stress 152.altered synaptic signalling-	RT RT	1	4	3.8E-1 3.8E-1		1.0E0 1.0E0	1.0E0 1.0E0
	GOTERM_CC_DIRECT	neurodegenerative disorders							8.8E-
<u> </u>	antian Observanta	pore complex	<u>RT</u>	1	3	4.3E-1	Fold	1.0E0	1
Anno	ation Cluster 176 GOTERM_CC_DIRECT	Enrichment Score: 1.13 eukaryotic translation initiation factor 4F	G	-	Count	P_Value	Change	Benjamini	2.0E-
	BIOCARTA	complex	<u>RT</u>	-	5	4.0E-2		2.3E-1	1 9.7E-
	GOTERM_BP_DIRECT	Eukaryotic protein translation nuclear-transcribed mRNA poly(A) tail	<u>RT</u>	•	10	4.4E-2		1.4E-1	2
		shortening	<u>RT</u>	i	9	1.0E-1		7.1E-1	6.8E- 1
	BIOCARTA	Internal Ribosome entry pathway	<u>RT</u>	i	5	1.6E-1		3.7E-1	2.6E- 1
Annot	ation Cluster 177	Enrichment Score: 1.13	G	· ·	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	domain:IQ 5	<u>RT</u>	i	6	1.4E-2	3.7E0	2.7E-1	2.6E- 1
	INTERPRO	<u>Dilute</u>	<u>RT</u>	i	4	8.8E-2	3.5E0	4.9E-1	4.5E- 1
	UP_SEQ_FEATURE	domain:Dilute	<u>RT</u>	i .	4	1.0E-1	3.4E0	1.0E0	9.6E- 1
	SMART	SM01132	<u>RT</u>	i	4	2.4E-1	2.3E0	9.5E-1	8.6E- 1
Annot	ation Cluster 178	Enrichment Score: 1.12	G	170	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	region of interest:Bridging helix	<u>RT</u>	i	3	5.8E-2	·	8.4E-1	8.1E- 1

Annot	ation Cluster 1	Enrichment Score: ?	G	·	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	RNA polymerase Rpb1, domain 1	<u>RT</u>	i	3	7.0E-2	<u> </u>	4.1E-1	3.7E-
	INTERPRO	RNA polymerase Rpb1, domain 5	<u>RT</u>	i	3	7.0E-2	6.2E0	4.1E-1	3.7E-
	INTERPRO	RNA polymerase Rpb1, domain 4	<u>RT</u>	1	3	7.0E-2	6.2E0	4.1E-1	3.7E-
	INTERPRO	RNA polymerase, N-terminal	RT		3	7.0E-2	6.2E0	4.1E-1	1 3.7E-
	INTERPRO	RNA polymerase, alpha subunit	RT		3	7.0E-2		4.1E-1	1 3.7E-
	INTERPRO	RNA polymerase Rpb1, domain 3	RT		3	7.0E-2		4.1E-1	1 3.7E-
	SMART								1 6.2E-
Anna	totion Charton 470	RPOLA N	RT	1	3	1.5E-1	Fold	6.9E-1	1
Anno	INTERPRO	Proprotein convertase, P	G RT		Count 6	P_Value 1.7E-3	Change	Benjamini 2.1E-2	1.9E-
	INTERPRO								2 7.1E-
	INTERPRO	Peptidase S8, subtilisin, Asp-active site	<u>RT</u>		5	7.7E-3		7.7E-2	2 7.1E-
	INTERPRO	Peptidase S8, subtilisin, Ser-active site	<u>RT</u>	1	6	7.7E-3		7.7E-2	7.1E-
	INTERPRO	Peptidase S8, subtilisin, His-active site	<u>RT</u>	•	6	7.7E-3	4.1E0	7.7E-2	2
		Peptidase S8, subtilisin-related	<u>RT</u>	i	6	1.3E-2	3.7E0	1.3E-1	1.1E- 1
	INTERPRO	Peptidase S8/S53 domain	<u>RT</u>	i	6	2.1E-2	3.4E0	1.7E-1	1.6E- 1
	GOTERM_BP_DIRECT	peptide biosynthetic process	<u>RT</u>	i	4	3.7E-2	4.7E0	3.7E-1	3.6E- 1
	INTERPRO	<u>Proteinase inhibitor, propeptide</u>	<u>RT</u>	i	6	1.3E-1	2.2E0	6.4E-1	5.8E- 1
	GOTERM_BP_DIRECT	peptide hormone processing	<u>RT</u>	i .	5	2.8E-1	1.9E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	protein processing	<u>RT</u>	i	11	8.0E-1	9.0E-1	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	signal peptide processing	<u>RT</u>	i .	4	8.2E-1	9.5E-1	1.0E0	9.6E-
	UP_KEYWORDS	Serine protease	<u>RT</u>	<u> </u>	8	1.0E0	3.9E-1		1.0E0
	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		1.0E0 1.0E0
Annot	tation Cluster 180	Enrichment Score: 1.11	G	-	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_MF_DIRECT	MAP kinase kinase activity	<u>RT</u>	i	7	8.2E-3	3.5E0	6.9E-2	6.2E- 2
	UP_SEQ_FEATURE	site:Cleavage; by anthrax lethal factor	<u>RT</u>	i .	3	2.2E-1	3.4E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	proteolysis in other organism	<u>RT</u>	i	3	2.7E-1	3.0E0	1.0E0	9.6E-
Annot	tation Cluster 181	Enrichment Score: 1.1	G	To the second se	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	zinc finger region:TFIIB-type	<u>RT</u>	i	3	5.8E-2		8.4E-1	8.1E- 1
	INTERPRO	Transcription factor TFIIB	<u>RT</u>	i .	3	7.0E-2	6.2E0	4.1E-1	3.7E-
	INTERPRO	Zinc finger, TFIIB-type	<u>RT</u>		3	1.2E-1	4.6E0	6.4E-1	5.8E-
Annot	tation Cluster 182	Enrichment Score: 1.07	G	- 	Count	P_Value	Fold	Benjamini	1 FDR
	GOTERM_BP_DIRECT	rRNA methylation	RT		7	2.9E-2	Change	3.2E-1	3.1E-
	INTERPRO	Ribosomal RNA adenine methylase	RT		3	7.0E-2		4.1E-1	1 3.7E-
	INTERPRO	transferase Ribosomal RNA adenine methylase			3	7.0E-2		4.1E-1	1 3.7E-
	SMART	transferase, N-terminal	<u>RT</u>						1 6.2E-
	GOTERM_MF_DIRECT	rADc rRNA (adenine-N6,N6-)-dimethyltransferase	<u>RT</u>		3	1.5E-1		6.9E-1	1 7.0E-
		<u>activity</u>	RT	1	3	2.0E-1	Fold	7.8E-1	1
Annot	ation Cluster 183	Enrichment Score: 1.07 Ubiquitin-associated/translation elongation	G	-	Count	P_Value	Change	:	FDR 7.1E-
		factor EF1B, N-terminal, eukaryote	<u>RT</u>	i	15		2.1E0		2
	UP_SEQ_FEATURE	domain:UBA	<u>RT</u>	•	13	1.0E-2	2.2E0	2.2E-1	2.1E- 1
	GOTERM_BP_DIRECT	regulation of proteasomal ubiquitin- dependent protein catabolic process	<u>RT</u>	i	6	3.8E-2	3.0E0	3.8E-1	3.6E- 1
	INTERPRO	<u>Ubiquilin</u>	<u>RT</u>	i	4	5.7E-2	4.1E0	4.0E-1	3.7E- 1
	INTERPRO	Heat shock chaperonin-binding	<u>RT</u>	1	5	6.3E-2	3.1E0	4.1E-1	3.7E- 1
	GOTERM_MF_DIRECT	polyubiquitin binding	<u>RT</u>	i .	8	7.7E-2	2.1E0	3.9E-1	3.5E- 1
	SMART	STI1	<u>RT</u>	i .	5	2.1E-1	2.0E0	8.9E-1	8.1E- 1
	SMART	<u>UBA</u>	<u>RT</u>	i	10	2.7E-1	1.4E0	1.0E0	9.1E- 1
	INTERPRO	<u>UBA-like</u>	<u>RT</u>	i e	11	4.9E-1	1.2E0	1.0E0	9.1E- 1
	GOTERM_CC_DIRECT	<u>autophagosome</u>	RT		7		6.9E-1		9.5E-
									1

nota	ation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Citaliye	Benjamini	i FD
nota	ation Cluster 184	Enrichment Score: 1.06	G	13	Count	P_Value	Fold Change	Benjamini	i FD
	GOTERM_CC_DIRECT	<u>actomyosin</u>	<u>RT</u>	i	7	5.9E-3	3.7E0	4.8E-2	4.2 2
	GOTERM_CC_DIRECT	myosin II filament	<u>RT</u>	1	3	6.6E-2	6.4E0	3.3E-1	2.9
	GOTERM_CC_DIRECT	myosin II complex	<u>RT</u>		4	8.3E-2	3.6E0	4.0E-1	3.
	GOTERM_BP_DIRECT				7	3.0E-1	1 550	1.0E0	1 9.
	UP_KEYWORDS	actomyosin structure organization	<u>RT</u>						1 7.
	- CI_KETWOKBO	<u>Cell shape</u>	<u>RT</u>	i	5	5.0E-1		1.0E0	1
nota	ation Cluster 185	Enrichment Score: 1.06	G		Count	P_Value	Fold Change	Benjamini	4
	GOTERM_BP_DIRECT	histone H2A monoubiquitination	<u>RT</u>	i	6	3.8E-2	3.0E0	3.8E-1	3. 1
	GOTERM_BP_DIRECT	UV-damage excision repair	<u>RT</u>	i	5	9.9E-2	2.7E0	6.9E-1	6. 1
	GOTERM_CC_DIRECT	Cul4B-RING E3 ubiquitin ligase complex	<u>RT</u>	1	3	1.8E-1	3.8E0	6.7E-1	5.
nota	ation Cluster 186	Enrichment Score: 1.05	G	178	Count	P_Value	Fold Change	Benjamini	i FI
	GOTERM_BP_DIRECT	activation of JNKK activity	RT	1	4	6.4E-2	Change	5.5E-1	5.
	INTERPRO	Mitogen-activated protein (MAP) kinase		_					1 3.
	GOTERM_MF_DIRECT	kinase kinase, 9/10/11	<u>RT</u>		3	7.0E-2		4.1E-1	1
		JUN kinase kinase kinase activity	<u>RT</u>	i	3	7.5E-2	6.0E0	3.9E-1	3.
	PIR_SUPERFAMILY	<u>mitogen-activated protein kinase kinase</u> <u>kinase, types 9/10/11</u>	<u>RT</u>	i	3	8.8E-2	5.4E0	6.9E-1	6. 1
	UP_SEQ_FEATURE	domain:Leucine-zipper 1	<u>RT</u>	i	4	1.3E-1	3.0E0	1.0E0	9.
	UP_SEQ_FEATURE	domain:Leucine-zipper 2	<u>RT</u>	i	4	1.3E-1	3.0E0	1.0E0	9.
nota	ation Cluster 187	Enrichment Score: 1.03	G	17 8	Count	P_Value	Fold	Benjamini	Ŧ
	GOTERM_BP_DIRECT	regulation of interferon-gamma-mediated	RT	-	9	3.8E-4	Onlange	1.0E-2	9
	GOTERM_BP_DIRECT	signaling pathway JAK-STAT cascade involved in growth		•					3 2.
		hormone signaling pathway	<u>RT</u>	•	9	1.4E-3	3.6E0	3.0E-2	2
	BIOCARTA	Stat3 Signaling Pathway	<u>RT</u>	•	8	2.3E-3	3.0E0	1.7E-2	1. 2
	UP_SEQ_FEATURE	domain:SH2; atypical	<u>RT</u>	1	5	5.4E-3	5.7E0	1.2E-1	1.
	INTERPRO	<u>Tyrosine-protein kinase, non-receptor</u> <u>Jak/Tyk2</u>	<u>RT</u>	1	4	1.5E-2	6.2E0	1.3E-1	1.
	PIR_SUPERFAMILY	tyrosine-protein kinase, Jak/Tyk2 type	<u>RT</u>	4	4	2.1E-2	5.4E0	2.9E-1	2.
	BIOCARTA	IL22 Soluble Receptor Signaling Pathway	RT		9	3.1E-2	2 1F0	1.1E-1	1 7.
	INTERPRO			_					2 2.
		MyTH4 domain	<u>RT</u>	•	5	4.3E-2	3.4E0	3.2E-1	1
	UP_SEQ_FEATURE	domain:MyTH4 1	<u>RT</u>	1	3	5.8E-2	6.8E0	8.4E-1	8. 1
	UP_SEQ_FEATURE	domain:MyTH4 2	<u>RT</u>	1	3	5.8E-2	6.8E0	8.4E-1	8. 1
	BBID	48.mice minus JAKs and STATs	<u>RT</u>	•	8	6.1E-2		1.0E0	1.
	BBID SMART	75.Stats activators of Apoptosis	<u>RT</u>		4 5	1.4E-1 1.6E-1		1.0E0 7.0E-1	1. 6.
	GOTERM_MF_DIRECT	MyTH4	<u>RT</u>						1 7.
		growth hormone receptor binding	<u>RT</u>	i	3	2.0E-1	3.6E0	7.8E-1	1
	BIOCARTA	IL-10 Anti-inflammatory Signaling Pathway	<u>RT</u>	1	7	2.3E-1	1.6E0	4.7E-1	3. 1
	BIOCARTA	IFN gamma signaling pathway	<u>RT</u>	i	4	3.1E-1	2.0E0	5.9E-1	4.
	GOTERM_MF_DIRECT	CCR5 chemokine receptor binding	<u>RT</u>	1	3	4.0E-1	2.2E0	1.0E0	8.
	INTERPRO	FERM domain	<u>RT</u>		10	4.4E-1	1.2E0	1.0E0	9.
	INTERPRO	Band 4.1 domain	RT	_	10	4.4E-1		1.0E0	1 9
	BBID	12.IL-6 type cytok-signal-transduct	RT	1	8	5.1E-1		1.0E0	1 1.
	INTERPRO	FERM central domain	RT		9	5.9E-1		1.0E0	9.
	BBID	11.IL-6 gp130-Jak-STAT	RT		3	6.0E-1		1.0E0	1
	UP_SEQ_FEATURE	domain:FERM	RT	i	7		9.7E-1		9.
	BIOCARTA	<u>IFN alpha signaling pathway</u>	<u>RT</u>		3	8.5E-1	1.0E0	1.0E0	8.
	SMART								1 9.
		B41 EEDM/acyl CoA binding protein 3 bolical	<u>RT</u>	i	10		8.0E-1		1
	INTERPRO	FERM/acyl-CoA-binding protein, 3-helical bundle	<u>RT</u>	i	5	9.7E-1	6.2E-1	1.0E0	9
ıota	ntion Cluster 188	Enrichment Score: 1.03	G	13	Count	P_Value	Fold Change	Benjamini	F
	KEGG_PATHWAY	Non-homologous end-joining	<u>RT</u>	i	7	2.5E-2	2.8E0	4.6E-2	2. 2
	GOTERM_CC_DIRECT	nonhomologous end joining complex	<u>RT</u>	i	4	1.2E-1	3.2E0	4.9E-1	4. 1
	GOTERM_BP_DIRECT								7.

				-			Fold		
	ation Cluster 1 GOTERM_BP_DIRECT	Enrichment Score: ?	G	-	Count	P_Value	Change	•	9.6E
		regulation of smooth muscle cell proliferation	<u>RT</u>		4	1.8E-1	Fold	1.0E0	1
	ation Cluster 189	Enrichment Score: 1.03	G	N .	Count	P_Value	Fold Change	Benjamin	
	UP_KEYWORDS	Elongation factor	<u>RT</u>	i	10	2.3E-2	2.3E0	9.3E-2	7.2E 2
	GOTERM_BP_DIRECT	translational elongation	<u>RT</u>	i	6	1.7E-1	2.0E0	9.8E-1	9.4E 1
	GOTERM_MF_DIRECT	translation elongation factor activity	<u>RT</u>	i	9	2.0E-1	1.6E0	7.9E-1	7.0E 1
Annota	ation Cluster 190	Enrichment Score: 1.01	G	™	Count	P_Value	Fold Change	Benjamin	i FDR
	UP_KEYWORDS	Innate immunity	<u>RT</u>	i .	53	1.1E-2	1.4E0	4.6E-2	3.6E 2
	GOTERM_BP_DIRECT	innate immune response	<u>RT</u>	■	82	1.5E-1	1.1E0	8.8E-1	8.4E 1
	UP_KEYWORDS	<u>Immunity</u>	<u>RT</u>	•	73	5.6E-1	1.0E0	1.0E0	7.8E
Annota	ntion Cluster 191	Enrichment Score: 1.01	G	N.	Count	P_Value	Fold Change	Benjamin	Ť
	BIOCARTA	E2F1 Destruction Pathway	<u>RT</u>	i	7	7.1E-2	•	2.0E-1	1.4E
	BIOCARTA	Regulation of p27 Phosphorylation during Cell	RT		8	9.5E-2	1.9E0	2.5E-1	1 1.8E
_ _	BIOCARTA	Cycle Progression Cyclin E Destruction Pathway	RT		6	1.4E-1		3.3E-1	1 2.4E
	otion Christian 402					1	Fold		1
	ution Cluster 192 UP_SEQ_FEATURE	Enrichment Score: 1	G		Count	P_Value	Change	=	2.5E
	INTERPRO	domain:C2	<u>RT</u>	•	21	1.4E-2		2.6E-1	1 4.0E
_	SMART	C2 calcium-dependent membrane targeting	<u>RT</u>	•	35	7.5E-2		4.3E-1	1
	ation Cluster 193	C2 Enrichment Score: 0.98	RT G	*	18 Count	1.0E0 P_Value	5.8E-1	Roniamin	1.0E
	BIOCARTA	IL22 Soluble Receptor Signaling Pathway	RT		9	3.1E-2	Change	1.1E-1	7.8
	BBID	48.mice minus JAKs and STATs	RT		8	6.1E-2		1.0E0	2 1.0E
	GOTERM_BP_DIRECT	JAK-STAT cascade	<u>RT</u>	1	10	7.8E-2	1.9E0	5.9E-1	5.6E
	INTERPRO	STAT transcription factor, coiled coil	<u>RT</u>	i	4	8.8E-2	3.5E0	4.9E-1	4.5E
	INTERPRO	STAT transcription factor, protein interaction	<u>RT</u>		4	8.8E-2	3.5E0	4.9E-1	4.5E
_ _	INTERPRO	STAT transcription factor, DNA-binding,	RT		4	8.8E-2		4.9E-1	1 4.5E
_ 	INTERPRO	subdomain STAT transcription factor, all-alpha	RT		4	8.8E-2		4.9E-1	1 4.5E
 	INTERPRO								1 4.5E
	INTERPRO	STAT transcription factor, DNA-binding	<u>RT</u>		4	8.8E-2		4.9E-1	1 4.5E
	BIOCARTA	STAT transcription factor, core	<u>RT</u>	•	4	8.8E-2	3.5E0	4.9E-1	1
		IL-10 Anti-inflammatory Signaling Pathway	<u>RT</u>	i	7	2.3E-1	1.6E0	4.7E-1	3.4E
	SMART	<u>SM00964</u>	<u>RT</u>	i .	4	2.4E-1	2.3E0	9.5E-1	8.6E 1
	INTERPRO	p53-like transcription factor, DNA-binding	<u>RT</u>	i	9	4.2E-1	1.3E0	1.0E0	9.1E 1
Annota	ation Cluster 194	Enrichment Score: 0.98	G	15	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_BP_DIRECT	positive regulation of protein metabolic process	<u>RT</u>	i	5	3.2E-2	3.7E0	3.4E-1	3.3E 1
	GOTERM_BP_DIRECT	cellular response to laminar fluid shear stress	<u>RT</u>	i .	4	1.4E-1	3.0E0	8.2E-1	7.9E 1
	GOTERM_BP_DIRECT	negative regulation of heterotypic cell-cell adhesion	<u>RT</u>	1	4	1.4E-1	3.0E0	8.2E-1	7.9E
	GOTERM_BP_DIRECT	negative regulation of response to cytokine stimulus	<u>RT</u>	i	3	2.0E-1	3.6E0	1.0E0	9.6E
Annota	ntion Cluster 195	Enrichment Score: 0.97	G	To the second se	Count	P_Value	Fold Change	Benjamin	1
	GOTERM_CC_DIRECT	Swr1 complex	<u>RT</u>	i	5	4.0E-2	Change	2.3E-1	2.0
7	GOTERM_CC_DIRECT	NuA4 histone acetyltransferase complex	RT		7	5.1E-2		2.8E-1	1 2.5E
	GOTERM_BP_DIRECT	histone H2A acetylation	RT		5	2.4E-1			1 9.6E
	GOTERM_BP_DIRECT							1.0E0	1 9.6E
		histone H4 acetylation	<u>RT</u>	i	8	2.6E-1	:	1.0E0	1
nach	ution Cluster 196 UP_SEQ_FEATURE	Enrichment Score: 0.97	G	-			Change		8.1E
		repeat:REM 1	<u>RT</u>	i	3	5.8E-2	6.8E0	8.4E-1	1
	IID CENTINE	repeat:REM 2	<u>RT</u>	i	3	5.8E-2	6.8E0	8.4E-1	8.1E 1
	UP_SEQ_FEATURE								8.1
	UP_SEQ_FEATURE	repeat:REM 3	<u>RT</u>	i	3	5.8E-2	6.8E0	8.4E-1	1
			RT RT	i i	3	5.8E-2 1.2E-1		8.4E-1 6.4E-1	1
	UP_SEQ_FEATURE	repeat:REM 3					3.1E0		1 5.8E

Annota	ation Cluster 1	Enrichment Score: ?	G	N.	Count	P_Value	Fold Change	Benjamini	FDR
Annota	ation Cluster 197	Enrichment Score: 0.95	G	100	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	Zinc finger, PHD-finger	<u>RT</u>	1	21	2.4E-2	1.6E0	1.9E-1	1.7E
	INTERPRO	Zinc finger, PHD-type	<u>RT</u>	•	23	2.4E-2	1.6E0	1.9E-1	1.7E
	UP_SEQ_FEATURE	zinc finger region:PHD-type 2	<u>RT</u>		9	6.3E-2	2.0E0	9.0E-1	8.7E
ے ا	UP_SEQ_FEATURE	zinc finger region:PHD-type 1	RT	_	9	1.0E-1		1.0E0	1 9.6E
_ _	UP_SEQ_FEATURE								1 9.6E
	INTERPRO	zinc finger region:PHD-type	<u>RT</u>	•	12	1.3E-1		1.0E0	1 9.1E
		Zinc finger, FYVE/PHD-type	<u>RT</u>	•	27	2.6E-1	1.2E0	1.0E0	1
	INTERPRO	Zinc finger, PHD-type, conserved site	<u>RT</u>	•	13	3.9E-1	1.2E0	1.0E0	9.1E 1
	SMART	<u>PHD</u>	<u>RT</u>	Ē	23	5.3E-1	1.1E0	1.0E0	9.1E 1
nnota	ation Cluster 198	Enrichment Score: 0.95	G	-	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	Histone H2B	<u>RT</u>	i	12	6.0E-4	3.1E0	8.2E-3	7.5E 3
	SMART	<u>H2B</u>	<u>RT</u>	•	12	1.9E-2	2.0E0	1.6E-1	1.4E
	GOTERM_BP_DIRECT	innate immune response in mucosa	RT	4	7	2.4E-1	1.7E0	1.0E0	9.6E
_ 	GOTERM_BP_DIRECT	antibacterial humoral response	RT		7	7 8F-1	9.4E-1	1 0F0	1 9.6E
	UP_KEYWORDS	Antibiotic	RT		4	1.0E0	2.9E-1		1 1.0E
	UP_KEYWORDS	Antimicrobial	<u>RT</u>	i	4	1.0E0	2.5E-1	1.0E0	1.0E
nnota	ation Cluster 199	Enrichment Score: 0.95	G	- 1	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	region of interest:Domain A	<u>RT</u>	1	3	5.8E-2	6.8E0	8.4E-1	8.1E 1
	UP_SEQ_FEATURE	region of interest:Domain B	<u>RT</u>	i	3	5.8E-2	6.8E0	8.4E-1	8.1E
	INTERPRO	Domain of unknown function DUF3452, retinoblastoma-associated	<u>RT</u>	i	3	7.0E-2	6.2E0	4.1E-1	3.7E
1	INTERPRO	Retinoblastoma-associated protein, B-box	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E
) 1	INTERPRO	Retinoblastoma-associated protein, A-box		-	3	7.0E-2		4.1E-1	1 3.7E
J	INTERPRO		<u>RT</u>						1 3.7E
J		Rb C-terminal	<u>RT</u>	•	3	7.0E-2	6.2E0	4.1E-1	1
	SMART	SM01367	<u>RT</u>	•	3	1.5E-1	4.1E0	6.9E-1	6.2E 1
	SMART	SM01368	<u>RT</u>	i	3	1.5E-1	4.1E0	6.9E-1	6.2E 1
	SMART	SM01369	<u>RT</u>	i	3	1.5E-1	4.1E0	6.9E-1	6.2E
	GOTERM_BP_DIRECT	regulation of lipid kinase activity	<u>RT</u>	1	3	2.0E-1	3.6E0	1.0E0	9.6E
	UP_SEQ_FEATURE	region of interest:Spacer	<u>RT</u>		4	7.1E-1	1.1E0	1.0E0	9.6E
nnota	ation Cluster 200	Enrichment Score: 0.94	G	178	Count	P_Value	Fold	Benjamini	1 FDR
)	GOTERM_MF_DIRECT	nucleosomal DNA binding		_	15		Change 1.9E0		1.0E
J	INTERPRO		<u>RT</u>					1.2E-1	1 8.0E
J		Histone H3	<u>RT</u>		6	1.8E-1	2.0E0	8.8E-1	1
)	SMART	<u>H3</u>	<u>RT</u>	i	6	5.2E-1		1.0E0	9.1E 1
nnota	ation Cluster 201	Enrichment Score: 0.92	G	-13	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	regulation of actin polymerization or depolymerization	<u>RT</u>	i	4	9.9E-2	3.4E0	6.9E-1	6.6E 1
	INTERPRO	DEK, C-terminal	<u>RT</u>	1	3	1.2E-1	4.6E0	6.4E-1	5.8E
	GOTERM_BP_DIRECT	regulation of lamellipodium assembly	<u>RT</u>	4	4	1.4E-1	3.0E0	8.2E-1	7.9E
nnota	ation Cluster 202	Enrichment Score: 0.91	G	<u> </u>	Count	P_Value	Fold	Benjamini	1
7	GOTERM_MF_DIRECT	cysteine-type endopeptidase inhibitor activity		-	9		Change 2.3E0		1.6E
	GOTERM_BP_DIRECT	involved in apoptotic process regulation of nucleotide-binding	<u>KI</u>	•	9	2.01-2	2.320	1.02-1	1
		oligomerization domain containing signaling pathway	<u>RT</u>	i	3	7.6E-2	5.9E0	5.8E-1	5.5E 1
	UP_SEQ_FEATURE	repeat:BIR 1	<u>RT</u>	i	3	1.1E-1	5.1E0	1.0E0	9.6E
	UP_SEQ_FEATURE	repeat:BIR 2	<u>RT</u>	1	3	1.1E-1	5.1E0	1.0E0	9.6E
1	UP_SEQ_FEATURE				3	1.1E-1		1.0E0	1 9.6E
)	INTERPRO	repeat:BIR 3 <u>Baculoviral inhibition of apoptosis protein</u>	<u>RT</u>						1 5.8E
		<u>repeat</u>	<u>RT</u>	1	4	1.2E-1	3.1E0	6.4E-1	1
	GOTERM_BP_DIRECT	<u>inhibition of cysteine-type endopeptidase</u> <u>activity involved in apoptotic process</u>	<u>RT</u>	1	4	1.8E-1	2.6E0	1.0E0	9.6E 1
	SMART	BIR	<u>RT</u>	1	4	3.1E-1	2.0E0	1.0E0	9.1E 1
	GOTERM_BP_DIRECT	regulation of innate immune response	<u>RT</u>	1	4	3.8E-1	1.8E0	1.0E0	9.6E
									_

Annot	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	Rap protein signal transduction	<u>RT</u>	i	6	1.6E-2	-	2.1E-1	2.0E-
	GOTERM_BP_DIRECT	microvillus assembly	<u>RT</u>	i	6	1.5E-1	2.1E0	8.5E-1	8.1E- 1
	GOTERM_CC_DIRECT	recycling endosome membrane	<u>RT</u>	i	6	8.4E-1	8.7E-1	1.0E0	8.8E- 1
Annot	ation Cluster 204	Enrichment Score: 0.9	G	17	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	Brix domain	<u>RT</u>	i	4	5.7E-2		4.0E-1	3.7E-
	UP_SEQ_FEATURE	domain:Brix	<u>RT</u>	i .	4	7.0E-2	3.9E0	9.7E-1	9.3E- 1
	SMART	SM00879	<u>RT</u>		4	1.6E-1	2.7E0	7.0E-1	6.4E-
	INTERPRO	Anticodon-binding	<u>RT</u>	•	4	4.0E-1	1.8E0	1.0E0	9.1E-
Annot	ation Cluster 205	Enrichment Score: 0.89	G		Count	P_Value	Fold Change	Benjamini	1 FDR
	UP_SEQ_FEATURE	domain:PDZ	<u>RT</u>	i	26	2.1E-2	Onlange	4.0E-1	3.9E-
	INTERPRO	PDZ domain	RT	•	32	1.2E-1	1.3E0	6.3E-1	5.8E-
	SMART	<u>PDZ</u>	RT		32	8.8E-1	8.7E-1	1.0E0	9.1E-
Annot	ation Cluster 206	Enrichment Score: 0.88	G		Count	P_Value	Fold	Benjamini	1 FDR
	GOTERM_CC_DIRECT	endoplasmic reticulum chaperone complex	RT .		5	8.0E-2	Onlange	3.9E-1	3.4E-
	GOTERM_BP_DIRECT	protein folding in endoplasmic reticulum	RT		5	1.6E-1		9.3E-1	1 8.9E-
	UP_SEQ_FEATURE	short sequence motif:Prevents secretion from	RT		13	1.8E-1		1.0E0	1 9.6E-
Annot	ation Cluster 207	Enrichment Score: 0.88	G	•	1	P_Value	Fold	Benjamini	1 FDR
	UP_SEQ_FEATURE	region of interest: Autoinhibitory domain	RT .	i	4	4.5E-2	Change	7.4E-1	7.2E-
	GOTERM_MF_DIRECT	calmodulin-dependent protein kinase activity	RT RT		8	6.2E-2		3.5E-1	1 3.1E-
	BIOCARTA	Ca++/ Calmodulin-dependent Protein Kinase		:					1 8.5E-
Annat	otion Charter 200	Activation	<u>RT</u>	•	4	1	9.4E-1 Fold		1
Annot	ation Cluster 208 GOTERM_MF_DIRECT	Enrichment Score: 0.86	G	i	Count	P_Value	Change	Benjamini	3.1E-
	INTERPRO	ubiquitin conjugating enzyme binding	<u>RT</u>	_	10	6.3E-2		3.5E-1	1 4.2E-
	UP_SEQ_FEATURE	Zinc finger, C6HC-type	<u>RT</u>		6	8.0E-2		4.6E-1	1 9.6E-
	UP_SEQ_FEATURE	zinc finger region:RING-type 1; atypical	<u>RT</u>		4	1.0E-1		1.0E0	1 9.6E-
	UP_SEQ_FEATURE	zinc finger region:IBR-type	<u>RT</u>	i	5	1.1E-1		1.0E0	1
		zinc finger region:RING-type 2	<u>RT</u>	i	4	2.5E-1	2.3E0	1.0E0	9.6E- 1
	SMART	<u>IBR</u>	<u>RT</u>	i	5	4.6E-1	•	1.0E0	9.1E- 1
Annot	ation Cluster 209	Enrichment Score: 0.86	G	N .	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	domain:KEN	<u>RT</u>	i	3	5.8E-2	6.8E0	8.4E-1	8.1E- 1
	INTERPRO	KEN domain	<u>RT</u>	i	3	7.0E-2	6.2E0	4.1E-1	3.7E- 1
	INTERPRO	PUB domain	<u>RT</u>	i	3	2.5E-1	3.1E0	1.0E0	9.1E- 1
	SMART	<u>PUG</u>	<u>RT</u>	i	3	3.6E-1		1.0E0	9.1E- 1
Annot	ation Cluster 210	Enrichment Score: 0.85	G		Count	P_Value	Fold Change	Benjamini	
	GOTERM_CC_DIRECT	spectrin-associated cytoskeleton	<u>RT</u>	i	5	2.5E-2	4.0E0	1.5E-1	1.3E- 1
	UP_KEYWORDS	Elliptocytosis	<u>RT</u>	i	3	3.3E-1	2.6E0	9.1E-1	7.1E- 1
	UP_KEYWORDS	Hereditary hemolytic anemia	<u>RT</u>	i	7	3.5E-1		9.5E-1	7.3E- 1
Annot	ation Cluster 211	Enrichment Score: 0.84	G	17	Count	P_Value	Fold Change	Benjamini	
	UP_KEYWORDS	Glycolysis	<u>RT</u>	i	11	1.0E-2	2.4E0	4.4E-2	3.4E- 2
	INTERPRO	Enolase, C-terminal	<u>RT</u>	i	4	3.2E-2	5.0E0	2.4E-1	2.2E- 1
	GOTERM_CC_DIRECT	phosphopyruvate hydratase complex	<u>RT</u>	i	4	5.4E-2	4.2E0	2.9E-1	2.5E- 1
	INTERPRO	<u>Enolase</u>	<u>RT</u>	i	4	5.7E-2	4.1E0	4.0E-1	3.7E- 1
	INTERPRO	Enolase, N-terminal	<u>RT</u>	i	4	5.7E-2	4.1E0	4.0E-1	3.7E- 1
	GOTERM_BP_DIRECT	canonical glycolysis	<u>RT</u>	i .	9	5.9E-2	2.0E0	5.2E-1	5.0E- 1
	GOTERM_MF_DIRECT	phosphopyruvate hydratase activity	<u>RT</u>	i	4	6.3E-2	4.0E0	3.5E-1	3.1E- 1
	INTERPRO	Enolase, conserved site	<u>RT</u>	1	3	7.0E-2	6.2E0	4.1E-1	3.7E- 1
	SMART	SM01192	<u>RT</u>	i	4	9.9E-2	3.3E0	5.3E-1	4.8E-

Anno	tation Cluster 1	Enrichment Score: ?	G	N N	Count	P_Value	Fold Change	Benjamin	i FDR
	GOTERM_BP_DIRECT	g <u>lycolytic process</u>	<u>RT</u>	i	10	1.1E-1	1.7E0	7.3E-1	7.0E- 1
	PIR_SUPERFAMILY	<u>enolase</u>	<u>RT</u>	i	3	1.6E-1	4.1E0	1.0E0	1.0E0
	SMART	SM01193	<u>RT</u>	1	4	1.6E-1	2.7E0	7.0E-1	6.4E- 1
	BIOCARTA	<u>Glycolysis Pathway</u>	<u>RT</u>	i	5	4.3E-1	1.5E0	7.3E-1	5.2E- 1
	GOTERM_BP_DIRECT	<u>gluconeogenesis</u>	<u>RT</u>	i e	8	6.3E-1	1.1E0	1.0E0	9.6E- 1
	KEGG_PATHWAY	Biosynthesis of amino acids	<u>RT</u>		12	8.4E-1	8.6E-1	1.0E0	8.4E- 1
	KEGG_PATHWAY	<u>Glycolysis / Gluconeogenesis</u>	<u>RT</u>	4	11	8.6E-1	8.5E-1	1.0E0	8.6E-
	KEGG_PATHWAY	Carbon metabolism	RT		15		6.9E-1		1 9.8E-
	UP_SEQ_FEATURE	binding site:Substrate	RT		20	1.0E0	4.5E-1		1 1.0E0
Anno	tation Cluster 212	Enrichment Score: 0.83	G	· ·	Count	P_Value	Fold	Baniamin	1
	UP_SEQ_FEATURE	zinc finger region:CXXC-type	<u>RT</u>	i	5	4.7E-2	3.4E0	7.7E-1	7.4E-
	INTERPRO	Zinc finger, CXXC-type	<u>RT</u>	1	5	1.1E-1	2.6E0	6.3E-1	5.7E-
	INTERPRO	Leucine-rich repeat, cysteine-containing	RT		6		2.0E0	8.8E-1	1 8.0E-
	SMART	<u>subtype</u>							1 9.1E-
		LRR CC	<u>RT</u>	i	6	1	1.3E0	1.0E0	1
Anno	tation Cluster 213	Enrichment Score: 0.83	G	- T	Count	P_Value	Change	_	
	UP_SEQ_FEATURE	domain:HSA	<u>RT</u>	1	3	1.1E-1	5.1E0	1.0E0	9.6E- 1
	INTERPRO	Helicase/SANT-associated, DNA binding	<u>RT</u>	i e	3	1.2E-1	4.6E0	6.4E-1	5.8E- 1
	SMART	<u>HSA</u>	<u>RT</u>	i e	3	2.5E-1	3.0E0	9.9E-1	9.0E- 1
Anno	tation Cluster 214	Enrichment Score: 0.82	G	178	Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	JAB1/Mov34/MPN/PAD-1	<u>RT</u>	1	7	6.7E-3	3.6E0	7.2E-2	6.6E- 2
	UP_SEQ_FEATURE	domain:MPN	<u>RT</u>	i	6	2.2E-2	3.4E0	4.0E-1	3.9E-
	SMART	JAB MPN	<u>RT</u>	1	7	3.2E-2	2.6E0	2.5E-1	2.3E-
	UP_SEQ_FEATURE	short sequence motif:JAMM motif	RT		4		3.9E0	9.7E-1	1 9.3E-
	INTERPRO								1 5.8E-
	GOTERM_MF_DIRECT	Rpn11/EIF3F C-terminal domain metallopeptidase activity	RT RT		3	1.2E-1 1.0E0	4.6E0 4.4E-1	6.4E-1	1 1.0E0
	GOTERM_MF_DIRECT	thiol-dependent ubiquitin-specific protease	RT		5	1.0E0		1.0E0	1.0E0
	UP_SEQ_FEATURE	<u>activity</u> metal ion-binding site:Zinc; catalytic	RT		4	1.0E0	2.1E-1	1.0E0	1.0E0
	UP_KEYWORDS	<u>Metalloprotease</u>	<u>RT</u>	i	5	1.0E0	2.3E-1 Fold	1.0E0	1.0E0
Anno	tation Cluster 215	Enrichment Score: 0.82	G	<u> </u>	Count	P_Value	Change	Benjamin	
	GOTERM_BP_DIRECT	positive regulation of cyclin-dependent protein serine/threonine kinase activity	<u>RT</u>	•	9	3.8E-2	2.2E0	3.8E-1	3.6E- 1
	GOTERM_MF_DIRECT	<u>cyclin-dependent protein serine/threonine</u> <u>kinase regulator activity</u>	<u>RT</u>	i	5	2.4E-1	2.0E0	9.0E-1	8.1E- 1
	GOTERM_BP_DIRECT	<u>positive regulation of phosphorylation of RNA</u> <u>polymerase II C-terminal domain</u>	<u>RT</u>	i e	3	4.0E-1	2.2E0	1.0E0	9.6E- 1
Anno	tation Cluster 216	Enrichment Score: 0.81	G	178	Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	Adenylate kinase, active site lid domain	<u>RT</u>	1	3	1.2E-1	4.6E0	6.4E-1	5.8E-
	INTERPRO	Adenylate kinase	<u>RT</u>	1	4	1.7E-1	2.8E0	8.2E-1	7.5E-
	GOTERM_MF_DIRECT	adenylate kinase activity	<u>RT</u>		4	1.8E-1	2.6E0	7.5E-1	1 6.7E-
Anno	tation Cluster 217	Enrichment Score: 0.8	G	· ·	Count	P_Value	Fold	Panjamin	i FDR
	GOTERM_BP_DIRECT	positive regulation of cell adhesion mediated	RT		7		Change	1.8E-1	1.7E-
	UP_SEQ_FEATURE	<u>by integrin</u>					3.2E0		1 9.6E-
		domain:SH2 1	<u>RT</u>	1	3		1.7E0		1
	UP_SEQ_FEATURE	domain:SH2 2	<u>RT</u>	i	3	5.4E-1	1.7E0	1.0E0	9.6E- 1
Anno	tation Cluster 218	Enrichment Score: 0.8	G	**	Count	P_Value	Fold Change	Benjamin	
	UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A2	<u>RT</u>	i	3	1.6E-1	4.1E0	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A3	<u>RT</u>	i	3	1.6E-1	4.1E0	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	chain:Putative uncharacterized protein C21orf81	<u>RT</u>	1	3	1.6E-1	4.1E0	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing	<u>RT</u>	1	3	1.6E-1	4.1E0	1.0E0	9.6E-
Anno	tation Cluster 219	protein 20A1 Enrichment Score: 0.8	G	 	Count	P_Value	Fold	Bereienstein	i FDR
	UP_SEQ_FEATURE	active site: Phosphoserine intermediate	RT .	1	6		Change 4.1E0	2.0E-1	1.9E-
	INTERPRO	·							1 1.1E-
		Alkaline phosphatase, active site	<u>RT</u>	i	4	1.5E-2	6.2E0	1.3E-1	1

Ann	otation Cluster 1	Enrichment Score: ?	G	· N	Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	Alkaline phosphatase	<u>RT</u>	i	4	1.5E-2		1.3E-1	1.1E- 1
	SMART	<u>alkPPc</u>	<u>RT</u>	1	4	4.9E-2	4.1E0	3.0E-1	2.7E-
	GOTERM_MF_DIRECT	alkaline phosphatase activity	<u>RT</u>		4	6.3E-2	4.0E0	3.5E-1	1 3.1E-
	UP_SEQ_FEATURE	lipid moiety-binding region:GPI-anchor	RT		3	2.2E-1		1.0E0	1 9.6E-
	KEGG_PATHWAY	amidated aspartate							1 2.8E-
	INTERPRO	Folate biosynthesis	<u>RT</u>		5	2.8E-1		4.3E-1	1 9.1E-
	INTERPRO	Alkaline phosphatase-like, alpha/beta/alpha	<u>RT</u>	•	4	9.0E-1	8.0E-1	1.0E0	1
		Alkaline-phosphatase-like, core domain	<u>RT</u>	i	4	9.1E-1	7.7E-1	1.0E0	9.1E- 1
	UP_SEQ_FEATURE	lipid moiety-binding region:GPI-anchor amidated serine	<u>RT</u>	1	4	9.9E-1	5.0E-1	1.0E0	9.9E- 1
	UP_KEYWORDS GOTERM_CC_DIRECT	GPI-anchor anchored component of membrane	RT RT		8	1.0E0 1.0E0	4.0E-1 3.4E-1		1.0E0 1.0E0
Ann	otation Cluster 220	Enrichment Score: 0.79	G	**		P_Value	Fold	Benjamin	
	GOTERM_BP_DIRECT	regulation of establishment of endothelial barrier	<u>RT</u>	i	5	1.8E-2	4.2E0	2.2E-1	2.1E-
	GOTERM_BP_DIRECT	negative regulation of bicellular tight junction	<u>RT</u>	1	3	1.3E-1	4.4E0	8.2E-1	7.9E-
	GOTERM_BP_DIRECT	assembly negative regulation of myosin-light-chain-	RT	1	3	2.0E-1	3.6F0	1.0E0	9.6E-
	GOTERM_BP_DIRECT	phosphatase activity cortical actin cytoskeleton organization	RT		6	3.8E-1		1.0E0	1 9.6E-
	GOTERM_BP_DIRECT	establishment of protein localization to							1 9.6E-
		<u>plasma membrane</u>	<u>RT</u>		8	5.8E-1	Fold	1.0E0	1
Ann	otation Cluster 221 GOTERM_BP_DIRECT	Enrichment Score: 0.79	G	-	Count	P_Value	Change	Benjamin	3.1E-
		isotype switching	RT		7	2.9E-2		3.2E-1	1
	OMIM_DISEASE GOTERM_MF_DIRECT	Mismatch repair cancer syndrome guanine/thymine mispair binding	RT RT	:	3	8.2E-2 1.3E-1	5.9E0 4 5E0	5.9E-1	1.0E0 5.3E-
	GOTERM_BP_DIRECT	somatic hypermutation of immunoglobulin							1 9.6E-
	UP_KEYWORDS	<u>genes</u>	<u>RT</u>		5	2.8E-1		1.0E0	1 7.8E-
	GOTERM_MF_DIRECT	Hereditary nonpolyposis colorectal cancer	<u>RT</u>		3	3.9E-1	2.3E0	1.0E0	1
	GOTERM_WIF_DIRECT	mismatched DNA binding	<u>RT</u>	i	3	5.7E-1		1.0E0	8.9E- 1
Ann	otation Cluster 222	Enrichment Score: 0.78	G	1	Count	P_Value	Fold Change	Benjamin	
	UP_SEQ_FEATURE	repeat:WD 8	<u>RT</u>	i	15	4.9E-2	1.7E0	8.1E-1	7.8E- 1
	INTERPRO	<u>Quinonprotein alcohol dehydrogenase-like</u> <u>superfamily</u>	<u>RT</u>	1	13	7.5E-2	1.7E0	4.4E-1	4.0E- 1
	UP_SEQ_FEATURE	repeat:WD 9	<u>RT</u>	1	11	1.0E-1	1.7E0	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	repeat:WD 11	<u>RT</u>	i .	8	1.4E-1	1.8E0	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	repeat:WD 10	<u>RT</u>	1	8	1.6E-1	1.8E0	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	repeat:WD 13	<u>RT</u>	i .	5	2.7E-1	1.9E0	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	repeat:WD 12	<u>RT</u>	1	5	4.1E-1	1.5E0	1.0E0	9.6E-
	UP_SEQ_FEATURE	repeat:WD 14	RT	1	3	6.3E-1	1.5E0	1.0E0	1 9.6E-
Ann	otation Cluster 223	Enrichment Score: 0.78	G	·	Count	P_Value	Fold	Benjamini	i FDR
	GOTERM_BP_DIRECT	sulfate assimilation	RT .		5	3.2E-2	Change	3.4E-1	3.3E-
	GOTERM_MF_DIRECT	oxidoreductase activity, acting on a sulfur							1 5.3E-
	INTERPRO	group of donors, disulfide as acceptor	<u>RT</u>		4	1.4E-1		5.9E-1	1 8.1E-
	GOTERM_BP_DIRECT	<u>Thioredoxin</u>	<u>RT</u>		3	1.9E-1		8.9E-1	1
		glycerol ether metabolic process	<u>RT</u>	1	3	2.0E-1	3.6E0	1.0E0	9.6E- 1
	GOTERM_MF_DIRECT	protein disulfide oxidoreductase activity	<u>RT</u>	i	4	7.9E-1	9.9E-1	1.0E0	8.9E- 1
Ann	otation Cluster 224	Enrichment Score: 0.76	G	17	Count	P_Value	Fold Change	Benjamin	
	GOTERM_BP_DIRECT	beta-catenin destruction complex disassembly	<u>RT</u>	i	7	1.5E-1	1.9E0	8.9E-1	8.5E- 1
	GOTERM_CC_DIRECT	beta-catenin destruction complex	<u>RT</u>	i	5	1.7E-1	2.3E0	6.5E-1	5.7E- 1
	GOTERM_BP_DIRECT	beta-catenin destruction complex assembly	<u>RT</u>	i .	3	2.0E-1	3.6E0	1.0E0	9.6E- 1
Ann	otation Cluster 225	Enrichment Score: 0.76	G	To the second se	Count	P_Value	Fold Change	Benjamin	
	PIR_SUPERFAMILY	heat shock protein, HSP90/HTPG types	<u>RT</u>	i	4	2.1E-2		2.9E-1	2.9E-
	INTERPRO	Heat shock protein Hsp90, conserved site	<u>RT</u>	i .	3	1.2E-1	4.6E0	6.4E-1	5.8E-
	INTERPRO	Heat shock protein Hsp90, N-terminal	RT		4	1.7E-1		8.2E-1	1 7.5E-
	INTERPRO	Heat shock protein Hsp90	RT		4	2.6E-1		1.0E0	1 9.1E-
		THE STOCK PROCESS TISH TO	<u>KI</u>		7	Z.UL-1	2.310	1.000	1

Annota	ation Cluster 1	Enrichment Score: ?	G	100	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	<u>Histidine kinase-like ATPase, ATP-binding</u> domain	<u>RT</u>	i	7	4.5E-1	Change	1.0E0	9.1E- 1
	SMART	HATPase c	<u>RT</u>	i .	4	5.3E-1	1.5E0	1.0E0	9.1E-
Annota	ation Cluster 226	Enrichment Score: 0.76	G	To the second se	Count	P_Value	Fold Change	Benjamini	_
	UP_SEQ_FEATURE	repeat:RCC1 7	<u>RT</u>	i	4	1.0E-1	·	1.0E0	9.6E- 1
	INTERPRO	Regulator of chromosome condensation,	<u>RT</u>		7	1.1E-1	2.1E0	6.0E-1	5.5E-
	UP_SEQ_FEATURE	RCC1 repeat:RCC1 5	RT		6	1.1E-1		1.0E0	1 9.6E-
	INTERPRO	Regulator of chromosome condensation	RT		7	1.3E-1		6.6E-1	1 6.0E-
	UP_SEQ_FEATURE	1/beta-lactamase-inhibitor protein II repeat:RCC1 4	RT		6	1.3E-1		1.0E0	1 9.6E-
	UP_SEQ_FEATURE	repeat:RCC1 1	RT		6	1.6E-1		1.0E0	1 9.6E-
	UP_SEQ_FEATURE	repeat:RCC1 2	RT	-	6	1.6E-1		1.0E0	1 9.6E-
	UP_SEQ_FEATURE	repeat:RCC1 3	RT		6	1.6E-1		1.0E0	1 9.6E-
	UP_SEQ_FEATURE								1 9.6E-
	COG_ONTOLOGY	repeat:RCC1 6 Cell division and chromosome partitioning /	<u>RT</u>		4	3.0E-1		1.0E0	1
		Cytoskeleton	<u>RT</u>		5	1.0E0	5.1E-1 Fold		1.0EC
Annota	ation Cluster 227 INTERPRO	Enrichment Score: 0.74 Carbamoyl-phosphate synthetase large	G	-	Count	P_Value	Change	Benjamini	FDR 4.5E-
	INTERPRO	subunit-like, ATP-binding domain	<u>RT</u>	1	4	8.8E-2		4.9E-1	1 4.5E-
	INTERPRO	ATP-grasp fold, subdomain 2	<u>RT</u>		7	9.0E-2	2.2E0	5.0E-1	1 6.7E-
		ATP-grasp fold	<u>RT</u>	i	5	1.4E-1		7.3E-1	1
	INTERPRO	<u>Pre-ATP-grasp domain</u>	<u>RT</u>	i	5	1.8E-1	2.2E0	8.7E-1	8.0E- 1
	INTERPRO	ATP-grasp fold, subdomain 1	<u>RT</u>	i	5	2.1E-1	2.1E0	1.0E0	9.1E- 1
	INTERPRO	Rudiment single hybrid motif	<u>RT</u>	1	3	2.5E-1	3.1E0	1.0E0	9.1E- 1
	UP_SEQ_FEATURE	domain:ATP-grasp	<u>RT</u>	i	3	5.9E-1	•	1.0E0	9.6E- 1
Annota	ation Cluster 228	Enrichment Score: 0.74			Count	P_Value	Fold Change	Benjamini	FDR
							Change		:
	KEGG_PATHWAY	Hedgehog signaling pathway	RT	i	12	8.1E-3		1.6E-2	8.1E- 3
	KEGG_PATHWAY BIOCARTA	Hedgehog signaling pathway Repression of Pain Sensation by the Transcriptional Regulator DREAM	RT RT	_	12 10	8.1E-3 1.5E-2	2.3E0	1.6E-2 6.3E-2	3
		Repression of Pain Sensation by the		i			2.3E0 2.2E0		3 4.5E- 2
	BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM	<u>RT</u>	i i	10	1.5E-2	2.3E0 2.2E0 1.9E0	6.3E-2	3 4.5E- 2 9.7E- 2
	BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway	RT RT	i i	10	1.5E-2 4.4E-2	2.3E0 2.2E0 1.9E0 1.9E0	6.3E-2 1.4E-1	3 4.5E- 2 9.7E- 2 4.3E- 1
	BIOCARTA BIOCARTA GOTERM_CC_DIRECT	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate	RT RT RT	i i i	10 10 8	1.5E-2 4.4E-2 1.2E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0	6.3E-2 1.4E-1 4.9E-1	3 4.5E-2 9.7E-2 4.3E-1 2.6E-1
	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors	RT RT RT RT		10 10 8 9	1.5E-2 4.4E-2 1.2E-1 1.6E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1	3 4.5E-2 9.7E-2 4.3E-1 2.6E-1 5.9E-1
	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase	RT RT RT RT RT		10 10 8 9	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0 2.7E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1	3 4.5E-2 9.7E-2 4.3E-1 2.6E-1 5.9E-1
	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS GOTERM_CC_DIRECT	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase of CARM1 Cystic fibrosis transmembrane conductance	RT RT RT RT RT RT RT		10 10 8 9 8 3 6	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1 3.0E-1 3.5E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0 2.7E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1 8.8E-1 6.5E-1	3 4.5E-2 9.7E-2 4.3E-1 2.6E-1 5.9E-1 7.7E-1 4.6E-1
	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS GOTERM_CC_DIRECT BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase of CARM1 Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway	RT RT RT RT RT RT RT		10 10 8 9 8 3 6	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1 3.0E-1 3.5E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 2.7E0 1.5E0 1.5E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1 8.8E-1 6.5E-1	3 4.5E-2 9.7E-2 4.3E-1 2.6E-1 5.9E-1 7.7E-1 4.6E-1
	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS GOTERM_CC_DIRECT BIOCARTA BIOCARTA BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase of CARM1 Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway Phospholipase C-epsilon pathway	RT RT RT RT RT RT RT RT RT		10 10 8 9 8 3 6 6	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1 3.0E-1 3.5E-1 3.5E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0 1.5E0 1.5E0 1.5E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1 8.8E-1 6.5E-1 6.5E-1	3 4.5E-2 9.7E-2 4.3E-1 2.6E-1 5.9E-1 4.6E-1 4.6E-1
	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS GOTERM_CC_DIRECT BIOCARTA BIOCARTA BIOCARTA BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase of CARM1 Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway Phospholipase C-epsilon pathway Attenuation of GPCR Signaling	RT		10 10 8 9 8 3 6 6 6	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1 3.0E-1 3.5E-1 3.5E-1 4.3E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0 1.5E0 1.5E0 1.4E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1 8.8E-1 6.5E-1 6.5E-1 7.3E-1	3 4.5E-2 9.7E-2 4.3E-1 2.6E-1 5.9E-1 4.6E-1 4.6E-1 5.2E-1
	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS GOTERM_CC_DIRECT BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase of CARM1 Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway Phospholipase C-epsilon pathway Attenuation of GPCR Signaling GATA3 participate in activating the Th2 cytokine genes expression	RT		10 10 8 9 8 3 6 6 6 6 7	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1 3.0E-1 3.5E-1 3.5E-1 4.3E-1 4.3E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0 1.5E0 1.5E0 1.4E0 1.3E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1 8.8E-1 6.5E-1 6.5E-1 7.3E-1 7.3E-1	3 4.5E-2 9.7E-2 4.3E-1 2.6E-1 5.9E-1 4.6E-1 4.6E-1 5.2E-1
	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS GOTERM_CC_DIRECT BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase of CARM1 Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway Phospholipase C-epsilon pathway Attenuation of GPCR Signaling GATA3 participate in activating the Th2 cytokine genes expression mCalpain and friends in Cell motility	RT		10 10 8 9 8 3 6 6 6	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1 3.0E-1 3.5E-1 3.5E-1 4.3E-1 4.3E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0 1.5E0 1.5E0 1.4E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1 8.8E-1 6.5E-1 6.5E-1 7.3E-1 7.3E-1	3 4.5E-2 9.7E-2 4.3E-1 2.6E-1 5.9E-1 4.6E-1 4.6E-1 5.2E-1
	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS GOTERM_CC_DIRECT BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase of CARM1 Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway Phospholipase C-epsilon pathway Attenuation of GPCR Signaling GATA3 participate in activating the Th2 cytokine genes expression mCalpain and friends in Cell motility Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell	RT		10 10 8 9 8 3 6 6 6 6 7	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1 3.0E-1 3.5E-1 3.5E-1 4.3E-1 4.3E-1 4.4E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0 1.5E0 1.5E0 1.4E0 1.3E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1 8.8E-1 6.5E-1 6.5E-1 7.3E-1 7.3E-1 7.3E-1	3 4.5E-2 9.7E-2 4.3E-1 2.6E-1 5.9E-1 4.6E-1 4.6E-1 5.2E-1 5.2E-1
	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS GOTERM_CC_DIRECT BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase of CARM1 Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway. Phospholipase C-epsilon pathway Attenuation of GPCR Signaling GATA3 participate in activating the Th2 cytokine genes expression mCalpain and friends in Cell motility Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor Stathmin and breast cancer resistance to	RT		10 10 8 9 8 3 6 6 6 6 7	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1 3.0E-1 3.5E-1 3.5E-1 4.3E-1 4.3E-1 4.4E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0 1.5E0 1.5E0 1.5E0 1.4E0 1.3E0 1.2E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1 8.8E-1 6.5E-1 6.5E-1 7.3E-1 7.3E-1 7.3E-1	3 4.5E-2 9.7E-2 4.3E-1 2.6E-1 5.9E-1 4.6E-1 4.6E-1 5.2E-1 5.2E-1 5.2E-1
	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS GOTERM_CC_DIRECT BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase of CARM1 Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway. Phospholipase C-epsilon pathway Attenuation of GPCR Signaling GATA3 participate in activating the Th2 cytokine genes expression mCalpain and friends in Cell motility Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor	RT R		10 10 8 9 8 3 6 6 6 6 7 9	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1 3.0E-1 3.5E-1 3.5E-1 4.3E-1 4.3E-1 4.4E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0 2.7E0 1.5E0 1.5E0 1.4E0 1.3E0 1.2E0 1.1E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1 8.8E-1 6.5E-1 6.5E-1 7.3E-1 7.3E-1 7.3E-1 7.3E-1	3 4.5E-2 9.7E-2 4.3E-1 2.6E-1 5.9E-1 4.6E-1 4.6E-1 5.2E-1 5.2E-1 5.2E-1 6.7E-1
	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS GOTERM_CC_DIRECT BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase of CARM1 Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway Phospholipase C-epsilon pathway Attenuation of GPCR Signaling GATA3 participate in activating the Th2 cytokine genes expression mCalpain and friends in Cell motility Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor Stathmin and breast cancer resistance to antimicrotubule agents	RT R		10 10 8 9 8 3 6 6 6 6 7 9	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1 3.0E-1 3.5E-1 3.5E-1 4.3E-1 4.3E-1 4.4E-1 4.4E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0 1.5E0 1.5E0 1.4E0 1.3E0 1.2E0 1.1E0 Fold Change	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1 8.8E-1 6.5E-1 6.5E-1 7.3E-1 7.3E-1 7.3E-1 7.3E-1 9.4E-1	3 4.5E-2 9.7E-2 4.3E-1 2.6E-1 5.9E-1 4.6E-1 4.6E-1 5.2E-1 5.2E-1 5.2E-1 6.7E-1
	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS GOTERM_CC_DIRECT BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase of CARM1 Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway. Phospholipase C-epsilon pathway Attenuation of GPCR Signaling GATA3 participate in activating the Th2 cytokine genes expression mCalpain and friends in Cell motility Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor Stathmin and breast cancer resistance to antimicrotubule agents Enrichment Score: 0.72	RT R		10 10 8 9 8 3 6 6 7 9 9 Count	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1 3.0E-1 3.5E-1 4.3E-1 4.3E-1 4.4E-1 4.4E-1 6.1E-1 P_Value	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0 2.7E0 1.5E0 1.5E0 1.4E0 1.3E0 1.2E0 1.1E0 Fold Change 1.7E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1 8.8E-1 6.5E-1 6.5E-1 7.3E-1 7.3E-1 7.3E-1 7.3E-1 9.4E-1 Benjamini	3 4.5E-2 9.7E-2 4.3E-1 5.9E-1 7.7E-1 4.6E-1 4.6E-1 5.2E-1 5.2E-1 5.2E-1 5.2E-1 5.2E-1 5.2E-1 8.5E-1
	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS GOTERM_CC_DIRECT BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase of CARM1 Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway Phospholipase C-epsilon pathway Attenuation of GPCR Signaling GATA3 participate in activating the Th2 cytokine genes expression mCalpain and friends in Cell motility Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor Stathmin and breast cancer resistance to antimicrotubule agents Enrichment Score: 0.72 Presenilin action in Notch and Wnt signaling	RT R		10 10 8 9 8 3 6 6 6 7 9 9 9 Count 8	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1 3.0E-1 3.5E-1 4.3E-1 4.3E-1 4.4E-1 6.1E-1 P_Value 1.4E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0 2.7E0 1.5E0 1.5E0 1.4E0 1.3E0 1.2E0 1.1E0 Fold Change 1.7E0 1.9E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1 8.8E-1 6.5E-1 6.5E-1 7.3E-1 7.3E-1 7.3E-1 7.3E-1 9.4E-1 Benjamini 3.3E-1	3 4.5E-2 9.7E-2 4.3E-1 2.6E-1 7.7E-1 4.6E-1 4.6E-1 5.2E-1 5.2E-1 5.2E-1 5.2E-1 5.2E-1 1 6.7E-1 1 8.5E-1
	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS GOTERM_CC_DIRECT BIOCARTA GOTERM_CC_DIRECT BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase of CARM1 Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway Phospholipase C-epsilon pathway Attenuation of GPCR Signaling GATA3 participate in activating the Th2 cytokine genes expression mCalpain and friends in Cell motility Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor Stathmin and breast cancer resistance to antimicrotubule agents Enrichment Score: 0.72 Presenilin action in Notch and Wnt signaling beta-catenin destruction complex disassembly	RI R		10 10 8 9 8 3 6 6 6 7 9 9 Count 8 7	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1 3.0E-1 3.5E-1 3.5E-1 4.3E-1 4.3E-1 4.4E-1 6.1E-1 P_Value 1.4E-1 1.5E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0 1.5E0 1.5E0 1.4E0 1.3E0 1.2E0 1.1E0 Fold Change 1.7E0 1.9E0 2.3E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1 8.8E-1 6.5E-1 6.5E-1 7.3E-1 7.3E-1 7.3E-1 9.4E-1 Benjamini 3.3E-1 8.9E-1	3 4.5E-2 9.7E-2 4.3E-1 2.6E-1 7.7E-1 4.6E-1 4.6E-1 5.2E-1 5.2E-1 5.2E-1 6.7E-1 7.3E-1 3.6E-1
Annota	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS GOTERM_CC_DIRECT BIOCARTA GOTERM_CC_DIRECT GOTERM_CC_DIRECT BIOCARTA BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase of CARM1 Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway Phospholipase C-epsilon pathway Attenuation of GPCR Signaling GATA3 participate in activating the Th2 cytokine genes expression mCalpain and friends in Cell motility Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor Stathmin and breast cancer resistance to antimicrotubule agents Enrichment Score: 0.72 Presenilin action in Notch and Wnt signaling beta-catenin destruction complex disassembly. Wnt signalosome	RI R		10 10 8 9 8 3 6 6 6 7 9 9 Count 8 7 4 8	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1 3.0E-1 3.5E-1 3.5E-1 4.3E-1 4.3E-1 4.4E-1 4.4E-1 1.4E-1 1.4E-1 1.5E-1 2.4E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0 2.7E0 1.5E0 1.5E0 1.4E0 1.3E0 1.2E0 1.1E0 Fold Change 1.7E0 1.9E0 2.3E0 1.5E0 1.5E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1 8.8E-1 6.5E-1 6.5E-1 7.3E-1 7.3E-1 7.3E-1 9.4E-1 Benjamini 3.3E-1 8.9E-1 8.9E-1	3 4.5E-2 9.7E-2 4.3E-1 5.9E-1 7.7E-1 4.6E-1 4.6E-1 5.2E-1 5.2E-1 5.2E-1 6.7E-1 7.3E-1 7.3E-1 1 3.6E-1
Annota	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS GOTERM_CC_DIRECT BIOCARTA GOTERM_CC_DIRECT GOTERM_CC_DIRECT BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase of CARM1 Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway Phospholipase C-epsilon pathway Attenuation of GPCR Signaling GATA3 participate in activating the Th2 cytokine genes expression mCalpain and friends in Cell motility Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor Stathmin and breast cancer resistance to antimicrotubule agents Enrichment Score: 0.72 Presenilin action in Notch and Wnt signaling beta-catenin destruction complex disassembly Wnt signalosome Multi-step Regulation of Transcription by Pitx2	RI R		10 10 8 9 8 3 6 6 6 7 9 9 Count 8 7 4 8	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1 3.0E-1 3.5E-1 4.3E-1 4.3E-1 4.4E-1 6.1E-1 P_Value 1.4E-1 1.5E-1 2.4E-1 2.5E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0 1.5E0 1.5E0 1.4E0 1.3E0 1.2E0 1.1E0 Fold Change 1.9E0 2.3E0 1.5E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1 8.8E-1 6.5E-1 6.5E-1 7.3E-1 7.3E-1 7.3E-1 9.4E-1 Benjamini 3.3E-1 8.9E-1 8.9E-1 5.0E-1	4.5E-2 9.7E-2 4.3E-1 2.6E-1 5.9E-1 4.6E-1 4.6E-1 5.2E-1 5.2E-1 5.2E-1 5.2E-1 7.7E-1 7.3E-1 7.3E-1 7.3E-1
Annota	BIOCARTA BIOCARTA GOTERM_CC_DIRECT BIOCARTA UP_KEYWORDS GOTERM_CC_DIRECT BIOCARTA GOTERM_CC_DIRECT GOTERM_CC_DIRECT BIOCARTA CATION Cluster 229 BIOCARTA GOTERM_CC_DIRECT BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM Sonic Hedgehog (Shh) Pathway. ciliary base Regulation of ck1/cdk5 by type 1 glutamate receptors cAMP cAMP-dependent protein kinase complex Transcription Regulation by Methyltransferase of CARM1 Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway. Phospholipase C-epsilon pathway. Attenuation of GPCR Signaling. GATA3 participate in activating the Th2 cytokine genes expression mCalpain and friends in Cell motility. Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor Stathmin and breast cancer resistance to antimicrotubule agents Enrichment Score: 0.72 Presenilin action in Notch and Wnt signaling. beta-catenin destruction complex disassembly. Wnt signalosome Multi-step Regulation of Transcription by Pitx2 Enrichment Score: 0.72	RI R		10 10 8 9 8 3 6 6 6 7 9 9 9 Count 8 7 4 8	1.5E-2 4.4E-2 1.2E-1 1.6E-1 2.6E-1 3.0E-1 3.5E-1 3.5E-1 4.3E-1 4.3E-1 4.4E-1 6.1E-1 P_Value 1.4E-1 2.4E-1 2.5E-1	2.3E0 2.2E0 1.9E0 1.9E0 1.6E0 1.5E0 2.7E0 1.5E0 1.5E0 1.4E0 1.3E0 1.2E0 1.1E0 Fold Change 1.7E0 1.9E0 2.3E0 1.5E0 Fold Change 6.2E0	6.3E-2 1.4E-1 4.9E-1 3.6E-1 7.6E-1 8.8E-1 6.5E-1 6.5E-1 7.3E-1 7.3E-1 7.3E-1 7.3E-1 8.9E-1 8.9E-1 8.3E-1 5.0E-1	3 4.5E-2 9.7E-2 4.3E-1 5.9E-1 7.7E-1 4.6E-1 4.6E-1 5.2E-1 5.2E-1 5.2E-1 5.2E-1 1 5.2E-1 1 5.2E-1 1 7.7E-1 1 3.6E-1 1 8.5E-1

	tion Cluster 1	Enrichment Score: ?	G	- 1	Count	P_Value	Fold Change	Benjamini	
	GOTERM_BP_DIRECT	DNA-templated transcription, initiation	<u>RT</u>	•	8	4.1E-1	1.3E0	1.0E0	9.6 1
ota	tion Cluster 231	Enrichment Score: 0.71	G	100	Count	P_Value	Fold Change	Benjamini	i FD
	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 1	<u>RT</u>	1	8	3.3E-2	2.5E0	5.7E-1	5.5 1
	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 2	<u>RT</u>	•	8	3.3E-2	2.5E0	5.7E-1	5.5 1
	GOTERM_MF_DIRECT	calcium-transporting ATPase activity	<u>RT</u>	1	5	4.9E-2	3.3E0	2.8E-1	2.5
	INTERPRO	Protein kinase C, alpha/beta/gamma types	RT		3	7.0E-2	6.2E0	4.1E-1	1 3.7
	PIR_SUPERFAMILY	protein kinase C, alpha/beta/gamma types	RT		3	8.8E-2		6.9E-1	1 6.8
	GOTERM_BP_DIRECT	negative regulation of glial cell apoptotic		-					1 6.6
	UP_SEQ_FEATURE	process metal ion-binding site:Calcium 2; via carbonyl	<u>RT</u>		4	9.9E-2		6.9E-1	1 9.6
	GOTERM_MF_DIRECT	oxygen	<u>RT</u>	•	10	1.1E-1	1.7E0	1.0E0	1
		<u>calcium-dependent protein kinase C activity</u>	<u>RT</u>	•	3	1.3E-1	4.5E0	5.9E-1	5.3
	UP_SEQ_FEATURE	metal ion-binding site:Calcium 2	<u>RT</u>	•	11	3.2E-1	1.3E0	1.0E0	9.6 1
	UP_SEQ_FEATURE	metal ion-binding site:Calcium 1	<u>RT</u>	•	9	3.8E-1	1.3E0	1.0E0	9.6 1
	UP_SEQ_FEATURE	metal ion-binding site:Calcium 3; via carbonyl oxygen	<u>RT</u>	1	4	6.1E-1	1.3E0	1.0E0	9.6 1
	UP_SEQ_FEATURE	metal ion-binding site:Calcium 1; via carbonyl oxygen	<u>RT</u>	1	4	8.7E-1	8.5E-1	1.0E0	9.6 1
	UP_SEQ_FEATURE	metal ion-binding site:Calcium 3	<u>RT</u>	1	4	8.7E-1	8.5E-1	1.0E0	9.6
	GOTERM_BP_DIRECT	cellular calcium ion homeostasis	<u>RT</u>		11	9.6E-1	7.0E-1	1.0E0	9.6
	UP_KEYWORDS	<u>Calcium transport</u>	RT	i e	5	1.0E0	3.5E-1		1 1.0
ota	tion Cluster 232	Enrichment Score: 0.7		100	Count	P_Value	Fold Change	Benjamini	i FD
	GOTERM_CC_DIRECT	rDNA heterochromatin	<u>RT</u>	1	3	1.2E-1		4.9E-1	4.3
	GOTERM_CC_DIRECT	chromatin silencing complex	<u>RT</u>	1	4	1.6E-1	2.8E0	6.2E-1	5.4 1
	GOTERM_BP_DIRECT	chromatin silencing at rDNA	<u>RT</u>		8	4.4E-1	1.3E0	1.0E0	9.6
ota	tion Cluster 233	Enrichment Score: 0.69	G		Count	P_Value	Fold	Benjamini	1 i FD
	UP_SEQ_FEATURE	zinc finger region:Btk-type	RT	1	4	1.3E-1	Change	1.0E0	9.0
	INTERPRO	Zinc finger, Btk motif	RT	-	4	1.7E-1		8.2E-1	1 7.5
	SMART								1 9.:
_		BTK	RT		4	3.9E-1	Fold	1.0E0	1
	BIOCARTA	Enrichment Score: 0.69 AKAP95 role in mitosis and chromosome	G	- The state of the	Count	P_Value	Change		1.3
		dynamics	<u>RT</u>	•	8	6.1E-2	2.0E0	1.8E-1	1
	BIOCARTA	Protein Kinase A at the Centrosome	<u>RT</u>	•	8	1.9E-1	1.6E0	4.1E-1	2.9
	BIOCARTA	Rho-Selective Guanine Exchange Factor AKAP13 Mediates Stress Fiber Formation	<u>RT</u>	i	4	7.6E-1	1.1E0	1.0E0	7.6 1
ota	tion Cluster 235	Enrichment Score: 0.69	G	-13	Count	P_Value	Fold Change	Benjamini	i FD
	GOTERM_BP_DIRECT	<u>positive regulation of chemokine biosynthetic</u> <u>process</u>	<u>RT</u>	1	7	2.6E-3	4.1E0	5.0E-2	4.8 2
	GOTERM_BP_DIRECT	positive regulation of calcidiol 1- monooxygenase activity	<u>RT</u>	1	3	7.6E-2	5.9E0	5.8E-1	5.5 1
	GOTERM_BP_DIRECT	positive regulation of membrane protein ectodomain proteolysis	<u>RT</u>	1	4	4.8E-1	1.6E0	1.0E0	9.6 1
	KEGG_PATHWAY	Graft-versus-host disease	<u>RT</u>	1	5	9.0E-1	7.9E-1	1.0E0	9.0 1
	KEGG_PATHWAY	Type I diabetes mellitus	RT	4	6	9.3E-1	7.4E-1	1.0E0	9.3
	GOTERM_BP_DIRECT	regulation of insulin secretion	RT		8		7.1E-1		1 9.6
	tion Cluster 236		G	- 198		P_Value			1
	UP_SEQ_FEATURE	Enrichment Score: 0.67		-					7.:
	UP_SEQ_FEATURE	repeat:1-2	<u>RT</u>	1	10		2.1E0		1 8.1
		repeat:1-1	<u>RT</u>	•	10	5.2E-2	2.0E0	8.4E-1	1
	UP_SEQ_FEATURE	region of interest:2 X 16 AA Gly-rich approximate repeats	<u>RT</u>	1	3	2.2E-1	3.4E0	1.0E0	9.6
	UP_SEQ_FEATURE	region of interest:2 X 19 AA perfect repeats	<u>RT</u>	i	3	2.2E-1	3.4E0	1.0E0	9.6 1
	UP_SEQ_FEATURE	repeat:2-1	<u>RT</u>	1	7	3.3E-1	1.5E0	1.0E0	9.6 1
	UP_SEQ_FEATURE	repeat:2-2	<u>RT</u>	4	7	3.8E-1	1.4E0	1.0E0	9.6 1
	UP_SEQ_FEATURE	repeat:1-4	<u>RT</u>	1	4	5.4E-1	1.4E0	1.0E0	9.6
	UP_SEQ_FEATURE	repeat:1-3	<u>RT</u>		4	5.8E-1	1.4E0	1.0E0	9.6
ota	tion Cluster 237	Enrichment Score: 0.67	G	- -	Count	:	:	:	1 i FD
. 6	don Glaster 237	Enrichment Score. 0.07		- V	Count	P_Value	Change	- Jenjamini	

Annot	tation Cluster 1	Enrichment Score: ?	G	13	Count	P_Value	Fold Change	Benjamini	i FDR
	GOTERM_MF_DIRECT	aspartic-type endopeptidase activity	<u>RT</u>	1	10	8.9E-2	1.8E0	4.5E-1	4.0E
	INTERPRO	Aspartic peptidase	<u>RT</u>	1	8	1.3E-1	1.8E0	6.7E-1	6.1E
	INTERPRO	Peptidase A1	RT		4	2.1E-1	2.5E0	9.9E-1	9.18
_ 	INTERPRO	Propeptide, peptidase A1	RT	- -	3	3.2E-1		1.0E0	1 9.1E
	UP_KEYWORDS								1 7.8E
	INTERPRO	Aspartyl protease	<u>RT</u>	•	4	6.1E-1	1.3E0	1.0E0	1
		Peptidase aspartic, active site	<u>RT</u>	i	4	6.8E-1		1.0E0	9.1E 1
Annot	UP_SEQ_FEATURE tation Cluster 238	propeptide:Activation peptide Enrichment Score: 0.66	RT G		4 Count	1.0E0	3.6E-1 Fold		1.0E
Annot	UP_KEYWORDS					P_Value	Onlange		2.8E
	GOTERM_BP_DIRECT	Purine biosynthesis	<u>RT</u>	1	5	1.1E-1		3.6E-1	1 9.6E
		<u>purine nucleobase biosynthetic process</u>	<u>RT</u>	•	3	2.0E-1	3.6E0	1.0E0	1
	GOTERM_BP_DIRECT	'de novo' IMP biosynthetic process	<u>RT</u>	1	3	2.7E-1	3.0E0	1.0E0	9.6l 1
	GOTERM_BP_DIRECT	<u>purine ribonucleoside monophosphate</u> <u>biosynthetic process</u>	<u>RT</u>	1	4	3.8E-1	1.8E0	1.0E0	9.6l 1
Annot	tation Cluster 239	Enrichment Score: 0.66		100	Count	P_Value	Fold Change	Benjamin	i FDF
	UP_SEQ_FEATURE	domain:PDZ	<u>RT</u>	1	26	2.1E-2	1.6E0	4.0E-1	3.9I 1
	UP_SEQ_FEATURE	short sequence motif:LD motif 1	<u>RT</u>	i	3	5.8E-2	6.8E0	8.4E-1	8.1
	UP_SEQ_FEATURE	short sequence motif:LD motif 2	RT		3	5.8E-2	6.8E0	8.4E-1	8.1
7	UP_SEQ_FEATURE	short sequence motif:LD motif 3	RT	- -	3	5.8E-2		8.4E-1	1 8.1
	UP_SEQ_FEATURE								1 9.6
_	UP_SEQ_FEATURE	domain:LIM zinc-binding 3	<u>RT</u>		6	3.0E-1	1.6E0	1.0E0	1 9.6
		domain:LIM zinc-binding	<u>RT</u>	i	5	3.0E-1	1.8E0	1.0E0	1
	UP_KEYWORDS	<u>LIM domain</u>	<u>RT</u>	•	13	3.5E-1	1.2E0	9.6E-1	7.4 1
	UP_SEQ_FEATURE	domain:LIM zinc-binding 4	<u>RT</u>	1	3	5.0E-1	1.9E0	1.0E0	9.6 1
	INTERPRO	Zinc finger, LIM-type	<u>RT</u>	i .	13	5.0E-1	1.1E0	1.0E0	9.1 1
	UP_SEQ_FEATURE	domain:LIM zinc-binding 1	<u>RT</u>	1	8	6.1E-1	1.1E0	1.0E0	9.6 1
	UP_SEQ_FEATURE	domain:LIM zinc-binding 2	RT		8	6.1E-1	1.1E0	1.0E0	9.6
	SMART	<u>LIM</u>	RT		13	9.6E-1	7.3E-1		9.6 1
Annot	tation Cluster 240	Enrichment Score: 0.65	G	17	Count	P_Value	Fold Change	Benjamin	Ť
	UP_SEQ_FEATURE	domain:PUA	RT	i	3	1.6E-1		1.0E0	9.6
_ 	INTERPRO	Pseudouridine synthase/archaeosine	RT		3	1.9E-1	3 7F0	8.9E-1	8.1
ے ا	INTERPRO	<u>transglycosylase</u>		_					1 9.1
		PUA-like domain	RT	i	5	3.7E-1		1.0E0	1
nnot	tation Cluster 241 GOTERM_CC_DIRECT	Enrichment Score: 0.65	G					Doniomin	i FDI
					Count	P_Value	Fold Change	Benjamin	4.2
		<u>calcineurin complex</u>	<u>RT</u>	i	Count 3	P_Value 1.2E-1	Change	4.9E-1	1
	GOTERM_BP_DIRECT	calcineurin complex positive regulation of NFAT protein import into nucleus	RT RT				Change 4.8E0		1
		positive regulation of NFAT protein import			3	1.2E-1	4.8E0 2.4E0	4.9E-1	1 9.6 1
Annot	GOTERM_BP_DIRECT	positive regulation of NFAT protein import into nucleus	<u>RT</u>	i	3	1.2E-1 2.3E-1	4.8E0 2.4E0 2.2E0	4.9E-1 1.0E0	9.6 1 9.6 1
Innot	GOTERM_BP_DIRECT GOTERM_BP_DIRECT	positive regulation of NFAT protein import into nucleus calcineurin-NFAT signaling cascade Enrichment Score: 0.65 Small Leucine-rich Proteoglycan (SLRP)	RT RT	i i	3 4 3	1.2E-1 2.3E-1 4.0E-1	4.8E0 2.4E0 2.2E0 Fold Change	4.9E-1 1.0E0 1.0E0	9.6 1 9.6 1
annot	GOTERM_BP_DIRECT GOTERM_BP_DIRECT tation Cluster 242	positive regulation of NFAT protein import into nucleus calcineurin-NFAT signaling cascade Enrichment Score: 0.65	RT RT G	i i i	3 4 3 Count	1.2E-1 2.3E-1 4.0E-1 P_Value	2.4E0 2.2E0 Fold Change 3.0E0	4.9E-1 1.0E0 1.0E0 Benjamini	1 9.6 1 9.6 1 FD 4.7 2 3.6
nnot	GOTERM_BP_DIRECT GOTERM_BP_DIRECT tation Cluster 242 BIOCARTA	positive regulation of NFAT protein import into nucleus calcineurin-NFAT signaling cascade Enrichment Score: 0.65 Small Leucine-rich Proteoglycan (SLRP) molecules keratan sulfate catabolic process glycosylation site:N-linked (GlcNAc)	RT RT G RT RT	i i i	3 4 3 Count	1.2E-1 2.3E-1 4.0E-1 P_Value 1.6E-2 3.8E-2	Change 4.8E0 2.4E0 2.2E0 Fold Change 3.0E0 3.0E0	4.9E-1 1.0E0 1.0E0 Benjamini 6.6E-2 3.8E-1	1 9.6 1 9.6 1 FD 4.7 2 3.6
nnot	GOTERM_BP_DIRECT GOTERM_BP_DIRECT tation Cluster 242 BIOCARTA GOTERM_BP_DIRECT	positive regulation of NFAT protein import into nucleus calcineurin-NFAT signaling cascade Enrichment Score: 0.65 Small Leucine-rich Proteoglycan (SLRP) molecules keratan sulfate catabolic process glycosylation site:N-linked (GlcNAc) (keratan sulfate)	RT RT G RT RT RT	i i i	3 4 3 Count 6 6 3	1.2E-1 2.3E-1 4.0E-1 P_Value 1.6E-2 3.8E-2 5.8E-2	Change 4.8E0 2.4E0 2.2E0 Fold Change 3.0E0 3.0E0 6.8E0	4.9E-1 1.0E0 1.0E0 Benjamini 6.6E-2 3.8E-1 8.4E-1	1 9.6 1 9.6 1 FD 4.7 2 3.6 1 8.1
annot	GOTERM_BP_DIRECT GOTERM_BP_DIRECT tation Cluster 242 BIOCARTA GOTERM_BP_DIRECT UP_SEQ_FEATURE UP_KEYWORDS	positive regulation of NFAT protein import into nucleus calcineurin-NFAT signaling cascade Enrichment Score: 0.65 Small Leucine-rich Proteoglycan (SLRP) molecules keratan sulfate catabolic process glycosylation site:N-linked (GlcNAc) (keratan sulfate) Proteoglycan	RT RT G RT RT RT RT		3 4 3 Count 6 6 3 11	1.2E-1 2.3E-1 4.0E-1 P_Value 1.6E-2 3.8E-2 5.8E-2 1.7E-1	Change 4.8E0 2.4E0 2.2E0 Fold Change 3.0E0 3.0E0 6.8E0 1.5E0	4.9E-1 1.0E0 1.0E0 Benjamini 6.6E-2 3.8E-1 8.4E-1 5.2E-1	1 9.6 1 9.6 1 4.7 2 3.6 1 8.1 1 4.0 1
nnnot	GOTERM_BP_DIRECT GOTERM_BP_DIRECT tation Cluster 242 BIOCARTA GOTERM_BP_DIRECT UP_SEQ_FEATURE UP_KEYWORDS GOTERM_BP_DIRECT	positive regulation of NFAT protein import into nucleus calcineurin-NFAT signaling cascade Enrichment Score: 0.65 Small Leucine-rich Proteoglycan (SLRP) molecules keratan sulfate catabolic process glycosylation site:N-linked (GlcNAc) (keratan sulfate) Proteoglycan keratan sulfate biosynthetic process	RT RT G RT RT RT		3 4 3 Count 6 6 3 11	1.2E-1 2.3E-1 4.0E-1 P_Value 1.6E-2 3.8E-2 5.8E-2 1.7E-1 5.2E-1	Change 4.8E0 2.4E0 2.2E0 Fold Change 3.0E0 6.8E0 1.5E0 1.3E0	4.9E-1 1.0E0 1.0E0 Benjamini 6.6E-2 3.8E-1 8.4E-1 5.2E-1 1.0E0	1 9.6 1 9.6 1 4.7 2 3.6 1 8.1 1 9.6 1
Annot	GOTERM_BP_DIRECT GOTERM_BP_DIRECT tation Cluster 242 BIOCARTA GOTERM_BP_DIRECT UP_SEQ_FEATURE UP_KEYWORDS GOTERM_BP_DIRECT GOTERM_CC_DIRECT	positive regulation of NFAT protein import into nucleus calcineurin-NFAT signaling cascade Enrichment Score: 0.65 Small Leucine-rich Proteoglycan (SLRP) molecules keratan sulfate catabolic process glycosylation site:N-linked (GlcNAc) (keratan sulfate) Proteoglycan	RT RT G RT RT RT RT		3 4 3 Count 6 6 3 11	1.2E-1 2.3E-1 4.0E-1 P_Value 1.6E-2 3.8E-2 5.8E-2 1.7E-1 5.2E-1	Change 4.8E0 2.4E0 2.2E0 Fold Change 3.0E0 3.0E0 6.8E0 1.5E0	4.9E-1 1.0E0 1.0E0 Benjamini 6.6E-2 3.8E-1 8.4E-1 5.2E-1 1.0E0	9.6 1 9.6 1 4.7 2 3.6 1 4.0 1 9.6 1 8.1 1 8.8 1
Annot	GOTERM_BP_DIRECT GOTERM_BP_DIRECT tation Cluster 242 BIOCARTA GOTERM_BP_DIRECT UP_SEQ_FEATURE UP_KEYWORDS GOTERM_BP_DIRECT	positive regulation of NFAT protein import into nucleus calcineurin-NFAT signaling cascade Enrichment Score: 0.65 Small Leucine-rich Proteoglycan (SLRP) molecules keratan sulfate catabolic process glycosylation site:N-linked (GlcNAc) (keratan sulfate) Proteoglycan keratan sulfate biosynthetic process	RT RT RT RT RT RT RT RT		3 4 3 Count 6 6 3 11	1.2E-1 2.3E-1 4.0E-1 P_Value 1.6E-2 3.8E-2 5.8E-2 1.7E-1 5.2E-1 7.0E-1	Change 4.8E0 2.4E0 2.2E0 Fold Change 3.0E0 6.8E0 1.5E0 1.3E0	4.9E-1 1.0E0 1.0E0 Benjamin 6.6E-2 3.8E-1 8.4E-1 5.2E-1 1.0E0 1.0E0	1 9.6 1 9.6 1 4.7 2 3.6 1 8.1 1 9.6 1 8.8
Annot	GOTERM_BP_DIRECT GOTERM_BP_DIRECT tation Cluster 242 BIOCARTA GOTERM_BP_DIRECT UP_SEQ_FEATURE UP_KEYWORDS GOTERM_BP_DIRECT GOTERM_CC_DIRECT	positive regulation of NFAT protein import into nucleus calcineurin-NFAT signaling cascade Enrichment Score: 0.65 Small Leucine-rich Proteoglycan (SLRP) molecules keratan sulfate catabolic process glycosylation site:N-linked (GlcNAc) (keratan sulfate) Proteoglycan keratan sulfate biosynthetic process lysosomal lumen	RT RT RT RT RT RT RT RT		3 4 3 Count 6 6 3 11 6 13	1.2E-1 2.3E-1 4.0E-1 P_Value 1.6E-2 3.8E-2 5.8E-2 1.7E-1 5.2E-1 7.0E-1 7.6E-1	Change 4.8E0 2.4E0 2.2E0 Fold Change 3.0E0 6.8E0 1.5E0 1.3E0 9.7E-1	4.9E-1 1.0E0 1.0E0 Benjamini 6.6E-2 3.8E-1 8.4E-1 5.2E-1 1.0E0 1.0E0 1.0E0	1 9.6 1 9.6 1 4.7 2 3.6 1 8.1 1 9.6 1 8.8 1 8.8 1
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT tation Cluster 242 BIOCARTA GOTERM_BP_DIRECT UP_SEQ_FEATURE UP_KEYWORDS GOTERM_BP_DIRECT GOTERM_CC_DIRECT GOTERM_CC_DIRECT	positive regulation of NFAT protein import into nucleus calcineurin-NFAT signaling cascade Enrichment Score: 0.65 Small Leucine-rich Proteoglycan (SLRP) molecules keratan sulfate catabolic process glycosylation site:N-linked (GlcNAc) (keratan sulfate) Proteoglycan keratan sulfate biosynthetic process lysosomal lumen Golgi lumen	RT RT RT RT RT RT RT RT RT		3 4 3 Count 6 6 3 11 6 13	1.2E-1 2.3E-1 4.0E-1 P_Value 1.6E-2 3.8E-2 5.8E-2 1.7E-1 5.2E-1 7.0E-1 7.6E-1	Change 4.8E0 2.4E0 2.2E0 Fold Change 3.0E0 6.8E0 1.5E0 1.3E0 9.7E-1 9.3E-1 8.1E-1 5.1E-1	4.9E-1 1.0E0 1.0E0 Benjamini 6.6E-2 3.8E-1 8.4E-1 1.0E0 1.0E0 1.0E0 1.0E0	1 9.6 1 9.6 1 4.7 2 3.6 1 8.1 1 9.6 1 8.8 1 8.8 1
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT tation Cluster 242 BIOCARTA GOTERM_BP_DIRECT UP_SEQ_FEATURE UP_KEYWORDS GOTERM_BP_DIRECT GOTERM_CC_DIRECT UP_KEYWORDS UP_KEYWORDS UP_KEYWORDS tation Cluster 243	positive regulation of NFAT protein import into nucleus calcineurin-NFAT signaling cascade Enrichment Score: 0.65 Small Leucine-rich Proteoglycan (SLRP) molecules keratan sulfate catabolic process glycosylation site:N-linked (GlcNAc) (keratan sulfate) Proteoglycan keratan sulfate biosynthetic process lysosomal lumen Golgi lumen Sulfation	RT		3 4 3 Count 6 6 3 11 6 13 14 6	1.2E-1 2.3E-1 4.0E-1 P_Value 1.6E-2 3.8E-2 5.8E-2 1.7E-1 5.2E-1 7.0E-1 7.6E-1 8.8E-1	Change 4.8E0 2.4E0 2.2E0 Fold Change 3.0E0 3.0E0 6.8E0 1.5E0 1.3E0 9.7E-1 9.3E-1 8.1E-1 5.1E-1	4.9E-1 1.0E0 1.0E0 Benjamini 6.6E-2 3.8E-1 8.4E-1 1.0E0 1.0E0 1.0E0 1.0E0	9.6 1 9.6 1 4.7 2 3.6 1 4.0 1 9.6 1 8.1 1 8.8 1 8.8 1 1.0
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT tation Cluster 242 BIOCARTA GOTERM_BP_DIRECT UP_SEQ_FEATURE UP_KEYWORDS GOTERM_BP_DIRECT GOTERM_CC_DIRECT UP_KEYWORDS UP_KEYWORDS UP_KEYWORDS	positive regulation of NFAT protein import into nucleus calcineurin-NFAT signaling cascade Enrichment Score: 0.65 Small Leucine-rich Proteoglycan (SLRP) molecules keratan sulfate catabolic process glycosylation site:N-linked (GlcNAc) (keratan sulfate) Proteoglycan keratan sulfate biosynthetic process lysosomal lumen Golgi lumen Sulfation Extracellular matrix	RT		3 4 3 Count 6 6 3 11 6 13 14 6 19	1.2E-1 2.3E-1 4.0E-1 P_Value 1.6E-2 3.8E-2 5.8E-2 1.7E-1 7.0E-1 7.6E-1 8.8E-1 1.0E0	Change 4.8E0 2.4E0 2.2E0 Fold Change 3.0E0 3.0E0 6.8E0 1.5E0 1.3E0 9.7E-1 9.3E-1 8.1E-1 5.1E-1 Fold Change	4.9E-1 1.0E0 1.0E0 Benjamin 6.6E-2 3.8E-1 8.4E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	9.6 1 9.6 1 4.7 2 3.6 1 4.0 1 9.6 1 8.1 1 8.8 1 8.8 1 1.0 1 1.0
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT tation Cluster 242 BIOCARTA GOTERM_BP_DIRECT UP_SEQ_FEATURE UP_KEYWORDS GOTERM_BP_DIRECT GOTERM_CC_DIRECT UP_KEYWORDS UP_KEYWORDS UP_KEYWORDS tation Cluster 243	positive regulation of NFAT protein import into nucleus calcineurin-NFAT signaling cascade Enrichment Score: 0.65 Small Leucine-rich Proteoglycan (SLRP) molecules keratan sulfate catabolic process glycosylation site:N-linked (GlcNAc) (keratan sulfate) Proteoglycan keratan sulfate biosynthetic process lysosomal lumen Golgi lumen Sulfation Extracellular matrix Enrichment Score: 0.64	RT RT G RT RT RT RT RT RT RT RT RT G		3 4 3 Count 6 6 3 11 6 13 14 6 19 Count	1.2E-1 2.3E-1 4.0E-1 P_Value 1.6E-2 3.8E-2 5.8E-2 1.7E-1 5.2E-1 7.0E-1 7.6E-1 8.8E-1 1.0E0 P_Value	Change 4.8E0 2.4E0 2.2E0 Fold Change 3.0E0 6.8E0 1.5E0 1.3E0 9.7E-1 9.3E-1 8.1E-1 5.1E-1 Fold Change 3.4E0	4.9E-1 1.0E0 1.0E0 Benjamini 6.6E-2 3.8E-1 8.4E-1 5.2E-1 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini	9.66 1 9.61 4.72 3.66 1 8.1 1 9.66 1 8.8 1 8.8 1 1.0 6.6

Anno	otation Cluster 1	Enrichment Score: ?	G	To the second se	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_BP_DIRECT	positive regulation of sodium ion transport	<u>RT</u>	i	5	4.0E-1		1.0E0	9.6E- 1
	GOTERM_MF_DIRECT	sodium channel regulator activity	<u>RT</u>	i	7	4.5E-1	1.3E0	1.0E0	8.9E- 1
Anno	otation Cluster 244	Enrichment Score: 0.64	G	17	Count	P_Value	Fold Change	Benjamini	
	GOTERM_MF_DIRECT	GKAP/Homer scaffold activity	<u>RT</u>	i	3	1.3E-1		5.9E-1	5.3E- 1
	GOTERM_BP_DIRECT	vocalization behavior	<u>RT</u>	1	5	2.0E-1	2.1E0	1.0E0	9.6E-
	GOTERM_BP_DIRECT	adult behavior	RT	1	6	4.5E-1	1.4E0	1.0E0	1 9.6E-
Anno	otation Cluster 245	Enrichment Score: 0.63	G		Count	P_Value	Fold	Daniamini	1 FDR
	GOTERM_BP_DIRECT	type I interferon signaling pathway	RT		15	1.8E-1	Change	1.0E0	9.6E-
	UP_KEYWORDS	Antiviral defense	RT		21	2.4E-1		7.1E-1	1 5.5E-
	GOTERM_BP_DIRECT	defense response to virus	RT		32	2.9E-1		1.0E0	1 9.6E-
Anno	otation Cluster 246	Enrichment Score: 0.63	G	-	Count	P_Value	Fold	Daniamini	1 EDR
	GOTERM_BP_DIRECT	lung-associated mesenchyme development	RT		5	7.3E-2	Change	5.8E-1	5.5E-
	GOTERM_BP_DIRECT	branching involved in salivary gland							1 9.6E-
	GOTERM_BP_DIRECT	<u>morphogenesis</u>	<u>RT</u>		4	2.8E-1		1.0E0	1 9.6E-
		midbrain development	<u>RT</u>	1	6	6.2E-1	Fold	1.0E0	1
Anno	otation Cluster 247 KEGG_PATHWAY	Enrichment Score: 0.63	G	-	Count	P_Value	Change		FDR 9.3E-
	GOTERM_MF_DIRECT	<u>Circadian rhythm</u>	<u>RT</u>	•	13	9.3E-3	2.2E0	1.8E-2	3 1.1E-
		AMP-activated protein kinase activity	<u>RT</u>	i	5	1.8E-2	4.3E0	1.2E-1	1
	GOTERM_CC_DIRECT	nucleotide-activated protein kinase complex	<u>RT</u>	i	6	1.9E-2	3.5E0	1.2E-1	1.1E- 1
	UP_SEQ_FEATURE	domain:CBS 3	<u>RT</u>	i	3	5.8E-2	6.8E0	8.4E-1	8.1E- 1
	UP_SEQ_FEATURE	domain:CBS 4	<u>RT</u>	i	3	5.8E-2	6.8E0	8.4E-1	8.1E- 1
	BIOCARTA	Reversal of Insulin Resistance by Leptin	<u>RT</u>	i	7	1.1E-1	1.9E0	2.9E-1	2.0E- 1
	GOTERM_BP_DIRECT	carnitine shuttle	<u>RT</u>	i	4	1.8E-1	2.6E0	1.0E0	9.6E- 1
	UP_KEYWORDS	Fatty acid biosynthesis	<u>RT</u>	i .	10	3.4E-1	1.3E0	9.4E-1	7.3E- 1
	GOTERM_BP_DIRECT	fatty acid biosynthetic process	<u>RT</u>	1	9	6.7E-1	1.0E0	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	domain:CBS 1	<u>RT</u>	i .	3	7.6E-1	1.1E0	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	domain:CBS 2	<u>RT</u>	i	3	7.6E-1	1.1E0	1.0E0	9.6E- 1
	UP_KEYWORDS	CBS domain	<u>RT</u>	1	3	8.1E-1	1.0E0	1.0E0	8.1E- 1
	INTERPRO	<u>Cystathionine beta-synthase, core</u>	<u>RT</u>	1	3	8.6E-1	9.3E-1	1.0E0	9.1E-
	SMART	<u>CBS</u>	RT		3	8.9F-1	8.7E-1	1.0E0	1 9.1E-
	UP_KEYWORDS	Fatty acid metabolism	RT		13		7.2E-1		1 9.6E-
	UP_KEYWORDS	<u>Lipid biosynthesis</u>	RT		11	1.0E0	4.8E-1		1 1.0E0
	UP_KEYWORDS	<u>Lipid metabolism</u>	<u>RT</u>	i	19	1.0E0	3.0E-1 Fold		1.0E0
Anno	otation Cluster 248	Enrichment Score: 0.63	G	1	Count	P_Value	Change	Benjamini	
	GOTERM_BP_DIRECT	positive regulation of interleukin-12 production	<u>RT</u>	•	8	1.2E-1	1.9E0	7.7E-1	7.4E- 1
	GOTERM_BP_DIRECT	positive regulation of interleukin-10 production	<u>RT</u>	i	7	1.8E-1	1.8E0	1.0E0	9.6E- 1
	BIOCARTA	Dendritic cells in regulating TH1 and TH2 Development	<u>RT</u>	i	8	6.2E-1		9.5E-1	6.7E- 1
Anno	otation Cluster 249	Enrichment Score: 0.63	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	KEGG_PATHWAY	Dorso-ventral axis formation	<u>RT</u>	i e	12	8.1E-3	2.3E0	1.6E-2	8.1E- 3
	UP_SEQ_FEATURE	repeat:LNR 3	<u>RT</u>	i	4	1.1E-2	6.8E0	2.2E-1	2.1E- 1
	INTERPRO	Notch, NOD domain	<u>RT</u>	i	4	1.5E-2	6.2E0	1.3E-1	1.1E- 1
	INTERPRO	Notch, NODP domain	<u>RT</u>	i .	4	1.5E-2	6.2E0	1.3E-1	1.1E- 1
	UP_SEQ_FEATURE	repeat:LNR 1	<u>RT</u>	i .	4	2.5E-2	5.5E0	4.4E-1	4.3E- 1
	UP_SEQ_FEATURE	repeat:LNR 2	<u>RT</u>	i	4	2.5E-2	5.5E0	4.4E-1	4.3E-
	UP_SEQ_FEATURE	domain:EGF-like 28	<u>RT</u>	i	4	2.5E-2	5.5E0	4.4E-1	4.3E-
	SMART	<u>SM01338</u>	<u>RT</u>	i e	4	4.9E-2	4.1E0	3.0E-1	2.7E-
	SMART	<u>SM01339</u>	RT		4	4.9E-2		3.0E-1	1 2.7E-
	UP_SEQ_FEATURE	domain:EGF-like 29			3		6.8E0		1 8.1E-
				•					1

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

	ation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamin	
	SMART	<u>HMG</u>	<u>RT</u>	1	14	5.9E-1	1.1E0	1.0E0	9.1 1
not	ation Cluster 251	Enrichment Score: 0.61	G	178	Count	P_Value	Fold Change	Benjamin	i FD
	INTERPRO	Actin-related protein 3 (Arp3)	<u>RT</u>	i	3	7.0E-2	•	4.1E-1	3.7
	GOTERM_CC_DIRECT	Arp2/3 protein complex	<u>RT</u>		4	2.9E-1	2 1F0	8.6E-1	7.!
	GOTERM_BP_DIRECT			-					1 9.0
		Arp2/3 complex-mediated actin nucleation	<u>RT</u>		4	7.4E-1		1.0E0	1
ıot	ation Cluster 252	Enrichment Score: 0.6	G		Count	P_Value	Fold Change	Benjamin	
	INTERPRO	Natriuretic peptide receptor	<u>RT</u>	i	3	7.0E-2	6.2E0	4.1E-1	3. 1
	GOTERM_MF_DIRECT	natriuretic peptide receptor activity	<u>RT</u>	i	3	7.5E-2	6.0E0	3.9E-1	3. ₄
	GOTERM_MF_DIRECT	hormone binding	<u>RT</u>	1	4	2.8E-1	2.2E0	1.0E0	8. 1
	INTERPRO	Extracellular ligand-binding receptor	<u>RT</u>		5	8.5E-1	8.6E-1	1.0E0	9.
	GOTERM_MF_DIRECT								1 8.
		peptide hormone binding	<u>RT</u>		4	1	8.8E-1	1	1
ota	ation Cluster 253	Enrichment Score: 0.59	G		Count	P_Value	Change	Benjamin	_
	BBID BBID	108.Regulating glucose transport 104.Insulin signaling	RT RT		7 9	1.1E-1 2.5E-1	1.9E0 1.4E0	1.0E0 1.0E0	1. 1.
	BBID	105.Signaling glucose uptake	RT	i	6	2.8E-1		1.0E0	1.
	BBID	106.Glycogen synthase-synthesis	<u>RT</u>	1	5	3.3E-1		1.0E0	1.
	BBID	107.mRNA translation-protein synthesis	<u>RT</u>		7	4.1E-1	Fold	1.0E0	1.
ota	ation Cluster 254	Enrichment Score: 0.58	G	-	Count	P_Value	Change	Benjamin	_
	GOTERM_BP_DIRECT	execution phase of apoptosis	<u>RT</u>	i	7	4.0E-2	2.6E0	3.9E-1	3. 1
	BIOCARTA	Role of Mitochondria in Apoptotic Signaling	<u>RT</u>	i	12	7.0E-2	1.7E0	2.0E-1	1. 1
	BIOCARTA	<u>D4-GDI Signaling Pathway</u>	<u>RT</u>		8	9.5E-2	1.9E0	2.5E-1	1. 1
	GOTERM_MF_DIRECT	death receptor binding	<u>RT</u>		6	1.2E-1	2.2E0	5.5E-1	4.
	INTERPRO								1 8.
		Peptidase C14, caspase precursor p45, core	<u>RT</u>	•	5	1.8E-1		8.7E-1	1
	BBID INTERPRO	86.Apoptosis Nematode& Vert Peptidase C14, ICE, catalytic subunit p20,	RT		6	2.0E-1		1.0E0	1. 9.
	INTERPRO	active site	<u>RT</u>	•	4	2.1E-1	2.5E0	9.9E-1	1
		Peptidase C14, ICE, catalytic subunit p20	<u>RT</u>	i	5	2.1E-1	2.1E0	1.0E0	9. 1
	GOTERM_BP_DIRECT	response to cobalt ion	<u>RT</u>	i	3	2.7E-1	3.0E0	1.0E0	9. 1
	INTERPRO	Peptidase C14, caspase non-catalytic subunit p10	<u>RT</u>	1	4	3.0E-1	2.1E0	1.0E0	9. 1
	GOTERM_CC_DIRECT	death-inducing signaling complex	<u>RT</u>	4	3	3.0E-1	2.7E0	8.8E-1	7.
	GOTERM_MF_DIRECT	cysteine-type endopeptidase activity involved		-	4			1.050	1 8.
	BIOCARTA	in apoptotic process	<u>RT</u>	•	4	3.8E-1	1.8EU	1.0E0	1
	BIOCARIA	Caspase Cascade in Apoptosis	<u>RT</u>	•	10	3.8E-1	1.3E0	7.0E-1	4. 1
	SMART	CASc	<u>RT</u>	1	5	4.0E-1	1.6E0	1.0E0	9. 1
	BBID	72.IAP interaction with cell death pathways	<u>RT</u>	1	6	7.0E-1	1.1E0	1.0E0	1.
	BBID	150.caspase and NFKB activation	<u>RT</u>	i	6	8.1E-1	9.6E-1	1.0E0	1.
	GOTERM_MF_DIRECT	<u>cysteine-type endopeptidase activity</u>	<u>RT</u>	•	9	8.3E-1	8.8E-1	1.0E0	8. 1
	UP_KEYWORDS	<u>Thiol protease</u>	<u>RT</u>	Ē.	9	1.0E0	4.0E-1	1.0E0	1.
ot	ation Cluster 255	Enrichment Score: 0.58	G		Count	P_Value	Fold Change	Benjamin	i Fl
	GOTERM_BP_DIRECT	beta-catenin destruction complex disassembly	<u>RT</u>	i	7	1.5E-1	1.9E0	8.9E-1	8. 1
	INTERPRO	DIX domain	<u>RT</u>		3	2.5E-1	3.1E0	1.0E0	9. 1
	UP_SEQ_FEATURE	domain:DIX	<u>RT</u>	-	3	2.7E-1	2 9F0	1.0E0	9.
	SMART			•					1 9.
		DAX	<u>RT</u>	i	3	4.6E-1	Fold	1.0E0	1
ota	ation Cluster 256	Enrichment Score: 0.57	G	100	Count	P_Value	Fold Change	Benjamin	i Fl
	GOTERM_MF_DIRECT	RNA polymerase II transcription factor activity, TBP-class protein binding, involved in preinitiation complex assembly	<u>RT</u>	i	3	7.5E-2	6.0E0	3.9E-1	3. 1
	GOTERM_CC_DIRECT	transcription factor TFIID complex	<u>RT</u>	i	9	2.0E-1	1.6E0	7.3E-1	6. 1
	GOTERM_MF_DIRECT	transcription factor activity, RNA polymerase II core promoter sequence-specific binding involved in preinitiation complex assembly	<u>RT</u>	i	3	4.6E-1	2.0E0	1.0E0	8. 1
	GOTERM_BP_DIRECT	RNA polymerase II transcriptional	<u>RT</u>	1	3	7.5E-1	1.2E0	1.0E0	9.
ot:	ation Cluster 257	preinitiation complex assembly Enrichment Score: 0.57	G	-	Count	P_Value	Fold		1 i Fi
	UP_SEQ_FEATURE						-	•	9.
		zinc finger region:CR-type	<u>RT</u>	i	3	1.1E-1	5.1EU	1.0E0	1
	UP_SEQ_FEATURE	repeat:CXXCXGXG motif	<u>RT</u>	1	3	1 1F-1	5.1E0	1.0E0	9.

NITERPRO	Annota	ition Cluster 1	Enrichment Score: ?	G	·	Count	P_Value	Fold	Benjamini	i FDR
MITERINO CENTER MITE		INTERPRO	Chaperone DnaJ			3		Change		5.8E-
NTERPRO		INTERPRO				4	1.7E-1	2.8E0	8.2E-1	7.5E-
INTERPRO		INTERPRO			-					1 7.5E-
MYERPRO		INTERPRO			-					1 8.1E-
W. SEG, PEATURE Committee		INTERPRO								1 9.1E-
MTERPRO		UP SEO FEATURE								
SMART Deal R.										1
Monteston Coulant 2011 Section			<u>DnaJ domain</u>	<u>RT</u>	•	8	7.4E-1	9.7E-1	1.0E0	1
GOTERAL RP_DIRECT ambrook hindrich morthopereds ET 7 3.51 1.550 1.050 7.00		SMARI	_			8	1	Fold	1	1
GOTERALIP-DIRECT solutional social morphophosphases ET 7 3.51-1 3.51-1 1.600 5.6	Annota							Change		
GOTEMA_MP_DIRECT Closer Section Sectio				<u>RT</u>		3	7.6E-2	5.9E0	5.8E-1	1
Amoutation Cluster 250 DOTERN_MP_DRECT Seloments Bores 0.56 COUNT P_VAIN Find F			embryonic hindlimb morphogenesis	<u>RT</u>	i	7	3.3E-1	1.5E0	1.0E0	1
GOTERN_MP_DRECT Informerson RNA Information RT		GOTERM_BP_DIRECT	embryonic forelimb morphogenesis	<u>RT</u>	i	5	8.1E-1	•	1.0E0	9.6E- 1
GOTERM_BP_DIRECT Selement ministerate with a between tender and in the selement an	Annota		Enrichment Score: 0.56	G	Maria de la companya della companya	Count	P_Value	Fold Change	Benjamin	
UP_KEYWORDS Descontants consents RT		GOTERM_MF_DIRECT	telomerase RNA binding	<u>RT</u>	i	6	1.2E-1	2.2E0	5.5E-1	4.9E- 1
INTERPRO DAL directed DNA polymerase, family B. Interpro DAL directed DNA polymerase, family B. Interpro DAL directed DNA polymerase, family B. Interpro DAL directed DNA polymerase activity B. Interpro DAL directed DNA polym		GOTERM_BP_DIRECT	telomere maintenance via telomerase	<u>RT</u>	i	5	3.6E-1	1.6E0	1.0E0	9.6E- 1
NTERPRO BRCT domain: BCCT 1 RT		UP_KEYWORDS	<u>Dyskeratosis congenita</u>	<u>RT</u>	i .	3	4.9E-1	1.9E0	1.0E0	7.8E- 1
UP_SEQ_FEATURE domain_BRCT 1 RT	Annota	ition Cluster 260	Enrichment Score: 0.56		To the second se	Count	P_Value	Fold Change	Benjamin	i FDR
UP_SEQ_FEATURE UP_SEQ_FEATURE Domain-BRCT 2 RT		INTERPRO	BRCT domain	<u>RT</u>	i	8	1.5E-1	1.8E0	7.7E-1	7.0E- 1
SMART BRCT RI		UP_SEQ_FEATURE	domain:BRCT 1	<u>RT</u>	i .	4	2.5E-1	2.3E0	1.0E0	9.6E- 1
SMART BRCT RT		UP_SEQ_FEATURE	domain:BRCT 2	<u>RT</u>	i	4	2.5E-1	2.3E0	1.0E0	9.6E-
UP_SEQ_FEATURE domain:BRCT RT		SMART	<u>BRCT</u>	<u>RT</u>	i	7	2.7E-1	1.6E0	1.0E0	9.1E-
Annotation Cluster 261		UP_SEQ_FEATURE	domain:BRCT	<u>RT</u>	i .	3	6.3E-1	1.5E0	1.0E0	9.6E-
INTERPRO DMA-directed DMA polymerase, family B, RT	Annota	ition Cluster 261	Enrichment Score: 0.56	G	·	Count	P_Value		Benjamin	
INTERPRO DiAk-directed DNA polymerase, family B, multifunctional domain multifunctional multifunctional domain multifunctional multifunctio		INTERPRO				3	<u> </u>	Change	6.4E-1	5.8E-
INTERPRO DNA-directed DNA polymerase, family B RI		INTERPRO	DNA-directed DNA polymerase, family B,	<u>RT</u>		3	1.2E-1	4.6E0	6.4E-1	5.8E-
GOTERM_MF_DIRECT 3-5' exonuclease activity. RT		INTERPRO		<u>RT</u>	i .	3	1.2E-1	4.6E0	6.4E-1	5.8E-
SMART POLBC RT		GOTERM_MF_DIRECT	<u>3'-5' exonuclease activity</u>	<u>RT</u>	i	6	2.0E-1	1.9E0	7.9E-1	7.1E-
UP_KEYWORDS DNA-directed DNA polymerase RT		SMART	<u>POLBc</u>	<u>RT</u>		3	2.5E-1	3.0E0	9.9E-1	9.0E-
GOTERM_MF_DIRECT DNA-directed DNA polymerase activity I P_KEYWORDS dFe-4S RI		UP_KEYWORDS	DNA-directed DNA polymerase	RT		6	2.7E-1	1.7E0	7.6E-1	5.9E-
UP_KEYWORDS 4Fe-4S RT		GOTERM_MF_DIRECT				7	3.6E-1	1.4E0	1.0E0	8.9E-
GOTERM_MF_DIRECT 4 iron, 4 sulfur cluster binding RT i 7, 3E-1 9,9E-1 1,0E0 8,9 1 op_KEYWORDS Iron-sulfur RT i 7, 3E-1 9,9E-1 1,0E0 8,9 Annotation Cluster 262 Enrichment Score: 0.55 Count P_value Fold Change Benjamin FDI BIOCARTA Nitric Oxide Signaling Pathway RT i 1,5E-1 1,5E-1 1,5E-0 3,5E-1 1, BIOCARTA Effects of calcineurin in Keratinocyte Differentiation BIOCARTA Role of MEF2D in T-cell Apoptosis RT i 7,57E-1 1,2E0 8,9E-1 3,7 Annotation Cluster 263 Enrichment Score: 0.55 GOTERM_CC_DIRECT L'eappaB/NF-kappaB complex RT i 4,3E-2 5,1E0 1,8E-1 1, INTERPRO REI i 4,3E-2 5,1E0 1,8E-1 1, INTERPRO Rel homology domain RT i 4,2E-1 2,5E0 9,9E-1 9,1 INTERPRO P_SS-Like transcription factor, DNA-binding RT i 6,5E-1 1,2E0 1,0E0 9,1 INTERPRO Cell surface receptor IPT/TIG RT i 6,5E-1 1,2E0 1,0E0 9,1 INTERPRO Cell surface receptor IPT/TIG RT i 6,5E-1 1,2E0 1,0E0 9,1 INTERPRO COTERM_MF_DIRECT COUNT P_Value Fold Change REI 1,0E0 9,1 RI i 6,5E-1 1,2E0 1,0E0 9,1		UP_KEYWORDS								7.8E-
UP_KEYWORDS Iron-sulfur RT		GOTERM_MF_DIRECT								1 8.9E-
Annotation Cluster 262		UP_KEYWORDS								1 8.9E-
BIOCARTA Nitric Oxide Signaling Pathway RT						:	•		:	1
BIOCARTA	Annota							Change		2.5E-
BIOCARTA Role of MEF2D in T-cell Apoptosis RT										1 3.7E-
Annotation Cluster 263			Differentiation	<u>RT</u>	1	9			5.2E-1	1
GOTERM_CC_DIRECT I-kappaB/NF-kappaB complex RT		BIOURIA	Role of MEF2D in T-cell Apoptosis		1	:	:		:	6.3E- 1
INTERPRO NF-kappa-B/Rel/Dorsal RT	Annota		Enrichment Score: 0.55	G		Count	P_Value	Change	Benjamin	
INTERPRO Rel homology domain RT			<u>I-kappaB/NF-kappaB complex</u>	<u>RT</u>	i	4	3.0E-2	5.1E0	1.8E-1	1.6E- 1
UP_SEQ_FEATURE domain:RHD RT 3 3.9E-1 2.3E0 1.0E0 9.6 1 INTERPRO p53-like transcription factor, DNA-binding RT P53-like transcription factor, DNA-binding RT OCEll surface receptor IPT/TIG RT GOTERM_MF_DIRECT transcriptional activator activity, RNA polymerase II distal enhancer sequence-specific binding			NF-kappa-B/Rel/Dorsal	<u>RT</u>	i	4	3.2E-2	5.0E0	2.4E-1	_
INTERPRO p53-like transcription factor, DNA-binding RT 9 4.2E-1 1.3E0 1.0E0 1 INTERPRO Cell surface receptor IPT/TIG RT GOTERM_MF_DIRECT transcriptional activator activity, RNA polymerase II distal enhancer sequence-specific binding EMART		INTERPRO	Rel homology domain	<u>RT</u>	i	4	2.1E-1	2.5E0	9.9E-1	9.1E- 1
INTERPRO Cell surface receptor IPT/TIG GOTERM_MF_DIRECT transcriptional activator activity, RNA polymerase II distal enhancer sequence- specific binding SMART 9 4.2E-1 1.3E0 1.0E0 1 1 5 5.8E-1 1.2E0 1.0E0 1 8.9 1		UP_SEQ_FEATURE	domain:RHD	<u>RT</u>	i	3	3.9E-1	2.3E0	1.0E0	9.6E- 1
GOTERM_MF_DIRECT transcriptional activator activity, RNA polymerase II distal enhancer sequence- specific binding transcriptional activator activity, RNA polymerase II distal enhancer sequence- specific binding		INTERPRO	p53-like transcription factor, DNA-binding	<u>RT</u>	i	9	4.2E-1	1.3E0	1.0E0	9.1E- 1
GOTERM_MF_DIRECT transcriptional activator activity, RNA polymerase II distal enhancer sequence- specific binding transcriptional activator activity, RNA polymerase II distal enhancer sequence- specific binding		INTERPRO	Cell surface receptor IPT/TIG	<u>RT</u>	i .	6	5.8E-1	1.2E0	1.0E0	9.1E- 1
specific binding		GOTERM_MF_DIRECT		RT	•	5	6.2F-1	1.2F0	1.0E0	8.9E-
TOT Y 3		SMART	specific binding							1 9.3E-
IPT RT 5 9.3E-1 7.5E-1 1.0E0 9.3			141	<u>RT</u>	•	5	9.3E-1	7.5E-1	1.0E0	

Annota	ation Cluster 1	Enrichment Score: ?	G	™	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	Immunoglobulin E-set	<u>RT</u>	ī	12	9.7E-1	7.0E-1	1.0E0	9.7E- 1
Annota	ation Cluster 264	Enrichment Score: 0.54	G	13	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:BRO1	<u>RT</u>	i	3	2.2E-1	3.4E0	1.0E0	9.6E- 1
	INTERPRO	BRO1 domain	<u>RT</u>	i contract of	3	2.5E-1	3.1E0	1.0E0	9.1E- 1
	SMART	SM01041	<u>RT</u>	i contract of	3	4.6E-1	2.0E0	1.0E0	9.1E- 1
Annota	ation Cluster 265	Enrichment Score: 0.51	G	1	Count	P_Value	Fold Change	Benjamini	FDR
	UP_KEYWORDS	<u>Glycogen metabolism</u>	<u>RT</u>	i .	8	7.3E-2	2.1E0	2.5E-1	2.0E- 1
	GOTERM_BP_DIRECT	g <u>lycogen metabolic process</u>	<u>RT</u>	i .	8	2.1E-1	1.6E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	entrainment of circadian clock by photoperiod	<u>RT</u>	i .	4	6.8E-1	1.2E0	1.0E0	9.6E- 1
	UP_KEYWORDS	<u>Carbohydrate metabolism</u>	<u>RT</u>	i .	11	8.9E-1	8.0E-1	1.0E0	8.9E-
Annota	ation Cluster 266	Enrichment Score: 0.5	G	To the second se	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	Zinc finger, TFIIS-type	<u>RT</u>	i	3	2.5E-1		1.0E0	9.1E- 1
	UP_SEQ_FEATURE	zinc finger region:TFIIS-type	<u>RT</u>	i	3	2.7E-1	2.9E0	1.0E0	9.6E-
	SMART	<u>ZnF_C2C2</u>	<u>RT</u>	i	3	4.6E-1	2.0E0	1.0E0	9.1E-
Annota	ation Cluster 267	Enrichment Score: 0.48	G	M	Count	P_Value	Fold Change	Benjamini	
	GOTERM_BP_DIRECT	social behavior	<u>RT</u>	i	12	1.8E-1		9.8E-1	9.4E- 1
	GOTERM_BP_DIRECT	positive regulation of excitatory postsynaptic potential	<u>RT</u>	i	5	4.4E-1	1.5E0	1.0E0	9.6E-
	GOTERM_BP_DIRECT	adult behavior	<u>RT</u>		6	4.5E-1	1.4E0	1.0E0	9.6E-
Annota	ation Cluster 268	Enrichment Score: 0.46	G	™	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:KH	RT		6	7.3E-2	Change	1.0E0	9.6E-
	INTERPRO	<u>K Homology domain</u>	RT	•	10	1.5E-1	1.6E0	7.4E-1	1 6.8E-
	INTERPRO	K Homology domain, type 1	RT		10	2.7E-1		1.0E0	9.1E-
	SMART	<u>KH</u>	RT		10	6.1E-1		1.0E0	9.1E-
	UP_SEQ_FEATURE	domain:KH 3	RT		3	6.7E-1		1.0E0	1 9.6E-
	UP_SEQ_FEATURE	domain:KH 1	RT		4	7.1E-1		1.0E0	1 9.6E-
	UP_SEQ_FEATURE	domain:KH 2	RT		4	7.1E-1		1.0E0	1 9.6E-
Annota	ation Cluster 269	Enrichment Score: 0.44	G	- -	1	P_Value	Fold	Benjamini	1 FDR
	UP_SEQ_FEATURE	domain:MATH	RT		4	2.5E-1	Change	1.0E0	9.6E-
	INTERPRO	MATH	RT		4	3.0E-1		1.0E0	1 9.1E-
	INTERPRO	TRAF-like	RT		6	3.8E-1		1.0E0	1 9.1E-
	SMART	MATH.	RT		4	6.0E-1		1.0E0	1 9.1E-
Annota	ation Cluster 270	Enrichment Score: 0.44	G	· -	1	P_Value	Fold	Benjamini	1 FDR
	UP_SEQ_FEATURE	domain:SWIRM	RT		3	2.2E-1	Change	1.0E0	9.6E-
	INTERPRO	SWIRM domain	RT		3	2.5E-1		1.0E0	1 9.1E-
	INTERPRO	SANT domain	RT		6	4.1E-1		1.0E0	1 9.1E-
	UP_SEQ_FEATURE	domain:SANT	RT		3	7.9E-1		1.0E0	1 9.6E-
Annote	ation Cluster 271	Enrichment Score: 0.42	C	1				Benjamini	1
	GOTERM_BP_DIRECT	positive regulation of guanylate cyclase	RT	i	7		Change 3.8E0		8.1E-
	INTERPRO	activity			3			4.1E-1	2 3.7E-
	GOTERM_MF_DIRECT	Nitric oxide synthase, oxygenase domain	RT DT			7.0E-2			1 3.4E-
	UP_SEQ_FEATURE	nitric-oxide synthase activity	<u>RT</u>		3	7.5E-2		3.9E-1	1 9.6E-
	INTERPRO	domain:Flavodoxin-like	<u>RT</u>	1	4	1.0E-1		1.0E0	1 5.8E-
	INTERPRO	Flavodoxin/nitric oxide synthase	<u>RT</u>	•	4	1.2E-1		6.4E-1	5.8E-
		<u>Flavodoxin</u>	<u>RT</u>	•	4	1.2E-1		6.4E-1	1
	GOTERM_MF_DIRECT	<u>tetrahydrobiopterin binding</u>	<u>RT</u>	i	3	1.3E-1		5.9E-1	5.3E- 1
	GOTERM_MF_DIRECT	NADP binding	<u>RT</u>	•	9	2.2E-1	1.5E0	8.7E-1	7.8E- 1
	INTERPRO	FAD-binding, type 1	<u>RT</u>	i	3	2.5E-1	3.1E0	1.0E0	9.1E- 1

Annota	ation Cluster 1	Enrichment Score: ?	G	100	Count	P_Value	Fold Change	Benjamir	i FDR
	INTERPRO	NADPH-cytochrome p450 reductase, FAD-	RT	1	3	2 5F-1	-	1.0E0	9.1E
	UP_SEQ_FEATURE	<u>binding, alpha-helical domain-3</u>		•					1 9.6E
	or _ore_rearone	nucleotide phosphate-binding region:FMN	<u>RT</u>	i	4	3.0E-1	2.1E0	1.0E0	1
	INTERPRO	Oxidoreductase FAD/NAD(P)-binding	<u>RT</u>	i	4	3.0E-1	2.1E0	1.0E0	9.1E ⁻
	GOTERM_MF_DIRECT	arginine binding	<u>RT</u>	1	3	3.3E-1	2.6E0	1.0E0	8.9E
	GOTERM_BP_DIRECT	positive regulation of vacadilation	DT		7	2 65 1	1.4E0	1 050	1 9.6E
	COTEDM DD DIDECT	positive regulation of vasodilation	<u>RT</u>	•	/	3.0E-1	1.40	1.0E0	1
	GOTERM_BP_DIRECT	nitric oxide biosynthetic process	<u>RT</u>	i	4	3.8E-1	1.8E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	arginine catabolic process	<u>RT</u>	1	3	4.0E-1	2.2E0	1.0E0	9.6E-
	GOTERM_BP_DIRECT	nitric oxide mediated signal transduction	<u>RT</u>		5	4.0E-1	1.6E0	1.0E0	9.6E
	INTERPRO	Flavoprotein pyridine nucleotide cytochrome		-		4.45.4	2.450	1.050	1 9.1E
	COTEDN ME DIDECT	reductase	<u>RT</u>	•	3	4.4E-1	2.1E0	1.0E0	1
	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>	1	4	5.4E-1	1.4E0	1.0E0	9.6E
	KEGG_PATHWAY	Arginine biosynthesis	<u>RT</u>		5	5.6E-1	1.3E0	8.3E-1	5.6E
	UP_KEYWORDS			-	4	C 1E 1	1 250	1.050	1 7.8E
	INTERRO	FMN	<u>RT</u>	•	4	0.16-1	1.3E0	1.0E0	1
	INTERPRO	<u>Ferredoxin reductase-type FAD-binding</u> <u>domain</u>	<u>RT</u>	i	4	6.1E-1	1.3E0	1.0E0	9.1E- 1
	INTERPRO	Riboflavin synthase-like beta-barrel	<u>RT</u>	1	4	6.1E-1	1.3E0	1.0E0	9.1E ⁻
	GOTERM_BP_DIRECT	negative regulation of blood pressure	<u>RT</u>		4	9.0E-1	7.9E-1	1.0E0	9.6E
	UP_SEQ_FEATURE			-					1 9.6E
		nucleotide phosphate-binding region:FAD	<u>RT</u>	•	7	9.1E-1	7.7E-1	1.0E0	1
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:NADP	<u>RT</u>	i .	8	9.3E-1	7.4E-1	1.0E0	9.6E [.]
	UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	<u>RT</u>	1	8	9.9E-1	5.5E-1	1.0E0	9.9E
	GOTERM_MF_DIRECT	heme binding	<u>RT</u>	1	13	1.0E0	5.7E-1	1.0E0	1.0E
	KEGG_PATHWAY	Arginine and proline metabolism	<u>RT</u>	1	4	1.0E0	4.2E-1		1.0E
	COG_ONTOLOGY GOTERM_MF_DIRECT	Inorganic ion transport and metabolism flavin adenine dinucleotide binding	RT RT	1	5 4	1.0E0 1.0E0	4.7E-1 3.7E-1		1.0E
	UP_KEYWORDS	Heme	RT		9	1.0E0	4.7E-1		1.0E
	UP_KEYWORDS	FAD	<u>RT</u>	1	6	1.0E0	3.7E-1	1.0E0	1.0E
	UP_KEYWORDS UP_KEYWORDS	<u>Flavoprotein</u>	RT DT	i.	6 10	1.0E0 1.0E0	3.4E-1 3.7E-1		1.0E
Annot	ation Cluster 272	NADP Enrichment Score: 0.42	RT G		Count		Fold	Danismin	
	GOTERM_MF_DIRECT						Change		2.5E-
		calcium-transporting ATPase activity	<u>RT</u>	i	5	4.9E-2	3.3E0	2.8E-1	1
	INTERPRO	<u>Calcium-transporting P-type ATPase,</u> <u>subfamily IIA, SERCA-type</u>	<u>RT</u>	i	3	7.0E-2	6.2E0	4.1E-1	3.7E- 1
	UP_SEQ_FEATURE	metal ion-binding site:Calcium 2; via carbonyl	<u>RT</u>	1	10	1.1E-1	1.7E0	1.0E0	9.6E
	GOTERM_CC_DIRECT	oxygen	рт		3	4 2E 1	2 150	1 050	8.8E
	COTERM CC DIRECT	platelet dense tubular network membrane	<u>RT</u>	_	3	4.3E-1	2.1E0	1.0E0	1
	GOTERM_CC_DIRECT	sarcoplasmic reticulum membrane	<u>RT</u>	i	7	4.5E-1	1.3E0	1.0E0	8.8E- 1
	GOTERM_CC_DIRECT	sarcoplasmic reticulum	<u>RT</u>	1	7	4.5E-1	1.3E0	1.0E0	8.8E-
	UP_KEYWORDS	Sarcoplasmic reticulum	<u>RT</u>		6	7.1E-1	1.0E0	1.0E0	7.8E
	GOTERM_BP_DIRECT								1 9.6E
		cellular calcium ion homeostasis	<u>RT</u>		11		7.0E-1		1
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT	calcium ion transport calcium ion transmembrane transport	RT RT		6 10	1.0E0 1.0E0	4.7E-1 5.0E-1		1.0E
	UP_KEYWORDS	Calcium transport	RT	i	5	1.0E0	3.5E-1		1.0E
Annota	ation Cluster 273	Enrichment Score: 0.41	G	100	Count	P_Value	Fold Change	Benjamir	i FDR
	GOTERM_BP_DIRECT	actin crosslink formation	<u>RT</u>	i	4	2.8E-1		1.0E0	9.6E
	GOTERM_BP_DIRECT				7				1 9.6E
		actin filament bundle assembly	<u>RT</u>	i	/		1.4E0	1.000	1
	GOTERM RP DIRECT				3	5 2F-1	1.8E0	1.0E0	9.6E 1
	GOTERM_BP_DIRECT	actin filament network formation	<u>RT</u>	i		J.ZL-1			
Annota	GOTERM_BP_DIRECT ation Cluster 274	actin filament network formation Enrichment Score: 0.4	RT G	·	Count		Fold	Benjamir	ii FDR
Annota						P_Value	Fold		9.6E
Annota	ation Cluster 274	Enrichment Score: 0.4 domain:SANT 1	G RT	i i	Count	P_Value 3.9E-1	Fold Change 2.3E0	1.0E0	9.6E
Annota	ation Cluster 274 UP_SEQ_FEATURE UP_SEQ_FEATURE	Enrichment Score: 0.4	G	i i	Count	P_Value 3.9E-1	Fold Change		9.6E 1 9.6E 1
Annota	ation Cluster 274 UP_SEQ_FEATURE	Enrichment Score: 0.4 domain:SANT 1	G RT	i i	Count	3.9E-1 3.9E-1 4.1E-1	Fold Change 2.3E0 2.3E0 1.4E0	1.0E0 1.0E0	9.6E 1 9.6E 1
	ation Cluster 274 UP_SEQ_FEATURE UP_SEQ_FEATURE	Enrichment Score: 0.4 domain:SANT 1 domain:SANT 2	G RT RT	i i	3 3	3.9E-1 3.9E-1 4.1E-1	Fold Change 2.3E0 2.3E0 1.4E0	1.0E0 1.0E0 1.0E0	9.6E- 1 9.6E- 1 9.1E- 1
	ation Cluster 274 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO	Enrichment Score: 0.4 domain:SANT 1 domain:SANT 2 SANT domain	G RT RT RT	i i i	2 Count 3 3 6	3.9E-1 3.9E-1 4.1E-1 P_Value	Fold Change 2.3E0 2.3E0 1.4E0 Fold Change	1.0E0 1.0E0 1.0E0	9.6E-1 9.6E-1 1 9.1E-1 1 ii FDR
	ation Cluster 274 UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO ation Cluster 275	Enrichment Score: 0.4 domain:SANT 1 domain:SANT 2 SANT domain Enrichment Score: 0.4 Postsynaptic cell membrane	RT RT RT RT RT		Count 3 6 Count 33	3.9E-1 3.9E-1 4.1E-1 P_Value 1.3E-1	Fold Change 2.3E0 2.3E0 1.4E0 Fold Change 1.3E0	1.0E0 1.0E0 1.0E0 Benjamir 4.1E-1	9.6E-1 9.6E-1 1 9.1E-1
	up_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE INTERPRO ation Cluster 275 UP_KEYWORDS	Enrichment Score: 0.4 domain:SANT 1 domain:SANT 2 SANT domain Enrichment Score: 0.4	RT RT RT G	i i i	Count 3 3 6 Count	P_Value 3.9E-1 4.1E-1 P_Value 1.3E-1 2.0E-1	Fold Change 2.3E0 2.3E0 1.4E0 Fold Change 1.3E0	1.0E0 1.0E0 1.0E0 Benjamir 4.1E-1 7.4E-1	9.6E-1 9.6E-1 9.1E-1 1 FDR

Annota	ation Cluster 1	Enrichment Score: ?	G	· · · · · · · · · · · · · · · · · · ·	Count	P_Value	Fold	Benjamini	FDR
	UP_KEYWORDS	<u>Synapse</u>	RT	-	48		Change 9.2E-1		8.0E
	UP_KEYWORDS	Cell junction	RT		88		8.9E-1		1 9.1E
	GOTERM_CC_DIRECT								1 9.4E
		cell junction	<u>RT</u>	i	62	1	8.6E-1	!	1
Annota	ation Cluster 276	Enrichment Score: 0.4	G		Count	P_Value	Change	Benjamini	
	BBID BBID	68.Mitogen signaling in growth control 2.Cytokine Receptors	RT RT		4 4	3.8E-1 3.8E-1		1.0E0 1.0E0	1.0E 1.0E
	BBID	54.T-cell anergy	<u>RT</u>	i	8	4.3E-1		1.0E0	1.0E
Annota	ation Cluster 277	Enrichment Score: 0.39	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	Sirtuin family, catalytic core small domain	<u>RT</u>	i	3	2.5E-1	3.1E0	1.0E0	9.1E 1
	UP_SEQ_FEATURE	domain:Deacetylase sirtuin-type	<u>RT</u>	i .	3	2.7E-1	2.9E0	1.0E0	9.6E 1
	INTERPRO	Sirtuin family, catalytic core domain	<u>RT</u>	1	3	3.2E-1	2.7E0	1.0E0	9.1E 1
	INTERPRO	Sirtuin family	<u>RT</u>	1	3	3.2E-1	2.7E0	1.0E0	9.1E
	GOTERM_MF_DIRECT	NAD+ binding	RT	1	3	6.7E-1	1 4F0	1.0E0	1 8.9E
	UP_SEQ_FEATURE								1 9.8E
		nucleotide phosphate-binding region:NAD	<u>RT</u>	i	7	1	6.0E-1		1
Annota	ation Cluster 278	Enrichment Score: 0.39	G		Count	P_Value	Fold Change	Benjamini	
	GOTERM_CC_DIRECT	RISC complex	<u>RT</u>	i	4	2.4E-1	2.3E0	8.3E-1	7.3E 1
	GOTERM_CC_DIRECT	RISC-loading complex	<u>RT</u>	i .	3	3.0E-1	2.7E0	8.8E-1	7.7E 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	9.6E
	GOTERM_BP_DIRECT	pre-miRNA processing	<u>RT</u>	1	4	3.8E-1	1.8E0	1.0E0	9.6E
	GOTERM_BP_DIRECT	production of miRNAs involved in gene	RT		3	4.0E-1		1.0E0	1 9.6E
	UP_SEQ_FEATURE	silencing by miRNA		•					1 9.6E
		domain:PAZ	<u>RT</u>	•	3	4.4E-1	2.0E0	1.0E0	1
	INTERPRO	Argonaute/Dicer protein, PAZ	<u>RT</u>	1	3	5.0E-1	1.9E0	1.0E0	9.1E 1
	BIOCARTA	<u>Dicer Pathway</u>	<u>RT</u>	1	3	5.3E-1	1.8E0	8.4E-1	6.0E 1
	SMART	<u>SM00949</u>	<u>RT</u>	i -	3	6.9E-1	1.4E0	1.0E0	9.1E 1
Annota	ation Cluster 279	Enrichment Score: 0.39	G	**	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:DOC	<u>RT</u>	i	3	3.3E-1		1.0E0	9.6E
	INTERPRO	Anaphase-promoting complex, subunit	<u>RT</u>		3	3.8E-1	2.3E0	1.0E0	9.1E
	SMART	10/DOC domain			3	5.5E-1		1.0E0	1 9.1E
		<u>SM01337</u>	<u>RT</u>	•	3	5.5E-1	1.70	1.000	
Annota				-			Fold		1
	ation Cluster 280	Enrichment Score: 0.39	G	To the second se	Count	P_Value	Fold Change	Benjamini	
	GOTERM_BP_DIRECT	protein ADP-ribosylation	G RT	i	Count	P_Value 1.3E-1	Change	Benjamini 8.2E-1	7.9E 1
				-			Change 2.0E0		7.9E
	GOTERM_BP_DIRECT	protein ADP-ribosylation negative regulation of telomere maintenance	RT	i	7	1.3E-1	2.0E0 3.6E0	8.2E-1	7.9E 1 9.6E
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening	RT RT	i i	7	1.3E-1 2.0E-1	2.0E0 3.6E0 1.5E0	8.2E-1 1.0E0	7.9E 1 9.6E 1 8.9E
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening NAD+ ADP-ribosyltransferase activity domain:PARP catalytic Poly(ADP-ribose) polymerase, catalytic	RT RT RT	i i	7 3 7	1.3E-1 2.0E-1 3.3E-1	2.0E0 3.6E0 1.5E0 1.2E0	8.2E-1 1.0E0 1.0E0	7.9E 1 9.6E 1 8.9E 1 9.6E 1
	GOTERM_BP_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening NAD+ ADP-ribosyltransferase activity domain:PARP catalytic	RT RT RT RT	i i	7 3 7 3	1.3E-1 2.0E-1 3.3E-1 7.4E-1	2.0E0 3.6E0 1.5E0 1.2E0	8.2E-1 1.0E0 1.0E0 1.0E0	7.9E 1 9.6E 1 8.9E 1 9.6E
Annota	GOTERM_BP_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening NAD+ ADP-ribosyltransferase activity domain:PARP catalytic Poly(ADP-ribose) polymerase, catalytic domain	RT RT RT RT RT	i i	7 3 7 3 3	1.3E-1 2.0E-1 3.3E-1 7.4E-1 7.9E-1	2.0E0 3.6E0 1.5E0 1.1E0 1.5E-1 Fold	8.2E-1 1.0E0 1.0E0 1.0E0	7.9E 1 9.6E 1 8.9E 1 9.6E 1 9.1E 1
Annota	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO UP_KEYWORDS	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening NAD+ ADP-ribosyltransferase activity domain:PARP catalytic Poly(ADP-ribose) polymerase, catalytic domain Glycosyltransferase	RI RI RI RI RI RI	i i i i	7 3 7 3 3 5	1.3E-1 2.0E-1 3.3E-1 7.4E-1 7.9E-1 1.0E0	2.0E0 3.6E0 1.5E0 1.1E0 1.5E-1 Fold Change	8.2E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	7.9E 1 9.6E 1 8.9E 1 9.6E 1 1.0E FDR 9.6E
Annota	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO UP_KEYWORDS ation Cluster 281	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening NAD+ ADP-ribosyltransferase activity domain:PARP catalytic Poly(ADP-ribose) polymerase, catalytic domain Glycosyltransferase Enrichment Score: 0.37 zinc finger region:RanBP2-type	RT RT RT RT RT RT RT RT		7 3 7 3 3 5 Count	1.3E-1 2.0E-1 3.3E-1 7.4E-1 7.9E-1 1.0E0 P_Value 2.7E-1	2.0E0 3.6E0 1.5E0 1.2E0 1.1E0 1.5E-1 Fold Change 1.9E0	8.2E-1 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini 1.0E0	7.9E 1 9.6E 1 9.6E 1 9.1E 1 1.0E FDR 9.6E 1 9.1E
Annota	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO UP_KEYWORDS ation Cluster 281 UP_SEQ_FEATURE	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening NAD+ ADP-ribosyltransferase activity domain:PARP catalytic Poly(ADP-ribose) polymerase, catalytic domain Glycosyltransferase Enrichment Score: 0.37 zinc finger region:RanBP2-type Zinc finger, RanBP2-type	RT		7 3 7 3 3 5 Count 5	1.3E-1 2.0E-1 3.3E-1 7.4E-1 7.9E-1 1.0E0 P_Value 2.7E-1 3.8E-1	2.0E0 3.6E0 1.5E0 1.1E0 1.5E-1 Fold Change 1.9E0 1.5E0	8.2E-1 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0	7.9E 1 9.6E 1 8.9E 1 9.6E 1 1.0E FDR 9.6E 1 9.1E 1
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO UP_KEYWORDS ation Cluster 281 UP_SEQ_FEATURE INTERPRO SMART	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening NAD+ ADP-ribosyltransferase activity domain:PARP catalytic Poly(ADP-ribose) polymerase, catalytic domain Glycosyltransferase Enrichment Score: 0.37 zinc finger region:RanBP2-type Zinc finger, RanBP2-type ZnF RBZ	RT		7 3 7 3 5 Count 5 6 5	1.3E-1 2.0E-1 3.3E-1 7.4E-1 7.9E-1 1.0E0 P_Value 2.7E-1 3.8E-1 7.6E-1	2.0E0 3.6E0 1.5E0 1.2E0 1.1E0 1.5E-1 Fold Change 1.9E0 1.5E0 1.0E0	8.2E-1 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0	7.9E 1 9.6E 1 9.6E 1 9.1E 1 1.0E FDR 9.6E 1 9.1E 1 9.1E 1
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO UP_KEYWORDS ation Cluster 281 UP_SEQ_FEATURE INTERPRO SMART	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening NAD+ ADP-ribosyltransferase activity domain:PARP catalytic Poly(ADP-ribose) polymerase, catalytic domain Glycosyltransferase Enrichment Score: 0.37 zinc finger region:RanBP2-type Zinc finger, RanBP2-type	RT		7 3 7 3 3 5 Count 5	1.3E-1 2.0E-1 3.3E-1 7.4E-1 7.9E-1 1.0E0 P_Value 2.7E-1 3.8E-1	2.0E0 3.6E0 1.5E0 1.1E0 1.5E-1 Fold Change 1.9E0 1.5E0 1.0E0	8.2E-1 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0	7.9E 1 9.6E 1 9.6E 1 9.1E 1 9.1E 1 9.1E 1 FDR
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO UP_KEYWORDS ation Cluster 281 UP_SEQ_FEATURE INTERPRO SMART ation Cluster 282 UP_KEYWORDS	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening NAD+ ADP-ribosyltransferase activity domain:PARP catalytic Poly(ADP-ribose) polymerase, catalytic domain Glycosyltransferase Enrichment Score: 0.37 zinc finger region:RanBP2-type Zinc finger, RanBP2-type ZnF RBZ	RT		7 3 7 3 5 Count 5 6 5	1.3E-1 2.0E-1 3.3E-1 7.4E-1 7.9E-1 1.0E0 P_Value 2.7E-1 3.8E-1 7.6E-1	2.0E0 3.6E0 1.5E0 1.2E0 1.1E0 1.5E-1 Fold Change 1.9E0 1.5E0 1.0E0 Fold Change	8.2E-1 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0	7.9E 1 9.6E 1 9.6E 1 9.1E 1 1.0E FDR 9.6E 1 9.1E 1 9.1E 1
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO UP_KEYWORDS ation Cluster 281 UP_SEQ_FEATURE INTERPRO SMART	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening NAD+ ADP-ribosyltransferase activity domain:PARP catalytic Poly(ADP-ribose) polymerase, catalytic domain Glycosyltransferase Enrichment Score: 0.37 zinc finger region:RanBP2-type Zinc finger, RanBP2-type ZnF_RBZ Enrichment Score: 0.37	RT R		7 3 7 3 3 5 Count 5 6 5	1.3E-1 2.0E-1 3.3E-1 7.4E-1 7.9E-1 1.0E0 P_Value 2.7E-1 3.8E-1 7.6E-1 P_Value	2.0E0 3.6E0 1.5E0 1.2E0 1.1E0 1.5E-1 Fold Change 1.9E0 1.0E0 Fold Change 6.9E0	8.2E-1 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0 Benjamini	7.9E 1 9.6E 1 9.6E 1 9.1E 1 1.0E FDR 9.6E 1 9.1E 1 9.1E 1 1.6E 1
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO UP_KEYWORDS ation Cluster 281 UP_SEQ_FEATURE INTERPRO SMART ation Cluster 282 UP_KEYWORDS	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening NAD+ ADP-ribosyltransferase activity domain: PARP catalytic Poly(ADP-ribose) polymerase, catalytic domain Glycosyltransferase Enrichment Score: 0.37 zinc finger region: RanBP2-type Zinc finger, RanBP2-type ZnF_RBZ Enrichment Score: 0.37 Bernard Soulier syndrome	RT R		7 3 7 3 3 5 Count 5 6 5 Count 3	1.3E-1 2.0E-1 3.3E-1 7.4E-1 7.9E-1 1.0E0 P_Value 2.7E-1 3.8E-1 7.6E-1 P_Value 5.7E-2 3.6E-1	2.0E0 3.6E0 1.5E0 1.2E0 1.1E0 1.5E-1 Fold Change 1.9E0 1.0E0 Fold Change 6.9E0	8.2E-1 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 Benjamini 2.1E-1 1.0E0	7.9E 1 9.6E 1 9.6E 1 9.1E 1 1.0E FDR 9.6E 1 9.1E 1 9.6E 1 9.1E 1 8.5E
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO UP_KEYWORDS ation Cluster 281 UP_SEQ_FEATURE INTERPRO SMART ation Cluster 282 UP_KEYWORDS GOTERM_BP_DIRECT	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening NAD+ ADP-ribosyltransferase activity domain:PARP catalytic Poly(ADP-ribose) polymerase, catalytic domain Glycosyltransferase Enrichment Score: 0.37 zinc finger region:RanBP2-type Zinc finger, RanBP2-type ZnF_RBZ Enrichment Score: 0.37 Bernard Soulier syndrome blood coagulation, intrinsic pathway Blood coagulation	RT R		7 3 7 3 3 5 Count 5 6 5 Count 3 5	1.3E-1 2.0E-1 3.3E-1 7.4E-1 7.9E-1 1.0E0 P_Value 2.7E-1 3.8E-1 7.6E-1 P_Value 5.7E-2 3.6E-1 8.5E-1	2.0E0 3.6E0 1.5E0 1.2E0 1.1E0 1.5E-1 Fold Change 1.9E0 1.0E0 Fold Change 6.9E0 1.6E0 8.6E-1	8.2E-1 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 Benjamini 2.1E-1 1.0E0 1.0E0	7.9E 1 9.6E 1 9.6E 1 9.1E 1 1.0E FDR 9.1E 1 9.1E 1 9.1E 1 8.5E 1 8.5E
	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO UP_KEYWORDS ation Cluster 281 UP_SEQ_FEATURE INTERPRO SMART ation Cluster 282 UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening NAD+ ADP-ribosyltransferase activity domain:PARP catalytic Poly(ADP-ribose) polymerase, catalytic domain Glycosyltransferase Enrichment Score: 0.37 zinc finger region:RanBP2-type Zinc finger, RanBP2-type ZnF RBZ Enrichment Score: 0.37 Bernard Soulier syndrome blood coagulation, intrinsic pathway	RT R		7 3 7 3 3 5 Count 5 6 5 Count 3 5	1.3E-1 2.0E-1 3.3E-1 7.4E-1 7.9E-1 1.0E0 P_Value 2.7E-1 3.8E-1 7.6E-1 P_Value 5.7E-2 3.6E-1 8.5E-1	2.0E0 3.6E0 1.5E0 1.1E0 1.5E-1 Fold Change 1.9E0 1.5E0 1.0E0 Fold Change 6.9E0 1.6E0	8.2E-1 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	7.9E 1 9.6E 1 9.6E 1 9.1E 1 1.0E FDR 9.6E 1 9.1E 1 9.1E 1 8.5E 1 8.5E 1
Annota	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO UP_KEYWORDS ation Cluster 281 UP_SEQ_FEATURE INTERPRO SMART ation Cluster 282 UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS UP_KEYWORDS UP_KEYWORDS UP_KEYWORDS	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening NAD+ ADP-ribosyltransferase activity domain:PARP catalytic Poly(ADP-ribose) polymerase, catalytic domain Glycosyltransferase Enrichment Score: 0.37 zinc finger region:RanBP2-type Zinc finger, RanBP2-type ZnF RBZ Enrichment Score: 0.37 Bernard Soulier syndrome blood coagulation, intrinsic pathway Blood coagulation Hemostasis	RT R		7 3 7 3 3 5 Count 5 6 5 6 7	1.3E-1 2.0E-1 3.3E-1 7.4E-1 7.9E-1 1.0E0 P_Value 2.7E-1 3.8E-1 7.6E-1 P_Value 5.7E-2 3.6E-1 8.5E-1 8.5E-1	Change 2.0E0 3.6E0 1.5E0 1.2E0 1.1E0 1.5E-1 Fold Change 1.9E0 1.5E0 1.0E0 Fold Change 6.9E0 1.6E0 8.6E-1 8.6E-1 4.2E-1	8.2E-1 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	7.9E 1 9.6E 1 9.6E 1 9.1E 1 1.0E FDR 9.1E 1 9.1E 1 9.1E 1 8.5E 1 8.5E 1 1.0E
Annota	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO UP_KEYWORDS ation Cluster 281 UP_SEQ_FEATURE INTERPRO SMART ation Cluster 282 UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS UP_KEYWORDS UP_KEYWORDS KEGG_PATHWAY	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening NAD+ ADP-ribosyltransferase activity domain: PARP catalytic Poly(ADP-ribose) polymerase, catalytic domain Glycosyltransferase Enrichment Score: 0.37 zinc finger region:RanBP2-type Zinc finger, RanBP2-type ZnF RBZ Enrichment Score: 0.37 Bernard Soulier syndrome blood coagulation, intrinsic pathway Blood coagulation Hemostasis ECM-receptor interaction	RT R		7 3 7 3 3 5 Count 5 6 5 6 7	1.3E-1 2.0E-1 3.3E-1 7.4E-1 7.9E-1 1.0E0 P_Value 2.7E-1 3.8E-1 7.6E-1 P_Value 5.7E-2 3.6E-1 8.5E-1 1.0E0	Change 2.0E0 3.6E0 1.5E0 1.2E0 1.1E0 1.5E-1 Fold Change 1.9E0 1.0E0 Fold Change 6.9E0 1.6E0 8.6E-1 8.6E-1 4.2E-1 Fold Change	8.2E-1 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	7.9E 1 9.6E 1 9.6E 1 9.1E 1 1.0E FDR 9.1E 1 9.1E 1 9.1E 1 1.6E 1 9.6E 1 8.5E 1 1.0E FDR
Annota	GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_MF_DIRECT UP_SEQ_FEATURE INTERPRO UP_KEYWORDS ation Cluster 281 UP_SEQ_FEATURE INTERPRO SMART ation Cluster 282 UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS UP_KEYWORDS UP_KEYWORDS KEGG_PATHWAY ation Cluster 283	protein ADP-ribosylation negative regulation of telomere maintenance via telomere lengthening. NAD+ ADP-ribosyltransferase activity domain:PARP catalytic Poly(ADP-ribose) polymerase, catalytic domain Glycosyltransferase Enrichment Score: 0.37 zinc finger region:RanBP2-type Zinc finger, RanBP2-type ZnF_RBZ Enrichment Score: 0.37 Bernard Soulier syndrome blood coagulation, intrinsic pathway Blood coagulation Hemostasis ECM-receptor interaction Enrichment Score: 0.36	RT R		7 3 7 3 3 5 Count 5 6 5 Count 7 Count 7 Count	1.3E-1 2.0E-1 3.3E-1 7.4E-1 7.9E-1 1.0E0 P_Value 2.7E-1 3.8E-1 7.6E-1 P_Value 5.7E-2 3.6E-1 8.5E-1 1.0E0 P_Value	Change 2.0E0 3.6E0 1.5E0 1.2E0 1.1E0 1.5E-1 Fold Change 1.9E0 1.0E0 Fold Change 6.9E0 1.6E0 8.6E-1 8.6E-1 4.2E-1 Fold Change	8.2E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 Benjamini 1.0E0	7.9E 1 9.6E 1 9.6E 1 9.1E 1 1.0E FDR 9.1E 1 9.1E 1 9.1E 1 1.6E 1 9.6E 1 8.5E 1 1.0E FDR

Annota	ation Cluster 1	Enrichment Score: ?	G	·	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	repeat:HEAT 7	<u>RT</u>	i	6	2.7E-1		1.0E0	9.6E-
	UP_SEQ_FEATURE			_					1 9.6E-
		repeat:HEAT 8	<u>RT</u>	•	5	3.0E-1	1.8E0	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	9.6E- 1
	UP_SEQ_FEATURE	repeat:HEAT 11	<u>RT</u>	i	3	5.0E-1	1.9E0	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	repeat:HEAT 5	<u>RT</u>		6	6.0E-1	1 2F0	1.0E0	9.6E-
	UP_SEQ_FEATURE								1 9.6E-
		repeat:HEAT 1	<u>RT</u>	•	8	7.7E-1	9.4E-1	1.0E0	1
	UP_SEQ_FEATURE	repeat:HEAT 2	<u>RT</u>	i	8	7.7E-1	9.4E-1	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	repeat:HEAT 4	<u>RT</u>	i	6	7.8E-1	9.5E-1	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	repeat:HEAT 3	<u>RT</u>	1	6	8.8E-1	8.2E-1	1.0E0	9.6E- 1
Annota	ntion Cluster 284	Enrichment Score: 0.36	G	17	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	region of interest:Interaction with KCND2	<u>RT</u>	i	4	1.1E-2	Change	2.2E-1	2.1E-
	UP_SEQ_FEATURE								1 2.1E-
		domain:EF-hand 1; degenerate	<u>RT</u>	i	4	1.1E-2	6.8E0	2.2E-1	1
	GOTERM_BP_DIRECT	regulation of potassium ion transmembrane transport	<u>RT</u>	i	4	4.8E-1	1.6E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	cardiac conduction	<u>RT</u>	i	6	9.0E-1	7.9E-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-
	UP_KEYWORDS	Potassium	RT	-	12	9 9F-1	6.4E-1	1 0F0	1 9.9E-
	GOTERM_CC_DIRECT								1 9.9E-
		voltage-gated potassium channel complex	<u>RT</u>	•	8	9.9E-1	5.8E-1	1.0E0	1
	GOTERM_MF_DIRECT	potassium channel activity	<u>RT</u>	i e	3	9.9E-1	4.8E-1	1.0E0	9.9E- 1
	UP_KEYWORDS	Potassium transport	<u>RT</u>	i contraction	10	9.9E-1	5.9E-1	1.0E0	9.9E- 1
	UP_KEYWORDS	Potassium channel	<u>RT</u>	i e	4	1.0E0	3.7E-1		1.0E0
	GOTERM_BP_DIRECT UP_KEYWORDS	potassium ion transmembrane transport Voltage-gated channel	RT RT		5 4	1.0E0 1.0E0	2.4E-1 1.8E-1		1.0E0 1.0E0
Annota	ation Cluster 285	Enrichment Score: 0.34	G	178	Count	P_Value	Fold	Benjamini	
	GOTERM_BP_DIRECT	positive regulation of chemokine biosynthetic	RT	:	7	2.6E-3	Change	5.0E-2	4.8E-
	GOTERM_BP_DIRECT	process positive regulation of MHC class II							2 3.3E-
		biosynthetic process	<u>RT</u>	•	5	3.2E-2	3.7EU	3.4E-1	1
	KEGG_PATHWAY	African trypanosomiasis	<u>RT</u>	i	12	4.0E-2	1.9E0	7.0E-2	4.0E- 2
	KEGG_PATHWAY	<u>Malaria</u>	<u>RT</u>	i .	15	7.4E-2	1.6E0	1.3E-1	7.4E- 2
	GOTERM_BP_DIRECT	defense response to protozoan	<u>RT</u>	i	7	8.7E-2	2.2E0	6.4E-1	6.2E- 1
	KEGG_PATHWAY	Inflammatory bowel disease (IBD)	<u>RT</u>		18	9.5E-2	1.5E0	1.6E-1	9.5E-
	BBID	111.Stress influences immunity	RT	:	5	1.3E-1		1.0E0	2 1.0E0
	BBID	112.StressandCRHinfluence	RT	i	5	1.3E-1		1.0E0	1.0E0
	BBID	19.Cytokine microglia	RT DT		7	1.7E-1		1.0E0	1.0E0
	BBID BBID	18.Cytokine astocytes 56.Macrophage regulation of CD4+T cells	RT RT		9	1.9E-1 2.8E-1		1.0E0 1.0E0	1.0E0 1.0E0
	BBID	58.(CD40L) immnosurveillance	<u>RT</u>	1	8	3.6E-1		1.0E0	1.0E0
	GOTERM_BP_DIRECT	<u>positive regulation of isotype switching to IgG isotypes</u>	<u>RT</u>	i	3	4.0E-1	2.2E0	1.0E0	9.6E- 1
	BBID	22.Cytokine-chemokine CNS	<u>RT</u>	i	6	4.6E-1		1.0E0	1.0E0
	BBID BBID	20.Cytokine oligodendrocytes 21.Cytokine neurons	RT RT		3	4.7E-1 4.7E-1		1.0E0 1.0E0	1.0E0 1.0E0
	BBID	113.Th1andTh2cells	RT	i	4	5.0E-1		1.0E0	1.0E0
	GOTERM_BP_DIRECT	negative regulation of growth of symbiont in host	<u>RT</u>	1	4	5.2E-1	1.5E0	1.0E0	9.6E- 1
	BBID	80.T cell Activation	<u>RT</u>	i .	10	6.0E-1	1.1E0	1.0E0	1.0E0
	BBID	35.Chemokines EAE Autoreactive T Cells	<u>RT</u>	i	4	6.1E-1		1.0E0	1.0E0
	BIOCARTA	<u>Dendritic cells in regulating TH1 and TH2</u> <u>Development</u>	<u>RT</u>	1	8	6.2E-1		9.5E-1	6.7E- 1
	BBID KEGG_PATHWAY	88.Alternatively Activated APC	<u>RT</u>	1	5	6.2E-1		1.0E0	1.0E0
		Rheumatoid arthritis	<u>RT</u>	1	17	6.4E-1	1.0E0	9.2E-1	6.4E- 1
	INTERPRO	Four-helical cytokine, core	<u>RT</u>	i .	8	7.4E-1	9.7E-1	1.0E0	9.1E- 1
	BIOCARTA	Regulation of hematopoiesis by cytokines	<u>RT</u>	i .	5	7.8E-1	1.0E0	1.0E0	7.8E- 1
	BIOCARTA	Cytokine Network	<u>RT</u>	•	7	7.8E-1	9.7E-1	1.0E0	7.8E-
	BIOCARTA			_					1 7.9E-
		Cytokines and Inflammatory Response	<u>RT</u>	•	9	7.9E-1	9.4E-1	1.000	1
	INTERDED								0 1 -
	INTERPRO BBID	Four-helical cytokine-like, core 76.Sig trans Ca2 Calcineurin NF-AT	RT RT	1	8		9.2E-1 1.2E0		9.1E- 1 1.0E0

Annot	tation Cluster 1	Enrichment Score: ?	G	**	Count	P_Value	Fold Change	Benjamini	FDR
	KEGG_PATHWAY	Intestinal immune network for IgA production	<u>RT</u>	i	8	8.3E-1	8.8E-1	1.0E0	8.3E- 1
	BIOCARTA	Antigen Dependent B Cell Activation	<u>RT</u>		4	Ω 5F-1	9.4E-1	1 0E0	8.5E-
	BBID	59.L-type Ca2+ Tat immune cells	RT	:	3	8.6E-1		1.0E0	1 1.0E0
	KEGG_PATHWAY	Allograft rejection	RT		6		8.4E-1		8.7E-
	BBID	97.Immune injury MS-lesions MS antigen	RT		5		8.5E-1		1 1.0E0
	KEGG_PATHWAY	Graft-versus-host disease	RT	-	5		7.9E-1		9.0E-
	BIOCARTA				3				1 9.2E-
		Adhesion and Diapedesis of Granulocytes	<u>RT</u>	•	4	9.2E-1	8.1E-1	1.0E0	1
	UP_KEYWORDS	Growth factor	<u>RT</u>	i e	15	9.2E-1	7.9E-1	1.0E0	9.2E- 1
	BBID	15.T-cell polarization-chemokine receptors	<u>RT</u>	i contraction	5	9.2E-1	8.0E-1	1.0E0	1.0E0
	BIOCARTA	<u>Selective expression of chemokine receptors</u> <u>during T-cell polarization</u>	<u>RT</u>	i .	7	9.4E-1	7.6E-1	1.0E0	9.4E- 1
	KEGG_PATHWAY	<u>Asthma</u>	<u>RT</u>	i	4	9.5E-1	6.9E-1	1.0E0	9.5E-
	BIOCARTA	Cells and Molecules involved in local acute	RT		4	0 EE 1	7.2E-1	1.050	1 9.5E-
	BBID	inflammatory response			4				1
	BBID BIOCARTA	5.B7 CD40 B-cell activa	RT DT		3		6.8E-1		1.0E0 9.7E-
	DIOCADTA	Role of Tob in T-cell activation	<u>RT</u>	•	4	9.7E-1	6.4E-1	1.0E0	1
	BIOCARTA	Th1/Th2 Differentiation	<u>RT</u>	i	4	9.8E-1	6.1E-1	1.0E0	9.8E- 1
	GOTERM_MF_DIRECT	growth factor activity	<u>RT</u>	i contraction	19	9.8E-1	7.0E-1	1.0E0	9.8E- 1
	KEGG_PATHWAY	Autoimmune thyroid disease	<u>RT</u>	i	4	1.0E0	4.0E-1	1.0E0	1.0E0
	GOTERM_MF_DIRECT	cytokine activity	<u>RT</u>	i	14	1.0E0	4.7E-1		1.0E0
	UP_KEYWORDS KEGG_PATHWAY	<u>Cytokine</u> <u>Cytokine-cytokine receptor interaction</u>	RT RT		12 16	1.0E0 1.0E0	4.3E-1 3.4E-1		1.0E0 1.0E0
	GOTERM_BP_DIRECT	immune response	RT		31	1.0E0	4.4E-1		1.0E0
Annot	tation Cluster 286	Enrichment Score: 0.33	G	**	Count	P_Value	Fold Change	Benjamini	FDR
	BIOCARTA	Caspase Cascade in Apoptosis	RT	i	10	3.8E-1	•	7.0E-1	4.9E-
	UP_SEQ_FEATURE								1 9.6E-
		domain:CARD	<u>RT</u>	1	6	4.2E-1	1.4E0	1.0E0	1
	INTERPRO	Caspase Recruitment	<u>RT</u>	1	6	5.1E-1	1.3E0	1.0E0	9.1E- 1
	SMART	<u>CARD</u>	<u>RT</u>	1	4	6.0E-1	1.4E0	1.0E0	9.1E-
Annot	tation Cluster 287	Enrichment Score: 0.32	G	178	Count	P_Value	Fold	Benjamini	EDP
Annoc	INTERPRO			-			Change		9.1E-
		Exportin-1/Importin-beta-like	<u>RT</u>	•	3	2.5E-1	3.1E0	1.0E0	1
	COTEDM ME DIDECT								0.05
	GOTERM_MF_DIRECT	Ran GTPase binding	<u>RT</u>	i	7	3.9E-1	1.4E0	1.0E0	8.9E- 1
	GOTERM_MF_DIRECT INTERPRO	Ran GTPase binding Importin-beta, N-terminal	<u>RT</u> <u>RT</u>	i i	7	3.9E-1 5.3E-1		1.0E0 1.0E0	
		Importin-beta, N-terminal	<u>RT</u>	•			1.5E0		1 9.1E- 1 9.6E-
	INTERPRO	Importin-beta, N-terminal domain:Importin N-terminal	RT RT	i i	4	5.3E-1 6.3E-1	1.5E0 1.5E0	1.0E0 1.0E0	1 9.1E- 1 9.6E- 1
	INTERPRO UP_SEQ_FEATURE	Importin-beta, N-terminal domain:Importin N-terminal SM00913	<u>RT</u>	i i i	4	5.3E-1	1.5E0 1.5E0 1.0E0	1.0E0	1 9.1E- 1 9.6E-
Annot	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288	Importin-beta, N-terminal domain:Importin N-terminal	RT RT	i i	4	5.3E-1 6.3E-1	1.5E0 1.5E0 1.0E0	1.0E0 1.0E0	9.1E- 1 9.6E- 1 9.1E- 1
Annot	INTERPRO UP_SEQ_FEATURE SMART	Importin-beta, N-terminal domain:Importin N-terminal SM00913	RT RT RT	i i i	4 3 4	5.3E-1 6.3E-1 7.9E-1	1.5E0 1.5E0 1.0E0 Fold Change	1.0E0 1.0E0 1.0E0	9.1E- 1 9.6E- 1 9.1E- 1
Annot	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32	RT RT RT G	i i i	4 3 4 Count	5.3E-1 6.3E-1 7.9E-1 P_Value	1.5E0 1.5E0 1.0E0 Fold Change 2.1E0	1.0E0 1.0E0 1.0E0 Benjamini	9.1E-1 9.6E-1 9.1E-1 FDR 9.1E-1 9.1E-1
Annot	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat	RT RT RT G RT RT		4 3 4 Count 4 3	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 5.0E-1	1.5E0 1.0E0 1.0E0 Fold Change 2.1E0 1.9E0	1.0E0 1.0E0 1.0E0 Benjamini 1.0E0	9.1E- 1 9.6E- 1 9.1E- 1 FDR 9.1E- 1
	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG FLMN	RT RT RT G RT RT RT		4 3 4 Count	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 5.0E-1 7.5E-1	1.5E0 1.5E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0	1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0	9.1E-1 9.6E-1 9.1E-1 FDR 9.1E-1 9.1E-1
	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART tation Cluster 289	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat	RT RT RT G RT RT		4 3 4 Count 4 3	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 5.0E-1	1.5E0 1.5E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0	1.0E0 1.0E0 1.0E0 Benjamini 1.0E0	9.1E-1 9.6E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1
	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG FLMN	RT RT RT G RT RT RT		4 3 4 Count 4 3	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 5.0E-1 7.5E-1	1.5E0 1.0E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0 Fold Change	1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0	9.1E-1 9.6E-1 9.1E-1 FDR 9.1E-1 9.1E-1
	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART tation Cluster 289	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG FLMN Enrichment Score: 0.28	RT RT RT G RT RT RT CG		4 3 4 Count 4 3 Count	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 5.0E-1 7.5E-1 P_Value	1.5E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0 Fold Change	1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0 Benjamini	9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 2.9E-2
	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART tation Cluster 289 INTERPRO	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG FLMN Enrichment Score: 0.28 Immunoglobulin I-set Immunoglobulin subtype 2	RT		4 3 4 Count 4 3 Count 37 42	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 5.0E-1 7.5E-1 P_Value 2.7E-3 4.8E-1	1.5E0 1.0E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0 Fold Change 1.6E0 1.0E0	1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 Benjamini 3.2E-2 1.0E0	9.1E-1 9.6E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.9.E-1
	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART tation Cluster 289 INTERPRO INTERPRO UP_SEQ_FEATURE	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG FLMN Enrichment Score: 0.28 Immunoglobulin I-set Immunoglobulin subtype 2 domain:Ig-like C2-type 3	RT		4 3 4 Count 4 3 3 Count 37 42 18	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 5.0E-1 7.5E-1 P_Value 2.7E-3 4.8E-1 7.1E-1	1.5E0 1.0E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0 Fold Change 1.6E0 1.0E0 9.6E-1	1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 Benjamini 3.2E-2 1.0E0 1.0E0	9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.9.E-1
	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART tation Cluster 289 INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG FLMN Enrichment Score: 0.28 Immunoglobulin I-set Immunoglobulin subtype 2	RT		4 3 4 Count 4 3 Count 37 42	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 5.0E-1 7.5E-1 P_Value 2.7E-3 4.8E-1 7.1E-1	1.5E0 1.0E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0 Fold Change 1.6E0 1.0E0	1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 Benjamini 3.2E-2 1.0E0 1.0E0	9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.6E-1
	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART tation Cluster 289 INTERPRO INTERPRO UP_SEQ_FEATURE	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG FLMN Enrichment Score: 0.28 Immunoglobulin I-set Immunoglobulin subtype 2 domain:Ig-like C2-type 3	RT		4 3 4 Count 4 3 3 Count 37 42 18	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 5.0E-1 7.5E-1 P_Value 2.7E-3 4.8E-1 7.1E-1 9.3E-1	1.5E0 1.0E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0 Fold Change 1.6E0 1.0E0 9.6E-1	1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 Benjamini 3.2E-2 1.0E0 1.0E0 1.0E0	9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.6E-1
Annot	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART tation Cluster 289 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG FLMN Enrichment Score: 0.28 Immunoglobulin I-set Immunoglobulin subtype 2 domain:Ig-like C2-type 3 domain:Ig-like C2-type 1 domain:Ig-like C2-type 2 IGC2	RT		4 3 4 Count 4 3 3 Count 37 42 18 24 24 42	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 5.0E-1 7.5E-1 P_Value 2.7E-3 4.8E-1 7.1E-1 9.3E-1	1.5E0 1.5E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0 Fold Change 1.6E0 1.0E0 9.6E-1 8.1E-1 8.1E-1 6.8E-1	1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.6E-1 9.6E-1
Annot	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART tation Cluster 289 INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_KEYWORDS	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG FLMN Enrichment Score: 0.28 Immunoglobulin I-set Immunoglobulin subtype 2 domain:Ig-like C2-type 3 domain:Ig-like C2-type 1 domain:Ig-like C2-type 2 IGC2 Immunoglobulin domain	RT R		4 3 4 Count 4 3 3 Count 37 42 18 24 42 49	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 7.5E-1 P_Value 2.7E-3 4.8E-1 7.1E-1 9.3E-1 1.0E0 1.0E0	1.5E0 1.5E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0 Fold Change 1.6E0 1.0E0 9.6E-1 8.1E-1 8.1E-1 6.8E-1 6.2E-1	1.0E0 1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 Benjamini 3.2E-2 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.6E-1 1,0E0
Annot	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART tation Cluster 289 INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG FLMN Enrichment Score: 0.28 Immunoglobulin I-set Immunoglobulin subtype 2 domain:Ig-like C2-type 3 domain:Ig-like C2-type 1 domain:Ig-like C2-type 2 IGC2	RT R		4 3 4 Count 4 3 3 Count 37 42 18 24 24 42	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 5.0E-1 7.5E-1 P_Value 2.7E-3 4.8E-1 7.1E-1 9.3E-1 1.0E0	1.5E0 1.5E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0 Fold Change 1.6E0 1.0E0 9.6E-1 8.1E-1 8.1E-1 6.8E-1	1.0E0	1 9.1E-1 9.6E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 1 9.6E-1 1 9.6E-1 1.0E0 1.0E0
Annot	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART tation Cluster 289 INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_KEYWORDS INTERPRO	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG FLMN Enrichment Score: 0.28 Immunoglobulin I-set Immunoglobulin subtype 2 domain:Ig-like C2-type 3 domain:Ig-like C2-type 1 domain:Ig-like C2-type 2 IGC2 Immunoglobulin domain Immunoglobulin subtype	RT R		4 3 4 Count 4 3 3 Count 37 42 18 24 42 49 47	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 7.5E-1 P_Value 2.7E-3 4.8E-1 7.1E-1 9.3E-1 1.0E0 1.0E0 1.0E0	1.5E0 1.5E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0 Fold Change 1.6E0 1.0E0 9.6E-1 8.1E-1 6.8E-1 6.2E-1 5.9E-1	1.0E0	1 9.1E-1 9.6E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.6E-1 1.0E0 1.0E0 1.0E0
Annot	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART tation Cluster 289 INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_KEYWORDS INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG FLMN Enrichment Score: 0.28 Immunoglobulin I-set Immunoglobulin subtype 2 domain:Ig-like C2-type 3 domain:Ig-like C2-type 1 domain:Ig-like C2-type 2 IGC2 Immunoglobulin domain Immunoglobulin subtype Immunoglobulin-like fold	RT R		4 3 4 Count 4 3 3 Count 37 42 18 24 42 49 47 85	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 5.0E-1 7.5E-1 P_Value 2.7E-3 4.8E-1 7.1E-1 9.3E-1 1.0E0 1.0E0 1.0E0 1.0E0	1.5E0 1.5E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0 Fold Change 1.6E0 1.0E0 9.6E-1 8.1E-1 6.8E-1 6.2E-1 5.9E-1 5.5E-1 4.1E-1 3.8E-1	1.0E0	1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.6E-1 1.0E0 1.0E0 1.0E0
Annot	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART tation Cluster 289 INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_KEYWORDS INTERPRO	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG FLMN Enrichment Score: 0.28 Immunoglobulin I-set Immunoglobulin subtype 2 domain:Ig-like C2-type 3 domain:Ig-like C2-type 1 domain:Ig-like C2-type 2 IGC2 Immunoglobulin domain Immunoglobulin subtype Immunoglobulin-like fold Immunoglobulin-like domain	RT R		4 3 4 Count 4 3 3 Count 37 42 18 24 42 49 47 85 51	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 7.5E-1 P_Value 2.7E-3 4.8E-1 7.1E-1 9.3E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	1.5E0 1.5E0 1.0E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0 Fold Change 1.6E0 1.0E0 9.6E-1 8.1E-1 8.1E-1 6.8E-1 6.2E-1 5.9E-1 5.5E-1 4.1E-1 3.8E-1	1.0E0	1 9.1E-1 9.6E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.6E-1 1.0E0 1.0E0 1.0E0 1.0E0
Annot	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART tation Cluster 289 INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_KEYWORDS INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO SMART	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG FLMN Enrichment Score: 0.28 Immunoglobulin I-set Immunoglobulin subtype 2 domain:Ig-like C2-type 3 domain:Ig-like C2-type 1 domain:Ig-like C2-type 2 IGc2 Immunoglobulin domain Immunoglobulin subtype Immunoglobulin-like fold Immunoglobulin-like domain IG	RT R		4 3 4 Count 4 3 3 Count 37 42 18 24 42 49 47 85 51 47	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 5.0E-1 7.5E-1 P_Value 2.7E-3 4.8E-1 7.1E-1 9.3E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	1.5E0 1.5E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0 Fold Change 1.6E0 1.0E0 9.6E-1 8.1E-1 8.1E-1 6.8E-1 6.2E-1 5.9E-1 5.5E-1 4.1E-1 3.8E-1 Fold Change	1.0E0	1 9.1E-1 9.6E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.6E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0
Annot	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART tation Cluster 289 INTERPRO INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_KEYWORDS INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO SMART tation Cluster 290	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG_FLMN Enrichment Score: 0.28 Immunoglobulin I-set Immunoglobulin subtype 2 domain:Ig-like C2-type 3 domain:Ig-like C2-type 1 domain:Ig-like C2-type 2 IGc2 Immunoglobulin domain Immunoglobulin subtype Immunoglobulin-like fold Immunoglobulin-like domain IG Enrichment Score: 0.27 SMAD protein complex assembly type I transforming growth factor beta	RT R		4 3 4 Count 4 3 3 Count 37 42 18 24 42 49 47 85 51 47 Count 3	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 7.5E-1 P_Value 2.7E-3 4.8E-1 7.1E-1 9.3E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 4.0E-1	1.5E0 1.5E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0 Fold Change 1.6E0 1.0E0 9.6E-1 8.1E-1 6.8E-1 6.2E-1 5.9E-1 5.5E-1 4.1E-1 3.8E-1 Fold Change 2.2E0	1.0E0	1 9.1E-1 9.6E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.6E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0
Annot	INTERPRO UP_SEQ_FEATURE SMART tation Cluster 288 INTERPRO INTERPRO SMART tation Cluster 289 INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_KEYWORDS INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO INTERPRO SMART tation Cluster 290 GOTERM_BP_DIRECT GOTERM_MF_DIRECT	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG FLMN Enrichment Score: 0.28 Immunoglobulin I-set Immunoglobulin subtype 2 domain:Ig-like C2-type 3 domain:Ig-like C2-type 1 domain:Ig-like C2-type 2 IGC2 Immunoglobulin domain Immunoglobulin subtype Immunoglobulin-like fold Immunoglobulin-like domain IG Enrichment Score: 0.27 SMAD protein complex assembly type I transforming growth factor beta receptor binding.	RI R		4 3 4 Count 4 3 3 Count 37 42 18 24 42 49 47 85 51 47 Count 3 3	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 7.5E-1 P_Value 2.7E-3 4.8E-1 7.1E-1 9.3E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 4.0E-1 4.6E-1	1.5E0 1.5E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0 Fold Change 1.6E0 1.0E0 9.6E-1 8.1E-1 6.8E-1 6.2E-1 5.9E-1 5.5E-1 4.1E-1 3.8E-1 Fold Change 2.2E0 2.0E0	1.0E0	1 9.1E-1 9.6E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 1 9.6E-1 1 9.6E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0
Annot	INTERPRO UP_SEQ_FEATURE SMART Tation Cluster 288 INTERPRO INTERPRO SMART Tation Cluster 289 INTERPRO INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART UP_KEYWORDS INTERPRO INTERPRO INTERPRO INTERPRO SMART Tation Cluster 290 GOTERM_BP_DIRECT	Importin-beta, N-terminal domain:Importin N-terminal SM00913 Enrichment Score: 0.32 Filamin/ABP280 repeat-like Filamin/ABP280 repeat IG_FLMN Enrichment Score: 0.28 Immunoglobulin I-set Immunoglobulin subtype 2 domain:Ig-like C2-type 3 domain:Ig-like C2-type 1 domain:Ig-like C2-type 2 IGc2 Immunoglobulin domain Immunoglobulin subtype Immunoglobulin-like fold Immunoglobulin-like domain IG Enrichment Score: 0.27 SMAD protein complex assembly type I transforming growth factor beta	RT R		4 3 4 Count 4 3 3 Count 37 42 18 24 42 49 47 85 51 47 Count 3	5.3E-1 6.3E-1 7.9E-1 P_Value 3.0E-1 7.5E-1 P_Value 2.7E-3 4.8E-1 7.1E-1 9.3E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 4.0E-1 4.6E-1	1.5E0 1.5E0 1.0E0 Fold Change 2.1E0 1.9E0 1.2E0 Fold Change 1.6E0 1.0E0 9.6E-1 8.1E-1 6.8E-1 6.2E-1 5.9E-1 5.5E-1 4.1E-1 3.8E-1 Fold Change 2.2E0	1.0E0	1 9.1E-1 9.6E-1 9.1E-1 9.1E-1 9.1E-1 9.1E-1 9.6E-1 1 9.6E-1 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0

	ation Cluster 1	Enrichment Score: ?	G	· ·	Count	P_Value	Fold Change	Benjamini	FDR
Annota	ation Cluster 291	Enrichment Score: 0.24	G	·	Count	P_Value	Fold	Benjamini	FDR
	UP_SEQ_FEATURE	short sequence motif:"KMSKS" region	<u>RT</u>	i	5	2.0E-1		1.0E0	9.6E- 1
	UP_SEQ_FEATURE	short sequence motif:"HIGH" region	<u>RT</u>	i .	5	2.7E-1	1.9E0	1.0E0	9.6E-
	INTERPRO	Aminoacyl-tRNA synthetase, class I,	<u>RT</u>		4	4.4E-1	1.7E0	1.0E0	9.1E-
	INTERPRO	<u>conserved site</u> <u>Glutathione S-transferase, C-terminal</u>	RT	•	5	5.2E-1	1.3E0	1.0E0	1 9.1E-
	INTERPRO	Rossmann-like alpha/beta/alpha sandwich	RT		8	5.3E-1		1.0E0	1 9.1E-
	GOTERM_MF_DIRECT	fold		-	4				1 8.9E-
	INTERPRO	aminoacyl-tRNA ligase activity Aminoacyl-tRNA synthetase, class 1a,	<u>RT</u>			5.6E-1		1.0E0	1 9.1E-
	UP_KEYWORDS	anticodon-binding	<u>RT</u>		3	6.4E-1		1.0E0	1 8.2E-
	INTERPRO	Aminoacyl-tRNA synthetase	<u>RT</u>	•	5	8.2E-1	9.0E-1	1.0E0	1
		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	9.6E- 1
	GOTERM_BP_DIRECT	tRNA aminoacylation for protein translation	<u>RT</u>	1	5	9.2E-1	7.4E-1	1.0E0	9.6E- 1
Annote	KEGG_PATHWAY ation Cluster 292	Aminoacyl-tRNA biosynthesis Enrichment Score: 0.23	RT G	·	5 Count	1.0E0	3.9E-1 Fold		1.0E0
Annota	UP_SEQ_FEATURE			_	Count	P_Value	Onlange	Benjamini	9.6E-
	INTERPRO	domain:MIF4G	<u>RT</u>		3	4.4E-1		1.0E0	1 9.1E-
	INTERPRO	MIF4G-like, type 3	<u>RT</u>		3	5.0E-1	1.9E0	1.0E0	1
		MIF4-like, type 1/2/3	<u>RT</u>	i	3	7.2E-1	1.2E0	1.0E0	9.1E- 1
	SMART	MIF4G	<u>RT</u>	i	3	7.5E-1		1.0E0	9.1E- 1
Annota	ation Cluster 293	Enrichment Score: 0.23	G	·	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	domain:MBD	<u>RT</u>	i	3	5.0E-1	1.9E0	1.0E0	9.6E- 1
	INTERPRO	Methyl-CpG DNA binding	<u>RT</u>	i	3	5.5E-1	1.7E0	1.0E0	9.1E- 1
	INTERPRO	DNA-binding, integrase-type	<u>RT</u>	i	3	5.5E-1	1.7E0	1.0E0	9.1E- 1
	SMART	MBD	<u>RT</u>	i .	3	7.9E-1	1.1E0	1.0E0	9.1E- 1
Annota	ation Cluster 294	Enrichment Score: 0.23	G	™	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	region of interest:Heparin-binding	<u>RT</u>	1	5	3.4E-1	1 750	1.050	9.6E-
				•	5	3.4E-1	1.760	1.0E0	1
	GOTERM_BP_DIRECT	organ induction	RT		3	6.3E-1		1.0E0	1 9.6E- 1
				-		6.3E-1		1.0E0	1
Annota	GOTERM_BP_DIRECT	organ induction	<u>RT</u>	•	3	6.3E-1 9.8E-1	1.5E0 6.2E-1	1.0E0	1 9.6E- 1 9.8E- 1
Annota	GOTERM_BP_DIRECT UP_KEYWORDS	organ induction Heparin-binding	RT RT	i i	3 8	6.3E-1	1.5E0 6.2E-1 Fold Change	1.0E0 1.0E0	9.6E- 1 9.8E- 1 FDR 9.1E-
Annota	GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 295	organ induction Heparin-binding Enrichment Score: 0.23	RT RT	i i	3 8 Count	6.3E-1 9.8E-1 P_Value	1.5E0 6.2E-1 Fold Change 2.7E0	1.0E0 1.0E0 Benjamini	9.6E- 1 9.8E- 1 FDR 9.1E- 1 9.6E-
Annota	GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 295 INTERPRO	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha domain:IBB	RT RT G RT RT	i i	3 8 Count	6.3E-1 9.8E-1 P_Value 3.2E-1 3.3E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0	1.0E0 1.0E0 Benjamini 1.0E0 1.0E0	1 9.6E- 1 9.8E- 1 FDR 9.1E- 1 9.6E- 1
Annota	GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 295 INTERPRO UP_SEQ_FEATURE	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha	RT RT G RT	i i	3 8 Count 3	6.3E-1 9.8E-1 P_Value 3.2E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0 1.5E0	1.0E0 1.0E0 Benjamini 1.0E0 1.0E0	1 9.6E- 1 9.8E- 1 FDR 9.1E- 1 9.6E- 1
Annota	GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 295 INTERPRO UP_SEQ_FEATURE GOTERM_BP_DIRECT	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha domain:IBB NLS-bearing protein import into nucleus	RT RT G RT RT RT	i i	3 8 Count 3 3	6.3E-1 9.8E-1 P_Value 3.2E-1 3.3E-1 3.5E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0 1.5E0 2.3E0	1.0E0 1.0E0 Benjamini 1.0E0 1.0E0	1 9.6E- 1 9.8E- 1 FDR 9.1E- 1 9.6E- 1
Annota	GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 295 INTERPRO UP_SEQ_FEATURE GOTERM_BP_DIRECT PIR_SUPERFAMILY	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha domain:IBB NLS-bearing protein import into nucleus importin subunit alpha	RT RT RT RT RT RT RT RT RT		3 Count 3 3 6 3	6.3E-1 9.8E-1 P_Value 3.2E-1 3.3E-1 3.5E-1 3.8E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0 1.5E0 2.3E0 1.5E0	1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0	1 9.6E- 1 9.8E- 1 9.1E- 1 9.6E- 1 1.0E0 9.6E-
Annota	GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 295 INTERPRO UP_SEQ_FEATURE GOTERM_BP_DIRECT PIR_SUPERFAMILY UP_SEQ_FEATURE	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha domain:IBB NLS-bearing protein import into nucleus importin subunit alpha repeat:ARM 8	RT RT RT RT RT RT RT RT RT		3 8 Count 3 3 6 3 5	6.3E-1 9.8E-1 P_Value 3.2E-1 3.3E-1 3.5E-1 4.1E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0 1.5E0 2.3E0 1.5E0 2.1E0	1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0 1.0E0	1 9.6E- 1 9.8E- 1 9.1E- 1 9.6E- 1 1.0E0 9.6E- 1 9.6E- 1
Annota	GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 295 INTERPRO UP_SEQ_FEATURE GOTERM_BP_DIRECT PIR_SUPERFAMILY UP_SEQ_FEATURE INTERPRO	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha domain:IBB NLS-bearing protein import into nucleus importin subunit alpha repeat:ARM 8 Importin-alpha, importin-beta-binding domain	RT RT RT RT RT RT RT RT RT		3 Count 3 3 6 3 5 3	6.3E-1 9.8E-1 P_Value 3.2E-1 3.3E-1 3.5E-1 4.1E-1 4.4E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0 1.5E0 2.3E0 1.5E0 2.1E0 1.4E0	1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	1 9.6E-1 9.8E-1 FDR 9.1E-1 9.6E-1 1.0E0 9.6E-1 1.9.1E-1
Annota	GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 295 INTERPRO UP_SEQ_FEATURE GOTERM_BP_DIRECT PIR_SUPERFAMILY UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha domain:IBB NLS-bearing protein import into nucleus importin subunit alpha repeat:ARM 8 Importin-alpha, importin-beta-binding domain repeat:ARM 7	RT		3 8 Count 3 3 6 3 5 5	6.3E-1 9.8E-1 P_Value 3.2E-1 3.3E-1 3.5E-1 4.1E-1 4.4E-1 4.8E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0 1.5E0 2.3E0 1.5E0 2.1E0 1.4E0 1.3E0	1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	1 9.6E-1 9.8E-1 1 9.1E-1 9.6E-1 1.0E0 9.6E-1 9.1E-1
Annota	GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 295 INTERPRO UP_SEQ_FEATURE GOTERM_BP_DIRECT PIR_SUPERFAMILY UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha domain:IBB NLS-bearing protein import into nucleus importin subunit alpha repeat:ARM 8 Importin-alpha, importin-beta-binding domain repeat:ARM 7 repeat:ARM 6 repeat:ARM 5	RT		3 8 Count 3 3 6 3 5 5 5	6.3E-1 9.8E-1 P_Value 3.2E-1 3.3E-1 3.5E-1 4.1E-1 4.4E-1 4.8E-1 5.4E-1 6.3E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0 1.5E0 2.3E0 1.5E0 2.1E0 1.4E0 1.3E0 1.2E0	1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	1 9.6E-1 9.8E-1 9.1E-1 9.6E-1 1.0E0 9.6E-1 1.9.6E-1 9.6E-1
Annota	GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 295 INTERPRO UP_SEQ_FEATURE GOTERM_BP_DIRECT PIR_SUPERFAMILY UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha domain:IBB NLS-bearing protein import into nucleus importin subunit alpha repeat:ARM 8 Importin-alpha, importin-beta-binding domain repeat:ARM 7 repeat:ARM 6 repeat:ARM 5 repeat:ARM 4	RT		3 8 Count 3 3 6 3 5 5 5 5	6.3E-1 9.8E-1 P_Value 3.2E-1 3.3E-1 3.5E-1 4.1E-1 4.4E-1 4.8E-1 5.4E-1 6.3E-1 6.9E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0 1.5E0 2.3E0 1.5E0 2.1E0 1.4E0 1.3E0 1.2E0 1.1E0	1.0E0 1.0E0 Benjamini 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	1 9.6E-1 9.8E-1 9.1E-1 9.6E-1 1.0E0 9.6E-1 9.6E-1 9.6E-1 9.6E-1
Annota	GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 295 INTERPRO UP_SEQ_FEATURE GOTERM_BP_DIRECT PIR_SUPERFAMILY UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha domain:IBB NLS-bearing protein import into nucleus importin subunit alpha repeat:ARM 8 Importin-alpha, importin-beta-binding domain repeat:ARM 7 repeat:ARM 6 repeat:ARM 5 repeat:ARM 4 nuclear localization sequence binding.	RT R		3 8 Count 3 3 6 3 5 5 5 5 5	6.3E-1 9.8E-1 P_Value 3.2E-1 3.3E-1 3.5E-1 4.1E-1 4.4E-1 4.8E-1 5.4E-1 6.3E-1 6.9E-1 7.1E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0 1.5E0 2.3E0 1.5E0 1.4E0 1.3E0 1.2E0 1.1E0 1.1E0	1.0E0	1 9.6E-1 9.8E-1 1 9.1E-1 9.6E-1 1.0E0 9.6E-1 9.6E-1 9.6E-1 9.6E-1
Annota	GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 295 INTERPRO UP_SEQ_FEATURE GOTERM_BP_DIRECT PIR_SUPERFAMILY UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE GOTERM_MF_DIRECT	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha domain:IBB NLS-bearing protein import into nucleus importin subunit alpha repeat:ARM 8 Importin-alpha, importin-beta-binding domain repeat:ARM 7 repeat:ARM 6 repeat:ARM 5 repeat:ARM 4 nuclear localization sequence binding repeat:ARM 9	RT R		3 8 Count 3 3 6 3 5 5 5 5 5 5 3	6.3E-1 9.8E-1 P_Value 3.2E-1 3.3E-1 3.5E-1 4.1E-1 4.4E-1 4.8E-1 5.4E-1 6.3E-1 6.9E-1 7.1E-1 7.6E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0 1.5E0 2.3E0 1.5E0 1.4E0 1.4E0 1.1E0 1.1E0 1.1E0 1.1E0	1.0E0	1 9.6E-1 9.8E-1 9.1E-1 9.6E-1 1.0E0 9.6E-1 9.6E-1 9.6E-1 9.6E-1 9.6E-1 9.6E-1
Annota	GOTERM_BP_DIRECT UP_KEYWORDS Ation Cluster 295 INTERPRO UP_SEQ_FEATURE GOTERM_BP_DIRECT PIR_SUPERFAMILY UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha domain:IBB NLS-bearing protein import into nucleus importin subunit alpha repeat:ARM 8 Importin-alpha, importin-beta-binding domain repeat:ARM 7 repeat:ARM 6 repeat:ARM 5 repeat:ARM 4 nuclear localization sequence binding repeat:ARM 9 repeat:ARM 3	RI R		3 8 Count 3 3 6 3 5 5 5 5 5 5 5 5 5	6.3E-1 9.8E-1 P_Value 3.2E-1 3.3E-1 3.5E-1 4.1E-1 4.4E-1 4.4E-1 5.4E-1 6.3E-1 6.9E-1 7.1E-1 7.6E-1 7.9E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0 1.5E0 2.3E0 1.5E0 2.1E0 1.4E0 1.3E0 1.2E0 1.1E0 1.1E0 9.5E-1	1.0E0	1 9.6E-1 9.8E-1 9.1E-1 9.6E-1 1.0E0 9.6E-1 9.6E-1 9.6E-1 9.6E-1 9.6E-1 9.6E-1 9.6E-1
Annota	GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 295 INTERPRO UP_SEQ_FEATURE GOTERM_BP_DIRECT PIR_SUPERFAMILY UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha domain:IBB NLS-bearing protein import into nucleus importin subunit alpha repeat:ARM 8 Importin-alpha, importin-beta-binding domain repeat:ARM 7 repeat:ARM 6 repeat:ARM 5 repeat:ARM 4 nuclear localization sequence binding repeat:ARM 9 repeat:ARM 3 repeat:ARM 2	RT R		3 8 Count 3 3 6 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	6.3E-1 9.8E-1 P_Value 3.2E-1 3.3E-1 3.5E-1 4.1E-1 4.4E-1 4.8E-1 5.4E-1 6.3E-1 7.1E-1 7.6E-1 7.9E-1 8.1E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0 1.5E0 2.3E0 1.5E0 1.4E0 1.4E0 1.1E0 1.1E0 1.1E0 9.5E-1	1.0E0	1 9.6E-1 1 9.8E-1 1 9.6E-1 1 9.6E-1 1,0E0 9.6E-1 1 9.6E-1 1 9.6E-1 1 9.6E-1 1 9.6E-1 1 9.6E-1
Annota	GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 295 INTERPRO UP_SEQ_FEATURE GOTERM_BP_DIRECT PIR_SUPERFAMILY UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha domain:IBB NLS-bearing protein import into nucleus importin subunit alpha repeat:ARM 8 Importin-alpha, importin-beta-binding domain repeat:ARM 7 repeat:ARM 6 repeat:ARM 5 repeat:ARM 4 nuclear localization sequence binding repeat:ARM 9 repeat:ARM 3	RI R		3 8 Count 3 3 6 3 5 5 5 5 5 5 5 5 5	6.3E-1 9.8E-1 P_Value 3.2E-1 3.3E-1 3.5E-1 4.1E-1 4.4E-1 4.8E-1 5.4E-1 6.3E-1 7.1E-1 7.6E-1 7.9E-1 8.1E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0 1.5E0 2.3E0 1.5E0 2.1E0 1.4E0 1.3E0 1.2E0 1.1E0 1.1E0 9.5E-1	1.0E0	1 9.6E-1 9.8E-1 9.1E-1 9.6E-1 1.0E0 9.6E-1 1.0E0 9.6E-1 9.6E-1 9.6E-1 9.6E-1 1.0E0
Annota	GOTERM_BP_DIRECT UP_KEYWORDS Ation Cluster 295 INTERPRO UP_SEQ_FEATURE GOTERM_BP_DIRECT PIR_SUPERFAMILY UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha domain:IBB NLS-bearing protein import into nucleus importin subunit alpha repeat:ARM 8 Importin-alpha, importin-beta-binding domain repeat:ARM 7 repeat:ARM 6 repeat:ARM 5 repeat:ARM 4 nuclear localization sequence binding repeat:ARM 9 repeat:ARM 3 repeat:ARM 2	RT R		3 8 Count 3 3 6 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	6.3E-1 9.8E-1 P_Value 3.2E-1 3.3E-1 3.5E-1 4.1E-1 4.4E-1 4.8E-1 5.4E-1 6.3E-1 7.1E-1 7.6E-1 7.9E-1 8.1E-1 9.3E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0 1.5E0 2.3E0 1.5E0 1.4E0 1.4E0 1.1E0 1.1E0 1.1E0 9.5E-1	1.0E0	1 9.6E-1 9.8E-1 9.1E-1 9.6E-1 1.0E0 9.6E-1 9.6E-1 9.6E-1 9.6E-1 9.6E-1 9.6E-1 9.6E-1 9.6E-1 9.6E-1
Annota	GOTERM_BP_DIRECT UP_KEYWORDS ation Cluster 295 INTERPRO UP_SEQ_FEATURE GOTERM_BP_DIRECT PIR_SUPERFAMILY UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE SMART	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha domain:IBB NLS-bearing protein import into nucleus importin subunit alpha repeat:ARM 8 Importin-alpha, importin-beta-binding domain repeat:ARM 7 repeat:ARM 6 repeat:ARM 5 repeat:ARM 4 nuclear localization sequence binding repeat:ARM 9 repeat:ARM 3 repeat:ARM 2 Armadillo repeat:ARM 1 ARM	RI R		3 8 Count 3 3 6 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	6.3E-1 9.8E-1 P_Value 3.2E-1 3.3E-1 3.5E-1 3.8E-1 4.1E-1 4.4E-1 4.4E-1 5.4E-1 6.3E-1 7.1E-1 7.6E-1 7.9E-1 8.1E-1 9.3E-1 9.9E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0 1.5E0 2.3E0 1.5E0 2.1E0 1.4E0 1.3E0 1.1E0 1.1E0 1.1E0 1.1E0 1.1E0 1.1E0 5.2E-1 7.2E-1 6.6E-1 5.2E-1	1.0E0	1 9.6E-1 1 9.8E-1 1 9.6E-1 1 9.6E-1 1.0E0 9.6E-1 1 9.6E-1 1 9.6E-1 1 9.6E-1 1 9.6E-1 1 9.6E-1 1 9.6E-1 1 9.6E-1 1 9.6E-1
	GOTERM_BP_DIRECT UP_KEYWORDS Ation Cluster 295 INTERPRO UP_SEQ_FEATURE GOTERM_BP_DIRECT PIR_SUPERFAMILY UP_SEQ_FEATURE INTERPRO UP_SEQ_FEATURE	organ induction Heparin-binding Enrichment Score: 0.23 Importin subunit alpha domain:IBB NLS-bearing protein import into nucleus importin subunit alpha repeat:ARM 8 Importin-alpha, importin-beta-binding domain repeat:ARM 6 repeat:ARM 6 repeat:ARM 5 repeat:ARM 4 nuclear localization sequence binding repeat:ARM 9 repeat:ARM 3 repeat:ARM 2 Armadillo repeat:ARM 1	RI R		3 8 Count 3 3 6 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	6.3E-1 9.8E-1 P_Value 3.2E-1 3.3E-1 3.5E-1 3.8E-1 4.1E-1 4.4E-1 4.4E-1 5.4E-1 6.3E-1 7.1E-1 7.6E-1 7.9E-1 8.1E-1 9.3E-1	1.5E0 6.2E-1 Fold Change 2.7E0 2.6E0 1.5E0 2.3E0 1.5E0 1.4E0 1.4E0 1.1E0 1.1E0 1.1E0 1.1E0 1.1E0 1.1E0 5.2E-1 5.0E-1	1.0E0	1 9.6E-1 1 9.8E-1 9.1E-1 9.6E-1 1.0E0 9.6E-1 9.6E-1 9.6E-1 9.6E-1 9.6E-1 9.6E-1 9.6E-1 9.6E-1 1 9.6E-1 1 9.6E-1 1 9.6E-1

nnot	tation Cluster 1	Enrichment Score: ?	G	15	Count	P_Value	Fold Change	Benjamin	i FC
	UP_SEQ_FEATURE	zinc finger region:ZZ-type	<u>RT</u>	1	4	4.6E-1	1.6E0	1.0E0	9. 1
)	INTERPRO	Zinc finger, ZZ-type	<u>RT</u>	i	4	5.7E-1	1.4E0	1.0E0	9. 1
)	SMART	ZnF ZZ	<u>RT</u>	1	4	7.9E-1	1.0E0	1.0E0	9. 1
nnot	tation Cluster 297	Enrichment Score: 0.23	G	™	Count	P_Value	Fold Change	Benjamin	i FC
	GOTERM_MF_DIRECT	protein-hormone receptor activity	<u>RT</u>	i	3	7.5E-2		3.9E-1	3. 1
	INTERPRO	G protein-coupled receptor, rhodopsin-like	<u>RT</u>	i	7	1.0E0	6.0E-2	1.0E0	1.
) 1	INTERPRO GOTERM_MF_DIRECT	GPCR, rhodopsin-like, 7TM G-protein coupled receptor activity	RT RT		7 10	1.0E0 1.0E0	5.9E-2 8.4E-2		1. 1.
))	UP_KEYWORDS	G-protein coupled receptor G-protein coupled receptor	RT	1	11	1.0E0	9.0E-2		1.
not	tation Cluster 298	Enrichment Score: 0.22		· Marian Company	Count	P_Value	Fold Change	Benjamin	i F
	INTERPRO	Cyclic nucleotide-binding, conserved site	<u>RT</u>	i	5	2.5E-1	1.9E0	1.0E0	9
	INTERPRO	Cyclic nucleotide-binding domain	<u>RT</u>	1	7	5.1E-1	1.2E0	1.0E0	9
	INTERPRO	Cyclic nucleotide-binding-like	<u>RT</u>	1	7	5.9E-1	1.1E0	1.0E0	9
	UP_KEYWORDS	cAMP-binding	RT	•	3	7.3E-1	1 2F0	1.0E0	1 7
	INTERPRO			-	7				1 9
	GOTERM_MF_DIRECT	RmlC-like jelly roll fold	<u>RT</u>				9.2E-1		1 8
		<u>cAMP binding</u>	<u>RT</u>	•	4	7.9E-1	9.9E-1	1.0E0	1
	SMART	<u>cNMP</u>	<u>RT</u>	i	7	8.1E-1	9.2E-1	1.0E0	1
not	tation Cluster 299	Enrichment Score: 0.21	G	N Company	Count	P_Value	Fold Change	Benjamin	i F
	GOTERM_CC_DIRECT	nuclear pore	<u>RT</u>	i .	14	3.4E-1	1.2E0	9.5E-1	8
	UP_KEYWORDS	Nuclear pore complex	<u>RT</u>	i	7	7.6E-1	9.6E-1	1.0E0	7 1
	UP_KEYWORDS	Translocation	<u>RT</u>	1	9	9.4E-1	7.4E-1	1.0E0	9
not	tation Cluster 300	Enrichment Score: 0.2	G	170	Count	P_Value	Fold Change	Benjamin	
	UP_SEQ_FEATURE	chain:Histone H2A type 1-D	RT	i	3	6.3E-1	Onlange	1.0E0	9
	UP_SEQ_FEATURE	chain:Histone H3.1	RT		3	6.3E-1		1.0E0	1 9
	UP_SEQ_FEATURE								1 9
		chain:Histone H3.2	<u>RT</u>		3	6.3E-1	1.5EU	1.0E0	1
				198			Fold		
not	tation Cluster 301	Enrichment Score: 0.19	G	N .		P_Value	Change	Benjamin	_
not	UP_KEYWORDS	Enrichment Score: 0.19 <u>Vision</u>	G RT	i i	Count 20	P_Value 3.1E-1	Change	Benjamin 8.8E-1	6
not	UP_KEYWORDS GOTERM_BP_DIRECT	<u>Vision</u> <u>visual perception</u>	RT RT		20 29	3.1E-1 8.9E-1	1.2E0 8.5E-1	8.8E-1 1.0E0	6 1 9
	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS	Vision visual perception Sensory transduction	RT RT RT	i i	20 29 22	3.1E-1 8.9E-1 1.0E0	1.2E0 8.5E-1 2.5E-1	8.8E-1 1.0E0 1.0E0	6 1 9 1
	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302	Vision visual perception Sensory transduction Enrichment Score: 0.18	RT RT RT G		20 29 22 Count	3.1E-1 8.9E-1 1.0E0 P_Value	1.2E0 8.5E-1 2.5E-1 Fold Change	8.8E-1 1.0E0 1.0E0 Benjamin	6 1 9 1 1
	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO	Vision visual perception Sensory transduction	RT RT RT	i i	20 29 22	3.1E-1 8.9E-1 1.0E0	1.2E0 8.5E-1 2.5E-1 Fold Change	8.8E-1 1.0E0 1.0E0	66 11 11 11 11 19
	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO UP_SEQ_FEATURE	Vision visual perception Sensory transduction Enrichment Score: 0.18	RT RT RT G		20 29 22 Count	3.1E-1 8.9E-1 1.0E0 P_Value	1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0	8.8E-1 1.0E0 1.0E0 Benjamin	6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO	Vision visual perception Sensory transduction Enrichment Score: 0.18 Forkhead-associated (FHA) domain	RT RT RT G		20 29 22 Count	3.1E-1 8.9E-1 1.0E0 P_Value 5.6E-1	1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0	8.8E-1 1.0E0 1.0E0 Benjamin 1.0E0	66 11 11 11 11 11 12 13 14 14 15 16 17 17 18 18 18 18 18 18 18 18 18 18 18 18 18
	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO UP_SEQ_FEATURE	Vision visual perception Sensory transduction Enrichment Score: 0.18 Forkhead-associated (FHA) domain domain:FHA	RT RT G RT RT G		20 29 22 Count 7	3.1E-1 8.9E-1 1.0E0 P_Value 5.6E-1 6.0E-1	1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0	8.8E-1 1.0E0 1.0E0 Benjamin 1.0E0 1.0E0	66 11 11 11 11 11 12 13 14 14 15 16 17 17 18 18 18 18 18 18 18 18 18 18 18 18 18
not	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO UP_SEQ_FEATURE INTERPRO	Vision Visual perception Sensory transduction Enrichment Score: 0.18 Forkhead-associated (FHA) domain domain:FHA SMAD/FHA domain	RT RT RT G RT RT RT		20 29 22 Count 7 6 9	3.1E-1 8.9E-1 1.0E0 P_Value 5.6E-1 6.0E-1	Change 1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0 1.2E0 1.1E0 8.8E-1	8.8E-1 1.0E0 1.0E0 Benjamin 1.0E0 1.0E0 1.0E0	66 11 11 11 11 12 13 14 14 15 16 17 17 18 18 18 18 18 18 18 18 18 18 18 18 18
not	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO UP_SEQ_FEATURE INTERPRO SMART	Vision Visual perception Sensory transduction Enrichment Score: 0.18 Forkhead-associated (FHA) domain domain:FHA SMAD/FHA domain FHA	RT RT RT G RT RT RT		20 29 22 Count 7 6 9	3.1E-1 8.9E-1 1.0E0 P_Value 5.6E-1 6.0E-1 6.4E-1 8.5E-1	1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0 1.2E0 1.1E0 8.8E-1 Fold Change	8.8E-1 1.0E0 1.0E0 Benjamin 1.0E0 1.0E0 1.0E0	61 11 11 11 11 11 11 11 11 11 11 11 11 1
not	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO UP_SEQ_FEATURE INTERPRO SMART tation Cluster 303	Vision visual perception Sensory transduction Enrichment Score: 0.18 Forkhead-associated (FHA) domain domain:FHA SMAD/FHA domain FHA Enrichment Score: 0.18	RT RT G RT RT RT RT RT G G G		20 29 22 Count 7 6 9 5 Count	3.1E-1 8.9E-1 1.0E0 P_Value 5.6E-1 6.0E-1 6.4E-1 8.5E-1 P_Value 2.2E-1	1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0 1.2E0 1.1E0 8.8E-1 Fold Change	8.8E-1 1.0E0 1.0E0 Benjamin 1.0E0 1.0E0 1.0E0 Benjamin 1.0E0	61 91 1 1 91 91 91 91 91
not	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO UP_SEQ_FEATURE INTERPRO SMART tation Cluster 303 UP_SEQ_FEATURE	Vision visual perception Sensory transduction Enrichment Score: 0.18 Forkhead-associated (FHA) domain domain:FHA SMAD/FHA domain FHA Enrichment Score: 0.18 binding site:NAD; via carbonyl oxygen	RT RT G RT RT RT RT RT RT RT		20 29 22 Count 7 6 9 5 Count	3.1E-1 8.9E-1 1.0E0 P_Value 5.6E-1 6.0E-1 8.5E-1 P_Value 2.2E-1 9.0E-1	1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0 1.2E0 1.1E0 8.8E-1 Fold Change	8.8E-1 1.0E0 1.0E0 Benjamin 1.0E0 1.0E0 1.0E0 Benjamin 1.0E0 1.0E0	9 1 1 1 9 1 1 1 9 1 1 1 9 1 1 1 9 1 1 1 1 9 1
not	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO UP_SEQ_FEATURE INTERPRO SMART tation Cluster 303 UP_SEQ_FEATURE GOTERM_MF_DIRECT	Vision visual perception Sensory transduction Enrichment Score: 0.18 Forkhead-associated (FHA) domain domain:FHA SMAD/FHA domain FHA Enrichment Score: 0.18 binding site:NAD; via carbonyl oxygen NAD binding binding site:NAD	RT		20 29 22 Count 7 6 9 5 Count 3 5 5	3.1E-1 8.9E-1 1.0E0 P_Value 5.6E-1 6.0E-1 6.4E-1 8.5E-1 P_Value 2.2E-1 9.0E-1 9.7E-1	Change 1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0 1.2E0 1.1E0 8.8E-1 Fold Change 3.4E0 7.8E-1 6.3E-1	8.8E-1 1.0E0 1.0E0 Benjamin 1.0E0 1.0E0 1.0E0 Benjamin 1.0E0 1.0E0 1.0E0	6 1 9 1 1 1 9 1 1 1 9 1 1 1 9 1 1 1 9 1 1 1 9 1
not	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO UP_SEQ_FEATURE INTERPRO SMART tation Cluster 303 UP_SEQ_FEATURE GOTERM_MF_DIRECT UP_SEQ_FEATURE UP_SEQ_FEATURE	Vision visual perception Sensory transduction Enrichment Score: 0.18 Forkhead-associated (FHA) domain domain:FHA SMAD/FHA domain FHA Enrichment Score: 0.18 binding site:NAD; via carbonyl oxygen NAD binding binding site:NAD nucleotide phosphate-binding region:NAD	RT R		20 29 22 Count 7 6 9 5 Count 3 5 7	3.1E-1 8.9E-1 1.0E0 P_Value 5.6E-1 6.0E-1 6.4E-1 8.5E-1 P_Value 2.2E-1 9.0E-1 9.7E-1 9.8E-1	Change 1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0 1.1E0 8.8E-1 Fold Change 3.4E0 7.8E-1 6.3E-1 Fold	8.8E-1 1.0E0 1.0E0 Benjamin 1.0E0 1.0E0 1.0E0 Benjamin 1.0E0 1.0E0 1.0E0 1.0E0	6 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1
not	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO UP_SEQ_FEATURE INTERPRO SMART tation Cluster 303 UP_SEQ_FEATURE GOTERM_MF_DIRECT UP_SEQ_FEATURE	Vision visual perception Sensory transduction Enrichment Score: 0.18 Forkhead-associated (FHA) domain domain:FHA SMAD/FHA domain FHA Enrichment Score: 0.18 binding site:NAD; via carbonyl oxygen NAD binding binding site:NAD nucleotide phosphate-binding region:NAD Enrichment Score: 0.18	RT R		20 29 22 Count 7 6 9 5 Count 3 5 7 Count	3.1E-1 8.9E-1 1.0E0 P_Value 5.6E-1 6.0E-1 6.4E-1 8.5E-1 P_Value 2.2E-1 9.0E-1 9.7E-1 9.8E-1 P_Value	Change 1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0 1.1E0 8.8E-1 Fold Change 3.4E0 7.8E-1 6.3E-1 Fold Change	8.8E-1 1.0E0 1.0E0 Benjamin 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 Benjamin	61 91 11 91 91 91 91 91 91 91
not	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO UP_SEQ_FEATURE INTERPRO SMART tation Cluster 303 UP_SEQ_FEATURE GOTERM_MF_DIRECT UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE SMART tation Cluster 304 GOTERM_BP_DIRECT	Vision visual perception Sensory transduction Enrichment Score: 0.18 Forkhead-associated (FHA) domain domain:FHA SMAD/FHA domain FHA Enrichment Score: 0.18 binding site:NAD; via carbonyl oxygen NAD binding binding site:NAD nucleotide phosphate-binding region:NAD Enrichment Score: 0.18 ATP hydrolysis coupled proton transport	RT R		20 29 22 Count 7 6 9 5 Count 3 5 7 Count 8	3.1E-1 8.9E-1 1.0E0 P_Value 5.6E-1 6.0E-1 6.4E-1 8.5E-1 P_Value 2.2E-1 9.0E-1 9.7E-1 9.8E-1 P_Value 2.9E-1	Change 1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0 1.2E0 1.1E0 8.8E-1 Fold Change 3.4E0 7.8E-1 6.0E-1 Fold Change	8.8E-1 1.0E0 1.0E0 Benjamin 1.0E0	6 1 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
not	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO UP_SEQ_FEATURE INTERPRO SMART tation Cluster 303 UP_SEQ_FEATURE GOTERM_MF_DIRECT UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE tation Cluster 304 GOTERM_BP_DIRECT UP_KEYWORDS	Vision visual perception Sensory transduction Enrichment Score: 0.18 Forkhead-associated (FHA) domain domain:FHA SMAD/FHA domain FHA Enrichment Score: 0.18 binding site:NAD; via carbonyl oxygen NAD binding binding site:NAD nucleotide phosphate-binding region:NAD Enrichment Score: 0.18 ATP hydrolysis coupled proton transport Hydrogen ion transport	RT R		20 29 22 Count 7 6 9 5 Count 3 5 7 Count 8 4	3.1E-1 8.9E-1 1.0E0 P_Value 5.6E-1 6.0E-1 6.4E-1 8.5E-1 P_Value 2.2E-1 9.0E-1 9.7E-1 9.8E-1 P_Value 2.9E-1	Change 1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0 1.1E0 8.8E-1 Fold Change 3.4E0 7.8E-1 6.3E-1 6.0E-1 Fold Change	8.8E-1 1.0E0 1.0E0 Benjamin 1.0E0	6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
not	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO UP_SEQ_FEATURE INTERPRO SMART tation Cluster 303 UP_SEQ_FEATURE GOTERM_MF_DIRECT UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE tation Cluster 304 GOTERM_BP_DIRECT UP_KEYWORDS KEGG_PATHWAY	Vision Visual perception Sensory transduction Enrichment Score: 0.18 Forkhead-associated (FHA) domain domain:FHA SMAD/FHA domain FHA Enrichment Score: 0.18 binding site:NAD; via carbonyl oxygen NAD binding binding site:NAD nucleotide phosphate-binding region:NAD Enrichment Score: 0.18 ATP hydrolysis coupled proton transport Hydrogen ion transport Oxidative phosphorylation	RI R		20 29 22 Count 7 6 9 5 Count 3 5 7 Count 8 4 5	3.1E-1 8.9E-1 1.0E0 P_Value 5.6E-1 6.0E-1 6.4E-1 8.5E-1 P_Value 2.2E-1 9.0E-1 9.7E-1 9.8E-1 P_Value 2.9E-1 1.0E0	Change 1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0 1.1E0 8.8E-1 Fold Change 3.4E0 7.8E-1 6.3E-1 6.0E-1 Fold Change 1.5E0 5.6E-1 2.0E-1	8.8E-1 1.0E0	6 1 9 1 9 1 9 1 9 1 9 1 1 9 1 1 1 1 1 1
not	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO UP_SEQ_FEATURE INTERPRO SMART tation Cluster 303 UP_SEQ_FEATURE GOTERM_MF_DIRECT UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE tation Cluster 304 GOTERM_BP_DIRECT UP_KEYWORDS	Vision visual perception Sensory transduction Enrichment Score: 0.18 Forkhead-associated (FHA) domain domain:FHA SMAD/FHA domain FHA Enrichment Score: 0.18 binding site:NAD; via carbonyl oxygen NAD binding binding site:NAD nucleotide phosphate-binding region:NAD Enrichment Score: 0.18 ATP hydrolysis coupled proton transport Hydrogen ion transport	RI R		20 29 22 Count 7 6 9 5 Count 3 5 7 Count 8 4 5 Count	3.1E-1 8.9E-1 1.0E0 P_Value 5.6E-1 6.0E-1 6.4E-1 8.5E-1 P_Value 2.2E-1 9.0E-1 9.7E-1 9.8E-1 P_Value 2.9E-1 1.0E0 P_Value	Change 1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0 1.1E0 8.8E-1 Fold Change 3.4E0 7.8E-1 6.3E-1 6.0E-1 Fold Change 1.5E0 5.6E-1 2.0E-1 Fold Change	8.8E-1 1.0E0 Benjamin 1.0E0 1.0E0 Benjamin 1.0E0	6 1 9 1 9 1 9 1 9 1 9 1 1 1 1 1 1 1 1 1
not	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO UP_SEQ_FEATURE INTERPRO SMART tation Cluster 303 UP_SEQ_FEATURE GOTERM_MF_DIRECT UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE TOTAL CLUSTER 304 GOTERM_BP_DIRECT UP_KEYWORDS KEGG_PATHWAY tation Cluster 305 BIOCARTA	Vision visual perception Sensory transduction Enrichment Score: 0.18 Forkhead-associated (FHA) domain domain: FHA SMAD/FHA domain FHA Enrichment Score: 0.18 binding site: NAD; via carbonyl oxygen NAD binding binding site: NAD nucleotide phosphate-binding region: NAD Enrichment Score: 0.18 ATP hydrolysis coupled proton transport Hydrogen ion transport Oxidative phosphorylation Enrichment Score: 0.17 TACI and BCMA stimulation of B cell immune responses.	RI R		20 29 22 Count 7 6 9 5 Count 3 5 7 Count 8 4 5 Count 6	3.1E-1 8.9E-1 1.0E0 P_Value 5.6E-1 6.0E-1 6.4E-1 8.5E-1 P_Value 2.2E-1 9.0E-1 9.7E-1 9.8E-1 P_Value 2.9E-1 1.0E0 P_Value 5.8E-1	Change 1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0 1.2E0 1.1E0 8.8E-1 Fold Change 3.4E0 7.8E-1 6.3E-1 6.0E-1 Fold Change 1.5E0 5.6E-1 2.0E-1 Fold Change	8.8E-1 1.0E0 Benjamin 1.0E0 1.0E0 Benjamin 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0 1.0E0	6 1 9 1 1 9 1 9 1 9 1 9 1 1 1 1 6 1 1 1 1
not	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO UP_SEQ_FEATURE INTERPRO SMART tation Cluster 303 UP_SEQ_FEATURE GOTERM_MF_DIRECT UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE tation Cluster 304 GOTERM_BP_DIRECT UP_KEYWORDS KEGG_PATHWAY tation Cluster 305 BIOCARTA GOTERM_BP_DIRECT	Vision visual perception Sensory transduction Enrichment Score: 0.18 Forkhead-associated (FHA) domain domain: FHA SMAD/FHA domain FHA Enrichment Score: 0.18 binding site: NAD; via carbonyl oxygen NAD binding binding site: NAD nucleotide phosphate-binding region: NAD Enrichment Score: 0.18 ATP hydrolysis coupled proton transport Hydrogen ion transport Oxidative phosphorylation Enrichment Score: 0.17 TACI and BCMA stimulation of B cell immune	RI R		20 29 22 Count 7 6 9 5 Count 3 5 7 Count 8 4 5 Count	3.1E-1 8.9E-1 1.0E0 P_Value 5.6E-1 6.0E-1 6.4E-1 8.5E-1 P_Value 2.2E-1 9.0E-1 9.7E-1 9.8E-1 P_Value 2.9E-1 1.0E0 P_Value	Change 1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0 1.2E0 1.1E0 8.8E-1 Fold Change 3.4E0 7.8E-1 6.3E-1 6.0E-1 Fold Change 1.5E0 5.6E-1 2.0E-1 Fold Change	8.8E-1 1.0E0 Benjamin 1.0E0 1.0E0 Benjamin 1.0E0	6 1 9 1 9 1 9 1 9 1 9 1 9 1 1 1 6 1 9 1 1 9 1 1 1 1
inot	UP_KEYWORDS GOTERM_BP_DIRECT UP_KEYWORDS tation Cluster 302 INTERPRO UP_SEQ_FEATURE INTERPRO SMART tation Cluster 303 UP_SEQ_FEATURE GOTERM_MF_DIRECT UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE UP_SEQ_FEATURE TOTAL CLUSTER 304 GOTERM_BP_DIRECT UP_KEYWORDS KEGG_PATHWAY tation Cluster 305 BIOCARTA	Vision visual perception Sensory transduction Enrichment Score: 0.18 Forkhead-associated (FHA) domain domain: FHA SMAD/FHA domain FHA Enrichment Score: 0.18 binding site: NAD; via carbonyl oxygen NAD binding binding site: NAD nucleotide phosphate-binding region: NAD Enrichment Score: 0.18 ATP hydrolysis coupled proton transport Hydrogen ion transport Oxidative phosphorylation Enrichment Score: 0.17 TACI and BCMA stimulation of B cell immune responses. membrane protein intracellular domain	RI R		20 29 22 Count 7 6 9 5 Count 3 5 7 Count 8 4 5 Count 6	3.1E-1 8.9E-1 1.0E0 P_Value 5.6E-1 6.0E-1 8.5E-1 P_Value 2.2E-1 9.0E-1 9.7E-1 9.8E-1 1.0E0 P_Value 5.8E-1 6.1E-1 7.3E-1	Change 1.2E0 8.5E-1 2.5E-1 Fold Change 1.2E0 1.1E0 8.8E-1 Fold Change 3.4E0 7.8E-1 6.3E-1 6.0E-1 Fold Change 1.5E0 5.6E-1 2.0E-1 Fold Change 1.2E0 1.3E0	8.8E-1 1.0E0 Benjamin 1.0E0	6 1 9 1 1 9 1 9 1 9 1 9 1 1 1 1 1 1 1 1

Annota	ation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
	UP_KEYWORDS	Steroid-binding	<u>RT</u>	i	5	1.9E-1	2.1E0	5.9E-1	4.6E-
	UP_SEQ_FEATURE	region of interest:Steroid-binding	<u>RT</u>	i	3	2.2E-1	3.4E0	1.0E0	9.6E-
	INTERPRO	Zinc finger, NHR/GATA-type	<u>RT</u>		13	2.2E-1	1.4E0	1.0E0	9.1E-
	UP_SEQ_FEATURE	region of interest: Modulating	<u>RT</u>		3	6.3E-1	1.5E0	1.0E0	9.6E-
	GOTERM_MF_DIRECT	steroid binding	RT		5	6.9E-1		1.0E0	1 8.9E-
	UP_SEQ_FEATURE	zinc finger region:NR C4-type	RT	-	6		9.1E-1		1 9.6E-
	UP_SEQ_FEATURE								1 9.6E-
	INTERPRO	DNA-binding region: Nuclear receptor	<u>RT</u>		6		9.1E-1		1 9.1E-
	INTERPRO	Zinc finger, nuclear hormone receptor-type	<u>RT</u>		6		8.1E-1		1 9.1E-
	INTERPRO	Steroid hormone receptor Nuclear hormone receptor, ligand-binding,	<u>RT</u>		6	9.0E-1	7.9E-1	1.0E0	9.1E-
		core	<u>RT</u>	i	6	9.1E-1	7.7E-1	1.0E0	1
	UP_SEQ_FEATURE	region of interest:Hinge	<u>RT</u>	i	3	9.3E-1	7.3E-1	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	region of interest:Ligand-binding	<u>RT</u>	i	3	9.5E-1	6.8E-1	1.0E0	9.6E- 1
	GOTERM_MF_DIRECT	RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding	<u>RT</u>	i	4	9.5E-1	6.6E-1	1.0E0	9.5E- 1
	GOTERM_MF_DIRECT	steroid hormone receptor activity	<u>RT</u>	i .	6	9.7E-1	6.4E-1	1.0E0	9.7E- 1
	GOTERM_BP_DIRECT	steroid hormone mediated signaling pathway	<u>RT</u>	i .	5	9.9E-1	5.2E-1	1.0E0	9.9E- 1
	SMART	ZnF_C4	<u>RT</u>	i .	6	9.9E-1	5.3E-1	1.0E0	9.9E- 1
	SMART	HOLI	<u>RT</u>	i	6	1.0E0	5.1E-1	1.0E0	1.0E0
Annota	ation Cluster 307	Enrichment Score: 0.16	G	™	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	domain:OPR	<u>RT</u>	i	3	5.4E-1	1.7E0	1.0E0	9.6E- 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	9.1E- 1
Annot	ation Cluster 308	Enrichment Score: 0.15	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_CC_DIRECT	mitochondrial small ribosomal subunit	<u>RT</u>	i	5	5.7E-1	1.3E0	1.0E0	8.8E- 1
	GOTERM_BP_DIRECT	mitochondrial translational elongation	<u>RT</u>	1	14	7.0E-1	9.8E-1	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	mitochondrial translation	<u>RT</u>	i	6	7.5E-1	9.9E-1	1.0E0	9.6E-
	GOTERM_BP_DIRECT	mitochondrial translational termination	<u>RT</u>	1	13	8.1E-1	9.0E-1	1.0E0	9.6E-
Annot	ation Cluster 309	Enrichment Score: 0.15	G	T.	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	Patatin/Phospholipase A2-related	RT	1	3	4.4E-1	Change	1.0E0	9.1E-
	INTERPRO	Acyl transferase/acyl	RT		3	8.1E-1	1.0E0	1.0E0	1 9.1E-
	KEGG_PATHWAY	hydrolase/lysophospholipase Glycerophospholipid metabolism	<u>RT</u>	i	5	1.0E0	2.7E-1		1 1.0E0
Annot	ation Cluster 310	Enrichment Score: 0.14	G	170	Count	P_Value	Fold Change	Benjamini	FDR
	BIOCARTA	Role of PI3K subunit p85 in regulation of Actin Organization and Cell Migration	<u>RT</u>	i .	7	4.3E-1	1.3E0	7.3E-1	5.2E- 1
	BIOCARTA	How does salmonella hijack a cell	<u>RT</u>	i .	4	8.5E-1	9.4E-1	1.0E0	8.5E- 1
	BIOCARTA	Y branching of actin filaments	<u>RT</u>	i	3	1.0E0	4.3E-1	1.0E0	1.0E0
Annota	ation Cluster 311	Enrichment Score: 0.13	G	15	Count	P_Value	Fold Change	Benjamini	
	GOTERM_BP_DIRECT	histone H4-K16 acetylation	<u>RT</u>	i	4	6.8E-1	1.2E0	1.0E0	9.6E- 1
	GOTERM_CC_DIRECT	histone acetyltransferase complex	<u>RT</u>	1	4	7.2E-1	1.1E0	1.0E0	8.8E- 1
	GOTERM_BP_DIRECT	histone H4-K5 acetylation	<u>RT</u>	i	3	7.8E-1	1.1E0	1.0E0	9.6E- 1
	GOTERM_BP_DIRECT	histone H4-K8 acetylation	<u>RT</u>	1	3	7.8E-1	1.1E0	1.0E0	9.6E- 1
Annot	ation Cluster 312	Enrichment Score: 0.12	G	-	Count	P_Value	Fold Change	Benjamini	
	KEGG_PATHWAY	One carbon pool by folate	<u>RT</u>	i	5			8.3E-1	5.6E- 1
	UP_KEYWORDS	One-carbon metabolism	<u>RT</u>	i	3	7.3E-1	1.2E0	1.0E0	7.8E-
	GOTERM_BP_DIRECT	folic acid metabolic process	RT	1	3	8.3E-1	9.9E-1	1.0E0	9.6E-
	GOTERM_BP_DIRECT	one-carbon metabolic process	RT		3		5.9E-1		1 9.7E-
						1	Fold	1	1 EDB
Appet	ation Cluster 343	Enrichment Score: 0.11			Count	2 4/4-11-2		- HONDON	
Annota	ation Cluster 313 GOTERM_BP_DIRECT	Enrichment Score: 0.11	G DT	-	Count		Cilalige	:	9.6E-
Annota		Enrichment Score: 0.11 negative regulation of viral transcription negative regulation of viral release from host	RT RT	i i	Count 3	6.7E-1 7.8E-1	1.4E0	1.0E0 1.0E0	

Annot	ation Cluster 1	Enrichment Score: ?	G	To the second se	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	zinc finger region:B box-type	<u>RT</u>	i	8	8.9E-1	8.0E-1	1.0E0	9.6E- 1
Annot	ation Cluster 314	Enrichment Score: 0.11	G	17	Count	P_Value	Fold Change	Benjamini	
	INTERPRO	Phospholipid-transporting P-type ATPase,	RT	i	3	6.9E-1	Change	1.0E0	9.1E-
	GOTERM_MF_DIRECT	subfamily IV phospholipid-translocating ATPase activity	RT		3	7.1E-1	1.3E0	1.0E0	1 8.9E-
	GOTERM_BP_DIRECT	phospholipid translocation	RT		4	7.4E-1		1.0E0	1 9.6E-
	UP_KEYWORDS	<u>Lipid transport</u>	RT		4	1.0E0		1.0E0	1 1.0E0
Annot	ation Cluster 315	Enrichment Score: 0.11	G	17	Count	P_Value	Fold Change	Benjamini	FDR
	GOTERM_MF_DIRECT	cAMP response element binding	<u>RT</u>	i	4	3.8E-1	1.8E0	1.0E0	8.9E- 1
	INTERPRO	Basic-leucine zipper domain	<u>RT</u>	i .	5	9.8E-1	5.7E-1	1.0E0	9.8E- 1
	SMART	<u>BRLZ</u>	<u>RT</u>	i	5	1.0E0	4.0E-1	1.0E0	1.0E0
	UP_SEQ_FEATURE	DNA-binding region:Basic motif	<u>RT</u>	i e	10	1.0E0	4.2E-1 Fold		1.0E0
Annot	up_SEQ_FEATURE	Enrichment Score: 0.1	G	-	Count	P_Value	Change	Benjamini	9.6E-
	INTERPRO	domain:SAP	<u>RT</u>	•	4	7.1E-1	1.1E0	1.0E0	1
		SAP domain	<u>RT</u>	i	4	7.7E-1	1.0E0	1.0E0	9.1E- 1
	SMART	SAP	<u>RT</u>	i	4	9.5E-1	7.1E-1	1.0E0	9.5E- 1
Annot	ation Cluster 317	Enrichment Score: 0.09	G	17	Count	P_Value	Fold Change	Benjamini	
	UP_SEQ_FEATURE	domain:CS	<u>RT</u>	i	3	7.0E-1	1.3E0	1.0E0	9.6E- 1
	INTERPRO	CS-like domain	<u>RT</u>	1	3	7.9E-1	1.1E0	1.0E0	9.1E- 1
	INTERPRO	HSP20-like chaperone	<u>RT</u>	i	3	9.5E-1	6.6E-1	1.0E0	9.5E- 1
Annot	ation Cluster 318	Enrichment Score: 0.06	G	13	Count	P_Value	Fold Change	Benjamini	FDR
	UP_KEYWORDS	Nuclear pore complex	<u>RT</u>	i	7	7.6E-1	9.6E-1	1.0E0	7.8E-
	GOTERM_BP_DIRECT	tRNA export from nucleus	<u>RT</u>	i	4	9.2E-1	7.4E-1	1.0E0	9.6E-
	GOTERM_BP_DIRECT	regulation of glucose transport	<u>RT</u>	1	4	9.3E-1	7.2E-1	1.0E0	9.6E-
Annot	ation Cluster 319	Enrichment Score: 0.05	G	178	Count	P_Value	Fold Change	Benjamini	1 FDR
	UP_SEQ_FEATURE	domain:Ig-like 3	RT		3	7.9E-1	Change	1.0E0	9.6E-
	UP_SEQ_FEATURE	domain:Ig-like 1	RT		3	9.4F-1	7.0E-1	1.0F0	1 9.6E-
	UP_SEQ_FEATURE	domain:Ig-like 2	RT		3		7.0E-1		1 9.6E-
Annot	ation Cluster 320	Enrichment Score: 0.05	G		Count	P_Value	Fold	Benjamini	1 EDR
	GOTERM_MF_DIRECT	3',5'-cyclic-nucleotide phosphodiesterase	RT	i	4	7.7E-1	Change	1.0E0	8.9E-
	INTERPRO	activity 2.E. cyclic pyclostide phosphodiostorace		-					1 9.1E-
	INTERPRO	3'5'-cyclic nucleotide phosphodiesterase 3'5'-cyclic nucleotide phosphodiesterase,	<u>RT</u>		3		9.8E-1		1 9.1E-
	INTERPRO	conserved site 3'5'-cyclic nucleotide phosphodiesterase,	<u>RT</u>		3		8.9E-1		1 9.1E-
	INTERPRO	catalytic domain	<u>RT</u>	1	3	8.9E-1	8.5E-1	1.0E0	1
		HD/PDEase domain	<u>RT</u>	i	3	9.1E-1	8.1E-1	1.0E0	9.1E- 1
	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 1	RT	i	3	9.3E-1	7.3E-1	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 2	<u>RT</u>	i	3	9.3E-1	7.3E-1	1.0E0	9.6E- 1
	SMART	HDc	<u>RT</u>	i	3	9.9E-1	5.3E-1	1.0E0	9.9E- 1
Annot	ation Cluster 321	Enrichment Score: 0.05	G	13	Count	P_Value	Fold Change	Benjamini	FDR
	UP_SEQ_FEATURE	domain:DEP	<u>RT</u>	i	3	7.9E-1	1.1E0	1.0E0	9.6E- 1
	INTERPRO	DEP domain	<u>RT</u>	i	3	9.1E-1	8.1E-1	1.0E0	9.1E- 1
	SMART	<u>DEP</u>	<u>RT</u>	i	3	9.8E-1	5.5E-1	1.0E0	9.8E- 1
Annot	ation Cluster 322	Enrichment Score: 0.04	G	TN .	Count	P_Value	Fold Change	Benjamini	FDR
	INTERPRO	Kelch-like protein, gigaxonin	<u>RT</u>	i	7	6.9E-1		1.0E0	9.1E- 1
	GOTERM_CC_DIRECT	Cul3-RING ubiquitin ligase complex	<u>RT</u>	i .	10	7.5E-1	9.5E-1	1.0E0	8.8E-
	PIR_SUPERFAMILY	kelch-like protein, gigaxonin type	<u>RT</u>	i	7	8.1E-1	9.1E-1	1.0E0	1.0E0
	INTERPRO	Galactose oxidase, beta-propeller	<u>RT</u>	i	4	8.7E-1	8.5E-1	1.0E0	9.1E- 1
	UP_SEQ_FEATURE	repeat:Kelch 6	<u>RT</u>	i	6	9.0E-1	7.9E-1	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	repeat:Kelch 5	<u>RT</u>	i	7	9.4E-1	7.2E-1	1.0E0	9.6E- 1
	UP_SEQ_FEATURE	domain:BACK	<u>RT</u>	i	3	9.5E-1	6.8E-1	1.0E0	9.6E- 1

Annota	ation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	BTB/Kelch-associated	RT		7	9.5E-1	7.0E-1	1.0E0	9.5E
	UP_SEQ_FEATURE	repeat:Kelch 4	RT		7		6.8E-1		1 9.6E
	INTERPRO								1 9.6E
		Kelch repeat type 1	<u>RT</u>	•	7	9.6E-1	6.8E-1	1.0E0	1
	UP_SEQ_FEATURE	repeat:Kelch 1	<u>RT</u>	1	7	9.6E-1	6.7E-1	1.0E0	9.6E
	UP_SEQ_FEATURE	repeat:Kelch 2	<u>RT</u>	1	7	9.6E-1	6.7E-1	1.0E0	9.6E
	UP_SEQ_FEATURE	repeat:Kelch 3	<u>RT</u>	1	7	9.6E-1	6.7E-1	1.0E0	9.6E
	UP_KEYWORDS	<u>Kelch repeat</u>	<u>RT</u>	4	7	9.6E-1	6.7E-1	1.0E0	9.6E
	INTERPRO			-					1 9.9E
 	SMART	Kelch-type beta propeller Kelch	<u>RT</u> <u>RT</u>		4 7	1.0E0	4.7E-1 4.9E-1		1 1.0E
	SMART	<u>SM00875</u>	RT	i	7	1.0E0	4.7E-1		1.0E
Annota	ation Cluster 323	Enrichment Score: 0.03		100	Count	P_Value	Fold Change	Benjamin	i FDR
	INTERPRO	<u>Heparin-binding growth factor/Fibroblast</u> growth factor	<u>RT</u>	i	3	8.9E-1	8.5E-1	-	9.1E 1
7	INTERPRO	Cytokine, IL-1-like	RT		4	9.2F-1	7.5E-1	1.0F0	9.2E
_	SMART			_					1 9.8E
		<u>FGF</u>	RT		3	9.8E-1	5.5E-1	1	1
nnota	ation Cluster 324	Enrichment Score: 0.02	G	<u> </u>	Count	P_Value	Fold Change	Benjamin	
	UP_SEQ_FEATURE	domain:G-patch	<u>RT</u>	1	3	8.7E-1	8.9E-1	1.0E0	9.6E 1
	INTERPRO	<u>G-patch domain</u>	<u>RT</u>	1	3	9.7E-1	5.8E-1	1.0E0	9.7E 1
	SMART	<u>G_patch</u>	<u>RT</u>	i	3	1.0E0	3.9E-1	1.0E0	1.0E
nnota	ation Cluster 325	Enrichment Score: 0.02		100	Count	P_Value	Fold Change	Benjamin	i FDR
	UP_KEYWORDS	Host cell receptor for virus entry	<u>RT</u>	i	7		7.5E-1		9.2E
\neg	GOTERM_BP_DIRECT	viral entry into host cell	<u>RT</u>		10	9.4F-1	7.4E-1	1.0F0	9.6E
	GOTERM_MF_DIRECT								1 9.8E
		<u>virus receptor activity</u>	<u>RT</u>	i	7	9.8E-1	6.0E-1	1.0E0	1
nnota	ation Cluster 326	Enrichment Score: 0.02	G	-	Count	P_Value	Fold Change	Benjamin	
	UP_KEYWORDS	<u>Cilium biogenesis/degradation</u>	<u>RT</u>	i	17	9.3E-1	7.9E-1	1.0E0	9.3E 1
	GOTERM_BP_DIRECT	<u>cilium morphogenesis</u>	<u>RT</u>	1	18	9.4E-1	7.8E-1	1.0E0	9.6E 1
	GOTERM_BP_DIRECT	<u>cilium assembly</u>	<u>RT</u>	4	14	9.8E-1	6.7E-1	1.0E0	9.8E
nnota	ation Cluster 327	Enrichment Score: 0.02	G	-	Count	P_Value	Fold	Daniamin	1 EDP
	UP_SEQ_FEATURE						Change		9.6E
		domain:LisH	<u>RT</u>	i	3	9.3E-1	7.3E-1	1.0E0	1
	INTERPRO	<u>LisH dimerisation motif</u>	<u>RT</u>	1	3	9.5E-1	6.6E-1	1.0E0	9.5E 1
	SMART	<u>LisH</u>	<u>RT</u>	i	3	9.9E-1	5.3E-1	1.0E0	9.9E 1
Annota	ation Cluster 328	Enrichment Score: 0.01	G	178	Count	P_Value	Fold Change	Benjamin	i FDR
7	INTERPRO	Zinc finger, B-box	RT		11	8.7E-1	8.3E-1	-	9.1E
ے ا	UP_SEQ_FEATURE			<u>-</u>					1 9.6E
		zinc finger region:B box-type	<u>RT</u>	•	8		8.0E-1		1
	UP_SEQ_FEATURE	domain:B30.2/SPRY	<u>RT</u>	•	10	9.6E-1	7.0E-1	1.0E0	9.6E 1
	INTERPRO	SPla/RYanodine receptor SPRY	<u>RT</u>	1	10	9.8E-1	6.6E-1	1.0E0	9.8E 1
	INTERPRO	B30.2/SPRY domain	<u>RT</u>	•	10	9.9E-1	6.3E-1	1.0E0	9.9E 1
	INTERPRO	SPRY-associated	RT		4	9.9E-1	5.0E-1	1.0E0	9.9E
	SMART	BBOX	RT		10		5.5E-1		1 1.0E
	INTERPRO	<u>Butyrophylin-like</u>	<u>RT</u>		5	1.0E0	4.3E-1	1.0E0	1.0E
	SMART SMART	PRY SPRY	RT RT		4 10	1.0E0 1.0E0	3.3E-1 4.4E-1		1.0E
	INTERPRO	Concanavalin A-like lectin/glucanase,	RT		13	1.0E0	3.5E-1		1.0E
	akian Classassassassassassassassassassassassass	<u>subgroup</u>				1	Fold	Di.	1
nnota	ation Cluster 329	Enrichment Score: 0.01	G	_	Count	P_Value	Change	•	
	UP_SEQ_FEATURE	zinc finger region:FYVE-type	<u>RT</u>	1	4	9.4E-1	7.0E-1	1.0E0	9.6E 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>	i	3	9.8E-1	5.5E-1	1.0E0	9.8E
	SMART	<u>FYVE</u>	RT	1	3	1.0E0	4.2E-1		1 1.0E
nnota	ation Cluster 330	Enrichment Score: 0.01	G	178	Count	P_Value	Fold	Daniamin	1
	GOTERM_MF_DIRECT	histone demethylase activity	<u>RT</u>	i	3	9.2E-1	7.8E-1	=	9.2E
	UP_SEQ_FEATURE								1 9.6E
	I	domain:JmjC	<u>RT</u>		3	9.6E-1	6.4E-1	1.0E0	9.00

ınot	tation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamin	i FDF
)	INTERPRO	<u>JmjC domain</u>	<u>RT</u>	i	3	9.8E-1	5.6E-1	1.0E0	9.8
	SMART	<u>JmjC</u>	RT	1	3	1.0E0	4.2E-1	1.0E0	1.0
	UP_KEYWORDS	<u>Dioxygenase</u>	RT	i	5	1.0E0	4.1E-1		1.0
not	tation Cluster 331	Enrichment Score: 0.01	G	100	Count	P_Value	Fold Change	Benjamin	i FDI
	INTERPRO	Ras-association	RT		4	0 7F-1	6.2E-1	•	9.7
	UD SEO FEATURE	<u>Nas association</u>	<u>KI</u>	•	7	J./L-1	0.2L-1	1.020	1
	UP_SEQ_FEATURE	domain:Ras-associating	<u>RT</u>	i	3	9.7E-1	6.0E-1	1.0E0	9.7 1
	SMART	<u>RA</u>	<u>RT</u>	i	3	1.0E0	4.2E-1	1.0E0	1.0
not	tation Cluster 332	Enrichment Score: 0	G	- 13	Count	P_Value	Fold Change	Benjamin	i FDI
	UP_SEQ_FEATURE	repeat:22	RT	1	4	9.5E-1	6.6E-1	1.0E0	9.6
	UP_SEQ_FEATURE	·		-					1 9.6
		repeat:21	<u>RT</u>	•	4	9.6E-1	6.3E-1	1.0E0	1
	UP_SEQ_FEATURE	repeat:24	<u>RT</u>	i	3	9.7E-1	6.0E-1	1.0E0	9.7 1
	UP_SEQ_FEATURE	repeat:20	<u>RT</u>	4	4	9.7F-1	5.9E-1	1.0F0	9.7
	UP_SEQ_FEATURE	Topodit 20			·				1 9.8
	OF_SEQ_FEATORE	repeat:19	<u>RT</u>	•	4	9.8E-1	5.7E-1	1.0E0	1
	UP_SEQ_FEATURE	repeat:18	<u>RT</u>	1	4	9.8E-1	5.6E-1	1.0E0	9.8 1
	UP_SEQ_FEATURE	report 1	DT	_	27	0.05.1	7 25 1	1.050	9.9
		repeat:1	<u>RT</u>	•	27	9.90-1	7.2E-1	1.000	1
	UP_SEQ_FEATURE	repeat:2	<u>RT</u>	•	27	9.9E-1	7.1E-1	1.0E0	9.9 1
	UP_SEQ_FEATURE	repeat:17	<u>RT</u>	1	4	9.9E-1	4.9E-1	1.0E0	9.9
	UP_SEQ_FEATURE	repeat:16	RT		4	1.0E0	4.5E-1		1
	UP_SEQ_FEATURE	repeat:8	RT		10	1.0E0	5.5E-1		1.0
	UP_SEQ_FEATURE	repeat:9	<u>RT</u>	1	8	1.0E0	5.1E-1	1.0E0	1.0
	UP_SEQ_FEATURE	repeat:6	<u>RT</u>	•	12	1.0E0	5.6E-1		1.0
	UP_SEQ_FEATURE	repeat:10	<u>RT</u>		7	1.0E0	4.9E-1		1.0
	UP_SEQ_FEATURE UP_SEQ_FEATURE	repeat:11 repeat:7	RT RT		6 10	1.0E0 1.0E0	4.6E-1 5.1E-1		1.0
	UP_SEQ_FEATURE	repeat:3	RT		19	1.0E0	5.8E-1		1.0
	UP_SEQ_FEATURE	repeat:12	RT	i	5	1.0E0	4.0E-1	1.0E0	1.0
	UP_SEQ_FEATURE	repeat:15	<u>RT</u>	1	4	1.0E0	3.7E-1		1.0
	UP_SEQ_FEATURE	repeat:4	RT DT		15	1.0E0	5.3E-1		1.0
	UP_SEQ_FEATURE UP_SEQ_FEATURE	repeat:14 repeat:5	RT RT		4 11	1.0E0 1.0E0	3.4E-1 4.7E-1		1.0
	UP_SEQ_FEATURE	repeat:13	RT	i i	4	1.0E0	3.2E-1		1.0
not	tation Cluster 333	Enrichment Score: 0	G	178	Count	P_Value	Fold Change	Benjamin	i FD
	UP_SEQ_FEATURE	damain DU			25		Onlange		9.9
		domain:PH	<u>RT</u>		25		7.0E-1		1
	INTERPRO INTERPRO	Pleckstrin homology domain	RT DT	1	25	1.0E0	5.7E-1 5.8E-1		1.0
	SMART	<u>Pleckstrin homology-like domain</u> <u>PH</u>	RT RT		40 24	1.0E0 1.0E0	3.7E-1		1.0
not	tation Cluster 334	Enrichment Score: 0	G	100	Count	P_Value	Fold	Benjamin	
	GOTERM_CC_DIRECT		RT	-	9	1.0E0	Change 5.5E-1		1.0
	UP_KEYWORDS	<u>peroxisome</u> <u>Peroxisome</u>	RT		6	1.0E0	4.2E-1		1.0
	KEGG_PATHWAY	<u>Peroxisome</u>	RT		6	1.0E0	3.8E-1		1.0
101	tation Cluster 335	Enrichment Score: 0	G	100	Count	P_Value	Fold Change	Benjamin	i FD
	GOTERM_CC_DIRECT	mitach and ripl matrix	рт		27	0.0E.1		-	9.9
		mitochondrial matrix	<u>RT</u>		37		7.2E-1		1
	UP_SEQ_FEATURE GOTERM_CC_DIRECT	transit peptide: Mitochondrion mitochondrial inner membrane	RT RT		39 37	1.0E0 1.0E0	5.5E-1 5.3E-1		1.0
	UP_KEYWORDS	<u>Transit peptide</u>	RT		43	1.0E0 1.0E0	5.5E-1		1.0
	UP_KEYWORDS	<u>Mitochondrion</u>	RT		109	1.0E0	6.7E-1		1.0
101	tation Cluster 336	Enrichment Score: 0	G	100	Count	P_Value	Fold Change	Benjamin	i FD
	INTERPRO	Chemokine interleukin-8-like domain	RT	i	3	1.0E0	4.0E-1	-	1.0
	GOTERM_MF_DIRECT	chemokine activity	RT	i	3	1.0E0	3.6E-1		1.0
	GOTERM_BP_DIRECT	chemokine-mediated signaling pathway	<u>RT</u>	1	4	1.0E0	3.3E-1		1.0
	SMART	SCY	RT DT	1	3	1.0E0	2.8E-1		1.0
	BBID	109.Chemokine families	<u>RT</u>	-	3	1.0E0	3.0E-1 Fold	Danie de la	1.0
ot	tation Cluster 337	Enrichment Score: 0	G		Count	P_Value	Change	_	
	UP_SEQ_FEATURE GOTERM_BP_DIRECT	domain:DH	RT DT		4	1.0E0	4.0E-1		1.0
	INTERPRO	regulation of Rho protein signal transduction Dbl homology (DH) domain	RT RT		6 4	1.0E0 1.0E0	4.4E-1 3.5E-1		1.0
	GOTERM_MF_DIRECT	Rho guanyl-nucleotide exchange factor	RT		4	1.0E0	3.1E-1		1.0
		<u>activity</u>							
	GOTERM_MF_DIRECT SMART	<u>guanyl-nucleotide exchange factor activity</u> <u>RhoGEF</u>	RT PT		6 4	1.0E0 1.0E0	3.0E-1 2.4E-1		1.0
	UP_KEYWORDS	Knoger Guanine-nucleotide releasing factor	RT RT		4 5	1.0E0 1.0E0	2.4E-1 2.3E-1		1.0
าดเ	tation Cluster 338	Enrichment Score: 0	G		Count	P_Value	Fold	Danie de la	
							Change	1.0E0	1.0
	UP_SEQ_FEATURE	domain:Rho-GAP	RT		3	1.0E0	7 11 -	110-11	

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