

Supplemental Table 3

Category	Term	Count	%	F _E	P _{value}	Benjamini
Cluster 1	Enrichment Score: 4.1					
SP_PIR_KEYWORDS	ATP	6	14	26.6	2.488E-06	1.31E-04
SP_PIR_KEYWORDS	nucleotide-binding	13	30	5.3	2.549E-06	8.92E-05
GOTERM_MF_FAT	GO:0000166~nucleotide binding	19	44	3.1	4.379E-06	7.00E-04
SP_PIR_KEYWORDS	atp-binding	11	26	5.7	1.275E-05	3.35E-04
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	16	37	3.2	3.434E-05	2.74E-03
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	14	33	3.4	8.096E-05	4.31E-03
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	14	33	3.4	8.630E-05	3.45E-03
GOTERM_MF_FAT	GO:0001882~nucleoside binding	14	33	3.4	9.428E-05	3.01E-03
GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	13	30	2.8	1.142E-03	2.26E-02
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	13	30	2.8	1.142E-03	2.26E-02
GOTERM_MF_FAT	GO:0005524~ATP binding	11	26	2.9	2.681E-03	4.66E-02
GOTERM_MF_FAT	GO:0032559~adenyl ribonucleotide binding	11	26	2.9	2.734E-03	4.29E-02
Cluster 2	Enrichment Score: 3.8					
SP_PIR_KEYWORDS	ATP	6	14	26.6	2.488E-06	1.31E-04
INTERPRO	IPR018181:Heat shock protein 70, conserved site	4	9	80.9	1.295E-05	1.77E-03
INTERPRO	IPR013126:Heat shock protein 70	4	9	74.7	1.679E-05	1.15E-03
INTERPRO	IPR001023:Heat shock protein Hsp70	4	9	74.7	1.679E-05	1.15E-03
SP_PIR_KEYWORDS	stress response	4	9	52.5	5.333E-05	9.33E-04
PIRSF_SUPERFAMILY	PIRSF002581:chaperone HSP70	4	9	38.5	1.022E-04	2.55E-03
SP_PIR_KEYWORDS	molecular chaperone	3	7	129.4	2.125E-04	2.03E-03
GOTERM_BP_FAT	GO:0009266~response to temperature stimulus	5	12	13.6	4.247E-04	4.07E-02
GOTERM_BP_FAT	GO:0009628~response to abiotic stimulus	6	14	5.6	3.710E-03	1.41E-01
GOTERM_BP_FAT	GO:0009408~response to heat	4	9	11.7	4.410E-03	1.53E-01
KEGG_PATHWAY	dme04144:Endocytosis	5	12	6.1	6.423E-03	9.21E-02
Cluster 3	Enrichment Score: 3.7					
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	10	23	9.1	7.510E-07	3.67E-04
KEGG_PATHWAY	dme00010:Glycolysis / Gluconeogenesis	7	16	13.2	5.805E-06	1.74E-04
SP_PIR_KEYWORDS	glycolysis	4	9	50.3	6.082E-05	9.12E-04
GOTERM_BP_FAT	GO:0044275~cellular carbohydrate catabolic process	5	12	19.5	1.054E-04	2.54E-02
GOTERM_BP_FAT	GO:0046164~alcohol catabolic process	5	12	19.5	1.054E-04	2.54E-02
GOTERM_BP_FAT	GO:0006006~glucose metabolic process	5	12	16.3	2.124E-04	2.56E-02
SP_PIR_KEYWORDS	gluconeogenesis	3	7	129.4	2.125E-04	2.03E-03
UP_SEQ_FEATURE	binding site:Substrate	5	12	12.4	5.004E-04	2.98E-02
GOTERM_BP_FAT	GO:0006096~glycolysis	4	9	22.7	6.440E-04	5.11E-02
GOTERM_BP_FAT	GO:0016052~carbohydrate catabolic process	5	12	12.0	6.922E-04	4.72E-02
GOTERM_BP_FAT	GO:0019318~hexose metabolic process	5	12	11.7	7.573E-04	4.53E-02
GOTERM_BP_FAT	GO:0006007~glucose catabolic process	4	9	18.5	1.182E-03	6.22E-02
GOTERM_BP_FAT	GO:0019320~hexose catabolic process	4	9	18.5	1.182E-03	6.22E-02
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	5	12	10.2	1.242E-03	5.90E-02
GOTERM_BP_FAT	GO:0046365~monosaccharide catabolic process	4	9	18.0	1.264E-03	5.47E-02
Cluster 4	Enrichment Score: 3.3					
SP_PIR_KEYWORDS	oxidoreductase	12	28	6.5	1.125E-06	1.18E-04
GOTERM_BP_FAT	GO:0055114~oxidation reduction	12	28	3.8	1.338E-04	2.16E-02
GOTERM_MF_FAT	GO:0048037~cofactor binding	7	16	7.5	2.576E-04	6.85E-03
GOTERM_MF_FAT	GO:0050662~coenzyme binding	6	14	8.5	5.262E-04	1.26E-02
GOTERM_MF_FAT	GO:0051287~NAD or NADH binding	3	7	14.8	1.639E-02	1.98E-01
GOTERM_MF_FAT	GO:0050660~FAD binding	3	7	9.7	3.605E-02	3.07E-01
Cluster 5	Enrichment Score: 2.9					
SP_PIR_KEYWORDS	cytoplasm	9	21	6.2	6.569E-05	8.62E-04
SP_PIR_KEYWORDS	cytoskeleton	4	9	13.6	2.949E-03	2.19E-02
GOTERM_CC_FAT	GO:0015629~actin cytoskeleton	4	9	8.1	1.115E-02	3.15E-01
Cluster 6	Enrichment Score: 2.1					
SP_PIR_KEYWORDS	Redox-active center	3	7	60.4	1.045E-03	8.41E-03
GOTERM_BP_FAT	GO:0042592~homeostatic process	5	12	6.1	8.060E-03	2.46E-01
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	4	9	7.2	1.689E-02	4.26E-01
GOTERM_BP_FAT	GO:0045454~cell redox homeostasis	3	7	11.2	2.769E-02	4.97E-01
Cluster 7	Enrichment Score: 1.8					
SP_PIR_KEYWORDS	actin-binding	3	7	19.7	9.668E-03	6.57E-02
GOTERM_MF_FAT	GO:0008092~cytoskeletal protein binding	5	12	4.5	2.165E-02	2.36E-01
GOTERM_MF_FAT	GO:0003779~actin binding	4	9	6.5	2.180E-02	2.23E-01
Cluster 8	Enrichment Score: 1.6					
GOTERM_CC_FAT	GO:0005739~mitochondrion	9	21	2.8	8.600E-03	3.53E-01
GOTERM_CC_FAT	GO:0044429~mitochondrial part	7	16	3.0	2.025E-02	4.03E-01
GOTERM_BP_FAT	GO:0006119~oxidative phosphorylation	4	9	6.0	2.658E-02	5.00E-01
GOTERM_CC_FAT	GO:0031966~mitochondrial membrane	5	12	3.7	3.916E-02	5.54E-01
GOTERM_CC_FAT	GO:0005740~mitochondrial envelope	5	12	3.4	4.839E-02	5.66E-01