3 d Functional Annotation Chart

Input proteins: 181 significantly regulated proteins

Criteria: Fold enrichment > 1.5 and p-value < 0.05

132 terms were identified, table is sorted by p-value

Term	**Category**	**Number of te**	**% of input pro**	**Fold enrichment**	**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
Acetylation	SP_PIR_KEYWORDS	69	40,12	3,12	5,20E-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
Phosphoprotein	SP_PIR_KEYWORDS	99	57,56	1,65	1,41E-09
Protein biosynthesis	SP_PIR_KEYWORDS	13	7,56	9,82	8,24E-09
Ribosome	SP_PIR_KEYWORDS	7	4,07	31,96	5,81E-08
Cytoplasm	SP_PIR_KEYWORDS	57	33,14	1,98	2,08E-07
Intracellular non-membrane-bounded organelle	GOTERM_CC_FAT	41	23,84	2,02	8,06E-06
Non-membrane-bounded organelle	GOTERM_CC_FAT	41	23,84	2,02	8,06E-06
Small ribosomal subunit	GOTERM_CC_FAT	6	3,49	19,60	1,13E-05
Coenzyme metabolic process	GOTERM_BP_FAT	10	5,81	6,74	1,67E-05
Oxidation reduction	GOTERM_BP_FAT	21	12,21	3,01	1,78E-05
Mitochondrion	SP_PIR_KEYWORDS	22	12,79	2,92	1,89E-05
Cytosolic ribosome	GOTERM_CC_FAT	5	2,91	26,31	3,14E-05
Ribosomal subunit	GOTERM_CC_FAT	7	4,07	10,05	6,40E-05
Mitochondrion	GOTERM_CC_FAT	30	17,44	2,15	8,39E-05
Glutathione metabolic process	GOTERM_BP_FAT	5	2,91	20,08	9,77E-05
Oxidoreductase	SP_PIR_KEYWORDS	17	9,88	3,12	1,10E-04
Cofactor metabolic process	GOTERM_BP_FAT	10	5,81	5,29	1,11E-04
rRNA binding	GOTERM_MF_FAT	5	2,91	19,36	1,12E-04
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
Translation, ribosomal structure and biogenesis	COG_ONTOLOGY	7	4,07	7,96	1,28E-04
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
rRNA-binding	SP_PIR_KEYWORDS	4	2,33	28,01	3,49E-04
Generation of precursor metabolites and energy	GOTERM_BP_FAT	11	6,40	4,06	3,70E-04
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
Valine, leucine and isoleucine biosynthesis	KEGG_PATHWAY	4	2,33	22,44	6,00E-04
Peptide metabolic process	GOTERM_BP_FAT	5	2,91	12,68	6,07E-04
Cytosol	GOTERM_CC_FAT	16	9,30	2,76	6,20E-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
Glutathione metabolism	KEGG_PATHWAY	6	3,49	7,12	1,36E-03
Organelle inner membrane	GOTERM_CC_FAT	11	6,40	3,34	1,63E-03
Aminoacyl-tRNA ligase activity	GOTERM_MF_FAT	5	2,91	9,68	1,69E-03
Ligase activity, forming aminoacyl-tRNA and related compounds	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
Nucleic acid-binding, OB-fold	INTERPRO	5	2,91	9,28	2,02E-03
Response to oxidative stress	GOTERM_BP_FAT	6	3,49	6,65	2,03E-03
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
Cofactor binding	GOTERM_MF_FAT	9	5,23	3,70	2,95E-03
Acetyl-CoA metabolic process	GOTERM_BP_FAT	4	2,33	12,43	3,90E-03
Mitochondrial inner membrane	GOTERM_CC_FAT	10	5,81	3,20	3,93E-03
Aminoacyl-tRNA biosynthesis	KEGG_PATHWAY	5	2,91	7,35	4,35E-03
Regulation of epithelial cell proliferation involved in prostate gland development	GOTERM_BP_FAT	3	1,74	28,91	4,49E-03
Mitochondrial membrane	GOTERM_CC_FAT	11	6,40	2,83	5,31E-03
Actin-binding	SP_PIR_KEYWORDS	8	4,65	3,72	5,81E-03
Valine, leucine and isoleucine degradation	KEGG_PATHWAY	5	2,91	6,71	6,04E-03
RNA binding	SP_PIR_KEYWORDS	3	1,74	24,24	6,49E-03
RNA-binding	SP_PIR_KEYWORDS	12	6,98	2,60	6,56E-03
Nucleotide binding	GOTERM_MF_FAT	36	20,93	1,53	7,49E-03
Mitochondrial envelope	GOTERM_CC_FAT	11	6,40	2,66	8,02E-03
Vitamin binding	GOTERM_MF_FAT	6	3,49	4,61	9,60E-03
"KMSKS" region	UP_SEQ_FEATURE	3	1,74	18,96	1,05E-02
Nucleotide-binding	SP_PIR_KEYWORDS	26	15,12	1,67	1,09E-02
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
Proteoglycan	SP_PIR_KEYWORDS	4	2,33	8,40	1,18E-02
Actin binding	GOTERM_MF_FAT	9	5,23	2,90	1,22E-02
RNA binding	GOTERM_MF_FAT	15	8,72	2,07	1,27E-02
Citrate cycle (TCA cycle)	KEGG_PATHWAY	4	2,33	7,96	1,30E-02
Blood vessel development	GOTERM_BP_FAT	8	4,65	3,16	1,32E-02
Cytoskeletal protein binding	GOTERM_MF_FAT	11	6,40	2,47	1,34E-02
"HIGH" region	UP_SEQ_FEATURE	3	1,74	16,73	1,34E-02
Tricarboxylic acid cycle	SP_PIR_KEYWORDS	3	1,74	16,58	1,37E-02
Proteasome	SP_PIR_KEYWORDS	4	2,33	7,78	1,45E-02
Vasculature development	GOTERM_BP_FAT	8	4,65	3,08	1,49E-02
Electron transport	SP_PIR_KEYWORDS	5	2,91	5,25	1,50E-02
Sulfur metabolic process	GOTERM_BP_FAT	5	2,91	5,13	1,61E-02
Posttranslational modification, protein turnover, chaperones	COG_ONTOLOGY	6	3,49	3,71	1,67E-02
Thioredoxin fold	INTERPRO	5	2,91	5,08	1,68E-02
Energy derivation by oxidation of organic compounds	GOTERM_BP_FAT	5	2,91	4,92	1,85E-02
ATP-binding	SP_PIR_KEYWORDS	21	12,21	1,71	1,95E-02
Repeat:1	UP_SEQ_FEATURE	6	3,49	3,84	1,99E-02
Soluble fraction	GOTERM_CC_FAT	5	2,91	4,78	2,02E-02
Angiogenesis	SP_PIR_KEYWORDS	4	2,33	6,78	2,10E-02
Repeat:2	UP_SEQ_FEATURE	6	3,49	3,77	2,15E-02
Repeat:4	UP_SEQ_FEATURE	5	2,91	4,69	2,17E-02
Proteasome complex	GOTERM_CC_FAT	4	2,33	6,53	2,28E-02
Repeat:8	UP_SEQ_FEATURE	4	2,33	6,54	2,29E-02
Positive regulation of phagocytosis	GOTERM_BP_FAT	3	1,74	12,57	2,31E-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
Binding site: NADP	UP_SEQ_FEATURE	3	1,74	11,85	2,59E-02
Regulation of phagocytosis	GOTERM_BP_FAT	3	1,74	11,56	2,71E-02
Regulation of epithelial cell proliferation	GOTERM_BP_FAT	4	2,33	6,12	2,71E-02
Duplication	SP_PIR_KEYWORDS	5	2,91	4,38	2,73E-02
Pyruvate metabolism	KEGG_PATHWAY	4	2,33	6,02	2,74E-02
Glyoxylate bypass	SP_PIR_KEYWORDS	2	1,16	70,02	2,81E-02
Coenzyme biosynthetic process	GOTERM_BP_FAT	4	2,33	6,02	2,83E-02
Cytosolic part	GOTERM_CC_FAT	4	2,33	6,01	2,83E-02
Electron transport chain	GOTERM_BP_FAT	5	2,91	4,30	2,85E-02
Coenzyme binding	GOTERM_MF_FAT	6	3,49	3,48	2,86E-02
tRNA metabolic process	GOTERM_BP_FAT	5	2,91	4,26	2,94E-02
Glutathione S-transferase, C-terminal-like	INTERPRO	3	1,74	10,77	3,11E-02
Aerobic respiration	GOTERM_BP_FAT	3	1,74	10,71	3,13E-02
Cross-link: Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin)	UP_SEQ_FEATURE	6	3,49	3,39	3,21E-02
Repeat:7	UP_SEQ_FEATURE	4	2,33	5,66	3,33E-02
Fatty acid metabolism	KEGG_PATHWAY	4	2,33	5,48	3,49E-02
Adenyl nucleotide binding	GOTERM_MF_FAT	25	14,53	1,51	3,55E-02
Coenzyme catabolic process	GOTERM_BP_FAT	3	1,74	9,97	3,57E-02
Ligase activity, forming carbon-sulfur bonds	GOTERM_MF_FAT	3	1,74	9,96	3,58E-02
Class II aldolase/adducin, N-terminal	INTERPRO	2	1,16	53,83	3,64E-02
Microvillus	GOTERM_CC_FAT	3	1,74	9,80	3,68E-02
Plasminogen activation	SP_PIR_KEYWORDS	2	1,16	52,51	3,73E-02
Epithelial cell differentiation	GOTERM_BP_FAT	5	2,91	3,92	3,83E-02
Repeat:6	UP_SEQ_FEATURE	4	2,33	5,34	3,85E-02
Purine nucleoside binding	GOTERM_MF_FAT	25	14,53	1,50	3,87E-02
Proteasome	KEGG_PATHWAY	4	2,33	5,25	3,90E-02
Aminoacyl-tRNA synthetase, class I, conserved site	INTERPRO	3	1,74	9,50	3,92E-02
Glutathione S-transferase/chloride channel, C-terminal	INTERPRO	3	1,74	9,50	3,92E-02
Lipid metabolism	SP_PIR_KEYWORDS	5	2,91	3,86	4,04E-02
Extracellular space	GOTERM_CC_FAT	11	6,40	2,04	4,21E-02
Cofactor catabolic process	GOTERM_BP_FAT	3	1,74	9,03	4,27E-02
Reproductive structure development	GOTERM_BP_FAT	5	2,91	3,71	4,54E-02
NADP	SP_PIR_KEYWORDS	5	2,91	3,70	4,59E-02
Enzyme inhibitor activity	GOTERM_MF_FAT	7	4,07	2,68	4,62E-02
GST C-terminal	UP_SEQ_FEATURE	3	1,74	8,62	4,67E-02
Positive regulation of endocytosis	GOTERM_BP_FAT	3	1,74	8,50	4,77E-02
Isopeptide bond	SP_PIR_KEYWORDS	7	4,07	2,65	4,83E-02
Angiogenesis	GOTERM_BP_FAT	5	2,91	3,62	4,86E-02

6 d Functional Annotation Chart
Input proteins: 158 significantly regulated proteins
Criteria: Fold enrichment > 1.5 and p-value < 0.05
105 terms were identified, table is sorted by p-value

Term	**Category**	**Number of te**	**% of input pr**	**Fold enrichm**	**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
Acetylation	SP_PIR_KEYWORDS	61	40,13	3,08	1,20E-16
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
Protein biosynthesis	SP_PIR_KEYWORDS	14	9,21	11,83	1,75E-10
Ribonucleoprotein complex	GOTERM_CC_FAT	23	15,13	5,28	2,47E-10
Cytoplasm	SP_PIR_KEYWORDS	53	34,87	2,06	1,40E-07
Ribosome	SP_PIR_KEYWORDS	6	3,95	30,64	1,20E-06
Phosphoprotein	SP_PIR_KEYWORDS	81	53,29	1,51	6,43E-06
LIM	SMART	7	4,61	12,52	1,70E-05
Aminoacyl-tRNA synthetase	SP_PIR_KEYWORDS	6	3,95	18,07	1,85E-05
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
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
Amino acid activation	GOTERM_BP_FAT	6	3,95	14,65	5,07E-05
tRNA aminoacylation for protein translation	GOTERM_BP_FAT	6	3,95	14,65	5,07E-05
tRNA aminoacylation	GOTERM_BP_FAT	6	3,95	14,65	5,07E-05
rRNA binding	GOTERM_MF_FAT	5	3,29	22,88	5,84E-05
Ligase activity, forming aminoacyl-tRNA and related c	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 ligase activity	GOTERM_MF_FAT	6	3,95	13,73	6,94E-05
LIM zinc-binding 3	UP_SEQ_FEATURE	5	3,29	20,27	9,65E-05
rRNA-binding	SP_PIR_KEYWORDS	4	2,63	31,32	2,50E-04
Aminoacyl-tRNA biosynthesis	KEGG_PATHWAY	6	3,95	10,00	2,80E-04
Plasminogen activation	SP_PIR_KEYWORDS	3	1,97	88,10	4,22E-04
Cytosolic ribosome	GOTERM_CC_FAT	4	2,63	23,55	5,88E-04
Translation, ribosomal structure and biogenesis	COG_ONTOLOGY	5	3,29	9,24	1,24E-03
LIM zinc-binding 2	UP_SEQ_FEATURE	5	3,29	10,54	1,25E-03
LIM zinc-binding 1	UP_SEQ_FEATURE	5	3,29	10,54	1,25E-03
Coenzyme metabolic process	GOTERM_BP_FAT	7	4,61	5,50	1,67E-03
Small ribosomal subunit	GOTERM_CC_FAT	4	2,63	14,62	2,44E-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
Ribosomal subunit	GOTERM_CC_FAT	5	3,29	8,03	3,36E-03
Actin cytoskeleton organization	GOTERM_BP_FAT	7	4,61	4,76	3,42E-03
Actin binding	GOTERM_MF_FAT	9	5,92	3,43	4,58E-03
LIM zinc-binding 4	UP_SEQ_FEATURE	3	1,97	28,75	4,59E-03
Actin filament-based process	GOTERM_BP_FAT	7	4,61	4,47	4,69E-03
Cofactor metabolic process	GOTERM_BP_FAT	7	4,61	4,32	5,51E-03
Fibrinolysis Pathway	BIOCARTA	3	1,97	23,11	5,92E-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
Oxidoreductase	SP_PIR_KEYWORDS	12	7,89	2,46	9,43E-03
TSP1	SMART	4	2,63	8,97	9,54E-03
Valine, leucine and isoleucine biosynthesis	KEGG_PATHWAY	3	1,97	19,08	9,97E-03
"HIGH" region	UP_SEQ_FEATURE	3	1,97	18,60	1,09E-02
Tricarboxylic acid cycle	SP_PIR_KEYWORDS	3	1,97	18,55	1,11E-02
Ligase	SP_PIR_KEYWORDS	8	5,26	3,24	1,18E-02
Nucleic acid-binding, OB-fold	INTERPRO	4	2,63	8,39	1,18E-02
Thrombospondin, type 1 repeat	INTERPRO	4	2,63	8,25	1,24E-02
Pept_C1	SMART	3	1,97	17,26	1,25E-02
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
Cytosol	GOTERM_CC_FAT	12	7,89	2,32	1,37E-02
Endopeptidase activity	GOTERM_MF_FAT	10	6,58	2,61	1,40E-02
Peptidase C1A, papain C-terminal	INTERPRO	3	1,97	15,87	1,50E-02
Oxidation reduction	GOTERM_BP_FAT	13	8,55	2,17	1,56E-02
Cell adhesion	SP_PIR_KEYWORDS	9	5,92	2,78	1,57E-02
Tricarboxylic acid cycle	GOTERM_BP_FAT	3	1,97	14,65	1,73E-02
Prevents secretion from ER	UP_SEQ_FEATURE	4	2,63	7,15	1,82E-02
Glutathione metabolic process	GOTERM_BP_FAT	3	1,97	14,04	1,88E-02
Acetyl-CoA catabolic process	GOTERM_BP_FAT	3	1,97	14,04	1,88E-02

Peptidase C1A, papain	INTERPRO	3	1,97	13,52	2,03E-02
Cytoplasmic vesicle	GOTERM_CC_FAT	11	7,24	2,29	2,07E-02
Glyoxylate and dicarboxylate metabolism	KEGG_PATHWAY	3	1,97	13,12	2,08E-02
Cytosolic part	GOTERM_CC_FAT	4	2,63	6,73	2,11E-02
Aerobic respiration	GOTERM_BP_FAT	3	1,97	12,48	2,35E-02
Vesicle	GOTERM_CC_FAT	11	7,24	2,25	2,36E-02
Carbohydrate binding	GOTERM_MF_FAT	8	5,26	2,77	2,48E-02
Cysteine proteinase	SP_PIR_KEYWORDS	2	1,32	78,31	2,52E-02
Glyoxylate bypass	SP_PIR_KEYWORDS	2	1,32	78,31	2,52E-02
Protein folding	GOTERM_BP_FAT	5	3,29	4,42	2,61E-02
Thrombin signaling and protease-activated receptors	BIOCARTA	3	1,97	10,88	2,65E-02
Cytoskeleton	SP_PIR_KEYWORDS	11	7,24	2,22	2,65E-02
TSP type-1 3	UP_SEQ_FEATURE	3	1,97	11,71	2,66E-02
Coenzyme catabolic process	GOTERM_BP_FAT	3	1,97	11,62	2,69E-02
Zymogen	SP_PIR_KEYWORDS	6	3,95	3,54	2,71E-02
Proteasomal protein catabolic process	GOTERM_BP_FAT	3	1,97	11,23	2,86E-02
Proteasomal ubiquitin-dependent protein catabolic pr	GOTERM_BP_FAT	3	1,97	11,23	2,86E-02
Endoplasmic reticulum lumen	GOTERM_CC_FAT	4	2,63	5,89	2,99E-02
Acetyl-CoA metabolic process	GOTERM_BP_FAT	3	1,97	10,87	3,04E-02
Calponin	INTERPRO	2	1,32	60,83	3,23E-02
Cofactor catabolic process	GOTERM_BP_FAT	3	1,97	10,53	3,23E-02
Rho cell motility signaling pathway	BIOCARTA	3	1,97	9,73	3,27E-02
Lysosome	SP_PIR_KEYWORDS	5	3,29	4,08	3,38E-02
Glutathione metabolism	KEGG_PATHWAY	4	2,63	5,38	3,65E-02
Antigen processing and presentation	KEGG_PATHWAY	5	3,29	3,84	3,91E-02
Guanine nucleotide-binding protein, beta subunit	INTERPRO	2	1,32	48,67	4,02E-02
Cytoplasmic membrane-bounded vesicle	GOTERM_CC_FAT	9	5,92	2,30	4,04E-02
Response to oxidative stress	GOTERM_BP_FAT	4	2,63	5,16	4,17E-02
Rossmann-like alpha/beta/alpha sandwich fold	INTERPRO	3	1,97	9,12	4,22E-02
Membrane-bounded vesicle	GOTERM_CC_FAT	9	5,92	2,27	4,33E-02
Peptide metabolic process	GOTERM_BP_FAT	3	1,97	8,87	4,42E-02
RPTP-like protein binding	GOTERM_MF_FAT	2	1,32	43,93	4,44E-02
TSP type-1 2	UP_SEQ_FEATURE	3	1,97	8,78	4,51E-02
TSP type-1 1	UP_SEQ_FEATURE	3	1,97	8,78	4,51E-02
Aminoacyl-tRNA synthetase, class Ia	INTERPRO	2	1,32	40,55	4,80E-02
Valyl/Leucyl/Isoleucyl-tRNA synthetase, class I, anticod	INTERPRO	2	1,32	40,55	4,80E-02
Endoplasmic reticulum, targeting sequence	INTERPRO	3	1,97	8,49	4,81E-02
Protein degradation	SP_PIR_KEYWORDS	2	1,32	39,15	4,97E-02

9 d Functional Annotation Chart
Input proteins: 363 significantly regulated proteins
Criteria: Fold enrichment > 1.5 and p-value < 0.05
271 terms were identified, table is sorted by p-value

Term	**Category**	**Number of te**	**% of input pro**	**Fold enrichme**	**p-value**
Acetylation	SP_PIR_KEYWORDS	136	39,08	3,03	4,40E-35
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
Cytoplasm	SP_PIR_KEYWORDS	118	33,91	2,02	7,58E-15
Ribonucleoprotein complex	GOTERM_CC_FAT	41	11,78	4,14	2,85E-14
Proteasome	SP_PIR_KEYWORDS	15	4,31	14,38	1,21E-12
Protein biosynthesis	SP_PIR_KEYWORDS	21	6,03	7,82	2,54E-12
Proteasome complex	GOTERM_CC_FAT	15	4,31	12,07	1,28E-11
Cytosol	GOTERM_CC_FAT	39	11,21	3,31	1,22E-10
Ribosome	SP_PIR_KEYWORDS	10	2,87	22,50	2,12E-10
LIM	SMART	14	4,02	10,60	4,37E-10
Proteasome	KEGG_PATHWAY	14	4,02	9,50	9,56E-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
Intracellular non-membrane-bounded organelle	GOTERM_CC_FAT	74	21,26	1,80	2,73E-07
Non-membrane-bounded organelle	GOTERM_CC_FAT	74	21,26	1,80	2,73E-07
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
Aminoacyl-tRNA synthetase	SP_PIR_KEYWORDS	9	2,59	11,94	6,40E-07
LIM zinc-binding 3	UP_SEQ_FEATURE	8	2,30	14,33	8,99E-07
Cell-substrate junction	GOTERM_CC_FAT	11	3,16	7,78	1,23E-06
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
Anchoring junction	GOTERM_CC_FAT	14	4,02	5,31	2,17E-06
Endoplasmic reticulum lumen	GOTERM_CC_FAT	11	3,16	7,13	2,78E-06
Focal adhesion	GOTERM_CC_FAT	10	2,87	8,19	2,96E-06
Amino acid activation	GOTERM_BP_FAT	9	2,59	9,46	3,89E-06
tRNA aminoacylation	GOTERM_BP_FAT	9	2,59	9,46	3,89E-06
tRNA aminoacylation for protein translation	GOTERM_BP_FAT	9	2,59	9,46	3,89E-06
Prevents secretion from ER	UP_SEQ_FEATURE	10	2,87	7,89	4,16E-06
Ligase activity, forming carbon-oxygen bonds	GOTERM_MF_FAT	9	2,59	8,99	5,75E-06
Ligase activity, forming aminoacyl-tRNA and related co	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
rRNA-binding	SP_PIR_KEYWORDS	6	1,72	20,70	6,61E-06
rRNA binding	GOTERM_MF_FAT	7	2,01	13,99	7,47E-06
Coenzyme metabolic process	GOTERM_BP_FAT	14	4,02	4,73	8,03E-06
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
Ribosomal subunit	GOTERM_CC_FAT	10	2,87	7,07	1,03E-05
Endoplasmic reticulum, targeting sequence	INTERPRO	8	2,30	9,95	1,33E-05
Cofactor metabolic process	GOTERM_BP_FAT	15	4,31	3,99	2,46E-05
Cytoskeleton	SP_PIR_KEYWORDS	28	8,05	2,49	2,55E-05
Plasminogen activation	SP_PIR_KEYWORDS	4	1,15	51,75	2,80E-05
Cytosolic ribosome	GOTERM_CC_FAT	6	1,72	15,55	2,92E-05
Basolateral plasma membrane	GOTERM_CC_FAT	13	3,74	4,30	4,85E-05
Cytosolic part	GOTERM_CC_FAT	9	2,59	6,67	5,45E-05
Posttranslational modification, protein turnover, chape	COG_ONTOLOGY	12	3,45	4,19	5,83E-05
Lysosome	SP_PIR_KEYWORDS	12	3,45	4,31	1,11E-04
Endoplasmic reticulum part	GOTERM_CC_FAT	16	4,60	3,23	1,32E-04
Cytoskeletal protein binding	GOTERM_MF_FAT	22	6,32	2,55	1,53E-04
Glutathione S-transferase, C-terminal-like	INTERPRO	6	1,72	10,70	2,12E-04
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
Aminoacyl-tRNA biosynthesis	KEGG_PATHWAY	8	2,30	6,07	2,74E-04
Protein folding	GOTERM_BP_FAT	11	3,16	4,19	2,95E-04
Oxidation reduction	GOTERM_BP_FAT	29	8,33	2,09	3,14E-04
Oxidoreductase	SP_PIR_KEYWORDS	25	7,18	2,26	3,20E-04
Small ribosomal subunit	GOTERM_CC_FAT	6	1,72	9,65	3,34E-04
Cell adhesion	SP_PIR_KEYWORDS	19	5,46	2,59	4,44E-04
Zymogen	SP_PIR_KEYWORDS	13	3,74	3,38	4,97E-04

tRNA metabolic process	GOTERM_BP_FAT	10	2,87	4,28	5,42E-04
Cytoplasmic vesicle	GOTERM_CC_FAT	24	6,90	2,20	5,64E-04
Concanavalin A-like lectin/glucanase, subgroup	INTERPRO	8	2,30	5,56	5,76E-04
Translation, ribosomal structure and biogenesis	COG_ONTOLOGY	8	2,30	5,14	6,07E-04
Actin cytoskeleton organization	GOTERM_BP_FAT	12	3,45	3,52	6,23E-04
Cell junction	SP_PIR_KEYWORDS	19	5,46	2,51	6,32E-04
GST C-terminal	UP_SEQ_FEATURE	6	1,72	8,47	6,33E-04
Glucose metabolic process	GOTERM_BP_FAT	11	3,16	3,80	6,41E-04
Vesicle	GOTERM_CC_FAT	24	6,90	2,16	7,52E-04
Thioredoxin fold	INTERPRO	9	2,59	4,54	8,27E-04
Basement membrane	GOTERM_CC_FAT	8	2,30	5,11	9,17E-04
Sorb	SMART	3	0,86	56,02	9,28E-04
Sorbin-like	INTERPRO	3	0,86	53,50	1,03E-03
Glutathione metabolism	KEGG_PATHWAY	8	2,30	4,90	1,04E-03
Generation of precursor metabolites and energy	GOTERM_BP_FAT	15	4,31	2,78	1,04E-03
Actin filament-based process	GOTERM_BP_FAT	12	3,45	3,30	1,06E-03
Cell junction	GOTERM_CC_FAT	22	6,32	2,18	1,15E-03
RNA-binding	SP_PIR_KEYWORDS	21	6,03	2,24	1,23E-03
Endopeptidase activity	GOTERM_MF_FAT	20	5,75	2,28	1,30E-03
Fibrinolysis Pathway	BIOCARTA	4	1,15	15,82	1,35E-03
SoHo	UP_SEQ_FEATURE	3	0,86	46,57	1,35E-03
LIM zinc-binding 4	UP_SEQ_FEATURE	4	1,15	16,94	1,41E-03
Cellular carbohydrate catabolic process	GOTERM_BP_FAT	7	2,01	5,64	1,43E-03
Endoplasmic reticulum	SP_PIR_KEYWORDS	26	7,47	1,98	1,53E-03
Lysosome	GOTERM_CC_FAT	12	3,45	3,15	1,54E-03
Pyruvate metabolism	KEGG_PATHWAY	7	2,01	5,44	1,54E-03
:NADP	UP_SEQ_FEATURE	5	1,44	9,70	1,56E-03
Regulation of phagocytosis	GOTERM_BP_FAT	5	1,44	9,67	1,59E-03
Lytic vacuole	GOTERM_CC_FAT	12	3,45	3,13	1,61E-03
RNA binding	GOTERM_MF_FAT	27	7,76	1,93	1,69E-03
Glutathione S-transferase, C-terminal	INTERPRO	5	1,44	9,55	1,70E-03
NADP	SP_PIR_KEYWORDS	10	2,87	3,64	1,75E-03
Tropomyosin	INTERPRO	3	0,86	40,13	2,03E-03
Calponin	INTERPRO	3	0,86	40,13	2,03E-03
Class II aldolase/adducin, N-terminal	INTERPRO	3	0,86	40,13	2,03E-03
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
PINT	SMART	4	1,15	14,00	2,59E-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
Proteasome component region PCI	INTERPRO	4	1,15	13,38	3,00E-03
Cytoskeleton organization	GOTERM_BP_FAT	16	4,60	2,37	3,14E-03
ncRNA metabolic process	GOTERM_BP_FAT	12	3,45	2,87	3,16E-03
Extracellular matrix part	GOTERM_CC_FAT	8	2,30	4,06	3,50E-03
Aminoacyl-tRNA synthetase, class I, conserved site	INTERPRO	5	1,44	7,87	3,53E-03
Glutathione S-transferase/chloride channel, C-termina	INTERPRO	5	1,44	7,87	3,53E-03
"KMSKS" region	UP_SEQ_FEATURE	4	1,15	12,42	3,66E-03
Valine, leucine and isoleucine biosynthesis	KEGG_PATHWAY	4	1,15	11,59	4,09E-03
Energy derivation by oxidation of organic compounds	GOTERM_BP_FAT	8	2,30	3,95	4,11E-03
Regulation of endocytosis	GOTERM_BP_FAT	6	1,72	5,58	4,23E-03
Cysteine and glycine-rich protein	PIR_SUPERFAMILY	3	0,86	27,36	4,29E-03
Tropomyosin	PIR_SUPERFAMILY	3	0,86	27,36	4,29E-03
Vacuole	GOTERM_CC_FAT	12	3,45	2,74	4,42E-03
Cellular glucan metabolic process	GOTERM_BP_FAT	5	1,44	7,33	4,51E-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
Protease	SP_PIR_KEYWORDS	20	5,75	2,03	4,80E-03
26S proteasome subunit P45	INTERPRO	3	0,86	26,75	4,94E-03
WHEP-TRS	INTERPRO	3	0,86	26,75	4,94E-03
Positive regulation of endocytosis	GOTERM_BP_FAT	5	1,44	7,11	5,03E-03
Cellular homeostasis	GOTERM_BP_FAT	16	4,60	2,26	5,09E-03
Soluble fraction	GOTERM_CC_FAT	8	2,30	3,77	5,25E-03
Protein degradation	SP_PIR_KEYWORDS	3	0,86	25,88	5,27E-03
"HIGH" region	UP_SEQ_FEATURE	4	1,15	10,96	5,29E-03
Glycogen metabolism	SP_PIR_KEYWORDS	4	1,15	10,89	5,46E-03
Cell attachment site	UP_SEQ_FEATURE	7	2,01	4,29	5,73E-03
Proteasome, subunit alpha/beta	INTERPRO	4	1,15	10,70	5,78E-03
Peptidase activity	GOTERM_MF_FAT	24	6,90	1,83	6,18E-03
PCI	UP_SEQ_FEATURE	4	1,15	10,35	6,25E-03
Monosaccharide metabolic process	GOTERM_BP_FAT	11	3,16	2,78	6,37E-03
Rossmann-like alpha/beta/alpha sandwich fold	INTERPRO	5	1,44	6,69	6,38E-03
Carbohydrate catabolic process	GOTERM_BP_FAT	7	2,01	4,18	6,48E-03
Redox-active center	SP_PIR_KEYWORDS	5	1,44	6,63	6,55E-03

Energy reserve metabolic process	GOTERM_BP_FAT	5	1,44	6,53	6,83E-03
Threonine protease	SP_PIR_KEYWORDS	4	1,15	9,86	7,29E-03
Pept_C1	SMART	4	1,15	9,74	7,48E-03
Peptidase activity, acting on L-amino acid peptides	GOTERM_MF_FAT	23	6,61	1,83	7,48E-03
Cofactor binding	GOTERM_MF_FAT	12	3,45	2,55	7,65E-03
Proteasome core complex	GOTERM_CC_FAT	4	1,15	9,33	8,39E-03
Peptidase C1A, papain C-terminal	INTERPRO	4	1,15	9,30	8,61E-03
Chaperonin-containing T-complex	GOTERM_CC_FAT	3	0,86	20,00	8,89E-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
Laminin G, subdomain 1	INTERPRO	3	0,86	20,06	9,00E-03
Calmodulin binding	GOTERM_MF_FAT	8	2,30	3,37	9,65E-03
Negative regulation of angiogenesis	GOTERM_BP_FAT	4	1,15	8,79	9,98E-03
Coenzyme biosynthetic process	GOTERM_BP_FAT	6	1,72	4,53	1,02E-02
Stress response	SP_PIR_KEYWORDS	5	1,44	5,75	1,08E-02
Ligase	SP_PIR_KEYWORDS	13	3,74	2,32	1,08E-02
Iintramolecular oxidoreductase activity, transposing 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
Positive regulation of phagocytosis	GOTERM_BP_FAT	4	1,15	8,41	1,13E-02
Cellular polysaccharide metabolic process	GOTERM_BP_FAT	5	1,44	5,62	1,16E-02
Lysosome	KEGG_PATHWAY	10	2,87	2,68	1,16E-02
Proton donor	UP_SEQ_FEATURE	10	2,87	2,69	1,23E-02
Cell adhesion	GOTERM_BP_FAT	21	6,03	1,81	1,25E-02
Glutathione metabolic process	GOTERM_BP_FAT	4	1,15	8,06	1,27E-02
Biological adhesion	GOTERM_BP_FAT	21	6,03	1,81	1,27E-02
NAD or NADH binding	GOTERM_MF_FAT	5	1,44	5,45	1,29E-02
Sulfur metabolic process	GOTERM_BP_FAT	7	2,01	3,60	1,30E-02
Vitamin binding	GOTERM_MF_FAT	8	2,30	3,17	1,31E-02
Carbohydrate metabolism	SP_PIR_KEYWORDS	6	1,72	4,25	1,33E-02
Peptidase C1A, papain	INTERPRO	4	1,15	7,93	1,35E-02
Regulation of angiogenesis	GOTERM_BP_FAT	5	1,44	5,37	1,36E-02
Intramolecular oxidoreductase activity, interconverting	GOTERM_MF_FAT	3	0,86	15,99	1,41E-02
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
Calmodulin-binding	SP_PIR_KEYWORDS	7	2,01	3,52	1,47E-02
Extracellular matrix	GOTERM_CC_FAT	14	4,02	2,11	1,55E-02
Heat shock protein Hsp70	INTERPRO	3	0,86	14,59	1,70E-02
Heat shock protein 70	INTERPRO	3	0,86	14,59	1,70E-02
Coenzyme binding	GOTERM_MF_FAT	9	2,59	2,70	1,86E-02
Negative regulation of neuron apoptosis	GOTERM_BP_FAT	5	1,44	4,84	1,94E-02
Erythrocyte homeostasis	GOTERM_BP_FAT	5	1,44	4,74	2,07E-02
Protein kinase C binding	GOTERM_MF_FAT	3	0,86	13,08	2,09E-02
Coenzyme catabolic process	GOTERM_BP_FAT	4	1,15	6,67	2,13E-02
GLECT	SMART	3	0,86	12,93	2,15E-02
Endoplasmic reticulum	GOTERM_CC_FAT	28	8,05	1,56	2,16E-02
Hexose catabolic process	GOTERM_BP_FAT	5	1,44	4,65	2,20E-02
Glucose catabolic process	GOTERM_BP_FAT	5	1,44	4,65	2,20E-02
Metal ion-binding site:Iron (heme proximal ligand)	UP_SEQ_FEATURE	3	0,86	12,70	2,21E-02
Iron	SP_PIR_KEYWORDS	13	3,74	2,10	2,25E-02
Nucleic acid-binding, OB-fold	INTERPRO	5	1,44	4,61	2,28E-02
Protein complex binding	GOTERM_MF_FAT	6	1,72	3,69	2,30E-02
NAD(P)-binding domain	INTERPRO	8	2,30	2,83	2,32E-02
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
Molecular chaperone t-complex-type	PIR_SUPERFAMILY	3	0,86	12,16	2,35E-02
Galectin, carbohydrate recognition domain	INTERPRO	3	0,86	12,35	2,36E-02
Heat shock protein 70, conserved site	INTERPRO	3	0,86	12,35	2,36E-02
Hydrogen peroxide catabolic process	GOTERM_BP_FAT	3	0,86	12,09	2,44E-02
Cellular response to hydrogen peroxide	GOTERM_BP_FAT	3	0,86	12,09	2,44E-02
Monosaccharide catabolic process	GOTERM_BP_FAT	5	1,44	4,48	2,49E-02
Response to unfolded protein	GOTERM_BP_FAT	5	1,44	4,48	2,49E-02
RNA binding	SP_PIR_KEYWORDS	3	0,86	11,94	2,51E-02
Extracellular region part	GOTERM_CC_FAT	26	7,47	1,57	2,53E-02
Acetyl-CoA metabolic process	GOTERM_BP_FAT	4	1,15	6,24	2,54E-02
Proteinaceous extracellular matrix	GOTERM_CC_FAT	13	3,74	2,04	2,59E-02
Ubl conjugation	SP_PIR_KEYWORDS	18	5,17	1,78	2,60E-02
Cellular amino acid derivative metabolic process	GOTERM_BP_FAT	8	2,30	2,74	2,68E-02
Ubiquitin-dependent protein catabolic process	GOTERM_BP_FAT	8	2,30	2,74	2,68E-02
Chaperonin Cpn60/TCP-1	INTERPRO	3	0,86	11,46	2,72E-02
Basement membrane	SP_PIR_KEYWORDS	4	1,15	6,09	2,73E-02
Cofactor catabolic process	GOTERM_BP_FAT	4	1,15	6,04	2,76E-02
Regulation of vesicle-mediated transport	GOTERM_BP_FAT	6	1,72	3,50	2,83E-02
Platelet Amyloid Precursor Protein Pathway	BIOCARTA	3	0,86	10,55	2,89E-02

Protein phosphatase inhibitor	SP_PIR_KEYWORDS	3	0,86	11,09	2,89E-02
Thioredoxin-like	INTERPRO	4	1,15	5,94	2,91E-02
Angiogenesis	SP_PIR_KEYWORDS	5	1,44	4,17	3,15E-02
Allosteric enzyme	SP_PIR_KEYWORDS	4	1,15	5,75	3,17E-02
Actin cytoskeleton	GOTERM_CC_FAT	10	2,87	2,28	3,21E-02
Cell-cell junction	GOTERM_CC_FAT	9	2,59	2,43	3,23E-02
Vacuole organization	GOTERM_BP_FAT	4	1,15	5,69	3,24E-02
NADP metabolic process	GOTERM_BP_FAT	3	0,86	10,36	3,27E-02
Growth factor binding	SP_PIR_KEYWORDS	3	0,86	10,35	3,29E-02
Oxygen binding	GOTERM_MF_FAT	3	0,86	10,28	3,32E-02
Response to oxidative stress	GOTERM_BP_FAT	6	1,72	3,33	3,37E-02
Response to protein stimulus	GOTERM_BP_FAT	6	1,72	3,33	3,37E-02
Polysome	GOTERM_CC_FAT	3	0,86	10,00	3,49E-02
EF-hand 5	UP_SEQ_FEATURE	3	0,86	9,98	3,51E-02
Contractile fiber part	GOTERM_CC_FAT	6	1,72	3,26	3,68E-02
Glucose-6-phosphate dehydrogenase, active site	INTERPRO	2	0,57	53,50	3,69E-02
Myristoylated alanine-rich C-kinase substrate MARCKS	INTERPRO	2	0,57	53,50	3,69E-02
Aspartic proteinase	SP_PIR_KEYWORDS	2	0,57	51,75	3,82E-02
Cell redox homeostasis	GOTERM_BP_FAT	5	1,44	3,90	3,88E-02
Aminoacyl-tRNA synthetase, class II, conserved region	INTERPRO	3	0,86	9,44	3,92E-02
Cofactor biosynthetic process	GOTERM_BP_FAT	6	1,72	3,19	3,98E-02
Repeat:1	UP_SEQ_FEATURE	8	2,30	2,52	4,02E-02
Positive regulation of cellular component organization	GOTERM_BP_FAT	7	2,01	2,77	4,05E-02
Pentose biosynthetic process	GOTERM_BP_FAT	2	0,57	48,36	4,08E-02
Pinocytosis	GOTERM_BP_FAT	2	0,57	48,36	4,08E-02
Response to inorganic substance	GOTERM_BP_FAT	6	1,72	3,15	4,14E-02
Regulation of cell growth	GOTERM_BP_FAT	6	1,72	3,15	4,14E-02
Cysteine-type endopeptidase activity	GOTERM_MF_FAT	5	1,44	3,81	4,18E-02
Cell killing	GOTERM_BP_FAT	3	0,86	9,07	4,20E-02
Muscle thin filament tropomyosin	GOTERM_CC_FAT	2	0,57	46,66	4,23E-02
Proteasome regulatory particle	GOTERM_CC_FAT	2	0,57	46,66	4,23E-02
Second lumenal domain	UP_SEQ_FEATURE	2	0,57	46,57	4,24E-02
Cleavage; by collagenase	UP_SEQ_FEATURE	2	0,57	46,57	4,24E-02
Beta-galactoside	UP_SEQ_FEATURE	2	0,57	46,57	4,24E-02
Calmodulin-binding (PSD)	UP_SEQ_FEATURE	2	0,57	46,57	4,24E-02
RGSL	UP_SEQ_FEATURE	2	0,57	46,57	4,24E-02
First lumenal domain	UP_SEQ_FEATURE	2	0,57	46,57	4,24E-02
7S domain	UP_SEQ_FEATURE	2	0,57	46,57	4,24E-02
Response to hypoxia	GOTERM_BP_FAT	5	1,44	3,78	4,28E-02
Peptide metabolic process	GOTERM_BP_FAT	4	1,15	5,09	4,30E-02
SM00121: IB	SMART	3	0,86	8,85	4,39E-02
Repeat:2	UP_SEQ_FEATURE	8	2,30	2,47	4,40E-02
Internal side of plasma membrane	GOTERM_CC_FAT	12	3,45	1,95	4,43E-02
Alcohol catabolic process	GOTERM_BP_FAT	5	1,44	3,72	4,49E-02
Response to oxygen levels	GOTERM_BP_FAT	5	1,44	3,72	4,49E-02
Pleckstrin homology-type	INTERPRO	11	3,16	2,04	4,49E-02
glycosylation site: N-linked (GlcNAc...) (high mannose)	UP_SEQ_FEATURE	3	0,86	8,73	4,50E-02
Myofibril	GOTERM_CC_FAT	6	1,72	3,08	4,52E-02
NAD	SP_PIR_KEYWORDS	8	2,30	2,45	4,56E-02
Pentose phosphate pathway	KEGG_PATHWAY	4	1,15	4,90	4,59E-02
Cellular amide metabolic process	GOTERM_BP_FAT	4	1,15	4,96	4,59E-02
Actin binding	SP_PIR_KEYWORDS	3	0,86	8,63	4,62E-02
Extracellular space	GOTERM_CC_FAT	18	5,17	1,64	4,72E-02
Ubiquitin binding	GOTERM_MF_FAT	3	0,86	8,47	4,76E-02
Insulin-like growth factor-binding protein, IGFBP	INTERPRO	3	0,86	8,45	4,81E-02
Aldehyde dehydrogenase, N-terminal	INTERPRO	3	0,86	8,45	4,81E-02
Aldehyde dehydrogenase	INTERPRO	3	0,86	8,45	4,81E-02
Antioxidant activity	GOTERM_MF_FAT	4	1,15	4,80	4,98E-02