

Functional Annotation Clustering

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Current Gene List: Naive secretomes















































Current Background: Homo sapiens

101 DAVID IDs

Options Classification Stringency

44 Cluster(s)

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Annotation Cluster 1		Enrichment Score: 5.67			Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	protein biosynthesis	RT		14	1.7E-11	2.0E-9
<input type="checkbox"/>	GOTERM_BP_FAT	translational elongation	RT		12	3.1E-11	3.1E-8
<input type="checkbox"/>	GOTERM_MF_FAT	structural molecule activity	RT		22	1.8E-9	4.9E-7
<input type="checkbox"/>	SP_PIR_KEYWORDS	ribosome	RT		9	4.1E-9	3.2E-7
<input type="checkbox"/>	GOTERM_CC_FAT	cytosolic ribosome	RT		9	1.0E-7	2.0E-5
<input type="checkbox"/>	GOTERM_BP_FAT	translation	RT		14	1.3E-7	2.2E-5
<input type="checkbox"/>	GOTERM_CC_FAT	cytosolic small ribosomal subunit	RT		7	3.5E-7	3.4E-5
<input type="checkbox"/>	GOTERM_CC_FAT	cytosol	RT		27	1.1E-6	7.3E-5
<input type="checkbox"/>	GOTERM_CC_FAT	cytosolic part	RT		10	1.3E-6	6.3E-5
<input type="checkbox"/>	GOTERM_CC_FAT	ribosomal subunit	RT		9	3.4E-6	1.1E-4
<input type="checkbox"/>	GOTERM_CC_FAT	small ribosomal subunit	RT		7	5.4E-6	1.5E-4
<input type="checkbox"/>	SP_PIR_KEYWORDS	ribosomal protein	RT		9	6.2E-6	2.5E-4
<input type="checkbox"/>	SP_PIR_KEYWORDS	blocked amino end	RT		7	8.4E-6	2.9E-4
<input type="checkbox"/>	SP_PIR_KEYWORDS	ribonucleoprotein	RT		10	1.5E-5	4.5E-4
<input type="checkbox"/>	KEGG_PATHWAY	Ribosome	RT		8	1.6E-5	1.0E-3
<input type="checkbox"/>	GOTERM_CC_FAT	ribosome	RT		10	2.2E-5	4.8E-4
<input type="checkbox"/>	GOTERM_MF_FAT	structural constituent of ribosome	RT		9	2.3E-5	2.0E-3
<input type="checkbox"/>	GOTERM_CC_FAT	ribonucleoprotein complex	RT		11	3.6E-3	4.9E-2
<input type="checkbox"/>	GOTERM_MF_FAT	RNA binding	RT		7	3.9E-1	9.9E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	rna-binding	RT		3	7.8E-1	1.0E0
Annotation Cluster 2		Enrichment Score: 3.4			Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	actin-binding	RT		12	6.5E-8	3.9E-6
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of actin cytoskeleton organization	RT		9	8.1E-8	4.0E-5
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of actin polymerization or depolymerization	RT		8	1.0E-7	3.3E-5
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of actin filament-based process	RT		9	1.1E-7	2.6E-5
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of actin filament length	RT		8	1.3E-7	2.5E-5
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of actin filament polymerization	RT		7	1.0E-6	1.5E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cytoskeleton organization	RT		9	2.1E-6	2.6E-4
<input type="checkbox"/>	GOTERM_CC_FAT	actin cytoskeleton	RT		12	3.1E-6	1.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein polymerization	RT		7	4.1E-6	4.5E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of organelle organization	RT		10	8.5E-6	8.4E-4
<input type="checkbox"/>	GOTERM_CC_FAT	Arp2/3 protein complex	RT		4	1.2E-5	3.0E-4
<input type="checkbox"/>	GOTERM_MF_FAT	actin binding	RT		12	1.7E-5	2.2E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein complex assembly	RT		7	2.1E-5	1.9E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cellular component biogenesis	RT		8	3.0E-5	2.5E-3
<input type="checkbox"/>	SP_PIR_KEYWORDS	actin capping	RT		4	1.2E-4	3.0E-3
<input type="checkbox"/>	GOTERM_MF_FAT	structural constituent of cytoskeleton	RT		6	1.7E-4	1.1E-2
<input type="checkbox"/>	GOTERM_MF_FAT	cytoskeletal protein binding	RT		13	2.0E-4	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cellular component size	RT		9	3.0E-4	2.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	actin filament capping	RT		4	3.4E-4	2.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of actin filament depolymerization	RT		4	4.4E-4	2.9E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	cytoskeleton	RT		12	4.7E-4	9.2E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of actin filament	RT		4	6.3E-4	3.6E-2

<input type="checkbox"/>	GOTERM_BP_FAT	depolymerization	RT		4	7.0E-4	3.8E-2			
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of actin filament polymerization	RT		4	7.0E-4	3.8E-2			
<input type="checkbox"/>	GOTERM_BP_FAT	cell motion	RT		11	7.7E-4	3.9E-2			
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of protein polymerization	RT		4	7.8E-4	3.8E-2			
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of protein complex assembly	RT		4	1.2E-3	5.4E-2			
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of protein complex disassembly	RT		4	2.1E-3	8.8E-2			
<input type="checkbox"/>	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT		31	3.1E-3	4.6E-2			
<input type="checkbox"/>	GOTERM_CC_FAT	non-membrane-bounded organelle	RT		31	3.1E-3	4.6E-2			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein complex disassembly	RT		4	4.0E-3	1.5E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of cytoskeleton organization	RT		4	5.0E-3	1.7E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of organelle organization	RT		4	1.5E-2	3.7E-1			
<input type="checkbox"/>	KEGG_PATHWAY	Regulation of actin cytoskeleton	RT		7	1.6E-2	2.9E-1			
<input type="checkbox"/>	KEGG_PATHWAY	Pathogenic Escherichia coli infection	RT		4	1.7E-2	2.3E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	cell cortex part	RT		4	2.1E-2	1.6E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	cytoskeleton	RT		17	3.4E-2	2.1E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	cytoskeletal part	RT		13	3.7E-2	2.2E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	cortical cytoskeleton	RT		3	4.8E-2	2.5E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	actin cytoskeleton organization	RT		5	5.4E-2	6.4E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of cellular component organization	RT		4	6.0E-2	6.6E-1			
<input type="checkbox"/>	KEGG_PATHWAY	Fc gamma R-mediated phagocytosis	RT		4	6.3E-2	5.5E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	actin filament-based process	RT		5	6.5E-2	6.8E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	cell cortex	RT		4	8.6E-2	3.7E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	cell projection organization	RT		5	2.0E-1	9.0E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	cytoskeleton organization	RT		5	2.9E-1	9.5E-1			
Annotation Cluster 3					Enrichment Score: 2.51	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	pigment granule	RT		7	4.0E-5	7.9E-4			
<input type="checkbox"/>	GOTERM_CC_FAT	melanosome	RT		7	4.0E-5	7.9E-4			
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic membrane-bounded vesicle	RT		11	5.6E-3	7.2E-2			
<input type="checkbox"/>	GOTERM_CC_FAT	membrane-bounded vesicle	RT		11	7.0E-3	8.3E-2			
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic vesicle	RT		11	1.6E-2	1.6E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	vesicle	RT		11	2.1E-2	1.6E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	secretory granule	RT		4	1.4E-1	5.0E-1			
Annotation Cluster 4					Enrichment Score: 2.08	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	eukaryotic translation elongation factor 1 complex	RT		3	4.9E-4	8.9E-3			
<input type="checkbox"/>	SP_PIR_KEYWORDS	elongation factor	RT		3	5.3E-3	6.1E-2			
<input type="checkbox"/>	GOTERM_MF_FAT	translation elongation factor activity	RT		3	1.2E-2	3.7E-1			
<input type="checkbox"/>	GOTERM_MF_FAT	translation factor activity, nucleic acid binding	RT		3	1.5E-1	9.2E-1			
Annotation Cluster 5					Enrichment Score: 2.02	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	structural constituent of cytoskeleton	RT		6	1.7E-4	1.1E-2			
<input type="checkbox"/>	SP_PIR_KEYWORDS	actin binding	RT		4	1.2E-3	1.8E-2			
<input type="checkbox"/>	GOTERM_CC_FAT	sarcomere	RT		4	3.3E-2	2.2E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	myofibril	RT		4	4.5E-2	2.5E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	contractile fiber part	RT		4	4.7E-2	2.5E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	contractile fiber	RT		4	5.5E-2	2.7E-1			
Annotation Cluster 6					Enrichment Score: 1.85	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	signal	RT		31	8.2E-4	1.5E-2			
<input type="checkbox"/>	UP_SEQ_FEATURE	signal peptide	RT		31	9.2E-4	1.9E-1			
<input type="checkbox"/>	SP_PIR_KEYWORDS	disulfide bond	RT		27	3.5E-3	4.3E-2			
<input type="checkbox"/>	UP_SEQ_FEATURE	disulfide bond	RT		26	4.8E-3	4.2E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular region	RT		23	2.3E-2	1.7E-1			
<input type="checkbox"/>	SP_PIR_KEYWORDS	Secreted	RT		15	5.4E-2	3.3E-1			
<input type="checkbox"/>	SP_PIR_KEYWORDS	glycoprotein	RT		27	2.3E-1	7.7E-1			
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		24	4.1E-1	1.0E0			
Annotation Cluster 7					Enrichment Score: 1.79	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	EGF_CA	RT		5	1.2E-3	5.8E-2			
<input type="checkbox"/>	INTERPRO	EGF-like domain	RT		5	1.2E-3	5.8E-2			

<input type="checkbox"/>	INTERPRO	EGF-like region, conserved site	RT		8	1.6E-3	3.7E-1
<input type="checkbox"/>	INTERPRO	EGF-like calcium-binding	RT		5	2.4E-3	2.9E-1
<input type="checkbox"/>	INTERPRO	EGF-like calcium-binding, conserved site	RT		5	2.4E-3	2.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain: EGF-like 6; calcium-binding	RT		3	7.5E-3	5.0E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	extracellular matrix	RT		6	8.5E-3	8.8E-2
<input type="checkbox"/>	INTERPRO	EGF calcium-binding	RT		4	8.5E-3	5.6E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	calcium	RT		11	8.9E-3	8.9E-2
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular matrix	RT		8	1.1E-2	1.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain: EGF-like 4; calcium-binding	RT		3	1.3E-2	6.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain: EGF-like 3; calcium-binding	RT		3	1.6E-2	6.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain: EGF-like 5; calcium-binding	RT		3	1.6E-2	6.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular region part	RT		14	1.8E-2	1.6E-1
<input type="checkbox"/>	INTERPRO	EGF-type aspartate/asparagine hydroxylation conserved site	RT		4	1.9E-2	7.5E-1
<input type="checkbox"/>	GOTERM_MF_FAT	extracellular matrix structural constituent	RT		4	2.2E-2	5.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	calcium ion binding	RT		13	2.6E-2	5.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	proteinaceous extracellular matrix	RT		7	2.7E-2	1.9E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	egf-like domain	RT		5	3.2E-2	2.3E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	Secreted	RT		15	5.4E-2	3.3E-1
<input type="checkbox"/>	SMART	EGF	RT		3	2.5E-1	9.8E-1
<input type="checkbox"/>	INTERPRO	EGF-like, type 3	RT		3	3.1E-1	1.0E0
<input type="checkbox"/>	INTERPRO	EGF-like	RT		3	3.3E-1	1.0E0

Annotation Cluster 8		Enrichment Score: 1.77			Count	P_Value	Benjamini
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<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif: Prevents secretion from ER	RT		5	2.6E-4	1.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	endoplasmic reticulum lumen	RT		4	1.9E-2	1.6E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	endoplasmic reticulum	RT		9	3.2E-2	2.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	endoplasmic reticulum	RT		13	3.9E-2	2.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	endoplasmic reticulum part	RT		5	2.3E-1	6.7E-1

Annotation Cluster 9		Enrichment Score: 1.64			Count	P_Value	Benjamini
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<input type="checkbox"/>	SP_PIR_KEYWORDS	nadp	RT		6	1.3E-3	2.0E-2
<input type="checkbox"/>	GOTERM_MF_FAT	oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor	RT		3	7.7E-3	2.9E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	oxidoreductase	RT		9	9.0E-3	8.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	oxidation reduction	RT		10	1.9E-2	4.0E-1
<input type="checkbox"/>	INTERPRO	NAD(P)-binding domain	RT		4	5.7E-2	9.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	cofactor binding	RT		5	9.7E-2	8.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	coenzyme binding	RT		3	3.6E-1	9.9E-1

Annotation Cluster 10		Enrichment Score: 1.42			Count	P_Value	Benjamini
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<input type="checkbox"/>	SP_PIR_KEYWORDS	plasma	RT		5	1.4E-3	2.0E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	duplication	RT		6	6.8E-3	7.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	acute inflammatory response	RT		4	2.4E-2	4.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to wounding	RT		7	1.2E-1	8.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	inflammatory response	RT		4	3.3E-1	9.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	defense response	RT		6	3.4E-1	9.6E-1

Annotation Cluster 11		Enrichment Score: 1.36			Count	P_Value	Benjamini
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<input type="checkbox"/>	SP_PIR_KEYWORDS	gangliosidosis	RT		3	2.6E-4	5.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	glycosphingolipid metabolic process	RT		4	5.6E-4	3.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	glycolipid metabolic process	RT		4	9.5E-4	4.4E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	lysosome	RT		6	1.1E-3	1.8E-2
<input type="checkbox"/>	KEGG_PATHWAY	Lysosome	RT		6	5.0E-3	1.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	sphingolipid metabolic process	RT		4	1.2E-2	3.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	membrane lipid metabolic process	RT		4	1.4E-2	3.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	lysosome	RT		6	1.7E-2	1.6E-1
<input type="checkbox"/>	GOTERM_CC_FAT	lytic vacuole	RT		6	1.7E-2	1.6E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	zymogen	RT		5	2.3E-2	1.8E-1
<input type="checkbox"/>	GOTERM_CC_FAT	vacuole	RT		6	3.4E-2	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	propeptide: Activation peptide	RT		3	5.6E-2	9.5E-1
<input type="checkbox"/>	GOTERM_MF_FAT	enzyme activator activity	RT		5	2.1E-1	9.6E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	Protease	RT		5	2.4E-1	7.9E-1

<input type="checkbox"/>	GOTERM_BP_FAT	lipid localization	RT		3	2.6E-1	9.3E-1			
<input type="checkbox"/>	SP_PIR_KEYWORDS	hydrolase	RT		11	2.9E-1	8.4E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	proteolysis	RT		9	3.4E-1	9.6E-1			
<input type="checkbox"/>	GOTERM_MF_FAT	serine-type peptidase activity	RT		3	3.6E-1	9.9E-1			
<input type="checkbox"/>	GOTERM_MF_FAT	serine hydrolase activity	RT		3	3.6E-1	9.9E-1			
<input type="checkbox"/>	GOTERM_MF_FAT	endopeptidase activity	RT		4	4.9E-1	1.0E0			
<input type="checkbox"/>	GOTERM_MF_FAT	peptidase activity, acting on L-amino acid peptides	RT		5	5.4E-1	1.0E0			
<input type="checkbox"/>	GOTERM_MF_FAT	peptidase activity	RT		5	5.8E-1	1.0E0			
<input type="checkbox"/>	GOTERM_CC_FAT	integral to membrane	RT		7	1.0E0	1.0E0			
Annotation Cluster 12					Enrichment Score: 1.34	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	NADP metabolic process	RT		3	4.4E-3	1.6E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	nicotinamide nucleotide metabolic process	RT		3	2.6E-2	4.9E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	nicotinamide metabolic process	RT		3	2.6E-2	4.9E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	alkaloid metabolic process	RT		3	2.7E-2	4.9E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	pyridine nucleotide metabolic process	RT		3	2.9E-2	4.9E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	oxidoreduction coenzyme metabolic process	RT		3	4.2E-2	6.0E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	cellular amide metabolic process	RT		3	4.8E-2	6.2E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	secondary metabolic process	RT		3	8.8E-2	7.3E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	coenzyme metabolic process	RT		3	2.5E-1	9.3E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	cofactor metabolic process	RT		3	3.5E-1	9.6E-1			
Annotation Cluster 13					Enrichment Score: 1.19	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	cellular response to reactive oxygen species	RT		3	1.5E-2	3.7E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	cellular response to oxidative stress	RT		3	3.0E-2	4.9E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	cellular response to stress	RT		8	6.5E-2	6.8E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	response to reactive oxygen species	RT		3	8.1E-2	7.1E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	response to oxidative stress	RT		4	8.4E-2	7.2E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	response to inorganic substance	RT		3	3.7E-1	9.7E-1			
Annotation Cluster 14					Enrichment Score: 1.19	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	cell motion	RT		11	7.7E-4	3.9E-2			
<input type="checkbox"/>	GOTERM_BP_FAT	cell migration	RT		4	2.5E-1	9.3E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	localization of cell	RT		4	3.0E-1	9.5E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	cell motility	RT		4	3.0E-1	9.5E-1			
Annotation Cluster 15					Enrichment Score: 1.19	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	gonad development	RT		4	3.3E-2	5.2E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	reproductive structure development	RT		4	4.5E-2	6.1E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	development of primary sexual characteristics	RT		4	4.6E-2	6.0E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	female gonad development	RT		3	6.1E-2	6.7E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	sex differentiation	RT		4	7.0E-2	6.9E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	female sex differentiation	RT		3	7.0E-2	6.9E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	development of primary female sexual characteristics	RT		3	7.0E-2	6.9E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	reproductive developmental process	RT		4	2.3E-1	9.1E-1			
Annotation Cluster 16					Enrichment Score: 1.12	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	enzyme inhibitor activity	RT		6	4.1E-2	6.7E-1			
<input type="checkbox"/>	GOTERM_MF_FAT	endopeptidase inhibitor activity	RT		4	8.2E-2	8.5E-1			
<input type="checkbox"/>	GOTERM_MF_FAT	peptidase inhibitor activity	RT		4	9.2E-2	8.6E-1			
<input type="checkbox"/>	SP_PIR_KEYWORDS	protease inhibitor	RT		3	1.1E-1	5.2E-1			
Annotation Cluster 17					Enrichment Score: 1.03	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	isopeptide bond	RT		6	2.6E-2	2.0E-1			
<input type="checkbox"/>	UP_SEQ_FEATURE	cross-link: Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin)	RT		4	8.7E-2	9.7E-1			
<input type="checkbox"/>	SP_PIR_KEYWORDS	ubl conjugation	RT		5	3.7E-1	9.1E-1			
Annotation Cluster 18					Enrichment Score: 1.03	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of DNA repair	RT		3	8.3E-3	2.5E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cellular response to stress	RT		4	2.7E-2	4.9E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of binding	RT		4	7.2E-2	6.9E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of transcription factor activity	RT		3	1.4E-1	8.3E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of DNA metabolic process	RT		3	1.6E-1	8.7E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of DNA binding	RT		3	1.8E-1	8.8E-1			

<input type="checkbox"/>	GOTERM_BP_FAT	regulation of transcription	RT		3	1.0E0	1.0E0			
Annotation Cluster 19					Enrichment Score: 0.97			Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	EF-Hand type	RT		5	4.9E-2	9.5E-1			
<input type="checkbox"/>	UP_SEQ_FEATURE	domain: EF-hand 1	RT		4	7.0E-2	9.5E-1			
<input type="checkbox"/>	UP_SEQ_FEATURE	domain: EF-hand 2	RT		4	7.0E-2	9.5E-1			
<input type="checkbox"/>	UP_SEQ_FEATURE	domain: EF-hand 3	RT		3	8.7E-2	9.6E-1			
<input type="checkbox"/>	UP_SEQ_FEATURE	calcium-binding region: 2	RT		3	1.2E-1	9.9E-1			
<input type="checkbox"/>	INTERPRO	EF-HAND 2	RT		4	1.3E-1	9.9E-1			
<input type="checkbox"/>	INTERPRO	EF-HAND 1	RT		4	1.3E-1	9.8E-1			
<input type="checkbox"/>	UP_SEQ_FEATURE	calcium-binding region: 1	RT		3	1.4E-1	9.9E-1			
<input type="checkbox"/>	SMART	EFh	RT		3	1.5E-1	9.4E-1			
<input type="checkbox"/>	INTERPRO	Calcium-binding EF-hand	RT		3	2.0E-1	1.0E0			
Annotation Cluster 20					Enrichment Score: 0.95			Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	EGF-like region, conserved site	RT		8	1.6E-3	3.7E-1			
<input type="checkbox"/>	SP_PIR_KEYWORDS	extracellular matrix	RT		6	8.5E-3	8.8E-2			
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular matrix	RT		8	1.1E-2	1.3E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	proteinaceous extracellular matrix	RT		7	2.7E-2	1.9E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	basement membrane	RT		3	1.1E-1	4.2E-1			
<input type="checkbox"/>	KEGG_PATHWAY	Small cell lung cancer	RT		3	1.9E-1	8.9E-1			
<input type="checkbox"/>	KEGG_PATHWAY	ECM-receptor interaction	RT		3	1.9E-1	8.9E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular matrix part	RT		3	2.0E-1	6.4E-1			
<input type="checkbox"/>	KEGG_PATHWAY	Pathways in cancer	RT		5	3.9E-1	9.9E-1			
<input type="checkbox"/>	KEGG_PATHWAY	Focal adhesion	RT		3	5.8E-1	1.0E0			
<input type="checkbox"/>	SP_PIR_KEYWORDS	cell adhesion	RT		3	6.5E-1	9.9E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	cell adhesion	RT		3	9.4E-1	1.0E0			
<input type="checkbox"/>	GOTERM_BP_FAT	biological adhesion	RT		3	9.4E-1	1.0E0			
Annotation Cluster 21					Enrichment Score: 0.92			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	organelle lumen	RT		19	9.0E-2	3.8E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	membrane-enclosed lumen	RT		19	1.0E-1	4.2E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	intracellular organelle lumen	RT		17	1.9E-1	6.2E-1			
Annotation Cluster 22					Enrichment Score: 0.89			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of hydrolase activity	RT		6	5.4E-3	1.8E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of peptidase activity	RT		4	1.7E-2	3.8E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of hydrolase activity	RT		7	1.9E-2	4.1E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	activation of caspase activity	RT		3	4.5E-2	6.1E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of peptidase activity	RT		3	5.3E-2	6.4E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of caspase activity	RT		3	5.3E-2	6.4E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of caspase activity	RT		3	8.8E-2	7.3E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of endopeptidase activity	RT		3	9.4E-2	7.4E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of apoptosis	RT		7	3.9E-1	9.7E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of programmed cell death	RT		7	4.0E-1	9.7E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell death	RT		7	4.1E-1	9.7E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	cell death	RT		5	6.7E-1	1.0E0			
<input type="checkbox"/>	GOTERM_BP_FAT	death	RT		5	6.7E-1	1.0E0			
<input type="checkbox"/>	GOTERM_BP_FAT	apoptosis	RT		3	9.0E-1	1.0E0			
<input type="checkbox"/>	GOTERM_BP_FAT	programmed cell death	RT		3	9.0E-1	1.0E0			
Annotation Cluster 23					Enrichment Score: 0.73			Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	calcium	RT		11	8.9E-3	8.9E-2			
<input type="checkbox"/>	GOTERM_MF_FAT	calcium ion binding	RT		13	2.6E-2	5.5E-1			
<input type="checkbox"/>	GOTERM_MF_FAT	cation binding	RT		21	9.9E-1	1.0E0			
<input type="checkbox"/>	GOTERM_MF_FAT	ion binding	RT		21	9.9E-1	1.0E0			
<input type="checkbox"/>	GOTERM_MF_FAT	metal ion binding	RT		20	9.9E-1	1.0E0			
Annotation Cluster 24					Enrichment Score: 0.64			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	cellular homeostasis	RT		7	7.3E-2	6.9E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	cellular cation homeostasis	RT		5	7.6E-2	7.0E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	cation homeostasis	RT		5	1.1E-1	7.7E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	cellular di-, tri-valent inorganic cation homeostasis	RT		4	1.7E-1	8.8E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	di-, tri-valent inorganic cation homeostasis	RT		4	1.9E-1	8.9E-1			

<input type="checkbox"/>	GOTERM_BP_FAT	cellular ion homeostasis	RT		5	2.1E-1	9.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cellular chemical homeostasis	RT		5	2.2E-1	9.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	membrane organization	RT		5	2.2E-1	9.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	ion homeostasis	RT		5	2.6E-1	9.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cellular calcium ion homeostasis	RT		3	3.2E-1	9.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	calcium ion homeostasis	RT		3	3.3E-1	9.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	homeostatic process	RT		7	3.3E-1	9.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cellular metal ion homeostasis	RT		3	3.5E-1	9.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	metal ion homeostasis	RT		3	3.7E-1	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	chemical homeostasis	RT		5	4.0E-1	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cell proliferation	RT		3	7.6E-1	1.0E0

Annotation Cluster 25		Enrichment Score: 0.61	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	vitamin binding	RT		3	2.3E-1	9.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	carboxylic acid biosynthetic process	RT		3	2.5E-1	9.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	organic acid biosynthetic process	RT		3	2.5E-1	9.3E-1



Annotation Cluster 26		Enrichment Score: 0.6	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of molecular function	RT		10	1.1E-2	3.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of catalytic activity	RT		9	1.6E-2	3.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of ubiquitin-protein ligase activity	RT		3	7.2E-2	6.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of ligase activity	RT		3	7.7E-2	7.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of ubiquitin-protein ligase activity	RT		3	8.6E-2	7.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of ligase activity	RT		3	9.2E-2	7.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of protein ubiquitination	RT		3	9.8E-2	7.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein ubiquitination	RT		3	1.3E-1	8.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of protein modification process	RT		3	1.7E-1	8.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein modification process	RT		4	2.8E-1	9.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of cellular protein metabolic process	RT		3	3.1E-1	9.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of protein metabolic process	RT		3	3.3E-1	9.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of protein modification process	RT		3	3.3E-1	9.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	proteolysis	RT		9	3.4E-1	9.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cellular protein metabolic process	RT		3	4.3E-1	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of protein metabolic process	RT		3	4.5E-1	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cellular macromolecule catabolic process	RT		6	4.8E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	macromolecule catabolic process	RT		6	5.5E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cellular protein metabolic process	RT		4	5.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	modification-dependent protein catabolic process	RT		4	7.1E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	RT		4	7.1E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	RT		4	7.3E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	cellular protein catabolic process	RT		4	7.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	protein catabolic process	RT		4	7.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of macromolecule metabolic process	RT		4	8.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of macromolecule metabolic process	RT		3	9.7E-1	1.0E0

Annotation Cluster 27		Enrichment Score: 0.59	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	intracellular transport	RT		9	5.4E-2	6.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	protein localization	RT		9	1.9E-1	8.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	protein transport	RT		8	2.0E-1	9.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	establishment of protein localization	RT		8	2.1E-1	9.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cellular protein localization	RT		5	2.6E-1	9.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cellular macromolecule localization	RT		5	2.6E-1	9.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	intracellular protein transport	RT		4	4.2E-1	9.8E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	protein transport	RT		4	4.6E-1	9.5E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	transport	RT		6	9.4E-1	1.0E0

Annotation Cluster 28		Enrichment Score: 0.59	G		Count	P_Value	Benjamini
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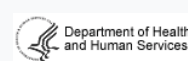
<input type="checkbox"/>	GOTERM_MF_FAT	identical protein binding	RT		9	8.0E-2	8.7E-1			
<input type="checkbox"/>	GOTERM_MF_FAT	protein homodimerization activity	RT		4	4.2E-1	9.9E-1			
<input type="checkbox"/>	GOTERM_MF_FAT	protein dimerization activity	RT		5	5.3E-1	1.0E0			
Annotation Cluster 29					Enrichment Score: 0.57	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of I-kappaB kinase/NF-kappaB cascade	RT		3	1.2E-1	8.1E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of I-kappaB kinase/NF-kappaB cascade	RT		3	1.5E-1	8.5E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein kinase cascade	RT		4	2.1E-1	9.0E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of protein kinase cascade	RT		3	2.8E-1	9.4E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of signal transduction	RT		3	5.6E-1	9.9E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cell communication	RT		3	6.2E-1	1.0E0			
Annotation Cluster 30					Enrichment Score: 0.57	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	activation of immune response	RT		3	1.2E-1	8.0E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of immune response	RT		3	2.3E-1	9.1E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of response to stimulus	RT		3	4.4E-1	9.8E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of immune system process	RT		3	4.4E-1	9.8E-1			
Annotation Cluster 31					Enrichment Score: 0.48	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	immune effector process	RT		3	2.1E-1	9.0E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	innate immune response	RT		3	2.2E-1	9.0E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	defense response	RT		6	3.4E-1	9.6E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	immune response	RT		4	8.2E-1	1.0E0			
Annotation Cluster 32					Enrichment Score: 0.44	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	ATP	RT		4	1.2E-1	5.6E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	ATP metabolic process	RT		3	1.4E-1	8.4E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	purine ribonucleoside triphosphate metabolic process	RT		3	1.7E-1	8.7E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	ribonucleoside triphosphate metabolic process	RT		3	1.7E-1	8.8E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	purine nucleoside triphosphate metabolic process	RT		3	1.8E-1	8.8E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	nucleoside triphosphate metabolic process	RT		3	2.0E-1	9.0E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	purine ribonucleotide metabolic process	RT		3	2.2E-1	9.0E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial matrix	RT		4	2.2E-1	6.6E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial lumen	RT		4	2.2E-1	6.6E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	ribonucleotide metabolic process	RT		3	2.4E-1	9.2E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	purine nucleotide metabolic process	RT		3	3.3E-1	9.6E-1			
<input type="checkbox"/>	SP_PIR_KEYWORDS	nucleotide-binding	RT		11	3.8E-1	9.2E-1			
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial part	RT		6	4.2E-1	8.8E-1			
<input type="checkbox"/>	SP_PIR_KEYWORDS	ligase	RT		3	4.7E-1	9.5E-1			
<input type="checkbox"/>	SP_PIR_KEYWORDS	atp-binding	RT		6	8.3E-1	1.0E0			
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT		4	8.9E-1	1.0E0			
<input type="checkbox"/>	GOTERM_MF_FAT	ATP binding	RT		8	9.1E-1	1.0E0			
<input type="checkbox"/>	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT		8	9.1E-1	1.0E0			
<input type="checkbox"/>	GOTERM_MF_FAT	adenyl nucleotide binding	RT		8	9.4E-1	1.0E0			
<input type="checkbox"/>	GOTERM_MF_FAT	purine nucleoside binding	RT		8	9.4E-1	1.0E0			
<input type="checkbox"/>	GOTERM_MF_FAT	nucleoside binding	RT		8	9.5E-1	1.0E0			
Annotation Cluster 33					Enrichment Score: 0.38	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	cellular component morphogenesis	RT		5	2.4E-1	9.2E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	cell morphogenesis involved in differentiation	RT		3	4.6E-1	9.8E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	cell morphogenesis	RT		3	6.6E-1	1.0E0			
Annotation Cluster 34					Enrichment Score: 0.36	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	response to organic substance	RT		8	1.7E-1	8.8E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	response to hormone stimulus	RT		3	6.8E-1	1.0E0			
<input type="checkbox"/>	GOTERM_BP_FAT	response to endogenous stimulus	RT		3	7.3E-1	1.0E0			
Annotation Cluster 35					Enrichment Score: 0.35	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	cellular response to stress	RT		8	6.5E-2	6.8E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of apoptosis	RT		7	3.9E-1	9.7E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of programmed cell death	RT		7	4.0E-1	9.7E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell death	RT		7	4.1E-1	9.7E-1			
<input type="checkbox"/>	GOTERM_BP_FAT	induction of apoptosis	RT		3	6.0E-1	1.0E0			

<input type="checkbox"/>	GOTERM_BP_FAT	induction of programmed cell death	RT		3	6.0E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of apoptosis	RT		3	7.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of programmed cell death	RT		3	7.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cell death	RT		3	7.6E-1	1.0E0
Annotation Cluster 36 Enrichment Score: 0.32					Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	RT		5	6.9E-2	9.6E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	gtp-binding	RT		5	9.3E-2	4.8E-1
<input type="checkbox"/>	GOTERM_MF_FAT	GTPase activity	RT		4	1.8E-1	9.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	GTP binding	RT		5	2.6E-1	9.7E-1
<input type="checkbox"/>	GOTERM_MF_FAT	guanyl nucleotide binding	RT		5	2.8E-1	9.7E-1
<input type="checkbox"/>	GOTERM_MF_FAT	guanyl ribonucleotide binding	RT		5	2.8E-1	9.7E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	nucleotide-binding	RT		11	3.8E-1	9.2E-1
<input type="checkbox"/>	GOTERM_MF_FAT	ribonucleotide binding	RT		12	7.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	purine ribonucleotide binding	RT		12	7.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	purine nucleotide binding	RT		12	8.1E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	nucleotide binding	RT		14	8.1E-1	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	atp-binding	RT		6	8.3E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT		4	8.9E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	ATP binding	RT		8	9.1E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT		8	9.1E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	adenyl nucleotide binding	RT		8	9.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	purine nucleoside binding	RT		8	9.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	nucleoside binding	RT		8	9.5E-1	1.0E0
Annotation Cluster 37 Enrichment Score: 0.31					Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	anti-apoptosis	RT		3	3.7E-1	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of apoptosis	RT		7	3.9E-1	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of programmed cell death	RT		7	4.0E-1	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell death	RT		7	4.1E-1	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of apoptosis	RT		3	6.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of programmed cell death	RT		3	6.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of cell death	RT		3	6.7E-1	1.0E0
Annotation Cluster 38 Enrichment Score: 0.3					Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrion	RT		13	8.4E-2	3.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial part	RT		6	4.2E-1	8.8E-1
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear envelope	RT		3	4.3E-1	8.9E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	mitochondrion	RT		6	4.4E-1	9.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	organelle envelope	RT		6	4.5E-1	9.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	envelope	RT		6	4.6E-1	9.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	organelle inner membrane	RT		3	6.8E-1	9.8E-1
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial membrane	RT		3	7.8E-1	9.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial envelope	RT		3	8.0E-1	9.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	endomembrane system	RT		5	8.2E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_FAT	organelle membrane	RT		5	9.6E-1	1.0E0
Annotation Cluster 39 Enrichment Score: 0.14					Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	iron	RT		3	4.4E-1	9.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	iron ion binding	RT		3	6.4E-1	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	metal-binding	RT		7	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	transition metal ion binding	RT		8	1.0E0	1.0E0
Annotation Cluster 40 Enrichment Score: 0.11					Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	gamete generation	RT		3	7.1E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	sexual reproduction	RT		3	7.9E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	reproductive process in a multicellular organism	RT		3	8.2E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	multicellular organism reproduction	RT		3	8.2E-1	1.0E0
Annotation Cluster 41 Enrichment Score: 0.09					Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	macromolecular complex assembly	RT		4	8.0E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	macromolecular complex subunit organization	RT		4	8.3E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	protein complex assembly	RT		3	8.3E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	protein complex biogenesis	RT		2	9.2E-1	1.0E0

Annotation Cluster 42		Enrichment Score: 0.02	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	protein complex biogenesis	RT		3	8.3E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	cognition	RT		4	9.3E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	neurological system process	RT		5	9.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	sensory perception	RT		3	9.7E-1	1.0E0
Annotation Cluster 43		Enrichment Score: 0.01	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	phosphorylation	RT		3	9.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	phosphorus metabolic process	RT		3	9.9E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	phosphate metabolic process	RT		3	9.9E-1	1.0E0
Annotation Cluster 44		Enrichment Score: 0	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	transmembrane region	RT		3	1.0E0	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	transmembrane	RT		3	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_FAT	integral to membrane	RT		7	1.0E0	1.0E0

87 terms were not clustered.

Please cite [Nature Protocols 2009; 4\(1\):44](#) & [Genome Biology 2003; 4\(5\):P3](#) within any publication that makes use of any methods inspired by **DAVID**.



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Functional Annotation Clustering

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Current Gene List: **Primed secretomes**














































Current Background: **Homo sapiens**

83 DAVID IDs

Options Classification Stringency



























































29 Cluster(s)

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Annotation Cluster 1		Enrichment Score: 3.76	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	acetylation	RT		24	1.2E-7	2.0E-5
<input type="checkbox"/>	GOTERM_CC_FAT	cytoskeleton	RT		15	3.9E-4	1.0E-2
<input type="checkbox"/>	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT		19	4.4E-3	6.7E-2
<input type="checkbox"/>	GOTERM_CC_FAT	non-membrane-bounded organelle	RT		19	4.4E-3	6.7E-2
Annotation Cluster 2		Enrichment Score: 3.46	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular region	RT		21	1.5E-5	2.3E-3
<input type="checkbox"/>	SP_PIR_KEYWORDS	signal	RT		23	2.0E-5	1.1E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	signal peptide	RT		23	2.2E-5	5.2E-3
<input type="checkbox"/>	SP_PIR_KEYWORDS	Secreted	RT		16	3.4E-5	1.4E-3
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular region part	RT		14	3.6E-5	1.9E-3
<input type="checkbox"/>	SP_PIR_KEYWORDS	glycoprotein	RT		22	3.7E-3	4.9E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	disulfide bond	RT		16	1.1E-2	9.3E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		20	1.2E-2	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	disulfide bond	RT		15	1.9E-2	7.7E-1
Annotation Cluster 3		Enrichment Score: 3.1	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	extracellular matrix	RT		9	2.9E-7	2.4E-5
<input type="checkbox"/>	GOTERM_CC_FAT	proteinaceous extracellular matrix	RT		9	2.2E-5	1.7E-3
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular matrix	RT		9	3.8E-5	1.5E-3
<input type="checkbox"/>	SP_PIR_KEYWORDS	trimer	RT		4	4.9E-5	1.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	collagen metabolic process	RT		4	1.3E-4	7.9E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	collagen	RT		5	1.4E-4	3.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	multicellular organismal macromolecule metabolic process	RT		4	1.8E-4	5.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	collagen	RT		4	3.0E-4	9.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT	multicellular organismal metabolic process	RT		4	3.0E-4	6.1E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	Ehlers-Danlos syndrome	RT		3	4.0E-4	8.3E-3
<input type="checkbox"/>	GOTERM_CC_FAT	fibrillar collagen	RT		3	8.9E-4	2.0E-2
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular matrix part	RT		5	9.5E-4	1.8E-2
<input type="checkbox"/>	INTERPRO	Collagen triple helix repeat	RT		4	2.2E-3	1.2E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	triple helix	RT		3	3.3E-3	4.8E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	hydroxylysine	RT		3	3.3E-3	4.8E-2
<input type="checkbox"/>	GOTERM_MF_FAT	extracellular matrix structural constituent	RT		4	3.5E-3	1.2E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	hydroxyproline	RT		3	4.7E-3	5.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	collagen fibril organization	RT		3	4.7E-3	3.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	extracellular matrix organization	RT		4	5.9E-3	3.4E-1
<input type="checkbox"/>	KEGG_PATHWAY	ECM-receptor interaction	RT		4	6.1E-3	9.3E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	hydroxylation	RT		3	1.6E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	extracellular structure organization	RT		4	2.0E-2	6.0E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	coiled coil	RT		9	1.9E-1	6.5E-1
Annotation Cluster 4		Enrichment Score: 3.06	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	trimer	RT		4	4.9E-5	1.6E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:TSP N-terminal	RT		3	1.8E-3	2.5E-1
<input type="checkbox"/>	INTERPRO	Laminin G, thrombospondin-type, N-terminal	RT		3	2.0E-3	1.6E-1
<input type="checkbox"/>	SMART	TSPN	RT		3	3.2E-3	6.3E-2
Annotation Cluster 5		Enrichment Score: 2.65	G		Count	P_Value	Benjamini

<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Hemopexin-like 2	RT		3	1.8E-3	2.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Hemopexin-like 1	RT		3	1.8E-3	2.5E-1
<input type="checkbox"/>	INTERPRO	Hemopexin/matrixin_repeat	RT		3	2.2E-3	9.2E-2
<input type="checkbox"/>	INTERPRO	Hemopexin/matrixin_conserved_site	RT		3	2.2E-3	9.2E-2
<input type="checkbox"/>	INTERPRO	Hemopexin/matrixin	RT		3	2.2E-3	9.2E-2
<input type="checkbox"/>	SMART	HX	RT		3	3.5E-3	4.6E-2
Annotation Cluster 6 Enrichment Score: 2.19					Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	polysaccharide binding	RT		5	2.1E-3	9.4E-2
<input type="checkbox"/>	GOTERM_MF_FAT	pattern binding	RT		5	2.1E-3	9.4E-2
<input type="checkbox"/>	GOTERM_MF_FAT	heparin binding	RT		4	5.7E-3	1.5E-1
<input type="checkbox"/>	KEGG_PATHWAY	ECM-receptor interaction	RT		4	6.1E-3	9.3E-2
<input type="checkbox"/>	GOTERM_MF_FAT	glycosaminoglycan binding	RT		4	1.3E-2	2.7E-1
<input type="checkbox"/>	GOTERM_MF_FAT	carbohydrate binding	RT		5	3.6E-2	3.8E-1
Annotation Cluster 7 Enrichment Score: 2.14					Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Cell attachment site	RT		6	4.4E-6	2.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	cell adhesion	RT		9	3.0E-3	3.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	biological adhesion	RT		9	3.0E-3	2.7E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	cell adhesion	RT		6	6.0E-3	6.8E-2
<input type="checkbox"/>	INTERPRO	EGF-like_type_3	RT		4	2.2E-2	5.3E-1
<input type="checkbox"/>	INTERPRO	EGF-like	RT		4	2.4E-2	5.0E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	egf-like domain	RT		4	2.6E-2	1.8E-1
<input type="checkbox"/>	SMART	EGF	RT		4	4.2E-2	3.5E-1
<input type="checkbox"/>	INTERPRO	EGF	RT		3	5.8E-2	7.2E-1
<input type="checkbox"/>	INTERPRO	EGF-like_region_conserved_site	RT		4	6.0E-2	7.0E-1
Annotation Cluster 8 Enrichment Score: 2.08					Count	P_Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	Focal adhesion	RT		8	1.9E-5	6.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	actin filament-based process	RT		6	1.6E-3	2.2E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	cytoskeleton	RT		7	7.8E-3	7.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	actin cytoskeleton organization	RT		5	8.3E-3	4.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	maintenance of protein location in cell	RT		3	9.3E-3	4.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	maintenance of location in cell	RT		3	1.3E-2	4.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	maintenance of protein location	RT		3	1.3E-2	4.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cytoskeleton organization	RT		6	1.9E-2	6.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	maintenance of location	RT		3	2.2E-2	6.0E-1
<input type="checkbox"/>	GOTERM_MF_FAT	actin binding	RT		5	2.8E-2	3.9E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	actin-binding	RT		4	3.1E-2	1.9E-1
<input type="checkbox"/>	GOTERM_MF_FAT	cytoskeletal protein binding	RT		5	1.0E-1	6.6E-1
Annotation Cluster 9 Enrichment Score: 1.45					Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	calcium ion binding	RT		12	2.8E-4	2.0E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	calcium	RT		10	3.1E-4	7.4E-3
<input type="checkbox"/>	GOTERM_MF_FAT	metal ion binding	RT		13	8.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	cation binding	RT		13	8.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	ion binding	RT		13	8.7E-1	1.0E0
Annotation Cluster 10 Enrichment Score: 1.37					Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 2	RT		4	1.4E-2	7.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand 1	RT		4	1.4E-2	7.3E-1
<input type="checkbox"/>	INTERPRO	EF-HAND_2	RT		4	2.8E-2	5.0E-1
<input type="checkbox"/>	INTERPRO	Calcium-binding_EF-hand	RT		3	7.1E-2	7.2E-1
<input type="checkbox"/>	SMART	EFh	RT		3	1.0E-1	6.0E-1
<input type="checkbox"/>	INTERPRO	EF-HAND_1	RT		3	1.4E-1	9.1E-1
Annotation Cluster 11 Enrichment Score: 1.33					Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	epidermis development	RT		4	2.7E-2	6.5E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	disease mutation	RT		10	2.9E-2	1.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	ectoderm development	RT		4	3.3E-2	6.8E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	coiled coil	RT		9	1.9E-1	6.5E-1
Annotation Cluster 12 Enrichment Score: 1					Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	pigment granule	RT		3	4.4E-2	3.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	melanosome	RT		3	4.4E-2	3.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT						

<input type="checkbox"/>		cytoplasmic membrane-bounded vesicle	RT		6	5.4E-2	4.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	membrane-bounded vesicle	RT		6	6.1E-2	4.6E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic vesicle	RT		6	9.2E-2	5.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	vesicle	RT		6	1.1E-1	6.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	secretory granule	RT		3	1.5E-1	6.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic vesicle part	RT		3	1.6E-1	6.8E-1
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrion	RT		4	7.9E-1	1.0E0
Annotation Cluster 13 Enrichment Score: 0.97 G					Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	RNA binding	RT		7	4.0E-2	3.8E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	protein biosynthesis	RT		3	9.5E-2	4.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	translation	RT		3	3.3E-1	9.9E-1
Annotation Cluster 14 Enrichment Score: 0.91 G					Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of protein metabolic process	RT		4	2.9E-2	6.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of cellular protein metabolic process	RT		3	1.3E-1	9.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cellular protein metabolic process	RT		4	2.4E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of macromolecule metabolic process	RT		5	2.6E-1	9.9E-1
Annotation Cluster 15 Enrichment Score: 0.82 G					Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	protein kinase binding	RT		3	9.5E-2	6.6E-1
<input type="checkbox"/>	GOTERM_MF_FAT	kinase binding	RT		3	1.3E-1	7.1E-1
<input type="checkbox"/>	GOTERM_MF_FAT	enzyme binding	RT		4	2.8E-1	8.9E-1
Annotation Cluster 16 Enrichment Score: 0.77 G					Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	zymogen	RT		4	1.9E-2	1.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular space	RT		7	4.2E-2	4.0E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	metal-binding	RT		4	9.9E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	transition metal ion binding	RT		4	1.0E0	1.0E0
Annotation Cluster 17 Enrichment Score: 0.77 G					Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	macromolecular complex assembly	RT		6	8.5E-2	9.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	protein complex biogenesis	RT		5	1.0E-1	9.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	protein complex assembly	RT		5	1.0E-1	9.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	macromolecular complex subunit organization	RT		6	1.1E-1	9.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cellular macromolecular complex subunit organization	RT		4	1.3E-1	9.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cellular macromolecular complex assembly	RT		3	3.1E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of transcription	RT		3	1.0E0	1.0E0
Annotation Cluster 18 Enrichment Score: 0.69 G					Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular space	RT		7	4.2E-2	4.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to endogenous stimulus	RT		3	4.2E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	response to organic substance	RT		4	4.8E-1	1.0E0
Annotation Cluster 19 Enrichment Score: 0.68 G					Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	sexual reproduction	RT		5	7.9E-2	9.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	gamete generation	RT		4	1.6E-1	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	reproductive developmental process	RT		3	2.4E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	multicellular organism reproduction	RT		4	2.5E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	reproductive process in a multicellular organism	RT		4	2.5E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	spermatogenesis	RT		3	3.0E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	male gamete generation	RT		3	3.0E-1	9.9E-1
Annotation Cluster 20 Enrichment Score: 0.66 G					Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	Ras protein signal transduction	RT		3	5.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT		3	2.9E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	intracellular signaling cascade	RT		5	6.6E-1	1.0E0
Annotation Cluster 21 Enrichment Score: 0.64 G					Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cellular component organization	RT		5	3.8E-3	2.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	internal side of plasma membrane	RT		4	1.2E-1	6.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	plasma membrane part	RT		9	6.0E-1	9.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	plasma membrane	RT		14	7.0E-1	9.9E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	cell membrane	RT		6	7.4E-1	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	membrane	RT		10	1.0E0	1.0E0

Annotation Cluster 22		Enrichment Score: 0.63			G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	RT				4	4.8E-2	9.6E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	gtp-binding	RT				4	6.2E-2	3.2E-1
<input type="checkbox"/>	GOTERM_MF_FAT	GTP binding	RT				4	1.4E-1	7.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	guanyl ribonucleotide binding	RT				4	1.5E-1	7.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	guanyl nucleotide binding	RT				4	1.5E-1	7.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	GTPase activity	RT				3	1.7E-1	7.5E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	nucleotide-binding	RT				6	5.0E-1	9.6E-1
<input type="checkbox"/>	GOTERM_MF_FAT	purine nucleotide binding	RT				8	5.3E-1	9.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	microtubule cytoskeleton	RT				3	6.2E-1	9.9E-1
<input type="checkbox"/>	GOTERM_MF_FAT	purine ribonucleotide binding	RT				7	6.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	ribonucleotide binding	RT				7	6.5E-1	1.0E0
Annotation Cluster 23		Enrichment Score: 0.54			G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	RNA binding	RT				7	4.0E-2	3.8E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	rna-binding	RT				5	6.1E-2	3.3E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	ribonucleoprotein	RT				3	1.8E-1	6.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	organelle lumen	RT				10	2.4E-1	8.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	membrane-enclosed lumen	RT				10	2.6E-1	8.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	nucleolus	RT				5	2.7E-1	8.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	ribonucleoprotein complex	RT				4	3.0E-1	8.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	intracellular organelle lumen	RT				8	5.1E-1	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	RNA processing	RT				3	5.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear lumen	RT				6	6.5E-1	9.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	nucleoplasm	RT				3	8.5E-1	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	nucleus	RT				9	9.3E-1	1.0E0
Annotation Cluster 24		Enrichment Score: 0.52			G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	intracellular transport	RT				6	8.2E-2	9.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	protein targeting	RT				3	1.8E-1	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cellular protein localization	RT				4	1.8E-1	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cellular macromolecule localization	RT				4	1.8E-1	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	protein localization	RT				6	2.0E-1	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	induction of apoptosis	RT				3	3.1E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	induction of programmed cell death	RT				3	3.2E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of apoptosis	RT				5	3.2E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of programmed cell death	RT				5	3.3E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell death	RT				5	3.3E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	intracellular protein transport	RT				3	3.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of apoptosis	RT				3	4.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of programmed cell death	RT				3	4.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cell death	RT				3	4.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	establishment of protein localization	RT				4	5.2E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	protein transport	RT				3	7.6E-1	1.0E0
Annotation Cluster 25		Enrichment Score: 0.5			G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	synapse part	RT				3	2.4E-1	8.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	mutagenesis site	RT				8	3.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_FAT	synapse	RT				3	3.9E-1	9.1E-1
Annotation Cluster 26		Enrichment Score: 0.46			G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	zymogen	RT				4	1.9E-2	1.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	endopeptidase activity	RT				3	3.9E-1	9.6E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	Protease	RT				3	3.9E-1	9.1E-1
<input type="checkbox"/>	GOTERM_MF_FAT	peptidase activity, acting on L-amino acid peptides	RT				3	5.9E-1	9.9E-1
<input type="checkbox"/>	GOTERM_MF_FAT	peptidase activity	RT				3	6.1E-1	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	proteolysis	RT				4	7.3E-1	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	hydrolase	RT				4	8.1E-1	1.0E0
Annotation Cluster 27		Enrichment Score: 0.16			G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	nucleotide binding	RT				11	2.6E-1	8.9E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	nucleotide-binding	RT				6	5.0E-1	9.6E-1
<input type="checkbox"/>	GOTERM_MF_FAT	purine nucleotide binding	RT				8	5.3E-1	9.9E-1

<input type="checkbox"/>	GOTERM_MF_FAT	purine ribonucleotide binding	RT		7	6.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	ribonucleotide binding	RT		7	6.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_BP_FAT	cell cycle	RT		3	7.7E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	adenyl nucleotide binding	RT		4	9.3E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	purine nucleoside binding	RT		4	9.3E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	nucleoside binding	RT		4	9.4E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	ATP binding	RT		3	9.7E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT		3	9.8E-1	1.0E0
Annotation Cluster 28					Enrichment Score: 0.09	G	
<input type="checkbox"/>	GOTERM_CC_FAT	cell fraction	RT		4	7.8E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_FAT	membrane fraction	RT		3	8.2E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_FAT	insoluble fraction	RT		3	8.3E-1	1.0E0
Annotation Cluster 29					Enrichment Score: 0	G	
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain: Cytoplasmic	RT		3	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	transmembrane region	RT		3	1.0E0	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	transmembrane	RT		3	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_FAT	intrinsic to membrane	RT		6	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_FAT	integral to membrane	RT		5	1.0E0	1.0E0

50 terms were not clustered.

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