

Table 3. Up-regulated proteins and their gene ontologies

Protein name	Time point (h) ^{a)}	Spot ^{b)}	Gene Ontology ^{c)}	GO number
1. Metabolism				
Triosephosphate isomerase	↑ 2	89	F: triose-phosphate isomerase activity	04807
Phosphoglycerate kinase 1	↑ 16	60	P: glycolysis	06096
			P: phosphorylation	16310
			F: ATP binding	05524
			F: phosphoglycerate kinase activity	04618
Phosphoglycerate mutase 1	↑ 16	85	P: glycolysis	06096
			F: bisphosphoglycerate mutase activity	04082
			F: bisphosphoglycerate phosphatase activity	04083
			F: phosphoglycerate mutase activity	04619
			C: cytosol	05829
Spermidine synthase	↑ 120	73	F:spermidine synthase activity	04766
2. Energy				
Ubiquinol-cytochrome-c reductase complex core protein I	↑ 2	48	P: aerobic respiration	09060
			P: electron transport	06118
			P: oxidative phosphorylation	06119
			F: ubiquinol-cytochrome-c reductase activity	08121
			C: mitochondrial electron transport chain	05746
Dihydrolipoyl dehydrogenase	↑↑ 16	36	F: dihydrolipoyl dehydrogenase activity	04148
			C: mitochondrion	05739
3. Cell growth, cell division, DNA synthesis				
Inosine-5'-monophosphate dehydrogenase 2	↑ 16	35	F: IMP dehydrogenase activity	03938
4. Transcription				
RuvB-like 1	↑↑ 16	41	P: regulation of transcription from RNA polymerase II promoter	06357
			P: spermatogenesis	07283
			F:DNA helicase activity	03678
			F: protein binding	05515
			C: nucleus	05634
			C:TIP60 histone acetyltransferase complex	35267
Heterogeneous nuclear	↑ 24	46	P: RNA processing	06396

ribonucleoprotein H			F: poly(U) binding	08266
			C: heterogeneous nuclear ribonucleoprotein complex	30530
Heterogeneous nuclear ribonucleoprotein K	↑ 48	24	F: protein binding	05515
ATP-dependent DNA helicase 2 subunit 1	↑ 48	15	P: DNA ligation	06266
			P: double-strand break repair via nonhomologous end-joining	06303
			P: positive regulation of transcription, DNA-dependent	45893
			F: ATP-dependent DNA helicase activity	04003
			F: double-stranded DNA binding	03690
			F: protein binding	05515
			C: membrane fraction	05624
			C: nucleus	05634
Spliceosome RNA helicase BAT1	↑↑ 48 ↑ 72	38	P: mRNA-nucleus export	06406
			P: nuclear mRNA splicing, via spliceosome	00398
			F: ATP-dependent RNA helicase activity	04004
			F: protein self binding	42802
			C: nucleus	05634
ATP-dependent RNA helicase DDX39	↑↑ 48 ↑ 120	39	P: mRNA-nucleus export	06406
			P: nuclear mRNA splicing, via spliceosome	00398
			F: ATP-dependent RNA helicase activity	04004
			F: protein binding	05515
			C: nucleus	05634
5. Protein synthesis				
60S acidic ribosomal protein P0	↑ 9 ↑ 16	65	P: protein biosynthesis	06412
			F: protein binding	05515
			F: RNA binding	03723
			F: structural constituent of ribosome	03735
			C: cytosolic large ribosomal subunit (sensu Eukaryota)	05842
Aspartyl-tRNA synthetase	↑ 24	43	P: protein biosynthesis	06412
			P: protein complex assembly	06461
			F: aminoacylase activity	04046
			F: aspartate-tRNA ligase activity	04815
			C: cytoplasm	05737
			C: soluble fraction	05625

Elongation factor 2	↑ 24 ^{d)}	9	none	
6. Protein destination				
Peptidyl-prolyl cis-trans isomerase A	↑↑ 24 ^{d)}	108	P: protein folding	06457
			P: regulation of viral genome replication	45069
			F: cyclosporin A binding	16018
			F: unfolded protein binding	51082
			F: virion binding	46790
			C: cytoplasm	05737
Protein disulfide-isomerase A3	↑ 12	31	P: protein-ER retention	06621
			P: protein-nucleus import	06606
			P: signal transduction	07165
			F: cysteine-type endopeptidase activity	04197
			F: phospholipase C activity	04629
			F: protein disulfide isomerase activity	03756
60 kDa heat shock protein	↑ 12	25	P: mitochondrial matrix protein import	30150
			P: protein folding	06457
			P: regulation of apoptosis	42981
			P: response to unfolded protein	06986
			F: ATP binding	05524
			C: mitochondrion	05739
T-complex protein 1 subunit ε	↑ 72	27	F: protein binding	05515
7. Redox balance				
Peroxiredoxin-1	↑ 16	101	P: cell proliferation	08283
	↑↑ 48		P: skeletal development	01501
Glutathione S-transferase P	↑ 120	93	P: anti-apoptosis	06916
			P: central nervous system development	07417
8. Intracellular transport				
GTP-binding nuclear protein Ran	↑ 24 ^{d)}	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				
Rab GDP dissociation inhibitor β	\uparrow 72	50	P: signal transduction	07165
			F: Rab GDP-dissociation inhibitor activity	05093
			C: cell surface	09986
			C: cytoplasm	05737
Interleukin-25	$\uparrow\uparrow$ 120	110	none	
10. Cellular organization				
Coronin-1A	$\uparrow\uparrow$ 16	33	P: mitosis	07067
			F: structural molecule activity	05198
			C: actin cytoskeleton	15629
			C: lysosomal membrane	05765
Actin, cytoplasmic 1	\uparrow 48	54	F: protein binding	05515
			C:TIP60 histone acetyltransferase complex	35267
Actin, cytoplasmic 1	\uparrow 120	83		
Lamin-B1	$\uparrow\uparrow$ 48	17	F: structural molecule activity	05198
	$\uparrow\uparrow$ 72		C: lamin filament	05638
	\uparrow 120			

- a) Time point(s) in hours for up-regulation. The \uparrow arrow indicates that the fold difference for up-regulation is from two to four, whereas the $\uparrow\uparrow$ double arrow indicates that the protein is up-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 down-regulated in other time point (see Table 4.)