

Table 4. Down-regulated proteins and their gene ontologies

Protein name	Time point (h) ^{a)}	Spot ^{b)}	Gene Ontology ^{c)}	GO number
1. Metabolism				
Fructose-bisphosphate aldolase C	↓↓ 16	62	P: fructose metabolism F: fructose-bisphosphate aldolase activity	06000 04332
L-lactate dehydrogenase B chain	↓ 16	67	F: L-lactate dehydrogenase activity	04459
Maleate dehydrogenase	↓ 48	69	F: malic enzyme activity C: cytosol	04470 05829
Phosphoglycerate mutase 1	↓↓ 48 ↓↓ 72 ↓↓ 120	87	P: glycolysis F: bisphosphoglycerate mutase activity F: bisphosphoglycerate phosphatase activity F: phosphoglycerate mutase activity C: cytosol	06096 04082 04083 04619 05829
2. Energy (no down-regulated proteins)				
3. Cell growth, cell division, DNA synthesis				
Deoxyuridine 5'-triphosphate nucleotidohydrolase	↓ 2 ↓↓ 16	103	P: DNA replication P: nucleobase, nucleoside, nucleotide and nucleic acid metabolism F: dUTP diphosphatase activity C: mitochondrion C: nucleus	06260 06139 04170 05739 05634
Nucleoside diphosphate kinase A	↓↓ 16	104	P: negative regulation of cell proliferation P: nucleoside triphosphate biosynthesis P: regulation of apoptosis F: ATP binding F: deoxyribonuclease activity F: DNA binding F: magnesium ion binding F: nucleoside-diphosphate kinase activity C: cytoplasm C: nucleus	08285 09142 42981 05524 04536 03677 00287 04550 05737 05634

4. Transcription				
RuvB-like 1	↓↓ 48	42	P: regulation of transcription from RNA polymerase II promoter P: spermatogenesis F: DNA helicase activity F: protein binding C: nucleus C: TIP60 histone acetyltransferase complex	06357 07283 03678 05515 05634 35267
Heterogeneous nuclear ribonucleoprotein A2/B1	↓ 120	70	P: nuclear mRNA splicing, via spliceosome F: protein binding F: RNA binding C: heterogeneous nuclear ribonucleoprotein complex C: spliceosome complex	00398 05515 03723 30530 05681
5. Protein synthesis				
Elongation factor 2	↓ 2	7	none	
Tryptophanyl-tRNA synthetase	↓ 16	40	P: protein biosynthesis P: negative regulation of cell proliferation P: tryptophanyl-tRNA aminoacylation C: cytoplasm C: soluble fraction	06412 08285 06436 05737 05625
Elongation factor 2	↓ 120 ^{d)}	9	none	
6. Protein destination				
Peptidyl-prolyl cis-trans isomerase A	↓ 2 ^{d)}	108	P: protein folding P: regulation of viral genome replication F: cyclosporin A binding F: unfolded protein binding F: virion binding C: cytoplasm C: cytoplasm	06457 45069 16018 51082 46790 05737 05737
Proteasome activator complex subunit 1	↓ 16	77	C: proteasome complex (sensu Eukaryota)	00502
Proteasome activator complex subunit 2	↓ 16	75	C: proteasome complex (sensu Eukaryota)	00502
Proteasome subunit α type 2	↓ 48	98	C: proteasome complex (sensu Eukaryota)	00502
Transitional endoplasmic reticulum ATPase	↓ 48	4	P: caspase activation P: double-strand break repair P: ER-associated protein catabolism	06919 06302 30433

P: establishment of protein localization	45184
P: protein ubiquitination	16567
P: regulation of apoptosis	42981
P: retrograde protein transport	30970
P: unfolded protein response	30968
F: ATP binding	05524
F: ATPase activity	16887
F: protein binding	05515
C: cytosol	05829
C: endoplasmic reticulum	05783
C: microsome	05792
C: nucleus	05634

7. Redox balance				
Glutathione S-transferase P	↓ 16	94	P: anti-apoptosis	06916
			P: central nervous system development	07417
Superoxide dismutase [Cu-Zn]	↓↓ 16	106	P: neurogenesis	07399
			F: copper, zinc superoxide dismutase activity	04785
8. Intracellular transport				
Voltage-dependent anion-selective channel protein 1	↓ 12	79	P: anion transport	06820
			P: apoptotic program	08632
			F: apoptogenic cytochrome c release channel activity	15283
			F: voltage-gated anion channel porin activity	15482
			C: mitochondrial outer membrane	05741
GTP-binding nuclear protein Ran	↓ 72 ^{b)}	100	P: DNA metabolism	06259
			P: mitosis	07067
			P: mitotic spindle organization and biogenesis	07052
			P: positive regulation of transcription, DNA-dependent	45893
			P: protein-nucleus export	06611
			P: regulation of cell cycle	00074
			P: RNA-nucleus export	06405
			P: signal transduction	07165
			F: androgen receptor binding	50681
			F: chromatin binding	03682
			F: GTP binding	05525

F: GTPase activity	03924
F: protein binding	05515
C: cytoplasm	05737
C: nuclear pore	05643

9. Signal transduction

Growth factor receptor-bound protein 2	↓ 16 ↓ 72	97	P: Ras protein signal transduction P: insulin receptor signaling pathway P: cell-cell signaling P: epidermal growth factor receptor signaling pathway F: epidermal growth factor receptor binding F: protein binding F: SH3/SH2 adaptor activity C: cytosol	07265 08286 07267 07173 05154 05515 05070 05829
DJ-1 protein	↓ 16 ↓ 24 ↓↓ 72	102	P: Ras protein signal transduction C: cytoplasm C: nucleus	07265 05737 05634
Peroxiredoxin-4	↓ 24	84	P: I-κB phosphorylation F: thioredoxin peroxidase activity	07252 08379

10. Cellular organization

Stathmin	↓ 2 ↓↓ 72	107	P: intracellular signaling cascade P: microtubule depolymerization P: mitotic spindle organization and biogenesis F: signal transducer activity F: tubulin binding	07242 07019 07052 04871 15631
Heat-shock protein β-1	↓ 16	88	P: regulation of translational initiation P: response to unfolded protein C: cell surface C: cytoplasm	06446 06986 09986 05737
Lamin-B1	↓↓ 16	18	F: structural molecule activity C: lamin filament	05198 05638
Plastin-2	↓ 16	21	F: actin binding F: calcium ion binding C: cytosol	03779 05509 05829
Actin, cytoplasmic 2	↓ 24	95	none	

Actin, cytoplasmic 1	↓ 24	56		
	↓ 24	57	F: protein binding	05515
	↓ 48	57	C: TIP60 histone acetyltransferase complex	35267
Coronin-1A	↓↓ 48	34	P: mitosis	07067
	↓↓ 72		F: structural molecule activity	05198
	↓↓ 120		C: actin cytoskeleton	15629
			C: lysosomal membrane	05765

- a) Time point(s) in hours for down-regulation. The ↓ arrow indicates that the fold difference for down-regulation is from two to four, whereas the ↓↓ double arrow indicates that the protein is down-regulated more than fourfold.
- b) Spot numbers refer to those in Fig. 1.
- c) F stands for molecular function, P for biological process and C for cellular component.
- d) The protein is also up-regulated in other time point (see Table 3.)