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## Functional Annotation Clustering

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Current Gene List: [List\\_1](#)

Current Background: Homo sapiens

1960 DAVID IDs








































Options Classification Stringency High ▼

Rerun using options

Create Sublist

507 Cluster(s)

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Annotation Cluster 1		Enrichment Score: 19.33	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">tyrosine-protein kinase</a>	<a href="#">RT</a>		56	5.0E-26	2.9E-24
<input type="checkbox"/>	INTERPRO	<a href="#">Tyrosine protein kinase, active site</a>	<a href="#">RT</a>		50	1.5E-21	3.9E-18
<input type="checkbox"/>	INTERPRO	<a href="#">Tyrosine protein kinase</a>	<a href="#">RT</a>		53	2.1E-19	2.7E-16
<input type="checkbox"/>	SMART	<a href="#">TyrKc</a>	<a href="#">RT</a>		53	4.2E-17	1.6E-14
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">protein tyrosine kinase activity</a>	<a href="#">RT</a>		65	3.3E-16	5.4E-13
Annotation Cluster 2		Enrichment Score: 19.15	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">hemopoietic or lymphoid organ development</a>	<a href="#">RT</a>		94	1.2E-20	3.2E-18
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">hemopoiesis</a>	<a href="#">RT</a>		88	2.3E-20	5.7E-18
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">immune system development</a>	<a href="#">RT</a>		94	1.2E-18	1.7E-16
Annotation Cluster 3		Enrichment Score: 18.97	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of phosphorus metabolic process</a>	<a href="#">RT</a>		140	7.0E-20	1.4E-17
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of phosphate metabolic process</a>	<a href="#">RT</a>		140	7.0E-20	1.4E-17
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of phosphorylation</a>	<a href="#">RT</a>		135	2.4E-19	3.9E-17
Annotation Cluster 4		Enrichment Score: 18.33	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell death</a>	<a href="#">RT</a>		200	4.1E-19	6.1E-17
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of apoptosis</a>	<a href="#">RT</a>		198	4.2E-19	6.1E-17
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of programmed cell death</a>	<a href="#">RT</a>		199	5.9E-19	8.4E-17
Annotation Cluster 5		Enrichment Score: 17.23	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">protein amino acid phosphorylation</a>	<a href="#">RT</a>		173	4.0E-19	6.2E-17
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">phosphorus metabolic process</a>	<a href="#">RT</a>		226	1.8E-18	2.3E-16
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">phosphate metabolic process</a>	<a href="#">RT</a>		226	1.8E-18	2.3E-16
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">phosphorylation</a>	<a href="#">RT</a>		188	1.0E-15	8.7E-14
Annotation Cluster 6		Enrichment Score: 16.92	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">chemical homeostasis</a>	<a href="#">RT</a>		149	1.7E-21	6.1E-19
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ion homeostasis</a>	<a href="#">RT</a>		121	3.5E-18	4.2E-16
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular ion homeostasis</a>	<a href="#">RT</a>		111	7.4E-17	1.1E-14
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular chemical homeostasis</a>	<a href="#">RT</a>		112	9.1E-17	1.1E-14
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular homeostasis</a>	<a href="#">RT</a>		125	6.0E-15	4.7E-13
Annotation Cluster 7		Enrichment Score: 16.15	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:ATP	<a href="#">RT</a>		132	6.7E-22	6.4E-19
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase	<a href="#">RT</a>		112	5.0E-18	2.9E-15
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase, ATP binding site</a>	<a href="#">RT</a>		114	3.4E-16	2.8E-13
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase, core</a>	<a href="#">RT</a>		116	1.7E-15	1.1E-12
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">protein kinase activity</a>	<a href="#">RT</a>		145	9.1E-13	7.5E-10
Annotation Cluster 8		Enrichment Score: 14.61	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">metal ion homeostasis</a>	<a href="#">RT</a>		76	1.6E-17	1.7E-15
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular metal ion homeostasis</a>	<a href="#">RT</a>		72	3.2E-16	3.2E-14
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">calcium ion homeostasis</a>	<a href="#">RT</a>		70	3.6E-16	3.1E-14

<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular calcium ion homeostasis</a>	RT		68	1.0E-15	8.8E-14
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">di-, tri-valent inorganic cation homeostasis</a>	RT		80	2.3E-15	2.0E-13
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cation homeostasis</a>	RT		89	7.5E-15	5.9E-13
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular di-, tri-valent inorganic cation homeostasis</a>	RT		74	1.3E-13	8.4E-12
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular cation homeostasis</a>	RT		79	3.0E-13	1.7E-11
Annotation Cluster 9		Enrichment Score: 14.36	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cell migration</a>	RT		89	7.0E-16	6.0E-14
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cell motility</a>	RT		93	1.1E-14	8.3E-13
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">localization of cell</a>	RT		93	1.1E-14	8.3E-13
Annotation Cluster 10		Enrichment Score: 13.84	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cAMP-mediated signaling</a>	RT		45	4.6E-15	3.9E-13
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cyclic-nucleotide-mediated signaling</a>	RT		54	5.9E-15	4.7E-13
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">G-protein signaling, coupled to cyclic nucleotide second messenger</a>	RT		49	3.9E-14	2.6E-12
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">G-protein signaling, coupled to cAMP nucleotide second messenger</a>	RT		41	4.2E-14	2.8E-12
Annotation Cluster 11		Enrichment Score: 13.82	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of biosynthetic process</a>	RT		180	8.3E-20	1.7E-17
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cellular biosynthetic process</a>	RT		177	2.3E-19	3.7E-17
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of macromolecule biosynthetic process</a>	RT		164	2.2E-16	2.2E-14
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of nitrogen compound metabolic process</a>	RT		161	5.1E-16	5.1E-14
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	RT		151	8.6E-14	5.6E-12
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of transcription from RNA polymerase II promoter</a>	RT		102	4.7E-13	2.6E-11
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of gene expression</a>	RT		141	5.0E-13	2.7E-11
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of transcription</a>	RT		133	2.2E-11	8.5E-10
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of RNA metabolic process</a>	RT		118	2.4E-11	9.3E-10
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of transcription, DNA-dependent</a>	RT		117	3.0E-11	1.1E-9
Annotation Cluster 12		Enrichment Score: 13.11	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of kinase activity</a>	RT		102	3.4E-14	2.3E-12
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of transferase activity</a>	RT		104	8.6E-14	5.7E-12
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of protein kinase activity</a>	RT		98	1.7E-13	1.0E-11
Annotation Cluster 13		Enrichment Score: 12.71	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of locomotion</a>	RT		70	1.2E-15	1.0E-13
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell migration</a>	RT		59	2.1E-12	1.0E-10
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell motion</a>	RT		64	3.0E-12	1.4E-10
Annotation Cluster 14		Enrichment Score: 12.27	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of protein kinase activity</a>	RT		73	1.5E-13	9.6E-12
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of kinase activity</a>	RT		74	3.5E-13	2.0E-11
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of transferase activity</a>	RT		74	2.9E-12	1.3E-10
Annotation Cluster 15		Enrichment Score: 12.16	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of apoptosis</a>	RT		99	3.5E-13	2.0E-11
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of programmed cell death</a>	RT		99	9.0E-13	4.8E-11
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of cell death</a>	RT		99	1.1E-12	5.6E-11
Annotation Cluster 16		Enrichment Score: 11.92	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of locomotion</a>	RT		45	1.9E-14	1.4E-12
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cell migration</a>	RT		39	7.7E-12	3.3E-10
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cell motion</a>	RT		41	1.2E-11	5.0E-10
Annotation Cluster 17		Enrichment Score: 11.61	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cyclase activity</a>	RT		43	7.9E-13	4.3E-11
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of adenylate cyclase activity</a>	RT		42	1.1E-12	5.9E-11
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of lyase activity</a>	RT		43	1.8E-12	8.8E-11
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cAMP biosynthetic process</a>	RT		43	1.8E-12	8.8E-11
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cyclic nucleotide biosynthetic process</a>	RT		45	2.6E-12	1.2E-10

<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of nucleotide biosynthetic process</a>	RT		45	2.6E-12	1.2E-10
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cAMP metabolic process</a>	RT		43	3.9E-12	1.7E-10
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of nucleotide metabolic process</a>	RT		46	5.3E-12	2.3E-10
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cyclic nucleotide metabolic process</a>	RT		45	7.8E-12	3.3E-10
Annotation Cluster 18		Enrichment Score: 11.02	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">vasculature development</a>	RT		77	1.3E-12	6.9E-11
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">blood vessel development</a>	RT		75	3.0E-12	1.4E-10
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">blood vessel morphogenesis</a>	RT		64	2.1E-10	7.1E-9
Annotation Cluster 19		Enrichment Score: 10.99	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of phosphate metabolic process</a>	RT		44	2.4E-13	1.4E-11
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of phosphorus metabolic process</a>	RT		44	2.4E-13	1.4E-11
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of phosphorylation</a>	RT		43	3.4E-13	2.0E-11
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of protein amino acid phosphorylation</a>	RT		40	1.5E-12	7.7E-11
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of protein modification process</a>	RT		49	4.0E-6	6.8E-5
Annotation Cluster 20		Enrichment Score: 10.8	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of adenylate cyclase activity</a>	RT		30	6.5E-12	2.8E-10
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cyclase activity</a>	RT		30	1.1E-11	4.7E-10
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">activation of adenylate cyclase activity</a>	RT		29	2.6E-11	9.7E-10
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of lyase activity</a>	RT		30	3.4E-11	1.3E-9
Annotation Cluster 21		Enrichment Score: 10.68	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cell death</a>	RT		110	1.7E-11	6.8E-10
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of apoptosis</a>	RT		109	1.8E-11	7.2E-10
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of programmed cell death</a>	RT		109	2.9E-11	1.1E-9
Annotation Cluster 22		Enrichment Score: 10.07	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell activation</a>	RT		59	1.1E-11	4.5E-10
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of leukocyte activation</a>	RT		56	3.8E-11	1.4E-9
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of lymphocyte activation</a>	RT		49	1.5E-9	4.6E-8
Annotation Cluster 23		Enrichment Score: 9.85	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of body fluid levels</a>	RT		51	1.8E-11	7.1E-10
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">blood coagulation</a>	RT		40	2.3E-10	7.6E-9
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">coagulation</a>	RT		40	2.3E-10	7.6E-9
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">hemostasis</a>	RT		41	4.2E-10	1.4E-8
Annotation Cluster 24		Enrichment Score: 9.66	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of leukocyte activation</a>	RT		42	5.2E-11	1.9E-9
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cell activation</a>	RT		43	6.9E-11	2.4E-9
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of lymphocyte activation</a>	RT		37	2.9E-9	8.3E-8
Annotation Cluster 25		Enrichment Score: 9.43	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">vesicle</a>	RT		143	1.1E-10	3.6E-9
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">membrane-bounded vesicle</a>	RT		126	1.3E-10	4.0E-9
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytoplasmic membrane-bounded vesicle</a>	RT		120	1.1E-9	2.7E-8
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytoplasmic vesicle</a>	RT		135	1.2E-9	2.7E-8
Annotation Cluster 26		Enrichment Score: 8.79	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of neurological system process</a>	RT		52	1.5E-10	5.2E-9
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of transmission of nerve impulse</a>	RT		48	3.7E-9	1.1E-7
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of synaptic transmission</a>	RT		45	7.7E-9	2.1E-7
Annotation Cluster 27		Enrichment Score: 8.25	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">vesicle lumen</a>	RT		24	8.2E-10	2.1E-8
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytoplasmic membrane-bounded vesicle lumen</a>	RT		23	1.9E-9	4.3E-8
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">platelet alpha granule lumen</a>	RT		20	1.2E-7	2.0E-6
Annotation Cluster 28		Enrichment Score: 8.16	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">sarcomere</a>	RT		37	8.8E-10	2.2E-8
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">myofibril</a>	RT		39	3.1E-9	6.6E-8
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">contractile fiber part</a>	RT		38	1.9E-8	3.9E-7

<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">contractile fiber</a>	<a href="#">RT</a>		39	4.4E-8	8.1E-7
Annotation Cluster 29		Enrichment Score: 7.81	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of behavior</a>	<a href="#">RT</a>		20	5.4E-9	1.5E-7
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of chemotaxis</a>	<a href="#">RT</a>		18	1.3E-8	3.5E-7
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of behavior</a>	<a href="#">RT</a>		23	1.6E-8	4.1E-7
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of chemotaxis</a>	<a href="#">RT</a>		18	5.1E-8	1.2E-6
Annotation Cluster 30		Enrichment Score: 7.11	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">heparin binding</a>	<a href="#">RT</a>		38	5.5E-9	9.9E-7
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">polysaccharide binding</a>	<a href="#">RT</a>		46	1.8E-7	1.6E-5
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">pattern binding</a>	<a href="#">RT</a>		46	1.8E-7	1.6E-5
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">glycosaminoglycan binding</a>	<a href="#">RT</a>		43	2.0E-7	1.8E-5
Annotation Cluster 31		Enrichment Score: 6.89	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of leukocyte proliferation</a>	<a href="#">RT</a>		25	5.0E-8	1.2E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of mononuclear cell proliferation</a>	<a href="#">RT</a>		25	5.0E-8	1.2E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of leukocyte proliferation</a>	<a href="#">RT</a>		31	1.6E-7	3.6E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of mononuclear cell proliferation</a>	<a href="#">RT</a>		31	1.6E-7	3.6E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of lymphocyte proliferation</a>	<a href="#">RT</a>		24	1.6E-7	3.7E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of lymphocyte proliferation</a>	<a href="#">RT</a>		30	4.4E-7	9.1E-6
Annotation Cluster 32		Enrichment Score: 6.77	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of adenylate cyclase activity by G-protein signaling pathway</a>	<a href="#">RT</a>		20	1.7E-7	3.8E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">activation of adenylate cyclase activity by G-protein signaling pathway</a>	<a href="#">RT</a>		20	1.7E-7	3.8E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of adenylate cyclase activity involved in G-protein signaling</a>	<a href="#">RT</a>		20	1.7E-7	3.8E-6
Annotation Cluster 33		Enrichment Score: 6.76	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of phospholipase activity</a>	<a href="#">RT</a>		29	3.6E-8	9.0E-7
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of phospholipase activity</a>	<a href="#">RT</a>		28	7.5E-8	1.8E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">activation of phospholipase C activity</a>	<a href="#">RT</a>		27	7.7E-8	1.8E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of phospholipase C activity</a>	<a href="#">RT</a>		27	7.7E-8	1.8E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of lipase activity</a>	<a href="#">RT</a>		32	1.1E-7	2.4E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of lipase activity</a>	<a href="#">RT</a>		28	5.5E-7	1.1E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">activation of phospholipase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger</a>	<a href="#">RT</a>		21	5.0E-6	8.3E-5
Annotation Cluster 34		Enrichment Score: 6.75	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Alpha-2	<a href="#">RT</a>		13	6.8E-8	2.4E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Alpha-1	<a href="#">RT</a>		13	6.8E-8	2.4E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Connecting peptide	<a href="#">RT</a>		17	3.1E-7	1.0E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ig-like C1-type	<a href="#">RT</a>		17	7.1E-7	2.0E-4
Annotation Cluster 35		Enrichment Score: 6.55	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	<a href="#">mitogen</a>	<a href="#">RT</a>		19	8.6E-9	1.2E-7
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell division</a>	<a href="#">RT</a>		21	7.5E-7	1.5E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cell division</a>	<a href="#">RT</a>		18	3.4E-6	5.9E-5
Annotation Cluster 36		Enrichment Score: 6.52	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Type I diabetes mellitus</a>	<a href="#">RT</a>		26	2.3E-8	4.8E-7
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Allograft rejection</a>	<a href="#">RT</a>		23	8.4E-8	1.6E-6
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Graft-versus-host disease</a>	<a href="#">RT</a>		21	1.4E-5	1.6E-4
Annotation Cluster 37		Enrichment Score: 6.49	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">respiratory tube development</a>	<a href="#">RT</a>		35	1.7E-7	3.8E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">lung development</a>	<a href="#">RT</a>		34	2.6E-7	5.5E-6
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">respiratory system development</a>	<a href="#">RT</a>		35	7.8E-7	1.5E-5
Annotation Cluster 38		Enrichment Score: 6.46	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:II	<a href="#">RT</a>		14	3.4E-7	1.1E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:III	<a href="#">RT</a>		14	3.4E-7	1.1E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:I	<a href="#">RT</a>		14	3.4E-7	1.1E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:IV	<a href="#">RT</a>		14	3.4E-7	1.1E-4