3 d Functional Annotation Cluster
Input proteins: 181 significantly regulated proteins
Criteria: Enrichment score > 1.5
9 functional cluster were identified, clusters are sorted by enrichment score

Annotation Cluster 1 **Enrichment Score: 14.94**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Ribosome	KEGG_PATHWAY	24	13,95	16,64	1,41E-22
Ribosomal protein	SP_PIR_KEYWORDS	24	13,95	14,24	7,35E-20
Structural constituent of ribosome	GOTERM_MF_FAT	23	13,37	14,15	3,75E-19
Translation	GOTERM_BP_FAT	29	16,86	8,76	1,41E-18
Ribosome	GOTERM_CC_FAT	24	13,95	11,84	2,80E-18
Ribonucleoprotein	SP_PIR_KEYWORDS	26	15,12	10,27	4,69E-18
Ribonucleoprotein complex	GOTERM_CC_FAT	29	16,86	5,95	2,88E-14
Structural molecule activity	GOTERM_MF_FAT	29	16,86	5,99	2,92E-14
Non-membrane-bounded organelle	GOTERM_CC_FAT	41	23,84	2,02	8,06E-06
Intracellular non-membrane-bounded organelle	GOTERM_CC_FAT	41	23,84	2,02	8,06E-06

Annotation Cluster 2 **Enrichment Score: 2.99**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Mitochondrion	SP_PIR_KEYWORDS	22	12,79	2,92	1,89E-05
Mitochondrion	GOTERM_CC_FAT	30	17,44	2,15	8,39E-05
Mitochondrial part	GOTERM_CC_FAT	17	9,88	3,07	1,15E-04
Transit peptide	SP_PIR_KEYWORDS	15	8,72	3,45	1,17E-04
Transit peptide:Mitochondrion	UP_SEQ_FEATURE	15	8,72	3,17	2,78E-04
Mitochondrial lumen	GOTERM_CC_FAT	9	5,23	5,23	3,13E-04
Mitochondrial matrix	GOTERM_CC_FAT	9	5,23	5,23	3,13E-04
Organelle inner membrane	GOTERM_CC_FAT	11	6,40	3,34	1,63E-03
Mitochondrial inner membrane	GOTERM_CC_FAT	10	5,81	3,20	3,93E-03
Mitochondrial membrane	GOTERM_CC_FAT	11	6,40	2,83	5,31E-03
Mitochondrial envelope	GOTERM_CC_FAT	11	6,40	2,66	8,02E-03
Organelle envelope	GOTERM_CC_FAT	13	7,56	2,28	1,11E-02
Envelope	GOTERM_CC_FAT	13	7,56	2,27	1,14E-02
Organelle membrane	GOTERM_CC_FAT	14	8,14	1,64	8,13E-02

Annotation Cluster 3 **Enrichment Score: 2.71**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Protein biosynthesis	SP_PIR_KEYWORDS	13	7,56	9,82	8,24E-09
Ligase	SP_PIR_KEYWORDS	11	6,40	3,98	4,52E-04
Aminoacyl-tRNA synthetase	SP_PIR_KEYWORDS	5	2,91	13,46	4,92E-04
tRNA aminoacylation for protein translation	GOTERM_BP_FAT	5	2,91	10,47	1,26E-03
tRNA aminoacylation	GOTERM_BP_FAT	5	2,91	10,47	1,26E-03
Amino acid activation	GOTERM_BP_FAT	5	2,91	10,47	1,26E-03
Ligase activity, forming aminoacyl-tRNA and related co	GOTERM_MF_FAT	5	2,91	9,68	1,69E-03
Ligase activity, forming carbon-oxygen bonds	GOTERM_MF_FAT	5	2,91	9,68	1,69E-03
Aminoacyl-tRNA ligase activity	GOTERM_MF_FAT	5	2,91	9,68	1,69E-03
Aminoacyl-tRNA biosynthesis	KEGG_PATHWAY	5	2,91	7,35	4,35E-03
"KMSKS" region	UP_SEQ_FEATURE	3	1,74	18,96	1,05E-02
"HIGH" region	UP_SEQ_FEATURE	3	1,74	16,73	1,34E-02
tRNA metabolic process	GOTERM_BP_FAT	5	2,91	4,26	2,94E-02
Aminoacyl-tRNA synthetase, class I, conserved site	INTERPRO	3	1,74	9,50	3,92E-02
Rossmann-like alpha/beta/alpha sandwich fold	INTERPRO	3	1,74	8,07	5,26E-02
ncRNA metabolic process	GOTERM_BP_FAT	6	3,49	2,86	5,79E-02

Annotation Cluster 4 **Enrichment Score: 2.64**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Coenzyme metabolic process	GOTERM_BP_FAT	10	5,81	6,74	1,67E-05
Glutathione metabolic process	GOTERM_BP_FAT	5	2,91	20,08	9,77E-05
Cofactor metabolic process	GOTERM_BP_FAT	10	5,81	5,29	1,11E-04
Peptide metabolic process	GOTERM_BP_FAT	5	2,91	12,68	6,07E-04
Glutathione metabolism	KEGG_PATHWAY	6	3,49	7,12	1,36E-03
Sulfur metabolic process	GOTERM_BP_FAT	5	2,91	5,13	1,61E-02
Thioredoxin fold	INTERPRO	5	2,91	5,08	1,68E-02
Coenzyme biosynthetic process	GOTERM_BP_FAT	4	2,33	6,02	2,83E-02
Cellular amino acid derivative metabolic process	GOTERM_BP_FAT	5	2,91	3,42	5,79E-02
Cofactor biosynthetic process	GOTERM_BP_FAT	4	2,33	4,24	6,76E-02

Annotation Cluster 5 **Enrichment Score: 1.71**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Generation of precursor metabolites and energy	GOTERM_BP_FAT	11	6,40	4,06	3,70E-04
Electron transport	SP_PIR_KEYWORDS	5	2,91	5,25	1,50E-02
Electron transport chain	GOTERM_BP_FAT	5	2,91	4,30	2,85E-02
Transport	SP_PIR_KEYWORDS	10	5,81	0,67	9,67E-01

Annotation Cluster 6 **Enrichment Score: 1.70**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Mitochondrial lumen	GOTERM_CC_FAT	9	5,23255814	5,23	3,13E-04
Mitochondrial matrix	GOTERM_CC_FAT	9	5,23255814	5,23	3,13E-04
Intracellular organelle lumeN	GOTERM_CC_FAT	18	10,46511628	1,50	8,31E-02
Organelle lumen	GOTERM_CC_FAT	18	10,46511628	1,50	8,47E-02
Membrane-enclosed lumen	GOTERM_CC_FAT	18	10,46511628	1,45	1,06E-01
Nuclear lumen	GOTERM_CC_FAT	8	4,651162791	0,86	8,26E-01

Annotation Cluster 7 **Enrichment Score: 1.67**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
AMP-dependent synthetase and ligase	INTERPRO	4	2,33	14,35	2,61E-03
Fatty acid metabolism	SP_PIR_KEYWORDS	5	2,91	8,61	2,66E-03
Fatty acid metabolism	KEGG_PATHWAY	4	2,33	5,48	3,49E-02
Lipid metabolism	SP_PIR_KEYWORDS	5	2,91	3,86	4,04E-02
Lipid metabolism	COG_ONTOLOGY	4	2,33	3,65	8,53E-02
Fatty acid metabolic process	GOTERM_BP_FAT	5	2,91	2,62	1,22E-01

Annotation Cluster 8 **Enrichment Score: 1.64**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Acetyl-CoA metabolic process	GOTERM_BP_FAT	4	2,33	12,43	3,90E-03
Citrate cycle (TCA cycle)	KEGG_PATHWAY	4	2,33	7,96	1,30E-02
Tricarboxylic acid cycle	SP_PIR_KEYWORDS	3	1,74	16,58	1,37E-02
Energy derivation by oxidation of organic compounds	GOTERM_BP_FAT	5	2,91	4,92	1,85E-02
Tricarboxylic acid cycle	GOTERM_BP_FAT	3	1,74	12,57	2,31E-02
Acetyl-CoA catabolic process	GOTERM_BP_FAT	3	1,74	12,05	2,51E-02
Aerobic respiration	GOTERM_BP_FAT	3	1,74	10,71	3,13E-02
Coenzyme catabolic process	GOTERM_BP_FAT	3	1,74	9,97	3,57E-02
Cofactor catabolic process	GOTERM_BP_FAT	3	1,74	9,03	4,27E-02
Cellular respiration	GOTERM_BP_FAT	3	1,74	4,90	1,24E-01

Annotation Cluster 9 **Enrichment Score: 1.51**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Thioredoxin fold	INTERPRO	5	2,91	5,08	1,68E-02
Glutathione S-transferase, C-terminal-like	INTERPRO	3	1,74	10,77	3,11E-02
Glutathione S-transferase/chloride channel, C-termina	INTERPRO	3	1,74	9,50	3,92E-02
GST C-terminal	UP_SEQ_FEATURE	3	1,74	8,62	4,67E-02

6 d Functional Annotation Cluster

Input proteins: 158 significantly regulated proteins

Criteria: Enrichment score > 1.5

12 functional cluster were identified, clusters are sorted by enrichment score

Annotation Cluster 1	**Enrichment Score: 12.72**				
Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Ribosome	KEGG_PATHWAY	21	13,82	16,51	1,49E-19
Translation	GOTERM_BP_FAT	28	18,42	9,86	2,34E-19
Ribosomal protein	SP_PIR_KEYWORDS	21	13,82	13,94	3,65E-17
Structural constituent of ribosome	GOTERM_MF_FAT	20	13,16	14,55	7,46E-17
Ribosome	GOTERM_CC_FAT	21	13,82	11,59	9,61E-16
Ribonucleoprotein	SP_PIR_KEYWORDS	21	13,82	9,27	1,04E-13
Structural molecule activity	GOTERM_MF_FAT	23	15,13	5,61	7,97E-11
Ribonucleoprotein complex	GOTERM_CC_FAT	23	15,13	5,28	2,47E-10
Intracellular non-membrane-bounded organelle	GOTERM_CC_FAT	37	24,34	2,04	1,87E-05
Non-membrane-bounded organelle	GOTERM_CC_FAT	37	24,34	2,04	1,87E-05

Annotation Cluster 2	**Enrichment Score: 3.67**				
Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Ribosome	SP_PIR_KEYWORDS	6	3,95	30,64	1,20E-06
Small ribosomal subunit	GOTERM_CC_FAT	4	2,63	14,62	2,44E-03
Ribosomal subunit	GOTERM_CC_FAT	5	3,29	8,03	3,36E-03

Annotation Cluster 3	**Enrichment Score: 2.89**				
Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
LIM	SMART	7	4,61	12,52	1,70E-05
Zinc finger, LIM-type	INTERPRO	7	4,61	11,51	3,13E-05
LIM domain	SP_PIR_KEYWORDS	7	4,61	11,26	3,54E-05
LIM zinc-binding 3	UP_SEQ_FEATURE	5	3,29	20,27	9,65E-05
LIM zinc-binding 1	UP_SEQ_FEATURE	5	3,29	10,54	1,25E-03
LIM zinc-binding 2	UP_SEQ_FEATURE	5	3,29	10,54	1,25E-03
LIM zinc-binding 4	UP_SEQ_FEATURE	3	1,97	28,75	4,59E-03
Zinc	SP_PIR_KEYWORDS	14	9,21	0,87	8,19E-01
Zinc ion binding	GOTERM_MF_FAT	15	9,87	0,78	9,22E-01

Annotation Cluster 4	**Enrichment Score: 2.46**				
Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
rRNA binding	GOTERM_MF_FAT	5	3,29	22,88	5,84E-05
rRNA-binding	SP_PIR_KEYWORDS	4	2,63	31,32	2,50E-04
RNA binding	GOTERM_MF_FAT	11	7,24	1,80	8,24E-02
RNA-binding	SP_PIR_KEYWORDS	8	5,26	1,94	1,18E-01

Annotation Cluster 5	**Enrichment Score: 1.99**				
Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Protein biosynthesis	SP_PIR_KEYWORDS	14	9,21	11,83	1,75E-10
Aminoacyl-tRNA synthetase	SP_PIR_KEYWORDS	6	3,95	18,07	1,85E-05
tRNA aminoacylation for protein translation	GOTERM_BP_FAT	6	3,95	14,65	5,07E-05
Amino acid activation	GOTERM_BP_FAT	6	3,95	14,65	5,07E-05
tRNA aminoacylation	GOTERM_BP_FAT	6	3,95	14,65	5,07E-05
Aminoacyl-tRNA ligase activity	GOTERM_MF_FAT	6	3,95	13,73	6,94E-05
Ligase activity, forming aminoacyl-tRNA and related co	GOTERM_MF_FAT	6	3,95	13,73	6,94E-05
Ligase activity, forming carbon-oxygen bonds	GOTERM_MF_FAT	6	3,95	13,73	6,94E-05
Aminoacyl-tRNA biosynthesis	KEGG_PATHWAY	6	3,95	10,00	2,80E-04
Translation, ribosomal structure and biogenesis	COG_ONTOLOGY	5	3,29	9,24	1,24E-03
Aminoacyl-tRNA synthetase, class I, conserved site	INTERPRO	4	2,63	14,31	2,65E-03
tRNA metabolic process	GOTERM_BP_FAT	6	3,95	5,96	3,25E-03
"KMSKS" region	UP_SEQ_FEATURE	3	1,97	21,08	8,55E-03
ncRNA metabolic process	GOTERM_BP_FAT	7	4,61	3,89	9,02E-03
"HIGH" region	UP_SEQ_FEATURE	3	1,97	18,60	1,09E-02
Ligase	SP_PIR_KEYWORDS	8	5,26	3,24	1,18E-02
Rossmann-like alpha/beta/alpha sandwich fold	INTERPRO	3	1,97	9,12	4,22E-02
Nucleotide binding	GOTERM_MF_FAT	26	17,11	1,31	1,20E-01
Nucleotide-binding	SP_PIR_KEYWORDS	19	12,50	1,37	1,47E-01
ATP-binding	SP_PIR_KEYWORDS	15	9,87	1,37	2,00E-01
Purine nucleotide binding	GOTERM_MF_FAT	21	13,82	1,23	2,41E-01
ATP	UP_SEQ_FEATURE	8	5,26	1,55	2,55E-01
Adenyl nucleotide binding	GOTERM_MF_FAT	17	11,18	1,22	3,09E-01
Purine nucleoside binding	GOTERM_MF_FAT	17	11,18	1,21	3,22E-01
Nucleoside binding	GOTERM_MF_FAT	17	11,18	1,20	3,31E-01
Ribonucleotide binding	GOTERM_MF_FAT	19	12,50	1,16	3,55E-01
Purine ribonucleotide binding	GOTERM_MF_FAT	19	12,50	1,16	3,55E-01
ATP binding	GOTERM_MF_FAT	15	9,87	1,14	4,30E-01

Adenyl ribonucleotide binding	GOTERM_MF_FAT	15	9,87	1,13	4,48E-01
ATP	UP_SEQ_FEATURE	7	4,61	0,81	8,63E-01
Protein kinase, core	INTERPRO	3	1,97	0,74	9,13E-01
Protein kinase	UP_SEQ_FEATURE	3	1,97	0,66	9,42E-01
Protein kinase activity	GOTERM_MF_FAT	3	1,97	0,57	9,71E-01
Kinase	SP_PIR_KEYWORDS	3	1,97	0,50	9,84E-01

Annotation Cluster 6 **Enrichment Score: 1.99**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Actin cytoskeleton organization	GOTERM_BP_FAT	7	4,61	4,76	3,42E-03
Actin filament-based process	GOTERM_BP_FAT	7	4,61	4,47	4,69E-03
Cytoskeleton organization	GOTERM_BP_FAT	7	4,61	2,41	6,90E-02

Annotation Cluster 7 **Enrichment Score: 1.64**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
TSP1	SMART	4	2,63	8,97	9,54E-03
Thrombospondin, type 1 repeat	INTERPRO	4	2,63	8,25	1,24E-02
TSP type-1 3	UP_SEQ_FEATURE	3	1,97	11,71	2,66E-02
TSP type-1 1	UP_SEQ_FEATURE	3	1,97	8,78	4,51E-02
TSP type-1 2	UP_SEQ_FEATURE	3	1,97	8,78	4,51E-02

Annotation Cluster 8 **Enrichment Score: 1.61**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Actin binding	GOTERM_MF_FAT	9	5,92	3,43	4,58E-03
Actin-binding	SP_PIR_KEYWORDS	7	4,61	3,64	1,26E-02
Cytoskeletal protein binding	GOTERM_MF_FAT	10	6,58	2,65	1,27E-02
Cytoskeleton	SP_PIR_KEYWORDS	11	7,24	2,22	2,65E-02
Cytoskeleton	GOTERM_CC_FAT	12	7,89	1,13	4,82E-01

Annotation Cluster 9 **Enrichment Score: 1.59**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Coenzyme metabolic process	GOTERM_BP_FAT	7	4,61	5,50	1,67E-03
Cofactor metabolic process	GOTERM_BP_FAT	7	4,61	4,32	5,51E-03
Glutathione metabolic process	GOTERM_BP_FAT	3	1,97	14,04	1,88E-02
Glutathione metabolism	KEGG_PATHWAY	4	2,63	5,38	3,65E-02
Peptide metabolic process	GOTERM_BP_FAT	3	1,97	8,87	4,42E-02
Cellular amino acid derivative metabolic process	GOTERM_BP_FAT	4	2,63	3,19	1,29E-01
Sulfur metabolic process	GOTERM_BP_FAT	3	1,97	3,58	2,02E-01

Annotation Cluster 10 **Enrichment Score: 1.59**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Oxidoreductase	SP_PIR_KEYWORDS	12	7,89	2,46	9,43E-03
Oxidation reduction	GOTERM_BP_FAT	13	8,55	2,17	1,56E-02
Substrate	UP_SEQ_FEATURE	6	3,95	2,30	1,19E-01

Annotation Cluster 11 **Enrichment Score: 1.52**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Cytoplasmic vesicle	GOTERM_CC_FAT	11	7,24	2,29	2,07E-02
Vesicle	GOTERM_CC_FAT	11	7,24	2,25	2,36E-02
Cytoplasmic membrane-bounded vesicle	GOTERM_CC_FAT	9	5,92	2,30	4,04E-02
Membrane-bounded vesicle	GOTERM_CC_FAT	9	5,92	2,27	4,33E-02

Annotation Cluster 12 **Enrichment Score: 1.51**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Coenzyme metabolic process	GOTERM_BP_FAT	7	4,61	5,50	1,67E-03
Cofactor metabolic process	GOTERM_BP_FAT	7	4,61	4,32	5,51E-03
Tricarboxylic acid cycle	SP_PIR_KEYWORDS	3	1,97	18,55	1,11E-02
Tricarboxylic acid cycle	GOTERM_BP_FAT	3	1,97	14,65	1,73E-02
Acetyl-CoA catabolic process	GOTERM_BP_FAT	3	1,97	14,04	1,88E-02
Glyoxylate and dicarboxylate metabolism	KEGG_PATHWAY	3	1,97	13,12	2,08E-02
Aerobic respiration	GOTERM_BP_FAT	3	1,97	12,48	2,35E-02
Coenzyme catabolic process	GOTERM_BP_FAT	3	1,97	11,62	2,69E-02
Acetyl-CoA metabolic process	GOTERM_BP_FAT	3	1,97	10,87	3,04E-02
Cofactor catabolic process	GOTERM_BP_FAT	3	1,97	10,53	3,23E-02
Energy derivation by oxidation of organic compounds	GOTERM_BP_FAT	4	2,63	4,58	5,58E-02
Citrate cycle (TCA cycle)	KEGG_PATHWAY	3	1,97	6,77	7,03E-02
Cellular respiration	GOTERM_BP_FAT	3	1,97	5,71	9,57E-02
Coenzyme biosynthetic process	GOTERM_BP_FAT	3	1,97	5,26	1,10E-01
Cofactor biosynthetic process	GOTERM_BP_FAT	3	1,97	3,70	1,92E-01
Generation of precursor metabolites and energy	GOTERM_BP_FAT	5	3,29	2,15	2,00E-01

9 d Functional Annotation Cluster

Input proteins: 363 significantly regulated proteins
Criteria: Enrichment score > 1.5
25 functional cluster were identified, clusters are sorted by enrichment score

Annotation Cluster 1 **Enrichment Score: 17.28**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Ribosome	KEGG_PATHWAY	33	9,48	11,82	1,28E-26
Translation	GOTERM_BP_FAT	44	12,64	6,67	3,23E-23
Structural constituent of ribosome	GOTERM_MF_FAT	32	9,20	10,17	2,06E-22
Ribosomal protein	SP_PIR_KEYWORDS	33	9,48	9,65	3,82E-22
Ribonucleoprotein	SP_PIR_KEYWORDS	37	10,63	7,20	2,18E-20
Ribosome	GOTERM_CC_FAT	33	9,48	8,02	7,01E-20
Structural molecule activity	GOTERM_MF_FAT	43	12,36	4,58	1,43E-16
Ribonucleoprotein complex	GOTERM_CC_FAT	41	11,78	4,14	2,85E-14
Non-membrane-bounded organelle	GOTERM_CC_FAT	74	21,26	1,80	2,73E-07
Intracellular non-membrane-bounded organelle	GOTERM_CC_FAT	74	21,26	1,80	2,73E-07

Annotation Cluster 2 **Enrichment Score: 6.22**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
LIM	SMART	14	4,02	10,60	4,37E-10
Zinc finger, LIM-type	INTERPRO	14	4,02	10,12	9,73E-10
LIM domain	SP_PIR_KEYWORDS	14	4,02	9,92	1,23E-09
LIM zinc-binding 2	UP_SEQ_FEATURE	12	3,45	11,18	6,54E-09
LIM zinc-binding 1	UP_SEQ_FEATURE	12	3,45	11,18	6,54E-09
LIM zinc-binding 3	UP_SEQ_FEATURE	8	2,30	14,33	8,99E-07
Zinc	SP_PIR_KEYWORDS	30	8,62	0,82	9,21E-01
Zinc ion binding	GOTERM_MF_FAT	33	9,48	0,75	9,82E-01

Annotation Cluster 3 **Enrichment Score: 5.03**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Adherens junction	GOTERM_CC_FAT	14	4,02	6,16	3,89E-07
Cell-substrate adherens junction	GOTERM_CC_FAT	11	3,16	8,41	5,76E-07
Cell-substrate junction	GOTERM_CC_FAT	11	3,16	7,78	1,23E-06
Anchoring junction	GOTERM_CC_FAT	14	4,02	5,31	2,17E-06
Focal adhesion	GOTERM_CC_FAT	10	2,87	8,19	2,96E-06
Basolateral plasma membrane	GOTERM_CC_FAT	13	3,74	4,30	4,85E-05
Cell junction	SP_PIR_KEYWORDS	19	5,46	2,51	6,32E-04
Cell junction	GOTERM_CC_FAT	22	6,32	2,18	1,15E-03

Annotation Cluster 4 **Enrichment Score: 4.40**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Protein biosynthesis	SP_PIR_KEYWORDS	21	6,03	7,82	2,54E-12
Aminoacyl-tRNA synthetase	SP_PIR_KEYWORDS	9	2,59	11,94	6,40E-07
tRNA aminoacylation for protein translation	GOTERM_BP_FAT	9	2,59	9,46	3,89E-06
tRNA aminoacylation	GOTERM_BP_FAT	9	2,59	9,46	3,89E-06
Amino acid activation	GOTERM_BP_FAT	9	2,59	9,46	3,89E-06
Ligase activity, forming aminoacyl-tRNA and related co	GOTERM_MF_FAT	9	2,59	8,99	5,75E-06
Ligase activity, forming carbon-oxygen bonds	GOTERM_MF_FAT	9	2,59	8,99	5,75E-06
Aminoacyl-tRNA ligase activity	GOTERM_MF_FAT	9	2,59	8,99	5,75E-06
Aminoacyl-tRNA biosynthesis	KEGG_PATHWAY	8	2,30	6,07	2,74E-04
tRNA metabolic process	GOTERM_BP_FAT	10	2,87	4,28	5,42E-04
ncRNA metabolic process	GOTERM_BP_FAT	12	3,45	2,87	3,16E-03
Aminoacyl-tRNA synthetase, class I, conserved site	INTERPRO	5	1,44	7,87	3,53E-03
"KMSKS" region	UP_SEQ_FEATURE	4	1,15	12,42	3,66E-03
"HIGH" region	UP_SEQ_FEATURE	4	1,15	10,96	5,29E-03
Rossmann-like alpha/beta/alpha sandwich fold	INTERPRO	5	1,44	6,69	6,38E-03
Ligase	SP_PIR_KEYWORDS	13	3,74	2,32	1,08E-02

Annotation Cluster 5 **Enrichment Score: 4.18**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Melanosome	GOTERM_CC_FAT	12	3,45	6,59	1,81E-06
Pigment granule	GOTERM_CC_FAT	12	3,45	6,59	1,81E-06
Cytoplasmic membrane-bounded vesicle	GOTERM_CC_FAT	22	6,32	2,48	2,20E-04
Membrane-bounded vesicle	GOTERM_CC_FAT	22	6,32	2,44	2,68E-04
Cytoplasmic vesicle	GOTERM_CC_FAT	24	6,90	2,20	5,64E-04
Vesicle	GOTERM_CC_FAT	24	6,90	2,16	7,52E-04

Annotation Cluster 6 **Enrichment Score: 4.03**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Endoplasmic reticulum lumen	GOTERM_CC_FAT	11	3,16	7,13	2,78E-06
Prevents secretion from ER	UP_SEQ_FEATURE	10	2,87	7,89	4,16E-06
Endoplasmic reticulum, targeting sequence	INTERPRO	8	2,30	9,95	1,33E-05

Endoplasmic reticulum part	GOTERM_CC_FAT	16	4,60	3,23	1,32E-04
Endoplasmic reticulum	SP_PIR_KEYWORDS	26	7,47	1,98	1,53E-03
Endoplasmic reticulum	GOTERM_CC_FAT	28	8,05	1,56	2,16E-02

Annotation Cluster 7 **Enrichment Score: 3.95**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Actin-binding	SP_PIR_KEYWORDS	17	4,89	3,89	8,44E-06
Actin binding	GOTERM_MF_FAT	20	5,75	3,33	9,28E-06
Cytoskeleton	SP_PIR_KEYWORDS	28	8,05	2,49	2,55E-05
Cytoskeletal protein binding	GOTERM_MF_FAT	22	6,32	2,55	1,53E-04
Cytoskeleton	GOTERM_CC_FAT	33	9,48	1,37	5,56E-02

Annotation Cluster 8 **Enrichment Score: 3.28**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Coenzyme metabolic process	GOTERM_BP_FAT	14	4,02	4,73	8,03E-06
Cofactor metabolic process	GOTERM_BP_FAT	15	4,31	3,99	2,46E-05
Coenzyme biosynthetic process	GOTERM_BP_FAT	6	1,72	4,53	1,02E-02
Cofactor biosynthetic process	GOTERM_BP_FAT	6	1,72	3,19	3,98E-02

Annotation Cluster 9 **Enrichment Score: 2.89**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Actin cytoskeleton organization	GOTERM_BP_FAT	12	3,45	3,52	6,23E-04
Actin filament-based process	GOTERM_BP_FAT	12	3,45	3,30	1,06E-03
Cytoskeleton organization	GOTERM_BP_FAT	16	4,60	2,37	3,14E-03

Annotation Cluster 10 **Enrichment Score: 2.77**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Lysosome	SP_PIR_KEYWORDS	12	3,45	4,31	1,11E-04
Lysosome	GOTERM_CC_FAT	12	3,45	3,15	1,54E-03
Lytic vacuole	GOTERM_CC_FAT	12	3,45	3,13	1,61E-03
Vacuole	GOTERM_CC_FAT	12	3,45	2,74	4,42E-03
Lysosome	KEGG_PATHWAY	10	2,87	2,68	1,16E-02

Annotation Cluster 11 **Enrichment Score: 2.58**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Proteasome	SP_PIR_KEYWORDS	15	4,31	14,38	1,21E-12
Proteasome complex	GOTERM_CC_FAT	15	4,31	12,07	1,28E-11
Proteasome	KEGG_PATHWAY	14	4,02	9,50	9,56E-10
Protease	SP_PIR_KEYWORDS	20	5,75	2,03	4,80E-03
Proteasomal ubiquitin-dependent protein catabolic pr	GOTERM_BP_FAT	4	1,15	6,45	2,33E-02
Proteasomal protein catabolic process	GOTERM_BP_FAT	4	1,15	6,45	2,33E-02
Ubiquitin-dependent protein catabolic process	GOTERM_BP_FAT	8	2,30	2,74	2,68E-02
Macromolecule catabolic process	GOTERM_BP_FAT	17	4,89	1,26	2,78E-01
Proteolysis	GOTERM_BP_FAT	25	7,18	1,17	3,01E-01
Protein catabolic process	GOTERM_BP_FAT	14	4,02	1,22	3,62E-01
Cellular protein catabolic process	GOTERM_BP_FAT	12	3,45	1,08	5,52E-01
Cellular macromolecule catabolic process	GOTERM_BP_FAT	13	3,74	1,03	6,05E-01
Proteolysis involved in cellular protein catabolic proces	GOTERM_BP_FAT	11	3,16	1,00	6,67E-01
Modification-dependent protein catabolic process	GOTERM_BP_FAT	9	2,59	0,86	8,27E-01
Modification-dependent macromolecule catabolic pro	GOTERM_BP_FAT	9	2,59	0,86	8,27E-01
Ubl conjugation pathway	SP_PIR_KEYWORDS	6	1,72	0,64	9,58E-01

Annotation Cluster 12 **Enrichment Score: 2.44**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
PINT	SMART	4	1,15	14,00	2,59E-03
Proteasome component region PCI	INTERPRO	4	1,15	13,38	3,00E-03
PCI	UP_SEQ_FEATURE	4	1,15	10,35	6,25E-03

Annotation Cluster 13 **Enrichment Score: 2.38**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Cell adhesion	SP_PIR_KEYWORDS	19	5,46	2,59	4,44E-04
Cell adhesion	GOTERM_BP_FAT	21	6,03	1,81	1,25E-02
Biological adhesion	GOTERM_BP_FAT	21	6,03	1,81	1,27E-02

Annotation Cluster 14 **Enrichment Score: 2.30**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Glucose metabolic process	GOTERM_BP_FAT	11	3,16	3,80	6,41E-04
Generation of precursor metabolites and energy	GOTERM_BP_FAT	15	4,31	2,78	1,04E-03
Hexose metabolic process	GOTERM_BP_FAT	11	3,16	3,15	2,65E-03
Polysaccharide metabolic process	GOTERM_BP_FAT	8	2,30	4,20	2,89E-03
Energy derivation by oxidation of organic compounds	GOTERM_BP_FAT	8	2,30	3,95	4,11E-03
Glycogen metabolic process	GOTERM_BP_FAT	5	1,44	7,33	4,51E-03
Glucan metabolic process	GOTERM_BP_FAT	5	1,44	7,33	4,51E-03

Cellular glucan metabolic process	GOTERM_BP_FAT	5	1,44	7,33	4,51E-03
Glycogen metabolism	SP_PIR_KEYWORDS	4	1,15	10,89	5,46E-03
Monosaccharide metabolic process	GOTERM_BP_FAT	11	3,16	2,78	6,37E-03
Energy reserve metabolic process	GOTERM_BP_FAT	5	1,44	6,53	6,83E-03
Cellular polysaccharide metabolic process	GOTERM_BP_FAT	5	1,44	5,62	1,16E-02
Carbohydrate metabolism	SP_PIR_KEYWORDS	6	1,72	4,25	1,33E-02
Starch and sucrose metabolism	KEGG_PATHWAY	4	1,15	3,54	1,01E-01

Annotation Cluster 15 **Enrichment Score: 2.14**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
NADP	UP_SEQ_FEATURE	5	1,44	9,70	1,56E-03
NADP	SP_PIR_KEYWORDS	10	2,87	3,64	1,75E-03
NADP	UP_SEQ_FEATURE	4	1,15	3,05	1,42E-01

Annotation Cluster 16 **Enrichment Score: 2.11**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Protein folding	GOTERM_BP_FAT	11	3,16	4,19	2,95E-04
Molecular chaperone	SP_PIR_KEYWORDS	4	1,15	14,79	2,20E-03
Chaperone	SP_PIR_KEYWORDS	10	2,87	3,45	2,54E-03
Chaperonin-containing T-complex	GOTERM_CC_FAT	3	0,86	20,00	8,89E-03
Chaperone, tailless complex polypeptide 1	INTERPRO	3	0,86	16,05	1,41E-02
Chaperonin TCP-1, conserved site	INTERPRO	3	0,86	16,05	1,41E-02
Molecular chaperone t-complex-type	PIR_SUPERFAMILY	3	0,86	12,16	2,35E-02
Chaperonin Cpn60/TCP-1	INTERPRO	3	0,86	11,46	2,72E-02
Unfolded protein binding	GOTERM_MF_FAT	5	1,44	3,43	5,76E-02

Annotation Cluster 17 **Enrichment Score: 2.07**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Zymogen	SP_PIR_KEYWORDS	13	3,74	3,38	4,97E-04
Endopeptidase activity	GOTERM_MF_FAT	20	5,75	2,28	1,30E-03
Protease	SP_PIR_KEYWORDS	20	5,75	2,03	4,80E-03
Peptidase activity	GOTERM_MF_FAT	24	6,90	1,83	6,18E-03
Peptidase activity, acting on L-amino acid peptides	GOTERM_MF_FAT	23	6,61	1,83	7,48E-03
Hydrolase	SP_PIR_KEYWORDS	38	10,92	1,31	7,13E-02
Proteolysis	GOTERM_BP_FAT	25	7,18	1,17	3,01E-01

Annotation Cluster 18 **Enrichment Score: 1.95**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Endoplasmic reticulum, targeting sequence	INTERPRO	8	2,30	9,95	1,33E-05
Redox-active center	SP_PIR_KEYWORDS	5	1,44	6,63	6,55E-03
Intramolecular oxidoreductase activity, transposing S-S	GOTERM_MF_FAT	3	0,86	17,99	1,11E-02
Protein disulfide isomerase activity	GOTERM_MF_FAT	3	0,86	17,99	1,11E-02
Intramolecular oxidoreductase activity, interconverting	GOTERM_MF_FAT	3	0,86	15,99	1,41E-02
Thioredoxin-like	INTERPRO	4	1,15	5,94	2,91E-02
Cell redox homeostasis	GOTERM_BP_FAT	5	1,44	3,90	3,88E-02
Thioredoxin domain	INTERPRO	3	0,86	6,17	8,40E-02
Intramolecular oxidoreductase activity	GOTERM_MF_FAT	3	0,86	3,79	1,86E-01

Annotation Cluster 19 **Enrichment Score: 1.94**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Glutathione metabolism	KEGG_PATHWAY	8	2,30	4,90	1,04E-03
Glutathione metabolic process	GOTERM_BP_FAT	4	1,15	8,06	1,27E-02
Sulfur metabolic process	GOTERM_BP_FAT	7	2,01	3,60	1,30E-02
Cellular amino acid derivative metabolic process	GOTERM_BP_FAT	8	2,30	2,74	2,68E-02
Peptide metabolic process	GOTERM_BP_FAT	4	1,15	5,09	4,30E-02

Annotation Cluster 20 **Enrichment Score: 1.91**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Cofactor binding	GOTERM_MF_FAT	12	3,45	2,55	7,65E-03
NAD or NADH binding	GOTERM_MF_FAT	5	1,44	5,45	1,29E-02
Coenzyme binding	GOTERM_MF_FAT	9	2,59	2,70	1,86E-02

Annotation Cluster 21 **Enrichment Score: 1.86**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Basement membrane	GOTERM_CC_FAT	8	2,30	5,11	9,17E-04
Extracellular matrix part	GOTERM_CC_FAT	8	2,30	4,06	3,50E-03
Cell attachment site	UP_SEQ_FEATURE	7	2,01	4,29	5,73E-03
Extracellular matrix	GOTERM_CC_FAT	14	4,02	2,11	1,55E-02
Proteinaceous extracellular matrix	GOTERM_CC_FAT	13	3,74	2,04	2,59E-02
Basement membrane	SP_PIR_KEYWORDS	4	1,15	6,09	2,73E-02
Extracellular matrix	SP_PIR_KEYWORDS	9	2,59	2,19	5,47E-02
Extracellular matrix structural constituent	GOTERM_MF_FAT	3	0,86	4,80	1,28E-01

Annotation Cluster 22 **Enrichment Score: 1.79**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Proteasome, subunit alpha/beta	INTERPRO	4	1,15	10,70	5,78E-03
Threonine protease	SP_PIR_KEYWORDS	4	1,15	9,86	7,29E-03
Proteasome core complex	GOTERM_CC_FAT	4	1,15	9,33	8,39E-03
Threonine-type endopeptidase activity	GOTERM_MF_FAT	4	1,15	9,14	8,94E-03
Threonine-type peptidase activity	GOTERM_MF_FAT	4	1,15	9,14	8,94E-03
Proteolysis involved in cellular protein catabolic proces	GOTERM_BP_FAT	11	3,16	1,00	6,67E-01

Annotation Cluster 23 **Enrichment Score: 1.78**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Stress response	SP_PIR_KEYWORDS	5	1,44	5,75	1,08E-02
Heat shock protein 70	INTERPRO	3	0,86	14,59	1,70E-02
Heat shock protein Hsp70	INTERPRO	3	0,86	14,59	1,70E-02
Heat shock protein 70, conserved site	INTERPRO	3	0,86	12,35	2,36E-02

Annotation Cluster 24 **Enrichment Score: 1.74**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Glucose metabolic process	GOTERM_BP_FAT	11	3,16	3,80	6,41E-04
Cellular carbohydrate catabolic process	GOTERM_BP_FAT	7	2,01	5,64	1,43E-03
Hexose metabolic process	GOTERM_BP_FAT	11	3,16	3,15	2,65E-03
Monosaccharide metabolic process	GOTERM_BP_FAT	11	3,16	2,78	6,37E-03
Carbohydrate catabolic process	GOTERM_BP_FAT	7	2,01	4,18	6,48E-03
Glucose catabolic process	GOTERM_BP_FAT	5	1,44	4,65	2,20E-02
Hexose catabolic process	GOTERM_BP_FAT	5	1,44	4,65	2,20E-02
Monosaccharide catabolic process	GOTERM_BP_FAT	5	1,44	4,48	2,49E-02
Alcohol catabolic process	GOTERM_BP_FAT	5	1,44	3,72	4,49E-02
Glycolysis / Gluconeogenesis	KEGG_PATHWAY	6	1,72	2,81	6,01E-02
Carbohydrate transport and metabolism	COG_ONTOLOGY	3	0,86	4,16	1,56E-01
Glycolysis	SP_PIR_KEYWORDS	3	0,86	3,70	1,94E-01
Glycolysis	GOTERM_BP_FAT	3	0,86	3,30	2,30E-01

Annotation Cluster 25 **Enrichment Score: 1.68**

Term	Category	Number of ter	% of input pro	Fold enrichme	p-value
Glutathione S-transferase, C-terminal-like	INTERPRO	6	1,72	10,70	2,12E-04
GST C-terminal	UP_SEQ_FEATURE	6	1,72	8,47	6,33E-04
Glutathione metabolism	KEGG_PATHWAY	8	2,30	4,90	1,04E-03
Glutathione S-transferase, C-terminal	INTERPRO	5	1,44	9,55	1,70E-03
Glutathione S-transferase/chloride channel, C-termina	INTERPRO	5	1,44	7,87	3,53E-03
GST N-terminal	UP_SEQ_FEATURE	3	0,86	6,35	7,97E-02
Glutathione S-transferase, N-terminal	INTERPRO	3	0,86	5,94	8,96E-02
Glutathione transferase	PIR_SUPERFAMILY	3	0,86	5,76	9,36E-02
Glutathione transferase activity	GOTERM_MF_FAT	3	0,86	5,54	1,01E-01
Transferase activity, transferring alkyl or aryl (other tha	GOTERM_MF_FAT	3	0,86	2,72	3,02E-01
Metabolism of xenobiotics by cytochrome P450	KEGG_PATHWAY	3	0,86	1,45	6,16E-01
Drug metabolism	KEGG_PATHWAY	3	0,86	1,28	6,85E-01