Functional Annotation Clustering Of Genes Induced By Kit

http://david.abcc.ncifcrf.gov/summary.jsp

DAVID Bioinformatics Resources 2008
National Institute of Allergy and Infectious Diseases (NIAID), NIH

Functional Annotation Clustering Of Genes Upregulated >2 in WT BMMCs

Help and Manual

Current Gene List: wt up >2
1633 DAVID IDs

Options **Classification Stringency** Medium

Rerun using options Create Sublist

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	Annotation Cluster 1	Enrichment Score: 24.15	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	intracellular part	RT	985	1.6E-45	1.3E-42
☐	GOTERM_CC_ALL	intracellular	RT	1007	5.9E-40	2.3E-37
☐	GOTERM_CC_ALL	intracellular membrane-bound organelle	RT	777	2.2E-35	5.8E-33
☐	GOTERM_CC_ALL	membrane-bound organelle	RT	777	3.6E-35	6.9E-33
☐	GOTERM_CC_ALL	intracellular organelle	RT	840	2.5E-33	3.8E-31
☐	GOTERM_CC_ALL	organelle	RT	840	3.6E-33	4.7E-31
☐	GOTERM_CC_ALL	nucleus	RT	518	1.8E-23	2.0E-21
☐	GOTERM_CC_ALL	cytoplasm	RT	655	3.8E-22	2.9E-20
☐	SP_PIR_KEYWORDS	nucleus	RT	419	1.4E-19	3.1E-17
☐	GOTERM_CC_ALL	cell	RT	1176	2.2E-13	9.6E-12
☐	GOTERM_CC_ALL	cell part	RT	1176	2.2E-13	9.6E-12
☐	GOTERM_BP_ALL	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	381	9.1E-7	1.4E-4
☐	GOTERM_BP_ALL	biopolymer metabolic process	RT	450	3.7E-2	5.9E-1
	Annotation Cluster 2	Enrichment Score: 15.69	G 🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	cell cycle	RT	104	3.2E-26	1.4E-23
☐	SP_PIR_KEYWORDS	cell division	RT	66	9.0E-22	2.6E-19
☐	GOTERM_BP_ALL	cell cycle	RT	152	9.3E-22	4.8E-18
☐	GOTERM_BP_ALL	cell division	RT	76	4.4E-21	1.1E-17
☐	SP_PIR_KEYWORDS	mitosis	RT	48	1.4E-18	2.4E-16
☐	GOTERM_BP_ALL	cell cycle process	RT	119	5.1E-16	7.2E-13
☐	GOTERM_BP_ALL	cell cycle phase	RT	75	1.1E-15	1.1E-12
☐	GOTERM_BP_ALL	M phase	RT	66	6.5E-15	5.5E-12
☐	GOTERM_BP_ALL	mitotic cell cycle	RT	66	1.2E-14	8.9E-12
☐	GOTERM_BP_ALL	mitosis	RT	54	6.5E-14	4.2E-11
☐	GOTERM_BP_ALL	M phase of mitotic cell cycle	RT	54	8.3E-14	4.8E-11
☐	GOTERM_BP_ALL	regulation of progression through cell cycle	RT	68	1.3E-7	2.3E-5
☐	GOTERM_BP_ALL	regulation of cell cycle	RT	68	1.8E-7	2.9E-5
	Annotation Cluster 3	Enrichment Score: 14.14	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	chromosome	RT	79	4.0E-16	3.1E-14
☐	GOTERM_CC_ALL	chromosomal part	RT	70	9.2E-15	5.9E-13
☐	GOTERM_CC_ALL	chromosome, pericentric region	RT	30	1.1E-13	5.5E-12
	Annotation Cluster 4	Enrichment Score: 13.07	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	intracellular organelle part	RT	358	6.7E-23	6.5E-21
☐	GOTERM_CC_ALL	organelle part	RT	359	7.6E-23	6.5E-21
☐	GOTERM_CC_ALL	non-membrane-bound organelle	RT	219	4.4E-14	2.6E-12
☐	GOTERM_CC_ALL	intracellular non-membrane-bound organelle	RT	219	4.4E-14	2.6E-12
☐	GOTERM_CC_ALL	macromolecular complex	RT	284	1.7E-13	8.3E-12

☐	GOTERM_CC_ALL	cytoskeletal part	RT		82	4.4E-6	9.9E-5
☐	GOTERM_CC_ALL	cytoskeleton	RT		104	4.3E-3	5.6E-2
	Annotation Cluster 5	Enrichment Score: 12.68	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	nucleotide binding	RT		290	2.6E-18	7.0E-15
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT		211	2.1E-16	2.4E-14
☐	SP_PIR_KEYWORDS	atp-binding	RT		171	1.1E-14	9.1E-13
☐	GOTERM_MF_ALL	ribonucleotide binding	RT		242	2.9E-14	2.6E-11
☐	GOTERM_MF_ALL	purine ribonucleotide binding	RT		242	2.9E-14	2.6E-11
☐	GOTERM_MF_ALL	purine nucleotide binding	RT		247	1.2E-13	6.5E-11
☐	GOTERM_MF_ALL	ATP binding	RT		201	5.2E-13	2.3E-10
☐	GOTERM_MF_ALL	adenyl ribonucleotide binding	RT		202	9.0E-13	3.4E-10
☐	GOTERM_MF_ALL	adenyl nucleotide binding	RT		207	4.2E-12	1.4E-9
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT		91	1.5E-4	2.0E-1
	Annotation Cluster 6	Enrichment Score: 11.27	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	RNA processing	RT		84	2.2E-13	1.1E-10
☐	SP_PIR_KEYWORDS	rna-binding	RT		81	3.2E-12	2.3E-10
☐	GOTERM_MF_ALL	RNA binding	RT		103	2.2E-10	4.5E-8
	Annotation Cluster 7	Enrichment Score: 8.51	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	chaperone	RT		38	1.9E-11	1.3E-9
☐	GOTERM_BP_ALL	protein folding	RT		51	4.4E-10	1.3E-7
☐	GOTERM_MF_ALL	unfolded protein binding	RT		22	3.7E-6	6.1E-4
	Annotation Cluster 8	Enrichment Score: 7.6	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cellular metabolic process	RT		748	9.8E-12	3.6E-9
☐	GOTERM_BP_ALL	primary metabolic process	RT		747	1.8E-11	6.3E-9
☐	GOTERM_BP_ALL	metabolic process	RT		809	1.6E-10	4.8E-8
☐	GOTERM_BP_ALL	cellular process	RT		1053	6.9E-10	1.8E-7
☐	GOTERM_BP_ALL	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		381	9.1E-7	1.4E-4
☐	GOTERM_BP_ALL	macromolecule metabolic process	RT		628	9.7E-6	1.1E-3
☐	GOTERM_BP_ALL	biopolymer metabolic process	RT		450	3.7E-2	5.9E-1
	Annotation Cluster 9	Enrichment Score: 7.48	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	nucleoside-triphosphatase activity	RT		97	1.9E-11	5.7E-9
☐	GOTERM_MF_ALL	pyrophosphatase activity	RT		100	2.1E-11	5.7E-9
☐	GOTERM_MF_ALL	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	RT		100	3.7E-11	9.0E-9
☐	GOTERM_MF_ALL	hydrolase activity, acting on acid anhydrides	RT		100	5.1E-11	1.1E-8
☐	GOTERM_MF_ALL	ATPase activity, coupled	RT		44	2.8E-4	2.8E-2
☐	GOTERM_MF_ALL	hydrolase activity	RT		240	2.9E-4	2.6E-2
☐	GOTERM_MF_ALL	ATPase activity	RT		48	6.7E-4	5.0E-2
	Annotation Cluster 10	Enrichment Score: 6.55	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	biosynthetic process	RT		196	2.8E-13	1.3E-10
☐	GOTERM_BP_ALL	cellular biosynthetic process	RT		142	5.7E-9	1.2E-6
☐	SP_PIR_KEYWORDS	protein biosynthesis	RT		33	4.4E-7	1.7E-5
☐	GOTERM_BP_ALL	translation	RT		65	7.2E-4	3.7E-2
☐	GOTERM_BP_ALL	macromolecule biosynthetic process	RT		88	3.6E-3	1.4E-1
	Annotation Cluster 11	Enrichment Score: 6.34	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	RNA processing	RT		84	2.2E-13	1.1E-10
☐	SP_PIR_KEYWORDS	mrna splicing	RT		40	2.8E-9	1.4E-7
☐	GOTERM_CC_ALL	ribonucleoprotein complex	RT		76	1.3E-8	4.6E-7
☐	SP_PIR_KEYWORDS	mrna processing	RT		43	1.3E-7	5.3E-6
☐	GOTERM_BP_ALL	RNA splicing	RT		42	1.6E-7	2.7E-5

☐	GOTERM_BP_ALL	mRNA metabolic process	RT	▮		53	3.0E-7	4.7E-5
☐	GOTERM_BP_ALL	mRNA processing	RT	▮		46	2.7E-6	3.6E-4
☐	SP_PIR_KEYWORDS	spliceosome	RT	▮		25	1.1E-5	3.3E-4
☐	GOTERM_CC_ALL	spliceosome	RT	▮		29	1.5E-5	3.1E-4
☐	GOTERM_BP_ALL	RNA splicing, via transesterification reactions	RT	▮		16	1.4E-4	1.0E-2
☐	GOTERM_BP_ALL	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	RT	▮		16	1.4E-4	1.0E-2
☐	GOTERM_BP_ALL	nuclear mRNA splicing, via spliceosome	RT	▮		16	1.4E-4	1.0E-2
	Annotation Cluster 12	Enrichment Score: 6.3	G		🟩	Count	P_Value	Benjamini
☐	SMART	RRM	RT	▮		39	4.3E-9	2.6E-6
☐	GOTERM_BP_ALL	mRNA metabolic process	RT	▮		53	3.0E-7	4.7E-5
☐	INTERPRO	RNA recognition motif, RNP-1	RT	▮		36	3.8E-7	7.4E-4
☐	INTERPRO	Nucleotide-binding, alpha-beta plait	RT	▮		33	7.8E-6	1.1E-2
☐	UP_SEQ_FEATURE	domain:RRM	RT	▮		18	8.1E-6	1.4E-2
	Annotation Cluster 13	Enrichment Score: 6.01	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Biosynthesis of steroids	RT	▮		20	1.9E-14	2.0E-12
☐	SP_PIR_KEYWORDS	lipid synthesis	RT	▮		32	1.4E-12	1.1E-10
☐	GOTERM_BP_ALL	sterol biosynthetic process	RT	▮		20	2.8E-12	1.2E-9
☐	GOTERM_BP_ALL	cholesterol biosynthetic process	RT	▮		16	4.8E-10	1.3E-7
☐	SP_PIR_KEYWORDS	sterol biosynthesis	RT	▮		14	3.3E-9	1.6E-7
☐	GOTERM_BP_ALL	lipid biosynthetic process	RT	▮		53	4.3E-8	7.7E-6
☐	SP_PIR_KEYWORDS	steroid biosynthesis	RT	▮		16	5.7E-8	2.5E-6
☐	SP_PIR_KEYWORDS	cholesterol biosynthesis	RT	▮		11	8.3E-8	3.4E-6
☐	GOTERM_BP_ALL	steroid biosynthetic process	RT	▮		23	1.1E-6	1.5E-4
☐	GOTERM_BP_ALL	sterol metabolic process	RT	▮		23	1.7E-6	2.4E-4
☐	GOTERM_BP_ALL	cholesterol metabolic process	RT	▮		19	7.1E-5	5.7E-3
☐	GOTERM_BP_ALL	alcohol metabolic process	RT	▮		48	8.5E-5	6.6E-3
☐	GOTERM_BP_ALL	isoprenoid biosynthetic process	RT	▮		9	1.7E-4	1.2E-2
☐	GOTERM_BP_ALL	steroid metabolic process	RT	▮		27	2.5E-3	1.0E-1
☐	GOTERM_BP_ALL	isoprenoid metabolic process	RT	▮		9	9.8E-3	2.8E-1
☐	SP_PIR_KEYWORDS	Isoprene biosynthesis	RT	▮		4	3.1E-2	2.8E-1
☐	GOTERM_BP_ALL	cellular lipid metabolic process	RT	▮		63	7.4E-2	7.6E-1
☐	GOTERM_BP_ALL	lipid metabolic process	RT	▮		67	2.2E-1	9.7E-1
	Annotation Cluster 14	Enrichment Score: 5.86	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	ribonucleoprotein complex biogenesis and assembly	RT	▮		53	2.3E-11	7.5E-9
☐	GOTERM_BP_ALL	ribosome biogenesis and assembly	RT	▮		30	3.5E-6	4.4E-4
☐	GOTERM_BP_ALL	rRNA processing	RT	▮		18	1.9E-5	2.1E-3
☐	GOTERM_BP_ALL	rRNA metabolic process	RT	▮		18	2.4E-5	2.5E-3
☐	SP_PIR_KEYWORDS	rrna processing	RT	▮		14	1.4E-4	3.3E-3
	Annotation Cluster 15	Enrichment Score: 5.63	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	cell cycle control	RT	▮		16	3.6E-10	2.1E-8
☐	GOTERM_MF_ALL	cyclin-dependent protein kinase regulator activity	RT	▮		14	1.5E-8	2.8E-6
☐	PIR_SUPERFAMILY	PIRSF001771:cyclin, A/B/D/E types	RT	▮		10	7.6E-8	2.4E-4
☐	INTERPRO	Cyclin, C-terminal	RT	▮		11	1.4E-7	8.0E-4
☐	INTERPRO	Cyclin, A/B/D/E	RT	▮		9	1.4E-7	4.1E-4
☐	SMART	CYCLIN	RT	▮		14	3.6E-7	7.2E-5
☐	INTERPRO	Cyclin, N-terminal	RT	▮		12	8.5E-6	9.9E-3
☐	INTERPRO	Cyclin	RT	▮		13	9.2E-6	8.9E-3

☐	**SP_PIR_KEYWORDS**	cyclin	RT	19	1.9E-5	5.3E-4
☐	**KEGG_PATHWAY**	p53 signaling pathway	RT	21	2.3E-5	9.5E-4
☐	**GOTERM_MF_ALL**	protein kinase regulator activity	RT	19	3.4E-5	5.4E-3
☐	**INTERPRO**	Cyclin-related	RT	12	7.7E-5	4.4E-2
☐	**GOTERM_MF_ALL**	kinase regulator activity	RT	20	2.0E-4	2.3E-2
☐	**INTERPRO**	Cyclin D	RT	4	2.6E-3	5.6E-1
	Annotation Cluster 16	Enrichment Score: 5.33	G	Count	P_Value	Benjamini
☐	**SMART**	AAA	RT	24	1.0E-7	3.1E-5
☐	**INTERPRO**	AAA ATPase, core	RT	14	3.2E-5	2.3E-2
☐	**INTERPRO**	AAA+ ATPase, core	RT	19	3.2E-5	2.1E-2
	Annotation Cluster 17	Enrichment Score: 4.94	G	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	repeat:WD 5	RT	31	9.0E-7	1.3E-2
☐	**UP_SEQ_FEATURE**	repeat:WD 4	RT	32	1.4E-6	9.7E-3
☐	**UP_SEQ_FEATURE**	repeat:WD 3	RT	32	4.9E-6	2.3E-2
☐	**UP_SEQ_FEATURE**	repeat:WD 6	RT	25	5.3E-6	1.9E-2
☐	**UP_SEQ_FEATURE**	repeat:WD 2	RT	32	6.9E-6	1.9E-2
☐	**UP_SEQ_FEATURE**	repeat:WD 1	RT	32	6.9E-6	1.9E-2
☐	**SMART**	WD40	RT	36	1.1E-5	1.3E-3
☐	**UP_SEQ_FEATURE**	repeat:WD 7	RT	18	6.8E-5	1.0E-1
☐	**INTERPRO**	WD40 repeat	RT	35	1.9E-4	8.7E-2
☐	**SP_PIR_KEYWORDS**	wd repeat	RT	40	1.9E-4	4.2E-3
	Annotation Cluster 18	Enrichment Score: 4.83	G	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	nuclear membrane part	RT	22	1.7E-7	5.5E-6
☐	**GOTERM_CC_ALL**	nuclear membrane	RT	22	4.0E-7	1.2E-5
☐	**SP_PIR_KEYWORDS**	mrna transport	RT	16	2.4E-6	7.8E-5
☐	**GOTERM_CC_ALL**	nuclear pore	RT	18	3.0E-6	7.3E-5
☐	**GOTERM_CC_ALL**	pore complex	RT	19	3.4E-6	7.9E-5
☐	**GOTERM_BP_ALL**	mRNA transport	RT	18	8.8E-6	1.1E-3
☐	**SP_PIR_KEYWORDS**	translocation	RT	18	8.8E-6	2.7E-4
☐	**GOTERM_BP_ALL**	nucleobase, nucleoside, nucleotide and nucleic acid transport	RT	19	2.0E-5	2.1E-3
☐	**GOTERM_CC_ALL**	nuclear envelope	RT	28	2.1E-5	4.1E-4
☐	**GOTERM_BP_ALL**	establishment of RNA localization	RT	18	3.0E-5	2.9E-3
☐	**GOTERM_BP_ALL**	RNA transport	RT	18	3.0E-5	2.9E-3
☐	**GOTERM_BP_ALL**	nucleic acid transport	RT	18	3.0E-5	2.9E-3
☐	**GOTERM_BP_ALL**	RNA localization	RT	18	3.8E-5	3.5E-3
☐	**GOTERM_CC_ALL**	endomembrane system	RT	58	2.5E-4	4.4E-3
☐	**GOTERM_BP_ALL**	intracellular protein transport across a membrane	RT	15	3.5E-4	2.1E-2
☐	**SP_PIR_KEYWORDS**	nuclear pore complex	RT	9	9.7E-4	1.8E-2
	Annotation Cluster 19	Enrichment Score: 4.14	G	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	protein biosynthesis	RT	33	4.4E-7	1.7E-5
☐	**SP_PIR_KEYWORDS**	aminoacyl-tRNA synthetase	RT	16	8.1E-7	2.8E-5
☐	**GOTERM_BP_ALL**	tRNA metabolic process	RT	28	2.9E-6	3.7E-4
☐	**KEGG_PATHWAY**	Aminoacyl-tRNA biosynthesis	RT	14	2.9E-5	1.0E-3
☐	**SP_PIR_KEYWORDS**	ligase	RT	43	7.7E-5	1.9E-3
☐	**GOTERM_MF_ALL**	ligase activity, forming carbon-oxygen bonds	RT	16	3.1E-4	2.7E-2
☐	**GOTERM_MF_ALL**	aminoacyl-tRNA ligase activity	RT	16	3.1E-4	2.7E-2
☐	**GOTERM_MF_ALL**	ligase activity, forming aminoacyl-tRNA and related compounds	RT	16	3.1E-4	2.7E-2
☐	**GOTERM_BP_ALL**	amino acid activation	RT	15	6.3E-4	3.4E-2

☐	GOTERM_BP_ALL	tRNA aminoacylation for protein translation	RT		15	6.3E-4	3.4E-2
☐	GOTERM_BP_ALL	tRNA aminoacylation	RT		15	6.3E-4	3.4E-2
☐	GOTERM_BP_ALL	amino acid metabolic process	RT		41	1.2E-3	5.8E-2
	Annotation Cluster 20	Enrichment Score: 3.92	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	intracellular transport	RT		114	1.0E-9	2.6E-7
☐	GOTERM_BP_ALL	cellular localization	RT		133	1.5E-8	3.1E-6
☐	GOTERM_BP_ALL	establishment of cellular localization	RT		129	4.0E-8	7.6E-6
☐	GOTERM_BP_ALL	cellular component organization and biogenesis	RT		302	9.8E-7	1.5E-4
☐	GOTERM_BP_ALL	macromolecule localization	RT		114	1.9E-5	2.1E-3
☐	GOTERM_BP_ALL	intracellular protein transport	RT		66	1.2E-4	8.9E-3
☐	GOTERM_BP_ALL	protein localization	RT		106	1.5E-4	1.0E-2
☐	GOTERM_BP_ALL	establishment of protein localization	RT		97	3.8E-4	2.3E-2
☐	SP_PIR_KEYWORDS	protein transport	RT		58	4.2E-4	8.5E-3
☐	GOTERM_BP_ALL	protein targeting	RT		40	4.8E-4	2.7E-2
☐	GOTERM_MF_ALL	protein transporter activity	RT		28	1.0E-3	7.1E-2
☐	GOTERM_BP_ALL	protein transport	RT		89	1.6E-3	7.3E-2
☐	GOTERM_BP_ALL	localization	RT		294	7.5E-2	7.7E-1
☐	SP_PIR_KEYWORDS	transport	RT		133	8.4E-2	5.4E-1
☐	GOTERM_BP_ALL	establishment of localization	RT		260	8.8E-2	8.1E-1
☐	GOTERM_BP_ALL	transport	RT		250	1.3E-1	8.9E-1
	Annotation Cluster 21	Enrichment Score: 3.7	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein-RNA complex assembly	RT		23	1.0E-5	1.1E-3
☐	GOTERM_BP_ALL	cellular component assembly	RT		61	3.0E-4	1.8E-2
☐	GOTERM_BP_ALL	macromolecular complex assembly	RT		50	2.6E-3	1.1E-1
	Annotation Cluster 22	Enrichment Score: 3.67	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	lipid synthesis	RT		32	1.4E-12	1.1E-10
☐	SP_PIR_KEYWORDS	fatty acid biosynthesis	RT		14	3.6E-5	9.9E-4
☐	GOTERM_BP_ALL	fatty acid biosynthetic process	RT		16	1.2E-3	5.5E-2
☐	GOTERM_BP_ALL	organic acid biosynthetic process	RT		16	2.1E-3	9.2E-2
☐	GOTERM_BP_ALL	carboxylic acid biosynthetic process	RT		16	2.1E-3	9.2E-2
☐	GOTERM_BP_ALL	monocarboxylic acid metabolic process	RT		26	2.4E-1	9.7E-1
☐	GOTERM_BP_ALL	fatty acid metabolic process	RT		18	3.5E-1	9.9E-1
	Annotation Cluster 23	Enrichment Score: 3.65	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	nuclear part	RT		160	1.7E-10	6.7E-9
☐	GOTERM_CC_ALL	nucleolus	RT		38	1.4E-9	5.3E-8
☐	GOTERM_CC_ALL	organelle lumen	RT		107	3.2E-4	5.5E-3
☐	GOTERM_CC_ALL	membrane-enclosed lumen	RT		107	3.2E-4	5.5E-3
☐	GOTERM_CC_ALL	nuclear lumen	RT		93	1.5E-3	2.3E-2
☐	GOTERM_CC_ALL	nucleoplasm	RT		60	3.5E-1	8.9E-1
☐	GOTERM_CC_ALL	nucleoplasm part	RT		53	5.6E-1	9.8E-1
☐	GOTERM_CC_ALL	transcription factor complex	RT		34	9.1E-1	1.0E0
	Annotation Cluster 24	Enrichment Score: 3.58	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	lyase activity	RT		33	6.5E-5	9.1E-3
☐	GOTERM_MF_ALL	hydro-lyase activity	RT		16	1.4E-4	1.7E-2
☐	GOTERM_MF_ALL	carbon-oxygen lyase activity	RT		17	2.8E-4	2.8E-2
☐	GOTERM_MF_ALL	pseudouridylate synthase activity	RT		6	1.9E-3	1.0E-1
	Annotation Cluster 25	Enrichment Score: 3.54	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	organelle envelope	RT		69	1.6E-6	4.1E-5
☐	GOTERM_CC_ALL	envelope	RT		69	2.0E-6	5.2E-5

☐	GOTERM_CC_ALL	organelle membrane	RT	▮		94	2.3E-6	5.6E-5
☐	GOTERM_CC_ALL	organelle inner membrane	RT	▮		39	2.1E-3	3.0E-2
☐	GOTERM_CC_ALL	mitochondrial part	RT	▮		47	5.7E-3	7.2E-2
☐	GOTERM_CC_ALL	mitochondrial envelope	RT	▮		41	6.6E-3	8.1E-2
☐	GOTERM_CC_ALL	mitochondrial membrane	RT	▮		38	9.3E-3	1.1E-1
☐	GOTERM_CC_ALL	mitochondrial inner membrane	RT	▮		35	9.9E-3	1.1E-1
	Annotation Cluster 26	Enrichment Score: 3.32	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	DNA replication initiation	RT	▮		13	4.9E-9	1.1E-6
☐	SMART	MCM	RT	▮		7	3.8E-6	5.7E-4
☐	UP_SEQ_FEATURE	domain:MCM	RT	▮		7	7.9E-6	1.6E-2
☐	INTERPRO	MCM	RT	▮		7	1.1E-5	9.3E-3
☐	INTERPRO	Nucleic acid-binding, OB-fold	RT	▮		14	1.9E-4	8.3E-2
☐	GOTERM_MF_ALL	DNA-dependent ATPase activity	RT	▮		12	2.6E-4	2.7E-2
☐	SP_PIR_KEYWORDS	DNA replication initiation	RT	▮		5	3.3E-4	7.0E-3
☐	GOTERM_MF_ALL	single-stranded DNA binding	RT	▮		10	1.8E-3	9.9E-2
☐	GOTERM_BP_ALL	DNA duplex unwinding	RT	▮		6	4.9E-3	1.6E-1
☐	GOTERM_BP_ALL	DNA geometric change	RT	▮		6	4.9E-3	1.6E-1
☐	GOTERM_BP_ALL	DNA unwinding during replication	RT	▮		6	4.9E-3	1.6E-1
☐	SP_PIR_KEYWORDS	heterohexamer	RT	▮		3	2.4E-2	2.5E-1
☐	GOTERM_MF_ALL	DNA helicase activity	RT	▮		4	3.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc finger	RT	▮		7	7.5E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 3.25	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	response to DNA damage stimulus	RT	▮		46	2.0E-5	2.1E-3
☐	GOTERM_BP_ALL	DNA repair	RT	▮		36	3.0E-4	1.8E-2
☐	GOTERM_BP_ALL	response to endogenous stimulus	RT	▮		46	4.2E-4	2.4E-2
☐	SP_PIR_KEYWORDS	DNA damage	RT	▮		26	1.1E-3	1.9E-2
☐	SP_PIR_KEYWORDS	DNA repair	RT	▮		23	3.4E-3	5.1E-2
☐	GOTERM_BP_ALL	response to stress	RT	▮		102	3.5E-3	1.4E-1
	Annotation Cluster 28	Enrichment Score: 3.2	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	nitrogen compound biosynthetic process	RT	▮		22	2.2E-4	1.4E-2
☐	GOTERM_BP_ALL	amine biosynthetic process	RT	▮		18	3.4E-4	2.0E-2
☐	GOTERM_BP_ALL	amino acid biosynthetic process	RT	▮		12	3.5E-3	1.4E-1
	Annotation Cluster 29	Enrichment Score: 3.19	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein-RNA complex assembly	RT	▮		23	1.0E-5	1.1E-3
☐	GOTERM_MF_ALL	translation initiation factor activity	RT	▮		18	1.1E-3	7.2E-2
☐	SP_PIR_KEYWORDS	initiation factor	RT	▮		16	1.1E-3	1.9E-2
☐	GOTERM_BP_ALL	translational initiation	RT	▮		14	1.4E-3	6.7E-2
☐	GOTERM_MF_ALL	translation factor activity, nucleic acid binding	RT	▮		23	1.5E-3	9.3E-2
☐	GOTERM_MF_ALL	translation regulator activity	RT	▮		23	2.9E-3	1.4E-1
	Annotation Cluster 30	Enrichment Score: 3.17	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	nucleocytoplasmic transport	RT	▮		25	2.2E-4	1.4E-2
☐	GOTERM_BP_ALL	nuclear transport	RT	▮		25	2.5E-4	1.6E-2
☐	GOTERM_BP_ALL	protein targeting	RT	▮		40	4.8E-4	2.7E-2
☐	GOTERM_BP_ALL	protein import	RT	▮		19	5.0E-4	2.8E-2
☐	GOTERM_BP_ALL	nuclear import	RT	▮		16	1.8E-3	8.2E-2
☐	GOTERM_BP_ALL	protein import into nucleus	RT	▮		15	3.8E-3	1.4E-1
	Annotation Cluster 31	Enrichment Score: 3.17	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	chromosome segregation	RT	▮		22	1.8E-8	3.5E-6
☐	GOTERM_BP_ALL	mitotic sister chromatid segregation	RT	▮		9	8.0E-4	4.0E-2
☐	GOTERM_BP_ALL	sister chromatid segregation	RT	▮		9	1.1E-3	5.4E-2

☐	**GOTERM_BP_ALL**	mitotic chromosome condensation	RT		6	9.8E-3	2.8E-1
☐	**GOTERM_BP_ALL**	chromosome condensation	RT		7	1.1E-2	2.9E-1
☐	**SP_PIR_KEYWORDS**	dna condensation	RT		4	5.7E-2	4.3E-1
	Annotation Cluster 32	Enrichment Score: 3.11	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	mitochondrion	RT		122	1.0E-5	2.1E-4
☐	**GOTERM_CC_ALL**	mitochondrial part	RT		47	5.7E-3	7.2E-2
☐	**SP_PIR_KEYWORDS**	Mitochondrion	RT		76	8.2E-3	1.1E-1
	Annotation Cluster 33	Enrichment Score: 2.98	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	nucleotide binding	RT		20	1.5E-4	3.5E-3
☐	**SP_PIR_KEYWORDS**	P-loop	RT		20	1.8E-4	4.0E-3
☐	**SP_PIR_KEYWORDS**	GTP binding	RT		9	4.0E-2	3.4E-1
	Annotation Cluster 34	Enrichment Score: 2.89	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	microtubule cytoskeleton	RT		60	7.5E-8	2.5E-6
☐	**GOTERM_CC_ALL**	microtubule	RT		41	6.3E-7	1.8E-5
☐	**GOTERM_CC_ALL**	cytoskeletal part	RT		82	4.4E-6	9.9E-5
☐	**GOTERM_BP_ALL**	microtubule-based process	RT		40	5.4E-6	6.7E-4
☐	**SP_PIR_KEYWORDS**	microtubule	RT		28	4.3E-4	8.4E-3
☐	**GOTERM_BP_ALL**	microtubule-based movement	RT		20	3.1E-3	1.3E-1
☐	**GOTERM_BP_ALL**	cytoskeleton-dependent intracellular transport	RT		22	3.8E-3	1.4E-1
☐	**GOTERM_BP_ALL**	cytoskeleton organization and biogenesis	RT		66	3.9E-3	1.4E-1
☐	**GOTERM_CC_ALL**	cytoskeleton	RT		104	4.3E-3	5.6E-2
☐	**SMART**	KISc	RT		9	4.7E-3	2.7E-1
☐	**INTERPRO**	Kinesin, motor region	RT		9	1.4E-2	9.4E-1
☐	**GOTERM_MF_ALL**	microtubule motor activity	RT		13	3.0E-2	6.5E-1
☐	**SP_PIR_KEYWORDS**	motor protein	RT		15	4.2E-2	3.5E-1
☐	**GOTERM_CC_ALL**	kinesin complex	RT		6	1.7E-1	7.0E-1
☐	**GOTERM_MF_ALL**	motor activity	RT		17	2.0E-1	9.8E-1
☐	**GOTERM_CC_ALL**	microtubule associated complex	RT		13	2.1E-1	7.5E-1
	Annotation Cluster 35	Enrichment Score: 2.77	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	amino acid and derivative metabolic process	RT		51	5.3E-4	2.9E-2
☐	**GOTERM_BP_ALL**	nitrogen compound metabolic process	RT		60	1.0E-3	5.0E-2
☐	**GOTERM_BP_ALL**	amino acid metabolic process	RT		41	1.2E-3	5.8E-2
☐	**GOTERM_BP_ALL**	amine metabolic process	RT		55	2.1E-3	9.2E-2
☐	**GOTERM_BP_ALL**	carboxylic acid metabolic process	RT		67	4.0E-3	1.5E-1
☐	**GOTERM_BP_ALL**	organic acid metabolic process	RT		67	4.2E-3	1.5E-1
	Annotation Cluster 36	Enrichment Score: 2.69	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	snoRNA binding	RT		6	2.8E-4	2.7E-2
☐	**GOTERM_CC_ALL**	small nucleolar ribonucleoprotein complex	RT		7	2.0E-3	2.9E-2
☐	**GOTERM_CC_ALL**	nucleolar part	RT		9	1.6E-2	1.6E-1
	Annotation Cluster 37	Enrichment Score: 2.55	G	🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	domain:RRM 1	RT		15	3.2E-4	3.0E-1
☐	**UP_SEQ_FEATURE**	domain:RRM 2	RT		15	3.2E-4	3.0E-1
☐	**UP_SEQ_FEATURE**	domain:RRM 3	RT		5	2.1E-1	1.0E0
	Annotation Cluster 38	Enrichment Score: 2.5	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Chaperonin Cpn60	RT		6	9.3E-4	2.9E-1
☐	**INTERPRO**	Chaperonin TCP-1	RT		6	1.6E-3	4.2E-1
☐	**GOTERM_CC_ALL**	chaperonin-containing T-complex	RT		5	3.5E-3	4.7E-2
☐	**PIR_SUPERFAMILY**	PIRSF002584:molecular chaperone t-complex-type	RT		6	3.6E-3	9.4E-1
☐	**INTERPRO**	Chaperonin Cpn60/TCP-1	RT		5	1.7E-2	9.5E-1

	Annotation Cluster 39	Enrichment Score: 2.47	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	ligase	RT	43	7.7E-5	1.9E-3
☐	GOTERM_MF_ALL	ligase activity	RT	50	2.3E-3	1.2E-1
☐	GOTERM_MF_ALL	ligase activity, forming carbon-nitrogen bonds	RT	21	2.2E-1	9.9E-1

	Annotation Cluster 40	Enrichment Score: 2.46	G	Count	P_Value	Benjamini
☐	BIOCARTA	Cell Cycle	RT	13	5.7E-5	8.0E-3
☐	BIOCARTA	E2F1 Destruction Pathway	RT	6	3.1E-3	1.4E-1
☐	BIOCARTA	Regulation of p27 Phosphorylation during Cell Cycle Progression	RT	6	9.0E-3	3.1E-1
☐	BIOCARTA	Cyclin E Destruction Pathway	RT	5	1.3E-2	3.8E-1
☐	BIOCARTA	Influence of Ras and Rho proteins on G1 to S Transition	RT	9	2.4E-2	4.9E-1

	Annotation Cluster 41	Enrichment Score: 2.4	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	transferase activity, transferring one-carbon groups	RT	31	2.1E-4	2.3E-2
☐	GOTERM_MF_ALL	methyltransferase activity	RT	30	3.4E-4	2.7E-2
☐	SP_PIR_KEYWORDS	methyltransferase	RT	21	4.0E-3	5.6E-2
☐	GOTERM_MF_ALL	S-adenosylmethionine-dependent methyltransferase activity	RT	13	3.6E-2	6.9E-1
☐	SP_PIR_KEYWORDS	s-adenosyl-l-methionine	RT	11	1.0E-1	5.8E-1

	Annotation Cluster 42	Enrichment Score: 2.38	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	short sequence motif:Histidine box-3	RT	4	4.1E-3	9.6E-1
☐	UP_SEQ_FEATURE	short sequence motif:Histidine box-2	RT	4	4.1E-3	9.6E-1
☐	UP_SEQ_FEATURE	short sequence motif:Histidine box-1	RT	4	4.1E-3	9.6E-1

	Annotation Cluster 43	Enrichment Score: 2.37	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	GTPase activity	RT	30	7.6E-5	1.0E-2
☐	GOTERM_MF_ALL	guanyl nucleotide binding	RT	49	1.4E-3	9.2E-2
☐	GOTERM_MF_ALL	guanyl ribonucleotide binding	RT	49	1.4E-3	9.2E-2
☐	GOTERM_MF_ALL	GTP binding	RT	48	1.7E-3	9.7E-2
☐	SP_PIR_KEYWORDS	GTP-binding	RT	39	7.4E-3	1.0E-1
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	RT	29	6.6E-2	1.0E0
☐	INTERPRO	Small GTP-binding protein domain	RT	17	2.0E-1	1.0E0

	Annotation Cluster 44	Enrichment Score: 2.37	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:Thioredoxin 1	RT	6	2.1E-4	2.4E-1
☐	UP_SEQ_FEATURE	domain:Thioredoxin 2	RT	6	2.1E-4	2.4E-1
☐	INTERPRO	Disulphide isomerase	RT	5	2.8E-4	1.0E-1
☐	UP_SEQ_FEATURE	short sequence motif:Prevents secretion from ER	RT	12	1.2E-3	6.7E-1
☐	SP_PIR_KEYWORDS	redox-active center	RT	11	1.5E-3	2.4E-2
☐	INTERPRO	Thioredoxin domain	RT	8	2.9E-3	5.8E-1
☐	GOTERM_MF_ALL	intramolecular oxidoreductase activity	RT	12	2.9E-3	1.4E-1
☐	PIR_SUPERFAMILY	PIRSF001487:protein disulfide-isomerase	RT	5	3.4E-3	9.7E-1
☐	GOTERM_MF_ALL	protein disulfide isomerase activity	RT	5	3.6E-3	1.6E-1
☐	UP_SEQ_FEATURE	site:Contributes to redox potential value	RT	4	4.1E-3	9.6E-1
☐	GOTERM_BP_ALL	cell redox homeostasis	RT	12	7.9E-3	2.3E-1
☐	INTERPRO	Thioredoxin-related	RT	8	9.4E-3	8.7E-1
☐	UP_SEQ_FEATURE	domain:Thioredoxin 3	RT	3	3.0E-2	1.0E0
☐	INTERPRO	Endoplasmic reticulum targeting sequence	RT	10	4.1E-2	9.9E-1
☐	GOTERM_MF_ALL	electron carrier activity	RT	25	8.0E-2	8.7E-1
☐	INTERPRO	Thioredoxin fold	RT	11	1.6E-1	1.0E0

	Annotation Cluster 45	Enrichment Score: 2.3	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	meiotic cell cycle	RT	17	2.1E-3	9.2E-2
☐	GOTERM_BP_ALL	meiosis	RT	16	4.8E-3	1.6E-1

☐	GOTERM_BP_ALL	M phase of meiotic cell cycle	RT	16	4.8E-3	1.6E-1
☐	GOTERM_BP_ALL	meiosis I	RT	8	1.3E-2	3.3E-1
	Annotation Cluster 46	Enrichment Score: 2.25	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	replication fork	RT	12	6.8E-6	1.5E-4
☐	GOTERM_CC_ALL	replisome	RT	5	1.3E-2	1.4E-1
☐	GOTERM_CC_ALL	nuclear replication fork	RT	5	1.3E-2	1.4E-1
☐	GOTERM_CC_ALL	nuclear replisome	RT	5	1.3E-2	1.4E-1
☐	GOTERM_CC_ALL	alpha DNA polymerase:primase complex	RT	3	4.3E-2	3.1E-1
☐	GOTERM_MF_ALL	DNA primase activity	RT	3	4.4E-2	7.5E-1
	Annotation Cluster 47	Enrichment Score: 2.25	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	nucleotidyltransferase activity	RT	23	8.7E-4	6.3E-2
☐	GOTERM_MF_ALL	DNA-directed RNA polymerase activity	RT	11	1.8E-3	9.9E-2
☐	SP_PIR_KEYWORDS	dna-directed rna polymerase	RT	10	2.3E-3	3.7E-2
☐	KEGG_PATHWAY	RNA polymerase	RT	5	2.9E-1	8.3E-1
	Annotation Cluster 48	Enrichment Score: 2.09	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	pseudouridylate synthase activity	RT	6	1.9E-3	1.0E-1
☐	GOTERM_BP_ALL	tRNA processing	RT	12	1.2E-2	3.2E-1
☐	SP_PIR_KEYWORDS	trna processing	RT	9	2.4E-2	2.5E-1
	Annotation Cluster 49	Enrichment Score: 2.06	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Transcription factor E2F/dimerisation partner (TDP)	RT	7	1.5E-4	7.5E-2
☐	INTERPRO	E2F Family	RT	6	2.4E-4	9.4E-2
☐	UP_SEQ_FEATURE	short sequence motif:DEF box	RT	4	9.5E-3	1.0E0
☐	UP_SEQ_FEATURE	region of interest:Cyclin A/CDK2 binding	RT	3	3.0E-2	1.0E0
☐	PIR_SUPERFAMILY	PIRSF019596:transcription factor E2F	RT	3	5.9E-2	1.0E0
☐	UP_SEQ_FEATURE	region of interest:Dimerization	RT	4	7.7E-2	1.0E0
☐	UP_SEQ_FEATURE	region of interest:Transactivation	RT	3	8.7E-2	1.0E0
	Annotation Cluster 50	Enrichment Score: 2	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein polymerization	RT	15	8.8E-5	6.8E-3
☐	COG_ONTOLOGY	Cytoskeleton	RT	13	4.3E-4	1.7E-2
☐	PIR_SUPERFAMILY	PIRSF002306:tubulin	RT	8	1.7E-3	9.3E-1
☐	INTERPRO	Tubulin/FtsZ, GTPase	RT	6	7.6E-3	8.4E-1
☐	INTERPRO	Tubulin/FtsZ, C-terminal	RT	6	7.6E-3	8.4E-1
☐	INTERPRO	Tubulin	RT	6	3.3E-2	9.8E-1
☐	INTERPRO	Alpha tubulin	RT	3	9.2E-2	1.0E0
☐	KEGG_PATHWAY	Gap junction	RT	14	2.0E-1	7.9E-1
☐	GOTERM_MF_ALL	structural constituent of cytoskeleton	RT	9	4.8E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 1.96	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	heterocycle metabolic process	RT	18	1.8E-3	8.2E-2
☐	GOTERM_BP_ALL	nucleobase metabolic process	RT	7	4.7E-3	1.6E-1
☐	GOTERM_BP_ALL	aromatic compound metabolic process	RT	17	1.5E-1	9.2E-1
	Annotation Cluster 52	Enrichment Score: 1.94	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	macromolecule metabolic process	RT	628	9.7E-6	1.1E-3
☐	GOTERM_BP_ALL	protein metabolic process	RT	346	6.8E-5	5.5E-3
☐	GOTERM_BP_ALL	cellular protein metabolic process	RT	329	1.6E-4	1.1E-2
☐	GOTERM_BP_ALL	cellular macromolecule metabolic process	RT	329	4.7E-4	2.7E-2
☐	GOTERM_BP_ALL	biopolymer modification	RT	158	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	protein modification process	RT	148	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	phosphate metabolic process	RT	80	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	phosphorus metabolic process	RT	80	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	post-translational protein modification	RT	126	7.0E-1	1.0E0

	Annotation Cluster 53	Enrichment Score: 1.93	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	DNA topoisomerase (ATP-hydrolyzing) activity	RT	▮		5	6.1E-3	2.5E-1
☐	SMART	HATPase_c	RT	▮		6	8.1E-3	3.6E-1
☐	GOTERM_MF_ALL	DNA topoisomerase activity	RT	▮		5	1.4E-2	4.3E-1
☐	GOTERM_BP_ALL	DNA topological change	RT	▮		5	2.8E-2	5.2E-1
	Annotation Cluster 54	Enrichment Score: 1.91	G		🟩	Count	P_Value	Benjamini
☐	BIOCARTA	Role of Ran in mitotic spindle regulation	RT	▮		8	1.3E-4	9.2E-3
☐	BIOCARTA	Cycling of Ran in nucleocytoplasmic transport	RT	▮		4	3.4E-2	5.9E-1
☐	BIOCARTA	Sumoylation by RanBP2 Regulates Transcriptional Repression	RT	▮		3	4.4E-1	9.6E-1
	Annotation Cluster 55	Enrichment Score: 1.82	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Rotamase	RT	▮		10	2.9E-3	4.5E-2
☐	GOTERM_MF_ALL	peptidyl-prolyl cis-trans isomerase activity	RT	▮		10	3.5E-3	1.6E-1
☐	GOTERM_MF_ALL	cis-trans isomerase activity	RT	▮		10	4.3E-3	1.8E-1
☐	UP_SEQ_FEATURE	domain:PPIase cyclophilin-type	RT	▮		5	2.9E-2	1.0E0
☐	INTERPRO	Peptidyl-prolyl cis-trans isomerase, cyclophilin-type	RT	▮		5	5.7E-2	9.9E-1
☐	PIR_SUPERFAMILY	PIRSF001467:peptidylprolyl isomerase	RT	▮		3	1.7E-1	1.0E0
	Annotation Cluster 56	Enrichment Score: 1.79	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	release of cytochrome c from mitochondria	RT	▮		8	6.6E-5	5.5E-3
☐	GOTERM_BP_ALL	apoptotic mitochondrial changes	RT	▮		8	4.1E-3	1.5E-1
☐	GOTERM_BP_ALL	induction of apoptosis by intracellular signals	RT	▮		7	6.5E-2	7.5E-1
☐	GOTERM_BP_ALL	negative regulation of fibroblast proliferation	RT	▮		3	7.3E-2	7.7E-1
☐	GOTERM_BP_ALL	regulation of fibroblast proliferation	RT	▮		4	1.2E-1	8.7E-1
☐	GOTERM_BP_ALL	fibroblast proliferation	RT	▮		4	1.2E-1	8.7E-1
	Annotation Cluster 57	Enrichment Score: 1.74	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	mitochondrial membrane organization and biogenesis	RT	▮		10	8.9E-5	6.7E-3
☐	GOTERM_BP_ALL	mitochondrial transport	RT	▮		10	1.7E-3	7.6E-2
☐	INTERPRO	Zinc finger, Tim10/DDP-type	RT	▮		4	1.8E-2	9.5E-1
☐	GOTERM_CC_ALL	mitochondrial intermembrane space protein transporter complex	RT	▮		4	2.0E-2	1.8E-1
☐	GOTERM_BP_ALL	protein import into mitochondrial inner membrane	RT	▮		4	2.2E-2	4.6E-1
☐	GOTERM_CC_ALL	mitochondrial intermembrane space	RT	▮		5	3.2E-2	2.5E-1
☐	GOTERM_BP_ALL	inner mitochondrial membrane organization and biogenesis	RT	▮		4	3.2E-2	5.6E-1
☐	GOTERM_BP_ALL	protein import into mitochondrion	RT	▮		4	6.0E-2	7.2E-1
☐	GOTERM_BP_ALL	protein targeting to mitochondrion	RT	▮		4	7.7E-2	7.7E-1
☐	UP_SEQ_FEATURE	short sequence motif:Twin CX3C motif	RT	▮		3	8.7E-2	1.0E0
☐	GOTERM_CC_ALL	organelle envelope lumen	RT	▮		5	1.7E-1	6.9E-1
	Annotation Cluster 58	Enrichment Score: 1.69	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	compositionally biased region:Arg/Ser-rich (RS domain)	RT	▮		6	1.1E-3	6.3E-1
☐	GOTERM_BP_ALL	spliceosome assembly	RT	▮		7	2.5E-2	5.0E-1
☐	GOTERM_MF_ALL	RNA splicing factor activity, transesterification mechanism	RT	▮		5	3.3E-2	6.7E-1
☐	GOTERM_BP_ALL	mRNA splice site selection	RT	▮		5	4.6E-2	6.5E-1
☐	UP_SEQ_FEATURE	compositionally biased region:Gly-rich (hinge region)	RT	▮		3	8.7E-2	1.0E0
	Annotation Cluster 59	Enrichment Score: 1.69	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	centrosome	RT	▮		13	6.7E-3	8.2E-2
☐	GOTERM_CC_ALL	microtubule organizing center part	RT	▮		6	3.6E-2	2.7E-1
☐	GOTERM_CC_ALL	microtubule organizing center	RT	▮		13	3.6E-2	2.7E-1

	Annotation Cluster 60	Enrichment Score: 1.64	G	Count	P_Value	Benjamini
☐	BIOCARTA	Cyclins and Cell Cycle Regulation	RT	13	3.6E-5	1.0E-2
☐	BIOCARTA	Cell Cycle	RT	13	5.7E-5	8.0E-3
☐	BIOCARTA	p53 Signaling Pathway	RT	10	9.5E-5	9.0E-3
☐	GOTERM_CC_ALL	cyclin-dependent protein kinase holoenzyme complex	RT	6	2.7E-4	4.7E-3
☐	KEGG_PATHWAY	Bladder cancer	RT	12	1.4E-2	2.3E-1
☐	KEGG_PATHWAY	Small cell lung cancer	RT	19	2.3E-2	2.9E-1
☐	BIOCARTA	Influence of Ras and Rho proteins on G1 to S Transition	RT	9	2.4E-2	4.9E-1
☐	KEGG_PATHWAY	Chronic myeloid leukemia	RT	14	1.1E-1	6.5E-1
☐	KEGG_PATHWAY	Glioma	RT	11	1.8E-1	7.9E-1
☐	KEGG_PATHWAY	Prostate cancer	RT	15	1.9E-1	7.9E-1
☐	KEGG_PATHWAY	Non-small cell lung cancer	RT	10	2.1E-1	7.7E-1
☐	KEGG_PATHWAY	Pancreatic cancer	RT	12	2.5E-1	8.2E-1
☐	KEGG_PATHWAY	Thyroid cancer	RT	6	2.7E-1	8.2E-1
☐	KEGG_PATHWAY	Melanoma	RT	10	4.8E-1	9.4E-1
☐	KEGG_PATHWAY	Endometrial cancer	RT	7	6.0E-1	9.6E-1
☐	KEGG_PATHWAY	Acute myeloid leukemia	RT	6	8.6E-1	1.0E0

	Annotation Cluster 61	Enrichment Score: 1.64	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	nucleobase biosynthetic process	RT	5	4.0E-3	1.5E-1
☐	GOTERM_BP_ALL	nucleobase metabolic process	RT	7	4.7E-3	1.6E-1
☐	GOTERM_BP_ALL	pyrimidine base metabolic process	RT	4	4.5E-2	6.5E-1
☐	GOTERM_BP_ALL	'de novo' pyrimidine base biosynthetic process	RT	3	7.3E-2	7.7E-1
☐	GOTERM_BP_ALL	pyrimidine base biosynthetic process	RT	3	1.0E-1	8.4E-1

	Annotation Cluster 62	Enrichment Score: 1.59	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	viral reproductive process	RT	9	6.7E-5	5.5E-3
☐	GOTERM_BP_ALL	viral reproduction	RT	9	2.7E-4	1.7E-2
☐	GOTERM_BP_ALL	viral infectious cycle	RT	7	6.5E-4	3.4E-2
☐	GOTERM_BP_ALL	interaction with host	RT	3	7.3E-2	7.7E-1
☐	GOTERM_BP_ALL	viral genome replication	RT	3	7.3E-2	7.7E-1
☐	GOTERM_BP_ALL	interspecies interaction between organisms	RT	3	2.8E-1	9.8E-1
☐	GOTERM_BP_ALL	symbiosis, encompassing mutualism through parasitism	RT	3	2.8E-1	9.8E-1
☐	GOTERM_BP_ALL	reproductive process	RT	17	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	multi-organism process	RT	8	1.0E0	1.0E0

	Annotation Cluster 63	Enrichment Score: 1.59	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	cell cortex	RT	12	8.0E-3	9.6E-2
☐	GOTERM_CC_ALL	cortical cytoskeleton	RT	7	1.1E-2	1.3E-1
☐	GOTERM_CC_ALL	cell cortex part	RT	9	1.3E-2	1.4E-1
☐	GOTERM_CC_ALL	cell division site part	RT	4	2.9E-2	2.4E-1
☐	GOTERM_CC_ALL	cell division site	RT	4	2.9E-2	2.4E-1
☐	GOTERM_CC_ALL	contractile ring	RT	3	6.8E-2	4.2E-1
☐	GOTERM_CC_ALL	cortical actin cytoskeleton	RT	4	1.1E-1	5.5E-1

	Annotation Cluster 64	Enrichment Score: 1.57	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	nucleobase, nucleoside and nucleotide metabolic process	RT	44	2.6E-6	3.5E-4
☐	GOTERM_BP_ALL	nucleotide metabolic process	RT	39	4.2E-5	3.8E-3
☐	GOTERM_BP_ALL	nucleotide biosynthetic process	RT	30	4.7E-5	4.1E-3
☐	GOTERM_BP_ALL	purine nucleotide biosynthetic process	RT	20	1.2E-4	8.8E-3
☐	GOTERM_BP_ALL	purine nucleotide metabolic process	RT	21	2.1E-4	1.4E-2
☐	GOTERM_BP_ALL	ribonucleotide metabolic process	RT	20	4.4E-4	2.5E-2

☐	GOTERM_CC_ALL	proton-transporting two-sector ATPase complex, catalytic domain	RT	▮	6	5.5E-4	9.1E-3
☐	GOTERM_BP_ALL	ribonucleotide biosynthetic process	RT	▮	18	6.6E-4	3.4E-2
☐	GOTERM_BP_ALL	nucleoside triphosphate metabolic process	RT	▮	17	1.0E-3	5.0E-2
☐	GOTERM_CC_ALL	proton-transporting ATP synthase complex, catalytic core F(1)	RT	▮	5	3.5E-3	4.7E-2
☐	GOTERM_BP_ALL	nucleoside triphosphate biosynthetic process	RT	▮	14	4.4E-3	1.5E-1
☐	GOTERM_BP_ALL	purine ribonucleotide biosynthetic process	RT	▮	15	5.0E-3	1.6E-1
☐	GOTERM_BP_ALL	purine ribonucleotide metabolic process	RT	▮	16	5.5E-3	1.8E-1
☐	GOTERM_BP_ALL	ribonucleoside triphosphate metabolic process	RT	▮	14	5.9E-3	1.9E-1
☐	SP_PIR_KEYWORDS	cf(1)	RT	▮	4	1.3E-2	1.5E-1
☐	GOTERM_BP_ALL	coenzyme metabolic process	RT	▮	27	1.5E-2	3.6E-1
☐	GOTERM_BP_ALL	ribonucleoside triphosphate biosynthetic process	RT	▮	12	1.8E-2	4.1E-1
☐	GOTERM_BP_ALL	cofactor metabolic process	RT	▮	31	2.2E-2	4.6E-1
☐	GOTERM_BP_ALL	purine ribonucleoside triphosphate metabolic process	RT	▮	12	2.8E-2	5.2E-1
☐	GOTERM_CC_ALL	proton-transporting ATP synthase complex	RT	▮	6	3.0E-2	2.4E-1
☐	GOTERM_BP_ALL	purine nucleoside triphosphate metabolic process	RT	▮	12	3.5E-2	5.8E-1
☐	GOTERM_BP_ALL	purine nucleoside triphosphate biosynthetic process	RT	▮	11	3.8E-2	6.0E-1
☐	GOTERM_BP_ALL	purine ribonucleoside triphosphate biosynthetic process	RT	▮	11	3.8E-2	6.0E-1
☐	GOTERM_BP_ALL	coenzyme biosynthetic process	RT	▮	16	4.0E-2	6.1E-1
☐	GOTERM_BP_ALL	cofactor biosynthetic process	RT	▮	18	4.0E-2	6.2E-1
☐	SP_PIR_KEYWORDS	hydrogen ion transport	RT	▮	9	4.5E-2	3.7E-1
☐	SP_PIR_KEYWORDS	ATP synthesis	RT	▮	6	8.5E-2	5.4E-1
☐	GOTERM_MF_ALL	primary active transmembrane transporter activity	RT	▮	20	9.3E-2	8.9E-1
☐	GOTERM_MF_ALL	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT	▮	20	9.3E-2	8.9E-1
☐	GOTERM_BP_ALL	ATP synthesis coupled proton transport	RT	▮	8	1.0E-1	8.4E-1
☐	GOTERM_BP_ALL	ATP metabolic process	RT	▮	9	1.1E-1	8.6E-1
☐	GOTERM_MF_ALL	hydrogen ion transporting ATP synthase activity, rotational mechanism	RT	▮	8	1.2E-1	9.4E-1
☐	GOTERM_MF_ALL	hydrogen ion transporting ATPase activity, rotational mechanism	RT	▮	8	1.4E-1	9.5E-1
☐	GOTERM_BP_ALL	proton transport	RT	▮	11	1.4E-1	9.0E-1
☐	GOTERM_MF_ALL	cation-transporting ATPase activity	RT	▮	9	1.5E-1	9.6E-1
☐	GOTERM_BP_ALL	ATP biosynthetic process	RT	▮	8	1.5E-1	9.1E-1
☐	GOTERM_BP_ALL	nucleoside phosphate metabolic process	RT	▮	8	1.5E-1	9.1E-1
☐	GOTERM_CC_ALL	proton-transporting two-sector ATPase complex	RT	▮	8	1.6E-1	6.8E-1
☐	GOTERM_BP_ALL	hydrogen transport	RT	▮	11	1.9E-1	9.5E-1
☐	KEGG_PATHWAY	Oxidative phosphorylation	RT	▮	17	2.6E-1	8.2E-1
☐	GOTERM_MF_ALL	inorganic cation transmembrane transporter activity	RT	▮	17	2.8E-1	9.9E-1
☐	GOTERM_BP_ALL	oxidative phosphorylation	RT	▮	8	3.2E-1	9.9E-1
☐	GOTERM_MF_ALL	ATPase activity, coupled to transmembrane movement of substances	RT	▮	15	3.7E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity, coupled to movement of substances	RT	▮	15	3.7E-1	1.0E0
☐	GOTERM_MF_ALL	active transmembrane transporter activity	RT	▮	35	3.7E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity, coupled to transmembrane movement of ions	RT	▮	11	3.9E-1	1.0E0
☐	GOTERM_MF_ALL	hydrogen ion transmembrane transporter activity	RT	▮	12	3.9E-1	1.0E0
☐	GOTERM_MF_ALL	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane	RT	▮	15	4.0E-1	1.0E0

		movement of substances				
☐	GOTERM_MF_ALL	monovalent inorganic cation transmembrane transporter activity	RT	12	4.4E-1	1.0E0
☐	GOTERM_MF_ALL	hydrogen-exporting ATPase activity, phosphorylative mechanism	RT	3	7.0E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	6	7.4E-1	1.0E0
☐	GOTERM_BP_ALL	monovalent inorganic cation transport	RT	17	1.0E0	1.0E0
	Annotation Cluster 65	Enrichment Score: 1.54	G	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	One carbon pool by folate	RT	10	1.6E-5	8.3E-4
☐	SP_PIR_KEYWORDS	one-carbon metabolism	RT	7	9.5E-4	1.8E-2
☐	GOTERM_BP_ALL	amino acid biosynthetic process	RT	12	3.5E-3	1.4E-1
☐	GOTERM_BP_ALL	folic acid and derivative biosynthetic process	RT	5	4.0E-3	1.5E-1
☐	GOTERM_MF_ALL	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines	RT	8	7.4E-3	2.9E-1
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	RT	6	8.8E-3	3.2E-1
☐	SP_PIR_KEYWORDS	amino-acid biosynthesis	RT	7	9.8E-3	1.3E-1
☐	KEGG_PATHWAY	Glyoxylate and dicarboxylate metabolism	RT	6	2.1E-2	2.9E-1
☐	INTERPRO	Tetrahydrofolate dehydrogenase/cyclohydrolase	RT	3	2.2E-2	9.6E-1
☐	GOTERM_MF_ALL	methenyltetrahydrofolate cyclohydrolase activity	RT	3	2.4E-2	5.8E-1
☐	GOTERM_MF_ALL	methylenetetrahydrofolate dehydrogenase (NADP+) activity	RT	3	2.4E-2	5.8E-1
☐	GOTERM_MF_ALL	methylenetetrahydrofolate dehydrogenase activity	RT	3	2.4E-2	5.8E-1
☐	GOTERM_BP_ALL	folic acid and derivative metabolic process	RT	5	2.8E-2	5.2E-1
☐	GOTERM_BP_ALL	methionine biosynthetic process	RT	4	4.5E-2	6.5E-1
☐	GOTERM_BP_ALL	methionine metabolic process	RT	4	4.5E-2	6.5E-1
☐	GOTERM_BP_ALL	histidine family amino acid biosynthetic process	RT	3	4.7E-2	6.5E-1
☐	GOTERM_BP_ALL	histidine biosynthetic process	RT	3	4.7E-2	6.5E-1
☐	GOTERM_BP_ALL	aspartate family amino acid biosynthetic process	RT	5	5.7E-2	7.2E-1
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on the CH-NH group of donors	RT	6	7.3E-2	8.5E-1
☐	GOTERM_BP_ALL	aspartate family amino acid metabolic process	RT	5	8.2E-2	7.9E-1
☐	GOTERM_BP_ALL	sulfur amino acid biosynthetic process	RT	4	1.2E-1	8.7E-1
☐	COG_ONTOLOGY	Coenzyme metabolism	RT	7	1.6E-1	9.3E-1
☐	GOTERM_BP_ALL	histidine family amino acid metabolic process	RT	4	1.6E-1	9.3E-1
☐	GOTERM_BP_ALL	histidine metabolic process	RT	4	1.6E-1	9.3E-1
☐	GOTERM_BP_ALL	sulfur amino acid metabolic process	RT	4	2.6E-1	9.8E-1
☐	GOTERM_BP_ALL	sulfur compound biosynthetic process	RT	5	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	sulfur metabolic process	RT	7	7.9E-1	1.0E0
	Annotation Cluster 66	Enrichment Score: 1.52	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of DNA replication	RT	5	6.6E-3	2.0E-1
☐	GOTERM_BP_ALL	regulation of DNA replication	RT	6	9.8E-3	2.8E-1
☐	GOTERM_BP_ALL	negative regulation of DNA metabolic process	RT	5	4.6E-2	6.5E-1
☐	GOTERM_BP_ALL	DNA integrity checkpoint	RT	6	7.9E-2	7.8E-1
☐	GOTERM_BP_ALL	regulation of DNA metabolic process	RT	6	1.0E-1	8.4E-1
	Annotation Cluster 67	Enrichment Score: 1.51	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	nucleobase metabolic process	RT	7	4.7E-3	1.6E-1
☐	INTERPRO	Phosphoribosyltransferase	RT	4	6.7E-2	1.0E0
☐	INTERPRO	Purine/pyrimidine phosphoribosyl	RT	3	9.2E-2	1.0E0

☐		transferase	RT			
	Annotation Cluster 68	Enrichment Score: 1.48	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	nucleotidyltransferase activity	RT	23	8.7E-4	6.3E-2
☐	GOTERM_MF_ALL	DNA-directed DNA polymerase activity	RT	8	1.4E-2	4.3E-1
☐	KEGG_PATHWAY	DNA polymerase	RT	8	1.8E-2	2.7E-1
☐	SP_PIR_KEYWORDS	Nucleotidyltransferase	RT	13	2.8E-2	2.7E-1
☐	SP_PIR_KEYWORDS	DNA-directed DNA polymerase	RT	6	3.2E-2	2.9E-1
☐	INTERPRO	DNA polymerase, B region	RT	3	4.2E-2	9.9E-1
☐	INTERPRO	DNA polymerase B, exonuclease	RT	3	4.2E-2	9.9E-1
☐	SMART	POLBc	RT	3	6.6E-2	9.1E-1
☐	INTERPRO	DNA-directed DNA polymerase B	RT	3	9.2E-2	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C4-type	RT	8	1.5E-1	1.0E0
☐	GOTERM_MF_ALL	3'-5' exonuclease activity	RT	5	1.9E-1	9.8E-1
	Annotation Cluster 69	Enrichment Score: 1.47	G	Count	P_Value	Benjamini
☐	INTERPRO	Heat shock protein Hsp70	RT	5	1.7E-2	9.5E-1
☐	INTERPRO	Heat shock protein 70	RT	5	2.3E-2	9.6E-1
☐	SP_PIR_KEYWORDS	stress response	RT	9	5.7E-2	4.3E-1
☐	PIR_SUPERFAMILY	PIRSF002581:chaperone HSP70	RT	4	6.2E-2	1.0E0
	Annotation Cluster 70	Enrichment Score: 1.46	G	Count	P_Value	Benjamini
☐	SMART	HELICc	RT	16	1.2E-3	1.1E-1
☐	SMART	DEXDc	RT	17	1.8E-3	1.4E-1
☐	GOTERM_MF_ALL	helicase activity	RT	24	3.2E-3	1.5E-1
☐	SP_PIR_KEYWORDS	helicase	RT	19	1.4E-2	1.6E-1
☐	INTERPRO	RNA helicase, DEAD-box type, Q motif	RT	8	1.7E-2	9.6E-1
☐	INTERPRO	DNA/RNA helicase, C-terminal	RT	14	2.1E-2	9.7E-1
☐	INTERPRO	DEAD-like helicase, N-terminal	RT	14	4.2E-2	9.8E-1
☐	UP_SEQ_FEATURE	domain:Helicase ATP-binding	RT	11	4.4E-2	1.0E0
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT	13	5.6E-2	9.9E-1
☐	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT	9	5.8E-2	9.9E-1
☐	UP_SEQ_FEATURE	domain:Helicase C-terminal	RT	10	7.0E-2	1.0E0
☐	GOTERM_MF_ALL	ATP-dependent helicase activity	RT	15	8.2E-2	8.7E-1
☐	UP_SEQ_FEATURE	short sequence motif:Q motif	RT	6	1.4E-1	1.0E0
☐	INTERPRO	RNA helicase, ATP-dependent, DEAD-box type	RT	5	2.3E-1	1.0E0
☐	INTERPRO	SNF2-related	RT	5	2.3E-1	1.0E0
☐	UP_SEQ_FEATURE	short sequence motif:DEAD box	RT	4	4.6E-1	1.0E0
	Annotation Cluster 71	Enrichment Score: 1.43	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor	RT	7	1.4E-3	8.9E-2
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on the CH-CH group of donors	RT	8	8.5E-2	8.8E-1
☐	INTERPRO	Alcohol dehydrogenase, zinc-binding	RT	3	4.2E-1	1.0E0
	Annotation Cluster 72	Enrichment Score: 1.42	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:GST-like	RT	3	3.0E-2	1.0E0
☐	INTERPRO	Glutathione S-transferase, C-terminal-like	RT	6	3.3E-2	9.8E-1
☐	INTERPRO	Glutathione S-transferase, C-terminal	RT	6	5.5E-2	9.9E-1
	Annotation Cluster 73	Enrichment Score: 1.41	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	deoxyribonucleotide metabolic process	RT	6	4.9E-3	1.6E-1
☐	GOTERM_BP_ALL	deoxyribonucleoside diphosphate metabolic process	RT	3	7.3E-2	7.7E-1
☐	GOTERM_BP_ALL	nucleoside diphosphate metabolic process	RT	4	1.6E-1	9.3E-1
	Annotation Cluster 74	Enrichment Score: 1.4	G	Count	P_Value	Benjamini

☐	**GOTERM_BP_ALL**	glutamine family amino acid metabolic process	RT	▮		9	1.9E-2	4.3E-1
☐	**GOTERM_BP_ALL**	glutamine metabolic process	RT	▮		6	2.8E-2	5.2E-1
☐	**SP_PIR_KEYWORDS**	Glutamine amidotransferase	RT	▮		4	5.7E-2	4.3E-1
☐	**INTERPRO**	Glutamine amidotransferase, class-II	RT	▮		4	8.3E-2	1.0E0
	Annotation Cluster 75	Enrichment Score: 1.37	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	pyrimidine nucleotide biosynthetic process	RT	▮		10	5.7E-5	4.9E-3
☐	**GOTERM_BP_ALL**	pyrimidine nucleotide metabolic process	RT	▮		11	6.7E-5	5.5E-3
☐	**GOTERM_BP_ALL**	pyrimidine nucleoside triphosphate metabolic process	RT	▮		7	3.4E-3	1.3E-1
☐	**GOTERM_MF_ALL**	nucleobase, nucleoside, nucleotide kinase activity	RT	▮		9	2.3E-2	5.9E-1
☐	**GOTERM_BP_ALL**	pyrimidine ribonucleotide biosynthetic process	RT	▮		5	2.8E-2	5.2E-1
☐	**SMART**	NDK	RT	▮		4	3.2E-2	7.6E-1
☐	**GOTERM_BP_ALL**	pyrimidine ribonucleotide metabolic process	RT	▮		5	3.6E-2	5.9E-1
☐	**INTERPRO**	Nucleoside diphosphate kinase, core	RT	▮		4	5.2E-2	9.9E-1
☐	**GOTERM_MF_ALL**	phosphotransferase activity, phosphate group as acceptor	RT	▮		7	5.9E-2	8.3E-1
☐	**GOTERM_BP_ALL**	CTP biosynthetic process	RT	▮		4	7.7E-2	7.7E-1
☐	**GOTERM_BP_ALL**	CTP metabolic process	RT	▮		4	7.7E-2	7.7E-1
☐	**GOTERM_BP_ALL**	pyrimidine ribonucleoside triphosphate metabolic process	RT	▮		4	7.7E-2	7.7E-1
☐	**GOTERM_BP_ALL**	pyrimidine ribonucleoside triphosphate biosynthetic process	RT	▮		4	7.7E-2	7.7E-1
☐	**UP_SEQ_FEATURE**	active site:Pros-phosphohistidine intermediate	RT	▮		3	1.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Nucleotide metabolism	RT	▮		4	2.3E-1	8.4E-1
☐	**GOTERM_MF_ALL**	nucleoside diphosphate kinase activity	RT	▮		3	2.3E-1	9.9E-1
☐	**GOTERM_BP_ALL**	UTP metabolic process	RT	▮		3	2.4E-1	9.7E-1
☐	**GOTERM_BP_ALL**	UTP biosynthetic process	RT	▮		3	2.4E-1	9.7E-1
☐	**GOTERM_BP_ALL**	GTP metabolic process	RT	▮		3	2.4E-1	9.7E-1
☐	**GOTERM_BP_ALL**	GTP biosynthetic process	RT	▮		3	2.4E-1	9.7E-1
☐	**GOTERM_MF_ALL**	nucleotide kinase activity	RT	▮		3	5.0E-1	1.0E0
	Annotation Cluster 76	Enrichment Score: 1.36	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	glucose catabolic process	RT	▮		14	5.1E-3	1.7E-1
☐	**GOTERM_BP_ALL**	monosaccharide catabolic process	RT	▮		14	5.9E-3	1.9E-1
☐	**GOTERM_BP_ALL**	hexose catabolic process	RT	▮		14	5.9E-3	1.9E-1
☐	**GOTERM_BP_ALL**	alcohol catabolic process	RT	▮		14	7.7E-3	2.3E-1
☐	**GOTERM_BP_ALL**	glycolysis	RT	▮		12	1.2E-2	3.2E-1
☐	**GOTERM_BP_ALL**	cellular carbohydrate catabolic process	RT	▮		14	2.9E-2	5.3E-1
☐	**GOTERM_BP_ALL**	hexose metabolic process	RT	▮		22	4.1E-2	6.3E-1
☐	**GOTERM_BP_ALL**	carbohydrate catabolic process	RT	▮		14	4.2E-2	6.2E-1
☐	**GOTERM_BP_ALL**	monosaccharide metabolic process	RT	▮		22	4.7E-2	6.5E-1
☐	**GOTERM_BP_ALL**	glucose metabolic process	RT	▮		17	5.9E-2	7.2E-1
☐	**SP_PIR_KEYWORDS**	glycolysis	RT	▮		8	8.7E-2	5.4E-1
☐	**GOTERM_BP_ALL**	cellular carbohydrate metabolic process	RT	▮		31	2.7E-1	9.8E-1
☐	**SP_PIR_KEYWORDS**	gluconeogenesis	RT	▮		3	3.0E-1	9.0E-1
☐	**KEGG_PATHWAY**	Glycolysis / Gluconeogenesis	RT	▮		8	4.9E-1	9.4E-1
☐	**GOTERM_BP_ALL**	carbohydrate metabolic process	RT	▮		40	5.1E-1	1.0E0
	Annotation Cluster 77	Enrichment Score: 1.36	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	heterochromatin	RT	▮		11	2.0E-3	2.9E-2
☐	**GOTERM_CC_ALL**	nuclear heterochromatin	RT	▮		5	1.5E-1	6.6E-1
☐	**GOTERM_CC_ALL**	nuclear chromatin	RT	▮		5	2.9E-1	8.3E-1

	Annotation Cluster 78	Enrichment Score: 1.36	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	one-carbon compound metabolic process	RT	23	2.6E-5	2.6E-3
☐	GOTERM_BP_ALL	biopolymer methylation	RT	11	2.7E-2	5.2E-1
☐	GOTERM_BP_ALL	methylation	RT	11	3.8E-2	6.0E-1
☐	GOTERM_BP_ALL	DNA alkylation	RT	5	1.5E-1	9.1E-1
☐	GOTERM_BP_ALL	DNA methylation	RT	5	1.5E-1	9.1E-1
☐	GOTERM_BP_ALL	DNA modification	RT	5	2.0E-1	9.6E-1
☐	GOTERM_BP_ALL	regulation of gene expression, epigenetic	RT	8	2.7E-1	9.8E-1
☐	GOTERM_BP_ALL	gene silencing	RT	5	4.4E-1	1.0E0
	Annotation Cluster 79	Enrichment Score: 1.32	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	stress-induced protein	RT	5	3.7E-3	5.3E-2
☐	SP_PIR_KEYWORDS	heat shock	RT	5	3.7E-3	5.3E-2
☐	GOTERM_BP_ALL	response to protein stimulus	RT	15	4.4E-3	1.6E-1
☐	GOTERM_BP_ALL	response to unfolded protein	RT	15	4.4E-3	1.6E-1
☐	PIR_SUPERFAMILY	PIRSF002583:heat shock protein, HSP90/HTPG types	RT	4	4.4E-3	9.4E-1
☐	SMART	HATPase_c	RT	6	8.1E-3	3.6E-1
☐	INTERPRO	Heat shock protein Hsp90	RT	4	1.1E-2	9.0E-1
☐	SP_PIR_KEYWORDS	estrogen-induced protein	RT	3	2.4E-2	2.5E-1
☐	GOTERM_MF_ALL	TPR domain binding	RT	3	4.4E-2	7.5E-1
☐	INTERPRO	ATP-binding region, ATPase-like	RT	5	4.7E-2	9.9E-1
☐	SP_PIR_KEYWORDS	stress response	RT	9	5.7E-2	4.3E-1
☐	GOTERM_MF_ALL	nitric-oxide synthase regulator activity	RT	3	7.0E-2	8.6E-1
☐	GOTERM_BP_ALL	response to heat	RT	6	1.0E-1	8.4E-1
☐	GOTERM_BP_ALL	response to temperature stimulus	RT	8	1.0E-1	8.4E-1
☐	GOTERM_BP_ALL	regulation of nitric oxide biosynthetic process	RT	4	1.2E-1	8.7E-1
☐	GOTERM_BP_ALL	response to chemical stimulus	RT	44	2.2E-1	9.7E-1
☐	GOTERM_BP_ALL	positive regulation of nitric oxide biosynthetic process	RT	3	2.4E-1	9.7E-1
☐	GOTERM_BP_ALL	nitric oxide biosynthetic process	RT	4	4.0E-1	1.0E0
☐	GOTERM_BP_ALL	nitric oxide metabolic process	RT	4	4.0E-1	1.0E0
☐	GOTERM_BP_ALL	response to biotic stimulus	RT	20	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of biosynthetic process	RT	5	9.1E-1	1.0E0
	Annotation Cluster 80	Enrichment Score: 1.32	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	pyrimidine nucleoside triphosphate metabolic process	RT	7	3.4E-3	1.3E-1
☐	GOTERM_BP_ALL	deoxyribonucleotide metabolic process	RT	6	4.9E-3	1.6E-1
☐	GOTERM_BP_ALL	pyrimidine deoxyribonucleotide metabolic process	RT	4	3.2E-2	5.6E-1
☐	GOTERM_BP_ALL	pyrimidine nucleoside metabolic process	RT	4	6.0E-2	7.2E-1
☐	GOTERM_BP_ALL	pyrimidine deoxyribonucleotide biosynthetic process	RT	3	7.3E-2	7.7E-1
☐	GOTERM_BP_ALL	pyrimidine deoxyribonucleoside triphosphate metabolic process	RT	3	1.0E-1	8.4E-1
☐	GOTERM_BP_ALL	pyrimidine deoxyribonucleoside metabolic process	RT	3	1.0E-1	8.4E-1
☐	GOTERM_BP_ALL	deoxyribonucleotide biosynthetic process	RT	3	1.0E-1	8.4E-1
☐	GOTERM_BP_ALL	deoxyribonucleoside metabolic process	RT	3	1.3E-1	9.0E-1
☐	GOTERM_BP_ALL	deoxyribonucleoside triphosphate metabolic process	RT	3	1.7E-1	9.3E-1
	Annotation Cluster 81	Enrichment Score: 1.31	G	Count	P_Value	Benjamini
☐	INTERPRO	Glyceraldehyde 3-phosphate dehydrogenase	RT	4	1.8E-2	9.5E-1
☐	GOTERM_MF_ALL	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity	RT	4	2.0E-2	5.4E-1
☐	GOTERM_MF_ALL	glyceraldehyde-3-phosphate	RT	4	2.0E-2	5.4E-1

☐		dehydrogenase activity					
☐	GOTERM_MF_ALL	NAD binding	RT		7	3.8E-2	7.0E-1
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	RT		6	1.5E-1	9.6E-1
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on the aldehyde or oxo group of donors	RT		6	3.2E-1	1.0E0
	Annotation Cluster 82	Enrichment Score: 1.29	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell cycle checkpoint	RT		11	2.1E-3	9.2E-2
☐	GOTERM_BP_ALL	regulation of mitosis	RT		10	1.9E-2	4.3E-1
☐	GOTERM_BP_ALL	DNA damage response, signal transduction	RT		9	3.5E-2	5.8E-1
☐	BIOCARTA	RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage	RT		5	4.6E-2	6.4E-1
☐	GOTERM_BP_ALL	DNA integrity checkpoint	RT		6	7.9E-2	7.8E-1
☐	BIOCARTA	Cell Cycle	RT		6	1.6E-1	9.1E-1
☐	GOTERM_BP_ALL	mitotic cell cycle checkpoint	RT		5	1.6E-1	9.3E-1
☐	GOTERM_BP_ALL	DNA damage checkpoint	RT		4	3.4E-1	9.9E-1
	Annotation Cluster 83	Enrichment Score: 1.29	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	cortical cytoskeleton	RT		7	1.1E-2	1.3E-1
☐	GOTERM_CC_ALL	filamentous actin	RT		4	5.5E-2	3.6E-1
☐	GOTERM_CC_ALL	actin filament	RT		5	2.2E-1	7.7E-1
	Annotation Cluster 84	Enrichment Score: 1.27	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	L-serine metabolic process	RT		4	2.2E-2	4.6E-1
☐	GOTERM_BP_ALL	serine family amino acid metabolic process	RT		6	2.8E-2	5.2E-1
☐	KEGG_PATHWAY	Glycine, serine and threonine metabolism	RT		8	2.6E-1	8.1E-1
	Annotation Cluster 85	Enrichment Score: 1.26	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	mitochondrial inner membrane presequence translocase complex	RT		4	2.9E-2	2.4E-1
☐	GOTERM_CC_ALL	mitochondrial intermembrane space	RT		5	3.2E-2	2.5E-1
☐	GOTERM_MF_ALL	macromolecule transmembrane transporter activity	RT		5	3.3E-2	6.7E-1
☐	GOTERM_MF_ALL	P-P-bond-hydrolysis-driven protein transmembrane transporter activity	RT		5	3.3E-2	6.7E-1
☐	GOTERM_MF_ALL	protein transmembrane transporter activity	RT		5	1.5E-1	9.6E-1
☐	GOTERM_CC_ALL	organelle envelope lumen	RT		5	1.7E-1	6.9E-1
	Annotation Cluster 86	Enrichment Score: 1.26	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	DNA damage response, signal transduction by p53 class mediator	RT		6	1.7E-2	4.0E-1
☐	GOTERM_BP_ALL	DNA damage response, signal transduction	RT		9	3.5E-2	5.8E-1
☐	GOTERM_BP_ALL	induction of apoptosis by intracellular signals	RT		7	6.5E-2	7.5E-1
☐	GOTERM_BP_ALL	DNA damage response, signal transduction resulting in induction of apoptosis	RT		4	2.4E-1	9.7E-1
	Annotation Cluster 87	Enrichment Score: 1.25	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	purine biosynthesis	RT		7	3.4E-4	7.1E-3
☐	GOTERM_BP_ALL	nucleoside monophosphate biosynthetic process	RT		6	2.2E-2	4.6E-1
☐	GOTERM_BP_ALL	nucleoside monophosphate metabolic process	RT		6	2.8E-2	5.2E-1
☐	GOTERM_BP_ALL	ribonucleoside monophosphate biosynthetic process	RT		5	5.7E-2	7.2E-1
☐	GOTERM_BP_ALL	ribonucleoside monophosphate metabolic process	RT		5	6.9E-2	7.6E-1
☐	GOTERM_BP_ALL	purine nucleoside monophosphate biosynthetic process	RT		3	2.8E-1	9.8E-1
☐	GOTERM_BP_ALL	purine ribonucleoside monophosphate biosynthetic process	RT		3	2.8E-1	9.8E-1
☐	GOTERM_BP_ALL	purine nucleoside monophosphate metabolic process	RT		3	3.1E-1	9.9E-1

☐	GOTERM_BP_ALL	purine ribonucleoside monophosphate metabolic process	RT		3	3.1E-1	9.9E-1
	Annotation Cluster 88	Enrichment Score: 1.24	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:CH 2	RT		7	1.3E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:CH 1	RT		7	1.3E-2	1.0E0
☐	INTERPRO	Actin-binding, actinin-type	RT		6	7.4E-2	1.0E0
☐	SMART	CH	RT		9	8.3E-2	9.4E-1
☐	UP_SEQ_FEATURE	domain:Actin-binding	RT		4	1.7E-1	1.0E0
☐	INTERPRO	Calponin-like actin-binding	RT		9	1.8E-1	1.0E0
	Annotation Cluster 89	Enrichment Score: 1.24	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Mitochondrion	RT		76	8.2E-3	1.1E-1
☐	UP_SEQ_FEATURE	transit peptide:Mitochondrion	RT		34	1.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	transit peptide	RT		41	1.8E-1	7.7E-1
	Annotation Cluster 90	Enrichment Score: 1.21	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein depolymerization	RT		10	7.4E-3	2.2E-1
☐	GOTERM_BP_ALL	regulation of actin polymerization and/or depolymerization	RT		10	1.0E-2	2.9E-1
☐	GOTERM_BP_ALL	regulation of actin cytoskeleton organization and biogenesis	RT		10	1.2E-2	3.2E-1
☐	GOTERM_BP_ALL	regulation of actin filament length	RT		10	1.2E-2	3.2E-1
☐	GOTERM_BP_ALL	regulation of cellular component size	RT		10	1.4E-2	3.6E-1
☐	GOTERM_BP_ALL	actin polymerization and/or depolymerization	RT		11	1.6E-2	3.9E-1
☐	GOTERM_BP_ALL	regulation of cytoskeleton organization and biogenesis	RT		10	2.2E-2	4.6E-1
☐	GOTERM_BP_ALL	regulation of organelle organization and biogenesis	RT		10	2.2E-2	4.6E-1
☐	GOTERM_BP_ALL	actin filament depolymerization	RT		7	2.5E-2	5.0E-1
☐	GOTERM_BP_ALL	regulation of actin filament depolymerization	RT		7	2.5E-2	5.0E-1
☐	GOTERM_BP_ALL	negative regulation of cellular component organization and biogenesis	RT		9	3.5E-2	5.8E-1
☐	GOTERM_BP_ALL	regulation of cellular component organization and biogenesis	RT		13	3.5E-2	5.8E-1
☐	GOTERM_BP_ALL	actin filament capping	RT		6	5.9E-2	7.2E-1
☐	GOTERM_BP_ALL	negative regulation of actin filament depolymerization	RT		6	5.9E-2	7.2E-1
☐	SMART	GEL	RT		3	1.1E-1	9.6E-1
☐	INTERPRO	Gelsolin region	RT		4	1.2E-1	1.0E0
☐	GOTERM_BP_ALL	barbed-end actin filament capping	RT		5	1.5E-1	9.1E-1
☐	INTERPRO	Gelsolin	RT		3	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	actin filament polymerization	RT		5	1.8E-1	9.4E-1
☐	UP_SEQ_FEATURE	repeat:Gelsolin-like 1	RT		3	2.0E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:Gelsolin-like 2	RT		3	2.0E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:Gelsolin-like 3	RT		3	2.0E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of protein metabolic process	RT		12	2.0E-1	9.6E-1
☐	SP_PIR_KEYWORDS	actin capping	RT		4	2.3E-1	8.4E-1
☐	GOTERM_BP_ALL	actin cytoskeleton organization and biogenesis	RT		22	2.8E-1	9.8E-1
☐	GOTERM_BP_ALL	actin filament-based process	RT		23	3.0E-1	9.8E-1
☐	GOTERM_BP_ALL	regulation of protein metabolic process	RT		30	3.3E-1	9.9E-1
	Annotation Cluster 91	Enrichment Score: 1.16	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	establishment of organelle localization	RT		8	1.3E-2	3.3E-1
☐	GOTERM_BP_ALL	organelle localization	RT		9	2.3E-2	4.6E-1
☐	GOTERM_BP_ALL	establishment of chromosome localization	RT		3	1.0E-1	8.4E-1
☐	GOTERM_BP_ALL	chromosome localization	RT		3	1.0E-1	8.4E-1
☐	GOTERM_BP_ALL	positive regulation of progression through	RT		3	5.1E-1	1.0E0

☐		cell cycle	RT				
	Annotation Cluster 92	Enrichment Score: 1.14	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	meiosis I	RT		8	1.3E-2	3.3E-1
☐	GOTERM_BP_ALL	meiotic prophase I	RT		3	1.7E-1	9.3E-1
☐	GOTERM_BP_ALL	prophase	RT		3	1.7E-1	9.3E-1
	Annotation Cluster 93	Enrichment Score: 1.13	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	glutamine family amino acid metabolic process	RT		9	1.9E-2	4.3E-1
☐	GOTERM_BP_ALL	proline biosynthetic process	RT		3	7.3E-2	7.7E-1
☐	GOTERM_BP_ALL	proline metabolic process	RT		3	1.3E-1	9.0E-1
☐	GOTERM_BP_ALL	glutamine family amino acid biosynthetic process	RT		4	1.6E-1	9.3E-1
	Annotation Cluster 94	Enrichment Score: 1.13	G	🟩	Count	P_Value	Benjamini
☐	SMART	Sm	RT		6	1.0E-2	4.1E-1
☐	INTERPRO	Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core	RT		6	2.2E-2	9.7E-1
☐	INTERPRO	Like-Sm ribonucleoprotein, core	RT		6	2.7E-2	9.7E-1
☐	GOTERM_BP_ALL	mRNA catabolic process	RT		6	1.8E-1	9.4E-1
☐	GOTERM_BP_ALL	RNA catabolic process	RT		6	2.8E-1	9.8E-1
☐	GOTERM_BP_ALL	mRNA catabolic process, nonsense-mediated decay	RT		3	5.7E-1	1.0E0
	Annotation Cluster 95	Enrichment Score: 1.12	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	nucleobase, nucleoside, nucleotide kinase activity	RT		9	2.3E-2	5.9E-1
☐	GOTERM_MF_ALL	deoxynucleoside kinase activity	RT		3	7.0E-2	8.6E-1
☐	GOTERM_MF_ALL	nucleoside kinase activity	RT		3	2.7E-1	9.9E-1
	Annotation Cluster 96	Enrichment Score: 1.12	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	actin-binding	RT		26	1.8E-2	2.0E-1
☐	GOTERM_MF_ALL	actin binding	RT		34	5.6E-2	8.2E-1
☐	GOTERM_CC_ALL	actin cytoskeleton	RT		27	7.1E-2	4.2E-1
☐	GOTERM_MF_ALL	cytoskeletal protein binding	RT		45	7.8E-2	8.6E-1
☐	SP_PIR_KEYWORDS	cytoskeleton	RT		30	4.5E-1	9.6E-1
	Annotation Cluster 97	Enrichment Score: 1.11	G	🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Selenoamino acid metabolism	RT		10	3.6E-3	9.0E-2
☐	KEGG_PATHWAY	Aminophosphonate metabolism	RT		7	4.2E-3	9.4E-2
☐	GOTERM_BP_ALL	biopolymer methylation	RT		11	2.7E-2	5.2E-1
☐	KEGG_PATHWAY	Naphthalene and anthracene degradation	RT		6	3.6E-2	3.8E-1
☐	GOTERM_MF_ALL	S-adenosylmethionine-dependent methyltransferase activity	RT		13	3.6E-2	6.9E-1
☐	GOTERM_BP_ALL	methylation	RT		11	3.8E-2	6.0E-1
☐	GOTERM_BP_ALL	peptidyl-arginine methylation	RT		3	4.7E-2	6.5E-1
☐	KEGG_PATHWAY	Tyrosine metabolism	RT		11	5.7E-2	4.8E-1
☐	KEGG_PATHWAY	Histidine metabolism	RT		9	6.7E-2	4.9E-1
☐	GOTERM_MF_ALL	arginine N-methyltransferase activity	RT		3	7.0E-2	8.6E-1
☐	GOTERM_MF_ALL	protein-arginine N-methyltransferase activity	RT		3	7.0E-2	8.6E-1
☐	GOTERM_MF_ALL	histone-arginine N-methyltransferase activity	RT		3	7.0E-2	8.6E-1
☐	GOTERM_BP_ALL	peptidyl-arginine modification	RT		3	7.3E-2	7.7E-1
☐	PIR_SUPERFAMILY	PIRSF037127:type 1 arginine N-methyltransferase	RT		3	9.1E-2	1.0E0
☐	UP_SEQ_FEATURE	binding site:S-adenosyl-L-methionine	RT		4	1.7E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid methylation	RT		6	2.1E-1	9.6E-1
☐	GOTERM_BP_ALL	protein amino acid alkylation	RT		6	2.1E-1	9.6E-1
☐	KEGG_PATHWAY	Tryptophan metabolism	RT		9	2.3E-1	7.9E-1
☐	GOTERM_MF_ALL	histone methyltransferase activity	RT		5	2.3E-1	9.9E-1

☐	**UP_SEQ_FEATURE**	binding site:S-adenosyl-L-methionine; via carbonyl oxygen	RT	3	2.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	protein methyltransferase activity	RT	6	2.8E-1	9.9E-1
☐	**GOTERM_MF_ALL**	N-methyltransferase activity	RT	6	3.0E-1	1.0E0
☐	**KEGG_PATHWAY**	Androgen and estrogen metabolism	RT	8	3.6E-1	8.8E-1
	Annotation Cluster 98	Enrichment Score: 1.07	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	release of cytochrome c from mitochondria	RT	8	6.6E-5	5.5E-3
☐	**GOTERM_BP_ALL**	mitochondrial membrane organization and biogenesis	RT	10	8.9E-5	6.7E-3
☐	**GOTERM_BP_ALL**	mitochondrion organization and biogenesis	RT	17	2.4E-3	1.0E-1
☐	**GOTERM_BP_ALL**	apoptotic mitochondrial changes	RT	8	4.1E-3	1.5E-1
☐	**GOTERM_BP_ALL**	caspase activation via cytochrome c	RT	4	7.2E-3	2.2E-1
☐	**GOTERM_BP_ALL**	regulation of caspase activity	RT	10	1.7E-2	4.0E-1
☐	**GOTERM_BP_ALL**	apoptotic program	RT	12	2.3E-2	4.6E-1
☐	**GOTERM_BP_ALL**	caspase activation	RT	7	3.0E-2	5.4E-1
☐	**BIOCARTA**	Apoptotic Signaling in Response to DNA Damage	RT	7	3.9E-2	6.1E-1
☐	**GOTERM_BP_ALL**	positive regulation of caspase activity	RT	7	5.7E-2	7.2E-1
☐	**UP_SEQ_FEATURE**	short sequence motif:BH1	RT	4	5.8E-2	1.0E0
☐	**UP_SEQ_FEATURE**	short sequence motif:BH2	RT	4	7.7E-2	1.0E0
☐	**INTERPRO**	BCL2-like apoptosis inhibitor	RT	4	1.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of mitochondrial membrane potential	RT	3	1.3E-1	9.0E-1
☐	**GOTERM_BP_ALL**	positive regulation of hydrolase activity	RT	7	1.7E-1	9.3E-1
☐	**UP_SEQ_FEATURE**	short sequence motif:BH3	RT	4	1.7E-1	1.0E0
☐	**BIOCARTA**	Caspase Cascade in Apoptosis	RT	6	1.8E-1	9.2E-1
☐	**SMART**	BCL	RT	4	2.0E-1	9.9E-1
☐	**BIOCARTA**	Stress Induction of HSP Regulation	RT	4	2.4E-1	9.1E-1
☐	**INTERPRO**	Apoptosis regulator Bcl-2, BH	RT	4	2.6E-1	1.0E0
☐	**BIOCARTA**	Role of Mitochondria in Apoptotic Signaling	RT	5	3.3E-1	9.5E-1
☐	**BIOCARTA**	Telomeres, Telomerase, Cellular Aging, and Immortality	RT	4	4.3E-1	9.7E-1
☐	**BIOCARTA**	HIV-I Nef	RT	8	5.9E-1	9.7E-1
☐	**KEGG_PATHWAY**	Amyotrophic lateral sclerosis (ALS)	RT	3	6.8E-1	9.7E-1
☐	**KEGG_PATHWAY**	Neurodegenerative Diseases	RT	5	6.8E-1	9.7E-1
☐	**BIOCARTA**	Induction of apoptosis through DR3 and DR4/5 Death Receptors	RT	4	7.6E-1	9.9E-1
☐	**BIOCARTA**	Ceramide Signaling Pathway	RT	3	8.3E-1	9.9E-1
☐	**GOTERM_BP_ALL**	positive regulation of catalytic activity	RT	15	8.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of hydrolase activity	RT	11	9.1E-1	1.0E0
☐	**KEGG_PATHWAY**	Apoptosis	RT	7	9.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of membrane potential	RT	3	9.7E-1	1.0E0
	Annotation Cluster 99	Enrichment Score: 1.06	G	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	pseudouridylate synthase activity	RT	6	1.9E-3	1.0E-1
☐	**GOTERM_BP_ALL**	tRNA modification	RT	4	4.5E-2	6.5E-1
☐	**GOTERM_BP_ALL**	pseudouridine synthesis	RT	4	6.0E-2	7.2E-1
☐	**GOTERM_BP_ALL**	RNA modification	RT	6	6.9E-2	7.6E-1
☐	**GOTERM_BP_ALL**	tRNA pseudouridine synthesis	RT	3	7.3E-2	7.7E-1
☐	**GOTERM_MF_ALL**	intramolecular transferase activity	RT	5	4.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	tRNA-pseudouridine synthase activity	RT	3	5.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	pseudouridine synthase activity	RT	3	6.4E-1	1.0E0
	Annotation Cluster 100	Enrichment Score: 1.05	G	Count	P_Value	Benjamini

☐	GOTERM_MF_ALL	steroid hormone receptor binding	RT	▮		4	5.7E-2	8.2E-1
☐	GOTERM_MF_ALL	hormone receptor binding	RT	▮		6	7.3E-2	8.5E-1
☐	GOTERM_MF_ALL	estrogen receptor binding	RT	▮		3	9.8E-2	9.0E-1
☐	GOTERM_MF_ALL	nuclear hormone receptor binding	RT	▮		5	1.5E-1	9.6E-1
	Annotation Cluster 101	Enrichment Score: 1.04	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	virion	RT	▮		6	5.1E-2	3.4E-1
☐	GOTERM_CC_ALL	virion part	RT	▮		6	5.1E-2	3.4E-1
☐	GOTERM_CC_ALL	viral capsid	RT	▮		5	1.2E-1	5.8E-1
☐	INTERPRO	ENV polyprotein (coat polyprotein)	RT	▮		3	2.2E-1	1.0E0
	Annotation Cluster 102	Enrichment Score: 1.03	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	pentosyltransferase	RT	▮		3	7.0E-2	4.9E-1
☐	SP_PIR_KEYWORDS	salvage pathway	RT	▮		3	7.0E-2	4.9E-1
☐	GOTERM_BP_ALL	purine nucleoside metabolic process	RT	▮		3	1.7E-1	9.3E-1
	Annotation Cluster 103	Enrichment Score: 1.02	G		🟩	Count	P_Value	Benjamini
☐	SMART	STI1	RT	▮		5	2.7E-3	1.9E-1
☐	INTERPRO	Heat shock chaperonin-binding	RT	▮		5	5.3E-3	7.9E-1
☐	UP_SEQ_FEATURE	domain:UBA 2	RT	▮		3	8.7E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:UBA 1	RT	▮		3	8.7E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:Ubiquitin-like	RT	▮		5	2.1E-1	1.0E0
☐	SMART	UBQ	RT	▮		6	3.2E-1	1.0E0
☐	SMART	UBA	RT	▮		4	3.4E-1	1.0E0
☐	INTERPRO	Ubiquitin	RT	▮		6	4.2E-1	1.0E0
☐	INTERPRO	Ubiquitin-associated/translation elongation factor EF1B, N-terminal	RT	▮		5	5.7E-1	1.0E0
	Annotation Cluster 104	Enrichment Score: 1.02	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	protein kinase C binding	RT	▮		4	3.0E-2	6.5E-1
☐	GOTERM_MF_ALL	enzyme binding	RT	▮		27	6.4E-2	8.5E-1
☐	GOTERM_MF_ALL	kinase binding	RT	▮		11	2.0E-1	9.8E-1
☐	GOTERM_MF_ALL	protein kinase binding	RT	▮		10	2.1E-1	9.8E-1
	Annotation Cluster 105	Enrichment Score: 1.02	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:KH 3	RT	▮		4	4.2E-2	1.0E0
☐	SMART	KH	RT	▮		6	7.3E-2	9.2E-1
☐	INTERPRO	K Homology	RT	▮		6	1.2E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:KH 1	RT	▮		4	1.2E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:KH 2	RT	▮		4	1.2E-1	1.0E0
☐	INTERPRO	K Homology, type 1	RT	▮		6	1.3E-1	1.0E0
	Annotation Cluster 106	Enrichment Score: 1.02	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cellular macromolecule catabolic process	RT	▮		40	3.4E-3	1.3E-1
☐	GOTERM_BP_ALL	macromolecule catabolic process	RT	▮		42	5.9E-2	7.2E-1
☐	GOTERM_BP_ALL	cellular catabolic process	RT	▮		55	6.1E-2	7.2E-1
☐	GOTERM_BP_ALL	ubiquitin-dependent protein catabolic process	RT	▮		20	7.3E-2	7.6E-1
☐	GOTERM_BP_ALL	modification-dependent protein catabolic process	RT	▮		20	8.6E-2	8.0E-1
☐	GOTERM_BP_ALL	modification-dependent macromolecule catabolic process	RT	▮		20	8.6E-2	8.0E-1
☐	GOTERM_BP_ALL	proteolysis involved in cellular protein catabolic process	RT	▮		20	1.0E-1	8.4E-1
☐	GOTERM_BP_ALL	cellular protein catabolic process	RT	▮		20	1.1E-1	8.6E-1
☐	GOTERM_BP_ALL	biopolymer catabolic process	RT	▮		28	4.0E-1	1.0E0
☐	GOTERM_BP_ALL	catabolic process	RT	▮		58	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	protein catabolic process	RT	▮		21	4.6E-1	1.0E0
	Annotation Cluster 107	Enrichment Score: 1.01	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	dolichyl-diphosphooligosaccharide-protein	RT	▮		5	3.6E-3	1.6E-1

☐		glycotransferase activity	RT				
☐	GOTERM_MF_ALL	oligosaccharyl transferase activity	RT		5	3.6E-3	1.6E-1
☐	GOTERM_BP_ALL	protein amino acid N-linked glycosylation via asparagine	RT		5	1.0E-2	2.9E-1
☐	GOTERM_BP_ALL	peptidyl-asparagine modification	RT		5	1.0E-2	2.9E-1
☐	GOTERM_MF_ALL	transferase activity, transferring pentosyl groups	RT		10	1.2E-2	4.1E-1
☐	GOTERM_BP_ALL	protein amino acid N-linked glycosylation	RT		6	6.9E-2	7.6E-1
☐	GOTERM_CC_ALL	oligosaccharyl transferase complex	RT		3	1.3E-1	6.0E-1
☐	GOTERM_MF_ALL	transferase activity, transferring glycosyl groups	RT		28	1.3E-1	9.4E-1
☐	GOTERM_BP_ALL	glycoprotein biosynthetic process	RT		11	4.0E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid glycosylation	RT		10	4.1E-1	1.0E0
☐	GOTERM_BP_ALL	biopolymer glycosylation	RT		10	4.5E-1	1.0E0
☐	KEGG_PATHWAY	Glycan structures - biosynthesis 1	RT		14	5.1E-1	9.4E-1
☐	SP_PIR_KEYWORDS	glycosyltransferase	RT		18	5.1E-1	9.8E-1
☐	KEGG_PATHWAY	N-Glycan biosynthesis	RT		6	5.3E-1	9.4E-1
☐	GOTERM_MF_ALL	transferase activity, transferring hexosyl groups	RT		15	5.4E-1	1.0E0
☐	GOTERM_BP_ALL	glycoprotein metabolic process	RT		12	5.5E-1	1.0E0
	Annotation Cluster 108	Enrichment Score: 0.99	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	interphase	RT		11	4.7E-2	6.5E-1
☐	GOTERM_BP_ALL	interphase of mitotic cell cycle	RT		11	4.7E-2	6.5E-1
☐	GOTERM_BP_ALL	S phase	RT		4	9.6E-2	8.3E-1
☐	GOTERM_BP_ALL	S phase of mitotic cell cycle	RT		4	9.6E-2	8.3E-1
☐	GOTERM_BP_ALL	G1/S transition of mitotic cell cycle	RT		4	5.5E-1	1.0E0
	Annotation Cluster 109	Enrichment Score: 0.97	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	maintenance of localization	RT		6	4.1E-2	6.2E-1
☐	GOTERM_BP_ALL	maintenance of cellular localization	RT		4	1.2E-1	8.7E-1
☐	GOTERM_BP_ALL	maintenance of protein localization	RT		4	1.2E-1	8.7E-1
☐	GOTERM_BP_ALL	maintenance of cellular protein localization	RT		3	2.4E-1	9.7E-1
	Annotation Cluster 110	Enrichment Score: 0.95	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	nuclear envelope-endoplasmic reticulum network	RT		18	1.5E-2	1.6E-1
☐	GOTERM_CC_ALL	endoplasmic reticulum part	RT		19	1.6E-2	1.6E-1
☐	GOTERM_CC_ALL	endoplasmic reticulum membrane	RT		17	2.2E-2	2.0E-1
☐	GOTERM_CC_ALL	integral to endoplasmic reticulum membrane	RT		6	1.9E-1	7.2E-1
☐	GOTERM_CC_ALL	intrinsic to endoplasmic reticulum membrane	RT		6	2.8E-1	8.2E-1
☐	GOTERM_CC_ALL	integral to organelle membrane	RT		6	8.3E-1	1.0E0
☐	GOTERM_CC_ALL	intrinsic to organelle membrane	RT		6	8.9E-1	1.0E0
	Annotation Cluster 111	Enrichment Score: 0.92	G	🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Polyunsaturated fatty acid biosynthesis	RT		6	3.6E-2	3.8E-1
☐	GOTERM_MF_ALL	stearoyl-CoA 9-desaturase activity	RT		3	7.0E-2	8.6E-1
☐	INTERPRO	Fatty acid desaturase, type 1, N-terminal	RT		3	9.2E-2	1.0E0
☐	INTERPRO	Fatty acid desaturase, type 1	RT		3	1.2E-1	1.0E0
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	RT		3	1.3E-1	9.4E-1
☐	KEGG_PATHWAY	PPAR signaling pathway	RT		7	8.7E-1	1.0E0
	Annotation Cluster 112	Enrichment Score: 0.89	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	heat shock protein binding	RT		11	3.3E-2	6.7E-1
☐	INTERPRO	Molecular chaperone, heat shock protein, Hsp40, DnaJ	RT		7	6.7E-2	9.9E-1
☐	SMART	DnaJ	RT		7	1.0E-1	9.5E-1

☐	INTERPRO	Heat shock protein DnaJ, N-terminal	RT	▮	7	1.5E-1	1.0E0
☐	INTERPRO	Heat shock protein DnaJ	RT	▮	4	2.6E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:J	RT	▮	4	5.4E-1	1.0E0
	Annotation Cluster 113	Enrichment Score: 0.87	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	pyridoxal phosphate	RT	▮	12	1.4E-2	1.6E-1
☐	UP_SEQ_FEATURE	binding site:Pyridoxal phosphate (covalent)	RT	▮	8	5.7E-2	1.0E0
☐	GOTERM_MF_ALL	vitamin binding	RT	▮	16	8.7E-2	8.8E-1
☐	GOTERM_MF_ALL	transferase activity, transferring nitrogenous groups	RT	▮	7	1.6E-1	9.6E-1
☐	SP_PIR_KEYWORDS	aminotransferase	RT	▮	5	1.6E-1	7.4E-1
☐	GOTERM_MF_ALL	pyridoxal phosphate binding	RT	▮	8	1.6E-1	9.6E-1
☐	GOTERM_MF_ALL	transaminase activity	RT	▮	6	2.5E-1	9.9E-1
☐	INTERPRO	Aminotransferase, class I and II	RT	▮	3	3.9E-1	1.0E0
☐	INTERPRO	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	RT	▮	4	5.7E-1	1.0E0
	Annotation Cluster 114	Enrichment Score: 0.87	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Cyclin D	RT	▮	4	2.6E-3	5.6E-1
☐	KEGG_PATHWAY	Wnt signaling pathway	RT	▮	12	9.6E-1	1.0E0
☐	KEGG_PATHWAY	Jak-STAT signaling pathway	RT	▮	8	1.0E0	1.0E0
	Annotation Cluster 115	Enrichment Score: 0.86	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	exonuclease activity	RT	▮	12	1.0E-2	3.5E-1
☐	SP_PIR_KEYWORDS	Exonuclease	RT	▮	8	2.8E-2	2.7E-1
☐	GOTERM_MF_ALL	nuclease activity	RT	▮	20	7.5E-2	8.5E-1
☐	GOTERM_MF_ALL	endodeoxyribonuclease activity	RT	▮	3	2.3E-1	9.9E-1
☐	SP_PIR_KEYWORDS	Endonuclease	RT	▮	7	3.3E-1	9.1E-1
☐	SP_PIR_KEYWORDS	nuclease	RT	▮	9	4.0E-1	9.5E-1
☐	GOTERM_MF_ALL	endonuclease activity	RT	▮	10	4.0E-1	1.0E0
☐	GOTERM_MF_ALL	deoxyribonuclease activity	RT	▮	3	4.7E-1	1.0E0
	Annotation Cluster 116	Enrichment Score: 0.86	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of RNA metabolic process	RT	▮	6	2.2E-2	4.6E-1
☐	GOTERM_BP_ALL	regulation of mRNA stability	RT	▮	3	3.1E-1	9.9E-1
☐	GOTERM_BP_ALL	regulation of RNA stability	RT	▮	3	3.8E-1	1.0E0
	Annotation Cluster 117	Enrichment Score: 0.85	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	polyamine biosynthetic process	RT	▮	4	2.2E-2	4.6E-1
☐	INTERPRO	Ornithine decarboxylase	RT	▮	3	4.2E-2	9.9E-1
☐	GOTERM_BP_ALL	polyamine metabolic process	RT	▮	5	6.9E-2	7.6E-1
☐	GOTERM_BP_ALL	biogenic amine biosynthetic process	RT	▮	6	9.1E-2	8.1E-1
☐	SP_PIR_KEYWORDS	Polyamine biosynthesis	RT	▮	3	9.9E-2	5.8E-1
☐	INTERPRO	Orn/DAP/Arg decarboxylase 2	RT	▮	3	1.2E-1	1.0E0
☐	GOTERM_BP_ALL	amino acid derivative biosynthetic process	RT	▮	6	1.6E-1	9.3E-1
☐	SP_PIR_KEYWORDS	decarboxylase	RT	▮	5	1.7E-1	7.7E-1
☐	GOTERM_MF_ALL	carboxy-lyase activity	RT	▮	6	1.8E-1	9.7E-1
☐	GOTERM_MF_ALL	carbon-carbon lyase activity	RT	▮	7	2.4E-1	9.9E-1
☐	GOTERM_BP_ALL	amino acid derivative metabolic process	RT	▮	11	3.8E-1	9.9E-1
☐	KEGG_PATHWAY	Urea cycle and metabolism of amino groups	RT	▮	5	5.0E-1	9.4E-1
☐	GOTERM_BP_ALL	biogenic amine metabolic process	RT	▮	8	5.9E-1	1.0E0
	Annotation Cluster 118	Enrichment Score: 0.85	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	superoxide dismutase activity	RT	▮	4	5.7E-2	8.2E-1
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on superoxide radicals as acceptor	RT	▮	4	5.7E-2	8.2E-1
☐	GOTERM_MF_ALL	copper, zinc superoxide dismutase	RT	▮	3	1.3E-1	9.4E-1

		activity						
☐	GOTERM_BP_ALL	superoxide metabolic process	RT			4	3.2E-1	9.9E-1
☐	GOTERM_BP_ALL	oxygen and reactive oxygen species metabolic process	RT			5	4.4E-1	1.0E0
	Annotation Cluster 119	Enrichment Score: 0.84		G	🟩	Count	P_Value	Benjamini
☐	SMART	TPR	RT			16	8.0E-3	3.8E-1
☐	INTERPRO	Tetratricopeptide region	RT			16	2.5E-2	9.7E-1
☐	INTERPRO	Tetratricopeptide TPR-1	RT			13	4.1E-2	9.9E-1
☐	SP_PIR_KEYWORDS	TPR repeat	RT			17	5.5E-2	4.2E-1
☐	INTERPRO	Tetratricopeptide-like helical	RT			16	6.0E-2	1.0E0
☐	INTERPRO	Tetratricopeptide TPR2	RT			8	1.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 3	RT			9	1.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 2	RT			9	2.4E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 1	RT			9	2.4E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 9	RT			3	2.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 8	RT			4	3.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 4	RT			6	3.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 7	RT			4	5.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 6	RT			4	5.7E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 5	RT			4	5.9E-1	1.0E0
	Annotation Cluster 120	Enrichment Score: 0.83		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	anti-apoptosis	RT			18	1.8E-2	4.2E-1
☐	GOTERM_BP_ALL	negative regulation of programmed cell death	RT			25	1.3E-1	8.9E-1
☐	GOTERM_BP_ALL	negative regulation of apoptosis	RT			24	1.6E-1	9.3E-1
☐	GOTERM_BP_ALL	regulation of programmed cell death	RT			47	4.1E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of apoptosis	RT			46	4.3E-1	1.0E0
	Annotation Cluster 121	Enrichment Score: 0.83		G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	proteasome	RT			14	8.2E-4	1.6E-2
☐	KEGG_PATHWAY	Proteasome	RT			8	5.4E-2	4.8E-1
☐	GOTERM_CC_ALL	proteasome complex (sensu Eukaryota)	RT			6	1.7E-1	7.0E-1
☐	INTERPRO	Peptidase T1A, proteasome beta-subunit	RT			3	2.9E-1	1.0E0
☐	INTERPRO	20S proteasome, A and B subunits	RT			3	5.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	Threonine protease	RT			3	5.6E-1	9.8E-1
☐	GOTERM_CC_ALL	proteasome core complex (sensu Eukaryota)	RT			3	5.8E-1	9.8E-1
☐	GOTERM_MF_ALL	threonine endopeptidase activity	RT			3	6.1E-1	1.0E0
	Annotation Cluster 122	Enrichment Score: 0.81		G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	porin	RT			8	1.4E-2	1.6E-1
☐	GOTERM_CC_ALL	outer membrane	RT			14	2.7E-2	2.3E-1
☐	GOTERM_MF_ALL	porin activity	RT			6	9.6E-2	8.9E-1
☐	GOTERM_MF_ALL	wide pore channel activity	RT			6	3.8E-1	1.0E0
☐	GOTERM_MF_ALL	passive transmembrane transporter activity	RT			13	1.0E0	1.0E0
☐	GOTERM_MF_ALL	channel activity	RT			13	1.0E0	1.0E0
	Annotation Cluster 123	Enrichment Score: 0.8		G	🟩	Count	P_Value	Benjamini
☐	BIOCARTA	RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage	RT			5	4.6E-2	6.4E-1
☐	GOTERM_MF_ALL	cyclin-dependent protein kinase activity	RT			6	1.2E-1	9.4E-1
☐	PIR_SUPERFAMILY	PIRSF000564:kinase-related transforming protein	RT			4	7.0E-1	1.0E0
	Annotation Cluster 124	Enrichment Score: 0.8		G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	lysosome	RT			17	7.1E-2	4.8E-1
☐	GOTERM_CC_ALL	vacuole	RT			24	1.8E-1	7.0E-1

☐	GOTERM_CC_ALL	lysosome	RT		21	2.3E-1	7.7E-1
☐	GOTERM_CC_ALL	lytic vacuole	RT		21	2.3E-1	7.7E-1
	Annotation Cluster 125	Enrichment Score: 0.78	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	repeat:1-1	RT		4	1.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:2-1	RT		4	1.5E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:1-2	RT		4	1.7E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:2-2	RT		4	1.7E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:1-3	RT		3	2.0E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:2-3	RT		3	2.0E-1	1.0E0
	Annotation Cluster 126	Enrichment Score: 0.78	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	transferase activity	RT		211	6.3E-5	9.3E-3
☐	SP_PIR_KEYWORDS	transferase	RT		152	1.2E-3	2.0E-2
☐	GOTERM_MF_ALL	transferase activity, transferring phosphorus-containing groups	RT		120	2.8E-3	1.4E-1
☐	GOTERM_MF_ALL	kinase activity	RT		95	6.9E-2	8.6E-1
☐	SMART	S_TKc	RT		33	1.4E-1	9.8E-1
☐	INTERPRO	Serine/threonine protein kinase	RT		24	1.6E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase, active site	RT		28	1.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	kinase	RT		71	2.9E-1	8.9E-1
☐	SP_PIR_KEYWORDS	Serine/threonine-protein kinase	RT		36	3.5E-1	9.3E-1
☐	UP_SEQ_FEATURE	binding site:ATP	RT		42	3.7E-1	1.0E0
☐	UP_SEQ_FEATURE	active site:Proton acceptor	RT		50	5.6E-1	1.0E0
☐	GOTERM_MF_ALL	phosphotransferase activity, alcohol group as acceptor	RT		64	5.9E-1	1.0E0
☐	GOTERM_BP_ALL	phosphate metabolic process	RT		80	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	phosphorus metabolic process	RT		80	6.1E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Protein kinase	RT		35	6.4E-1	1.0E0
☐	INTERPRO	Protein kinase, core	RT		30	6.6E-1	1.0E0
☐	GOTERM_MF_ALL	protein serine/threonine kinase activity	RT		42	7.2E-1	1.0E0
☐	GOTERM_MF_ALL	protein kinase activity	RT		51	7.8E-1	1.0E0
☐	GOTERM_BP_ALL	phosphorylation	RT		63	7.9E-1	1.0E0
☐	GOTERM_MF_ALL	protein-tyrosine kinase activity	RT		23	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid phosphorylation	RT		49	9.5E-1	1.0E0
	Annotation Cluster 127	Enrichment Score: 0.74	G	🟩	Count	P_Value	Benjamini
☐	SMART	PHB	RT		3	1.6E-1	9.8E-1
☐	PIR_SUPERFAMILY	PIRSF005651:membrane protease subunits, stomatin/prohibitin homologs	RT		3	1.7E-1	1.0E0
☐	INTERPRO	Band 7 protein	RT		3	2.2E-1	1.0E0
	Annotation Cluster 128	Enrichment Score: 0.74	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	centrosome organization and biogenesis	RT		4	1.4E-1	9.0E-1
☐	GOTERM_BP_ALL	microtubule organizing center organization and biogenesis	RT		4	1.6E-1	9.3E-1
☐	GOTERM_BP_ALL	centrosome cycle	RT		3	2.8E-1	9.8E-1
	Annotation Cluster 129	Enrichment Score: 0.69	G	🟩	Count	P_Value	Benjamini
☐	SMART	DSRM	RT		5	9.5E-2	9.5E-1
☐	INTERPRO	Double-stranded RNA-binding-like	RT		4	2.3E-1	1.0E0
☐	GOTERM_MF_ALL	double-stranded RNA binding	RT		6	2.5E-1	9.9E-1
☐	INTERPRO	Double-stranded RNA binding	RT		4	3.1E-1	1.0E0
	Annotation Cluster 130	Enrichment Score: 0.69	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	double-strand break repair	RT		5	2.0E-1	9.6E-1
☐	GOTERM_BP_ALL	recombinational repair	RT		3	2.0E-1	9.6E-1
☐	GOTERM_BP_ALL	double-strand break repair via homologous recombination	RT		3	2.0E-1	9.6E-1

	Annotation Cluster 131	Enrichment Score: 0.67	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	chromosome organization and biogenesis	RT	43	2.0E-2	4.4E-1
☐	GOTERM_BP_ALL	DNA packaging	RT	28	2.8E-1	9.8E-1
☐	GOTERM_BP_ALL	establishment and/or maintenance of chromatin architecture	RT	26	3.8E-1	9.9E-1
☐	GOTERM_BP_ALL	chromatin modification	RT	19	4.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	Chromatin regulator	RT	11	4.8E-1	9.7E-1
	Annotation Cluster 132	Enrichment Score: 0.67	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of cellular component organization and biogenesis	RT	9	3.5E-2	5.8E-1
☐	GOTERM_BP_ALL	microtubule polymerization or depolymerization	RT	4	2.1E-1	9.6E-1
☐	GOTERM_BP_ALL	microtubule depolymerization	RT	3	3.5E-1	9.9E-1
☐	GOTERM_BP_ALL	negative regulation of microtubule polymerization or depolymerization	RT	3	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of microtubule polymerization or depolymerization	RT	3	4.5E-1	1.0E0
	Annotation Cluster 133	Enrichment Score: 0.66	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell proliferation	RT	64	6.2E-2	7.3E-1
☐	GOTERM_BP_ALL	positive regulation of cell proliferation	RT	23	3.5E-1	9.9E-1
☐	GOTERM_BP_ALL	regulation of cell proliferation	RT	38	4.7E-1	1.0E0
	Annotation Cluster 134	Enrichment Score: 0.66	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	metal ion-binding site:Manganese	RT	6	6.0E-2	1.0E0
☐	GOTERM_MF_ALL	manganese ion binding	RT	16	2.1E-1	9.8E-1
☐	SP_PIR_KEYWORDS	Manganese	RT	15	2.3E-1	8.4E-1
☐	GOTERM_MF_ALL	UDP-glycosyltransferase activity	RT	8	8.0E-1	1.0E0
	Annotation Cluster 135	Enrichment Score: 0.65	G	Count	P_Value	Benjamini
☐	INTERPRO	Importin-beta, N-terminal	RT	5	3.8E-2	9.9E-1
☐	GOTERM_BP_ALL	protein import into nucleus, docking	RT	5	4.6E-2	6.5E-1
☐	UP_SEQ_FEATURE	domain:Importin N-terminal	RT	4	1.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:HEAT 6	RT	4	2.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:HEAT 5	RT	4	3.5E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:HEAT 4	RT	4	4.0E-1	1.0E0
☐	GOTERM_BP_ALL	cellular protein complex assembly	RT	6	4.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:HEAT 3	RT	4	4.3E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:HEAT 1	RT	4	4.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:HEAT 2	RT	4	4.6E-1	1.0E0
	Annotation Cluster 136	Enrichment Score: 0.65	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	er-golgi transport	RT	12	2.5E-2	2.5E-1
☐	GOTERM_BP_ALL	ER to Golgi vesicle-mediated transport	RT	10	9.1E-2	8.1E-1
☐	GOTERM_BP_ALL	Golgi vesicle transport	RT	12	1.9E-1	9.5E-1
☐	GOTERM_BP_ALL	secretion by cell	RT	27	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	secretion	RT	29	7.5E-1	1.0E0
☐	GOTERM_BP_ALL	secretory pathway	RT	20	7.6E-1	1.0E0
	Annotation Cluster 137	Enrichment Score: 0.65	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	poly(A) binding	RT	3	1.3E-1	9.4E-1
☐	GOTERM_MF_ALL	mRNA binding	RT	6	2.1E-1	9.8E-1
☐	GOTERM_MF_ALL	single-stranded RNA binding	RT	3	4.1E-1	1.0E0
	Annotation Cluster 138	Enrichment Score: 0.65	G	Count	P_Value	Benjamini
☐	INTERPRO	Flavodoxin-like fold	RT	3	2.2E-2	9.6E-1
☐	GOTERM_MF_ALL	NAD(P)H dehydrogenase (quinone) activity	RT	3	2.4E-2	5.8E-1
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor	RT	7	2.0E-1	9.8E-1

☐	GOTERM_MF_ALL	oxidoreductase activity, acting on NADH or NADPH	RT	8	3.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	ubiquinone	RT	5	4.9E-1	9.7E-1
☐	GOTERM_MF_ALL	NADH dehydrogenase activity	RT	4	7.1E-1	1.0E0
☐	GOTERM_MF_ALL	NADH dehydrogenase (quinone) activity	RT	4	7.1E-1	1.0E0
☐	GOTERM_MF_ALL	NADH dehydrogenase (ubiquinone) activity	RT	4	7.1E-1	1.0E0
	Annotation Cluster 139	Enrichment Score: 0.63	G	Count	P_Value	Benjamini
☐	INTERPRO	MAP kinase phosphatase	RT	4	3.9E-2	9.9E-1
☐	SMART	RHOD	RT	5	5.5E-2	9.0E-1
☐	INTERPRO	Dual specificity protein phosphatase (MAP kinase phosphatase)	RT	3	6.5E-2	9.9E-1
☐	GOTERM_MF_ALL	MAP kinase phosphatase activity	RT	4	7.3E-2	8.5E-1
☐	GOTERM_MF_ALL	MAP kinase tyrosine/serine/threonine phosphatase activity	RT	4	7.3E-2	8.5E-1
☐	UP_SEQ_FEATURE	domain:Rhodanese	RT	4	1.2E-1	1.0E0
☐	GOTERM_MF_ALL	phosphoric monoester hydrolase activity	RT	28	1.5E-1	9.6E-1
☐	SMART	DSPc	RT	5	1.9E-1	9.9E-1
☐	GOTERM_MF_ALL	phosphoprotein phosphatase activity	RT	18	2.3E-1	9.9E-1
☐	INTERPRO	Rhodanese-like	RT	4	2.3E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid dephosphorylation	RT	15	2.6E-1	9.8E-1
☐	INTERPRO	Protein-tyrosine phosphatase, dual specificity	RT	5	2.7E-1	1.0E0
☐	GOTERM_MF_ALL	protein tyrosine/serine/threonine phosphatase activity	RT	6	2.8E-1	9.9E-1
☐	GOTERM_MF_ALL	protein tyrosine phosphatase activity	RT	11	3.0E-1	1.0E0
☐	GOTERM_MF_ALL	hydrolase activity, acting on ester bonds	RT	61	3.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	protein phosphatase	RT	12	3.9E-1	9.4E-1
☐	INTERPRO	Protein-tyrosine phosphatase, Tyr-specific/dual-specificity type	RT	9	4.1E-1	1.0E0
☐	GOTERM_MF_ALL	phosphoric ester hydrolase activity	RT	30	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	dephosphorylation	RT	15	4.3E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Tyrosine-protein phosphatase	RT	6	4.7E-1	1.0E0
☐	BIOCARTA	Regulation of MAP Kinase Pathways Through Dual Specificity Phosphatases	RT	3	4.9E-1	9.7E-1
☐	UP_SEQ_FEATURE	active site:Phosphocysteine intermediate	RT	7	5.0E-1	1.0E0
☐	SMART	PTPc	RT	3	7.9E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase, receptor/non-receptor type	RT	3	8.7E-1	1.0E0
	Annotation Cluster 140	Enrichment Score: 0.62	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	region of interest:Autoinhibitory domain	RT	3	1.2E-1	1.0E0
☐	GOTERM_MF_ALL	calmodulin-dependent protein kinase activity	RT	4	1.8E-1	9.7E-1
☐	UP_SEQ_FEATURE	region of interest:Calmodulin-binding	RT	5	6.5E-1	1.0E0
	Annotation Cluster 141	Enrichment Score: 0.59	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	repeat:5	RT	11	8.1E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:2	RT	17	1.0E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:3	RT	14	1.1E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:4	RT	12	1.1E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:1	RT	16	1.4E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:6	RT	8	2.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:11	RT	5	3.3E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:8	RT	6	3.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:10	RT	5	3.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:9	RT	5	3.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:13	RT	4	4.6E-1	1.0E0

☐	UP_SEQ_FEATURE	repeat:12	RT		4	4.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:7	RT		6	5.3E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:14	RT		3	6.8E-1	1.0E0
	Annotation Cluster 142	Enrichment Score: 0.59	G	🟩	Count	P_Value	Benjamini
☐	BIOCARTA	Cell Cycle	RT		6	1.6E-1	9.1E-1
☐	BIOCARTA	Role of BRCA1, BRCA2 and ATR in Cancer Susceptibility	RT		5	2.4E-1	9.2E-1
☐	BIOCARTA	ATM Signaling Pathway	RT		4	4.7E-1	9.7E-1
	Annotation Cluster 143	Enrichment Score: 0.59	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Pre-ATP-grasp fold	RT		3	1.5E-1	1.0E0
☐	INTERPRO	ATP-grasp fold	RT		3	3.2E-1	1.0E0
☐	INTERPRO	ATP-grasp fold, subdomain 2	RT		3	3.6E-1	1.0E0
	Annotation Cluster 144	Enrichment Score: 0.58	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	I-kappaB kinase/NF-kappaB cascade	RT		10	1.6E-1	9.3E-1
☐	GOTERM_BP_ALL	positive regulation of I-kappaB kinase/NF-kappaB cascade	RT		7	1.7E-1	9.3E-1
☐	GOTERM_BP_ALL	regulation of I-kappaB kinase/NF-kappaB cascade	RT		7	2.0E-1	9.5E-1
☐	GOTERM_BP_ALL	positive regulation of signal transduction	RT		8	8.9E-1	1.0E0
	Annotation Cluster 145	Enrichment Score: 0.57	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell death	RT		82	5.7E-2	7.2E-1
☐	GOTERM_BP_ALL	death	RT		82	5.7E-2	7.2E-1
☐	SP_PIR_KEYWORDS	apoptosis	RT		32	9.2E-2	5.6E-1
☐	GOTERM_BP_ALL	programmed cell death	RT		77	1.0E-1	8.4E-1
☐	GOTERM_BP_ALL	apoptosis	RT		75	1.2E-1	8.7E-1
☐	GOTERM_BP_ALL	regulation of programmed cell death	RT		47	4.1E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of apoptosis	RT		46	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	cell development	RT		106	8.9E-1	1.0E0
☐	GOTERM_BP_ALL	cell differentiation	RT		149	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	cellular developmental process	RT		149	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	developmental process	RT		226	1.0E0	1.0E0
	Annotation Cluster 146	Enrichment Score: 0.55	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	methylation-dependent chromatin silencing	RT		3	7.3E-2	7.7E-1
☐	GOTERM_BP_ALL	chromatin remodeling	RT		9	7.7E-2	7.8E-1
☐	GOTERM_BP_ALL	regulation of gene expression, epigenetic	RT		8	2.7E-1	9.8E-1
☐	GOTERM_BP_ALL	covalent chromatin modification	RT		7	3.1E-1	9.9E-1
☐	GOTERM_BP_ALL	gene silencing	RT		5	4.4E-1	1.0E0
☐	GOTERM_BP_ALL	chromatin silencing	RT		3	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	heterochromatin formation	RT		3	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	chromatin assembly	RT		8	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of gene expression, epigenetic	RT		3	5.4E-1	1.0E0
	Annotation Cluster 147	Enrichment Score: 0.53	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	blocked amino end	RT		8	7.0E-2	4.8E-1
☐	SMART	ARF	RT		4	2.0E-1	9.9E-1
☐	SP_PIR_KEYWORDS	myristylation	RT		5	2.5E-1	8.6E-1
☐	INTERPRO	ADP-ribosylation factor	RT		4	2.6E-1	1.0E0
☐	INTERPRO	ARF/SAR superfamily	RT		4	4.6E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001711:ADP-ribosylation factor	RT		4	5.1E-1	1.0E0
☐	UP_SEQ_FEATURE	lipid moiety-binding region:N-myristoyl glycine	RT		5	9.6E-1	1.0E0
	Annotation Cluster 148	Enrichment Score: 0.52	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cellular response to stimulus	RT		6	1.5E-1	9.1E-1

☐	GOTERM_BP_ALL	cellular response to extracellular stimulus	RT	3	3.1E-1	9.9E-1
☐	GOTERM_BP_ALL	response to extracellular stimulus	RT	3	6.0E-1	1.0E0
	Annotation Cluster 149	Enrichment Score: 0.5	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	ruffle	RT	9	6.4E-2	4.1E-1
☐	GOTERM_CC_ALL	leading edge	RT	10	5.2E-1	9.7E-1
☐	GOTERM_CC_ALL	cell projection	RT	26	9.8E-1	1.0E0
	Annotation Cluster 150	Enrichment Score: 0.49	G	Count	P_Value	Benjamini
☐	INTERPRO	Mitochondrial brown fat uncoupling protein	RT	4	8.3E-2	1.0E0
☐	INTERPRO	Mitochondrial substrate carrier	RT	6	2.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:Solcar 2	RT	4	4.0E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:Solcar 1	RT	4	4.0E-1	1.0E0
☐	INTERPRO	Mitochondrial carrier protein	RT	4	4.3E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:Solcar 3	RT	3	6.6E-1	1.0E0
	Annotation Cluster 151	Enrichment Score: 0.49	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	nuclear lamina	RT	4	4.1E-2	3.0E-1
☐	INTERPRO	Intermediate filament, C-terminal	RT	3	4.2E-2	9.9E-1
☐	GOTERM_CC_ALL	lamin filament	RT	3	6.8E-2	4.2E-1
☐	BIOCARTA	Caspase Cascade in Apoptosis	RT	6	1.8E-1	9.2E-1
☐	GOTERM_CC_ALL	nuclear inner membrane	RT	3	2.3E-1	7.7E-1
☐	BIOCARTA	TNFR1 Signaling Pathway	RT	6	3.4E-1	9.5E-1
☐	BIOCARTA	FAS signaling pathway (CD95)	RT	6	3.6E-1	9.5E-1
☐	SP_PIR_KEYWORDS	intermediate filament	RT	5	8.5E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002282:cytoskeletal keratin	RT	4	9.0E-1	1.0E0
☐	INTERPRO	Intermediate filament protein	RT	4	9.4E-1	1.0E0
☐	GOTERM_CC_ALL	intermediate filament	RT	6	9.8E-1	1.0E0
☐	GOTERM_CC_ALL	intermediate filament cytoskeleton	RT	6	9.8E-1	1.0E0
☐	KEGG_PATHWAY	Cell Communication	RT	6	1.0E0	1.0E0
	Annotation Cluster 152	Enrichment Score: 0.49	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	general RNA polymerase II transcription factor activity	RT	4	1.5E-1	9.6E-1
☐	KEGG_PATHWAY	Basal transcription factors	RT	6	2.9E-1	8.3E-1
☐	GOTERM_MF_ALL	RNA polymerase II transcription factor activity	RT	8	7.6E-1	1.0E0
	Annotation Cluster 153	Enrichment Score: 0.49	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	ER-nuclear signaling pathway	RT	6	9.1E-2	8.1E-1
☐	BIOCARTA	Cadmium induces DNA synthesis and proliferation in macrophages	RT	5	1.5E-1	9.2E-1
☐	GOTERM_BP_ALL	cell aging	RT	4	2.4E-1	9.7E-1
☐	BIOCARTA	BTG family proteins and cell cycle regulation	RT	4	2.4E-1	9.1E-1
☐	KEGG_PATHWAY	Thyroid cancer	RT	6	2.7E-1	8.2E-1
☐	BIOCARTA	WNT Signaling Pathway	RT	5	4.3E-1	9.7E-1
☐	BIOCARTA	Regulation of transcriptional activity by PML	RT	4	5.1E-1	9.7E-1
☐	GOTERM_BP_ALL	aging	RT	4	5.7E-1	1.0E0
☐	KEGG_PATHWAY	Endometrial cancer	RT	7	6.0E-1	9.6E-1
☐	KEGG_PATHWAY	Acute myeloid leukemia	RT	6	8.6E-1	1.0E0
	Annotation Cluster 154	Enrichment Score: 0.46	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	vesicle coat	RT	9	6.4E-2	4.1E-1
☐	GOTERM_CC_ALL	coated vesicle membrane	RT	9	8.6E-2	4.7E-1
☐	GOTERM_CC_ALL	cytoplasmic vesicle membrane	RT	10	1.5E-1	6.6E-1
☐	GOTERM_CC_ALL	coated membrane	RT	9	1.5E-1	6.6E-1
☐	GOTERM_CC_ALL	membrane coat	RT	9	1.5E-1	6.6E-1

☐	GOTERM_CC_ALL	clathrin vesicle coat	RT		6	1.9E-1	7.2E-1
☐	UP_SEQ_FEATURE	domain:MHD	RT		3	2.0E-1	1.0E0
☐	GOTERM_CC_ALL	clathrin adaptor complex	RT		5	2.0E-1	7.5E-1
☐	GOTERM_CC_ALL	AP-type membrane coat adaptor complex	RT		5	2.0E-1	7.5E-1
☐	SP_PIR_KEYWORDS	coated pit	RT		5	2.1E-1	8.2E-1
☐	INTERPRO	Clathrin adaptor, mu subunit, C-terminal	RT		3	2.2E-1	1.0E0
☐	GOTERM_CC_ALL	clathrin coated vesicle membrane	RT		6	2.2E-1	7.7E-1
☐	GOTERM_CC_ALL	clathrin coat	RT		6	2.6E-1	8.1E-1
☐	GOTERM_CC_ALL	cytoplasmic vesicle part	RT		10	2.6E-1	8.1E-1
☐	GOTERM_CC_ALL	vesicle membrane	RT		11	2.6E-1	8.1E-1
☐	GOTERM_BP_ALL	protein complex assembly	RT		19	3.3E-1	9.9E-1
☐	INTERPRO	Clathrin/coatomer adaptor, adaptin-like, N-terminal	RT		3	3.6E-1	1.0E0
☐	GOTERM_CC_ALL	transport vesicle membrane	RT		4	4.0E-1	9.2E-1
☐	GOTERM_CC_ALL	coated pit	RT		6	4.0E-1	9.2E-1
☐	GOTERM_CC_ALL	Golgi-associated vesicle membrane	RT		4	4.2E-1	9.3E-1
☐	GOTERM_CC_ALL	Golgi-associated vesicle	RT		6	4.6E-1	9.5E-1
☐	GOTERM_CC_ALL	clathrin coat of trans-Golgi network vesicle	RT		3	4.9E-1	9.6E-1
☐	GOTERM_CC_ALL	trans-Golgi network transport vesicle membrane	RT		3	5.2E-1	9.7E-1
☐	GOTERM_CC_ALL	transport vesicle	RT		5	5.7E-1	9.8E-1
☐	GOTERM_CC_ALL	coated vesicle	RT		11	6.7E-1	9.9E-1
☐	GOTERM_CC_ALL	Golgi apparatus part	RT		15	7.1E-1	9.9E-1
☐	GOTERM_CC_ALL	trans-Golgi network transport vesicle	RT		3	7.2E-1	9.9E-1
☐	GOTERM_CC_ALL	cytoplasmic membrane-bound vesicle	RT		19	8.3E-1	1.0E0
☐	GOTERM_CC_ALL	clathrin-coated vesicle	RT		8	8.4E-1	1.0E0
☐	GOTERM_CC_ALL	cytoplasmic vesicle	RT		26	8.7E-1	1.0E0
☐	GOTERM_CC_ALL	membrane-bound vesicle	RT		19	8.7E-1	1.0E0
☐	GOTERM_CC_ALL	vesicle	RT		26	9.0E-1	1.0E0
☐	GOTERM_CC_ALL	Golgi membrane	RT		6	9.6E-1	1.0E0
	Annotation Cluster 155	Enrichment Score: 0.46	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	repeat:ARM 2	RT		5	1.7E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ARM 3	RT		5	1.7E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ARM 4	RT		4	2.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ARM 8	RT		3	3.6E-1	1.0E0
☐	SMART	ARM	RT		4	4.0E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ARM 6	RT		3	4.4E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ARM 7	RT		3	4.4E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ARM 5	RT		3	4.7E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ARM 1	RT		3	5.1E-1	1.0E0
☐	INTERPRO	Armadillo	RT		4	5.3E-1	1.0E0
	Annotation Cluster 156	Enrichment Score: 0.46	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	GTP-binding	RT		39	7.4E-3	1.0E-1
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	RT		29	6.6E-2	1.0E0
☐	INTERPRO	Small GTP-binding protein domain	RT		17	2.0E-1	1.0E0
☐	SMART	RHO	RT		3	4.6E-1	1.0E0
☐	INTERPRO	Ras GTPase	RT		14	5.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	prenylation	RT		14	5.2E-1	9.8E-1
☐	INTERPRO	Ras small GTPase, Rho type	RT		3	5.7E-1	1.0E0
☐	INTERPRO	Ras	RT		11	5.7E-1	1.0E0

☐	**UP_SEQ_FEATURE**	short sequence motif:Effector region	RT	▮		7	8.7E-1	1.0E0
☐	**UP_SEQ_FEATURE**	lipid moiety-binding region:S-geranylgeranyl cysteine	RT	▮		6	9.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	small GTPase mediated signal transduction	RT	▮		28	9.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	propeptide:Removed in mature form	RT	▮		6	1.0E0	1.0E0
	Annotation Cluster 157	Enrichment Score: 0.46	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	tumor necrosis factor receptor superfamily binding	RT	▮		4	3.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	tumor necrosis factor receptor binding	RT	▮		4	3.0E-1	1.0E0
☐	**SMART**	TNF	RT	▮		3	3.6E-1	1.0E0
☐	**INTERPRO**	Tumor Necrosis Factor	RT	▮		3	4.5E-1	1.0E0
	Annotation Cluster 158	Enrichment Score: 0.46	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	pigment metabolic process	RT	▮		7	1.3E-1	8.9E-1
☐	**GOTERM_BP_ALL**	pigment biosynthetic process	RT	▮		6	1.6E-1	9.3E-1
☐	**GOTERM_BP_ALL**	secondary metabolic process	RT	▮		7	3.6E-1	9.9E-1
☐	**GOTERM_BP_ALL**	heme metabolic process	RT	▮		3	5.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	porphyrin metabolic process	RT	▮		3	6.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	tetrapyrrole metabolic process	RT	▮		3	6.5E-1	1.0E0
	Annotation Cluster 159	Enrichment Score: 0.45	G		🟩	Count	P_Value	Benjamini
☐	**SMART**	UBCc	RT	▮		9	2.5E-2	6.9E-1
☐	**INTERPRO**	Ubiquitin-conjugating enzyme, E2	RT	▮		8	9.9E-2	1.0E0
☐	**GOTERM_MF_ALL**	ligase activity, forming carbon-nitrogen bonds	RT	▮		21	2.2E-1	9.9E-1
☐	**PIR_SUPERFAMILY**	PIRSF001567:ubiquitin-protein ligase E2	RT	▮		4	2.7E-1	1.0E0
☐	**UP_SEQ_FEATURE**	active site:Glycyl thioester intermediate	RT	▮		5	5.0E-1	1.0E0
☐	**KEGG_PATHWAY**	Ubiquitin mediated proteolysis	RT	▮		15	6.6E-1	9.7E-1
☐	**GOTERM_MF_ALL**	acid-amino acid ligase activity	RT	▮		13	7.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	ubiquitin-protein ligase activity	RT	▮		11	7.1E-1	1.0E0
☐	**KEGG_PATHWAY**	Parkinson's disease	RT	▮		3	7.3E-1	9.8E-1
☐	**GOTERM_MF_ALL**	small protein conjugating enzyme activity	RT	▮		11	7.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	small conjugating protein ligase activity	RT	▮		11	7.6E-1	1.0E0
	Annotation Cluster 160	Enrichment Score: 0.43	G		🟩	Count	P_Value	Benjamini
☐	**SMART**	ANX	RT	▮		3	2.8E-1	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF002359:annexin I	RT	▮		3	2.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	annexin	RT	▮		3	3.4E-1	9.2E-1
☐	**INTERPRO**	Annexin	RT	▮		3	3.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	calcium/phospholipid-binding	RT	▮		3	3.7E-1	9.4E-1
☐	**GOTERM_MF_ALL**	calcium-dependent phospholipid binding	RT	▮		3	6.8E-1	1.0E0
	Annotation Cluster 161	Enrichment Score: 0.43	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	ABC transporter related	RT	▮		7	8.4E-2	1.0E0
☐	**UP_SEQ_FEATURE**	domain:ABC transporter 2	RT	▮		3	5.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:ABC transporter 1	RT	▮		3	5.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	nucleotide phosphate-binding region:ATP 2	RT	▮		3	5.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	nucleotide phosphate-binding region:ATP 1	RT	▮		3	5.4E-1	1.0E0
	Annotation Cluster 162	Enrichment Score: 0.43	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	positive regulation of myeloid leukocyte differentiation	RT	▮		5	1.5E-2	3.7E-1
☐	**GOTERM_BP_ALL**	positive regulation of osteoclast differentiation	RT	▮		4	2.2E-2	4.6E-1
☐	**GOTERM_BP_ALL**	positive regulation of myeloid cell differentiation	RT	▮		6	3.4E-2	5.8E-1
☐	**GOTERM_BP_ALL**	regulation of myeloid leukocyte differentiation	RT	▮		6	7.9E-2	7.8E-1
☐	**GOTERM_BP_ALL**	regulation of osteoclast differentiation	RT	▮		5	1.1E-1	8.6E-1

☐	GOTERM_BP_ALL	regulation of myeloid cell differentiation	RT		8	1.5E-1	9.1E-1
☐	GOTERM_BP_ALL	myeloid leukocyte differentiation	RT		8	1.9E-1	9.5E-1
☐	GOTERM_BP_ALL	osteoclast differentiation	RT		5	2.0E-1	9.6E-1
☐	GOTERM_BP_ALL	myeloid cell differentiation	RT		14	2.6E-1	9.8E-1
☐	GOTERM_BP_ALL	hemopoiesis	RT		24	5.4E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of developmental process	RT		9	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cell differentiation	RT		6	6.6E-1	1.0E0
☐	GOTERM_BP_ALL	immune system development	RT		26	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	hemopoietic or lymphoid organ development	RT		24	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	leukocyte differentiation	RT		13	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	bone mineralization	RT		3	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	immune system process	RT		60	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	cartilage development	RT		3	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	ossification	RT		6	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	biomineral formation	RT		6	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	bone remodeling	RT		6	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell differentiation	RT		11	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	skeletal development	RT		11	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of developmental process	RT		18	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	tissue development	RT		18	1.0E0	1.0E0
☐	GOTERM_BP_ALL	tissue remodeling	RT		6	1.0E0	1.0E0
	Annotation Cluster 163	Enrichment Score: 0.41	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Poly(ADP-ribose) polymerase, catalytic region	RT		3	3.6E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid ADP-ribosylation	RT		4	3.7E-1	9.9E-1
☐	GOTERM_MF_ALL	NAD+ ADP-ribosyltransferase activity	RT		3	4.4E-1	1.0E0
	Annotation Cluster 164	Enrichment Score: 0.41	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	in utero embryonic development	RT		16	1.9E-1	9.5E-1
☐	GOTERM_BP_ALL	chordate embryonic development	RT		24	3.3E-1	9.9E-1
☐	GOTERM_BP_ALL	embryonic development ending in birth or egg hatching	RT		24	3.6E-1	9.9E-1
☐	GOTERM_BP_ALL	embryonic development	RT		34	9.5E-1	1.0E0
	Annotation Cluster 165	Enrichment Score: 0.41	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	protein dimerization activity	RT		32	1.6E-1	9.6E-1
☐	GOTERM_MF_ALL	protein homodimerization activity	RT		15	4.8E-1	1.0E0
☐	GOTERM_MF_ALL	identical protein binding	RT		24	7.7E-1	1.0E0
	Annotation Cluster 166	Enrichment Score: 0.4	G	🟩	Count	P_Value	Benjamini
☐	BIOCARTA	How Progesterone Initiates the Oocyte Maturation	RT		10	1.6E-3	8.5E-2
☐	SP_PIR_KEYWORDS	GTP binding	RT		9	4.0E-2	3.4E-1
☐	BIOCARTA	Signaling Pathway from G-Protein Families	RT		8	5.5E-2	6.8E-1
☐	GOTERM_CC_ALL	heterotrimeric G-protein complex	RT		7	1.2E-1	6.0E-1
☐	BIOCARTA	Corticosteroids and cardioprotection	RT		5	1.8E-1	9.3E-1
☐	INTERPRO	Guanine nucleotide binding protein (G-protein), alpha subunit	RT		4	1.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	thiolester bond	RT		4	2.0E-1	8.1E-1
☐	BIOCARTA	CCR3 signaling in Eosinophils	RT		6	2.0E-1	9.1E-1
☐	GOTERM_CC_ALL	extrinsic to plasma membrane	RT		8	2.7E-1	8.1E-1
☐	BIOCARTA	CXCR4 Signaling Pathway	RT		6	2.8E-1	9.4E-1
☐	BIOCARTA	Activation of cAMP-dependent protein kinase, PKA	RT		3	2.9E-1	9.4E-1
☐	BIOCARTA	Attenuation of GPCR Signaling	RT		3	2.9E-1	9.4E-1

☐	**BIOCARTA**	Roles of ?-arrestin-dependent Recruitment of Src Kinases in GPCR Signaling	RT	5	3.3E-1	9.5E-1
☐	**BIOCARTA**	ChREBP regulation by carbohydrates and cAMP	RT	3	3.4E-1	9.4E-1
☐	**INTERPRO**	G protein alpha subunit, helical insertion	RT	3	3.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	signal transduction	RT	3	4.1E-1	9.5E-1
☐	**SP_PIR_KEYWORDS**	heterotrimer	RT	4	4.3E-1	9.6E-1
☐	**BIOCARTA**	Erk1/Erk2 Mapk Signaling pathway	RT	6	4.8E-1	9.7E-1
☐	**BIOCARTA**	?-arrestins in GPCR Desensitization	RT	3	4.9E-1	9.7E-1
☐	**PIR_SUPERFAMILY**	PIRSF002400:GTP-binding regulatory protein Gs alpha chain	RT	3	4.9E-1	1.0E0
☐	**GOTERM_CC_ALL**	extrinsic to membrane	RT	8	5.7E-1	9.8E-1
☐	**BIOCARTA**	Transcription factor CREB and its extracellular signals	RT	4	6.1E-1	9.7E-1
☐	**BIOCARTA**	fMLP induced chemokine gene expression in HMC-1 cells	RT	5	6.3E-1	9.8E-1
☐	**BIOCARTA**	T Cell Receptor Signaling Pathway	RT	6	6.5E-1	9.8E-1
☐	**BIOCARTA**	NFAT and Hypertrophy of the heart (Transcription in the broken heart)	RT	6	6.9E-1	9.8E-1
☐	**BIOCARTA**	Role of ?-arrestins in the activation and targeting of MAP kinases	RT	3	7.1E-1	9.9E-1
☐	**BIOCARTA**	Bioactive Peptide Induced Signaling Pathway	RT	5	7.4E-1	9.9E-1
☐	**GOTERM_BP_ALL**	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	RT	4	7.5E-1	1.0E0
☐	**BIOCARTA**	Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor	RT	3	7.7E-1	9.9E-1
☐	**GOTERM_BP_ALL**	phosphoinositide-mediated signaling	RT	5	7.8E-1	1.0E0
☐	**BIOCARTA**	BCR Signaling Pathway	RT	4	8.0E-1	9.9E-1
☐	**BIOCARTA**	Fc Epsilon Receptor I Signaling in Mast Cells	RT	4	8.5E-1	1.0E0
☐	**KEGG_PATHWAY**	Taste transduction	RT	3	8.7E-1	1.0E0
☐	**BIOCARTA**	Links between Pyk2 and Map Kinases	RT	3	9.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	second-messenger-mediated signaling	RT	10	9.4E-1	1.0E0
☐	**BIOCARTA**	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling	RT	3	9.4E-1	1.0E0
☐	**KEGG_PATHWAY**	Long-term depression	RT	6	9.5E-1	1.0E0
☐	**KEGG_PATHWAY**	GnRH signaling pathway	RT	7	9.7E-1	1.0E0
☐	**KEGG_PATHWAY**	Melanogenesis	RT	7	9.8E-1	1.0E0
☐	**KEGG_PATHWAY**	Long-term potentiation	RT	3	1.0E0	1.0E0
☐	**KEGG_PATHWAY**	Calcium signaling pathway	RT	9	1.0E0	1.0E0
	Annotation Cluster 167	Enrichment Score: 0.4	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of lipid kinase activity	RT	5	1.0E-2	2.9E-1
☐	**GOTERM_BP_ALL**	negative regulation of catalytic activity	RT	9	2.2E-1	9.7E-1
☐	**GOTERM_BP_ALL**	inactivation of MAPK activity	RT	3	2.8E-1	9.8E-1
☐	**GOTERM_BP_ALL**	negative regulation of protein kinase activity	RT	7	2.8E-1	9.8E-1
☐	**GOTERM_BP_ALL**	negative regulation of kinase activity	RT	7	2.8E-1	9.8E-1
☐	**GOTERM_BP_ALL**	negative regulation of MAP kinase activity	RT	4	2.9E-1	9.8E-1
☐	**GOTERM_BP_ALL**	negative regulation of transferase activity	RT	7	3.1E-1	9.9E-1
☐	**GOTERM_BP_ALL**	regulation of a molecular function	RT	42	3.7E-1	9.9E-1
☐	**GOTERM_BP_ALL**	regulation of kinase activity	RT	18	5.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of MAP kinase activity	RT	8	5.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of catalytic activity	RT	35	5.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of transferase activity	RT	18	5.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of protein kinase activity	RT	15	7.4E-1	1.0E0

☐	GOTERM_BP_ALL	activation of MAPK activity	RT	3	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of kinase activity	RT	8	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of MAP kinase activity	RT	3	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of transferase activity	RT	8	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of protein kinase activity	RT	6	9.8E-1	1.0E0
	Annotation Cluster 168	Enrichment Score: 0.4	G	Count	P_Value	Benjamini
☐	BIOCARTA	Signaling Pathway from G-Protein Families	RT	8	5.5E-2	6.8E-1
☐	GOTERM_BP_ALL	regulation of neuron apoptosis	RT	9	7.7E-2	7.8E-1
☐	BIOCARTA	Regulation of Splicing through Sam68	RT	4	1.0E-1	8.6E-1
☐	BIOCARTA	METS affect on Macrophage Differentiation	RT	6	1.1E-1	8.7E-1
☐	GOTERM_BP_ALL	neuron apoptosis	RT	9	1.3E-1	8.9E-1
☐	BIOCARTA	Cadmium induces DNA synthesis and proliferation in macrophages	RT	5	1.5E-1	9.2E-1
☐	GOTERM_BP_ALL	negative regulation of neuron apoptosis	RT	6	1.6E-1	9.3E-1
☐	BIOCARTA	IL 6 signaling pathway	RT	6	2.0E-1	9.1E-1
☐	SP_PIR_KEYWORDS	proto-oncogene	RT	11	2.8E-1	8.8E-1
☐	BIOCARTA	IGF-1 Signaling Pathway	RT	5	3.3E-1	9.5E-1
☐	BIOCARTA	TPO Signaling Pathway	RT	5	4.3E-1	9.7E-1
☐	BIOCARTA	Insulin Signaling Pathway	RT	5	4.3E-1	9.7E-1
☐	BIOCARTA	Nerve growth factor pathway (NGF)	RT	4	5.1E-1	9.7E-1
☐	BIOCARTA	Role of EGF Receptor Transactivation by GPCRs in Cardiac Hypertrophy	RT	4	5.1E-1	9.7E-1
☐	KEGG_PATHWAY	Renal cell carcinoma	RT	10	5.1E-1	9.4E-1
☐	BIOCARTA	Signaling of Hepatocyte Growth Factor Receptor	RT	6	5.5E-1	9.7E-1
☐	BIOCARTA	PDGF Signaling Pathway	RT	5	5.8E-1	9.7E-1
☐	BIOCARTA	EGF Signaling Pathway	RT	5	5.8E-1	9.7E-1
☐	KEGG_PATHWAY	Endometrial cancer	RT	7	6.0E-1	9.6E-1
☐	BIOCARTA	IL-2 Receptor Beta Chain in T cell Activation	RT	6	6.0E-1	9.8E-1
☐	BIOCARTA	EPO Signaling Pathway	RT	4	6.1E-1	9.7E-1
☐	BIOCARTA	Inhibition of Cellular Proliferation by Gleevec	RT	4	6.1E-1	9.7E-1
☐	BIOCARTA	T Cell Receptor Signaling Pathway	RT	6	6.5E-1	9.8E-1
☐	BIOCARTA	IL 2 signaling pathway	RT	4	6.9E-1	9.8E-1
☐	BIOCARTA	Sprouty regulation of tyrosine kinase signals	RT	3	7.1E-1	9.9E-1
☐	BIOCARTA	IL 3 signaling pathway	RT	3	7.4E-1	9.9E-1
☐	BIOCARTA	BCR Signaling Pathway	RT	4	8.0E-1	9.9E-1
☐	KEGG_PATHWAY	Insulin signaling pathway	RT	14	8.1E-1	9.9E-1
☐	BIOCARTA	Fc Epsilon Receptor I Signaling in Mast Cells	RT	4	8.5E-1	1.0E0
☐	KEGG_PATHWAY	Acute myeloid leukemia	RT	6	8.6E-1	1.0E0
☐	KEGG_PATHWAY	ErbB signaling pathway	RT	7	9.5E-1	1.0E0
☐	BIOCARTA	MAPKinase Signaling Pathway	RT	7	9.8E-1	1.0E0
	Annotation Cluster 169	Enrichment Score: 0.4	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	blastocyst development	RT	6	2.3E-1	9.7E-1
☐	GOTERM_BP_ALL	blastocyst growth	RT	3	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	developmental growth	RT	5	7.3E-1	1.0E0
	Annotation Cluster 170	Enrichment Score: 0.38	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	DNA-directed RNA polymerase complex	RT	3	4.0E-1	9.2E-1
☐	GOTERM_CC_ALL	nuclear DNA-directed RNA polymerase complex	RT	3	4.0E-1	9.2E-1
☐	GOTERM_CC_ALL	RNA polymerase complex	RT	3	4.6E-1	9.5E-1
	Annotation Cluster 171	Enrichment Score: 0.36	G	Count	P_Value	Benjamini

☐	**BIOCARTA**	IL 6 signaling pathway	RT		6	2.0E-1	9.1E-1
☐	**INTERPRO**	Basic leucine zipper	RT		3	4.8E-1	1.0E0
☐	**SMART**	BRLZ	RT		5	5.5E-1	1.0E0
☐	**INTERPRO**	Basic-leucine zipper (bZIP) transcription factor	RT		5	6.6E-1	1.0E0
	Annotation Cluster 172	Enrichment Score: 0.36	G	🟩	Count	P_Value	Benjamini
☐	**SMART**	CBS	RT		3	3.9E-1	1.0E0
☐	**INTERPRO**	Cystathionine beta-synthase, core	RT		3	4.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:CBS 1	RT		3	4.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:CBS 2	RT		3	4.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	cbs domain	RT		3	5.0E-1	9.7E-1
	Annotation Cluster 173	Enrichment Score: 0.36	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	estrogen receptor signaling pathway	RT		3	1.7E-1	9.3E-1
☐	**GOTERM_BP_ALL**	intracellular receptor-mediated signaling pathway	RT		4	6.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	steroid hormone receptor signaling pathway	RT		3	7.5E-1	1.0E0
	Annotation Cluster 174	Enrichment Score: 0.36	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	acetyl-CoA metabolic process	RT		6	2.5E-1	9.7E-1
☐	**GOTERM_BP_ALL**	cellular respiration	RT		5	3.5E-1	9.9E-1
☐	**GOTERM_BP_ALL**	cofactor catabolic process	RT		5	4.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	tricarboxylic acid cycle	RT		4	4.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	acetyl-CoA catabolic process	RT		4	4.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	aerobic respiration	RT		4	4.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Tricarboxylic acid cycle	RT		3	5.6E-1	9.8E-1
☐	**GOTERM_BP_ALL**	coenzyme catabolic process	RT		4	5.7E-1	1.0E0
☐	**KEGG_PATHWAY**	Citrate cycle (TCA cycle)	RT		4	5.8E-1	9.5E-1
	Annotation Cluster 175	Enrichment Score: 0.35	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		381	9.1E-7	1.4E-4
☐	**GOTERM_BP_ALL**	gene expression	RT		296	2.5E-1	9.7E-1
☐	**GOTERM_BP_ALL**	RNA metabolic process	RT		250	2.6E-1	9.8E-1
☐	**GOTERM_MF_ALL**	nucleic acid binding	RT		280	5.5E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Transcription	RT		114	7.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	DNA binding	RT		165	9.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Transcription regulation	RT		103	9.5E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	dna-binding	RT		102	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cellular process	RT		306	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	biological regulation	RT		373	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	regulation of biological process	RT		336	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	transcription regulator activity	RT		84	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	regulation of metabolic process	RT		191	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	transcription	RT		166	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	RNA biosynthetic process	RT		152	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	transcription factor activity	RT		52	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		161	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	transcription, DNA-dependent	RT		150	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cellular metabolic process	RT		174	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	regulation of transcription	RT		152	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	regulation of transcription, DNA-dependent	RT		143	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	regulation of gene expression	RT		163	1.0E0	1.0E0

	Annotation Cluster 176	Enrichment Score: 0.35	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	chaperone cofactor-dependent protein folding	RT	3	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	'de novo' protein folding	RT	3	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	'de novo' posttranslational protein folding	RT	3	4.8E-1	1.0E0
	Annotation Cluster 177	Enrichment Score: 0.34	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of nucleocytoplasmic transport	RT	4	2.9E-1	9.8E-1
☐	GOTERM_BP_ALL	regulation of intracellular protein transport	RT	3	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of protein import into nucleus	RT	3	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of intracellular transport	RT	3	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of protein transport	RT	3	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of transport	RT	6	9.8E-1	1.0E0
	Annotation Cluster 178	Enrichment Score: 0.34	G 🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Iron transport	RT	4	2.8E-1	8.8E-1
☐	GOTERM_BP_ALL	transition metal ion transport	RT	8	3.0E-1	9.9E-1
☐	GOTERM_BP_ALL	iron ion transport	RT	4	5.2E-1	1.0E0
☐	GOTERM_BP_ALL	di-, tri-valent inorganic cation transport	RT	6	1.0E0	1.0E0
	Annotation Cluster 179	Enrichment Score: 0.34	G 🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	translation regulation	RT	5	2.8E-1	8.8E-1
☐	GOTERM_BP_ALL	regulation of protein metabolic process	RT	30	3.3E-1	9.9E-1
☐	GOTERM_BP_ALL	regulation of biosynthetic process	RT	19	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of translation	RT	14	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cellular biosynthetic process	RT	15	7.0E-1	1.0E0
	Annotation Cluster 180	Enrichment Score: 0.33	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	positive regulation of apoptosis	RT	23	3.4E-1	9.9E-1
☐	GOTERM_BP_ALL	positive regulation of programmed cell death	RT	23	3.6E-1	9.9E-1
☐	GOTERM_BP_ALL	regulation of programmed cell death	RT	47	4.1E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of apoptosis	RT	46	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	induction of apoptosis	RT	15	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	induction of programmed cell death	RT	15	6.9E-1	1.0E0
	Annotation Cluster 181	Enrichment Score: 0.31	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	chromatin assembly or disassembly	RT	14	1.8E-1	9.4E-1
☐	GOTERM_BP_ALL	chromatin assembly	RT	8	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	protein-DNA complex assembly	RT	8	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	nucleosome assembly	RT	5	8.0E-1	1.0E0
	Annotation Cluster 182	Enrichment Score: 0.31	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	phospholipid biosynthetic process	RT	11	9.5E-2	8.3E-1
☐	GOTERM_BP_ALL	phosphoinositide biosynthetic process	RT	5	2.0E-1	9.6E-1
☐	GOTERM_BP_ALL	glycerophospholipid biosynthetic process	RT	6	2.3E-1	9.7E-1
☐	GOTERM_BP_ALL	membrane lipid biosynthetic process	RT	11	2.4E-1	9.7E-1
☐	GOTERM_BP_ALL	phosphatidylinositol metabolic process	RT	3	3.1E-1	9.9E-1
☐	GOTERM_BP_ALL	phospholipid metabolic process	RT	14	5.2E-1	1.0E0
☐	GOTERM_BP_ALL	phosphoinositide metabolic process	RT	6	5.5E-1	1.0E0
☐	GOTERM_BP_ALL	GPI anchor biosynthetic process	RT	3	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	glycerophospholipid metabolic process	RT	7	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	GPI anchor metabolic process	RT	3	6.7E-1	1.0E0
☐	KEGG_PATHWAY	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	RT	3	7.1E-1	9.8E-1
☐	GOTERM_BP_ALL	membrane lipid metabolic process	RT	15	7.8E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid lipidation	RT	4	8.7E-1	1.0E0
☐	GOTERM_BP_ALL	lipoprotein biosynthetic process	RT	4	8.9E-1	1.0E0

☐	KEGG_PATHWAY	Glycan structures - biosynthesis 2	RT	5	9.1E-1	1.0E0
☐	GOTERM_BP_ALL	lipoprotein metabolic process	RT	5	9.2E-1	1.0E0
	Annotation Cluster 183	Enrichment Score: 0.3	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	Ran GTPase binding	RT	3	1.3E-1	9.4E-1
☐	GOTERM_MF_ALL	Ras GTPase binding	RT	5	7.6E-1	1.0E0
☐	GOTERM_MF_ALL	small GTPase binding	RT	5	7.9E-1	1.0E0
☐	GOTERM_MF_ALL	GTPase binding	RT	5	8.2E-1	1.0E0
	Annotation Cluster 184	Enrichment Score: 0.3	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	aminopeptidase activity	RT	6	2.8E-1	9.9E-1
☐	SP_PIR_KEYWORDS	aminopeptidase	RT	4	4.1E-1	9.5E-1
☐	GOTERM_MF_ALL	exopeptidase activity	RT	9	7.0E-1	1.0E0
☐	GOTERM_MF_ALL	metalloexopeptidase activity	RT	5	7.9E-1	1.0E0
	Annotation Cluster 185	Enrichment Score: 0.29	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein secretion	RT	7	2.1E-1	9.6E-1
☐	GOTERM_BP_ALL	regulation of protein secretion	RT	3	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of secretion	RT	4	9.6E-1	1.0E0
	Annotation Cluster 186	Enrichment Score: 0.29	G	Count	P_Value	Benjamini
☐	SMART	LDLa	RT	5	3.2E-1	1.0E0
☐	INTERPRO	Low density lipoprotein-receptor, class A	RT	5	4.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	endocytosis	RT	5	9.4E-1	1.0E0
	Annotation Cluster 187	Enrichment Score: 0.28	G	Count	P_Value	Benjamini
☐	BIOCARTA	p38 MAPK Signaling Pathway	RT	8	1.5E-1	9.1E-1
☐	BIOCARTA	MAPKinase Signaling Pathway	RT	7	9.8E-1	1.0E0
☐	KEGG_PATHWAY	VEGF signaling pathway	RT	5	9.9E-1	1.0E0
	Annotation Cluster 188	Enrichment Score: 0.28	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	sugar binding	RT	22	2.7E-1	9.9E-1
☐	SP_PIR_KEYWORDS	lectin	RT	18	3.0E-1	8.9E-1
☐	GOTERM_MF_ALL	carbohydrate binding	RT	29	4.8E-1	1.0E0
☐	SMART	CLECT	RT	9	6.6E-1	1.0E0
☐	INTERPRO	Type II antifreeze protein	RT	4	6.8E-1	1.0E0
☐	INTERPRO	C-type lectin	RT	9	8.2E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:C-type lectin	RT	5	8.4E-1	1.0E0
	Annotation Cluster 189	Enrichment Score: 0.27	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	positive regulation of cell motility	RT	4	4.0E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of locomotion	RT	4	4.0E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of cell motility	RT	4	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of locomotion	RT	4	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cell migration	RT	3	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of cell migration	RT	3	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell motility	RT	8	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	locomotion	RT	9	6.2E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of locomotion	RT	8	6.6E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell migration	RT	6	7.9E-1	1.0E0
	Annotation Cluster 190	Enrichment Score: 0.27	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	polypeptide N-acetylgalactosaminyltransferase activity	RT	3	3.7E-1	1.0E0
☐	UP_SEQ_FEATURE	region of interest:Catalytic subdomain A	RT	3	4.4E-1	1.0E0
☐	UP_SEQ_FEATURE	region of interest:Catalytic subdomain B	RT	3	4.4E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Ricin B-type lectin	RT	3	4.7E-1	1.0E0
☐	SMART	RICIN	RT	3	5.6E-1	1.0E0
☐	KEGG_PATHWAY	O-Glycan biosynthesis	RT	4	5.8E-1	9.5E-1

☐	INTERPRO	Ricin B lectin	RT	▮		3	6.6E-1	1.0E0
☐	GOTERM_MF_ALL	acetylgalactosaminyltransferase activity	RT	▮		3	6.8E-1	1.0E0
☐	GOTERM_MF_ALL	UDP-glycosyltransferase activity	RT	▮		8	8.0E-1	1.0E0
	Annotation Cluster 191	Enrichment Score: 0.26	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	blood vessel development	RT	▮		25	3.9E-1	1.0E0
☐	GOTERM_BP_ALL	vasculature development	RT	▮		25	4.1E-1	1.0E0
☐	GOTERM_BP_ALL	angiogenesis	RT	▮		17	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	blood vessel morphogenesis	RT	▮		21	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	anatomical structure formation	RT	▮		18	8.0E-1	1.0E0
☐	GOTERM_BP_ALL	organ morphogenesis	RT	▮		38	9.9E-1	1.0E0
	Annotation Cluster 192	Enrichment Score: 0.26	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	calmodulin-binding	RT	▮		11	4.0E-1	9.5E-1
☐	GOTERM_MF_ALL	calmodulin binding	RT	▮		11	6.3E-1	1.0E0
☐	UP_SEQ_FEATURE	region of interest:Calmodulin-binding	RT	▮		5	6.5E-1	1.0E0
	Annotation Cluster 193	Enrichment Score: 0.26	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	pentose-phosphate shunt	RT	▮		3	1.7E-1	9.3E-1
☐	GOTERM_BP_ALL	NADP metabolic process	RT	▮		3	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	nicotinamide metabolic process	RT	▮		3	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	pyridine nucleotide metabolic process	RT	▮		3	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	water-soluble vitamin metabolic process	RT	▮		4	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	vitamin metabolic process	RT	▮		4	9.7E-1	1.0E0
	Annotation Cluster 194	Enrichment Score: 0.26	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	mitochondrial ribosome	RT	▮		5	4.7E-1	9.5E-1
☐	GOTERM_CC_ALL	organellar ribosome	RT	▮		5	4.7E-1	9.5E-1
☐	GOTERM_CC_ALL	mitochondrial matrix	RT	▮		6	6.4E-1	9.9E-1
☐	GOTERM_CC_ALL	mitochondrial lumen	RT	▮		6	6.4E-1	9.9E-1
	Annotation Cluster 195	Enrichment Score: 0.25	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	organic anion transport	RT	▮		3	2.4E-1	9.7E-1
☐	GOTERM_MF_ALL	neutral amino acid transmembrane transporter activity	RT	▮		3	2.7E-1	9.9E-1
☐	GOTERM_MF_ALL	solute:sodium symporter activity	RT	▮		6	3.6E-1	1.0E0
☐	GOTERM_MF_ALL	solute:cation symporter activity	RT	▮		7	3.9E-1	1.0E0
☐	GOTERM_MF_ALL	monocarboxylic acid transmembrane transporter activity	RT	▮		3	4.1E-1	1.0E0
☐	GOTERM_MF_ALL	carboxylic acid transmembrane transporter activity	RT	▮		8	4.3E-1	1.0E0
☐	GOTERM_MF_ALL	organic acid transmembrane transporter activity	RT	▮		8	4.5E-1	1.0E0
☐	GOTERM_MF_ALL	anion:cation symporter activity	RT	▮		3	5.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	amino-acid transport	RT	▮		3	5.0E-1	9.7E-1
☐	SP_PIR_KEYWORDS	Symport	RT	▮		9	5.3E-1	9.8E-1
☐	GOTERM_MF_ALL	organic acid:sodium symporter activity	RT	▮		3	5.9E-1	1.0E0
☐	GOTERM_MF_ALL	amino acid transmembrane transporter activity	RT	▮		5	6.5E-1	1.0E0
☐	GOTERM_MF_ALL	symporter activity	RT	▮		13	6.7E-1	1.0E0
☐	GOTERM_MF_ALL	secondary active transmembrane transporter activity	RT	▮		15	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	carboxylic acid transport	RT	▮		5	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	organic acid transport	RT	▮		5	8.9E-1	1.0E0
☐	GOTERM_BP_ALL	amino acid transport	RT	▮		3	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	amine transport	RT	▮		3	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	sodium ion transport	RT	▮		3	1.0E0	1.0E0
	Annotation Cluster 196	Enrichment Score: 0.25	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	lipid transport	RT	▮		6	4.2E-1	9.5E-1

☐	GOTERM_MF_ALL	lipid transporter activity	RT	6	5.6E-1	1.0E0
☐	GOTERM_BP_ALL	lipid transport	RT	8	7.4E-1	1.0E0
	Annotation Cluster 197	Enrichment Score: 0.25	G	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF001135:trypsin	RT	10	1.8E-1	1.0E0
☐	GOTERM_BP_ALL	cytolysis	RT	5	2.0E-1	9.6E-1
☐	SP_PIR_KEYWORDS	serine proteinase	RT	8	2.1E-1	8.2E-1
☐	UP_SEQ_FEATURE	domain:Peptidase S1	RT	9	3.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	cytolysis	RT	3	4.4E-1	9.6E-1
☐	UP_SEQ_FEATURE	propeptide:Activation peptide	RT	7	5.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	Zymogen	RT	18	5.5E-1	9.8E-1
☐	UP_SEQ_FEATURE	active site:Charge relay system	RT	12	7.1E-1	1.0E0
☐	SMART	Tryp_SPc	RT	9	7.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	serine protease	RT	12	7.4E-1	1.0E0
☐	GOTERM_MF_ALL	serine-type endopeptidase activity	RT	16	7.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	T-cell	RT	3	7.9E-1	1.0E0
☐	INTERPRO	Peptidase S1 and S6, chymotrypsin/Hap	RT	9	8.6E-1	1.0E0
☐	GOTERM_MF_ALL	serine-type peptidase activity	RT	16	8.7E-1	1.0E0
☐	GOTERM_MF_ALL	serine hydrolase activity	RT	16	8.7E-1	1.0E0
☐	INTERPRO	Peptidase S1A, chymotrypsin	RT	8	9.0E-1	1.0E0
☐	GOTERM_MF_ALL	endopeptidase activity	RT	26	1.0E0	1.0E0
	Annotation Cluster 198	Enrichment Score: 0.25	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	thiol protease	RT	14	1.8E-1	7.8E-1
☐	GOTERM_MF_ALL	small conjugating protein-specific protease activity	RT	7	5.4E-1	1.0E0
☐	GOTERM_MF_ALL	cysteine-type peptidase activity	RT	15	6.5E-1	1.0E0
☐	GOTERM_MF_ALL	ubiquitin thiolesterase activity	RT	6	6.5E-1	1.0E0
☐	GOTERM_MF_ALL	ubiquitin-specific protease activity	RT	6	6.8E-1	1.0E0
☐	INTERPRO	Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2	RT	4	7.7E-1	1.0E0
☐	GOTERM_MF_ALL	thiolester hydrolase activity	RT	7	7.9E-1	1.0E0
	Annotation Cluster 199	Enrichment Score: 0.25	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	solute:sodium symporter activity	RT	6	3.6E-1	1.0E0
☐	GOTERM_MF_ALL	solute:cation symporter activity	RT	7	3.9E-1	1.0E0
☐	GOTERM_MF_ALL	neurotransmitter:sodium symporter activity	RT	3	6.1E-1	1.0E0
☐	GOTERM_MF_ALL	neurotransmitter transporter activity	RT	3	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	neurotransmitter transport	RT	3	9.7E-1	1.0E0
	Annotation Cluster 200	Enrichment Score: 0.24	G	Count	P_Value	Benjamini
☐	SMART	RAS	RT	3	5.4E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF037165:ras protein	RT	3	5.5E-1	1.0E0
☐	INTERPRO	Ras small GTPase, Ras type	RT	3	6.4E-1	1.0E0
	Annotation Cluster 201	Enrichment Score: 0.23	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	monosaccharide biosynthetic process	RT	4	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	alcohol biosynthetic process	RT	4	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	carbohydrate biosynthetic process	RT	9	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	hexose biosynthetic process	RT	3	7.2E-1	1.0E0
	Annotation Cluster 202	Enrichment Score: 0.23	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	transport	RT	133	8.4E-2	5.4E-1
☐	GOTERM_BP_ALL	proton transport	RT	11	1.4E-1	9.0E-1
☐	GOTERM_BP_ALL	hydrogen transport	RT	11	1.9E-1	9.5E-1
☐	GOTERM_MF_ALL	inorganic cation transmembrane transporter activity	RT	17	2.8E-1	9.9E-1

☐	GOTERM_MF_ALL	substrate-specific transporter activity	RT			83	7.3E-1	1.0E0
☐	GOTERM_MF_ALL	transporter activity	RT			111	7.9E-1	1.0E0
☐	GOTERM_MF_ALL	transmembrane transporter activity	RT			65	9.7E-1	1.0E0
☐	GOTERM_MF_ALL	substrate-specific transmembrane transporter activity	RT			54	9.8E-1	1.0E0
☐	GOTERM_MF_ALL	ion transmembrane transporter activity	RT			41	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	ion transport	RT			27	1.0E0	1.0E0
☐	GOTERM_MF_ALL	cation transmembrane transporter activity	RT			29	1.0E0	1.0E0
☐	GOTERM_BP_ALL	monovalent inorganic cation transport	RT			17	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cation transport	RT			29	1.0E0	1.0E0
☐	GOTERM_BP_ALL	ion transport	RT			43	1.0E0	1.0E0
☐	GOTERM_BP_ALL	metal ion transport	RT			17	1.0E0	1.0E0
	Annotation Cluster 203	Enrichment Score: 0.23	G		🟩	Count	P_Value	Benjamini
☐	BIOCARTA	Cadmium induces DNA synthesis and proliferation in macrophages	RT			5	1.5E-1	9.2E-1
☐	KEGG_PATHWAY	B cell receptor signaling pathway	RT			10	4.1E-1	9.1E-1
☐	BIOCARTA	Regulation of transcriptional activity by PML	RT			4	5.1E-1	9.7E-1
☐	KEGG_PATHWAY	T cell receptor signaling pathway	RT			9	9.1E-1	1.0E0
☐	BIOCARTA	Keratinocyte Differentiation	RT			4	9.4E-1	1.0E0
☐	KEGG_PATHWAY	Fc epsilon RI signaling pathway	RT			6	9.5E-1	1.0E0
☐	KEGG_PATHWAY	Natural killer cell mediated cytotoxicity	RT			8	1.0E0	1.0E0
	Annotation Cluster 204	Enrichment Score: 0.22	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of synaptic plasticity	RT			5	2.2E-1	9.7E-1
☐	GOTERM_BP_ALL	regulation of synapse structure and activity	RT			5	2.7E-1	9.8E-1
☐	GOTERM_BP_ALL	regulation of neuronal synaptic plasticity	RT			3	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	synaptic transmission	RT			7	1.0E0	1.0E0
☐	GOTERM_BP_ALL	transmission of nerve impulse	RT			8	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cell-cell signaling	RT			10	1.0E0	1.0E0
☐	GOTERM_BP_ALL	neurological system process	RT			17	1.0E0	1.0E0
	Annotation Cluster 205	Enrichment Score: 0.22	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	ribosomal protein	RT			18	4.2E-1	9.5E-1
☐	GOTERM_CC_ALL	ribosome	RT			17	5.7E-1	9.8E-1
☐	GOTERM_MF_ALL	structural constituent of ribosome	RT			16	6.0E-1	1.0E0
☐	KEGG_PATHWAY	Ribosome	RT			7	9.4E-1	1.0E0
	Annotation Cluster 206	Enrichment Score: 0.21	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Elongation factor	RT			4	3.8E-1	9.4E-1
☐	GOTERM_MF_ALL	translation elongation factor activity	RT			4	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	translational elongation	RT			3	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	biopolymer biosynthetic process	RT			3	9.4E-1	1.0E0
	Annotation Cluster 207	Enrichment Score: 0.2	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	fad	RT			10	5.3E-1	9.8E-1
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:FAD	RT			4	5.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	flavoprotein	RT			10	6.0E-1	9.9E-1
☐	GOTERM_MF_ALL	FAD binding	RT			5	8.3E-1	1.0E0
	Annotation Cluster 208	Enrichment Score: 0.19	G		🟩	Count	P_Value	Benjamini
☐	SMART	ETS	RT			3	5.8E-1	1.0E0
☐	INTERPRO	Ets	RT			3	6.6E-1	1.0E0
☐	UP_SEQ_FEATURE	DNA-binding region:ETS	RT			3	6.8E-1	1.0E0
	Annotation Cluster 209	Enrichment Score: 0.19	G		🟩	Count	P_Value	Benjamini
☐	BIOCARTA	Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia	RT			4	5.4E-1	9.6E-1

☐	BIOCARTA	mCalpain and friends in Cell motility	RT		3	6.1E-1	9.7E-1
☐	BIOCARTA	Integrin Signaling Pathway	RT		4	8.2E-1	9.9E-1
	Annotation Cluster 210	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	RT		4	4.1E-1	1.0E0
☐	GOTERM_MF_ALL	endoribonuclease activity, producing 5'-phosphomonoesters	RT		3	6.4E-1	1.0E0
☐	GOTERM_MF_ALL	ribonuclease activity	RT		5	8.3E-1	1.0E0
☐	GOTERM_MF_ALL	endoribonuclease activity	RT		3	9.1E-1	1.0E0
	Annotation Cluster 211	Enrichment Score: 0.17	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	response to UV	RT		4	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	response to radiation	RT		9	7.1E-1	1.0E0
☐	GOTERM_BP_ALL	response to light stimulus	RT		6	8.5E-1	1.0E0
	Annotation Cluster 212	Enrichment Score: 0.17	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	UDP-galactosyltransferase activity	RT		3	5.0E-1	1.0E0
☐	GOTERM_MF_ALL	galactosyltransferase activity	RT		3	7.6E-1	1.0E0
☐	GOTERM_MF_ALL	UDP-glycosyltransferase activity	RT		8	8.0E-1	1.0E0
	Annotation Cluster 213	Enrichment Score: 0.17	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Porin, eukaryotic type	RT		3	6.5E-2	9.9E-1
☐	GOTERM_CC_ALL	organelle outer membrane	RT		5	3.3E-1	8.7E-1
☐	GOTERM_CC_ALL	mitochondrial outer membrane	RT		4	4.9E-1	9.6E-1
☐	GOTERM_MF_ALL	anion transmembrane transporter activity	RT		8	9.0E-1	1.0E0
☐	GOTERM_MF_ALL	anion channel activity	RT		4	9.2E-1	1.0E0
☐	GOTERM_MF_ALL	voltage-gated ion channel activity	RT		3	1.0E0	1.0E0
☐	GOTERM_MF_ALL	voltage-gated channel activity	RT		3	1.0E0	1.0E0
☐	GOTERM_MF_ALL	ion channel activity	RT		8	1.0E0	1.0E0
☐	GOTERM_MF_ALL	cation channel activity	RT		4	1.0E0	1.0E0
☐	GOTERM_MF_ALL	substrate specific channel activity	RT		8	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	Ionic channel	RT		4	1.0E0	1.0E0
☐	GOTERM_MF_ALL	gated channel activity	RT		3	1.0E0	1.0E0
	Annotation Cluster 214	Enrichment Score: 0.17	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of cell size	RT		4	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of cell growth	RT		3	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of growth	RT		4	7.5E-1	1.0E0
	Annotation Cluster 215	Enrichment Score: 0.16	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	response to oxidative stress	RT		8	3.3E-1	9.9E-1
☐	GOTERM_MF_ALL	antioxidant activity	RT		5	7.8E-1	1.0E0
☐	GOTERM_MF_ALL	peroxidase activity	RT		3	9.2E-1	1.0E0
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on peroxide as acceptor	RT		3	9.2E-1	1.0E0
	Annotation Cluster 216	Enrichment Score: 0.16	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of metabolic process	RT		43	2.6E-1	9.8E-1
☐	GOTERM_BP_ALL	negative regulation of biological process	RT		96	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		28	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of cellular process	RT		89	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of cellular metabolic process	RT		32	7.0E-1	1.0E0
☐	GOTERM_MF_ALL	transcription repressor activity	RT		14	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of transcription	RT		22	9.1E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of transcription, DNA-dependent	RT		15	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of transcription from RNA polymerase II promoter	RT		9	9.8E-1	1.0E0

	Annotation Cluster 217	Enrichment Score: 0.16	G 🟩	Count	P_Value	Benjamini
☐	**SMART**	HLH	RT	9	5.4E-1	1.0E0
☐	**INTERPRO**	Basic helix-loop-helix dimerisation region bHLH	RT	9	6.9E-1	1.0E0
☐	**INTERPRO**	Helix-loop-helix DNA-binding	RT	7	7.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Helix-loop-helix motif	RT	8	7.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	DNA-binding region:Basic motif	RT	10	8.4E-1	1.0E0
	Annotation Cluster 218	Enrichment Score: 0.16	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	cell migration	RT	28	6.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell motility	RT	33	7.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	localization of cell	RT	33	7.1E-1	1.0E0
	Annotation Cluster 219	Enrichment Score: 0.15	G 🟩	Count	P_Value	Benjamini
☐	**SMART**	Pept_C1	RT	3	4.9E-1	1.0E0
☐	**INTERPRO**	Peptidase C1A, papain C-terminal	RT	3	5.7E-1	1.0E0
☐	**INTERPRO**	Peptidase C1A, papain	RT	3	6.8E-1	1.0E0
☐	**INTERPRO**	Peptidase, cysteine peptidase active site	RT	3	9.2E-1	1.0E0
☐	**GOTERM_MF_ALL**	cysteine-type endopeptidase activity	RT	4	1.0E0	1.0E0
	Annotation Cluster 220	Enrichment Score: 0.15	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	lymphocyte homeostasis	RT	3	6.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	leukocyte homeostasis	RT	3	7.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	homeostasis of number of cells	RT	3	7.9E-1	1.0E0
	Annotation Cluster 221	Enrichment Score: 0.14	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	positive regulation of biological process	RT	100	4.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of cellular process	RT	86	5.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	33	6.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of transcription	RT	32	6.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	transcription activator activity	RT	19	7.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of metabolic process	RT	41	7.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of transcription, DNA-dependent	RT	23	8.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of cellular metabolic process	RT	35	9.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of transcription from RNA polymerase II promoter	RT	12	1.0E0	1.0E0
	Annotation Cluster 222	Enrichment Score: 0.14	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	embryonic epithelial tube formation	RT	6	4.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	neural tube formation	RT	5	5.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	neural plate morphogenesis	RT	5	5.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	neural plate development	RT	5	6.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	morphogenesis of embryonic epithelium	RT	6	6.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	neural tube development	RT	5	7.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	primary neural tube formation	RT	3	8.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	morphogenesis of an epithelium	RT	8	9.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	tube development	RT	13	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	tube morphogenesis	RT	9	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	embryonic morphogenesis	RT	9	1.0E0	1.0E0
	Annotation Cluster 223	Enrichment Score: 0.13	G 🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	Myosin	RT	4	6.4E-1	9.9E-1
☐	**GOTERM_CC_ALL**	myosin complex	RT	6	6.7E-1	9.9E-1
☐	**SMART**	MYSc	RT	3	6.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Myosin head-like	RT	3	6.8E-1	1.0E0
☐	**INTERPRO**	Myosin head, motor region	RT	3	7.7E-1	1.0E0

☐	**SMART**	IQ	RT	5	8.3E-1	1.0E0
☐	**INTERPRO**	IQ calmodulin-binding region	RT	4	9.6E-1	1.0E0
	Annotation Cluster 224	Enrichment Score: 0.13	G	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	microbody	RT	8	6.9E-1	9.9E-1
☐	**GOTERM_CC_ALL**	peroxisome	RT	8	6.9E-1	9.9E-1
☐	**SP_PIR_KEYWORDS**	peroxisome	RT	7	7.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	short sequence motif:Microbody targeting signal	RT	3	8.3E-1	1.0E0
	Annotation Cluster 225	Enrichment Score: 0.13	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	hair cycle process	RT	4	6.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	molting cycle process	RT	4	6.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	hair follicle development	RT	4	6.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	hair cycle	RT	4	6.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	molting cycle	RT	4	6.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	epidermis development	RT	8	8.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	ectoderm development	RT	8	8.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	epidermis morphogenesis	RT	3	9.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	tissue morphogenesis	RT	3	1.0E0	1.0E0
	Annotation Cluster 226	Enrichment Score: 0.13	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	membrane organization and biogenesis	RT	28	3.4E-1	9.9E-1
☐	**SP_PIR_KEYWORDS**	endocytosis	RT	5	9.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	endocytosis	RT	11	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	membrane invagination	RT	11	9.8E-1	1.0E0
	Annotation Cluster 227	Enrichment Score: 0.13	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	lymphocyte proliferation	RT	9	5.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	mononuclear cell proliferation	RT	9	5.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	B cell activation	RT	9	6.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	leukocyte activation	RT	21	7.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	lymphocyte activation	RT	19	7.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell activation	RT	22	7.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	B cell proliferation	RT	3	7.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	T cell activation	RT	10	9.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	T cell proliferation	RT	4	9.5E-1	1.0E0
	Annotation Cluster 228	Enrichment Score: 0.13	G	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	enzyme activator activity	RT	23	4.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	GTPase activator activity	RT	13	8.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	GTPase regulator activity	RT	22	9.8E-1	1.0E0
	Annotation Cluster 229	Enrichment Score: 0.12	G	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	microsome	RT	15	5.9E-1	9.8E-1
☐	**GOTERM_CC_ALL**	vesicular fraction	RT	15	6.4E-1	9.9E-1
☐	**SP_PIR_KEYWORDS**	microsome	RT	8	8.0E-1	1.0E0
☐	**GOTERM_CC_ALL**	cell fraction	RT	44	8.5E-1	1.0E0
☐	**GOTERM_CC_ALL**	membrane fraction	RT	36	9.3E-1	1.0E0
	Annotation Cluster 230	Enrichment Score: 0.12	G	Count	P_Value	Benjamini
☐	**SMART**	PSI	RT	4	6.8E-1	1.0E0
☐	**SMART**	Sema	RT	3	7.1E-1	1.0E0
☐	**INTERPRO**	Plexin	RT	3	7.9E-1	1.0E0
☐	**INTERPRO**	Plexin/semaphorin/integrin	RT	4	8.0E-1	1.0E0
☐	**INTERPRO**	Semaphorin/CD100 antigen	RT	3	8.0E-1	1.0E0
	Annotation Cluster 231	Enrichment Score: 0.12	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	inner ear receptor cell differentiation	RT	4	4.5E-1	1.0E0

☐	GOTERM_BP_ALL	mechanoreceptor differentiation	RT	▮		4	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	ear development	RT	▮		5	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	inner ear development	RT	▮		4	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	sensory organ development	RT	▮		6	1.0E0	1.0E0
	Annotation Cluster 232	Enrichment Score: 0.12	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	acetyltransferase activity	RT	▮		8	4.3E-1	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring acyl groups	RT	▮		16	7.2E-1	1.0E0
☐	GOTERM_MF_ALL	N-acetyltransferase activity	RT	▮		5	7.6E-1	1.0E0
☐	GOTERM_MF_ALL	N-acyltransferase activity	RT	▮		5	8.5E-1	1.0E0
☐	GOTERM_MF_ALL	acyltransferase activity	RT	▮		13	8.8E-1	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring groups other than amino-acyl groups	RT	▮		13	8.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	acyltransferase	RT	▮		8	9.7E-1	1.0E0
	Annotation Cluster 233	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	chemotaxis	RT	▮		7	4.5E-1	9.6E-1
☐	INTERPRO	Small chemokine, C-C	RT	▮		3	6.2E-1	1.0E0
☐	GOTERM_BP_ALL	chemotaxis	RT	▮		11	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	taxis	RT	▮		11	6.3E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001950:small inducible chemokine, C/CC types	RT	▮		3	6.7E-1	1.0E0
☐	GOTERM_MF_ALL	chemokine activity	RT	▮		4	7.5E-1	1.0E0
☐	GOTERM_MF_ALL	chemokine receptor binding	RT	▮		4	7.7E-1	1.0E0
☐	SMART	SCY	RT	▮		3	8.0E-1	1.0E0
☐	GOTERM_MF_ALL	G-protein-coupled receptor binding	RT	▮		5	8.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	pyrrolidone carboxylic acid	RT	▮		3	8.7E-1	1.0E0
☐	INTERPRO	Small chemokine, interleukin-8-like	RT	▮		3	8.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	inflammatory response	RT	▮		5	8.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	cytokine	RT	▮		10	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	locomotory behavior	RT	▮		13	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	behavior	RT	▮		18	1.0E0	1.0E0
	Annotation Cluster 234	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	iron ion homeostasis	RT	▮		4	4.0E-1	1.0E0
☐	GOTERM_BP_ALL	cellular iron ion homeostasis	RT	▮		4	4.0E-1	1.0E0
☐	GOTERM_BP_ALL	cellular homeostasis	RT	▮		25	5.3E-1	1.0E0
☐	GOTERM_BP_ALL	elevation of cytosolic calcium ion concentration	RT	▮		3	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of biological quality	RT	▮		66	6.4E-1	1.0E0
☐	GOTERM_BP_ALL	cytosolic calcium ion homeostasis	RT	▮		3	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	cellular di-, tri-valent inorganic cation homeostasis	RT	▮		9	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	di-, tri-valent inorganic cation homeostasis	RT	▮		9	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	cellular cation homeostasis	RT	▮		9	8.9E-1	1.0E0
☐	GOTERM_BP_ALL	cellular calcium ion homeostasis	RT	▮		5	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	cation homeostasis	RT	▮		9	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	calcium ion homeostasis	RT	▮		5	9.1E-1	1.0E0
☐	GOTERM_BP_ALL	homeostatic process	RT	▮		28	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	cellular metal ion homeostasis	RT	▮		5	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	metal ion homeostasis	RT	▮		5	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	cellular chemical homeostasis	RT	▮		12	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	cellular ion homeostasis	RT	▮		12	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	ion homeostasis	RT	▮		12	9.8E-1	1.0E0

☐	GOTERM_BP_ALL	chemical homeostasis	RT	▮		13	1.0E0	1.0E0
	Annotation Cluster 235	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	SMART	RING	RT	▮		18	6.8E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:RING-type	RT	▮		11	7.4E-1	1.0E0
☐	INTERPRO	Zinc finger, RING/FYVE/PHD-type	RT	▮		12	8.1E-1	1.0E0
☐	INTERPRO	Zinc finger, RING-type	RT	▮		17	8.9E-1	1.0E0
	Annotation Cluster 236	Enrichment Score: 0.1	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of JNK cascade	RT	▮		3	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	MAPKKK cascade	RT	▮		11	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	JNK cascade	RT	▮		4	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	stress-activated protein kinase signaling pathway	RT	▮		4	8.8E-1	1.0E0
	Annotation Cluster 237	Enrichment Score: 0.1	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	immunoglobulin production	RT	▮		4	7.5E-1	1.0E0
☐	GOTERM_BP_ALL	production of molecular mediator of immune response	RT	▮		4	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	somatic recombination of immunoglobulin gene segments	RT	▮		3	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	somatic cell DNA recombination	RT	▮		3	8.0E-1	1.0E0
☐	GOTERM_BP_ALL	somatic diversification of immune receptors via germline recombination within a single locus	RT	▮		3	8.0E-1	1.0E0
☐	GOTERM_BP_ALL	somatic diversification of immunoglobulins	RT	▮		3	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	somatic diversification of immune receptors	RT	▮		3	8.4E-1	1.0E0
	Annotation Cluster 238	Enrichment Score: 0.1	G		🟩	Count	P_Value	Benjamini
☐	SMART	SOCS	RT	▮		3	7.4E-1	1.0E0
☐	INTERPRO	SOCS protein, C-terminal	RT	▮		3	8.3E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:SOCS box	RT	▮		3	8.3E-1	1.0E0
	Annotation Cluster 239	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	exopeptidase activity	RT	▮		9	7.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	carboxypeptidase	RT	▮		3	8.1E-1	1.0E0
☐	GOTERM_MF_ALL	carboxypeptidase activity	RT	▮		3	9.3E-1	1.0E0
	Annotation Cluster 240	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	glucose transport	RT	▮		3	8.0E-1	1.0E0
☐	GOTERM_BP_ALL	carbohydrate transport	RT	▮		6	8.1E-1	1.0E0
☐	GOTERM_BP_ALL	hexose transport	RT	▮		3	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	monosaccharide transport	RT	▮		3	8.2E-1	1.0E0
	Annotation Cluster 241	Enrichment Score: 0.08	G		🟩	Count	P_Value	Benjamini
☐	SMART	SANT	RT	▮		4	7.9E-1	1.0E0
☐	INTERPRO	Myb, DNA-binding	RT	▮		3	8.0E-1	1.0E0
☐	INTERPRO	SANT, DNA-binding	RT	▮		4	8.8E-1	1.0E0
	Annotation Cluster 242	Enrichment Score: 0.08	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	EF hand	RT	▮		5	3.2E-1	9.1E-1
☐	SMART	EFh	RT	▮		12	8.5E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:EF-hand 1	RT	▮		8	9.3E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:EF-hand 2	RT	▮		8	9.3E-1	1.0E0
☐	UP_SEQ_FEATURE	calcium-binding region:2	RT	▮		5	9.7E-1	1.0E0
☐	INTERPRO	Calcium-binding EF-hand	RT	▮		11	9.7E-1	1.0E0
☐	UP_SEQ_FEATURE	calcium-binding region:1	RT	▮		5	9.7E-1	1.0E0
☐	INTERPRO	EF-Hand type	RT	▮		8	1.0E0	1.0E0
	Annotation Cluster 243	Enrichment Score: 0.08	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	cholesterol metabolism	RT	▮		3	6.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	steroid metabolism	RT	▮		3	8.3E-1	1.0E0

☐	SP_PIR_KEYWORDS	lipid metabolism	RT		5	9.9E-1	1.0E0
	Annotation Cluster 244	Enrichment Score: 0.08	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT		6	7.4E-1	1.0E0
☐	INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	RT		3	8.2E-1	1.0E0
☐	COG_ONTOLOGY	Inorganic ion transport and metabolism	RT		6	9.7E-1	1.0E0
	Annotation Cluster 245	Enrichment Score: 0.08	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Sterile alpha motif-type	RT		6	6.2E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:SAM	RT		3	9.0E-1	1.0E0
☐	SMART	SAM	RT		4	9.2E-1	1.0E0
☐	INTERPRO	Sterile alpha motif SAM	RT		4	9.6E-1	1.0E0
	Annotation Cluster 246	Enrichment Score: 0.07	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	lung development	RT		6	8.0E-1	1.0E0
☐	GOTERM_BP_ALL	respiratory tube development	RT		6	8.1E-1	1.0E0
☐	GOTERM_BP_ALL	tube development	RT		13	9.8E-1	1.0E0
	Annotation Cluster 247	Enrichment Score: 0.07	G	🟩	Count	P_Value	Benjamini
☐	SMART	HMG	RT		4	7.9E-1	1.0E0
☐	INTERPRO	High mobility group box, HMG1/HMG2	RT		4	8.6E-1	1.0E0
☐	INTERPRO	High mobility group box, HMG	RT		3	9.3E-1	1.0E0
	Annotation Cluster 248	Enrichment Score: 0.06	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	male sex differentiation	RT		4	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	development of primary male sexual characteristics	RT		3	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	development of primary sexual characteristics	RT		4	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	sex differentiation	RT		5	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	gonad development	RT		3	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive structure development	RT		3	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive developmental process	RT		5	9.9E-1	1.0E0
	Annotation Cluster 249	Enrichment Score: 0.06	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	focal adhesion	RT		3	7.8E-1	1.0E0
☐	GOTERM_CC_ALL	cell-substrate adherens junction	RT		3	8.4E-1	1.0E0
☐	GOTERM_CC_ALL	adherens junction	RT		5	8.7E-1	1.0E0
☐	GOTERM_CC_ALL	cell-matrix junction	RT		3	8.8E-1	1.0E0
☐	GOTERM_CC_ALL	basolateral plasma membrane	RT		4	9.8E-1	1.0E0
	Annotation Cluster 250	Enrichment Score: 0.06	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	sugar transport	RT		3	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	carbohydrate transport	RT		6	8.1E-1	1.0E0
☐	GOTERM_MF_ALL	sugar:hydrogen ion symporter activity	RT		3	9.1E-1	1.0E0
☐	GOTERM_MF_ALL	sugar transmembrane transporter activity	RT		3	9.1E-1	1.0E0
☐	GOTERM_MF_ALL	carbohydrate transmembrane transporter activity	RT		3	9.2E-1	1.0E0
	Annotation Cluster 251	Enrichment Score: 0.06	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of anatomical structure morphogenesis	RT		4	8.7E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell morphogenesis	RT		4	8.7E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell shape	RT		4	8.7E-1	1.0E0
	Annotation Cluster 252	Enrichment Score: 0.06	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	chemotaxis	RT		11	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	taxis	RT		11	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	response to wounding	RT		22	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	inflammatory response	RT		13	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	response to external stimulus	RT		32	1.0E0	1.0E0

☐	**GOTERM_BP_ALL**	immune response	RT	▮		25	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	defense response	RT	▮		22	1.0E0	1.0E0
	Annotation Cluster 253	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	humoral immune response	RT	▮		7	5.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	complement activation	RT	▮		4	7.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	activation of plasma proteins during acute inflammatory response	RT	▮		4	7.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	immune effector process	RT	▮		12	7.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	activation of immune response	RT	▮		5	9.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of immune response	RT	▮		5	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	acute inflammatory response	RT	▮		4	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of immune system process	RT	▮		5	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of immune response	RT	▮		5	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	regulation of immune system process	RT	▮		5	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of multicellular organismal process	RT	▮		5	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	regulation of multicellular organismal process	RT	▮		14	1.0E0	1.0E0
	Annotation Cluster 254	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of cell growth	RT	▮		9	7.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cell size	RT	▮		11	8.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell growth	RT	▮		10	8.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of growth	RT	▮		12	9.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	growth	RT	▮		19	9.7E-1	1.0E0
	Annotation Cluster 255	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	B cell activation	RT	▮		9	6.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of B cell activation	RT	▮		3	7.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of B cell activation	RT	▮		4	8.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of lymphocyte activation	RT	▮		5	9.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of lymphocyte activation	RT	▮		7	9.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cell activation	RT	▮		7	9.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of T cell activation	RT	▮		4	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of lymphocyte proliferation	RT	▮		3	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of mononuclear cell proliferation	RT	▮		3	9.9E-1	1.0E0
	Annotation Cluster 256	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	proteolysis	RT	▮		62	8.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	protease	RT	▮		39	8.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	peptidase activity	RT	▮		51	9.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	endopeptidase activity	RT	▮		26	1.0E0	1.0E0
	Annotation Cluster 257	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Variant SH3	RT	▮		6	5.1E-1	1.0E0
☐	**SMART**	SH2	RT	▮		6	9.2E-1	1.0E0
☐	**SMART**	SH3	RT	▮		10	9.5E-1	1.0E0
☐	**INTERPRO**	SH2 motif	RT	▮		6	9.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	sh2 domain	RT	▮		6	9.8E-1	1.0E0
☐	**INTERPRO**	Src homology-3	RT	▮		10	9.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	SH3 domain	RT	▮		10	9.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:SH3	RT	▮		4	1.0E0	1.0E0
	Annotation Cluster 258	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	basement membrane	RT	▮		6	7.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	extracellular matrix organization and	RT	▮		6	7.4E-1	1.0E0

☐		biogenesis	RT	6	7.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	basement membrane	RT	3	8.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	extracellular structure organization and biogenesis	RT	8	9.1E-1	1.0E0
☐	**GOTERM_CC_ALL**	extracellular matrix part	RT	6	9.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	extracellular matrix structural constituent	RT	3	9.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	extracellular matrix	RT	7	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	proteinaceous extracellular matrix	RT	9	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	extracellular matrix	RT	9	1.0E0	1.0E0
	Annotation Cluster 259	Enrichment Score: 0.05	G	Count	P_Value	Benjamini
☐	**BIOCARTA**	Role of MAL in Rho-Mediated Activation of SRF	RT	3	8.1E-1	9.9E-1
☐	**BIOCARTA**	Ras Signaling Pathway	RT	3	8.3E-1	9.9E-1
☐	**KEGG_PATHWAY**	VEGF signaling pathway	RT	5	9.9E-1	1.0E0
☐	**KEGG_PATHWAY**	Axon guidance	RT	9	9.9E-1	1.0E0
	Annotation Cluster 260	Enrichment Score: 0.04	G	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	enzyme inhibitor activity	RT	20	6.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	endopeptidase inhibitor activity	RT	8	9.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	protease inhibitor activity	RT	8	9.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	serine-type endopeptidase inhibitor activity	RT	5	9.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	protease inhibitor	RT	3	1.0E0	1.0E0
	Annotation Cluster 261	Enrichment Score: 0.03	G	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	glycosidase	RT	4	9.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrolase activity, hydrolyzing O-glycosyl compounds	RT	6	9.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrolase activity, acting on glycosyl bonds	RT	7	9.6E-1	1.0E0
	Annotation Cluster 262	Enrichment Score: 0.03	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	sensory perception of sound	RT	6	7.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	sensory perception of mechanical stimulus	RT	6	8.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	sensory perception	RT	10	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	transmission of nerve impulse	RT	8	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	neurological system process	RT	17	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	system process	RT	24	1.0E0	1.0E0
	Annotation Cluster 263	Enrichment Score: 0.02	G	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	domain:C2 1	RT	3	9.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:C2 2	RT	3	9.2E-1	1.0E0
☐	**SMART**	C2	RT	6	9.6E-1	1.0E0
☐	**INTERPRO**	C2 calcium-dependent membrane targeting	RT	6	9.9E-1	1.0E0
	Annotation Cluster 264	Enrichment Score: 0.02	G	Count	P_Value	Benjamini
☐	**SMART**	ANK	RT	13	8.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:ANK 3	RT	6	9.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:ANK 1	RT	6	9.7E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:ANK 2	RT	6	9.7E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:ANK 5	RT	3	9.8E-1	1.0E0
☐	**INTERPRO**	Ankyrin	RT	10	9.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:ANK 4	RT	3	9.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	ank repeat	RT	10	9.9E-1	1.0E0
	Annotation Cluster 265	Enrichment Score: 0.02	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	immune effector process	RT	12	7.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	leukocyte mediated immunity	RT	6	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	B cell mediated immunity	RT	4	9.8E-1	1.0E0

☐	**GOTERM_BP_ALL**	immunoglobulin mediated immune response	RT	3	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	lymphocyte mediated immunity	RT	4	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	RT	4	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	adaptive immune response	RT	4	1.0E0	1.0E0
	Annotation Cluster 266	Enrichment Score: 0.02	G 🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	EGF calcium-binding	RT	5	8.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:EGF-like 2; calcium-binding	RT	3	8.8E-1	1.0E0
☐	**SMART**	EGF_CA	RT	5	9.1E-1	1.0E0
☐	**INTERPRO**	Aspartic acid and asparagine hydroxylation site	RT	5	9.5E-1	1.0E0
☐	**INTERPRO**	EGF-like calcium-binding	RT	5	9.6E-1	1.0E0
☐	**SMART**	EGF	RT	7	9.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:EGF-like 1	RT	3	9.9E-1	1.0E0
☐	**INTERPRO**	EGF-like	RT	5	1.0E0	1.0E0
☐	**INTERPRO**	EGF-like, type 3	RT	7	1.0E0	1.0E0
☐	**INTERPRO**	EGF	RT	7	1.0E0	1.0E0
☐	**INTERPRO**	EGF-like region	RT	9	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	egf-like domain	RT	7	1.0E0	1.0E0
	Annotation Cluster 267	Enrichment Score: 0.02	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of protein amino acid phosphorylation	RT	4	9.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of amino acid metabolic process	RT	4	9.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of amine metabolic process	RT	4	9.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of protein metabolic process	RT	6	9.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of phosphorylation	RT	4	9.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of phosphorus metabolic process	RT	4	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of phosphate metabolic process	RT	4	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	multi-organism process	RT	8	1.0E0	1.0E0
	Annotation Cluster 268	Enrichment Score: 0.02	G 🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	Dioxygenase	RT	3	9.2E-1	1.0E0
☐	**GOTERM_MF_ALL**	dioxygenase activity	RT	3	9.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	RT	3	9.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	RT	3	9.8E-1	1.0E0
	Annotation Cluster 269	Enrichment Score: 0.01	G 🟩	Count	P_Value	Benjamini
☐	**SMART**	LIM	RT	3	9.5E-1	1.0E0
☐	**INTERPRO**	Zinc finger, LIM-type	RT	3	9.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	lim domain	RT	3	9.8E-1	1.0E0
	Annotation Cluster 270	Enrichment Score: 0.01	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	amino acid catabolic process	RT	3	9.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	nitrogen compound catabolic process	RT	3	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	amine catabolic process	RT	3	9.8E-1	1.0E0
	Annotation Cluster 271	Enrichment Score: 0.01	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	wound healing	RT	6	9.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	blood coagulation	RT	3	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	coagulation	RT	3	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of body fluid levels	RT	4	9.8E-1	1.0E0

☐	**GOTERM_BP_ALL**	hemostasis	RT	▮		3	9.9E-1	1.0E0
	Annotation Cluster 272	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	repeat:LRR 6	RT	▮		5	9.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:LRR 5	RT	▮		5	9.7E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:LRR 3	RT	▮		6	9.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:LRR 1	RT	▮		6	9.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:LRR 2	RT	▮		6	9.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:LRR 4	RT	▮		5	9.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:LRR 8	RT	▮		3	9.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:LRR 7	RT	▮		3	9.9E-1	1.0E0
☐	**INTERPRO**	Leucine-rich repeat	RT	▮		7	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	leucine-rich repeat	RT	▮		8	1.0E0	1.0E0
	Annotation Cluster 273	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	myoblast differentiation	RT	▮		3	9.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	skeletal muscle development	RT	▮		6	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	skeletal muscle fiber development	RT	▮		3	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	muscle fiber development	RT	▮		3	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	muscle cell differentiation	RT	▮		3	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	striated muscle development	RT	▮		6	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	muscle development	RT	▮		8	1.0E0	1.0E0
	Annotation Cluster 274	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	tube morphogenesis	RT	▮		9	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	branching morphogenesis of a tube	RT	▮		3	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	morphogenesis of a branching structure	RT	▮		3	9.9E-1	1.0E0
	Annotation Cluster 275	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	G-protein signaling, coupled to cAMP nucleotide second messenger	RT	▮		3	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	G-protein signaling, coupled to cyclic nucleotide second messenger	RT	▮		3	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	cAMP-mediated signaling	RT	▮		3	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	cyclic-nucleotide-mediated signaling	RT	▮		3	9.9E-1	1.0E0
	Annotation Cluster 276	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	Ras protein signal transduction	RT	▮		13	9.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	small GTPase regulator activity	RT	▮		10	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	regulation of Ras protein signal transduction	RT	▮		6	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	regulation of small GTPase mediated signal transduction	RT	▮		8	1.0E0	1.0E0
	Annotation Cluster 277	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of blood pressure	RT	▮		3	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	blood circulation	RT	▮		5	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	circulatory system process	RT	▮		5	1.0E0	1.0E0
	Annotation Cluster 278	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	heparin-binding	RT	▮		3	9.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	heparin binding	RT	▮		3	9.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	glycosaminoglycan binding	RT	▮		4	9.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	polysaccharide binding	RT	▮		4	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	pattern binding	RT	▮		4	1.0E0	1.0E0
	Annotation Cluster 279	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	potassium	RT	▮		5	9.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	potassium ion binding	RT	▮		5	9.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	alkali metal ion binding	RT	▮		8	1.0E0	1.0E0
	Annotation Cluster 280	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini

☐	**UP_SEQ_FEATURE**	domain:Fibronectin type-III 1	RT	▮		4	9.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Fibronectin type-III 2	RT	▮		4	9.8E-1	1.0E0
☐	**SMART**	FN3	RT	▮		7	9.9E-1	1.0E0
☐	**INTERPRO**	Fibronectin, type III	RT	▮		7	1.0E0	1.0E0
☐	**INTERPRO**	Fibronectin, type III-like fold	RT	▮		5	1.0E0	1.0E0
	Annotation Cluster 281	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**SMART**	IG	RT	▮		13	9.6E-1	1.0E0
☐	**INTERPRO**	Immunoglobulin subtype	RT	▮		13	9.8E-1	1.0E0
☐	**INTERPRO**	Immunoglobulin	RT	▮		6	1.0E0	1.0E0
☐	**INTERPRO**	Immunoglobulin V-set	RT	▮		5	1.0E0	1.0E0
☐	**INTERPRO**	Immunoglobulin-like	RT	▮		16	1.0E0	1.0E0
☐	**INTERPRO**	Immunoglobulin-like fold	RT	▮		16	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	immunoglobulin domain	RT	▮		11	1.0E0	1.0E0
	Annotation Cluster 282	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	collagen	RT	▮		4	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	phosphate transport	RT	▮		4	9.9E-1	1.0E0
☐	**INTERPRO**	Collagen triple helix repeat	RT	▮		3	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	inorganic anion transport	RT	▮		7	1.0E0	1.0E0
	Annotation Cluster 283	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	spermatogenesis	RT	▮		11	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	male gamete generation	RT	▮		11	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	reproduction	RT	▮		29	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	gamete generation	RT	▮		14	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	sexual reproduction	RT	▮		16	1.0E0	1.0E0
	Annotation Cluster 284	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**SMART**	PH	RT	▮		10	9.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:PH	RT	▮		5	1.0E0	1.0E0
☐	**INTERPRO**	Pleckstrin homology-type	RT	▮		12	1.0E0	1.0E0
☐	**INTERPRO**	Pleckstrin-like	RT	▮		10	1.0E0	1.0E0
	Annotation Cluster 285	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	visual perception	RT	▮		5	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	sensory perception of light stimulus	RT	▮		5	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	sensory perception	RT	▮		10	1.0E0	1.0E0
	Annotation Cluster 286	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	transcription from RNA polymerase II promoter	RT	▮		32	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of transcription from RNA polymerase II promoter	RT	▮		12	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	regulation of transcription from RNA polymerase II promoter	RT	▮		26	1.0E0	1.0E0
	Annotation Cluster 287	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of cytokine biosynthetic process	RT	▮		3	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	cytokine biosynthetic process	RT	▮		3	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	cytokine metabolic process	RT	▮		3	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	cytokine production	RT	▮		3	1.0E0	1.0E0
	Annotation Cluster 288	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	cell-cell adhesion	RT	▮		16	9.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	cell adhesion	RT	▮		19	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	biological adhesion	RT	▮		36	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	cell adhesion	RT	▮		36	1.0E0	1.0E0
	Annotation Cluster 289	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	forebrain development	RT	▮		5	9.9E-1	1.0E0

☐	GOTERM_BP_ALL	brain development	RT	6	1.0E0	1.0E0
☐	GOTERM_BP_ALL	central nervous system development	RT	8	1.0E0	1.0E0
	Annotation Cluster 290	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	nucleotide receptor activity, G-protein coupled	RT	3	9.8E-1	1.0E0
☐	GOTERM_MF_ALL	nucleotide receptor activity	RT	3	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	peptide receptor activity	RT	3	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	transducer	RT	12	1.0E0	1.0E0
☐	INTERPRO	Rhodopsin-like GPCR superfamily	RT	4	1.0E0	1.0E0
☐	KEGG_PATHWAY	Neuroactive ligand-receptor interaction	RT	6	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	g-protein coupled receptor	RT	7	1.0E0	1.0E0
☐	GOTERM_MF_ALL	rhodopsin-like receptor activity	RT	7	1.0E0	1.0E0
☐	GOTERM_MF_ALL	G-protein coupled receptor activity	RT	7	1.0E0	1.0E0
☐	GOTERM_MF_ALL	transmembrane receptor activity	RT	16	1.0E0	1.0E0
	Annotation Cluster 291	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell differentiation	RT	149	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	cellular developmental process	RT	149	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	developmental process	RT	226	1.0E0	1.0E0
☐	GOTERM_BP_ALL	organ development	RT	90	1.0E0	1.0E0
☐	GOTERM_BP_ALL	anatomical structure morphogenesis	RT	72	1.0E0	1.0E0
☐	GOTERM_BP_ALL	system development	RT	115	1.0E0	1.0E0
☐	GOTERM_BP_ALL	anatomical structure development	RT	137	1.0E0	1.0E0
☐	GOTERM_BP_ALL	multicellular organismal development	RT	146	1.0E0	1.0E0
☐	GOTERM_BP_ALL	multicellular organismal process	RT	172	1.0E0	1.0E0
	Annotation Cluster 292	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	intracellular signaling cascade	RT	91	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	signal transduction	RT	157	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cell communication	RT	163	1.0E0	1.0E0
	Annotation Cluster 293	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	heme	RT	5	1.0E0	1.0E0
☐	GOTERM_MF_ALL	tetrapyrrole binding	RT	7	1.0E0	1.0E0
☐	GOTERM_MF_ALL	heme binding	RT	7	1.0E0	1.0E0
	Annotation Cluster 294	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	apical junction complex	RT	3	1.0E0	1.0E0
☐	GOTERM_CC_ALL	apicolateral plasma membrane	RT	3	1.0E0	1.0E0
☐	GOTERM_CC_ALL	intercellular junction	RT	4	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	cell junction	RT	9	1.0E0	1.0E0
	Annotation Cluster 295	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	generation of neurons	RT	19	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cellular morphogenesis during differentiation	RT	9	1.0E0	1.0E0
☐	GOTERM_BP_ALL	neurogenesis	RT	20	1.0E0	1.0E0
☐	GOTERM_BP_ALL	neuron differentiation	RT	15	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cell morphogenesis	RT	30	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cellular structure morphogenesis	RT	30	1.0E0	1.0E0
☐	GOTERM_BP_ALL	axonogenesis	RT	6	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cell part morphogenesis	RT	13	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cell projection organization and biogenesis	RT	13	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cell projection morphogenesis	RT	13	1.0E0	1.0E0
☐	GOTERM_BP_ALL	neuron morphogenesis during differentiation	RT	6	1.0E0	1.0E0
☐	GOTERM_BP_ALL	neurite morphogenesis	RT	6	1.0E0	1.0E0

☐	**GOTERM_BP_ALL**	neurite development	RT	7	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	nervous system development	RT	37	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	neuron development	RT	8	1.0E0	1.0E0
	Annotation Cluster 296	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 2	RT	5	1.0E0	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 1	RT	5	1.0E0	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 3	RT	4	1.0E0	1.0E0
☐	**INTERPRO**	Zinc finger, C2H2-type/integrase, DNA-binding	RT	5	1.0E0	1.0E0
	Annotation Cluster 297	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	postsynaptic membrane	RT	3	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	synapse part	RT	3	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	synapse	RT	6	1.0E0	1.0E0
	Annotation Cluster 298	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	integral to plasma membrane	RT	32	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	intrinsic to plasma membrane	RT	32	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	plasma membrane part	RT	72	1.0E0	1.0E0
	Annotation Cluster 299	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	synapse	RT	4	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	cell junction	RT	9	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	synapse	RT	6	1.0E0	1.0E0
	Annotation Cluster 300	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	**SMART**	ZnF_C2H2	RT	10	1.0E0	1.0E0
☐	**INTERPRO**	Zinc finger, C2H2-like	RT	10	1.0E0	1.0E0
☐	**INTERPRO**	Zinc finger, C2H2-type/integrase, DNA-binding	RT	5	1.0E0	1.0E0
☐	**INTERPRO**	Zinc finger, C2H2-type	RT	10	1.0E0	1.0E0
	Annotation Cluster 301	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	metal-binding	RT	147	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	transition metal ion binding	RT	154	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	zinc	RT	90	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	metal ion binding	RT	250	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	ion binding	RT	254	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	zinc ion binding	RT	110	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	zinc-finger	RT	60	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	cation binding	RT	209	1.0E0	1.0E0
	Annotation Cluster 302	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	transmembrane region	RT	169	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	membrane part	RT	349	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	integral to membrane	RT	299	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	intrinsic to membrane	RT	299	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	transmembrane	RT	228	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	membrane	RT	446	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	membrane	RT	302	1.0E0	1.0E0
	Annotation Cluster 303	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	transmembrane region	RT	169	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	extracellular space	RT	119	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	extracellular region part	RT	122	1.0E0	1.0E0
☐	**UP_SEQ_FEATURE**	topological domain:Cytoplasmic	RT	103	1.0E0	1.0E0
☐	**UP_SEQ_FEATURE**	topological domain:Extracellular	RT	70	1.0E0	1.0E0
☐	**UP_SEQ_FEATURE**	disulfide bond	RT	89	1.0E0	1.0E0

☐	**GOTERM_CC_ALL**	extracellular region	RT	▬		124	1.0E0	1.0E0
☐	**UP_SEQ_FEATURE**	glycosylation site:N-linked (GlcNAc...)	RT	▬		123	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	signal	RT	▬		119	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	glycoprotein	RT	▬		159	1.0E0	1.0E0
☐	**UP_SEQ_FEATURE**	signal peptide	RT	▬		99	1.0E0	1.0E0
	Annotation Cluster 304	**Enrichment Score: 0**	**G**		🟩	**Count**	**P_Value**	**Benjamini**
☐	**SP_PIR_KEYWORDS**	receptor	RT	▬		57	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	signal transducer activity	RT	▬		93	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	molecular transducer activity	RT	▬		93	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	receptor activity	RT	▬		70	1.0E0	1.0E0

647 terms were not clustered.

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					Count	P_Value	Benjamini
	Annotation Cluster 1	Enrichment Score: 48.89	G		Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	intracellular part	RT		1024	4.2E-74	3.3E-71
☐	GOTERM_CC_ALL	intracellular	RT		1048	9.4E-70	3.6E-67
☐	GOTERM_CC_ALL	intracellular membrane-bound organelle	RT		839	3.6E-65	9.3E-63
☐	GOTERM_CC_ALL	membrane-bound organelle	RT		839	6.8E-65	1.3E-62
☐	GOTERM_CC_ALL	intracellular organelle	RT		896	3.5E-61	5.4E-59
☐	GOTERM_CC_ALL	organelle	RT		896	5.8E-61	7.5E-59
☐	GOTERM_CC_ALL	nucleus	RT		601	5.2E-55	5.7E-53
☐	SP_PIR_KEYWORDS	nucleus	RT		491	2.7E-43	2.3E-40
☐	GOTERM_CC_ALL	cytoplasm	RT		627	5.0E-18	2.3E-16
☐	GOTERM_CC_ALL	cell part	RT		1160	1.1E-16	4.3E-15
☐	GOTERM_CC_ALL	cell	RT		1160	1.1E-16	4.3E-15
	Annotation Cluster 2	Enrichment Score: 27.48	G		Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	intracellular organelle part	RT		387	2.4E-34	2.4E-32
☐	GOTERM_CC_ALL	organelle part	RT		387	6.7E-34	5.8E-32
☐	GOTERM_CC_ALL	macromolecular complex	RT		322	4.0E-26	2.6E-24
☐	GOTERM_CC_ALL	non-membrane-bound organelle	RT		249	3.5E-25	2.1E-23
☐	GOTERM_CC_ALL	intracellular non-membrane-bound organelle	RT		249	3.5E-25	2.1E-23
☐	GOTERM_CC_ALL	nuclear part	RT		198	1.7E-24	8.6E-23
	Annotation Cluster 3	Enrichment Score: 21.18	G		Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell cycle	RT		165	3.4E-29	5.8E-26
☐	SP_PIR_KEYWORDS	cell cycle	RT		106	9.7E-28	2.8E-25
☐	GOTERM_BP_ALL	cell cycle phase	RT		92	6.3E-27	6.5E-24
☐	GOTERM_BP_ALL	mitotic cell cycle	RT		81	7.7E-25	4.4E-22
☐	SP_PIR_KEYWORDS	mitosis	RT		55	9.1E-25	1.6E-22
☐	GOTERM_BP_ALL	M phase	RT		80	1.6E-24	8.2E-22
☐	GOTERM_BP_ALL	cell cycle process	RT		132	3.7E-23	1.7E-20
☐	GOTERM_BP_ALL	cell division	RT		78	3.8E-23	1.6E-20
☐	SP_PIR_KEYWORDS	cell division	RT		67	1.1E-22	1.6E-20
☐	GOTERM_BP_ALL	M phase of mitotic cell cycle	RT		66	1.4E-22	5.4E-20
☐	GOTERM_BP_ALL	mitosis	RT		65	5.4E-22	1.9E-19
☐	GOTERM_BP_ALL	regulation of progression through cell cycle	RT		64	1.1E-6	9.7E-5
☐	GOTERM_BP_ALL	regulation of cell cycle	RT		64	1.5E-6	1.2E-4
	Annotation Cluster 4	Enrichment Score: 21.09	G		Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	chromosome	RT		95	3.2E-26	2.3E-24
☐	GOTERM_CC_ALL	chromosomal part	RT		82	2.1E-22	9.9E-21
☐	GOTERM_CC_ALL	chromosome, pericentric region	RT		33	8.3E-17	4.6E-15
	Annotation Cluster 5	Enrichment Score: 16.18	G		Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cellular metabolic process	RT		784	2.4E-25	2.1E-22

☐	**GOTERM_BP_ALL**	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		452	6.9E-25	4.4E-22
☐	**GOTERM_BP_ALL**	primary metabolic process	RT		774	2.1E-22	7.7E-20
☐	**GOTERM_BP_ALL**	metabolic process	RT		830	2.2E-20	7.1E-18
☐	**GOTERM_BP_ALL**	cellular process	RT		1036	3.7E-13	6.8E-11
☐	**GOTERM_BP_ALL**	macromolecule metabolic process	RT		655	1.5E-12	2.5E-10
☐	**GOTERM_BP_ALL**	gene expression	RT		356	2.1E-8	2.3E-6
☐	**GOTERM_BP_ALL**	biopolymer metabolic process	RT		494	3.9E-8	4.2E-6
	Annotation Cluster 6	Enrichment Score: 15.06	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	ribonucleoprotein complex biogenesis and assembly	RT		73	6.4E-25	4.7E-22
☐	**GOTERM_BP_ALL**	ribosome biogenesis and assembly	RT		49	4.5E-19	1.4E-16
☐	**GOTERM_BP_ALL**	rRNA processing	RT		27	1.5E-12	2.4E-10
☐	**GOTERM_BP_ALL**	rRNA metabolic process	RT		27	2.4E-12	3.8E-10
☐	**SP_PIR_KEYWORDS**	rrna processing	RT		21	4.9E-10	2.0E-8
	Annotation Cluster 7	Enrichment Score: 14.71	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	nucleotide binding	RT		298	9.8E-23	1.3E-19
☐	**SP_PIR_KEYWORDS**	atp-binding	RT		177	2.7E-17	2.9E-15
☐	**GOTERM_MF_ALL**	adenyl ribonucleotide binding	RT		210	2.0E-16	1.5E-13
☐	**GOTERM_MF_ALL**	ATP binding	RT		208	2.1E-16	1.2E-13
☐	**GOTERM_MF_ALL**	adenyl nucleotide binding	RT		216	4.8E-16	2.0E-13
☐	**GOTERM_MF_ALL**	purine ribonucleotide binding	RT		240	3.0E-15	1.0E-12
☐	**GOTERM_MF_ALL**	ribonucleotide binding	RT		240	3.0E-15	1.0E-12
☐	**SP_PIR_KEYWORDS**	nucleotide-binding	RT		205	5.4E-15	4.6E-13
☐	**GOTERM_MF_ALL**	purine nucleotide binding	RT		246	6.6E-15	2.0E-12
☐	**UP_SEQ_FEATURE**	nucleotide phosphate-binding region:ATP	RT		89	5.0E-5	6.9E-2
	Annotation Cluster 8	Enrichment Score: 14.49	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	RNA processing	RT		115	1.0E-31	5.3E-28
☐	**GOTERM_BP_ALL**	RNA splicing	RT		54	2.1E-14	4.9E-12
☐	**SP_PIR_KEYWORDS**	mrna splicing	RT		48	3.1E-14	2.2E-12
☐	**SP_PIR_KEYWORDS**	mrna processing	RT		55	4.8E-14	3.2E-12
☐	**GOTERM_BP_ALL**	mRNA metabolic process	RT		66	1.1E-13	2.3E-11
☐	**GOTERM_BP_ALL**	mRNA processing	RT		60	3.2E-13	6.3E-11
☐	**GOTERM_CC_ALL**	spliceosome	RT		38	1.4E-10	3.4E-9
☐	**SP_PIR_KEYWORDS**	spliceosome	RT		32	7.5E-10	3.0E-8
	Annotation Cluster 9	Enrichment Score: 12.28	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	DNA metabolic process	RT		146	2.0E-27	2.5E-24
☐	**GOTERM_BP_ALL**	DNA repair	RT		61	4.4E-17	1.1E-14
☐	**GOTERM_BP_ALL**	response to DNA damage stimulus	RT		67	1.6E-15	3.8E-13
☐	**SP_PIR_KEYWORDS**	DNA damage	RT		45	1.1E-13	6.8E-12
☐	**GOTERM_BP_ALL**	response to endogenous stimulus	RT		68	3.2E-13	6.2E-11
☐	**SP_PIR_KEYWORDS**	DNA repair	RT		41	1.8E-12	9.9E-11
☐	**GOTERM_BP_ALL**	response to stress	RT		104	6.7E-4	2.7E-2
☐	**GOTERM_BP_ALL**	response to stimulus	RT		135	1.0E0	1.0E0
	Annotation Cluster 10	Enrichment Score: 10.92	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	tRNA metabolic process	RT		44	2.2E-17	6.2E-15
☐	**GOTERM_BP_ALL**	tRNA processing	RT		23	7.7E-10	9.3E-8
☐	**SP_PIR_KEYWORDS**	trna processing	RT		17	1.1E-7	2.9E-6
	Annotation Cluster 11	Enrichment Score: 10.68	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	biosynthetic process	RT		204	2.7E-17	7.4E-15
☐	**GOTERM_BP_ALL**	cellular biosynthetic process	RT		157	2.2E-14	5.0E-12

☐	**GOTERM_BP_ALL**	translation	RT	81	7.4E-9	8.3E-7
☐	**GOTERM_BP_ALL**	macromolecule biosynthetic process	RT	96	4.4E-5	2.6E-3
	Annotation Cluster 12	Enrichment Score: 9.58	G	Count	P_Value	Benjamini
☐	**SMART**	RRM	RT	45	3.5E-14	2.1E-11
☐	**INTERPRO**	RNA recognition motif, RNP-1	RT	40	1.4E-9	8.3E-6
☐	**INTERPRO**	Nucleotide-binding, alpha-beta plait	RT	39	4.2E-9	1.2E-5
☐	**UP_SEQ_FEATURE**	domain:RRM	RT	21	2.2E-8	3.1E-4
	Annotation Cluster 13	Enrichment Score: 8.53	G	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	chaperone	RT	37	6.7E-11	2.9E-9
☐	**GOTERM_BP_ALL**	protein folding	RT	51	1.6E-10	2.3E-8
☐	**GOTERM_MF_ALL**	unfolded protein binding	RT	22	2.3E-6	2.2E-4
	Annotation Cluster 14	Enrichment Score: 8.33	G	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	mitochondrion	RT	150	7.1E-14	2.5E-12
☐	**SP_PIR_KEYWORDS**	Mitochondrion	RT	109	2.2E-11	9.9E-10
☐	**GOTERM_CC_ALL**	mitochondrial part	RT	61	3.8E-7	7.3E-6
☐	**SP_PIR_KEYWORDS**	transit peptide	RT	54	8.4E-4	1.3E-2
	Annotation Cluster 15	Enrichment Score: 8.11	G	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	nucleoside-triphosphatase activity	RT	94	4.6E-11	1.1E-8
☐	**GOTERM_MF_ALL**	pyrophosphatase activity	RT	97	4.8E-11	1.1E-8
☐	**GOTERM_MF_ALL**	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	RT	97	8.0E-11	1.6E-8
☐	**GOTERM_MF_ALL**	hydrolase activity, acting on acid anhydrides	RT	97	1.1E-10	2.1E-8
☐	**GOTERM_MF_ALL**	ATPase activity, coupled	RT	50	1.3E-6	1.5E-4
☐	**GOTERM_MF_ALL**	ATPase activity	RT	55	2.3E-6	2.2E-4
☐	**GOTERM_MF_ALL**	hydrolase activity	RT	241	2.9E-5	2.3E-3
	Annotation Cluster 16	Enrichment Score: 7.89	G	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	nuclear membrane part	RT	28	2.5E-12	8.2E-11
☐	**GOTERM_CC_ALL**	nuclear pore	RT	25	4.7E-12	1.5E-10
☐	**GOTERM_CC_ALL**	nuclear membrane	RT	28	8.6E-12	2.5E-10
☐	**SP_PIR_KEYWORDS**	mrna transport	RT	22	1.1E-11	5.1E-10
☐	**GOTERM_BP_ALL**	mRNA transport	RT	25	2.3E-11	3.4E-9
☐	**GOTERM_CC_ALL**	pore complex	RT	25	7.2E-11	2.0E-9
☐	**GOTERM_BP_ALL**	nucleobase, nucleoside, nucleotide and nucleic acid transport	RT	26	1.5E-10	2.1E-8
☐	**GOTERM_BP_ALL**	RNA transport	RT	25	2.0E-10	2.6E-8
☐	**GOTERM_BP_ALL**	nucleic acid transport	RT	25	2.0E-10	2.6E-8
☐	**GOTERM_BP_ALL**	establishment of RNA localization	RT	25	2.0E-10	2.6E-8
☐	**GOTERM_BP_ALL**	RNA localization	RT	25	2.9E-10	3.7E-8
☐	**GOTERM_BP_ALL**	nucleocytoplasmic transport	RT	35	7.2E-10	8.9E-8
☐	**GOTERM_BP_ALL**	nuclear transport	RT	35	9.3E-10	1.1E-7
☐	**GOTERM_CC_ALL**	nuclear envelope	RT	35	2.8E-9	6.6E-8
☐	**SP_PIR_KEYWORDS**	translocation	RT	21	6.4E-8	1.9E-6
☐	**GOTERM_BP_ALL**	protein targeting	RT	48	3.8E-7	3.5E-5
☐	**GOTERM_BP_ALL**	intracellular protein transport across a membrane	RT	19	6.9E-7	6.3E-5
☐	**GOTERM_BP_ALL**	protein import	RT	23	2.7E-6	2.2E-4
☐	**SP_PIR_KEYWORDS**	nuclear pore complex	RT	11	2.3E-5	4.7E-4
☐	**GOTERM_BP_ALL**	nuclear import	RT	19	4.0E-5	2.4E-3
☐	**GOTERM_BP_ALL**	protein import into nucleus	RT	18	9.6E-5	5.3E-3
☐	**GOTERM_BP_ALL**	intracellular protein transport	RT	65	9.7E-5	5.3E-3
☐	**SP_PIR_KEYWORDS**	protein transport	RT	59	2.0E-4	3.6E-3

☐	GOTERM_CC_ALL	endomembrane system	RT	▬		51	6.2E-3	6.2E-2
	Annotation Cluster 17	Enrichment Score: 6.41	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	envelope	RT	▬		84	2.9E-12	9.2E-11
☐	GOTERM_CC_ALL	organelle envelope	RT	▬		83	5.1E-12	1.5E-10
☐	GOTERM_CC_ALL	mitochondrial part	RT	▬		61	3.8E-7	7.3E-6
☐	GOTERM_CC_ALL	organelle membrane	RT	▬		90	1.1E-5	1.7E-4
☐	GOTERM_CC_ALL	organelle inner membrane	RT	▬		45	2.2E-5	3.1E-4
☐	GOTERM_CC_ALL	mitochondrial envelope	RT	▬		48	6.1E-5	8.4E-4
☐	GOTERM_CC_ALL	mitochondrial inner membrane	RT	▬		42	7.7E-5	1.0E-3
☐	GOTERM_CC_ALL	mitochondrial membrane	RT	▬		45	8.6E-5	1.1E-3
	Annotation Cluster 18	Enrichment Score: 6.37	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Pyrimidine metabolism	RT	▬		37	3.3E-15	7.0E-13
☐	KEGG_PATHWAY	Purine metabolism	RT	▬		39	1.5E-9	8.1E-8
☐	KEGG_PATHWAY	DNA polymerase	RT	▬		12	7.4E-6	2.2E-4
☐	GOTERM_MF_ALL	DNA-directed DNA polymerase activity	RT	▬		12	2.0E-5	1.7E-3
☐	GOTERM_MF_ALL	nucleotidyltransferase activity	RT	▬		26	2.9E-5	2.3E-3
☐	SP_PIR_KEYWORDS	DNA-directed DNA polymerase	RT	▬		9	2.2E-4	3.9E-3
☐	SP_PIR_KEYWORDS	Nucleotidyltransferase	RT	▬		17	5.5E-4	9.1E-3
	Annotation Cluster 19	Enrichment Score: 6.26	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	nucleolus	RT	▬		49	3.1E-17	1.3E-15
☐	GOTERM_CC_ALL	organelle lumen	RT	▬		132	1.0E-10	2.7E-9
☐	GOTERM_CC_ALL	membrane-enclosed lumen	RT	▬		132	1.0E-10	2.7E-9
☐	GOTERM_CC_ALL	nuclear lumen	RT	▬		106	1.4E-6	2.4E-5
☐	GOTERM_CC_ALL	nucleoplasm	RT	▬		63	1.8E-1	7.1E-1
☐	GOTERM_CC_ALL	nucleoplasm part	RT	▬		58	2.4E-1	8.1E-1
☐	GOTERM_CC_ALL	transcription factor complex	RT	▬		33	9.2E-1	1.0E0
	Annotation Cluster 20	Enrichment Score: 6.08	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	ribonucleoprotein complex	RT	▬		114	1.2E-27	9.4E-26
☐	SP_PIR_KEYWORDS	ribonucleoprotein	RT	▬		68	3.9E-17	3.7E-15
☐	SP_PIR_KEYWORDS	ribosomal protein	RT	▬		40	7.3E-8	2.0E-6
☐	GOTERM_CC_ALL	ribosome	RT	▬		38	9.8E-7	1.8E-5
☐	GOTERM_MF_ALL	structural constituent of ribosome	RT	▬		36	2.0E-6	2.0E-4
☐	GOTERM_CC_ALL	mitochondrial ribosome	RT	▬		14	1.8E-5	2.7E-4
☐	GOTERM_CC_ALL	organellar ribosome	RT	▬		14	1.8E-5	2.7E-4
☐	GOTERM_CC_ALL	mitochondrial lumen	RT	▬		16	1.8E-4	2.2E-3
☐	GOTERM_CC_ALL	mitochondrial matrix	RT	▬		16	1.8E-4	2.2E-3
☐	GOTERM_CC_ALL	ribosomal subunit	RT	▬		13	1.2E-2	1.1E-1
☐	GOTERM_CC_ALL	organellar large ribosomal subunit	RT	▬		5	5.8E-2	3.7E-1
☐	GOTERM_CC_ALL	mitochondrial large ribosomal subunit	RT	▬		5	5.8E-2	3.7E-1
☐	GOTERM_CC_ALL	large ribosomal subunit	RT	▬		6	1.6E-1	6.9E-1
☐	GOTERM_MF_ALL	structural molecule activity	RT	▬		59	1.8E-1	9.6E-1
	Annotation Cluster 21	Enrichment Score: 5.99	G		🟩	Count	P_Value	Benjamini
☐	SMART	AAA	RT	▬		23	7.4E-8	1.5E-5
☐	INTERPRO	AAA ATPase, core	RT	▬		16	6.8E-7	9.8E-4
☐	INTERPRO	AAA+ ATPase, core	RT	▬		19	2.1E-5	1.5E-2
	Annotation Cluster 22	Enrichment Score: 5.86	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	tRNA metabolic process	RT	▬		44	2.2E-17	6.2E-15
☐	SP_PIR_KEYWORDS	protein biosynthesis	RT	▬		36	9.2E-9	3.1E-7
☐	SP_PIR_KEYWORDS	aminoacyl-tRNA synthetase	RT	▬		18	1.4E-8	4.6E-7
☐	GOTERM_BP_ALL	tRNA aminoacylation	RT	▬		20	3.4E-7	3.3E-5

☐	GOTERM_BP_ALL	tRNA aminoacylation for protein translation	RT			20	3.4E-7	3.3E-5
☐	GOTERM_BP_ALL	amino acid activation	RT			20	3.4E-7	3.3E-5
☐	KEGG_PATHWAY	Aminoacyl-tRNA biosynthesis	RT			15	7.0E-7	3.0E-5
☐	GOTERM_MF_ALL	ligase activity, forming carbon-oxygen bonds	RT			20	7.5E-7	1.0E-4
☐	GOTERM_MF_ALL	ligase activity, forming aminoacyl-tRNA and related compounds	RT			20	7.5E-7	1.0E-4
☐	GOTERM_MF_ALL	aminoacyl-tRNA ligase activity	RT			20	7.5E-7	1.0E-4
☐	SP_PIR_KEYWORDS	ligase	RT			46	5.9E-6	1.3E-4
☐	GOTERM_BP_ALL	amino acid and derivative metabolic process	RT			56	9.5E-6	7.0E-4
☐	GOTERM_BP_ALL	nitrogen compound metabolic process	RT			65	2.7E-5	1.6E-3
☐	GOTERM_BP_ALL	amino acid metabolic process	RT			45	4.3E-5	2.6E-3
☐	GOTERM_MF_ALL	ligase activity	RT			55	5.9E-5	4.2E-3
☐	GOTERM_BP_ALL	amine metabolic process	RT			59	1.2E-4	6.1E-3
☐	GOTERM_BP_ALL	carboxylic acid metabolic process	RT			67	2.1E-3	7.2E-2
☐	GOTERM_BP_ALL	organic acid metabolic process	RT			67	2.2E-3	7.5E-2
☐	INTERPRO	Aminoacyl-tRNA synthetase, class I	RT			8	8.0E-3	6.2E-1
	Annotation Cluster 23	Enrichment Score: 5.63	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	nuclease activity	RT			37	1.2E-8	1.9E-6
☐	GOTERM_MF_ALL	exonuclease activity	RT			21	2.0E-8	3.2E-6
☐	SP_PIR_KEYWORDS	Exonuclease	RT			15	4.1E-7	1.0E-5
☐	SP_PIR_KEYWORDS	Exosome	RT			6	5.8E-4	9.5E-3
☐	SP_PIR_KEYWORDS	nuclease	RT			17	1.2E-3	1.7E-2
	Annotation Cluster 24	Enrichment Score: 5.61	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Biosynthesis of steroids	RT			17	1.5E-11	1.0E-9
☐	GOTERM_BP_ALL	sterol biosynthetic process	RT			19	2.4E-11	3.5E-9
☐	SP_PIR_KEYWORDS	lipid synthesis	RT			28	1.2E-9	4.6E-8
☐	SP_PIR_KEYWORDS	sterol biosynthesis	RT			14	3.0E-9	1.1E-7
☐	SP_PIR_KEYWORDS	steroid biosynthesis	RT			16	5.1E-8	1.5E-6
☐	GOTERM_BP_ALL	cholesterol biosynthetic process	RT			14	5.3E-8	5.5E-6
☐	GOTERM_BP_ALL	sterol metabolic process	RT			23	1.1E-6	9.6E-5
☐	SP_PIR_KEYWORDS	cholesterol biosynthesis	RT			10	1.3E-6	2.9E-5
☐	GOTERM_BP_ALL	lipid biosynthetic process	RT			48	1.8E-6	1.5E-4
☐	GOTERM_BP_ALL	steroid biosynthetic process	RT			22	2.7E-6	2.2E-4
☐	GOTERM_BP_ALL	isoprenoid biosynthetic process	RT			10	1.7E-5	1.2E-3
☐	GOTERM_BP_ALL	cholesterol metabolic process	RT			18	1.7E-4	8.8E-3
☐	GOTERM_BP_ALL	alcohol metabolic process	RT			44	6.5E-4	2.6E-2
☐	GOTERM_BP_ALL	steroid metabolic process	RT			28	7.9E-4	3.1E-2
☐	GOTERM_BP_ALL	isoprenoid metabolic process	RT			10	2.2E-3	7.5E-2
☐	GOTERM_BP_ALL	cellular lipid metabolic process	RT			59	1.4E-1	9.2E-1
☐	GOTERM_BP_ALL	lipid metabolic process	RT			60	4.8E-1	1.0E0
	Annotation Cluster 25	Enrichment Score: 4.89	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	chromosome segregation	RT			27	5.5E-13	9.5E-11
☐	GOTERM_BP_ALL	mitotic sister chromatid segregation	RT			11	1.5E-5	1.0E-3
☐	GOTERM_BP_ALL	sister chromatid segregation	RT			11	2.3E-5	1.5E-3
☐	GOTERM_BP_ALL	mitotic chromosome condensation	RT			7	1.4E-3	5.1E-2
☐	GOTERM_BP_ALL	chromosome condensation	RT			8	1.9E-3	6.8E-2
☐	SP_PIR_KEYWORDS	dna condensation	RT			5	9.3E-3	1.1E-1
	Annotation Cluster 26	Enrichment Score: 4.84	G		🟩	Count	P_Value	Benjamini
☐	SMART	WD40	RT			42	1.2E-9	3.5E-7

☐	INTERPRO	WD40 repeat	RT			38	7.6E-6	8.7E-3
☐	UP_SEQ_FEATURE	repeat:WD 4	RT			29	1.2E-5	3.2E-2
☐	SP_PIR_KEYWORDS	wd repeat	RT			43	1.6E-5	3.3E-4
☐	UP_SEQ_FEATURE	repeat:WD 2	RT			30	1.7E-5	3.4E-2
☐	UP_SEQ_FEATURE	repeat:WD 1	RT			30	1.7E-5	3.4E-2
☐	UP_SEQ_FEATURE	repeat:WD 5	RT			27	2.6E-5	4.6E-2
☐	UP_SEQ_FEATURE	repeat:WD 3	RT			29	3.5E-5	5.4E-2
☐	UP_SEQ_FEATURE	repeat:WD 6	RT			21	2.2E-4	2.5E-1
☐	UP_SEQ_FEATURE	repeat:WD 7	RT			14	4.0E-3	9.6E-1
	Annotation Cluster 27	Enrichment Score: 4.77	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	transferase activity, transferring one-carbon groups	RT			39	3.4E-8	5.0E-6
☐	GOTERM_MF_ALL	methyltransferase activity	RT			38	6.4E-8	9.1E-6
☐	SP_PIR_KEYWORDS	methyltransferase	RT			25	9.5E-5	1.8E-3
☐	GOTERM_MF_ALL	S-adenosylmethionine-dependent methyltransferase activity	RT			16	1.9E-3	8.7E-2
☐	SP_PIR_KEYWORDS	s-adenosyl-l-methionine	RT			15	3.4E-3	4.3E-2
	Annotation Cluster 28	Enrichment Score: 4.6	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein-RNA complex assembly	RT			25	4.4E-7	4.0E-5
☐	GOTERM_BP_ALL	nuclear mRNA splicing, via spliceosome	RT			17	2.6E-5	1.7E-3
☐	GOTERM_BP_ALL	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	RT			17	2.6E-5	1.7E-3
☐	GOTERM_BP_ALL	RNA splicing, via transesterification reactions	RT			17	2.6E-5	1.7E-3
☐	GOTERM_BP_ALL	spliceosome assembly	RT			9	1.2E-3	4.7E-2
	Annotation Cluster 29	Enrichment Score: 4.54	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	replication fork	RT			15	6.1E-9	1.4E-7
☐	GOTERM_CC_ALL	nuclear chromosome part	RT			24	3.9E-8	8.1E-7
☐	KEGG_PATHWAY	DNA polymerase	RT			12	7.4E-6	2.2E-4
☐	GOTERM_CC_ALL	replisome	RT			8	1.0E-5	1.6E-4
☐	GOTERM_CC_ALL	nuclear replisome	RT			8	1.0E-5	1.6E-4
☐	GOTERM_CC_ALL	nuclear replication fork	RT			8	1.0E-5	1.6E-4
☐	GOTERM_CC_ALL	alpha DNA polymerase:primase complex	RT			4	2.6E-3	2.8E-2
☐	GOTERM_MF_ALL	DNA primase activity	RT			3	4.2E-2	6.7E-1
☐	GOTERM_CC_ALL	DNA replication factor A complex	RT			3	6.6E-2	4.0E-1
	Annotation Cluster 30	Enrichment Score: 4.51	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein-RNA complex assembly	RT			25	4.4E-7	4.0E-5
☐	GOTERM_BP_ALL	cellular component assembly	RT			61	1.4E-4	7.3E-3
☐	GOTERM_BP_ALL	macromolecular complex assembly	RT			52	4.7E-4	2.1E-2
	Annotation Cluster 31	Enrichment Score: 4.03	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	carbon-oxygen lyase activity	RT			18	5.7E-5	4.2E-3
☐	GOTERM_MF_ALL	lyase activity	RT			32	8.9E-5	6.1E-3
☐	GOTERM_MF_ALL	hydro-lyase activity	RT			16	9.8E-5	6.5E-3
☐	GOTERM_MF_ALL	pseudouridylate synthase activity	RT			7	1.5E-4	9.7E-3
	Annotation Cluster 32	Enrichment Score: 3.97	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	spindle	RT			19	4.5E-7	8.5E-6
☐	GOTERM_BP_ALL	regulation of mitosis	RT			13	4.3E-4	1.9E-2
☐	GOTERM_CC_ALL	spindle pole	RT			7	6.3E-3	6.2E-2
	Annotation Cluster 33	Enrichment Score: 3.85	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	DNA replication initiation	RT			13	3.5E-9	4.1E-7
☐	INTERPRO	Nucleic acid-binding, OB-fold	RT			18	2.1E-7	4.1E-4
☐	SMART	MCM	RT			7	2.1E-6	2.5E-4

☐	**UP_SEQ_FEATURE**	domain:MCM	RT	7	5.6E-6	3.9E-2
☐	**INTERPRO**	MCM	RT	7	9.4E-6	7.8E-3
☐	**SP_PIR_KEYWORDS**	DNA replication initiation	RT	5	3.2E-4	5.6E-3
☐	**GOTERM_MF_ALL**	single-stranded DNA binding	RT	10	1.4E-3	6.9E-2
☐	**GOTERM_BP_ALL**	DNA geometric change	RT	6	4.4E-3	1.3E-1
☐	**GOTERM_BP_ALL**	DNA duplex unwinding	RT	6	4.4E-3	1.3E-1
☐	**GOTERM_BP_ALL**	DNA unwinding during replication	RT	6	4.4E-3	1.3E-1
☐	**SP_PIR_KEYWORDS**	heterohexamer	RT	3	2.4E-2	2.2E-1
☐	**SP_PIR_KEYWORDS**	zinc finger	RT	7	7.4E-1	1.0E0
	Annotation Cluster 34	Enrichment Score: 3.74	G	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	domain:RRM 2	RT	17	9.5E-6	4.4E-2
☐	**UP_SEQ_FEATURE**	domain:RRM 1	RT	17	9.5E-6	4.4E-2
☐	**UP_SEQ_FEATURE**	domain:RRM 3	RT	6	6.8E-2	1.0E0
	Annotation Cluster 35	Enrichment Score: 3.58	G	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	centrosome	RT	17	4.7E-5	6.6E-4
☐	**GOTERM_CC_ALL**	microtubule organizing center	RT	18	2.4E-4	2.9E-3
☐	**GOTERM_CC_ALL**	microtubule organizing center part	RT	8	1.6E-3	1.8E-2
	Annotation Cluster 36	Enrichment Score: 3.41	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	protein-RNA complex assembly	RT	25	4.4E-7	4.0E-5
☐	**GOTERM_BP_ALL**	translational initiation	RT	15	3.2E-4	1.5E-2
☐	**GOTERM_MF_ALL**	translation initiation factor activity	RT	18	7.6E-4	3.9E-2
☐	**GOTERM_MF_ALL**	translation factor activity, nucleic acid binding	RT	22	2.4E-3	1.1E-1
☐	**SP_PIR_KEYWORDS**	initiation factor	RT	15	3.0E-3	3.8E-2
☐	**GOTERM_MF_ALL**	translation regulator activity	RT	22	4.4E-3	1.7E-1
	Annotation Cluster 37	Enrichment Score: 3.38	G	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	microtubule cytoskeleton	RT	63	2.3E-9	5.7E-8
☐	**GOTERM_CC_ALL**	microtubule	RT	43	4.7E-8	9.5E-7
☐	**SP_PIR_KEYWORDS**	microtubule	RT	35	3.6E-7	9.1E-6
☐	**GOTERM_BP_ALL**	microtubule-based process	RT	40	2.8E-6	2.2E-4
☐	**SMART**	KISc	RT	12	1.7E-5	1.5E-3
☐	**GOTERM_CC_ALL**	cytoskeletal part	RT	76	7.4E-5	1.0E-3
☐	**INTERPRO**	Kinesin, motor region	RT	12	1.9E-4	7.4E-2
☐	**GOTERM_BP_ALL**	microtubule cytoskeleton organization and biogenesis	RT	18	4.1E-4	1.8E-2
☐	**GOTERM_BP_ALL**	microtubule-based movement	RT	21	9.2E-4	3.5E-2
☐	**GOTERM_BP_ALL**	cytoskeleton-dependent intracellular transport	RT	22	2.7E-3	8.9E-2
☐	**GOTERM_MF_ALL**	microtubule motor activity	RT	14	1.0E-2	3.1E-1
☐	**SP_PIR_KEYWORDS**	motor protein	RT	16	1.9E-2	2.0E-1
☐	**GOTERM_CC_ALL**	microtubule associated complex	RT	14	1.2E-1	5.8E-1
☐	**GOTERM_CC_ALL**	cytoskeleton	RT	89	1.4E-1	6.5E-1
☐	**GOTERM_CC_ALL**	kinesin complex	RT	6	1.6E-1	6.9E-1
☐	**GOTERM_MF_ALL**	motor activity	RT	17	1.7E-1	9.5E-1
☐	**GOTERM_BP_ALL**	cytoskeleton organization and biogenesis	RT	53	1.7E-1	9.5E-1
	Annotation Cluster 38	Enrichment Score: 3.34	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	intracellular transport	RT	106	5.1E-8	5.4E-6
☐	**GOTERM_BP_ALL**	cellular component organization and biogenesis	RT	298	2.8E-7	2.8E-5
☐	**GOTERM_BP_ALL**	protein targeting	RT	48	3.8E-7	3.5E-5
☐	**GOTERM_BP_ALL**	establishment of cellular localization	RT	118	3.9E-6	3.0E-4
☐	**GOTERM_BP_ALL**	cellular localization	RT	120	4.6E-6	3.5E-4

☐	GOTERM_BP_ALL	intracellular protein transport	RT	65	9.7E-5	5.3E-3
☐	SP_PIR_KEYWORDS	protein transport	RT	59	2.0E-4	3.6E-3
☐	GOTERM_BP_ALL	macromolecule localization	RT	106	2.2E-4	1.1E-2
☐	GOTERM_BP_ALL	establishment of protein localization	RT	89	3.9E-3	1.2E-1
☐	GOTERM_BP_ALL	protein localization	RT	95	4.5E-3	1.4E-1
☐	GOTERM_BP_ALL	protein transport	RT	84	4.9E-3	1.4E-1
☐	SP_PIR_KEYWORDS	transport	RT	119	4.8E-1	9.9E-1
☐	GOTERM_BP_ALL	establishment of localization	RT	231	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	transport	RT	221	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	localization	RT	252	8.6E-1	1.0E0
	Annotation Cluster 39	Enrichment Score: 3.33	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	helicase activity	RT	36	6.9E-9	1.2E-6
☐	SMART	DEXDc	RT	23	2.5E-7	3.8E-5
☐	SP_PIR_KEYWORDS	helicase	RT	29	6.2E-7	1.5E-5
☐	GOTERM_MF_ALL	ATP-dependent helicase activity	RT	25	7.5E-6	6.7E-4
☐	SMART	HELICc	RT	19	8.7E-6	8.7E-4
☐	INTERPRO	DEAD-like helicase, N-terminal	RT	20	1.2E-4	6.5E-2
☐	UP_SEQ_FEATURE	domain:Helicase ATP-binding	RT	14	1.4E-3	7.7E-1
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT	16	3.8E-3	5.1E-1
☐	INTERPRO	DNA/RNA helicase, C-terminal	RT	15	6.8E-3	5.8E-1
☐	UP_SEQ_FEATURE	domain:Helicase C-terminal	RT	12	7.9E-3	1.0E0
☐	INTERPRO	SNF2-related	RT	8	8.0E-3	6.2E-1
☐	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT	10	1.9E-2	8.7E-1
☐	UP_SEQ_FEATURE	short sequence motif:Q motif	RT	5	2.7E-1	1.0E0
☐	INTERPRO	RNA helicase, DEAD-box type, Q motif	RT	5	2.7E-1	1.0E0
☐	UP_SEQ_FEATURE	short sequence motif:DEAD box	RT	4	4.2E-1	1.0E0
	Annotation Cluster 40	Enrichment Score: 3.32	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	snoRNA binding	RT	6	2.5E-4	1.4E-2
☐	GOTERM_CC_ALL	nucleolar part	RT	12	2.5E-4	2.9E-3
☐	GOTERM_CC_ALL	small nucleolar ribonucleoprotein complex	RT	7	1.8E-3	1.9E-2
	Annotation Cluster 41	Enrichment Score: 3.25	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	nucleoside monophosphate biosynthetic process	RT	10	9.8E-6	7.1E-4
☐	GOTERM_BP_ALL	nucleoside monophosphate metabolic process	RT	10	1.7E-5	1.2E-3
☐	GOTERM_BP_ALL	ribonucleoside monophosphate biosynthetic process	RT	9	3.1E-5	1.9E-3
☐	GOTERM_BP_ALL	ribonucleoside monophosphate metabolic process	RT	9	5.4E-5	3.1E-3
☐	SP_PIR_KEYWORDS	purine biosynthesis	RT	7	3.3E-4	5.6E-3
☐	GOTERM_BP_ALL	purine ribonucleoside monophosphate biosynthetic process	RT	5	1.4E-2	3.2E-1
☐	GOTERM_BP_ALL	purine nucleoside monophosphate biosynthetic process	RT	5	1.4E-2	3.2E-1
☐	GOTERM_BP_ALL	purine ribonucleoside monophosphate metabolic process	RT	5	1.9E-2	4.0E-1
☐	GOTERM_BP_ALL	purine nucleoside monophosphate metabolic process	RT	5	1.9E-2	4.0E-1
	Annotation Cluster 42	Enrichment Score: 3.19	G	Count	P_Value	Benjamini
☐	INTERPRO	Chaperonin Cpn60	RT	7	6.1E-5	3.8E-2
☐	INTERPRO	Chaperonin TCP-1	RT	7	1.2E-4	5.8E-2
☐	PIR_SUPERFAMILY	PIRSF002584:molecular chaperone t-complex-type	RT	7	2.3E-4	3.0E-1
☐	GOTERM_CC_ALL	chaperonin-containing T-complex	RT	6	2.4E-4	2.9E-3
☐	INTERPRO	Chaperonin Cpn60/TCP-1	RT	6	2.2E-3	4.1E-1

☐	GOTERM_CC_ALL	cytosolic part	RT	15	7.5E-2	4.3E-1
	Annotation Cluster 43	Enrichment Score: 3.1	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	cell cycle control	RT	15	4.5E-9	1.6E-7
☐	GOTERM_MF_ALL	cyclin-dependent protein kinase regulator activity	RT	10	8.8E-5	6.2E-3
☐	INTERPRO	Cyclin, C-terminal	RT	8	1.9E-4	7.1E-2
☐	PIR_SUPERFAMILY	PIRSF001771:cyclin, A/B/D/E types	RT	7	2.3E-4	3.0E-1
☐	INTERPRO	Cyclin, A/B/D/E	RT	6	8.0E-4	2.1E-1
☐	SMART	CYCLIN	RT	9	1.4E-3	8.1E-2
☐	INTERPRO	Cyclin	RT	9	4.6E-3	5.6E-1
☐	INTERPRO	Cyclin-related	RT	9	5.7E-3	5.5E-1
☐	INTERPRO	Cyclin, N-terminal	RT	8	6.4E-3	5.9E-1
☐	GOTERM_MF_ALL	protein kinase regulator activity	RT	14	7.2E-3	2.5E-1
☐	GOTERM_MF_ALL	kinase regulator activity	RT	16	7.6E-3	2.6E-1
☐	KEGG_PATHWAY	p53 signaling pathway	RT	14	9.0E-3	1.5E-1
☐	SP_PIR_KEYWORDS	cyclin	RT	12	3.6E-2	3.0E-1
	Annotation Cluster 44	Enrichment Score: 3.08	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	meiotic cell cycle	RT	19	1.8E-4	9.1E-3
☐	GOTERM_BP_ALL	meiosis	RT	18	4.8E-4	2.1E-2
☐	GOTERM_BP_ALL	M phase of meiotic cell cycle	RT	18	4.8E-4	2.1E-2
☐	GOTERM_BP_ALL	meiosis I	RT	8	1.1E-2	2.8E-1
	Annotation Cluster 45	Enrichment Score: 3.08	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	isomerase	RT	30	1.2E-6	2.8E-5
☐	GOTERM_MF_ALL	isomerase activity	RT	35	1.5E-6	1.6E-4
☐	SP_PIR_KEYWORDS	Rotamase	RT	12	1.4E-4	2.7E-3
☐	GOTERM_MF_ALL	peptidyl-prolyl cis-trans isomerase activity	RT	12	1.5E-4	9.7E-3
☐	GOTERM_MF_ALL	cis-trans isomerase activity	RT	12	2.0E-4	1.2E-2
☐	UP_SEQ_FEATURE	domain:PPIase cyclophilin-type	RT	5	2.4E-2	1.0E0
☐	INTERPRO	Peptidyl-prolyl cis-trans isomerase, cyclophilin-type	RT	5	5.2E-2	9.7E-1
☐	PIR_SUPERFAMILY	PIRSF001467:peptidylprolyl isomerase	RT	3	1.4E-1	1.0E0
☐	INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type	RT	4	1.5E-1	1.0E0
	Annotation Cluster 46	Enrichment Score: 3.07	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	nucleobase metabolic process	RT	10	9.8E-6	7.1E-4
☐	GOTERM_BP_ALL	heterocycle metabolic process	RT	19	4.8E-4	2.0E-2
☐	GOTERM_BP_ALL	purine base metabolic process	RT	6	5.8E-4	2.4E-2
☐	GOTERM_BP_ALL	aromatic compound metabolic process	RT	16	2.0E-1	9.7E-1
	Annotation Cluster 47	Enrichment Score: 2.95	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	nucleotidyltransferase activity	RT	26	2.9E-5	2.3E-3
☐	GOTERM_MF_ALL	DNA-directed RNA polymerase activity	RT	12	3.3E-4	1.8E-2
☐	SP_PIR_KEYWORDS	dna-directed rna polymerase	RT	10	2.2E-3	3.0E-2
☐	KEGG_PATHWAY	RNA polymerase	RT	6	7.4E-2	5.4E-1
	Annotation Cluster 48	Enrichment Score: 2.94	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	kinetochore	RT	12	2.2E-6	3.7E-5
☐	GOTERM_CC_ALL	condensed chromosome kinetochore	RT	4	1.9E-2	1.6E-1
☐	GOTERM_CC_ALL	condensed chromosome, pericentric region	RT	4	3.9E-2	2.8E-1
	Annotation Cluster 49	Enrichment Score: 2.85	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	proteasome	RT	15	2.1E-4	3.8E-3
☐	KEGG_PATHWAY	Proteasome	RT	10	1.9E-3	4.0E-2
☐	GOTERM_CC_ALL	proteasome complex (sensu Eukaryota)	RT	9	7.0E-3	6.7E-2

					Count	P_Value	Benjamini
	Annotation Cluster 50	Enrichment Score: 2.77	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell cycle checkpoint	RT		12	4.2E-4	1.9E-2
☐	GOTERM_BP_ALL	regulation of mitosis	RT		13	4.3E-4	1.9E-2
☐	GOTERM_BP_ALL	spindle checkpoint	RT		5	1.9E-3	6.8E-2
☐	GOTERM_BP_ALL	mitotic cell cycle checkpoint	RT		8	3.5E-3	1.1E-1
☐	GOTERM_BP_ALL	mitotic cell cycle spindle assembly checkpoint	RT		4	1.2E-2	3.0E-1
	Annotation Cluster 51	Enrichment Score: 2.73	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Phosphoribosyltransferase	RT		8	8.1E-6	7.8E-3
☐	GOTERM_BP_ALL	nucleoside monophosphate biosynthetic process	RT		10	9.8E-6	7.1E-4
☐	GOTERM_BP_ALL	nucleoside monophosphate metabolic process	RT		10	1.7E-5	1.2E-3
☐	GOTERM_BP_ALL	ribonucleoside monophosphate biosynthetic process	RT		9	3.1E-5	1.9E-3
☐	GOTERM_BP_ALL	ribonucleoside monophosphate metabolic process	RT		9	5.4E-5	3.1E-3
☐	SP_PIR_KEYWORDS	nucleotide biosynthesis	RT		6	5.8E-4	9.5E-3
☐	INTERPRO	Phosphoribosyl pyrophosphate synthetase	RT		3	3.9E-2	9.4E-1
☐	GOTERM_MF_ALL	lipoate-protein ligase activity	RT		3	6.6E-2	7.6E-1
☐	INTERPRO	Ribose-phosphate pyrophosphokinase	RT		3	8.7E-2	9.9E-1
☐	GOTERM_MF_ALL	ribose phosphate diphosphokinase activity	RT		3	1.2E-1	9.1E-1
☐	GOTERM_MF_ALL	diphosphotransferase activity	RT		3	1.5E-1	9.4E-1
☐	GOTERM_MF_ALL	carbohydrate kinase activity	RT		5	2.8E-1	9.9E-1
	Annotation Cluster 52	Enrichment Score: 2.73	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of DNA metabolic process	RT		8	1.7E-4	8.9E-3
☐	GOTERM_BP_ALL	negative regulation of DNA replication	RT		6	5.8E-4	2.4E-2
☐	GOTERM_BP_ALL	regulation of DNA replication	RT		7	1.4E-3	5.1E-2
☐	GOTERM_BP_ALL	regulation of DNA metabolic process	RT		9	2.2E-3	7.4E-2
☐	GOTERM_BP_ALL	DNA integrity checkpoint	RT		6	7.2E-2	7.7E-1
	Annotation Cluster 53	Enrichment Score: 2.67	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	outer membrane	RT		21	1.6E-5	2.4E-4
☐	SP_PIR_KEYWORDS	nuclear pore complex	RT		11	2.3E-5	4.7E-4
☐	SP_PIR_KEYWORDS	porin	RT		12	2.6E-5	5.2E-4
☐	GOTERM_MF_ALL	porin activity	RT		10	3.6E-4	2.0E-2
☐	GOTERM_MF_ALL	nucleocytoplasmic transporter activity	RT		5	8.5E-3	2.7E-1
☐	GOTERM_MF_ALL	wide pore channel activity	RT		10	1.4E-2	3.8E-1
☐	GOTERM_MF_ALL	passive transmembrane transporter activity	RT		14	1.0E0	1.0E0
☐	GOTERM_MF_ALL	channel activity	RT		14	1.0E0	1.0E0
	Annotation Cluster 54	Enrichment Score: 2.66	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	DNA helicase activity	RT		11	1.2E-5	1.0E-3
☐	GOTERM_MF_ALL	ATP-dependent DNA helicase activity	RT		7	4.9E-4	2.6E-2
☐	SMART	DEXDc2	RT		4	2.6E-3	1.2E-1
☐	SMART	HELICc2	RT		4	2.6E-3	1.2E-1
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding, DinG/Rad3-type	RT		4	5.5E-3	5.5E-1
☐	INTERPRO	Helicase, ATP-dependent, c2 type	RT		4	5.5E-3	5.5E-1
☐	INTERPRO	DNA helicase (DNA repair), Rad3 type	RT		4	5.5E-3	5.5E-1
☐	INTERPRO	DEAD2	RT		4	5.5E-3	5.5E-1
☐	COG_ONTOLOGY	Transcription / DNA replication, recombination, and repair	RT		5	3.1E-2	5.6E-1
	Annotation Cluster 55	Enrichment Score: 2.51	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	interphase of mitotic cell cycle	RT		16	2.0E-4	9.9E-3
☐	GOTERM_BP_ALL	interphase	RT		16	2.0E-4	9.9E-3

☐	GOTERM_BP_ALL	S phase	RT		7	3.3E-4	1.5E-2
☐	GOTERM_BP_ALL	S phase of mitotic cell cycle	RT		7	3.3E-4	1.5E-2
☐	GOTERM_BP_ALL	regulation of progression through mitotic cell cycle	RT		7	2.2E-2	4.5E-1
☐	GOTERM_BP_ALL	regulation of progression through S phase	RT		3	1.6E-1	9.4E-1
☐	GOTERM_BP_ALL	regulation of S phase of mitotic cell cycle	RT		3	1.6E-1	9.4E-1
	Annotation Cluster 56	Enrichment Score: 2.5	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	WHEP-TRS	RT		5	2.5E-4	8.2E-2
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II	RT		6	3.3E-3	4.7E-1
☐	INTERPRO	Anticodon-binding	RT		5	4.8E-3	5.6E-1
☐	INTERPRO	Aminoacyl-tRNA synthetase, class II (G, H, P and S)	RT		4	2.5E-2	9.1E-1
	Annotation Cluster 57	Enrichment Score: 2.47	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	WHEP-TRS	RT		5	2.5E-4	8.2E-2
☐	INTERPRO	S15/NS1, RNA-binding	RT		4	2.4E-3	3.9E-1
☐	INTERPRO	Aminoacyl-tRNA synthetase, class I	RT		8	8.0E-3	6.2E-1
☐	INTERPRO	Rossmann-like alpha/beta/alpha sandwich fold	RT		7	2.9E-2	9.3E-1
	Annotation Cluster 58	Enrichment Score: 2.46	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	short sequence motif:Histidine box-1	RT		4	3.5E-3	9.5E-1
☐	UP_SEQ_FEATURE	short sequence motif:Histidine box-2	RT		4	3.5E-3	9.5E-1
☐	UP_SEQ_FEATURE	short sequence motif:Histidine box-3	RT		4	3.5E-3	9.5E-1
	Annotation Cluster 59	Enrichment Score: 2.45	G	🟩	Count	P_Value	Benjamini
☐	SMART	Sm	RT		7	1.1E-3	6.9E-2
☐	INTERPRO	Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core	RT		7	4.0E-3	5.2E-1
☐	INTERPRO	Like-Sm ribonucleoprotein, core	RT		7	5.3E-3	5.9E-1
☐	GOTERM_BP_ALL	mRNA catabolic process	RT		9	6.8E-3	1.8E-1
	Annotation Cluster 60	Enrichment Score: 2.45	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	double-strand break repair	RT		9	1.2E-3	4.7E-2
☐	GOTERM_BP_ALL	double-strand break repair via homologous recombination	RT		5	6.0E-3	1.7E-1
☐	GOTERM_BP_ALL	recombinational repair	RT		5	6.0E-3	1.7E-1
	Annotation Cluster 61	Enrichment Score: 2.44	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	endonuclease activity	RT		20	1.9E-4	1.1E-2
☐	GOTERM_MF_ALL	tRNA-specific ribonuclease activity	RT		6	1.6E-3	7.6E-2
☐	GOTERM_MF_ALL	ribonuclease activity	RT		14	2.8E-3	1.2E-1
☐	GOTERM_MF_ALL	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	RT		8	5.0E-3	1.9E-1
☐	GOTERM_MF_ALL	ribonuclease P activity	RT		5	5.5E-3	2.0E-1
☐	GOTERM_MF_ALL	endoribonuclease activity, producing 5'-phosphomonoesters	RT		7	1.3E-2	3.7E-1
☐	GOTERM_MF_ALL	endoribonuclease activity	RT		9	3.0E-2	5.7E-1
	Annotation Cluster 62	Enrichment Score: 2.41	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	centrosome organization and biogenesis	RT		7	9.1E-4	3.5E-2
☐	GOTERM_BP_ALL	microtubule organizing center organization and biogenesis	RT		7	1.4E-3	5.1E-2
☐	GOTERM_BP_ALL	centrosome cycle	RT		6	1.8E-3	6.6E-2
☐	GOTERM_BP_ALL	centrosome duplication	RT		3	9.8E-2	8.5E-1
	Annotation Cluster 63	Enrichment Score: 2.39	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	lipid synthesis	RT		28	1.2E-9	4.6E-8
☐	SP_PIR_KEYWORDS	fatty acid biosynthesis	RT		12	6.8E-4	1.1E-2
☐	GOTERM_BP_ALL	fatty acid biosynthetic process	RT		13	1.7E-2	3.8E-1
☐	KEGG_PATHWAY	Polyunsaturated fatty acid biosynthesis	RT		6	1.9E-2	2.5E-1
☐	GOTERM_BP_ALL	organic acid biosynthetic process	RT		13	2.6E-2	4.9E-1

☐	GOTERM_BP_ALL	carboxylic acid biosynthetic process	RT	13	2.6E-2	4.9E-1
☐	GOTERM_BP_ALL	monocarboxylic acid metabolic process	RT	21	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	fatty acid metabolic process	RT	15	6.3E-1	1.0E0
	Annotation Cluster 64	Enrichment Score: 2.27	G	Count	P_Value	Benjamini
☐	BIOCARTA	Cyclins and Cell Cycle Regulation	RT	11	2.0E-4	2.9E-2
☐	BIOCARTA	E2F1 Destruction Pathway	RT	6	1.3E-3	1.1E-1
☐	BIOCARTA	Regulation of p27 Phosphorylation during Cell Cycle Progression	RT	6	3.9E-3	1.5E-1
☐	BIOCARTA	Cell Cycle	RT	9	6.1E-3	2.0E-1
☐	BIOCARTA	Cyclin E Destruction Pathway	RT	5	6.8E-3	1.9E-1
☐	BIOCARTA	Influence of Ras and Rho proteins on G1 to S Transition	RT	8	2.7E-2	4.0E-1
☐	BIOCARTA	p53 Signaling Pathway	RT	5	1.1E-1	7.6E-1
	Annotation Cluster 65	Enrichment Score: 2.13	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	452	6.9E-25	4.4E-22
☐	GOTERM_BP_ALL	gene expression	RT	356	2.1E-8	2.3E-6
☐	GOTERM_MF_ALL	nucleic acid binding	RT	340	1.4E-6	1.6E-4
☐	GOTERM_BP_ALL	RNA metabolic process	RT	285	7.9E-5	4.5E-3
☐	GOTERM_MF_ALL	DNA binding	RT	184	2.2E-1	9.8E-1
☐	SP_PIR_KEYWORDS	Transcription	RT	109	8.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	Transcription regulation	RT	96	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	transcription	RT	177	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of metabolic process	RT	192	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	166	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of cellular process	RT	290	1.0E0	1.0E0
☐	GOTERM_BP_ALL	RNA biosynthetic process	RT	156	1.0E0	1.0E0
☐	GOTERM_BP_ALL	transcription, DNA-dependent	RT	154	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of cellular metabolic process	RT	181	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of gene expression	RT	172	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of transcription	RT	158	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of biological process	RT	314	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of transcription, DNA-dependent	RT	145	1.0E0	1.0E0
☐	GOTERM_BP_ALL	biological regulation	RT	344	1.0E0	1.0E0
☐	GOTERM_MF_ALL	transcription regulator activity	RT	72	1.0E0	1.0E0
	Annotation Cluster 66	Enrichment Score: 2.07	G	Count	P_Value	Benjamini
☐	INTERPRO	RecA bacterial DNA recombination	RT	5	1.5E-3	3.3E-1
☐	INTERPRO	Rad51, C-terminal	RT	4	5.5E-3	5.5E-1
☐	PIR_SUPERFAMILY	PIRSF005856:DNA repair and recombination protein, Rad51 type	RT	3	7.6E-2	1.0E0
	Annotation Cluster 67	Enrichment Score: 2.02	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	establishment of organelle localization	RT	9	2.8E-3	9.1E-2
☐	GOTERM_BP_ALL	establishment of chromosome localization	RT	4	1.2E-2	3.0E-1
☐	GOTERM_BP_ALL	chromosome localization	RT	4	1.2E-2	3.0E-1
☐	GOTERM_BP_ALL	organelle localization	RT	9	1.9E-2	4.1E-1
	Annotation Cluster 68	Enrichment Score: 2.01	G	Count	P_Value	Benjamini
☐	INTERPRO	Phosphoribosyltransferase	RT	8	8.1E-6	7.8E-3
☐	GOTERM_BP_ALL	nucleoside metabolic process	RT	12	1.8E-5	1.2E-3
☐	GOTERM_BP_ALL	purine base metabolic process	RT	6	5.8E-4	2.4E-2
☐	INTERPRO	Purine/pyrimidine phosphoribosyl transferase	RT	5	7.0E-4	1.9E-1
☐	GOTERM_BP_ALL	ribonucleoside metabolic process	RT	5	6.0E-3	1.7E-1

☐	GOTERM_MF_ALL	transferase activity, transferring pentosyl groups	RT	▮		10	1.0E-2	3.1E-1
☐	GOTERM_BP_ALL	purine ribonucleoside metabolic process	RT	▮		4	1.2E-2	3.0E-1
☐	GOTERM_BP_ALL	adenine salvage	RT	▮		3	2.4E-2	4.6E-1
☐	GOTERM_BP_ALL	adenine metabolic process	RT	▮		3	2.4E-2	4.6E-1
☐	GOTERM_BP_ALL	purine base salvage	RT	▮		3	2.4E-2	4.6E-1
☐	GOTERM_BP_ALL	purine nucleoside metabolic process	RT	▮		4	3.0E-2	5.2E-1
☐	GOTERM_BP_ALL	purine ribonucleoside salvage	RT	▮		3	4.4E-2	6.3E-1
☐	GOTERM_BP_ALL	purine salvage	RT	▮		3	4.4E-2	6.3E-1
☐	GOTERM_BP_ALL	nucleoside salvage	RT	▮		3	4.4E-2	6.3E-1
☐	SP_PIR_KEYWORDS	purine salvage	RT	▮		3	4.4E-2	3.5E-1
☐	SP_PIR_KEYWORDS	salvage pathway	RT	▮		3	6.9E-2	4.8E-1
☐	SP_PIR_KEYWORDS	pentosyltransferase	RT	▮		3	6.9E-2	4.8E-1
☐	GOTERM_BP_ALL	metabolic compound salvage	RT	▮		3	1.3E-1	9.1E-1
☐	GOTERM_BP_ALL	grooming behavior	RT	▮		3	1.3E-1	9.1E-1
	Annotation Cluster 69	Enrichment Score: 1.98	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	exosome (RNase complex)	RT	▮		8	1.4E-4	1.9E-3
☐	GOTERM_MF_ALL	3'-5' exonuclease activity	RT	▮		10	1.9E-4	1.2E-2
☐	SP_PIR_KEYWORDS	Exosome	RT	▮		6	5.8E-4	9.5E-3
☐	INTERPRO	Exoribonuclease, phosphorolytic domain 1	RT	▮		4	1.7E-2	8.4E-1
☐	GOTERM_MF_ALL	3'-5'-exoribonuclease activity	RT	▮		4	5.2E-2	7.3E-1
☐	GOTERM_MF_ALL	exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	RT	▮		5	8.2E-2	8.2E-1
☐	INTERPRO	Exoribonuclease, phosphorolytic domain 2	RT	▮		3	8.7E-2	9.9E-1
☐	GOTERM_MF_ALL	exoribonuclease activity	RT	▮		4	1.2E-1	9.2E-1
☐	GOTERM_MF_ALL	exoribonuclease activity, producing 5'-phosphomonoesters	RT	▮		4	1.2E-1	9.2E-1
	Annotation Cluster 70	Enrichment Score: 1.89	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	nucleobase, nucleoside, nucleotide kinase activity	RT	▮		11	1.7E-3	8.0E-2
☐	GOTERM_MF_ALL	phosphotransferase activity, phosphate group as acceptor	RT	▮		8	1.7E-2	4.4E-1
☐	GOTERM_MF_ALL	nucleotide kinase activity	RT	▮		5	7.0E-2	7.7E-1
	Annotation Cluster 71	Enrichment Score: 1.88	G		🟩	Count	P_Value	Benjamini
☐	SMART	S1	RT	▮		5	6.2E-3	2.3E-1
☐	INTERPRO	S1, RNA binding	RT	▮		5	1.5E-2	8.2E-1
☐	UP_SEQ_FEATURE	domain:S1 motif	RT	▮		4	2.4E-2	1.0E0
	Annotation Cluster 72	Enrichment Score: 1.88	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	compositionally biased region:Arg/Ser-rich (RS domain)	RT	▮		6	8.1E-4	5.9E-1
☐	GOTERM_BP_ALL	spliceosome assembly	RT	▮		9	1.2E-3	4.7E-2
☐	GOTERM_BP_ALL	mRNA splice site selection	RT	▮		5	4.2E-2	6.3E-1
☐	UP_SEQ_FEATURE	compositionally biased region:Gly-rich (hinge region)	RT	▮		3	7.9E-2	1.0E0
☐	GOTERM_MF_ALL	RNA splicing factor activity, transesterification mechanism	RT	▮		4	1.2E-1	9.2E-1
	Annotation Cluster 73	Enrichment Score: 1.81	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	nuclear import	RT	▮		19	4.0E-5	2.4E-3
☐	GOTERM_BP_ALL	protein import into nucleus	RT	▮		18	9.6E-5	5.3E-3
☐	INTERPRO	Importin-beta, N-terminal	RT	▮		8	1.2E-4	5.9E-2
☐	GOTERM_BP_ALL	protein import into nucleus, docking	RT	▮		8	1.7E-4	8.9E-3
☐	INTERPRO	Armadillo-like helical	RT	▮		21	2.7E-4	8.4E-2
☐	UP_SEQ_FEATURE	domain:Importin N-terminal	RT	▮		7	4.8E-4	4.3E-1
☐	GOTERM_BP_ALL	cellular protein complex assembly	RT	▮		11	6.4E-3	1.8E-1
☐	GOTERM_BP_ALL	ribosomal protein import into nucleus	RT	▮		3	6.9E-2	7.6E-1

☐	UP_SEQ_FEATURE	repeat:HEAT 6	RT	5	7.8E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:HEAT 5	RT	5	1.3E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:HEAT 4	RT	5	1.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:HEAT 3	RT	5	1.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:HEAT 1	RT	5	2.0E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:HEAT 2	RT	5	2.0E-1	1.0E0
☐	COG_ONTOLOGY	Intracellular trafficking and secretion	RT	9	3.4E-1	9.6E-1
☐	UP_SEQ_FEATURE	repeat:HEAT 8	RT	3	3.7E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:HEAT 7	RT	3	4.4E-1	1.0E0
☐	GOTERM_BP_ALL	protein complex assembly	RT	15	7.0E-1	1.0E0
	Annotation Cluster 74	Enrichment Score: 1.81	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	inner membrane	RT	18	1.2E-3	1.7E-2
☐	GOTERM_BP_ALL	mitochondrion organization and biogenesis	RT	17	1.8E-3	6.5E-2
☐	GOTERM_BP_ALL	mitochondrial membrane organization and biogenesis	RT	8	2.6E-3	8.6E-2
☐	GOTERM_BP_ALL	inner mitochondrial membrane organization and biogenesis	RT	5	3.6E-3	1.1E-1
☐	GOTERM_CC_ALL	mitochondrial intermembrane space	RT	6	5.5E-3	5.6E-2
☐	GOTERM_BP_ALL	protein import into mitochondrion	RT	5	9.3E-3	2.4E-1
☐	GOTERM_CC_ALL	organelle envelope lumen	RT	7	1.6E-2	1.4E-1
☐	INTERPRO	Zinc finger, Tim10/DDP-type	RT	4	1.7E-2	8.4E-1
☐	GOTERM_CC_ALL	mitochondrial intermembrane space protein transporter complex	RT	4	1.9E-2	1.6E-1
☐	GOTERM_BP_ALL	mitochondrial transport	RT	8	2.0E-2	4.1E-1
☐	GOTERM_BP_ALL	protein import into mitochondrial inner membrane	RT	4	2.0E-2	4.2E-1
☐	GOTERM_CC_ALL	mitochondrial inner membrane presequence translocase complex	RT	4	2.8E-2	2.1E-1
☐	GOTERM_MF_ALL	macromolecule transmembrane transporter activity	RT	5	3.0E-2	5.7E-1
☐	GOTERM_MF_ALL	P-P-bond-hydrolysis-driven protein transmembrane transporter activity	RT	5	3.0E-2	5.7E-1
☐	GOTERM_CC_ALL	mitochondrial membrane part	RT	10	5.2E-2	3.4E-1
☐	GOTERM_BP_ALL	protein targeting to mitochondrion	RT	4	7.2E-2	7.7E-1
☐	UP_SEQ_FEATURE	short sequence motif:Twin CX3C motif	RT	3	7.9E-2	1.0E0
☐	GOTERM_MF_ALL	protein transmembrane transporter activity	RT	5	1.4E-1	9.4E-1
	Annotation Cluster 75	Enrichment Score: 1.8	G	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	One carbon pool by folate	RT	10	4.0E-6	1.4E-4
☐	GOTERM_BP_ALL	nitrogen compound biosynthetic process	RT	24	1.5E-5	1.1E-3
☐	GOTERM_BP_ALL	amine biosynthetic process	RT	20	2.1E-5	1.3E-3
☐	GOTERM_BP_ALL	amino acid biosynthetic process	RT	13	8.2E-4	3.2E-2
☐	SP_PIR_KEYWORDS	one-carbon metabolism	RT	7	9.1E-4	1.3E-2
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	RT	7	1.2E-3	5.9E-2
☐	SP_PIR_KEYWORDS	amino-acid biosynthesis	RT	8	1.9E-3	2.6E-2
☐	GOTERM_MF_ALL	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines	RT	8	6.3E-3	2.2E-1
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on the CH-NH group of donors	RT	7	2.0E-2	4.7E-1
☐	INTERPRO	Tetrahydrofolate dehydrogenase/cyclohydrolase	RT	3	2.1E-2	8.7E-1
☐	GOTERM_MF_ALL	methylenetetrahydrofolate dehydrogenase activity	RT	3	2.2E-2	5.0E-1
☐	GOTERM_MF_ALL	methylenetetrahydrofolate dehydrogenase (NADP+) activity	RT	3	2.2E-2	5.0E-1
☐	GOTERM_MF_ALL	methenyltetrahydrofolate cyclohydrolase				

					Count	P_Value	Benjamini
☐		activity	RT				
☐	GOTERM_BP_ALL	folic acid and derivative biosynthetic process	RT		4	3.0E-2	5.2E-1
☐	GOTERM_BP_ALL	methionine metabolic process	RT		4	4.2E-2	6.2E-1
☐	GOTERM_BP_ALL	methionine biosynthetic process	RT		4	4.2E-2	6.2E-1
☐	GOTERM_BP_ALL	histidine biosynthetic process	RT		3	4.4E-2	6.3E-1
☐	GOTERM_BP_ALL	histidine family amino acid biosynthetic process	RT		3	4.4E-2	6.3E-1
☐	KEGG_PATHWAY	Glyoxylate and dicarboxylate metabolism	RT		5	4.9E-2	4.1E-1
☐	GOTERM_BP_ALL	aspartate family amino acid biosynthetic process	RT		5	5.2E-2	6.7E-1
☐	GOTERM_BP_ALL	aspartate family amino acid metabolic process	RT		5	7.5E-2	7.8E-1
☐	GOTERM_BP_ALL	sulfur amino acid metabolic process	RT		5	8.9E-2	8.3E-1
☐	GOTERM_BP_ALL	sulfur amino acid biosynthetic process	RT		4	1.1E-1	8.8E-1
☐	GOTERM_BP_ALL	folic acid and derivative metabolic process	RT		4	1.1E-1	8.8E-1
☐	GOTERM_BP_ALL	histidine metabolic process	RT		3	4.0E-1	1.0E0
☐	GOTERM_BP_ALL	histidine family amino acid metabolic process	RT		3	4.0E-1	1.0E0
☐	COG_ONTOLOGY	Coenzyme metabolism	RT		6	4.6E-1	9.8E-1
☐	GOTERM_BP_ALL	sulfur metabolic process	RT		7	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	sulfur compound biosynthetic process	RT		4	7.7E-1	1.0E0
	Annotation Cluster 76	Enrichment Score: 1.75	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	macromolecule metabolic process	RT		655	1.5E-12	2.5E-10
☐	GOTERM_BP_ALL	cellular protein metabolic process	RT		311	1.8E-3	6.5E-2
☐	GOTERM_BP_ALL	cellular macromolecule metabolic process	RT		311	4.4E-3	1.3E-1
☐	GOTERM_BP_ALL	protein metabolic process	RT		318	6.8E-3	1.9E-1
☐	GOTERM_BP_ALL	biopolymer modification	RT		139	8.9E-1	1.0E0
☐	GOTERM_BP_ALL	phosphorus metabolic process	RT		68	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	phosphate metabolic process	RT		68	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	phosphorylation	RT		54	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	protein modification process	RT		126	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	post-translational protein modification	RT		105	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid phosphorylation	RT		43	9.9E-1	1.0E0
	Annotation Cluster 77	Enrichment Score: 1.75	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	L-serine metabolic process	RT		5	1.9E-3	6.8E-2
☐	GOTERM_BP_ALL	serine family amino acid metabolic process	RT		7	5.5E-3	1.6E-1
☐	GOTERM_BP_ALL	serine family amino acid biosynthetic process	RT		4	2.0E-2	4.2E-1
☐	SP_PIR_KEYWORDS	serine biosynthesis	RT		3	2.4E-2	2.2E-1
☐	GOTERM_BP_ALL	L-serine biosynthetic process	RT		3	4.4E-2	6.3E-1
☐	KEGG_PATHWAY	Glycine, serine and threonine metabolism	RT		8	1.5E-1	6.9E-1
	Annotation Cluster 78	Enrichment Score: 1.74	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell cycle checkpoint	RT		12	4.2E-4	1.9E-2
☐	BIOCARTA	Role of BRCA1, BRCA2 and ATR in Cancer Susceptibility	RT		8	2.6E-3	1.2E-1
☐	GOTERM_BP_ALL	DNA integrity checkpoint	RT		6	7.2E-2	7.7E-1
☐	GOTERM_BP_ALL	DNA damage response, signal transduction	RT		8	7.6E-2	7.8E-1
☐	GOTERM_BP_ALL	DNA damage checkpoint	RT		4	3.3E-1	9.9E-1
	Annotation Cluster 79	Enrichment Score: 1.72	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	pseudouridylate synthase activity	RT		7	1.5E-4	9.7E-3
☐	GOTERM_BP_ALL	RNA modification	RT		9	9.2E-4	3.6E-2
☐	GOTERM_BP_ALL	tRNA modification	RT		5	6.0E-3	1.7E-1
☐	GOTERM_BP_ALL	pseudouridine synthesis	RT		5	9.3E-3	2.4E-1

☐	GOTERM_BP_ALL	tRNA pseudouridine synthesis	RT	3	6.9E-2	7.6E-1
☐	GOTERM_MF_ALL	intramolecular transferase activity	RT	6	2.0E-1	9.7E-1
☐	GOTERM_MF_ALL	pseudouridine synthase activity	RT	4	3.4E-1	1.0E0
☐	GOTERM_MF_ALL	tRNA-pseudouridine synthase activity	RT	3	5.1E-1	1.0E0
	Annotation Cluster 80	Enrichment Score: 1.61	G	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF002306:tubulin	RT	8	9.0E-4	6.0E-1
☐	INTERPRO	Tubulin/FtsZ, C-terminal	RT	6	6.6E-3	5.8E-1
☐	INTERPRO	Tubulin/FtsZ, GTPase	RT	6	6.6E-3	5.8E-1
☐	GOTERM_BP_ALL	protein polymerization	RT	11	1.0E-2	2.6E-1
☐	COG_ONTOLOGY	Cytoskeleton	RT	10	5.0E-2	6.4E-1
☐	INTERPRO	Alpha tubulin	RT	3	8.7E-2	9.9E-1
☐	INTERPRO	Tubulin	RT	5	1.0E-1	1.0E0
☐	GOTERM_MF_ALL	structural constituent of cytoskeleton	RT	7	7.5E-1	1.0E0
	Annotation Cluster 81	Enrichment Score: 1.6	G	Count	P_Value	Benjamini
☐	SMART	TPR	RT	20	3.9E-5	2.9E-3
☐	INTERPRO	Tetratricopeptide-like helical	RT	21	9.9E-4	2.4E-1
☐	INTERPRO	Tetratricopeptide region	RT	19	1.5E-3	3.2E-1
☐	INTERPRO	Tetratricopeptide TPR-1	RT	16	2.3E-3	4.0E-1
☐	SP_PIR_KEYWORDS	TPR repeat	RT	20	6.6E-3	7.8E-2
☐	UP_SEQ_FEATURE	repeat:TPR 3	RT	11	3.1E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 1	RT	11	4.8E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 2	RT	11	4.8E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 9	RT	4	6.7E-2	1.0E0
☐	INTERPRO	Tetratricopeptide TPR2	RT	8	1.4E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 7	RT	5	2.5E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 4	RT	6	2.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 8	RT	4	2.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 6	RT	5	2.9E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 5	RT	5	3.2E-1	1.0E0
	Annotation Cluster 82	Enrichment Score: 1.59	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	short sequence motif:"KMSKS" region	RT	4	2.4E-2	1.0E0
☐	UP_SEQ_FEATURE	short sequence motif:"HIGH" region	RT	4	2.4E-2	1.0E0
☐	INTERPRO	Rossmann-like alpha/beta/alpha sandwich fold	RT	7	2.9E-2	9.3E-1
	Annotation Cluster 83	Enrichment Score: 1.56	G	Count	P_Value	Benjamini
☐	SMART	BRCT	RT	6	1.3E-2	4.1E-1
☐	INTERPRO	BRCT	RT	6	3.5E-2	9.6E-1
☐	UP_SEQ_FEATURE	domain:BRCT 1	RT	4	3.6E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:BRCT 2	RT	4	3.6E-2	1.0E0
	Annotation Cluster 84	Enrichment Score: 1.55	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Isoprene biosynthesis	RT	5	3.6E-3	4.4E-2
☐	GOTERM_MF_ALL	prenyltransferase activity	RT	6	4.8E-2	7.1E-1
☐	GOTERM_MF_ALL	transferase activity, transferring alkyl or aryl (other than methyl) groups	RT	9	1.3E-1	9.2E-1
	Annotation Cluster 85	Enrichment Score: 1.53	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	polyamine biosynthetic process	RT	6	1.1E-4	6.1E-3
☐	SP_PIR_KEYWORDS	Polyamine biosynthesis	RT	5	9.0E-4	1.3E-2
☐	KEGG_PATHWAY	Methionine metabolism	RT	7	9.2E-3	1.4E-1
☐	GOTERM_BP_ALL	polyamine metabolic process	RT	6	1.5E-2	3.5E-1
☐	GOTERM_BP_ALL	spermidine biosynthetic process	RT	3	2.4E-2	4.6E-1
☐	SP_PIR_KEYWORDS	spermidine biosynthesis	RT	3	2.4E-2	2.2E-1

☐	GOTERM_MF_ALL	carboxy-lyase activity	RT		8	2.4E-2	5.0E-1
☐	GOTERM_BP_ALL	biogenic amine biosynthetic process	RT		7	2.7E-2	5.0E-1
☐	INTERPRO	Ornithine decarboxylase	RT		3	3.9E-2	9.4E-1
☐	GOTERM_MF_ALL	carbon-carbon lyase activity	RT		9	4.8E-2	7.1E-1
☐	GOTERM_BP_ALL	amino acid derivative biosynthetic process	RT		7	5.8E-2	7.1E-1
☐	SP_PIR_KEYWORDS	decarboxylase	RT		6	6.2E-2	4.5E-1
☐	GOTERM_BP_ALL	spermidine metabolic process	RT		3	6.9E-2	7.6E-1
☐	SP_PIR_KEYWORDS	lyase	RT		17	7.1E-2	4.8E-1
☐	INTERPRO	Orn/DAP/Arg decarboxylase 2	RT		3	1.2E-1	1.0E0
☐	GOTERM_BP_ALL	amino acid derivative metabolic process	RT		13	1.4E-1	9.2E-1
☐	GOTERM_BP_ALL	biogenic amine metabolic process	RT		10	2.7E-1	9.9E-1
☐	KEGG_PATHWAY	Urea cycle and metabolism of amino groups	RT		5	3.7E-1	9.1E-1
	Annotation Cluster 86	Enrichment Score: 1.53	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	double-strand break repair	RT		9	1.2E-3	4.7E-2
☐	GOTERM_BP_ALL	double-strand break repair via nonhomologous end joining	RT		3	1.3E-1	9.1E-1
☐	GOTERM_BP_ALL	non-recombinational repair	RT		3	1.6E-1	9.4E-1
	Annotation Cluster 87	Enrichment Score: 1.53	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	DNA-directed DNA polymerase	RT		9	2.2E-4	3.9E-3
☐	INTERPRO	DNA polymerase, B region	RT		3	3.9E-2	9.4E-1
☐	INTERPRO	DNA polymerase B, exonuclease	RT		3	3.9E-2	9.4E-1
☐	SMART	POLBc	RT		3	5.5E-2	7.6E-1
☐	INTERPRO	DNA-directed DNA polymerase B	RT		3	8.7E-2	9.9E-1
☐	UP_SEQ_FEATURE	zinc finger region:C4-type	RT		6	4.2E-1	1.0E0
	Annotation Cluster 88	Enrichment Score: 1.52	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	molecular chaperone	RT		11	8.7E-7	2.0E-5
☐	INTERPRO	Heat shock protein Hsp70	RT		6	2.2E-3	4.1E-1
☐	SP_PIR_KEYWORDS	stress response	RT		12	2.4E-3	3.1E-2
☐	GOTERM_MF_ALL	TPR domain binding	RT		4	2.6E-3	1.1E-1
☐	PIR_SUPERFAMILY	PIRSF002583:heat shock protein, HSP90/HTPG types	RT		4	3.3E-3	9.2E-1
☐	SMART	HATPase_c	RT		6	5.3E-3	2.2E-1
☐	INTERPRO	Heat shock protein Hsp90	RT		4	1.0E-2	7.0E-1
☐	INTERPRO	Heat shock protein 70	RT		5	2.0E-2	8.7E-1
☐	SP_PIR_KEYWORDS	estrogen-induced protein	RT		3	2.4E-2	2.2E-1
☐	SP_PIR_KEYWORDS	stress-induced protein	RT		4	3.0E-2	2.6E-1
☐	SP_PIR_KEYWORDS	heat shock	RT		4	3.0E-2	2.6E-1
☐	GOTERM_BP_ALL	response to heat	RT		7	3.2E-2	5.4E-1
☐	INTERPRO	ATP-binding region, ATPase-like	RT		5	4.2E-2	9.6E-1
☐	GOTERM_BP_ALL	response to unfolded protein	RT		12	4.7E-2	6.5E-1
☐	GOTERM_BP_ALL	response to protein stimulus	RT		12	4.7E-2	6.5E-1
☐	PIR_SUPERFAMILY	PIRSF002581:chaperone HSP70	RT		4	4.8E-2	1.0E0
☐	GOTERM_MF_ALL	nitric-oxide synthase regulator activity	RT		3	6.6E-2	7.6E-1
☐	GOTERM_BP_ALL	response to temperature stimulus	RT		8	9.3E-2	8.4E-1
☐	GOTERM_BP_ALL	regulation of nitric oxide biosynthetic process	RT		4	1.1E-1	8.8E-1
☐	GOTERM_BP_ALL	positive regulation of nitric oxide biosynthetic process	RT		3	2.3E-1	9.8E-1
☐	GOTERM_BP_ALL	response to abiotic stimulus	RT		19	3.2E-1	9.9E-1
☐	GOTERM_BP_ALL	nitric oxide metabolic process	RT		4	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	nitric oxide biosynthetic process	RT		4	3.8E-1	1.0E0
☐	KEGG_PATHWAY	Antigen processing and presentation	RT		10	4.4E-1	9.4E-1

☐	GOTERM_BP_ALL	positive regulation of biosynthetic process	RT	▮		4	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	response to biotic stimulus	RT	▮		14	9.8E-1	1.0E0
	Annotation Cluster 89	Enrichment Score: 1.5	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	one-carbon compound metabolic process	RT	▮		24	4.9E-6	3.7E-4
☐	KEGG_PATHWAY	Selenoamino acid metabolism	RT	▮		10	1.1E-3	2.9E-2
☐	KEGG_PATHWAY	Aminophosphonate metabolism	RT	▮		7	1.8E-3	4.2E-2
☐	GOTERM_MF_ALL	histone methyltransferase activity	RT	▮		8	7.9E-3	2.6E-1
☐	GOTERM_BP_ALL	biopolymer methylation	RT	▮		12	8.6E-3	2.3E-1
☐	GOTERM_BP_ALL	methylation	RT	▮		12	1.3E-2	3.1E-1
☐	KEGG_PATHWAY	Naphthalene and anthracene degradation	RT	▮		6	1.9E-2	2.5E-1
☐	GOTERM_MF_ALL	protein methyltransferase activity	RT	▮		9	2.0E-2	4.7E-1
☐	GOTERM_BP_ALL	protein amino acid alkylation	RT	▮		8	3.1E-2	5.3E-1
☐	GOTERM_BP_ALL	protein amino acid methylation	RT	▮		8	3.1E-2	5.3E-1
☐	GOTERM_BP_ALL	peptidyl-arginine methylation	RT	▮		3	4.4E-2	6.3E-1
☐	GOTERM_MF_ALL	N-methyltransferase activity	RT	▮		8	6.1E-2	7.5E-1
☐	GOTERM_MF_ALL	arginine N-methyltransferase activity	RT	▮		3	6.6E-2	7.6E-1
☐	GOTERM_MF_ALL	protein-arginine N-methyltransferase activity	RT	▮		3	6.6E-2	7.6E-1
☐	GOTERM_MF_ALL	histone-arginine N-methyltransferase activity	RT	▮		3	6.6E-2	7.6E-1
☐	GOTERM_BP_ALL	peptidyl-arginine modification	RT	▮		3	6.9E-2	7.6E-1
☐	PIR_SUPERFAMILY	PIRSF037127:type 1 arginine N-methyltransferase	RT	▮		3	7.6E-2	1.0E0
☐	KEGG_PATHWAY	Tyrosine metabolism	RT	▮		9	1.1E-1	6.1E-1
☐	UP_SEQ_FEATURE	binding site:S-adenosyl-L-methionine	RT	▮		4	1.5E-1	1.0E0
☐	KEGG_PATHWAY	Histidine metabolism	RT	▮		7	1.7E-1	7.2E-1
☐	KEGG_PATHWAY	Androgen and estrogen metabolism	RT	▮		8	2.2E-1	8.1E-1
☐	GOTERM_BP_ALL	histone methylation	RT	▮		4	2.2E-1	9.8E-1
☐	GOTERM_BP_ALL	histone modification	RT	▮		7	2.3E-1	9.8E-1
☐	KEGG_PATHWAY	Tryptophan metabolism	RT	▮		8	2.3E-1	8.1E-1
☐	UP_SEQ_FEATURE	binding site:S-adenosyl-L-methionine; via carbonyl oxygen	RT	▮		3	2.6E-1	1.0E0
	Annotation Cluster 90	Enrichment Score: 1.5	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	nucleobase biosynthetic process	RT	▮		5	3.6E-3	1.1E-1
☐	GOTERM_BP_ALL	pyrimidine base metabolic process	RT	▮		4	4.2E-2	6.2E-1
☐	GOTERM_BP_ALL	'de novo' pyrimidine base biosynthetic process	RT	▮		3	6.9E-2	7.6E-1
☐	GOTERM_BP_ALL	pyrimidine base biosynthetic process	RT	▮		3	9.8E-2	8.5E-1
	Annotation Cluster 91	Enrichment Score: 1.5	G		🟩	Count	P_Value	Benjamini
☐	SMART	XPGN	RT	▮		3	2.4E-2	5.2E-1
☐	SMART	XPGI	RT	▮		3	2.4E-2	5.2E-1
☐	SMART	HhH2	RT	▮		3	2.4E-2	5.2E-1
☐	INTERPRO	Helix-hairpin-helix motif, class 2	RT	▮		3	3.9E-2	9.4E-1
☐	INTERPRO	XPG N-terminal	RT	▮		3	3.9E-2	9.4E-1
☐	INTERPRO	DNA repair protein (XPGC)/yeast Rad	RT	▮		3	3.9E-2	9.4E-1
☐	INTERPRO	XPG I	RT	▮		3	3.9E-2	9.4E-1
	Annotation Cluster 92	Enrichment Score: 1.47	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	RT	▮		7	1.2E-3	5.9E-2
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on the CH-NH group of donors	RT	▮		7	2.0E-2	4.7E-1
☐	INTERPRO	Delta 1-pyrroline-5-carboxylate reductase	RT	▮		3	2.1E-2	8.7E-1
☐	GOTERM_MF_ALL	pyrroline-5-carboxylate reductase activity	RT	▮		3	2.2E-2	5.0E-1
☐	PIR_SUPERFAMILY	PIRSF000193:pyrroline-5-carboxylate	RT	▮		3	2.6E-2	1.0E0

☐		reductase	RT			
☐	GOTERM_BP_ALL	glutamine family amino acid metabolic process	RT	8	4.7E-2	6.5E-1
☐	GOTERM_BP_ALL	proline biosynthetic process	RT	3	6.9E-2	7.6E-1
☐	INTERPRO	NADP oxidoreductase, coenzyme F420-dependent	RT	3	1.2E-1	1.0E0
☐	GOTERM_BP_ALL	proline metabolic process	RT	3	1.3E-1	9.1E-1
☐	GOTERM_BP_ALL	glutamine family amino acid biosynthetic process	RT	4	1.5E-1	9.4E-1
	Annotation Cluster 93	Enrichment Score: 1.43	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	organellar small ribosomal subunit	RT	4	2.8E-2	2.1E-1
☐	GOTERM_CC_ALL	mitochondrial small ribosomal subunit	RT	4	2.8E-2	2.1E-1
☐	GOTERM_CC_ALL	small ribosomal subunit	RT	7	6.7E-2	4.0E-1
	Annotation Cluster 94	Enrichment Score: 1.42	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	ubiquinone biosynthetic process	RT	4	3.0E-2	5.2E-1
☐	GOTERM_BP_ALL	ubiquinone metabolic process	RT	4	3.0E-2	5.2E-1
☐	SP_PIR_KEYWORDS	ubiquinone biosynthesis	RT	4	3.0E-2	2.6E-1
☐	GOTERM_BP_ALL	quinone cofactor biosynthetic process	RT	4	4.2E-2	6.2E-1
☐	KEGG_PATHWAY	Ubiquinone biosynthesis	RT	4	4.8E-2	4.4E-1
☐	GOTERM_BP_ALL	quinone cofactor metabolic process	RT	4	5.6E-2	7.0E-1
	Annotation Cluster 95	Enrichment Score: 1.41	G	Count	P_Value	Benjamini
☐	SMART	eIF1a	RT	3	3.8E-2	6.6E-1
☐	INTERPRO	Eukaryotic initiation factor 1A (eIF-1A)	RT	3	3.9E-2	9.4E-1
☐	INTERPRO	S1, IF1 type	RT	3	3.9E-2	9.4E-1
	Annotation Cluster 96	Enrichment Score: 1.35	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	RNA catabolic process	RT	10	6.2E-3	1.7E-1
☐	GOTERM_BP_ALL	mRNA catabolic process	RT	9	6.8E-3	1.8E-1
☐	GOTERM_BP_ALL	mRNA catabolic process, nonsense-mediated decay	RT	4	2.7E-1	9.9E-1
☐	SP_PIR_KEYWORDS	Nonsense-mediated mRNA decay	RT	3	3.4E-1	9.5E-1
	Annotation Cluster 97	Enrichment Score: 1.32	G	Count	P_Value	Benjamini
☐	INTERPRO	Transcription factor E2F/dimerisation partner (TDP)	RT	7	1.2E-4	5.8E-2
☐	INTERPRO	E2F Family	RT	6	2.1E-4	7.2E-2
☐	UP_SEQ_FEATURE	short sequence motif:DEF box	RT	4	8.1E-3	1.0E0
☐	UP_SEQ_FEATURE	region of interest:Cyclin A/CDK2 binding	RT	3	2.7E-2	1.0E0
☐	PIR_SUPERFAMILY	PIRSF019596:transcription factor E2F	RT	3	4.8E-2	1.0E0
☐	UP_SEQ_FEATURE	region of interest:Dimerization	RT	4	6.7E-2	1.0E0
☐	UP_SEQ_FEATURE	region of interest:Transactivation	RT	3	7.9E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:Leucine-zipper	RT	12	2.3E-1	1.0E0
☐	KEGG_PATHWAY	Glioma	RT	9	2.7E-1	8.5E-1
☐	KEGG_PATHWAY	Non-small cell lung cancer	RT	8	3.2E-1	8.9E-1
☐	KEGG_PATHWAY	Chronic myeloid leukemia	RT	9	5.1E-1	9.6E-1
☐	INTERPRO	Winged helix repressor DNA-binding	RT	10	5.9E-1	1.0E0
☐	KEGG_PATHWAY	Melanoma	RT	7	7.4E-1	9.9E-1
	Annotation Cluster 98	Enrichment Score: 1.32	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	chromosome organization and biogenesis	RT	50	2.9E-4	1.4E-2
☐	GOTERM_BP_ALL	chromatin remodeling	RT	10	2.8E-2	5.1E-1
☐	GOTERM_BP_ALL	covalent chromatin modification	RT	10	3.2E-2	5.3E-1
☐	GOTERM_BP_ALL	DNA packaging	RT	30	1.2E-1	9.0E-1
☐	GOTERM_BP_ALL	chromatin modification	RT	21	2.2E-1	9.8E-1
☐	GOTERM_BP_ALL	establishment and/or maintenance of chromatin architecture	RT	27	2.5E-1	9.9E-1
☐	SP_PIR_KEYWORDS	Chromatin regulator	RT	12	3.4E-1	9.5E-1

	Annotation Cluster 99	Enrichment Score: 1.3	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	deoxyribonucleotide metabolic process	RT	6	4.4E-3	1.3E-1
☐	GOTERM_BP_ALL	deoxyribonucleoside diphosphate metabolic process	RT	3	6.9E-2	7.6E-1
☐	GOTERM_BP_ALL	nucleoside diphosphate metabolic process	RT	3	4.0E-1	1.0E0
	Annotation Cluster 100	Enrichment Score: 1.29	G 🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	ubiquinone	RT	9	2.3E-2	2.3E-1
☐	SP_PIR_KEYWORDS	NAD	RT	24	2.7E-2	2.4E-1
☐	GOTERM_MF_ALL	NADH dehydrogenase (quinone) activity	RT	8	5.4E-2	7.2E-1
☐	GOTERM_MF_ALL	NADH dehydrogenase activity	RT	8	5.4E-2	7.2E-1
☐	GOTERM_MF_ALL	NADH dehydrogenase (ubiquinone) activity	RT	8	5.4E-2	7.2E-1
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on NADH or NADPH	RT	11	5.5E-2	7.2E-1
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor	RT	8	8.3E-2	8.2E-1
☐	KEGG_PATHWAY	Oxidative phosphorylation	RT	17	9.9E-2	5.9E-1
	Annotation Cluster 101	Enrichment Score: 1.28	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	deoxyribonucleotide metabolic process	RT	6	4.4E-3	1.3E-1
☐	GOTERM_BP_ALL	pyrimidine nucleoside triphosphate metabolic process	RT	6	1.5E-2	3.5E-1
☐	GOTERM_BP_ALL	pyrimidine deoxyribonucleotide metabolic process	RT	4	3.0E-2	5.2E-1
☐	GOTERM_BP_ALL	pyrimidine nucleoside metabolic process	RT	4	5.6E-2	7.0E-1
☐	GOTERM_BP_ALL	pyrimidine deoxyribonucleotide biosynthetic process	RT	3	6.9E-2	7.6E-1
☐	GOTERM_BP_ALL	pyrimidine deoxyribonucleoside triphosphate metabolic process	RT	3	9.8E-2	8.5E-1
☐	GOTERM_BP_ALL	pyrimidine deoxyribonucleoside metabolic process	RT	3	9.8E-2	8.5E-1
☐	GOTERM_BP_ALL	deoxyribonucleotide biosynthetic process	RT	3	9.8E-2	8.5E-1
☐	GOTERM_BP_ALL	deoxyribonucleoside metabolic process	RT	3	1.3E-1	9.1E-1
☐	GOTERM_BP_ALL	deoxyribonucleoside triphosphate metabolic process	RT	3	1.6E-1	9.4E-1
	Annotation Cluster 102	Enrichment Score: 1.27	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	heat shock protein binding	RT	12	1.1E-2	3.2E-1
☐	SMART	DnaJ	RT	8	2.5E-2	5.1E-1
☐	INTERPRO	Heat shock protein DnaJ, N-terminal	RT	8	5.7E-2	9.8E-1
☐	INTERPRO	Molecular chaperone, heat shock protein, Hsp40, DnaJ	RT	7	5.9E-2	9.8E-1
☐	UP_SEQ_FEATURE	domain:J	RT	4	5.0E-1	1.0E0
	Annotation Cluster 103	Enrichment Score: 1.27	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	pyrimidine nucleotide metabolic process	RT	10	3.2E-4	1.5E-2
☐	GOTERM_BP_ALL	pyrimidine nucleotide biosynthetic process	RT	9	3.3E-4	1.5E-2
☐	GOTERM_BP_ALL	pyrimidine nucleoside triphosphate metabolic process	RT	6	1.5E-2	3.5E-1
☐	GOTERM_BP_ALL	pyrimidine ribonucleotide biosynthetic process	RT	4	1.1E-1	8.8E-1
☐	GOTERM_BP_ALL	pyrimidine ribonucleotide metabolic process	RT	4	1.3E-1	9.1E-1
☐	GOTERM_BP_ALL	CTP biosynthetic process	RT	3	2.7E-1	9.9E-1
☐	GOTERM_BP_ALL	CTP metabolic process	RT	3	2.7E-1	9.9E-1
☐	GOTERM_BP_ALL	pyrimidine ribonucleoside triphosphate biosynthetic process	RT	3	2.7E-1	9.9E-1
☐	GOTERM_BP_ALL	pyrimidine ribonucleoside triphosphate metabolic process	RT	3	2.7E-1	9.9E-1
☐	GOTERM_BP_ALL	ribonucleoside triphosphate biosynthetic process	RT	8	2.8E-1	9.9E-1
☐	GOTERM_BP_ALL	ribonucleoside triphosphate metabolic process	RT	8	3.7E-1	1.0E0
	Annotation Cluster 104	Enrichment Score: 1.21	G 🟩	Count	P_Value	Benjamini

☐	**GOTERM_BP_ALL**	maintenance of fidelity during DNA-dependent DNA replication	RT		6	8.7E-3	2.3E-1
☐	**GOTERM_BP_ALL**	mismatch repair	RT		5	3.3E-2	5.5E-1
☐	**GOTERM_MF_ALL**	mismatched DNA binding	RT		3	2.2E-1	9.8E-1
☐	**GOTERM_MF_ALL**	double-stranded DNA binding	RT		5	2.4E-1	9.8E-1
	Annotation Cluster 105	Enrichment Score: 1.19	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	redox-active center	RT		10	5.1E-3	6.2E-2
☐	**GOTERM_BP_ALL**	cell redox homeostasis	RT		12	6.5E-3	1.8E-1
☐	**INTERPRO**	Thioredoxin domain	RT		7	1.1E-2	7.2E-1
☐	**PIR_SUPERFAMILY**	PIRSF001487:protein disulfide-isomerase	RT		4	2.3E-2	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Thioredoxin 2	RT		4	2.4E-2	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Thioredoxin 1	RT		4	2.4E-2	1.0E0
☐	**UP_SEQ_FEATURE**	short sequence motif:Prevents secretion from ER	RT		9	2.8E-2	1.0E0
☐	**INTERPRO**	Thioredoxin-related	RT		7	2.9E-2	9.3E-1
☐	**INTERPRO**	Disulphide isomerase	RT		3	6.2E-2	9.8E-1
☐	**INTERPRO**	Endoplasmic reticulum targeting sequence	RT		9	8.0E-2	9.9E-1
☐	**GOTERM_MF_ALL**	intramolecular oxidoreductase activity	RT		8	1.2E-1	9.2E-1
☐	**GOTERM_MF_ALL**	protein disulfide isomerase activity	RT		3	1.5E-1	9.4E-1
☐	**INTERPRO**	Thioredoxin fold	RT		10	2.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular homeostasis	RT		19	9.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	homeostatic process	RT		25	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of biological quality	RT		40	1.0E0	1.0E0
	Annotation Cluster 106	Enrichment Score: 1.18	G	🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	repeat:2-1	RT		5	3.2E-2	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:1-3	RT		4	3.6E-2	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:1-2	RT		5	4.1E-2	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:2-2	RT		5	4.1E-2	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:1-1	RT		4	1.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:1-4	RT		3	1.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:2-3	RT		3	1.8E-1	1.0E0
	Annotation Cluster 107	Enrichment Score: 1.18	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	meiosis I	RT		8	1.1E-2	2.8E-1
☐	**GOTERM_BP_ALL**	meiotic prophase I	RT		3	1.6E-1	9.4E-1
☐	**GOTERM_BP_ALL**	prophase	RT		3	1.6E-1	9.4E-1
	Annotation Cluster 108	Enrichment Score: 1.15	G	🟩	Count	P_Value	Benjamini
☐	**BIOCARTA**	RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage	RT		5	2.5E-2	4.0E-1
☐	**BIOCARTA**	Cell Cycle	RT		6	8.3E-2	7.5E-1
☐	**BIOCARTA**	cdc25 and chk1 Regulatory Pathway in response to DNA damage	RT		3	1.7E-1	8.1E-1
	Annotation Cluster 109	Enrichment Score: 1.12	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	hormone receptor binding	RT		7	2.0E-2	4.7E-1
☐	**GOTERM_MF_ALL**	nuclear hormone receptor binding	RT		6	4.8E-2	7.1E-1
☐	**GOTERM_MF_ALL**	thyroid hormone receptor binding	RT		3	1.5E-1	9.4E-1
☐	**GOTERM_MF_ALL**	steroid hormone receptor binding	RT		3	2.2E-1	9.8E-1
	Annotation Cluster 110	Enrichment Score: 1.11	G	🟩	Count	P_Value	Benjamini
☐	**SMART**	DSRM	RT		6	1.9E-2	4.9E-1
☐	**INTERPRO**	Double-stranded RNA-binding-like	RT		6	1.9E-2	8.7E-1
☐	**GOTERM_MF_ALL**	double-stranded RNA binding	RT		7	1.1E-1	8.9E-1
☐	**INTERPRO**	Double-stranded RNA binding	RT		5	1.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:DRBM 2	RT		3	2.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:DRBM 1	RT		3	2.2E-1	1.0E0

	Annotation Cluster 111	Enrichment Score: 1.11	G	🟩	Count	P_Value	Benjamini
☐	**SMART**	KH	RT	▮	7	1.5E-2	4.3E-1
☐	**INTERPRO**	K Homology	RT	▮	7	3.9E-2	9.7E-1
☐	**INTERPRO**	K Homology, type 1	RT	▮	7	4.5E-2	9.6E-1
☐	**UP_SEQ_FEATURE**	domain:KH 2	RT	▮	3	3.3E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:KH 1	RT	▮	3	3.3E-1	1.0E0
	Annotation Cluster 112	Enrichment Score: 1.08	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	biopolymer methylation	RT	▮	12	8.6E-3	2.3E-1
☐	**GOTERM_BP_ALL**	methylation	RT	▮	12	1.3E-2	3.1E-1
☐	**GOTERM_BP_ALL**	regulation of gene expression, epigenetic	RT	▮	10	6.6E-2	7.5E-1
☐	**GOTERM_BP_ALL**	DNA methylation	RT	▮	4	3.3E-1	9.9E-1
☐	**GOTERM_BP_ALL**	DNA alkylation	RT	▮	4	3.3E-1	9.9E-1
☐	**GOTERM_BP_ALL**	DNA modification	RT	▮	4	4.0E-1	1.0E0
	Annotation Cluster 113	Enrichment Score: 1.05	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	blastocyst growth	RT	▮	6	6.3E-3	1.7E-1
☐	**GOTERM_BP_ALL**	inner cell mass cell proliferation	RT	▮	4	3.0E-2	5.2E-1
☐	**GOTERM_BP_ALL**	blastocyst development	RT	▮	8	3.6E-2	5.8E-1
☐	**GOTERM_BP_ALL**	developmental growth	RT	▮	8	1.9E-1	9.7E-1
☐	**GOTERM_BP_ALL**	in utero embryonic development	RT	▮	14	3.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	growth	RT	▮	13	1.0E0	1.0E0
	Annotation Cluster 114	Enrichment Score: 1.05	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	heterochromatin	RT	▮	12	4.2E-4	4.8E-3
☐	**INTERPRO**	SNF2-related	RT	▮	8	8.0E-3	6.2E-1
☐	**GOTERM_BP_ALL**	chromatin remodeling	RT	▮	10	2.8E-2	5.1E-1
☐	**GOTERM_BP_ALL**	covalent chromatin modification	RT	▮	10	3.2E-2	5.3E-1
☐	**GOTERM_BP_ALL**	gene silencing	RT	▮	8	4.2E-2	6.3E-1
☐	**GOTERM_BP_ALL**	regulation of gene expression, epigenetic	RT	▮	10	6.6E-2	7.5E-1
☐	**GOTERM_BP_ALL**	methylation-dependent chromatin silencing	RT	▮	3	6.9E-2	7.6E-1
☐	**GOTERM_CC_ALL**	chromatin remodeling complex	RT	▮	5	1.1E-1	5.6E-1
☐	**GOTERM_CC_ALL**	SWI/SNF complex	RT	▮	3	1.2E-1	5.9E-1
☐	**GOTERM_BP_ALL**	chromatin silencing	RT	▮	4	1.7E-1	9.6E-1
☐	**GOTERM_BP_ALL**	heterochromatin formation	RT	▮	4	1.7E-1	9.6E-1
☐	**GOTERM_BP_ALL**	protein-DNA complex assembly	RT	▮	12	2.2E-1	9.8E-1
☐	**GOTERM_BP_ALL**	negative regulation of gene expression, epigenetic	RT	▮	4	2.5E-1	9.9E-1
☐	**GOTERM_BP_ALL**	chromatin assembly	RT	▮	9	3.2E-1	9.9E-1
☐	**GOTERM_BP_ALL**	chromatin assembly or disassembly	RT	▮	12	3.5E-1	1.0E0
☐	**BIOCARTA**	Control of Gene Expression by Vitamin D Receptor	RT	▮	5	3.7E-1	9.4E-1
☐	**GOTERM_BP_ALL**	nucleosome assembly	RT	▮	7	4.2E-1	1.0E0
☐	**BIOCARTA**	Chromatin Remodeling by hSWI/SNF ATP-dependent Complexes	RT	▮	3	6.0E-1	9.8E-1
	Annotation Cluster 115	Enrichment Score: 1.05	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	coenzyme metabolic process	RT	▮	24	5.4E-2	6.8E-1
☐	**GOTERM_BP_ALL**	coenzyme biosynthetic process	RT	▮	15	6.1E-2	7.3E-1
☐	**GOTERM_BP_ALL**	cofactor biosynthetic process	RT	▮	16	1.0E-1	8.6E-1
☐	**GOTERM_BP_ALL**	cofactor metabolic process	RT	▮	25	2.0E-1	9.7E-1
	Annotation Cluster 116	Enrichment Score: 1.03	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	nuclear chromatin	RT	▮	8	1.4E-2	1.3E-1
☐	**GOTERM_CC_ALL**	nuclear heterochromatin	RT	▮	6	4.8E-2	3.2E-1
☐	**SMART**	CHROMO	RT	▮	4	2.8E-1	1.0E0

☐	**INTERPRO**	Chromo	RT	4	3.9E-1	1.0E0
	Annotation Cluster 117	Enrichment Score: 1.02	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	polyol metabolic process	RT	6	4.5E-2	6.3E-1
☐	**GOTERM_BP_ALL**	glycerol metabolic process	RT	5	1.2E-1	9.0E-1
☐	**GOTERM_BP_ALL**	glycerol-3-phosphate metabolic process	RT	3	1.6E-1	9.4E-1
	Annotation Cluster 118	Enrichment Score: 0.98	G 🟩	Count	P_Value	Benjamini
☐	**SMART**	TUDOR	RT	5	6.2E-2	7.9E-1
☐	**INTERPRO**	Tudor	RT	5	7.4E-2	9.9E-1
☐	**UP_SEQ_FEATURE**	domain:Tudor	RT	3	1.4E-1	1.0E0
☐	**INTERPRO**	Maternal tudor protein	RT	3	1.8E-1	1.0E0
	Annotation Cluster 119	Enrichment Score: 0.94	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	nucleotide biosynthetic process	RT	32	3.6E-6	2.8E-4
☐	**GOTERM_BP_ALL**	nucleobase, nucleoside and nucleotide metabolic process	RT	41	1.8E-5	1.2E-3
☐	**GOTERM_BP_ALL**	purine nucleotide biosynthetic process	RT	20	8.1E-5	4.5E-3
☐	**GOTERM_BP_ALL**	nucleotide metabolic process	RT	37	1.2E-4	6.2E-3
☐	**GOTERM_BP_ALL**	purine nucleotide metabolic process	RT	20	4.2E-4	1.9E-2
☐	**GOTERM_BP_ALL**	ribonucleotide biosynthetic process	RT	18	4.8E-4	2.1E-2
☐	**GOTERM_BP_ALL**	ribonucleotide metabolic process	RT	18	2.3E-3	7.7E-2
☐	**GOTERM_BP_ALL**	purine ribonucleotide biosynthetic process	RT	13	2.4E-2	4.6E-1
☐	**GOTERM_BP_ALL**	purine ribonucleotide metabolic process	RT	13	5.0E-2	6.6E-1
☐	**GOTERM_BP_ALL**	coenzyme biosynthetic process	RT	15	6.1E-2	7.3E-1
☐	**GOTERM_CC_ALL**	proton-transporting ATP synthase complex, coupling factor F(o)	RT	4	6.7E-2	4.1E-1
☐	**GOTERM_CC_ALL**	proton-transporting two-sector ATPase complex, proton-transporting domain	RT	4	6.7E-2	4.1E-1
☐	**SP_PIR_KEYWORDS**	CF(0)	RT	4	7.2E-2	4.8E-1
☐	**GOTERM_CC_ALL**	proton-transporting ATP synthase complex	RT	5	9.5E-2	5.1E-1
☐	**GOTERM_BP_ALL**	nucleoside triphosphate biosynthetic process	RT	10	1.1E-1	8.7E-1
☐	**GOTERM_BP_ALL**	nucleoside triphosphate metabolic process	RT	11	1.3E-1	9.1E-1
☐	**GOTERM_BP_ALL**	ribonucleoside triphosphate biosynthetic process	RT	8	2.8E-1	9.9E-1
☐	**GOTERM_BP_ALL**	ribonucleoside triphosphate metabolic process	RT	8	3.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	hydrogen ion transport	RT	6	3.8E-1	9.6E-1
☐	**GOTERM_BP_ALL**	purine nucleoside triphosphate biosynthetic process	RT	7	4.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	purine ribonucleoside triphosphate biosynthetic process	RT	7	4.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	purine ribonucleoside triphosphate metabolic process	RT	7	5.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	purine nucleoside triphosphate metabolic process	RT	7	5.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	ATP synthesis coupled proton transport	RT	5	5.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	inorganic cation transmembrane transporter activity	RT	14	5.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	cation-transporting ATPase activity	RT	6	5.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT	14	5.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	primary active transmembrane transporter activity	RT	14	5.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrogen ion transporting ATP synthase activity, rotational mechanism	RT	5	5.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrogen ion transporting ATPase activity, rotational mechanism	RT	5	6.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	ATP biosynthetic process	RT	5	6.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	nucleoside phosphate metabolic process	RT	5	6.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	proton transport	RT	7	6.5E-1	1.0E0

☐	GOTERM_CC_ALL	proton-transporting two-sector ATPase complex	RT	▮		5	6.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	ATP synthesis	RT	▮		3	7.0E-1	1.0E0
☐	GOTERM_BP_ALL	ATP metabolic process	RT	▮		5	7.1E-1	1.0E0
☐	GOTERM_BP_ALL	hydrogen transport	RT	▮		7	7.3E-1	1.0E0
☐	GOTERM_BP_ALL	oxidative phosphorylation	RT	▮		5	8.0E-1	1.0E0
☐	GOTERM_MF_ALL	hydrogen ion transmembrane transporter activity	RT	▮		8	8.5E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity, coupled to transmembrane movement of ions	RT	▮		7	8.7E-1	1.0E0
☐	GOTERM_MF_ALL	monovalent inorganic cation transmembrane transporter activity	RT	▮		8	8.7E-1	1.0E0
☐	GOTERM_MF_ALL	active transmembrane transporter activity	RT	▮		26	8.9E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity, coupled to movement of substances	RT	▮		9	9.3E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity, coupled to transmembrane movement of substances	RT	▮		9	9.3E-1	1.0E0
☐	GOTERM_MF_ALL	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT	▮		9	9.4E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	▮		3	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	monovalent inorganic cation transport	RT	▮		12	1.0E0	1.0E0
	Annotation Cluster 120	Enrichment Score: 0.89	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	translational initiation	RT	▮		15	3.2E-4	1.5E-2
☐	GOTERM_BP_ALL	regulation of translational initiation	RT	▮		6	3.7E-2	5.9E-1
☐	SP_PIR_KEYWORDS	translation regulation	RT	▮		6	1.2E-1	6.5E-1
☐	GOTERM_BP_ALL	regulation of biosynthetic process	RT	▮		17	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cellular biosynthetic process	RT	▮		13	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of translation	RT	▮		12	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of protein metabolic process	RT	▮		22	8.7E-1	1.0E0
	Annotation Cluster 121	Enrichment Score: 0.89	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	repeat:WD 10	RT	▮		3	7.9E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 11	RT	▮		3	7.9E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 9	RT	▮		3	1.1E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 8	RT	▮		3	4.1E-1	1.0E0
	Annotation Cluster 122	Enrichment Score: 0.87	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	superoxide dismutase activity	RT	▮		4	5.2E-2	7.3E-1
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on superoxide radicals as acceptor	RT	▮		4	5.2E-2	7.3E-1
☐	GOTERM_MF_ALL	copper, zinc superoxide dismutase activity	RT	▮		3	1.2E-1	9.1E-1
☐	GOTERM_BP_ALL	superoxide metabolic process	RT	▮		4	3.0E-1	9.9E-1
☐	GOTERM_BP_ALL	oxygen and reactive oxygen species metabolic process	RT	▮		5	4.2E-1	1.0E0
	Annotation Cluster 123	Enrichment Score: 0.86	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Polyunsaturated fatty acid biosynthesis	RT	▮		6	1.9E-2	2.5E-1
☐	GOTERM_MF_ALL	stearoyl-CoA 9-desaturase activity	RT	▮		3	6.6E-2	7.6E-1
☐	INTERPRO	Fatty acid desaturase, type 1, N-terminal	RT	▮		3	8.7E-2	9.9E-1
☐	INTERPRO	Fatty acid desaturase, type 1	RT	▮		3	1.2E-1	1.0E0
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	RT	▮		3	1.2E-1	9.1E-1
☐	KEGG_PATHWAY	PPAR signaling pathway	RT	▮		8	5.9E-1	9.8E-1
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	RT	▮		8	9.6E-1	1.0E0
	Annotation Cluster 124	Enrichment Score: 0.83	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	proteasome complex (sensu Eukaryota)	RT	▮		9	7.0E-3	6.7E-2

☐	INTERPRO	20S proteasome, A and B subunits	RT	▮		4	2.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	Threonine protease	RT	▮		4	2.7E-1	9.0E-1
☐	INTERPRO	Peptidase T1A, proteasome beta-subunit	RT	▮		3	2.7E-1	1.0E0
☐	GOTERM_CC_ALL	proteasome core complex (sensu Eukaryota)	RT	▮		4	2.8E-1	8.7E-1
☐	GOTERM_MF_ALL	threonine endopeptidase activity	RT	▮		4	3.1E-1	9.9E-1
	Annotation Cluster 125	Enrichment Score: 0.82	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	histone methyltransferase activity	RT	▮		8	7.9E-3	2.6E-1
☐	GOTERM_MF_ALL	protein methyltransferase activity	RT	▮		9	2.0E-2	4.7E-1
☐	GOTERM_MF_ALL	N-methyltransferase activity	RT	▮		8	6.1E-2	7.5E-1
☐	SMART	SET	RT	▮		6	1.3E-1	9.5E-1
☐	SMART	PostSET	RT	▮		3	2.1E-1	9.8E-1
☐	INTERPRO	SET	RT	▮		6	2.7E-1	1.0E0
☐	INTERPRO	Post-SET zinc-binding region	RT	▮		3	3.1E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:SET	RT	▮		3	4.1E-1	1.0E0
☐	GOTERM_MF_ALL	histone-lysine N-methyltransferase activity	RT	▮		3	4.8E-1	1.0E0
☐	GOTERM_MF_ALL	lysine N-methyltransferase activity	RT	▮		3	4.8E-1	1.0E0
☐	GOTERM_MF_ALL	protein-lysine N-methyltransferase activity	RT	▮		3	4.8E-1	1.0E0
	Annotation Cluster 126	Enrichment Score: 0.81	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:Rhodanese	RT	▮		5	2.4E-2	1.0E0
☐	SMART	RHOD	RT	▮		5	4.0E-2	6.6E-1
☐	INTERPRO	Rhodanese-like	RT	▮		4	2.2E-1	1.0E0
☐	GOTERM_MF_ALL	protein tyrosine phosphatase activity	RT	▮		9	5.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	protein phosphatase	RT	▮		9	7.6E-1	1.0E0
	Annotation Cluster 127	Enrichment Score: 0.81	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	DNA-directed RNA polymerase complex	RT	▮		4	1.4E-1	6.5E-1
☐	GOTERM_CC_ALL	nuclear DNA-directed RNA polymerase complex	RT	▮		4	1.4E-1	6.5E-1
☐	GOTERM_CC_ALL	RNA polymerase complex	RT	▮		4	1.9E-1	7.3E-1
	Annotation Cluster 128	Enrichment Score: 0.8	G		🟩	Count	P_Value	Benjamini
☐	SMART	PHB	RT	▮		3	1.4E-1	9.5E-1
☐	PIR_SUPERFAMILY	PIRSF005651:membrane protease subunits, stomatin/prohibitin homologs	RT	▮		3	1.4E-1	1.0E0
☐	INTERPRO	Band 7 protein	RT	▮		3	2.1E-1	1.0E0
	Annotation Cluster 129	Enrichment Score: 0.78	G		🟩	Count	P_Value	Benjamini
☐	SMART	PINT	RT	▮		4	9.9E-2	9.1E-1
☐	INTERPRO	Proteasome component region PCI	RT	▮		4	1.5E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:PCI	RT	▮		3	2.9E-1	1.0E0
	Annotation Cluster 130	Enrichment Score: 0.77	G		🟩	Count	P_Value	Benjamini
☐	SMART	UBQ	RT	▮		7	1.2E-1	9.4E-1
☐	UP_SEQ_FEATURE	domain:Ubiquitin-like	RT	▮		5	1.8E-1	1.0E0
☐	INTERPRO	Ubiquitin	RT	▮		7	2.3E-1	1.0E0
	Annotation Cluster 131	Enrichment Score: 0.76	G		🟩	Count	P_Value	Benjamini
☐	BIOCARTA	RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage	RT	▮		5	2.5E-2	4.0E-1
☐	GOTERM_MF_ALL	cyclin-dependent protein kinase activity	RT	▮		5	2.6E-1	9.9E-1
☐	PIR_SUPERFAMILY	PIRSF000564:kinase-related transforming protein	RT	▮		3	8.4E-1	1.0E0
	Annotation Cluster 132	Enrichment Score: 0.75	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	maintenance of protein localization	RT	▮		4	1.1E-1	8.8E-1
☐	GOTERM_BP_ALL	maintenance of localization	RT	▮		5	1.2E-1	9.0E-1
☐	GOTERM_BP_ALL	maintenance of cellular protein localization	RT	▮		3	2.3E-1	9.8E-1

☐	GOTERM_BP_ALL	maintenance of cellular localization	RT	▮		3	3.4E-1	1.0E0
	Annotation Cluster 133	Enrichment Score: 0.72	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	GTPase activity	RT	▮		23	1.2E-2	3.5E-1
☐	GOTERM_MF_ALL	GTP binding	RT	▮		35	2.1E-1	9.8E-1
☐	GOTERM_MF_ALL	guanyl ribonucleotide binding	RT	▮		35	2.4E-1	9.8E-1
☐	GOTERM_MF_ALL	guanyl nucleotide binding	RT	▮		35	2.4E-1	9.8E-1
☐	SP_PIR_KEYWORDS	GTP-binding	RT	▮		27	4.6E-1	9.8E-1
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	RT	▮		19	6.9E-1	1.0E0
	Annotation Cluster 134	Enrichment Score: 0.72	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on sulfur group of donors	RT	▮		6	4.1E-2	6.7E-1
☐	GOTERM_MF_ALL	NADP binding	RT	▮		5	5.8E-2	7.4E-1
☐	INTERPRO	Mercuric reductase	RT	▮		3	6.2E-2	9.8E-1
☐	INTERPRO	Pyridine nucleotide-disulphide oxidoreductase, class I, active site	RT	▮		3	6.2E-2	9.8E-1
☐	INTERPRO	Pyridine nucleotide-disulphide oxidoreductase dimerisation region	RT	▮		3	1.2E-1	1.0E0
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on sulfur group of donors, NAD or NADP as acceptor	RT	▮		3	1.2E-1	9.1E-1
☐	INTERPRO	Pyridine nucleotide-disulphide oxidoreductase, NAD-binding region	RT	▮		3	3.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	fad	RT	▮		10	5.2E-1	9.9E-1
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:FAD	RT	▮		4	5.5E-1	1.0E0
☐	GOTERM_MF_ALL	antioxidant activity	RT	▮		6	5.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	flavoprotein	RT	▮		10	5.9E-1	1.0E0
☐	GOTERM_MF_ALL	FAD binding	RT	▮		6	6.6E-1	1.0E0
	Annotation Cluster 135	Enrichment Score: 0.71	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	transferase activity, transferring pentosyl groups	RT	▮		10	1.0E-2	3.1E-1
☐	GOTERM_MF_ALL	transferase activity, transferring glycosyl groups	RT	▮		19	7.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	glycosyltransferase	RT	▮		13	9.1E-1	1.0E0
	Annotation Cluster 136	Enrichment Score: 0.7	G		🟩	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF005673:pendulin	RT	▮		3	7.6E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:ARM 10; atypical	RT	▮		3	7.9E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:ARM 1; truncated	RT	▮		3	7.9E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:IBB	RT	▮		3	7.9E-2	1.0E0
☐	UP_SEQ_FEATURE	region of interest:NLS binding site (minor)	RT	▮		3	7.9E-2	1.0E0
☐	UP_SEQ_FEATURE	region of interest:NLS binding site (major)	RT	▮		3	7.9E-2	1.0E0
☐	INTERPRO	Importin-alpha-like, importin-beta-binding region	RT	▮		3	1.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ARM 4	RT	▮		4	2.3E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ARM 9	RT	▮		3	2.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ARM 8	RT	▮		3	3.3E-1	1.0E0
☐	SMART	ARM	RT	▮		4	3.4E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ARM 3	RT	▮		4	3.4E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ARM 2	RT	▮		4	3.4E-1	1.0E0
☐	COG_ONTOLOGY	Intracellular trafficking and secretion	RT	▮		9	3.4E-1	9.6E-1
☐	UP_SEQ_FEATURE	repeat:ARM 6	RT	▮		3	4.1E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ARM 7	RT	▮		3	4.1E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ARM 5	RT	▮		3	4.4E-1	1.0E0
☐	INTERPRO	Armadillo	RT	▮		4	5.0E-1	1.0E0
	Annotation Cluster 137	Enrichment Score: 0.67	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	poly(A) binding	RT	▮		3	1.2E-1	9.1E-1

☐	GOTERM_MF_ALL	mRNA binding	RT		6	2.0E-1	9.7E-1
☐	GOTERM_MF_ALL	single-stranded RNA binding	RT		3	3.9E-1	1.0E0
	Annotation Cluster 138	Enrichment Score: 0.67	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	transferase activity	RT		213	4.2E-6	3.9E-4
☐	SP_PIR_KEYWORDS	transferase	RT		150	1.6E-3	2.2E-2
☐	GOTERM_MF_ALL	transferase activity, transferring phosphorus-containing groups	RT		117	2.8E-3	1.2E-1
☐	GOTERM_MF_ALL	kinase activity	RT		88	1.6E-1	9.4E-1
☐	SMART	S_TKc	RT		27	3.4E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase, active site	RT		25	3.5E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase	RT		19	5.3E-1	1.0E0
☐	UP_SEQ_FEATURE	binding site:ATP	RT		37	5.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	kinase	RT		65	5.7E-1	9.9E-1
☐	SP_PIR_KEYWORDS	Serine/threonine-protein kinase	RT		32	6.3E-1	1.0E0
☐	UP_SEQ_FEATURE	active site:Proton acceptor	RT		44	7.5E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Protein kinase	RT		31	7.7E-1	1.0E0
☐	INTERPRO	Protein kinase, core	RT		27	7.9E-1	1.0E0
☐	GOTERM_MF_ALL	protein serine/threonine kinase activity	RT		38	8.5E-1	1.0E0
☐	GOTERM_MF_ALL	phosphotransferase activity, alcohol group as acceptor	RT		56	8.6E-1	1.0E0
☐	GOTERM_MF_ALL	protein kinase activity	RT		47	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	phosphorus metabolic process	RT		68	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	phosphate metabolic process	RT		68	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	phosphorylation	RT		54	9.6E-1	1.0E0
☐	GOTERM_MF_ALL	protein-tyrosine kinase activity	RT		20	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid phosphorylation	RT		43	9.9E-1	1.0E0
	Annotation Cluster 139	Enrichment Score: 0.66	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	electron carrier activity	RT		27	2.3E-2	4.9E-1
☐	GOTERM_BP_ALL	generation of precursor metabolites and energy	RT		47	6.2E-1	1.0E0
☐	GOTERM_BP_ALL	electron transport	RT		35	7.3E-1	1.0E0
	Annotation Cluster 140	Enrichment Score: 0.64	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	Ran GTPase binding	RT		4	1.9E-2	4.6E-1
☐	GOTERM_MF_ALL	Ras GTPase binding	RT		7	3.6E-1	1.0E0
☐	GOTERM_MF_ALL	small GTPase binding	RT		7	4.1E-1	1.0E0
☐	GOTERM_MF_ALL	GTPase binding	RT		7	4.6E-1	1.0E0
☐	GOTERM_MF_ALL	enzyme binding	RT		20	4.9E-1	1.0E0
	Annotation Cluster 141	Enrichment Score: 0.64	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	microtubule polymerization or depolymerization	RT		5	6.3E-2	7.4E-1
☐	GOTERM_BP_ALL	microtubule depolymerization	RT		4	1.1E-1	8.8E-1
☐	GOTERM_BP_ALL	negative regulation of microtubule polymerization or depolymerization	RT		4	1.3E-1	9.1E-1
☐	GOTERM_BP_ALL	regulation of microtubule polymerization or depolymerization	RT		4	1.7E-1	9.6E-1
☐	GOTERM_BP_ALL	protein depolymerization	RT		6	2.6E-1	9.9E-1
☐	GOTERM_BP_ALL	negative regulation of microtubule depolymerization	RT		3	3.0E-1	9.9E-1
☐	GOTERM_BP_ALL	regulation of microtubule depolymerization	RT		3	3.0E-1	9.9E-1
☐	GOTERM_BP_ALL	negative regulation of cellular component organization and biogenesis	RT		6	3.2E-1	9.9E-1
☐	GOTERM_BP_ALL	regulation of cellular component organization and biogenesis	RT		8	4.9E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of protein metabolic process	RT		8	7.0E-1	1.0E0
	Annotation Cluster 142	Enrichment Score: 0.63	G	🟩	Count	P_Value	Benjamini

☐	UP_SEQ_FEATURE	repeat:RCC1 6	RT	3	1.4E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:RCC1 5	RT	3	2.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:RCC1 4	RT	3	2.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:RCC1 3	RT	3	2.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:RCC1 2	RT	3	2.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:RCC1 1	RT	3	2.6E-1	1.0E0
	Annotation Cluster 143	Enrichment Score: 0.61	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Pre-ATP-grasp fold	RT	3	1.5E-1	1.0E0
☐	INTERPRO	ATP-grasp fold	RT	3	3.1E-1	1.0E0
☐	INTERPRO	ATP-grasp fold, subdomain 2	RT	3	3.4E-1	1.0E0
	Annotation Cluster 144	Enrichment Score: 0.6	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	DNA topoisomerase (ATP-hydrolyzing) activity	RT	3	1.9E-1	9.7E-1
☐	GOTERM_MF_ALL	DNA topoisomerase activity	RT	3	2.6E-1	9.9E-1
☐	GOTERM_BP_ALL	DNA topological change	RT	3	3.4E-1	1.0E0
	Annotation Cluster 145	Enrichment Score: 0.58	G 🟩	Count	P_Value	Benjamini
☐	SMART	EXOIII	RT	3	2.1E-1	9.8E-1
☐	INTERPRO	Exonuclease	RT	3	2.7E-1	1.0E0
☐	INTERPRO	Exonuclease, RNase T and DNA polymerase III	RT	3	3.1E-1	1.0E0
	Annotation Cluster 146	Enrichment Score: 0.58	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	viral reproductive process	RT	4	2.0E-1	9.7E-1
☐	GOTERM_BP_ALL	viral reproduction	RT	4	2.7E-1	9.9E-1
☐	GOTERM_BP_ALL	viral infectious cycle	RT	3	3.4E-1	1.0E0
	Annotation Cluster 147	Enrichment Score: 0.56	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	DNA damage response, signal transduction	RT	8	7.6E-2	7.8E-1
☐	GOTERM_BP_ALL	DNA damage response, signal transduction resulting in induction of apoptosis	RT	3	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	induction of apoptosis by intracellular signals	RT	4	5.5E-1	1.0E0
	Annotation Cluster 148	Enrichment Score: 0.56	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	I-kappaB kinase/NF-kappaB cascade	RT	11	7.6E-2	7.8E-1
☐	GOTERM_BP_ALL	positive regulation of I-kappaB kinase/NF-kappaB cascade	RT	7	1.5E-1	9.4E-1
☐	GOTERM_BP_ALL	regulation of I-kappaB kinase/NF-kappaB cascade	RT	7	1.8E-1	9.6E-1
☐	GOTERM_BP_ALL	positive regulation of signal transduction	RT	9	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	protein kinase cascade	RT	18	9.8E-1	1.0E0
	Annotation Cluster 149	Enrichment Score: 0.52	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	blastocyst growth	RT	6	6.3E-3	1.7E-1
☐	GOTERM_BP_ALL	glial cell differentiation	RT	5	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	gliogenesis	RT	5	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	central nervous system development	RT	9	1.0E0	1.0E0
☐	GOTERM_BP_ALL	neurogenesis	RT	13	1.0E0	1.0E0
	Annotation Cluster 150	Enrichment Score: 0.5	G 🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	pyridoxal phosphate	RT	10	7.2E-2	4.8E-1
☐	UP_SEQ_FEATURE	binding site:Pyridoxal phosphate (covalent)	RT	7	1.1E-1	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring nitrogenous groups	RT	6	2.8E-1	9.9E-1
☐	INTERPRO	Aminotransferase, class I and II	RT	3	3.7E-1	1.0E0
☐	GOTERM_MF_ALL	transaminase activity	RT	5	4.2E-1	1.0E0
☐	GOTERM_MF_ALL	pyridoxal phosphate binding	RT	6	4.4E-1	1.0E0
☐	GOTERM_MF_ALL	vitamin binding	RT	11	5.4E-1	1.0E0
☐	INTERPRO	Pyridoxal phosphate-dependent	RT	4	5.5E-1	1.0E0

☐		transferase, major region, subdomain 1	RT				
☐	SP_PIR_KEYWORDS	aminotransferase	RT		3	6.3E-1	1.0E0
	Annotation Cluster 151	Enrichment Score: 0.49	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	WW	RT		3	1.5E-1	1.0E0
☐	SMART	WW	RT		5	4.0E-1	1.0E0
☐	INTERPRO	WW/Rsp5/WWP	RT		5	5.8E-1	1.0E0
	Annotation Cluster 152	Enrichment Score: 0.49	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	acetyltransferase activity	RT		10	1.5E-1	9.4E-1
☐	GOTERM_BP_ALL	protein amino acid acetylation	RT		4	1.7E-1	9.6E-1
☐	GOTERM_BP_ALL	N-terminal protein amino acid modification	RT		3	2.0E-1	9.7E-1
☐	GOTERM_BP_ALL	protein amino acid acylation	RT		5	2.1E-1	9.7E-1
☐	GOTERM_MF_ALL	N-acyltransferase activity	RT		8	3.4E-1	1.0E0
☐	GOTERM_MF_ALL	N-acetyltransferase activity	RT		7	3.6E-1	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring acyl groups	RT		19	3.7E-1	1.0E0
☐	GOTERM_MF_ALL	acyltransferase activity	RT		17	4.8E-1	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring groups other than amino-acyl groups	RT		17	5.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	acyltransferase	RT		13	6.0E-1	1.0E0
☐	INTERPRO	GCN5-related N-acetyltransferase	RT		3	6.0E-1	1.0E0
	Annotation Cluster 153	Enrichment Score: 0.48	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	blastocyst development	RT		8	3.6E-2	5.8E-1
☐	GOTERM_BP_ALL	in utero embryonic development	RT		14	3.5E-1	1.0E0
☐	GOTERM_BP_ALL	chordate embryonic development	RT		21	5.5E-1	1.0E0
☐	GOTERM_BP_ALL	embryonic development ending in birth or egg hatching	RT		21	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	embryonic development	RT		33	9.5E-1	1.0E0
	Annotation Cluster 154	Enrichment Score: 0.48	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		38	4.8E-2	6.5E-1
☐	GOTERM_BP_ALL	negative regulation of metabolic process	RT		48	4.8E-2	6.5E-1
☐	GOTERM_BP_ALL	negative regulation of cellular metabolic process	RT		41	1.0E-1	8.6E-1
☐	GOTERM_BP_ALL	negative regulation of transcription	RT		30	3.0E-1	9.9E-1
☐	GOTERM_BP_ALL	negative regulation of transcription, DNA-dependent	RT		19	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of cellular process	RT		86	7.0E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of biological process	RT		92	7.0E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of transcription from RNA polymerase II promoter	RT		13	7.4E-1	1.0E0
☐	GOTERM_BP_ALL	transcription from RNA polymerase II promoter	RT		35	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of transcription from RNA polymerase II promoter	RT		29	9.8E-1	1.0E0
	Annotation Cluster 155	Enrichment Score: 0.48	G	🟩	Count	P_Value	Benjamini
☐	BIOCARTA	Apoptotic Signaling in Response to DNA Damage	RT		7	1.6E-2	3.7E-1
☐	BIOCARTA	Caspase Cascade in Apoptosis	RT		5	2.4E-1	8.8E-1
☐	BIOCARTA	TNFR1 Signaling Pathway	RT		4	6.3E-1	9.8E-1
☐	BIOCARTA	FAS signaling pathway (CD95)	RT		4	6.6E-1	9.8E-1
☐	BIOCARTA	HIV-I Nef	RT		5	8.6E-1	1.0E0
☐	KEGG_PATHWAY	Apoptosis	RT		5	9.8E-1	1.0E0
	Annotation Cluster 156	Enrichment Score: 0.47	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	ENV polyprotein (coat polyprotein)	RT		3	2.1E-1	1.0E0
☐	GOTERM_CC_ALL	virion part	RT		4	3.3E-1	9.1E-1
☐	GOTERM_CC_ALL	virion	RT		4	3.3E-1	9.1E-1

☐	**GOTERM_CC_ALL**	viral capsid	RT	3	5.7E-1	9.9E-1
	Annotation Cluster 157	Enrichment Score: 0.46	G	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	repeat:32	RT	3	1.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:29	RT	3	1.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:30	RT	3	1.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:31	RT	3	1.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:28	RT	3	1.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:23	RT	3	2.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:25	RT	3	2.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:26	RT	3	2.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:27	RT	3	2.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:22	RT	3	2.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:8	RT	6	3.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:9	RT	5	3.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:3	RT	11	3.5E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:20	RT	3	3.7E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:6	RT	7	3.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:4	RT	9	3.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:21	RT	3	4.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:17	RT	3	4.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:16	RT	3	4.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:7	RT	6	4.7E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:2	RT	12	5.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:11	RT	4	5.3E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:15	RT	3	5.7E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:10	RT	4	5.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:1	RT	11	6.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:14	RT	3	6.5E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:13	RT	3	7.0E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:12	RT	3	7.0E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:5	RT	6	7.0E-1	1.0E0
	Annotation Cluster 158	Enrichment Score: 0.46	G	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	repeat:Solcar 2	RT	5	1.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:Solcar 1	RT	5	1.6E-1	1.0E0
☐	**INTERPRO**	Mitochondrial brown fat uncoupling protein	RT	3	2.7E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:Solcar 3	RT	4	3.4E-1	1.0E0
☐	**INTERPRO**	Mitochondrial carrier protein	RT	4	4.1E-1	1.0E0
☐	**INTERPRO**	Mitochondrial substrate carrier	RT	5	4.5E-1	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF002458:ADP,ATP carrier protein	RT	3	6.4E-1	1.0E0
☐	**INTERPRO**	Adenine nucleotide translocator 1	RT	3	7.1E-1	1.0E0
	Annotation Cluster 159	Enrichment Score: 0.42	G	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	iron ion transmembrane transporter activity	RT	3	4.2E-2	6.7E-1
☐	**SP_PIR_KEYWORDS**	Iron transport	RT	5	1.0E-1	6.0E-1
☐	**GOTERM_MF_ALL**	di-, tri-valent inorganic cation transmembrane transporter activity	RT	6	1.7E-1	9.5E-1
☐	**GOTERM_MF_ALL**	transition metal ion transmembrane transporter activity	RT	5	1.8E-1	9.6E-1
☐	**GOTERM_BP_ALL**	iron ion transport	RT	5	2.7E-1	9.9E-1
☐	**GOTERM_BP_ALL**	transition metal ion transport	RT	7	4.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	inorganic cation transmembrane transporter activity	RT	14	5.6E-1	1.0E0

☐	GOTERM_BP_ALL	di-, tri-valent inorganic cation transport	RT	▮		7	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	metal ion transmembrane transporter activity	RT	▮		10	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cation transport	RT	▮		22	1.0E0	1.0E0
☐	GOTERM_MF_ALL	ion transmembrane transporter activity	RT	▮		29	1.0E0	1.0E0
☐	GOTERM_BP_ALL	metal ion transport	RT	▮		15	1.0E0	1.0E0
	Annotation Cluster 160	Enrichment Score: 0.4	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	filamentous actin	RT	▮		3	2.2E-1	7.9E-1
☐	GOTERM_CC_ALL	cortical cytoskeleton	RT	▮		4	3.1E-1	8.9E-1
☐	GOTERM_CC_ALL	cell cortex part	RT	▮		5	4.0E-1	9.5E-1
☐	GOTERM_CC_ALL	cell cortex	RT	▮		6	5.3E-1	9.8E-1
☐	GOTERM_CC_ALL	actin filament	RT	▮		3	7.1E-1	1.0E0
	Annotation Cluster 161	Enrichment Score: 0.4	G		🟩	Count	P_Value	Benjamini
☐	BIOCARTA	How Progesterone Initiates the Oocyte Maturation	RT	▮		9	2.0E-3	1.1E-1
☐	BIOCARTA	METS affect on Macrophage Differentiation	RT	▮		7	1.6E-2	3.7E-1
☐	BIOCARTA	Signaling Pathway from G-Protein Families	RT	▮		8	2.2E-2	4.1E-1
☐	BIOCARTA	Cadmium induces DNA synthesis and proliferation in macrophages	RT	▮		6	2.4E-2	4.1E-1
☐	BIOCARTA	Influence of Ras and Rho proteins on G1 to S Transition	RT	▮		8	2.7E-2	4.0E-1
☐	KEGG_PATHWAY	Bladder cancer	RT	▮		10	3.3E-2	3.5E-1
☐	KEGG_PATHWAY	Gap junction	RT	▮		14	8.2E-2	5.5E-1
☐	BIOCARTA	Transcription factor CREB and its extracellular signals	RT	▮		6	9.7E-2	7.5E-1
☐	BIOCARTA	Corticosteroids and cardioprotection	RT	▮		5	1.1E-1	7.6E-1
☐	BIOCARTA	CCR3 signaling in Eosinophils	RT	▮		6	1.1E-1	7.4E-1
☐	SP_PIR_KEYWORDS	nucleotide binding	RT	▮		12	1.3E-1	6.9E-1
☐	SP_PIR_KEYWORDS	P-loop	RT	▮		12	1.4E-1	7.0E-1
☐	BIOCARTA	Role of EGF Receptor Transactivation by GPCRs in Cardiac Hypertrophy	RT	▮		5	1.7E-1	8.1E-1
☐	BIOCARTA	Trka Receptor Signaling Pathway	RT	▮		4	1.9E-1	8.2E-1
☐	SP_PIR_KEYWORDS	GTP binding	RT	▮		7	2.0E-1	8.1E-1
☐	SP_PIR_KEYWORDS	thiolester bond	RT	▮		4	2.0E-1	8.1E-1
☐	BIOCARTA	Attenuation of GPCR Signaling	RT	▮		3	2.2E-1	8.5E-1
☐	KEGG_PATHWAY	Small cell lung cancer	RT	▮		13	2.2E-1	8.1E-1
☐	BIOCARTA	Inhibition of Cellular Proliferation by Gleevec	RT	▮		5	2.4E-1	8.8E-1
☐	BIOCARTA	Pertussis toxin-insensitive CCR5 Signaling in Macrophage	RT	▮		4	2.5E-1	8.8E-1
☐	KEGG_PATHWAY	Glioma	RT	▮		9	2.7E-1	8.5E-1
☐	KEGG_PATHWAY	Pancreatic cancer	RT	▮		10	3.2E-1	8.9E-1
☐	KEGG_PATHWAY	Non-small cell lung cancer	RT	▮		8	3.2E-1	8.9E-1
☐	BIOCARTA	The IGF-1 Receptor and Longevity	RT	▮		3	3.8E-1	9.4E-1
☐	BIOCARTA	IL-2 Receptor Beta Chain in T cell Activation	RT	▮		6	4.3E-1	9.5E-1
☐	INTERPRO	Guanine nucleotide binding protein (G-protein), alpha subunit	RT	▮		3	4.3E-1	1.0E0
☐	BIOCARTA	Roles of ?-arrestin-dependent Recruitment of Src Kinases in GPCR Signaling	RT	▮		4	4.4E-1	9.5E-1
☐	BIOCARTA	BCR Signaling Pathway	RT	▮		5	4.5E-1	9.5E-1
☐	KEGG_PATHWAY	Prostate cancer	RT	▮		11	4.5E-1	9.4E-1
☐	BIOCARTA	Ras Signaling Pathway	RT	▮		4	4.7E-1	9.6E-1
☐	KEGG_PATHWAY	Chronic myeloid leukemia	RT	▮		9	5.1E-1	9.6E-1
☐	BIOCARTA	NFAT and Hypertrophy of the heart (Transcription in the broken heart)	RT	▮		6	5.2E-1	9.7E-1
☐	BIOCARTA	Erk1/Erk2 Mapk Signaling pathway	RT	▮		5	5.2E-1	9.6E-1

☐	**BIOCARTA**	Fc Epsilon Receptor I Signaling in Mast Cells	RT	▮	5	5.2E-1	9.6E-1
☐	**BIOCARTA**	p38 MAPK Signaling Pathway	RT	▮	5	5.2E-1	9.6E-1
☐	**BIOCARTA**	Trefoil Factors Initiate Mucosal Healing	RT	▮	4	5.3E-1	9.6E-1
☐	**BIOCARTA**	TPO Signaling Pathway	RT	▮	4	5.3E-1	9.6E-1
☐	**BIOCARTA**	Role of Erk5 in Neuronal Survival	RT	▮	3	5.4E-1	9.6E-1
☐	**BIOCARTA**	CXCR4 Signaling Pathway	RT	▮	4	5.8E-1	9.8E-1
☐	**BIOCARTA**	Bioactive Peptide Induced Signaling Pathway	RT	▮	5	5.9E-1	9.8E-1
☐	**BIOCARTA**	IL 3 signaling pathway	RT	▮	3	6.3E-1	9.8E-1
☐	**BIOCARTA**	EGF Signaling Pathway	RT	▮	4	6.6E-1	9.8E-1
☐	**BIOCARTA**	PDGF Signaling Pathway	RT	▮	4	6.6E-1	9.8E-1
☐	**BIOCARTA**	Links between Pyk2 and Map Kinases	RT	▮	4	6.6E-1	9.8E-1
☐	**BIOCARTA**	Regulation of transcriptional activity by PML	RT	▮	3	6.6E-1	9.8E-1
☐	**BIOCARTA**	Nerve growth factor pathway (NGF)	RT	▮	3	6.6E-1	9.8E-1
☐	**BIOCARTA**	T Cell Receptor Signaling Pathway	RT	▮	5	6.7E-1	9.8E-1
☐	**BIOCARTA**	Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation	RT	▮	3	6.9E-1	9.8E-1
☐	**SP_PIR_KEYWORDS**	proto-oncogene	RT	▮	8	6.9E-1	1.0E0
☐	**BIOCARTA**	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling	RT	▮	4	7.0E-1	9.8E-1
☐	**BIOCARTA**	IGF-1 Signaling Pathway	RT	▮	3	7.1E-1	9.9E-1
☐	**BIOCARTA**	Role of MAL in Rho-Mediated Activation of SRF	RT	▮	3	7.1E-1	9.9E-1
☐	**BIOCARTA**	EPO Signaling Pathway	RT	▮	3	7.4E-1	9.9E-1
☐	**KEGG_PATHWAY**	Melanoma	RT	▮	7	7.4E-1	9.9E-1
☐	**BIOCARTA**	IL 6 signaling pathway	RT	▮	3	7.6E-1	9.9E-1
☐	**KEGG_PATHWAY**	Renal cell carcinoma	RT	▮	7	7.7E-1	1.0E0
☐	**BIOCARTA**	Insulin Signaling Pathway	RT	▮	3	7.8E-1	9.9E-1
☐	**KEGG_PATHWAY**	VEGF signaling pathway	RT	▮	7	8.0E-1	1.0E0
☐	**BIOCARTA**	IL 2 signaling pathway	RT	▮	3	8.0E-1	9.9E-1
☐	**KEGG_PATHWAY**	Thyroid cancer	RT	▮	3	8.1E-1	1.0E0
☐	**KEGG_PATHWAY**	GnRH signaling pathway	RT	▮	8	8.2E-1	1.0E0
☐	**KEGG_PATHWAY**	B cell receptor signaling pathway	RT	▮	6	8.3E-1	1.0E0
☐	**BIOCARTA**	Growth Hormone Signaling Pathway	RT	▮	3	8.6E-1	1.0E0
☐	**BIOCARTA**	Keratinocyte Differentiation	RT	▮	4	8.7E-1	1.0E0
☐	**KEGG_PATHWAY**	T cell receptor signaling pathway	RT	▮	8	8.8E-1	1.0E0
☐	**BIOCARTA**	fMLP induced chemokine gene expression in HMC-1 cells	RT	▮	3	8.8E-1	1.0E0
☐	**KEGG_PATHWAY**	Fc epsilon RI signaling pathway	RT	▮	6	8.8E-1	1.0E0
☐	**KEGG_PATHWAY**	Long-term depression	RT	▮	6	8.9E-1	1.0E0
☐	**KEGG_PATHWAY**	Endometrial cancer	RT	▮	4	9.1E-1	1.0E0
☐	**KEGG_PATHWAY**	Long-term potentiation	RT	▮	5	9.2E-1	1.0E0
☐	**KEGG_PATHWAY**	mTOR signaling pathway	RT	▮	4	9.2E-1	1.0E0
☐	**KEGG_PATHWAY**	Melanogenesis	RT	▮	7	9.4E-1	1.0E0
☐	**KEGG_PATHWAY**	Tight junction	RT	▮	9	9.4E-1	1.0E0
☐	**KEGG_PATHWAY**	Acute myeloid leukemia	RT	▮	4	9.5E-1	1.0E0
☐	**KEGG_PATHWAY**	ErbB signaling pathway	RT	▮	5	9.8E-1	1.0E0
☐	**KEGG_PATHWAY**	Axon guidance	RT	▮	7	9.9E-1	1.0E0
☐	**KEGG_PATHWAY**	Focal adhesion	RT	▮	12	9.9E-1	1.0E0
☐	**KEGG_PATHWAY**	MAPK signaling pathway	RT	▮	16	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	Palmitate	RT	▮	9	1.0E0	1.0E0

☐	**BIOCARTA**	MAPKinase Signaling Pathway	RT	4	1.0E0	1.0E0
☐	**KEGG_PATHWAY**	Natural killer cell mediated cytotoxicity	RT	5	1.0E0	1.0E0
☐	**KEGG_PATHWAY**	Regulation of actin cytoskeleton	RT	8	1.0E0	1.0E0
	Annotation Cluster 162	Enrichment Score: 0.37	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	release of cytochrome c from mitochondria	RT	3	3.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	apoptotic mitochondrial changes	RT	4	3.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	apoptotic program	RT	6	6.5E-1	1.0E0
	Annotation Cluster 163	Enrichment Score: 0.36	G	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	tumor necrosis factor receptor superfamily binding	RT	4	2.9E-1	9.9E-1
☐	**GOTERM_MF_ALL**	tumor necrosis factor receptor binding	RT	4	2.9E-1	9.9E-1
☐	**GOTERM_MF_ALL**	cytokine activity	RT	12	9.9E-1	1.0E0
	Annotation Cluster 164	Enrichment Score: 0.34	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	pigment biosynthetic process	RT	5	3.1E-1	9.9E-1
☐	**GOTERM_BP_ALL**	pigment metabolic process	RT	5	4.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	secondary metabolic process	RT	5	7.1E-1	1.0E0
	Annotation Cluster 165	Enrichment Score: 0.33	G	Count	P_Value	Benjamini
☐	**INTERPRO**	Porin, eukaryotic type	RT	3	6.2E-2	9.8E-1
☐	**GOTERM_CC_ALL**	organelle outer membrane	RT	6	1.5E-1	6.6E-1
☐	**GOTERM_CC_ALL**	mitochondrial outer membrane	RT	5	2.5E-1	8.3E-1
☐	**GOTERM_MF_ALL**	anion channel activity	RT	3	9.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	anion transmembrane transporter activity	RT	6	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	anion transport	RT	9	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	ion channel activity	RT	5	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	substrate specific channel activity	RT	5	1.0E0	1.0E0
	Annotation Cluster 166	Enrichment Score: 0.33	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	amyloid precursor protein metabolic process	RT	3	3.0E-1	9.9E-1
☐	**GOTERM_BP_ALL**	beta-amyloid metabolic process	RT	3	3.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	glycoprotein metabolic process	RT	8	9.2E-1	1.0E0
	Annotation Cluster 167	Enrichment Score: 0.32	G	Count	P_Value	Benjamini
☐	**INTERPRO**	Myb, DNA-binding	RT	5	3.1E-1	1.0E0
☐	**SMART**	SANT	RT	6	3.1E-1	1.0E0
☐	**INTERPRO**	SANT, DNA-binding	RT	6	5.3E-1	1.0E0
☐	**INTERPRO**	Homeodomain-related	RT	5	1.0E0	1.0E0
	Annotation Cluster 168	Enrichment Score: 0.31	G	Count	P_Value	Benjamini
☐	**SMART**	HMG	RT	6	3.1E-1	1.0E0
☐	**INTERPRO**	High mobility group box, HMG1/HMG2, subgroup	RT	3	4.6E-1	1.0E0
☐	**INTERPRO**	High mobility group box, HMG1/HMG2	RT	6	4.8E-1	1.0E0
☐	**INTERPRO**	High mobility group box, HMG	RT	4	7.9E-1	1.0E0
	Annotation Cluster 169	Enrichment Score: 0.31	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	cellular macromolecule catabolic process	RT	31	1.3E-1	9.1E-1
☐	**GOTERM_BP_ALL**	biopolymer catabolic process	RT	29	2.7E-1	9.9E-1
☐	**GOTERM_BP_ALL**	cellular catabolic process	RT	47	3.1E-1	9.9E-1
☐	**GOTERM_BP_ALL**	ubiquitin-dependent protein catabolic process	RT	16	3.2E-1	9.9E-1
☐	**GOTERM_BP_ALL**	modification-dependent macromolecule catabolic process	RT	16	3.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	modification-dependent protein catabolic process	RT	16	3.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	proteolysis involved in cellular protein catabolic process	RT	16	3.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	macromolecule catabolic process	RT	34	3.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular protein catabolic process	RT	16	4.0E-1	1.0E0

☐	GOTERM_MF_ALL	ubiquitin thiolesterase activity	RT		6	6.3E-1	1.0E0
☐	GOTERM_MF_ALL	thiolester hydrolase activity	RT		8	6.3E-1	1.0E0
☐	GOTERM_MF_ALL	ubiquitin-specific protease activity	RT		6	6.6E-1	1.0E0
☐	GOTERM_MF_ALL	small conjugating protein-specific protease activity	RT		6	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	protein catabolic process	RT		18	7.0E-1	1.0E0
☐	INTERPRO	Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2	RT		4	7.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	thiol protease	RT		9	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	catabolic process	RT		50	8.1E-1	1.0E0
☐	GOTERM_MF_ALL	cysteine-type peptidase activity	RT		11	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	proteolysis	RT		46	1.0E0	1.0E0
	Annotation Cluster 170	Enrichment Score: 0.31	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	endoplasmic reticulum part	RT		14	2.3E-1	8.0E-1
☐	SP_PIR_KEYWORDS	GPI-anchor biosynthesis	RT		3	2.7E-1	9.0E-1
☐	GOTERM_BP_ALL	phospholipid biosynthetic process	RT		9	2.7E-1	9.9E-1
☐	KEGG_PATHWAY	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	RT		4	3.3E-1	8.9E-1
☐	GOTERM_CC_ALL	nuclear envelope-endoplasmic reticulum network	RT		12	3.5E-1	9.2E-1
☐	GOTERM_BP_ALL	GPI anchor biosynthetic process	RT		4	3.5E-1	1.0E0
☐	GOTERM_BP_ALL	GPI anchor metabolic process	RT		4	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	phosphoinositide biosynthetic process	RT		4	4.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	Phospholipid biosynthesis	RT		4	4.3E-1	9.8E-1
☐	GOTERM_CC_ALL	endoplasmic reticulum membrane	RT		11	4.3E-1	9.6E-1
☐	GOTERM_BP_ALL	membrane lipid biosynthetic process	RT		9	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid lipidation	RT		6	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	lipoprotein biosynthetic process	RT		6	5.6E-1	1.0E0
☐	GOTERM_BP_ALL	glycerophospholipid biosynthetic process	RT		4	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	lipoprotein metabolic process	RT		7	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	phosphoinositide metabolic process	RT		4	8.7E-1	1.0E0
☐	GOTERM_BP_ALL	phospholipid metabolic process	RT		10	8.8E-1	1.0E0
☐	KEGG_PATHWAY	Glycan structures - biosynthesis 2	RT		4	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	glycerophospholipid metabolic process	RT		4	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	membrane lipid metabolic process	RT		11	9.7E-1	1.0E0
	Annotation Cluster 171	Enrichment Score: 0.31	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	dolichyl-diphosphooligosaccharide-protein glycotransferase activity	RT		3	1.5E-1	9.4E-1
☐	GOTERM_MF_ALL	oligosaccharyl transferase activity	RT		3	1.5E-1	9.4E-1
☐	GOTERM_BP_ALL	protein amino acid N-linked glycosylation via asparagine	RT		3	2.3E-1	9.8E-1
☐	GOTERM_BP_ALL	peptidyl-asparagine modification	RT		3	2.3E-1	9.8E-1
☐	KEGG_PATHWAY	N-Glycan biosynthesis	RT		6	3.8E-1	9.1E-1
☐	GOTERM_BP_ALL	protein amino acid N-linked glycosylation	RT		3	6.6E-1	1.0E0
☐	GOTERM_BP_ALL	glycoprotein biosynthetic process	RT		7	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	biopolymer glycosylation	RT		6	9.1E-1	1.0E0
☐	GOTERM_BP_ALL	glycoprotein metabolic process	RT		8	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid glycosylation	RT		5	9.6E-1	1.0E0
☐	KEGG_PATHWAY	Glycan structures - biosynthesis 1	RT		7	9.7E-1	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring hexosyl groups	RT		8	9.9E-1	1.0E0
	Annotation Cluster 172	Enrichment Score: 0.3	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of nucleocytoplasmic transport	RT		4	2.7E-1	9.9E-1
☐	GOTERM_BP_ALL	regulation of protein transport	RT		3	5.0E-1	1.0E0

☐	GOTERM_BP_ALL	regulation of transport	RT		7	9.4E-1	1.0E0
	Annotation Cluster 173	Enrichment Score: 0.29	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	tricarboxylic acid cycle	RT		4	4.0E-1	1.0E0
☐	GOTERM_BP_ALL	acetyl-CoA metabolic process	RT		5	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	acetyl-CoA catabolic process	RT		4	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	aerobic respiration	RT		4	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	coenzyme catabolic process	RT		4	5.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	Tricarboxylic acid cycle	RT		3	5.6E-1	9.9E-1
☐	GOTERM_BP_ALL	cellular respiration	RT		4	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	cofactor catabolic process	RT		4	6.3E-1	1.0E0
☐	KEGG_PATHWAY	Citrate cycle (TCA cycle)	RT		3	7.3E-1	9.9E-1
	Annotation Cluster 174	Enrichment Score: 0.28	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	response to UV	RT		5	2.5E-1	9.9E-1
☐	GOTERM_BP_ALL	response to radiation	RT		9	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	response to light stimulus	RT		6	8.4E-1	1.0E0
	Annotation Cluster 175	Enrichment Score: 0.26	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of Ras protein signal transduction	RT		3	1.3E-1	9.1E-1
☐	GOTERM_BP_ALL	negative regulation of small GTPase mediated signal transduction	RT		3	2.3E-1	9.8E-1
☐	GOTERM_BP_ALL	Ras protein signal transduction	RT		12	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of Ras protein signal transduction	RT		8	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of small GTPase mediated signal transduction	RT		9	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of signal transduction	RT		23	1.0E0	1.0E0
	Annotation Cluster 176	Enrichment Score: 0.25	G	🟩	Count	P_Value	Benjamini
☐	BIOCARTA	Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia	RT		4	4.1E-1	9.5E-1
☐	BIOCARTA	mCalpain and friends in Cell motility	RT		3	5.0E-1	9.7E-1
☐	BIOCARTA	Integrin Signaling Pathway	RT		3	8.8E-1	1.0E0
	Annotation Cluster 177	Enrichment Score: 0.25	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	ligase activity, forming carbon-nitrogen bonds	RT		21	1.8E-1	9.6E-1
☐	UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	RT		6	2.6E-1	1.0E0
☐	SMART	UBCc	RT		5	4.1E-1	1.0E0
☐	KEGG_PATHWAY	Ubiquitin mediated proteolysis	RT		13	6.4E-1	9.9E-1
☐	INTERPRO	Ubiquitin-conjugating enzyme, E2	RT		4	7.5E-1	1.0E0
☐	GOTERM_MF_ALL	ubiquitin-protein ligase activity	RT		9	8.7E-1	1.0E0
☐	GOTERM_MF_ALL	small protein conjugating enzyme activity	RT		9	8.9E-1	1.0E0
☐	GOTERM_MF_ALL	small conjugating protein ligase activity	RT		9	9.0E-1	1.0E0
☐	GOTERM_MF_ALL	acid-amino acid ligase activity	RT		10	9.1E-1	1.0E0
	Annotation Cluster 178	Enrichment Score: 0.24	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of caspase activity	RT		3	2.0E-1	9.7E-1
☐	GOTERM_BP_ALL	regulation of caspase activity	RT		6	3.6E-1	1.0E0
☐	GOTERM_BP_ALL	apoptotic program	RT		6	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	caspase activation	RT		3	7.0E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of caspase activity	RT		3	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of hydrolase activity	RT		3	8.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of hydrolase activity	RT		7	1.0E0	1.0E0
	Annotation Cluster 179	Enrichment Score: 0.23	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of MAP kinase activity	RT		4	2.7E-1	9.9E-1
☐	GOTERM_BP_ALL	negative regulation of catalytic activity	RT		8	3.4E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of protein kinase activity	RT		6	4.3E-1	1.0E0

☐	GOTERM_BP_ALL	negative regulation of kinase activity	RT	▮		6	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of transferase activity	RT	▮		6	4.7E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of kinase activity	RT	▮		15	7.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of MAP kinase activity	RT	▮		6	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of transferase activity	RT	▮		15	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of protein kinase activity	RT	▮		12	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of a molecular function	RT	▮		30	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of catalytic activity	RT	▮		24	9.8E-1	1.0E0
	Annotation Cluster 180	Enrichment Score: 0.23	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	nuclear envelope-endoplasmic reticulum network	RT	▮		12	3.5E-1	9.2E-1
☐	GOTERM_CC_ALL	endoplasmic reticulum membrane	RT	▮		11	4.3E-1	9.6E-1
☐	GOTERM_CC_ALL	integral to endoplasmic reticulum membrane	RT	▮		4	5.9E-1	9.9E-1
☐	GOTERM_CC_ALL	intrinsic to endoplasmic reticulum membrane	RT	▮		4	6.8E-1	1.0E0
☐	GOTERM_CC_ALL	integral to organelle membrane	RT	▮		6	8.2E-1	1.0E0
☐	GOTERM_CC_ALL	intrinsic to organelle membrane	RT	▮		6	8.8E-1	1.0E0
	Annotation Cluster 181	Enrichment Score: 0.22	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, RING/FYVE/PHD-type	RT	▮		15	4.5E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:RING-type	RT	▮		12	5.4E-1	1.0E0
☐	SMART	RING	RT	▮		17	6.1E-1	1.0E0
☐	INTERPRO	Zinc finger, RING-type	RT	▮		17	8.6E-1	1.0E0
	Annotation Cluster 182	Enrichment Score: 0.22	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	somatic hypermutation of immunoglobulin genes	RT	▮		3	2.0E-1	9.7E-1
☐	GOTERM_BP_ALL	somatic diversification of immune receptors via somatic mutation	RT	▮		3	2.0E-1	9.7E-1
☐	GOTERM_BP_ALL	immunoglobulin production	RT	▮		4	7.4E-1	1.0E0
☐	GOTERM_BP_ALL	production of molecular mediator of immune response	RT	▮		4	7.5E-1	1.0E0
☐	GOTERM_BP_ALL	somatic recombination of immunoglobulin gene segments	RT	▮		3	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	somatic diversification of immune receptors via germline recombination within a single locus	RT	▮		3	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	somatic cell DNA recombination	RT	▮		3	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	somatic diversification of immunoglobulins	RT	▮		3	8.0E-1	1.0E0
☐	GOTERM_BP_ALL	somatic diversification of immune receptors	RT	▮		3	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	immune effector process	RT	▮		6	1.0E0	1.0E0
	Annotation Cluster 183	Enrichment Score: 0.22	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	enzyme binding	RT	▮		20	4.9E-1	1.0E0
☐	GOTERM_MF_ALL	protein kinase binding	RT	▮		7	6.3E-1	1.0E0
☐	GOTERM_MF_ALL	kinase binding	RT	▮		7	7.3E-1	1.0E0
	Annotation Cluster 184	Enrichment Score: 0.21	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	glucose transport	RT	▮		4	5.5E-1	1.0E0
☐	GOTERM_BP_ALL	hexose transport	RT	▮		4	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	monosaccharide transport	RT	▮		4	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	carbohydrate transport	RT	▮		6	7.9E-1	1.0E0
	Annotation Cluster 185	Enrichment Score: 0.21	G		🟩	Count	P_Value	Benjamini
☐	SMART	BROMO	RT	▮		4	5.0E-1	1.0E0
☐	INTERPRO	Bromodomain	RT	▮		4	6.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	bromodomain	RT	▮		3	7.7E-1	1.0E0
	Annotation Cluster 186	Enrichment Score: 0.2	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	GTP binding	RT	▮		7	2.0E-1	8.1E-1

☐	**INTERPRO**	Small GTP-binding protein domain	**RT**	▮		10	8.8E-1	1.0E0
☐	**INTERPRO**	Ras GTPase	**RT**	▮		8	9.7E-1	1.0E0
☐	**INTERPRO**	Ras	**RT**	▮		6	9.7E-1	1.0E0
	Annotation Cluster 187	Enrichment Score: 0.17	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	positive regulation of locomotion	**RT**	▮		4	3.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of cell motility	**RT**	▮		4	3.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of cell migration	**RT**	▮		3	5.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	locomotion	**RT**	▮		6	9.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cell motility	**RT**	▮		5	9.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of locomotion	**RT**	▮		5	9.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cell migration	**RT**	▮		4	9.6E-1	1.0E0
	Annotation Cluster 188	Enrichment Score: 0.17	G		🟩	Count	P_Value	Benjamini
☐	**SMART**	CH	**RT**	▮		5	6.0E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:CH	**RT**	▮		3	6.5E-1	1.0E0
☐	**INTERPRO**	Calponin-like actin-binding	**RT**	▮		5	7.9E-1	1.0E0
	Annotation Cluster 189	Enrichment Score: 0.17	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	skeletal morphogenesis	**RT**	▮		4	4.0E-1	1.0E0
☐	**BIOCARTA**	Erk1/Erk2 Mapk Signaling pathway	**RT**	▮		5	5.2E-1	9.6E-1
☐	**GOTERM_BP_ALL**	skeletal development	**RT**	▮		7	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	embryonic morphogenesis	**RT**	▮		5	1.0E0	1.0E0
	Annotation Cluster 190	Enrichment Score: 0.17	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	phosphoric monoester hydrolase activity	**RT**	▮		25	3.0E-1	9.9E-1
☐	**GOTERM_MF_ALL**	protein tyrosine phosphatase activity	**RT**	▮		9	5.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein amino acid dephosphorylation	**RT**	▮		12	5.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	phosphoric ester hydrolase activity	**RT**	▮		27	5.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	phosphoprotein phosphatase activity	**RT**	▮		13	7.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	dephosphorylation	**RT**	▮		12	7.4E-1	1.0E0
☐	**SMART**	PTPc	**RT**	▮		3	7.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	protein phosphatase	**RT**	▮		9	7.6E-1	1.0E0
☐	**INTERPRO**	Protein-tyrosine phosphatase, Tyr-specific/dual-specificity type	**RT**	▮		6	8.3E-1	1.0E0
☐	**INTERPRO**	Protein-tyrosine phosphatase, receptor/non-receptor type	**RT**	▮		3	8.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	active site:Phosphocysteine intermediate	**RT**	▮		4	9.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Tyrosine-protein phosphatase	**RT**	▮		3	9.3E-1	1.0E0
	Annotation Cluster 191	Enrichment Score: 0.17	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	protein dimerization activity	**RT**	▮		25	6.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	protein homodimerization activity	**RT**	▮		13	6.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	identical protein binding	**RT**	▮		23	7.9E-1	1.0E0
	Annotation Cluster 192	Enrichment Score: 0.16	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	positive regulation of myeloid leukocyte differentiation	**RT**	▮		3	2.7E-1	9.9E-1
☐	**GOTERM_BP_ALL**	regulation of myeloid leukocyte differentiation	**RT**	▮		4	4.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of myeloid cell differentiation	**RT**	▮		3	5.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of osteoclast differentiation	**RT**	▮		3	5.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of myeloid cell differentiation	**RT**	▮		5	6.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	osteoclast differentiation	**RT**	▮		3	6.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	myeloid cell differentiation	**RT**	▮		9	8.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of developmental process	**RT**	▮		7	8.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	myeloid leukocyte differentiation	**RT**	▮		4	8.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of cell differentiation	**RT**	▮		4	9.2E-1	1.0E0

☐	GOTERM_BP_ALL	leukocyte differentiation	RT	9	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell differentiation	RT	7	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of developmental process	RT	13	1.0E0	1.0E0
	Annotation Cluster 193	Enrichment Score: 0.16	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	anti-apoptosis	RT	15	9.7E-2	8.5E-1
☐	GOTERM_BP_ALL	negative regulation of programmed cell death	RT	22	2.9E-1	9.9E-1
☐	GOTERM_BP_ALL	negative regulation of apoptosis	RT	20	4.4E-1	1.0E0
☐	GOTERM_BP_ALL	death	RT	68	4.9E-1	1.0E0
☐	GOTERM_BP_ALL	cell death	RT	68	4.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	apoptosis	RT	24	6.2E-1	1.0E0
☐	GOTERM_BP_ALL	programmed cell death	RT	62	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	apoptosis	RT	60	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of programmed cell death	RT	39	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of apoptosis	RT	37	8.7E-1	1.0E0
☐	GOTERM_BP_ALL	cell development	RT	85	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cellular developmental process	RT	118	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cell differentiation	RT	118	1.0E0	1.0E0
☐	GOTERM_BP_ALL	developmental process	RT	187	1.0E0	1.0E0
☐	GOTERM_BP_ALL	organ development	RT	66	1.0E0	1.0E0
☐	GOTERM_BP_ALL	anatomical structure morphogenesis	RT	50	1.0E0	1.0E0
☐	GOTERM_BP_ALL	multicellular organismal development	RT	122	1.0E0	1.0E0
☐	GOTERM_BP_ALL	system development	RT	85	1.0E0	1.0E0
☐	GOTERM_BP_ALL	anatomical structure development	RT	101	1.0E0	1.0E0
☐	GOTERM_BP_ALL	multicellular organismal process	RT	138	1.0E0	1.0E0
	Annotation Cluster 194	Enrichment Score: 0.16	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	transcription factor binding	RT	22	6.1E-1	1.0E0
☐	GOTERM_MF_ALL	transcription coactivator activity	RT	8	6.3E-1	1.0E0
☐	GOTERM_MF_ALL	transcription activator activity	RT	19	6.8E-1	1.0E0
☐	GOTERM_MF_ALL	transcription cofactor activity	RT	11	9.1E-1	1.0E0
	Annotation Cluster 195	Enrichment Score: 0.15	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	hair cycle process	RT	4	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	hair follicle development	RT	4	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	molting cycle process	RT	4	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	molting cycle	RT	4	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	hair cycle	RT	4	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	epidermis development	RT	8	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	ectoderm development	RT	8	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	tissue development	RT	15	1.0E0	1.0E0
	Annotation Cluster 196	Enrichment Score: 0.15	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	protein tyrosine phosphatase activity	RT	9	5.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	tyrosine-specific phosphatase	RT	3	7.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	phosphoric monoester hydrolase	RT	3	9.4E-1	1.0E0
	Annotation Cluster 197	Enrichment Score: 0.14	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	gluconeogenesis	RT	3	5.3E-1	1.0E0
☐	GOTERM_BP_ALL	pyruvate metabolic process	RT	3	6.6E-1	1.0E0
☐	GOTERM_BP_ALL	hexose biosynthetic process	RT	3	7.0E-1	1.0E0
☐	GOTERM_BP_ALL	monosaccharide biosynthetic process	RT	3	7.4E-1	1.0E0
☐	GOTERM_BP_ALL	alcohol biosynthetic process	RT	3	7.4E-1	1.0E0
☐	GOTERM_BP_ALL	glucose metabolic process	RT	9	8.1E-1	1.0E0

					Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	carbohydrate biosynthetic process	RT		6	9.4E-1	1.0E0
	Annotation Cluster 198	Enrichment Score: 0.14	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of neuron apoptosis	RT		5	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	neuron apoptosis	RT		5	7.4E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of neuron apoptosis	RT		3	7.9E-1	1.0E0
	Annotation Cluster 199	Enrichment Score: 0.14	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	microbody	RT		8	6.7E-1	1.0E0
☐	GOTERM_CC_ALL	peroxisome	RT		8	6.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	peroxisome	RT		7	7.5E-1	1.0E0
☐	UP_SEQ_FEATURE	short sequence motif:Microbody targeting signal	RT		3	8.1E-1	1.0E0
	Annotation Cluster 200	Enrichment Score: 0.14	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	anion:cation symporter activity	RT		3	4.8E-1	1.0E0
☐	GOTERM_MF_ALL	organic acid:sodium symporter activity	RT		3	5.7E-1	1.0E0
☐	GOTERM_MF_ALL	carboxylic acid transmembrane transporter activity	RT		7	5.7E-1	1.0E0
☐	GOTERM_MF_ALL	organic acid transmembrane transporter activity	RT		7	5.9E-1	1.0E0
☐	GOTERM_MF_ALL	solute:cation symporter activity	RT		5	7.3E-1	1.0E0
☐	GOTERM_MF_ALL	solute:sodium symporter activity	RT		4	7.5E-1	1.0E0
☐	GOTERM_MF_ALL	symporter activity	RT		10	9.0E-1	1.0E0
☐	GOTERM_MF_ALL	secondary active transmembrane transporter activity	RT		12	9.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	Symport	RT		5	9.6E-1	1.0E0
☐	GOTERM_MF_ALL	anion transmembrane transporter activity	RT		6	9.8E-1	1.0E0
	Annotation Cluster 201	Enrichment Score: 0.13	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	multicellular organismal homeostasis	RT		3	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	tissue homeostasis	RT		3	7.2E-1	1.0E0
☐	KEGG_PATHWAY	Renal cell carcinoma	RT		7	7.7E-1	1.0E0
	Annotation Cluster 202	Enrichment Score: 0.13	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cytolysis	RT		6	7.2E-2	7.7E-1
☐	SP_PIR_KEYWORDS	cytolysis	RT		3	4.4E-1	9.8E-1
☐	SP_PIR_KEYWORDS	serine proteinase	RT		6	5.4E-1	9.9E-1
☐	PIR_SUPERFAMILY	PIRSF001135:trypsin	RT		6	7.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	T-cell	RT		3	7.9E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Peptidase S1	RT		5	8.9E-1	1.0E0
☐	SMART	Tryp_SPc	RT		5	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	Zymogen	RT		11	9.8E-1	1.0E0
☐	UP_SEQ_FEATURE	active site:Charge relay system	RT		7	9.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	serine protease	RT		7	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	serine-type endopeptidase activity	RT		10	9.9E-1	1.0E0
☐	INTERPRO	Peptidase S1 and S6, chymotrypsin/Hap	RT		5	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	serine hydrolase activity	RT		10	1.0E0	1.0E0
☐	GOTERM_MF_ALL	serine-type peptidase activity	RT		10	1.0E0	1.0E0
☐	INTERPRO	Peptidase S1A, chymotrypsin	RT		4	1.0E0	1.0E0
☐	GOTERM_MF_ALL	endopeptidase activity	RT		22	1.0E0	1.0E0
	Annotation Cluster 203	Enrichment Score: 0.12	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:B30.2/SPRY	RT		4	4.8E-1	1.0E0
☐	SMART	SPRY	RT		4	8.2E-1	1.0E0
☐	INTERPRO	SPla/RYanodine receptor SPRY	RT		4	9.0E-1	1.0E0
☐	INTERPRO	B302, (SPRY)-like	RT		4	9.1E-1	1.0E0
	Annotation Cluster 204	Enrichment Score: 0.12	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	carboxylic acid transmembrane	RT		7	5.7E-1	1.0E0

		transporter activity					
☐	GOTERM_MF_ALL	organic acid transmembrane transporter activity	RT		7	5.9E-1	1.0E0
☐	GOTERM_MF_ALL	amino acid transmembrane transporter activity	RT		5	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	carboxylic acid transport	RT		5	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	organic acid transport	RT		5	8.7E-1	1.0E0
☐	GOTERM_BP_ALL	amino acid transport	RT		3	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	amine transport	RT		3	9.8E-1	1.0E0
	Annotation Cluster 205	Enrichment Score: 0.1	G	🟩	Count	P_Value	Benjamini
☐	SMART	Sema	RT		3	6.5E-1	1.0E0
☐	INTERPRO	Plexin	RT		3	7.7E-1	1.0E0
☐	INTERPRO	Semaphorin/CD100 antigen	RT		3	7.9E-1	1.0E0
☐	SMART	PSI	RT		3	8.3E-1	1.0E0
☐	INTERPRO	Plexin/semaphorin/integrin	RT		3	9.2E-1	1.0E0
	Annotation Cluster 206	Enrichment Score: 0.1	G	🟩	Count	P_Value	Benjamini
☐	SMART	S_TK_X	RT		4	7.1E-1	1.0E0
☐	INTERPRO	Protein kinase, C-terminal	RT		4	8.5E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:AGC-kinase C-terminal	RT		4	8.6E-1	1.0E0
	Annotation Cluster 207	Enrichment Score: 0.09	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	aminopeptidase	RT		3	6.8E-1	1.0E0
☐	GOTERM_MF_ALL	aminopeptidase activity	RT		4	6.9E-1	1.0E0
☐	GOTERM_MF_ALL	metalloexopeptidase activity	RT		4	9.0E-1	1.0E0
☐	GOTERM_MF_ALL	exopeptidase activity	RT		4	9.9E-1	1.0E0
	Annotation Cluster 208	Enrichment Score: 0.09	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	female gonad development	RT		5	5.2E-1	1.0E0
☐	GOTERM_BP_ALL	female sex differentiation	RT		5	5.6E-1	1.0E0
☐	GOTERM_BP_ALL	development of primary female sexual characteristics	RT		5	5.6E-1	1.0E0
☐	GOTERM_BP_ALL	development of primary sexual characteristics	RT		6	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	male sex differentiation	RT		3	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	gonad development	RT		5	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive structure development	RT		5	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	menstrual cycle phase	RT		3	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	menstrual cycle process	RT		3	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	sex differentiation	RT		7	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive developmental process	RT		7	9.1E-1	1.0E0
☐	GOTERM_BP_ALL	cell maturation	RT		6	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	menstrual cycle	RT		3	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	rhythmic process	RT		5	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	multicellular organism reproduction	RT		4	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive process in a multicellular organism	RT		4	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive process	RT		14	9.9E-1	1.0E0
	Annotation Cluster 209	Enrichment Score: 0.08	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	cholesterol metabolism	RT		3	6.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	steroid metabolism	RT		3	8.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	lipid metabolism	RT		5	9.9E-1	1.0E0
	Annotation Cluster 210	Enrichment Score: 0.08	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:SH3 1	RT		3	5.1E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:SH3 2	RT		3	5.4E-1	1.0E0
☐	INTERPRO	Variant SH3	RT		3	9.5E-1	1.0E0

☐	**SMART**	SH3	RT		6	1.0E0	1.0E0
☐	**INTERPRO**	Src homology-3	RT		6	1.0E0	1.0E0
☐	**UP_SEQ_FEATURE**	domain:SH3	RT		3	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	SH3 domain	RT		6	1.0E0	1.0E0
	Annotation Cluster 211	Enrichment Score: 0.08	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	chemokine receptor binding	RT		5	5.4E-1	1.0E0
☐	**INTERPRO**	Small chemokine, C-C	RT		3	6.0E-1	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF001950:small inducible chemokine, C/CC types	RT		3	6.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	leukocyte chemotaxis	RT		3	6.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	G-protein-coupled receptor binding	RT		6	7.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	chemokine activity	RT		4	7.3E-1	1.0E0
☐	**SMART**	SCY	RT		3	7.5E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	chemotaxis	RT		5	7.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	taxis	RT		9	8.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	chemotaxis	RT		9	8.2E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	pyrrolidone carboxylic acid	RT		3	8.6E-1	1.0E0
☐	**INTERPRO**	Small chemokine, interleukin-8-like	RT		3	8.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	inflammatory response	RT		4	9.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	cytokine activity	RT		12	9.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	cytokine	RT		8	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	locomotory behavior	RT		10	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	behavior	RT		17	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	inflammatory response	RT		9	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	response to wounding	RT		10	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	response to external stimulus	RT		17	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	defense response	RT		15	1.0E0	1.0E0
	Annotation Cluster 212	Enrichment Score: 0.08	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	hexose metabolic process	RT		14	6.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	monosaccharide metabolic process	RT		14	6.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	alcohol catabolic process	RT		6	7.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	glycolysis	RT		5	7.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	glucose metabolic process	RT		9	8.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	glucose catabolic process	RT		5	8.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	monosaccharide catabolic process	RT		5	8.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	hexose catabolic process	RT		5	8.5E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	glycolysis	RT		3	9.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular carbohydrate catabolic process	RT		5	9.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular carbohydrate metabolic process	RT		20	9.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	carbohydrate catabolic process	RT		5	9.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	carbohydrate metabolic process	RT		29	9.7E-1	1.0E0
☐	**KEGG_PATHWAY**	Glycolysis / Gluconeogenesis	RT		3	9.8E-1	1.0E0
	Annotation Cluster 213	Enrichment Score: 0.08	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	glycosidase	RT		5	7.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrolase activity, acting on glycosyl bonds	RT		9	8.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrolase activity, hydrolyzing O-glycosyl compounds	RT		6	9.3E-1	1.0E0
	Annotation Cluster 214	Enrichment Score: 0.07	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of cellular component organization and biogenesis	RT		8	4.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of actin polymerization and/or depolymerization	RT		3	8.9E-1	1.0E0

☐	GOTERM_BP_ALL	regulation of actin filament length	RT		3	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of actin cytoskeleton organization and biogenesis	RT		3	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cellular component size	RT		3	9.1E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cytoskeleton organization and biogenesis	RT		3	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of organelle organization and biogenesis	RT		3	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	actin polymerization and/or depolymerization	RT		3	9.5E-1	1.0E0
	Annotation Cluster 215	Enrichment Score: 0.07	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	electron transport	RT		5	5.2E-1	9.9E-1
☐	GOTERM_MF_ALL	tetrapyrrole binding	RT		6	1.0E0	1.0E0
☐	GOTERM_MF_ALL	heme binding	RT		6	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	heme	RT		4	1.0E0	1.0E0
	Annotation Cluster 216	Enrichment Score: 0.06	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	ER to Golgi vesicle-mediated transport	RT		6	6.2E-1	1.0E0
☐	GOTERM_BP_ALL	Golgi vesicle transport	RT		7	8.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	er-golgi transport	RT		5	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	secretion by cell	RT		15	1.0E0	1.0E0
☐	GOTERM_BP_ALL	secretory pathway	RT		11	1.0E0	1.0E0
☐	GOTERM_BP_ALL	secretion	RT		16	1.0E0	1.0E0
	Annotation Cluster 217	Enrichment Score: 0.06	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	carbohydrate transport	RT		6	7.9E-1	1.0E0
☐	GOTERM_MF_ALL	sugar:hydrogen ion symporter activity	RT		3	9.0E-1	1.0E0
☐	GOTERM_MF_ALL	sugar transmembrane transporter activity	RT		3	9.1E-1	1.0E0
☐	GOTERM_MF_ALL	carbohydrate transmembrane transporter activity	RT		3	9.1E-1	1.0E0
	Annotation Cluster 218	Enrichment Score: 0.06	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	developmental maturation	RT		8	8.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	mitogen	RT		3	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	cell maturation	RT		6	9.2E-1	1.0E0
	Annotation Cluster 219	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	patterning of blood vessels	RT		3	7.0E-1	1.0E0
☐	GOTERM_BP_ALL	lung development	RT		6	7.8E-1	1.0E0
☐	GOTERM_BP_ALL	respiratory tube development	RT		6	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	branching morphogenesis of a tube	RT		5	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	morphogenesis of a branching structure	RT		5	8.9E-1	1.0E0
☐	GOTERM_BP_ALL	embryonic pattern specification	RT		3	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	rhythmic process	RT		5	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	morphogenesis of an epithelium	RT		6	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	tube morphogenesis	RT		7	1.0E0	1.0E0
☐	GOTERM_BP_ALL	tube development	RT		9	1.0E0	1.0E0
☐	GOTERM_BP_ALL	pattern specification process	RT		5	1.0E0	1.0E0
	Annotation Cluster 220	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	angiogenesis	RT		5	5.0E-1	9.9E-1
☐	GOTERM_BP_ALL	angiogenesis	RT		10	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	blood vessel development	RT		14	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	vasculature development	RT		14	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	blood vessel morphogenesis	RT		11	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	anatomical structure formation	RT		11	1.0E0	1.0E0
☐	GOTERM_BP_ALL	organ morphogenesis	RT		24	1.0E0	1.0E0
	Annotation Cluster 221	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini

☐	SP_PIR_KEYWORDS	transport	RT		119	4.8E-1	9.9E-1
☐	GOTERM_MF_ALL	inorganic cation transmembrane transporter activity	RT		14	5.6E-1	1.0E0
☐	GOTERM_MF_ALL	transporter activity	RT		97	9.7E-1	1.0E0
☐	GOTERM_MF_ALL	substrate-specific transporter activity	RT		67	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	transmembrane transporter activity	RT		56	1.0E0	1.0E0
☐	GOTERM_MF_ALL	substrate-specific transmembrane transporter activity	RT		43	1.0E0	1.0E0
☐	GOTERM_MF_ALL	cation transmembrane transporter activity	RT		23	1.0E0	1.0E0
☐	GOTERM_BP_ALL	monovalent inorganic cation transport	RT		12	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	ion transport	RT		19	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cation transport	RT		22	1.0E0	1.0E0
☐	GOTERM_MF_ALL	ion transmembrane transporter activity	RT		29	1.0E0	1.0E0
☐	GOTERM_BP_ALL	metal ion transport	RT		15	1.0E0	1.0E0
☐	GOTERM_BP_ALL	ion transport	RT		31	1.0E0	1.0E0
	Annotation Cluster 222	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	SMART	Kelch	RT		3	9.0E-1	1.0E0
☐	INTERPRO	Kelch repeat type 1	RT		3	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	kelch repeat	RT		3	9.1E-1	1.0E0
	Annotation Cluster 223	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	amino acid catabolic process	RT		4	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	amine catabolic process	RT		4	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	nitrogen compound catabolic process	RT		4	9.3E-1	1.0E0
	Annotation Cluster 224	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	guanine-nucleotide releasing factor	RT		7	6.8E-1	1.0E0
☐	GOTERM_MF_ALL	Ras guanyl-nucleotide exchange factor activity	RT		7	7.4E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:DH	RT		3	7.8E-1	1.0E0
☐	INTERPRO	Guanine-nucleotide dissociation stimulator, CDC24	RT		3	8.1E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:PH	RT		8	8.9E-1	1.0E0
☐	GOTERM_MF_ALL	guanyl-nucleotide exchange factor activity	RT		10	9.0E-1	1.0E0
☐	SMART	RhoGEF	RT		3	9.0E-1	1.0E0
☐	GOTERM_MF_ALL	Rho guanyl-nucleotide exchange factor activity	RT		4	9.5E-1	1.0E0
☐	INTERPRO	DH	RT		3	9.6E-1	1.0E0
☐	GOTERM_MF_ALL	small GTPase regulator activity	RT		12	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of Ras protein signal transduction	RT		8	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	Rho protein signal transduction	RT		5	9.8E-1	1.0E0
☐	GOTERM_MF_ALL	GTPase regulator activity	RT		20	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of Rho protein signal transduction	RT		3	9.9E-1	1.0E0
☐	SMART	PH	RT		8	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of small GTPase mediated signal transduction	RT		9	1.0E0	1.0E0
☐	INTERPRO	Pleckstrin-like	RT		8	1.0E0	1.0E0
☐	INTERPRO	Pleckstrin homology-type	RT		7	1.0E0	1.0E0
	Annotation Cluster 225	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of programmed cell death	RT		39	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of apoptosis	RT		37	8.7E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of apoptosis	RT		15	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of programmed cell death	RT		15	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	induction of programmed cell death	RT		10	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	induction of apoptosis	RT		10	9.7E-1	1.0E0

	Annotation Cluster 226	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	diacylglycerol binding	RT		4	8.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	Phorbol-ester binding	RT		3	9.1E-1	1.0E0
☐	SMART	C1	RT		3	9.2E-1	1.0E0
☐	INTERPRO	Protein kinase C, phorbol ester/diacylglycerol binding	RT		3	9.7E-1	1.0E0
	Annotation Cluster 227	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of kinase activity	RT		15	7.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of transferase activity	RT		15	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of kinase activity	RT		5	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of transferase activity	RT		5	1.0E0	1.0E0
☐	GOTERM_BP_ALL	positive regulation of catalytic activity	RT		8	1.0E0	1.0E0
☐	GOTERM_BP_ALL	positive regulation of protein kinase activity	RT		3	1.0E0	1.0E0
	Annotation Cluster 228	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	heparin-binding	RT		5	7.7E-1	1.0E0
☐	GOTERM_MF_ALL	heparin binding	RT		5	8.8E-1	1.0E0
☐	GOTERM_MF_ALL	glycosaminoglycan binding	RT		6	9.1E-1	1.0E0
☐	GOTERM_MF_ALL	polysaccharide binding	RT		6	9.4E-1	1.0E0
☐	GOTERM_MF_ALL	pattern binding	RT		6	9.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	growth factor	RT		5	1.0E0	1.0E0
☐	GOTERM_MF_ALL	carbohydrate binding	RT		15	1.0E0	1.0E0
	Annotation Cluster 229	Enrichment Score: 0.03	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	heterotrimeric G-protein complex	RT		3	8.6E-1	1.0E0
☐	GOTERM_CC_ALL	extrinsic to plasma membrane	RT		4	9.0E-1	1.0E0
☐	GOTERM_CC_ALL	extrinsic to membrane	RT		4	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	second-messenger-mediated signaling	RT		5	1.0E0	1.0E0
	Annotation Cluster 230	Enrichment Score: 0.03	G	🟩	Count	P_Value	Benjamini
☐	SMART	BRLZ	RT		3	8.8E-1	1.0E0
☐	INTERPRO	Basic-leucine zipper (bZIP) transcription factor	RT		3	9.4E-1	1.0E0
☐	UP_SEQ_FEATURE	DNA-binding region:Basic motif	RT		6	9.9E-1	1.0E0
	Annotation Cluster 231	Enrichment Score: 0.03	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	actin binding	RT		20	8.9E-1	1.0E0
☐	GOTERM_MF_ALL	cytoskeletal protein binding	RT		28	9.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	actin-binding	RT		12	9.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	cytoskeleton	RT		19	9.9E-1	1.0E0
	Annotation Cluster 232	Enrichment Score: 0.03	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	lysosome	RT		8	9.2E-1	1.0E0
☐	GOTERM_CC_ALL	vacuole	RT		14	9.3E-1	1.0E0
☐	GOTERM_CC_ALL	lytic vacuole	RT		12	9.4E-1	1.0E0
☐	GOTERM_CC_ALL	lysosome	RT		12	9.4E-1	1.0E0
	Annotation Cluster 233	Enrichment Score: 0.03	G	🟩	Count	P_Value	Benjamini
☐	SMART	HLH	RT		6	8.5E-1	1.0E0
☐	INTERPRO	Helix-loop-helix DNA-binding	RT		5	9.2E-1	1.0E0
☐	INTERPRO	Basic helix-loop-helix dimerisation region bHLH	RT		6	9.4E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Helix-loop-helix motif	RT		4	9.9E-1	1.0E0
☐	UP_SEQ_FEATURE	DNA-binding region:Basic motif	RT		6	9.9E-1	1.0E0
	Annotation Cluster 234	Enrichment Score: 0.03	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	actin filament organization	RT		4	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	actin filament-based process	RT		12	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	actin cytoskeleton organization and	RT		11	9.9E-1	1.0E0

☐		biogenesis	RT	▮		11	9.9E-1	1.0E0
	Annotation Cluster 235	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	▮		28	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of transcription	RT	▮		27	8.9E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of metabolic process	RT	▮		36	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of biological process	RT	▮		83	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cellular process	RT	▮		72	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of transcription, DNA-dependent	RT	▮		19	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cellular metabolic process	RT	▮		30	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of transcription from RNA polymerase II promoter	RT	▮		11	1.0E0	1.0E0
	Annotation Cluster 236	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	dendrite morphogenesis	RT	▮		3	4.4E-1	1.0E0
☐	GOTERM_BP_ALL	dendrite development	RT	▮		3	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of neurogenesis	RT	▮		3	9.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	neurogenesis	RT	▮		5	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	cellular morphogenesis during differentiation	RT	▮		11	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	neurite morphogenesis	RT	▮		7	1.0E0	1.0E0
☐	GOTERM_BP_ALL	neuron morphogenesis during differentiation	RT	▮		7	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cell part morphogenesis	RT	▮		13	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cell projection organization and biogenesis	RT	▮		13	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cell projection morphogenesis	RT	▮		13	1.0E0	1.0E0
☐	GOTERM_BP_ALL	neurite development	RT	▮		8	1.0E0	1.0E0
☐	GOTERM_BP_ALL	neuron development	RT	▮		8	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cell morphogenesis	RT	▮		25	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cellular structure morphogenesis	RT	▮		25	1.0E0	1.0E0
☐	GOTERM_BP_ALL	axonogenesis	RT	▮		4	1.0E0	1.0E0
☐	GOTERM_BP_ALL	neurogenesis	RT	▮		13	1.0E0	1.0E0
☐	GOTERM_BP_ALL	neuron differentiation	RT	▮		9	1.0E0	1.0E0
☐	GOTERM_BP_ALL	generation of neurons	RT	▮		10	1.0E0	1.0E0
☐	GOTERM_BP_ALL	nervous system development	RT	▮		26	1.0E0	1.0E0
	Annotation Cluster 237	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cellular calcium ion homeostasis	RT	▮		5	8.9E-1	1.0E0
☐	GOTERM_BP_ALL	calcium ion homeostasis	RT	▮		5	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	cellular homeostasis	RT	▮		19	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	cellular di-, tri-valent inorganic cation homeostasis	RT	▮		7	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	cellular metal ion homeostasis	RT	▮		5	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	di-, tri-valent inorganic cation homeostasis	RT	▮		7	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	metal ion homeostasis	RT	▮		5	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	cellular cation homeostasis	RT	▮		7	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	cation homeostasis	RT	▮		7	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	cellular chemical homeostasis	RT	▮		7	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cellular ion homeostasis	RT	▮		7	1.0E0	1.0E0
☐	GOTERM_BP_ALL	ion homeostasis	RT	▮		7	1.0E0	1.0E0
☐	GOTERM_BP_ALL	chemical homeostasis	RT	▮		8	1.0E0	1.0E0
	Annotation Cluster 238	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	myeloid cell differentiation	RT	▮		9	8.2E-1	1.0E0

☐	**GOTERM_BP_ALL**	hemopoiesis	RT			16	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	immune system development	RT			19	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	leukocyte differentiation	RT			9	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	hemopoietic or lymphoid organ development	RT			16	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	immune system process	RT			43	1.0E0	1.0E0
	Annotation Cluster 239	Enrichment Score: 0.02		G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of cell shape	RT			3	9.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of anatomical structure morphogenesis	RT			3	9.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cell morphogenesis	RT			3	9.5E-1	1.0E0
	Annotation Cluster 240	Enrichment Score: 0.01		G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	JNK cascade	RT			3	9.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	stress-activated protein kinase signaling pathway	RT			3	9.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	MAPKKK cascade	RT			5	1.0E0	1.0E0
	Annotation Cluster 241	Enrichment Score: 0.01		G	🟩	Count	P_Value	Benjamini
☐	**SMART**	ANK	RT			10	9.3E-1	1.0E0
☐	**INTERPRO**	Ankyrin	RT			9	9.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	ank repeat	RT			6	1.0E0	1.0E0
	Annotation Cluster 242	Enrichment Score: 0.01		G	🟩	Count	P_Value	Benjamini
☐	**SMART**	EFh	RT			11	8.4E-1	1.0E0
☐	**INTERPRO**	Calcium-binding EF-hand	RT			11	9.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:EF-hand 1	RT			5	9.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:EF-hand 2	RT			5	9.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	calcium-binding region:2	RT			3	1.0E0	1.0E0
☐	**UP_SEQ_FEATURE**	calcium-binding region:1	RT			3	1.0E0	1.0E0
☐	**INTERPRO**	EF-Hand type	RT			6	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	calcium	RT			18	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	calcium ion binding	RT			23	1.0E0	1.0E0
	Annotation Cluster 243	Enrichment Score: 0.01		G	🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	repeat:LRR 3	RT			6	9.7E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:LRR 6	RT			4	9.7E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:LRR 1	RT			6	9.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:LRR 2	RT			6	9.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:LRR 4	RT			5	9.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:LRR 5	RT			4	9.8E-1	1.0E0
☐	**INTERPRO**	Leucine-rich repeat	RT			9	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	leucine-rich repeat	RT			8	1.0E0	1.0E0
	Annotation Cluster 244	Enrichment Score: 0.01		G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	microsome	RT			10	9.5E-1	1.0E0
☐	**GOTERM_CC_ALL**	vesicular fraction	RT			10	9.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	microsome	RT			4	9.9E-1	1.0E0
☐	**GOTERM_CC_ALL**	membrane fraction	RT			22	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	cell fraction	RT			25	1.0E0	1.0E0
	Annotation Cluster 245	Enrichment Score: 0.01		G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	mononuclear cell proliferation	RT			5	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	lymphocyte proliferation	RT			5	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	lymphocyte activation	RT			14	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	leukocyte differentiation	RT			9	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	leukocyte activation	RT			14	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	T cell differentiation	RT			3	9.9E-1	1.0E0

☐	**GOTERM_BP_ALL**	lymphocyte differentiation	RT	▮		5	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell activation	RT	▮		14	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	T cell activation	RT	▮		6	1.0E0	1.0E0
	Annotation Cluster 246	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Ras	RT	▮		6	9.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	prenylation	RT	▮		8	9.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	short sequence motif:Effector region	RT	▮		3	1.0E0	1.0E0
	Annotation Cluster 247	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	cell migration	RT	▮		20	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	localization of cell	RT	▮		22	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell motility	RT	▮		22	9.9E-1	1.0E0
	Annotation Cluster 248	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	spermatogenesis	RT	▮		4	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	male gamete generation	RT	▮		11	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	spermatogenesis	RT	▮		11	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	gamete generation	RT	▮		15	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	sexual reproduction	RT	▮		17	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	reproduction	RT	▮		27	1.0E0	1.0E0
	Annotation Cluster 249	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Intermediate filament protein	RT	▮		3	9.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	intermediate filament	RT	▮		3	9.8E-1	1.0E0
☐	**GOTERM_CC_ALL**	intermediate filament	RT	▮		4	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	intermediate filament cytoskeleton	RT	▮		4	1.0E0	1.0E0
	Annotation Cluster 250	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of phosphorylation	RT	▮		3	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of phosphate metabolic process	RT	▮		3	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of phosphorus metabolic process	RT	▮		3	9.9E-1	1.0E0
	Annotation Cluster 251	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	membrane organization and biogenesis	RT	▮		17	9.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	endocytosis	RT	▮		3	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	endocytosis	RT	▮		7	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	membrane invagination	RT	▮		7	1.0E0	1.0E0
	Annotation Cluster 252	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	gtpase activation	RT	▮		4	9.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	GTPase regulator activity	RT	▮		20	9.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	GTPase activator activity	RT	▮		8	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	enzyme activator activity	RT	▮		11	1.0E0	1.0E0
	Annotation Cluster 253	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	EGF calcium-binding	RT	▮		3	9.7E-1	1.0E0
☐	**SMART**	EGF_CA	RT	▮		3	9.9E-1	1.0E0
☐	**INTERPRO**	Aspartic acid and asparagine hydroxylation site	RT	▮		3	1.0E0	1.0E0
☐	**INTERPRO**	EGF-like calcium-binding	RT	▮		3	1.0E0	1.0E0
☐	**SMART**	EGF	RT	▮		4	1.0E0	1.0E0
☐	**INTERPRO**	EGF-like, type 3	RT	▮		4	1.0E0	1.0E0
☐	**INTERPRO**	EGF	RT	▮		4	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	egf-like domain	RT	▮		4	1.0E0	1.0E0
☐	**INTERPRO**	EGF-like region	RT	▮		4	1.0E0	1.0E0
	Annotation Cluster 254	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	sensory perception of sound	RT	▮		3	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	sensory perception of mechanical stimulus	RT	▮		3	1.0E0	1.0E0

☐	**GOTERM_BP_ALL**	sensory perception	RT	▮		6	1.0E0	1.0E0
	Annotation Cluster 255	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**SMART**	FN3	RT	▮		8	9.5E-1	1.0E0
☐	**INTERPRO**	Fibronectin, type III	RT	▮		8	9.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Fibronectin type-III 2	RT	▮		3	9.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Fibronectin type-III 1	RT	▮		3	9.9E-1	1.0E0
☐	**INTERPRO**	Immunoglobulin I-set	RT	▮		3	1.0E0	1.0E0
☐	**SMART**	IG	RT	▮		7	1.0E0	1.0E0
☐	**INTERPRO**	Fibronectin, type III-like fold	RT	▮		5	1.0E0	1.0E0
☐	**SMART**	IGc2	RT	▮		3	1.0E0	1.0E0
☐	**INTERPRO**	Immunoglobulin subtype	RT	▮		7	1.0E0	1.0E0
☐	**INTERPRO**	Immunoglobulin subtype 2	RT	▮		3	1.0E0	1.0E0
☐	**INTERPRO**	Immunoglobulin V-set	RT	▮		3	1.0E0	1.0E0
☐	**INTERPRO**	Immunoglobulin	RT	▮		3	1.0E0	1.0E0
☐	**INTERPRO**	Immunoglobulin-like	RT	▮		10	1.0E0	1.0E0
☐	**INTERPRO**	Immunoglobulin-like fold	RT	▮		9	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	immunoglobulin domain	RT	▮		8	1.0E0	1.0E0
	Annotation Cluster 256	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	G protein-coupled receptor	RT	▮		3	9.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	nucleotide receptor activity, G-protein coupled	RT	▮		3	9.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	nucleotide receptor activity	RT	▮		3	9.8E-1	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF002406:vertebrate rhodopsin	RT	▮		3	1.0E0	1.0E0
☐	**UP_SEQ_FEATURE**	lipid moiety-binding region:S-palmitoyl cysteine	RT	▮		5	1.0E0	1.0E0
☐	**INTERPRO**	Rhodopsin-like GPCR superfamily	RT	▮		6	1.0E0	1.0E0
☐	**KEGG_PATHWAY**	Neuroactive ligand-receptor interaction	RT	▮		4	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	rhodopsin-like receptor activity	RT	▮		5	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	transducer	RT	▮		7	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	g-protein coupled receptor	RT	▮		5	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	G-protein coupled receptor protein signaling pathway	RT	▮		14	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	G-protein coupled receptor activity	RT	▮		5	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	transmembrane receptor activity	RT	▮		11	1.0E0	1.0E0
	Annotation Cluster 257	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Concanavalin A-like lectin/glucanase, subgroup	RT	▮		3	9.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	carbohydrate binding	RT	▮		15	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	sugar binding	RT	▮		7	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	lectin	RT	▮		5	1.0E0	1.0E0
	Annotation Cluster 258	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	forebrain development	RT	▮		5	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	brain development	RT	▮		7	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	central nervous system development	RT	▮		9	1.0E0	1.0E0
	Annotation Cluster 259	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	basement membrane	RT	▮		3	9.9E-1	1.0E0
☐	**GOTERM_CC_ALL**	extracellular matrix part	RT	▮		3	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	extracellular matrix	RT	▮		5	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	proteinaceous extracellular matrix	RT	▮		5	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	extracellular matrix	RT	▮		5	1.0E0	1.0E0
	Annotation Cluster 260	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	protease	RT	▮		29	1.0E0	1.0E0

☐	GOTERM_BP_ALL	proteolysis	RT	▮		46	1.0E0	1.0E0
☐	GOTERM_MF_ALL	peptidase activity	RT	▮		42	1.0E0	1.0E0
☐	GOTERM_MF_ALL	endopeptidase activity	RT	▮		22	1.0E0	1.0E0
	Annotation Cluster 261	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	ossification	RT	▮		4	1.0E0	1.0E0
☐	GOTERM_BP_ALL	biomineral formation	RT	▮		4	1.0E0	1.0E0
☐	GOTERM_BP_ALL	bone remodeling	RT	▮		4	1.0E0	1.0E0
☐	GOTERM_BP_ALL	tissue remodeling	RT	▮		4	1.0E0	1.0E0
☐	GOTERM_BP_ALL	skeletal development	RT	▮		7	1.0E0	1.0E0
	Annotation Cluster 262	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of developmental process	RT	▮		4	1.0E0	1.0E0
☐	GOTERM_BP_ALL	negative regulation of cell differentiation	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of cell differentiation	RT	▮		7	1.0E0	1.0E0
	Annotation Cluster 263	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	potassium	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_MF_ALL	potassium ion binding	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_MF_ALL	alkali metal ion binding	RT	▮		6	1.0E0	1.0E0
	Annotation Cluster 264	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	RT	▮		5	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 3	RT	▮		4	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	RT	▮		4	1.0E0	1.0E0
	Annotation Cluster 265	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of cell size	RT	▮		5	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of cell growth	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cell growth	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of growth	RT	▮		5	1.0E0	1.0E0
	Annotation Cluster 266	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	cytoplasmic membrane-bound vesicle	RT	▮		10	1.0E0	1.0E0
☐	GOTERM_CC_ALL	membrane-bound vesicle	RT	▮		10	1.0E0	1.0E0
☐	GOTERM_CC_ALL	cytoplasmic vesicle	RT	▮		15	1.0E0	1.0E0
☐	GOTERM_CC_ALL	vesicle	RT	▮		15	1.0E0	1.0E0
	Annotation Cluster 267	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of lymphocyte activation	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of cell activation	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of multicellular organismal process	RT	▮		9	1.0E0	1.0E0
	Annotation Cluster 268	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	synaptic transmission	RT	▮		10	1.0E0	1.0E0
☐	GOTERM_BP_ALL	transmission of nerve impulse	RT	▮		10	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cell-cell signaling	RT	▮		11	1.0E0	1.0E0
☐	GOTERM_BP_ALL	neurological system process	RT	▮		15	1.0E0	1.0E0
☐	GOTERM_BP_ALL	system process	RT	▮		20	1.0E0	1.0E0
	Annotation Cluster 269	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of immune response	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of immune system process	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_BP_ALL	regulation of multicellular organismal process	RT	▮		9	1.0E0	1.0E0
	Annotation Cluster 270	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	GPI anchor binding	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_MF_ALL	phosphoinositide binding	RT	▮		5	1.0E0	1.0E0
☐	GOTERM_MF_ALL	phospholipid binding	RT	▮		6	1.0E0	1.0E0
☐	GOTERM_MF_ALL	lipid binding	RT	▮		15	1.0E0	1.0E0

	Annotation Cluster 271	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	zinc	RT	99	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	zinc-finger	RT	71	1.0E0	1.0E0
☐	GOTERM_MF_ALL	zinc ion binding	RT	118	1.0E0	1.0E0
☐	GOTERM_MF_ALL	transition metal ion binding	RT	154	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	metal-binding	RT	141	1.0E0	1.0E0
☐	GOTERM_MF_ALL	metal ion binding	RT	224	1.0E0	1.0E0
☐	GOTERM_MF_ALL	ion binding	RT	226	1.0E0	1.0E0
☐	GOTERM_MF_ALL	cation binding	RT	183	1.0E0	1.0E0
	Annotation Cluster 272	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	SMART	ZnF_C2H2	RT	8	1.0E0	1.0E0
☐	INTERPRO	Zinc finger, C2H2-type	RT	14	1.0E0	1.0E0
☐	INTERPRO	Zinc finger, C2H2-like	RT	8	1.0E0	1.0E0
	Annotation Cluster 273	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	integral to plasma membrane	RT	19	1.0E0	1.0E0
☐	GOTERM_CC_ALL	intrinsic to plasma membrane	RT	19	1.0E0	1.0E0
☐	GOTERM_CC_ALL	plasma membrane part	RT	36	1.0E0	1.0E0
	Annotation Cluster 274	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	cell adhesion	RT	6	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cell adhesion	RT	16	1.0E0	1.0E0
☐	GOTERM_BP_ALL	biological adhesion	RT	16	1.0E0	1.0E0
	Annotation Cluster 275	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	intracellular signaling cascade	RT	56	1.0E0	1.0E0
☐	GOTERM_BP_ALL	signal transduction	RT	108	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cell communication	RT	118	1.0E0	1.0E0
	Annotation Cluster 276	Enrichment Score: -0	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	topological domain:Extracellular	RT	35	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT	56	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT	67	1.0E0	1.0E0
	Annotation Cluster 277	Enrichment Score: -0	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	extracellular region	RT	90	1.0E0	1.0E0
☐	GOTERM_CC_ALL	extracellular region part	RT	87	1.0E0	1.0E0
☐	GOTERM_CC_ALL	extracellular space	RT	86	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	signal	RT	75	1.0E0	1.0E0
	Annotation Cluster 278	Enrichment Score: -0	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	receptor	RT	39	1.0E0	1.0E0
☐	GOTERM_MF_ALL	receptor activity	RT	53	1.0E0	1.0E0
☐	GOTERM_MF_ALL	signal transducer activity	RT	67	1.0E0	1.0E0
☐	GOTERM_MF_ALL	molecular transducer activity	RT	67	1.0E0	1.0E0
	Annotation Cluster 279	Enrichment Score: -0	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	membrane part	RT	256	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	transmembrane	RT	160	1.0E0	1.0E0
☐	GOTERM_CC_ALL	membrane	RT	341	1.0E0	1.0E0
☐	GOTERM_CC_ALL	integral to membrane	RT	231	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	membrane	RT	216	1.0E0	1.0E0
☐	GOTERM_CC_ALL	intrinsic to membrane	RT	231	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	transmembrane region	RT	111	1.0E0	1.0E0
	Annotation Cluster 280	Enrichment Score: -0	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	glycoprotein	RT	95	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	disulfide bond	RT	54	1.0E0	1.0E0

☐	**UP_SEQ_FEATURE**	signal peptide	**RT**	▬	57	1.0E0	1.0E0
☐	**UP_SEQ_FEATURE**	glycosylation site:N-linked (GlcNAc...)	**RT**	▬	67	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	signal	**RT**	▬	75	1.0E0	1.0E0

573 terms were not clustered.

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Functional Annotation Clustering Of Genes Upregulated >2 in WT But Not In WASP Deficient BMMCs

Help and Manual

Current Gene List: wt1 not wsp1 >2up
313 DAVID IDs

Options **Classification Stringency** Medium

Rerun using options   Create Sublist   Download File

	Annotation Cluster 1	Enrichment Score: 3.14	G	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	repeat:WD 7	RT	9	2.7E-5	3.1E-1
☐	**UP_SEQ_FEATURE**	repeat:WD 6	RT	10	7.5E-5	4.1E-1
☐	**UP_SEQ_FEATURE**	repeat:WD 5	RT	11	1.1E-4	4.2E-1
☐	**UP_SEQ_FEATURE**	repeat:WD 4	RT	11	2.0E-4	5.1E-1
☐	**UP_SEQ_FEATURE**	repeat:WD 3	RT	11	3.2E-4	5.9E-1
☐	**UP_SEQ_FEATURE**	repeat:WD 2	RT	11	3.6E-4	5.2E-1
☐	**UP_SEQ_FEATURE**	repeat:WD 1	RT	11	3.6E-4	5.2E-1
☐	**UP_SEQ_FEATURE**	repeat:WD 8	RT	4	2.7E-3	9.9E-1
☐	**SP_PIR_KEYWORDS**	wd repeat	RT	12	4.1E-3	5.1E-1
☐	**INTERPRO**	WD40 repeat	RT	9	2.8E-2	1.0E0
☐	**SMART**	WD40	RT	9	5.0E-2	1.0E0
	Annotation Cluster 2	Enrichment Score: 1.72	G	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	lectin	RT	12	1.8E-4	7.3E-2
☐	**GOTERM_MF_ALL**	sugar binding	RT	12	9.7E-4	9.2E-1
☐	**GOTERM_MF_ALL**	carbohydrate binding	RT	12	2.0E-2	9.0E-1
☐	**INTERPRO**	Type II antifreeze protein	RT	4	3.2E-2	1.0E0
☐	**INTERPRO**	C-type lectin	RT	5	1.5E-1	1.0E0
☐	**SMART**	CLECT	RT	5	1.7E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:C-type lectin	RT	3	3.2E-1	1.0E0
	Annotation Cluster 3	Enrichment Score: 1.49	G	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	cytoplasm	RT	135	1.9E-5	1.5E-2
☐	**GOTERM_CC_ALL**	cytoplasmic part	RT	78	6.6E-3	7.2E-1
☐	**GOTERM_CC_ALL**	cell	RT	239	1.2E-2	6.5E-1
☐	**GOTERM_CC_ALL**	cell part	RT	239	1.2E-2	6.5E-1
☐	**GOTERM_CC_ALL**	intracellular part	RT	172	4.0E-2	9.0E-1
☐	**GOTERM_CC_ALL**	intracellular	RT	179	5.8E-2	9.1E-1
☐	**GOTERM_CC_ALL**	intracellular membrane-bound organelle	RT	126	1.7E-1	9.8E-1
☐	**GOTERM_CC_ALL**	membrane-bound organelle	RT	126	1.8E-1	9.8E-1
☐	**GOTERM_CC_ALL**	intracellular organelle	RT	139	2.3E-1	9.9E-1
☐	**GOTERM_CC_ALL**	organelle	RT	139	2.4E-1	9.9E-1
☐	**GOTERM_CC_ALL**	nucleus	RT	76	4.8E-1	1.0E0
	Annotation Cluster 4	Enrichment Score: 1.45	G	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	lysosome	RT	8	5.9E-3	5.8E-1
☐	**GOTERM_CC_ALL**	lytic vacuole	RT	8	5.5E-2	9.2E-1
☐	**GOTERM_CC_ALL**	lysosome	RT	8	5.5E-2	9.2E-1
☐	**GOTERM_CC_ALL**	vacuole	RT	8	9.0E-2	9.3E-1
	Annotation Cluster 5	Enrichment Score: 1.43	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	protein metabolic process	RT	79	9.5E-4	9.9E-1
☐	**GOTERM_BP_ALL**	post-translational protein modification	RT	41	2.4E-3	1.0E0

☐	GOTERM_BP_ALL	protein modification process	RT	43	9.5E-3	1.0E0
☐	GOTERM_BP_ALL	cellular protein metabolic process	RT	71	9.6E-3	1.0E0
☐	GOTERM_BP_ALL	biopolymer modification	RT	44	1.1E-2	1.0E0
☐	GOTERM_BP_ALL	cellular macromolecule metabolic process	RT	71	1.3E-2	1.0E0
☐	GOTERM_BP_ALL	macromolecule metabolic process	RT	120	1.1E-1	1.0E0
☐	GOTERM_BP_ALL	cellular process	RT	201	1.1E-1	1.0E0
☐	GOTERM_BP_ALL	primary metabolic process	RT	133	2.0E-1	1.0E0
☐	GOTERM_BP_ALL	biopolymer metabolic process	RT	87	3.3E-1	1.0E0
☐	GOTERM_BP_ALL	metabolic process	RT	140	5.3E-1	1.0E0
☐	GOTERM_BP_ALL	cellular metabolic process	RT	126	5.4E-1	1.0E0
	Annotation Cluster 6	Enrichment Score: 1.36	G	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF002359:annexin I	RT	3	1.8E-2	1.0E0
☐	SP_PIR_KEYWORDS	annexin	RT	3	2.3E-2	7.9E-1
☐	INTERPRO	Annexin	RT	3	2.5E-2	1.0E0
☐	SMART	ANX	RT	3	2.6E-2	1.0E0
☐	SP_PIR_KEYWORDS	calcium/phospholipid-binding	RT	3	2.7E-2	7.9E-1
☐	GOTERM_MF_ALL	calcium-dependent phospholipid binding	RT	3	7.4E-2	9.9E-1
☐	GOTERM_MF_ALL	phospholipid binding	RT	5	5.9E-1	1.0E0
	Annotation Cluster 7	Enrichment Score: 1.35	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:KH 3	RT	3	1.1E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:KH 1	RT	3	2.5E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:KH 2	RT	3	2.5E-2	1.0E0
☐	INTERPRO	K Homology	RT	3	9.9E-2	1.0E0
☐	INTERPRO	K Homology, type 1	RT	3	1.0E-1	1.0E0
☐	SMART	KH	RT	3	1.1E-1	1.0E0
	Annotation Cluster 8	Enrichment Score: 1.33	G	Count	P_Value	Benjamini
☐	SMART	UBCc	RT	6	1.9E-3	6.9E-1
☐	PIR_SUPERFAMILY	PIRSF001567:ubiquitin-protein ligase E2	RT	4	5.0E-3	1.0E0
☐	GOTERM_MF_ALL	ubiquitin-protein ligase activity	RT	8	7.3E-3	8.1E-1
☐	INTERPRO	Ubiquitin-conjugating enzyme, E2	RT	5	8.2E-3	1.0E0
☐	GOTERM_MF_ALL	small protein conjugating enzyme activity	RT	8	8.3E-3	8.2E-1
☐	GOTERM_BP_ALL	ubiquitin cycle	RT	18	8.3E-3	1.0E0
☐	GOTERM_MF_ALL	small conjugating protein ligase activity	RT	8	9.4E-3	7.9E-1
☐	GOTERM_MF_ALL	acid-amino acid ligase activity	RT	8	1.7E-2	9.0E-1
☐	SP_PIR_KEYWORDS	Ubl conjugation pathway	RT	14	2.5E-2	7.9E-1
☐	KEGG_PATHWAY	Ubiquitin mediated proteolysis	RT	8	3.3E-2	6.9E-1
☐	GOTERM_MF_ALL	ligase activity, forming carbon-nitrogen bonds	RT	8	4.6E-2	9.8E-1
☐	GOTERM_BP_ALL	ubiquitin-dependent protein catabolic process	RT	7	4.7E-2	1.0E0
☐	GOTERM_BP_ALL	modification-dependent macromolecule catabolic process	RT	7	5.2E-2	1.0E0
☐	GOTERM_BP_ALL	modification-dependent protein catabolic process	RT	7	5.2E-2	1.0E0
☐	GOTERM_BP_ALL	proteolysis involved in cellular protein catabolic process	RT	7	5.6E-2	1.0E0
☐	GOTERM_BP_ALL	cellular macromolecule catabolic process	RT	10	5.7E-2	1.0E0
☐	GOTERM_BP_ALL	cellular protein catabolic process	RT	7	5.9E-2	1.0E0
☐	KEGG_PATHWAY	Parkinson's disease	RT	3	9.1E-2	8.1E-1
☐	GOTERM_BP_ALL	proteolysis	RT	19	1.1E-1	1.0E0
☐	UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	RT	3	1.6E-1	1.0E0
☐	GOTERM_BP_ALL	macromolecule catabolic process	RT	10	1.8E-1	1.0E0

☐	GOTERM_BP_ALL	protein catabolic process	RT		7	1.8E-1	1.0E0
☐	GOTERM_MF_ALL	ligase activity	RT		10	1.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	ligase	RT		7	3.1E-1	1.0E0
☐	GOTERM_BP_ALL	cellular catabolic process	RT		11	3.6E-1	1.0E0
☐	GOTERM_BP_ALL	biopolymer catabolic process	RT		7	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	catabolic process	RT		12	5.5E-1	1.0E0
	Annotation Cluster 9	Enrichment Score: 1.28	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	interaction with host	RT		3	3.3E-3	1.0E0
☐	GOTERM_BP_ALL	interspecies interaction between organisms	RT		3	1.7E-2	1.0E0
☐	GOTERM_BP_ALL	symbiosis, encompassing mutualism through parasitism	RT		3	1.7E-2	1.0E0
☐	GOTERM_BP_ALL	viral reproductive process	RT		3	3.8E-2	1.0E0
☐	GOTERM_BP_ALL	viral reproduction	RT		3	5.2E-2	1.0E0
☐	GOTERM_BP_ALL	reproductive process	RT		5	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	multi-organism process	RT		3	9.1E-1	1.0E0
	Annotation Cluster 10	Enrichment Score: 1.24	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell motility	RT		13	4.0E-2	1.0E0
☐	GOTERM_BP_ALL	localization of cell	RT		13	4.0E-2	1.0E0
☐	GOTERM_BP_ALL	cell migration	RT		10	1.2E-1	1.0E0
	Annotation Cluster 11	Enrichment Score: 1.24	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	intracellular transport	RT		23	7.7E-3	1.0E0
☐	GOTERM_BP_ALL	cellular localization	RT		25	3.2E-2	1.0E0
☐	GOTERM_BP_ALL	cellular component organization and biogenesis	RT		59	3.5E-2	1.0E0
☐	GOTERM_BP_ALL	establishment of cellular localization	RT		24	4.3E-2	1.0E0
☐	GOTERM_BP_ALL	protein localization	RT		22	5.8E-2	1.0E0
☐	GOTERM_BP_ALL	macromolecule localization	RT		22	8.0E-2	1.0E0
☐	GOTERM_BP_ALL	establishment of protein localization	RT		20	8.0E-2	1.0E0
☐	GOTERM_BP_ALL	protein transport	RT		19	8.4E-2	1.0E0
☐	GOTERM_BP_ALL	intracellular protein transport	RT		13	1.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	protein transport	RT		10	3.1E-1	1.0E0
	Annotation Cluster 12	Enrichment Score: 1.2	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	signal-anchor	RT		14	1.1E-2	6.8E-1
☐	SP_PIR_KEYWORDS	golgi apparatus	RT		16	1.2E-2	6.5E-1
☐	KEGG_PATHWAY	O-Glycan biosynthesis	RT		4	2.1E-2	9.0E-1
☐	GOTERM_MF_ALL	polypeptide N-acetylgalactosaminyltransferase activity	RT		3	2.6E-2	9.2E-1
☐	UP_SEQ_FEATURE	region of interest:Catalytic subdomain A	RT		3	3.3E-2	1.0E0
☐	UP_SEQ_FEATURE	region of interest:Catalytic subdomain B	RT		3	3.3E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:Ricin B-type lectin	RT		3	3.8E-2	1.0E0
☐	UP_SEQ_FEATURE	metal ion-binding site:Manganese	RT		3	7.0E-2	1.0E0
☐	INTERPRO	Ricin B lectin	RT		3	7.2E-2	1.0E0
☐	GOTERM_MF_ALL	acetylgalactosaminyltransferase activity	RT		3	7.4E-2	9.9E-1
☐	SP_PIR_KEYWORDS	Manganese	RT		6	7.5E-2	9.3E-1
☐	SMART	RICIN	RT		3	7.6E-2	1.0E0
☐	GOTERM_MF_ALL	manganese ion binding	RT		6	8.7E-2	1.0E0
☐	GOTERM_MF_ALL	UDP-glycosyltransferase activity	RT		5	9.9E-2	1.0E0
☐	KEGG_PATHWAY	Glycan structures - biosynthesis 1	RT		6	1.2E-1	8.4E-1
☐	GOTERM_MF_ALL	transferase activity, transferring glycosyl groups	RT		8	1.3E-1	1.0E0
☐	UP_SEQ_FEATURE	topological domain:Lumenal	RT		9	1.4E-1	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring hexosyl groups	RT		5	3.0E-1	1.0E0

☐	SP_PIR_KEYWORDS	glycosyltransferase	RT		5	4.3E-1	1.0E0
	Annotation Cluster 13	Enrichment Score: 1.19	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	response to stress	RT		26	1.0E-2	1.0E0
☐	GOTERM_BP_ALL	response to wounding	RT		10	1.4E-1	1.0E0
☐	GOTERM_BP_ALL	response to external stimulus	RT		13	2.0E-1	1.0E0
	Annotation Cluster 14	Enrichment Score: 1.17	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	cell fraction	RT		19	1.3E-2	6.2E-1
☐	GOTERM_CC_ALL	membrane fraction	RT		15	6.5E-2	9.2E-1
☐	GOTERM_CC_ALL	microsome	RT		7	7.7E-2	9.3E-1
☐	GOTERM_CC_ALL	vesicular fraction	RT		7	8.6E-2	9.3E-1
☐	SP_PIR_KEYWORDS	microsome	RT		4	2.7E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 1.14	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	CD9/CD37/CD63 antigen	RT		4	1.6E-2	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002419:CD9 antigen	RT		3	3.9E-2	1.0E0
☐	GOTERM_BP_ALL	reproductive process	RT		5	6.3E-1	1.0E0
	Annotation Cluster 16	Enrichment Score: 1.06	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	actin-binding	RT		8	4.3E-2	9.0E-1
☐	GOTERM_CC_ALL	actin cytoskeleton	RT		9	4.4E-2	9.0E-1
☐	GOTERM_MF_ALL	cytoskeletal protein binding	RT		13	4.9E-2	9.8E-1
☐	GOTERM_MF_ALL	actin binding	RT		10	5.8E-2	9.9E-1
☐	SP_PIR_KEYWORDS	cytoskeleton	RT		10	1.1E-1	9.7E-1
☐	GOTERM_BP_ALL	actin cytoskeleton organization and biogenesis	RT		7	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	actin filament-based process	RT		7	1.8E-1	1.0E0
☐	GOTERM_BP_ALL	cytoskeleton organization and biogenesis	RT		13	2.1E-1	1.0E0
	Annotation Cluster 17	Enrichment Score: 1.05	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	guanyl nucleotide binding	RT		14	8.5E-3	8.0E-1
☐	GOTERM_MF_ALL	guanyl ribonucleotide binding	RT		14	8.5E-3	8.0E-1
☐	SP_PIR_KEYWORDS	GTP-binding	RT		12	1.3E-2	6.5E-1
☐	GOTERM_MF_ALL	GTP binding	RT		13	1.7E-2	8.9E-1
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	RT		9	5.8E-2	1.0E0
☐	INTERPRO	Small GTP-binding protein domain	RT		6	1.1E-1	1.0E0
☐	INTERPRO	Ras GTPase	RT		6	1.1E-1	1.0E0
☐	GOTERM_BP_ALL	small GTPase mediated signal transduction	RT		11	2.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	prenylation	RT		5	2.5E-1	1.0E0
☐	INTERPRO	Ras	RT		4	3.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	lipoprotein	RT		13	3.4E-1	1.0E0
☐	UP_SEQ_FEATURE	short sequence motif:Effector region	RT		3	5.1E-1	1.0E0
☐	UP_SEQ_FEATURE	lipid moiety-binding region:S-geranylgeranyl cysteine	RT		3	5.4E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 1.05	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT		37	1.1E-2	6.5E-1
☐	GOTERM_MF_ALL	ribonucleotide binding	RT		40	5.3E-2	9.8E-1
☐	GOTERM_MF_ALL	purine ribonucleotide binding	RT		40	5.3E-2	9.8E-1
☐	GOTERM_MF_ALL	purine nucleotide binding	RT		41	6.0E-2	9.8E-1
☐	GOTERM_MF_ALL	nucleotide binding	RT		44	1.1E-1	1.0E0
☐	GOTERM_MF_ALL	ATP binding	RT		31	1.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	atp-binding	RT		25	1.4E-1	9.8E-1
☐	GOTERM_MF_ALL	adenyl ribonucleotide binding	RT		31	1.5E-1	1.0E0
☐	GOTERM_MF_ALL	adenyl nucleotide binding	RT		32	1.6E-1	1.0E0
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT		15	3.6E-1	1.0E0

	Annotation Cluster 19	Enrichment Score: 1.04	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	cell adhesion	RT	12	5.6E-2	9.0E-1
☐	GOTERM_BP_ALL	biological adhesion	RT	18	1.2E-1	1.0E0
☐	GOTERM_BP_ALL	cell adhesion	RT	18	1.2E-1	1.0E0

	Annotation Cluster 20	Enrichment Score: 1.04	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cellular component assembly	RT	13	7.4E-2	1.0E0
☐	GOTERM_BP_ALL	protein complex assembly	RT	7	9.4E-2	1.0E0
☐	GOTERM_BP_ALL	macromolecular complex assembly	RT	11	1.1E-1	1.0E0

	Annotation Cluster 21	Enrichment Score: 1.02	G	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Chronic myeloid leukemia	RT	7	9.9E-3	8.8E-1
☐	GOTERM_BP_ALL	ER-nuclear signaling pathway	RT	4	1.2E-2	1.0E0
☐	BIOCARTA	p53 Signaling Pathway	RT	4	1.3E-2	9.8E-1
☐	KEGG_PATHWAY	Pancreatic cancer	RT	6	3.2E-2	7.4E-1
☐	KEGG_PATHWAY	Renal cell carcinoma	RT	6	3.2E-2	7.4E-1
☐	GOTERM_BP_ALL	unfolded protein response	RT	3	4.3E-2	1.0E0
☐	KEGG_PATHWAY	Cell cycle	RT	7	4.4E-2	7.4E-1
☐	BIOCARTA	Cell Cycle	RT	4	4.5E-2	1.0E0
☐	KEGG_PATHWAY	Colorectal cancer	RT	6	4.8E-2	7.2E-1
☐	BIOCARTA	BTG family proteins and cell cycle regulation	RT	3	5.6E-2	1.0E0
☐	KEGG_PATHWAY	Glioma	RT	5	5.9E-2	7.6E-1
☐	KEGG_PATHWAY	p53 signaling pathway	RT	5	6.5E-2	7.6E-1
☐	KEGG_PATHWAY	Small cell lung cancer	RT	6	7.2E-2	7.6E-1
☐	KEGG_PATHWAY	Bladder cancer	RT	4	9.4E-2	8.0E-1
☐	KEGG_PATHWAY	Wnt signaling pathway	RT	7	1.3E-1	8.6E-1
☐	KEGG_PATHWAY	Endometrial cancer	RT	4	1.3E-1	8.5E-1
☐	GOTERM_BP_ALL	response to protein stimulus	RT	4	1.3E-1	1.0E0
☐	GOTERM_BP_ALL	response to unfolded protein	RT	4	1.3E-1	1.0E0
☐	KEGG_PATHWAY	Non-small cell lung cancer	RT	4	1.5E-1	8.7E-1
☐	KEGG_PATHWAY	Thyroid cancer	RT	3	1.6E-1	8.7E-1
☐	KEGG_PATHWAY	Prostate cancer	RT	5	1.8E-1	8.8E-1
☐	KEGG_PATHWAY	Focal adhesion	RT	8	2.0E-1	8.9E-1
☐	KEGG_PATHWAY	Melanoma	RT	4	2.5E-1	9.2E-1
☐	KEGG_PATHWAY	Regulation of actin cytoskeleton	RT	7	3.9E-1	9.8E-1
☐	KEGG_PATHWAY	Acute myeloid leukemia	RT	3	4.3E-1	9.9E-1
☐	KEGG_PATHWAY	ErbB signaling pathway	RT	3	6.2E-1	1.0E0
☐	GOTERM_BP_ALL	response to biotic stimulus	RT	5	6.2E-1	1.0E0
☐	KEGG_PATHWAY	Jak-STAT signaling pathway	RT	4	7.2E-1	1.0E0

	Annotation Cluster 22	Enrichment Score: 1.01	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	GTPase activity	RT	8	1.9E-2	9.0E-1
☐	GOTERM_CC_ALL	heterotrimeric G-protein complex	RT	4	3.3E-2	8.6E-1
☐	GOTERM_CC_ALL	extrinsic to plasma membrane	RT	4	9.2E-2	9.3E-1
☐	GOTERM_CC_ALL	extrinsic to membrane	RT	4	1.8E-1	9.8E-1
☐	SP_PIR_KEYWORDS	transducer	RT	6	8.8E-1	1.0E0

	Annotation Cluster 23	Enrichment Score: 1	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	nucleoside-triphosphatase activity	RT	21	1.3E-3	7.0E-1
☐	GOTERM_MF_ALL	pyrophosphatase activity	RT	21	2.3E-3	7.0E-1
☐	GOTERM_MF_ALL	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	RT	21	2.5E-3	6.7E-1
☐	GOTERM_MF_ALL	hydrolase activity, acting on acid anhydrides	RT	21	2.7E-3	6.4E-1

☐	**GOTERM_MF_ALL**	active transmembrane transporter activity	RT		15	4.3E-3	7.7E-1
☐	**GOTERM_MF_ALL**	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT		9	6.0E-3	8.0E-1
☐	**GOTERM_MF_ALL**	primary active transmembrane transporter activity	RT		9	6.0E-3	8.0E-1
☐	**GOTERM_CC_ALL**	proton-transporting ATP synthase complex, catalytic core F(1)	RT		3	8.9E-3	7.5E-1
☐	**GOTERM_CC_ALL**	proton-transporting two-sector ATPase complex, catalytic domain	RT		3	1.1E-2	7.1E-1
☐	**GOTERM_MF_ALL**	ATPase activity, coupled to movement of substances	RT		8	1.2E-2	8.5E-1
☐	**GOTERM_MF_ALL**	ATPase activity, coupled to transmembrane movement of substances	RT		8	1.2E-2	8.5E-1
☐	**GOTERM_MF_ALL**	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT		8	1.3E-2	8.5E-1
☐	**GOTERM_MF_ALL**	GTPase activity	RT		8	1.9E-2	9.0E-1
☐	**GOTERM_MF_ALL**	cation-transporting ATPase activity	RT		5	2.0E-2	8.9E-1
☐	**GOTERM_MF_ALL**	ATPase activity, coupled to transmembrane movement of ions	RT		6	3.0E-2	9.4E-1
☐	**GOTERM_BP_ALL**	localization	RT		66	4.2E-2	1.0E0
☐	**GOTERM_BP_ALL**	proton transport	RT		5	4.4E-2	1.0E0
☐	**GOTERM_BP_ALL**	ATP synthesis coupled proton transport	RT		4	4.4E-2	1.0E0
☐	**GOTERM_MF_ALL**	hydrogen ion transporting ATP synthase activity, rotational mechanism	RT		4	5.0E-2	9.8E-1
☐	**GOTERM_CC_ALL**	proton-transporting ATP synthase complex	RT		3	5.2E-2	9.2E-1
☐	**GOTERM_MF_ALL**	hydrogen ion transporting ATPase activity, rotational mechanism	RT		4	5.3E-2	9.8E-1
☐	**GOTERM_BP_ALL**	nucleoside phosphate metabolic process	RT		4	5.5E-2	1.0E0
☐	**GOTERM_BP_ALL**	ATP biosynthetic process	RT		4	5.5E-2	1.0E0
☐	**GOTERM_BP_ALL**	hydrogen transport	RT		5	5.6E-2	1.0E0
☐	**GOTERM_MF_ALL**	ATPase activity, coupled	RT		10	5.9E-2	9.8E-1
☐	**GOTERM_MF_ALL**	ATPase activity	RT		11	6.3E-2	9.9E-1
☐	**GOTERM_CC_ALL**	proton-transporting two-sector ATPase complex	RT		4	6.5E-2	9.3E-1
☐	**SP_PIR_KEYWORDS**	transport	RT		32	6.9E-2	9.2E-1
☐	**GOTERM_BP_ALL**	ATP metabolic process	RT		4	7.0E-2	1.0E0
☐	**SP_PIR_KEYWORDS**	ATP synthesis	RT		3	8.2E-2	9.4E-1
☐	**GOTERM_BP_ALL**	purine ribonucleoside triphosphate biosynthetic process	RT		4	8.7E-2	1.0E0
☐	**GOTERM_BP_ALL**	purine nucleoside triphosphate biosynthetic process	RT		4	8.7E-2	1.0E0
☐	**GOTERM_BP_ALL**	ribonucleoside triphosphate biosynthetic process	RT		4	9.1E-2	1.0E0
☐	**GOTERM_BP_ALL**	oxidative phosphorylation	RT		4	9.5E-2	1.0E0
☐	**GOTERM_BP_ALL**	purine ribonucleoside triphosphate metabolic process	RT		4	1.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	nucleoside triphosphate biosynthetic process	RT		4	1.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	ribonucleoside triphosphate metabolic process	RT		4	1.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	purine nucleoside triphosphate metabolic process	RT		4	1.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	symporter activity	RT		6	1.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	purine ribonucleotide biosynthetic process	RT		4	1.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	nucleoside triphosphate metabolic process	RT		4	1.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	cofactor biosynthetic process	RT		5	1.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	transport	RT		53	1.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	ribonucleotide biosynthetic process	RT		4	1.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	purine ribonucleotide metabolic process	RT		4	1.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	purine nucleotide biosynthetic process	RT		4	1.8E-1	1.0E0

☐	**GOTERM_BP_ALL**	establishment of localization	RT	54	1.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	hydrogen ion transport	RT	3	1.9E-1	9.9E-1
☐	**GOTERM_MF_ALL**	substrate-specific transporter activity	RT	22	2.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Symport	RT	4	2.1E-1	9.9E-1
☐	**GOTERM_BP_ALL**	cofactor metabolic process	RT	7	2.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	ribonucleotide metabolic process	RT	4	2.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	purine nucleotide metabolic process	RT	4	2.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrolase activity	RT	44	2.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	secondary active transmembrane transporter activity	RT	6	2.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	coenzyme biosynthetic process	RT	4	2.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	inorganic cation transmembrane transporter activity	RT	5	2.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	transporter activity	RT	27	3.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrogen ion transmembrane transporter activity	RT	4	3.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	monovalent inorganic cation transmembrane transporter activity	RT	4	3.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	3	3.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	coenzyme metabolic process	RT	5	4.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	substrate-specific transmembrane transporter activity	RT	15	4.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	nucleotide biosynthetic process	RT	4	4.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	transmembrane transporter activity	RT	17	5.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	monovalent inorganic cation transport	RT	6	6.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	cation transport	RT	9	6.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	ion transmembrane transporter activity	RT	11	7.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	nucleotide metabolic process	RT	4	7.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	generation of precursor metabolites and energy	RT	9	7.5E-1	1.0E0
☐	**KEGG_PATHWAY**	Oxidative phosphorylation	RT	3	7.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	cation transmembrane transporter activity	RT	8	7.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	nucleobase, nucleoside and nucleotide metabolic process	RT	4	7.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	ion transport	RT	7	8.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	ion transport	RT	11	8.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	metal ion transmembrane transporter activity	RT	3	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	metal ion transport	RT	4	9.8E-1	1.0E0
	Annotation Cluster 24	Enrichment Score: 0.99	G	Count	P_Value	Benjamini
☐	**KEGG_PATHWAY**	Huntington's disease	RT	4	2.6E-2	8.4E-1
☐	**GOTERM_BP_ALL**	anti-apoptosis	RT	6	4.4E-2	1.0E0
☐	**GOTERM_BP_ALL**	death	RT	21	4.7E-2	1.0E0
☐	**GOTERM_BP_ALL**	cell death	RT	21	4.7E-2	1.0E0
☐	**GOTERM_BP_ALL**	regulation of apoptosis	RT	15	4.8E-2	1.0E0
☐	**GOTERM_BP_ALL**	apoptosis	RT	20	5.1E-2	1.0E0
☐	**GOTERM_BP_ALL**	regulation of programmed cell death	RT	15	5.4E-2	1.0E0
☐	**SP_PIR_KEYWORDS**	apoptosis	RT	10	5.6E-2	9.1E-1
☐	**GOTERM_BP_ALL**	programmed cell death	RT	20	5.9E-2	1.0E0
☐	**GOTERM_BP_ALL**	negative regulation of apoptosis	RT	8	7.2E-2	1.0E0
☐	**GOTERM_BP_ALL**	negative regulation of programmed cell death	RT	8	7.8E-2	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of apoptosis	RT	8	9.5E-2	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of programmed cell death	RT	8	1.0E-1	1.0E0

☐	GOTERM_BP_ALL	induction of apoptosis by intracellular signals	RT		3	1.1E-1	1.0E0
☐	GOTERM_BP_ALL	cell differentiation	RT		41	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	cellular developmental process	RT		41	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of biological process	RT		25	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cellular process	RT		22	1.8E-1	1.0E0
☐	GOTERM_BP_ALL	induction of programmed cell death	RT		6	1.9E-1	1.0E0
☐	GOTERM_BP_ALL	induction of apoptosis	RT		6	1.9E-1	1.0E0
☐	GOTERM_BP_ALL	cell development	RT		28	2.0E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of neuron apoptosis	RT		3	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of cellular process	RT		22	2.6E-1	1.0E0
☐	GOTERM_BP_ALL	neuron apoptosis	RT		3	2.6E-1	1.0E0
☐	GOTERM_BP_ALL	developmental process	RT		58	3.8E-1	1.0E0
	Annotation Cluster 25	Enrichment Score: 0.96	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Cyclin, N-terminal	RT		3	8.2E-2	1.0E0
☐	INTERPRO	Cyclin	RT		3	1.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	cyclin	RT		4	1.2E-1	9.7E-1
☐	SMART	CYCLIN	RT		3	1.3E-1	1.0E0
	Annotation Cluster 26	Enrichment Score: 0.95	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of actin polymerization and/or depolymerization	RT		4	3.7E-2	1.0E0
☐	GOTERM_BP_ALL	regulation of actin filament length	RT		4	3.9E-2	1.0E0
☐	GOTERM_BP_ALL	regulation of actin cytoskeleton organization and biogenesis	RT		4	3.9E-2	1.0E0
☐	GOTERM_BP_ALL	regulation of cellular component size	RT		4	4.2E-2	1.0E0
☐	SP_PIR_KEYWORDS	actin-binding	RT		8	4.3E-2	9.0E-1
☐	GOTERM_BP_ALL	regulation of cytoskeleton organization and biogenesis	RT		4	5.0E-2	1.0E0
☐	GOTERM_BP_ALL	regulation of organelle organization and biogenesis	RT		4	5.0E-2	1.0E0
☐	GOTERM_BP_ALL	actin polymerization and/or depolymerization	RT		4	6.4E-2	1.0E0
☐	GOTERM_BP_ALL	actin filament capping	RT		3	6.6E-2	1.0E0
☐	GOTERM_BP_ALL	negative regulation of actin filament depolymerization	RT		3	6.6E-2	1.0E0
☐	GOTERM_BP_ALL	actin filament depolymerization	RT		3	7.7E-2	1.0E0
☐	GOTERM_BP_ALL	regulation of actin filament depolymerization	RT		3	7.7E-2	1.0E0
☐	GOTERM_BP_ALL	regulation of protein metabolic process	RT		10	7.7E-2	1.0E0
☐	GOTERM_BP_ALL	regulation of cellular component organization and biogenesis	RT		4	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	actin cytoskeleton organization and biogenesis	RT		7	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	protein depolymerization	RT		3	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of cellular component organization and biogenesis	RT		3	1.7E-1	1.0E0
☐	GOTERM_BP_ALL	actin filament-based process	RT		7	1.8E-1	1.0E0
☐	GOTERM_CC_ALL	ruffle	RT		3	2.2E-1	9.9E-1
☐	GOTERM_BP_ALL	negative regulation of protein metabolic process	RT		3	4.8E-1	1.0E0
☐	GOTERM_CC_ALL	leading edge	RT		3	5.4E-1	1.0E0
☐	GOTERM_CC_ALL	cell projection	RT		6	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of metabolic process	RT		6	8.7E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 0.93	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	intracellular signaling cascade	RT		33	1.9E-2	1.0E0
☐	GOTERM_BP_ALL	signal transduction	RT		58	7.7E-2	1.0E0
☐	GOTERM_BP_ALL	cell communication	RT		60	1.7E-1	1.0E0

☐	GOTERM_BP_ALL	cell surface receptor linked signal transduction	RT	▬		23	7.4E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 0.93	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of progression through cell cycle	RT	▬		12	8.4E-2	1.0E0
☐	GOTERM_BP_ALL	cell division	RT	▬		9	8.6E-2	1.0E0
☐	GOTERM_BP_ALL	regulation of cell cycle	RT	▬		12	8.7E-2	1.0E0
☐	GOTERM_BP_ALL	negative regulation of progression through cell cycle	RT	▬		6	1.1E-1	1.0E0
☐	GOTERM_BP_ALL	cell cycle	RT	▬		19	1.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	cell cycle	RT	▬		11	1.4E-1	9.8E-1
☐	SP_PIR_KEYWORDS	cell division	RT	▬		7	1.4E-1	9.7E-1
☐	GOTERM_BP_ALL	cell cycle process	RT	▬		15	2.0E-1	1.0E0
	Annotation Cluster 29	Enrichment Score: 0.88	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Flavodoxin-like fold	RT	▬		3	9.3E-4	1.0E0
☐	GOTERM_MF_ALL	NAD(P)H dehydrogenase (quinone) activity	RT	▬		3	9.7E-4	7.3E-1
☐	GOTERM_BP_ALL	response to oxidative stress	RT	▬		5	2.4E-2	1.0E0
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor	RT	▬		3	1.8E-1	1.0E0
☐	GOTERM_MF_ALL	cofactor binding	RT	▬		6	2.5E-1	1.0E0
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on NADH or NADPH	RT	▬		3	3.2E-1	1.0E0
☐	GOTERM_MF_ALL	coenzyme binding	RT	▬		4	4.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	fad	RT	▬		3	5.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	flavoprotein	RT	▬		3	5.6E-1	1.0E0
☐	GOTERM_MF_ALL	oxidoreductase activity	RT	▬		13	8.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	oxidoreductase	RT	▬		7	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	electron transport	RT	▬		5	9.4E-1	1.0E0
	Annotation Cluster 30	Enrichment Score: 0.87	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	lymphocyte homeostasis	RT	▬		3	5.6E-2	1.0E0
☐	GOTERM_BP_ALL	leukocyte homeostasis	RT	▬		3	9.3E-2	1.0E0
☐	GOTERM_BP_ALL	homeostasis of number of cells	RT	▬		3	1.0E-1	1.0E0
☐	GOTERM_BP_ALL	leukocyte activation	RT	▬		8	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	homeostatic process	RT	▬		8	5.2E-1	1.0E0
	Annotation Cluster 31	Enrichment Score: 0.8	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	protein heterodimerization activity	RT	▬		8	2.1E-3	7.6E-1
☐	GOTERM_MF_ALL	protein dimerization activity	RT	▬		13	5.0E-3	7.8E-1
☐	GOTERM_BP_ALL	embryonic placenta development	RT	▬		3	2.0E-2	1.0E0
☐	GOTERM_MF_ALL	protein homodimerization activity	RT	▬		7	5.1E-2	9.8E-1
☐	GOTERM_BP_ALL	in utero embryonic development	RT	▬		6	8.1E-2	1.0E0
☐	GOTERM_BP_ALL	placenta development	RT	▬		3	9.9E-2	1.0E0
☐	GOTERM_MF_ALL	identical protein binding	RT	▬		9	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of biological process	RT	▬		25	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cellular process	RT	▬		22	1.8E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cellular metabolic process	RT	▬		11	2.9E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of transcription	RT	▬		9	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	▬		9	3.3E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of metabolic process	RT	▬		11	3.7E-1	1.0E0
☐	GOTERM_BP_ALL	chordate embryonic development	RT	▬		6	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	embryonic development ending in birth or egg hatching	RT	▬		6	4.0E-1	1.0E0

☐	SP_PIR_KEYWORDS	DNA binding	RT	6	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of transcription, DNA-dependent	RT	6	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	embryonic development	RT	8	7.3E-1	1.0E0
☐	GOTERM_MF_ALL	transcription activator activity	RT	4	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of developmental process	RT	4	9.2E-1	1.0E0
	Annotation Cluster 32	Enrichment Score: 0.77	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	protein heterodimerization activity	RT	8	2.1E-3	7.6E-1
☐	GOTERM_BP_ALL	cell growth	RT	6	8.5E-2	1.0E0
☐	GOTERM_BP_ALL	regulation of cell size	RT	6	1.1E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell growth	RT	5	1.3E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of biological process	RT	25	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of growth	RT	3	1.7E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cellular process	RT	22	1.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of growth	RT	6	2.3E-1	1.0E0
☐	GOTERM_BP_ALL	growth	RT	8	2.5E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cellular metabolic process	RT	11	2.9E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of transcription	RT	9	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	9	3.3E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of metabolic process	RT	11	3.7E-1	1.0E0
☐	GOTERM_BP_ALL	cell morphogenesis	RT	12	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	cellular structure morphogenesis	RT	12	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of catalytic activity	RT	5	4.5E-1	1.0E0
	Annotation Cluster 33	Enrichment Score: 0.69	G	Count	P_Value	Benjamini
☐	INTERPRO	CD9/CD37/CD63 antigen	RT	4	1.6E-2	1.0E0
☐	GOTERM_CC_ALL	plasma membrane part	RT	29	2.2E-1	9.9E-1
☐	GOTERM_CC_ALL	integral to plasma membrane	RT	11	6.9E-1	1.0E0
☐	GOTERM_CC_ALL	intrinsic to plasma membrane	RT	11	7.2E-1	1.0E0
	Annotation Cluster 34	Enrichment Score: 0.67	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of a molecular function	RT	14	4.2E-2	1.0E0
☐	GOTERM_BP_ALL	regulation of catalytic activity	RT	12	7.1E-2	1.0E0
☐	GOTERM_BP_ALL	regulation of MAP kinase activity	RT	4	1.4E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of kinase activity	RT	3	2.1E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of protein kinase activity	RT	3	2.1E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of transferase activity	RT	3	2.3E-1	1.0E0
☐	GOTERM_BP_ALL	MAPKKK cascade	RT	5	2.4E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of catalytic activity	RT	3	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of protein kinase activity	RT	5	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of kinase activity	RT	5	4.1E-1	1.0E0
☐	GOTERM_BP_ALL	protein kinase cascade	RT	7	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of transferase activity	RT	5	4.4E-1	1.0E0
	Annotation Cluster 35	Enrichment Score: 0.64	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	lymphocyte proliferation	RT	5	7.9E-2	1.0E0
☐	GOTERM_BP_ALL	mononuclear cell proliferation	RT	5	7.9E-2	1.0E0
☐	GOTERM_BP_ALL	cell growth	RT	6	8.5E-2	1.0E0
☐	GOTERM_BP_ALL	cell activation	RT	9	9.8E-2	1.0E0
☐	GOTERM_BP_ALL	B cell activation	RT	5	1.0E-1	1.0E0
☐	GOTERM_BP_ALL	B cell proliferation	RT	3	1.0E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of B cell activation	RT	3	1.0E-1	1.0E0

☐	**GOTERM_BP_ALL**	regulation of cell size	RT	6	1.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	leukocyte activation	RT	8	1.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of B cell activation	RT	3	1.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of cell proliferation	RT	7	2.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	immune system process	RT	18	2.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	lymphocyte activation	RT	7	2.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of growth	RT	6	2.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	growth	RT	8	2.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cell proliferation	RT	10	2.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of mononuclear cell proliferation	RT	3	3.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of lymphocyte proliferation	RT	3	3.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	T cell proliferation	RT	3	3.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of lymphocyte activation	RT	3	3.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell proliferation	RT	12	4.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of catalytic activity	RT	5	4.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	T cell activation	RT	4	4.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of lymphocyte activation	RT	3	5.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cell activation	RT	3	5.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	reproductive process	RT	5	6.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of multicellular organismal process	RT	6	6.9E-1	1.0E0
	Annotation Cluster 36	Enrichment Score: 0.6	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	blood vessel morphogenesis	RT	9	3.6E-2	1.0E0
☐	**GOTERM_BP_ALL**	blood vessel development	RT	9	7.3E-2	1.0E0
☐	**GOTERM_BP_ALL**	vasculature development	RT	9	7.8E-2	1.0E0
☐	**GOTERM_BP_ALL**	cell differentiation	RT	41	1.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular developmental process	RT	41	1.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	angiogenesis	RT	6	1.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	organ morphogenesis	RT	14	2.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	anatomical structure formation	RT	7	2.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	anatomical structure morphogenesis	RT	25	3.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	developmental process	RT	58	3.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	system development	RT	31	6.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	anatomical structure development	RT	36	7.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	organ development	RT	24	7.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	multicellular organismal development	RT	38	7.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	multicellular organismal process	RT	49	8.2E-1	1.0E0
	Annotation Cluster 37	Enrichment Score: 0.58	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	chromatin binding	RT	7	2.4E-2	9.2E-1
☐	**GOTERM_CC_ALL**	heterochromatin	RT	3	1.6E-1	9.8E-1
☐	**BIOCARTA**	Control of Gene Expression by Vitamin D Receptor	RT	3	2.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	chromatin remodeling	RT	3	2.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	chromatin modification	RT	6	2.4E-1	1.0E0
☐	**GOTERM_CC_ALL**	chromosomal part	RT	8	2.7E-1	9.9E-1
☐	**SP_PIR_KEYWORDS**	Chromatin regulator	RT	4	3.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	chromatin assembly or disassembly	RT	4	3.0E-1	1.0E0
☐	**GOTERM_CC_ALL**	chromosome, pericentric region	RT	3	3.5E-1	1.0E0
☐	**GOTERM_CC_ALL**	chromatin	RT	5	3.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	DNA metabolic process	RT	14	3.7E-1	1.0E0

☐	**GOTERM_BP_ALL**	chromosome organization and biogenesis	RT		8	3.9E-1	1.0E0
☐	**GOTERM_CC_ALL**	chromosome	RT		8	4.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	establishment and/or maintenance of chromatin architecture	RT		6	4.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	DNA packaging	RT		6	5.0E-1	1.0E0
	Annotation Cluster 38	Enrichment Score: 0.58	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	cytoskeletal part	RT		16	8.1E-2	9.3E-1
☐	**GOTERM_CC_ALL**	cytoskeleton	RT		23	9.8E-2	9.2E-1
☐	**GOTERM_CC_ALL**	microtubule cytoskeleton	RT		10	1.4E-1	9.7E-1
☐	**GOTERM_BP_ALL**	microtubule-based process	RT		7	1.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	cytoskeleton organization and biogenesis	RT		13	2.1E-1	1.0E0
☐	**GOTERM_CC_ALL**	microtubule	RT		6	2.9E-1	9.9E-1
☐	**GOTERM_MF_ALL**	microtubule motor activity	RT		3	3.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	cytoskeleton-dependent intracellular transport	RT		4	3.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	motor activity	RT		4	4.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	motor protein	RT		3	5.1E-1	1.0E0
☐	**GOTERM_CC_ALL**	microtubule associated complex	RT		3	5.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	microtubule-based movement	RT		3	5.7E-1	1.0E0
	Annotation Cluster 39	Enrichment Score: 0.58	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	phosphatidylinositol metabolic process	RT		3	2.0E-2	1.0E0
☐	**GOTERM_BP_ALL**	glycerophospholipid biosynthetic process	RT		3	1.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	glycerophospholipid metabolic process	RT		4	1.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	phospholipid metabolic process	RT		5	2.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	phosphoinositide metabolic process	RT		3	2.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	phospholipid biosynthetic process	RT		3	3.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	membrane lipid metabolic process	RT		5	4.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	membrane lipid biosynthetic process	RT		3	4.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	lipid biosynthetic process	RT		6	5.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	lipid metabolic process	RT		11	7.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular lipid metabolic process	RT		9	8.0E-1	1.0E0
	Annotation Cluster 40	Enrichment Score: 0.53	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	anatomical structure formation	RT		7	2.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	wound healing	RT		4	2.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	blood coagulation	RT		3	3.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	coagulation	RT		3	3.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	hemostasis	RT		3	3.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of body fluid levels	RT		3	4.3E-1	1.0E0
	Annotation Cluster 41	Enrichment Score: 0.52	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	caspase activation	RT		3	8.2E-2	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of caspase activity	RT		3	1.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of hydrolase activity	RT		3	1.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of caspase activity	RT		3	1.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	apoptotic program	RT		3	3.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of catalytic activity	RT		5	4.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	response to DNA damage stimulus	RT		6	5.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	response to endogenous stimulus	RT		6	6.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	DNA repair	RT		4	7.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of hydrolase activity	RT		3	7.7E-1	1.0E0
	Annotation Cluster 42	Enrichment Score: 0.52	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	nucleocytoplasmic transport	RT		5	1.7E-1	1.0E0

☐	GOTERM_BP_ALL	nuclear transport	RT		5	1.8E-1	1.0E0
☐	GOTERM_BP_ALL	protein import into nucleus	RT		3	3.6E-1	1.0E0
☐	GOTERM_BP_ALL	nuclear import	RT		3	3.7E-1	1.0E0
☐	GOTERM_BP_ALL	protein import	RT		3	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	protein targeting	RT		6	4.5E-1	1.0E0
	Annotation Cluster 43	Enrichment Score: 0.51	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	intracellular organelle part	RT		51	2.7E-1	9.9E-1
☐	GOTERM_CC_ALL	organelle part	RT		51	2.8E-1	9.9E-1
☐	GOTERM_CC_ALL	intracellular non-membrane-bound organelle	RT		31	3.4E-1	1.0E0
☐	GOTERM_CC_ALL	non-membrane-bound organelle	RT		31	3.4E-1	1.0E0
	Annotation Cluster 44	Enrichment Score: 0.5	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	male gamete generation	RT		6	2.8E-1	1.0E0
☐	GOTERM_BP_ALL	spermatogenesis	RT		6	2.8E-1	1.0E0
☐	GOTERM_BP_ALL	sexual reproduction	RT		8	3.4E-1	1.0E0
☐	GOTERM_BP_ALL	reproduction	RT		11	3.4E-1	1.0E0
☐	GOTERM_BP_ALL	gamete generation	RT		7	3.4E-1	1.0E0
	Annotation Cluster 45	Enrichment Score: 0.5	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein complex assembly	RT		7	9.4E-2	1.0E0
☐	GOTERM_CC_ALL	cytoplasmic vesicle membrane	RT		4	1.3E-1	9.6E-1
☐	GOTERM_MF_ALL	protein transporter activity	RT		6	1.6E-1	1.0E0
☐	GOTERM_CC_ALL	cytoplasmic vesicle part	RT		4	1.7E-1	9.8E-1
☐	GOTERM_CC_ALL	secretory granule	RT		3	2.2E-1	9.9E-1
☐	GOTERM_CC_ALL	vesicle membrane	RT		4	2.2E-1	9.9E-1
☐	GOTERM_CC_ALL	vesicle coat	RT		3	2.2E-1	9.9E-1
☐	GOTERM_CC_ALL	coated vesicle membrane	RT		3	2.4E-1	9.9E-1
☐	GOTERM_CC_ALL	membrane coat	RT		3	2.9E-1	9.9E-1
☐	GOTERM_CC_ALL	coated membrane	RT		3	2.9E-1	9.9E-1
☐	GOTERM_CC_ALL	cytoplasmic vesicle	RT		8	4.3E-1	1.0E0
☐	GOTERM_CC_ALL	vesicle	RT		8	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	vesicle-mediated transport	RT		9	5.8E-1	1.0E0
☐	GOTERM_CC_ALL	endomembrane system	RT		8	6.0E-1	1.0E0
☐	GOTERM_CC_ALL	cytoplasmic membrane-bound vesicle	RT		5	6.5E-1	1.0E0
☐	GOTERM_CC_ALL	coated vesicle	RT		3	6.6E-1	1.0E0
☐	GOTERM_CC_ALL	membrane-bound vesicle	RT		5	6.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	cytoplasmic vesicle	RT		3	7.0E-1	1.0E0
	Annotation Cluster 46	Enrichment Score: 0.48	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	phosphoprotein phosphatase activity	RT		6	1.4E-1	1.0E0
☐	GOTERM_MF_ALL	protein tyrosine/serine/threonine phosphatase activity	RT		3	1.6E-1	1.0E0
☐	GOTERM_MF_ALL	protein tyrosine phosphatase activity	RT		4	2.2E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Tyrosine-protein phosphatase	RT		3	2.2E-1	1.0E0
☐	UP_SEQ_FEATURE	active site:Phosphocysteine intermediate	RT		3	3.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	protein phosphatase	RT		4	3.1E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid dephosphorylation	RT		4	4.0E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase, Tyr-specific/dual-specificity type	RT		3	4.2E-1	1.0E0
☐	GOTERM_MF_ALL	phosphoric monoester hydrolase activity	RT		6	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	dephosphorylation	RT		4	4.7E-1	1.0E0
☐	GOTERM_MF_ALL	phosphoric ester hydrolase activity	RT		6	6.4E-1	1.0E0
☐	GOTERM_MF_ALL	hydrolase activity, acting on ester bonds	RT		9	8.8E-1	1.0E0
	Annotation Cluster 47	Enrichment Score: 0.44	G	🟩	Count	P_Value	Benjamini

☐	**GOTERM_BP_ALL**	phosphate metabolic process	RT		22	1.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	phosphorus metabolic process	RT		22	1.1E-1	1.0E0
☐	**INTERPRO**	Serine/threonine protein kinase	RT		7	1.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	phosphorylation	RT		18	1.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	kinase activity	RT		21	1.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	phosphotransferase activity, alcohol group as acceptor	RT		17	2.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	protein kinase activity	RT		14	2.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	transferase activity, transferring phosphorus-containing groups	RT		22	3.0E-1	1.0E0
☐	**SMART**	S_TKc	RT		9	3.3E-1	1.0E0
☐	**UP_SEQ_FEATURE**	nucleotide phosphate-binding region:ATP	RT		15	3.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	protein serine/threonine kinase activity	RT		11	3.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein amino acid phosphorylation	RT		14	3.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	active site:Proton acceptor	RT		12	4.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	kinase	RT		15	4.3E-1	1.0E0
☐	**INTERPRO**	Serine/threonine protein kinase, active site	RT		6	4.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	transferase activity	RT		34	4.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	binding site:ATP	RT		9	5.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Protein kinase	RT		8	5.7E-1	1.0E0
☐	**INTERPRO**	Protein kinase, core	RT		7	5.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Serine/threonine-protein kinase	RT		7	6.4E-1	1.0E0
☐	**INTERPRO**	Tyrosine protein kinase	RT		3	6.5E-1	1.0E0
☐	**SMART**	TyrKc	RT		3	6.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	transferase	RT		22	7.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	protein-tyrosine kinase activity	RT		5	8.3E-1	1.0E0
	Annotation Cluster 48	Enrichment Score: 0.43	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	activator	RT		16	8.2E-3	6.4E-1
☐	**SP_PIR_KEYWORDS**	Transcription regulation	RT		33	4.4E-2	8.9E-1
☐	**SP_PIR_KEYWORDS**	Transcription	RT		33	5.5E-2	9.1E-1
☐	**GOTERM_BP_ALL**	biological regulation	RT		91	1.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cellular process	RT		76	1.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of biological process	RT		82	2.1E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	nucleus	RT		62	3.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	biopolymer metabolic process	RT		87	3.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	transcription factor activity	RT		19	3.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	transcription regulator activity	RT		25	4.4E-1	1.0E0
☐	**GOTERM_CC_ALL**	nucleus	RT		76	4.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of transcription, DNA-dependent	RT		39	5.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of metabolic process	RT		47	5.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	transcription, DNA-dependent	RT		39	6.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	RNA biosynthetic process	RT		39	6.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	RNA metabolic process	RT		46	6.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cellular metabolic process	RT		44	6.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		40	6.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of transcription	RT		39	7.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	transcription	RT		40	7.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of gene expression	RT		41	7.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	dna-binding	RT		22	7.6E-1	1.0E0

☐	GOTERM_BP_ALL	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		56	8.2E-1	1.0E0
☐	GOTERM_MF_ALL	DNA binding	RT		31	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	gene expression	RT		49	9.0E-1	1.0E0
☐	GOTERM_MF_ALL	nucleic acid binding	RT		42	9.9E-1	1.0E0
	Annotation Cluster 49	Enrichment Score: 0.43	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Basic helix-loop-helix dimerisation region bHLH	RT		4	2.7E-1	1.0E0
☐	SMART	HLH	RT		4	3.2E-1	1.0E0
☐	INTERPRO	Helix-loop-helix DNA-binding	RT		3	4.1E-1	1.0E0
☐	UP_SEQ_FEATURE	DNA-binding region:Basic motif	RT		4	4.1E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Helix-loop-helix motif	RT		3	4.8E-1	1.0E0
	Annotation Cluster 50	Enrichment Score: 0.43	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Variant SH3	RT		3	2.4E-1	1.0E0
☐	INTERPRO	SH2 motif	RT		4	3.1E-1	1.0E0
☐	BIOCARTA	Signaling of Hepatocyte Growth Factor Receptor	RT		3	3.1E-1	1.0E0
☐	SMART	SH2	RT		4	3.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	sh2 domain	RT		4	3.4E-1	1.0E0
☐	INTERPRO	Src homology-3	RT		5	4.2E-1	1.0E0
☐	SMART	SH3	RT		5	4.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	SH3 domain	RT		5	4.8E-1	1.0E0
☐	KEGG_PATHWAY	MAPK signaling pathway	RT		7	5.9E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 0.42	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Basic-leucine zipper (bZIP) transcription factor	RT		3	2.2E-1	1.0E0
☐	SMART	BRLZ	RT		3	2.5E-1	1.0E0
☐	GOTERM_MF_ALL	sequence-specific DNA binding	RT		6	9.5E-1	1.0E0
	Annotation Cluster 52	Enrichment Score: 0.42	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	myoblast differentiation	RT		3	1.9E-1	1.0E0
☐	GOTERM_BP_ALL	skeletal muscle development	RT		4	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	skeletal muscle fiber development	RT		3	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	muscle fiber development	RT		3	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	muscle cell differentiation	RT		3	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	muscle development	RT		5	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	striated muscle development	RT		4	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	cell-cell adhesion	RT		6	5.1E-1	1.0E0
	Annotation Cluster 53	Enrichment Score: 0.42	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell cycle checkpoint	RT		3	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	DNA damage response, signal transduction	RT		3	1.7E-1	1.0E0
☐	GOTERM_BP_ALL	M phase	RT		7	3.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	mitosis	RT		4	3.9E-1	1.0E0
☐	GOTERM_BP_ALL	mitosis	RT		5	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	M phase of mitotic cell cycle	RT		5	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	cell cycle phase	RT		7	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	response to DNA damage stimulus	RT		6	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	response to endogenous stimulus	RT		6	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	mitotic cell cycle	RT		5	6.8E-1	1.0E0
	Annotation Cluster 54	Enrichment Score: 0.4	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	M phase	RT		7	3.0E-1	1.0E0
☐	GOTERM_BP_ALL	M phase of meiotic cell cycle	RT		3	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	meiosis	RT		3	4.2E-1	1.0E0

☐	**GOTERM_BP_ALL**	meiotic cell cycle	RT	3	4.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell cycle phase	RT	7	4.6E-1	1.0E0
	Annotation Cluster 55	Enrichment Score: 0.4	G	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	membrane	RT	128	1.6E-2	6.5E-1
☐	**SP_PIR_KEYWORDS**	membrane	RT	91	5.1E-2	9.1E-1
☐	**GOTERM_CC_ALL**	membrane part	RT	99	9.3E-2	9.3E-1
☐	**SP_PIR_KEYWORDS**	transmembrane	RT	65	3.5E-1	1.0E0
☐	**UP_SEQ_FEATURE**	topological domain:Cytoplasmic	RT	38	3.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	topological domain:Extracellular	RT	29	4.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	transmembrane region	RT	48	4.4E-1	1.0E0
☐	**GOTERM_CC_ALL**	integral to membrane	RT	80	4.5E-1	1.0E0
☐	**GOTERM_CC_ALL**	intrinsic to membrane	RT	80	4.7E-1	1.0E0
☐	**UP_SEQ_FEATURE**	disulfide bond	RT	33	5.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	glycosylation site:N-linked (GlcNAc...)	RT	41	8.1E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	glycoprotein	RT	46	9.1E-1	1.0E0
☐	**GOTERM_CC_ALL**	extracellular region part	RT	29	9.9E-1	1.0E0
☐	**GOTERM_CC_ALL**	extracellular region	RT	30	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	extracellular space	RT	26	1.0E0	1.0E0
☐	**UP_SEQ_FEATURE**	signal peptide	RT	27	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	signal	RT	30	1.0E0	1.0E0
	Annotation Cluster 56	Enrichment Score: 0.39	G	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	Zymogen	RT	8	5.7E-2	8.9E-1
☐	**GOTERM_BP_ALL**	proteolysis	RT	19	1.1E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	thiol protease	RT	5	1.4E-1	9.8E-1
☐	**UP_SEQ_FEATURE**	propeptide:Activation peptide	RT	3	3.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	cysteine-type peptidase activity	RT	5	3.5E-1	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF001135:trypsin	RT	3	3.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Peptidase S1	RT	3	3.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	hydrolase	RT	26	4.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	active site:Charge relay system	RT	4	4.5E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	serine protease	RT	4	4.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	protease	RT	10	5.0E-1	1.0E0
☐	**INTERPRO**	Peptidase S1A, chymotrypsin	RT	3	6.2E-1	1.0E0
☐	**INTERPRO**	Peptidase S1 and S6, chymotrypsin/Hap	RT	3	6.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	serine-type endopeptidase activity	RT	4	6.9E-1	1.0E0
☐	**SMART**	Tryp_SPc	RT	3	6.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	peptidase activity	RT	12	7.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	serine hydrolase activity	RT	4	7.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	serine-type peptidase activity	RT	4	7.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	endopeptidase activity	RT	7	8.1E-1	1.0E0
	Annotation Cluster 57	Enrichment Score: 0.35	G	Count	P_Value	Benjamini
☐	**INTERPRO**	Immunoglobulin subtype	RT	7	2.1E-1	1.0E0
☐	**SMART**	IG	RT	7	3.1E-1	1.0E0
☐	**INTERPRO**	Immunoglobulin	RT	5	3.4E-1	1.0E0
☐	**INTERPRO**	Immunoglobulin-like	RT	7	6.1E-1	1.0E0
☐	**INTERPRO**	Immunoglobulin-like fold	RT	7	6.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	immunoglobulin domain	RT	5	9.0E-1	1.0E0
	Annotation Cluster 58	Enrichment Score: 0.34	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	glycolysis	RT	3	2.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	glucose catabolic process	RT	3	3.2E-1	1.0E0

☐	GOTERM_BP_ALL	monosaccharide catabolic process	RT	3	3.3E-1	1.0E0
☐	GOTERM_BP_ALL	hexose catabolic process	RT	3	3.3E-1	1.0E0
☐	GOTERM_BP_ALL	glucose metabolic process	RT	4	3.4E-1	1.0E0
☐	GOTERM_BP_ALL	alcohol catabolic process	RT	3	3.4E-1	1.0E0
☐	GOTERM_BP_ALL	cellular carbohydrate catabolic process	RT	3	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	alcohol metabolic process	RT	7	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	carbohydrate catabolic process	RT	3	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	hexose metabolic process	RT	4	5.2E-1	1.0E0
☐	GOTERM_BP_ALL	monosaccharide metabolic process	RT	4	5.3E-1	1.0E0
☐	GOTERM_BP_ALL	carbohydrate metabolic process	RT	6	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	cellular carbohydrate metabolic process	RT	4	9.0E-1	1.0E0
☐	GOTERM_MF_ALL	magnesium ion binding	RT	5	9.0E-1	1.0E0
	Annotation Cluster 59	Enrichment Score: 0.34	G 🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	basement membrane	RT	3	1.2E-1	9.7E-1
☐	SP_PIR_KEYWORDS	calcium binding	RT	3	2.8E-1	1.0E0
☐	GOTERM_BP_ALL	extracellular matrix organization and biogenesis	RT	3	3.4E-1	1.0E0
☐	GOTERM_BP_ALL	extracellular structure organization and biogenesis	RT	4	3.4E-1	1.0E0
☐	GOTERM_CC_ALL	basement membrane	RT	3	3.5E-1	1.0E0
☐	GOTERM_CC_ALL	extracellular matrix part	RT	3	5.8E-1	1.0E0
☐	GOTERM_CC_ALL	proteinaceous extracellular matrix	RT	5	7.9E-1	1.0E0
☐	GOTERM_CC_ALL	extracellular matrix	RT	5	8.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	extracellular matrix	RT	3	8.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	Secreted	RT	13	9.9E-1	1.0E0
	Annotation Cluster 60	Enrichment Score: 0.28	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	visual perception	RT	4	3.0E-1	1.0E0
☐	GOTERM_BP_ALL	sensory perception of light stimulus	RT	4	3.1E-1	1.0E0
☐	GOTERM_BP_ALL	sensory perception of sound	RT	3	3.6E-1	1.0E0
☐	GOTERM_BP_ALL	sensory perception of mechanical stimulus	RT	3	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	sensory perception	RT	5	7.8E-1	1.0E0
☐	GOTERM_BP_ALL	neurological system process	RT	7	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	system process	RT	7	9.9E-1	1.0E0
	Annotation Cluster 61	Enrichment Score: 0.27	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	translational initiation	RT	3	2.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	initiation factor	RT	3	3.6E-1	1.0E0
☐	GOTERM_MF_ALL	translation initiation factor activity	RT	3	4.4E-1	1.0E0
☐	GOTERM_BP_ALL	protein-RNA complex assembly	RT	3	4.7E-1	1.0E0
☐	GOTERM_MF_ALL	translation factor activity, nucleic acid binding	RT	3	6.5E-1	1.0E0
☐	GOTERM_MF_ALL	translation regulator activity	RT	3	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	translation	RT	7	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	ribonucleoprotein complex biogenesis and assembly	RT	3	9.0E-1	1.0E0
	Annotation Cluster 62	Enrichment Score: 0.27	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of protein metabolic process	RT	10	7.7E-2	1.0E0
☐	GOTERM_BP_ALL	regulation of translation	RT	4	5.4E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cellular biosynthetic process	RT	4	5.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of biosynthetic process	RT	4	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	biosynthetic process	RT	22	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	cellular biosynthetic process	RT	15	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	translation	RT	7	8.5E-1	1.0E0

☐	GOTERM_BP_ALL	macromolecule biosynthetic process	RT		10	9.0E-1	1.0E0
	Annotation Cluster 63	Enrichment Score: 0.25	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	nucleoplasm	RT		14	3.6E-1	1.0E0
☐	GOTERM_CC_ALL	nuclear lumen	RT		16	4.2E-1	1.0E0
☐	GOTERM_CC_ALL	organelle lumen	RT		17	5.1E-1	1.0E0
☐	GOTERM_CC_ALL	membrane-enclosed lumen	RT		17	5.1E-1	1.0E0
☐	GOTERM_CC_ALL	transcription factor complex	RT		9	5.9E-1	1.0E0
☐	GOTERM_CC_ALL	nucleoplasm part	RT		11	6.4E-1	1.0E0
☐	GOTERM_CC_ALL	nuclear part	RT		19	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	transcription from RNA polymerase II promoter	RT		6	9.4E-1	1.0E0
	Annotation Cluster 64	Enrichment Score: 0.25	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, PHD-type	RT		3	4.2E-1	1.0E0
☐	SMART	PHD	RT		3	4.6E-1	1.0E0
☐	SMART	RING	RT		5	6.8E-1	1.0E0
☐	INTERPRO	Zinc finger, RING-type	RT		4	7.9E-1	1.0E0
	Annotation Cluster 65	Enrichment Score: 0.23	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	immune effector process	RT		5	2.6E-1	1.0E0
☐	GOTERM_BP_ALL	activation of immune response	RT		3	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of immune response	RT		3	5.5E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of immune system process	RT		3	5.6E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of immune response	RT		3	6.2E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of immune system process	RT		3	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of multicellular organismal process	RT		3	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of multicellular organismal process	RT		6	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	inflammatory response	RT		4	8.0E-1	1.0E0
☐	GOTERM_BP_ALL	defense response	RT		5	9.7E-1	1.0E0
	Annotation Cluster 66	Enrichment Score: 0.2	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cellular homeostasis	RT		6	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	homeostatic process	RT		8	5.2E-1	1.0E0
☐	GOTERM_BP_ALL	cellular di-, tri-valent inorganic cation homeostasis	RT		3	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	di-, tri-valent inorganic cation homeostasis	RT		3	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	cellular chemical homeostasis	RT		4	6.4E-1	1.0E0
☐	GOTERM_BP_ALL	cellular ion homeostasis	RT		4	6.4E-1	1.0E0
☐	GOTERM_BP_ALL	cellular cation homeostasis	RT		3	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	cation homeostasis	RT		3	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	ion homeostasis	RT		4	7.1E-1	1.0E0
☐	GOTERM_BP_ALL	chemical homeostasis	RT		4	8.2E-1	1.0E0
	Annotation Cluster 67	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	mitochondrion organization and biogenesis	RT		4	1.8E-1	1.0E0
☐	GOTERM_CC_ALL	organelle membrane	RT		13	5.2E-1	1.0E0
☐	GOTERM_CC_ALL	organelle envelope	RT		8	6.7E-1	1.0E0
☐	GOTERM_CC_ALL	envelope	RT		8	6.7E-1	1.0E0
☐	GOTERM_CC_ALL	nuclear envelope	RT		3	6.8E-1	1.0E0
☐	GOTERM_CC_ALL	mitochondrial membrane	RT		5	7.5E-1	1.0E0
☐	GOTERM_CC_ALL	mitochondrial envelope	RT		5	8.0E-1	1.0E0
☐	GOTERM_CC_ALL	mitochondrial inner membrane	RT		4	8.4E-1	1.0E0
☐	GOTERM_CC_ALL	organelle inner membrane	RT		4	8.6E-1	1.0E0

☐	**GOTERM_CC_ALL**	mitochondrial part	RT	▮		5	8.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Mitochondrion	RT	▮		7	9.7E-1	1.0E0
	Annotation Cluster 68	Enrichment Score: 0.18	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	muscle development	RT	▮		5	4.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	myeloid cell differentiation	RT	▮		3	6.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	hemopoiesis	RT	▮		5	6.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	hemopoietic or lymphoid organ development	RT	▮		5	7.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	leukocyte differentiation	RT	▮		3	7.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	immune system development	RT	▮		5	7.8E-1	1.0E0
	Annotation Cluster 69	Enrichment Score: 0.16	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Pleckstrin-like	RT	▮		5	5.3E-1	1.0E0
☐	**SMART**	PH	RT	▮		5	6.0E-1	1.0E0
☐	**INTERPRO**	Pleckstrin homology-type	RT	▮		4	8.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	GTPase regulator activity	RT	▮		4	9.4E-1	1.0E0
	Annotation Cluster 70	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Magnesium	RT	▮		3	4.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	magnesium ion binding	RT	▮		5	9.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	magnesium	RT	▮		4	9.4E-1	1.0E0
	Annotation Cluster 71	Enrichment Score: 0.12	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	secretion	RT	▮		6	7.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	secretion by cell	RT	▮		5	7.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	secretory pathway	RT	▮		4	8.0E-1	1.0E0
	Annotation Cluster 72	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	generation of neurons	RT	▮		7	6.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	neuron differentiation	RT	▮		6	6.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	neurogenesis	RT	▮		7	6.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	nervous system development	RT	▮		12	6.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular morphogenesis during differentiation	RT	▮		3	8.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	neurite development	RT	▮		3	9.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell part morphogenesis	RT	▮		4	9.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell projection morphogenesis	RT	▮		4	9.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell projection organization and biogenesis	RT	▮		4	9.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	neuron development	RT	▮		3	9.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	central nervous system development	RT	▮		3	9.5E-1	1.0E0
	Annotation Cluster 73	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	mRNA processing	RT	▮		4	8.1E-1	1.0E0
☐	**SMART**	RRM	RT	▮		3	8.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	mRNA metabolic process	RT	▮		4	8.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	RNA processing	RT	▮		5	9.3E-1	1.0E0
	Annotation Cluster 74	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of signal transduction	RT	▮		7	8.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of small GTPase mediated signal transduction	RT	▮		3	8.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	GTPase regulator activity	RT	▮		4	9.4E-1	1.0E0
	Annotation Cluster 75	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	rna-binding	RT	▮		7	7.2E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	ribonucleoprotein	RT	▮		3	9.4E-1	1.0E0
☐	**GOTERM_CC_ALL**	ribonucleoprotein complex	RT	▮		3	1.0E0	1.0E0
	Annotation Cluster 76	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	carboxylic acid metabolic process	RT	▮		8	8.3E-1	1.0E0

☐	**GOTERM_BP_ALL**	organic acid metabolic process	**RT**		8	8.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	amino acid metabolic process	**RT**		4	8.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	amino acid and derivative metabolic process	**RT**		5	8.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	monocarboxylic acid metabolic process	**RT**		3	9.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	amine metabolic process	**RT**		5	9.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	nitrogen compound metabolic process	**RT**		5	9.5E-1	1.0E0
	Annotation Cluster 77	Enrichment Score: 0.03	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	receptor	**RT**		18	9.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	signal transducer activity	**RT**		26	9.2E-1	1.0E0
☐	**GOTERM_MF_ALL**	molecular transducer activity	**RT**		26	9.2E-1	1.0E0
☐	**GOTERM_MF_ALL**	receptor activity	**RT**		19	9.8E-1	1.0E0
	Annotation Cluster 78	Enrichment Score: 0.02	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	negative regulation of metabolic process	**RT**		6	8.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	**RT**		3	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	negative regulation of cellular metabolic process	**RT**		3	9.9E-1	1.0E0
	Annotation Cluster 79	Enrichment Score: 0.02	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Zinc finger, C2H2-like	**RT**		5	8.9E-1	1.0E0
☐	**SMART**	ZnF_C2H2	**RT**		5	9.4E-1	1.0E0
☐	**INTERPRO**	Zinc finger, C2H2-type/integrase, DNA-binding	**RT**		3	9.7E-1	1.0E0
☐	**INTERPRO**	Zinc finger, C2H2-type	**RT**		5	9.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	zinc-finger	**RT**		14	9.9E-1	1.0E0
	Annotation Cluster 80	Enrichment Score: 0.01	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	transducer	**RT**		6	8.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	rhodopsin-like receptor activity	**RT**		3	9.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	g-protein coupled receptor	**RT**		3	9.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	G-protein coupled receptor activity	**RT**		3	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	transmembrane receptor activity	**RT**		6	1.0E0	1.0E0
	Annotation Cluster 81	Enrichment Score: 0.01	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	metal ion binding	**RT**		54	9.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	ion binding	**RT**		55	9.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	cation binding	**RT**		48	9.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	zinc	**RT**		19	9.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	zinc-finger	**RT**		14	9.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	metal-binding	**RT**		28	9.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	transition metal ion binding	**RT**		30	9.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	zinc ion binding	**RT**		21	1.0E0	1.0E0

160 terms were not clustered.

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Functional Annotation Clustering Of Genes Upregulated >2 in WASP Deficient But Not In WT BMMCs

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					Count	P_Value	Benjamini
	Annotation Cluster 1	Enrichment Score: 9.14	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	nucleus	RT		91	2.2E-14	1.7E-11
☐	SP_PIR_KEYWORDS	nucleus	RT		82	9.3E-13	8.1E-10
☐	GOTERM_CC_ALL	intracellular organelle	RT		122	2.2E-12	8.4E-10
☐	GOTERM_CC_ALL	organelle	RT		122	2.3E-12	6.0E-10
☐	GOTERM_CC_ALL	intracellular part	RT		133	1.6E-11	3.0E-9
☐	GOTERM_CC_ALL	intracellular membrane-bound organelle	RT		112	2.6E-11	4.0E-9
☐	GOTERM_CC_ALL	membrane-bound organelle	RT		112	2.8E-11	3.7E-9
☐	GOTERM_CC_ALL	intracellular	RT		136	5.1E-11	5.6E-9
☐	GOTERM_CC_ALL	cell	RT		150	1.4E-4	7.8E-3
☐	GOTERM_CC_ALL	cell part	RT		150	1.4E-4	7.8E-3
☐	GOTERM_BP_ALL	cellular process	RT		140	2.2E-2	9.0E-1
	Annotation Cluster 2	Enrichment Score: 4.49	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	nucleus	RT		82	9.3E-13	8.1E-10
☐	GOTERM_BP_ALL	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		76	2.7E-9	6.9E-6
☐	GOTERM_BP_ALL	biopolymer metabolic process	RT		84	3.9E-6	2.9E-3
☐	GOTERM_BP_ALL	RNA metabolic process	RT		55	1.9E-5	1.2E-2
☐	GOTERM_BP_ALL	gene expression	RT		59	1.6E-4	4.5E-2
☐	GOTERM_BP_ALL	macromolecule metabolic process	RT		95	5.8E-4	1.2E-1
☐	GOTERM_BP_ALL	cellular metabolic process	RT		100	1.0E-2	7.1E-1
☐	GOTERM_BP_ALL	primary metabolic process	RT		100	1.0E-2	7.1E-1
☐	GOTERM_BP_ALL	cellular process	RT		140	2.2E-2	9.0E-1
☐	GOTERM_BP_ALL	metabolic process	RT		106	3.4E-2	9.6E-1
	Annotation Cluster 3	Enrichment Score: 4.35	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	intracellular organelle part	RT		57	4.6E-8	4.5E-6
☐	GOTERM_CC_ALL	organelle part	RT		57	5.4E-8	4.6E-6
☐	GOTERM_CC_ALL	nuclear part	RT		31	3.0E-6	2.1E-4
☐	GOTERM_CC_ALL	macromolecular complex	RT		41	4.1E-4	1.8E-2
☐	GOTERM_CC_ALL	intracellular non-membrane-bound organelle	RT		31	1.0E-3	3.7E-2
☐	GOTERM_CC_ALL	non-membrane-bound organelle	RT		31	1.0E-3	3.7E-2
☐	GOTERM_CC_ALL	protein complex	RT		26	1.1E-1	8.7E-1
	Annotation Cluster 4	Enrichment Score: 4.27	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	RNA processing	RT		24	3.4E-10	1.7E-6
☐	GOTERM_BP_ALL	mRNA processing	RT		18	5.0E-9	8.6E-6
☐	GOTERM_BP_ALL	mRNA metabolic process	RT		19	5.6E-9	7.2E-6
☐	SP_PIR_KEYWORDS	mrna processing	RT		16	2.1E-8	9.2E-6
☐	GOTERM_BP_ALL	RNA splicing	RT		15	7.4E-8	7.7E-5
☐	GOTERM_CC_ALL	spliceosome	RT		11	2.3E-6	1.8E-4
☐	SP_PIR_KEYWORDS	mrna splicing	RT		12	3.3E-6	9.7E-4

☐	**GOTERM_CC_ALL**	ribonucleoprotein complex	RT	17	2.5E-5	1.6E-3
☐	**SP_PIR_KEYWORDS**	spliceosome	RT	9	3.8E-5	6.5E-3
☐	**GOTERM_BP_ALL**	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	RT	7	6.4E-5	3.0E-2
☐	**GOTERM_BP_ALL**	RNA splicing, via transesterification reactions	RT	7	6.4E-5	3.0E-2
☐	**GOTERM_BP_ALL**	nuclear mRNA splicing, via spliceosome	RT	7	6.4E-5	3.0E-2
☐	**GOTERM_BP_ALL**	spliceosome assembly	RT	4	3.5E-3	4.8E-1
☐	**GOTERM_BP_ALL**	ribonucleoprotein complex biogenesis and assembly	RT	9	4.3E-3	5.2E-1
☐	**GOTERM_BP_ALL**	macromolecular complex assembly	RT	11	1.1E-2	7.3E-1
☐	**GOTERM_BP_ALL**	protein-RNA complex assembly	RT	5	2.2E-2	8.9E-1
☐	**GOTERM_BP_ALL**	cellular component assembly	RT	11	3.1E-2	9.5E-1
☐	**SMART**	RRM	RT	4	2.0E-1	1.0E0
☐	**INTERPRO**	Nucleotide-binding, alpha-beta plait	RT	4	2.5E-1	1.0E0
☐	**INTERPRO**	RNA recognition motif, RNP-1	RT	4	2.5E-1	1.0E0
	Annotation Cluster 5	Enrichment Score: 3.61	G	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	mitosis	RT	10	2.2E-5	4.7E-3
☐	**GOTERM_BP_ALL**	mitotic cell cycle	RT	13	6.5E-5	2.6E-2
☐	**GOTERM_BP_ALL**	cell cycle	RT	23	1.0E-4	3.6E-2
☐	**GOTERM_BP_ALL**	mitosis	RT	11	1.1E-4	3.6E-2
☐	**GOTERM_BP_ALL**	M phase of mitotic cell cycle	RT	11	1.1E-4	3.5E-2
☐	**GOTERM_BP_ALL**	cell cycle process	RT	20	1.2E-4	3.6E-2
☐	**SP_PIR_KEYWORDS**	cell cycle	RT	15	2.0E-4	2.5E-2
☐	**GOTERM_BP_ALL**	cell cycle phase	RT	13	3.0E-4	7.1E-2
☐	**SP_PIR_KEYWORDS**	cell division	RT	10	6.6E-4	6.1E-2
☐	**GOTERM_BP_ALL**	M phase	RT	11	1.0E-3	1.9E-1
☐	**GOTERM_BP_ALL**	cell division	RT	11	1.0E-3	1.9E-1
☐	**GOTERM_BP_ALL**	chromosome segregation	RT	5	5.4E-3	5.8E-1
	Annotation Cluster 6	Enrichment Score: 3.25	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	DNA metabolic process	RT	24	2.7E-6	2.3E-3
☐	**SP_PIR_KEYWORDS**	DNA damage	RT	10	6.8E-5	9.8E-3
☐	**SP_PIR_KEYWORDS**	DNA repair	RT	9	2.1E-4	2.3E-2
☐	**GOTERM_BP_ALL**	DNA repair	RT	11	2.2E-4	5.7E-2
☐	**GOTERM_BP_ALL**	response to endogenous stimulus	RT	13	2.4E-4	6.0E-2
☐	**GOTERM_BP_ALL**	response to DNA damage stimulus	RT	12	3.1E-4	7.1E-2
☐	**GOTERM_BP_ALL**	response to stress	RT	17	5.2E-2	9.9E-1
☐	**GOTERM_BP_ALL**	response to stimulus	RT	26	2.9E-1	1.0E0
	Annotation Cluster 7	Enrichment Score: 2.46	G	Count	P_Value	Benjamini
☐	**KEGG_PATHWAY**	Pyrimidine metabolism	RT	6	7.8E-4	1.5E-1
☐	**KEGG_PATHWAY**	DNA polymerase	RT	4	1.1E-3	1.1E-1
☐	**SP_PIR_KEYWORDS**	DNA-directed DNA polymerase	RT	4	1.9E-3	1.4E-1
☐	**GOTERM_MF_ALL**	DNA-directed DNA polymerase activity	RT	4	4.4E-3	1.0E0
☐	**KEGG_PATHWAY**	Purine metabolism	RT	6	6.3E-3	3.6E-1
☐	**GOTERM_MF_ALL**	nucleotidyltransferase activity	RT	6	1.1E-2	1.0E0
☐	**SP_PIR_KEYWORDS**	Nucleotidyltransferase	RT	5	1.2E-2	4.6E-1
	Annotation Cluster 8	Enrichment Score: 2.34	G	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	microtubule cytoskeleton	RT	13	2.6E-4	1.2E-2
☐	**GOTERM_CC_ALL**	centrosome	RT	6	5.6E-4	2.2E-2
☐	**GOTERM_CC_ALL**	microtubule organizing center	RT	6	1.5E-3	5.3E-2
☐	**GOTERM_BP_ALL**	centrosome cycle	RT	3	7.8E-3	6.5E-1

☐	**GOTERM_CC_ALL**	cytoskeletal part	RT	14	8.4E-3	2.1E-1
☐	**GOTERM_BP_ALL**	centrosome organization and biogenesis	RT	3	1.3E-2	7.6E-1
☐	**GOTERM_BP_ALL**	microtubule organizing center organization and biogenesis	RT	3	1.4E-2	7.8E-1
☐	**GOTERM_CC_ALL**	cytoskeleton	RT	16	7.3E-2	7.9E-1
	Annotation Cluster 9	Enrichment Score: 2.17	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	nuclear chromosome part	RT	7	1.7E-4	8.6E-3
☐	**GOTERM_CC_ALL**	nuclear chromosome	RT	7	4.9E-4	2.1E-2
☐	**GOTERM_CC_ALL**	chromosome	RT	11	3.7E-3	1.2E-1
☐	**GOTERM_CC_ALL**	chromosomal part	RT	10	4.7E-3	1.4E-1
☐	**GOTERM_CC_ALL**	chromosome, pericentric region	RT	5	6.8E-3	1.8E-1
☐	**GOTERM_CC_ALL**	condensed chromosome	RT	4	2.5E-2	4.6E-1
☐	**GOTERM_CC_ALL**	condensed nuclear chromosome	RT	3	6.2E-2	7.4E-1
☐	**GOTERM_CC_ALL**	chromatin	RT	4	2.8E-1	9.9E-1
	Annotation Cluster 10	Enrichment Score: 1.99	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	DNA-dependent DNA replication	RT	5	5.7E-3	5.8E-1
☐	**GOTERM_BP_ALL**	mismatch repair	RT	3	1.3E-2	7.6E-1
☐	**GOTERM_BP_ALL**	maintenance of fidelity during DNA-dependent DNA replication	RT	3	1.4E-2	7.8E-1
	Annotation Cluster 11	Enrichment Score: 1.79	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	76	2.7E-9	6.9E-6
☐	**GOTERM_BP_ALL**	biopolymer metabolic process	RT	84	3.9E-6	2.9E-3
☐	**GOTERM_BP_ALL**	RNA metabolic process	RT	55	1.9E-5	1.2E-2
☐	**GOTERM_BP_ALL**	gene expression	RT	59	1.6E-4	4.5E-2
☐	**GOTERM_MF_ALL**	nucleic acid binding	RT	48	1.7E-2	1.0E0
☐	**GOTERM_MF_ALL**	DNA binding	RT	31	5.6E-2	1.0E0
☐	**GOTERM_BP_ALL**	transcription	RT	37	6.7E-2	1.0E0
☐	**GOTERM_BP_ALL**	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	36	8.2E-2	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cellular metabolic process	RT	38	1.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	transcription, DNA-dependent	RT	33	1.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of gene expression	RT	36	1.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	RNA biosynthetic process	RT	33	1.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of transcription	RT	34	1.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of metabolic process	RT	38	1.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Transcription	RT	21	1.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of transcription, DNA-dependent	RT	31	2.2E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Transcription regulation	RT	20	2.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cellular process	RT	50	3.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of biological process	RT	50	6.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	biological regulation	RT	54	6.8E-1	1.0E0
	Annotation Cluster 12	Enrichment Score: 1.78	G 🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Tetratricopeptide-like helical	RT	7	1.3E-3	1.0E0
☐	**SMART**	TPR	RT	6	1.7E-3	6.3E-1
☐	**INTERPRO**	Tetratricopeptide region	RT	6	4.4E-3	1.0E0
☐	**INTERPRO**	Tetratricopeptide TPR-1	RT	5	1.0E-2	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:TPR 4	RT	4	1.1E-2	1.0E0
☐	**SP_PIR_KEYWORDS**	TPR repeat	RT	6	1.4E-2	4.8E-1
☐	**UP_SEQ_FEATURE**	repeat:TPR 3	RT	4	3.0E-2	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:TPR 2	RT	4	3.7E-2	1.0E0

☐	UP_SEQ_FEATURE	repeat:TPR 1	RT	4	3.7E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 7	RT	3	4.4E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 6	RT	3	5.0E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 5	RT	3	5.3E-2	1.0E0
☐	INTERPRO	Tetratricopeptide TPR2	RT	3	1.1E-1	1.0E0
	Annotation Cluster 13	Enrichment Score: 1.77	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	nucleocytoplasmic transport	RT	7	3.5E-3	4.9E-1
☐	GOTERM_BP_ALL	nuclear transport	RT	7	3.6E-3	4.8E-1
☐	GOTERM_BP_ALL	mRNA transport	RT	5	5.1E-3	5.7E-1
☐	GOTERM_BP_ALL	nucleic acid transport	RT	5	6.9E-3	6.3E-1
☐	GOTERM_BP_ALL	RNA transport	RT	5	6.9E-3	6.3E-1
☐	GOTERM_BP_ALL	establishment of RNA localization	RT	5	6.9E-3	6.3E-1
☐	GOTERM_BP_ALL	RNA localization	RT	5	7.3E-3	6.3E-1
☐	GOTERM_BP_ALL	nucleobase, nucleoside, nucleotide and nucleic acid transport	RT	5	8.6E-3	6.7E-1
☐	GOTERM_BP_ALL	nuclear export	RT	4	1.1E-2	7.2E-1
☐	SP_PIR_KEYWORDS	mrna transport	RT	4	1.5E-2	5.1E-1
☐	GOTERM_BP_ALL	nuclear import	RT	3	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	intracellular protein transport	RT	8	3.0E-1	1.0E0
☐	GOTERM_CC_ALL	endomembrane system	RT	5	6.5E-1	1.0E0
	Annotation Cluster 14	Enrichment Score: 1.7	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	microtubule cytoskeleton	RT	13	2.6E-4	1.2E-2
☐	GOTERM_CC_ALL	intracellular non-membrane-bound organelle	RT	31	1.0E-3	3.7E-2
☐	GOTERM_CC_ALL	non-membrane-bound organelle	RT	31	1.0E-3	3.7E-2
☐	SP_PIR_KEYWORDS	microtubule	RT	8	2.6E-3	1.6E-1
☐	GOTERM_CC_ALL	microtubule	RT	8	6.5E-3	1.8E-1
☐	GOTERM_CC_ALL	cytoskeletal part	RT	14	8.4E-3	2.1E-1
☐	GOTERM_CC_ALL	cytoskeleton	RT	16	7.3E-2	7.9E-1
☐	GOTERM_BP_ALL	microtubule-based process	RT	6	9.9E-2	1.0E0
☐	GOTERM_BP_ALL	microtubule cytoskeleton organization and biogenesis	RT	3	2.4E-1	1.0E0
☐	GOTERM_BP_ALL	microtubule-based movement	RT	3	3.7E-1	1.0E0
☐	GOTERM_BP_ALL	cytoskeleton organization and biogenesis	RT	8	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	cytoskeleton-dependent intracellular transport	RT	3	4.4E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 1.21	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	nucleocytoplasmic transport	RT	7	3.5E-3	4.9E-1
☐	GOTERM_BP_ALL	nuclear transport	RT	7	3.6E-3	4.8E-1
☐	GOTERM_CC_ALL	organelle envelope	RT	11	2.1E-2	4.1E-1
☐	GOTERM_CC_ALL	nuclear pore	RT	4	2.3E-2	4.4E-1
☐	GOTERM_CC_ALL	pore complex	RT	4	3.0E-2	5.1E-1
☐	GOTERM_CC_ALL	nuclear membrane part	RT	4	3.8E-2	5.9E-1
☐	GOTERM_CC_ALL	nuclear membrane	RT	4	4.3E-2	6.2E-1
☐	SP_PIR_KEYWORDS	protein transport	RT	10	6.0E-2	8.9E-1
☐	GOTERM_BP_ALL	protein transport	RT	13	1.5E-1	1.0E0
☐	GOTERM_CC_ALL	nuclear envelope	RT	4	1.7E-1	9.5E-1
☐	GOTERM_CC_ALL	organelle membrane	RT	11	1.8E-1	9.6E-1
☐	GOTERM_BP_ALL	establishment of protein localization	RT	13	2.0E-1	1.0E0
☐	GOTERM_BP_ALL	protein localization	RT	13	2.8E-1	1.0E0
☐	GOTERM_BP_ALL	intracellular protein transport	RT	8	3.0E-1	1.0E0
☐	GOTERM_CC_ALL	endomembrane system	RT	5	6.5E-1	1.0E0

	Annotation Cluster 16	Enrichment Score: 1.06	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	repeat:WD 6	RT	5	2.5E-2	1.0E0
☐	SMART	WD40	RT	6	3.7E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 5	RT	5	5.7E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 4	RT	5	7.0E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 3	RT	5	8.2E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 1	RT	5	8.6E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 2	RT	5	8.6E-2	1.0E0
☐	SP_PIR_KEYWORDS	wd repeat	RT	6	1.7E-1	9.9E-1
☐	UP_SEQ_FEATURE	repeat:WD 7	RT	3	1.8E-1	1.0E0
☐	INTERPRO	WD40 repeat	RT	4	3.8E-1	1.0E0
	Annotation Cluster 17	Enrichment Score: 0.95	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	outer membrane	RT	5	1.3E-2	2.9E-1
☐	GOTERM_MF_ALL	porin activity	RT	3	3.8E-2	1.0E0
☐	SP_PIR_KEYWORDS	porin	RT	3	5.0E-2	8.6E-1
☐	GOTERM_MF_ALL	wide pore channel activity	RT	3	9.1E-2	1.0E0
☐	GOTERM_MF_ALL	channel activity	RT	3	9.3E-1	1.0E0
☐	GOTERM_MF_ALL	passive transmembrane transporter activity	RT	3	9.3E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 0.92	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	decarboxylase	RT	3	3.6E-2	7.8E-1
☐	GOTERM_MF_ALL	carboxy-lyase activity	RT	3	5.5E-2	1.0E0
☐	GOTERM_MF_ALL	carbon-carbon lyase activity	RT	3	9.8E-2	1.0E0
☐	GOTERM_MF_ALL	lyase activity	RT	4	3.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	lyase	RT	3	4.3E-1	1.0E0
	Annotation Cluster 19	Enrichment Score: 0.83	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	10	1.4E-2	7.8E-1
☐	GOTERM_BP_ALL	negative regulation of cellular metabolic process	RT	10	3.3E-2	9.6E-1
☐	GOTERM_BP_ALL	negative regulation of metabolic process	RT	10	6.4E-2	1.0E0
☐	GOTERM_BP_ALL	negative regulation of transcription	RT	7	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of cellular process	RT	17	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of biological process	RT	17	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of transcription from RNA polymerase II promoter	RT	4	2.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of transcription from RNA polymerase II promoter	RT	7	4.4E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of transcription, DNA-dependent	RT	4	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	transcription from RNA polymerase II promoter	RT	7	5.4E-1	1.0E0
	Annotation Cluster 20	Enrichment Score: 0.82	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	ATP binding	RT	22	9.0E-2	1.0E0
☐	GOTERM_MF_ALL	adenyl ribonucleotide binding	RT	22	9.9E-2	1.0E0
☐	GOTERM_MF_ALL	nucleotide binding	RT	29	1.4E-1	1.0E0
☐	GOTERM_MF_ALL	adenyl nucleotide binding	RT	22	1.4E-1	1.0E0
☐	GOTERM_MF_ALL	purine ribonucleotide binding	RT	25	1.4E-1	1.0E0
☐	GOTERM_MF_ALL	ribonucleotide binding	RT	25	1.4E-1	1.0E0
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT	12	1.5E-1	1.0E0
☐	GOTERM_MF_ALL	purine nucleotide binding	RT	25	1.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	atp-binding	RT	17	2.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT	20	2.9E-1	1.0E0
	Annotation Cluster 21	Enrichment Score: 0.69	G	Count	P_Value	Benjamini

☐	GOTERM_MF_ALL	acid phosphatase activity	RT	3	1.3E-2	1.0E0
☐	GOTERM_MF_ALL	phosphoric monoester hydrolase activity	RT	3	7.6E-1	1.0E0
☐	GOTERM_MF_ALL	phosphoric ester hydrolase activity	RT	3	8.6E-1	1.0E0
	Annotation Cluster 22	Enrichment Score: 0.69	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:Helicase C-terminal	RT	3	1.3E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Helicase ATP-binding	RT	3	1.5E-1	1.0E0
☐	GOTERM_MF_ALL	helicase activity	RT	4	2.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	helicase	RT	3	4.1E-1	1.0E0
	Annotation Cluster 23	Enrichment Score: 0.68	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	envelope	RT	12	8.4E-3	2.1E-1
☐	GOTERM_CC_ALL	organelle envelope	RT	11	2.1E-2	4.1E-1
☐	GOTERM_CC_ALL	mitochondrial part	RT	9	4.3E-2	6.1E-1
☐	SP_PIR_KEYWORDS	Mitochondrion	RT	14	4.6E-2	8.5E-1
☐	GOTERM_CC_ALL	mitochondrial envelope	RT	7	1.2E-1	8.9E-1
☐	GOTERM_CC_ALL	mitochondrial inner membrane	RT	6	1.5E-1	9.4E-1
☐	GOTERM_CC_ALL	mitochondrion	RT	15	1.5E-1	9.4E-1
☐	GOTERM_CC_ALL	organelle inner membrane	RT	6	1.7E-1	9.6E-1
☐	GOTERM_CC_ALL	organelle membrane	RT	11	1.8E-1	9.6E-1
☐	GOTERM_CC_ALL	mitochondrial membrane	RT	6	2.0E-1	9.7E-1
☐	GOTERM_CC_ALL	cytoplasmic part	RT	36	6.2E-1	1.0E0
☐	GOTERM_MF_ALL	substrate-specific transmembrane transporter activity	RT	7	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	metal ion transport	RT	3	9.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	ion transport	RT	3	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	cation transport	RT	3	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	ion transmembrane transporter activity	RT	3	1.0E0	1.0E0
☐	GOTERM_BP_ALL	ion transport	RT	4	1.0E0	1.0E0
	Annotation Cluster 24	Enrichment Score: 0.61	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	membrane-enclosed lumen	RT	15	9.6E-2	8.6E-1
☐	GOTERM_CC_ALL	organelle lumen	RT	15	9.6E-2	8.6E-1
☐	GOTERM_CC_ALL	nuclear lumen	RT	12	2.2E-1	9.8E-1
☐	GOTERM_CC_ALL	nucleoplasm	RT	10	2.6E-1	9.9E-1
☐	GOTERM_CC_ALL	nucleoplasm part	RT	8	4.8E-1	1.0E0
☐	GOTERM_CC_ALL	transcription factor complex	RT	4	8.8E-1	1.0E0
	Annotation Cluster 25	Enrichment Score: 0.6	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein folding	RT	6	1.2E-1	1.0E0
☐	GOTERM_MF_ALL	isomerase activity	RT	4	2.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	isomerase	RT	3	4.5E-1	1.0E0
	Annotation Cluster 26	Enrichment Score: 0.6	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein ubiquitination	RT	5	5.7E-3	5.8E-1
☐	GOTERM_BP_ALL	protein modification by small protein conjugation	RT	5	8.6E-3	6.7E-1
☐	GOTERM_BP_ALL	ubiquitin cycle	RT	10	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	biopolymer modification	RT	19	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	protein modification process	RT	16	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	cellular protein metabolic process	RT	30	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	cellular macromolecule metabolic process	RT	30	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	protein metabolic process	RT	31	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	post-translational protein modification	RT	12	9.6E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 0.58	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	transferase activity, transferring phosphorus-containing groups	RT	18	7.6E-2	1.0E0

☐	GOTERM_MF_ALL	transferase activity	RT	28	8.5E-2	1.0E0
☐	GOTERM_MF_ALL	kinase activity	RT	12	4.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	transferase	RT	17	5.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	kinase	RT	8	7.9E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 0.55	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	protein transport	RT	10	6.0E-2	8.9E-1
☐	GOTERM_BP_ALL	intracellular transport	RT	14	8.3E-2	1.0E0
☐	GOTERM_BP_ALL	macromolecule localization	RT	16	8.6E-2	1.0E0
☐	GOTERM_BP_ALL	protein transport	RT	13	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	establishment of protein localization	RT	13	2.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	transport	RT	20	2.4E-1	1.0E0
☐	GOTERM_BP_ALL	establishment of cellular localization	RT	14	2.6E-1	1.0E0
☐	GOTERM_BP_ALL	protein import	RT	3	2.7E-1	1.0E0
☐	GOTERM_BP_ALL	protein localization	RT	13	2.8E-1	1.0E0
☐	GOTERM_BP_ALL	cellular localization	RT	14	2.9E-1	1.0E0
☐	GOTERM_BP_ALL	intracellular protein transport	RT	8	3.0E-1	1.0E0
☐	GOTERM_BP_ALL	protein targeting	RT	5	3.5E-1	1.0E0
☐	GOTERM_MF_ALL	protein transporter activity	RT	3	5.4E-1	1.0E0
☐	GOTERM_BP_ALL	protein complex assembly	RT	3	6.3E-1	1.0E0
☐	GOTERM_CC_ALL	endomembrane system	RT	5	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	transport	RT	30	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	establishment of localization	RT	30	7.4E-1	1.0E0
☐	GOTERM_BP_ALL	localization	RT	34	7.5E-1	1.0E0
	Annotation Cluster 29	Enrichment Score: 0.52	G	Count	P_Value	Benjamini
☐	INTERPRO	Thioredoxin domain	RT	3	2.6E-2	1.0E0
☐	INTERPRO	Thioredoxin-related	RT	3	3.7E-2	1.0E0
☐	GOTERM_BP_ALL	cell redox homeostasis	RT	3	1.4E-1	1.0E0
☐	INTERPRO	Thioredoxin fold	RT	3	2.1E-1	1.0E0
☐	GOTERM_BP_ALL	homeostatic process	RT	7	3.1E-1	1.0E0
☐	GOTERM_MF_ALL	electron carrier activity	RT	4	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of biological quality	RT	8	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	cellular homeostasis	RT	3	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	generation of precursor metabolites and energy	RT	4	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	electron transport	RT	3	9.6E-1	1.0E0
☐	GOTERM_MF_ALL	oxidoreductase activity	RT	4	1.0E0	1.0E0
	Annotation Cluster 30	Enrichment Score: 0.49	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	lung development	RT	3	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	respiratory tube development	RT	3	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	tube development	RT	3	7.3E-1	1.0E0
	Annotation Cluster 31	Enrichment Score: 0.46	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	ribonucleoprotein	RT	6	1.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	ribosomal protein	RT	4	3.6E-1	1.0E0
☐	GOTERM_CC_ALL	ribosome	RT	3	6.0E-1	1.0E0
	Annotation Cluster 32	Enrichment Score: 0.45	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	ligase activity, forming carbon-nitrogen bonds	RT	5	1.6E-1	1.0E0
☐	GOTERM_MF_ALL	ligase activity	RT	7	2.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	ligase	RT	5	3.7E-1	1.0E0
☐	GOTERM_MF_ALL	ubiquitin-protein ligase activity	RT	3	4.2E-1	1.0E0
☐	GOTERM_MF_ALL	small protein conjugating enzyme activity	RT	3	4.3E-1	1.0E0

☐	GOTERM_MF_ALL	small conjugating protein ligase activity	RT		▬	3	4.4E-1	1.0E0
☐	GOTERM_MF_ALL	acid-amino acid ligase activity	RT		▬	3	5.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	Ubl conjugation pathway	RT		▬	6	5.2E-1	1.0E0
	Annotation Cluster 33	Enrichment Score: 0.43		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	chromosome organization and biogenesis	RT		▬	7	2.1E-1	1.0E0
☐	GOTERM_BP_ALL	establishment and/or maintenance of chromatin architecture	RT		▬	5	3.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	Chromatin regulator	RT		▬	3	3.7E-1	1.0E0
☐	GOTERM_BP_ALL	DNA packaging	RT		▬	5	3.9E-1	1.0E0
☐	GOTERM_BP_ALL	chromatin modification	RT		▬	3	6.6E-1	1.0E0
	Annotation Cluster 34	Enrichment Score: 0.41		G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	apoptosis	RT		▬	7	1.1E-1	9.8E-1
☐	GOTERM_BP_ALL	apoptosis	RT		▬	13	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	programmed cell death	RT		▬	13	1.6E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cellular process	RT		▬	16	1.7E-1	1.0E0
☐	GOTERM_BP_ALL	death	RT		▬	13	1.9E-1	1.0E0
☐	GOTERM_BP_ALL	cell death	RT		▬	13	1.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of apoptosis	RT		▬	9	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of biological process	RT		▬	17	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of apoptosis	RT		▬	5	2.3E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of programmed cell death	RT		▬	9	2.3E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of programmed cell death	RT		▬	5	2.4E-1	1.0E0
☐	GOTERM_BP_ALL	cell development	RT		▬	15	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	cell differentiation	RT		▬	19	8.9E-1	1.0E0
☐	GOTERM_BP_ALL	cellular developmental process	RT		▬	19	8.9E-1	1.0E0
☐	GOTERM_BP_ALL	developmental process	RT		▬	28	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	system development	RT		▬	14	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	anatomical structure development	RT		▬	17	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	multicellular organismal development	RT		▬	19	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	organ development	RT		▬	9	1.0E0	1.0E0
☐	GOTERM_BP_ALL	multicellular organismal process	RT		▬	20	1.0E0	1.0E0
	Annotation Cluster 35	Enrichment Score: 0.41		G	🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	mTOR signaling pathway	RT		▬	3	8.1E-2	9.9E-1
☐	KEGG_PATHWAY	Renal cell carcinoma	RT		▬	3	1.4E-1	9.9E-1
☐	KEGG_PATHWAY	Pancreatic cancer	RT		▬	3	1.4E-1	9.9E-1
☐	KEGG_PATHWAY	VEGF signaling pathway	RT		▬	3	1.5E-1	9.9E-1
☐	GOTERM_BP_ALL	transmembrane receptor protein tyrosine kinase signaling pathway	RT		▬	5	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of apoptosis	RT		▬	5	2.3E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of programmed cell death	RT		▬	5	2.4E-1	1.0E0
☐	GOTERM_BP_ALL	homeostatic process	RT		▬	7	3.1E-1	1.0E0
☐	GOTERM_BP_ALL	enzyme linked receptor protein signaling pathway	RT		▬	6	3.3E-1	1.0E0
☐	GOTERM_BP_ALL	developmental maturation	RT		▬	3	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	anti-apoptosis	RT		▬	3	3.8E-1	1.0E0
☐	KEGG_PATHWAY	Focal adhesion	RT		▬	3	5.3E-1	1.0E0
☐	GOTERM_BP_ALL	blood vessel development	RT		▬	4	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	vasculature development	RT		▬	4	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	reproduction	RT		▬	6	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	cell morphogenesis	RT		▬	6	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	cellular structure morphogenesis	RT		▬	6	7.9E-1	1.0E0

☐	GOTERM_BP_ALL	regulation of biological quality	RT	8	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	tissue development	RT	3	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	organ morphogenesis	RT	4	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	anatomical structure morphogenesis	RT	7	1.0E0	1.0E0
	Annotation Cluster 36	Enrichment Score: 0.39	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of apoptosis	RT	9	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of programmed cell death	RT	9	2.3E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of apoptosis	RT	4	4.9E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of programmed cell death	RT	4	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	induction of programmed cell death	RT	3	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	induction of apoptosis	RT	3	6.1E-1	1.0E0
	Annotation Cluster 37	Enrichment Score: 0.34	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, C2H2-type	RT	7	4.2E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 3	RT	3	4.7E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	RT	3	5.0E-1	1.0E0
	Annotation Cluster 38	Enrichment Score: 0.32	G 🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	heparin-binding	RT	3	1.5E-1	9.9E-1
☐	GOTERM_MF_ALL	heparin binding	RT	3	1.9E-1	1.0E0
☐	GOTERM_MF_ALL	carbohydrate binding	RT	6	2.6E-1	1.0E0
☐	GOTERM_MF_ALL	glycosaminoglycan binding	RT	3	2.8E-1	1.0E0
☐	GOTERM_MF_ALL	polysaccharide binding	RT	3	3.1E-1	1.0E0
☐	GOTERM_MF_ALL	pattern binding	RT	3	3.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	growth factor	RT	3	4.8E-1	1.0E0
☐	GOTERM_MF_ALL	growth factor activity	RT	3	5.8E-1	1.0E0
☐	GOTERM_MF_ALL	receptor binding	RT	8	6.2E-1	1.0E0
☐	GOTERM_CC_ALL	extracellular space	RT	8	1.0E0	1.0E0
☐	GOTERM_CC_ALL	extracellular region part	RT	8	1.0E0	1.0E0
☐	GOTERM_CC_ALL	extracellular region	RT	8	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	signal peptide	RT	3	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	signal	RT	4	1.0E0	1.0E0
	Annotation Cluster 39	Enrichment Score: 0.25	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	amino acid derivative metabolic process	RT	3	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	amino acid and derivative metabolic process	RT	5	5.9E-1	1.0E0
☐	GOTERM_BP_ALL	amine metabolic process	RT	5	7.1E-1	1.0E0
☐	GOTERM_BP_ALL	nitrogen compound metabolic process	RT	5	7.7E-1	1.0E0
	Annotation Cluster 40	Enrichment Score: 0.23	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	cysteine-type peptidase activity	RT	4	2.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	thiol protease	RT	3	3.9E-1	1.0E0
☐	GOTERM_BP_ALL	macromolecule catabolic process	RT	6	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	cellular macromolecule catabolic process	RT	5	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	biopolymer catabolic process	RT	5	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	protein catabolic process	RT	4	4.7E-1	1.0E0
☐	GOTERM_BP_ALL	ubiquitin-dependent protein catabolic process	RT	3	5.3E-1	1.0E0
☐	GOTERM_BP_ALL	modification-dependent macromolecule catabolic process	RT	3	5.4E-1	1.0E0
☐	GOTERM_BP_ALL	modification-dependent protein catabolic process	RT	3	5.4E-1	1.0E0
☐	GOTERM_BP_ALL	proteolysis involved in cellular protein catabolic process	RT	3	5.6E-1	1.0E0
☐	GOTERM_BP_ALL	cellular protein catabolic process	RT	3	5.6E-1	1.0E0
☐	GOTERM_BP_ALL	cellular catabolic process	RT	5	8.4E-1	1.0E0

☐	GOTERM_BP_ALL	catabolic process	RT			6	8.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	protease	RT			4	9.4E-1	1.0E0
☐	GOTERM_MF_ALL	peptidase activity	RT			5	9.6E-1	1.0E0
☐	GOTERM_MF_ALL	endopeptidase activity	RT			3	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	proteolysis	RT			5	9.8E-1	1.0E0
	Annotation Cluster 41	Enrichment Score: 0.23	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, C2H2-type	RT			7	4.2E-1	1.0E0
☐	SMART	ZnF_C2H2	RT			4	6.5E-1	1.0E0
☐	INTERPRO	Zinc finger, C2H2-like	RT			4	7.7E-1	1.0E0
	Annotation Cluster 42	Enrichment Score: 0.22	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	nucleoside-triphosphatase activity	RT			8	4.0E-1	1.0E0
☐	GOTERM_MF_ALL	pyrophosphatase activity	RT			8	4.4E-1	1.0E0
☐	GOTERM_MF_ALL	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	RT			8	4.5E-1	1.0E0
☐	GOTERM_MF_ALL	hydrolase activity, acting on acid anhydrides	RT			8	4.6E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity	RT			5	5.0E-1	1.0E0
☐	GOTERM_MF_ALL	GTPase activity	RT			3	5.1E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity, coupled	RT			4	6.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	GTP-binding	RT			3	8.6E-1	1.0E0
☐	GOTERM_MF_ALL	GTP binding	RT			3	9.0E-1	1.0E0
☐	GOTERM_MF_ALL	guanyl nucleotide binding	RT			3	9.0E-1	1.0E0
☐	GOTERM_MF_ALL	guanyl ribonucleotide binding	RT			3	9.0E-1	1.0E0
	Annotation Cluster 43	Enrichment Score: 0.22	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	angiogenesis	RT			3	8.9E-2	9.5E-1
☐	GOTERM_BP_ALL	blood vessel development	RT			4	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	vasculature development	RT			4	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	angiogenesis	RT			3	6.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	differentiation	RT			5	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	reproduction	RT			6	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	blood vessel morphogenesis	RT			3	7.3E-1	1.0E0
☐	GOTERM_BP_ALL	anatomical structure formation	RT			3	7.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	Developmental protein	RT			5	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	organ morphogenesis	RT			4	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	anatomical structure morphogenesis	RT			7	1.0E0	1.0E0
	Annotation Cluster 44	Enrichment Score: 0.21	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	ligase activity	RT			7	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	cellular biosynthetic process	RT			11	7.4E-1	1.0E0
☐	GOTERM_BP_ALL	carboxylic acid metabolic process	RT			4	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	organic acid metabolic process	RT			4	9.5E-1	1.0E0
	Annotation Cluster 45	Enrichment Score: 0.19	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	glucose metabolic process	RT			3	4.1E-1	1.0E0
☐	GOTERM_BP_ALL	hexose metabolic process	RT			3	5.6E-1	1.0E0
☐	GOTERM_BP_ALL	monosaccharide metabolic process	RT			3	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	carbohydrate metabolic process	RT			6	5.9E-1	1.0E0
☐	GOTERM_BP_ALL	alcohol metabolic process	RT			4	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	cellular carbohydrate metabolic process	RT			3	8.7E-1	1.0E0
☐	GOTERM_BP_ALL	macromolecule biosynthetic process	RT			5	9.8E-1	1.0E0
	Annotation Cluster 46	Enrichment Score: 0.18	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	hydrolase activity, acting on ester bonds	RT			9	4.3E-1	1.0E0

☐	GOTERM_MF_ALL	hydrolase activity	RT	▬		23	7.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	hydrolase	RT	▬		13	8.9E-1	1.0E0
	Annotation Cluster 47	Enrichment Score: 0.16	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	gamete generation	RT	▬		4	6.2E-1	1.0E0
☐	GOTERM_BP_ALL	reproduction	RT	▬		6	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	male gamete generation	RT	▬		3	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	spermatogenesis	RT	▬		3	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	sexual reproduction	RT	▬		4	7.4E-1	1.0E0
	Annotation Cluster 48	Enrichment Score: 0.16	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	in utero embryonic development	RT	▬		3	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	chordate embryonic development	RT	▬		3	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	embryonic development ending in birth or egg hatching	RT	▬		3	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	embryonic development	RT	▬		5	8.1E-1	1.0E0
	Annotation Cluster 49	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	positive regulation of signal transduction	RT	▬		3	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	protein kinase cascade	RT	▬		4	7.0E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of signal transduction	RT	▬		4	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	intracellular signaling cascade	RT	▬		8	9.9E-1	1.0E0
	Annotation Cluster 50	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	symporter activity	RT	▬		3	4.9E-1	1.0E0
☐	GOTERM_MF_ALL	secondary active transmembrane transporter activity	RT	▬		3	6.4E-1	1.0E0
☐	GOTERM_MF_ALL	substrate-specific transmembrane transporter activity	RT	▬		7	8.6E-1	1.0E0
☐	GOTERM_MF_ALL	active transmembrane transporter activity	RT	▬		3	9.1E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	positive regulation of transcription	RT	▬		5	6.4E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	▬		5	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of transcription, DNA-dependent	RT	▬		4	7.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	activator	RT	▬		5	7.5E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cellular metabolic process	RT	▬		5	8.0E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of metabolic process	RT	▬		5	8.4E-1	1.0E0
	Annotation Cluster 52	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	lymphocyte activation	RT	▬		3	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	leukocyte activation	RT	▬		3	8.0E-1	1.0E0
☐	GOTERM_BP_ALL	immune system process	RT	▬		8	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	cell activation	RT	▬		3	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	immune system development	RT	▬		3	8.8E-1	1.0E0
	Annotation Cluster 53	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	transporter activity	RT	▬		14	7.2E-1	1.0E0
☐	GOTERM_MF_ALL	substrate-specific transporter activity	RT	▬		10	7.7E-1	1.0E0
☐	GOTERM_MF_ALL	transmembrane transporter activity	RT	▬		9	7.8E-1	1.0E0
☐	GOTERM_MF_ALL	substrate-specific transmembrane transporter activity	RT	▬		7	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	ion transport	RT	▬		4	1.0E0	1.0E0
	Annotation Cluster 54	Enrichment Score: 0.08	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell migration	RT	▬		4	7.4E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cell proliferation	RT	▬		3	7.5E-1	1.0E0
☐	GOTERM_BP_ALL	cell morphogenesis	RT	▬		6	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	cellular structure morphogenesis	RT	▬		6	7.9E-1	1.0E0

☐	GOTERM_BP_ALL	cell proliferation	RT		6	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	localization of cell	RT		4	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	cell motility	RT		4	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of progression through cell cycle	RT		4	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell cycle	RT		4	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell proliferation	RT		4	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	anatomical structure morphogenesis	RT		7	1.0E0	1.0E0
	Annotation Cluster 55	Enrichment Score: 0.08	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	zinc ion binding	RT		22	6.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc-finger	RT		15	6.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	zinc	RT		18	7.7E-1	1.0E0
☐	GOTERM_MF_ALL	transition metal ion binding	RT		25	7.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	metal-binding	RT		20	9.7E-1	1.0E0
☐	GOTERM_MF_ALL	cation binding	RT		28	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	metal ion binding	RT		30	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	ion binding	RT		30	1.0E0	1.0E0
	Annotation Cluster 56	Enrichment Score: 0.06	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cellular biosynthetic process	RT		11	7.4E-1	1.0E0
☐	GOTERM_BP_ALL	biosynthetic process	RT		13	8.7E-1	1.0E0
☐	GOTERM_BP_ALL	translation	RT		4	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	macromolecule biosynthetic process	RT		5	9.8E-1	1.0E0
	Annotation Cluster 57	Enrichment Score: 0.04	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	synaptic transmission	RT		3	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	transmission of nerve impulse	RT		3	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	cell-cell signaling	RT		3	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	neurological system process	RT		3	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	system process	RT		3	1.0E0	1.0E0
	Annotation Cluster 58	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell surface receptor linked signal transduction	RT		10	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	intracellular signaling cascade	RT		8	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	cell communication	RT		21	1.0E0	1.0E0
☐	GOTERM_BP_ALL	signal transduction	RT		18	1.0E0	1.0E0
	Annotation Cluster 59	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	phosphate metabolic process	RT		4	1.0E0	1.0E0
☐	GOTERM_BP_ALL	phosphorus metabolic process	RT		4	1.0E0	1.0E0
☐	GOTERM_BP_ALL	phosphorylation	RT		3	1.0E0	1.0E0
	Annotation Cluster 60	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	receptor	RT		6	1.0E0	1.0E0
☐	GOTERM_MF_ALL	receptor activity	RT		7	1.0E0	1.0E0
☐	GOTERM_MF_ALL	molecular transducer activity	RT		8	1.0E0	1.0E0
☐	GOTERM_MF_ALL	signal transducer activity	RT		8	1.0E0	1.0E0
	Annotation Cluster 61	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	integral to membrane	RT		25	1.0E0	1.0E0
☐	GOTERM_CC_ALL	intrinsic to membrane	RT		25	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	membrane	RT		28	1.0E0	1.0E0
☐	GOTERM_CC_ALL	membrane	RT		41	1.0E0	1.0E0
☐	GOTERM_CC_ALL	membrane part	RT		28	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	transmembrane	RT		14	1.0E0	1.0E0
	Annotation Cluster 62	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	transmembrane region	RT		8	1.0E0	1.0E0

☐	**UP_SEQ_FEATURE**	topological domain:Cytoplasmic	**RT**	▮	4	1.0E0	1.0E0
☐	**UP_SEQ_FEATURE**	glycosylation site:N-linked (GlcNAc...)	**RT**	▮	6	1.0E0	1.0E0

87 terms were not clustered.

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	Annotation Cluster 1	Enrichment Score: 9.43		Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	zinc-finger	RT	170	3.8E-15	3.3E-12
☐	GOTERM_MF_ALL	transition metal ion binding	RT	270	1.2E-11	3.2E-8
☐	GOTERM_MF_ALL	zinc ion binding	RT	224	5.2E-11	6.9E-8
☐	SP_PIR_KEYWORDS	zinc	RT	186	2.0E-10	8.6E-8
☐	GOTERM_MF_ALL	metal ion binding	RT	363	7.4E-9	6.6E-6
☐	SP_PIR_KEYWORDS	metal-binding	RT	231	1.8E-8	3.2E-6
☐	GOTERM_MF_ALL	ion binding	RT	365	4.1E-8	1.8E-5
☐	GOTERM_MF_ALL	cation binding	RT	332	1.3E-7	5.1E-5
	Annotation Cluster 2	Enrichment Score: 6.44		Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	nucleus	RT	404	1.8E-12	1.4E-9
☐	GOTERM_BP_ALL	transcription	RT	262	1.7E-11	8.7E-8
☐	GOTERM_BP_ALL	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	258	2.8E-11	7.1E-8
☐	GOTERM_BP_ALL	regulation of transcription	RT	254	3.2E-11	5.5E-8
☐	GOTERM_BP_ALL	regulation of transcription, DNA-dependent	RT	243	6.9E-11	9.0E-8
☐	GOTERM_BP_ALL	RNA biosynthetic process	RT	245	9.9E-11	1.0E-7
☐	GOTERM_BP_ALL	regulation of gene expression	RT	265	1.2E-10	1.0E-7
☐	GOTERM_BP_ALL	regulation of cellular process	RT	382	1.3E-10	9.5E-8
☐	GOTERM_BP_ALL	transcription, DNA-dependent	RT	244	1.4E-10	8.8E-8
☐	GOTERM_BP_ALL	biopolymer metabolic process	RT	446	2.6E-10	1.5E-7
☐	GOTERM_BP_ALL	regulation of cellular metabolic process	RT	272	2.8E-10	1.4E-7
☐	SP_PIR_KEYWORDS	nucleus	RT	318	7.0E-10	1.5E-7
☐	GOTERM_BP_ALL	regulation of metabolic process	RT	277	1.8E-9	8.6E-7
☐	GOTERM_MF_ALL	DNA binding	RT	218	8.7E-9	5.8E-6
☐	GOTERM_MF_ALL	nucleic acid binding	RT	315	1.1E-8	5.7E-6
☐	GOTERM_BP_ALL	regulation of biological process	RT	399	5.2E-8	2.2E-5
☐	GOTERM_BP_ALL	biological regulation	RT	428	1.6E-7	5.9E-5
☐	GOTERM_CC_ALL	intracellular	RT	748	5.5E-7	2.1E-4
☐	SP_PIR_KEYWORDS	Transcription	RT	146	7.2E-7	1.0E-4
☐	GOTERM_CC_ALL	membrane-bound organelle	RT	553	9.3E-7	2.4E-4
☐	GOTERM_CC_ALL	intracellular membrane-bound organelle	RT	552	1.1E-6	2.1E-4
☐	SP_PIR_KEYWORDS	Transcription regulation	RT	143	1.1E-6	1.3E-4
☐	GOTERM_BP_ALL	RNA metabolic process	RT	261	2.1E-6	6.1E-4
☐	SP_PIR_KEYWORDS	dna-binding	RT	143	2.2E-6	2.2E-4
☐	GOTERM_BP_ALL	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	320	8.9E-6	2.4E-3
☐	GOTERM_BP_ALL	cellular metabolic process	RT	601	1.6E-5	3.9E-3
☐	GOTERM_CC_ALL	intracellular part	RT	703	2.6E-5	4.0E-3
☐	GOTERM_BP_ALL	gene expression	RT	289	1.4E-4	2.5E-2

☐	GOTERM_CC_ALL	cell	RT		963	1.6E-4	1.8E-2
☐	GOTERM_CC_ALL	cell part	RT		963	1.6E-4	1.8E-2
☐	GOTERM_BP_ALL	cellular process	RT		867	1.9E-4	3.4E-2
☐	GOTERM_BP_ALL	macromolecule metabolic process	RT		521	3.6E-4	6.1E-2
☐	GOTERM_CC_ALL	organelle	RT		590	5.1E-4	4.8E-2
☐	GOTERM_BP_ALL	metabolic process	RT		646	5.1E-4	8.2E-2
☐	GOTERM_CC_ALL	intracellular organelle	RT		589	5.8E-4	4.9E-2
☐	GOTERM_MF_ALL	transcription regulator activity	RT		131	6.2E-4	1.4E-1
☐	GOTERM_MF_ALL	binding	RT		872	7.2E-4	1.4E-1
☐	GOTERM_BP_ALL	primary metabolic process	RT		586	9.1E-4	1.3E-1
☐	GOTERM_MF_ALL	transcription factor activity	RT		88	2.6E-2	9.1E-1
☐	GOTERM_MF_ALL	sequence-specific DNA binding	RT		50	4.7E-2	9.5E-1
	Annotation Cluster 3	Enrichment Score: 4.91	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Interferon alpha, beta and delta	RT		13	5.5E-11	1.6E-7
☐	PIR_SUPERFAMILY	PIRSF001934:interferon alpha	RT		13	1.4E-10	4.2E-7
☐	SMART	IFabd	RT		13	2.9E-10	1.8E-7
☐	SP_PIR_KEYWORDS	antiviral defense	RT		16	4.0E-10	1.2E-7
☐	INTERPRO	Interferon alpha	RT		11	1.6E-9	3.1E-6
☐	GOTERM_BP_ALL	response to virus	RT		19	7.8E-8	3.1E-5
☐	KEGG_PATHWAY	Regulation of autophagy	RT		13	7.3E-7	1.5E-4
☐	KEGG_PATHWAY	Cytokine-cytokine receptor interaction	RT		40	1.4E-6	1.5E-4
☐	KEGG_PATHWAY	Jak-STAT signaling pathway	RT		29	3.2E-6	2.3E-4
☐	KEGG_PATHWAY	Toll-like receptor signaling pathway	RT		23	3.7E-6	2.0E-4
☐	KEGG_PATHWAY	Natural killer cell mediated cytotoxicity	RT		21	9.3E-4	3.8E-2
☐	SP_PIR_KEYWORDS	cytokine	RT		26	1.1E-3	6.7E-2
☐	GOTERM_BP_ALL	multi-organism process	RT		31	1.9E-3	2.0E-1
☐	KEGG_PATHWAY	Antigen processing and presentation	RT		15	2.1E-3	7.1E-2
☐	GOTERM_BP_ALL	response to other organism	RT		23	2.5E-3	2.5E-1
☐	GOTERM_BP_ALL	response to biotic stimulus	RT		30	8.7E-3	5.3E-1
☐	INTERPRO	Four-helical cytokine, core	RT		12	1.0E-2	8.7E-1
☐	GOTERM_MF_ALL	cytokine activity	RT		28	1.9E-2	8.7E-1
☐	GOTERM_BP_ALL	defense response	RT		38	5.1E-1	1.0E0
☐	GOTERM_MF_ALL	receptor binding	RT		51	5.6E-1	1.0E0
	Annotation Cluster 4	Enrichment Score: 4.3	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, C2H2-type	RT		67	1.8E-6	2.1E-3
☐	INTERPRO	Zinc finger, C2H2-subtype	RT		33	3.1E-5	3.0E-2
☐	INTERPRO	KRAB box	RT		34	3.5E-5	2.9E-2
☐	COG_ONTOLOGY	General function prediction only	RT		84	5.2E-5	4.1E-3
☐	INTERPRO	Zinc finger, C2H2-type/integrase, DNA-binding	RT		43	7.4E-5	4.7E-2
☐	INTERPRO	Zinc finger, C2H2-like	RT		50	8.9E-5	5.0E-2
☐	SMART	KRAB	RT		36	2.3E-4	6.8E-2
☐	SMART	ZnF_C2H2	RT		57	2.5E-4	5.0E-2
	Annotation Cluster 5	Enrichment Score: 3.54	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	transcription factor binding	RT		39	3.3E-5	1.1E-2
☐	GOTERM_MF_ALL	transcription cofactor activity	RT		28	8.5E-5	2.5E-2
☐	GOTERM_MF_ALL	transcription coactivator activity	RT		17	6.8E-4	1.4E-1
☐	GOTERM_MF_ALL	transcription activator activity	RT		30	3.6E-3	4.4E-1
	Annotation Cluster 6	Enrichment Score: 3.36	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Protocadherin gamma	RT		22	6.9E-23	4.0E-19

☐	**INTERPRO**	Cadherin, N-terminal	RT	▬		22	1.4E-8	2.0E-5
☐	**INTERPRO**	Cadherin	RT	▬		23	4.2E-5	3.0E-2
☐	**SMART**	CA	RT	▬		23	3.8E-4	5.6E-2
☐	**GOTERM_CC_ALL**	cell fraction	RT	▬		55	2.3E-2	7.3E-1
☐	**GOTERM_CC_ALL**	membrane fraction	RT	▬		48	4.2E-2	8.7E-1
☐	**SP_PIR_KEYWORDS**	cell adhesion	RT	▬		35	7.1E-2	8.2E-1
☐	**GOTERM_BP_ALL**	homophilic cell adhesion	RT	▬		11	3.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	biological adhesion	RT	▬		56	4.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell adhesion	RT	▬		56	4.2E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	calcium	RT	▬		48	5.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell-cell adhesion	RT	▬		20	6.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	calcium ion binding	RT	▬		63	7.4E-1	1.0E0
	Annotation Cluster 7	Enrichment Score: 3.04	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	establishment and/or maintenance of chromatin architecture	RT	▬		44	6.5E-7	2.2E-4
☐	**GOTERM_BP_ALL**	DNA packaging	RT	▬		44	1.4E-6	4.6E-4
☐	**GOTERM_BP_ALL**	chromatin modification	RT	▬		33	1.2E-5	3.2E-3
☐	**GOTERM_BP_ALL**	chromosome organization and biogenesis	RT	▬		49	1.6E-5	3.8E-3
☐	**GOTERM_BP_ALL**	DNA metabolic process	RT	▬		78	5.8E-5	1.1E-2
☐	**GOTERM_BP_ALL**	chromatin assembly or disassembly	RT	▬		19	1.2E-3	1.6E-1
☐	**GOTERM_CC_ALL**	chromosome	RT	▬		41	1.5E-3	1.1E-1
☐	**SP_PIR_KEYWORDS**	Chromatin regulator	RT	▬		17	4.5E-3	2.1E-1
☐	**GOTERM_CC_ALL**	chromosomal part	RT	▬		35	4.8E-3	2.9E-1
☐	**GOTERM_BP_ALL**	organelle organization and biogenesis	RT	▬		84	7.4E-1	1.0E0
☐	**GOTERM_CC_ALL**	intracellular non-membrane-bound organelle	RT	▬		94	9.8E-1	1.0E0
☐	**GOTERM_CC_ALL**	non-membrane-bound organelle	RT	▬		94	9.8E-1	1.0E0
	Annotation Cluster 8	Enrichment Score: 2.2	G		🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	zinc finger region:RING-type	RT	▬		19	1.4E-3	1.0E0
☐	**INTERPRO**	Zinc finger, RING-type	RT	▬		31	3.9E-3	6.6E-1
☐	**INTERPRO**	Zinc finger, RING/FYVE/PHD-type	RT	▬		22	7.3E-3	8.2E-1
☐	**SMART**	RING	RT	▬		32	3.9E-2	7.8E-1
	Annotation Cluster 9	Enrichment Score: 2.08	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	ligand-dependent nuclear receptor activity	RT	▬		15	4.7E-4	1.2E-1
☐	**INTERPRO**	Nuclear hormone receptor, ligand-binding, core	RT	▬		12	7.0E-4	3.1E-1
☐	**INTERPRO**	Nuclear hormone receptor, ligand-binding	RT	▬		12	8.5E-4	3.4E-1
☐	**INTERPRO**	Zinc finger, nuclear hormone receptor-type	RT	▬		11	1.5E-3	4.7E-1
☐	**SMART**	HOLI	RT	▬		12	2.3E-3	2.4E-1
☐	**UP_SEQ_FEATURE**	region of interest:Modulating	RT	▬		6	2.5E-3	1.0E0
☐	**INTERPRO**	Steroid hormone receptor	RT	▬		11	2.6E-3	5.7E-1
☐	**GOTERM_MF_ALL**	steroid hormone receptor activity	RT	▬		13	3.5E-3	4.4E-1
☐	**UP_SEQ_FEATURE**	region of interest:Steroid-binding	RT	▬		4	3.6E-3	1.0E0
☐	**SMART**	ZnF_C4	RT	▬		11	4.5E-3	3.2E-1
☐	**INTERPRO**	Zinc finger, NHR/GATA-type	RT	▬		9	8.6E-3	8.3E-1
☐	**UP_SEQ_FEATURE**	zinc finger region:NR C4-type	RT	▬		8	2.0E-2	1.0E0
☐	**UP_SEQ_FEATURE**	DNA-binding region:Nuclear receptor	RT	▬		8	2.0E-2	1.0E0
☐	**SP_PIR_KEYWORDS**	Steroid-binding	RT	▬		5	2.9E-2	6.2E-1
☐	**GOTERM_MF_ALL**	steroid binding	RT	▬		10	3.4E-2	9.3E-1
☐	**UP_SEQ_FEATURE**	region of interest:Hinge	RT	▬		4	1.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Lipid-binding	RT	▬		9	2.9E-1	9.9E-1

☐	**UP_SEQ_FEATURE**	region of interest:Ligand-binding	RT	3	5.6E-1	1.0E0
	Annotation Cluster 10	Enrichment Score: 2.02	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	negative regulation of transcription	RT	40	5.5E-4	8.5E-2
☐	**GOTERM_MF_ALL**	transcription repressor activity	RT	27	1.1E-3	1.8E-1
☐	**GOTERM_BP_ALL**	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	41	1.1E-3	1.5E-1
☐	**GOTERM_BP_ALL**	negative regulation of cellular metabolic process	RT	46	1.1E-3	1.5E-1
☐	**GOTERM_BP_ALL**	negative regulation of transcription, DNA-dependent	RT	31	1.5E-3	1.8E-1
☐	**GOTERM_BP_ALL**	transcription from RNA polymerase II promoter	RT	57	1.7E-3	1.9E-1
☐	**GOTERM_BP_ALL**	negative regulation of cellular process	RT	101	3.4E-3	3.2E-1
☐	**GOTERM_MF_ALL**	transcription activator activity	RT	30	3.6E-3	4.4E-1
☐	**GOTERM_BP_ALL**	negative regulation of biological process	RT	105	7.1E-3	4.9E-1
☐	**GOTERM_BP_ALL**	negative regulation of metabolic process	RT	47	7.2E-3	4.9E-1
☐	**GOTERM_BP_ALL**	negative regulation of transcription from RNA polymerase II promoter	RT	22	7.8E-3	5.1E-1
☐	**GOTERM_BP_ALL**	regulation of transcription from RNA polymerase II promoter	RT	49	7.8E-3	5.0E-1
☐	**GOTERM_BP_ALL**	positive regulation of transcription	RT	39	2.9E-2	8.4E-1
☐	**GOTERM_BP_ALL**	positive regulation of cellular metabolic process	RT	47	3.3E-2	8.7E-1
☐	**GOTERM_BP_ALL**	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	39	3.8E-2	9.0E-1
☐	**GOTERM_BP_ALL**	positive regulation of metabolic process	RT	48	5.7E-2	9.4E-1
☐	**GOTERM_BP_ALL**	positive regulation of transcription, DNA-dependent	RT	31	8.2E-2	9.7E-1
☐	**GOTERM_BP_ALL**	positive regulation of cellular process	RT	85	8.4E-2	9.7E-1
☐	**GOTERM_BP_ALL**	positive regulation of transcription from RNA polymerase II promoter	RT	23	1.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of biological process	RT	90	2.3E-1	1.0E0
	Annotation Cluster 11	Enrichment Score: 1.87	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of odontogenesis	RT	4	1.9E-3	2.1E-1
☐	**GOTERM_BP_ALL**	regulation of odontogenesis of dentine-containing teeth	RT	4	8.2E-3	5.1E-1
☐	**GOTERM_BP_ALL**	positive regulation of odontogenesis of dentine-containing teeth	RT	3	1.8E-2	7.3E-1
☐	**GOTERM_BP_ALL**	positive regulation of odontogenesis	RT	3	1.8E-2	7.3E-1
☐	**GOTERM_BP_ALL**	odontogenesis of dentine-containing teeth	RT	8	2.7E-2	8.3E-1
☐	**GOTERM_BP_ALL**	odontogenesis	RT	8	4.5E-2	9.2E-1
	Annotation Cluster 12	Enrichment Score: 1.82	G	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	bromodomain	RT	8	6.1E-3	2.6E-1
☐	**INTERPRO**	Bromodomain	RT	9	6.2E-3	7.8E-1
☐	**SMART**	BROMO	RT	10	7.3E-3	4.3E-1
☐	**UP_SEQ_FEATURE**	domain:Bromo	RT	3	1.9E-1	1.0E0
	Annotation Cluster 13	Enrichment Score: 1.6	G	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	zinc finger region:ZZ-type	RT	4	1.7E-2	1.0E0
☐	**INTERPRO**	Zinc finger, ZZ-type	RT	5	2.4E-2	9.8E-1
☐	**SMART**	ZnF_ZZ	RT	5	3.8E-2	7.9E-1
	Annotation Cluster 14	Enrichment Score: 1.54	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	biotin biosynthetic process	RT	7	1.6E-6	4.8E-4
☐	**GOTERM_BP_ALL**	biotin metabolic process	RT	7	1.6E-5	3.7E-3
☐	**INTERPRO**	Biotin synthase	RT	4	1.7E-3	4.8E-1
☐	**INTERPRO**	Biotin and thiamin synthesis associated	RT	4	1.7E-3	4.8E-1
☐	**GOTERM_MF_ALL**	biotin synthase activity	RT	4	1.8E-3	2.7E-1

☐	**INTERPRO**	Elongator protein 3/MiaB/NifB	RT	▮		5	5.0E-3	7.3E-1
☐	**INTERPRO**	Radical SAM	RT	▮		5	5.0E-3	7.3E-1
☐	**SMART**	Elp3	RT	▮		5	8.4E-3	4.3E-1
☐	**GOTERM_MF_ALL**	2 iron, 2 sulfur cluster binding	RT	▮		6	1.0E-2	7.3E-1
☐	**GOTERM_BP_ALL**	water-soluble vitamin biosynthetic process	RT	▮		7	1.4E-2	6.8E-1
☐	**SP_PIR_KEYWORDS**	biotin biosynthesis	RT	▮		3	1.6E-2	4.6E-1
☐	**GOTERM_BP_ALL**	vitamin biosynthetic process	RT	▮		7	1.7E-2	7.3E-1
☐	**GOTERM_MF_ALL**	sulfurtransferase activity	RT	▮		4	2.8E-2	9.1E-1
☐	**SP_PIR_KEYWORDS**	s-adenosyl-l-methionine	RT	▮		11	3.4E-2	6.6E-1
☐	**SP_PIR_KEYWORDS**	iron-sulfur	RT	▮		7	7.1E-2	8.2E-1
☐	**SP_PIR_KEYWORDS**	4Fe-4S	RT	▮		5	8.0E-2	8.4E-1
☐	**GOTERM_MF_ALL**	4 iron, 4 sulfur cluster binding	RT	▮		5	9.9E-2	9.9E-1
☐	**GOTERM_BP_ALL**	sulfur compound biosynthetic process	RT	▮		7	1.2E-1	9.9E-1
☐	**GOTERM_MF_ALL**	metal cluster binding	RT	▮		7	1.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	iron-sulfur cluster binding	RT	▮		7	1.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	water-soluble vitamin metabolic process	RT	▮		7	1.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	sulfur metabolic process	RT	▮		10	1.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	vitamin metabolic process	RT	▮		9	2.3E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	2Fe-2S	RT	▮		3	3.2E-1	9.9E-1
☐	**COG_ONTOLOGY**	Coenzyme metabolism	RT	▮		5	3.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	heterocycle metabolic process	RT	▮		9	3.5E-1	1.0E0
☐	**INTERPRO**	Aldolase-type TIM barrel	RT	▮		4	4.3E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	iron	RT	▮		21	4.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	cofactor metabolic process	RT	▮		18	5.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	transferase activity, transferring sulfur-containing groups	RT	▮		5	6.2E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 1.54	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	MAD homology 1, Dwarfin-type	RT	▮		5	1.4E-2	9.3E-1
☐	**SMART**	DWA	RT	▮		5	2.3E-2	6.9E-1
☐	**PIR_SUPERFAMILY**	PIRSF018476:nuclear factor 1	RT	▮		3	4.2E-2	1.0E0
☐	**INTERPRO**	CTF/NF-I	RT	▮		3	5.1E-2	1.0E0
	Annotation Cluster 16	Enrichment Score: 1.51	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	AT-rich interaction region	RT	▮		6	2.0E-3	5.0E-1
☐	**SMART**	BRIGHT	RT	▮		6	3.9E-3	3.2E-1
☐	**INTERPRO**	Transcription factor jumonji	RT	▮		4	5.9E-2	1.0E0
☐	**SMART**	JmjC	RT	▮		5	7.0E-2	8.5E-1
☐	**INTERPRO**	Transcription factor jumonji, JmjN	RT	▮		3	7.2E-2	1.0E0
☐	**SMART**	JmjN	RT	▮		3	9.3E-2	9.1E-1
☐	**INTERPRO**	Transcription factor jumonji/aspartyl beta-hydroxylase	RT	▮		4	1.2E-1	1.0E0
	Annotation Cluster 17	Enrichment Score: 1.45	G		🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	Chromosomal protein	RT	▮		19	8.6E-4	5.6E-2
☐	**GOTERM_BP_ALL**	chromatin assembly or disassembly	RT	▮		19	1.2E-3	1.6E-1
☐	**PIR_SUPERFAMILY**	PIRSF002050:histone H2B	RT	▮		4	5.7E-3	1.0E0
☐	**GOTERM_BP_ALL**	chromatin assembly	RT	▮		13	9.2E-3	5.4E-1
☐	**GOTERM_CC_ALL**	chromatin	RT	▮		22	1.1E-2	4.9E-1
☐	**GOTERM_BP_ALL**	nucleosome assembly	RT	▮		11	1.3E-2	6.6E-1
☐	**INTERPRO**	Histone H2B	RT	▮		4	1.9E-2	9.7E-1
☐	**GOTERM_CC_ALL**	nucleosome	RT	▮		9	2.3E-2	7.0E-1
☐	**SMART**	H2B	RT	▮		4	2.8E-2	7.1E-1

☐	**SP_PIR_KEYWORDS**	Nucleosome core	RT		7	3.5E-2	6.6E-1
☐	**INTERPRO**	Histone core	RT		6	3.9E-2	1.0E0
☐	**SP_PIR_KEYWORDS**	citrullination	RT		4	5.7E-2	8.0E-1
☐	**PIR_SUPERFAMILY**	PIRSF002048:histone H2A	RT		3	1.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein-DNA complex assembly	RT		11	1.9E-1	1.0E0
☐	**INTERPRO**	Histone-fold	RT		5	3.5E-1	1.0E0
☐	**SMART**	H2A	RT		3	3.9E-1	9.9E-1
☐	**GOTERM_BP_ALL**	cellular component assembly	RT		34	4.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	macromolecular complex assembly	RT		27	6.5E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 1.45	G	🟩	Count	P_Value	Benjamini
☐	**PIR_SUPERFAMILY**	PIRSF002387:myelin proteolipid protein	RT		3	1.4E-2	1.0E0
☐	**INTERPRO**	Myelin proteolipid protein PLP	RT		3	5.1E-2	1.0E0
☐	**SMART**	PLP	RT		3	6.6E-2	8.6E-1
	Annotation Cluster 19	Enrichment Score: 1.44	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	retinal homeostasis	RT		4	1.9E-3	2.1E-1
☐	**GOTERM_BP_ALL**	multicellular organismal homeostasis	RT		5	1.6E-1	9.9E-1
☐	**GOTERM_BP_ALL**	tissue homeostasis	RT		5	1.6E-1	9.9E-1
	Annotation Cluster 20	Enrichment Score: 1.39	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	protein modification process	RT		169	3.0E-5	6.4E-3
☐	**GOTERM_BP_ALL**	post-translational protein modification	RT		149	4.8E-5	9.8E-3
☐	**GOTERM_BP_ALL**	biopolymer modification	RT		172	8.1E-5	1.5E-2
☐	**GOTERM_BP_ALL**	macromolecule metabolic process	RT		521	3.6E-4	6.1E-2
☐	**GOTERM_MF_ALL**	protein kinase activity	RT		65	5.9E-3	5.8E-1
☐	**SP_PIR_KEYWORDS**	Serine/threonine-protein kinase	RT		41	7.1E-3	2.8E-1
☐	**GOTERM_MF_ALL**	phosphotransferase activity, alcohol group as acceptor	RT		73	9.6E-3	7.2E-1
☐	**GOTERM_MF_ALL**	protein serine/threonine kinase activity	RT		53	1.1E-2	7.3E-1
☐	**GOTERM_BP_ALL**	protein amino acid phosphorylation	RT		66	1.6E-2	7.1E-1
☐	**UP_SEQ_FEATURE**	active site:Proton acceptor	RT		49	1.7E-2	1.0E0
☐	**GOTERM_MF_ALL**	transferase activity, transferring phosphorus-containing groups	RT		98	2.0E-2	8.7E-1
☐	**INTERPRO**	Serine/threonine protein kinase, active site	RT		30	2.3E-2	9.8E-1
☐	**GOTERM_MF_ALL**	kinase activity	RT		85	3.0E-2	9.1E-1
☐	**UP_SEQ_FEATURE**	domain:Protein kinase	RT		36	3.2E-2	1.0E0
☐	**SP_PIR_KEYWORDS**	transferase	RT		116	3.8E-2	6.7E-1
☐	**GOTERM_MF_ALL**	transferase activity	RT		160	3.9E-2	9.4E-1
☐	**GOTERM_BP_ALL**	phosphate metabolic process	RT		83	4.0E-2	9.1E-1
☐	**GOTERM_BP_ALL**	phosphorus metabolic process	RT		83	4.0E-2	9.1E-1
☐	**GOTERM_BP_ALL**	phosphorylation	RT		71	4.1E-2	9.1E-1
☐	**INTERPRO**	Serine/threonine protein kinase	RT		24	5.2E-2	1.0E0
☐	**UP_SEQ_FEATURE**	binding site:ATP	RT		37	5.8E-2	1.0E0
☐	**SP_PIR_KEYWORDS**	kinase	RT		66	6.4E-2	8.1E-1
☐	**INTERPRO**	Protein kinase, core	RT		35	8.6E-2	1.0E0
☐	**UP_SEQ_FEATURE**	nucleotide phosphate-binding region:ATP	RT		51	2.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	protein-tyrosine kinase activity	RT		30	2.2E-1	1.0E0
☐	**SMART**	S_TKc	RT		37	2.4E-1	9.8E-1
☐	**GOTERM_BP_ALL**	cellular protein metabolic process	RT		243	2.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	nucleotide binding	RT		162	2.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular macromolecule metabolic process	RT		243	3.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein metabolic process	RT		249	3.9E-1	1.0E0

☐	GOTERM_MF_ALL	ribonucleotide binding	RT	132	4.5E-1	1.0E0
☐	GOTERM_MF_ALL	purine ribonucleotide binding	RT	132	4.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT	102	4.6E-1	1.0E0
☐	GOTERM_MF_ALL	purine nucleotide binding	RT	137	4.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	atp-binding	RT	79	5.3E-1	1.0E0
☐	GOTERM_MF_ALL	adenyl ribonucleotide binding	RT	105	5.9E-1	1.0E0
☐	GOTERM_MF_ALL	adenyl nucleotide binding	RT	110	6.0E-1	1.0E0
☐	GOTERM_MF_ALL	ATP binding	RT	103	6.3E-1	1.0E0
	Annotation Cluster 21	Enrichment Score: 1.31	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	repeat:RCC1 4	RT	4	3.3E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:RCC1 3	RT	4	3.3E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:RCC1 2	RT	4	3.3E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:RCC1 1	RT	4	3.3E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:RCC1 5	RT	4	3.3E-2	1.0E0
☐	INTERPRO	Regulator of chromosome condensation, RCC1	RT	5	1.2E-1	1.0E0
☐	COG_ONTOLOGY	Cell division and chromosome partitioning / Cytoskeleton	RT	4	1.6E-1	1.0E0
	Annotation Cluster 22	Enrichment Score: 1.27	G	Count	P_Value	Benjamini
☐	INTERPRO	SANT, DNA-binding	RT	10	2.6E-2	9.8E-1
☐	SMART	SANT	RT	10	5.7E-2	8.3E-1
☐	INTERPRO	Myb, DNA-binding	RT	6	1.1E-1	1.0E0
	Annotation Cluster 23	Enrichment Score: 1.26	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	Ras protein signal transduction	RT	30	6.9E-4	1.0E-1
☐	GOTERM_BP_ALL	regulation of Ras protein signal transduction	RT	23	1.6E-3	1.9E-1
☐	GOTERM_BP_ALL	regulation of small GTPase mediated signal transduction	RT	26	4.6E-3	3.9E-1
☐	GOTERM_BP_ALL	small GTPase mediated signal transduction	RT	47	6.3E-3	4.7E-1
☐	GOTERM_MF_ALL	Ras GTPase activator activity	RT	12	1.2E-2	7.7E-1
☐	GOTERM_BP_ALL	regulation of Rab GTPase activity	RT	8	2.7E-2	8.3E-1
☐	GOTERM_BP_ALL	Rab protein signal transduction	RT	8	2.7E-2	8.3E-1
☐	GOTERM_BP_ALL	regulation of Rab protein signal transduction	RT	8	2.7E-2	8.3E-1
☐	GOTERM_BP_ALL	regulation of signal transduction	RT	47	3.5E-2	8.8E-1
☐	GOTERM_MF_ALL	small GTPase regulator activity	RT	24	3.5E-2	9.2E-1
☐	GOTERM_MF_ALL	Rab GTPase activator activity	RT	8	3.7E-2	9.3E-1
☐	INTERPRO	RabGAP/TBC	RT	7	4.9E-2	1.0E0
☐	GOTERM_BP_ALL	regulation of Ras GTPase activity	RT	8	6.1E-2	9.5E-1
☐	GOTERM_MF_ALL	guanyl-nucleotide exchange factor activity	RT	17	9.1E-2	9.9E-1
☐	SMART	TBC	RT	7	1.2E-1	9.2E-1
☐	GOTERM_MF_ALL	GTPase regulator activity	RT	32	1.8E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Rab-GAP TBC	RT	3	2.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of GTPase activity	RT	9	3.2E-1	1.0E0
☐	GOTERM_MF_ALL	GTPase activator activity	RT	16	3.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	gtpase activation	RT	8	4.8E-1	1.0E0
☐	GOTERM_MF_ALL	enzyme activator activity	RT	19	5.6E-1	1.0E0
☐	GOTERM_MF_ALL	enzyme regulator activity	RT	48	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of hydrolase activity	RT	10	8.5E-1	1.0E0
	Annotation Cluster 24	Enrichment Score: 1.22	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	zinc finger region:GATA-type	RT	3	3.0E-2	1.0E0
☐	INTERPRO	Zinc finger, GATA-type	RT	4	7.3E-2	1.0E0
☐	SMART	ZnF_GATA	RT	4	1.0E-1	9.0E-1

	Annotation Cluster 25	Enrichment Score: 1.21	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	biological rhythms	RT	▮		6	9.2E-3	3.3E-1
☐	UP_SEQ_FEATURE	region of interest:CSNK1E binding domain	RT	▮		3	1.6E-2	1.0E0
☐	UP_SEQ_FEATURE	region of interest:CRY binding domain	RT	▮		3	1.6E-2	1.0E0
☐	GOTERM_BP_ALL	two-component signal transduction system (phosphorelay)	RT	▮		7	1.7E-2	7.3E-1
☐	INTERPRO	PAC motif	RT	▮		6	2.8E-2	9.9E-1
☐	GOTERM_MF_ALL	protein histidine kinase activity	RT	▮		6	2.9E-2	9.0E-1
☐	GOTERM_MF_ALL	two-component sensor activity	RT	▮		5	4.7E-2	9.6E-1
☐	SMART	PAC	RT	▮		6	5.7E-2	8.4E-1
☐	KEGG_PATHWAY	Circadian rhythm	RT	▮		4	5.8E-2	5.7E-1
☐	GOTERM_MF_ALL	phosphotransferase activity, nitrogenous group as acceptor	RT	▮		6	6.2E-2	9.7E-1
☐	INTERPRO	PAS fold-3	RT	▮		5	6.3E-2	1.0E0
☐	INTERPRO	PAS	RT	▮		6	6.8E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:PAS 1	RT	▮		4	1.1E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:PAS 2	RT	▮		4	1.1E-1	1.0E0
☐	SMART	PAS	RT	▮		6	1.2E-1	9.2E-1
☐	GOTERM_BP_ALL	circadian rhythm	RT	▮		5	1.8E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:PAC	RT	▮		4	2.2E-1	1.0E0
☐	UP_SEQ_FEATURE	short sequence motif:Nuclear export signal	RT	▮		4	2.4E-1	1.0E0
☐	INTERPRO	PAS fold	RT	▮		3	5.1E-1	1.0E0
	Annotation Cluster 26	Enrichment Score: 1.21	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	histone modification	RT	▮		11	2.3E-3	2.3E-1
☐	GOTERM_BP_ALL	covalent chromatin modification	RT	▮		11	4.4E-3	3.8E-1
☐	SP_PIR_KEYWORDS	bromodomain	RT	▮		8	6.1E-3	2.6E-1
☐	KEGG_PATHWAY	Notch signaling pathway	RT	▮		9	1.5E-2	3.0E-1
☐	GOTERM_CC_ALL	histone acetyltransferase complex	RT	▮		4	4.5E-2	8.8E-1
☐	GOTERM_MF_ALL	histone acetyltransferase activity	RT	▮		5	4.7E-2	9.6E-1
☐	GOTERM_MF_ALL	lysine N-acetyltransferase activity	RT	▮		5	4.7E-2	9.6E-1
☐	GOTERM_BP_ALL	histone acetylation	RT	▮		4	5.0E-2	9.4E-1
☐	BIOCARTA	Control of Gene Expression by Vitamin D Receptor	RT	▮		7	6.4E-2	1.0E0
☐	GOTERM_BP_ALL	protein amino acid acetylation	RT	▮		4	1.3E-1	9.9E-1
☐	GOTERM_MF_ALL	N-acetyltransferase activity	RT	▮		8	1.3E-1	1.0E0
☐	GOTERM_MF_ALL	acetyltransferase activity	RT	▮		9	1.6E-1	1.0E0
☐	GOTERM_MF_ALL	N-acyltransferase activity	RT	▮		8	2.3E-1	1.0E0
☐	GOTERM_CC_ALL	kinetochore	RT	▮		4	2.7E-1	1.0E0
☐	BIOCARTA	The information-processing pathway at the IFN-beta enhancer	RT	▮		3	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid acylation	RT	▮		4	3.4E-1	1.0E0
☐	GOTERM_CC_ALL	chromosome, pericentric region	RT	▮		6	5.8E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 1.13	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	determination of left/right symmetry	RT	▮		8	1.5E-2	7.1E-1
☐	GOTERM_BP_ALL	determination of symmetry	RT	▮		8	1.8E-2	7.2E-1
☐	GOTERM_BP_ALL	determination of bilateral symmetry	RT	▮		8	1.8E-2	7.2E-1
☐	GOTERM_BP_ALL	pattern specification process	RT	▮		19	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	regionalization	RT	▮		11	7.3E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 1.13	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	repeat:ANK 9	RT	▮		5	9.1E-3	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 8	RT	▮		5	1.2E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 5	RT	▮		10	1.7E-2	1.0E0

☐	**UP_SEQ_FEATURE**	repeat:ANK 4	RT		10	3.8E-2	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:ANK 6	RT		7	5.8E-2	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:ANK 3	RT		11	6.1E-2	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:ANK 7	RT		5	7.5E-2	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:ANK 1	RT		11	1.3E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:ANK 2	RT		11	1.3E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	ank repeat	RT		19	1.9E-1	9.5E-1
☐	**INTERPRO**	Ankyrin	RT		14	6.4E-1	1.0E0
☐	**SMART**	ANK	RT		17	7.3E-1	1.0E0
	Annotation Cluster 29	Enrichment Score: 1.08	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	apoptosis	RT		29	4.2E-2	7.0E-1
☐	**GOTERM_BP_ALL**	apoptosis	RT		67	5.7E-2	9.4E-1
☐	**GOTERM_BP_ALL**	cell death	RT		70	6.2E-2	9.5E-1
☐	**GOTERM_BP_ALL**	death	RT		70	6.2E-2	9.5E-1
☐	**GOTERM_BP_ALL**	programmed cell death	RT		67	7.5E-2	9.6E-1
☐	**GOTERM_BP_ALL**	cell development	RT		112	7.9E-2	9.7E-1
☐	**GOTERM_BP_ALL**	regulation of apoptosis	RT		46	8.8E-2	9.7E-1
☐	**GOTERM_BP_ALL**	regulation of programmed cell death	RT		46	1.0E-1	9.8E-1
☐	**GOTERM_BP_ALL**	cellular developmental process	RT		157	1.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell differentiation	RT		157	1.7E-1	1.0E0
	Annotation Cluster 30	Enrichment Score: 1.07	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Zinc finger, CCCH-type	RT		9	2.0E-2	9.7E-1
☐	**SMART**	ZnF_C3H1	RT		9	5.3E-2	8.4E-1
☐	**UP_SEQ_FEATURE**	zinc finger region:C3H1-type 1	RT		3	2.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C3H1-type 2	RT		3	2.2E-1	1.0E0
	Annotation Cluster 31	Enrichment Score: 1.03	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	intracellular signaling cascade	RT		118	7.3E-3	4.9E-1
☐	**GOTERM_BP_ALL**	signal transduction	RT		225	6.9E-2	9.6E-1
☐	**GOTERM_BP_ALL**	cell communication	RT		239	1.7E-1	9.9E-1
☐	**GOTERM_BP_ALL**	cell surface receptor linked signal transduction	RT		96	8.8E-1	1.0E0
	Annotation Cluster 32	Enrichment Score: 1	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	LisH dimerisation motif	RT		6	5.2E-2	1.0E0
☐	**UP_SEQ_FEATURE**	domain:LisH	RT		4	5.4E-2	1.0E0
☐	**SMART**	LisH	RT		6	8.6E-2	9.0E-1
☐	**INTERPRO**	CTLH, C-terminal to LisH motif	RT		3	1.8E-1	1.0E0
☐	**SMART**	CTLH	RT		3	2.2E-1	9.7E-1
	Annotation Cluster 33	Enrichment Score: 0.98	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	BTB/POZ	RT		15	1.8E-2	9.6E-1
☐	**INTERPRO**	BTB/POZ-like	RT		17	6.8E-2	1.0E0
☐	**INTERPRO**	BTB/POZ fold	RT		16	1.2E-1	1.0E0
☐	**SMART**	BTB	RT		18	1.5E-1	9.3E-1
☐	**INTERPRO**	Kelch related	RT		7	2.0E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:BTB	RT		6	3.3E-1	1.0E0
	Annotation Cluster 34	Enrichment Score: 0.96	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	anti-apoptosis	RT		14	7.0E-2	9.6E-1
☐	**GOTERM_BP_ALL**	regulation of apoptosis	RT		46	8.8E-2	9.7E-1
☐	**GOTERM_BP_ALL**	regulation of programmed cell death	RT		46	1.0E-1	9.8E-1
☐	**GOTERM_BP_ALL**	negative regulation of apoptosis	RT		21	1.5E-1	9.9E-1
☐	**GOTERM_BP_ALL**	negative regulation of programmed cell death	RT		21	1.7E-1	9.9E-1

	Annotation Cluster 35	Enrichment Score: 0.96	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	repeat:Kelch 6	RT	5	2.6E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:Kelch 5	RT	5	4.0E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:Kelch 4	RT	5	5.6E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:Kelch 2	RT	5	6.5E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:Kelch 3	RT	5	6.5E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:Kelch 1	RT	5	6.5E-2	1.0E0
☐	SP_PIR_KEYWORDS	kelch repeat	RT	7	1.0E-1	8.8E-1
☐	INTERPRO	Kelch-type beta propeller	RT	6	1.6E-1	1.0E0
☐	INTERPRO	Kelch related	RT	7	2.0E-1	1.0E0
☐	SMART	Kelch	RT	8	2.4E-1	9.8E-1
☐	INTERPRO	Kelch repeat type 1	RT	6	2.5E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:BTB	RT	6	3.3E-1	1.0E0
☐	INTERPRO	BTB/Kelch-associated	RT	5	3.5E-1	1.0E0
	Annotation Cluster 36	Enrichment Score: 0.95	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	serine/threonine-specific protein kinase	RT	8	1.7E-2	4.6E-1
☐	SP_PIR_KEYWORDS	ATP	RT	18	1.3E-1	9.1E-1
☐	SP_PIR_KEYWORDS	autophosphorylation	RT	6	2.2E-1	9.7E-1
☐	SP_PIR_KEYWORDS	phosphotransferase	RT	13	3.1E-1	9.9E-1
	Annotation Cluster 37	Enrichment Score: 0.93	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein processing	RT	12	7.6E-2	9.6E-1
☐	GOTERM_BP_ALL	protein amino acid autophosphorylation	RT	7	1.3E-1	9.9E-1
☐	GOTERM_BP_ALL	protein autoprocessing	RT	7	1.6E-1	9.9E-1
	Annotation Cluster 38	Enrichment Score: 0.92	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of Ras protein signal transduction	RT	23	1.6E-3	1.9E-1
☐	GOTERM_BP_ALL	regulation of small GTPase mediated signal transduction	RT	26	4.6E-3	3.9E-1
☐	GOTERM_MF_ALL	small GTPase regulator activity	RT	24	3.5E-2	9.2E-1
☐	GOTERM_MF_ALL	guanyl-nucleotide exchange factor activity	RT	17	9.1E-2	9.9E-1
☐	SP_PIR_KEYWORDS	guanine-nucleotide releasing factor	RT	10	1.1E-1	8.8E-1
☐	GOTERM_MF_ALL	Ras guanyl-nucleotide exchange factor activity	RT	10	1.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of Rho protein signal transduction	RT	9	2.3E-1	1.0E0
☐	GOTERM_BP_ALL	Rho protein signal transduction	RT	11	2.6E-1	1.0E0
☐	GOTERM_MF_ALL	Rho guanyl-nucleotide exchange factor activity	RT	8	2.9E-1	1.0E0
☐	INTERPRO	Guanine-nucleotide dissociation stimulator, CDC24	RT	4	5.1E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:DH	RT	3	6.2E-1	1.0E0
☐	INTERPRO	DH	RT	5	6.5E-1	1.0E0
☐	SMART	RhoGEF	RT	5	7.6E-1	1.0E0
	Annotation Cluster 39	Enrichment Score: 0.91	G	Count	P_Value	Benjamini
☐	INTERPRO	Sulphatase	RT	4	5.9E-2	1.0E0
☐	GOTERM_MF_ALL	sulfuric ester hydrolase activity	RT	4	6.1E-2	9.7E-1
☐	INTERPRO	Alkaline phosphatase	RT	4	2.0E-1	1.0E0
☐	SMART	alkPPc	RT	4	3.1E-1	9.9E-1
	Annotation Cluster 40	Enrichment Score: 0.89	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:ELM2	RT	3	6.7E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:SANT	RT	3	1.4E-1	1.0E0
☐	INTERPRO	ELM2	RT	3	2.3E-1	1.0E0
	Annotation Cluster 41	Enrichment Score: 0.88	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	skeletal muscle development	RT	18	4.7E-3	3.8E-1

☐	GOTERM_BP_ALL	striated muscle development	RT	21	6.9E-3	4.9E-1
☐	GOTERM_BP_ALL	muscle development	RT	24	2.5E-2	8.1E-1
☐	GOTERM_BP_ALL	myoblast maturation	RT	6	4.3E-2	9.2E-1
☐	GOTERM_BP_ALL	cell maturation	RT	13	4.7E-2	9.3E-1
☐	GOTERM_BP_ALL	myoblast development	RT	6	5.0E-2	9.4E-1
☐	GOTERM_BP_ALL	skeletal muscle fiber development	RT	11	5.2E-2	9.4E-1
☐	GOTERM_BP_ALL	muscle fiber development	RT	11	5.2E-2	9.4E-1
☐	GOTERM_BP_ALL	myoblast differentiation	RT	8	5.5E-2	9.4E-1
☐	GOTERM_BP_ALL	muscle cell differentiation	RT	11	8.1E-2	9.7E-1
☐	GOTERM_BP_ALL	developmental maturation	RT	13	1.2E-1	9.9E-1
☐	GOTERM_BP_ALL	striated muscle cell differentiation	RT	6	1.4E-1	9.9E-1
☐	GOTERM_BP_ALL	myofibril assembly	RT	4	1.7E-1	9.9E-1
☐	GOTERM_BP_ALL	striated muscle cell development	RT	4	1.7E-1	9.9E-1
☐	GOTERM_BP_ALL	muscle cell development	RT	4	1.9E-1	1.0E0
☐	GOTERM_BP_ALL	actomyosin structure organization and biogenesis	RT	4	2.7E-1	1.0E0
☐	GOTERM_CC_ALL	myofibril	RT	7	5.6E-1	1.0E0
☐	GOTERM_CC_ALL	contractile fiber	RT	7	5.9E-1	1.0E0
☐	GOTERM_CC_ALL	contractile fiber part	RT	5	8.1E-1	1.0E0
☐	GOTERM_BP_ALL	actin filament-based process	RT	13	9.0E-1	1.0E0
☐	GOTERM_CC_ALL	sarcomere	RT	4	9.1E-1	1.0E0
☐	GOTERM_BP_ALL	actin cytoskeleton organization and biogenesis	RT	11	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	cytoskeleton organization and biogenesis	RT	27	9.9E-1	1.0E0
	Annotation Cluster 42	Enrichment Score: 0.87	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Caspase Recruitment	RT	5	7.3E-2	1.0E0
☐	SMART	CARD	RT	5	1.1E-1	9.1E-1
☐	UP_SEQ_FEATURE	domain:CARD	RT	3	3.1E-1	1.0E0
	Annotation Cluster 43	Enrichment Score: 0.87	G 🟩	Count	P_Value	Benjamini
☐	SMART	UBA	RT	6	9.8E-2	9.0E-1
☐	INTERPRO	Ubiquitin-associated/translation elongation factor EF1B, N-terminal	RT	7	1.3E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:UBA	RT	4	2.0E-1	1.0E0
	Annotation Cluster 44	Enrichment Score: 0.84	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	phospholipid metabolic process	RT	18	4.0E-2	9.1E-1
☐	GOTERM_BP_ALL	membrane lipid metabolic process	RT	20	1.0E-1	9.8E-1
☐	SP_PIR_KEYWORDS	Phospholipid biosynthesis	RT	5	1.3E-1	9.1E-1
☐	GOTERM_BP_ALL	phospholipid biosynthetic process	RT	9	1.6E-1	9.9E-1
☐	GOTERM_BP_ALL	membrane lipid biosynthetic process	RT	10	2.0E-1	1.0E0
☐	GOTERM_BP_ALL	glycerophospholipid biosynthetic process	RT	4	5.3E-1	1.0E0
	Annotation Cluster 45	Enrichment Score: 0.83	G 🟩	Count	P_Value	Benjamini
☐	SMART	CHROMO	RT	6	9.8E-2	9.0E-1
☐	INTERPRO	Chromo	RT	5	1.4E-1	1.0E0
☐	GOTERM_MF_ALL	chromatin binding	RT	13	2.5E-1	1.0E0
	Annotation Cluster 46	Enrichment Score: 0.83	G 🟩	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF038354:forkhead box O protein	RT	3	1.4E-2	1.0E0
☐	BIOCARTA	AKT Signaling Pathway	RT	5	1.5E-1	1.0E0
☐	INTERPRO	Fork head transcription factor	RT	6	1.8E-1	1.0E0
☐	SMART	FH	RT	6	2.6E-1	9.8E-1
☐	INTERPRO	Winged helix repressor DNA-binding	RT	11	3.2E-1	1.0E0
☐	UP_SEQ_FEATURE	DNA-binding region:Fork-head	RT	4	3.6E-1	1.0E0
	Annotation Cluster 47	Enrichment Score: 0.83	G 🟩	Count	P_Value	Benjamini

☐	UP_SEQ_FEATURE	repeat:WD 3	RT		16	5.1E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 2	RT		16	5.6E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 1	RT		16	5.6E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 4	RT		14	1.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	wd repeat	RT		24	1.2E-1	9.0E-1
☐	UP_SEQ_FEATURE	repeat:WD 5	RT		13	1.3E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 6	RT		10	1.9E-1	1.0E0
☐	INTERPRO	WD40 repeat	RT		18	3.9E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 7	RT		6	4.5E-1	1.0E0
☐	SMART	WD40	RT		20	6.0E-1	1.0E0
	Annotation Cluster 48	Enrichment Score: 0.81	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	telomeric DNA binding	RT		4	2.8E-2	9.1E-1
☐	GOTERM_MF_ALL	single-stranded DNA binding	RT		5	2.4E-1	1.0E0
☐	GOTERM_MF_ALL	structure-specific DNA binding	RT		6	5.5E-1	1.0E0
	Annotation Cluster 49	Enrichment Score: 0.75	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Pleckstrin homology-type	RT		25	1.1E-1	1.0E0
☐	INTERPRO	Pleckstrin-like	RT		22	1.4E-1	1.0E0
☐	SMART	PH	RT		23	3.5E-1	9.9E-1
	Annotation Cluster 50	Enrichment Score: 0.75	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of growth	RT		21	6.7E-2	9.5E-1
☐	GOTERM_BP_ALL	regulation of cell size	RT		16	1.3E-1	9.9E-1
☐	GOTERM_BP_ALL	growth	RT		28	1.5E-1	9.9E-1
☐	GOTERM_BP_ALL	cell growth	RT		14	2.0E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell growth	RT		11	3.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	growth regulation	RT		5	3.8E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 0.74	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	monocarboxylic acid metabolic process	RT		28	2.2E-2	7.8E-1
☐	GOTERM_BP_ALL	fatty acid metabolic process	RT		17	2.1E-1	1.0E0
☐	GOTERM_BP_ALL	carboxylic acid metabolic process	RT		42	4.7E-1	1.0E0
☐	GOTERM_BP_ALL	organic acid metabolic process	RT		42	4.9E-1	1.0E0
	Annotation Cluster 52	Enrichment Score: 0.72	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	carnitine O-palmitoyltransferase activity	RT		3	5.2E-2	9.5E-1
☐	GOTERM_MF_ALL	O-palmitoyltransferase activity	RT		3	5.2E-2	9.5E-1
☐	KEGG_PATHWAY	Fatty acid metabolism	RT		7	8.5E-2	6.9E-1
☐	GOTERM_MF_ALL	carnitine O-acyltransferase activity	RT		3	9.8E-2	1.0E0
☐	INTERPRO	Acyltransferase ChoActase/COT/CPT	RT		3	1.2E-1	1.0E0
☐	KEGG_PATHWAY	PPAR signaling pathway	RT		9	1.5E-1	8.4E-1
☐	SP_PIR_KEYWORDS	lipid metabolism	RT		12	1.8E-1	9.4E-1
☐	SP_PIR_KEYWORDS	Fatty acid metabolism	RT		6	3.0E-1	9.9E-1
☐	GOTERM_MF_ALL	palmitoyltransferase activity	RT		3	3.6E-1	1.0E0
☐	GOTERM_MF_ALL	O-acyltransferase activity	RT		4	4.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	outer membrane	RT		3	6.9E-1	1.0E0
☐	GOTERM_CC_ALL	outer membrane	RT		5	8.6E-1	1.0E0
	Annotation Cluster 53	Enrichment Score: 0.72	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	suckling behavior	RT		3	5.3E-2	9.4E-1
☐	GOTERM_BP_ALL	behavioral interaction between organisms	RT		4	2.5E-1	1.0E0
☐	GOTERM_BP_ALL	feeding behavior	RT		4	5.3E-1	1.0E0
	Annotation Cluster 54	Enrichment Score: 0.7	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, FYVE-type	RT		6	9.5E-2	1.0E0
☐	SMART	FYVE	RT		6	1.5E-1	9.4E-1

☐	**UP_SEQ_FEATURE**	zinc finger region:FYVE-type	RT	▮		3	5.4E-1	1.0E0
	Annotation Cluster 55	Enrichment Score: 0.7	G		🟩	Count	P_Value	Benjamini
☐	**PIR_SUPERFAMILY**	PIRSF001950:small inducible chemokine, C/CC types	RT	▮		5	5.3E-2	1.0E0
☐	**INTERPRO**	Small chemokine, interleukin-8-like	RT	▮		7	8.3E-2	1.0E0
☐	**INTERPRO**	Small chemokine, C-C	RT	▮		5	9.6E-2	1.0E0
☐	**GOTERM_MF_ALL**	chemokine activity	RT	▮		7	1.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	chemokine receptor binding	RT	▮		7	1.1E-1	1.0E0
☐	**SMART**	SCY	RT	▮		7	1.4E-1	9.4E-1
☐	**SP_PIR_KEYWORDS**	chemotaxis	RT	▮		8	1.5E-1	9.2E-1
☐	**GOTERM_MF_ALL**	G-protein-coupled receptor binding	RT	▮		8	2.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	locomotory behavior	RT	▮		19	3.9E-1	1.0E0
☐	**BIOCARTA**	Pertussis toxin-insensitive CCR5 Signaling in Macrophage	RT	▮		3	5.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	taxis	RT	▮		10	5.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	chemotaxis	RT	▮		10	5.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	behavior	RT	▮		26	5.8E-1	1.0E0
	Annotation Cluster 56	Enrichment Score: 0.69	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	leukocyte homeostasis	RT	▮		5	1.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	homeostasis of number of cells	RT	▮		5	2.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	lymphocyte homeostasis	RT	▮		4	2.3E-1	1.0E0
	Annotation Cluster 57	Enrichment Score: 0.69	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	small conjugating protein ligase activity	RT	▮		16	8.1E-2	9.9E-1
☐	**GOTERM_MF_ALL**	ubiquitin-protein ligase activity	RT	▮		15	1.0E-1	9.9E-1
☐	**GOTERM_MF_ALL**	ligase activity, forming carbon-nitrogen bonds	RT	▮		20	1.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	small protein conjugating enzyme activity	RT	▮		15	1.2E-1	1.0E0
☐	**GOTERM_MF_ALL**	ligase activity	RT	▮		34	1.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	acid-amino acid ligase activity	RT	▮		16	1.7E-1	1.0E0
☐	**SMART**	UBCc	RT	▮		7	2.7E-1	9.8E-1
☐	**SP_PIR_KEYWORDS**	ligase	RT	▮		21	4.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein modification by small protein conjugation	RT	▮		6	5.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein ubiquitination	RT	▮		5	6.8E-1	1.0E0
	Annotation Cluster 58	Enrichment Score: 0.68	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	chromosome, telomeric region	RT	▮		5	5.9E-2	9.1E-1
☐	**SP_PIR_KEYWORDS**	telomere	RT	▮		4	1.2E-1	9.0E-1
☐	**GOTERM_BP_ALL**	telomere maintenance	RT	▮		3	5.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	telomere organization and biogenesis	RT	▮		3	5.3E-1	1.0E0
	Annotation Cluster 59	Enrichment Score: 0.68	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	rhythmic process	RT	▮		12	6.2E-2	9.5E-1
☐	**GOTERM_BP_ALL**	development of primary sexual characteristics	RT	▮		10	8.6E-2	9.7E-1
☐	**GOTERM_BP_ALL**	reproductive developmental process	RT	▮		13	1.0E-1	9.8E-1
☐	**GOTERM_BP_ALL**	gonad development	RT	▮		9	1.1E-1	9.8E-1
☐	**GOTERM_BP_ALL**	sex differentiation	RT	▮		12	1.2E-1	9.9E-1
☐	**GOTERM_BP_ALL**	female sex differentiation	RT	▮		7	1.2E-1	9.9E-1
☐	**GOTERM_BP_ALL**	development of primary female sexual characteristics	RT	▮		7	1.2E-1	9.9E-1
☐	**GOTERM_BP_ALL**	reproductive structure development	RT	▮		9	1.2E-1	9.9E-1
☐	**GOTERM_BP_ALL**	menstrual cycle phase	RT	▮		6	1.4E-1	9.9E-1
☐	**GOTERM_BP_ALL**	menstrual cycle process	RT	▮		6	1.5E-1	9.9E-1
☐	**GOTERM_BP_ALL**	ovulation from ovarian follicle	RT	▮		3	1.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	ovulation	RT	▮		3	2.1E-1	1.0E0

☐	GOTERM_BP_ALL	female gonad development	RT	▮		6	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	menstrual cycle	RT	▮		6	2.7E-1	1.0E0
☐	GOTERM_BP_ALL	female gamete generation	RT	▮		5	2.8E-1	1.0E0
☐	GOTERM_BP_ALL	ovarian follicle development	RT	▮		4	2.9E-1	1.0E0
☐	GOTERM_BP_ALL	male sex differentiation	RT	▮		4	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	male gonad development	RT	▮		3	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	multicellular organism reproduction	RT	▮		7	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive process in a multicellular organism	RT	▮		7	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive process	RT	▮		19	5.9E-1	1.0E0
☐	GOTERM_BP_ALL	development of primary male sexual characteristics	RT	▮		3	6.2E-1	1.0E0
	Annotation Cluster 60	Enrichment Score: 0.66	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of multicellular organism growth	RT	▮		9	5.5E-2	9.4E-1
☐	GOTERM_BP_ALL	multicellular organism growth	RT	▮		9	1.1E-1	9.8E-1
☐	GOTERM_BP_ALL	negative regulation of multicellular organism growth	RT	▮		3	1.8E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of multicellular organism growth	RT	▮		3	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of growth	RT	▮		3	7.6E-1	1.0E0
	Annotation Cluster 61	Enrichment Score: 0.66	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:Death	RT	▮		5	7.5E-2	1.0E0
☐	INTERPRO	Death	RT	▮		6	9.5E-2	1.0E0
☐	SMART	DEATH	RT	▮		6	1.7E-1	9.4E-1
☐	UP_SEQ_FEATURE	repeat:TNFR-Cys 2	RT	▮		4	1.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TNFR-Cys 1	RT	▮		4	1.8E-1	1.0E0
☐	INTERPRO	DEATH-like	RT	▮		6	3.1E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TNFR-Cys 3	RT	▮		3	3.6E-1	1.0E0
☐	INTERPRO	TNFR/CD27/30/40/95 cysteine-rich region	RT	▮		4	4.5E-1	1.0E0
☐	SMART	TNFR	RT	▮		4	5.5E-1	1.0E0
	Annotation Cluster 62	Enrichment Score: 0.65	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	stress-activated protein kinase signaling pathway	RT	▮		8	1.1E-1	9.9E-1
☐	GOTERM_BP_ALL	MAPKKK cascade	RT	▮		14	2.7E-1	1.0E0
☐	GOTERM_BP_ALL	JNK cascade	RT	▮		6	3.6E-1	1.0E0
	Annotation Cluster 63	Enrichment Score: 0.65	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	immune system process	RT	▮		75	2.1E-2	7.6E-1
☐	GOTERM_BP_ALL	leukocyte activation	RT	▮		27	5.7E-2	9.4E-1
☐	GOTERM_BP_ALL	cell activation	RT	▮		28	7.0E-2	9.6E-1
☐	GOTERM_BP_ALL	B cell activation	RT	▮		13	7.5E-2	9.6E-1
☐	GOTERM_BP_ALL	lymphocyte activation	RT	▮		23	1.5E-1	9.9E-1
☐	GOTERM_BP_ALL	leukocyte differentiation	RT	▮		15	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	hemopoietic or lymphoid organ development	RT	▮		24	3.9E-1	1.0E0
☐	GOTERM_BP_ALL	immune system development	RT	▮		25	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	B cell differentiation	RT	▮		5	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	T cell activation	RT	▮		13	4.4E-1	1.0E0
☐	GOTERM_BP_ALL	hemopoiesis	RT	▮		21	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	lymphocyte differentiation	RT	▮		10	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	myeloid cell differentiation	RT	▮		10	5.4E-1	1.0E0
☐	GOTERM_BP_ALL	T cell differentiation	RT	▮		6	6.8E-1	1.0E0
	Annotation Cluster 64	Enrichment Score: 0.65	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:AGC-kinase C-terminal	RT	▮		7	1.4E-1	1.0E0

☐	INTERPRO	Protein kinase, C-terminal	RT	▮	7	2.3E-1	1.0E0
☐	SMART	S_TK_X	RT	▮	7	3.5E-1	9.9E-1
	Annotation Cluster 65	Enrichment Score: 0.63	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	viral capsid	RT	▮	4	2.1E-1	1.0E0
☐	GOTERM_CC_ALL	virion	RT	▮	4	2.5E-1	1.0E0
☐	GOTERM_CC_ALL	virion part	RT	▮	4	2.5E-1	1.0E0
	Annotation Cluster 66	Enrichment Score: 0.6	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	detection of stimulus	RT	▮	10	6.9E-2	9.6E-1
☐	GOTERM_BP_ALL	detection of light stimulus	RT	▮	5	1.3E-1	9.9E-1
☐	GOTERM_BP_ALL	detection of external stimulus	RT	▮	8	1.3E-1	9.9E-1
☐	GOTERM_BP_ALL	detection of abiotic stimulus	RT	▮	7	1.4E-1	9.9E-1
☐	GOTERM_BP_ALL	detection of stimulus during sensory perception	RT	▮	6	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	detection of light stimulus during sensory perception	RT	▮	4	2.7E-1	1.0E0
☐	GOTERM_BP_ALL	detection of light stimulus during visual perception	RT	▮	4	2.7E-1	1.0E0
☐	GOTERM_BP_ALL	detection of visible light	RT	▮	4	2.7E-1	1.0E0
☐	GOTERM_BP_ALL	visual perception	RT	▮	11	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	sensory perception of light stimulus	RT	▮	11	3.3E-1	1.0E0
☐	GOTERM_BP_ALL	response to radiation	RT	▮	10	3.7E-1	1.0E0
☐	GOTERM_BP_ALL	response to light stimulus	RT	▮	8	4.0E-1	1.0E0
☐	GOTERM_BP_ALL	phototransduction	RT	▮	3	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	response to abiotic stimulus	RT	▮	14	6.2E-1	1.0E0
	Annotation Cluster 67	Enrichment Score: 0.6	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of apoptosis	RT	▮	46	8.8E-2	9.7E-1
☐	GOTERM_BP_ALL	regulation of programmed cell death	RT	▮	46	1.0E-1	9.8E-1
☐	GOTERM_BP_ALL	induction of apoptosis	RT	▮	16	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	induction of programmed cell death	RT	▮	16	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of apoptosis	RT	▮	18	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of programmed cell death	RT	▮	18	5.3E-1	1.0E0
	Annotation Cluster 68	Enrichment Score: 0.6	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	protein methyltransferase activity	RT	▮	8	2.9E-2	9.1E-1
☐	GOTERM_MF_ALL	histone methyltransferase activity	RT	▮	5	1.5E-1	1.0E0
☐	GOTERM_MF_ALL	lysine N-methyltransferase activity	RT	▮	4	1.6E-1	1.0E0
☐	GOTERM_MF_ALL	protein-lysine N-methyltransferase activity	RT	▮	4	1.6E-1	1.0E0
☐	GOTERM_MF_ALL	histone-lysine N-methyltransferase activity	RT	▮	4	1.6E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:SET	RT	▮	3	2.8E-1	1.0E0
☐	GOTERM_MF_ALL	S-adenosylmethionine-dependent methyltransferase activity	RT	▮	8	3.5E-1	1.0E0
☐	GOTERM_MF_ALL	N-methyltransferase activity	RT	▮	5	3.8E-1	1.0E0
☐	INTERPRO	SET	RT	▮	5	3.9E-1	1.0E0
☐	GOTERM_MF_ALL	methyltransferase activity	RT	▮	14	5.0E-1	1.0E0
☐	SMART	SET	RT	▮	5	5.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	methyltransferase	RT	▮	10	5.1E-1	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring one-carbon groups	RT	▮	14	5.3E-1	1.0E0
	Annotation Cluster 69	Enrichment Score: 0.59	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	positive regulation of MAP kinase activity	RT	▮	8	6.8E-2	9.6E-1
☐	GOTERM_BP_ALL	positive regulation of transferase activity	RT	▮	15	8.6E-2	9.7E-1
☐	GOTERM_BP_ALL	regulation of a molecular function	RT	▮	40	1.4E-1	9.9E-1
☐	GOTERM_BP_ALL	positive regulation of protein kinase activity	RT	▮	13	1.6E-1	9.9E-1

☐	GOTERM_BP_ALL	positive regulation of kinase activity	RT	13	2.0E-1	1.0E0
☐	GOTERM_BP_ALL	activation of MAPK activity	RT	6	2.1E-1	1.0E0
☐	GOTERM_BP_ALL	MAPKKK cascade	RT	14	2.7E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of JNK activity	RT	3	2.7E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of transferase activity	RT	18	2.8E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of catalytic activity	RT	18	3.0E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of MAP kinase activity	RT	8	3.3E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of JNK activity	RT	3	3.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of catalytic activity	RT	31	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of kinase activity	RT	16	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of protein kinase activity	RT	15	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	apoptotic program	RT	3	9.6E-1	1.0E0
	Annotation Cluster 70	Enrichment Score: 0.59	G	Count	P_Value	Benjamini
☐	INTERPRO	Nuclear receptor ROR	RT	4	7.6E-3	8.2E-1
☐	GOTERM_BP_ALL	regulation of macrophage activation	RT	3	7.6E-2	9.6E-1
☐	SP_PIR_KEYWORDS	transcription factor	RT	8	8.1E-2	8.4E-1
☐	GOTERM_BP_ALL	cGMP metabolic process	RT	4	1.1E-1	9.8E-1
☐	GOTERM_BP_ALL	macrophage activation	RT	3	1.8E-1	1.0E0
☐	GOTERM_BP_ALL	cerebellar Purkinje cell differentiation	RT	3	2.1E-1	1.0E0
☐	GOTERM_BP_ALL	cerebellar Purkinje cell layer formation	RT	3	2.1E-1	1.0E0
☐	GOTERM_BP_ALL	cerebellar Purkinje cell layer morphogenesis	RT	3	2.1E-1	1.0E0
☐	GOTERM_BP_ALL	cerebellar cortex formation	RT	3	2.4E-1	1.0E0
☐	GOTERM_BP_ALL	cell differentiation in hindbrain	RT	3	2.4E-1	1.0E0
☐	GOTERM_BP_ALL	myeloid leukocyte activation	RT	5	2.6E-1	1.0E0
☐	GOTERM_BP_ALL	cerebellar Purkinje cell layer development	RT	3	3.0E-1	1.0E0
☐	GOTERM_BP_ALL	cerebellar cortex morphogenesis	RT	3	3.3E-1	1.0E0
☐	GOTERM_BP_ALL	cyclic nucleotide metabolic process	RT	5	3.4E-1	1.0E0
☐	GOTERM_BP_ALL	cerebellum morphogenesis	RT	3	3.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	disease mutation	RT	8	3.9E-1	1.0E0
☐	GOTERM_BP_ALL	hindbrain morphogenesis	RT	3	3.9E-1	1.0E0
☐	GOTERM_BP_ALL	cerebellar cortex development	RT	3	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	metencephalon development	RT	3	5.3E-1	1.0E0
☐	GOTERM_BP_ALL	cerebellum development	RT	3	5.3E-1	1.0E0
☐	GOTERM_BP_ALL	nitric oxide metabolic process	RT	3	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	nitric oxide biosynthetic process	RT	3	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	hindbrain development	RT	4	6.4E-1	1.0E0
☐	GOTERM_BP_ALL	nitrogen compound biosynthetic process	RT	4	9.9E-1	1.0E0
	Annotation Cluster 71	Enrichment Score: 0.59	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	membrane lipid metabolic process	RT	20	1.0E-1	9.8E-1
☐	GOTERM_BP_ALL	cellular lipid metabolic process	RT	49	2.5E-1	1.0E0
☐	GOTERM_BP_ALL	lipid metabolic process	RT	55	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	lipid biosynthetic process	RT	21	5.3E-1	1.0E0
	Annotation Cluster 72	Enrichment Score: 0.58	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Nucleotidyltransferase	RT	9	1.7E-1	9.4E-1
☐	SP_PIR_KEYWORDS	DNA-directed DNA polymerase	RT	4	1.9E-1	9.5E-1
☐	KEGG_PATHWAY	DNA polymerase	RT	4	2.6E-1	8.7E-1
☐	GOTERM_MF_ALL	nucleotidyltransferase activity	RT	12	3.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna replication	RT	8	3.3E-1	9.9E-1
☐	GOTERM_MF_ALL	DNA-directed DNA polymerase activity	RT	4	4.0E-1	1.0E0

	Annotation Cluster 73	Enrichment Score: 0.58	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	spermine catabolic process	RT		3	1.8E-2	7.3E-1
☐	GOTERM_BP_ALL	polyamine catabolic process	RT		3	5.3E-2	9.4E-1
☐	GOTERM_BP_ALL	spermine metabolic process	RT		3	1.0E-1	9.8E-1
☐	GOTERM_BP_ALL	amino acid derivative catabolic process	RT		4	1.5E-1	9.9E-1
☐	GOTERM_BP_ALL	biogenic amine catabolic process	RT		3	3.3E-1	1.0E0
☐	GOTERM_BP_ALL	polyamine metabolic process	RT		3	3.9E-1	1.0E0
☐	GOTERM_BP_ALL	biogenic amine metabolic process	RT		4	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	amine catabolic process	RT		3	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	nitrogen compound catabolic process	RT		3	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	amino acid derivative metabolic process	RT		4	9.8E-1	1.0E0
	Annotation Cluster 74	Enrichment Score: 0.58	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	myelin sheath	RT		3	4.9E-2	8.8E-1
☐	GOTERM_BP_ALL	myelination	RT		5	2.3E-1	1.0E0
☐	GOTERM_BP_ALL	ensheathment of neurons	RT		5	2.6E-1	1.0E0
☐	GOTERM_BP_ALL	axon ensheathment	RT		5	2.6E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of action potential	RT		5	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	transmission of nerve impulse	RT		15	9.5E-1	1.0E0
	Annotation Cluster 75	Enrichment Score: 0.58	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Protein kinase C, phorbol ester/diacylglycerol binding	RT		9	9.4E-2	1.0E0
☐	SMART	C1	RT		9	1.7E-1	9.5E-1
☐	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 1	RT		3	2.2E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 2	RT		3	2.2E-1	1.0E0
☐	GOTERM_MF_ALL	protein kinase C activity	RT		3	3.3E-1	1.0E0
☐	GOTERM_MF_ALL	diacylglycerol binding	RT		6	3.8E-1	1.0E0
☐	GOTERM_MF_ALL	phorbol ester receptor activity	RT		3	3.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	Phorbol-ester binding	RT		4	6.4E-1	1.0E0
	Annotation Cluster 76	Enrichment Score: 0.56	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	odontogenesis of dentine-containing teeth	RT		8	2.7E-2	8.3E-1
☐	GOTERM_BP_ALL	odontogenesis	RT		8	4.5E-2	9.2E-1
☐	GOTERM_BP_ALL	kidney development	RT		6	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	metanephros development	RT		4	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	urogenital system development	RT		6	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	ureteric bud development	RT		3	8.0E-1	1.0E0
	Annotation Cluster 77	Enrichment Score: 0.56	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	microbody membrane	RT		4	1.7E-1	1.0E0
☐	GOTERM_CC_ALL	peroxisomal membrane	RT		4	1.7E-1	1.0E0
☐	GOTERM_CC_ALL	microbody part	RT		4	2.1E-1	1.0E0
☐	GOTERM_CC_ALL	peroxisomal part	RT		4	2.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	peroxisome	RT		8	4.0E-1	1.0E0
☐	GOTERM_CC_ALL	microbody	RT		8	5.0E-1	1.0E0
☐	GOTERM_CC_ALL	peroxisome	RT		8	5.0E-1	1.0E0
	Annotation Cluster 78	Enrichment Score: 0.55	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	lysosomal transport	RT		3	1.8E-1	1.0E0
☐	GOTERM_BP_ALL	vacuolar transport	RT		4	1.9E-1	1.0E0
☐	GOTERM_BP_ALL	endosome transport	RT		3	6.4E-1	1.0E0
	Annotation Cluster 79	Enrichment Score: 0.55	G	🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Prostate cancer	RT		13	3.5E-2	4.7E-1
☐	KEGG_PATHWAY	Renal cell carcinoma	RT		11	4.2E-2	5.0E-1

☐	KEGG_PATHWAY	mTOR signaling pathway	RT		8	9.5E-2	7.1E-1
☐	KEGG_PATHWAY	Melanoma	RT		9	1.5E-1	8.4E-1
☐	KEGG_PATHWAY	Insulin signaling pathway	RT		14	1.8E-1	8.6E-1
☐	GOTERM_MF_ALL	phosphoinositide 3-kinase activity	RT		3	1.8E-1	1.0E0
☐	GOTERM_MF_ALL	1-phosphatidylinositol-3-kinase activity	RT		3	1.8E-1	1.0E0
☐	KEGG_PATHWAY	Chronic myeloid leukemia	RT		9	2.0E-1	8.6E-1
☐	GOTERM_CC_ALL	phosphoinositide 3-kinase complex	RT		3	2.0E-1	1.0E0
☐	KEGG_PATHWAY	Non-small cell lung cancer	RT		7	2.2E-1	8.8E-1
☐	KEGG_PATHWAY	B cell receptor signaling pathway	RT		8	2.3E-1	8.7E-1
☐	KEGG_PATHWAY	Small cell lung cancer	RT		10	2.4E-1	8.7E-1
☐	KEGG_PATHWAY	Type II diabetes mellitus	RT		6	2.7E-1	8.9E-1
☐	KEGG_PATHWAY	Glioma	RT		7	2.9E-1	8.9E-1
☐	KEGG_PATHWAY	Fc epsilon RI signaling pathway	RT		8	3.1E-1	8.9E-1
☐	KEGG_PATHWAY	Endometrial cancer	RT		6	3.4E-1	9.0E-1
☐	KEGG_PATHWAY	Focal adhesion	RT		17	3.8E-1	9.1E-1
☐	KEGG_PATHWAY	ErbB signaling pathway	RT		8	4.4E-1	9.3E-1
☐	KEGG_PATHWAY	T cell receptor signaling pathway	RT		9	4.4E-1	9.3E-1
☐	KEGG_PATHWAY	Acute myeloid leukemia	RT		6	4.6E-1	9.4E-1
☐	GOTERM_MF_ALL	inositol or phosphatidylinositol kinase activity	RT		4	4.8E-1	1.0E0
☐	GOTERM_MF_ALL	lipid kinase activity	RT		3	5.2E-1	1.0E0
☐	KEGG_PATHWAY	Phosphatidylinositol signaling system	RT		6	5.5E-1	9.7E-1
☐	KEGG_PATHWAY	Colorectal cancer	RT		7	5.7E-1	9.7E-1
☐	KEGG_PATHWAY	Leukocyte transendothelial migration	RT		9	5.8E-1	9.7E-1
☐	KEGG_PATHWAY	Pancreatic cancer	RT		6	6.4E-1	9.8E-1
☐	KEGG_PATHWAY	VEGF signaling pathway	RT		5	8.2E-1	9.9E-1
☐	GOTERM_CC_ALL	cytosolic part	RT		5	9.6E-1	1.0E0
	Annotation Cluster 80	Enrichment Score: 0.54	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	N-acetyltransferase activity	RT		8	1.3E-1	1.0E0
☐	GOTERM_MF_ALL	acetyltransferase activity	RT		9	1.6E-1	1.0E0
☐	GOTERM_MF_ALL	N-acyltransferase activity	RT		8	2.3E-1	1.0E0
☐	GOTERM_MF_ALL	acyltransferase activity	RT		16	3.8E-1	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring groups other than amino-acyl groups	RT		16	4.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	acyltransferase	RT		12	4.6E-1	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring acyl groups	RT		16	4.7E-1	1.0E0
	Annotation Cluster 81	Enrichment Score: 0.54	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Basic-leucine zipper (bZIP) transcription factor	RT		7	1.8E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Leucine-zipper	RT		10	1.9E-1	1.0E0
☐	SMART	BRLZ	RT		7	3.3E-1	9.9E-1
☐	UP_SEQ_FEATURE	DNA-binding region:Basic motif	RT		9	5.9E-1	1.0E0
	Annotation Cluster 82	Enrichment Score: 0.54	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	zinc finger region:B box-type	RT		6	4.5E-2	1.0E0
☐	INTERPRO	Zinc finger, B-box	RT		9	6.3E-2	1.0E0
☐	INTERPRO	B-box, C-terminal	RT		4	1.0E-1	1.0E0
☐	SMART	BBOX	RT		9	1.2E-1	9.2E-1
☐	SMART	BBC	RT		4	3.6E-1	9.9E-1
☐	UP_SEQ_FEATURE	domain:B30.2/SPRY	RT		3	5.8E-1	1.0E0
☐	INTERPRO	Butyrophylin-like	RT		4	6.2E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001733:rfp transforming protein	RT		3	6.6E-1	1.0E0

☐	INTERPRO	SPla/RYanodine receptor SPRY	RT		5	6.9E-1	1.0E0
☐	INTERPRO	B302, (SPRY)-like	RT		5	7.1E-1	1.0E0
☐	SMART	SPRY	RT		5	8.4E-1	1.0E0
	Annotation Cluster 83	Enrichment Score: 0.52	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Metal-dependent phosphohydrolase, HD region	RT		4	2.2E-1	1.0E0
☐	GOTERM_MF_ALL	3',5'-cyclic-nucleotide phosphodiesterase activity	RT		4	2.4E-1	1.0E0
☐	SMART	HDc	RT		4	2.9E-1	9.8E-1
☐	GOTERM_MF_ALL	cyclic-nucleotide phosphodiesterase activity	RT		4	2.9E-1	1.0E0
☐	INTERPRO	3'5'-cyclic nucleotide phosphodiesterase	RT		3	4.1E-1	1.0E0
☐	GOTERM_MF_ALL	phosphoric diester hydrolase activity	RT		7	4.1E-1	1.0E0
	Annotation Cluster 84	Enrichment Score: 0.52	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of cell motility	RT		11	8.6E-2	9.7E-1
☐	GOTERM_BP_ALL	regulation of cell migration	RT		10	9.3E-2	9.8E-1
☐	GOTERM_BP_ALL	regulation of locomotion	RT		11	1.1E-1	9.9E-1
☐	GOTERM_BP_ALL	locomotion	RT		11	1.7E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cell migration	RT		4	2.1E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cell motility	RT		4	2.9E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of locomotion	RT		4	2.9E-1	1.0E0
☐	GOTERM_BP_ALL	cell migration	RT		27	4.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	growth factor	RT		11	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	localization of cell	RT		28	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	cell motility	RT		28	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	cell-matrix adhesion	RT		6	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	cell-substrate adhesion	RT		6	8.0E-1	1.0E0
	Annotation Cluster 85	Enrichment Score: 0.52	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	positive regulation of cell adhesion	RT		5	4.0E-2	9.1E-1
☐	GOTERM_BP_ALL	bone remodeling	RT		13	2.0E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of ossification	RT		5	2.1E-1	1.0E0
☐	GOTERM_BP_ALL	ossification	RT		12	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	biomineral formation	RT		12	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	osteoblast differentiation	RT		5	2.3E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of bone remodeling	RT		5	2.8E-1	1.0E0
☐	GOTERM_BP_ALL	tissue remodeling	RT		13	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	cartilage development	RT		5	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell adhesion	RT		5	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	skeletal development	RT		15	7.3E-1	1.0E0
☐	GOTERM_BP_ALL	tissue development	RT		19	9.3E-1	1.0E0
	Annotation Cluster 86	Enrichment Score: 0.51	G	🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	SNARE interactions in vesicular transport	RT		5	2.4E-1	8.7E-1
☐	INTERPRO	Syntaxin, N-terminal	RT		3	2.6E-1	1.0E0
☐	INTERPRO	Target SNARE coiled-coil region	RT		4	3.0E-1	1.0E0
☐	SMART	SynN	RT		3	3.2E-1	9.9E-1
☐	INTERPRO	Syntaxin/epimorphin coiled-coil	RT		3	3.8E-1	1.0E0
☐	SMART	t_SNARE	RT		4	3.9E-1	9.9E-1
	Annotation Cluster 87	Enrichment Score: 0.5	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:F-box	RT		7	1.4E-1	1.0E0
☐	SMART	FBOX	RT		7	4.8E-1	1.0E0
☐	INTERPRO	Cyclin-like F-box	RT		6	4.8E-1	1.0E0
	Annotation Cluster 88	Enrichment Score: 0.49	G	🟩	Count	P_Value	Benjamini

☐	**SP_PIR_KEYWORDS**	thiol protease	RT		14	6.1E-2	8.1E-1
☐	**GOTERM_MF_ALL**	cysteine-type peptidase activity	RT		18	1.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	small conjugating protein-specific protease activity	RT		7	3.8E-1	1.0E0
☐	**INTERPRO**	Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2	RT		5	4.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	ubiquitin-specific protease activity	RT		6	5.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	thiolester hydrolase activity	RT		7	6.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	ubiquitin thiolesterase activity	RT		5	7.0E-1	1.0E0
	Annotation Cluster 89	Enrichment Score: 0.49	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	RNA recognition motif, RNP-1	RT		17	1.7E-1	1.0E0
☐	**SMART**	RRM	RT		21	2.1E-1	9.7E-1
☐	**INTERPRO**	Nucleotide-binding, alpha-beta plait	RT		16	2.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	rna-binding	RT		31	4.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	RNA binding	RT		40	8.9E-1	1.0E0
	Annotation Cluster 90	Enrichment Score: 0.48	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	adrenal gland development	RT		3	1.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	gland development	RT		8	3.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	endocrine system development	RT		5	5.8E-1	1.0E0
	Annotation Cluster 91	Enrichment Score: 0.47	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Phox-like	RT		7	1.3E-1	1.0E0
☐	**SMART**	PX	RT		7	2.1E-1	9.7E-1
☐	**GOTERM_MF_ALL**	lipid binding	RT		35	3.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	phosphoinositide binding	RT		14	6.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	phospholipid binding	RT		17	7.1E-1	1.0E0
	Annotation Cluster 92	Enrichment Score: 0.47	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Tetratricopeptide region	RT		13	7.3E-2	1.0E0
☐	**INTERPRO**	Tetratricopeptide-like helical	RT		13	1.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	TPR repeat	RT		13	1.5E-1	9.2E-1
☐	**SMART**	TPR	RT		13	2.0E-1	9.7E-1
☐	**INTERPRO**	Tetratricopeptide TPR-1	RT		9	2.5E-1	1.0E0
☐	**INTERPRO**	Tetratricopeptide TPR2	RT		6	3.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:TPR 8	RT		3	4.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:TPR 4	RT		4	5.0E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:TPR 3	RT		5	5.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:TPR 7	RT		3	5.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:TPR 1	RT		5	6.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:TPR 2	RT		5	6.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:TPR 6	RT		3	6.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:TPR 5	RT		3	6.4E-1	1.0E0
	Annotation Cluster 93	Enrichment Score: 0.47	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	RT		6	8.9E-2	9.9E-1
☐	**KEGG_PATHWAY**	Propanoate metabolism	RT		5	1.8E-1	8.6E-1
☐	**GOTERM_MF_ALL**	oxidoreductase activity, acting on the aldehyde or oxo group of donors	RT		6	2.1E-1	1.0E0
☐	**INTERPRO**	Aldehyde dehydrogenase	RT		3	2.9E-1	1.0E0
☐	**KEGG_PATHWAY**	Lysine degradation	RT		4	5.9E-1	9.7E-1
☐	**KEGG_PATHWAY**	Valine, leucine and isoleucine degradation	RT		4	6.1E-1	9.7E-1
☐	**KEGG_PATHWAY**	Butanoate metabolism	RT		4	7.1E-1	9.8E-1
☐	**KEGG_PATHWAY**	Bile acid biosynthesis	RT		3	7.2E-1	9.9E-1
	Annotation Cluster 94	Enrichment Score: 0.46	G	🟩	Count	P_Value	Benjamini

☐	**KEGG_PATHWAY**	Propanoate metabolism	RT		5	1.8E-1	8.6E-1
☐	**KEGG_PATHWAY**	Pyruvate metabolism	RT		5	3.7E-1	9.1E-1
☐	**KEGG_PATHWAY**	Glycolysis / Gluconeogenesis	RT		5	5.9E-1	9.7E-1
	Annotation Cluster 95	Enrichment Score: 0.46	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	insulin-like growth factor binding	RT		4	2.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:IGFBP N-terminal	RT		3	3.6E-1	1.0E0
☐	**SMART**	IB	RT		3	5.1E-1	1.0E0
	Annotation Cluster 96	Enrichment Score: 0.46	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Guanine-nucleotide dissociation stimulator CDC25	RT		4	3.0E-1	1.0E0
☐	**INTERPRO**	Ras guanine nucleotide exchange factor	RT		4	3.7E-1	1.0E0
☐	**SMART**	RasGEF	RT		4	3.9E-1	9.9E-1
	Annotation Cluster 97	Enrichment Score: 0.45	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	GTPase activity	RT		19	4.1E-2	9.4E-1
☐	**GOTERM_MF_ALL**	pyrophosphatase activity	RT		46	3.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	nucleoside-triphosphatase activity	RT		44	3.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	RT		46	4.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrolase activity, acting on acid anhydrides	RT		46	4.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	ATPase activity	RT		23	7.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	ATPase activity, coupled	RT		17	9.1E-1	1.0E0
	Annotation Cluster 98	Enrichment Score: 0.43	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	cell development	RT		112	7.9E-2	9.7E-1
☐	**GOTERM_BP_ALL**	cellular developmental process	RT		157	1.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell differentiation	RT		157	1.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	developmental process	RT		244	2.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	organ development	RT		111	5.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	system development	RT		134	6.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	multicellular organismal development	RT		172	7.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	anatomical structure development	RT		155	7.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	multicellular organismal process	RT		208	9.6E-1	1.0E0
	Annotation Cluster 99	Enrichment Score: 0.43	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	condensed chromosome, pericentric region	RT		3	1.4E-1	1.0E0
☐	**GOTERM_CC_ALL**	chromosome, pericentric region	RT		6	5.8E-1	1.0E0
☐	**GOTERM_CC_ALL**	condensed chromosome	RT		5	6.2E-1	1.0E0
	Annotation Cluster 100	Enrichment Score: 0.42	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of ARF protein signal transduction	RT		3	3.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	ARF guanyl-nucleotide exchange factor activity	RT		3	3.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	ARF protein signal transduction	RT		3	3.6E-1	1.0E0
☐	**INTERPRO**	SEC7-like	RT		3	3.8E-1	1.0E0
☐	**SMART**	Sec7	RT		3	4.5E-1	1.0E0
	Annotation Cluster 101	Enrichment Score: 0.41	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	acetyl-CoA biosynthetic process	RT		3	7.6E-2	9.6E-1
☐	**GOTERM_BP_ALL**	acetyl-CoA metabolic process	RT		3	7.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	coenzyme metabolic process	RT		9	9.7E-1	1.0E0
	Annotation Cluster 102	Enrichment Score: 0.41	G	🟩	Count	P_Value	Benjamini
☐	**KEGG_PATHWAY**	ABC transporters - General	RT		8	2.5E-2	3.9E-1
☐	**UP_SEQ_FEATURE**	nucleotide phosphate-binding region:ATP 2	RT		4	1.3E-1	1.0E0
☐	**UP_SEQ_FEATURE**	nucleotide phosphate-binding region:ATP 1	RT		4	1.3E-1	1.0E0

☐	UP_SEQ_FEATURE	domain:ABC transporter 2	RT		4	1.3E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:ABC transporter 1	RT		4	1.3E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:ABC transmembrane type-1 2	RT		3	1.7E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:ABC transmembrane type-1 1	RT		3	1.7E-1	1.0E0
☐	INTERPRO	ABC transporter, transmembrane region, type 1	RT		4	3.2E-1	1.0E0
☐	COG_ONTOLOGY	Defense mechanisms	RT		4	6.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotide binding	RT		7	6.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	P-loop	RT		7	6.2E-1	1.0E0
☐	BIOCARTA	Nuclear Receptors in Lipid Metabolism and Toxicity	RT		4	6.9E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity	RT		23	7.5E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity, coupled to movement of substances	RT		9	8.4E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity, coupled to transmembrane movement of substances	RT		9	8.4E-1	1.0E0
☐	GOTERM_MF_ALL	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT		9	8.6E-1	1.0E0
☐	GOTERM_MF_ALL	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT		9	9.1E-1	1.0E0
☐	GOTERM_MF_ALL	primary active transmembrane transporter activity	RT		9	9.1E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity, coupled	RT		17	9.1E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT		3	9.7E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity, coupled to transmembrane movement of ions	RT		4	9.8E-1	1.0E0
	Annotation Cluster 103	Enrichment Score: 0.4	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Protein phosphatase 2C, manganese/magnesium aspartate binding site	RT		3	2.6E-1	1.0E0
☐	GOTERM_MF_ALL	protein serine/threonine phosphatase activity	RT		5	3.1E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C	RT		3	3.2E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C, N-terminal	RT		3	3.8E-1	1.0E0
☐	INTERPRO	Protein phosphatase 2C-related	RT		3	4.1E-1	1.0E0
☐	GOTERM_MF_ALL	protein phosphatase type 2C activity	RT		3	4.7E-1	1.0E0
☐	SMART	PP2C_SIG	RT		3	4.8E-1	1.0E0
☐	SMART	PP2Cc	RT		3	4.8E-1	1.0E0
☐	GOTERM_CC_ALL	protein serine/threonine phosphatase complex	RT		3	6.2E-1	1.0E0
	Annotation Cluster 104	Enrichment Score: 0.39	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	GTPase activity	RT		19	4.1E-2	9.4E-1
☐	INTERPRO	Ras small GTPase, Rab type	RT		8	1.6E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001710:Ras-related protein Rab	RT		7	2.3E-1	1.0E0
☐	SMART	RAB	RT		8	2.7E-1	9.8E-1
☐	GOTERM_MF_ALL	GTP binding	RT		30	2.9E-1	1.0E0
☐	UP_SEQ_FEATURE	lipid moiety-binding region:S-geranylgeranyl cysteine	RT		9	3.0E-1	1.0E0
☐	GOTERM_MF_ALL	guanyl nucleotide binding	RT		30	3.2E-1	1.0E0
☐	GOTERM_MF_ALL	guanyl ribonucleotide binding	RT		30	3.2E-1	1.0E0
☐	INTERPRO	Ras	RT		11	3.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	prenylation	RT		12	4.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	GTP-binding	RT		22	5.2E-1	1.0E0
☐	INTERPRO	Ras GTPase	RT		12	5.5E-1	1.0E0
☐	UP_SEQ_FEATURE	short sequence motif:Effector region	RT		6	7.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	er-golgi transport	RT		4	8.6E-1	1.0E0

☐	**INTERPRO**	Small GTP-binding protein domain	RT	9	8.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	Golgi vesicle transport	RT	5	9.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	nucleotide phosphate-binding region:GTP	RT	11	9.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	ER to Golgi vesicle-mediated transport	RT	3	9.5E-1	1.0E0
	Annotation Cluster 105	Enrichment Score: 0.38	G	Count	P_Value	Benjamini
☐	**BIOCARTA**	NFkB activation by Nontypeable Hemophilus influenzae	RT	6	1.6E-1	1.0E0
☐	**BIOCARTA**	TGF beta signaling pathway	RT	4	2.9E-1	1.0E0
☐	**KEGG_PATHWAY**	Adherens junction	RT	5	8.0E-1	9.9E-1
☐	**KEGG_PATHWAY**	Cell cycle	RT	7	8.1E-1	9.9E-1
	Annotation Cluster 106	Enrichment Score: 0.38	G	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 3; atypical	RT	3	9.0E-2	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 1; atypical	RT	3	1.7E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 7	RT	6	2.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 2	RT	12	3.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 3	RT	11	4.3E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 4	RT	9	4.3E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 8	RT	5	4.5E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 6	RT	6	4.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 1	RT	11	4.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 5	RT	7	5.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:KRAB	RT	3	5.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 13	RT	3	5.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 9	RT	4	5.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 11	RT	3	6.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 12	RT	3	6.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 10	RT	3	7.7E-1	1.0E0
	Annotation Cluster 107	Enrichment Score: 0.38	G	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	domain:Rho-GAP	RT	4	3.0E-1	1.0E0
☐	**INTERPRO**	RhoGAP	RT	5	4.2E-1	1.0E0
☐	**SMART**	RhoGAP	RT	5	5.8E-1	1.0E0
	Annotation Cluster 108	Enrichment Score: 0.37	G	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	enzyme binding	RT	19	3.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	kinase binding	RT	8	4.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	protein kinase binding	RT	7	4.9E-1	1.0E0
	Annotation Cluster 109	Enrichment Score: 0.37	G	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	carbohydrate transmembrane transporter activity	RT	6	2.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	glucose transmembrane transporter activity	RT	3	2.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	monosaccharide transmembrane transporter activity	RT	3	3.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	hexose transmembrane transporter activity	RT	3	3.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	sugar:hydrogen ion symporter activity	RT	5	4.2E-1	1.0E0
☐	**GOTERM_MF_ALL**	sugar transmembrane transporter activity	RT	5	4.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	symporter activity	RT	13	4.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	carbohydrate transport	RT	7	4.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	secondary active transmembrane transporter activity	RT	15	6.1E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	sugar transport	RT	3	6.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	active transmembrane transporter activity	RT	24	8.2E-1	1.0E0
	Annotation Cluster 110	Enrichment Score: 0.37	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	interphase	RT	7	3.2E-1	1.0E0

☐	GOTERM_BP_ALL	interphase of mitotic cell cycle	RT		7	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	G1/S transition of mitotic cell cycle	RT		4	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	mitotic cell cycle	RT		18	7.8E-1	1.0E0
	Annotation Cluster 111	Enrichment Score: 0.36	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:Ubiquitin-like	RT		4	2.4E-1	1.0E0
☐	INTERPRO	Ubiquitin	RT		5	5.1E-1	1.0E0
☐	SMART	UBQ	RT		5	6.8E-1	1.0E0
	Annotation Cluster 112	Enrichment Score: 0.36	G	🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Glycosphingolipid biosynthesis - ganglioseries	RT		4	9.7E-2	7.0E-1
☐	INTERPRO	Glycosyl transferase, family 29	RT		4	2.0E-1	1.0E0
☐	GOTERM_MF_ALL	sialyltransferase activity	RT		4	2.0E-1	1.0E0
☐	GOTERM_CC_ALL	integral to Golgi membrane	RT		5	2.0E-1	1.0E0
☐	KEGG_PATHWAY	Glycan structures - biosynthesis 2	RT		7	2.2E-1	8.8E-1
☐	KEGG_PATHWAY	O-Glycan biosynthesis	RT		4	2.7E-1	8.8E-1
☐	GOTERM_CC_ALL	intrinsic to Golgi membrane	RT		5	3.0E-1	1.0E0
☐	GOTERM_CC_ALL	intrinsic to organelle membrane	RT		9	3.1E-1	1.0E0
☐	INTERPRO	Sialyltransferase	RT		3	3.2E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF005557:sialyltransferase	RT		3	3.3E-1	1.0E0
☐	GOTERM_CC_ALL	integral to organelle membrane	RT		8	3.5E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid O-linked glycosylation	RT		3	3.9E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid glycosylation	RT		8	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	biopolymer glycosylation	RT		8	5.5E-1	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring glycosyl groups	RT		19	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	glycoprotein metabolic process	RT		10	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	glycoprotein biosynthetic process	RT		8	6.3E-1	1.0E0
☐	GOTERM_CC_ALL	Golgi membrane	RT		8	6.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	glycosyltransferase	RT		13	7.3E-1	1.0E0
☐	KEGG_PATHWAY	Glycan structures - biosynthesis 1	RT		7	8.1E-1	9.9E-1
☐	SP_PIR_KEYWORDS	signal-anchor	RT		22	8.6E-1	1.0E0
☐	GOTERM_CC_ALL	Golgi apparatus part	RT		10	9.1E-1	1.0E0
☐	UP_SEQ_FEATURE	topological domain:Lumenal	RT		14	9.2E-1	1.0E0
☐	GOTERM_MF_ALL	UDP-glycosyltransferase activity	RT		5	9.5E-1	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring hexosyl groups	RT		7	9.8E-1	1.0E0
	Annotation Cluster 113	Enrichment Score: 0.35	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:WW	RT		3	1.9E-1	1.0E0
☐	SMART	WW	RT		5	6.3E-1	1.0E0
☐	INTERPRO	WW/Rsp5/WWP	RT		4	7.1E-1	1.0E0
	Annotation Cluster 114	Enrichment Score: 0.35	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	photoreceptor cell maintenance	RT		4	5.0E-2	9.4E-1
☐	GOTERM_BP_ALL	visual perception	RT		11	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	sensory perception of light stimulus	RT		11	3.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	Vision	RT		4	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	sensory perception	RT		19	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	neurological system process	RT		33	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	sensory transduction	RT		5	9.8E-1	1.0E0
	Annotation Cluster 115	Enrichment Score: 0.34	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of progression through cell cycle	RT		17	8.2E-2	9.7E-1
☐	GOTERM_BP_ALL	cell cycle	RT		58	5.7E-1	1.0E0

☐	**GOTERM_BP_ALL**	regulation of cell cycle	RT		30	5.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of progression through cell cycle	RT		29	6.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell cycle process	RT		45	6.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell cycle phase	RT		22	7.2E-1	1.0E0
	Annotation Cluster 116	Enrichment Score: 0.33	G	🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	domain:SAM	RT		6	1.2E-1	1.0E0
☐	**SMART**	SAM	RT		8	5.1E-1	1.0E0
☐	**INTERPRO**	Sterile alpha motif SAM	RT		7	5.1E-1	1.0E0
☐	**INTERPRO**	Sterile alpha motif homology 2	RT		3	7.2E-1	1.0E0
☐	**INTERPRO**	Sterile alpha motif-type	RT		3	9.5E-1	1.0E0
	Annotation Cluster 117	Enrichment Score: 0.32	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	positive regulation of cell differentiation	RT		7	3.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of myeloid cell differentiation	RT		3	4.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of myeloid cell differentiation	RT		5	5.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cell differentiation	RT		16	5.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of developmental process	RT		8	5.6E-1	1.0E0
	Annotation Cluster 118	Enrichment Score: 0.32	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	RT		6	4.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	dioxygenase activity	RT		6	4.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	RT		6	4.9E-1	1.0E0
	Annotation Cluster 119	Enrichment Score: 0.31	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	lysosome	RT		11	3.9E-1	1.0E0
☐	**GOTERM_CC_ALL**	vacuole	RT		17	5.0E-1	1.0E0
☐	**GOTERM_CC_ALL**	lytic vacuole	RT		15	5.3E-1	1.0E0
☐	**GOTERM_CC_ALL**	lysosome	RT		15	5.3E-1	1.0E0
	Annotation Cluster 120	Enrichment Score: 0.31	G	🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	domain:Kazal-like	RT		3	3.3E-1	1.0E0
☐	**INTERPRO**	Proteinase inhibitor I1, Kazal	RT		4	5.3E-1	1.0E0
☐	**SMART**	KAZAL	RT		4	6.7E-1	1.0E0
	Annotation Cluster 121	Enrichment Score: 0.3	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	neural tube formation	RT		6	2.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	neural plate morphogenesis	RT		6	2.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	neural plate development	RT		6	2.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	embryonic epithelial tube formation	RT		6	2.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	tube morphogenesis	RT		15	3.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	neural tube development	RT		6	4.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	morphogenesis of embryonic epithelium	RT		6	5.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	tube development	RT		17	5.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	morphogenesis of an epithelium	RT		10	5.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	in utero embryonic development	RT		10	6.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	neural tube closure	RT		3	7.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	primary neural tube formation	RT		3	7.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	embryonic development	RT		33	7.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	chordate embryonic development	RT		16	7.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	embryonic development ending in birth or egg hatching	RT		16	7.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	embryonic morphogenesis	RT		13	8.4E-1	1.0E0

	Annotation Cluster 122	Enrichment Score: 0.3	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:RRM 1	RT		5	5.0E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:RRM 2	RT		5	5.0E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:RRM 3	RT		3	5.2E-1	1.0E0
	Annotation Cluster 123	Enrichment Score: 0.3	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	ubiquitin-dependent protein catabolic process	RT		15	2.3E-1	1.0E0
☐	GOTERM_BP_ALL	modification-dependent protein catabolic process	RT		15	2.6E-1	1.0E0
☐	GOTERM_BP_ALL	modification-dependent macromolecule catabolic process	RT		15	2.6E-1	1.0E0
☐	GOTERM_BP_ALL	proteolysis involved in cellular protein catabolic process	RT		15	2.8E-1	1.0E0
☐	GOTERM_BP_ALL	cellular protein catabolic process	RT		15	3.0E-1	1.0E0
☐	INTERPRO	Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2	RT		5	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	biopolymer catabolic process	RT		21	6.6E-1	1.0E0
☐	GOTERM_BP_ALL	protein catabolic process	RT		16	6.6E-1	1.0E0
☐	GOTERM_MF_ALL	ubiquitin thiolesterase activity	RT		5	7.0E-1	1.0E0
☐	GOTERM_BP_ALL	cellular macromolecule catabolic process	RT		18	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	macromolecule catabolic process	RT		21	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	cellular catabolic process	RT		29	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	catabolic process	RT		35	9.9E-1	1.0E0
	Annotation Cluster 124	Enrichment Score: 0.3	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Plexin/semaphorin/integrin	RT		6	2.9E-1	1.0E0
☐	SMART	PSI	RT		6	4.1E-1	9.9E-1
☐	INTERPRO	Plexin	RT		4	4.5E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Sema	RT		3	5.2E-1	1.0E0
☐	INTERPRO	Semaphorin/CD100 antigen	RT		3	7.3E-1	1.0E0
☐	SMART	Sema	RT		3	8.1E-1	1.0E0
	Annotation Cluster 125	Enrichment Score: 0.28	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on heme group of donors, oxygen as acceptor	RT		4	3.3E-1	1.0E0
☐	GOTERM_MF_ALL	heme-copper terminal oxidase activity	RT		4	3.3E-1	1.0E0
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on heme group of donors	RT		4	3.3E-1	1.0E0
☐	GOTERM_MF_ALL	cytochrome-c oxidase activity	RT		4	3.3E-1	1.0E0
☐	GOTERM_MF_ALL	hydrogen ion transmembrane transporter activity	RT		6	9.3E-1	1.0E0
☐	GOTERM_MF_ALL	monovalent inorganic cation transmembrane transporter activity	RT		6	9.4E-1	1.0E0
☐	GOTERM_MF_ALL	inorganic cation transmembrane transporter activity	RT		7	9.8E-1	1.0E0
	Annotation Cluster 126	Enrichment Score: 0.28	G	🟩	Count	P_Value	Benjamini
☐	BIOCARTA	Regulation of hematopoiesis by cytokines	RT		3	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of osteoclast differentiation	RT		3	4.8E-1	1.0E0
☐	BIOCARTA	Cytokines and Inflammatory Response	RT		4	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of myeloid cell differentiation	RT		5	5.2E-1	1.0E0
☐	GOTERM_BP_ALL	myeloid leukocyte differentiation	RT		5	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of myeloid leukocyte differentiation	RT		3	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	osteoclast differentiation	RT		3	6.0E-1	1.0E0
	Annotation Cluster 127	Enrichment Score: 0.26	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	cytokine binding	RT		9	3.4E-1	1.0E0
☐	INTERPRO	Chemokine receptor	RT		3	3.8E-1	1.0E0
☐	GOTERM_MF_ALL	C-C chemokine receptor activity	RT		3	4.4E-1	1.0E0
☐	GOTERM_MF_ALL	C-C chemokine binding	RT		3	4.4E-1	1.0E0

☐	GOTERM_MF_ALL	chemokine receptor activity	RT	3	5.9E-1	1.0E0
☐	GOTERM_MF_ALL	chemokine binding	RT	3	6.1E-1	1.0E0
☐	GOTERM_MF_ALL	peptide binding	RT	9	8.8E-1	1.0E0
☐	GOTERM_MF_ALL	peptide receptor activity	RT	6	9.5E-1	1.0E0
	Annotation Cluster 128	Enrichment Score: 0.26	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	protein phosphatase	RT	12	1.8E-1	9.4E-1
☐	GOTERM_MF_ALL	phosphoprotein phosphatase activity	RT	15	3.0E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid dephosphorylation	RT	11	5.1E-1	1.0E0
☐	GOTERM_MF_ALL	phosphoric ester hydrolase activity	RT	24	5.7E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase, receptor/non-receptor type	RT	4	5.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	tyrosine-specific phosphatase	RT	3	6.0E-1	1.0E0
☐	GOTERM_MF_ALL	hydrolase activity, acting on ester bonds	RT	48	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	dephosphorylation	RT	11	6.7E-1	1.0E0
☐	SMART	PTPc	RT	4	6.9E-1	1.0E0
☐	GOTERM_MF_ALL	phosphoric monoester hydrolase activity	RT	18	6.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	phosphoric monoester hydrolase	RT	4	7.0E-1	1.0E0
☐	GOTERM_MF_ALL	protein tyrosine phosphatase activity	RT	7	7.0E-1	1.0E0
☐	INTERPRO	Protein-tyrosine phosphatase, Tyr-specific/dual-specificity type	RT	6	7.5E-1	1.0E0
	Annotation Cluster 129	Enrichment Score: 0.26	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:J	RT	4	3.2E-1	1.0E0
☐	INTERPRO	Heat shock protein DnaJ, N-terminal	RT	5	3.9E-1	1.0E0
☐	GOTERM_MF_ALL	heat shock protein binding	RT	6	4.6E-1	1.0E0
☐	SMART	DnaJ	RT	5	5.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	chaperone	RT	7	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	protein folding	RT	11	9.7E-1	1.0E0
	Annotation Cluster 130	Enrichment Score: 0.26	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	spermatid development	RT	5	3.5E-1	1.0E0
☐	GOTERM_BP_ALL	spermatid differentiation	RT	5	3.9E-1	1.0E0
☐	GOTERM_BP_ALL	gamete generation	RT	22	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	sexual reproduction	RT	25	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	reproduction	RT	36	6.2E-1	1.0E0
☐	GOTERM_BP_ALL	male gamete generation	RT	15	6.6E-1	1.0E0
☐	GOTERM_BP_ALL	spermatogenesis	RT	15	6.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	spermatogenesis	RT	5	8.7E-1	1.0E0
	Annotation Cluster 131	Enrichment Score: 0.25	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	deacetylase activity	RT	3	3.9E-1	1.0E0
☐	GOTERM_MF_ALL	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	RT	5	5.2E-1	1.0E0
☐	GOTERM_MF_ALL	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	RT	6	8.7E-1	1.0E0
	Annotation Cluster 132	Enrichment Score: 0.24	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	histone methylation	RT	3	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid methylation	RT	4	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid alkylation	RT	4	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	biopolymer methylation	RT	5	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	methylation	RT	5	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	one-carbon compound metabolic process	RT	7	7.4E-1	1.0E0
	Annotation Cluster 133	Enrichment Score: 0.24	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of B cell proliferation	RT	3	1.6E-1	9.9E-1
☐	GOTERM_BP_ALL	regulation of B cell proliferation	RT	4	2.7E-1	1.0E0

☐	GOTERM_BP_ALL	negative regulation of B cell activation	RT	▮		3	2.7E-1	1.0E0
☐	GOTERM_BP_ALL	B cell proliferation	RT	▮		4	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell activation	RT	▮		10	4.9E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of T cell proliferation	RT	▮		4	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	lymphocyte proliferation	RT	▮		8	5.5E-1	1.0E0
☐	GOTERM_BP_ALL	mononuclear cell proliferation	RT	▮		8	5.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of lymphocyte proliferation	RT	▮		6	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of mononuclear cell proliferation	RT	▮		6	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	T cell proliferation	RT	▮		6	5.9E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of lymphocyte proliferation	RT	▮		3	6.2E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of mononuclear cell proliferation	RT	▮		3	6.2E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of lymphocyte proliferation	RT	▮		4	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of B cell activation	RT	▮		4	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of mononuclear cell proliferation	RT	▮		4	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of lymphocyte activation	RT	▮		3	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of T cell proliferation	RT	▮		4	7.8E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of T cell activation	RT	▮		4	8.0E-1	1.0E0
☐	GOTERM_CC_ALL	external side of plasma membrane	RT	▮		9	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of lymphocyte activation	RT	▮		6	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of lymphocyte activation	RT	▮		4	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of T cell activation	RT	▮		4	9.6E-1	1.0E0
	Annotation Cluster 134	Enrichment Score: 0.24	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of phosphorylation	RT	▮		7	4.7E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of phosphorus metabolic process	RT	▮		7	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of phosphate metabolic process	RT	▮		7	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of amine metabolic process	RT	▮		4	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of amino acid metabolic process	RT	▮		4	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of protein amino acid phosphorylation	RT	▮		4	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of protein amino acid phosphorylation	RT	▮		6	5.2E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of amine metabolic process	RT	▮		6	5.3E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of amino acid metabolic process	RT	▮		6	5.3E-1	1.0E0
☐	GOTERM_BP_ALL	peptidyl-tyrosine modification	RT	▮		6	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	peptidyl-tyrosine phosphorylation	RT	▮		6	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	peptidyl-amino acid modification	RT	▮		10	6.4E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of peptidyl-tyrosine phosphorylation	RT	▮		3	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	amino acid metabolic process	RT	▮		14	9.8E-1	1.0E0
	Annotation Cluster 135	Enrichment Score: 0.24	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cytokine production	RT	▮		13	2.1E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cellular biosynthetic process	RT	▮		16	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of biosynthetic process	RT	▮		17	3.9E-1	1.0E0
☐	GOTERM_BP_ALL	interleukin-2 biosynthetic process	RT	▮		3	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of translation	RT	▮		6	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of translation	RT	▮		14	4.4E-1	1.0E0
☐	GOTERM_BP_ALL	interleukin-2 production	RT	▮		3	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cellular biosynthetic	RT	▮		6	4.9E-1	1.0E0

☐		process	RT			6	4.9E-1	1.0E0
☐	GOTERM_BP_ALL	cytokine metabolic process	RT			7	5.9E-1	1.0E0
☐	GOTERM_BP_ALL	cytokine biosynthetic process	RT			7	5.9E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of protein metabolic process	RT			8	6.4E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of biosynthetic process	RT			6	6.6E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cytokine biosynthetic process	RT			4	7.3E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of protein metabolic process	RT			20	8.0E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cytokine biosynthetic process	RT			5	8.1E-1	1.0E0
☐	GOTERM_BP_ALL	biosynthetic process	RT			83	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	macromolecule biosynthetic process	RT			42	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	translation	RT			23	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cellular biosynthetic process	RT			54	1.0E0	1.0E0
	Annotation Cluster 136	Enrichment Score: 0.24	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	mRNA splice site selection	RT			3	3.3E-1	1.0E0
☐	GOTERM_BP_ALL	nuclear mRNA splicing, via spliceosome	RT			6	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	RNA splicing, via transesterification reactions	RT			6	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	RT			6	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of translational initiation	RT			3	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	spliceosome assembly	RT			3	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	protein-RNA complex assembly	RT			6	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	translational initiation	RT			3	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	ribonucleoprotein complex biogenesis and assembly	RT			7	1.0E0	1.0E0
	Annotation Cluster 137	Enrichment Score: 0.22	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	cell projection part	RT			8	2.8E-1	1.0E0
☐	GOTERM_CC_ALL	neuron projection	RT			8	8.8E-1	1.0E0
☐	GOTERM_CC_ALL	dendrite	RT			3	9.2E-1	1.0E0
	Annotation Cluster 138	Enrichment Score: 0.22	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:Ras-associating	RT			3	3.3E-1	1.0E0
☐	INTERPRO	Ras-association	RT			3	7.8E-1	1.0E0
☐	SMART	RA	RT			3	8.6E-1	1.0E0
	Annotation Cluster 139	Enrichment Score: 0.21	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	mesenchymal cell development	RT			5	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	mesenchymal cell differentiation	RT			5	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	neural crest cell development	RT			3	7.8E-1	1.0E0
☐	GOTERM_BP_ALL	neural crest cell differentiation	RT			3	7.8E-1	1.0E0
	Annotation Cluster 140	Enrichment Score: 0.21	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	embryonic pattern specification	RT			6	3.6E-1	1.0E0
☐	GOTERM_BP_ALL	patterning of blood vessels	RT			3	6.2E-1	1.0E0
☐	GOTERM_BP_ALL	branching morphogenesis of a tube	RT			5	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	morphogenesis of a branching structure	RT			5	8.1E-1	1.0E0
	Annotation Cluster 141	Enrichment Score: 0.21	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	cytokine binding	RT			9	3.4E-1	1.0E0
☐	GOTERM_MF_ALL	interleukin receptor activity	RT			3	8.0E-1	1.0E0
☐	GOTERM_MF_ALL	interleukin binding	RT			3	8.7E-1	1.0E0
	Annotation Cluster 142	Enrichment Score: 0.2	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of biosynthetic process	RT			5	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of cellular biosynthetic process	RT			4	5.1E-1	1.0E0

☐	GOTERM_BP_ALL	negative regulation of translation	RT		3	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of protein metabolic process	RT		4	9.7E-1	1.0E0
	Annotation Cluster 143	Enrichment Score: 0.2	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	nuclear chromosome part	RT		7	4.8E-1	1.0E0
☐	GOTERM_CC_ALL	condensed chromosome	RT		5	6.2E-1	1.0E0
☐	GOTERM_CC_ALL	nuclear chromosome	RT		7	6.7E-1	1.0E0
☐	GOTERM_CC_ALL	nuclear chromatin	RT		3	6.7E-1	1.0E0
☐	GOTERM_CC_ALL	condensed nuclear chromosome	RT		3	7.7E-1	1.0E0
	Annotation Cluster 144	Enrichment Score: 0.2	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:PDZ	RT		6	5.0E-1	1.0E0
☐	INTERPRO	PDZ/DHR/GLGF	RT		10	6.2E-1	1.0E0
☐	SMART	PDZ	RT		10	8.3E-1	1.0E0
	Annotation Cluster 145	Enrichment Score: 0.19	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	cysteine-type peptidase activity	RT		18	1.4E-1	1.0E0
☐	GOTERM_BP_ALL	proteolysis	RT		49	9.0E-1	1.0E0
☐	GOTERM_MF_ALL	peptidase activity	RT		45	9.2E-1	1.0E0
☐	GOTERM_MF_ALL	endopeptidase activity	RT		27	9.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	protease	RT		27	9.7E-1	1.0E0
	Annotation Cluster 146	Enrichment Score: 0.19	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of cell differentiation	RT		16	5.3E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of developmental process	RT		8	5.6E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of cell differentiation	RT		8	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of developmental process	RT		23	7.1E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of developmental process	RT		8	8.3E-1	1.0E0
	Annotation Cluster 147	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	neuromuscular junction development	RT		3	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	synapse organization and biogenesis	RT		4	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	extracellular structure organization and biogenesis	RT		8	7.9E-1	1.0E0
	Annotation Cluster 148	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	meiosis I	RT		4	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	meiosis	RT		8	4.1E-1	1.0E0
☐	GOTERM_BP_ALL	M phase of meiotic cell cycle	RT		8	4.1E-1	1.0E0
☐	GOTERM_BP_ALL	meiotic cell cycle	RT		8	4.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	Meiosis	RT		3	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	cell cycle phase	RT		22	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	mitotic cell cycle	RT		18	7.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	mitosis	RT		8	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	M phase	RT		17	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	mitosis	RT		12	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	M phase of mitotic cell cycle	RT		12	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	cell division	RT		13	9.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	cell division	RT		9	9.8E-1	1.0E0
	Annotation Cluster 149	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	antigen processing and presentation	RT		9	2.6E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001990:class I histocompatibility antigen	RT		3	5.0E-1	1.0E0
☐	INTERPRO	MHC class I-like antigen recognition	RT		4	5.5E-1	1.0E0
☐	KEGG_PATHWAY	Type I diabetes mellitus	RT		5	6.6E-1	9.8E-1
☐	GOTERM_CC_ALL	MHC protein complex	RT		3	8.5E-1	1.0E0
☐	INTERPRO	Immunoglobulin/major histocompatibility	RT		5	8.7E-1	1.0E0

☐		complex motif	RT	▮				
☐	**INTERPRO**	Immunoglobulin C1-set	RT	▮		4	8.9E-1	1.0E0
☐	**KEGG_PATHWAY**	Cell adhesion molecules (CAMs)	RT	▮		8	9.0E-1	1.0E0
☐	**SMART**	IGc1	RT	▮		4	9.4E-1	1.0E0
	Annotation Cluster 150	Enrichment Score: 0.17	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	protein amino acid lipidation	RT	▮		5	5.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	lipoprotein biosynthetic process	RT	▮		5	6.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	lipoprotein metabolic process	RT	▮		5	8.4E-1	1.0E0
	Annotation Cluster 151	Enrichment Score: 0.17	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Guanylate kinase/L-type calcium channel region	RT	▮		3	5.6E-1	1.0E0
☐	**SMART**	GuKc	RT	▮		3	6.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:SH3	RT	▮		7	8.6E-1	1.0E0
	Annotation Cluster 152	Enrichment Score: 0.17	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	exopeptidase activity	RT	▮		9	5.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	carboxypeptidase A activity	RT	▮		3	6.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	metalloexopeptidase activity	RT	▮		5	6.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	metallocarboxypeptidase activity	RT	▮		3	7.2E-1	1.0E0
☐	**GOTERM_MF_ALL**	carboxypeptidase activity	RT	▮		3	8.8E-1	1.0E0
	Annotation Cluster 153	Enrichment Score: 0.17	G		🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	Endonuclease	RT	▮		6	3.4E-1	9.9E-1
☐	**GOTERM_MF_ALL**	endoribonuclease activity, producing 5'-phosphomonoesters	RT	▮		3	5.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	RT	▮		3	5.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	nuclease	RT	▮		6	6.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	endonuclease activity	RT	▮		6	8.2E-1	1.0E0
☐	**GOTERM_MF_ALL**	endoribonuclease activity	RT	▮		3	8.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	nuclease activity	RT	▮		9	8.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	ribonuclease activity	RT	▮		3	9.6E-1	1.0E0
	Annotation Cluster 154	Enrichment Score: 0.16	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	homeostatic process	RT	▮		34	2.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	cation homeostasis	RT	▮		11	5.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular homeostasis	RT	▮		21	5.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular iron ion homeostasis	RT	▮		3	5.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	iron ion homeostasis	RT	▮		3	5.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular cation homeostasis	RT	▮		10	6.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	di-, tri-valent inorganic cation homeostasis	RT	▮		9	6.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular di-, tri-valent inorganic cation homeostasis	RT	▮		8	7.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular chemical homeostasis	RT	▮		12	8.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular ion homeostasis	RT	▮		12	8.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	ion homeostasis	RT	▮		13	8.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	chemical homeostasis	RT	▮		15	9.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular metal ion homeostasis	RT	▮		4	9.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	metal ion homeostasis	RT	▮		4	9.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular calcium ion homeostasis	RT	▮		3	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	calcium ion homeostasis	RT	▮		3	9.8E-1	1.0E0
	Annotation Cluster 155	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	embryonic appendage morphogenesis	RT	▮		6	6.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	embryonic limb morphogenesis	RT	▮		6	6.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	appendage morphogenesis	RT	▮		6	6.9E-1	1.0E0

☐	GOTERM_BP_ALL	limb morphogenesis	RT	▮		6	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	limb development	RT	▮		6	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	appendage development	RT	▮		6	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	embryonic morphogenesis	RT	▮		13	8.4E-1	1.0E0
	Annotation Cluster 156	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Src homology-3	RT	▮		15	5.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	SH3 domain	RT	▮		15	6.1E-1	1.0E0
☐	SMART	SH3	RT	▮		15	8.3E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:SH3	RT	▮		7	8.6E-1	1.0E0
	Annotation Cluster 157	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	calcium-binding region:2	RT	▮		7	5.1E-1	1.0E0
☐	UP_SEQ_FEATURE	calcium-binding region:1	RT	▮		7	5.5E-1	1.0E0
☐	INTERPRO	Calcium-binding EF-hand	RT	▮		15	5.5E-1	1.0E0
☐	INTERPRO	EF-Hand type	RT	▮		12	7.8E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:EF-hand 1	RT	▮		7	8.0E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:EF-hand 2	RT	▮		7	8.1E-1	1.0E0
☐	SMART	EFh	RT	▮		15	8.3E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:EF-hand 3	RT	▮		3	9.4E-1	1.0E0
	Annotation Cluster 158	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	aminotransferase	RT	▮		3	5.3E-1	1.0E0
☐	GOTERM_MF_ALL	transaminase activity	RT	▮		3	8.0E-1	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring nitrogenous groups	RT	▮		3	8.3E-1	1.0E0
	Annotation Cluster 159	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of blood pressure	RT	▮		5	6.4E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of blood vessel size	RT	▮		4	7.0E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of tube size	RT	▮		4	7.0E-1	1.0E0
☐	GOTERM_BP_ALL	vascular process in circulatory system	RT	▮		4	7.0E-1	1.0E0
☐	GOTERM_BP_ALL	blood circulation	RT	▮		9	7.4E-1	1.0E0
☐	GOTERM_BP_ALL	circulatory system process	RT	▮		9	7.4E-1	1.0E0
	Annotation Cluster 160	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Iron transport	RT	▮		3	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	iron ion transport	RT	▮		3	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	transition metal ion transport	RT	▮		4	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	di-, tri-valent inorganic cation transport	RT	▮		8	9.5E-1	1.0E0
	Annotation Cluster 161	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF000050:cytochrome P450 CYP4B1	RT	▮		3	1.3E-1	1.0E0
☐	INTERPRO	Cytochrome P450	RT	▮		6	6.7E-1	1.0E0
☐	INTERPRO	Cytochrome P450, E-class, group I	RT	▮		5	7.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	monooxygenase	RT	▮		7	7.4E-1	1.0E0
☐	GOTERM_MF_ALL	monooxygenase activity	RT	▮		7	9.1E-1	1.0E0
☐	UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	RT	▮		4	9.1E-1	1.0E0
☐	GOTERM_MF_ALL	heme binding	RT	▮		9	9.5E-1	1.0E0
☐	GOTERM_MF_ALL	tetrapyrrole binding	RT	▮		9	9.5E-1	1.0E0
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	RT	▮		7	9.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	heme	RT	▮		6	9.6E-1	1.0E0
	Annotation Cluster 162	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	immunoglobulin production	RT	▮		4	6.4E-1	1.0E0
☐	GOTERM_BP_ALL	production of molecular mediator of immune response	RT	▮		4	6.6E-1	1.0E0

☐	GOTERM_BP_ALL	somatic recombination of immunoglobulin gene segments	RT	▮		3	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	somatic cell DNA recombination	RT	▮		3	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	somatic diversification of immune receptors via germline recombination within a single locus	RT	▮		3	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	somatic diversification of immunoglobulins	RT	▮		3	7.3E-1	1.0E0
☐	GOTERM_BP_ALL	somatic diversification of immune receptors	RT	▮		3	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	DNA recombination	RT	▮		6	8.1E-1	1.0E0
	Annotation Cluster 163	Enrichment Score: 0.15	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	extrinsic to plasma membrane	RT	▮		5	6.5E-1	1.0E0
☐	GOTERM_CC_ALL	extrinsic to membrane	RT	▮		6	7.1E-1	1.0E0
☐	GOTERM_CC_ALL	heterotrimeric G-protein complex	RT	▮		3	7.9E-1	1.0E0
	Annotation Cluster 164	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	K Homology	RT	▮		3	6.8E-1	1.0E0
☐	INTERPRO	K Homology, type 1	RT	▮		3	7.0E-1	1.0E0
☐	SMART	KH	RT	▮		3	7.8E-1	1.0E0
	Annotation Cluster 165	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	Rab GTPase binding	RT	▮		3	4.7E-1	1.0E0
☐	GOTERM_MF_ALL	Ras GTPase binding	RT	▮		4	8.1E-1	1.0E0
☐	GOTERM_MF_ALL	small GTPase binding	RT	▮		4	8.4E-1	1.0E0
☐	GOTERM_MF_ALL	GTPase binding	RT	▮		4	8.6E-1	1.0E0
	Annotation Cluster 166	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	mesoderm development	RT	▮		5	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	mesoderm formation	RT	▮		3	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	mesoderm morphogenesis	RT	▮		3	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	gastrulation	RT	▮		5	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	formation of primary germ layer	RT	▮		3	7.3E-1	1.0E0
☐	GOTERM_BP_ALL	tissue morphogenesis	RT	▮		3	9.9E-1	1.0E0
	Annotation Cluster 167	Enrichment Score: 0.13	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	damaged DNA binding	RT	▮		3	5.2E-1	1.0E0
☐	GOTERM_BP_ALL	response to endogenous stimulus	RT	▮		21	7.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	DNA repair	RT	▮		9	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	response to DNA damage stimulus	RT	▮		18	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	DNA repair	RT	▮		14	8.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	DNA damage	RT	▮		9	8.5E-1	1.0E0
	Annotation Cluster 168	Enrichment Score: 0.13	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Fibronectin, type III-like fold	RT	▮		14	5.5E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Fibronectin type-III 3	RT	▮		4	5.9E-1	1.0E0
☐	GOTERM_MF_ALL	transmembrane receptor protein tyrosine kinase activity	RT	▮		6	6.9E-1	1.0E0
☐	INTERPRO	Fibronectin, type III	RT	▮		12	7.7E-1	1.0E0
☐	SMART	FN3	RT	▮		13	8.6E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Fibronectin type-III 2	RT	▮		4	9.1E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Fibronectin type-III 1	RT	▮		4	9.1E-1	1.0E0
	Annotation Cluster 169	Enrichment Score: 0.12	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Tyrosine protein kinase	RT	▮		10	6.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	tyrosine-protein kinase	RT	▮		9	6.6E-1	1.0E0
☐	GOTERM_MF_ALL	transmembrane receptor protein tyrosine kinase activity	RT	▮		6	6.9E-1	1.0E0
☐	SMART	TyrKc	RT	▮		10	8.2E-1	1.0E0
☐	INTERPRO	Tyrosine protein kinase, active site	RT	▮		6	8.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	tyrosine-specific protein kinase	RT	▮		3	8.9E-1	1.0E0

	Annotation Cluster 170	Enrichment Score: 0.12	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	anatomical structure formation	RT	17	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	blood vessel development	RT	18	7.1E-1	1.0E0
☐	GOTERM_BP_ALL	vasculature development	RT	18	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	organ morphogenesis	RT	40	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	blood vessel morphogenesis	RT	14	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	angiogenesis	RT	10	9.0E-1	1.0E0

	Annotation Cluster 171	Enrichment Score: 0.12	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	nuclear mRNA splicing, via spliceosome	RT	6	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	RNA splicing, via transesterification reactions	RT	6	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	RT	6	4.6E-1	1.0E0
☐	GOTERM_CC_ALL	spliceosome	RT	10	6.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	mrna splicing	RT	10	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	mRNA metabolic process	RT	18	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	RNA splicing	RT	12	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	mRNA processing	RT	14	9.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	spliceosome	RT	5	9.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	mrna processing	RT	10	9.6E-1	1.0E0
☐	GOTERM_CC_ALL	ribonucleoprotein complex	RT	21	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	RNA processing	RT	15	1.0E0	1.0E0

	Annotation Cluster 172	Enrichment Score: 0.12	G	Count	P_Value	Benjamini
☐	INTERPRO	SNF2-related	RT	4	3.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	helicase	RT	9	6.2E-1	1.0E0
☐	GOTERM_MF_ALL	helicase activity	RT	10	7.5E-1	1.0E0
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT	6	7.7E-1	1.0E0
☐	SMART	DEXDc	RT	8	7.7E-1	1.0E0
☐	INTERPRO	DEAD-like helicase, N-terminal	RT	6	8.1E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, C-terminal	RT	5	8.7E-1	1.0E0
☐	SMART	HELICc	RT	6	8.9E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Helicase C-terminal	RT	3	8.9E-1	1.0E0
☐	GOTERM_MF_ALL	ATP-dependent helicase activity	RT	6	9.1E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Helicase ATP-binding	RT	3	9.1E-1	1.0E0

	Annotation Cluster 173	Enrichment Score: 0.12	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of cell activation	RT	10	4.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of immune system process	RT	10	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	immune effector process	RT	11	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	RT	8	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	adaptive immune response	RT	8	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of multicellular organismal process	RT	24	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of immune response	RT	9	6.9E-1	1.0E0
☐	GOTERM_BP_ALL	alpha-beta T cell activation	RT	3	7.8E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of multicellular organismal process	RT	9	8.0E-1	1.0E0
☐	GOTERM_BP_ALL	innate immune response	RT	7	8.0E-1	1.0E0
☐	GOTERM_BP_ALL	lymphocyte mediated immunity	RT	7	8.0E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of immune system process	RT	7	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	immunoglobulin mediated immune				

☐		response	RT			
☐	GOTERM_BP_ALL	leukocyte mediated immunity	RT	7	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	B cell mediated immunity	RT	5	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of immune response	RT	6	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	acute inflammatory response	RT	4	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	activation of immune response	RT	3	9.9E-1	1.0E0
	Annotation Cluster 174	Enrichment Score: 0.11	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	blood circulation	RT	9	7.4E-1	1.0E0
☐	GOTERM_BP_ALL	circulatory system process	RT	9	7.4E-1	1.0E0
☐	GOTERM_BP_ALL	heart contraction	RT	4	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	heart process	RT	4	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of heart contraction	RT	3	8.6E-1	1.0E0
	Annotation Cluster 175	Enrichment Score: 0.11	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	receptor	RT	91	5.8E-1	1.0E0
☐	GOTERM_MF_ALL	receptor activity	RT	109	8.2E-1	1.0E0
☐	GOTERM_MF_ALL	signal transducer activity	RT	126	8.8E-1	1.0E0
☐	GOTERM_MF_ALL	molecular transducer activity	RT	126	8.8E-1	1.0E0
	Annotation Cluster 176	Enrichment Score: 0.11	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of cell shape	RT	4	7.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell morphogenesis	RT	4	7.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of anatomical structure morphogenesis	RT	4	7.8E-1	1.0E0
	Annotation Cluster 177	Enrichment Score: 0.11	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	protein dimerization activity	RT	22	6.1E-1	1.0E0
☐	GOTERM_MF_ALL	protein homodimerization activity	RT	10	8.2E-1	1.0E0
☐	GOTERM_MF_ALL	identical protein binding	RT	16	9.6E-1	1.0E0
	Annotation Cluster 178	Enrichment Score: 0.11	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cholesterol metabolic process	RT	6	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	sterol metabolic process	RT	6	7.5E-1	1.0E0
☐	GOTERM_BP_ALL	steroid metabolic process	RT	11	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	alcohol metabolic process	RT	17	9.4E-1	1.0E0
	Annotation Cluster 179	Enrichment Score: 0.1	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	transit peptide:Mitochondrion	RT	19	6.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	Mitochondrion	RT	43	8.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	transit peptide	RT	25	8.3E-1	1.0E0
☐	GOTERM_CC_ALL	mitochondrion	RT	60	9.2E-1	1.0E0
	Annotation Cluster 180	Enrichment Score: 0.1	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	phagocytosis	RT	4	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	vesicle-mediated transport	RT	31	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	membrane invagination	RT	12	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	endocytosis	RT	12	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	membrane organization and biogenesis	RT	16	9.3E-1	1.0E0
	Annotation Cluster 181	Enrichment Score: 0.1	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:C2	RT	4	5.4E-1	1.0E0
☐	INTERPRO	C2 calcium-dependent membrane targeting	RT	6	9.6E-1	1.0E0
☐	SMART	C2	RT	6	9.9E-1	1.0E0
	Annotation Cluster 182	Enrichment Score: 0.09	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	endoplasmic reticulum part	RT	8	7.8E-1	1.0E0
☐	GOTERM_CC_ALL	endoplasmic reticulum membrane	RT	7	8.0E-1	1.0E0
☐	GOTERM_CC_ALL	intrinsic to endoplasmic reticulum membrane	RT	3	8.0E-1	1.0E0
☐	GOTERM_CC_ALL	nuclear envelope-endoplasmic reticulum				

☐		network	RT			7		
	Annotation Cluster 183	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	carbon-carbon lyase activity	RT			4	7.1E-1	1.0E0
☐	GOTERM_MF_ALL	carboxy-lyase activity	RT			3	7.4E-1	1.0E0
☐	GOTERM_MF_ALL	lyase activity	RT			7	9.9E-1	1.0E0
	Annotation Cluster 184	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	SH2 motif	RT			8	7.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	sh2 domain	RT			8	7.5E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:SH2	RT			4	8.7E-1	1.0E0
☐	SMART	SH2	RT			8	8.7E-1	1.0E0
	Annotation Cluster 185	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	DNA-binding region:HMG box	RT			3	6.8E-1	1.0E0
☐	INTERPRO	High mobility group box, HMG1/HMG2	RT			4	7.8E-1	1.0E0
☐	SMART	HMG	RT			4	8.9E-1	1.0E0
☐	INTERPRO	High mobility group box, HMG	RT			3	8.9E-1	1.0E0
	Annotation Cluster 186	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of I-kappaB kinase/NF-kappaB cascade	RT			4	6.6E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of I-kappaB kinase/NF-kappaB cascade	RT			3	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of signal transduction	RT			7	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	I-kappaB kinase/NF-kappaB cascade	RT			4	9.0E-1	1.0E0
	Annotation Cluster 187	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell morphogenesis	RT			42	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	cellular structure morphogenesis	RT			42	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	nervous system development	RT			51	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	cell projection morphogenesis	RT			21	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	cell projection organization and biogenesis	RT			21	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	cell part morphogenesis	RT			21	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	neurite development	RT			15	8.0E-1	1.0E0
☐	GOTERM_BP_ALL	axon guidance	RT			6	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	cellular morphogenesis during differentiation	RT			14	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	neuron development	RT			16	8.7E-1	1.0E0
☐	GOTERM_BP_ALL	neuron morphogenesis during differentiation	RT			11	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	neurite morphogenesis	RT			11	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	axonogenesis	RT			10	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	neuron differentiation	RT			19	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	neurogenesis	RT			23	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	generation of neurons	RT			20	9.7E-1	1.0E0
	Annotation Cluster 188	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	electron transport	RT			31	6.8E-1	1.0E0
☐	GOTERM_MF_ALL	oxidoreductase activity	RT			64	7.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	oxidoreductase	RT			32	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	generation of precursor metabolites and energy	RT			33	9.5E-1	1.0E0
	Annotation Cluster 189	Enrichment Score: 0.09	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	FAD binding	RT			5	7.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	fad	RT			7	7.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	flavoprotein	RT			7	7.9E-1	1.0E0
☐	GOTERM_MF_ALL	coenzyme binding	RT			8	8.9E-1	1.0E0
☐	GOTERM_MF_ALL	cofactor binding	RT			11	9.2E-1	1.0E0

	Annotation Cluster 190	Enrichment Score: 0.08	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	nucleotide receptor activity, G-protein coupled	RT	7	3.8E-1	1.0E0
☐	GOTERM_MF_ALL	nucleotide receptor activity	RT	7	4.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	transducer	RT	22	9.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	g-protein coupled receptor	RT	18	9.9E-1	1.0E0
☐	KEGG_PATHWAY	Neuroactive ligand-receptor interaction	RT	10	9.9E-1	1.0E0
☐	INTERPRO	Rhodopsin-like GPCR superfamily	RT	11	1.0E0	1.0E0
☐	GOTERM_MF_ALL	rhodopsin-like receptor activity	RT	17	1.0E0	1.0E0
☐	GOTERM_MF_ALL	G-protein coupled receptor activity	RT	21	1.0E0	1.0E0
☐	GOTERM_MF_ALL	transmembrane receptor activity	RT	41	1.0E0	1.0E0
☐	GOTERM_BP_ALL	G-protein coupled receptor protein signaling pathway	RT	31	1.0E0	1.0E0
	Annotation Cluster 191	Enrichment Score: 0.08	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Sushi/SCR/CCP	RT	4	7.7E-1	1.0E0
☐	SMART	CCP	RT	4	8.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	sushi	RT	3	8.6E-1	1.0E0
	Annotation Cluster 192	Enrichment Score: 0.08	G 🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	DNA-binding region:Basic motif	RT	9	5.9E-1	1.0E0
☐	INTERPRO	Basic helix-loop-helix dimerisation region bHLH	RT	7	8.1E-1	1.0E0
☐	SMART	HLH	RT	7	9.3E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Helix-loop-helix motif	RT	4	9.4E-1	1.0E0
☐	INTERPRO	Helix-loop-helix DNA-binding	RT	4	9.5E-1	1.0E0
	Annotation Cluster 193	Enrichment Score: 0.08	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	fatty acid biosynthetic process	RT	5	7.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	fatty acid biosynthesis	RT	3	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	organic acid biosynthetic process	RT	5	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	carboxylic acid biosynthetic process	RT	5	8.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	lipid synthesis	RT	4	9.5E-1	1.0E0
	Annotation Cluster 194	Enrichment Score: 0.07	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cofactor metabolic process	RT	18	5.6E-1	1.0E0
☐	GOTERM_BP_ALL	cofactor biosynthetic process	RT	6	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	coenzyme metabolic process	RT	9	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	coenzyme biosynthetic process	RT	4	9.9E-1	1.0E0
	Annotation Cluster 195	Enrichment Score: 0.07	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Laminin G, subdomain 2	RT	3	8.0E-1	1.0E0
☐	INTERPRO	Laminin G	RT	3	8.4E-1	1.0E0
☐	SMART	LamG	RT	3	9.0E-1	1.0E0
	Annotation Cluster 196	Enrichment Score: 0.07	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	antioxidant activity	RT	4	8.3E-1	1.0E0
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on peroxide as acceptor	RT	3	8.7E-1	1.0E0
☐	GOTERM_MF_ALL	peroxidase activity	RT	3	8.7E-1	1.0E0
	Annotation Cluster 197	Enrichment Score: 0.06	G 🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	region of interest:Calmodulin-binding	RT	3	8.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	calmodulin-binding	RT	6	8.7E-1	1.0E0
☐	GOTERM_MF_ALL	calmodulin binding	RT	7	9.0E-1	1.0E0
	Annotation Cluster 198	Enrichment Score: 0.06	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	hormone biosynthetic process	RT	3	8.1E-1	1.0E0
☐	GOTERM_BP_ALL	steroid biosynthetic process	RT	5	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	hormone metabolic process	RT	5	9.3E-1	1.0E0
	Annotation Cluster 199	Enrichment Score: 0.05	G 🟩	Count	P_Value	Benjamini

☐	GOTERM_CC_ALL	synaptic vesicle	RT		5	6.2E-1	1.0E0
☐	GOTERM_CC_ALL	vesicle	RT		22	8.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	cytoplasmic vesicle	RT		8	8.8E-1	1.0E0
☐	GOTERM_CC_ALL	cytoplasmic vesicle	RT		20	9.3E-1	1.0E0
☐	GOTERM_CC_ALL	membrane-bound vesicle	RT		14	9.5E-1	1.0E0
☐	GOTERM_CC_ALL	coated vesicle	RT		6	9.6E-1	1.0E0
☐	GOTERM_CC_ALL	clathrin-coated vesicle	RT		5	9.6E-1	1.0E0
☐	GOTERM_CC_ALL	cytoplasmic membrane-bound vesicle	RT		12	9.8E-1	1.0E0
	Annotation Cluster 200	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	pyruvate metabolic process	RT		3	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	glucose metabolic process	RT		7	8.9E-1	1.0E0
☐	GOTERM_BP_ALL	alcohol metabolic process	RT		17	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	hexose metabolic process	RT		8	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	monosaccharide metabolic process	RT		8	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	cellular carbohydrate metabolic process	RT		12	1.0E0	1.0E0
☐	GOTERM_BP_ALL	carbohydrate metabolic process	RT		17	1.0E0	1.0E0
	Annotation Cluster 201	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein targeting	RT		18	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	intracellular protein transport	RT		32	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	protein transport	RT		49	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	protein localization	RT		56	8.7E-1	1.0E0
☐	GOTERM_BP_ALL	macromolecule localization	RT		57	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	establishment of protein localization	RT		50	9.1E-1	1.0E0
☐	GOTERM_BP_ALL	intracellular transport	RT		43	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	protein transport	RT		18	1.0E0	1.0E0
☐	GOTERM_BP_ALL	establishment of cellular localization	RT		48	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cellular localization	RT		48	1.0E0	1.0E0
	Annotation Cluster 202	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	microsome	RT		6	8.7E-1	1.0E0
☐	GOTERM_CC_ALL	vesicular fraction	RT		10	8.8E-1	1.0E0
☐	GOTERM_CC_ALL	microsome	RT		9	9.2E-1	1.0E0
	Annotation Cluster 203	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	repeat:LRR 4	RT		6	7.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	leucine-rich repeat	RT		14	8.5E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 3	RT		6	8.5E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 1	RT		6	8.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 2	RT		6	8.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 9	RT		3	9.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 8	RT		3	9.3E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 5	RT		4	9.3E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 7	RT		3	9.5E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 6	RT		3	9.7E-1	1.0E0
	Annotation Cluster 204	Enrichment Score: 0.05	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	kinesin complex	RT		3	7.2E-1	1.0E0
☐	GOTERM_MF_ALL	microtubule motor activity	RT		5	8.2E-1	1.0E0
☐	GOTERM_MF_ALL	motor activity	RT		8	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	cytoskeleton-dependent intracellular transport	RT		7	9.2E-1	1.0E0
☐	GOTERM_CC_ALL	microtubule associated complex	RT		5	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	microtubule-based movement	RT		4	9.9E-1	1.0E0

☐	SP_PIR_KEYWORDS	motor protein	RT	▮		3	9.9E-1	1.0E0
	Annotation Cluster 205	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	translation elongation factor activity	RT	▮		3	7.2E-1	1.0E0
☐	GOTERM_MF_ALL	translation factor activity, nucleic acid binding	RT	▮		7	9.2E-1	1.0E0
☐	GOTERM_MF_ALL	translation regulator activity	RT	▮		7	9.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	initiation factor	RT	▮		3	9.7E-1	1.0E0
☐	GOTERM_MF_ALL	translation initiation factor activity	RT	▮		3	9.9E-1	1.0E0
	Annotation Cluster 206	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	basal lamina	RT	▮		3	6.5E-1	1.0E0
☐	GOTERM_CC_ALL	basement membrane	RT	▮		4	8.9E-1	1.0E0
☐	GOTERM_CC_ALL	extracellular matrix part	RT	▮		5	9.6E-1	1.0E0
☐	GOTERM_CC_ALL	extracellular matrix	RT	▮		12	1.0E0	1.0E0
☐	GOTERM_CC_ALL	proteinaceous extracellular matrix	RT	▮		10	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	extracellular matrix	RT	▮		4	1.0E0	1.0E0
	Annotation Cluster 207	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:EGF-like 3	RT	▮		4	6.4E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:EGF-like 2	RT	▮		4	7.3E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:EGF-like 1	RT	▮		4	8.8E-1	1.0E0
☐	INTERPRO	EGF-like	RT	▮		6	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	egf-like domain	RT	▮		9	9.9E-1	1.0E0
☐	INTERPRO	EGF	RT	▮		8	9.9E-1	1.0E0
☐	INTERPRO	Aspartic acid and asparagine hydroxylation site	RT	▮		3	9.9E-1	1.0E0
☐	INTERPRO	EGF-like, type 3	RT	▮		7	9.9E-1	1.0E0
☐	SMART	EGF	RT	▮		8	1.0E0	1.0E0
☐	INTERPRO	EGF-like region	RT	▮		9	1.0E0	1.0E0
	Annotation Cluster 208	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Leucine-rich repeat	RT	▮		13	8.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	leucine-rich repeat	RT	▮		14	8.5E-1	1.0E0
☐	INTERPRO	Leucine-rich repeat, typical subtype	RT	▮		5	9.8E-1	1.0E0
☐	SMART	LRR_TYP	RT	▮		5	9.9E-1	1.0E0
	Annotation Cluster 209	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of muscle contraction	RT	▮		3	7.8E-1	1.0E0
☐	GOTERM_BP_ALL	muscle contraction	RT	▮		4	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	muscle system process	RT	▮		4	9.8E-1	1.0E0
	Annotation Cluster 210	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	intercellular junction	RT	▮		10	8.0E-1	1.0E0
☐	GOTERM_CC_ALL	tight junction	RT	▮		4	9.1E-1	1.0E0
☐	GOTERM_CC_ALL	apical junction complex	RT	▮		4	9.7E-1	1.0E0
☐	GOTERM_CC_ALL	apicolateral plasma membrane	RT	▮		4	9.7E-1	1.0E0
	Annotation Cluster 211	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	second-messenger-mediated signaling	RT	▮		10	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	cAMP-mediated signaling	RT	▮		4	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	cyclic-nucleotide-mediated signaling	RT	▮		4	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	G-protein signaling, coupled to cAMP nucleotide second messenger	RT	▮		3	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	G-protein signaling, coupled to cyclic nucleotide second messenger	RT	▮		3	9.7E-1	1.0E0
	Annotation Cluster 212	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	inorganic anion transmembrane transporter activity	RT	▮		3	7.1E-1	1.0E0
☐	GOTERM_MF_ALL	anion transmembrane transporter activity	RT	▮		6	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	chloride transport	RT	▮		3	9.6E-1	1.0E0

☐	GOTERM_BP_ALL	inorganic anion transport	RT	▮		6	1.0E0	1.0E0
☐	GOTERM_BP_ALL	anion transport	RT	▮		7	1.0E0	1.0E0
	Annotation Cluster 213	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	eye development	RT	▮		7	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	camera-type eye development	RT	▮		4	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	sensory organ development	RT	▮		9	9.8E-1	1.0E0
	Annotation Cluster 214	Enrichment Score: 0.04	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	site:Reactive bond	RT	▮		3	6.8E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001630:serpin	RT	▮		3	8.0E-1	1.0E0
☐	INTERPRO	Protease inhibitor I4, serpin	RT	▮		3	9.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	Serine protease inhibitor	RT	▮		3	9.5E-1	1.0E0
☐	SMART	SERPIN	RT	▮		3	9.6E-1	1.0E0
☐	GOTERM_MF_ALL	serine-type endopeptidase inhibitor activity	RT	▮		5	9.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	protease inhibitor	RT	▮		3	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	endopeptidase inhibitor activity	RT	▮		6	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	protease inhibitor activity	RT	▮		6	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	enzyme inhibitor activity	RT	▮		8	1.0E0	1.0E0
	Annotation Cluster 215	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	transcription factor complex	RT	▮		30	8.3E-1	1.0E0
☐	GOTERM_CC_ALL	nucleoplasm part	RT	▮		39	8.5E-1	1.0E0
☐	GOTERM_CC_ALL	nucleoplasm	RT	▮		41	8.7E-1	1.0E0
☐	GOTERM_CC_ALL	nuclear lumen	RT	▮		46	9.6E-1	1.0E0
☐	GOTERM_CC_ALL	nuclear part	RT	▮		65	9.9E-1	1.0E0
☐	GOTERM_CC_ALL	organelle lumen	RT	▮		49	9.9E-1	1.0E0
☐	GOTERM_CC_ALL	membrane-enclosed lumen	RT	▮		49	9.9E-1	1.0E0
	Annotation Cluster 216	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	EGF-like, laminin	RT	▮		3	8.5E-1	1.0E0
☐	SMART	EGF_Lam	RT	▮		3	9.3E-1	1.0E0
☐	INTERPRO	EGF-like region	RT	▮		9	1.0E0	1.0E0
	Annotation Cluster 217	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	response to external stimulus	RT	▮		34	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	response to wounding	RT	▮		18	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	inflammatory response	RT	▮		12	9.8E-1	1.0E0
	Annotation Cluster 218	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	synapse part	RT	▮		8	8.2E-1	1.0E0
☐	GOTERM_CC_ALL	synapse	RT	▮		14	9.2E-1	1.0E0
☐	GOTERM_CC_ALL	cell junction	RT	▮		23	9.4E-1	1.0E0
☐	GOTERM_CC_ALL	postsynaptic membrane	RT	▮		5	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	Postsynaptic cell membrane	RT	▮		4	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	synapse	RT	▮		7	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	cell junction	RT	▮		13	9.9E-1	1.0E0
	Annotation Cluster 219	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	organelle membrane	RT	▮		44	8.1E-1	1.0E0
☐	GOTERM_CC_ALL	mitochondrial membrane	RT	▮		16	9.3E-1	1.0E0
☐	GOTERM_CC_ALL	mitochondrial envelope	RT	▮		17	9.4E-1	1.0E0
☐	GOTERM_CC_ALL	mitochondrial inner membrane	RT	▮		14	9.4E-1	1.0E0
☐	GOTERM_CC_ALL	organelle inner membrane	RT	▮		14	9.6E-1	1.0E0
☐	GOTERM_CC_ALL	mitochondrial part	RT	▮		18	9.8E-1	1.0E0
☐	GOTERM_CC_ALL	organelle envelope	RT	▮		22	9.9E-1	1.0E0

☐	GOTERM_CC_ALL	envelope	RT	22	9.9E-1	1.0E0
	Annotation Cluster 220	Enrichment Score: 0.03	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	phospholipase activity	RT	3	9.3E-1	1.0E0
☐	GOTERM_MF_ALL	lipase activity	RT	4	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	lipid catabolic process	RT	6	9.3E-1	1.0E0
☐	GOTERM_MF_ALL	carboxylesterase activity	RT	5	9.8E-1	1.0E0
	Annotation Cluster 221	Enrichment Score: 0.02	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein import	RT	5	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	protein import into nucleus	RT	4	9.1E-1	1.0E0
☐	GOTERM_BP_ALL	nuclear import	RT	4	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	nucleocytoplasmic transport	RT	4	1.0E0	1.0E0
☐	GOTERM_BP_ALL	nuclear transport	RT	4	1.0E0	1.0E0
	Annotation Cluster 222	Enrichment Score: 0.02	G	Count	P_Value	Benjamini
☐	INTERPRO	Immunoglobulin	RT	11	8.3E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Ig-like C2-type 2	RT	5	8.8E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Ig-like C2-type 1	RT	5	8.8E-1	1.0E0
☐	INTERPRO	Immunoglobulin-like fold	RT	24	9.2E-1	1.0E0
☐	INTERPRO	Immunoglobulin subtype 2	RT	8	9.6E-1	1.0E0
☐	INTERPRO	Immunoglobulin-like	RT	19	9.8E-1	1.0E0
☐	SMART	IGc2	RT	9	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	immunoglobulin domain	RT	18	9.9E-1	1.0E0
☐	INTERPRO	Immunoglobulin I-set	RT	4	9.9E-1	1.0E0
☐	INTERPRO	Immunoglobulin subtype	RT	9	1.0E0	1.0E0
☐	SMART	IG	RT	11	1.0E0	1.0E0
	Annotation Cluster 223	Enrichment Score: 0.02	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	microtubule-based process	RT	13	8.6E-1	1.0E0
☐	GOTERM_CC_ALL	microtubule cytoskeleton	RT	19	9.3E-1	1.0E0
☐	GOTERM_CC_ALL	microtubule	RT	10	9.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	microtubule	RT	7	9.7E-1	1.0E0
☐	GOTERM_CC_ALL	cytoskeleton	RT	47	1.0E0	1.0E0
☐	GOTERM_CC_ALL	cytoskeletal part	RT	25	1.0E0	1.0E0
	Annotation Cluster 224	Enrichment Score: 0.02	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	repeat:5	RT	3	9.4E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:3	RT	4	9.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:1	RT	5	9.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:2	RT	5	9.7E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:4	RT	3	9.7E-1	1.0E0
	Annotation Cluster 225	Enrichment Score: 0.02	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	di-, tri-valent inorganic cation transport	RT	8	9.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	calcium transport	RT	3	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	calcium ion transport	RT	5	9.8E-1	1.0E0
	Annotation Cluster 226	Enrichment Score: 0.02	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	sensory perception	RT	19	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	transmission of nerve impulse	RT	15	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	neurological system process	RT	33	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	synaptic transmission	RT	11	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	system process	RT	42	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	cell-cell signaling	RT	16	1.0E0	1.0E0
	Annotation Cluster 227	Enrichment Score: 0.02	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	wound healing	RT	5	9.5E-1	1.0E0

☐	GOTERM_BP_ALL	blood coagulation	RT	▮		3	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	coagulation	RT	▮		3	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	hemostasis	RT	▮		3	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of body fluid levels	RT	▮		3	9.9E-1	1.0E0
	Annotation Cluster 228	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein localization	RT	▮		56	8.7E-1	1.0E0
☐	GOTERM_BP_ALL	macromolecule localization	RT	▮		57	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	transport	RT	▮		61	1.0E0	1.0E0
☐	GOTERM_MF_ALL	transporter activity	RT	▮		63	1.0E0	1.0E0
☐	GOTERM_BP_ALL	transport	RT	▮		141	1.0E0	1.0E0
☐	GOTERM_BP_ALL	localization	RT	▮		168	1.0E0	1.0E0
☐	GOTERM_BP_ALL	establishment of localization	RT	▮		143	1.0E0	1.0E0
	Annotation Cluster 229	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	ATP metabolic process	RT	▮		3	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	purine ribonucleotide metabolic process	RT	▮		4	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	purine ribonucleoside triphosphate metabolic process	RT	▮		3	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	nucleobase, nucleoside and nucleotide metabolic process	RT	▮		12	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	ribonucleoside triphosphate metabolic process	RT	▮		3	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	purine nucleoside triphosphate metabolic process	RT	▮		3	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	nucleotide metabolic process	RT	▮		11	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	ribonucleotide metabolic process	RT	▮		4	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	purine nucleotide metabolic process	RT	▮		4	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	purine ribonucleotide biosynthetic process	RT	▮		3	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	nucleoside triphosphate metabolic process	RT	▮		3	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	ribonucleotide biosynthetic process	RT	▮		3	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	purine nucleotide biosynthetic process	RT	▮		3	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	nucleotide biosynthetic process	RT	▮		5	1.0E0	1.0E0
	Annotation Cluster 230	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	Golgi vesicle transport	RT	▮		5	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	secretory pathway	RT	▮		11	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	secretion	RT	▮		16	1.0E0	1.0E0
☐	GOTERM_BP_ALL	secretion by cell	RT	▮		12	1.0E0	1.0E0
	Annotation Cluster 231	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	actin binding	RT	▮		15	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	actin-binding	RT	▮		8	9.8E-1	1.0E0
☐	GOTERM_MF_ALL	cytoskeletal protein binding	RT	▮		21	9.8E-1	1.0E0
	Annotation Cluster 232	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	sugar binding	RT	▮		10	9.8E-1	1.0E0
☐	GOTERM_MF_ALL	carbohydrate binding	RT	▮		16	9.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	lectin	RT	▮		7	9.8E-1	1.0E0
	Annotation Cluster 233	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	neurotransmitter secretion	RT	▮		3	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	regulated secretory pathway	RT	▮		3	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	generation of a signal involved in cell-cell signaling	RT	▮		4	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of neurotransmitter levels	RT	▮		4	9.9E-1	1.0E0
	Annotation Cluster 234	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	inner ear development	RT	▮		3	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	sensory perception of sound	RT	▮		3	9.8E-1	1.0E0

☐	GOTERM_BP_ALL	sensory organ development	RT		9	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	ear development	RT		3	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	sensory perception of mechanical stimulus	RT		3	9.9E-1	1.0E0
	Annotation Cluster 235	Enrichment Score: 0.01	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	amino acid and derivative metabolic process	RT		19	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	amino acid metabolic process	RT		14	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	nitrogen compound metabolic process	RT		23	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	amine metabolic process	RT		20	9.9E-1	1.0E0
	Annotation Cluster 236	Enrichment Score: 0.01	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	sodium transport	RT		4	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	sodium ion transport	RT		6	9.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	sodium	RT		3	9.7E-1	1.0E0
☐	GOTERM_MF_ALL	sodium ion binding	RT		3	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	potassium transport	RT		3	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	potassium ion transport	RT		6	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	potassium	RT		3	1.0E0	1.0E0
☐	GOTERM_MF_ALL	potassium ion binding	RT		3	1.0E0	1.0E0
☐	GOTERM_MF_ALL	alkali metal ion binding	RT		5	1.0E0	1.0E0
☐	GOTERM_BP_ALL	monovalent inorganic cation transport	RT		11	1.0E0	1.0E0
	Annotation Cluster 237	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	heparin binding	RT		3	9.8E-1	1.0E0
☐	GOTERM_MF_ALL	pattern binding	RT		4	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	glycosaminoglycan binding	RT		3	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	polysaccharide binding	RT		3	1.0E0	1.0E0
	Annotation Cluster 238	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Homeobox	RT		9	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	Homeobox	RT		11	9.9E-1	1.0E0
☐	INTERPRO	Helix-turn-helix motif, lambda-like repressor	RT		3	9.9E-1	1.0E0
☐	UP_SEQ_FEATURE	DNA-binding region:Homeobox	RT		5	1.0E0	1.0E0
☐	SMART	HOX	RT		9	1.0E0	1.0E0
☐	INTERPRO	Homeodomain-related	RT		6	1.0E0	1.0E0
	Annotation Cluster 239	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	plasma membrane part	RT		78	9.9E-1	1.0E0
☐	GOTERM_CC_ALL	integral to plasma membrane	RT		32	9.9E-1	1.0E0
☐	GOTERM_CC_ALL	intrinsic to plasma membrane	RT		33	9.9E-1	1.0E0
	Annotation Cluster 240	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	lectin	RT		7	9.8E-1	1.0E0
☐	INTERPRO	C-type lectin	RT		3	1.0E0	1.0E0
☐	SMART	CLECT	RT		3	1.0E0	1.0E0
	Annotation Cluster 241	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	sodium ion transport	RT		6	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	metal ion transport	RT		18	1.0E0	1.0E0
☐	GOTERM_BP_ALL	monovalent inorganic cation transport	RT		11	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cation transport	RT		21	1.0E0	1.0E0
☐	GOTERM_MF_ALL	substrate-specific transporter activity	RT		48	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	ion transport	RT		16	1.0E0	1.0E0
☐	GOTERM_MF_ALL	substrate-specific transmembrane transporter activity	RT		32	1.0E0	1.0E0
☐	GOTERM_MF_ALL	cation transmembrane transporter activity	RT		17	1.0E0	1.0E0
☐	GOTERM_MF_ALL	transmembrane transporter activity	RT		39	1.0E0	1.0E0

☐	GOTERM_MF_ALL	ion transmembrane transporter activity	RT		24	1.0E0	1.0E0
☐	GOTERM_MF_ALL	transporter activity	RT		63	1.0E0	1.0E0
☐	GOTERM_BP_ALL	ion transport	RT		25	1.0E0	1.0E0
	Annotation Cluster 242	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	nuclear part	RT		65	9.9E-1	1.0E0
☐	GOTERM_CC_ALL	organelle part	RT		156	1.0E0	1.0E0
☐	GOTERM_CC_ALL	intracellular organelle part	RT		154	1.0E0	1.0E0
☐	GOTERM_CC_ALL	macromolecular complex	RT		119	1.0E0	1.0E0
	Annotation Cluster 243	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	calcium channel activity	RT		3	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	calcium ion transport	RT		5	9.8E-1	1.0E0
☐	GOTERM_MF_ALL	voltage-gated cation channel activity	RT		4	1.0E0	1.0E0
☐	GOTERM_MF_ALL	voltage-gated ion channel activity	RT		5	1.0E0	1.0E0
☐	GOTERM_MF_ALL	voltage-gated channel activity	RT		5	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	voltage-gated channel	RT		3	1.0E0	1.0E0
☐	GOTERM_MF_ALL	metal ion transmembrane transporter activity	RT		7	1.0E0	1.0E0
☐	GOTERM_MF_ALL	gated channel activity	RT		6	1.0E0	1.0E0
☐	GOTERM_MF_ALL	cation channel activity	RT		5	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	Ionic channel	RT		4	1.0E0	1.0E0
☐	GOTERM_MF_ALL	ion channel activity	RT		6	1.0E0	1.0E0
☐	GOTERM_MF_ALL	substrate specific channel activity	RT		6	1.0E0	1.0E0
☐	GOTERM_MF_ALL	passive transmembrane transporter activity	RT		6	1.0E0	1.0E0
☐	GOTERM_MF_ALL	channel activity	RT		6	1.0E0	1.0E0
	Annotation Cluster 244	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT		103	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	transmembrane	RT		219	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	membrane	RT		281	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	topological domain:Extracellular	RT		74	1.0E0	1.0E0
☐	GOTERM_CC_ALL	integral to membrane	RT		275	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	transmembrane region	RT		132	1.0E0	1.0E0
☐	GOTERM_CC_ALL	membrane part	RT		314	1.0E0	1.0E0
☐	GOTERM_CC_ALL	intrinsic to membrane	RT		276	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		126	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	disulfide bond	RT		86	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	signal peptide	RT		105	1.0E0	1.0E0
☐	GOTERM_CC_ALL	membrane	RT		388	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	glycoprotein	RT		161	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	signal	RT		130	1.0E0	1.0E0
	Annotation Cluster 245	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Peptidase S1 and S6, chymotrypsin/Hap	RT		3	1.0E0	1.0E0
☐	GOTERM_MF_ALL	serine hydrolase activity	RT		6	1.0E0	1.0E0
☐	GOTERM_MF_ALL	serine-type peptidase activity	RT		6	1.0E0	1.0E0
☐	GOTERM_MF_ALL	serine-type endopeptidase activity	RT		5	1.0E0	1.0E0
☐	SMART	Tryp_SPc	RT		3	1.0E0	1.0E0
	Annotation Cluster 246	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	signal peptide	RT		105	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	Secreted	RT		55	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	signal	RT		130	1.0E0	1.0E0
☐	GOTERM_CC_ALL	extracellular space	RT		96	1.0E0	1.0E0

☐	**GOTERM_CC_ALL**	extracellular region part	**RT**	▬	102	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	extracellular region	**RT**	▬	110	1.0E0	1.0E0

560 terms were not clustered.

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	Annotation Cluster 1	Enrichment Score: 5.75	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	zinc-finger	RT	173	9.0E-12	7.8E-9
☐	SP_PIR_KEYWORDS	zinc	RT	192	5.7E-8	2.5E-5
☐	GOTERM_MF_ALL	transition metal ion binding	RT	268	4.4E-7	1.2E-3
☐	SP_PIR_KEYWORDS	metal-binding	RT	245	5.9E-7	1.7E-4
☐	GOTERM_MF_ALL	zinc ion binding	RT	221	8.2E-7	1.1E-3
☐	GOTERM_MF_ALL	metal ion binding	RT	357	7.0E-4	2.7E-1
☐	GOTERM_MF_ALL	ion binding	RT	362	1.1E-3	3.4E-1
☐	GOTERM_MF_ALL	cation binding	RT	330	1.1E-3	3.1E-1
	Annotation Cluster 2	Enrichment Score: 4.51	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	immune system process	RT	106	1.6E-7	1.4E-4
☐	GOTERM_BP_ALL	immune response	RT	66	3.8E-5	9.3E-3
☐	GOTERM_BP_ALL	response to stimulus	RT	185	4.9E-3	3.3E-1
	Annotation Cluster 3	Enrichment Score: 3.95	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	lysosome	RT	25	3.7E-5	8.0E-3
☐	GOTERM_CC_ALL	vacuole	RT	36	4.7E-5	3.6E-2
☐	GOTERM_CC_ALL	lysosome	RT	31	3.1E-4	7.6E-2
☐	GOTERM_CC_ALL	lytic vacuole	RT	31	3.1E-4	7.6E-2
	Annotation Cluster 4	Enrichment Score: 3.46	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	establishment and/or maintenance of chromatin architecture	RT	49	6.1E-8	7.9E-5
☐	GOTERM_BP_ALL	DNA packaging	RT	49	1.5E-7	1.5E-4
☐	GOTERM_BP_ALL	chromatin modification	RT	36	4.2E-6	2.2E-3
☐	GOTERM_BP_ALL	chromosome organization and biogenesis	RT	52	1.7E-5	6.7E-3
☐	GOTERM_BP_ALL	chromatin assembly or disassembly	RT	20	1.3E-3	1.6E-1
☐	GOTERM_BP_ALL	DNA metabolic process	RT	75	3.0E-3	2.6E-1
☐	GOTERM_CC_ALL	chromatin	RT	25	4.7E-3	4.0E-1
☐	SP_PIR_KEYWORDS	Chromatin regulator	RT	18	5.6E-3	2.3E-1
☐	GOTERM_CC_ALL	chromosomal part	RT	35	2.1E-2	6.4E-1
☐	GOTERM_CC_ALL	chromosome	RT	39	2.2E-2	6.2E-1
☐	GOTERM_BP_ALL	organelle organization and biogenesis	RT	102	3.1E-1	9.8E-1
	Annotation Cluster 5	Enrichment Score: 3.35	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of cellular process	RT	131	1.7E-7	1.3E-4
☐	GOTERM_BP_ALL	negative regulation of biological process	RT	135	9.8E-7	6.3E-4
☐	GOTERM_MF_ALL	transcription repressor activity	RT	32	7.5E-5	6.5E-2
☐	GOTERM_BP_ALL	negative regulation of transcription	RT	41	1.5E-3	1.7E-1
☐	GOTERM_BP_ALL	negative regulation of transcription, DNA-dependent	RT	32	2.9E-3	2.6E-1
☐	GOTERM_BP_ALL	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	42	3.0E-3	2.7E-1
☐	GOTERM_BP_ALL	negative regulation of cellular metabolic process	RT	46	5.9E-3	3.5E-1

☐	GOTERM_BP_ALL	negative regulation of metabolic process	RT		49	1.3E-2	4.8E-1
☐	GOTERM_BP_ALL	negative regulation of transcription from RNA polymerase II promoter	RT		20	6.0E-2	8.0E-1
	Annotation Cluster 6	Enrichment Score: 3.33	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of cellular process	RT		411	1.8E-10	9.4E-7
☐	GOTERM_BP_ALL	biological regulation	RT		469	1.7E-8	4.3E-5
☐	GOTERM_BP_ALL	regulation of biological process	RT		431	5.2E-8	9.0E-5
☐	GOTERM_BP_ALL	biopolymer metabolic process	RT		452	9.2E-6	4.0E-3
☐	GOTERM_BP_ALL	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		244	3.4E-5	1.0E-2
☐	GOTERM_BP_ALL	regulation of cellular metabolic process	RT		263	3.5E-5	1.0E-2
☐	GOTERM_BP_ALL	regulation of transcription	RT		238	6.9E-5	1.4E-2
☐	GOTERM_BP_ALL	regulation of transcription, DNA-dependent	RT		227	9.8E-5	1.8E-2
☐	GOTERM_BP_ALL	regulation of metabolic process	RT		269	1.0E-4	1.8E-2
☐	GOTERM_BP_ALL	regulation of gene expression	RT		250	1.2E-4	2.0E-2
☐	GOTERM_BP_ALL	transcription	RT		243	1.2E-4	2.0E-2
☐	SP_PIR_KEYWORDS	Transcription regulation	RT		145	1.4E-4	2.0E-2
☐	GOTERM_BP_ALL	transcription, DNA-dependent	RT		228	1.5E-4	2.3E-2
☐	GOTERM_BP_ALL	RNA biosynthetic process	RT		228	1.7E-4	2.5E-2
☐	SP_PIR_KEYWORDS	Transcription	RT		146	2.3E-4	2.4E-2
☐	SP_PIR_KEYWORDS	dna-binding	RT		136	4.9E-3	2.1E-1
☐	GOTERM_BP_ALL	primary metabolic process	RT		627	6.1E-3	3.6E-1
☐	GOTERM_BP_ALL	macromolecule metabolic process	RT		549	9.9E-3	4.4E-1
☐	GOTERM_MF_ALL	DNA binding	RT		195	1.0E-2	7.5E-1
☐	GOTERM_CC_ALL	nucleus	RT		368	1.9E-2	6.8E-1
☐	GOTERM_MF_ALL	nucleic acid binding	RT		291	2.1E-2	8.3E-1
☐	GOTERM_BP_ALL	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		312	2.9E-2	6.4E-1
☐	GOTERM_MF_ALL	transcription regulator activity	RT		128	3.3E-2	9.1E-1
☐	GOTERM_BP_ALL	RNA metabolic process	RT		243	4.6E-2	7.5E-1
☐	SP_PIR_KEYWORDS	nucleus	RT		287	4.9E-2	6.9E-1
☐	GOTERM_MF_ALL	sequence-specific DNA binding	RT		49	1.9E-1	1.0E0
☐	GOTERM_BP_ALL	gene expression	RT		272	2.5E-1	9.6E-1
☐	GOTERM_MF_ALL	transcription factor activity	RT		84	2.9E-1	1.0E0
	Annotation Cluster 7	Enrichment Score: 3.06	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	apoptosis	RT		92	2.1E-5	7.7E-3
☐	GOTERM_BP_ALL	cell death	RT		95	3.5E-5	9.1E-3
☐	GOTERM_BP_ALL	death	RT		95	3.5E-5	9.1E-3
☐	GOTERM_BP_ALL	programmed cell death	RT		92	4.1E-5	9.5E-3
☐	GOTERM_BP_ALL	regulation of apoptosis	RT		66	5.8E-5	1.2E-2
☐	GOTERM_BP_ALL	regulation of programmed cell death	RT		66	9.0E-5	1.7E-2
☐	SP_PIR_KEYWORDS	apoptosis	RT		37	2.7E-3	1.7E-1
☐	GOTERM_BP_ALL	cell development	RT		134	3.4E-3	2.7E-1
☐	GOTERM_BP_ALL	negative regulation of apoptosis	RT		29	5.8E-3	3.5E-1
☐	GOTERM_BP_ALL	negative regulation of programmed cell death	RT		29	7.6E-3	3.9E-1
☐	GOTERM_BP_ALL	cellular developmental process	RT		186	1.1E-2	4.6E-1
☐	GOTERM_BP_ALL	cell differentiation	RT		186	1.1E-2	4.6E-1
☐	GOTERM_BP_ALL	anti-apoptosis	RT		17	1.8E-2	5.4E-1
☐	GOTERM_BP_ALL	developmental process	RT		282	3.3E-2	6.8E-1
	Annotation Cluster 8	Enrichment Score: 2.96	G	🟩	Count	P_Value	Benjamini

☐	GOTERM_BP_ALL	taxis	RT	25	2.7E-5	8.7E-3
☐	GOTERM_BP_ALL	chemotaxis	RT	25	2.7E-5	8.7E-3
☐	GOTERM_BP_ALL	response to chemical stimulus	RT	53	2.4E-3	2.3E-1
☐	GOTERM_BP_ALL	locomotory behavior	RT	31	3.8E-3	2.9E-1
☐	GOTERM_BP_ALL	response to external stimulus	RT	60	5.6E-3	3.5E-1
☐	GOTERM_BP_ALL	behavior	RT	38	4.5E-2	7.4E-1
	Annotation Cluster 9	Enrichment Score: 2.95	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein modification process	RT	188	2.6E-6	1.5E-3
☐	GOTERM_BP_ALL	biopolymer modification	RT	192	6.4E-6	3.0E-3
☐	GOTERM_BP_ALL	post-translational protein modification	RT	160	5.5E-5	1.2E-2
☐	GOTERM_BP_ALL	cellular metabolic process	RT	638	5.8E-4	7.6E-2
☐	GOTERM_BP_ALL	primary metabolic process	RT	627	6.1E-3	3.6E-1
☐	GOTERM_BP_ALL	macromolecule metabolic process	RT	549	9.9E-3	4.4E-1
☐	GOTERM_BP_ALL	cellular macromolecule metabolic process	RT	284	3.3E-2	6.8E-1
☐	GOTERM_BP_ALL	cellular protein metabolic process	RT	279	4.0E-2	7.1E-1
☐	GOTERM_BP_ALL	protein metabolic process	RT	288	6.5E-2	8.2E-1
	Annotation Cluster 10	Enrichment Score: 2.66	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	signal transduction	RT	276	4.5E-5	1.0E-2
☐	GOTERM_BP_ALL	cell communication	RT	291	4.8E-4	6.4E-2
☐	GOTERM_BP_ALL	intracellular signaling cascade	RT	127	8.3E-3	3.9E-1
☐	GOTERM_BP_ALL	cell surface receptor linked signal transduction	RT	128	1.2E-1	9.1E-1
	Annotation Cluster 11	Enrichment Score: 2.61	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of apoptosis	RT	66	5.8E-5	1.2E-2
☐	GOTERM_BP_ALL	regulation of programmed cell death	RT	66	9.0E-5	1.7E-2
☐	GOTERM_BP_ALL	induction of programmed cell death	RT	24	1.4E-2	4.9E-1
☐	GOTERM_BP_ALL	induction of apoptosis	RT	24	1.4E-2	4.9E-1
☐	GOTERM_BP_ALL	positive regulation of apoptosis	RT	29	1.4E-2	5.0E-1
☐	GOTERM_BP_ALL	positive regulation of programmed cell death	RT	29	1.7E-2	5.4E-1
	Annotation Cluster 12	Enrichment Score: 2.27	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	biopolymer metabolic process	RT	452	9.2E-6	4.0E-3
☐	GOTERM_BP_ALL	cellular process	RT	945	1.0E-4	1.8E-2
☐	GOTERM_CC_ALL	intracellular	RT	805	2.6E-4	9.5E-2
☐	GOTERM_BP_ALL	cellular metabolic process	RT	638	5.8E-4	7.6E-2
☐	GOTERM_CC_ALL	cell part	RT	1060	3.0E-3	3.7E-1
☐	GOTERM_CC_ALL	cell	RT	1060	3.0E-3	3.7E-1
☐	GOTERM_BP_ALL	primary metabolic process	RT	627	6.1E-3	3.6E-1
☐	GOTERM_BP_ALL	metabolic process	RT	690	6.3E-3	3.6E-1
☐	GOTERM_CC_ALL	intracellular part	RT	751	8.5E-3	4.8E-1
☐	GOTERM_BP_ALL	macromolecule metabolic process	RT	549	9.9E-3	4.4E-1
☐	GOTERM_CC_ALL	nucleus	RT	368	1.9E-2	6.8E-1
☐	GOTERM_CC_ALL	intracellular membrane-bound organelle	RT	565	1.9E-2	6.6E-1
☐	GOTERM_CC_ALL	cytoplasm	RT	494	2.0E-2	6.5E-1
☐	GOTERM_CC_ALL	membrane-bound organelle	RT	565	2.1E-2	6.3E-1
☐	GOTERM_BP_ALL	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	312	2.9E-2	6.4E-1
☐	GOTERM_CC_ALL	intracellular organelle	RT	604	3.5E-1	1.0E0
☐	GOTERM_CC_ALL	organelle	RT	604	3.8E-1	1.0E0
	Annotation Cluster 13	Enrichment Score: 2.15	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	positive regulation of cellular process	RT	109	4.3E-4	6.0E-2
☐	GOTERM_BP_ALL	regulation of transcription from RNA	RT	56	1.5E-3	1.7E-1

☐		polymerase II promoter					
☐	GOTERM_BP_ALL	transcription from RNA polymerase II promoter	RT		61	1.7E-3	1.9E-1
☐	GOTERM_BP_ALL	positive regulation of cellular metabolic process	RT		56	3.5E-3	2.7E-1
☐	GOTERM_BP_ALL	positive regulation of biological process	RT		112	1.0E-2	4.5E-1
☐	GOTERM_BP_ALL	positive regulation of transcription	RT		44	1.2E-2	4.7E-1
☐	GOTERM_BP_ALL	positive regulation of metabolic process	RT		56	1.2E-2	4.7E-1
☐	GOTERM_BP_ALL	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		44	1.6E-2	5.3E-1
☐	GOTERM_BP_ALL	positive regulation of transcription, DNA-dependent	RT		36	2.9E-2	6.4E-1
☐	GOTERM_BP_ALL	positive regulation of transcription from RNA polymerase II promoter	RT		26	1.3E-1	9.1E-1
	Annotation Cluster 14	Enrichment Score: 2.07	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	region of interest:Modulating	RT		7	7.5E-4	1.0E0
☐	UP_SEQ_FEATURE	region of interest:Hinge	RT		8	1.1E-3	1.0E0
☐	GOTERM_MF_ALL	ligand-dependent nuclear receptor activity	RT		15	1.2E-3	3.0E-1
☐	INTERPRO	Steroid hormone receptor	RT		12	1.7E-3	9.9E-1
☐	INTERPRO	Nuclear hormone receptor, ligand-binding, core	RT		12	1.7E-3	9.9E-1
☐	INTERPRO	Nuclear hormone receptor, ligand-binding	RT		12	2.1E-3	9.5E-1
☐	INTERPRO	Zinc finger, nuclear hormone receptor-type	RT		11	3.5E-3	8.9E-1
☐	SMART	HOLI	RT		12	3.8E-3	6.8E-1
☐	INTERPRO	Zinc finger, NHR/GATA-type	RT		10	4.9E-3	9.4E-1
☐	UP_SEQ_FEATURE	region of interest:Steroid-binding	RT		4	6.0E-3	1.0E0
☐	SMART	ZnF_C4	RT		11	7.0E-3	5.7E-1
☐	GOTERM_MF_ALL	steroid hormone receptor activity	RT		13	7.4E-3	7.3E-1
☐	UP_SEQ_FEATURE	DNA-binding region:Nuclear receptor	RT		9	1.6E-2	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:NR C4-type	RT		9	1.6E-2	1.0E0
☐	GOTERM_MF_ALL	steroid binding	RT		10	5.7E-2	9.6E-1
☐	SP_PIR_KEYWORDS	Steroid-binding	RT		4	1.5E-1	8.8E-1
☐	UP_SEQ_FEATURE	region of interest:Ligand-binding	RT		4	3.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	Lipid-binding	RT		8	5.6E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 2	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	immune system development	RT		41	1.7E-3	1.8E-1
☐	GOTERM_BP_ALL	hemopoietic or lymphoid organ development	RT		39	1.8E-3	1.8E-1
☐	GOTERM_BP_ALL	myeloid cell differentiation	RT		19	7.8E-3	3.9E-1
☐	GOTERM_BP_ALL	hemopoiesis	RT		33	1.2E-2	4.6E-1
☐	GOTERM_BP_ALL	leukocyte differentiation	RT		16	3.4E-1	9.8E-1
	Annotation Cluster 16	Enrichment Score: 1.97	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	receptor	RT		128	4.8E-3	2.2E-1
☐	GOTERM_MF_ALL	receptor activity	RT		154	9.2E-3	7.9E-1
☐	GOTERM_MF_ALL	signal transducer activity	RT		175	1.7E-2	8.3E-1
☐	GOTERM_MF_ALL	molecular transducer activity	RT		175	1.7E-2	8.3E-1
	Annotation Cluster 17	Enrichment Score: 1.96	G	🟩	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF002050:histone H2B	RT		6	2.8E-5	8.4E-2
☐	INTERPRO	Histone H2B	RT		6	2.1E-4	7.0E-1
☐	SMART	H2B	RT		6	3.3E-4	1.8E-1
☐	GOTERM_BP_ALL	chromatin assembly or disassembly	RT		20	1.3E-3	1.6E-1
☐	GOTERM_CC_ALL	chromatin	RT		25	4.7E-3	4.0E-1
☐	GOTERM_CC_ALL	nucleosome	RT		11	4.8E-3	3.7E-1

☐	SP_PIR_KEYWORDS	Chromosomal protein	RT	18	6.8E-3	2.6E-1
☐	GOTERM_BP_ALL	chromatin assembly	RT	14	7.1E-3	3.8E-1
☐	GOTERM_BP_ALL	nucleosome assembly	RT	12	8.5E-3	4.0E-1
☐	INTERPRO	Histone core	RT	7	1.7E-2	9.9E-1
☐	SP_PIR_KEYWORDS	Nucleosome core	RT	8	1.8E-2	4.4E-1
☐	GOTERM_CC_ALL	chromosomal part	RT	35	2.1E-2	6.4E-1
☐	GOTERM_CC_ALL	chromosome	RT	39	2.2E-2	6.2E-1
☐	GOTERM_BP_ALL	protein-DNA complex assembly	RT	13	9.6E-2	8.8E-1
☐	INTERPRO	Histone-fold	RT	6	2.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	Methylation	RT	17	3.0E-1	9.7E-1
☐	GOTERM_BP_ALL	cellular component assembly	RT	38	4.0E-1	9.9E-1
☐	GOTERM_BP_ALL	macromolecular complex assembly	RT	31	5.3E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 1.91	G	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, ZZ-type	RT	6	6.7E-3	9.6E-1
☐	SMART	ZnF_ZZ	RT	6	1.0E-2	5.9E-1
☐	UP_SEQ_FEATURE	zinc finger region:ZZ-type	RT	4	2.7E-2	1.0E0
	Annotation Cluster 19	Enrichment Score: 1.77	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	transcription cofactor activity	RT	25	4.1E-3	5.7E-1
☐	GOTERM_MF_ALL	transcription factor binding	RT	33	1.1E-2	7.4E-1
☐	GOTERM_MF_ALL	transcription activator activity	RT	28	3.6E-2	9.2E-1
☐	GOTERM_MF_ALL	transcription coactivator activity	RT	13	5.3E-2	9.6E-1
	Annotation Cluster 20	Enrichment Score: 1.77	G	Count	P_Value	Benjamini
☐	INTERPRO	Pleckstrin homology-type	RT	35	2.3E-3	9.3E-1
☐	INTERPRO	Pleckstrin-like	RT	28	2.6E-2	1.0E0
☐	SMART	PH	RT	29	8.2E-2	8.5E-1
	Annotation Cluster 21	Enrichment Score: 1.66	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	transmembrane receptor protein serine/threonine kinase signaling pathway	RT	16	7.8E-3	3.9E-1
☐	GOTERM_BP_ALL	transforming growth factor beta receptor signaling pathway	RT	10	2.9E-2	6.4E-1
☐	KEGG_PATHWAY	TGF-beta signaling pathway	RT	14	4.5E-2	5.3E-1
	Annotation Cluster 22	Enrichment Score: 1.62	G	Count	P_Value	Benjamini
☐	SMART	ZnF_A20	RT	4	1.4E-2	5.7E-1
☐	INTERPRO	Zinc finger, AN1-type	RT	4	1.7E-2	9.9E-1
☐	SMART	ZnF_AN1	RT	4	2.2E-2	7.1E-1
☐	INTERPRO	Zinc finger, A20-type	RT	3	6.2E-2	1.0E0
	Annotation Cluster 23	Enrichment Score: 1.62	G	Count	P_Value	Benjamini
☐	INTERPRO	KRAB box	RT	31	2.5E-3	9.1E-1
☐	SMART	KRAB	RT	32	9.7E-3	6.3E-1
☐	INTERPRO	Zinc finger, C2H2-subtype	RT	27	1.5E-2	9.9E-1
☐	INTERPRO	Zinc finger, C2H2-type	RT	54	2.9E-2	1.0E0
☐	INTERPRO	Zinc finger, C2H2-type/integrase, DNA-binding	RT	35	4.7E-2	1.0E0
☐	INTERPRO	Zinc finger, C2H2-like	RT	40	9.0E-2	1.0E0
☐	SMART	ZnF_C2H2	RT	46	1.1E-1	8.5E-1
	Annotation Cluster 24	Enrichment Score: 1.56	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	leukocyte chemotaxis	RT	8	3.2E-3	2.7E-1
☐	GOTERM_BP_ALL	leukocyte migration	RT	9	1.0E-2	4.4E-1
☐	GOTERM_BP_ALL	regulation of chemotaxis	RT	5	1.1E-2	4.6E-1
☐	GOTERM_BP_ALL	positive regulation of chemotaxis	RT	5	1.1E-2	4.6E-1
☐	GOTERM_BP_ALL	regulation of positive chemotaxis	RT	4	4.8E-2	7.6E-1
☐	GOTERM_BP_ALL	positive regulation of positive chemotaxis	RT	4	4.8E-2	7.6E-1

☐	GOTERM_BP_ALL	induction of positive chemotaxis	RT			4	4.8E-2	7.6E-1
☐	GOTERM_BP_ALL	positive chemotaxis	RT			4	6.2E-2	8.1E-1
☐	GOTERM_BP_ALL	neutrophil chemotaxis	RT			3	3.4E-1	9.8E-1
	Annotation Cluster 25	Enrichment Score: 1.53		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of cell differentiation	RT			29	3.2E-3	2.7E-1
☐	GOTERM_BP_ALL	regulation of myeloid cell differentiation	RT			11	5.9E-3	3.5E-1
☐	GOTERM_BP_ALL	myeloid cell differentiation	RT			19	7.8E-3	3.9E-1
☐	GOTERM_BP_ALL	negative regulation of myeloid cell differentiation	RT			6	3.0E-2	6.5E-1
☐	GOTERM_BP_ALL	regulation of developmental process	RT			34	1.1E-1	8.9E-1
☐	GOTERM_BP_ALL	negative regulation of cell differentiation	RT			13	1.3E-1	9.2E-1
☐	GOTERM_BP_ALL	negative regulation of developmental process	RT			13	3.1E-1	9.8E-1
	Annotation Cluster 26	Enrichment Score: 1.53		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein modification process	RT			188	2.6E-6	1.5E-3
☐	GOTERM_BP_ALL	biopolymer modification	RT			192	6.4E-6	3.0E-3
☐	GOTERM_BP_ALL	post-translational protein modification	RT			160	5.5E-5	1.2E-2
☐	SP_PIR_KEYWORDS	transferase	RT			147	1.4E-4	1.8E-2
☐	GOTERM_MF_ALL	transferase activity	RT			194	2.9E-4	1.4E-1
☐	GOTERM_MF_ALL	kinase activity	RT			100	2.9E-3	5.1E-1
☐	GOTERM_BP_ALL	protein amino acid phosphorylation	RT			74	5.2E-3	3.4E-1
☐	GOTERM_MF_ALL	transferase activity, transferring phosphorus-containing groups	RT			111	5.5E-3	6.5E-1
☐	SP_PIR_KEYWORDS	kinase	RT			80	7.0E-3	2.5E-1
☐	GOTERM_MF_ALL	phosphotransferase activity, alcohol group as acceptor	RT			79	9.6E-3	7.8E-1
☐	GOTERM_BP_ALL	phosphorylation	RT			80	1.5E-2	5.0E-1
☐	GOTERM_MF_ALL	protein serine/threonine kinase activity	RT			56	1.7E-2	8.1E-1
☐	GOTERM_MF_ALL	protein kinase activity	RT			66	2.6E-2	8.9E-1
☐	GOTERM_BP_ALL	phosphorus metabolic process	RT			91	2.8E-2	6.4E-1
☐	GOTERM_BP_ALL	phosphate metabolic process	RT			91	2.8E-2	6.4E-1
☐	UP_SEQ_FEATURE	active site:Proton acceptor	RT			54	4.5E-2	1.0E0
☐	INTERPRO	Protein kinase, core	RT			40	4.9E-2	1.0E0
☐	INTERPRO	Serine/threonine protein kinase, active site	RT			30	7.4E-2	1.0E0
☐	SP_PIR_KEYWORDS	Serine/threonine-protein kinase	RT			39	7.6E-2	7.6E-1
☐	GOTERM_MF_ALL	protein-tyrosine kinase activity	RT			35	1.1E-1	9.9E-1
☐	UP_SEQ_FEATURE	domain:Protein kinase	RT			38	1.1E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase	RT			23	1.8E-1	1.0E0
☐	UP_SEQ_FEATURE	binding site:ATP	RT			39	1.9E-1	1.0E0
☐	SMART	S_TKc	RT			39	2.5E-1	9.4E-1
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT			54	5.1E-1	1.0E0
☐	GOTERM_MF_ALL	adenyl nucleotide binding	RT			118	7.0E-1	1.0E0
☐	GOTERM_MF_ALL	adenyl ribonucleotide binding	RT			111	7.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	atp-binding	RT			83	7.5E-1	1.0E0
☐	GOTERM_MF_ALL	ATP binding	RT			109	7.7E-1	1.0E0
☐	GOTERM_MF_ALL	purine nucleotide binding	RT			141	7.8E-1	1.0E0
☐	GOTERM_MF_ALL	nucleotide binding	RT			161	7.9E-1	1.0E0
☐	GOTERM_MF_ALL	ribonucleotide binding	RT			134	8.2E-1	1.0E0
☐	GOTERM_MF_ALL	purine ribonucleotide binding	RT			134	8.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleotide-binding	RT			102	8.8E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 1.45		G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of Ras protein signal	RT			24	2.1E-3	2.1E-1

☐		transduction				
☐	GOTERM_BP_ALL	regulation of signal transduction	RT	56	3.8E-3	2.8E-1
☐	GOTERM_BP_ALL	Ras protein signal transduction	RT	29	5.0E-3	3.3E-1
☐	GOTERM_BP_ALL	regulation of small GTPase mediated signal transduction	RT	27	7.2E-3	3.7E-1
☐	GOTERM_MF_ALL	guanyl-nucleotide exchange factor activity	RT	22	1.0E-2	7.8E-1
☐	GOTERM_MF_ALL	Ras guanyl-nucleotide exchange factor activity	RT	14	1.9E-2	8.3E-1
☐	GOTERM_BP_ALL	small GTPase mediated signal transduction	RT	47	2.7E-2	6.4E-1
☐	INTERPRO	Guanine-nucleotide dissociation stimulator, CDC24	RT	8	2.7E-2	1.0E0
☐	GOTERM_MF_ALL	GTPase regulator activity	RT	40	3.0E-2	9.1E-1
☐	GOTERM_MF_ALL	Rho guanyl-nucleotide exchange factor activity	RT	12	3.2E-2	9.1E-1
☐	GOTERM_BP_ALL	regulation of Rho protein signal transduction	RT	12	5.1E-2	7.7E-1
☐	GOTERM_MF_ALL	small GTPase regulator activity	RT	25	5.2E-2	9.6E-1
☐	INTERPRO	Rho GTP exchange factor	RT	4	6.2E-2	1.0E0
☐	INTERPRO	DH	RT	9	1.1E-1	1.0E0
☐	GOTERM_BP_ALL	Rho protein signal transduction	RT	13	1.4E-1	9.3E-1
☐	SMART	RhoGEF	RT	9	1.7E-1	9.0E-1
☐	GOTERM_MF_ALL	enzyme regulator activity	RT	66	2.0E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:DH	RT	5	2.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	guanine-nucleotide releasing factor	RT	9	2.9E-1	9.6E-1
	Annotation Cluster 28	Enrichment Score: 1.43	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	response to external stimulus	RT	60	5.6E-3	3.5E-1
☐	GOTERM_BP_ALL	defense response	RT	56	1.0E-2	4.4E-1
☐	GOTERM_BP_ALL	inflammatory response	RT	28	6.4E-2	8.1E-1
☐	GOTERM_BP_ALL	response to wounding	RT	36	9.0E-2	8.7E-1
☐	GOTERM_BP_ALL	response to stress	RT	79	2.2E-1	9.6E-1
	Annotation Cluster 29	Enrichment Score: 1.41	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	zinc finger region:RING-type	RT	18	1.8E-2	1.0E0
☐	INTERPRO	Zinc finger, RING-type	RT	30	2.8E-2	1.0E0
☐	SMART	RING	RT	31	1.1E-1	8.6E-1
	Annotation Cluster 30	Enrichment Score: 1.4	G	Count	P_Value	Benjamini
☐	INTERPRO	AT-rich interaction region	RT	6	3.3E-3	9.1E-1
☐	SMART	BRIGHT	RT	6	5.1E-3	5.4E-1
☐	INTERPRO	Transcription factor jumonji	RT	4	7.7E-2	1.0E0
☐	SMART	JmjC	RT	5	8.4E-2	8.5E-1
☐	INTERPRO	Transcription factor jumonji, JmjN	RT	3	8.7E-2	1.0E0
☐	SMART	JmjN	RT	3	1.0E-1	8.8E-1
☐	INTERPRO	Transcription factor jumonji/aspartyl beta-hydroxylase	RT	4	1.5E-1	1.0E0
	Annotation Cluster 31	Enrichment Score: 1.39	G	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, CCCH-type	RT	10	1.3E-2	9.9E-1
☐	SMART	ZnF_C3H1	RT	10	3.0E-2	7.6E-1
☐	UP_SEQ_FEATURE	zinc finger region:C3H1-type 1	RT	4	8.2E-2	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C3H1-type 2	RT	4	8.2E-2	1.0E0
	Annotation Cluster 32	Enrichment Score: 1.38	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	positive regulation of cell adhesion	RT	6	1.2E-2	4.6E-1
☐	GOTERM_BP_ALL	regulation of cell adhesion	RT	10	7.6E-2	8.5E-1
☐	GOTERM_BP_ALL	regulation of cell-cell adhesion	RT	4	7.8E-2	8.5E-1
	Annotation Cluster 33	Enrichment Score: 1.37	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of progression				

☐		through cell cycle	RT	▮				
☐	GOTERM_BP_ALL	regulation of cell cycle	RT	▮		45	2.2E-2	6.0E-1
☐	GOTERM_BP_ALL	regulation of progression through cell cycle	RT	▮		43	4.4E-2	7.3E-1
☐	GOTERM_BP_ALL	cell cycle process	RT	▮		54	3.8E-1	9.9E-1
☐	GOTERM_BP_ALL	cell cycle	RT	▮		64	5.3E-1	1.0E0
	Annotation Cluster 34	Enrichment Score: 1.34	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	cysteine-type peptidase activity	RT	▮		24	1.3E-2	7.7E-1
☐	SP_PIR_KEYWORDS	thiol protease	RT	▮		17	1.8E-2	4.4E-1
☐	PIR_SUPERFAMILY	PIRSF001182:papain	RT	▮		5	2.2E-2	1.0E0
☐	INTERPRO	Peptidase C1A, papain C-terminal	RT	▮		6	2.9E-2	1.0E0
☐	INTERPRO	Peptidase, cysteine peptidase active site	RT	▮		9	4.0E-2	1.0E0
☐	GOTERM_MF_ALL	cysteine-type endopeptidase activity	RT	▮		15	4.2E-2	9.4E-1
☐	SMART	Pept_C1	RT	▮		6	5.1E-2	8.6E-1
☐	INTERPRO	Proteinase inhibitor I29, cathepsin propeptide	RT	▮		5	5.2E-2	1.0E0
☐	INTERPRO	Peptidase C1A, papain	RT	▮		6	6.7E-2	1.0E0
☐	SP_PIR_KEYWORDS	protease	RT	▮		35	8.6E-1	1.0E0
	Annotation Cluster 35	Enrichment Score: 1.34	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	lamellipodium	RT	▮		12	8.0E-3	5.0E-1
☐	GOTERM_CC_ALL	leading edge	RT	▮		16	1.5E-2	6.5E-1
☐	GOTERM_CC_ALL	cell projection	RT	▮		29	8.4E-1	1.0E0
	Annotation Cluster 36	Enrichment Score: 1.33	G		🟩	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF002387:myelin proteolipid protein	RT	▮		3	2.2E-2	1.0E0
☐	INTERPRO	Myelin proteolipid protein PLP	RT	▮		3	6.2E-2	1.0E0
☐	SMART	PLP	RT	▮		3	7.4E-2	8.8E-1
	Annotation Cluster 37	Enrichment Score: 1.31	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	repeat:BIR 3	RT	▮		4	1.1E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:BIR 1	RT	▮		4	1.1E-2	1.0E0
☐	UP_SEQ_FEATURE	repeat:BIR 2	RT	▮		4	1.1E-2	1.0E0
☐	INTERPRO	Proteinase inhibitor I32, inhibitor of apoptosis	RT	▮		4	3.6E-2	1.0E0
☐	SMART	BIR	RT	▮		4	4.6E-2	8.5E-1
☐	BIOCARTA	Role of Mitochondria in Apoptotic Signaling	RT	▮		4	5.1E-1	1.0E0
☐	BIOCARTA	Caspase Cascade in Apoptosis	RT	▮		4	5.4E-1	1.0E0
	Annotation Cluster 38	Enrichment Score: 1.29	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	histone modification	RT	▮		11	4.3E-3	3.1E-1
☐	GOTERM_BP_ALL	protein amino acid alkylation	RT	▮		9	7.1E-3	3.8E-1
☐	GOTERM_BP_ALL	protein amino acid methylation	RT	▮		9	7.1E-3	3.8E-1
☐	GOTERM_BP_ALL	covalent chromatin modification	RT	▮		11	8.0E-3	3.9E-1
☐	GOTERM_BP_ALL	histone methylation	RT	▮		6	1.6E-2	5.2E-1
☐	GOTERM_MF_ALL	protein methyltransferase activity	RT	▮		9	1.6E-2	8.2E-1
☐	GOTERM_BP_ALL	biopolymer methylation	RT	▮		11	1.6E-2	5.2E-1
☐	UP_SEQ_FEATURE	domain:Post-SET	RT	▮		4	1.8E-2	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:PHD-type 3	RT	▮		3	2.2E-2	1.0E0
☐	GOTERM_BP_ALL	methylation	RT	▮		11	2.3E-2	6.0E-1
☐	UP_SEQ_FEATURE	domain:SET	RT	▮		5	2.9E-2	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:PHD-type 2	RT	▮		5	3.7E-2	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:PHD-type 1	RT	▮		5	4.6E-2	1.0E0
☐	GOTERM_MF_ALL	lysine N-methyltransferase activity	RT	▮		5	6.2E-2	9.6E-1
☐	GOTERM_MF_ALL	protein-lysine N-methyltransferase activity	RT	▮		5	6.2E-2	9.6E-1

☐	**GOTERM_MF_ALL**	histone-lysine N-methyltransferase activity	RT	▮		5	6.2E-2	9.6E-1
☐	**GOTERM_MF_ALL**	histone methyltransferase activity	RT	▮		6	7.6E-2	9.7E-1
☐	**INTERPRO**	Post-SET zinc-binding region	RT	▮		4	9.4E-2	1.0E0
☐	**SMART**	PostSET	RT	▮		4	1.2E-1	8.5E-1
☐	**SP_PIR_KEYWORDS**	s-adenosyl-l-methionine	RT	▮		10	1.3E-1	8.5E-1
☐	**INTERPRO**	SET	RT	▮		7	1.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	one-carbon compound metabolic process	RT	▮		12	1.6E-1	9.4E-1
☐	**GOTERM_MF_ALL**	S-adenosylmethionine-dependent methyltransferase activity	RT	▮		10	1.8E-1	9.9E-1
☐	**SMART**	SET	RT	▮		7	1.9E-1	9.1E-1
☐	**GOTERM_MF_ALL**	N-methyltransferase activity	RT	▮		6	2.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	methyltransferase activity	RT	▮		17	3.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	transferase activity, transferring one-carbon groups	RT	▮		17	3.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	methyltransferase	RT	▮		11	5.1E-1	9.9E-1
	Annotation Cluster 39	Enrichment Score: 1.26	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Protein kinase C, phorbol ester/diacylglycerol binding	RT	▮		13	5.1E-3	9.3E-1
☐	**SMART**	C1	RT	▮		13	1.1E-2	5.7E-1
☐	**UP_SEQ_FEATURE**	zinc finger region:Phorbol-ester/DAG-type 1	RT	▮		5	1.7E-2	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:Phorbol-ester/DAG-type 2	RT	▮		5	1.7E-2	1.0E0
☐	**SP_PIR_KEYWORDS**	serine/threonine-specific protein kinase	RT	▮		8	2.9E-2	5.5E-1
☐	**GOTERM_MF_ALL**	diacylglycerol binding	RT	▮		10	3.1E-2	9.1E-1
☐	**SP_PIR_KEYWORDS**	phospholipid binding	RT	▮		4	7.5E-2	7.6E-1
☐	**GOTERM_MF_ALL**	protein kinase C activity	RT	▮		4	1.3E-1	9.9E-1
☐	**SP_PIR_KEYWORDS**	phorbol ester binding	RT	▮		3	1.4E-1	8.8E-1
☐	**GOTERM_MF_ALL**	phorbol ester receptor activity	RT	▮		4	1.7E-1	1.0E0
☐	**INTERPRO**	Protein kinase C	RT	▮		3	1.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:C2	RT	▮		6	2.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Phorbol-ester binding	RT	▮		6	3.0E-1	9.7E-1
	Annotation Cluster 40	Enrichment Score: 1.24	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Receptor activity modifying protein	RT	▮		3	2.1E-2	1.0E0
☐	**GOTERM_BP_ALL**	regulation of G-protein coupled receptor protein signaling pathway	RT	▮		6	4.3E-2	7.3E-1
☐	**GOTERM_MF_ALL**	coreceptor activity	RT	▮		3	2.1E-1	1.0E0
	Annotation Cluster 41	Enrichment Score: 1.19	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	cell-matrix adhesion	RT	▮		15	7.9E-3	3.9E-1
☐	**GOTERM_BP_ALL**	regulation of cell motility	RT	▮		13	3.4E-2	6.9E-1
☐	**GOTERM_BP_ALL**	regulation of locomotion	RT	▮		13	4.8E-2	7.5E-1
☐	**GOTERM_BP_ALL**	negative regulation of cell motility	RT	▮		6	5.9E-2	8.0E-1
☐	**GOTERM_BP_ALL**	negative regulation of locomotion	RT	▮		6	6.8E-2	8.3E-1
☐	**GOTERM_BP_ALL**	locomotion	RT	▮		13	8.5E-2	8.6E-1
☐	**GOTERM_BP_ALL**	regulation of cell migration	RT	▮		10	1.4E-1	9.2E-1
☐	**GOTERM_BP_ALL**	negative regulation of cell migration	RT	▮		3	5.2E-1	1.0E0
	Annotation Cluster 42	Enrichment Score: 1.19	G		🟩	Count	P_Value	Benjamini
☐	**BIOCARTA**	Control of Gene Expression by Vitamin D Receptor	RT	▮		8	4.3E-2	9.6E-1
☐	**BIOCARTA**	Role of PPAR-gamma Coactivators in Obesity and Thermogenesis	RT	▮		5	4.7E-2	9.0E-1
☐	**BIOCARTA**	Transcription Regulation by Methyltransferase of CARM1	RT	▮		4	1.4E-1	9.9E-1
	Annotation Cluster 43	Enrichment Score: 1.18	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	determination of left/right symmetry	RT	▮		8	2.4E-2	6.1E-1

☐	GOTERM_BP_ALL	determination of symmetry	RT	8	2.7E-2	6.4E-1
☐	GOTERM_BP_ALL	determination of bilateral symmetry	RT	8	2.7E-2	6.4E-1
☐	GOTERM_BP_ALL	dorsal/ventral pattern formation	RT	7	1.6E-1	9.4E-1
☐	GOTERM_BP_ALL	smoothened signaling pathway	RT	4	4.4E-1	9.9E-1
	Annotation Cluster 44	Enrichment Score: 1.18	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	chondrocyte differentiation	RT	7	3.0E-3	2.6E-1
☐	GOTERM_BP_ALL	regulation of chondrocyte differentiation	RT	3	4.0E-2	7.1E-1
☐	GOTERM_BP_ALL	negative regulation of chondrocyte differentiation	RT	3	4.0E-2	7.1E-1
☐	KEGG_PATHWAY	Hedgehog signaling pathway	RT	7	3.2E-1	8.4E-1
☐	KEGG_PATHWAY	Basal cell carcinoma	RT	4	8.7E-1	9.9E-1
	Annotation Cluster 45	Enrichment Score: 1.16	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell activation	RT	37	2.0E-3	2.0E-1
☐	GOTERM_BP_ALL	regulation of cell activation	RT	19	4.9E-3	3.3E-1
☐	GOTERM_BP_ALL	leukocyte activation	RT	33	7.7E-3	3.9E-1
☐	GOTERM_BP_ALL	regulation of lymphocyte proliferation	RT	12	2.0E-2	5.8E-1
☐	GOTERM_BP_ALL	regulation of mononuclear cell proliferation	RT	12	2.0E-2	5.8E-1
☐	GOTERM_BP_ALL	positive regulation of T cell proliferation	RT	8	2.4E-2	6.1E-1
☐	GOTERM_BP_ALL	regulation of lymphocyte activation	RT	15	5.8E-2	8.0E-1
☐	GOTERM_BP_ALL	lymphocyte activation	RT	27	5.9E-2	8.0E-1
☐	GOTERM_BP_ALL	regulation of T cell proliferation	RT	9	6.9E-2	8.3E-1
☐	GOTERM_BP_ALL	regulation of multicellular organismal process	RT	36	7.1E-2	8.3E-1
☐	GOTERM_BP_ALL	mononuclear cell proliferation	RT	13	7.4E-2	8.5E-1
☐	GOTERM_BP_ALL	lymphocyte proliferation	RT	13	7.4E-2	8.5E-1
☐	GOTERM_BP_ALL	positive regulation of lymphocyte proliferation	RT	8	8.1E-2	8.5E-1
☐	GOTERM_BP_ALL	positive regulation of mononuclear cell proliferation	RT	8	8.1E-2	8.5E-1
☐	GOTERM_BP_ALL	positive regulation of T cell activation	RT	9	8.2E-2	8.6E-1
☐	GOTERM_BP_ALL	T cell proliferation	RT	10	1.0E-1	9.0E-1
☐	GOTERM_BP_ALL	regulation of T cell activation	RT	11	1.5E-1	9.3E-1
☐	GOTERM_BP_ALL	positive regulation of lymphocyte activation	RT	10	1.7E-1	9.4E-1
☐	GOTERM_BP_ALL	positive regulation of activated T cell proliferation	RT	3	2.4E-1	9.7E-1
☐	GOTERM_BP_ALL	regulation of activated T cell proliferation	RT	3	2.8E-1	9.7E-1
☐	GOTERM_BP_ALL	T cell activation	RT	15	3.3E-1	9.8E-1
☐	GOTERM_BP_ALL	positive regulation of cell proliferation	RT	21	3.8E-1	9.9E-1
☐	GOTERM_BP_ALL	activated T cell proliferation	RT	3	4.1E-1	9.9E-1
☐	GOTERM_BP_ALL	regulation of lymphocyte differentiation	RT	4	4.2E-1	9.9E-1
	Annotation Cluster 46	Enrichment Score: 1.14	G	Count	P_Value	Benjamini
☐	INTERPRO	Protein kinase, C-terminal	RT	10	3.9E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:AGC-kinase C-terminal	RT	9	5.7E-2	1.0E0
☐	SMART	S_TK_X	RT	10	6.6E-2	8.9E-1
☐	INTERPRO	Serine/threonine protein kinase	RT	23	1.8E-1	1.0E0
	Annotation Cluster 47	Enrichment Score: 1.08	G	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, MYM-type	RT	3	6.2E-2	1.0E0
☐	INTERPRO	TRASH	RT	3	8.7E-2	1.0E0
☐	SMART	TRASH	RT	3	1.0E-1	8.8E-1
	Annotation Cluster 48	Enrichment Score: 1.07	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell migration	RT	36	5.8E-2	8.0E-1
☐	GOTERM_BP_ALL	cell motility	RT	40	1.0E-1	8.9E-1

☐	**GOTERM_BP_ALL**	localization of cell	RT	40	1.0E-1	8.9E-1
	Annotation Cluster 49	Enrichment Score: 1.03	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	multicellular organism growth	RT	10	7.6E-2	8.5E-1
☐	**GOTERM_BP_ALL**	regulation of multicellular organism growth	RT	9	8.2E-2	8.6E-1
☐	**GOTERM_BP_ALL**	regulation of growth	RT	21	1.3E-1	9.2E-1
	Annotation Cluster 50	Enrichment Score: 1.02	G	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	biological rhythms	RT	7	2.8E-3	1.6E-1
☐	**KEGG_PATHWAY**	Circadian rhythm	RT	5	2.0E-2	4.6E-1
☐	**UP_SEQ_FEATURE**	region of interest:CRY binding domain	RT	3	2.2E-2	1.0E0
☐	**UP_SEQ_FEATURE**	region of interest:CSNK1E binding domain	RT	3	2.2E-2	1.0E0
☐	**INTERPRO**	PAS	RT	7	3.4E-2	1.0E0
☐	**GOTERM_BP_ALL**	xenobiotic metabolic process	RT	5	3.5E-2	6.8E-1
☐	**GOTERM_MF_ALL**	protein histidine kinase activity	RT	6	4.2E-2	9.4E-1
☐	**INTERPRO**	PAC motif	RT	6	4.2E-2	1.0E0
☐	**GOTERM_BP_ALL**	response to xenobiotic stimulus	RT	5	5.3E-2	7.7E-1
☐	**SMART**	PAS	RT	7	5.9E-2	8.9E-1
☐	**GOTERM_MF_ALL**	two-component sensor activity	RT	5	6.2E-2	9.6E-1
☐	**SMART**	PAC	RT	6	7.1E-2	8.8E-1
☐	**GOTERM_MF_ALL**	phosphotransferase activity, nitrogenous group as acceptor	RT	6	8.6E-2	9.8E-1
☐	**INTERPRO**	PAS fold-3	RT	5	8.6E-2	1.0E0
☐	**GOTERM_BP_ALL**	circadian rhythm	RT	6	8.8E-2	8.7E-1
☐	**UP_SEQ_FEATURE**	short sequence motif:Nuclear export signal	RT	5	1.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:PAS 1	RT	4	1.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:PAS 2	RT	4	1.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	two-component signal transduction system (phosphorelay)	RT	5	2.0E-1	9.6E-1
☐	**UP_SEQ_FEATURE**	DNA-binding region:Basic motif	RT	13	2.8E-1	1.0E0
☐	**INTERPRO**	PAS fold	RT	4	2.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:PAC	RT	4	3.1E-1	1.0E0
☐	**INTERPRO**	Basic helix-loop-helix dimerisation region bHLH	RT	9	6.6E-1	1.0E0
☐	**SMART**	HLH	RT	9	8.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Helix-loop-helix motif	RT	6	8.3E-1	1.0E0
☐	**INTERPRO**	Helix-loop-helix DNA-binding	RT	5	9.2E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 1.01	G	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	NAD+ ADP-ribosyltransferase activity	RT	5	4.2E-2	9.4E-1
☐	**GOTERM_MF_ALL**	transferase activity, transferring pentosyl groups	RT	8	6.4E-2	9.6E-1
☐	**INTERPRO**	Poly(ADP-ribose) polymerase, catalytic region	RT	3	3.4E-1	1.0E0
	Annotation Cluster 52	Enrichment Score: 1	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	protein amino acid autophosphorylation	RT	8	8.1E-2	8.5E-1
☐	**GOTERM_BP_ALL**	protein autoprocessing	RT	8	1.1E-1	8.9E-1
☐	**GOTERM_BP_ALL**	protein processing	RT	12	1.2E-1	9.1E-1
	Annotation Cluster 53	Enrichment Score: 0.96	G	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	inflammation	RT	6	1.4E-2	4.0E-1
☐	**SP_PIR_KEYWORDS**	calcium binding	RT	10	4.4E-2	6.6E-1
☐	**PIR_SUPERFAMILY**	PIRSF002353:S-100 protein	RT	4	9.9E-2	1.0E0
☐	**INTERPRO**	S100/CaBP-9k-type, calcium binding, subdomain	RT	4	2.0E-1	1.0E0
☐	**INTERPRO**	S100/CaBP-9k-type, calcium binding	RT	4	2.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	EF hand	RT	4	4.9E-1	9.9E-1

	Annotation Cluster 54	Enrichment Score: 0.95	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell proliferation	RT	▮	61	3.8E-2	7.0E-1
☐	GOTERM_BP_ALL	regulation of cell proliferation	RT	▮	42	9.7E-2	8.8E-1
☐	GOTERM_BP_ALL	positive regulation of cell proliferation	RT	▮	21	3.8E-1	9.9E-1
	Annotation Cluster 55	Enrichment Score: 0.94	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Peptidoglycan-binding LysM	RT	▮	3	8.7E-2	1.0E0
☐	SMART	LysM	RT	▮	3	1.0E-1	8.8E-1
☐	GOTERM_BP_ALL	cell wall catabolic process	RT	▮	4	1.1E-1	9.0E-1
☐	GOTERM_BP_ALL	cell wall metabolic process	RT	▮	4	1.1E-1	9.0E-1
☐	GOTERM_BP_ALL	cell wall organization and biogenesis	RT	▮	4	1.3E-1	9.2E-1
☐	GOTERM_BP_ALL	external encapsulating structure organization and biogenesis	RT	▮	4	1.5E-1	9.4E-1
	Annotation Cluster 56	Enrichment Score: 0.93	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Basic-leucine zipper (bZIP) transcription factor	RT	▮	11	9.0E-3	9.8E-1
☐	SMART	BRLZ	RT	▮	11	2.6E-2	7.3E-1
☐	INTERPRO	Basic leucine zipper	RT	▮	4	2.0E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Leucine-zipper	RT	▮	11	2.4E-1	1.0E0
☐	UP_SEQ_FEATURE	DNA-binding region:Basic motif	RT	▮	13	2.8E-1	1.0E0
☐	GOTERM_MF_ALL	protein dimerization activity	RT	▮	28	2.8E-1	1.0E0
☐	INTERPRO	bZIP transcription factor, bZIP-1	RT	▮	4	3.4E-1	1.0E0
	Annotation Cluster 57	Enrichment Score: 0.93	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	phagocytosis, engulfment	RT	▮	6	3.4E-3	2.7E-1
☐	GOTERM_BP_ALL	positive regulation of inflammatory response	RT	▮	6	6.8E-3	3.7E-1
☐	GOTERM_BP_ALL	positive regulation of defense response	RT	▮	6	6.8E-3	3.7E-1
☐	GOTERM_BP_ALL	regulation of immune effector process	RT	▮	6	1.2E-2	4.6E-1
☐	GOTERM_BP_ALL	regulation of inflammatory response	RT	▮	8	1.7E-2	5.4E-1
☐	GOTERM_BP_ALL	regulation of defense response	RT	▮	8	1.7E-2	5.4E-1
☐	GOTERM_BP_ALL	regulation of phagocytosis	RT	▮	6	2.0E-2	5.8E-1
☐	GOTERM_BP_ALL	positive regulation of phagocytosis	RT	▮	6	2.0E-2	5.8E-1
☐	GOTERM_BP_ALL	positive regulation of immune effector process	RT	▮	5	2.1E-2	5.8E-1
☐	GOTERM_BP_ALL	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains.	RT	▮	6	2.4E-2	6.1E-1
☐	GOTERM_BP_ALL	regulation of adaptive immune response	RT	▮	6	2.4E-2	6.1E-1
☐	GOTERM_BP_ALL	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	RT	▮	5	3.5E-2	6.8E-1
☐	GOTERM_BP_ALL	positive regulation of adaptive immune response	RT	▮	5	3.5E-2	6.8E-1
☐	GOTERM_BP_ALL	regulation of lymphocyte mediated immunity	RT	▮	5	3.5E-2	6.8E-1
☐	GOTERM_BP_ALL	regulation of leukocyte mediated immunity	RT	▮	5	3.5E-2	6.8E-1
☐	GOTERM_BP_ALL	phagocytosis	RT	▮	8	3.6E-2	6.9E-1
☐	GOTERM_BP_ALL	positive regulation of endocytosis	RT	▮	6	6.8E-2	8.3E-1
☐	GOTERM_BP_ALL	positive regulation of lymphocyte mediated immunity	RT	▮	4	7.8E-2	8.5E-1
☐	GOTERM_BP_ALL	positive regulation of leukocyte mediated immunity	RT	▮	4	7.8E-2	8.5E-1
☐	GOTERM_BP_ALL	regulation of inflammatory response to antigenic stimulus	RT	▮	4	9.5E-2	8.8E-1
☐	GOTERM_BP_ALL	regulation of response to stimulus	RT	▮	8	1.1E-1	8.9E-1
☐	GOTERM_BP_ALL	inflammatory response to antigenic stimulus	RT	▮	4	1.3E-1	9.2E-1
☐	GOTERM_BP_ALL	adaptive immune response based on somatic recombination of immune	RT	▮	13	1.5E-1	9.3E-1

☐		receptors built from immunoglobulin superfamily domains		▮				
☐	GOTERM_BP_ALL	adaptive immune response	RT	▮		13	1.5E-1	9.3E-1
☐	GOTERM_BP_ALL	regulation of immunoglobulin mediated immune response	RT	▮		3	1.8E-1	9.5E-1
☐	GOTERM_BP_ALL	regulation of B cell mediated immunity	RT	▮		3	1.8E-1	9.5E-1
☐	GOTERM_BP_ALL	positive regulation of multicellular organismal process	RT	▮		15	2.0E-1	9.6E-1
☐	GOTERM_BP_ALL	positive regulation of inflammatory response to antigenic stimulus	RT	▮		3	2.1E-1	9.6E-1
☐	GOTERM_BP_ALL	phagocytosis, recognition	RT	▮		3	2.1E-1	9.6E-1
☐	GOTERM_BP_ALL	immune effector process	RT	▮		16	2.2E-1	9.6E-1
☐	GOTERM_BP_ALL	regulation of endocytosis	RT	▮		6	2.4E-1	9.7E-1
☐	GOTERM_BP_ALL	regulation of hypersensitivity	RT	▮		3	2.4E-1	9.7E-1
☐	GOTERM_BP_ALL	regulation of acute inflammatory response to antigenic stimulus	RT	▮		3	2.4E-1	9.7E-1
☐	GOTERM_BP_ALL	regulation of acute inflammatory response	RT	▮		3	2.4E-1	9.7E-1
☐	GOTERM_BP_ALL	positive regulation of transport	RT	▮		6	2.9E-1	9.8E-1
☐	GOTERM_BP_ALL	regulation of immune system process	RT	▮		13	3.0E-1	9.8E-1
☐	GOTERM_BP_ALL	hypersensitivity	RT	▮		3	3.1E-1	9.8E-1
☐	GOTERM_BP_ALL	acute inflammatory response to antigenic stimulus	RT	▮		3	3.1E-1	9.8E-1
☐	GOTERM_BP_ALL	lymphocyte mediated immunity	RT	▮		11	3.4E-1	9.8E-1
☐	GOTERM_BP_ALL	positive regulation of immune system process	RT	▮		11	3.7E-1	9.9E-1
☐	GOTERM_BP_ALL	regulation of immune response	RT	▮		12	3.9E-1	9.9E-1
☐	GOTERM_BP_ALL	leukocyte mediated immunity	RT	▮		11	4.1E-1	9.9E-1
☐	GOTERM_BP_ALL	positive regulation of immune response	RT	▮		10	4.9E-1	1.0E0
☐	GOTERM_BP_ALL	cell recognition	RT	▮		5	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	immunoglobulin mediated immune response	RT	▮		7	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	B cell mediated immunity	RT	▮		7	6.4E-1	1.0E0
☐	GOTERM_BP_ALL	acute inflammatory response	RT	▮		6	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	membrane invagination	RT	▮		13	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	endocytosis	RT	▮		13	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of transport	RT	▮		7	9.1E-1	1.0E0
☐	GOTERM_BP_ALL	membrane organization and biogenesis	RT	▮		18	9.2E-1	1.0E0
	Annotation Cluster 58	Enrichment Score: 0.92	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	growth	RT	▮		34	3.4E-2	6.9E-1
☐	GOTERM_BP_ALL	regulation of growth	RT	▮		21	1.3E-1	9.2E-1
☐	GOTERM_BP_ALL	cell growth	RT	▮		16	1.3E-1	9.2E-1
☐	GOTERM_BP_ALL	regulation of cell size	RT	▮		17	1.4E-1	9.3E-1
☐	GOTERM_BP_ALL	regulation of cell growth	RT	▮		12	2.9E-1	9.8E-1
	Annotation Cluster 59	Enrichment Score: 0.91	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	SH2 motif	RT	▮		15	8.3E-2	1.0E0
☐	SP_PIR_KEYWORDS	sh2 domain	RT	▮		15	8.5E-2	7.9E-1
☐	SMART	SH2	RT	▮		15	1.6E-1	9.0E-1
☐	UP_SEQ_FEATURE	domain:SH2	RT	▮		9	2.1E-1	1.0E0
	Annotation Cluster 60	Enrichment Score: 0.91	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	response to other organism	RT	▮		19	7.7E-2	8.5E-1
☐	GOTERM_BP_ALL	response to virus	RT	▮		9	9.0E-2	8.7E-1
☐	GOTERM_BP_ALL	multi-organism process	RT	▮		24	1.8E-1	9.5E-1
☐	GOTERM_BP_ALL	response to biotic stimulus	RT	▮		25	2.0E-1	9.6E-1
	Annotation Cluster 61	Enrichment Score: 0.9	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Prostate cancer	RT	▮		17	6.9E-3	3.9E-1

☐	**KEGG_PATHWAY**	Apoptosis	**RT**	▮	16	7.2E-3	3.2E-1
☐	**KEGG_PATHWAY**	Acute myeloid leukemia	**RT**	▮	12	1.7E-2	4.5E-1
☐	**KEGG_PATHWAY**	Melanoma	**RT**	▮	13	2.5E-2	4.8E-1
☐	**KEGG_PATHWAY**	Renal cell carcinoma	**RT**	▮	13	3.0E-2	5.1E-1
☐	**KEGG_PATHWAY**	Chronic myeloid leukemia	**RT**	▮	13	3.9E-2	5.6E-1
☐	**GOTERM_MF_ALL**	phosphatidylinositol-4,5-bisphosphate 3-kinase activity	**RT**	▮	3	3.9E-2	9.4E-1
☐	**PIR_SUPERFAMILY**	PIRSF000586:phosphatidylinositol 3-kinase	**RT**	▮	3	4.1E-2	1.0E0
☐	**KEGG_PATHWAY**	Toll-like receptor signaling pathway	**RT**	▮	16	4.1E-2	5.5E-1
☐	**KEGG_PATHWAY**	Glioma	**RT**	▮	11	4.4E-2	5.5E-1
☐	**GOTERM_MF_ALL**	1-phosphatidylinositol-3-kinase activity	**RT**	▮	4	4.7E-2	9.5E-1
☐	**GOTERM_MF_ALL**	phosphoinositide 3-kinase activity	**RT**	▮	4	4.7E-2	9.5E-1
☐	**KEGG_PATHWAY**	Focal adhesion	**RT**	▮	26	4.8E-2	5.0E-1
☐	**KEGG_PATHWAY**	Non-small cell lung cancer	**RT**	▮	10	5.7E-2	4.8E-1
☐	**GOTERM_CC_ALL**	phosphoinositide 3-kinase complex	**RT**	▮	4	5.8E-2	8.9E-1
☐	**KEGG_PATHWAY**	Small cell lung cancer	**RT**	▮	14	6.9E-2	5.3E-1
☐	**KEGG_PATHWAY**	B cell receptor signaling pathway	**RT**	▮	11	8.0E-2	5.5E-1
☐	**INTERPRO**	Phosphoinositide 3-kinase, ras-binding	**RT**	▮	3	8.7E-2	1.0E0
☐	**KEGG_PATHWAY**	Endometrial cancer	**RT**	▮	9	9.5E-2	6.0E-1
☐	**KEGG_PATHWAY**	T cell receptor signaling pathway	**RT**	▮	14	1.0E-1	6.1E-1
☐	**KEGG_PATHWAY**	mTOR signaling pathway	**RT**	▮	9	1.0E-1	6.0E-1
☐	**SMART**	PI3K_rbd	**RT**	▮	3	1.0E-1	8.8E-1
☐	**INTERPRO**	Phosphoinositide 3-kinase, C2	**RT**	▮	3	1.2E-1	1.0E0
☐	**SMART**	PI3K_C2	**RT**	▮	3	1.4E-1	8.8E-1
☐	**KEGG_PATHWAY**	Phosphatidylinositol signaling system	**RT**	▮	10	1.4E-1	6.9E-1
☐	**INTERPRO**	Phosphoinositide 3-kinase accessory region PIK	**RT**	▮	3	1.5E-1	1.0E0
☐	**SMART**	PI3Ka	**RT**	▮	3	1.7E-1	8.9E-1
☐	**INTERPRO**	Phosphatidylinositol Kinase	**RT**	▮	3	1.8E-1	1.0E0
☐	**KEGG_PATHWAY**	Pancreatic cancer	**RT**	▮	10	2.1E-1	7.7E-1
☐	**KEGG_PATHWAY**	Fc epsilon RI signaling pathway	**RT**	▮	10	2.2E-1	7.7E-1
☐	**GOTERM_BP_ALL**	phosphoinositide phosphorylation	**RT**	▮	3	2.4E-1	9.7E-1
☐	**KEGG_PATHWAY**	Type II diabetes mellitus	**RT**	▮	7	2.6E-1	8.1E-1
☐	**GOTERM_BP_ALL**	lipid modification	**RT**	▮	5	2.6E-1	9.7E-1
☐	**GOTERM_BP_ALL**	glycerophospholipid metabolic process	**RT**	▮	9	2.7E-1	9.7E-1
☐	**GOTERM_BP_ALL**	lipid phosphorylation	**RT**	▮	3	2.8E-1	9.7E-1
☐	**GOTERM_MF_ALL**	lipid kinase activity	**RT**	▮	4	2.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	inositol or phosphatidylinositol kinase activity	**RT**	▮	5	3.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:PI3K/PI4K	**RT**	▮	3	3.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	phosphoinositide-mediated signaling	**RT**	▮	7	3.5E-1	9.9E-1
☐	**KEGG_PATHWAY**	ErbB signaling pathway	**RT**	▮	10	3.5E-1	8.7E-1
☐	**INTERPRO**	Phosphatidylinositol 3- and 4-kinase, catalytic	**RT**	▮	3	4.0E-1	1.0E0
☐	**KEGG_PATHWAY**	Insulin signaling pathway	**RT**	▮	14	4.2E-1	8.7E-1
☐	**KEGG_PATHWAY**	Inositol phosphate metabolism	**RT**	▮	6	4.3E-1	8.8E-1
☐	**SMART**	PI3Kc	**RT**	▮	3	4.6E-1	9.9E-1
☐	**KEGG_PATHWAY**	Colorectal cancer	**RT**	▮	9	4.6E-1	8.9E-1
☐	**GOTERM_BP_ALL**	phosphoinositide metabolic process	**RT**	▮	6	4.7E-1	1.0E0
☐	**KEGG_PATHWAY**	Natural killer cell mediated cytotoxicity	**RT**	▮	13	4.8E-1	9.0E-1
☐	**KEGG_PATHWAY**	VEGF signaling pathway	**RT**	▮	7	7.0E-1	9.6E-1

☐	GOTERM_CC_ALL	cytosolic part	RT	▮		5	9.8E-1	1.0E0
	Annotation Cluster 62	Enrichment Score: 0.9	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of lymphocyte proliferation	RT	▮		12	2.0E-2	5.8E-1
☐	GOTERM_BP_ALL	regulation of mononuclear cell proliferation	RT	▮		12	2.0E-2	5.8E-1
☐	GOTERM_BP_ALL	regulation of lymphocyte activation	RT	▮		15	5.8E-2	8.0E-1
☐	GOTERM_BP_ALL	mononuclear cell proliferation	RT	▮		13	7.4E-2	8.5E-1
☐	GOTERM_BP_ALL	lymphocyte proliferation	RT	▮		13	7.4E-2	8.5E-1
☐	GOTERM_BP_ALL	negative regulation of B cell proliferation	RT	▮		3	1.8E-1	9.5E-1
☐	GOTERM_BP_ALL	negative regulation of lymphocyte proliferation	RT	▮		5	1.8E-1	9.5E-1
☐	GOTERM_BP_ALL	negative regulation of mononuclear cell proliferation	RT	▮		5	1.8E-1	9.5E-1
☐	GOTERM_BP_ALL	B cell proliferation	RT	▮		5	2.6E-1	9.7E-1
☐	GOTERM_BP_ALL	negative regulation of B cell activation	RT	▮		3	3.1E-1	9.8E-1
☐	GOTERM_BP_ALL	regulation of B cell proliferation	RT	▮		4	3.2E-1	9.8E-1
☐	GOTERM_BP_ALL	regulation of B cell activation	RT	▮		6	3.3E-1	9.8E-1
☐	GOTERM_BP_ALL	negative regulation of lymphocyte activation	RT	▮		5	3.4E-1	9.8E-1
	Annotation Cluster 63	Enrichment Score: 0.9	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	autophosphorylation	RT	▮		11	2.6E-3	1.7E-1
☐	SP_PIR_KEYWORDS	ATP	RT	▮		21	7.2E-2	7.5E-1
☐	GOTERM_MF_ALL	protein-tyrosine kinase activity	RT	▮		35	1.1E-1	9.9E-1
☐	INTERPRO	Tyrosine protein kinase, active site	RT	▮		13	1.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	phosphotransferase	RT	▮		16	1.5E-1	8.8E-1
☐	INTERPRO	Tyrosine protein kinase	RT	▮		15	1.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	tyrosine-protein kinase	RT	▮		14	1.8E-1	9.0E-1
☐	SP_PIR_KEYWORDS	tyrosine-specific protein kinase	RT	▮		7	2.2E-1	9.3E-1
☐	UP_SEQ_FEATURE	domain:Ig-like C2-type 3	RT	▮		8	3.0E-1	1.0E0
☐	SMART	TyrKc	RT	▮		15	3.3E-1	9.6E-1
☐	GOTERM_MF_ALL	transmembrane receptor protein tyrosine kinase activity	RT	▮		8	4.5E-1	1.0E0
	Annotation Cluster 64	Enrichment Score: 0.9	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of odontogenesis of dentine-containing teeth	RT	▮		4	1.0E-2	4.5E-1
☐	GOTERM_BP_ALL	regulation of ossification	RT	▮		8	1.2E-2	4.7E-1
☐	GOTERM_BP_ALL	odontogenesis of dentine-containing teeth	RT	▮		9	1.4E-2	5.0E-1
☐	GOTERM_BP_ALL	positive regulation of bone remodeling	RT	▮		4	1.7E-2	5.4E-1
☐	GOTERM_BP_ALL	positive regulation of ossification	RT	▮		4	1.7E-2	5.4E-1
☐	GOTERM_BP_ALL	BMP signaling pathway	RT	▮		8	2.0E-2	5.8E-1
☐	PIR_SUPERFAMILY	PIRSF500510:bone morphogenetic protein, BMP2/ BMP4 types	RT	▮		3	2.2E-2	1.0E0
☐	GOTERM_BP_ALL	cartilage development	RT	▮		11	2.3E-2	6.0E-1
☐	GOTERM_BP_ALL	regulation of bone remodeling	RT	▮		8	2.4E-2	6.1E-1
☐	GOTERM_BP_ALL	odontogenesis	RT	▮		9	2.5E-2	6.2E-1
☐	GOTERM_BP_ALL	regulation of osteoblast differentiation	RT	▮		5	2.7E-2	6.4E-1
☐	GOTERM_BP_ALL	positive regulation of cell differentiation	RT	▮		11	2.8E-2	6.4E-1
☐	GOTERM_BP_ALL	ossification	RT	▮		16	3.8E-2	7.0E-1
☐	GOTERM_BP_ALL	regulation of odontogenesis	RT	▮		3	4.0E-2	7.1E-1
☐	GOTERM_BP_ALL	biomineral formation	RT	▮		16	4.1E-2	7.1E-1
☐	GOTERM_BP_ALL	osteoblast differentiation	RT	▮		7	4.6E-2	7.5E-1
☐	SP_PIR_KEYWORDS	osteogenesis	RT	▮		5	5.0E-2	6.9E-1
☐	GOTERM_BP_ALL	positive regulation of bone mineralization	RT	▮		3	6.2E-2	8.1E-1
☐	GOTERM_BP_ALL	bone mineralization	RT	▮		7	6.8E-2	8.3E-1

☐	**GOTERM_BP_ALL**	bone remodeling	RT	16	6.9E-2	8.3E-1
☐	**GOTERM_BP_ALL**	ureteric bud branching	RT	5	7.5E-2	8.5E-1
☐	**GOTERM_BP_ALL**	regulation of bone mineralization	RT	5	8.8E-2	8.7E-1
☐	**GOTERM_BP_ALL**	urogenital system development	RT	12	9.3E-2	8.7E-1
☐	**GOTERM_BP_ALL**	mesoderm formation	RT	6	9.9E-2	8.9E-1
☐	**SP_PIR_KEYWORDS**	Chondrogenesis	RT	4	1.1E-1	8.2E-1
☐	**GOTERM_BP_ALL**	kidney development	RT	11	1.1E-1	9.0E-1
☐	**PIR_SUPERFAMILY**	PIRSF037272:bone morphogenetic protein	RT	4	1.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	mesoderm morphogenesis	RT	6	1.2E-1	9.1E-1
☐	**GOTERM_BP_ALL**	formation of primary germ layer	RT	6	1.4E-1	9.2E-1
☐	**GOTERM_BP_ALL**	positive regulation of developmental process	RT	12	1.4E-1	9.3E-1
☐	**GOTERM_BP_ALL**	positive regulation of osteoblast differentiation	RT	3	1.8E-1	9.5E-1
☐	**GOTERM_BP_ALL**	tissue remodeling	RT	16	1.9E-1	9.5E-1
☐	**GOTERM_BP_ALL**	branching morphogenesis of a tube	RT	9	1.9E-1	9.6E-1
☐	**GOTERM_BP_ALL**	tube morphogenesis	RT	17	2.4E-1	9.7E-1
☐	**INTERPRO**	Transforming growth factor beta (TGFb), N-terminal	RT	4	2.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	metanephros development	RT	7	2.4E-1	9.7E-1
☐	**GOTERM_BP_ALL**	morphogenesis of a branching structure	RT	9	2.5E-1	9.7E-1
☐	**INTERPRO**	Transforming growth factor-beta-related	RT	5	2.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	skeletal development	RT	21	2.8E-1	9.7E-1
☐	**GOTERM_BP_ALL**	mesoderm development	RT	7	2.9E-1	9.8E-1
☐	**KEGG_PATHWAY**	Hedgehog signaling pathway	RT	7	3.2E-1	8.4E-1
☐	**INTERPRO**	Transforming growth factor beta	RT	5	3.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	negative regulation of bone remodeling	RT	3	3.8E-1	9.9E-1
☐	**GOTERM_BP_ALL**	ureteric bud development	RT	5	4.0E-1	9.9E-1
☐	**SMART**	TGFB	RT	5	4.7E-1	9.9E-1
☐	**GOTERM_BP_ALL**	tube development	RT	19	5.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	negative regulation of multicellular organismal process	RT	4	6.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	growth factor activity	RT	14	6.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	tissue development	RT	25	7.3E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	growth factor	RT	10	7.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	tissue morphogenesis	RT	6	8.2E-1	1.0E0
☐	**KEGG_PATHWAY**	Basal cell carcinoma	RT	4	8.7E-1	9.9E-1
☐	**GOTERM_BP_ALL**	eye development	RT	6	9.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell fate commitment	RT	6	9.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	camera-type eye development	RT	3	9.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Cleavage on pair of basic residues	RT	10	9.9E-1	1.0E0
	Annotation Cluster 65	**Enrichment Score: 0.88**	**G** 🟩	**Count**	**P_Value**	**Benjamini**
☐	**GOTERM_BP_ALL**	regulation of transferase activity	RT	24	4.3E-2	7.3E-1
☐	**GOTERM_BP_ALL**	regulation of kinase activity	RT	23	5.2E-2	7.7E-1
☐	**GOTERM_BP_ALL**	regulation of a molecular function	RT	46	5.8E-2	8.0E-1
☐	**GOTERM_BP_ALL**	regulation of protein kinase activity	RT	22	5.9E-2	8.0E-1
☐	**GOTERM_BP_ALL**	regulation of catalytic activity	RT	40	8.6E-2	8.6E-1
☐	**GOTERM_BP_ALL**	positive regulation of transferase activity	RT	16	8.7E-2	8.7E-1
☐	**GOTERM_BP_ALL**	positive regulation of protein kinase activity	RT	15	9.0E-2	8.7E-1
☐	**GOTERM_BP_ALL**	positive regulation of kinase activity	RT	15	1.2E-1	9.0E-1
☐	**GOTERM_BP_ALL**	positive regulation of catalytic activity	RT	22	1.2E-1	9.1E-1

☐	GOTERM_BP_ALL	positive regulation of MAP kinase activity	RT		7	2.0E-1	9.6E-1
☐	GOTERM_BP_ALL	regulation of MAP kinase activity	RT		8	4.1E-1	9.9E-1
☐	GOTERM_BP_ALL	activation of MAPK activity	RT		4	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	MAPKKK cascade	RT		10	8.3E-1	1.0E0
	Annotation Cluster 66	Enrichment Score: 0.87	G	🟩	Count	P_Value	Benjamini
☐	BIOCARTA	The information-processing pathway at the IFN-beta enhancer	RT		5	3.4E-2	9.6E-1
☐	BIOCARTA	Control of Gene Expression by Vitamin D Receptor	RT		8	4.3E-2	9.6E-1
☐	GOTERM_BP_ALL	histone acetylation	RT		4	6.2E-2	8.1E-1
☐	GOTERM_BP_ALL	protein amino acid acylation	RT		6	6.8E-2	8.3E-1
☐	SMART	BROMO	RT		8	8.0E-2	8.7E-1
☐	INTERPRO	Bromodomain	RT		7	9.3E-2	1.0E0
☐	GOTERM_MF_ALL	N-acyltransferase activity	RT		10	9.4E-2	9.8E-1
☐	GOTERM_MF_ALL	N-acetyltransferase activity	RT		9	9.5E-2	9.8E-1
☐	KEGG_PATHWAY	Notch signaling pathway	RT		8	1.0E-1	5.9E-1
☐	SP_PIR_KEYWORDS	bromodomain	RT		6	1.0E-1	8.1E-1
☐	GOTERM_MF_ALL	acetyltransferase activity	RT		10	1.2E-1	9.9E-1
☐	GOTERM_BP_ALL	protein amino acid acetylation	RT		4	1.5E-1	9.4E-1
☐	GOTERM_MF_ALL	lysine N-acetyltransferase activity	RT		4	2.0E-1	1.0E0
☐	GOTERM_MF_ALL	histone acetyltransferase activity	RT		4	2.0E-1	1.0E0
☐	GOTERM_CC_ALL	histone acetyltransferase complex	RT		3	2.3E-1	9.9E-1
☐	BIOCARTA	Regulation of transcriptional activity by PML	RT		4	4.4E-1	1.0E0
☐	GOTERM_CC_ALL	kinetochore	RT		3	6.1E-1	1.0E0
☐	GOTERM_CC_ALL	chromosome, pericentric region	RT		4	9.3E-1	1.0E0
	Annotation Cluster 67	Enrichment Score: 0.87	G	🟩	Count	P_Value	Benjamini
☐	SMART	CHROMO	RT		7	4.4E-2	8.6E-1
☐	INTERPRO	Chromo	RT		6	6.7E-2	1.0E0
☐	GOTERM_MF_ALL	chromatin binding	RT		14	2.5E-1	1.0E0
☐	INTERPRO	SNF2-related	RT		4	4.4E-1	1.0E0
	Annotation Cluster 68	Enrichment Score: 0.86	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cellular developmental process	RT		186	1.1E-2	4.6E-1
☐	GOTERM_BP_ALL	cell differentiation	RT		186	1.1E-2	4.6E-1
☐	GOTERM_BP_ALL	developmental process	RT		282	3.3E-2	6.8E-1
☐	GOTERM_BP_ALL	organ development	RT		131	2.3E-1	9.6E-1
☐	GOTERM_BP_ALL	system development	RT		158	2.7E-1	9.7E-1
☐	GOTERM_BP_ALL	multicellular organismal development	RT		198	3.7E-1	9.9E-1
☐	GOTERM_BP_ALL	anatomical structure development	RT		179	4.5E-1	9.9E-1
☐	GOTERM_BP_ALL	anatomical structure morphogenesis	RT		101	6.2E-1	1.0E0
☐	GOTERM_BP_ALL	multicellular organismal process	RT		244	7.0E-1	1.0E0
	Annotation Cluster 69	Enrichment Score: 0.86	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	sulfuric ester hydrolase activity	RT		4	7.7E-2	9.7E-1
☐	INTERPRO	Sulphatase	RT		4	7.7E-2	1.0E0
☐	INTERPRO	Alkaline phosphatase	RT		5	8.6E-2	1.0E0
☐	SMART	alkPPc	RT		5	1.5E-1	9.0E-1
☐	COG_ONTOLOGY	Inorganic ion transport and metabolism	RT		8	6.9E-1	1.0E0
	Annotation Cluster 70	Enrichment Score: 0.85	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	lipid binding	RT		45	6.1E-2	9.7E-1
☐	GOTERM_MF_ALL	phospholipid binding	RT		25	1.7E-1	1.0E0
☐	GOTERM_MF_ALL	phosphoinositide binding	RT		19	2.7E-1	1.0E0
	Annotation Cluster 71	Enrichment Score: 0.84	G	🟩	Count	P_Value	Benjamini

☐	GOTERM_MF_ALL	N-acyltransferase activity	RT	▮		10	9.4E-2	9.8E-1
☐	GOTERM_MF_ALL	N-acetyltransferase activity	RT	▮		9	9.5E-2	9.8E-1
☐	GOTERM_MF_ALL	acetyltransferase activity	RT	▮		10	1.2E-1	9.9E-1
☐	GOTERM_MF_ALL	acyltransferase activity	RT	▮		20	1.6E-1	9.9E-1
☐	GOTERM_MF_ALL	transferase activity, transferring groups other than amino-acyl groups	RT	▮		20	1.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	acyltransferase	RT	▮		16	1.7E-1	8.9E-1
☐	GOTERM_MF_ALL	transferase activity, transferring acyl groups	RT	▮		20	2.3E-1	1.0E0
	Annotation Cluster 72	Enrichment Score: 0.81	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	STAT transcription factor, all-alpha	RT	▮		3	1.5E-1	1.0E0
☐	INTERPRO	STAT transcription factor, core	RT	▮		3	1.5E-1	1.0E0
☐	INTERPRO	STAT transcription factor, DNA-binding	RT	▮		3	1.5E-1	1.0E0
☐	INTERPRO	STAT transcription factor, DNA-binding, subdomain	RT	▮		3	1.5E-1	1.0E0
☐	INTERPRO	STAT transcription factor, protein interaction	RT	▮		3	1.5E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF015568:signal transducer and transcription activator STAT5A	RT	▮		3	1.5E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:SH2	RT	▮		9	2.1E-1	1.0E0
	Annotation Cluster 73	Enrichment Score: 0.81	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	lipoprotein biosynthetic process	RT	▮		9	9.0E-2	8.7E-1
☐	GOTERM_BP_ALL	protein amino acid lipidation	RT	▮		8	1.5E-1	9.3E-1
☐	GOTERM_BP_ALL	lipoprotein metabolic process	RT	▮		9	2.9E-1	9.8E-1
	Annotation Cluster 74	Enrichment Score: 0.8	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	lipid metabolism	RT	▮		14	1.1E-1	8.2E-1
☐	GOTERM_MF_ALL	carnitine O-acyltransferase activity	RT	▮		3	1.2E-1	9.9E-1
☐	GOTERM_MF_ALL	O-acyltransferase activity	RT	▮		6	1.3E-1	9.9E-1
☐	INTERPRO	Acyltransferase ChoActase/COT/CPT	RT	▮		3	1.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	Fatty acid metabolism	RT	▮		6	3.8E-1	9.8E-1
	Annotation Cluster 75	Enrichment Score: 0.8	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Endonuclease	RT	▮		11	9.4E-3	3.1E-1
☐	SP_PIR_KEYWORDS	nuclease	RT	▮		12	5.4E-2	6.9E-1
☐	GOTERM_MF_ALL	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 3'-phosphomonoesters	RT	▮		5	8.6E-2	9.8E-1
☐	GOTERM_MF_ALL	endonuclease activity	RT	▮		12	1.2E-1	9.9E-1
☐	GOTERM_MF_ALL	endoribonuclease activity	RT	▮		7	1.5E-1	9.9E-1
☐	GOTERM_MF_ALL	pancreatic ribonuclease activity	RT	▮		4	1.5E-1	9.9E-1
☐	INTERPRO	Pancreatic ribonuclease	RT	▮		4	1.5E-1	1.0E0
☐	GOTERM_MF_ALL	ribonuclease activity	RT	▮		9	1.6E-1	9.9E-1
☐	SMART	RNAse_Pc	RT	▮		4	1.9E-1	9.0E-1
☐	GOTERM_MF_ALL	endoribonuclease activity, producing 3'-phosphomonoesters	RT	▮		4	2.0E-1	1.0E0
☐	GOTERM_MF_ALL	nuclease activity	RT	▮		16	2.7E-1	1.0E0
☐	UP_SEQ_FEATURE	region of interest:Substrate binding	RT	▮		5	5.5E-1	1.0E0
☐	GOTERM_MF_ALL	endoribonuclease activity, producing 5'-phosphomonoesters	RT	▮		3	6.0E-1	1.0E0
☐	GOTERM_MF_ALL	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	RT	▮		3	6.4E-1	1.0E0
	Annotation Cluster 76	Enrichment Score: 0.8	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	polyamine catabolic process	RT	▮		4	5.6E-3	3.5E-1
☐	GOTERM_BP_ALL	spermine catabolic process	RT	▮		3	2.1E-2	5.8E-1
☐	GOTERM_BP_ALL	amino acid derivative catabolic process	RT	▮		5	5.3E-2	7.7E-1
☐	GOTERM_BP_ALL	spermine metabolic process	RT	▮		3	1.2E-1	9.0E-1
☐	GOTERM_BP_ALL	biogenic amine catabolic process	RT	▮		4	1.3E-1	9.2E-1

☐	GOTERM_BP_ALL	polyamine metabolic process	RT		4	1.8E-1	9.5E-1
☐	KEGG_PATHWAY	Urea cycle and metabolism of amino groups	RT		5	2.9E-1	8.3E-1
☐	GOTERM_BP_ALL	amine catabolic process	RT		6	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	nitrogen compound catabolic process	RT		6	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	biogenic amine metabolic process	RT		5	9.1E-1	1.0E0
☐	GOTERM_BP_ALL	amino acid derivative metabolic process	RT		6	9.1E-1	1.0E0
	Annotation Cluster 77	Enrichment Score: 0.79	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	peptidyl-tyrosine phosphorylation	RT		10	1.1E-1	9.0E-1
☐	GOTERM_BP_ALL	peptidyl-tyrosine modification	RT		10	1.1E-1	9.0E-1
☐	GOTERM_BP_ALL	regulation of phosphorylation	RT		10	1.4E-1	9.2E-1
☐	GOTERM_BP_ALL	regulation of protein amino acid phosphorylation	RT		9	1.4E-1	9.3E-1
☐	GOTERM_BP_ALL	regulation of amine metabolic process	RT		9	1.5E-1	9.3E-1
☐	GOTERM_BP_ALL	regulation of amino acid metabolic process	RT		9	1.5E-1	9.3E-1
☐	GOTERM_BP_ALL	positive regulation of protein amino acid phosphorylation	RT		6	1.6E-1	9.5E-1
☐	GOTERM_BP_ALL	positive regulation of amino acid metabolic process	RT		6	1.6E-1	9.5E-1
☐	GOTERM_BP_ALL	positive regulation of amine metabolic process	RT		6	1.6E-1	9.5E-1
☐	GOTERM_BP_ALL	regulation of phosphorus metabolic process	RT		10	1.7E-1	9.4E-1
☐	GOTERM_BP_ALL	regulation of phosphate metabolic process	RT		10	1.7E-1	9.4E-1
☐	GOTERM_BP_ALL	peptidyl-amino acid modification	RT		15	1.7E-1	9.4E-1
☐	GOTERM_BP_ALL	regulation of peptidyl-tyrosine phosphorylation	RT		5	4.8E-1	1.0E0
	Annotation Cluster 78	Enrichment Score: 0.78	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	transferase activity, transferring glycosyl groups	RT		32	1.0E-2	7.6E-1
☐	SP_PIR_KEYWORDS	glycosyltransferase	RT		24	3.4E-2	5.8E-1
☐	GOTERM_CC_ALL	integral to Golgi membrane	RT		7	4.1E-2	8.0E-1
☐	KEGG_PATHWAY	Glycan structures - biosynthesis 2	RT		10	5.7E-2	4.8E-1
☐	GOTERM_CC_ALL	intrinsic to Golgi membrane	RT		7	8.5E-2	9.4E-1
☐	GOTERM_MF_ALL	sialyltransferase activity	RT		5	8.6E-2	9.8E-1
☐	INTERPRO	Glycosyl transferase, family 29	RT		5	8.6E-2	1.0E0
☐	SP_PIR_KEYWORDS	signal-anchor	RT		37	9.6E-2	8.0E-1
☐	GOTERM_BP_ALL	glycoprotein metabolic process	RT		15	1.3E-1	9.2E-1
☐	INTERPRO	Sialyltransferase	RT		4	1.3E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid O-linked glycosylation	RT		4	1.8E-1	9.5E-1
☐	PIR_SUPERFAMILY	PIRSF005557:sialyltransferase	RT		4	1.8E-1	1.0E0
☐	GOTERM_BP_ALL	glycoprotein biosynthetic process	RT		12	1.9E-1	9.6E-1
☐	GOTERM_BP_ALL	protein amino acid glycosylation	RT		11	1.9E-1	9.6E-1
☐	GOTERM_BP_ALL	biopolymer glycosylation	RT		11	2.3E-1	9.6E-1
☐	GOTERM_CC_ALL	intrinsic to organelle membrane	RT		10	2.8E-1	1.0E0
☐	GOTERM_CC_ALL	integral to organelle membrane	RT		9	3.0E-1	9.9E-1
☐	GOTERM_MF_ALL	UDP-glycosyltransferase activity	RT		11	3.2E-1	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring hexosyl groups	RT		16	3.3E-1	1.0E0
☐	KEGG_PATHWAY	Glycosphingolipid biosynthesis - ganglioseries	RT		3	4.1E-1	8.7E-1
☐	UP_SEQ_FEATURE	topological domain:Lumenal	RT		23	5.0E-1	1.0E0
☐	GOTERM_CC_ALL	Golgi membrane	RT		10	5.1E-1	1.0E0
☐	GOTERM_CC_ALL	Golgi apparatus part	RT		13	7.9E-1	1.0E0
☐	GOTERM_CC_ALL	endomembrane system	RT		28	8.9E-1	1.0E0

				Count	P_Value	Benjamini
	Annotation Cluster 79	Enrichment Score: 0.78	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:ELM2	RT	3	9.2E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:SANT	RT	3	1.8E-1	1.0E0
☐	INTERPRO	ELM2	RT	3	2.8E-1	1.0E0
	Annotation Cluster 80	Enrichment Score: 0.76	G	Count	P_Value	Benjamini
☐	INTERPRO	Caspase Recruitment	RT	5	1.0E-1	1.0E0
☐	SMART	CARD	RT	5	1.3E-1	8.8E-1
☐	UP_SEQ_FEATURE	domain:CARD	RT	3	3.9E-1	1.0E0
	Annotation Cluster 81	Enrichment Score: 0.76	G	Count	P_Value	Benjamini
☐	INTERPRO	SANT, DNA-binding	RT	9	1.0E-1	1.0E0
☐	SMART	SANT	RT	9	1.6E-1	9.1E-1
☐	INTERPRO	Myb, DNA-binding	RT	5	3.1E-1	1.0E0
	Annotation Cluster 82	Enrichment Score: 0.76	G	Count	P_Value	Benjamini
☐	INTERPRO	uDENN	RT	3	1.5E-1	1.0E0
☐	SMART	uDENN	RT	3	1.7E-1	8.9E-1
☐	SMART	DENN	RT	3	2.1E-1	9.2E-1
	Annotation Cluster 83	Enrichment Score: 0.76	G	Count	P_Value	Benjamini
☐	INTERPRO	BTB/POZ	RT	15	4.0E-2	1.0E0
☐	INTERPRO	Kelch related	RT	9	6.7E-2	1.0E0
☐	INTERPRO	BTB/POZ-like	RT	16	2.1E-1	1.0E0
☐	INTERPRO	BTB/POZ fold	RT	16	2.2E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:BTB	RT	7	2.9E-1	1.0E0
☐	SMART	BTB	RT	17	3.1E-1	9.6E-1
☐	INTERPRO	BTB/Kelch-associated	RT	5	4.3E-1	1.0E0
	Annotation Cluster 84	Enrichment Score: 0.74	G	Count	P_Value	Benjamini
☐	INTERPRO	MAD homology 2, Dwarfin-type	RT	4	1.3E-1	1.0E0
☐	INTERPRO	MAD homology, MH1	RT	3	1.5E-1	1.0E0
☐	INTERPRO	Dwarfin	RT	3	1.5E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF037286:Smad protein	RT	3	1.5E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:MH1	RT	3	1.5E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:MH2	RT	3	1.5E-1	1.0E0
☐	SMART	DWB	RT	4	1.6E-1	9.1E-1
☐	BIOCARTA	CTCF	RT	5	2.2E-1	1.0E0
☐	INTERPRO	MAD homology 1, Dwarfin-type	RT	3	3.1E-1	1.0E0
☐	SMART	DWA	RT	3	3.5E-1	9.7E-1
	Annotation Cluster 85	Enrichment Score: 0.73	G	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF002549:transferrin	RT	3	6.4E-2	1.0E0
☐	SP_PIR_KEYWORDS	Iron transport	RT	5	8.3E-2	7.8E-1
☐	INTERPRO	Peptidase S60, transferrin lactoferrin	RT	3	8.7E-2	1.0E0
☐	SMART	TR_FER	RT	3	1.0E-1	8.8E-1
☐	GOTERM_BP_ALL	iron ion transport	RT	5	2.4E-1	9.7E-1
☐	GOTERM_BP_ALL	cellular iron ion homeostasis	RT	4	3.4E-1	9.8E-1
☐	GOTERM_BP_ALL	iron ion homeostasis	RT	4	3.4E-1	9.8E-1
☐	GOTERM_MF_ALL	ferric iron binding	RT	3	3.7E-1	1.0E0
☐	GOTERM_BP_ALL	transition metal ion transport	RT	6	5.7E-1	1.0E0
	Annotation Cluster 86	Enrichment Score: 0.73	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	chemotaxis	RT	11	2.3E-2	4.8E-1
☐	PIR_SUPERFAMILY	PIRSF001950:small inducible chemokine, C/CC types	RT	5	1.1E-1	1.0E0
☐	INTERPRO	Small chemokine, C-C	RT	5	1.3E-1	1.0E0
☐	INTERPRO	Small chemokine, interleukin-8-like	RT	6	2.6E-1	1.0E0

☐	**GOTERM_MF_ALL**	chemokine activity	RT	▮		6	2.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	chemokine receptor binding	RT	▮		6	3.1E-1	1.0E0
☐	**SMART**	SCY	RT	▮		6	3.3E-1	9.6E-1
☐	**GOTERM_MF_ALL**	G-protein-coupled receptor binding	RT	▮		6	6.8E-1	1.0E0
	Annotation Cluster 87	Enrichment Score: 0.72	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	retinal homeostasis	RT	▮		3	4.0E-2	7.1E-1
☐	**GOTERM_BP_ALL**	multicellular organismal homeostasis	RT	▮		4	4.2E-1	9.9E-1
☐	**GOTERM_BP_ALL**	tissue homeostasis	RT	▮		4	4.2E-1	9.9E-1
	Annotation Cluster 88	Enrichment Score: 0.72	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Acyl-CoA dehydrogenase/oxidase, N-terminal	RT	▮		4	1.1E-1	1.0E0
☐	**INTERPRO**	Acyl-CoA oxidase/dehydrogenase, type 1	RT	▮		4	1.1E-1	1.0E0
☐	**INTERPRO**	Acyl-CoA dehydrogenase/oxidase, central region	RT	▮		4	1.3E-1	1.0E0
☐	**INTERPRO**	Acyl-CoA oxidase/dehydrogenase, type1/2, C-terminal	RT	▮		4	1.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	acyl-CoA dehydrogenase activity	RT	▮		4	1.7E-1	1.0E0
☐	**INTERPRO**	Acyl-CoA dehydrogenase	RT	▮		3	2.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	FAD binding	RT	▮		7	4.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	oxidoreductase activity, acting on the CH-CH group of donors	RT	▮		5	4.9E-1	1.0E0
	Annotation Cluster 89	Enrichment Score: 0.71	G		🟩	Count	P_Value	Benjamini
☐	**PIR_SUPERFAMILY**	PIRSF002512:integrin, beta subunit	RT	▮		4	1.8E-2	1.0E0
☐	**INTERPRO**	Integrin beta subunit, subgroup	RT	▮		4	2.5E-2	1.0E0
☐	**INTERPRO**	Integrin beta subunit, N-terminal	RT	▮		4	3.6E-2	1.0E0
☐	**INTERPRO**	Integrin beta subunit, tail	RT	▮		4	3.6E-2	1.0E0
☐	**INTERPRO**	Integrin beta subunit	RT	▮		4	4.8E-2	1.0E0
☐	**INTERPRO**	Integrin beta subunit, C-terminal	RT	▮		4	4.8E-2	1.0E0
☐	**SMART**	INB	RT	▮		4	6.2E-2	8.8E-1
☐	**INTERPRO**	Integrin beta subunit, cytoplasmic	RT	▮		3	1.2E-1	1.0E0
☐	**INTERPRO**	Plexin/semaphorin/integrin	RT	▮		7	2.1E-1	1.0E0
☐	**SMART**	PSI	RT	▮		7	2.9E-1	9.6E-1
☐	**KEGG_PATHWAY**	ECM-receptor interaction	RT	▮		10	3.9E-1	8.8E-1
☐	**GOTERM_CC_ALL**	integrin complex	RT	▮		4	5.5E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:VWFA	RT	▮		3	7.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	integrin-mediated signaling pathway	RT	▮		7	7.5E-1	1.0E0
☐	**INTERPRO**	von Willebrand factor, type A	RT	▮		6	8.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Integrin	RT	▮		5	8.0E-1	1.0E0
☐	**INTERPRO**	EGF, extracellular	RT	▮		5	8.5E-1	1.0E0
☐	**SMART**	VWA	RT	▮		6	8.9E-1	1.0E0
☐	**GOTERM_CC_ALL**	receptor complex	RT	▮		5	9.2E-1	1.0E0
	Annotation Cluster 90	Enrichment Score: 0.71	G		🟩	Count	P_Value	Benjamini
☐	**PIR_SUPERFAMILY**	PIRSF038354:forkhead box O protein	RT	▮		3	2.2E-2	1.0E0
☐	**BIOCARTA**	AKT Signaling Pathway	RT	▮		7	2.6E-2	9.8E-1
☐	**INTERPRO**	Fork head transcription factor	RT	▮		5	4.3E-1	1.0E0
☐	**SMART**	FH	RT	▮		5	5.1E-1	9.9E-1
☐	**INTERPRO**	Winged helix repressor DNA-binding	RT	▮		10	5.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	DNA-binding region:Fork-head	RT	▮		3	7.4E-1	1.0E0
	Annotation Cluster 91	Enrichment Score: 0.71	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Nuclear receptor ROR	RT	▮		4	1.0E-2	9.8E-1
☐	**SP_PIR_KEYWORDS**	transcription factor	RT	▮		9	5.7E-2	7.0E-1
☐	**GOTERM_BP_ALL**	myeloid leukocyte activation	RT	▮		7	6.0E-2	8.0E-1

☐	**GOTERM_BP_ALL**	regulation of macrophage activation	RT	▮		3	8.8E-2	8.6E-1
☐	**GOTERM_BP_ALL**	cerebellar Purkinje cell layer development	RT	▮		4	1.1E-1	9.0E-1
☐	**GOTERM_BP_ALL**	cGMP metabolic process	RT	▮		4	1.3E-1	9.2E-1
☐	**GOTERM_BP_ALL**	cerebellar cortex development	RT	▮		4	2.0E-1	9.6E-1
☐	**GOTERM_BP_ALL**	cyclic nucleotide metabolic process	RT	▮		6	2.1E-1	9.6E-1
☐	**GOTERM_BP_ALL**	macrophage activation	RT	▮		3	2.1E-1	9.6E-1
☐	**GOTERM_BP_ALL**	cerebellar Purkinje cell layer formation	RT	▮		3	2.4E-1	9.7E-1
☐	**GOTERM_BP_ALL**	cerebellar Purkinje cell layer morphogenesis	RT	▮		3	2.4E-1	9.7E-1
☐	**GOTERM_BP_ALL**	cerebellar Purkinje cell differentiation	RT	▮		3	2.4E-1	9.7E-1
☐	**GOTERM_BP_ALL**	cerebellar cortex formation	RT	▮		3	2.8E-1	9.7E-1
☐	**GOTERM_BP_ALL**	cell differentiation in hindbrain	RT	▮		3	2.8E-1	9.7E-1
☐	**GOTERM_BP_ALL**	cerebellum development	RT	▮		4	2.9E-1	9.8E-1
☐	**GOTERM_BP_ALL**	metencephalon development	RT	▮		4	2.9E-1	9.8E-1
☐	**GOTERM_BP_ALL**	nitric oxide biosynthetic process	RT	▮		4	3.4E-1	9.8E-1
☐	**GOTERM_BP_ALL**	nitric oxide metabolic process	RT	▮		4	3.4E-1	9.8E-1
☐	**SP_PIR_KEYWORDS**	disease mutation	RT	▮		9	3.5E-1	9.7E-1
☐	**GOTERM_BP_ALL**	cerebellar cortex morphogenesis	RT	▮		3	3.8E-1	9.9E-1
☐	**GOTERM_BP_ALL**	cerebellum morphogenesis	RT	▮		3	4.1E-1	9.9E-1
☐	**GOTERM_BP_ALL**	hindbrain morphogenesis	RT	▮		3	4.4E-1	9.9E-1
☐	**GOTERM_BP_ALL**	hindbrain development	RT	▮		5	4.8E-1	1.0E0
	Annotation Cluster 92	Enrichment Score: 0.7	G		🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Calcium 3 (via carbonyl oxygen)	RT	▮		6	7.5E-3	1.0E0
☐	**UP_SEQ_FEATURE**	propeptide:Activation peptide	RT	▮		12	1.0E-2	1.0E0
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Calcium 4 (via carbonyl oxygen)	RT	▮		4	1.8E-2	1.0E0
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Zinc 2 (in inhibited form)	RT	▮		4	5.1E-2	1.0E0
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Zinc 2 (catalytic)	RT	▮		4	6.6E-2	1.0E0
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Calcium 1	RT	▮		7	9.2E-2	1.0E0
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Calcium 3	RT	▮		5	1.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Calcium 2	RT	▮		7	1.2E-1	1.0E0
☐	**INTERPRO**	Hemopexin	RT	▮		5	1.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	peptidoglycan metabolic process	RT	▮		5	1.3E-1	9.2E-1
☐	**SMART**	HX	RT	▮		5	1.7E-1	9.1E-1
☐	**SP_PIR_KEYWORDS**	collagen degradation	RT	▮		4	1.7E-1	9.0E-1
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Calcium 2 (via carbonyl oxygen)	RT	▮		5	1.7E-1	1.0E0
☐	**INTERPRO**	Peptidoglycan binding-like	RT	▮		4	2.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	collagen catabolic process	RT	▮		4	2.2E-1	9.6E-1
☐	**GOTERM_BP_ALL**	multicellular organismal protein catabolic process	RT	▮		4	2.2E-1	9.6E-1
☐	**GOTERM_BP_ALL**	protein digestion	RT	▮		4	2.2E-1	9.6E-1
☐	**GOTERM_BP_ALL**	multicellular organismal macromolecule metabolic process	RT	▮		4	2.2E-1	9.6E-1
☐	**GOTERM_BP_ALL**	multicellular organismal macromolecule catabolic process	RT	▮		4	2.2E-1	9.6E-1
☐	**GOTERM_BP_ALL**	multicellular organismal protein metabolic process	RT	▮		4	2.2E-1	9.6E-1
☐	**UP_SEQ_FEATURE**	domain:Hemopexin-like 4	RT	▮		4	2.3E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Hemopexin-like 3	RT	▮		4	2.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	collagen metabolic process	RT	▮		4	2.5E-1	9.6E-1
☐	**GOTERM_BP_ALL**	multicellular organismal catabolic process	RT	▮		4	2.5E-1	9.6E-1
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Zinc 1	RT	▮		7	2.5E-1	1.0E0

☐	**UP_SEQ_FEATURE**	domain:Hemopexin-like 2	RT	4	2.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Hemopexin-like 1	RT	4	2.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	metalloproteinase	RT	3	3.0E-1	9.7E-1
☐	**INTERPRO**	Peptidase, metallopeptidases	RT	4	3.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	multicellular organismal metabolic process	RT	4	3.4E-1	9.8E-1
☐	**PIR_SUPERFAMILY**	PIRSF001191:matrix metalloproteinase, stromelysin type	RT	3	3.8E-1	1.0E0
☐	**SMART**	ZnMc	RT	4	4.0E-1	9.8E-1
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Calcium 1 (via carbonyl oxygen)	RT	4	4.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	short sequence motif:Cysteine switch	RT	4	5.9E-1	1.0E0
☐	**INTERPRO**	Peptidase M10A and M12B, matrixin and adamalysin	RT	4	5.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	digestion	RT	4	7.9E-1	1.0E0
☐	**INTERPRO**	Peptidase M, neutral zinc metallopeptidases, zinc-binding site	RT	5	8.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	metalloendopeptidase activity	RT	6	9.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	metalloprotease	RT	5	1.0E0	1.0E0
	Annotation Cluster 93	Enrichment Score: 0.69	G	Count	P_Value	Benjamini
☐	**INTERPRO**	Spectrin repeat	RT	7	4.5E-2	1.0E0
☐	**INTERPRO**	Actin-binding, actinin-type	RT	6	6.7E-2	1.0E0
☐	**SMART**	SPEC	RT	7	6.8E-2	8.8E-1
☐	**UP_SEQ_FEATURE**	domain:CH 1	RT	4	2.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:CH 2	RT	4	2.6E-1	1.0E0
☐	**INTERPRO**	Calponin-like actin-binding	RT	8	2.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:Spectrin 4	RT	3	2.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:Spectrin 3	RT	3	3.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:Spectrin 1	RT	3	3.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:Spectrin 2	RT	3	3.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Actin-binding	RT	3	3.5E-1	1.0E0
☐	**SMART**	CH	RT	8	3.7E-1	9.7E-1
	Annotation Cluster 94	Enrichment Score: 0.69	G	Count	P_Value	Benjamini
☐	**INTERPRO**	Death	RT	7	5.2E-2	1.0E0
☐	**SMART**	DEATH	RT	7	8.7E-2	8.5E-1
☐	**UP_SEQ_FEATURE**	domain:Death	RT	4	3.1E-1	1.0E0
☐	**INTERPRO**	DEATH-like	RT	6	4.0E-1	1.0E0
☐	**BIOCARTA**	TNF/Stress Related Signaling	RT	4	6.3E-1	1.0E0
	Annotation Cluster 95	Enrichment Score: 0.69	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	cytokine production	RT	18	2.1E-2	5.8E-1
☐	**GOTERM_BP_ALL**	regulation of translation	RT	19	1.1E-1	9.0E-1
☐	**GOTERM_BP_ALL**	regulation of cellular biosynthetic process	RT	20	1.2E-1	9.0E-1
☐	**GOTERM_BP_ALL**	cytokine metabolic process	RT	11	1.3E-1	9.2E-1
☐	**GOTERM_BP_ALL**	cytokine biosynthetic process	RT	11	1.3E-1	9.2E-1
☐	**GOTERM_BP_ALL**	regulation of biosynthetic process	RT	21	1.7E-1	9.5E-1
☐	**GOTERM_BP_ALL**	positive regulation of translation	RT	8	1.8E-1	9.5E-1
☐	**GOTERM_BP_ALL**	interleukin-2 biosynthetic process	RT	4	2.0E-1	9.6E-1
☐	**GOTERM_BP_ALL**	positive regulation of interleukin-2 biosynthetic process	RT	3	2.1E-1	9.6E-1
☐	**GOTERM_BP_ALL**	interleukin-2 production	RT	4	2.2E-1	9.6E-1
☐	**GOTERM_BP_ALL**	positive regulation of cellular biosynthetic process	RT	8	2.3E-1	9.6E-1
☐	**GOTERM_BP_ALL**	regulation of cytokine biosynthetic process	RT	9	2.4E-1	9.7E-1
☐	**GOTERM_BP_ALL**	regulation of protein metabolic process	RT	29	2.4E-1	9.7E-1

☐	**GOTERM_BP_ALL**	regulation of interleukin-2 biosynthetic process	RT	▮		3	3.8E-1	9.9E-1
☐	**GOTERM_BP_ALL**	positive regulation of cytokine biosynthetic process	RT	▮		6	3.8E-1	9.9E-1
☐	**GOTERM_BP_ALL**	positive regulation of biosynthetic process	RT	▮		8	4.0E-1	9.9E-1
☐	**GOTERM_BP_ALL**	positive regulation of protein metabolic process	RT	▮		10	4.5E-1	9.9E-1
☐	**GOTERM_BP_ALL**	translation	RT	▮		29	9.8E-1	1.0E0
	Annotation Cluster 96	Enrichment Score: 0.68	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	GTPase activator activity	RT	▮		22	7.1E-2	9.7E-1
☐	**GOTERM_MF_ALL**	enzyme activator activity	RT	▮		26	1.5E-1	9.9E-1
☐	**GOTERM_MF_ALL**	Ras GTPase activator activity	RT	▮		9	2.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of GTPase activity	RT	▮		9	4.1E-1	9.9E-1
☐	**SP_PIR_KEYWORDS**	gtpase activation	RT	▮		9	4.4E-1	9.9E-1
	Annotation Cluster 97	Enrichment Score: 0.68	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of Rab GTPase activity	RT	▮		7	1.0E-1	8.9E-1
☐	**GOTERM_BP_ALL**	regulation of Rab protein signal transduction	RT	▮		7	1.0E-1	8.9E-1
☐	**GOTERM_BP_ALL**	Rab protein signal transduction	RT	▮		7	1.0E-1	8.9E-1
☐	**GOTERM_MF_ALL**	Rab GTPase activator activity	RT	▮		7	1.3E-1	9.9E-1
☐	**GOTERM_BP_ALL**	regulation of Ras GTPase activity	RT	▮		7	1.9E-1	9.5E-1
☐	**GOTERM_MF_ALL**	Ras GTPase activator activity	RT	▮		9	2.0E-1	1.0E0
☐	**SMART**	TBC	RT	▮		6	2.9E-1	9.6E-1
☐	**INTERPRO**	RabGAP/TBC	RT	▮		5	3.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of GTPase activity	RT	▮		9	4.1E-1	9.9E-1
☐	**GOTERM_BP_ALL**	regulation of hydrolase activity	RT	▮		13	6.5E-1	1.0E0
	Annotation Cluster 98	Enrichment Score: 0.68	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of cyclic nucleotide metabolic process	RT	▮		3	1.8E-1	9.5E-1
☐	**GOTERM_BP_ALL**	cyclic nucleotide metabolic process	RT	▮		6	2.1E-1	9.6E-1
☐	**GOTERM_BP_ALL**	regulation of nucleotide metabolic process	RT	▮		3	2.4E-1	9.7E-1
	Annotation Cluster 99	Enrichment Score: 0.68	G		🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	hydrogen peroxide	RT	▮		3	3.8E-2	6.2E-1
☐	**KEGG_PATHWAY**	Methane metabolism	RT	▮		4	4.8E-2	5.2E-1
☐	**GOTERM_BP_ALL**	response to oxidative stress	RT	▮		10	7.0E-2	8.3E-1
☐	**GOTERM_BP_ALL**	hydrogen peroxide catabolic process	RT	▮		3	1.2E-1	9.0E-1
☐	**GOTERM_BP_ALL**	oxygen and reactive oxygen species metabolic process	RT	▮		6	1.9E-1	9.6E-1
☐	**GOTERM_BP_ALL**	hydrogen peroxide metabolic process	RT	▮		3	2.1E-1	9.6E-1
☐	**GOTERM_BP_ALL**	response to reactive oxygen species	RT	▮		4	2.5E-1	9.6E-1
☐	**GOTERM_BP_ALL**	response to hydrogen peroxide	RT	▮		3	3.1E-1	9.8E-1
☐	**SP_PIR_KEYWORDS**	Peroxidase	RT	▮		4	3.3E-1	9.7E-1
☐	**GOTERM_MF_ALL**	oxidoreductase activity, acting on peroxide as acceptor	RT	▮		5	5.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	peroxidase activity	RT	▮		5	5.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	antioxidant activity	RT	▮		6	5.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Iron (heme axial ligand)	RT	▮		7	6.3E-1	1.0E0
	Annotation Cluster 100	Enrichment Score: 0.67	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	chondrocyte differentiation	RT	▮		7	3.0E-3	2.6E-1
☐	**GOTERM_BP_ALL**	lung development	RT	▮		5	8.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	respiratory tube development	RT	▮		5	8.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell fate commitment	RT	▮		6	9.6E-1	1.0E0
	Annotation Cluster 101	Enrichment Score: 0.66	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	post-Golgi vesicle-mediated transport	RT	▮		4	1.1E-1	9.0E-1

☐	GOTERM_BP_ALL	Golgi to plasma membrane transport	RT		3	1.2E-1	9.0E-1
☐	GOTERM_BP_ALL	Golgi vesicle transport	RT		7	7.7E-1	1.0E0
	Annotation Cluster 102	Enrichment Score: 0.66	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:UBX	RT		3	1.2E-1	1.0E0
☐	INTERPRO	UBX	RT		3	2.8E-1	1.0E0
☐	SMART	UBX	RT		3	3.2E-1	9.6E-1
	Annotation Cluster 103	Enrichment Score: 0.65	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	sterol homeostasis	RT		4	2.2E-1	9.6E-1
☐	GOTERM_BP_ALL	cholesterol homeostasis	RT		4	2.2E-1	9.6E-1
☐	GOTERM_BP_ALL	lipid homeostasis	RT		4	2.2E-1	9.6E-1
	Annotation Cluster 104	Enrichment Score: 0.65	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	C-C chemokine receptor activity	RT		5	7.3E-2	9.7E-1
☐	GOTERM_MF_ALL	C-C chemokine binding	RT		5	7.3E-2	9.7E-1
☐	GOTERM_MF_ALL	cytokine binding	RT		12	1.1E-1	9.9E-1
☐	GOTERM_MF_ALL	chemokine receptor activity	RT		5	1.6E-1	1.0E0
☐	INTERPRO	Chemokine receptor	RT		4	1.7E-1	1.0E0
☐	GOTERM_MF_ALL	chemokine binding	RT		5	1.8E-1	1.0E0
☐	GOTERM_MF_ALL	peptide receptor activity	RT		10	6.6E-1	1.0E0
☐	GOTERM_MF_ALL	peptide binding	RT		12	7.0E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF002406:vertebrate rhodopsin	RT		4	9.7E-1	1.0E0
	Annotation Cluster 105	Enrichment Score: 0.65	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	cytokine	RT		24	1.8E-2	4.5E-1
☐	GOTERM_MF_ALL	cytokine activity	RT		24	2.3E-1	1.0E0
☐	GOTERM_MF_ALL	growth factor activity	RT		14	6.9E-1	1.0E0
☐	GOTERM_MF_ALL	receptor binding	RT		49	8.8E-1	1.0E0
	Annotation Cluster 106	Enrichment Score: 0.65	G	🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Glycolysis / Gluconeogenesis	RT		9	1.2E-1	6.3E-1
☐	KEGG_PATHWAY	Propanoate metabolism	RT		5	2.9E-1	8.3E-1
☐	KEGG_PATHWAY	Pyruvate metabolism	RT		6	3.3E-1	8.4E-1
	Annotation Cluster 107	Enrichment Score: 0.64	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	gastrulation	RT		10	7.6E-2	8.5E-1
☐	GOTERM_BP_ALL	gastrulation with mouth forming second	RT		4	3.9E-1	9.9E-1
☐	GOTERM_BP_ALL	gastrulation (sensu Vertebrata)	RT		4	3.9E-1	9.9E-1
	Annotation Cluster 108	Enrichment Score: 0.64	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Regulator of chromosome condensation, RCC1	RT		5	1.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:RCC1 2	RT		3	2.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:RCC1 3	RT		3	2.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:RCC1 4	RT		3	2.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:RCC1 5	RT		3	2.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:RCC1 1	RT		3	2.2E-1	1.0E0
☐	COG_ONTOLOGY	Cell division and chromosome partitioning / Cytoskeleton	RT		3	4.3E-1	1.0E0
	Annotation Cluster 109	Enrichment Score: 0.63	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	aspartate family amino acid biosynthetic process	RT		4	1.5E-1	9.4E-1
☐	GOTERM_BP_ALL	aspartate family amino acid metabolic process	RT		4	2.0E-1	9.6E-1
☐	GOTERM_BP_ALL	nitrogen compound biosynthetic process	RT		12	2.1E-1	9.6E-1
☐	GOTERM_BP_ALL	amino acid biosynthetic process	RT		7	2.2E-1	9.6E-1
☐	SP_PIR_KEYWORDS	amino-acid biosynthesis	RT		4	2.6E-1	9.5E-1
☐	GOTERM_BP_ALL	amine biosynthetic process	RT		8	4.4E-1	9.9E-1
	Annotation Cluster 110	Enrichment Score: 0.63	G	🟩	Count	P_Value	Benjamini

☐	GOTERM_MF_ALL	DNA topoisomerase (ATP-hydrolyzing) activity	RT		3	1.8E-1	1.0E0
☐	GOTERM_MF_ALL	DNA topoisomerase activity	RT		3	2.4E-1	1.0E0
☐	GOTERM_BP_ALL	DNA topological change	RT		3	3.1E-1	9.8E-1
	Annotation Cluster 111	Enrichment Score: 0.63	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of myeloid cell differentiation	RT		11	5.9E-3	3.5E-1
☐	GOTERM_BP_ALL	regulation of osteoclast differentiation	RT		4	2.5E-1	9.6E-1
☐	GOTERM_BP_ALL	regulation of myeloid leukocyte differentiation	RT		4	3.7E-1	9.9E-1
☐	GOTERM_BP_ALL	osteoclast differentiation	RT		4	3.7E-1	9.9E-1
☐	BIOCARTA	Regulation of hematopoiesis by cytokines	RT		3	5.6E-1	1.0E0
☐	BIOCARTA	Cytokines and Inflammatory Response	RT		4	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	myeloid leukocyte differentiation	RT		5	6.4E-1	1.0E0
	Annotation Cluster 112	Enrichment Score: 0.62	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	antigen processing and presentation of peptide antigen	RT		7	9.4E-2	8.8E-1
☐	GOTERM_BP_ALL	antigen processing and presentation of exogenous antigen	RT		5	1.6E-1	9.5E-1
☐	GOTERM_BP_ALL	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	RT		4	2.2E-1	9.6E-1
☐	GOTERM_BP_ALL	antigen processing and presentation of exogenous peptide antigen	RT		4	2.5E-1	9.6E-1
☐	GOTERM_BP_ALL	antigen processing and presentation of peptide antigen via MHC class II	RT		3	4.7E-1	1.0E0
☐	GOTERM_BP_ALL	antigen processing and presentation of exogenous peptide antigen via MHC class II	RT		3	4.7E-1	1.0E0
	Annotation Cluster 113	Enrichment Score: 0.62	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of cyclin-dependent protein kinase activity	RT		3	1.8E-1	9.5E-1
☐	GOTERM_BP_ALL	negative regulation of protein kinase activity	RT		7	2.2E-1	9.6E-1
☐	GOTERM_BP_ALL	negative regulation of kinase activity	RT		7	2.2E-1	9.6E-1
☐	GOTERM_BP_ALL	regulation of cyclin-dependent protein kinase activity	RT		4	2.2E-1	9.6E-1
☐	GOTERM_BP_ALL	negative regulation of transferase activity	RT		7	2.4E-1	9.7E-1
☐	GOTERM_BP_ALL	negative regulation of catalytic activity	RT		7	4.5E-1	9.9E-1
	Annotation Cluster 114	Enrichment Score: 0.61	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	microbody	RT		11	2.0E-1	9.9E-1
☐	GOTERM_CC_ALL	peroxisome	RT		11	2.0E-1	9.9E-1
☐	SP_PIR_KEYWORDS	peroxisome	RT		9	3.7E-1	9.8E-1
	Annotation Cluster 115	Enrichment Score: 0.6	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Target SNARE coiled-coil region	RT		6	5.8E-2	1.0E0
☐	SMART	t_SNARE	RT		6	8.2E-2	8.6E-1
☐	KEGG_PATHWAY	SNARE interactions in vesicular transport	RT		6	1.9E-1	7.7E-1
☐	INTERPRO	Syntaxin, N-terminal	RT		3	3.1E-1	1.0E0
☐	SMART	SynN	RT		3	3.5E-1	9.7E-1
☐	UP_SEQ_FEATURE	domain:t-SNARE coiled-coil homology	RT		3	3.9E-1	1.0E0
☐	INTERPRO	Syntaxin/epimorphin coiled-coil	RT		3	4.4E-1	1.0E0
☐	GOTERM_MF_ALL	protein transporter activity	RT		10	9.3E-1	1.0E0
	Annotation Cluster 116	Enrichment Score: 0.6	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	WW/Rsp5/WWP	RT		7	2.1E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:WW	RT		3	2.5E-1	1.0E0
☐	SMART	WW	RT		7	3.0E-1	9.6E-1
	Annotation Cluster 117	Enrichment Score: 0.59	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	protein kinase activator activity	RT		3	2.1E-1	1.0E0
☐	GOTERM_MF_ALL	protein kinase regulator activity	RT		9	2.4E-1	1.0E0

☐	GOTERM_MF_ALL	kinase activator activity	RT	▮	3	3.4E-1	1.0E0
	Annotation Cluster 118	Enrichment Score: 0.58	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	vacuolar membrane	RT	▮	4	2.3E-1	9.9E-1
☐	GOTERM_CC_ALL	lysosomal membrane	RT	▮	3	2.3E-1	9.9E-1
☐	GOTERM_CC_ALL	vacuolar part	RT	▮	4	3.3E-1	1.0E0
	Annotation Cluster 119	Enrichment Score: 0.58	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	basolateral plasma membrane	RT	▮	11	1.3E-1	9.8E-1
☐	GOTERM_CC_ALL	cell-matrix junction	RT	▮	6	2.3E-1	9.9E-1
☐	GOTERM_CC_ALL	focal adhesion	RT	▮	5	2.6E-1	9.9E-1
☐	GOTERM_CC_ALL	cell-substrate adherens junction	RT	▮	5	3.4E-1	1.0E0
☐	GOTERM_CC_ALL	adherens junction	RT	▮	7	5.0E-1	1.0E0
	Annotation Cluster 120	Enrichment Score: 0.58	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regionalization	RT	▮	17	2.0E-1	9.6E-1
☐	GOTERM_BP_ALL	pattern specification process	RT	▮	25	2.3E-1	9.6E-1
☐	GOTERM_BP_ALL	anterior/posterior pattern formation	RT	▮	10	4.1E-1	9.9E-1
	Annotation Cluster 121	Enrichment Score: 0.57	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	TPR repeat	RT	▮	16	5.4E-2	7.0E-1
☐	INTERPRO	Tetratricopeptide region	RT	▮	14	7.5E-2	1.0E0
☐	INTERPRO	Tetratricopeptide-like helical	RT	▮	14	1.5E-1	1.0E0
☐	SMART	TPR	RT	▮	14	1.8E-1	9.0E-1
☐	INTERPRO	Tetratricopeptide TPR-1	RT	▮	10	2.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 3	RT	▮	7	3.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 1	RT	▮	7	3.9E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 2	RT	▮	7	3.9E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 4	RT	▮	5	3.9E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 7	RT	▮	4	4.1E-1	1.0E0
☐	INTERPRO	Tetratricopeptide TPR2	RT	▮	6	4.5E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 6	RT	▮	4	4.5E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 5	RT	▮	4	4.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:TPR 8	RT	▮	3	5.1E-1	1.0E0
	Annotation Cluster 122	Enrichment Score: 0.56	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	selenium binding	RT	▮	6	1.1E-1	9.9E-1
☐	SP_PIR_KEYWORDS	selenium	RT	▮	4	3.3E-1	9.7E-1
☐	SP_PIR_KEYWORDS	selenocysteine	RT	▮	3	5.7E-1	1.0E0
	Annotation Cluster 123	Enrichment Score: 0.56	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Spectrin repeat	RT	▮	7	4.5E-2	1.0E0
☐	INTERPRO	Actin-binding, actinin-type	RT	▮	6	6.7E-2	1.0E0
☐	SMART	SPEC	RT	▮	7	6.8E-2	8.8E-1
☐	GOTERM_CC_ALL	sarcomere	RT	▮	5	8.5E-1	1.0E0
☐	GOTERM_CC_ALL	contractile fiber part	RT	▮	5	8.7E-1	1.0E0
☐	GOTERM_CC_ALL	myofibril	RT	▮	5	9.1E-1	1.0E0
☐	GOTERM_CC_ALL	contractile fiber	RT	▮	5	9.2E-1	1.0E0
	Annotation Cluster 124	Enrichment Score: 0.55	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	amino acid and derivative metabolic process	RT	▮	35	1.7E-1	9.4E-1
☐	GOTERM_BP_ALL	amino acid metabolic process	RT	▮	28	1.8E-1	9.5E-1
☐	GOTERM_BP_ALL	nitrogen compound metabolic process	RT	▮	42	2.2E-1	9.6E-1
☐	GOTERM_BP_ALL	amine metabolic process	RT	▮	38	2.8E-1	9.7E-1
☐	GOTERM_BP_ALL	carboxylic acid metabolic process	RT	▮	48	3.2E-1	9.8E-1
☐	GOTERM_BP_ALL	organic acid metabolic process	RT	▮	48	3.3E-1	9.8E-1
☐	GOTERM_BP_ALL	monocarboxylic acid metabolic process	RT	▮	19	6.9E-1	1.0E0

	Annotation Cluster 125	Enrichment Score: 0.54	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	viral capsid	RT	4	2.6E-1	9.9E-1
☐	GOTERM_CC_ALL	virion	RT	4	3.0E-1	1.0E0
☐	GOTERM_CC_ALL	virion part	RT	4	3.0E-1	1.0E0
	Annotation Cluster 126	Enrichment Score: 0.52	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of growth	RT	7	1.4E-1	9.2E-1
☐	GOTERM_BP_ALL	regulation of cell growth	RT	12	2.9E-1	9.8E-1
☐	GOTERM_BP_ALL	negative regulation of cell growth	RT	4	3.9E-1	9.9E-1
☐	GOTERM_BP_ALL	negative regulation of cell size	RT	4	5.1E-1	1.0E0
	Annotation Cluster 127	Enrichment Score: 0.52	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	steroid metabolism	RT	6	1.6E-1	8.8E-1
☐	GOTERM_BP_ALL	cholesterol metabolic process	RT	9	2.7E-1	9.7E-1
☐	SP_PIR_KEYWORDS	cholesterol metabolism	RT	4	3.6E-1	9.8E-1
☐	GOTERM_BP_ALL	sterol metabolic process	RT	9	3.6E-1	9.9E-1
☐	GOTERM_BP_ALL	steroid metabolic process	RT	15	4.7E-1	1.0E0
	Annotation Cluster 128	Enrichment Score: 0.52	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cholesterol transport	RT	4	2.2E-1	9.6E-1
☐	GOTERM_BP_ALL	sterol transport	RT	4	2.5E-1	9.6E-1
☐	GOTERM_BP_ALL	lipid transport	RT	9	5.1E-1	1.0E0
	Annotation Cluster 129	Enrichment Score: 0.52	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	UDP-galactosyltransferase activity	RT	4	2.0E-1	1.0E0
☐	GOTERM_MF_ALL	UDP-glycosyltransferase activity	RT	11	3.2E-1	1.0E0
☐	GOTERM_MF_ALL	galactosyltransferase activity	RT	4	4.6E-1	1.0E0
	Annotation Cluster 130	Enrichment Score: 0.51	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	myelin sheath	RT	3	5.9E-2	8.8E-1
☐	GOTERM_BP_ALL	myelination	RT	5	2.8E-1	9.8E-1
☐	GOTERM_BP_ALL	ensheathment of neurons	RT	5	3.2E-1	9.8E-1
☐	GOTERM_BP_ALL	axon ensheathment	RT	5	3.2E-1	9.8E-1
☐	GOTERM_BP_ALL	regulation of action potential	RT	5	5.3E-1	1.0E0
☐	GOTERM_BP_ALL	transmission of nerve impulse	RT	15	9.8E-1	1.0E0
	Annotation Cluster 131	Enrichment Score: 0.5	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	membrane lipid biosynthetic process	RT	11	1.7E-1	9.4E-1
☐	GOTERM_BP_ALL	cellular lipid metabolic process	RT	53	2.6E-1	9.7E-1
☐	GOTERM_BP_ALL	membrane lipid metabolic process	RT	19	2.6E-1	9.7E-1
☐	GOTERM_BP_ALL	glycerophospholipid metabolic process	RT	9	2.7E-1	9.7E-1
☐	GOTERM_BP_ALL	phospholipid metabolic process	RT	15	2.8E-1	9.7E-1
☐	GOTERM_BP_ALL	phospholipid biosynthetic process	RT	8	3.6E-1	9.9E-1
☐	GOTERM_BP_ALL	lipid metabolic process	RT	58	4.0E-1	9.9E-1
☐	GOTERM_BP_ALL	lipid biosynthetic process	RT	20	7.7E-1	1.0E0
	Annotation Cluster 132	Enrichment Score: 0.49	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	flagellum biogenesis	RT	3	8.8E-2	8.6E-1
☐	GOTERM_BP_ALL	flagellum organization and biogenesis	RT	3	1.2E-1	9.0E-1
☐	GOTERM_BP_ALL	spermatid development	RT	5	4.2E-1	9.9E-1
☐	GOTERM_BP_ALL	spermatid differentiation	RT	5	4.6E-1	9.9E-1
☐	GOTERM_BP_ALL	cell projection biogenesis	RT	5	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	microtubule cytoskeleton organization and biogenesis	RT	6	8.0E-1	1.0E0
	Annotation Cluster 133	Enrichment Score: 0.48	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	glutamine family amino acid metabolic process	RT	6	2.1E-1	9.6E-1
☐	GOTERM_BP_ALL	glutamine metabolic process	RT	4	2.2E-1	9.6E-1
☐	KEGG_PATHWAY	Glutamate metabolism	RT	3	7.9E-1	9.8E-1

	Annotation Cluster 134	Enrichment Score: 0.47	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	adrenal gland development	RT	▮		3	2.1E-1	9.6E-1
☐	GOTERM_BP_ALL	gland development	RT	▮		9	2.8E-1	9.7E-1
☐	GOTERM_BP_ALL	endocrine system development	RT	▮		5	6.5E-1	1.0E0
	Annotation Cluster 135	Enrichment Score: 0.47	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Butyrophylin-like	RT	▮		7	1.4E-1	1.0E0
☐	INTERPRO	Zinc finger, B-box	RT	▮		8	2.0E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:B box-type	RT	▮		5	2.1E-1	1.0E0
☐	INTERPRO	SPla/RYanodine receptor SPRY	RT	▮		8	2.5E-1	1.0E0
☐	SMART	BBOX	RT	▮		8	2.8E-1	9.6E-1
☐	INTERPRO	B302, (SPRY)-like	RT	▮		8	2.8E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:B30.2/SPRY	RT	▮		4	4.1E-1	1.0E0
☐	SMART	SPRY	RT	▮		8	4.2E-1	9.8E-1
☐	PIR_SUPERFAMILY	PIRSF001733:rfp transforming protein	RT	▮		4	5.4E-1	1.0E0
☐	INTERPRO	SPRY-associated	RT	▮		3	7.6E-1	1.0E0
☐	SMART	PRY	RT	▮		3	8.5E-1	1.0E0
	Annotation Cluster 136	Enrichment Score: 0.47	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	cytokine binding	RT	▮		12	1.1E-1	9.9E-1
☐	GOTERM_MF_ALL	interleukin receptor activity	RT	▮		5	3.9E-1	1.0E0
☐	GOTERM_MF_ALL	interleukin binding	RT	▮		5	5.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	cytokine receptor	RT	▮		3	5.9E-1	1.0E0
	Annotation Cluster 137	Enrichment Score: 0.46	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of multicellular organism growth	RT	▮		9	8.2E-2	8.6E-1
☐	GOTERM_BP_ALL	positive regulation of multicellular organism growth	RT	▮		3	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of growth	RT	▮		3	8.0E-1	1.0E0
	Annotation Cluster 138	Enrichment Score: 0.46	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	mRNA catabolic process, deadenylation-dependent decay	RT	▮		3	1.2E-1	9.0E-1
☐	GOTERM_BP_ALL	regulation of mRNA stability	RT	▮		3	2.8E-1	9.7E-1
☐	GOTERM_BP_ALL	regulation of RNA stability	RT	▮		3	3.4E-1	9.8E-1
☐	GOTERM_BP_ALL	regulation of RNA metabolic process	RT	▮		3	4.7E-1	1.0E0
☐	GOTERM_BP_ALL	mRNA catabolic process	RT	▮		4	5.3E-1	1.0E0
☐	GOTERM_BP_ALL	RNA catabolic process	RT	▮		4	6.5E-1	1.0E0
	Annotation Cluster 139	Enrichment Score: 0.46	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	Rab GTPase binding	RT	▮		5	8.6E-2	9.8E-1
☐	GOTERM_MF_ALL	Ras GTPase binding	RT	▮		6	5.1E-1	1.0E0
☐	GOTERM_MF_ALL	small GTPase binding	RT	▮		6	5.6E-1	1.0E0
☐	GOTERM_MF_ALL	GTPase binding	RT	▮		6	6.1E-1	1.0E0
	Annotation Cluster 140	Enrichment Score: 0.45	G		🟩	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF000615:tyrosine-protein kinase, CSF-1/PDGF receptor type	RT	▮		4	1.1E-2	1.0E0
☐	INTERPRO	Receptor tyrosine kinase, class III, conserved region	RT	▮		4	4.8E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:Ig-like C2-type 2	RT	▮		12	1.3E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Ig-like C2-type 1	RT	▮		12	1.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	tyrosine-specific protein kinase	RT	▮		7	2.2E-1	9.3E-1
☐	UP_SEQ_FEATURE	domain:Ig-like C2-type 3	RT	▮		8	3.0E-1	1.0E0
☐	GOTERM_MF_ALL	transmembrane receptor protein tyrosine kinase activity	RT	▮		8	4.5E-1	1.0E0
☐	INTERPRO	Immunoglobulin-like fold	RT	▮		34	5.3E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Ig-like C2-type 5	RT	▮		4	5.7E-1	1.0E0
☐	INTERPRO	Immunoglobulin	RT	▮		15	5.7E-1	1.0E0

☐	UP_SEQ_FEATURE	domain:Ig-like C2-type 4	RT		4	6.5E-1	1.0E0
☐	INTERPRO	Immunoglobulin V-set	RT		14	6.6E-1	1.0E0
☐	INTERPRO	Immunoglobulin subtype	RT		18	7.4E-1	1.0E0
☐	SMART	IG	RT		21	8.3E-1	1.0E0
☐	INTERPRO	Immunoglobulin-like	RT		27	8.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	immunoglobulin domain	RT		26	8.6E-1	1.0E0
☐	INTERPRO	Immunoglobulin subtype 2	RT		9	9.7E-1	1.0E0
☐	SMART	IGc2	RT		10	9.8E-1	1.0E0
	Annotation Cluster 141	Enrichment Score: 0.45	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Guanylate kinase	RT		4	2.7E-1	1.0E0
☐	INTERPRO	Guanylate kinase/L-type calcium channel region	RT		4	3.4E-1	1.0E0
☐	SMART	GuKc	RT		4	4.0E-1	9.8E-1
☐	UP_SEQ_FEATURE	domain:Guanylate kinase-like	RT		3	4.5E-1	1.0E0
	Annotation Cluster 142	Enrichment Score: 0.44	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	homeostatic process	RT		43	3.8E-2	7.0E-1
☐	GOTERM_BP_ALL	cation homeostasis	RT		15	1.7E-1	9.5E-1
☐	GOTERM_BP_ALL	di-, tri-valent inorganic cation homeostasis	RT		13	2.3E-1	9.6E-1
☐	GOTERM_BP_ALL	cellular cation homeostasis	RT		14	2.3E-1	9.7E-1
☐	GOTERM_BP_ALL	cellular homeostasis	RT		26	2.8E-1	9.7E-1
☐	GOTERM_BP_ALL	cellular di-, tri-valent inorganic cation homeostasis	RT		12	3.0E-1	9.8E-1
☐	GOTERM_BP_ALL	chemical homeostasis	RT		24	3.3E-1	9.8E-1
☐	GOTERM_BP_ALL	ion homeostasis	RT		19	4.3E-1	9.9E-1
☐	GOTERM_BP_ALL	cellular ion homeostasis	RT		17	4.6E-1	9.9E-1
☐	GOTERM_BP_ALL	cellular chemical homeostasis	RT		17	4.6E-1	9.9E-1
☐	GOTERM_BP_ALL	elevation of cytosolic calcium ion concentration	RT		3	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	cytosolic calcium ion homeostasis	RT		3	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	cellular metal ion homeostasis	RT		7	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	metal ion homeostasis	RT		7	7.0E-1	1.0E0
☐	GOTERM_BP_ALL	cellular calcium ion homeostasis	RT		6	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	calcium ion homeostasis	RT		6	7.4E-1	1.0E0
	Annotation Cluster 143	Enrichment Score: 0.44	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Guanine-nucleotide dissociation stimulator CDC25	RT		5	1.6E-1	1.0E0
☐	SMART	RasGEF	RT		5	2.1E-1	9.2E-1
☐	INTERPRO	Ras guanine nucleotide exchange factor	RT		4	4.4E-1	1.0E0
☐	INTERPRO	Guanine nucleotide exchange factor for Ras-like GTPases, N-terminal	RT		3	6.4E-1	1.0E0
☐	SMART	RasGEFN	RT		3	7.0E-1	1.0E0
	Annotation Cluster 144	Enrichment Score: 0.43	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	repeat:ANK 1	RT		11	2.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 2	RT		11	2.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 9	RT		3	2.9E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 7	RT		4	3.1E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 8	RT		3	3.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	ank repeat	RT		19	3.3E-1	9.7E-1
☐	UP_SEQ_FEATURE	repeat:ANK 5	RT		7	3.4E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 3	RT		9	3.8E-1	1.0E0
☐	INTERPRO	Ankyrin	RT		18	3.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:ANK 4	RT		7	4.7E-1	1.0E0

☐	**SMART**	ANK	RT	20	5.5E-1	9.9E-1
☐	**UP_SEQ_FEATURE**	repeat:ANK 6	RT	4	6.6E-1	1.0E0
	Annotation Cluster 145	Enrichment Score: 0.43	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	lymphocyte homeostasis	RT	4	2.7E-1	9.7E-1
☐	**GOTERM_BP_ALL**	regulation of B cell activation	RT	6	3.3E-1	9.8E-1
☐	**GOTERM_BP_ALL**	leukocyte homeostasis	RT	4	4.4E-1	9.9E-1
☐	**GOTERM_BP_ALL**	homeostasis of number of cells	RT	4	4.8E-1	1.0E0
	Annotation Cluster 146	Enrichment Score: 0.43	G	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	synaptosome	RT	5	1.4E-1	8.7E-1
☐	**GOTERM_CC_ALL**	synaptosome	RT	6	4.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	synapse	RT	13	7.4E-1	1.0E0
	Annotation Cluster 147	Enrichment Score: 0.42	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	lymphocyte mediated immunity	RT	11	3.4E-1	9.8E-1
☐	**GOTERM_BP_ALL**	leukocyte mediated cytotoxicity	RT	4	3.4E-1	9.8E-1
☐	**GOTERM_BP_ALL**	cell killing	RT	4	3.7E-1	9.9E-1
☐	**GOTERM_BP_ALL**	regulation of leukocyte mediated cytotoxicity	RT	3	4.1E-1	9.9E-1
☐	**GOTERM_BP_ALL**	regulation of cell killing	RT	3	4.1E-1	9.9E-1
☐	**GOTERM_BP_ALL**	leukocyte mediated immunity	RT	11	4.1E-1	9.9E-1
	Annotation Cluster 148	Enrichment Score: 0.42	G	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	SH3 domain	RT	20	2.8E-1	9.6E-1
☐	**UP_SEQ_FEATURE**	domain:SH3	RT	13	3.0E-1	1.0E0
☐	**INTERPRO**	Src homology-3	RT	18	4.2E-1	1.0E0
☐	**SMART**	SH3	RT	19	5.7E-1	9.9E-1
	Annotation Cluster 149	Enrichment Score: 0.42	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	hexose metabolic process	RT	17	2.2E-1	9.6E-1
☐	**GOTERM_BP_ALL**	monosaccharide metabolic process	RT	17	2.4E-1	9.7E-1
☐	**GOTERM_BP_ALL**	glucose metabolic process	RT	12	3.7E-1	9.9E-1
☐	**GOTERM_BP_ALL**	alcohol metabolic process	RT	27	4.0E-1	9.9E-1
☐	**GOTERM_BP_ALL**	carbohydrate metabolic process	RT	37	5.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular carbohydrate metabolic process	RT	22	8.0E-1	1.0E0
	Annotation Cluster 150	Enrichment Score: 0.42	G	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	dioxygenase activity	RT	7	3.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	RT	7	3.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	RT	7	3.9E-1	1.0E0
	Annotation Cluster 151	Enrichment Score: 0.42	G	Count	P_Value	Benjamini
☐	**INTERPRO**	Metal-dependent phosphohydrolase, HD region	RT	4	2.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	3',5'-cyclic-nucleotide phosphodiesterase activity	RT	4	2.9E-1	1.0E0
☐	**SMART**	HDc	RT	4	3.2E-1	9.6E-1
☐	**GOTERM_MF_ALL**	cyclic-nucleotide phosphodiesterase activity	RT	4	3.4E-1	1.0E0
☐	**INTERPRO**	3'5'-cyclic nucleotide phosphodiesterase	RT	3	4.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	phosphoric diester hydrolase activity	RT	5	8.3E-1	1.0E0
	Annotation Cluster 152	Enrichment Score: 0.41	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	platelet activation	RT	4	1.1E-1	9.0E-1
☐	**GOTERM_BP_ALL**	hemostasis	RT	8	3.0E-1	9.8E-1
☐	**GOTERM_BP_ALL**	blood coagulation	RT	7	4.2E-1	9.9E-1
☐	**GOTERM_BP_ALL**	coagulation	RT	7	4.3E-1	9.9E-1
☐	**SP_PIR_KEYWORDS**	blood coagulation	RT	4	5.4E-1	1.0E0

☐	GOTERM_BP_ALL	regulation of body fluid levels	RT		8	5.4E-1	1.0E0
☐	GOTERM_BP_ALL	wound healing	RT		8	7.1E-1	1.0E0
	Annotation Cluster 153	Enrichment Score: 0.41	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	anatomical structure formation	RT		25	1.1E-1	9.0E-1
☐	GOTERM_BP_ALL	angiogenesis	RT		16	4.2E-1	9.9E-1
☐	GOTERM_BP_ALL	blood vessel development	RT		22	4.9E-1	1.0E0
☐	GOTERM_BP_ALL	blood vessel morphogenesis	RT		19	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	vasculature development	RT		22	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	organ morphogenesis	RT		47	5.7E-1	1.0E0
	Annotation Cluster 154	Enrichment Score: 0.41	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	rhythmic process	RT		14	2.5E-2	6.2E-1
☐	GOTERM_BP_ALL	menstrual cycle phase	RT		6	1.8E-1	9.5E-1
☐	GOTERM_BP_ALL	menstrual cycle process	RT		6	1.9E-1	9.6E-1
☐	GOTERM_BP_ALL	ovulation from ovarian follicle	RT		3	2.1E-1	9.6E-1
☐	GOTERM_BP_ALL	ovulation	RT		3	2.4E-1	9.7E-1
☐	GOTERM_BP_ALL	female gonad development	RT		6	2.8E-1	9.7E-1
☐	GOTERM_BP_ALL	development of primary female sexual characteristics	RT		6	3.1E-1	9.8E-1
☐	GOTERM_BP_ALL	female sex differentiation	RT		6	3.1E-1	9.8E-1
☐	GOTERM_BP_ALL	menstrual cycle	RT		6	3.3E-1	9.8E-1
☐	GOTERM_BP_ALL	female gamete generation	RT		4	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	gonad development	RT		6	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	ovarian follicle development	RT		3	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive structure development	RT		6	6.4E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive developmental process	RT		9	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive process in a multicellular organism	RT		7	6.6E-1	1.0E0
☐	GOTERM_BP_ALL	multicellular organism reproduction	RT		7	6.6E-1	1.0E0
☐	GOTERM_BP_ALL	sex differentiation	RT		8	7.0E-1	1.0E0
☐	GOTERM_BP_ALL	development of primary sexual characteristics	RT		6	7.1E-1	1.0E0
☐	GOTERM_BP_ALL	epithelial cell differentiation	RT		3	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive process	RT		16	9.2E-1	1.0E0
	Annotation Cluster 155	Enrichment Score: 0.41	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	vesicle	RT		35	1.8E-1	9.9E-1
☐	GOTERM_CC_ALL	cytoplasmic vesicle	RT		34	1.9E-1	9.9E-1
☐	SP_PIR_KEYWORDS	cytoplasmic vesicle	RT		15	2.3E-1	9.4E-1
☐	GOTERM_CC_ALL	membrane-bound vesicle	RT		23	4.4E-1	1.0E0
☐	GOTERM_CC_ALL	cytoplasmic membrane-bound vesicle	RT		22	4.5E-1	1.0E0
☐	GOTERM_CC_ALL	synaptic vesicle	RT		6	5.1E-1	1.0E0
☐	GOTERM_CC_ALL	clathrin-coated vesicle	RT		8	7.8E-1	1.0E0
☐	GOTERM_CC_ALL	coated vesicle	RT		8	8.9E-1	1.0E0
	Annotation Cluster 156	Enrichment Score: 0.4	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	NF-kappa-B/Rel/dorsal	RT		3	2.4E-1	1.0E0
☐	INTERPRO	Rel homology	RT		3	2.8E-1	1.0E0
☐	INTERPRO	Cell surface receptor IPT/TIG	RT		4	5.7E-1	1.0E0
☐	SMART	IPT	RT		4	6.6E-1	1.0E0
	Annotation Cluster 157	Enrichment Score: 0.39	G	🟩	Count	P_Value	Benjamini
☐	BIOCARTA	AKT Signaling Pathway	RT		7	2.6E-2	9.8E-1
☐	BIOCARTA	NFkB activation by Nontypeable Hemophilus influenzae	RT		8	4.3E-2	9.6E-1
☐	BIOCARTA	Acetylation and Deacetylation of RelA in The Nucleus	RT		5	1.2E-1	9.9E-1

☐	**BIOCARTA**	Activation of PKC through G protein coupled receptor	RT	▮		3	1.6E-1	9.9E-1
☐	**BIOCARTA**	Erythropoietin mediated neuroprotection through NF-kB	RT	▮		4	2.0E-1	1.0E0
☐	**BIOCARTA**	Double Stranded RNA Induced Gene Expression	RT	▮		3	3.9E-1	1.0E0
☐	**BIOCARTA**	ATM Signaling Pathway	RT	▮		4	4.1E-1	1.0E0
☐	**BIOCARTA**	The 4-1BB-dependent immune response	RT	▮		4	4.4E-1	1.0E0
☐	**BIOCARTA**	Signal transduction through IL1R	RT	▮		5	4.4E-1	9.9E-1
☐	**BIOCARTA**	Influence of Ras and Rho proteins on G1 to S Transition	RT	▮		5	4.4E-1	9.9E-1
☐	**BIOCARTA**	Induction of apoptosis through DR3 and DR4/5 Death Receptors	RT	▮		5	4.7E-1	9.9E-1
☐	**BIOCARTA**	CD40L Signaling Pathway	RT	▮		3	5.9E-1	1.0E0
☐	**BIOCARTA**	Cadmium induces DNA synthesis and proliferation in macrophages	RT	▮		3	5.9E-1	1.0E0
☐	**BIOCARTA**	TNF/Stress Related Signaling	RT	▮		4	6.3E-1	1.0E0
☐	**BIOCARTA**	CXCR4 Signaling Pathway	RT	▮		4	6.5E-1	1.0E0
☐	**BIOCARTA**	Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages	RT	▮		4	6.5E-1	1.0E0
☐	**BIOCARTA**	HIV-I Nef	RT	▮		7	6.5E-1	1.0E0
☐	**BIOCARTA**	TNFR2 Signaling Pathway	RT	▮		3	6.9E-1	1.0E0
☐	**BIOCARTA**	Neuropeptides VIP and PACAP inhibit the apoptosis of activated T cells	RT	▮		3	6.9E-1	1.0E0
☐	**BIOCARTA**	fMLP induced chemokine gene expression in HMC-1 cells	RT	▮		4	7.6E-1	1.0E0
☐	**BIOCARTA**	NF-kB Signaling Pathway	RT	▮		3	7.7E-1	1.0E0
☐	**BIOCARTA**	T Cell Receptor Signaling Pathway	RT	▮		4	8.9E-1	1.0E0
☐	**BIOCARTA**	Keratinocyte Differentiation	RT	▮		3	9.7E-1	1.0E0
☐	**BIOCARTA**	MAPKinase Signaling Pathway	RT	▮		4	1.0E0	1.0E0
	Annotation Cluster 158	Enrichment Score: 0.39	G		🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	region of interest:Heparin-binding	RT	▮		4	1.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	heparin binding	RT	▮		8	3.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	pattern binding	RT	▮		11	4.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	polysaccharide binding	RT	▮		10	4.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	glycosaminoglycan binding	RT	▮		8	6.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	heparin-binding	RT	▮		5	7.1E-1	1.0E0
	Annotation Cluster 159	Enrichment Score: 0.38	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	striated muscle development	RT	▮		16	2.2E-1	9.6E-1
☐	**GOTERM_BP_ALL**	regulation of myoblast differentiation	RT	▮		3	2.4E-1	9.7E-1
☐	**GOTERM_BP_ALL**	skeletal muscle development	RT	▮		12	3.3E-1	9.8E-1
☐	**GOTERM_BP_ALL**	muscle cell differentiation	RT	▮		9	3.4E-1	9.8E-1
☐	**GOTERM_BP_ALL**	muscle development	RT	▮		18	4.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	myoblast differentiation	RT	▮		5	5.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	muscle fiber development	RT	▮		6	7.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	skeletal muscle fiber development	RT	▮		6	7.4E-1	1.0E0
	Annotation Cluster 160	Enrichment Score: 0.38	G		🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	domain:C2	RT	▮		6	2.4E-1	1.0E0
☐	**INTERPRO**	C2 calcium-dependent membrane targeting	RT	▮		12	4.7E-1	1.0E0
☐	**SMART**	C2	RT	▮		12	6.5E-1	1.0E0
	Annotation Cluster 161	Enrichment Score: 0.38	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	ubiquitin ligase complex	RT	▮		7	2.5E-1	9.9E-1
☐	**GOTERM_MF_ALL**	ligase activity	RT	▮		34	3.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	ubiquitin-protein ligase activity	RT	▮		13	3.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	ligase activity, forming carbon-nitrogen	RT	▮		18	3.8E-1	1.0E0

☐		bonds	RT				
☐	GOTERM_MF_ALL	small protein conjugating enzyme activity	RT		13	4.0E-1	1.0E0
☐	GOTERM_MF_ALL	small conjugating protein ligase activity	RT		13	4.4E-1	1.0E0
☐	GOTERM_MF_ALL	acid-amino acid ligase activity	RT		14	4.8E-1	1.0E0
☐	SMART	UBCc	RT		6	5.0E-1	9.9E-1
☐	SP_PIR_KEYWORDS	ligase	RT		19	7.9E-1	1.0E0
	Annotation Cluster 162	Enrichment Score: 0.37	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	repeat:WD 3	RT		15	2.4E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 1	RT		15	2.5E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 2	RT		15	2.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	wd repeat	RT		24	2.5E-1	9.5E-1
☐	UP_SEQ_FEATURE	repeat:WD 5	RT		12	4.1E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 4	RT		12	5.0E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 6	RT		9	5.1E-1	1.0E0
☐	INTERPRO	WD40 repeat	RT		16	7.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:WD 7	RT		5	7.8E-1	1.0E0
☐	SMART	WD40	RT		19	7.9E-1	1.0E0
	Annotation Cluster 163	Enrichment Score: 0.37	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Phox-like	RT		6	3.4E-1	1.0E0
☐	SMART	PX	RT		6	4.3E-1	9.8E-1
☐	UP_SEQ_FEATURE	domain:PX	RT		3	5.4E-1	1.0E0
	Annotation Cluster 164	Enrichment Score: 0.36	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	condensed chromosome, pericentric region	RT		3	1.7E-1	9.9E-1
☐	GOTERM_CC_ALL	condensed chromosome	RT		6	5.1E-1	1.0E0
☐	GOTERM_CC_ALL	chromosome, pericentric region	RT		4	9.3E-1	1.0E0
	Annotation Cluster 165	Enrichment Score: 0.36	G	🟩	Count	P_Value	Benjamini
☐	BIOCARTA	PTEN dependent cell cycle arrest and apoptosis	RT		5	2.7E-1	9.9E-1
☐	BIOCARTA	Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway	RT		4	4.1E-1	1.0E0
☐	BIOCARTA	mTOR Signaling Pathway	RT		4	4.4E-1	1.0E0
☐	BIOCARTA	Regulation of eIF4e and p70 S6 Kinase	RT		3	7.2E-1	1.0E0
	Annotation Cluster 166	Enrichment Score: 0.36	G	🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Propanoate metabolism	RT		5	2.9E-1	8.3E-1
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on the aldehyde or oxo group of donors	RT		5	4.7E-1	1.0E0
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	RT		4	5.0E-1	1.0E0
☐	KEGG_PATHWAY	Valine, leucine and isoleucine degradation	RT		5	5.3E-1	9.1E-1
	Annotation Cluster 167	Enrichment Score: 0.36	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein oligomerization	RT		7	2.7E-1	9.7E-1
☐	GOTERM_BP_ALL	protein homooligomerization	RT		5	3.6E-1	9.9E-1
☐	GOTERM_BP_ALL	protein complex assembly	RT		12	8.8E-1	1.0E0
	Annotation Cluster 168	Enrichment Score: 0.35	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	region of interest:Calmodulin-binding	RT		6	3.1E-1	1.0E0
☐	GOTERM_MF_ALL	calmodulin-dependent protein kinase activity	RT		3	4.0E-1	1.0E0
☐	GOTERM_MF_ALL	calmodulin binding	RT		11	5.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	calmodulin-binding	RT		9	5.8E-1	1.0E0
	Annotation Cluster 169	Enrichment Score: 0.35	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	carbon-carbon lyase activity	RT		8	9.4E-2	9.8E-1
☐	GOTERM_MF_ALL	carboxy-lyase activity	RT		4	5.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	decarboxylase	RT		3	6.1E-1	1.0E0

☐	**GOTERM_MF_ALL**	lyase activity	RT		14	7.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	lyase	RT		9	7.9E-1	1.0E0
	Annotation Cluster 170	Enrichment Score: 0.35	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	RhoGAP	RT		6	3.1E-1	1.0E0
☐	**SMART**	RhoGAP	RT		6	4.3E-1	9.8E-1
☐	**UP_SEQ_FEATURE**	domain:Rho-GAP	RT		3	6.8E-1	1.0E0
	Annotation Cluster 171	Enrichment Score: 0.34	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	cellular catabolic process	RT		47	1.8E-1	9.5E-1
☐	**GOTERM_BP_ALL**	catabolic process	RT		59	1.8E-1	9.5E-1
☐	**GOTERM_BP_ALL**	biopolymer catabolic process	RT		27	3.1E-1	9.8E-1
☐	**GOTERM_BP_ALL**	macromolecule catabolic process	RT		32	4.0E-1	9.9E-1
☐	**GOTERM_BP_ALL**	protein catabolic process	RT		20	4.1E-1	9.9E-1
☐	**GOTERM_MF_ALL**	ubiquitin-specific protease activity	RT		7	4.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	small conjugating protein-specific protease activity	RT		7	4.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	proteolysis involved in cellular protein catabolic process	RT		14	5.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular protein catabolic process	RT		14	5.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	ubiquitin-dependent protein catabolic process	RT		13	5.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	thiolester hydrolase activity	RT		8	5.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	ubiquitin thiolesterase activity	RT		6	5.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	modification-dependent protein catabolic process	RT		13	6.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	modification-dependent macromolecule catabolic process	RT		13	6.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular macromolecule catabolic process	RT		23	6.1E-1	1.0E0
☐	**INTERPRO**	Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2	RT		4	7.5E-1	1.0E0
	Annotation Cluster 172	Enrichment Score: 0.34	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	cofactor biosynthetic process	RT		12	4.1E-1	9.9E-1
☐	**GOTERM_BP_ALL**	coenzyme metabolic process	RT		17	4.6E-1	9.9E-1
☐	**GOTERM_BP_ALL**	coenzyme biosynthetic process	RT		10	4.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	cofactor metabolic process	RT		20	5.2E-1	1.0E0
	Annotation Cluster 173	Enrichment Score: 0.34	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Kelch related	RT		9	6.7E-2	1.0E0
☐	**INTERPRO**	BTB/Kelch-associated	RT		5	4.3E-1	1.0E0
☐	**INTERPRO**	Kelch-type beta propeller	RT		4	6.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	kelch repeat	RT		4	7.2E-1	1.0E0
☐	**SMART**	Kelch	RT		5	8.0E-1	1.0E0
☐	**INTERPRO**	Kelch repeat type 1	RT		3	9.0E-1	1.0E0
	Annotation Cluster 174	Enrichment Score: 0.33	G	🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	short sequence motif:Cell attachment site	RT		9	1.4E-1	1.0E0
☐	**INTERPRO**	von Willebrand factor, type C	RT		3	8.4E-1	1.0E0
☐	**SMART**	VWC	RT		3	8.8E-1	1.0E0
	Annotation Cluster 175	Enrichment Score: 0.33	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	detection of biotic stimulus	RT		3	2.8E-1	9.7E-1
☐	**GOTERM_BP_ALL**	detection of external stimulus	RT		7	3.2E-1	9.8E-1
☐	**GOTERM_BP_ALL**	detection of stimulus	RT		7	4.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	detection of light stimulus	RT		3	6.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	detection of abiotic stimulus	RT		4	7.6E-1	1.0E0
	Annotation Cluster 176	Enrichment Score: 0.33	G	🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	domain:NTR	RT		3	4.2E-1	1.0E0
☐	**INTERPRO**	Netrin, C-terminal	RT		3	4.6E-1	1.0E0

☐	**SMART**	C345C	RT	▮		3	5.2E-1	9.9E-1
	Annotation Cluster 177	Enrichment Score: 0.33	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Retinoid X receptor	RT	▮		3	2.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	tRNA-pseudouridine synthase activity	RT	▮		3	4.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	intramolecular transferase activity	RT	▮		4	5.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	pseudouridine synthase activity	RT	▮		3	6.0E-1	1.0E0
	Annotation Cluster 178	Enrichment Score: 0.33	G		🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	glycosidase	RT	▮		7	3.5E-1	9.8E-1
☐	**GOTERM_MF_ALL**	hydrolase activity, acting on glycosyl bonds	RT	▮		11	5.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrolase activity, hydrolyzing O-glycosyl compounds	RT	▮		9	5.6E-1	1.0E0
	Annotation Cluster 179	Enrichment Score: 0.33	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of I-kappaB kinase/NF-kappaB cascade	RT	▮		6	2.9E-1	9.8E-1
☐	**GOTERM_BP_ALL**	I-kappaB kinase/NF-kappaB cascade	RT	▮		8	3.4E-1	9.8E-1
☐	**GOTERM_BP_ALL**	positive regulation of I-kappaB kinase/NF-kappaB cascade	RT	▮		4	6.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of signal transduction	RT	▮		9	7.1E-1	1.0E0
	Annotation Cluster 180	Enrichment Score: 0.33	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	UDP-glycosyltransferase activity	RT	▮		11	3.2E-1	1.0E0
☐	**KEGG_PATHWAY**	O-Glycan biosynthesis	RT	▮		4	3.9E-1	8.8E-1
☐	**KEGG_PATHWAY**	Glycan structures - biosynthesis 1	RT	▮		8	8.6E-1	9.9E-1
	Annotation Cluster 181	Enrichment Score: 0.32	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	T cell activation	RT	▮		15	3.3E-1	9.8E-1
☐	**GOTERM_BP_ALL**	leukocyte differentiation	RT	▮		16	3.4E-1	9.8E-1
☐	**GOTERM_BP_ALL**	lymphocyte differentiation	RT	▮		11	4.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	alpha-beta T cell activation	RT	▮		4	5.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	T cell differentiation	RT	▮		6	7.5E-1	1.0E0
	Annotation Cluster 182	Enrichment Score: 0.32	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	antigen processing and presentation	RT	▮		13	3.1E-2	6.7E-1
☐	**INTERPRO**	MHC class I-like antigen recognition	RT	▮		5	3.9E-1	1.0E0
☐	**KEGG_PATHWAY**	Antigen processing and presentation	RT	▮		9	4.5E-1	8.8E-1
☐	**GOTERM_CC_ALL**	MHC protein complex	RT	▮		5	4.9E-1	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF001990:class I histocompatibility antigen	RT	▮		3	6.3E-1	1.0E0
☐	**INTERPRO**	Immunoglobulin C1-set	RT	▮		6	6.7E-1	1.0E0
☐	**INTERPRO**	MHC class I, alpha chain, alpha1 and alpha2	RT	▮		3	7.1E-1	1.0E0
☐	**SMART**	IGc1	RT	▮		6	7.5E-1	1.0E0
☐	**GOTERM_CC_ALL**	MHC class I protein complex	RT	▮		3	7.6E-1	1.0E0
☐	**KEGG_PATHWAY**	Type I diabetes mellitus	RT	▮		5	8.0E-1	9.8E-1
☐	**INTERPRO**	Immunoglobulin/major histocompatibility complex motif	RT	▮		6	8.3E-1	1.0E0
	Annotation Cluster 183	Enrichment Score: 0.32	G		🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	short sequence motif:BH3	RT	▮		3	3.5E-1	1.0E0
☐	**INTERPRO**	Apoptosis regulator Bcl-2, BH	RT	▮		3	5.2E-1	1.0E0
☐	**SMART**	BCL	RT	▮		3	6.1E-1	1.0E0
	Annotation Cluster 184	Enrichment Score: 0.31	G		🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	2Fe-2S	RT	▮		3	3.7E-1	9.7E-1
☐	**SP_PIR_KEYWORDS**	iron-sulfur	RT	▮		5	4.2E-1	9.9E-1
☐	**GOTERM_MF_ALL**	2 iron, 2 sulfur cluster binding	RT	▮		3	4.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	metal cluster binding	RT	▮		5	6.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	iron-sulfur cluster binding	RT	▮		5	6.1E-1	1.0E0
	Annotation Cluster 185	Enrichment Score: 0.31	G		🟩	Count	P_Value	Benjamini

☐	GOTERM_BP_ALL	protein import into nucleus, translocation	RT	▮		5	3.5E-2	6.8E-1
☐	GOTERM_BP_ALL	protein import into nucleus	RT	▮		7	5.4E-1	1.0E0
☐	GOTERM_BP_ALL	nuclear import	RT	▮		7	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	protein import	RT	▮		7	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	nucleocytoplasmic transport	RT	▮		7	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	nuclear transport	RT	▮		7	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	protein targeting	RT	▮		15	9.6E-1	1.0E0
	Annotation Cluster 186	Enrichment Score: 0.31	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Bile acid biosynthesis	RT	▮		6	1.8E-1	7.5E-1
☐	KEGG_PATHWAY	Lysine degradation	RT	▮		4	7.3E-1	9.7E-1
☐	KEGG_PATHWAY	Butanoate metabolism	RT	▮		3	9.4E-1	1.0E0
	Annotation Cluster 187	Enrichment Score: 0.3	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	coenzyme binding	RT	▮		13	4.4E-1	1.0E0
☐	GOTERM_MF_ALL	FAD binding	RT	▮		7	4.4E-1	1.0E0
☐	GOTERM_MF_ALL	cofactor binding	RT	▮		16	6.4E-1	1.0E0
	Annotation Cluster 188	Enrichment Score: 0.3	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:FERM	RT	▮		5	2.5E-1	1.0E0
☐	INTERPRO	FERM-type 3-helical bundle	RT	▮		5	4.5E-1	1.0E0
☐	INTERPRO	Ezrin/radixin/moesin ERM	RT	▮		3	4.6E-1	1.0E0
☐	INTERPRO	Band 4.1, N-terminal	RT	▮		4	7.4E-1	1.0E0
☐	SMART	B41	RT	▮		4	8.4E-1	1.0E0
	Annotation Cluster 189	Enrichment Score: 0.29	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	microbody membrane	RT	▮		3	4.8E-1	1.0E0
☐	GOTERM_CC_ALL	peroxisomal membrane	RT	▮		3	4.8E-1	1.0E0
☐	GOTERM_CC_ALL	microbody part	RT	▮		3	5.4E-1	1.0E0
☐	GOTERM_CC_ALL	peroxisomal part	RT	▮		3	5.4E-1	1.0E0
	Annotation Cluster 190	Enrichment Score: 0.29	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	glucose transmembrane transporter activity	RT	▮		3	3.1E-1	1.0E0
☐	GOTERM_MF_ALL	carbohydrate transmembrane transporter activity	RT	▮		6	3.2E-1	1.0E0
☐	GOTERM_MF_ALL	hexose transmembrane transporter activity	RT	▮		3	3.4E-1	1.0E0
☐	GOTERM_MF_ALL	monosaccharide transmembrane transporter activity	RT	▮		3	3.4E-1	1.0E0
☐	GOTERM_BP_ALL	carbohydrate transport	RT	▮		8	4.1E-1	9.9E-1
☐	GOTERM_MF_ALL	sugar:hydrogen ion symporter activity	RT	▮		5	4.9E-1	1.0E0
☐	GOTERM_MF_ALL	sugar transmembrane transporter activity	RT	▮		5	5.1E-1	1.0E0
☐	GOTERM_MF_ALL	secondary active transmembrane transporter activity	RT	▮		16	6.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	sugar transport	RT	▮		3	7.5E-1	1.0E0
☐	GOTERM_MF_ALL	symporter activity	RT	▮		11	7.9E-1	1.0E0
☐	GOTERM_MF_ALL	active transmembrane transporter activity	RT	▮		26	8.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	Symport	RT	▮		6	8.6E-1	1.0E0
	Annotation Cluster 191	Enrichment Score: 0.29	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	vesicle docking during exocytosis	RT	▮		3	4.1E-1	9.9E-1
☐	GOTERM_BP_ALL	membrane docking	RT	▮		3	4.4E-1	9.9E-1
☐	GOTERM_BP_ALL	vesicle docking	RT	▮		3	4.4E-1	9.9E-1
☐	GOTERM_BP_ALL	exocytosis	RT	▮		6	9.2E-1	1.0E0
	Annotation Cluster 192	Enrichment Score: 0.28	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	ABC transporters - General	RT	▮		7	1.5E-1	6.9E-1
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP 2	RT	▮		3	4.5E-1	1.0E0
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP 1	RT	▮		3	4.5E-1	1.0E0

☐	**UP_SEQ_FEATURE**	domain:ABC transporter 1	RT	▮		3	4.5E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:ABC transporter 2	RT	▮		3	4.5E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	nucleotide binding	RT	▮		8	5.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	P-loop	RT	▮		8	5.7E-1	1.0E0
☐	**BIOCARTA**	Nuclear Receptors in Lipid Metabolism and Toxicity	RT	▮		5	5.8E-1	1.0E0
☐	**INTERPRO**	ABC transporter related	RT	▮		3	8.1E-1	1.0E0
☐	**SMART**	AAA	RT	▮		6	9.4E-1	1.0E0
☐	**INTERPRO**	AAA+ ATPase, core	RT	▮		4	9.5E-1	1.0E0
	Annotation Cluster 193	Enrichment Score: 0.28	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	PDZ/DHR/GLGF	RT	▮		13	3.8E-1	1.0E0
☐	**SMART**	PDZ	RT	▮		13	5.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:PDZ	RT	▮		6	6.6E-1	1.0E0
	Annotation Cluster 194	Enrichment Score: 0.27	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	dystrophin-associated glycoprotein complex	RT	▮		3	3.0E-1	1.0E0
☐	**GOTERM_CC_ALL**	basal lamina	RT	▮		4	4.4E-1	1.0E0
☐	**GOTERM_CC_ALL**	basement membrane	RT	▮		6	6.7E-1	1.0E0
☐	**GOTERM_CC_ALL**	extracellular matrix part	RT	▮		6	9.4E-1	1.0E0
	Annotation Cluster 195	Enrichment Score: 0.27	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	ubiquitin ligase complex	RT	▮		7	2.5E-1	9.9E-1
☐	**GOTERM_BP_ALL**	protein ubiquitination	RT	▮		5	7.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein modification by small protein conjugation	RT	▮		5	8.2E-1	1.0E0
	Annotation Cluster 196	Enrichment Score: 0.27	G		🟩	Count	P_Value	Benjamini
☐	**BIOCARTA**	Multi-Drug Resistance Factors	RT	▮		3	1.1E-1	9.9E-1
☐	**KEGG_PATHWAY**	ABC transporters - General	RT	▮		7	1.5E-1	6.9E-1
☐	**INTERPRO**	ABC transporter, transmembrane region, type 1	RT	▮		4	3.9E-1	1.0E0
☐	**COG_ONTOLOGY**	Defense mechanisms	RT	▮		5	3.9E-1	1.0E0
☐	**INTERPRO**	ABC transporter, transmembrane region	RT	▮		3	5.2E-1	1.0E0
☐	**BIOCARTA**	Nuclear Receptors in Lipid Metabolism and Toxicity	RT	▮		5	5.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	ATPase activity, coupled to movement of substances	RT	▮		10	8.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	ATPase activity, coupled to transmembrane movement of substances	RT	▮		10	8.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT	▮		10	8.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT	▮		10	9.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	primary active transmembrane transporter activity	RT	▮		10	9.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	▮		4	9.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	ATPase activity, coupled to transmembrane movement of ions	RT	▮		5	9.7E-1	1.0E0
	Annotation Cluster 197	Enrichment Score: 0.26	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	GPS	RT	▮		4	3.9E-1	1.0E0
☐	**SMART**	GPS	RT	▮		4	4.8E-1	9.9E-1
☐	**UP_SEQ_FEATURE**	domain:GPS	RT	▮		3	5.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	neuropeptide signaling pathway	RT	▮		8	6.3E-1	1.0E0
☐	**INTERPRO**	GPCR, family 2, secretin-like	RT	▮		4	8.0E-1	1.0E0
	Annotation Cluster 198	Enrichment Score: 0.26	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	aminopeptidase activity	RT	▮		5	4.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	exopeptidase activity	RT	▮		9	6.2E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	aminopeptidase	RT	▮		3	6.4E-1	1.0E0

	Annotation Cluster 199	Enrichment Score: 0.25	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	nuclear chromosome part	RT	8	4.1E-1	1.0E0
☐	GOTERM_CC_ALL	condensed chromosome	RT	6	5.1E-1	1.0E0
☐	GOTERM_CC_ALL	condensed nuclear chromosome	RT	4	5.9E-1	1.0E0
☐	GOTERM_CC_ALL	nuclear chromosome	RT	8	6.3E-1	1.0E0
☐	GOTERM_CC_ALL	nuclear chromatin	RT	3	7.3E-1	1.0E0
	Annotation Cluster 200	Enrichment Score: 0.25	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	cytoskeletal protein binding	RT	36	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	actin polymerization and/or depolymerization	RT	6	4.3E-1	9.9E-1
☐	GOTERM_MF_ALL	actin binding	RT	24	5.5E-1	1.0E0
☐	GOTERM_BP_ALL	actin filament-based process	RT	18	6.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	actin-binding	RT	14	7.3E-1	1.0E0
☐	GOTERM_BP_ALL	actin cytoskeleton organization and biogenesis	RT	15	7.9E-1	1.0E0
	Annotation Cluster 201	Enrichment Score: 0.25	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Zymogen	RT	20	2.3E-1	9.4E-1
☐	GOTERM_BP_ALL	proteolysis	RT	60	6.4E-1	1.0E0
☐	GOTERM_MF_ALL	peptidase activity	RT	57	6.5E-1	1.0E0
☐	GOTERM_MF_ALL	endopeptidase activity	RT	36	7.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	protease	RT	35	8.6E-1	1.0E0
	Annotation Cluster 202	Enrichment Score: 0.24	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	somatic recombination of immunoglobulin gene segments	RT	4	4.6E-1	9.9E-1
☐	GOTERM_BP_ALL	immunoglobulin production	RT	5	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	production of molecular mediator of immune response	RT	5	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	somatic cell DNA recombination	RT	4	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	somatic diversification of immune receptors via germline recombination within a single locus	RT	4	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	somatic diversification of immunoglobulins	RT	4	5.3E-1	1.0E0
☐	GOTERM_BP_ALL	somatic diversification of immune receptors	RT	4	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	isotype switching	RT	3	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	immunoglobulin production during immune response	RT	3	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	somatic recombination of immunoglobulin genes during immune response	RT	3	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	somatic diversification of immunoglobulins during immune response	RT	3	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	immunoglobulin mediated immune response	RT	7	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	B cell mediated immunity	RT	7	6.4E-1	1.0E0
☐	GOTERM_BP_ALL	DNA recombination	RT	5	9.4E-1	1.0E0
	Annotation Cluster 203	Enrichment Score: 0.24	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	axon guidance	RT	10	3.3E-1	9.8E-1
☐	GOTERM_BP_ALL	neurite development	RT	21	3.8E-1	9.9E-1
☐	GOTERM_BP_ALL	neuron development	RT	23	4.2E-1	9.9E-1
☐	GOTERM_BP_ALL	neuron differentiation	RT	28	4.9E-1	1.0E0
☐	GOTERM_BP_ALL	axonogenesis	RT	15	5.9E-1	1.0E0
☐	GOTERM_BP_ALL	neurite morphogenesis	RT	16	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	neuron morphogenesis during differentiation	RT	16	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	nervous system development	RT	57	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	cell morphogenesis	RT	45	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	cellular structure morphogenesis	RT	45	6.1E-1	1.0E0

☐	**GOTERM_BP_ALL**	generation of neurons	RT		29	6.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	neurogenesis	RT		31	6.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular morphogenesis during differentiation	RT		17	6.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell projection morphogenesis	RT		24	7.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell projection organization and biogenesis	RT		24	7.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell part morphogenesis	RT		24	7.2E-1	1.0E0
	Annotation Cluster 204	Enrichment Score: 0.24	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	negative regulation of biosynthetic process	RT		5	5.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	negative regulation of translation	RT		4	5.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	negative regulation of cellular biosynthetic process	RT		4	5.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	negative regulation of protein metabolic process	RT		7	7.8E-1	1.0E0
	Annotation Cluster 205	Enrichment Score: 0.24	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	iron ion binding	RT		29	4.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	iron	RT		22	5.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	heme	RT		10	7.2E-1	1.0E0
	Annotation Cluster 206	Enrichment Score: 0.23	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of gene expression, epigenetic	RT		6	5.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	DNA methylation	RT		3	5.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	DNA alkylation	RT		3	5.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	DNA modification	RT		3	6.5E-1	1.0E0
	Annotation Cluster 207	Enrichment Score: 0.22	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	translation elongation factor activity	RT		5	2.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Elongation factor	RT		4	3.3E-1	9.7E-1
☐	**GOTERM_MF_ALL**	translation factor activity, nucleic acid binding	RT		11	6.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	translation regulator activity	RT		11	6.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	initiation factor	RT		5	8.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	translation initiation factor activity	RT		5	9.3E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	protein biosynthesis	RT		5	1.0E0	1.0E0
	Annotation Cluster 208	Enrichment Score: 0.22	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	nucleotide receptor activity, G-protein coupled	RT		9	1.8E-1	9.9E-1
☐	**GOTERM_MF_ALL**	nucleotide receptor activity	RT		9	1.9E-1	1.0E0
☐	**INTERPRO**	P2 purinoceptor	RT		3	4.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	g-protein coupled receptor	RT		28	8.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	transducer	RT		31	8.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	G-protein coupled receptor activity	RT		34	8.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	rhodopsin-like receptor activity	RT		27	8.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	transmembrane receptor activity	RT		60	9.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	G-protein coupled receptor protein signaling pathway	RT		47	9.2E-1	1.0E0
☐	**INTERPRO**	Rhodopsin-like GPCR superfamily	RT		14	9.9E-1	1.0E0
	Annotation Cluster 209	Enrichment Score: 0.21	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	tyrosine-specific phosphatase	RT		4	3.8E-1	9.8E-1
☐	**INTERPRO**	Protein-tyrosine phosphatase, receptor/non-receptor type	RT		5	4.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrolase activity, acting on ester bonds	RT		55	4.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	protein tyrosine phosphatase activity	RT		9	5.0E-1	1.0E0
☐	**SMART**	PTPc	RT		5	5.1E-1	9.9E-1
☐	**INTERPRO**	Protein-tyrosine phosphatase, Tyr-specific/dual-specificity type	RT		8	5.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	phosphoprotein phosphatase activity	RT		13	6.6E-1	1.0E0

☐	**SP_PIR_KEYWORDS**	protein phosphatase	RT		9	6.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	active site:Phosphocysteine intermediate	RT		5	7.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein amino acid dephosphorylation	RT		10	7.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	phosphoric monoester hydrolase activity	RT		19	7.5E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	phosphoric monoester hydrolase	RT		4	7.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	phosphoric ester hydrolase activity	RT		23	8.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	dephosphorylation	RT		10	8.6E-1	1.0E0
	Annotation Cluster 210	Enrichment Score: 0.21	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of translational initiation	RT		4	2.7E-1	9.7E-1
☐	**SP_PIR_KEYWORDS**	translation regulation	RT		4	4.5E-1	9.9E-1
☐	**GOTERM_BP_ALL**	translational initiation	RT		4	8.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein-RNA complex assembly	RT		6	8.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	ribonucleoprotein complex biogenesis and assembly	RT		6	1.0E0	1.0E0
	Annotation Cluster 211	Enrichment Score: 0.21	G	🟩	Count	P_Value	Benjamini
☐	**BIOCARTA**	TGF beta signaling pathway	RT		4	3.7E-1	1.0E0
☐	**KEGG_PATHWAY**	Adherens junction	RT		8	5.0E-1	9.0E-1
☐	**BIOCARTA**	WNT Signaling Pathway	RT		3	8.3E-1	1.0E0
☐	**KEGG_PATHWAY**	Cell cycle	RT		6	9.7E-1	1.0E0
	Annotation Cluster 212	Enrichment Score: 0.2	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	response to UV	RT		4	4.4E-1	9.9E-1
☐	**GOTERM_BP_ALL**	response to radiation	RT		10	4.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	nucleotide-excision repair	RT		3	6.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	response to light stimulus	RT		7	6.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	response to abiotic stimulus	RT		14	7.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	DNA repair	RT		8	9.3E-1	1.0E0
	Annotation Cluster 213	Enrichment Score: 0.2	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	aminotransferase	RT		3	5.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	transaminase activity	RT		4	6.2E-1	1.0E0
☐	**GOTERM_MF_ALL**	transferase activity, transferring nitrogenous groups	RT		4	6.8E-1	1.0E0
	Annotation Cluster 214	Enrichment Score: 0.2	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	sexual reproduction	RT		28	5.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	gamete generation	RT		23	5.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	spermatogenesis	RT		16	6.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	male gamete generation	RT		16	6.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	reproduction	RT		37	7.5E-1	1.0E0
	Annotation Cluster 215	Enrichment Score: 0.2	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Cyclin	RT		4	5.3E-1	1.0E0
☐	**INTERPRO**	Cyclin-related	RT		4	5.5E-1	1.0E0
☐	**SMART**	CYCLIN	RT		4	6.4E-1	1.0E0
☐	**INTERPRO**	Cyclin, N-terminal	RT		3	6.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	cyclin	RT		5	8.2E-1	1.0E0
	Annotation Cluster 216	Enrichment Score: 0.19	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	muscle system process	RT		9	5.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	muscle contraction	RT		9	5.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of muscle contraction	RT		3	8.2E-1	1.0E0
	Annotation Cluster 217	Enrichment Score: 0.18	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	carbohydrate transport	RT		8	4.1E-1	9.9E-1
☐	**GOTERM_BP_ALL**	glucose transport	RT		3	7.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	hexose transport	RT		3	7.8E-1	1.0E0

☐	GOTERM_BP_ALL	monosaccharide transport	RT		3	7.8E-1	1.0E0
	Annotation Cluster 218	Enrichment Score: 0.18	G		Count	P_Value	Benjamini
☐	INTERPRO	Ras small GTPase, Rab type	RT		8	2.3E-1	1.0E0
☐	SMART	RAB	RT		8	3.3E-1	9.6E-1
☐	PIR_SUPERFAMILY	PIRSF001710:Ras-related protein Rab	RT		7	4.3E-1	1.0E0
☐	UP_SEQ_FEATURE	lipid moiety-binding region:S-geranylgeranyl cysteine	RT		8	6.4E-1	1.0E0
☐	INTERPRO	Ras	RT		10	6.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	prenylation	RT		11	7.5E-1	1.0E0
☐	INTERPRO	Small GTP-binding protein domain	RT		11	8.0E-1	1.0E0
☐	GOTERM_MF_ALL	GTP binding	RT		25	8.3E-1	1.0E0
☐	GOTERM_MF_ALL	guanyl ribonucleotide binding	RT		25	8.5E-1	1.0E0
☐	GOTERM_MF_ALL	guanyl nucleotide binding	RT		25	8.5E-1	1.0E0
☐	UP_SEQ_FEATURE	short sequence motif:Effector region	RT		6	8.6E-1	1.0E0
☐	INTERPRO	Ras GTPase	RT		10	8.8E-1	1.0E0
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	RT		14	9.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	GTP-binding	RT		18	9.4E-1	1.0E0
	Annotation Cluster 219	Enrichment Score: 0.17	G		Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF036848:conserved protein with F-box/LRR-repeat, Skp2 type	RT		3	9.1E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:F-box	RT		7	2.5E-1	1.0E0
☐	SMART	FBOX	RT		8	3.7E-1	9.7E-1
☐	INTERPRO	Cyclin-like F-box	RT		7	4.0E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 3	RT		7	8.7E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 12	RT		3	8.7E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 1	RT		7	8.9E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 2	RT		7	8.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	leucine-rich repeat	RT		15	8.9E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 4	RT		6	8.9E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 11	RT		3	9.1E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 5	RT		5	9.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 10	RT		3	9.3E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 9	RT		3	9.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 8	RT		3	9.7E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 7	RT		3	9.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:LRR 6	RT		3	9.9E-1	1.0E0
	Annotation Cluster 220	Enrichment Score: 0.17	G		Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	sulfur amino acid metabolic process	RT		3	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	sulfur metabolic process	RT		7	7.1E-1	1.0E0
☐	GOTERM_BP_ALL	sulfur compound biosynthetic process	RT		3	9.0E-1	1.0E0
	Annotation Cluster 221	Enrichment Score: 0.16	G		Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	hexose biosynthetic process	RT		3	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	monosaccharide biosynthetic process	RT		3	7.1E-1	1.0E0
☐	GOTERM_BP_ALL	alcohol biosynthetic process	RT		3	7.1E-1	1.0E0
	Annotation Cluster 222	Enrichment Score: 0.16	G		Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	photoreceptor cell maintenance	RT		3	2.4E-1	9.7E-1
☐	GOTERM_BP_ALL	visual perception	RT		5	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	sensory perception of light stimulus	RT		5	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	sensory perception	RT		13	1.0E0	1.0E0
	Annotation Cluster 223	Enrichment Score: 0.16	G		Count	P_Value	Benjamini
☐	INTERPRO	Calcium-binding EF-hand	RT		16	6.1E-1	1.0E0

☐	INTERPRO	EF-Hand type	RT		15	6.2E-1	1.0E0
☐	UP_SEQ_FEATURE	calcium-binding region:2	RT		7	6.8E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:EF-hand 1	RT		9	7.2E-1	1.0E0
☐	UP_SEQ_FEATURE	calcium-binding region:1	RT		7	7.2E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:EF-hand 2	RT		9	7.3E-1	1.0E0
☐	SMART	EFh	RT		16	8.3E-1	1.0E0
	Annotation Cluster 224	Enrichment Score: 0.15	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	synapse	RT		22	4.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	synapse	RT		13	7.4E-1	1.0E0
☐	GOTERM_CC_ALL	cell junction	RT		30	7.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	cell junction	RT		18	9.5E-1	1.0E0
	Annotation Cluster 225	Enrichment Score: 0.15	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	DNA/RNA helicase, ATP-dependent, DEAH-box type	RT		4	3.9E-1	1.0E0
☐	INTERPRO	SNF2-related	RT		4	4.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	helicase	RT		11	4.8E-1	9.9E-1
☐	GOTERM_MF_ALL	helicase activity	RT		12	6.3E-1	1.0E0
☐	GOTERM_MF_ALL	ATP-dependent helicase activity	RT		8	7.8E-1	1.0E0
☐	INTERPRO	DNA/RNA helicase, C-terminal	RT		6	8.2E-1	1.0E0
☐	SMART	DEXDc	RT		8	8.3E-1	1.0E0
☐	SMART	HELICc	RT		7	8.3E-1	1.0E0
☐	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT		6	8.4E-1	1.0E0
☐	INTERPRO	DEAD-like helicase, N-terminal	RT		6	8.8E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Helicase C-terminal	RT		3	9.4E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Helicase ATP-binding	RT		3	9.5E-1	1.0E0
	Annotation Cluster 226	Enrichment Score: 0.15	G	🟩	Count	P_Value	Benjamini
☐	INTERPRO	Heat shock protein DnaJ, N-terminal	RT		5	4.7E-1	1.0E0
☐	GOTERM_MF_ALL	heat shock protein binding	RT		6	5.4E-1	1.0E0
☐	SMART	DnaJ	RT		5	6.1E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:J	RT		3	7.0E-1	1.0E0
☐	INTERPRO	Molecular chaperone, heat shock protein, Hsp40, DnaJ	RT		3	7.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	chaperone	RT		5	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	protein folding	RT		8	1.0E0	1.0E0
	Annotation Cluster 227	Enrichment Score: 0.15	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	plasma membrane part	RT		110	5.1E-1	1.0E0
☐	GOTERM_CC_ALL	integral to plasma membrane	RT		46	8.2E-1	1.0E0
☐	GOTERM_CC_ALL	intrinsic to plasma membrane	RT		47	8.4E-1	1.0E0
	Annotation Cluster 228	Enrichment Score: 0.15	G	🟩	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF000050:cytochrome P450 CYP4B1	RT		3	1.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	heme	RT		10	7.2E-1	1.0E0
☐	INTERPRO	Cytochrome P450	RT		6	7.6E-1	1.0E0
☐	INTERPRO	Cytochrome P450, E-class, group I	RT		5	8.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	monooxygenase	RT		6	9.2E-1	1.0E0
☐	GOTERM_MF_ALL	tetrapyrrole binding	RT		10	9.5E-1	1.0E0
☐	GOTERM_MF_ALL	heme binding	RT		10	9.5E-1	1.0E0
☐	GOTERM_MF_ALL	monooxygenase activity	RT		6	9.8E-1	1.0E0
	Annotation Cluster 229	Enrichment Score: 0.15	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	circulatory system process	RT		12	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	blood circulation	RT		12	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of blood vessel size	RT		4	7.6E-1	1.0E0

☐	GOTERM_BP_ALL	regulation of tube size	RT	▮		4	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	vascular process in circulatory system	RT	▮		4	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	heart process	RT	▮		4	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	heart contraction	RT	▮		4	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of blood pressure	RT	▮		4	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of heart contraction	RT	▮		3	8.9E-1	1.0E0
	Annotation Cluster 230	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Sterile alpha motif homology 2	RT	▮		4	5.3E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:SAM	RT	▮		4	6.3E-1	1.0E0
☐	INTERPRO	Sterile alpha motif SAM	RT	▮		6	7.7E-1	1.0E0
☐	SMART	SAM	RT	▮		6	8.5E-1	1.0E0
☐	INTERPRO	Sterile alpha motif-type	RT	▮		4	9.0E-1	1.0E0
	Annotation Cluster 231	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	glutathione transferase activity	RT	▮		3	6.0E-1	1.0E0
☐	KEGG_PATHWAY	Glutathione metabolism	RT	▮		4	6.6E-1	9.6E-1
☐	GOTERM_MF_ALL	transferase activity, transferring alkyl or aryl (other than methyl) groups	RT	▮		5	7.3E-1	1.0E0
☐	KEGG_PATHWAY	Metabolism of xenobiotics by cytochrome P450	RT	▮		4	9.4E-1	1.0E0
	Annotation Cluster 232	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Fructose and mannose metabolism	RT	▮		6	3.6E-1	8.7E-1
☐	GOTERM_BP_ALL	glucose metabolic process	RT	▮		12	3.7E-1	9.9E-1
☐	GOTERM_BP_ALL	carbohydrate catabolic process	RT	▮		7	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	cellular carbohydrate catabolic process	RT	▮		6	8.1E-1	1.0E0
☐	GOTERM_BP_ALL	glycolysis	RT	▮		4	8.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	glycolysis	RT	▮		3	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	glucose catabolic process	RT	▮		4	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	monosaccharide catabolic process	RT	▮		4	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	hexose catabolic process	RT	▮		4	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	alcohol catabolic process	RT	▮		4	9.3E-1	1.0E0
	Annotation Cluster 233	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	actin polymerization and/or depolymerization	RT	▮		6	4.3E-1	9.9E-1
☐	GOTERM_BP_ALL	regulation of cellular component organization and biogenesis	RT	▮		7	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of actin filament depolymerization	RT	▮		3	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	actin filament capping	RT	▮		3	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	actin filament depolymerization	RT	▮		3	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of actin filament depolymerization	RT	▮		3	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cellular component size	RT	▮		4	7.1E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of protein metabolic process	RT	▮		7	7.8E-1	1.0E0
☐	GOTERM_BP_ALL	protein depolymerization	RT	▮		3	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of actin polymerization and/or depolymerization	RT	▮		3	8.7E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of cellular component organization and biogenesis	RT	▮		3	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of actin cytoskeleton organization and biogenesis	RT	▮		3	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of actin filament length	RT	▮		3	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cytoskeleton organization and biogenesis	RT	▮		3	9.1E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of organelle organization and biogenesis	RT	▮		3	9.1E-1	1.0E0
	Annotation Cluster 234	Enrichment Score: 0.13	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	amino sugar metabolic process	RT	▮		4	4.6E-1	9.9E-1

☐	**GOTERM_BP_ALL**	cellular polysaccharide metabolic process	RT	▮		3	9.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	polysaccharide metabolic process	RT	▮		3	9.5E-1	1.0E0
	Annotation Cluster 235	Enrichment Score: 0.13	G		🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	phosphatidylinositol linkage	RT	▮		3	3.0E-1	9.7E-1
☐	**UP_SEQ_FEATURE**	lipid moiety-binding region:GPI-anchor amidated serine	RT	▮		3	9.1E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	gpi-anchor	RT	▮		7	9.2E-1	1.0E0
☐	**GOTERM_MF_ALL**	GPI anchor binding	RT	▮		7	9.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	propeptide:Removed in mature form	RT	▮		8	9.8E-1	1.0E0
	Annotation Cluster 236	Enrichment Score: 0.12	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	neural tube development	RT	▮		6	4.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	neural tube formation	RT	▮		4	7.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	neural plate morphogenesis	RT	▮		4	7.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	neural plate development	RT	▮		4	7.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	embryonic epithelial tube formation	RT	▮		4	7.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	neural tube closure	RT	▮		3	7.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	primary neural tube formation	RT	▮		3	8.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	morphogenesis of embryonic epithelium	RT	▮		4	9.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	morphogenesis of an epithelium	RT	▮		7	9.4E-1	1.0E0
	Annotation Cluster 237	Enrichment Score: 0.12	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	secondary metabolic process	RT	▮		5	6.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	pigment biosynthetic process	RT	▮		3	7.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	pigment metabolic process	RT	▮		3	8.4E-1	1.0E0
	Annotation Cluster 238	Enrichment Score: 0.12	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	mitochondrial outer membrane	RT	▮		3	7.1E-1	1.0E0
☐	**GOTERM_CC_ALL**	organelle outer membrane	RT	▮		3	7.6E-1	1.0E0
☐	**GOTERM_CC_ALL**	outer membrane	RT	▮		6	8.1E-1	1.0E0
	Annotation Cluster 239	Enrichment Score: 0.12	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	sugar binding	RT	▮		17	6.3E-1	1.0E0
☐	**INTERPRO**	Type II antifreeze protein	RT	▮		4	6.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	lectin	RT	▮		13	7.0E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:C-type lectin	RT	▮		4	8.7E-1	1.0E0
☐	**INTERPRO**	C-type lectin	RT	▮		8	8.8E-1	1.0E0
☐	**SMART**	CLECT	RT	▮		9	8.9E-1	1.0E0
	Annotation Cluster 240	Enrichment Score: 0.12	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	RT	▮		45	7.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrolase activity, acting on acid anhydrides	RT	▮		45	7.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	pyrophosphatase activity	RT	▮		44	7.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	nucleoside-triphosphatase activity	RT	▮		42	7.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	ATPase activity	RT	▮		24	8.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	ATPase activity, coupled	RT	▮		20	8.5E-1	1.0E0
	Annotation Cluster 241	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	response to bacterium	RT	▮		8	6.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	antimicrobial	RT	▮		4	7.5E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	antibiotic	RT	▮		3	8.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	defense response to bacterium	RT	▮		4	9.2E-1	1.0E0
	Annotation Cluster 242	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Nucleotide-binding, alpha-beta plait	RT	▮		14	6.1E-1	1.0E0
☐	**INTERPRO**	RNA recognition motif, RNP-1	RT	▮		14	6.2E-1	1.0E0
☐	**SMART**	RRM	RT	▮		16	7.8E-1	1.0E0

☐	SP_PIR_KEYWORDS	rna-binding	RT		25	9.6E-1	1.0E0
☐	GOTERM_MF_ALL	RNA binding	RT		34	1.0E0	1.0E0
	Annotation Cluster 243	Enrichment Score: 0.1	G	🟩	Count	P_Value	Benjamini
☐	KEGG_PATHWAY	Long-term potentiation	RT		6	7.3E-1	9.7E-1
☐	KEGG_PATHWAY	Melanogenesis	RT		8	7.9E-1	9.8E-1
☐	KEGG_PATHWAY	Wnt signaling pathway	RT		11	8.4E-1	9.9E-1
	Annotation Cluster 244	Enrichment Score: 0.1	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	kinesin complex	RT		5	3.0E-1	1.0E0
☐	GOTERM_MF_ALL	microtubule motor activity	RT		6	7.5E-1	1.0E0
☐	INTERPRO	Kinesin, motor region	RT		3	8.4E-1	1.0E0
☐	GOTERM_CC_ALL	microtubule associated complex	RT		7	8.7E-1	1.0E0
☐	SMART	KISc	RT		3	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	cytoskeleton-dependent intracellular transport	RT		8	9.0E-1	1.0E0
☐	GOTERM_MF_ALL	motor activity	RT		8	9.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	motor protein	RT		3	1.0E0	1.0E0
☐	GOTERM_BP_ALL	microtubule-based movement	RT		3	1.0E0	1.0E0
	Annotation Cluster 245	Enrichment Score: 0.1	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	transition metal ion transport	RT		6	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	di-, tri-valent inorganic cation transport	RT		10	8.9E-1	1.0E0
☐	GOTERM_BP_ALL	metal ion transport	RT		18	1.0E0	1.0E0
	Annotation Cluster 246	Enrichment Score: 0.09	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell recognition	RT		5	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	single fertilization	RT		3	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	fertilization	RT		3	9.6E-1	1.0E0
	Annotation Cluster 247	Enrichment Score: 0.09	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	macromolecule biosynthetic process	RT		59	6.4E-1	1.0E0
☐	GOTERM_BP_ALL	biosynthetic process	RT		105	7.1E-1	1.0E0
☐	GOTERM_BP_ALL	translation	RT		29	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	cellular biosynthetic process	RT		65	9.8E-1	1.0E0
	Annotation Cluster 248	Enrichment Score: 0.09	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	vesicle membrane	RT		7	7.5E-1	1.0E0
☐	GOTERM_CC_ALL	cytoplasmic vesicle part	RT		6	7.8E-1	1.0E0
☐	GOTERM_CC_ALL	cytoplasmic vesicle membrane	RT		4	9.3E-1	1.0E0
	Annotation Cluster 249	Enrichment Score: 0.09	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	disulfide bond	RT		139	5.1E-1	1.0E0
☐	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		188	6.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	glycoprotein	RT		242	6.1E-1	1.0E0
☐	UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT		138	8.8E-1	1.0E0
☐	UP_SEQ_FEATURE	transmembrane region	RT		181	9.0E-1	1.0E0
☐	UP_SEQ_FEATURE	signal peptide	RT		156	9.4E-1	1.0E0
☐	GOTERM_CC_ALL	extracellular space	RT		154	9.7E-1	1.0E0
☐	GOTERM_CC_ALL	extracellular region part	RT		159	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	signal	RT		180	9.9E-1	1.0E0
☐	GOTERM_CC_ALL	extracellular region	RT		163	1.0E0	1.0E0
	Annotation Cluster 250	Enrichment Score: 0.09	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	neural tube development	RT		6	4.9E-1	1.0E0
☐	GOTERM_BP_ALL	embryonic development ending in birth or egg hatching	RT		14	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	chordate embryonic development	RT		13	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	in utero embryonic development	RT		5	1.0E0	1.0E0

	Annotation Cluster 251	Enrichment Score: 0.09	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	interphase of mitotic cell cycle	RT	6	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	interphase	RT	6	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	M phase of meiotic cell cycle	RT	7	6.6E-1	1.0E0
☐	GOTERM_BP_ALL	meiosis	RT	7	6.6E-1	1.0E0
☐	GOTERM_BP_ALL	meiotic cell cycle	RT	7	6.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	Meiosis	RT	3	7.3E-1	1.0E0
☐	GOTERM_BP_ALL	G1/S transition of mitotic cell cycle	RT	3	7.4E-1	1.0E0
☐	GOTERM_BP_ALL	cell cycle phase	RT	17	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	M phase	RT	13	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	mitotic cell cycle	RT	12	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	cell division	RT	8	1.0E0	1.0E0
☐	GOTERM_BP_ALL	cell division	RT	11	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	mitosis	RT	4	1.0E0	1.0E0
☐	GOTERM_BP_ALL	mitosis	RT	7	1.0E0	1.0E0
☐	GOTERM_BP_ALL	M phase of mitotic cell cycle	RT	7	1.0E0	1.0E0
	Annotation Cluster 252	Enrichment Score: 0.09	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	pyridine nucleotide metabolic process	RT	3	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	vitamin metabolic process	RT	5	8.9E-1	1.0E0
☐	GOTERM_BP_ALL	water-soluble vitamin metabolic process	RT	3	9.3E-1	1.0E0
	Annotation Cluster 253	Enrichment Score: 0.08	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	hormone biosynthetic process	RT	4	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	hormone metabolic process	RT	6	8.9E-1	1.0E0
☐	GOTERM_BP_ALL	steroid biosynthetic process	RT	4	9.6E-1	1.0E0
	Annotation Cluster 254	Enrichment Score: 0.08	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	vesicular fraction	RT	13	7.4E-1	1.0E0
☐	GOTERM_CC_ALL	microsome	RT	12	7.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	microsome	RT	5	9.7E-1	1.0E0
	Annotation Cluster 255	Enrichment Score: 0.08	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	repeat:4	RT	6	7.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:5	RT	5	7.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:7	RT	4	7.8E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:3	RT	7	7.9E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:6	RT	4	8.4E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:8	RT	3	8.6E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:1	RT	7	9.2E-1	1.0E0
☐	UP_SEQ_FEATURE	repeat:2	RT	7	9.3E-1	1.0E0
	Annotation Cluster 256	Enrichment Score: 0.08	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	viral nucleoprotein	RT	4	5.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	ribonucleoprotein	RT	5	1.0E0	1.0E0
☐	GOTERM_CC_ALL	ribonucleoprotein complex	RT	10	1.0E0	1.0E0
	Annotation Cluster 257	Enrichment Score: 0.08	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:EGF-like 1	RT	8	3.8E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:EGF-like 2	RT	6	4.5E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:EGF-like 3	RT	4	7.6E-1	1.0E0
☐	INTERPRO	Aspartic acid and asparagine hydroxylation site	RT	5	9.4E-1	1.0E0
☐	INTERPRO	EGF-like calcium-binding	RT	5	9.5E-1	1.0E0
☐	INTERPRO	EGF	RT	11	9.6E-1	1.0E0
☐	INTERPRO	EGF-like	RT	7	9.6E-1	1.0E0
☐	INTERPRO	EGF-like, type 3	RT	10	9.7E-1	1.0E0

☐	**INTERPRO**	EGF calcium-binding	RT	▮		3	9.7E-1	1.0E0
☐	**INTERPRO**	EGF-like region	RT	▮		14	9.8E-1	1.0E0
☐	**SMART**	EGF_CA	RT	▮		5	9.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	egf-like domain	RT	▮		11	9.8E-1	1.0E0
☐	**SMART**	EGF	RT	▮		11	9.8E-1	1.0E0
	Annotation Cluster 258	Enrichment Score: 0.08	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	inorganic anion transmembrane transporter activity	RT	▮		4	5.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	anion transmembrane transporter activity	RT	▮		6	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	anion transport	RT	▮		7	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	inorganic anion transport	RT	▮		5	1.0E0	1.0E0
	Annotation Cluster 259	Enrichment Score: 0.08	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	nucleotide metabolic process	RT	▮		21	3.3E-1	9.8E-1
☐	**GOTERM_BP_ALL**	nucleobase, nucleoside and nucleotide metabolic process	RT	▮		22	3.4E-1	9.8E-1
☐	**GOTERM_BP_ALL**	nucleoside triphosphate metabolic process	RT	▮		7	6.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	purine ribonucleoside triphosphate metabolic process	RT	▮		5	7.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	purine nucleoside triphosphate metabolic process	RT	▮		5	8.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	ribonucleoside triphosphate metabolic process	RT	▮		5	8.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	purine ribonucleotide metabolic process	RT	▮		6	8.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	ATP metabolic process	RT	▮		4	8.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	purine ribonucleotide biosynthetic process	RT	▮		5	8.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	purine ribonucleoside triphosphate biosynthetic process	RT	▮		4	8.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	purine nucleoside triphosphate biosynthetic process	RT	▮		4	8.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	ribonucleotide metabolic process	RT	▮		6	8.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	ribonucleoside triphosphate biosynthetic process	RT	▮		4	8.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	purine nucleotide metabolic process	RT	▮		6	9.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	ribonucleotide biosynthetic process	RT	▮		5	9.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	nucleoside triphosphate biosynthetic process	RT	▮		4	9.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrogen ion transporting ATP synthase activity, rotational mechanism	RT	▮		3	9.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrogen ion transporting ATPase activity, rotational mechanism	RT	▮		3	9.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	nucleoside phosphate metabolic process	RT	▮		3	9.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	ATP biosynthetic process	RT	▮		3	9.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	purine nucleotide biosynthetic process	RT	▮		5	9.2E-1	1.0E0
☐	**GOTERM_CC_ALL**	proton-transporting two-sector ATPase complex	RT	▮		3	9.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	nucleotide biosynthetic process	RT	▮		9	9.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrogen ion transmembrane transporter activity	RT	▮		6	9.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	cation-transporting ATPase activity	RT	▮		3	9.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	monovalent inorganic cation transmembrane transporter activity	RT	▮		6	9.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	ATPase activity, coupled to transmembrane movement of ions	RT	▮		5	9.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	inorganic cation transmembrane transporter activity	RT	▮		8	9.7E-1	1.0E0
☐	**KEGG_PATHWAY**	Oxidative phosphorylation	RT	▮		6	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	proton transport	RT	▮		3	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	hydrogen transport	RT	▮		3	9.9E-1	1.0E0
	Annotation Cluster 260	Enrichment Score: 0.07	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	immune response-activating cell surface	RT	▮		3	8.0E-1	1.0E0

☐		receptor signaling pathway				
☐	GOTERM_BP_ALL	immune response-regulating cell surface receptor signaling pathway	RT	3	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	immune response-activating signal transduction	RT	3	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	immune response-regulating signal transduction	RT	3	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	activation of immune response	RT	5	9.1E-1	1.0E0
	Annotation Cluster 261	Enrichment Score: 0.07		Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	damaged DNA binding	RT	3	5.7E-1	1.0E0
☐	GOTERM_BP_ALL	response to endogenous stimulus	RT	21	8.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	DNA damage	RT	9	9.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	DNA repair	RT	8	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	response to DNA damage stimulus	RT	17	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	DNA repair	RT	11	9.8E-1	1.0E0
	Annotation Cluster 262	Enrichment Score: 0.07		Count	P_Value	Benjamini
☐	INTERPRO	Sulphotransferase	RT	3	7.4E-1	1.0E0
☐	GOTERM_MF_ALL	sulfotransferase activity	RT	3	8.9E-1	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring sulfur-containing groups	RT	3	9.5E-1	1.0E0
	Annotation Cluster 263	Enrichment Score: 0.06		Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT	188	6.0E-1	1.0E0
☐	GOTERM_CC_ALL	membrane part	RT	386	7.8E-1	1.0E0
☐	UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT	138	8.8E-1	1.0E0
☐	GOTERM_CC_ALL	integral to membrane	RT	334	9.0E-1	1.0E0
☐	UP_SEQ_FEATURE	transmembrane region	RT	181	9.0E-1	1.0E0
☐	GOTERM_CC_ALL	intrinsic to membrane	RT	335	9.1E-1	1.0E0
☐	GOTERM_CC_ALL	membrane	RT	478	9.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	membrane	RT	336	9.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	transmembrane	RT	260	9.4E-1	1.0E0
☐	UP_SEQ_FEATURE	topological domain:Extracellular	RT	100	9.5E-1	1.0E0
	Annotation Cluster 264	Enrichment Score: 0.06		Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell adhesion	RT	53	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	biological adhesion	RT	53	8.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	cell adhesion	RT	21	9.8E-1	1.0E0
	Annotation Cluster 265	Enrichment Score: 0.05		Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	embryonic limb morphogenesis	RT	5	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	embryonic appendage morphogenesis	RT	5	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	appendage morphogenesis	RT	5	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	limb morphogenesis	RT	5	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	appendage development	RT	5	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	limb development	RT	5	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	embryonic morphogenesis	RT	13	9.1E-1	1.0E0
	Annotation Cluster 266	Enrichment Score: 0.05		Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein localization	RT	64	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	protein transport	RT	55	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	establishment of protein localization	RT	57	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	macromolecule localization	RT	64	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	intracellular protein transport	RT	32	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	intracellular transport	RT	51	9.1E-1	1.0E0
☐	GOTERM_BP_ALL	establishment of cellular localization	RT	60	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	cellular localization	RT	60	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	protein transport	RT	22	9.9E-1	1.0E0

	Annotation Cluster 267	Enrichment Score: 0.05	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	High mobility group box, HMG1/HMG2	RT	4	8.4E-1	1.0E0
☐	SMART	HMG	RT	4	9.1E-1	1.0E0
☐	INTERPRO	High mobility group box, HMG	RT	3	9.3E-1	1.0E0
	Annotation Cluster 268	Enrichment Score: 0.05	G 🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	microtubule	RT	11	8.1E-1	1.0E0
☐	GOTERM_BP_ALL	microtubule-based process	RT	14	8.8E-1	1.0E0
☐	GOTERM_CC_ALL	microtubule	RT	13	9.0E-1	1.0E0
☐	GOTERM_CC_ALL	microtubule cytoskeleton	RT	22	9.0E-1	1.0E0
☐	GOTERM_CC_ALL	cytoskeletal part	RT	28	1.0E0	1.0E0
	Annotation Cluster 269	Enrichment Score: 0.05	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	Golgi vesicle transport	RT	7	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	ER to Golgi vesicle-mediated transport	RT	3	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	er-golgi transport	RT	3	9.7E-1	1.0E0
	Annotation Cluster 270	Enrichment Score: 0.04	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	extracellular matrix	RT	21	8.8E-1	1.0E0
☐	GOTERM_CC_ALL	proteinaceous extracellular matrix	RT	20	9.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	extracellular matrix	RT	13	9.3E-1	1.0E0
	Annotation Cluster 271	Enrichment Score: 0.04	G 🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	oxidoreductase	RT	39	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	electron transport	RT	30	8.8E-1	1.0E0
☐	GOTERM_MF_ALL	oxidoreductase activity	RT	65	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	generation of precursor metabolites and energy	RT	32	9.9E-1	1.0E0
	Annotation Cluster 272	Enrichment Score: 0.04	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	eye morphogenesis	RT	4	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	eye development	RT	6	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	sensory organ development	RT	10	9.8E-1	1.0E0
	Annotation Cluster 273	Enrichment Score: 0.04	G 🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	Golgi vesicle transport	RT	7	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	secretory pathway	RT	14	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	secretion by cell	RT	17	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	secretion	RT	20	9.8E-1	1.0E0
	Annotation Cluster 274	Enrichment Score: 0.04	G 🟩	Count	P_Value	Benjamini
☐	INTERPRO	Fibronectin, type III-like fold	RT	13	8.0E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Fibronectin type-III 3	RT	3	8.9E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Fibronectin type-III 1	RT	4	9.6E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Fibronectin type-III 2	RT	4	9.6E-1	1.0E0
☐	INTERPRO	Fibronectin, type III	RT	10	9.6E-1	1.0E0
☐	SMART	FN3	RT	11	9.8E-1	1.0E0
	Annotation Cluster 275	Enrichment Score: 0.04	G 🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	lipid degradation	RT	5	7.9E-1	1.0E0
☐	GOTERM_MF_ALL	phospholipase activity	RT	3	9.5E-1	1.0E0
☐	GOTERM_MF_ALL	lipase activity	RT	4	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	lipid catabolic process	RT	6	9.6E-1	1.0E0
☐	GOTERM_MF_ALL	carboxylesterase activity	RT	6	9.6E-1	1.0E0
	Annotation Cluster 276	Enrichment Score: 0.03	G 🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	site:Reactive bond	RT	3	7.7E-1	1.0E0
☐	PIR_SUPERFAMILY	PIRSF001630:serpin	RT	3	8.9E-1	1.0E0
☐	INTERPRO	Protease inhibitor I4, serpin	RT	3	9.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	protease inhibitor	RT	4	9.7E-1	1.0E0

☐	**SMART**	SERPIN	RT	▮		3	9.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Serine protease inhibitor	RT	▮		3	9.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	serine-type endopeptidase inhibitor activity	RT	▮		5	9.8E-1	1.0E0
	Annotation Cluster 277	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	endopeptidase inhibitor activity	RT	▮		10	8.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	protease inhibitor activity	RT	▮		10	9.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	enzyme inhibitor activity	RT	▮		15	9.1E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	protease inhibitor	RT	▮		4	9.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	serine-type endopeptidase inhibitor activity	RT	▮		5	9.8E-1	1.0E0
	Annotation Cluster 278	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of anatomical structure morphogenesis	RT	▮		3	9.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cell shape	RT	▮		3	9.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cell morphogenesis	RT	▮		3	9.4E-1	1.0E0
	Annotation Cluster 279	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 1	RT	▮		9	8.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 2	RT	▮		8	9.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 4	RT	▮		5	9.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:C2H2-type 3	RT	▮		6	9.9E-1	1.0E0
	Annotation Cluster 280	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	inner ear development	RT	▮		4	9.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	inner ear morphogenesis	RT	▮		3	9.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	ear development	RT	▮		4	9.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	ear morphogenesis	RT	▮		3	9.6E-1	1.0E0
	Annotation Cluster 281	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	synapse part	RT	▮		8	8.9E-1	1.0E0
☐	**GOTERM_CC_ALL**	postsynaptic membrane	RT	▮		5	9.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Postsynaptic cell membrane	RT	▮		4	9.9E-1	1.0E0
	Annotation Cluster 282	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	intrinsic to endoplasmic reticulum membrane	RT	▮		3	8.5E-1	1.0E0
☐	**GOTERM_CC_ALL**	endoplasmic reticulum part	RT	▮		6	9.7E-1	1.0E0
☐	**GOTERM_CC_ALL**	endoplasmic reticulum membrane	RT	▮		5	9.8E-1	1.0E0
☐	**GOTERM_CC_ALL**	nuclear envelope-endoplasmic reticulum network	RT	▮		5	9.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	RT	▮		6	9.9E-1	1.0E0
	Annotation Cluster 283	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	neuropeptide Y receptor activity	RT	▮		3	8.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	neuropeptide binding	RT	▮		3	9.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	neuropeptide receptor activity	RT	▮		3	9.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	neurotransmitter receptor activity	RT	▮		3	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	neurotransmitter binding	RT	▮		3	1.0E0	1.0E0
	Annotation Cluster 284	Enrichment Score: 0.02	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	transcription factor complex	RT	▮		33	8.5E-1	1.0E0
☐	**GOTERM_CC_ALL**	nucleoplasm	RT	▮		42	9.6E-1	1.0E0
☐	**GOTERM_CC_ALL**	nucleoplasm part	RT	▮		39	9.6E-1	1.0E0
☐	**GOTERM_CC_ALL**	nuclear lumen	RT	▮		46	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	organelle lumen	RT	▮		50	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	membrane-enclosed lumen	RT	▮		50	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	nuclear part	RT	▮		61	1.0E0	1.0E0
	Annotation Cluster 285	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini

☐	**UP_SEQ_FEATURE**	transit peptide:Mitochondrion	RT	▮		17	9.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	transit peptide	RT	▮		24	9.6E-1	1.0E0
☐	**GOTERM_CC_ALL**	mitochondrion	RT	▮		64	9.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Mitochondrion	RT	▮		39	9.9E-1	1.0E0
	Annotation Cluster 286	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	nuclear mRNA splicing, via spliceosome	RT	▮		3	9.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	RT	▮		3	9.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	RNA splicing, via transesterification reactions	RT	▮		3	9.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	RNA splicing	RT	▮		6	1.0E0	1.0E0
	Annotation Cluster 287	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	tRNA aminoacylation	RT	▮		3	9.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	amino acid activation	RT	▮		3	9.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	tRNA aminoacylation for protein translation	RT	▮		3	9.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	ligase activity, forming aminoacyl-tRNA and related compounds	RT	▮		3	9.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	aminoacyl-tRNA ligase activity	RT	▮		3	9.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	ligase activity, forming carbon-oxygen bonds	RT	▮		3	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	tRNA metabolic process	RT	▮		4	1.0E0	1.0E0
	Annotation Cluster 288	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Zinc finger, LIM-type	RT	▮		3	9.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	lim domain	RT	▮		3	9.8E-1	1.0E0
☐	**SMART**	LIM	RT	▮		3	9.9E-1	1.0E0
	Annotation Cluster 289	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	organelle membrane	RT	▮		45	9.3E-1	1.0E0
☐	**GOTERM_CC_ALL**	mitochondrial envelope	RT	▮		18	9.7E-1	1.0E0
☐	**GOTERM_CC_ALL**	mitochondrial membrane	RT	▮		16	9.8E-1	1.0E0
☐	**GOTERM_CC_ALL**	mitochondrial part	RT	▮		20	9.9E-1	1.0E0
☐	**GOTERM_CC_ALL**	mitochondrial inner membrane	RT	▮		13	9.9E-1	1.0E0
☐	**GOTERM_CC_ALL**	organelle inner membrane	RT	▮		13	9.9E-1	1.0E0
☐	**GOTERM_CC_ALL**	organelle envelope	RT	▮		23	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	envelope	RT	▮		23	1.0E0	1.0E0
	Annotation Cluster 290	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	active transmembrane transporter activity	RT	▮		26	8.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	ion transport	RT	▮		21	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	metal ion transport	RT	▮		18	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	cation transport	RT	▮		23	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	substrate-specific transporter activity	RT	▮		53	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	monovalent inorganic cation transport	RT	▮		11	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	cation transmembrane transporter activity	RT	▮		20	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	ion transmembrane transporter activity	RT	▮		28	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	substrate-specific transmembrane transporter activity	RT	▮		35	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	transmembrane transporter activity	RT	▮		41	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	transporter activity	RT	▮		69	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	ion transport	RT	▮		32	1.0E0	1.0E0
	Annotation Cluster 291	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	active site:Charge relay system	RT	▮		7	9.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	serine-type peptidase activity	RT	▮		11	9.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	serine hydrolase activity	RT	▮		11	9.9E-1	1.0E0

☐	**INTERPRO**	Peptidase S1A, chymotrypsin	RT		5	9.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	serine protease	RT		6	9.9E-1	1.0E0
☐	**INTERPRO**	Peptidase S1 and S6, chymotrypsin/Hap	RT		5	9.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	serine-type endopeptidase activity	RT		9	9.9E-1	1.0E0
☐	**SMART**	Tryp_SPc	RT		5	1.0E0	1.0E0
	Annotation Cluster 292	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	potassium	RT		5	9.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	potassium ion binding	RT		5	9.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	potassium transport	RT		3	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	potassium ion transport	RT		6	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	alkali metal ion binding	RT		7	1.0E0	1.0E0
	Annotation Cluster 293	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	transmission of nerve impulse	RT		15	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	synaptic transmission	RT		11	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell-cell signaling	RT		20	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	neurological system process	RT		30	1.0E0	1.0E0
	Annotation Cluster 294	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	sodium	RT		3	9.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	sodium transport	RT		3	9.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	sodium ion binding	RT		3	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	sodium ion transport	RT		4	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	alkali metal ion binding	RT		7	1.0E0	1.0E0
	Annotation Cluster 295	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	voltage-gated potassium channel complex	RT		3	9.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	ligand-gated channel activity	RT		4	9.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	ligand-gated ion channel activity	RT		4	9.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	voltage-gated potassium channel activity	RT		3	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	potassium ion transport	RT		6	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	voltage-gated ion channel activity	RT		5	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	voltage-gated channel activity	RT		5	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	voltage-gated cation channel activity	RT		3	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	voltage-gated channel	RT		3	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	potassium channel activity	RT		3	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	gated channel activity	RT		9	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	cation channel activity	RT		7	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	metal ion transmembrane transporter activity	RT		9	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	Ionic channel	RT		7	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	ion channel activity	RT		9	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	substrate specific channel activity	RT		9	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	passive transmembrane transporter activity	RT		9	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	channel activity	RT		9	1.0E0	1.0E0
	Annotation Cluster 296	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	non-membrane-bound organelle	RT		99	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	intracellular non-membrane-bound organelle	RT		99	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	organelle part	RT		160	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	intracellular organelle part	RT		159	1.0E0	1.0E0
	Annotation Cluster 297	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	mRNA metabolic process	RT		12	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	mRNA processing	RT		10	1.0E0	1.0E0

☐	**GOTERM_BP_ALL**	RNA splicing	RT		6	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	RNA processing	RT		13	1.0E0	1.0E0
	Annotation Cluster 298	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Homeobox	RT		7	1.0E0	1.0E0
☐	**UP_SEQ_FEATURE**	DNA-binding region:Homeobox	RT		4	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	Homeobox	RT		8	1.0E0	1.0E0
☐	**INTERPRO**	Homeodomain-related	RT		5	1.0E0	1.0E0
☐	**SMART**	HOX	RT		7	1.0E0	1.0E0
	Annotation Cluster 299	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	localization	RT		206	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	transport	RT		77	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	transport	RT		168	1.0E0	1.0E0
☐	**GOTERM_BP_ALL**	establishment of localization	RT		171	1.0E0	1.0E0
☐	**GOTERM_MF_ALL**	transporter activity	RT		69	1.0E0	1.0E0
	Annotation Cluster 300	Enrichment Score: 0	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	RNA splicing	RT		6	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	mrna splicing	RT		3	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	mrna processing	RT		3	1.0E0	1.0E0

650 terms were not clustered.

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377 DAVID IDs

Options **Classification Stringency** Medium

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	Annotation Cluster 1	Enrichment Score: 5	G		Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	nucleus	RT		123	2.9E-13	2.3E-10
☐	GOTERM_CC_ALL	intracellular membrane-bound organelle	RT		157	4.1E-10	1.6E-7
☐	GOTERM_CC_ALL	membrane-bound organelle	RT		157	4.5E-10	1.2E-7
☐	GOTERM_CC_ALL	intracellular organelle	RT		168	2.3E-9	4.4E-7
☐	GOTERM_CC_ALL	organelle	RT		168	2.5E-9	3.8E-7
☐	SP_PIR_KEYWORDS	nucleus	RT		91	2.6E-8	2.2E-5
☐	GOTERM_CC_ALL	intracellular	RT		193	3.4E-8	4.4E-6
☐	GOTERM_CC_ALL	intracellular part	RT		185	9.4E-8	1.0E-5
☐	GOTERM_BP_ALL	transcription	RT		72	3.4E-7	5.9E-4
☐	GOTERM_BP_ALL	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		70	9.2E-7	1.2E-3
☐	GOTERM_BP_ALL	regulation of transcription	RT		69	1.0E-6	1.0E-3
☐	GOTERM_BP_ALL	RNA biosynthetic process	RT		67	1.3E-6	1.1E-3
☐	GOTERM_BP_ALL	regulation of gene expression	RT		71	2.5E-6	1.8E-3
☐	GOTERM_BP_ALL	transcription, DNA-dependent	RT		66	2.6E-6	1.7E-3
☐	GOTERM_BP_ALL	regulation of transcription, DNA-dependent	RT		65	3.7E-6	2.1E-3
☐	GOTERM_BP_ALL	regulation of cellular metabolic process	RT		72	5.3E-6	2.5E-3
☐	SP_PIR_KEYWORDS	Transcription	RT		45	6.4E-6	2.8E-3
☐	GOTERM_BP_ALL	RNA metabolic process	RT		74	6.5E-6	2.6E-3
☐	GOTERM_BP_ALL	regulation of cellular process	RT		96	1.2E-5	4.3E-3
☐	GOTERM_BP_ALL	regulation of metabolic process	RT		73	1.2E-5	4.0E-3
☐	GOTERM_MF_ALL	nucleic acid binding	RT		82	1.9E-5	4.9E-2
☐	GOTERM_BP_ALL	biopolymer metabolic process	RT		110	2.0E-5	6.6E-3
☐	GOTERM_BP_ALL	gene expression	RT		82	2.1E-5	6.4E-3
☐	SP_PIR_KEYWORDS	Transcription regulation	RT		43	2.1E-5	6.1E-3
☐	GOTERM_BP_ALL	regulation of biological process	RT		102	2.4E-5	6.9E-3
☐	SP_PIR_KEYWORDS	repressor	RT		17	4.2E-5	9.0E-3
☐	GOTERM_BP_ALL	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		86	4.6E-5	1.1E-2
☐	GOTERM_BP_ALL	cellular metabolic process	RT		149	7.4E-5	1.7E-2
☐	GOTERM_BP_ALL	metabolic process	RT		161	9.3E-5	2.1E-2
☐	GOTERM_MF_ALL	DNA binding	RT		56	1.4E-4	7.2E-2
☐	GOTERM_BP_ALL	biological regulation	RT		105	2.6E-4	4.3E-2
☐	GOTERM_BP_ALL	macromolecule metabolic process	RT		130	6.0E-4	9.2E-2
☐	GOTERM_BP_ALL	primary metabolic process	RT		145	6.5E-4	9.6E-2
☐	GOTERM_BP_ALL	cellular process	RT		201	1.9E-3	2.4E-1
☐	SP_PIR_KEYWORDS	dna-binding	RT		36	3.8E-3	2.8E-1
☐	GOTERM_MF_ALL	transcription regulator activity	RT		36	4.1E-3	6.3E-1

☐	GOTERM_CC_ALL	cell part	RT	225	4.5E-3	3.2E-1
☐	GOTERM_CC_ALL	cell	RT	225	4.5E-3	3.2E-1
☐	GOTERM_CC_ALL	cytoplasm	RT	113	1.4E-2	6.3E-1
☐	GOTERM_MF_ALL	transcription factor activity	RT	26	1.6E-2	9.5E-1
☐	GOTERM_MF_ALL	binding	RT	199	2.0E-2	9.7E-1
☐	GOTERM_MF_ALL	sequence-specific DNA binding	RT	15	5.0E-2	1.0E0
	Annotation Cluster 2	Enrichment Score: 3.76	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	zinc ion binding	RT	58	1.9E-5	2.6E-2
☐	GOTERM_MF_ALL	transition metal ion binding	RT	68	2.1E-5	1.4E-2
☐	SP_PIR_KEYWORDS	zinc-finger	RT	41	4.9E-5	8.4E-3
☐	SP_PIR_KEYWORDS	zinc	RT	48	7.2E-5	1.0E-2
☐	GOTERM_MF_ALL	metal ion binding	RT	87	4.9E-4	1.7E-1
☐	GOTERM_MF_ALL	ion binding	RT	88	6.2E-4	1.9E-1
☐	SP_PIR_KEYWORDS	metal-binding	RT	57	6.9E-4	7.2E-2
☐	GOTERM_MF_ALL	cation binding	RT	78	2.8E-3	5.6E-1
	Annotation Cluster 3	Enrichment Score: 2.82	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	biotin biosynthetic process	RT	7	2.0E-10	1.0E-6
☐	GOTERM_BP_ALL	biotin metabolic process	RT	7	2.3E-9	5.9E-6
☐	GOTERM_BP_ALL	water-soluble vitamin biosynthetic process	RT	7	4.9E-6	2.5E-3
☐	GOTERM_BP_ALL	vitamin biosynthetic process	RT	7	6.2E-6	2.7E-3
☐	INTERPRO	Biotin synthase	RT	4	1.9E-5	5.4E-2
☐	INTERPRO	Biotin and thiamin synthesis associated	RT	4	1.9E-5	5.4E-2
☐	GOTERM_MF_ALL	biotin synthase activity	RT	4	2.0E-5	1.8E-2
☐	GOTERM_BP_ALL	sulfur compound biosynthetic process	RT	7	1.0E-4	2.1E-2
☐	GOTERM_BP_ALL	water-soluble vitamin metabolic process	RT	7	2.1E-4	3.7E-2
☐	GOTERM_MF_ALL	sulfurtransferase activity	RT	4	4.0E-4	1.6E-1
☐	INTERPRO	Elongator protein 3/MiaB/NifB	RT	4	5.4E-4	6.5E-1
☐	INTERPRO	Radical SAM	RT	4	5.4E-4	6.5E-1
☐	SP_PIR_KEYWORDS	biotin biosynthesis	RT	3	8.5E-4	7.9E-2
☐	SMART	Elp3	RT	4	8.6E-4	4.0E-1
☐	COG_ONTOLOGY	Coenzyme metabolism	RT	5	1.8E-3	1.3E-1
☐	GOTERM_BP_ALL	vitamin metabolic process	RT	7	1.9E-3	2.4E-1
☐	GOTERM_BP_ALL	monocarboxylic acid metabolic process	RT	12	2.4E-3	2.8E-1
☐	GOTERM_BP_ALL	sulfur metabolic process	RT	7	3.1E-3	3.3E-1
☐	GOTERM_MF_ALL	2 iron, 2 sulfur cluster binding	RT	4	3.5E-3	6.1E-1
☐	GOTERM_BP_ALL	heterocycle metabolic process	RT	7	3.7E-3	3.8E-1
☐	SP_PIR_KEYWORDS	4Fe-4S	RT	4	5.9E-3	3.5E-1
☐	GOTERM_MF_ALL	4 iron, 4 sulfur cluster binding	RT	4	7.1E-3	7.9E-1
☐	INTERPRO	Aldolase-type TIM barrel	RT	4	1.5E-2	1.0E0
☐	SP_PIR_KEYWORDS	iron-sulfur	RT	4	2.8E-2	8.3E-1
☐	SP_PIR_KEYWORDS	s-adenosyl-l-methionine	RT	5	3.0E-2	8.3E-1
☐	GOTERM_MF_ALL	metal cluster binding	RT	4	5.3E-2	1.0E0
☐	GOTERM_MF_ALL	iron-sulfur cluster binding	RT	4	5.3E-2	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring sulfur-containing groups	RT	4	6.7E-2	1.0E0
☐	GOTERM_BP_ALL	cofactor metabolic process	RT	8	9.2E-2	1.0E0
☐	GOTERM_BP_ALL	carboxylic acid metabolic process	RT	13	1.9E-1	1.0E0
☐	GOTERM_BP_ALL	organic acid metabolic process	RT	13	1.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	iron	RT	6	4.4E-1	1.0E0
☐	GOTERM_MF_ALL	iron ion binding	RT	7	4.7E-1	1.0E0

☐	GOTERM_BP_ALL	biosynthetic process	RT	21	7.3E-1	1.0E0
☐	GOTERM_BP_ALL	cellular biosynthetic process	RT	15	7.8E-1	1.0E0
	Annotation Cluster 4	Enrichment Score: 1.93	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	skeletal muscle fiber development	RT	9	3.4E-5	8.8E-3
☐	GOTERM_BP_ALL	muscle fiber development	RT	9	3.4E-5	8.8E-3
☐	GOTERM_BP_ALL	myoblast differentiation	RT	7	1.1E-4	2.3E-2
☐	GOTERM_BP_ALL	skeletal muscle development	RT	10	1.2E-4	2.4E-2
☐	GOTERM_BP_ALL	muscle development	RT	13	1.3E-4	2.5E-2
☐	GOTERM_BP_ALL	striated muscle development	RT	11	1.9E-4	3.4E-2
☐	GOTERM_BP_ALL	muscle cell differentiation	RT	8	4.1E-4	6.6E-2
☐	GOTERM_BP_ALL	myoblast maturation	RT	5	9.0E-4	1.3E-1
☐	GOTERM_BP_ALL	myoblast development	RT	5	1.0E-3	1.4E-1
☐	GOTERM_BP_ALL	cell maturation	RT	7	4.9E-3	4.6E-1
☐	GOTERM_BP_ALL	developmental maturation	RT	7	1.1E-2	7.3E-1
☐	GOTERM_BP_ALL	striated muscle cell differentiation	RT	4	2.4E-2	9.2E-1
☐	GOTERM_BP_ALL	myofibril assembly	RT	3	4.0E-2	9.8E-1
☐	GOTERM_BP_ALL	striated muscle cell development	RT	3	4.0E-2	9.8E-1
☐	GOTERM_BP_ALL	muscle cell development	RT	3	4.4E-2	9.9E-1
☐	GOTERM_BP_ALL	actomyosin structure organization and biogenesis	RT	3	6.2E-2	1.0E0
☐	GOTERM_BP_ALL	protein complex assembly	RT	4	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	macromolecular complex assembly	RT	7	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	cellular component assembly	RT	8	5.9E-1	1.0E0
☐	GOTERM_BP_ALL	actin cytoskeleton organization and biogenesis	RT	4	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	actin filament-based process	RT	4	7.1E-1	1.0E0
☐	GOTERM_MF_ALL	actin binding	RT	4	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	cytoskeleton organization and biogenesis	RT	7	8.8E-1	1.0E0
☐	GOTERM_MF_ALL	cytoskeletal protein binding	RT	4	9.7E-1	1.0E0
	Annotation Cluster 5	Enrichment Score: 1.86	G	Count	P_Value	Benjamini
☐	INTERPRO	LisH dimerisation motif	RT	4	1.1E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:LisH	RT	3	1.5E-2	1.0E0
☐	SMART	LisH	RT	4	1.6E-2	9.9E-1
	Annotation Cluster 6	Enrichment Score: 1.66	G	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, C2H2-type	RT	19	1.4E-3	7.9E-1
☐	INTERPRO	Zinc finger, C2H2-like	RT	12	4.9E-2	1.0E0
☐	SMART	ZnF_C2H2	RT	14	5.3E-2	1.0E0
☐	INTERPRO	Zinc finger, C2H2-type/integrase, DNA-binding	RT	10	6.6E-2	1.0E0
	Annotation Cluster 7	Enrichment Score: 1.6	G	Count	P_Value	Benjamini
☐	PIR_SUPERFAMILY	PIRSF018476:nuclear factor 1	RT	3	1.5E-3	9.9E-1
☐	INTERPRO	CTF/NF-I	RT	3	2.8E-3	9.3E-1
☐	INTERPRO	MAD homology 1, Dwarfin-type	RT	3	2.0E-2	1.0E0
☐	SMART	DWA	RT	3	2.7E-2	9.8E-1
☐	GOTERM_BP_ALL	DNA replication	RT	5	2.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna replication	RT	3	3.6E-1	1.0E0
	Annotation Cluster 8	Enrichment Score: 1.5	G	Count	P_Value	Benjamini
☐	SMART	UBA	RT	4	1.8E-2	9.7E-1
☐	INTERPRO	Ubiquitin-associated/translation elongation factor EF1B, N-terminal	RT	4	4.1E-2	1.0E0
☐	UP_SEQ_FEATURE	domain:UBA	RT	3	4.3E-2	1.0E0
	Annotation Cluster 9	Enrichment Score: 1.19	G	Count	P_Value	Benjamini

☐	GOTERM_BP_ALL	negative regulation of transcription, DNA-dependent	RT	▬		10	1.4E-2	8.1E-1
☐	GOTERM_BP_ALL	negative regulation of transcription from RNA polymerase II promoter	RT	▬		8	1.8E-2	8.7E-1
☐	UP_SEQ_FEATURE	mutagenesis site	RT	▬		13	2.0E-2	1.0E0
☐	GOTERM_MF_ALL	transcription corepressor activity	RT	▬		5	2.4E-2	9.8E-1
☐	GOTERM_MF_ALL	transcription factor binding	RT	▬		10	2.7E-2	9.9E-1
☐	GOTERM_BP_ALL	negative regulation of transcription	RT	▬		11	3.1E-2	9.6E-1
☐	GOTERM_BP_ALL	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	▬		11	4.5E-2	9.9E-1
☐	GOTERM_BP_ALL	transcription from RNA polymerase II promoter	RT	▬		14	7.9E-2	1.0E0
☐	GOTERM_MF_ALL	transcription repressor activity	RT	▬		7	8.5E-2	1.0E0
☐	GOTERM_BP_ALL	negative regulation of cellular metabolic process	RT	▬		11	1.0E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of transcription from RNA polymerase II promoter	RT	▬		12	1.3E-1	1.0E0
☐	GOTERM_MF_ALL	transcription cofactor activity	RT	▬		6	1.4E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of metabolic process	RT	▬		11	1.8E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of cellular process	RT	▬		20	3.6E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of biological process	RT	▬		21	3.9E-1	1.0E0
	Annotation Cluster 10	Enrichment Score: 1.15	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	rna-binding	RT	▬		13	3.4E-2	8.1E-1
☐	INTERPRO	Nucleotide-binding, alpha-beta plait	RT	▬		7	5.5E-2	1.0E0
☐	INTERPRO	RNA recognition motif, RNP-1	RT	▬		7	5.6E-2	1.0E0
☐	SMART	RRM	RT	▬		8	7.8E-2	1.0E0
☐	GOTERM_MF_ALL	RNA binding	RT	▬		14	2.3E-1	1.0E0
	Annotation Cluster 11	Enrichment Score: 1.05	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	germ cell development	RT	▬		4	3.1E-2	9.6E-1
☐	GOTERM_BP_ALL	gamete generation	RT	▬		10	4.0E-2	9.8E-1
☐	GOTERM_BP_ALL	reproduction	RT	▬		14	6.4E-2	1.0E0
☐	GOTERM_BP_ALL	sexual reproduction	RT	▬		10	9.8E-2	1.0E0
☐	GOTERM_BP_ALL	spermatogenesis	RT	▬		6	2.5E-1	1.0E0
☐	GOTERM_BP_ALL	male gamete generation	RT	▬		6	2.5E-1	1.0E0
	Annotation Cluster 12	Enrichment Score: 1.03	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	BTB/POZ	RT	▬		6	2.6E-2	1.0E0
☐	INTERPRO	BTB/POZ-like	RT	▬		6	8.9E-2	1.0E0
☐	INTERPRO	BTB/POZ fold	RT	▬		6	9.1E-2	1.0E0
☐	SMART	BTB	RT	▬		6	1.7E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:BTB	RT	▬		3	1.9E-1	1.0E0
	Annotation Cluster 13	Enrichment Score: 1.03	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	chromatin modification	RT	▬		9	1.5E-2	8.3E-1
☐	SP_PIR_KEYWORDS	Chromatin regulator	RT	▬		6	3.1E-2	8.2E-1
☐	GOTERM_BP_ALL	establishment and/or maintenance of chromatin architecture	RT	▬		9	7.2E-2	1.0E0
☐	GOTERM_BP_ALL	DNA packaging	RT	▬		9	8.2E-2	1.0E0
☐	GOTERM_BP_ALL	DNA metabolic process	RT	▬		16	1.4E-1	1.0E0
☐	GOTERM_BP_ALL	chromosome organization and biogenesis	RT	▬		9	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	organelle organization and biogenesis	RT	▬		18	7.7E-1	1.0E0
	Annotation Cluster 14	Enrichment Score: 0.85	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	steroid binding	RT	▬		4	8.0E-2	1.0E0
☐	GOTERM_MF_ALL	steroid hormone receptor activity	RT	▬		4	1.0E-1	1.0E0
☐	GOTERM_MF_ALL	ligand-dependent nuclear receptor activity	RT	▬		4	1.1E-1	1.0E0
☐	INTERPRO	Nuclear hormone receptor, ligand-						

		binding, core						
☐	INTERPRO	Nuclear hormone receptor, ligand-binding	RT	▮		3	2.0E-1	1.0E0
☐	SMART	HOLI	RT	▮		3	2.4E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 0.82	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, C2H2-type/integrase, DNA-binding	RT	▮		10	6.6E-2	1.0E0
☐	INTERPRO	Zinc finger, C2H2-subtype	RT	▮		7	1.2E-1	1.0E0
☐	SMART	KRAB	RT	▮		7	2.5E-1	1.0E0
☐	INTERPRO	KRAB box	RT	▮		6	2.7E-1	1.0E0
	Annotation Cluster 16	Enrichment Score: 0.82	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	in utero embryonic development	RT	▮		7	2.4E-2	9.3E-1
☐	GOTERM_BP_ALL	sex differentiation	RT	▮		5	8.3E-2	1.0E0
☐	GOTERM_BP_ALL	chordate embryonic development	RT	▮		8	9.7E-2	1.0E0
☐	GOTERM_BP_ALL	embryonic development ending in birth or egg hatching	RT	▮		8	1.0E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive developmental process	RT	▮		5	1.0E-1	1.0E0
☐	GOTERM_BP_ALL	embryonic development	RT	▮		13	1.0E-1	1.0E0
☐	GOTERM_BP_ALL	development of primary sexual characteristics	RT	▮		4	1.2E-1	1.0E0
☐	GOTERM_BP_ALL	heart morphogenesis	RT	▮		3	1.3E-1	1.0E0
☐	GOTERM_BP_ALL	blood vessel development	RT	▮		7	2.5E-1	1.0E0
☐	GOTERM_BP_ALL	vasculature development	RT	▮		7	2.6E-1	1.0E0
☐	GOTERM_BP_ALL	gonad development	RT	▮		3	2.9E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive structure development	RT	▮		3	3.1E-1	1.0E0
☐	UP_SEQ_FEATURE	compositionally biased region:Poly-Ala	RT	▮		5	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive process	RT	▮		5	6.0E-1	1.0E0
	Annotation Cluster 17	Enrichment Score: 0.81	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of cell differentiation	RT	▮		5	9.3E-2	1.0E0
☐	GOTERM_BP_ALL	negative regulation of developmental process	RT	▮		5	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of developmental process	RT	▮		9	1.7E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell differentiation	RT	▮		6	2.4E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 0.79	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	ubiquitin cycle	RT	▮		14	8.9E-2	1.0E0
☐	SP_PIR_KEYWORDS	Ubl conjugation pathway	RT	▮		11	1.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	ligase	RT	▮		8	1.3E-1	1.0E0
☐	GOTERM_MF_ALL	ligase activity	RT	▮		9	2.7E-1	1.0E0
☐	GOTERM_BP_ALL	post-translational protein modification	RT	▮		28	3.2E-1	1.0E0
	Annotation Cluster 19	Enrichment Score: 0.76	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	signal sequence binding	RT	▮		3	1.5E-2	9.5E-1
☐	GOTERM_MF_ALL	peptide binding	RT	▮		4	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	intracellular protein transport	RT	▮		7	7.9E-1	1.0E0
	Annotation Cluster 20	Enrichment Score: 0.69	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	IQ calmodulin-binding region	RT	▮		4	1.3E-1	1.0E0
☐	SMART	IQ	RT	▮		4	2.0E-1	1.0E0
☐	GOTERM_MF_ALL	calmodulin binding	RT	▮		4	3.3E-1	1.0E0
	Annotation Cluster 21	Enrichment Score: 0.64	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of anatomical structure morphogenesis	RT	▮		3	2.3E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell shape	RT	▮		3	2.3E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell morphogenesis	RT	▮		3	2.3E-1	1.0E0
	Annotation Cluster 22	Enrichment Score: 0.64	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	ossification	RT	▮		5	1.2E-1	1.0E0
☐	GOTERM_BP_ALL	biomineral formation	RT	▮		5	1.2E-1	1.0E0

☐	GOTERM_BP_ALL	bone remodeling	RT	5	1.5E-1	1.0E0
☐	GOTERM_BP_ALL	tissue remodeling	RT	5	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	skeletal development	RT	5	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	tissue development	RT	6	6.4E-1	1.0E0
	Annotation Cluster 23	Enrichment Score: 0.61	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	RT	5	1.5E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 3	RT	4	3.1E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	RT	4	3.3E-1	1.0E0
	Annotation Cluster 24	Enrichment Score: 0.59	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	RNA splicing	RT	7	1.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	mrna splicing	RT	6	1.2E-1	9.9E-1
☐	GOTERM_BP_ALL	mRNA metabolic process	RT	8	2.0E-1	1.0E0
☐	GOTERM_BP_ALL	mRNA processing	RT	7	2.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	mrna processing	RT	6	2.4E-1	1.0E0
☐	GOTERM_BP_ALL	nuclear mRNA splicing, via spliceosome	RT	3	2.6E-1	1.0E0
☐	GOTERM_BP_ALL	RNA splicing, via transesterification reactions	RT	3	2.6E-1	1.0E0
☐	GOTERM_BP_ALL	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	RT	3	2.6E-1	1.0E0
☐	GOTERM_CC_ALL	spliceosome	RT	4	4.0E-1	1.0E0
☐	GOTERM_BP_ALL	RNA processing	RT	8	5.2E-1	1.0E0
☐	GOTERM_CC_ALL	ribonucleoprotein complex	RT	8	6.1E-1	1.0E0
	Annotation Cluster 25	Enrichment Score: 0.57	G	Count	P_Value	Benjamini
☐	INTERPRO	HECT	RT	3	7.2E-2	1.0E0
☐	SMART	HECTc	RT	3	1.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	ligase	RT	8	1.3E-1	1.0E0
☐	GOTERM_MF_ALL	ligase activity	RT	9	2.7E-1	1.0E0
☐	GOTERM_MF_ALL	ligase activity, forming carbon-nitrogen bonds	RT	5	3.9E-1	1.0E0
☐	GOTERM_MF_ALL	small conjugating protein ligase activity	RT	4	3.9E-1	1.0E0
☐	GOTERM_MF_ALL	acid-amino acid ligase activity	RT	4	4.7E-1	1.0E0
☐	GOTERM_MF_ALL	ubiquitin-protein ligase activity	RT	3	6.4E-1	1.0E0
☐	GOTERM_MF_ALL	small protein conjugating enzyme activity	RT	3	6.5E-1	1.0E0
	Annotation Cluster 26	Enrichment Score: 0.55	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	organ development	RT	32	1.2E-1	1.0E0
☐	GOTERM_BP_ALL	cellular developmental process	RT	39	1.7E-1	1.0E0
☐	GOTERM_BP_ALL	cell differentiation	RT	39	1.7E-1	1.0E0
☐	GOTERM_BP_ALL	developmental process	RT	57	3.1E-1	1.0E0
☐	GOTERM_BP_ALL	system development	RT	34	3.6E-1	1.0E0
☐	GOTERM_BP_ALL	anatomical structure development	RT	39	3.9E-1	1.0E0
☐	GOTERM_BP_ALL	multicellular organismal development	RT	42	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	multicellular organismal process	RT	51	6.0E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 0.53	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell proliferation	RT	15	1.1E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of cell proliferation	RT	6	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell proliferation	RT	7	6.8E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 0.53	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	wd repeat	RT	7	2.1E-1	1.0E0
☐	INTERPRO	WD40 repeat	RT	6	2.7E-1	1.0E0
☐	SMART	WD40	RT	6	4.6E-1	1.0E0
	Annotation Cluster 29	Enrichment Score: 0.47	G	Count	P_Value	Benjamini

☐	**SP_PIR_KEYWORDS**	wd repeat	RT	7	2.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:WD 3	RT	4	3.3E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:WD 1	RT	4	3.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:WD 2	RT	4	3.4E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:WD 4	RT	3	5.7E-1	1.0E0
	Annotation Cluster 30	Enrichment Score: 0.46	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	Ras protein signal transduction	RT	8	5.8E-2	1.0E0
☐	**GOTERM_BP_ALL**	regulation of Ras protein signal transduction	RT	5	2.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	small GTPase regulator activity	RT	6	2.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	small GTPase mediated signal transduction	RT	10	2.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of small GTPase mediated signal transduction	RT	5	4.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	GTPase regulator activity	RT	7	5.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of signal transduction	RT	9	5.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	guanyl-nucleotide exchange factor activity	RT	3	7.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	enzyme regulator activity	RT	9	9.1E-1	1.0E0
	Annotation Cluster 31	Enrichment Score: 0.45	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	detection of stimulus during sensory perception	RT	3	1.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	detection of abiotic stimulus	RT	3	1.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	detection of external stimulus	RT	3	2.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	detection of stimulus	RT	3	3.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	sensory perception	RT	6	5.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	response to abiotic stimulus	RT	4	5.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	response to external stimulus	RT	7	8.7E-1	1.0E0
	Annotation Cluster 32	Enrichment Score: 0.43	G	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	nucleoside-triphosphatase activity	RT	13	2.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	pyrophosphatase activity	RT	13	2.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	RT	13	2.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrolase activity, acting on acid anhydrides	RT	13	2.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	ATPase activity	RT	7	4.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	ATPase activity, coupled	RT	5	7.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrolase activity	RT	32	8.8E-1	1.0E0
	Annotation Cluster 33	Enrichment Score: 0.43	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	embryonic appendage morphogenesis	RT	3	3.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	embryonic limb morphogenesis	RT	3	3.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	limb morphogenesis	RT	3	3.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	appendage morphogenesis	RT	3	3.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	appendage development	RT	3	3.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	limb development	RT	3	3.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	embryonic morphogenesis	RT	5	4.4E-1	1.0E0
	Annotation Cluster 34	Enrichment Score: 0.42	G	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	repeat:ANK 5	RT	3	2.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:ANK 4	RT	3	2.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	ubl conjugation	RT	8	2.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:ANK 3	RT	3	3.5E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:ANK 1	RT	3	4.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	repeat:ANK 2	RT	3	4.2E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	ank repeat	RT	4	6.3E-1	1.0E0

☐	**SMART**	ANK	RT	4	7.8E-1	1.0E0
	Annotation Cluster 35	Enrichment Score: 0.4	G	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	nucleotide binding	RT	43	9.0E-2	1.0E0
☐	**UP_SEQ_FEATURE**	nucleotide phosphate-binding region:ATP	RT	15	9.0E-2	1.0E0
☐	**BIOCARTA**	MAPKinase Signaling Pathway	RT	4	1.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein modification process	RT	34	1.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	purine ribonucleotide binding	RT	34	2.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	ribonucleotide binding	RT	34	2.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	biopolymer modification	RT	34	2.5E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Serine/threonine-protein kinase	RT	9	2.6E-1	1.0E0
☐	**INTERPRO**	Serine/threonine protein kinase	RT	6	2.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Protein kinase	RT	8	3.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	purine nucleotide binding	RT	34	3.1E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	nucleotide-binding	RT	26	3.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	post-translational protein modification	RT	28	3.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	active site:Proton acceptor	RT	10	3.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular protein metabolic process	RT	56	3.5E-1	1.0E0
☐	**UP_SEQ_FEATURE**	binding site:ATP	RT	8	3.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein metabolic process	RT	58	3.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	ATP binding	RT	26	3.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular macromolecule metabolic process	RT	56	3.9E-1	1.0E0
☐	**KEGG_PATHWAY**	MAPK signaling pathway	RT	5	4.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	adenyl ribonucleotide binding	RT	26	4.1E-1	1.0E0
☐	**INTERPRO**	Serine/threonine protein kinase, active site	RT	6	4.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein amino acid phosphorylation	RT	13	4.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	protein serine/threonine kinase activity	RT	10	4.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	protein kinase activity	RT	12	4.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	protein-tyrosine kinase activity	RT	7	4.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	atp-binding	RT	19	4.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	adenyl nucleotide binding	RT	26	5.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	phosphorylation	RT	14	5.1E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	transferase	RT	23	5.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	phosphate metabolic process	RT	16	5.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	phosphorus metabolic process	RT	16	5.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	magnesium ion binding	RT	7	6.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	transferase activity	RT	31	6.2E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	magnesium	RT	6	6.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	phosphotransferase activity, alcohol group as acceptor	RT	12	6.8E-1	1.0E0
☐	**INTERPRO**	Protein kinase, core	RT	6	7.1E-1	1.0E0
☐	**SMART**	S_TKc	RT	7	7.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	transferase activity, transferring phosphorus-containing groups	RT	16	7.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	kinase activity	RT	13	8.5E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	kinase	RT	10	8.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein kinase cascade	RT	3	9.6E-1	1.0E0
	Annotation Cluster 36	Enrichment Score: 0.4	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	eye development	RT	4	2.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	camera-type eye development	RT	3	3.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	sensory organ development	RT	4	6.4E-1	1.0E0

	Annotation Cluster 37	Enrichment Score: 0.4	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	GTPase activity	RT		5	2.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	GTP-binding	RT		7	3.3E-1	1.0E0
☐	GOTERM_MF_ALL	GTP binding	RT		8	3.5E-1	1.0E0
☐	GOTERM_MF_ALL	guanyl ribonucleotide binding	RT		8	3.7E-1	1.0E0
☐	GOTERM_MF_ALL	guanyl nucleotide binding	RT		8	3.7E-1	1.0E0
☐	INTERPRO	Ras	RT		3	5.9E-1	1.0E0
☐	INTERPRO	Ras GTPase	RT		3	7.1E-1	1.0E0
	Annotation Cluster 38	Enrichment Score: 0.39	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	germ cell migration	RT		3	6.2E-3	5.3E-1
☐	GOTERM_BP_ALL	tube morphogenesis	RT		7	5.3E-2	9.9E-1
☐	GOTERM_BP_ALL	tube development	RT		8	7.5E-2	1.0E0
☐	GOTERM_BP_ALL	embryonic development	RT		13	1.0E-1	1.0E0
☐	GOTERM_BP_ALL	lymphocyte activation	RT		7	2.0E-1	1.0E0
☐	GOTERM_BP_ALL	hemopoietic or lymphoid organ development	RT		8	2.0E-1	1.0E0
☐	GOTERM_BP_ALL	T cell activation	RT		5	2.4E-1	1.0E0
☐	GOTERM_BP_ALL	leukocyte activation	RT		7	2.5E-1	1.0E0
☐	GOTERM_BP_ALL	blood vessel development	RT		7	2.5E-1	1.0E0
☐	GOTERM_BP_ALL	immune system development	RT		8	2.5E-1	1.0E0
☐	GOTERM_BP_ALL	vasculature development	RT		7	2.6E-1	1.0E0
☐	GOTERM_BP_ALL	hemopoiesis	RT		7	2.7E-1	1.0E0
☐	GOTERM_BP_ALL	leukocyte differentiation	RT		5	2.9E-1	1.0E0
☐	GOTERM_BP_ALL	cell activation	RT		7	2.9E-1	1.0E0
☐	GOTERM_BP_ALL	lymphocyte differentiation	RT		4	3.1E-1	1.0E0
☐	GOTERM_BP_ALL	branching morphogenesis of a tube	RT		3	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	morphogenesis of a branching structure	RT		3	3.5E-1	1.0E0
☐	GOTERM_BP_ALL	brain development	RT		5	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	blood vessel morphogenesis	RT		5	4.9E-1	1.0E0
☐	GOTERM_BP_ALL	locomotory behavior	RT		5	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	anatomical structure formation	RT		5	5.3E-1	1.0E0
☐	GOTERM_BP_ALL	angiogenesis	RT		4	5.4E-1	1.0E0
☐	GOTERM_BP_ALL	pattern specification process	RT		5	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	cell migration	RT		6	6.4E-1	1.0E0
☐	GOTERM_BP_ALL	central nervous system development	RT		5	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	cell morphogenesis	RT		9	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	cellular structure morphogenesis	RT		9	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	organ morphogenesis	RT		9	7.5E-1	1.0E0
☐	GOTERM_BP_ALL	nervous system development	RT		11	7.5E-1	1.0E0
☐	GOTERM_BP_ALL	immune system process	RT		12	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	cell motility	RT		6	7.8E-1	1.0E0
☐	GOTERM_BP_ALL	localization of cell	RT		6	7.8E-1	1.0E0
☐	KEGG_PATHWAY	Cytokine-cytokine receptor interaction	RT		3	8.1E-1	1.0E0
☐	GOTERM_BP_ALL	cellular morphogenesis during differentiation	RT		3	8.8E-1	1.0E0
☐	GOTERM_BP_ALL	cell projection morphogenesis	RT		4	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	cell projection organization and biogenesis	RT		4	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	cell part morphogenesis	RT		4	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	anatomical structure morphogenesis	RT		17	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	immune response	RT		6	9.1E-1	1.0E0

☐	GOTERM_BP_ALL	generation of neurons	RT	▮		4	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	neurogenesis	RT	▮		4	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	neuron differentiation	RT	▮		3	9.7E-1	1.0E0
	Annotation Cluster 39	Enrichment Score: 0.38	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	thiol protease	RT	▮		4	2.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	protease	RT	▮		10	4.1E-1	1.0E0
☐	GOTERM_MF_ALL	cysteine-type endopeptidase activity	RT	▮		3	5.2E-1	1.0E0
☐	GOTERM_MF_ALL	cysteine-type peptidase activity	RT	▮		4	5.5E-1	1.0E0
	Annotation Cluster 40	Enrichment Score: 0.37	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	gtpase activation	RT	▮		4	1.8E-1	1.0E0
☐	GOTERM_MF_ALL	small GTPase regulator activity	RT	▮		6	2.6E-1	1.0E0
☐	GOTERM_MF_ALL	Ras GTPase activator activity	RT	▮		3	3.2E-1	1.0E0
☐	GOTERM_MF_ALL	GTPase regulator activity	RT	▮		7	5.3E-1	1.0E0
☐	GOTERM_MF_ALL	enzyme activator activity	RT	▮		5	5.8E-1	1.0E0
☐	GOTERM_MF_ALL	GTPase activator activity	RT	▮		4	5.9E-1	1.0E0
☐	GOTERM_MF_ALL	enzyme regulator activity	RT	▮		9	9.1E-1	1.0E0
	Annotation Cluster 41	Enrichment Score: 0.37	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	ubiquitin-dependent protein catabolic process	RT	▮		5	2.4E-1	1.0E0
☐	GOTERM_BP_ALL	modification-dependent protein catabolic process	RT	▮		5	2.5E-1	1.0E0
☐	GOTERM_BP_ALL	modification-dependent macromolecule catabolic process	RT	▮		5	2.5E-1	1.0E0
☐	GOTERM_BP_ALL	proteolysis involved in cellular protein catabolic process	RT	▮		5	2.7E-1	1.0E0
☐	GOTERM_BP_ALL	cellular protein catabolic process	RT	▮		5	2.7E-1	1.0E0
☐	GOTERM_BP_ALL	protein catabolic process	RT	▮		6	2.9E-1	1.0E0
☐	GOTERM_BP_ALL	proteolysis	RT	▮		14	4.9E-1	1.0E0
☐	GOTERM_BP_ALL	biopolymer catabolic process	RT	▮		6	5.2E-1	1.0E0
☐	GOTERM_BP_ALL	cellular macromolecule catabolic process	RT	▮		5	7.0E-1	1.0E0
☐	GOTERM_BP_ALL	macromolecule catabolic process	RT	▮		6	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	catabolic process	RT	▮		7	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	cellular catabolic process	RT	▮		5	9.7E-1	1.0E0
	Annotation Cluster 42	Enrichment Score: 0.36	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	peroxisome	RT	▮		3	4.0E-1	1.0E0
☐	GOTERM_CC_ALL	microbody	RT	▮		3	4.5E-1	1.0E0
☐	GOTERM_CC_ALL	peroxisome	RT	▮		3	4.5E-1	1.0E0
	Annotation Cluster 43	Enrichment Score: 0.35	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	protein dimerization activity	RT	▮		8	2.1E-1	1.0E0
☐	GOTERM_MF_ALL	protein homodimerization activity	RT	▮		4	4.7E-1	1.0E0
☐	GOTERM_MF_ALL	identical protein binding	RT	▮		4	8.8E-1	1.0E0
	Annotation Cluster 44	Enrichment Score: 0.33	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Src homology-3	RT	▮		5	3.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	SH3 domain	RT	▮		5	4.2E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:SH3	RT	▮		3	5.4E-1	1.0E0
☐	SMART	SH3	RT	▮		5	5.4E-1	1.0E0
	Annotation Cluster 45	Enrichment Score: 0.31	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	positive regulation of cellular process	RT	▮		20	2.7E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of biological process	RT	▮		21	3.9E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of transcription, DNA-dependent	RT	▮		7	4.1E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of transcription	RT	▮		8	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid	RT	▮		8	4.4E-1	1.0E0

		metabolic process						
☐	GOTERM_BP_ALL	positive regulation of cellular metabolic process	RT	▮		9	5.2E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of metabolic process	RT	▮		9	5.9E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of transcription from RNA polymerase II promoter	RT	▮		4	7.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	DNA binding	RT	▮		4	8.1E-1	1.0E0
	Annotation Cluster 46	Enrichment Score: 0.31	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	glycoprotein metabolic process	RT	▮		4	3.4E-1	1.0E0
☐	UP_SEQ_FEATURE	topological domain:Lumenal	RT	▮		6	3.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	glycosyltransferase	RT	▮		5	3.7E-1	1.0E0
☐	KEGG_PATHWAY	Glycan structures - biosynthesis 1	RT	▮		3	3.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	golgi apparatus	RT	▮		9	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid glycosylation	RT	▮		3	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	biopolymer glycosylation	RT	▮		3	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	glycoprotein biosynthetic process	RT	▮		3	5.0E-1	1.0E0
☐	GOTERM_CC_ALL	Golgi apparatus	RT	▮		11	5.7E-1	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring glycosyl groups	RT	▮		5	5.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	signal-anchor	RT	▮		5	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	macromolecule biosynthetic process	RT	▮		7	9.9E-1	1.0E0
	Annotation Cluster 47	Enrichment Score: 0.29	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of growth	RT	▮		5	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell size	RT	▮		4	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	growth	RT	▮		6	5.4E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell growth	RT	▮		3	5.6E-1	1.0E0
☐	GOTERM_BP_ALL	cell growth	RT	▮		3	6.6E-1	1.0E0
	Annotation Cluster 48	Enrichment Score: 0.29	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	fatty acid metabolic process	RT	▮		5	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	lipid biosynthetic process	RT	▮		6	4.7E-1	1.0E0
☐	GOTERM_BP_ALL	cellular lipid metabolic process	RT	▮		10	6.4E-1	1.0E0
☐	GOTERM_BP_ALL	lipid metabolic process	RT	▮		11	7.0E-1	1.0E0
	Annotation Cluster 49	Enrichment Score: 0.25	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	non-membrane-bound organelle	RT	▮		27	5.1E-1	1.0E0
☐	GOTERM_CC_ALL	intracellular non-membrane-bound organelle	RT	▮		27	5.1E-1	1.0E0
☐	GOTERM_CC_ALL	cytoskeleton	RT	▮		15	6.8E-1	1.0E0
	Annotation Cluster 50	Enrichment Score: 0.25	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	chemotaxis	RT	▮		3	2.6E-1	1.0E0
☐	GOTERM_BP_ALL	behavior	RT	▮		7	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	locomotory behavior	RT	▮		5	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	chemotaxis	RT	▮		3	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	taxis	RT	▮		3	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	response to chemical stimulus	RT	▮		6	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	response to external stimulus	RT	▮		7	8.7E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 0.23	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	growth factor	RT	▮		4	3.7E-1	1.0E0
☐	GOTERM_MF_ALL	growth factor activity	RT	▮		4	5.6E-1	1.0E0
☐	GOTERM_MF_ALL	receptor binding	RT	▮		7	9.7E-1	1.0E0
	Annotation Cluster 52	Enrichment Score: 0.22	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	membrane organization and biogenesis	RT	▮		6	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	endocytosis	RT	▮		4	6.2E-1	1.0E0
☐	GOTERM_BP_ALL	membrane invagination	RT	▮		4	6.2E-1	1.0E0

☐	**GOTERM_BP_ALL**	vesicle-mediated transport	RT	▬		8	6.7E-1	1.0E0
	Annotation Cluster 53	Enrichment Score: 0.22	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	visual perception	RT	▬		4	2.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	sensory perception of light stimulus	RT	▬		4	2.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	sensory perception	RT	▬		6	5.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	neurological system process	RT	▬		9	7.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	synaptic transmission	RT	▬		4	7.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	transmission of nerve impulse	RT	▬		4	8.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	system process	RT	▬		10	8.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell-cell signaling	RT	▬		4	9.6E-1	1.0E0
	Annotation Cluster 54	Enrichment Score: 0.2	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Calcium-binding EF-hand	RT	▬		5	3.9E-1	1.0E0
☐	**SMART**	EFh	RT	▬		5	5.5E-1	1.0E0
☐	**INTERPRO**	EF-Hand type	RT	▬		3	7.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	calcium ion binding	RT	▬		10	9.6E-1	1.0E0
	Annotation Cluster 55	Enrichment Score: 0.19	G		🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	protease	RT	▬		10	4.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	proteolysis	RT	▬		14	4.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	peptidase activity	RT	▬		12	6.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	endopeptidase activity	RT	▬		8	6.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	hydrolase activity	RT	▬		32	8.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	hydrolase	RT	▬		16	9.6E-1	1.0E0
	Annotation Cluster 56	Enrichment Score: 0.18	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	nucleoplasm part	RT	▬		12	4.3E-1	1.0E0
☐	**GOTERM_CC_ALL**	nucleoplasm	RT	▬		12	5.1E-1	1.0E0
☐	**GOTERM_CC_ALL**	nuclear lumen	RT	▬		13	6.5E-1	1.0E0
☐	**GOTERM_CC_ALL**	transcription factor complex	RT	▬		8	6.6E-1	1.0E0
☐	**GOTERM_CC_ALL**	nuclear part	RT	▬		18	7.0E-1	1.0E0
☐	**GOTERM_CC_ALL**	organelle lumen	RT	▬		14	7.1E-1	1.0E0
☐	**GOTERM_CC_ALL**	membrane-enclosed lumen	RT	▬		14	7.1E-1	1.0E0
☐	**GOTERM_CC_ALL**	protein complex	RT	▬		21	9.8E-1	1.0E0
	Annotation Cluster 57	Enrichment Score: 0.18	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	synapse	RT	▬		6	4.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	synapse	RT	▬		4	5.3E-1	1.0E0
☐	**GOTERM_CC_ALL**	postsynaptic membrane	RT	▬		3	5.6E-1	1.0E0
☐	**GOTERM_CC_ALL**	synapse part	RT	▬		3	6.2E-1	1.0E0
☐	**GOTERM_CC_ALL**	cell junction	RT	▬		7	6.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	cell junction	RT	▬		5	7.1E-1	1.0E0
☐	**GOTERM_CC_ALL**	plasma membrane	RT	▬		19	9.9E-1	1.0E0
☐	**GOTERM_CC_ALL**	plasma membrane part	RT	▬		13	1.0E0	1.0E0
	Annotation Cluster 58	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Immunoglobulin subtype 2	RT	▬		4	5.1E-1	1.0E0
☐	**INTERPRO**	Immunoglobulin I-set	RT	▬		3	5.6E-1	1.0E0
☐	**SMART**	IGc2	RT	▬		4	6.6E-1	1.0E0
☐	**INTERPRO**	Immunoglobulin	RT	▬		3	7.8E-1	1.0E0
☐	**INTERPRO**	Immunoglobulin-like fold	RT	▬		6	7.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	immunoglobulin domain	RT	▬		4	9.4E-1	1.0E0
☐	**INTERPRO**	Immunoglobulin-like	RT	▬		4	9.5E-1	1.0E0
	Annotation Cluster 59	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	generation of precursor metabolites and energy	RT	▬		9	7.1E-1	1.0E0

☐	GOTERM_BP_ALL	electron transport	RT	▮		7	7.3E-1	1.0E0
☐	GOTERM_MF_ALL	oxidoreductase activity	RT	▮		14	7.3E-1	1.0E0
	Annotation Cluster 60	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	ATPase activity	RT	▮		7	4.7E-1	1.0E0
☐	GOTERM_CC_ALL	organelle membrane	RT	▮		12	5.5E-1	1.0E0
☐	GOTERM_CC_ALL	mitochondrial inner membrane	RT	▮		5	6.3E-1	1.0E0
☐	GOTERM_CC_ALL	organelle inner membrane	RT	▮		5	6.6E-1	1.0E0
☐	GOTERM_CC_ALL	mitochondrial membrane	RT	▮		5	7.0E-1	1.0E0
☐	GOTERM_CC_ALL	mitochondrial envelope	RT	▮		5	7.6E-1	1.0E0
☐	GOTERM_CC_ALL	mitochondrion	RT	▮		14	8.1E-1	1.0E0
☐	GOTERM_CC_ALL	mitochondrial part	RT	▮		5	8.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	Mitochondrion	RT	▮		8	9.1E-1	1.0E0
☐	GOTERM_CC_ALL	organelle envelope	RT	▮		5	9.4E-1	1.0E0
☐	GOTERM_CC_ALL	envelope	RT	▮		5	9.4E-1	1.0E0
	Annotation Cluster 61	Enrichment Score: 0.13	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	Golgi membrane	RT	▮		3	5.4E-1	1.0E0
☐	GOTERM_CC_ALL	Golgi apparatus part	RT	▮		3	8.0E-1	1.0E0
☐	GOTERM_CC_ALL	endomembrane system	RT	▮		5	9.1E-1	1.0E0
	Annotation Cluster 62	Enrichment Score: 0.13	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cytoskeleton-dependent intracellular transport	RT	▮		3	6.3E-1	1.0E0
☐	GOTERM_CC_ALL	microtubule cytoskeleton	RT	▮		6	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	microtubule-based process	RT	▮		4	6.8E-1	1.0E0
☐	GOTERM_CC_ALL	microtubule	RT	▮		3	8.5E-1	1.0E0
☐	GOTERM_CC_ALL	cytoskeletal part	RT	▮		7	9.1E-1	1.0E0
	Annotation Cluster 63	Enrichment Score: 0.11	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	protein transporter activity	RT	▮		4	5.2E-1	1.0E0
☐	GOTERM_BP_ALL	protein transport	RT	▮		13	5.6E-1	1.0E0
☐	GOTERM_BP_ALL	macromolecule localization	RT	▮		15	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	establishment of protein localization	RT	▮		13	6.4E-1	1.0E0
☐	GOTERM_BP_ALL	protein localization	RT	▮		14	6.5E-1	1.0E0
☐	SP_PIR_KEYWORDS	protein transport	RT	▮		7	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	intracellular protein transport	RT	▮		7	7.9E-1	1.0E0
☐	GOTERM_BP_ALL	protein targeting	RT	▮		4	8.0E-1	1.0E0
☐	GOTERM_BP_ALL	intracellular transport	RT	▮		10	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	establishment of cellular localization	RT	▮		12	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	cellular localization	RT	▮		12	9.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	transport	RT	▮		16	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	transport	RT	▮		34	9.8E-1	1.0E0
☐	GOTERM_MF_ALL	transporter activity	RT	▮		15	9.8E-1	1.0E0
☐	GOTERM_BP_ALL	establishment of localization	RT	▮		34	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	localization	RT	▮		38	9.9E-1	1.0E0
	Annotation Cluster 64	Enrichment Score: 0.1	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell division	RT	▮		6	4.4E-1	1.0E0
☐	GOTERM_BP_ALL	M phase	RT	▮		4	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	mitotic cell cycle	RT	▮		4	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	cell cycle	RT	▮		11	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	mitosis	RT	▮		3	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	M phase of mitotic cell cycle	RT	▮		3	8.5E-1	1.0E0
☐	GOTERM_BP_ALL	cell cycle phase	RT	▮		4	9.0E-1	1.0E0

☐	GOTERM_BP_ALL	cell cycle process	RT	8	9.0E-1	1.0E0
	Annotation Cluster 65	Enrichment Score: 0.1	G	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	nuclear part	RT	18	7.0E-1	1.0E0
☐	GOTERM_CC_ALL	intracellular organelle part	RT	40	7.7E-1	1.0E0
☐	GOTERM_CC_ALL	organelle part	RT	40	7.8E-1	1.0E0
☐	GOTERM_CC_ALL	macromolecular complex	RT	29	9.5E-1	1.0E0
	Annotation Cluster 66	Enrichment Score: 0.1	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	cell cycle	RT	7	5.9E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of progression through cell cycle	RT	3	7.1E-1	1.0E0
☐	GOTERM_BP_ALL	cell cycle	RT	11	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of progression through cell cycle	RT	5	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	cell cycle process	RT	8	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell cycle	RT	5	9.0E-1	1.0E0
	Annotation Cluster 67	Enrichment Score: 0.1	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell development	RT	26	2.7E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of apoptosis	RT	3	8.7E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of programmed cell death	RT	3	8.7E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of apoptosis	RT	6	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of programmed cell death	RT	6	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	apoptosis	RT	9	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	programmed cell death	RT	9	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	death	RT	9	9.5E-1	1.0E0
☐	GOTERM_BP_ALL	cell death	RT	9	9.5E-1	1.0E0
	Annotation Cluster 68	Enrichment Score: 0.07	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Homeobox	RT	4	7.7E-1	1.0E0
☐	INTERPRO	Homeobox	RT	3	8.5E-1	1.0E0
☐	SMART	HOX	RT	3	9.3E-1	1.0E0
	Annotation Cluster 69	Enrichment Score: 0.07	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of biological quality	RT	11	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	cellular homeostasis	RT	4	8.3E-1	1.0E0
☐	GOTERM_BP_ALL	homeostatic process	RT	5	9.0E-1	1.0E0
	Annotation Cluster 70	Enrichment Score: 0.06	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	intracellular signaling cascade	RT	20	7.2E-1	1.0E0
☐	GOTERM_BP_ALL	cell surface receptor linked signal transduction	RT	19	9.1E-1	1.0E0
☐	GOTERM_BP_ALL	signal transduction	RT	39	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	cell communication	RT	43	9.3E-1	1.0E0
	Annotation Cluster 71	Enrichment Score: 0.06	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	transit peptide:Mitochondrion	RT	4	7.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	Mitochondrion	RT	8	9.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	transit peptide	RT	4	9.6E-1	1.0E0
	Annotation Cluster 72	Enrichment Score: 0.04	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	structural constituent of ribosome	RT	3	8.0E-1	1.0E0
☐	GOTERM_CC_ALL	ribosome	RT	3	8.2E-1	1.0E0
☐	GOTERM_MF_ALL	structural molecule activity	RT	7	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	macromolecule biosynthetic process	RT	7	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	translation	RT	4	9.9E-1	1.0E0
	Annotation Cluster 73	Enrichment Score: 0.03	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	cell adhesion	RT	5	8.4E-1	1.0E0
☐	GOTERM_BP_ALL	cell-cell adhesion	RT	3	9.4E-1	1.0E0

☐	GOTERM_BP_ALL	cell adhesion	RT	8	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	biological adhesion	RT	8	9.6E-1	1.0E0
	Annotation Cluster 74	Enrichment Score: 0.02	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	secretory pathway	RT	3	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	secretion by cell	RT	3	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	secretion	RT	3	9.8E-1	1.0E0
	Annotation Cluster 75	Enrichment Score: 0.02	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	metal ion transmembrane transporter activity	RT	4	8.7E-1	1.0E0
☐	GOTERM_MF_ALL	substrate-specific transporter activity	RT	13	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	metal ion transport	RT	5	9.3E-1	1.0E0
☐	GOTERM_BP_ALL	cation transport	RT	6	9.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	ion transport	RT	5	9.5E-1	1.0E0
☐	GOTERM_MF_ALL	cation transmembrane transporter activity	RT	5	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	monovalent inorganic cation transport	RT	3	9.7E-1	1.0E0
☐	GOTERM_MF_ALL	substrate-specific transmembrane transporter activity	RT	8	9.8E-1	1.0E0
☐	GOTERM_MF_ALL	transporter activity	RT	15	9.8E-1	1.0E0
☐	GOTERM_MF_ALL	transmembrane transporter activity	RT	9	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	ion transmembrane transporter activity	RT	6	9.9E-1	1.0E0
☐	GOTERM_BP_ALL	ion transport	RT	7	9.9E-1	1.0E0
	Annotation Cluster 76	Enrichment Score: 0.02	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	response to DNA damage stimulus	RT	3	9.4E-1	1.0E0
☐	GOTERM_BP_ALL	response to endogenous stimulus	RT	3	9.6E-1	1.0E0
☐	GOTERM_BP_ALL	response to stress	RT	8	9.9E-1	1.0E0
	Annotation Cluster 77	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	molecular transducer activity	RT	21	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	signal transducer activity	RT	21	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	receptor activity	RT	17	9.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	receptor	RT	12	9.9E-1	1.0E0
	Annotation Cluster 78	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT	20	9.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	membrane	RT	57	9.9E-1	1.0E0
☐	UP_SEQ_FEATURE	transmembrane region	RT	22	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	transmembrane	RT	37	1.0E0	1.0E0
☐	GOTERM_CC_ALL	membrane	RT	75	1.0E0	1.0E0
☐	GOTERM_CC_ALL	membrane part	RT	52	1.0E0	1.0E0
☐	GOTERM_CC_ALL	integral to membrane	RT	41	1.0E0	1.0E0
☐	GOTERM_CC_ALL	intrinsic to membrane	RT	41	1.0E0	1.0E0
	Annotation Cluster 79	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT	20	9.7E-1	1.0E0
☐	UP_SEQ_FEATURE	disulfide bond	RT	16	9.9E-1	1.0E0
☐	UP_SEQ_FEATURE	transmembrane region	RT	22	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	topological domain:Extracellular	RT	10	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	signal peptide	RT	17	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT	18	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	signal	RT	21	1.0E0	1.0E0
☐	SP_PIR_KEYWORDS	glycoprotein	RT	20	1.0E0	1.0E0
	Annotation Cluster 80	Enrichment Score: 0	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Secreted	RT	10	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	signal peptide	RT	17	1.0E0	1.0E0

☐	**GOTERM_CC_ALL**	extracellular region	**RT**	▬	20	1.0E0	1.0E0
☐	**SP_PIR_KEYWORDS**	signal	**RT**	▬	21	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	extracellular space	**RT**	▬	15	1.0E0	1.0E0
☐	**GOTERM_CC_ALL**	extracellular region part	**RT**	▬	16	1.0E0	1.0E0

137 terms were not clustered.

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Functional Annotation Clustering Of Genes Downregulated <0.5 in WASP Deficient But Not In WT BMMCs

Help and Manual

Current Gene List: wsp1 not wt1 <.5lo

519 DAVID IDs

Options **Classification Stringency** Medium

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					Count	P_Value	Benjamini
	Annotation Cluster 1	Enrichment Score: 4.49	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	response to external stimulus	RT		31	2.7E-7	1.4E-3
☐	GOTERM_BP_ALL	taxis	RT		14	9.2E-7	2.4E-3
☐	GOTERM_BP_ALL	chemotaxis	RT		14	9.2E-7	2.4E-3
☐	GOTERM_BP_ALL	locomotory behavior	RT		15	1.7E-4	1.1E-1
☐	GOTERM_BP_ALL	behavior	RT		16	4.4E-3	4.3E-1
☐	GOTERM_BP_ALL	response to chemical stimulus	RT		18	7.0E-3	5.3E-1
	Annotation Cluster 2	Enrichment Score: 4.27	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	response to external stimulus	RT		31	2.7E-7	1.4E-3
☐	GOTERM_BP_ALL	defense response	RT		25	7.1E-5	7.1E-2
☐	GOTERM_BP_ALL	response to wounding	RT		19	2.2E-4	1.2E-1
☐	GOTERM_BP_ALL	response to stress	RT		35	2.2E-4	1.1E-1
☐	GOTERM_BP_ALL	inflammatory response	RT		15	4.9E-4	1.9E-1
	Annotation Cluster 3	Enrichment Score: 2.32	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	extracellular space	RT		66	5.5E-4	3.5E-1
☐	UP_SEQ_FEATURE	disulfide bond	RT		55	1.4E-3	1.0E0
☐	GOTERM_CC_ALL	extracellular region part	RT		66	2.2E-3	2.9E-1
☐	SP_PIR_KEYWORDS	glycoprotein	RT		82	3.8E-3	4.8E-1
☐	GOTERM_CC_ALL	extracellular region	RT		67	5.7E-3	5.2E-1
☐	UP_SEQ_FEATURE	signal peptide	RT		60	1.6E-2	1.0E0
☐	SP_PIR_KEYWORDS	signal	RT		68	1.9E-2	7.2E-1
☐	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		64	2.5E-2	1.0E0
	Annotation Cluster 4	Enrichment Score: 2.14	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	receptor	RT		44	5.3E-4	1.1E-1
☐	GOTERM_MF_ALL	receptor activity	RT		51	1.3E-3	6.8E-1
☐	GOTERM_MF_ALL	molecular transducer activity	RT		56	3.1E-3	8.1E-1
☐	GOTERM_MF_ALL	signal transducer activity	RT		56	3.1E-3	8.1E-1
☐	GOTERM_BP_ALL	cell surface receptor linked signal transduction	RT		40	3.1E-2	8.3E-1
☐	GOTERM_BP_ALL	signal transduction	RT		68	5.7E-2	9.1E-1
☐	GOTERM_BP_ALL	cell communication	RT		72	9.2E-2	9.5E-1
	Annotation Cluster 5	Enrichment Score: 2.12	G	🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	heterodimer	RT		8	5.6E-5	4.7E-2
☐	SP_PIR_KEYWORDS	calcium binding	RT		8	1.8E-4	7.3E-2
☐	SP_PIR_KEYWORDS	inflammation	RT		4	6.2E-3	4.9E-1
☐	PIR_SUPERFAMILY	PIRSF002353:S-100 protein	RT		3	4.0E-2	1.0E0
☐	INTERPRO	S100/CaBP-9k-type, calcium binding, subdomain	RT		3	5.8E-2	1.0E0
☐	INTERPRO	S100/CaBP-9k-type, calcium binding	RT		3	7.6E-2	1.0E0
☐	SP_PIR_KEYWORDS	EF hand	RT		3	1.4E-1	9.4E-1
	Annotation Cluster 6	Enrichment Score: 2	G	🟩	Count	P_Value	Benjamini

☐	**GOTERM_BP_ALL**	negative regulation of cell motility	**RT**		5	1.9E-3	3.8E-1
☐	**GOTERM_BP_ALL**	negative regulation of locomotion	**RT**		5	2.2E-3	3.7E-1
☐	**GOTERM_BP_ALL**	regulation of cell motility	**RT**		7	6.7E-3	5.2E-1
☐	**GOTERM_BP_ALL**	regulation of locomotion	**RT**		7	8.5E-3	5.6E-1
☐	**GOTERM_BP_ALL**	locomotion	**RT**		7	1.3E-2	6.8E-1
☐	**GOTERM_BP_ALL**	localization of cell	**RT**		16	1.4E-2	6.9E-1
☐	**GOTERM_BP_ALL**	cell motility	**RT**		16	1.4E-2	6.9E-1
☐	**GOTERM_BP_ALL**	regulation of cell migration	**RT**		4	1.9E-1	9.9E-1
	Annotation Cluster 7	Enrichment Score: 1.88	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	leukocyte chemotaxis	**RT**		5	1.6E-3	3.7E-1
☐	**GOTERM_BP_ALL**	leukocyte migration	**RT**		5	7.2E-3	5.4E-1
☐	**GOTERM_BP_ALL**	induction of positive chemotaxis	**RT**		3	1.9E-2	7.4E-1
☐	**GOTERM_BP_ALL**	positive regulation of positive chemotaxis	**RT**		3	1.9E-2	7.4E-1
☐	**GOTERM_BP_ALL**	regulation of positive chemotaxis	**RT**		3	1.9E-2	7.4E-1
☐	**GOTERM_BP_ALL**	positive regulation of chemotaxis	**RT**		3	2.2E-2	7.8E-1
☐	**GOTERM_BP_ALL**	regulation of chemotaxis	**RT**		3	2.2E-2	7.8E-1
☐	**GOTERM_BP_ALL**	positive chemotaxis	**RT**		3	2.2E-2	7.8E-1
	Annotation Cluster 8	Enrichment Score: 1.86	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	lysosome	**RT**		11	2.0E-4	5.5E-2
☐	**GOTERM_CC_ALL**	vacuole	**RT**		13	1.5E-3	4.4E-1
☐	**GOTERM_CC_ALL**	lytic vacuole	**RT**		12	1.8E-3	3.7E-1
☐	**GOTERM_CC_ALL**	lysosome	**RT**		12	1.8E-3	3.7E-1
☐	**UP_SEQ_FEATURE**	propeptide:Activation peptide	**RT**		7	2.0E-3	1.0E0
☐	**PIR_SUPERFAMILY**	PIRSF001182:papain	**RT**		4	3.5E-3	1.0E0
☐	**INTERPRO**	Proteinase inhibitor I29, cathepsin propeptide	**RT**		4	5.6E-3	1.0E0
☐	**INTERPRO**	Peptidase C1A, papain C-terminal	**RT**		4	1.0E-2	1.0E0
☐	**SMART**	Pept_C1	**RT**		4	1.3E-2	9.8E-1
☐	**SP_PIR_KEYWORDS**	Zymogen	**RT**		10	1.8E-2	7.4E-1
☐	**INTERPRO**	Peptidase C1A, papain	**RT**		4	1.9E-2	1.0E0
☐	**SP_PIR_KEYWORDS**	thiol protease	**RT**		6	7.8E-2	9.0E-1
☐	**INTERPRO**	Peptidase, cysteine peptidase active site	**RT**		4	7.9E-2	1.0E0
☐	**KEGG_PATHWAY**	Antigen processing and presentation	**RT**		5	1.6E-1	9.1E-1
☐	**GOTERM_MF_ALL**	cysteine-type endopeptidase activity	**RT**		5	1.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	endopeptidase activity	**RT**		13	2.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	cysteine-type peptidase activity	**RT**		6	2.9E-1	1.0E0
	Annotation Cluster 9	Enrichment Score: 1.82	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	apoptosis	**RT**		28	1.9E-3	3.8E-1
☐	**GOTERM_BP_ALL**	death	**RT**		29	2.1E-3	3.9E-1
☐	**GOTERM_BP_ALL**	cell death	**RT**		29	2.1E-3	3.9E-1
☐	**GOTERM_BP_ALL**	programmed cell death	**RT**		28	2.5E-3	3.7E-1
☐	**GOTERM_BP_ALL**	regulation of apoptosis	**RT**		21	2.6E-3	3.7E-1
☐	**GOTERM_BP_ALL**	regulation of programmed cell death	**RT**		21	3.1E-3	4.0E-1
☐	**GOTERM_BP_ALL**	cell development	**RT**		41	5.9E-3	5.0E-1
☐	**GOTERM_BP_ALL**	positive regulation of cellular process	**RT**		32	8.5E-3	5.7E-1
☐	**GOTERM_BP_ALL**	positive regulation of apoptosis	**RT**		11	1.6E-2	7.3E-1
☐	**GOTERM_BP_ALL**	positive regulation of biological process	**RT**		34	1.7E-2	7.3E-1
☐	**GOTERM_BP_ALL**	positive regulation of programmed cell death	**RT**		11	1.8E-2	7.3E-1
☐	**GOTERM_BP_ALL**	induction of programmed cell death	**RT**		9	2.6E-2	8.0E-1
☐	**GOTERM_BP_ALL**	induction of apoptosis	**RT**		9	2.6E-2	8.0E-1

☐	GOTERM_BP_ALL	negative regulation of apoptosis	RT	10	2.7E-2	8.1E-1
☐	GOTERM_BP_ALL	negative regulation of programmed cell death	RT	10	3.0E-2	8.3E-1
☐	SP_PIR_KEYWORDS	apoptosis	RT	11	5.5E-2	8.7E-1
☐	GOTERM_BP_ALL	cellular developmental process	RT	50	6.7E-2	9.2E-1
☐	GOTERM_BP_ALL	cell differentiation	RT	50	6.7E-2	9.2E-1
☐	GOTERM_BP_ALL	positive regulation of cellular metabolic process	RT	13	2.4E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of metabolic process	RT	13	3.2E-1	1.0E0
	Annotation Cluster 10	Enrichment Score: 1.79	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	positive regulation of defense response	RT	4	3.7E-3	4.2E-1
☐	GOTERM_BP_ALL	positive regulation of inflammatory response	RT	4	3.7E-3	4.2E-1
☐	GOTERM_BP_ALL	regulation of defense response	RT	4	3.1E-2	8.3E-1
☐	GOTERM_BP_ALL	regulation of inflammatory response	RT	4	3.1E-2	8.3E-1
☐	GOTERM_BP_ALL	regulation of response to stimulus	RT	4	8.0E-2	9.4E-1
	Annotation Cluster 11	Enrichment Score: 1.66	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	integrin binding	RT	6	2.6E-4	5.0E-1
☐	GOTERM_MF_ALL	protein complex binding	RT	6	9.7E-3	8.4E-1
☐	UP_SEQ_FEATURE	short sequence motif:Cell attachment site	RT	4	1.5E-1	1.0E0
☐	KEGG_PATHWAY	Cell Communication	RT	4	6.1E-1	1.0E0
	Annotation Cluster 12	Enrichment Score: 1.64	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	germ cell development	RT	7	1.7E-4	1.2E-1
☐	GOTERM_BP_ALL	myeloid cell differentiation	RT	9	3.1E-3	3.9E-1
☐	GOTERM_BP_ALL	erythrocyte differentiation	RT	4	5.5E-2	9.1E-1
☐	GOTERM_BP_ALL	positive regulation of cell differentiation	RT	3	3.6E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of developmental process	RT	3	5.8E-1	1.0E0
	Annotation Cluster 13	Enrichment Score: 1.52	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	bone mineralization	RT	6	7.5E-4	2.4E-1
☐	GOTERM_BP_ALL	regulation of bone mineralization	RT	5	7.8E-4	2.4E-1
☐	GOTERM_BP_ALL	hemopoietic or lymphoid organ development	RT	15	2.2E-3	3.7E-1
☐	GOTERM_BP_ALL	hemopoiesis	RT	14	2.6E-3	3.6E-1
☐	GOTERM_BP_ALL	myeloid cell differentiation	RT	9	3.1E-3	3.9E-1
☐	GOTERM_BP_ALL	regulation of myeloid cell differentiation	RT	6	3.3E-3	3.9E-1
☐	GOTERM_BP_ALL	regulation of ossification	RT	5	3.7E-3	4.1E-1
☐	GOTERM_BP_ALL	immune system development	RT	15	3.9E-3	4.1E-1
☐	GOTERM_BP_ALL	positive regulation of bone mineralization	RT	3	4.4E-3	4.3E-1
☐	GOTERM_BP_ALL	regulation of bone remodeling	RT	5	5.9E-3	4.9E-1
☐	GOTERM_BP_ALL	positive regulation of ossification	RT	3	9.1E-3	5.7E-1
☐	GOTERM_BP_ALL	positive regulation of bone remodeling	RT	3	9.1E-3	5.7E-1
☐	GOTERM_BP_ALL	regulation of cell differentiation	RT	10	2.1E-2	7.7E-1
☐	GOTERM_BP_ALL	ossification	RT	7	2.7E-2	8.1E-1
☐	GOTERM_BP_ALL	biomineral formation	RT	7	2.8E-2	8.2E-1
☐	GOTERM_BP_ALL	skeletal development	RT	10	3.0E-2	8.3E-1
☐	GOTERM_BP_ALL	regulation of osteoblast differentiation	RT	3	3.6E-2	8.4E-1
☐	GOTERM_BP_ALL	bone remodeling	RT	7	3.8E-2	8.6E-1
☐	GOTERM_BP_ALL	negative regulation of bone remodeling	RT	3	4.0E-2	8.6E-1
☐	GOTERM_BP_ALL	erythrocyte differentiation	RT	4	5.5E-2	9.1E-1
☐	GOTERM_BP_ALL	negative regulation of cell differentiation	RT	6	5.9E-2	9.2E-1
☐	GOTERM_BP_ALL	tissue remodeling	RT	7	7.2E-2	9.3E-1
☐	SP_PIR_KEYWORDS	cytokine	RT	8	7.3E-2	8.9E-1

☐	**GOTERM_BP_ALL**	negative regulation of myeloid cell differentiation	RT	▮	3	7.4E-2	9.3E-1
☐	**GOTERM_BP_ALL**	negative regulation of developmental process	RT	▮	6	1.1E-1	9.7E-1
☐	**GOTERM_BP_ALL**	regulation of developmental process	RT	▮	11	1.2E-1	9.8E-1
☐	**GOTERM_BP_ALL**	transmembrane receptor protein serine/threonine kinase signaling pathway	RT	▮	5	1.2E-1	9.7E-1
☐	**GOTERM_BP_ALL**	osteoblast differentiation	RT	▮	3	1.4E-1	9.8E-1
☐	**GOTERM_BP_ALL**	BMP signaling pathway	RT	▮	3	1.6E-1	9.9E-1
☐	**GOTERM_CC_ALL**	proteinaceous extracellular matrix	RT	▮	10	1.6E-1	1.0E0
☐	**GOTERM_CC_ALL**	extracellular matrix	RT	▮	10	1.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	negative regulation of multicellular organismal process	RT	▮	3	1.9E-1	9.9E-1
☐	**GOTERM_BP_ALL**	tissue development	RT	▮	10	2.2E-1	9.9E-1
☐	**GOTERM_MF_ALL**	cytokine activity	RT	▮	7	3.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	receptor binding	RT	▮	14	6.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	growth factor activity	RT	▮	4	7.1E-1	1.0E0
	Annotation Cluster 14	Enrichment Score: 1.39	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	calcium binding	RT	▮	8	1.8E-4	7.3E-2
☐	**GOTERM_BP_ALL**	muscle system process	RT	▮	3	6.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	muscle contraction	RT	▮	3	6.1E-1	1.0E0
	Annotation Cluster 15	Enrichment Score: 1.38	G	🟩	Count	P_Value	Benjamini
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Calcium 3 (via carbonyl oxygen)	RT	▮	5	3.2E-4	9.9E-1
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Calcium 4 (via carbonyl oxygen)	RT	▮	4	4.1E-4	9.5E-1
☐	**UP_SEQ_FEATURE**	propeptide:Activation peptide	RT	▮	7	2.0E-3	1.0E0
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Calcium 1	RT	▮	5	9.5E-3	1.0E0
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Calcium 2	RT	▮	5	1.3E-2	1.0E0
☐	**GOTERM_BP_ALL**	peptidoglycan metabolic process	RT	▮	4	1.3E-2	6.8E-1
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Calcium 3	RT	▮	4	1.4E-2	1.0E0
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Calcium 2 (via carbonyl oxygen)	RT	▮	4	2.0E-2	1.0E0
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Zinc 2 (in inhibited form)	RT	▮	3	2.2E-2	1.0E0
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Zinc 2 (catalytic)	RT	▮	3	2.6E-2	1.0E0
☐	**SP_PIR_KEYWORDS**	metalloproteinase	RT	▮	3	3.0E-2	8.1E-1
☐	**INTERPRO**	Peptidoglycan binding-like	RT	▮	3	5.8E-2	1.0E0
☐	**SP_PIR_KEYWORDS**	extracellular matrix	RT	▮	9	7.1E-2	8.9E-1
☐	**UP_SEQ_FEATURE**	domain:Hemopexin-like 3	RT	▮	3	7.2E-2	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Hemopexin-like 4	RT	▮	3	7.2E-2	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Hemopexin-like 1	RT	▮	3	7.9E-2	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Hemopexin-like 2	RT	▮	3	7.9E-2	1.0E0
☐	**INTERPRO**	Hemopexin	RT	▮	3	9.0E-2	1.0E0
☐	**SMART**	HX	RT	▮	3	9.4E-2	1.0E0
☐	**INTERPRO**	Peptidase, metallopeptidases	RT	▮	3	9.6E-2	1.0E0
☐	**SMART**	ZnMc	RT	▮	3	1.0E-1	1.0E0
☐	**INTERPRO**	Peptidase M10A and M12B, matrixin and adamalysin	RT	▮	3	1.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	short sequence motif:Cysteine switch	RT	▮	3	1.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Zinc 1	RT	▮	3	3.1E-1	1.0E0
☐	**INTERPRO**	Peptidase M, neutral zinc metallopeptidases, zinc-binding site	RT	▮	3	4.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	metalloendopeptidase activity	RT	▮	3	6.5E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	metalloprotease	RT	▮	3	7.6E-1	1.0E0
	Annotation Cluster 16	Enrichment Score: 1.31	G	🟩	Count	P_Value	Benjamini

☐	GOTERM_BP_ALL	regulation of kinase activity	RT	10	1.4E-2	7.0E-1
☐	GOTERM_BP_ALL	regulation of transferase activity	RT	10	1.8E-2	7.4E-1
☐	GOTERM_BP_ALL	regulation of protein kinase activity	RT	9	3.1E-2	8.3E-1
☐	GOTERM_BP_ALL	negative regulation of protein kinase activity	RT	4	8.0E-2	9.4E-1
☐	GOTERM_BP_ALL	negative regulation of kinase activity	RT	4	8.0E-2	9.4E-1
☐	GOTERM_BP_ALL	negative regulation of transferase activity	RT	4	8.9E-2	9.5E-1
☐	GOTERM_BP_ALL	negative regulation of catalytic activity	RT	4	1.5E-1	9.8E-1
	Annotation Cluster 17	Enrichment Score: 1.27	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	negative regulation of progression through cell cycle	RT	10	3.2E-3	3.9E-1
☐	GOTERM_BP_ALL	regulation of progression through cell cycle	RT	16	1.5E-2	7.2E-1
☐	GOTERM_BP_ALL	regulation of cell cycle	RT	16	1.6E-2	7.3E-1
☐	GOTERM_BP_ALL	cell cycle process	RT	18	1.3E-1	9.8E-1
☐	GOTERM_BP_ALL	cell cycle	RT	19	3.3E-1	1.0E0
☐	SP_PIR_KEYWORDS	cell cycle	RT	8	6.7E-1	1.0E0
	Annotation Cluster 18	Enrichment Score: 1.24	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	lipid binding	RT	16	3.2E-2	9.9E-1
☐	GOTERM_MF_ALL	phospholipid binding	RT	10	6.2E-2	1.0E0
☐	GOTERM_MF_ALL	phosphoinositide binding	RT	8	9.6E-2	1.0E0
	Annotation Cluster 19	Enrichment Score: 1.23	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	zinc-finger	RT	39	1.3E-2	6.4E-1
☐	SP_PIR_KEYWORDS	zinc	RT	46	2.3E-2	7.6E-1
☐	GOTERM_MF_ALL	transition metal ion binding	RT	65	3.7E-2	9.9E-1
☐	SP_PIR_KEYWORDS	metal-binding	RT	57	6.9E-2	9.0E-1
☐	GOTERM_MF_ALL	cation binding	RT	84	8.7E-2	1.0E0
☐	GOTERM_MF_ALL	zinc ion binding	RT	51	8.9E-2	1.0E0
☐	GOTERM_MF_ALL	ion binding	RT	90	1.4E-1	1.0E0
☐	GOTERM_MF_ALL	metal ion binding	RT	87	1.8E-1	1.0E0
	Annotation Cluster 20	Enrichment Score: 1.22	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	pancreatic ribonuclease activity	RT	4	4.6E-3	7.9E-1
☐	INTERPRO	Pancreatic ribonuclease	RT	4	4.7E-3	1.0E0
☐	SMART	RNAse_Pc	RT	4	5.1E-3	9.6E-1
☐	GOTERM_MF_ALL	endoribonuclease activity, producing 3'-phosphomonoesters	RT	4	6.5E-3	8.0E-1
☐	GOTERM_MF_ALL	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 3'-phosphomonoesters	RT	4	8.8E-3	8.6E-1
☐	GOTERM_MF_ALL	ribonuclease activity	RT	5	4.6E-2	9.9E-1
☐	GOTERM_MF_ALL	endoribonuclease activity	RT	4	6.3E-2	1.0E0
☐	UP_SEQ_FEATURE	active site:Proton donor	RT	5	2.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	nuclease	RT	4	2.2E-1	9.8E-1
☐	UP_SEQ_FEATURE	region of interest:Substrate binding	RT	3	2.8E-1	1.0E0
☐	GOTERM_MF_ALL	endonuclease activity	RT	4	2.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	Endonuclease	RT	3	3.0E-1	9.9E-1
☐	GOTERM_MF_ALL	nuclease activity	RT	5	3.9E-1	1.0E0
☐	GOTERM_MF_ALL	hydrolase activity, acting on ester bonds	RT	10	9.3E-1	1.0E0
	Annotation Cluster 21	Enrichment Score: 1.21	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	RT	5	3.7E-2	9.9E-1
☐	GOTERM_MF_ALL	dioxygenase activity	RT	5	3.7E-2	9.9E-1
☐	GOTERM_MF_ALL	oxidoreductase activity, acting on single donors with incorporation of molecular	RT	5	3.9E-2	9.9E-1

		oxygen				
☐	GOTERM_MF_ALL	iron ion binding	RT	10	2.5E-1	1.0E0
	Annotation Cluster 22	Enrichment Score: 1.2	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	germ cell development	RT	7	1.7E-4	1.2E-1
☐	GOTERM_BP_ALL	gamete generation	RT	11	5.3E-2	9.0E-1
☐	GOTERM_BP_ALL	sexual reproduction	RT	12	7.2E-2	9.3E-1
☐	GOTERM_BP_ALL	reproduction	RT	13	2.9E-1	1.0E0
☐	GOTERM_BP_ALL	male gamete generation	RT	5	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	spermatogenesis	RT	5	6.0E-1	1.0E0
	Annotation Cluster 23	Enrichment Score: 1.17	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell-substrate adhesion	RT	8	2.2E-3	3.4E-1
☐	KEGG_PATHWAY	ECM-receptor interaction	RT	8	7.3E-3	7.9E-1
☐	GOTERM_BP_ALL	cell-matrix adhesion	RT	7	7.6E-3	5.4E-1
☐	PIR_SUPERFAMILY	PIRSF002512:integrin, beta subunit	RT	3	1.2E-2	1.0E0
☐	INTERPRO	Integrin beta subunit, subgroup	RT	3	1.2E-2	1.0E0
☐	INTERPRO	Integrin beta subunit, tail	RT	3	1.6E-2	1.0E0
☐	INTERPRO	Integrin beta subunit, N-terminal	RT	3	1.6E-2	1.0E0
☐	INTERPRO	Integrin beta subunit, C-terminal	RT	3	1.9E-2	1.0E0
☐	INTERPRO	Integrin beta subunit	RT	3	1.9E-2	1.0E0
☐	SMART	INB	RT	3	2.0E-2	9.8E-1
☐	GOTERM_BP_ALL	cell adhesion	RT	23	3.5E-2	8.4E-1
☐	GOTERM_BP_ALL	biological adhesion	RT	23	3.5E-2	8.4E-1
☐	KEGG_PATHWAY	Focal adhesion	RT	10	7.0E-2	8.5E-1
☐	SP_PIR_KEYWORDS	duplication	RT	6	1.3E-1	9.4E-1
☐	SP_PIR_KEYWORDS	Integrin	RT	4	1.6E-1	9.5E-1
☐	GOTERM_CC_ALL	integrin complex	RT	3	1.6E-1	1.0E0
☐	INTERPRO	von Willebrand factor, type A	RT	4	2.4E-1	1.0E0
☐	SMART	VWA	RT	4	2.7E-1	1.0E0
☐	INTERPRO	Plexin/semaphorin/integrin	RT	3	2.8E-1	1.0E0
☐	GOTERM_BP_ALL	integrin-mediated signaling pathway	RT	4	2.8E-1	1.0E0
☐	SMART	PSI	RT	3	2.9E-1	1.0E0
☐	SP_PIR_KEYWORDS	cell adhesion	RT	10	3.2E-1	9.9E-1
☐	KEGG_PATHWAY	Cell adhesion molecules (CAMs)	RT	5	5.0E-1	9.9E-1
☐	GOTERM_CC_ALL	receptor complex	RT	3	5.1E-1	1.0E0
☐	GOTERM_MF_ALL	identical protein binding	RT	7	5.9E-1	1.0E0
☐	KEGG_PATHWAY	Regulation of actin cytoskeleton	RT	5	8.0E-1	1.0E0
	Annotation Cluster 24	Enrichment Score: 1.15	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	pattern binding	RT	10	4.7E-4	4.7E-1
☐	GOTERM_MF_ALL	polysaccharide binding	RT	9	1.3E-3	5.9E-1
☐	GOTERM_MF_ALL	heparin binding	RT	7	4.1E-3	7.9E-1
☐	GOTERM_MF_ALL	carbohydrate binding	RT	15	5.6E-3	8.1E-1
☐	GOTERM_BP_ALL	chondrocyte differentiation	RT	4	6.4E-3	5.1E-1
☐	GOTERM_MF_ALL	glycosaminoglycan binding	RT	7	1.4E-2	9.1E-1
☐	GOTERM_BP_ALL	cartilage development	RT	5	3.4E-2	8.4E-1
☐	GOTERM_BP_ALL	anatomical structure formation	RT	10	4.2E-2	8.6E-1
☐	UP_SEQ_FEATURE	region of interest:Heparin-binding	RT	3	4.7E-2	1.0E0
☐	GOTERM_BP_ALL	angiogenesis	RT	8	6.0E-2	9.2E-1
☐	SP_PIR_KEYWORDS	heparin-binding	RT	4	1.2E-1	9.4E-1
☐	GOTERM_BP_ALL	blood vessel development	RT	9	1.4E-1	9.8E-1
☐	GOTERM_BP_ALL	vasculature development	RT	9	1.5E-1	9.8E-1

☐	GOTERM_BP_ALL	blood vessel morphogenesis	RT		8	1.5E-1	9.8E-1
☐	GOTERM_BP_ALL	branching morphogenesis of a tube	RT		4	1.6E-1	9.9E-1
☐	GOTERM_BP_ALL	morphogenesis of a branching structure	RT		4	1.9E-1	9.9E-1
☐	GOTERM_BP_ALL	lung development	RT		4	1.9E-1	9.9E-1
☐	GOTERM_BP_ALL	respiratory tube development	RT		4	2.0E-1	9.9E-1
☐	GOTERM_BP_ALL	heart development	RT		7	2.2E-1	9.9E-1
☐	GOTERM_BP_ALL	tube morphogenesis	RT		6	2.3E-1	9.9E-1
☐	GOTERM_BP_ALL	tube development	RT		7	2.8E-1	1.0E0
☐	GOTERM_BP_ALL	sensory organ development	RT		6	3.6E-1	1.0E0
☐	GOTERM_BP_ALL	central nervous system development	RT		7	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	brain development	RT		5	6.1E-1	1.0E0
☐	GOTERM_BP_ALL	organ morphogenesis	RT		12	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	cell fate commitment	RT		3	6.7E-1	1.0E0
	Annotation Cluster 25	Enrichment Score: 1.14	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regulation of a molecular function	RT		18	8.1E-3	5.6E-1
☐	GOTERM_BP_ALL	regulation of kinase activity	RT		10	1.4E-2	7.0E-1
☐	GOTERM_BP_ALL	regulation of transferase activity	RT		10	1.8E-2	7.4E-1
☐	GOTERM_BP_ALL	regulation of catalytic activity	RT		15	2.6E-2	8.1E-1
☐	GOTERM_BP_ALL	regulation of protein kinase activity	RT		9	3.1E-2	8.3E-1
☐	GOTERM_BP_ALL	positive regulation of catalytic activity	RT		6	3.7E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of protein kinase activity	RT		4	4.2E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of kinase activity	RT		4	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of transferase activity	RT		4	4.8E-1	1.0E0
	Annotation Cluster 26	Enrichment Score: 1.11	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	UDP-galactosyltransferase activity	RT		4	6.5E-3	8.0E-1
☐	GOTERM_MF_ALL	galactosyltransferase activity	RT		4	2.5E-2	9.8E-1
☐	SP_PIR_KEYWORDS	signal-anchor	RT		14	3.1E-2	7.9E-1
☐	SP_PIR_KEYWORDS	glycosyltransferase	RT		9	4.1E-2	8.5E-1
☐	KEGG_PATHWAY	Glycan structures - biosynthesis 2	RT		5	5.5E-2	8.6E-1
☐	GOTERM_MF_ALL	UDP-glycosyltransferase activity	RT		6	6.0E-2	1.0E0
☐	GOTERM_MF_ALL	transferase activity, transferring glycosyl groups	RT		10	7.2E-2	1.0E0
☐	KEGG_PATHWAY	Glycosphingolipid biosynthesis - neo-lactoseries	RT		3	7.2E-2	8.3E-1
☐	GOTERM_BP_ALL	glycoprotein metabolic process	RT		6	1.1E-1	9.7E-1
☐	GOTERM_BP_ALL	protein amino acid glycosylation	RT		5	1.1E-1	9.7E-1
☐	GOTERM_MF_ALL	transferase activity, transferring hexosyl groups	RT		7	1.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	golgi apparatus	RT		14	1.2E-1	9.3E-1
☐	GOTERM_BP_ALL	biopolymer glycosylation	RT		5	1.2E-1	9.7E-1
☐	GOTERM_BP_ALL	glycoprotein biosynthetic process	RT		5	1.5E-1	9.8E-1
☐	UP_SEQ_FEATURE	topological domain:Lumenal	RT		8	3.5E-1	1.0E0
☐	GOTERM_CC_ALL	Golgi apparatus	RT		14	4.6E-1	1.0E0
	Annotation Cluster 27	Enrichment Score: 1.01	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	developmental process	RT		80	2.0E-2	7.4E-1
☐	GOTERM_BP_ALL	cellular developmental process	RT		50	6.7E-2	9.2E-1
☐	GOTERM_BP_ALL	cell differentiation	RT		50	6.7E-2	9.2E-1
☐	GOTERM_BP_ALL	anatomical structure development	RT		54	8.2E-2	9.4E-1
☐	GOTERM_BP_ALL	organ development	RT		39	9.0E-2	9.5E-1
☐	GOTERM_BP_ALL	system development	RT		46	1.1E-1	9.7E-1
☐	GOTERM_BP_ALL	anatomical structure morphogenesis	RT		31	2.0E-1	9.9E-1

☐	GOTERM_BP_ALL	multicellular organismal process	RT	69	2.3E-1	9.9E-1
☐	GOTERM_BP_ALL	multicellular organismal development	RT	54	2.5E-1	1.0E0
	Annotation Cluster 28	Enrichment Score: 0.99	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	collagen degradation	RT	3	5.0E-2	8.9E-1
☐	GOTERM_BP_ALL	multicellular organismal macromolecule catabolic process	RT	3	6.2E-2	9.2E-1
☐	GOTERM_BP_ALL	multicellular organismal protein metabolic process	RT	3	6.2E-2	9.2E-1
☐	GOTERM_BP_ALL	collagen catabolic process	RT	3	6.2E-2	9.2E-1
☐	GOTERM_BP_ALL	protein digestion	RT	3	6.2E-2	9.2E-1
☐	GOTERM_BP_ALL	multicellular organismal macromolecule metabolic process	RT	3	6.2E-2	9.2E-1
☐	GOTERM_BP_ALL	multicellular organismal protein catabolic process	RT	3	6.2E-2	9.2E-1
☐	GOTERM_BP_ALL	collagen metabolic process	RT	3	6.8E-2	9.2E-1
☐	GOTERM_BP_ALL	multicellular organismal catabolic process	RT	3	6.8E-2	9.2E-1
☐	GOTERM_BP_ALL	multicellular organismal metabolic process	RT	3	9.4E-2	9.6E-1
☐	GOTERM_BP_ALL	digestion	RT	3	2.8E-1	1.0E0
☐	GOTERM_BP_ALL	biopolymer catabolic process	RT	7	5.3E-1	1.0E0
☐	GOTERM_BP_ALL	protein catabolic process	RT	5	6.5E-1	1.0E0
	Annotation Cluster 29	Enrichment Score: 0.99	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	nucleotide catabolic process	RT	4	1.1E-2	6.4E-1
☐	GOTERM_BP_ALL	nucleotide metabolic process	RT	7	2.8E-1	1.0E0
☐	GOTERM_BP_ALL	nucleobase, nucleoside and nucleotide metabolic process	RT	7	3.3E-1	1.0E0
	Annotation Cluster 30	Enrichment Score: 0.99	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein modification process	RT	47	2.2E-2	7.8E-1
☐	GOTERM_BP_ALL	cellular macromolecule metabolic process	RT	79	3.2E-2	8.3E-1
☐	GOTERM_BP_ALL	biopolymer modification	RT	47	4.0E-2	8.6E-1
☐	GOTERM_BP_ALL	protein metabolic process	RT	80	4.6E-2	8.8E-1
☐	GOTERM_BP_ALL	cellular protein metabolic process	RT	75	7.6E-2	9.4E-1
☐	GOTERM_MF_ALL	catalytic activity	RT	126	8.6E-2	1.0E0
☐	GOTERM_BP_ALL	metabolic process	RT	172	1.7E-1	9.9E-1
☐	GOTERM_BP_ALL	primary metabolic process	RT	155	2.0E-1	9.9E-1
☐	GOTERM_BP_ALL	cellular metabolic process	RT	153	2.8E-1	1.0E0
☐	GOTERM_BP_ALL	macromolecule metabolic process	RT	133	3.3E-1	1.0E0
☐	GOTERM_BP_ALL	biopolymer metabolic process	RT	97	5.5E-1	1.0E0
	Annotation Cluster 31	Enrichment Score: 0.95	G	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	propeptide:Activation peptide	RT	7	2.0E-3	1.0E0
☐	SP_PIR_KEYWORDS	Zymogen	RT	10	1.8E-2	7.4E-1
☐	SP_PIR_KEYWORDS	hydrolase	RT	35	1.1E-1	9.4E-1
☐	SP_PIR_KEYWORDS	protease	RT	15	1.3E-1	9.4E-1
☐	GOTERM_MF_ALL	endopeptidase activity	RT	13	2.5E-1	1.0E0
☐	GOTERM_BP_ALL	proteolysis	RT	18	3.7E-1	1.0E0
☐	GOTERM_MF_ALL	peptidase activity	RT	15	6.3E-1	1.0E0
☐	GOTERM_MF_ALL	hydrolase activity	RT	43	7.8E-1	1.0E0
	Annotation Cluster 32	Enrichment Score: 0.9	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	antimicrobial	RT	4	7.0E-2	9.0E-1
☐	GOTERM_BP_ALL	response to other organism	RT	7	9.6E-2	9.6E-1
☐	GOTERM_BP_ALL	response to bacterium	RT	5	1.2E-1	9.7E-1
☐	GOTERM_BP_ALL	response to biotic stimulus	RT	9	1.3E-1	9.7E-1
☐	GOTERM_BP_ALL	defense response to bacterium	RT	4	1.5E-1	9.8E-1
☐	SP_PIR_KEYWORDS	antibiotic	RT	3	1.8E-1	9.7E-1

☐	GOTERM_BP_ALL	multi-organism process	RT		8	1.9E-1	9.9E-1
	Annotation Cluster 33	Enrichment Score: 0.89	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	cell proliferation	RT		19	5.5E-2	9.1E-1
☐	GOTERM_BP_ALL	positive regulation of cell proliferation	RT		8	1.8E-1	9.9E-1
☐	GOTERM_BP_ALL	regulation of cell proliferation	RT		12	2.2E-1	9.9E-1
	Annotation Cluster 34	Enrichment Score: 0.89	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	profilin binding	RT		3	9.2E-3	8.5E-1
☐	GOTERM_BP_ALL	actin polymerization and/or depolymerization	RT		5	2.2E-2	7.6E-1
☐	GOTERM_BP_ALL	actin filament-based process	RT		9	7.7E-2	9.4E-1
☐	GOTERM_BP_ALL	actin cytoskeleton organization and biogenesis	RT		8	1.3E-1	9.8E-1
☐	GOTERM_CC_ALL	focal adhesion	RT		3	1.4E-1	1.0E0
☐	GOTERM_CC_ALL	adherens junction	RT		4	1.7E-1	1.0E0
☐	GOTERM_CC_ALL	cell-substrate adherens junction	RT		3	1.7E-1	1.0E0
☐	GOTERM_CC_ALL	cell-matrix junction	RT		3	2.0E-1	1.0E0
☐	GOTERM_CC_ALL	basolateral plasma membrane	RT		4	2.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	actin-binding	RT		5	5.1E-1	1.0E0
☐	GOTERM_CC_ALL	cell junction	RT		7	8.3E-1	1.0E0
	Annotation Cluster 35	Enrichment Score: 0.89	G	🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:SET	RT		3	4.1E-2	1.0E0
☐	INTERPRO	SET	RT		3	2.3E-1	1.0E0
☐	SMART	SET	RT		3	2.4E-1	1.0E0
	Annotation Cluster 36	Enrichment Score: 0.88	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	histone modification	RT		4	7.3E-2	9.3E-1
☐	GOTERM_BP_ALL	covalent chromatin modification	RT		4	8.9E-2	9.5E-1
☐	SP_PIR_KEYWORDS	bromodomain	RT		3	1.3E-1	9.4E-1
☐	INTERPRO	Bromodomain	RT		3	1.9E-1	1.0E0
☐	SMART	BROMO	RT		3	2.3E-1	1.0E0
	Annotation Cluster 37	Enrichment Score: 0.88	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	menstrual cycle phase	RT		4	3.9E-2	8.6E-1
☐	GOTERM_BP_ALL	menstrual cycle process	RT		4	4.2E-2	8.6E-1
☐	GOTERM_BP_ALL	female gonad development	RT		4	5.8E-2	9.2E-1
☐	GOTERM_BP_ALL	development of primary female sexual characteristics	RT		4	6.5E-2	9.2E-1
☐	GOTERM_BP_ALL	female sex differentiation	RT		4	6.5E-2	9.2E-1
☐	GOTERM_BP_ALL	menstrual cycle	RT		4	6.9E-2	9.2E-1
☐	GOTERM_BP_ALL	rhythmic process	RT		5	1.0E-1	9.6E-1
☐	GOTERM_BP_ALL	gonad development	RT		4	1.4E-1	9.8E-1
☐	GOTERM_BP_ALL	reproductive structure development	RT		4	1.5E-1	9.8E-1
☐	GOTERM_BP_ALL	development of primary sexual characteristics	RT		4	1.8E-1	9.9E-1
☐	GOTERM_BP_ALL	multicellular organism reproduction	RT		4	2.3E-1	9.9E-1
☐	GOTERM_BP_ALL	reproductive process in a multicellular organism	RT		4	2.3E-1	9.9E-1
☐	GOTERM_BP_ALL	sex differentiation	RT		4	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive developmental process	RT		4	3.7E-1	1.0E0
☐	GOTERM_BP_ALL	reproductive process	RT		4	8.9E-1	1.0E0
	Annotation Cluster 38	Enrichment Score: 0.87	G	🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	diacylglycerol binding	RT		4	1.0E-1	1.0E0
☐	INTERPRO	Protein kinase C, phorbol ester/diacylglycerol binding	RT		4	1.5E-1	1.0E0
☐	SMART	C1	RT		4	1.6E-1	1.0E0
	Annotation Cluster 39	Enrichment Score: 0.86	G	🟩	Count	P_Value	Benjamini

☐	**GOTERM_BP_ALL**	chromatin modification	RT		10	1.7E-2	7.2E-1
☐	**GOTERM_BP_ALL**	establishment and/or maintenance of chromatin architecture	RT		11	4.1E-2	8.6E-1
☐	**GOTERM_BP_ALL**	DNA packaging	RT		11	4.8E-2	8.9E-1
☐	**GOTERM_BP_ALL**	chromosome organization and biogenesis	RT		12	9.3E-2	9.6E-1
☐	**INTERPRO**	Zinc finger, PHD-type	RT		4	2.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	organelle organization and biogenesis	RT		28	2.9E-1	1.0E0
☐	**SMART**	PHD	RT		4	3.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Chromatin regulator	RT		4	3.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	DNA metabolic process	RT		13	7.0E-1	1.0E0
	Annotation Cluster 40	Enrichment Score: 0.85	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of multicellular organism growth	RT		4	1.1E-1	9.6E-1
☐	**GOTERM_BP_ALL**	multicellular organism growth	RT		4	1.4E-1	9.8E-1
☐	**GOTERM_BP_ALL**	regulation of growth	RT		7	1.8E-1	9.9E-1
	Annotation Cluster 41	Enrichment Score: 0.84	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Zinc finger, RING/FYVE/PHD-type	RT		8	5.3E-2	1.0E0
☐	**INTERPRO**	Zinc finger, RING-type	RT		9	1.4E-1	1.0E0
☐	**SMART**	RING	RT		9	2.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	zinc finger region:RING-type	RT		5	2.7E-1	1.0E0
	Annotation Cluster 42	Enrichment Score: 0.84	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	platelet activation	RT		3	3.6E-2	8.4E-1
☐	**GOTERM_BP_ALL**	blood coagulation	RT		4	1.4E-1	9.8E-1
☐	**GOTERM_BP_ALL**	coagulation	RT		4	1.4E-1	9.8E-1
☐	**GOTERM_BP_ALL**	hemostasis	RT		4	1.5E-1	9.8E-1
☐	**GOTERM_BP_ALL**	regulation of body fluid levels	RT		4	2.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	wound healing	RT		4	3.3E-1	1.0E0
	Annotation Cluster 43	Enrichment Score: 0.83	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Basic-leucine zipper (bZIP) transcription factor	RT		4	9.6E-2	1.0E0
☐	**SMART**	BRLZ	RT		4	1.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Leucine-zipper	RT		5	1.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	protein dimerization activity	RT		10	1.6E-1	1.0E0
☐	**UP_SEQ_FEATURE**	DNA-binding region:Basic motif	RT		5	2.7E-1	1.0E0
	Annotation Cluster 44	Enrichment Score: 0.81	G	🟩	Count	P_Value	Benjamini
☐	**KEGG_PATHWAY**	TGF-beta signaling pathway	RT		7	2.5E-2	8.3E-1
☐	**GOTERM_BP_ALL**	regionalization	RT		8	4.0E-2	8.6E-1
☐	**GOTERM_BP_ALL**	transmembrane receptor protein serine/threonine kinase signaling pathway	RT		5	1.2E-1	9.7E-1
☐	**GOTERM_BP_ALL**	mesoderm formation	RT		3	1.3E-1	9.8E-1
☐	**GOTERM_BP_ALL**	pattern specification process	RT		9	1.4E-1	9.8E-1
☐	**GOTERM_BP_ALL**	mesoderm morphogenesis	RT		3	1.4E-1	9.8E-1
☐	**GOTERM_BP_ALL**	gastrulation	RT		4	1.4E-1	9.8E-1
☐	**GOTERM_BP_ALL**	formation of primary germ layer	RT		3	1.5E-1	9.8E-1
☐	**GOTERM_BP_ALL**	dorsal/ventral pattern formation	RT		3	2.4E-1	9.9E-1
☐	**GOTERM_BP_ALL**	urogenital system development	RT		4	2.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	mesoderm development	RT		3	3.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	kidney development	RT		3	4.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	tissue morphogenesis	RT		3	5.1E-1	1.0E0
	Annotation Cluster 45	Enrichment Score: 0.8	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	myeloid cell differentiation	RT		9	3.1E-3	3.9E-1
☐	**GOTERM_BP_ALL**	regulation of myeloid cell differentiation	RT		6	3.3E-3	3.9E-1
☐	**GOTERM_BP_ALL**	cell activation	RT		11	4.8E-2	8.9E-1

☐	**GOTERM_BP_ALL**	regulation of T cell activation	RT	▮		5	9.4E-2	9.5E-1
☐	**GOTERM_BP_ALL**	positive regulation of T cell activation	RT	▮		4	1.1E-1	9.6E-1
☐	**GOTERM_BP_ALL**	T cell proliferation	RT	▮		4	1.6E-1	9.9E-1
☐	**GOTERM_BP_ALL**	positive regulation of T cell proliferation	RT	▮		3	1.7E-1	9.9E-1
☐	**GOTERM_BP_ALL**	positive regulation of cell proliferation	RT	▮		8	1.8E-1	9.9E-1
☐	**GOTERM_BP_ALL**	regulation of lymphocyte activation	RT	▮		5	1.8E-1	9.9E-1
☐	**GOTERM_BP_ALL**	T cell activation	RT	▮		6	1.9E-1	9.9E-1
☐	**GOTERM_BP_ALL**	anti-apoptosis	RT	▮		5	1.9E-1	9.9E-1
☐	**GOTERM_BP_ALL**	positive regulation of lymphocyte activation	RT	▮		4	2.0E-1	9.9E-1
☐	**GOTERM_BP_ALL**	regulation of cell activation	RT	▮		5	2.0E-1	9.9E-1
☐	**GOTERM_BP_ALL**	positive regulation of lymphocyte proliferation	RT	▮		3	2.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of mononuclear cell proliferation	RT	▮		3	2.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	leukocyte activation	RT	▮		8	2.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	lymphocyte proliferation	RT	▮		4	3.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	mononuclear cell proliferation	RT	▮		4	3.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of T cell proliferation	RT	▮		3	3.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	lymphocyte activation	RT	▮		7	3.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of lymphocyte proliferation	RT	▮		3	4.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of mononuclear cell proliferation	RT	▮		3	4.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	leukocyte differentiation	RT	▮		4	6.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	lymphocyte differentiation	RT	▮		3	6.9E-1	1.0E0
	Annotation Cluster 46	Enrichment Score: 0.77	G		🟩	Count	P_Value	Benjamini
☐	**PIR_SUPERFAMILY**	PIRSF000615:tyrosine-protein kinase, CSF-1/PDGF receptor type	RT	▮		3	8.5E-3	1.0E0
☐	**INTERPRO**	Receptor tyrosine kinase, class III, conserved region	RT	▮		3	1.9E-2	1.0E0
☐	**SP_PIR_KEYWORDS**	proto-oncogene	RT	▮		6	3.8E-2	8.5E-1
☐	**SP_PIR_KEYWORDS**	autophosphorylation	RT	▮		4	6.3E-2	8.9E-1
☐	**GOTERM_BP_ALL**	transmembrane receptor protein tyrosine kinase signaling pathway	RT	▮		8	1.3E-1	9.8E-1
☐	**SP_PIR_KEYWORDS**	ATP	RT	▮		7	1.5E-1	9.5E-1
☐	**INTERPRO**	Tyrosine protein kinase, active site	RT	▮		5	1.7E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Ig-like C2-type 3	RT	▮		4	1.8E-1	1.0E0
☐	**KEGG_PATHWAY**	Hematopoietic cell lineage	RT	▮		5	1.8E-1	9.3E-1
☐	**GOTERM_MF_ALL**	transmembrane receptor protein tyrosine kinase activity	RT	▮		4	2.2E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	tyrosine-protein kinase	RT	▮		5	2.3E-1	9.8E-1
☐	**INTERPRO**	Immunoglobulin subtype 2	RT	▮		6	2.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	tyrosine-specific protein kinase	RT	▮		3	2.7E-1	9.9E-1
☐	**INTERPRO**	Tyrosine protein kinase	RT	▮		5	2.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Ig-like C2-type 1	RT	▮		4	3.2E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:Ig-like C2-type 2	RT	▮		4	3.2E-1	1.0E0
☐	**SMART**	TyrKc	RT	▮		5	3.3E-1	1.0E0
☐	**SMART**	IGc2	RT	▮		6	3.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	immunoglobulin domain	RT	▮		9	4.9E-1	1.0E0
☐	**INTERPRO**	Immunoglobulin	RT	▮		5	4.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	phosphotransferase	RT	▮		4	5.4E-1	1.0E0
	Annotation Cluster 47	Enrichment Score: 0.73	G		🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Zinc finger, ZZ-type	RT	▮		3	4.2E-2	1.0E0
☐	**SMART**	ZnF_ZZ	RT	▮		3	4.4E-2	9.9E-1

☐	SP_PIR_KEYWORDS	activator	RT	15	5.2E-2	8.8E-1
☐	BIOCARTA	IL-7 Signal Transduction	RT	3	1.1E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of transcription from RNA polymerase II promoter	RT	13	2.1E-1	9.9E-1
☐	GOTERM_BP_ALL	transcription from RNA polymerase II promoter	RT	14	2.3E-1	9.9E-1
☐	GOTERM_BP_ALL	positive regulation of cellular metabolic process	RT	13	2.4E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of transcription, DNA-dependent	RT	9	3.0E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of metabolic process	RT	13	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of transcription	RT	9	4.9E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	9	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	positive regulation of transcription from RNA polymerase II promoter	RT	6	5.5E-1	1.0E0
	Annotation Cluster 48	Enrichment Score: 0.72	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	regionalization	RT	8	4.0E-2	8.6E-1
☐	GOTERM_BP_ALL	pattern specification process	RT	9	1.4E-1	9.8E-1
☐	GOTERM_BP_ALL	protein amino acid alkylation	RT	3	1.7E-1	9.9E-1
☐	GOTERM_BP_ALL	protein amino acid methylation	RT	3	1.7E-1	9.9E-1
☐	GOTERM_BP_ALL	one-carbon compound metabolic process	RT	4	3.1E-1	1.0E0
☐	GOTERM_BP_ALL	anterior/posterior pattern formation	RT	4	3.2E-1	1.0E0
☐	GOTERM_BP_ALL	biopolymer methylation	RT	3	3.3E-1	1.0E0
☐	GOTERM_BP_ALL	methylation	RT	3	3.5E-1	1.0E0
	Annotation Cluster 49	Enrichment Score: 0.71	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	transferase	RT	41	1.1E-2	6.1E-1
☐	GOTERM_BP_ALL	protein modification process	RT	47	2.2E-2	7.8E-1
☐	INTERPRO	Protein kinase, C-terminal	RT	5	3.0E-2	1.0E0
☐	GOTERM_BP_ALL	cellular macromolecule metabolic process	RT	79	3.2E-2	8.3E-1
☐	SMART	S_TK_X	RT	5	3.3E-2	9.8E-1
☐	GOTERM_BP_ALL	enzyme linked receptor protein signaling pathway	RT	13	3.4E-2	8.4E-1
☐	GOTERM_BP_ALL	biopolymer modification	RT	47	4.0E-2	8.6E-1
☐	GOTERM_BP_ALL	protein metabolic process	RT	80	4.6E-2	8.8E-1
☐	SP_PIR_KEYWORDS	kinase	RT	23	5.1E-2	8.8E-1
☐	GOTERM_MF_ALL	transferase activity	RT	50	5.4E-2	1.0E0
☐	UP_SEQ_FEATURE	active site:Proton acceptor	RT	18	5.5E-2	1.0E0
☐	GOTERM_BP_ALL	cellular protein metabolic process	RT	75	7.6E-2	9.4E-1
☐	UP_SEQ_FEATURE	domain:AGC-kinase C-terminal	RT	4	1.0E-1	1.0E0
☐	GOTERM_MF_ALL	kinase activity	RT	25	1.5E-1	1.0E0
☐	GOTERM_MF_ALL	protein-tyrosine kinase activity	RT	11	1.6E-1	1.0E0
☐	GOTERM_MF_ALL	protein serine/threonine kinase activity	RT	15	1.7E-1	1.0E0
☐	GOTERM_BP_ALL	protein amino acid phosphorylation	RT	18	2.0E-1	9.9E-1
☐	GOTERM_MF_ALL	transferase activity, transferring phosphorus-containing groups	RT	27	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	post-translational protein modification	RT	35	2.3E-1	9.9E-1
☐	INTERPRO	Protein kinase, core	RT	11	2.3E-1	1.0E0
☐	GOTERM_MF_ALL	phosphotransferase activity, alcohol group as acceptor	RT	19	2.7E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:Protein kinase	RT	11	2.8E-1	1.0E0
☐	GOTERM_BP_ALL	phosphorylation	RT	19	2.9E-1	1.0E0
☐	INTERPRO	Serine/threonine protein kinase	RT	7	3.1E-1	1.0E0
☐	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT	17	3.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	Serine/threonine-protein kinase	RT	10	3.4E-1	1.0E0

☐	**UP_SEQ_FEATURE**	binding site:ATP	RT	11	3.7E-1	1.0E0
☐	**SMART**	S_TKc	RT	10	4.2E-1	1.0E0
☐	**GOTERM_MF_ALL**	protein kinase activity	RT	15	4.4E-1	1.0E0
☐	**INTERPRO**	Serine/threonine protein kinase, active site	RT	7	4.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	phosphorus metabolic process	RT	20	4.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	phosphate metabolic process	RT	20	4.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	atp-binding	RT	22	6.2E-1	1.0E0
☐	**GOTERM_MF_ALL**	adenyl nucleotide binding	RT	27	8.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	ATP binding	RT	25	8.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	nucleotide-binding	RT	24	8.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	adenyl ribonucleotide binding	RT	25	8.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	nucleotide binding	RT	35	9.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	purine nucleotide binding	RT	30	9.5E-1	1.0E0
☐	**GOTERM_MF_ALL**	ribonucleotide binding	RT	28	9.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	purine ribonucleotide binding	RT	28	9.6E-1	1.0E0
	Annotation Cluster 50	Enrichment Score: 0.7	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	carbohydrate catabolic process	RT	6	3.2E-2	8.3E-1
☐	**GOTERM_BP_ALL**	carbohydrate metabolic process	RT	16	3.4E-2	8.4E-1
☐	**KEGG_PATHWAY**	Glycolysis / Gluconeogenesis	RT	5	5.5E-2	8.6E-1
☐	**GOTERM_BP_ALL**	cellular carbohydrate catabolic process	RT	5	8.8E-2	9.5E-1
☐	**KEGG_PATHWAY**	Fructose and mannose metabolism	RT	4	1.0E-1	8.3E-1
☐	**GOTERM_BP_ALL**	macromolecule catabolic process	RT	11	2.0E-1	9.9E-1
☐	**GOTERM_BP_ALL**	hexose metabolic process	RT	6	2.2E-1	9.9E-1
☐	**SP_PIR_KEYWORDS**	glycolysis	RT	3	2.2E-1	9.8E-1
☐	**GOTERM_BP_ALL**	monosaccharide metabolic process	RT	6	2.3E-1	9.9E-1
☐	**GOTERM_BP_ALL**	alcohol metabolic process	RT	9	2.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	glycolysis	RT	3	3.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	glucose catabolic process	RT	3	4.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	hexose catabolic process	RT	3	4.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	monosaccharide catabolic process	RT	3	4.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular carbohydrate metabolic process	RT	8	4.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	alcohol catabolic process	RT	3	4.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	glucose metabolic process	RT	4	4.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular macromolecule catabolic process	RT	7	5.1E-1	1.0E0
	Annotation Cluster 51	Enrichment Score: 0.69	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of cellular component organization and biogenesis	RT	6	1.9E-2	7.5E-1
☐	**GOTERM_BP_ALL**	actin polymerization and/or depolymerization	RT	5	2.2E-2	7.6E-1
☐	**GOTERM_BP_ALL**	actin filament-based process	RT	9	7.7E-2	9.4E-1
☐	**GOTERM_BP_ALL**	actin filament capping	RT	3	8.7E-2	9.5E-1
☐	**GOTERM_BP_ALL**	negative regulation of actin filament depolymerization	RT	3	8.7E-2	9.5E-1
☐	**GOTERM_BP_ALL**	regulation of actin filament depolymerization	RT	3	1.0E-1	9.6E-1
☐	**GOTERM_BP_ALL**	actin filament depolymerization	RT	3	1.0E-1	9.6E-1
☐	**SP_PIR_KEYWORDS**	cytoskeleton	RT	11	1.2E-1	9.4E-1
☐	**GOTERM_BP_ALL**	actin cytoskeleton organization and biogenesis	RT	8	1.3E-1	9.8E-1
☐	**GOTERM_MF_ALL**	actin binding	RT	10	1.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein depolymerization	RT	3	2.0E-1	9.9E-1
☐	**GOTERM_BP_ALL**	regulation of actin polymerization and/or depolymerization	RT	3	2.1E-1	9.9E-1

☐	GOTERM_MF_ALL	cytoskeletal protein binding	RT	▮		12	2.2E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of actin filament length	RT	▮		3	2.2E-1	9.9E-1
☐	GOTERM_BP_ALL	negative regulation of cellular component organization and biogenesis	RT	▮		3	2.2E-1	9.9E-1
☐	GOTERM_BP_ALL	regulation of actin cytoskeleton organization and biogenesis	RT	▮		3	2.2E-1	9.9E-1
☐	GOTERM_BP_ALL	regulation of cellular component size	RT	▮		3	2.3E-1	9.9E-1
☐	GOTERM_BP_ALL	regulation of organelle organization and biogenesis	RT	▮		3	2.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cytoskeleton organization and biogenesis	RT	▮		3	2.5E-1	1.0E0
☐	GOTERM_BP_ALL	cytoskeleton organization and biogenesis	RT	▮		14	2.8E-1	1.0E0
☐	GOTERM_CC_ALL	actin cytoskeleton	RT	▮		7	3.0E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of protein metabolic process	RT	▮		8	4.1E-1	1.0E0
☐	SP_PIR_KEYWORDS	actin-binding	RT	▮		5	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	negative regulation of protein metabolic process	RT	▮		3	5.7E-1	1.0E0
☐	GOTERM_CC_ALL	cytoskeleton	RT	▮		14	9.4E-1	1.0E0
☐	GOTERM_CC_ALL	intracellular non-membrane-bound organelle	RT	▮		23	9.7E-1	1.0E0
☐	GOTERM_CC_ALL	non-membrane-bound organelle	RT	▮		23	9.7E-1	1.0E0
☐	GOTERM_CC_ALL	cytoskeletal part	RT	▮		6	9.9E-1	1.0E0
	Annotation Cluster 52	Enrichment Score: 0.68	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Proteinase inhibitor I25, cystatin	RT	▮		3	8.3E-2	1.0E0
☐	SMART	CY	RT	▮		3	8.7E-2	1.0E0
☐	GOTERM_MF_ALL	enzyme inhibitor activity	RT	▮		7	3.5E-1	1.0E0
☐	GOTERM_MF_ALL	endopeptidase inhibitor activity	RT	▮		5	3.9E-1	1.0E0
☐	GOTERM_MF_ALL	protease inhibitor activity	RT	▮		5	4.0E-1	1.0E0
	Annotation Cluster 53	Enrichment Score: 0.64	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	lamellipodium	RT	▮		6	7.4E-3	5.6E-1
☐	GOTERM_CC_ALL	leading edge	RT	▮		7	1.7E-2	7.6E-1
☐	INTERPRO	Pleckstrin homology-type	RT	▮		11	3.8E-2	1.0E0
☐	GOTERM_BP_ALL	regulation of signal transduction	RT	▮		16	5.8E-2	9.2E-1
☐	INTERPRO	Pleckstrin-like	RT	▮		8	1.9E-1	1.0E0
☐	GOTERM_MF_ALL	guanyl-nucleotide exchange factor activity	RT	▮		6	2.0E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of Rho protein signal transduction	RT	▮		4	2.1E-1	9.9E-1
☐	SMART	PH	RT	▮		8	2.5E-1	1.0E0
☐	GOTERM_MF_ALL	Ras guanyl-nucleotide exchange factor activity	RT	▮		4	2.6E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of small GTPase mediated signal transduction	RT	▮		6	3.5E-1	1.0E0
☐	INTERPRO	DH	RT	▮		3	3.6E-1	1.0E0
☐	GOTERM_BP_ALL	Rho protein signal transduction	RT	▮		4	3.6E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of Ras protein signal transduction	RT	▮		5	3.6E-1	1.0E0
☐	SMART	RhoGEF	RT	▮		3	3.7E-1	1.0E0
☐	GOTERM_MF_ALL	Rho guanyl-nucleotide exchange factor activity	RT	▮		3	4.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	cell projection	RT	▮		3	5.0E-1	1.0E0
☐	GOTERM_MF_ALL	GTPase regulator activity	RT	▮		8	6.0E-1	1.0E0
☐	GOTERM_BP_ALL	Ras protein signal transduction	RT	▮		5	6.1E-1	1.0E0
☐	GOTERM_MF_ALL	small GTPase regulator activity	RT	▮		5	6.3E-1	1.0E0
☐	GOTERM_CC_ALL	cell projection	RT	▮		6	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	small GTPase mediated signal transduction	RT	▮		6	9.4E-1	1.0E0
	Annotation Cluster 54	Enrichment Score: 0.64	G		🟩	Count	P_Value	Benjamini

☐	**GOTERM_BP_ALL**	positive regulation of transcription factor activity	RT	▮		3	9.4E-2	9.6E-1
☐	**GOTERM_MF_ALL**	transcription cofactor activity	RT	▮		7	1.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of transcription factor activity	RT	▮		3	1.5E-1	9.8E-1
☐	**GOTERM_MF_ALL**	transcription factor binding	RT	▮		9	1.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	transcription corepressor activity	RT	▮		3	4.0E-1	1.0E0
☐	**GOTERM_MF_ALL**	transcription activator activity	RT	▮		6	5.2E-1	1.0E0
☐	**GOTERM_MF_ALL**	transcription coactivator activity	RT	▮		3	5.5E-1	1.0E0
	Annotation Cluster 55	Enrichment Score: 0.61	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	positive regulation of phagocytosis	RT	▮		3	6.2E-2	9.2E-1
☐	**GOTERM_BP_ALL**	regulation of phagocytosis	RT	▮		3	6.2E-2	9.2E-1
☐	**GOTERM_BP_ALL**	positive regulation of endocytosis	RT	▮		3	1.1E-1	9.6E-1
☐	**GOTERM_BP_ALL**	phagocytosis	RT	▮		3	1.9E-1	9.9E-1
☐	**GOTERM_BP_ALL**	regulation of endocytosis	RT	▮		3	2.1E-1	9.9E-1
☐	**GOTERM_BP_ALL**	positive regulation of transport	RT	▮		3	2.3E-1	9.9E-1
☐	**GOTERM_BP_ALL**	regulation of transport	RT	▮		4	4.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	membrane organization and biogenesis	RT	▮		7	4.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	endocytosis	RT	▮		5	5.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	membrane invagination	RT	▮		5	5.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	vesicle-mediated transport	RT	▮		7	9.2E-1	1.0E0
	Annotation Cluster 56	Enrichment Score: 0.6	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of G-protein coupled receptor protein signaling pathway	RT	▮		5	1.4E-3	3.5E-1
☐	**INTERPRO**	Receptor activity modifying protein	RT	▮		3	1.4E-3	1.0E0
☐	**GOTERM_MF_ALL**	coreceptor activity	RT	▮		3	1.9E-2	9.6E-1
☐	**GOTERM_MF_ALL**	protein transporter activity	RT	▮		4	6.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	intracellular transport	RT	▮		13	8.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	intracellular protein transport	RT	▮		7	9.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	establishment of cellular localization	RT	▮		13	9.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular localization	RT	▮		13	9.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein transport	RT	▮		9	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein localization	RT	▮		10	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	establishment of protein localization	RT	▮		9	9.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	protein transport	RT	▮		4	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	macromolecule localization	RT	▮		10	9.9E-1	1.0E0
	Annotation Cluster 57	Enrichment Score: 0.57	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	plasma membrane part	RT	▮		33	2.0E-1	1.0E0
☐	**GOTERM_CC_ALL**	integral to plasma membrane	RT	▮		16	2.9E-1	1.0E0
☐	**GOTERM_CC_ALL**	intrinsic to plasma membrane	RT	▮		16	3.3E-1	1.0E0
	Annotation Cluster 58	Enrichment Score: 0.57	G		🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	chondrocyte differentiation	RT	▮		4	6.4E-3	5.1E-1
☐	**GOTERM_BP_ALL**	cartilage development	RT	▮		5	3.4E-2	8.4E-1
☐	**GOTERM_BP_ALL**	positive regulation of amino acid metabolic process	RT	▮		3	1.7E-1	9.9E-1
☐	**GOTERM_BP_ALL**	positive regulation of amine metabolic process	RT	▮		3	1.7E-1	9.9E-1
☐	**GOTERM_BP_ALL**	positive regulation of protein amino acid phosphorylation	RT	▮		3	1.7E-1	9.9E-1
☐	**GOTERM_BP_ALL**	regulation of protein amino acid phosphorylation	RT	▮		3	3.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of amine metabolic process	RT	▮		3	3.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of amino acid metabolic process	RT	▮		3	3.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	nitrogen compound metabolic process	RT	▮		11	4.2E-1	1.0E0

☐	GOTERM_BP_ALL	regulation of phosphorylation	RT	3	4.4E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of phosphorus metabolic process	RT	3	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of phosphate metabolic process	RT	3	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	amine metabolic process	RT	10	4.6E-1	1.0E0
☐	GOTERM_BP_ALL	amino acid metabolic process	RT	7	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	amino acid and derivative metabolic process	RT	8	5.8E-1	1.0E0
☐	GOTERM_BP_ALL	carboxylic acid metabolic process	RT	9	8.6E-1	1.0E0
☐	GOTERM_BP_ALL	organic acid metabolic process	RT	9	8.6E-1	1.0E0
	Annotation Cluster 59	Enrichment Score: 0.55	G	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	steroid binding	RT	4	1.3E-1	1.0E0
☐	INTERPRO	Nuclear hormone receptor, ligand-binding, core	RT	3	2.8E-1	1.0E0
☐	INTERPRO	Steroid hormone receptor	RT	3	2.8E-1	1.0E0
☐	INTERPRO	Nuclear hormone receptor, ligand-binding	RT	3	2.8E-1	1.0E0
☐	SMART	HOLI	RT	3	2.9E-1	1.0E0
☐	GOTERM_MF_ALL	steroid hormone receptor activity	RT	3	4.1E-1	1.0E0
☐	GOTERM_MF_ALL	ligand-dependent nuclear receptor activity	RT	3	4.2E-1	1.0E0
	Annotation Cluster 60	Enrichment Score: 0.54	G	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	biological regulation	RT	121	1.4E-3	3.4E-1
☐	GOTERM_BP_ALL	regulation of cellular process	RT	101	4.1E-3	4.2E-1
☐	GOTERM_BP_ALL	regulation of biological process	RT	109	5.0E-3	4.6E-1
☐	SP_PIR_KEYWORDS	Transcription regulation	RT	33	1.9E-1	9.7E-1
☐	SP_PIR_KEYWORDS	Transcription	RT	33	2.1E-1	9.8E-1
☐	GOTERM_BP_ALL	regulation of metabolic process	RT	59	3.4E-1	1.0E0
☐	GOTERM_MF_ALL	transcription regulator activity	RT	31	3.5E-1	1.0E0
☐	GOTERM_BP_ALL	transcription, DNA-dependent	RT	48	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cellular metabolic process	RT	55	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	RNA biosynthetic process	RT	48	4.5E-1	1.0E0
☐	GOTERM_BP_ALL	transcription	RT	51	4.7E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of transcription, DNA-dependent	RT	47	4.8E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	50	4.9E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of transcription	RT	49	4.9E-1	1.0E0
☐	GOTERM_MF_ALL	sequence-specific DNA binding	RT	12	5.1E-1	1.0E0
☐	GOTERM_BP_ALL	biopolymer metabolic process	RT	97	5.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of gene expression	RT	51	5.7E-1	1.0E0
☐	SP_PIR_KEYWORDS	dna-binding	RT	28	5.7E-1	1.0E0
☐	GOTERM_MF_ALL	transcription factor activity	RT	20	6.1E-1	1.0E0
☐	GOTERM_CC_ALL	nucleus	RT	83	6.5E-1	1.0E0
☐	GOTERM_MF_ALL	DNA binding	RT	39	7.9E-1	1.0E0
☐	GOTERM_MF_ALL	nucleic acid binding	RT	62	8.0E-1	1.0E0
☐	GOTERM_BP_ALL	RNA metabolic process	RT	51	8.0E-1	1.0E0
☐	SP_PIR_KEYWORDS	nucleus	RT	61	8.2E-1	1.0E0
☐	GOTERM_BP_ALL	gene expression	RT	58	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	62	9.3E-1	1.0E0
	Annotation Cluster 61	Enrichment Score: 0.54	G	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	immune response	RT	9	1.0E-2	6.3E-1
☐	GOTERM_BP_ALL	positive regulation of multicellular organismal process	RT	7	5.7E-2	9.1E-1

☐	**SP_PIR_KEYWORDS**	innate immunity	RT	3	2.9E-1	9.9E-1
☐	**GOTERM_BP_ALL**	innate immune response	RT	4	3.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	immune effector process	RT	5	3.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of immune system process	RT	4	3.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of immune system process	RT	4	4.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	activation of immune response	RT	3	5.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	lymphocyte mediated immunity	RT	3	6.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	positive regulation of immune response	RT	3	6.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	leukocyte mediated immunity	RT	3	6.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of immune response	RT	3	7.1E-1	1.0E0
	Annotation Cluster 62	Enrichment Score: 0.52	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	cytokine production	RT	6	1.1E-1	9.7E-1
☐	**GOTERM_BP_ALL**	cytokine metabolic process	RT	3	5.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	cytokine biosynthetic process	RT	3	5.0E-1	1.0E0
	Annotation Cluster 63	Enrichment Score: 0.52	G 🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	transmembrane	RT	78	2.0E-1	9.7E-1
☐	**UP_SEQ_FEATURE**	transmembrane region	RT	58	2.1E-1	1.0E0
☐	**UP_SEQ_FEATURE**	topological domain:Cytoplasmic	RT	44	2.9E-1	1.0E0
☐	**GOTERM_CC_ALL**	integral to membrane	RT	94	2.9E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	membrane	RT	95	3.0E-1	9.9E-1
☐	**GOTERM_CC_ALL**	intrinsic to membrane	RT	94	3.1E-1	1.0E0
☐	**GOTERM_CC_ALL**	membrane part	RT	105	3.1E-1	1.0E0
☐	**GOTERM_CC_ALL**	membrane	RT	128	4.3E-1	1.0E0
☐	**UP_SEQ_FEATURE**	topological domain:Extracellular	RT	32	4.7E-1	1.0E0
	Annotation Cluster 64	Enrichment Score: 0.51	G 🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	protein amino acid acylation	RT	3	1.1E-1	9.6E-1
☐	**GOTERM_MF_ALL**	N-acyltransferase activity	RT	4	1.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	acyltransferase activity	RT	6	3.3E-1	1.0E0
☐	**GOTERM_MF_ALL**	N-acetyltransferase activity	RT	3	3.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	transferase activity, transferring groups other than amino-acyl groups	RT	6	3.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	transferase activity, transferring acyl groups	RT	6	3.7E-1	1.0E0
☐	**COG_ONTOLOGY**	Lipid metabolism	RT	3	4.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	acetyltransferase activity	RT	3	4.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	acyltransferase	RT	4	5.6E-1	1.0E0
	Annotation Cluster 65	Enrichment Score: 0.48	G 🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	lectin	RT	7	1.2E-1	9.4E-1
☐	**GOTERM_MF_ALL**	sugar binding	RT	7	2.6E-1	1.0E0
☐	**SMART**	CLECT	RT	4	5.1E-1	1.0E0
☐	**INTERPRO**	C-type lectin	RT	3	7.3E-1	1.0E0
	Annotation Cluster 66	Enrichment Score: 0.48	G 🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	repressor	RT	11	9.7E-2	9.3E-1
☐	**GOTERM_MF_ALL**	transcription repressor activity	RT	7	1.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	negative regulation of metabolic process	RT	12	2.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	negative regulation of transcription	RT	8	4.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT	8	4.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	negative regulation of transcription, DNA-dependent	RT	6	4.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	negative regulation of cellular metabolic process	RT	9	5.0E-1	1.0E0

☐	**GOTERM_BP_ALL**	negative regulation of transcription from RNA polymerase II promoter	RT		4	6.4E-1	1.0E0
	Annotation Cluster 67	Enrichment Score: 0.48	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	protein amino acid autophosphorylation	RT		3	2.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein autoprocessing	RT		3	2.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	protein processing	RT		3	5.6E-1	1.0E0
	Annotation Cluster 68	Enrichment Score: 0.46	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	lung development	RT		4	1.9E-1	9.9E-1
☐	**GOTERM_BP_ALL**	respiratory tube development	RT		4	2.0E-1	9.9E-1
☐	**GOTERM_BP_ALL**	heart development	RT		7	2.2E-1	9.9E-1
☐	**GOTERM_BP_ALL**	muscle cell differentiation	RT		4	2.3E-1	9.9E-1
☐	**GOTERM_BP_ALL**	myoblast differentiation	RT		3	2.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	striated muscle development	RT		5	3.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	skeletal muscle development	RT		4	4.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	muscle fiber development	RT		3	4.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	skeletal muscle fiber development	RT		3	4.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	embryonic development ending in birth or egg hatching	RT		6	5.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	muscle development	RT		5	5.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	chordate embryonic development	RT		5	7.1E-1	1.0E0
	Annotation Cluster 69	Enrichment Score: 0.46	G	🟩	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	cholesterol metabolism	RT		3	9.8E-2	9.2E-1
☐	**SP_PIR_KEYWORDS**	steroid metabolism	RT		3	1.6E-1	9.6E-1
☐	**GOTERM_BP_ALL**	alcohol metabolic process	RT		9	2.7E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	lipid metabolism	RT		4	3.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	cholesterol metabolic process	RT		3	4.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	sterol metabolic process	RT		3	5.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	steroid metabolic process	RT		4	6.5E-1	1.0E0
☐	**GOTERM_CC_ALL**	membrane fraction	RT		8	8.9E-1	1.0E0
	Annotation Cluster 70	Enrichment Score: 0.46	G	🟩	Count	P_Value	Benjamini
☐	**INTERPRO**	Butyrophylin-like	RT		3	2.3E-1	1.0E0
☐	**INTERPRO**	Zinc finger, B-box	RT		3	3.5E-1	1.0E0
☐	**SMART**	BBOX	RT		3	3.6E-1	1.0E0
☐	**INTERPRO**	SPla/RYanodine receptor SPRY	RT		3	3.8E-1	1.0E0
☐	**INTERPRO**	B302, (SPRY)-like	RT		3	4.0E-1	1.0E0
☐	**SMART**	SPRY	RT		3	4.3E-1	1.0E0
	Annotation Cluster 71	Enrichment Score: 0.45	G	🟩	Count	P_Value	Benjamini
☐	**KEGG_PATHWAY**	Long-term potentiation	RT		4	2.5E-1	9.5E-1
☐	**KEGG_PATHWAY**	Melanogenesis	RT		5	2.5E-1	9.5E-1
☐	**KEGG_PATHWAY**	Wnt signaling pathway	RT		4	7.3E-1	1.0E0
	Annotation Cluster 72	Enrichment Score: 0.44	G	🟩	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	growth	RT		13	1.7E-2	7.2E-1
☐	**GOTERM_BP_ALL**	cell migration	RT		13	3.6E-2	8.4E-1
☐	**GOTERM_BP_ALL**	axon guidance	RT		5	1.2E-1	9.7E-1
☐	**GOTERM_BP_ALL**	cell growth	RT		6	1.4E-1	9.8E-1
☐	**GOTERM_BP_ALL**	regulation of cell size	RT		6	1.8E-1	9.9E-1
☐	**GOTERM_BP_ALL**	cellular structure morphogenesis	RT		14	3.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	cell morphogenesis	RT		14	3.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	nervous system development	RT		16	4.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	cytoskeleton-dependent intracellular transport	RT		4	4.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	axonogenesis	RT		5	4.9E-1	1.0E0

☐	GOTERM_BP_ALL	neuron morphogenesis during differentiation	RT	▮		5	5.4E-1	1.0E0
☐	GOTERM_BP_ALL	neurite morphogenesis	RT	▮		5	5.4E-1	1.0E0
☐	GOTERM_BP_ALL	generation of neurons	RT	▮		8	6.2E-1	1.0E0
☐	GOTERM_BP_ALL	cellular morphogenesis during differentiation	RT	▮		5	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	neuron differentiation	RT	▮		7	6.5E-1	1.0E0
☐	GOTERM_BP_ALL	regulation of cell growth	RT	▮		3	6.7E-1	1.0E0
☐	GOTERM_BP_ALL	neurite development	RT	▮		5	6.8E-1	1.0E0
☐	GOTERM_BP_ALL	neurogenesis	RT	▮		8	7.0E-1	1.0E0
☐	GOTERM_BP_ALL	cell part morphogenesis	RT	▮		6	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	cell projection morphogenesis	RT	▮		6	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	cell projection organization and biogenesis	RT	▮		6	7.6E-1	1.0E0
☐	GOTERM_BP_ALL	neuron development	RT	▮		5	7.7E-1	1.0E0
	Annotation Cluster 73	Enrichment Score: 0.44	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	phosphoinositide binding	RT	▮		8	9.6E-2	1.0E0
☐	SP_PIR_KEYWORDS	gpi-anchor	RT	▮		3	6.9E-1	1.0E0
☐	GOTERM_MF_ALL	GPI anchor binding	RT	▮		3	7.3E-1	1.0E0
	Annotation Cluster 74	Enrichment Score: 0.43	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	domain:SAM	RT	▮		3	2.1E-1	1.0E0
☐	INTERPRO	Sterile alpha motif SAM	RT	▮		3	4.8E-1	1.0E0
☐	SMART	SAM	RT	▮		3	5.1E-1	1.0E0
	Annotation Cluster 75	Enrichment Score: 0.37	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	sensory organ development	RT	▮		6	3.6E-1	1.0E0
☐	GOTERM_BP_ALL	inner ear development	RT	▮		3	4.3E-1	1.0E0
☐	GOTERM_BP_ALL	ear development	RT	▮		3	4.8E-1	1.0E0
	Annotation Cluster 76	Enrichment Score: 0.35	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	cytoplasmic vesicle	RT	▮		10	2.8E-1	1.0E0
☐	GOTERM_CC_ALL	vesicle	RT	▮		10	3.1E-1	1.0E0
☐	GOTERM_CC_ALL	cytoplasmic membrane-bound vesicle	RT	▮		7	4.0E-1	1.0E0
☐	GOTERM_CC_ALL	membrane-bound vesicle	RT	▮		7	4.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	cytoplasmic vesicle	RT	▮		4	5.4E-1	1.0E0
☐	GOTERM_CC_ALL	clathrin-coated vesicle	RT	▮		3	6.5E-1	1.0E0
☐	GOTERM_CC_ALL	coated vesicle	RT	▮		3	7.3E-1	1.0E0
	Annotation Cluster 77	Enrichment Score: 0.34	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Immunoglobulin V-set	RT	▮		7	1.5E-1	1.0E0
☐	INTERPRO	Immunoglobulin subtype 2	RT	▮		6	2.7E-1	1.0E0
☐	SMART	IGc2	RT	▮		6	3.4E-1	1.0E0
☐	SP_PIR_KEYWORDS	immunoglobulin domain	RT	▮		9	4.9E-1	1.0E0
☐	INTERPRO	Immunoglobulin	RT	▮		5	4.9E-1	1.0E0
☐	INTERPRO	Immunoglobulin-like fold	RT	▮		9	6.1E-1	1.0E0
☐	INTERPRO	Immunoglobulin-like	RT	▮		8	6.7E-1	1.0E0
☐	INTERPRO	Immunoglobulin subtype	RT	▮		5	7.3E-1	1.0E0
☐	SMART	IG	RT	▮		5	8.2E-1	1.0E0
	Annotation Cluster 78	Enrichment Score: 0.33	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	integral to organelle membrane	RT	▮		4	2.2E-1	1.0E0
☐	GOTERM_CC_ALL	intrinsic to organelle membrane	RT	▮		4	2.7E-1	1.0E0
☐	GOTERM_CC_ALL	endomembrane system	RT	▮		7	8.4E-1	1.0E0
☐	GOTERM_CC_ALL	organelle membrane	RT	▮		8	9.8E-1	1.0E0
	Annotation Cluster 79	Enrichment Score: 0.32	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Variant SH3	RT	▮		3	3.2E-1	1.0E0

☐	**SP_PIR_KEYWORDS**	SH3 domain	RT	6	3.9E-1	1.0E0
☐	**SMART**	SH3	RT	6	4.4E-1	1.0E0
☐	**INTERPRO**	Src homology-3	RT	5	5.8E-1	1.0E0
☐	**UP_SEQ_FEATURE**	domain:SH3	RT	3	7.5E-1	1.0E0
	Annotation Cluster 80	Enrichment Score: 0.32	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	embryonic limb morphogenesis	RT	3	4.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	embryonic appendage morphogenesis	RT	3	4.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	appendage morphogenesis	RT	3	4.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	limb morphogenesis	RT	3	4.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	appendage development	RT	3	4.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	limb development	RT	3	4.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	embryonic morphogenesis	RT	5	6.0E-1	1.0E0
	Annotation Cluster 81	Enrichment Score: 0.31	G	Count	P_Value	Benjamini
☐	**GOTERM_CC_ALL**	cytoplasm	RT	127	1.1E-1	1.0E0
☐	**GOTERM_CC_ALL**	intracellular membrane-bound organelle	RT	139	3.1E-1	1.0E0
☐	**GOTERM_CC_ALL**	membrane-bound organelle	RT	139	3.1E-1	1.0E0
☐	**GOTERM_CC_ALL**	intracellular	RT	191	4.8E-1	1.0E0
☐	**GOTERM_CC_ALL**	intracellular part	RT	179	5.9E-1	1.0E0
☐	**GOTERM_CC_ALL**	cytoplasmic part	RT	67	6.2E-1	1.0E0
☐	**GOTERM_CC_ALL**	nucleus	RT	83	6.5E-1	1.0E0
☐	**GOTERM_CC_ALL**	intracellular organelle	RT	147	7.1E-1	1.0E0
☐	**GOTERM_CC_ALL**	organelle	RT	147	7.1E-1	1.0E0
☐	**GOTERM_CC_ALL**	cell part	RT	259	7.6E-1	1.0E0
☐	**GOTERM_CC_ALL**	cell	RT	259	7.6E-1	1.0E0
	Annotation Cluster 82	Enrichment Score: 0.31	G	Count	P_Value	Benjamini
☐	**GOTERM_MF_ALL**	endopeptidase activity	RT	13	2.5E-1	1.0E0
☐	**UP_SEQ_FEATURE**	active site:Charge relay system	RT	5	3.0E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	serine protease	RT	5	3.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	serine hydrolase activity	RT	6	4.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	serine-type peptidase activity	RT	6	4.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	serine-type endopeptidase activity	RT	5	6.1E-1	1.0E0
☐	**INTERPRO**	Peptidase S1A, chymotrypsin	RT	3	7.3E-1	1.0E0
☐	**INTERPRO**	Peptidase S1 and S6, chymotrypsin/Hap	RT	3	7.5E-1	1.0E0
☐	**SMART**	Tryp_SPc	RT	3	7.9E-1	1.0E0
	Annotation Cluster 83	Enrichment Score: 0.3	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	membrane lipid biosynthetic process	RT	4	2.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	phospholipid biosynthetic process	RT	3	4.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	membrane lipid metabolic process	RT	5	5.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	phospholipid metabolic process	RT	4	5.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	lipid metabolic process	RT	14	6.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	lipid biosynthetic process	RT	6	6.4E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular lipid metabolic process	RT	12	6.5E-1	1.0E0
	Annotation Cluster 84	Enrichment Score: 0.27	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	tube morphogenesis	RT	6	2.3E-1	9.9E-1
☐	**GOTERM_BP_ALL**	neural tube development	RT	3	3.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	embryonic development ending in birth or egg hatching	RT	6	5.2E-1	1.0E0
☐	**GOTERM_BP_ALL**	chordate embryonic development	RT	5	7.1E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	differentiation	RT	5	9.3E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	Developmental protein	RT	5	1.0E0	1.0E0
	Annotation Cluster 85	Enrichment Score: 0.22	G	Count	P_Value	Benjamini

☐	UP_SEQ_FEATURE	domain:EF-hand 1	RT	▮		4	4.5E-1	1.0E0
☐	UP_SEQ_FEATURE	domain:EF-hand 2	RT	▮		4	4.5E-1	1.0E0
☐	INTERPRO	Calcium-binding EF-hand	RT	▮		4	7.7E-1	1.0E0
☐	SMART	EFh	RT	▮		4	8.2E-1	1.0E0
	Annotation Cluster 86	Enrichment Score: 0.21	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	peptide binding	RT	▮		5	3.8E-1	1.0E0
☐	GOTERM_BP_ALL	G-protein coupled receptor protein signaling pathway	RT	▮		16	4.1E-1	1.0E0
☐	GOTERM_MF_ALL	peptide receptor activity	RT	▮		4	4.6E-1	1.0E0
☐	GOTERM_MF_ALL	transmembrane receptor activity	RT	▮		19	4.7E-1	1.0E0
☐	GOTERM_BP_ALL	neuropeptide signaling pathway	RT	▮		3	5.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	transducer	RT	▮		8	7.8E-1	1.0E0
☐	GOTERM_MF_ALL	G-protein coupled receptor activity	RT	▮		9	7.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	g-protein coupled receptor	RT	▮		7	8.0E-1	1.0E0
☐	GOTERM_MF_ALL	rhodopsin-like receptor activity	RT	▮		7	8.2E-1	1.0E0
☐	INTERPRO	Rhodopsin-like GPCR superfamily	RT	▮		3	9.8E-1	1.0E0
	Annotation Cluster 87	Enrichment Score: 0.2	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	coenzyme metabolic process	RT	▮		5	5.2E-1	1.0E0
☐	GOTERM_BP_ALL	coenzyme biosynthetic process	RT	▮		3	6.3E-1	1.0E0
☐	GOTERM_BP_ALL	cofactor metabolic process	RT	▮		5	7.0E-1	1.0E0
☐	GOTERM_BP_ALL	cofactor biosynthetic process	RT	▮		3	7.1E-1	1.0E0
	Annotation Cluster 88	Enrichment Score: 0.19	G		🟩	Count	P_Value	Benjamini
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	RT	▮		4	5.8E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	RT	▮		4	5.8E-1	1.0E0
☐	UP_SEQ_FEATURE	zinc finger region:C2H2-type 3	RT	▮		3	7.9E-1	1.0E0
	Annotation Cluster 89	Enrichment Score: 0.17	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Tetratricopeptide region	RT	▮		3	6.4E-1	1.0E0
☐	SMART	TPR	RT	▮		3	6.8E-1	1.0E0
☐	INTERPRO	Tetratricopeptide-like helical	RT	▮		3	7.0E-1	1.0E0
	Annotation Cluster 90	Enrichment Score: 0.17	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	Palmitate	RT	▮		5	5.8E-1	1.0E0
☐	UP_SEQ_FEATURE	lipid moiety-binding region:S-palmitoyl cysteine	RT	▮		4	6.4E-1	1.0E0
☐	KEGG_PATHWAY	Neuroactive ligand-receptor interaction	RT	▮		6	7.6E-1	1.0E0
☐	SP_PIR_KEYWORDS	lipoprotein	RT	▮		11	7.6E-1	1.0E0
	Annotation Cluster 91	Enrichment Score: 0.16	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	protein complex assembly	RT	▮		5	5.0E-1	1.0E0
☐	GOTERM_BP_ALL	macromolecular complex assembly	RT	▮		7	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	cellular component assembly	RT	▮		7	8.8E-1	1.0E0
	Annotation Cluster 92	Enrichment Score: 0.16	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	sh2 domain	RT	▮		3	6.9E-1	1.0E0
☐	INTERPRO	SH2 motif	RT	▮		3	6.9E-1	1.0E0
☐	SMART	SH2	RT	▮		3	7.2E-1	1.0E0
	Annotation Cluster 93	Enrichment Score: 0.14	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	ligase activity	RT	▮		9	5.0E-1	1.0E0
☐	GOTERM_MF_ALL	ubiquitin-protein ligase activity	RT	▮		3	7.6E-1	1.0E0
☐	GOTERM_MF_ALL	ligase activity, forming carbon-nitrogen bonds	RT	▮		4	7.6E-1	1.0E0
☐	GOTERM_MF_ALL	small protein conjugating enzyme activity	RT	▮		3	7.7E-1	1.0E0
☐	GOTERM_MF_ALL	small conjugating protein ligase activity	RT	▮		3	7.8E-1	1.0E0
☐	GOTERM_MF_ALL	acid-amino acid ligase activity	RT	▮		3	8.3E-1	1.0E0
	Annotation Cluster 94	Enrichment Score: 0.13	G		🟩	Count	P_Value	Benjamini

☐	**GOTERM_BP_ALL**	chemical homeostasis	RT	7	4.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	ion homeostasis	RT	4	8.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular homeostasis	RT	5	8.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular chemical homeostasis	RT	3	9.0E-1	1.0E0
☐	**GOTERM_BP_ALL**	cellular ion homeostasis	RT	3	9.0E-1	1.0E0
	Annotation Cluster 95	Enrichment Score: 0.12	G	Count	P_Value	Benjamini
☐	**SP_PIR_KEYWORDS**	heme	RT	4	4.9E-1	1.0E0
☐	**UP_SEQ_FEATURE**	metal ion-binding site:Iron (heme axial ligand)	RT	3	5.1E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	iron	RT	6	6.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	oxidoreductase activity	RT	16	8.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	heme binding	RT	3	8.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	tetrapyrrole binding	RT	3	8.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	electron transport	RT	7	8.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	oxidoreductase	RT	8	9.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	generation of precursor metabolites and energy	RT	8	9.4E-1	1.0E0
	Annotation Cluster 96	Enrichment Score: 0.12	G	Count	P_Value	Benjamini
☐	**INTERPRO**	Nucleotide-binding, alpha-beta plait	RT	4	6.8E-1	1.0E0
☐	**INTERPRO**	RNA recognition motif, RNP-1	RT	4	6.8E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	rna-binding	RT	8	7.2E-1	1.0E0
☐	**SMART**	RRM	RT	4	7.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	RNA binding	RT	8	9.8E-1	1.0E0
	Annotation Cluster 97	Enrichment Score: 0.11	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	regulation of protein metabolic process	RT	8	4.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of translation	RT	3	8.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of cellular biosynthetic process	RT	3	8.7E-1	1.0E0
☐	**GOTERM_BP_ALL**	regulation of biosynthetic process	RT	3	9.1E-1	1.0E0
☐	**GOTERM_BP_ALL**	translation	RT	6	9.7E-1	1.0E0
	Annotation Cluster 98	Enrichment Score: 0.07	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	transition metal ion transport	RT	3	3.6E-1	1.0E0
☐	**GOTERM_BP_ALL**	di-, tri-valent inorganic cation transport	RT	4	6.1E-1	1.0E0
☐	**GOTERM_MF_ALL**	inorganic cation transmembrane transporter activity	RT	4	6.3E-1	1.0E0
☐	**GOTERM_BP_ALL**	cation transport	RT	9	8.4E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	ion transport	RT	8	8.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	substrate-specific transporter activity	RT	17	8.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	metal ion transport	RT	6	9.4E-1	1.0E0
☐	**GOTERM_MF_ALL**	metal ion transmembrane transporter activity	RT	4	9.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	localization	RT	53	9.5E-1	1.0E0
☐	**GOTERM_BP_ALL**	ion transport	RT	11	9.6E-1	1.0E0
☐	**GOTERM_MF_ALL**	transporter activity	RT	21	9.6E-1	1.0E0
☐	**SP_PIR_KEYWORDS**	transport	RT	20	9.7E-1	1.0E0
☐	**GOTERM_MF_ALL**	cation transmembrane transporter activity	RT	6	9.8E-1	1.0E0
☐	**GOTERM_BP_ALL**	transport	RT	42	9.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	substrate-specific transmembrane transporter activity	RT	10	9.8E-1	1.0E0
☐	**GOTERM_MF_ALL**	ion transmembrane transporter activity	RT	8	9.9E-1	1.0E0
☐	**GOTERM_BP_ALL**	establishment of localization	RT	42	9.9E-1	1.0E0
☐	**GOTERM_MF_ALL**	transmembrane transporter activity	RT	11	9.9E-1	1.0E0
	Annotation Cluster 99	Enrichment Score: 0.06	G	Count	P_Value	Benjamini
☐	**GOTERM_BP_ALL**	macromolecule biosynthetic process	RT	14	7.5E-1	1.0E0

☐	GOTERM_BP_ALL	biosynthetic process	RT	▬		25	7.7E-1	1.0E0
☐	GOTERM_BP_ALL	translation	RT	▬		6	9.7E-1	1.0E0
☐	GOTERM_BP_ALL	cellular biosynthetic process	RT	▬		13	9.9E-1	1.0E0
	Annotation Cluster 100	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	condensed chromosome	RT	▬		3	3.3E-1	1.0E0
☐	GOTERM_CC_ALL	chromosome	RT	▬		7	6.8E-1	1.0E0
☐	GOTERM_CC_ALL	chromosomal part	RT	▬		6	7.2E-1	1.0E0
☐	GOTERM_CC_ALL	transcription factor complex	RT	▬		7	9.1E-1	1.0E0
☐	GOTERM_CC_ALL	nucleoplasm	RT	▬		9	9.5E-1	1.0E0
☐	GOTERM_CC_ALL	nucleoplasm part	RT	▬		8	9.6E-1	1.0E0
☐	GOTERM_CC_ALL	nuclear lumen	RT	▬		10	9.8E-1	1.0E0
☐	GOTERM_CC_ALL	organelle lumen	RT	▬		11	9.9E-1	1.0E0
☐	GOTERM_CC_ALL	membrane-enclosed lumen	RT	▬		11	9.9E-1	1.0E0
☐	GOTERM_CC_ALL	nuclear part	RT	▬		14	9.9E-1	1.0E0
☐	GOTERM_CC_ALL	protein complex	RT	▬		22	1.0E0	1.0E0
☐	GOTERM_CC_ALL	intracellular organelle part	RT	▬		31	1.0E0	1.0E0
☐	GOTERM_CC_ALL	organelle part	RT	▬		31	1.0E0	1.0E0
☐	GOTERM_CC_ALL	macromolecular complex	RT	▬		24	1.0E0	1.0E0
	Annotation Cluster 101	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	EGF-like	RT	▬		3	7.6E-1	1.0E0
☐	INTERPRO	EGF-like region	RT	▬		5	7.8E-1	1.0E0
☐	INTERPRO	EGF-like, type 3	RT	▬		3	9.0E-1	1.0E0
☐	INTERPRO	EGF	RT	▬		3	9.1E-1	1.0E0
☐	SMART	EGF	RT	▬		3	9.2E-1	1.0E0
☐	SP_PIR_KEYWORDS	egf-like domain	RT	▬		3	9.3E-1	1.0E0
	Annotation Cluster 102	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, C2H2-like	RT	▬		7	8.1E-1	1.0E0
☐	SMART	ZnF_C2H2	RT	▬		7	8.9E-1	1.0E0
☐	INTERPRO	Zinc finger, C2H2-type	RT	▬		8	9.0E-1	1.0E0
	Annotation Cluster 103	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	microsome	RT	▬		3	8.5E-1	1.0E0
☐	GOTERM_CC_ALL	vesicular fraction	RT	▬		3	8.7E-1	1.0E0
☐	GOTERM_CC_ALL	membrane fraction	RT	▬		8	8.9E-1	1.0E0
	Annotation Cluster 104	Enrichment Score: 0.06	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	wd repeat	RT	▬		5	7.4E-1	1.0E0
☐	INTERPRO	WD40 repeat	RT	▬		3	9.4E-1	1.0E0
☐	SMART	WD40	RT	▬		3	9.6E-1	1.0E0
	Annotation Cluster 105	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	sensory perception	RT	▬		5	8.7E-1	1.0E0
☐	GOTERM_BP_ALL	system process	RT	▬		12	8.9E-1	1.0E0
☐	GOTERM_BP_ALL	neurological system process	RT	▬		9	9.0E-1	1.0E0
	Annotation Cluster 106	Enrichment Score: 0.05	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	ATPase activity, coupled to transmembrane movement of substances	RT	▬		3	8.0E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity, coupled to movement of substances	RT	▬		3	8.0E-1	1.0E0
☐	GOTERM_MF_ALL	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT	▬		3	8.1E-1	1.0E0
☐	GOTERM_MF_ALL	primary active transmembrane transporter activity	RT	▬		3	8.4E-1	1.0E0
☐	GOTERM_MF_ALL	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT	▬		3	8.4E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity, coupled	RT	▬		4	9.4E-1	1.0E0

☐	GOTERM_MF_ALL	active transmembrane transporter activity	RT	▮		5	9.5E-1	1.0E0
☐	GOTERM_MF_ALL	pyrophosphatase activity	RT	▮		8	9.6E-1	1.0E0
☐	GOTERM_MF_ALL	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	RT	▮		8	9.6E-1	1.0E0
☐	GOTERM_MF_ALL	hydrolase activity, acting on acid anhydrides	RT	▮		8	9.6E-1	1.0E0
☐	GOTERM_MF_ALL	ATPase activity	RT	▮		4	9.7E-1	1.0E0
☐	GOTERM_MF_ALL	nucleoside-triphosphatase activity	RT	▮		7	9.7E-1	1.0E0
	Annotation Cluster 107	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_BP_ALL	neurological system process	RT	▮		9	9.0E-1	1.0E0
☐	GOTERM_BP_ALL	transmission of nerve impulse	RT	▮		4	9.2E-1	1.0E0
☐	GOTERM_BP_ALL	cell-cell signaling	RT	▮		5	9.6E-1	1.0E0
	Annotation Cluster 108	Enrichment Score: 0.03	G		🟩	Count	P_Value	Benjamini
☐	INTERPRO	Zinc finger, C2H2-type/integrase, DNA-binding	RT	▮		5	8.9E-1	1.0E0
☐	INTERPRO	KRAB box	RT	▮		3	9.4E-1	1.0E0
☐	SMART	KRAB	RT	▮		3	9.6E-1	1.0E0
	Annotation Cluster 109	Enrichment Score: 0.01	G		🟩	Count	P_Value	Benjamini
☐	SP_PIR_KEYWORDS	ion transport	RT	▮		8	8.4E-1	1.0E0
☐	GOTERM_MF_ALL	gated channel activity	RT	▮		3	9.8E-1	1.0E0
☐	SP_PIR_KEYWORDS	Ionic channel	RT	▮		3	9.8E-1	1.0E0
☐	GOTERM_MF_ALL	ion transmembrane transporter activity	RT	▮		8	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	ion channel activity	RT	▮		3	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	substrate specific channel activity	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_MF_ALL	passive transmembrane transporter activity	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_MF_ALL	channel activity	RT	▮		3	1.0E0	1.0E0
	Annotation Cluster 110	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_CC_ALL	mitochondrial envelope	RT	▮		3	9.9E-1	1.0E0
☐	GOTERM_CC_ALL	organelle envelope	RT	▮		4	9.9E-1	1.0E0
☐	GOTERM_CC_ALL	envelope	RT	▮		4	9.9E-1	1.0E0
☐	GOTERM_CC_ALL	mitochondrial part	RT	▮		3	1.0E0	1.0E0
	Annotation Cluster 111	Enrichment Score: 0	G		🟩	Count	P_Value	Benjamini
☐	GOTERM_MF_ALL	GTP binding	RT	▮		3	9.9E-1	1.0E0
☐	GOTERM_MF_ALL	guanyl ribonucleotide binding	RT	▮		3	1.0E0	1.0E0
☐	GOTERM_MF_ALL	guanyl nucleotide binding	RT	▮		3	1.0E0	1.0E0

215 terms were not clustered.

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