Table S2. Functional annotation clustering of cytosol enriched proteins

Annotation Cluster 1 Enrichment Score: 10.380168698390056

Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_BP_FAT	GO:0006007~glucose catabolic process	12	9.09	5.5E-12	21.70
GOTERM_BP_FAT	GO:0019320~hexose catabolic process	12	9.09	4.0E-11	18.24
GOTERM_BP_FAT	GO:0046365~monosaccharide catabolic process	12	9.09	5.6E-11	17.72
GOTERM_BP_FAT	GO:0046164~alcohol catabolic process	12	9.09	2.4E-10	15.54

Annotation Cluster 2 Enrichment Score: 8.911831563001835

Category	Term	Count	%	PValue	Fold Enrichment
SP_PIR_KEYWORDS	glycolysis	10	7.58	1.4E-11	33.12
GOTERM_BP_FAT	GO:0006096~glycolysis	10	7.58	4.6E-10	22.31
KEGG_PATHWAY	hsa00010:Glycolysis / Gluconeogenesis	10	7.58	2.9E-07	10.46

Annotation Cluster 3 Enrichment Score: 8.028021927784092

Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_BP_FAT	GO:0044275~cellular carbohydrate catabolic process	13	9.85	2.2E-11	16.04
GOTERM_BP_FAT	GO:0016052~carbohydrate catabolic process	13	9.85	4.4E-10	12.51
GOTERM_BP_FAT	GO:0006006~glucose metabolic process	13	9.85	2.2E-08	8.91
GOTERM_BP_FAT	GO:0019318~hexose metabolic process	13	9.85	2.7E-07	7.10
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	13	9.85	1.3E-06	6.14

Annotation Cluster 4 Enrichment Score: 6.117884930664276

Category	Term	Count	%	PValue	Fold Enrichment
SP_PIR_KEYWORDS	ribosome	10	7.58	1.6E-09	19.96
GOTERM_CC_FAT	GO:0022626~cytosolic ribosome	10	7.58	3.1E-08	14.09
SP_PIR_KEYWORDS	ribosomal protein	10	7.58	5.7E-06	7.75
KEGG_PATHWAY	hsa03010:Ribosome	10	7.58	7.1E-06	7.22
SP_PIR_KEYWORDS	ribonucleoprotein	10	7.58	1.3E-04	5.22

Annotation Cluster 5 Enrichment Score: 5.177701919800204

Category	Term	Count	%	PValue	Fold Enrichment
SP_PIR_KEYWORDS	endonexin fold	5	3.79	6.5E-07	66.24
SMART	SM00335:ANX	5	3.79	7.2E-07	64.85
SP_PIR_KEYWORDS	annexin	5	3.79	2.0E-06	52.04
UP_SEQ_FEATURE	repeat:Annexin 1	5	3.79	2.0E-06	51.71
UP_SEQ_FEATURE	repeat:Annexin 3	5	3.79	2.0E-06	51.71
UP_SEQ_FEATURE	repeat:Annexin 2	5	3.79	2.0E-06	51.71
UP_SEQ_FEATURE	repeat:Annexin 4	5	3.79	2.0E-06	51.71
SP_PIR_KEYWORDS	calcium/phospholipid-binding	5	3.79	2.6E-06	48.57
INTERPRO	IPR018252:Annexin repeat, conserved site	5	3.79	3.4E-06	45.07

INTERPRO	IPR018502:Annexin repeat	5	3.79	3.4E-06	45.07
INTERPRO	IPR001464:Annexin	5	3.79	3.4E-06	45.07
GOTERM_MF_FAT	GO:0004859~phospholipase inhibitor activity	5	3.79	3.6E-06	43.63
GOTERM_MF_FAT	GO:0055102~lipase inhibitor activity	5	3.79	9.7E-06	34.90
SP_PIR_KEYWORDS	phospholipid binding	5	3.79	1.4E-05	33.12
PIR_SUPERFAMILY	PIRSF002359:annexin I	5	3.79	1.5E-05	30.21
GOTERM_MF_FAT	GO:0005544~calcium-dependent phospholipid binding	5	3.79	9.8E-05	20.13
GOTERM_MF_FAT	GO:0005543~phospholipid binding	5	3.79	8.7E-02	2.96

Annotation Cluster 6 Enrichment Score: 4.793971688099384

Category	Term	Count	%	PValue	Fold Enrichment
UP_SEQ_FEATURE	repeat:HEAT 6	6	4.55	1.7E-06	28.96
UP_SEQ_FEATURE	repeat:HEAT 5	6	4.55	3.9E-06	24.82
UP_SEQ_FEATURE	repeat:HEAT 4	6	4.55	1.1E-05	20.20
UP_SEQ_FEATURE	repeat:HEAT 3	6	4.55	2.3E-05	17.38
UP_SEQ_FEATURE	repeat:HEAT 2	6	4.55	4.8E-05	14.98
UP_SEQ_FEATURE	repeat:HEAT 1	6	4.55	4.8E-05	14.98
INTERPRO	IPR000357:HEAT	6	4.55	7.1E-05	13.77

Annotation Cluster 7 Enrichment Score: 4.641813968720388

Category	Term	Count	%	PValue	Fold Enrichment
SMART	SM00101:14_3_3	4	3.03	5.1E-06	103.76
UP_SEQ_FEATURE	site:Interaction with phosphoserine on interacting protein	4	3.03	1.1E-05	82.74
INTERPRO	IPR000308:14-3-3 protein	4	3.03	1.6E-05	72.12
PIR_SUPERFAMILY	PIRSF000868:14-3-3	4	3.03	8.3E-05	41.43
PIR_SUPERFAMILY	PIRSF000868:14-3-3 protein	4	3.03	8.3E-05	41.43

Annotation Cluster 8 Enrichment Score: 4.460457489749598

Category	Term	Count	%	PValue	Fold Enrichment
UP_SEQ_FEATURE	domain:Importin N-terminal	5	3.79	2.0E-06	51.71
INTERPRO	IPR001494:Importin-beta, N-terminal	5	3.79	4.7E-06	42.07
GOTERM_BP_FAT	GO:0000059~protein import into nucleus, docking	5	3.79	1.7E-05	30.84
GOTERM_MF_FAT	GO:0008565~protein transporter activity	5	3.79	9.3E-03	6.02

Annotation Cluster 9 Enrichment Score: 4.145530740431766

Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	21	15.91	6.4E-05	2.74
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	21	15.91	7.4E-05	2.71
GOTERM_BP_FAT	GO:0010941~regulation of cell death	21	15.91	7.7E-05	2.70

Annotation Cluster 10 Enrichment Score: 3.9005096948506717

Category	Term	Count	%	PValue	Fold Enrichment

INTERPRO	IPR013126:Heat shock protein 70	4	3.03	9.9E-05	42.07
INTERPRO	IPR001023:Heat shock protein Hsp70	4	3.03	9.9E-05	42.07
INTERPRO	IPR018181:Heat shock protein 70, conserved site	4	3.03	2.0E-04	33.65

Annotation Cluster 11 Enrichment Score: 3.234845013098904

Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_BP_FAT	GO:0043066~negative regulation of apoptosis	12	9.09	5.3E-04	3.55
GOTERM_BP_FAT	GO:0043069~negative regulation of programmed cell death	12	9.09	6.0E-04	3.51
GOTERM_BP_FAT	GO:0060548~negative regulation of cell death	12	9.09	6.1E-04	3.50

Annotation Cluster 12 Enrichment Score: 3.155627276223362

Category	Term	Count	%	PValue	Fold Enrichment
UP_SEQ_FEATURE	repeat:HEAT 23	3	2.27	2.8E-04	108.60
UP_SEQ_FEATURE	repeat:HEAT 22	3	2.27	2.8E-04	108.60
UP_SEQ_FEATURE	repeat:HEAT 21	3	2.27	2.8E-04	108.60
UP_SEQ_FEATURE	repeat:HEAT 20	3	2.27	2.8E-04	108.60
UP_SEQ_FEATURE	repeat:HEAT 24	3	2.27	2.8E-04	108.60
UP_SEQ_FEATURE	repeat:HEAT 16	3	2.27	2.8E-04	108.60
UP_SEQ_FEATURE	repeat:HEAT 17	3	2.27	2.8E-04	108.60
UP_SEQ_FEATURE	repeat:HEAT 18	3	2.27	2.8E-04	108.60
UP_SEQ_FEATURE	repeat:HEAT 19	3	2.27	2.8E-04	108.60
UP_SEQ_FEATURE	repeat:HEAT 15	3	2.27	9.6E-04	62.06
UP_SEQ_FEATURE	repeat:HEAT 14	3	2.27	1.6E-03	48.27
UP_SEQ_FEATURE	repeat:HEAT 13	3	2.27	2.0E-03	43.44
UP_SEQ_FEATURE	repeat:HEAT 12	3	2.27	2.0E-03	43.44
UP_SEQ_FEATURE	repeat:HEAT 11	3	2.27	2.5E-03	39.49
UP_SEQ_FEATURE	repeat:HEAT 9	3	2.27	4.6E-03	28.96
UP_SEQ_FEATURE	repeat:HEAT 10	3	2.27	4.6E-03	28.96

Annotation Cluster 13 Enrichment Score: 3.098788033864193

Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_BP_FAT	GO:0043623~cellular protein complex assembly	10	7.58	2.3E-05	6.47
GOTERM_BP_FAT	GO:0034622~cellular macromolecular complex assembly	10	7.58	3.2E-03	3.30
GOTERM_BP_FAT	GO:0034621~cellular macromolecular complex subunit organization	10	7.58	6.8E-03	2.94

Annotation Cluster 14 Enrichment Score: 3.0058451605448546

Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	32	24.24	7.7E-04	1.82
GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	32	24.24	7.7E-04	1.82
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	32	24.24	1.6E-03	1.75

Annotation Cluster 15 Enrichment Score: 2.986663397389544

Category	Term	Count	%	PValue	Fold Enrichment
UP_SEQ_FEATURE	active site:Cysteine sulfenic acid (-SOH) intermediate	4	3.03	6.2E-06	96.53
INTERPRO	IPR000866:Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	4	3.03	1.6E-05	72.12
SP_PIR_KEYWORDS	antioxidant	4	3.03	2.5E-05	64.76
GOTERM_MF_FAT	GO:0051920~peroxiredoxin activity	4	3.03	4.5E-05	52.35
SP_PIR_KEYWORDS	peroxidase	4	3.03	6.4E-04	23.32
UP_SEQ_FEATURE	domain:Thioredoxin	4	3.03	1.5E-03	17.55
GOTERM_BP_FAT	GO:0034614~cellular response to reactive oxygen species	4	3.03	2.8E-03	13.98
INTERPRO	IPR017936:Thioredoxin-like	4	3.03	2.8E-03	14.02
SP_PIR_KEYWORDS	Redox-active center	4	3.03	2.9E-03	13.88
GOTERM_MF_FAT	GO:0004601~peroxidase activity	4	3.03	3.4E-03	13.09
GOTERM_MF_FAT	GO:0016684~oxidoreductase activity, acting on peroxide as acceptor	4	3.03	3.4E-03	13.09
GOTERM_BP_FAT	GO:0034599~cellular response to oxidative stress	4	3.03	7.7E-03	9.76
GOTERM_MF_FAT	GO:0016209~antioxidant activity	4	3.03	9.9E-03	8.91
GOTERM_BP_FAT	GO:0045454~cell redox homeostasis	4	3.03	2.2E-02	6.66
GOTERM_BP_FAT	GO:0000302~response to reactive oxygen species	4	3.03	3.4E-02	5.59

Annotation Cluster 16 Enrichment Score: 2.9553752490507255

Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_BP_FAT	GO:0046496~nicotinamide nucleotide metabolic process	5	3.79	5.4E-04	13.11
GOTERM_BP_FAT	GO:0006769~nicotinamide metabolic process	5	3.79	5.4E-04	13.11
GOTERM_BP_FAT	GO:0009820~alkaloid metabolic process	5	3.79	5.9E-04	12.79
GOTERM_BP_FAT	GO:0019362~pyridine nucleotide metabolic process	5	3.79	6.5E-04	12.48
GOTERM_BP_FAT	GO:0006733~oxidoreduction coenzyme metabolic process	5	3.79	1.5E-03	10.08
GOTERM_BP_FAT	GO:0043603~cellular amide metabolic process	5	3.79	1.9E-03	9.36
GOTERM_BP_FAT	GO:0019748~secondary metabolic process	5	3.79	6.7E-03	6.64

Annotation Cluster 17 Enrichment Score: 2.9081886504762418

Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_CC_FAT	GO:0005643~nuclear pore	6	4.55	6.1E-04	8.67
GOTERM_BP_FAT	GO:0006606~protein import into nucleus	6	4.55	1.3E-03	7.32
GOTERM_BP_FAT	GO:0051170~nuclear import	6	4.55	1.5E-03	7.15
GOTERM_BP_FAT	GO:0034504~protein localization in nucleus	6	4.55	2.0E-03	6.69

Annotation Cluster 18 Enrichment Score: 2.893563616432318

Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_BP_FAT	GO:0070271~protein complex biogenesis	15	11.36	3.0E-04	3.11
GOTERM_BP_FAT	GO:0006461~protein complex assembly	15	11.36	3.0E-04	3.11
GOTERM_BP_FAT	GO:0065003~macromolecular complex assembly	15	11.36	4.1E-03	2.37
GOTERM_BP_FAT	GO:0043933~macromolecular complex subunit organization	15	11.36	7.2E-03	2.22

Annotation Cluster 19	Enrichment Score: 2.8087837900394588

Category	Term	Count	%	PValue	Fold Enrichment
SMART	SM00262:GEL	3	2.27	7.8E-04	68.09
UP_SEQ_FEATURE	repeat:Gelsolin-like 1	3	2.27	1.3E-03	54.30
UP_SEQ_FEATURE	repeat:Gelsolin-like 2	3	2.27	1.3E-03	54.30
UP_SEQ_FEATURE	repeat:Gelsolin-like 3	3	2.27	1.3E-03	54.30
INTERPRO	IPR007122:Gelsolin	3	2.27	1.7E-03	47.33
INTERPRO	IPR007123:Gelsolin region	3	2.27	5.2E-03	27.04

Annotation Cluster 20	Enrichment Score: 2.7952415595592583

Category	Term	Count	%	PValue	Fold Enrichment
SP_PIR_KEYWORDS	pentose shunt	3	2.27	1.4E-04	145.72
GOTERM_BP_FAT	GO:0006098~pentose-phosphate shunt	3	2.27	3.1E-03	34.96
GOTERM_BP_FAT	GO:0006739~NADP metabolic process	3	2.27	9.8E-03	19.66

Annotation Cluster 21	Enrichment Score: 2.350023807460341

Category	Term	Count	%	PValue	Fold Enrichment
INTERPRO	IPR002194:Chaperonin TCP-1, conserved site	3	2.27	2.6E-03	37.86
INTERPRO	IPR017998:Chaperone, tailless complex polypeptide 1	3	2.27	3.2E-03	34.42
INTERPRO	IPR002423:Chaperonin Cpn60/TCP-1	3	2.27	6.0E-03	25.24
PIR_SUPERFAMILY	PIRSF002584:molecular chaperone t-complex-type	3	2.27	7.7E-03	21.75

Annotation Cluster 22	Enrichment Score: 1.9426658366719283

Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_BP_FAT	GO:0032507~maintenance of protein location in cell	4	3.03	6.8E-03	10.23
GOTERM_BP_FAT	GO:0045185~maintenance of protein location	4	3.03	1.0E-02	8.74
GOTERM_BP_FAT	GO:0051651~maintenance of location in cell	4	3.03	1.0E-02	8.74
GOTERM_BP_FAT	GO:0051235~maintenance of location	4	3.03	2.3E-02	6.55

Annotation Cluster 23	Enrichment Score: 1.9076713225639956

Category	Term	Count	%	PValue	Fold Enrichment
INTERPRO	IPR019479:Peroxiredoxin, C-terminal	3	2.27	6.0E-04	75.72
PIR_SUPERFAMILY	PIRSF000239:alkyl hydroperoxide reductase C22 protein	3	2.27	1.8E-03	43.51
GOTERM_BP_FAT	GO:0042744~hydrogen peroxide catabolic process	3	2.27	1.1E-02	18.51
GOTERM_BP_FAT	GO:0070301~cellular response to hydrogen peroxide	3	2.27	1.2E-02	17.48
GOTERM_BP_FAT	GO:0042743~hydrogen peroxide metabolic process	3	2.27	2.3E-02	12.58
GOTERM_BP_FAT	GO:0042542~response to hydrogen peroxide	3	2.27	9.8E-02	5.62
GOTERM_BP_FAT	GO:0006800~oxygen and reactive oxygen species metabolic process	3	2.27	1.3E-01	4.70

Annotation Cluster 24	Enrichment Score: 1.7055341777652488

Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_MF_FAT	GO:0032559~adenyl ribonucleotide binding	24	18.18	1.3E-02	1.68

GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	24	18.18	2.3E-02	1.59
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	24	18.18	2.6E-02	1.57