

Supplementary Table 2. Gene products identified by both transcriptomics and MS-based proteomics

Protein name	UniProt Acc. No. ^{a)}	GenBank Acc. No. ^{b)}	Gene name	Spot ^{c)}	Time point protein (h) ^{d,e)}	Time point mRNA (h) ^{e)}	Gene Ontology ^{f)}	GO number
Group 1								
Aspartyl-tRNA synthetase	P14868	AA481562	DARS	43	↑ 24	↑↑ 48 ↑↑ 70 ↑↑ 124	P: aspartyl-tRNA aminoacylation P: protein biosynthesis P: protein complex assembly F: aminoacylase activity F: aspartate-tRNA ligase activity C: cytoplasm C: soluble fraction	06422 06412 06461 04046 04815 05737 05625
Heterogeneous nuclear ribonucleoprotein K	P61978	W85697	HNRPK	24	↑ 48	↑↑ 96	F: protein binding	05515
T-complex protein 1 subunit ε	P48643	AA629692	CCT5	27	↑ 72	↑↑ 124	F: protein binding	05515
Plastin-2	P13796	W73144	LCP1	21 20	↓ 16 ↔	↓↓ 48 ↓↓ 70 ↓↓ 96 ↓↓ 124	F: actin binding F: calcium ion binding C: cytosol	03779 05509 05829
Maleate dehydrogenase, cytoplasmic	P40925	AA403295	MDH1	69	↓ 48	↓↓ 124	F: malic enzyme activity C: cytosol	04470 05829
Proteasome activator complex subunit 1	Q06323	T47815	PSME1	77	↓ 16	↓↓ 16 ↓↓ 24 ↓↓ 48 ↓↓ 70 ↓↓ 96	C: cytoplasm C: proteasome complex (sensu Eukaryota)	05737 00502
Group 2								
Coronin-1A	P31146	AA047478	CORO1A	33 34	↑↑ 16 ↓↓ 48 ↓↓ 72 ↓↓ 120	↔	P: mitosis F: structural molecule activity C: actin cytoskeleton C: lysosomal membrane	07067 05198 15629 05765
Dihydrolipoyl dehydrogenase	P09622	AA447748	DLD	36	↓↓ 16	↔	F: dihydrolipoyl dehydrogenase activity	04148

							C:mitochondrion	05739
Fructose-bisphosphate aldolase C	P09972	R39463	ALDOC	62	↓ ↓ 16	↔	P: fructose metabolism	06000
							F: fructose-bisphosphate aldolase activity	04332
Growth factor receptor-bound protein 2	P62993	AA449831	GRB2	97	↓ 16 ↓ 72	↔	P: Ras protein signal transduction	07265
							P: cell-cell signaling	07267
							P: insulin receptor signalling pathway	08286
							P: epidermal growth factor receptor signaling pathway	07173
							F: epidermal growth factor receptor binding	05154
							F: protein binding	05515
							F: SH3/SH2 adaptor activity	05070
							C: cytosol	05829
GTP-binding nuclear protein Ran	P62826	AA456636	RAN	100	↑ 24 ↓ 72	↔	P: androgen receptor signalling pathway	30521
							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
							F: transcription coactivator activity	03713
							C: cytoplasm	05737
							C: nuclear pore	05643
Heterogeneous nuclear ribonucleoprotein H	P31943	W96058	HNRPH1	46 47	↑ 24 ↔	↔	P: RNA processing	06396
							F: poly(U) binding	08266

							C: heterogeneous nuclear ribonucleoprotein complex	30530
Nucleoside diphosphate kinase A	P15531	AA644092	NME1	104	↓↓ 16	↔	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: nucleus	08285 09142 42981 05524 04536 03677 00287 04550 05634
Peroxiredoxin-4	Q13162	AA45966	PRDX4	84	↓ 24	↔	P: I-kappaB phosphorylation F: thioredoxin peroxidase activity	07252 08379
Phosphoglycerate mutase 1	P18669	AA676970	PGAM1	85 86 87	↑ 16 ↔ ↓↓ 48 ↓↓ 70 ↓↓ 96 ↓↓ 120	↔	P: glycolysis F: bisphosphoglycerate mutase activity F: bisphosphoglycerate phosphatase activity F: phosphoglycerate mutase activity C: cytosol	06096 04082 04083 04619 05829
Proteasome activator complex subunit 2	Q9UL46	H65395	PSME2	75	↓ 16	↔	C: proteasome complex (sensu Eukaryota)	00502
Group 3								
ATP-dependent DNA helicase 2 subunit 1	P12956	AA486207	G22P1	15	↑ 48	↓↓ 48 ↓↓ 96 ↓↓ 124	P: DNA ligation P: double-strand break repair via nonhomologous end-joining P: positive regulation of transcription F: ATP-dependent DNA helicase activity F: double-stranded DNA binding F: protein binding C: membrane fraction C: nucleus C: transcription factor complex	06266 06303 45893 04003 03690 05515 05624 05634 05667
Elongation factor 2	P13639	R43766	EEF2	7 8 and 10	↓ 2 ↔	↓↓ 12 ↓↓ 48	none	

				9	↑ 24 ↓ 120	↓↓ 96		
Glutathione S-transferase P	P09211	R33642	GSTP1	93 94	↑ 120 ↓ 16	↓↓ 48 ↓↓ 124	P: anti-apoptosis P: central nervous system development C: cytoplasm	06916 07417 05737
Peroxiredoxin-1	Q06830	AA775803	PRDX1	101	↑ 16 ↑↑ 48	↓↓ 70 ↓↓ 96	P: cell proliferation P: skeletal development	08283 01501
Rab GDP dissociation inhibitor β	P50395	R92806	GDI2	50	↑ 72	↓↓ 48 ↓↓ 70 ↓↓ 96 ↓↓ 124	P: signal transduction F: Rab GDP-dissociation inhibitor activity C: cell surface C: cytoplasm	07165 05093 09986 05737
Spermidine synthase	P19623	AA669545	SRM	73	↑ 120	↓↓ 70	F: spermidine synthase activity	04766
Tryptophanyl-tRNA synthetase	P23381	AA664040	WARS	40	↓ 16	↑↑ 4	P: protein biosynthesis P: negative regulation of cell proliferation P: tryptophanyl-tRNA aminoacylation C: cytoplasm C: soluble fraction	06412 08285 06436 05737 05625
Voltage-dependent anion-selective channel protein 1	P21796	AA044059	VDAC1	79	↓ 12	↑↑ 1	P: anion transport P: apoptotic program F: apoptogenic cytochrome c release channel activity F: voltage-gated anion channel porin activity C: mitochondrial outer membrane	06820 08632 15283 15482 05741
Group 4								
ATP-dependent DNA helicase 2 subunit 2	P13010	AA775355	XRCC5	11	out	↓↓ 24 ↓↓ 48 ↓↓ 70 ↓↓ 96 ↓↓ 124	P: DNA recombination P: double-strand break repair F: ATP-dependent DNA helicase activity F: double-stranded DNA binding F: protein binding C: nucleus	06310 06302 04003 03690 05515 05634
ATP-synthase β-chain	P06576	AA708298	ATP5B	44	↔	↓↓ 24 ↓↓ 48 ↓↓ 70	F: protein binding F: transporter activity C: proton-transporting ATP synthase	05515 05215 05753

						↓↓ 96	complex (sensu Eukaryota)	
						↓↓ 124	C: proton-transporting ATP synthase, catalytic core (sensu Eukaryota)	05754
Endoplasmin	P14625	AA598758	TRA1	2	↔	↓↓ 48	P: anti-apoptosis	06916
						↓↓ 70	P: protein transport	15031
							P: response to hypoxia	01666
							F: calcium ion binding	05509
							F: low-density lipoprotein receptor binding	50750
							F: protein binding	05515
							F: RNA binding	03723
							F: virion binding	46790
							C: cytosol	05829
							C: endoplasmic reticulum lumen	05788
							C: endoplasmic reticulum membrane	05789
							C: microsome	05792
							C: perinuclear region	48471
F-actin capping protein β subunit	P47756	AA430524	CAPZB	76	↔	↑↑ 70	P: cell motility	06928
						↑↑ 96	F: actin binding	03779
						↑↑ 124	C: F-actin capping protein complex	08290
Glycyl-tRNA synthetase	P41250	AA629909	GARS	12	↔	↓↓ 70	F: glycine-tRNA ligase activity	04820
						↓↓ 96	C: cytoplasm	05737
						↓↓ 124	C: soluble fraction	05625
Heat shock protein 75 kDa	Q12931	AA497020	TRAP1	16	↔	↓↓ 9	F: tumor necrosis factor receptor binding	05164
Isocitrate dehydrogenase [NAD] subunit α	P50213	AA464139	IDH3A	61	↔	↓↓ 4	P: carbohydrate metabolism	05975
						↓↓ 12		
						↓↓ 16		
						↓↓ 48		
						↓↓ 124		
Nucleophosmin	P06748	AA669758	NPM1	63	out	↓↓ 70	P: activation of NF- κ B transcription factor	51092
						↓↓ 96	P: anti-apoptosis	06916
							P: cell aging	07569
							P: centrosome cycle	07098
							P: intracellular protein transport	06886

							P: negative regulation of cell proliferation	08285
							P: nucleocytoplasmic transport	06913
							P: response to stress	06950
							P: ribosome assembly	42255
							P: signal transduction	07165
							F: NF-κB binding	51059
							F: protein heterodimerization activity	46982
							F: protein homodimerization activity	42803
							F: RNA binding	03723
							F: Tat protein binding	30957
							F: transcription coactivator activity	03713
							F: unfolded protein binding	51082
							C: centrosome	05813
							C: cytoplasm	05737
							C: nucleolus	05730
Rho GDP-dissociation inhibitor 2	P52566	AA487426	ARHGDIB	92	↔	↓↓ 12 ↓↓ 48 ↓↓ 70 ↓↓ 124	P: actin cytoskeleton organization and biogenesis P: cell motility P: development P: immune response P: negative regulation of cell adhesion P: Rho protein signal transduction F: Rho GDP-dissociation inhibitor activity C: cytoplasm C: cytoplasmic membrane-bound vesicle C: cytoskeleton	30036 06928 07275 06955 07162 07266 05094 05737 16023 05856
Stress-induced-phosphoprotein 1	P31948	AA487427	STIP1	23	mix	↑↑ 48 ↑↑ 124	P: response to stress C: Golgi apparatus C: nucleus	06950 05794 05634
Succinate dehydrogenase [ubiquinone] flavoprotein subunit	P31040	T70043	SDHA	19	↔	↓↓ 24 ↓↓ 48 ↓↓ 70 ↓↓ 96 ↓↓ 124	P: tricarboxylic acid cycle F: electron transporter activity C: mitochondrion	06099 05489 05739

Tubulin α -1	P04687	AA865469	TUBA3	37	\leftrightarrow	$\downarrow\downarrow$ 70 $\downarrow\downarrow$ 96 $\downarrow\downarrow$ 124	none	
Tyrosine-protein kinase BTK	Q06187	N57766	BTK	66	\leftrightarrow	$\downarrow\downarrow$ 70	P: calcium-mediated signaling P: induction of apoptosis by extracellular signals P: intracellular signaling cascade P: mesoderm development P: protein amino acid phosphorylation F: ATP binding F: protein binding F: protein-tyrosine kinase activity C: cytoplasm C: lipid raft	19722 08624 07242 07498 06468 05524 05515 04713 05737 45121
14-3-3 protein ϵ	P62258	N21624	YWHAE	71	out	$\uparrow\uparrow$ 1 $\uparrow\uparrow$ 48	F: protein binding	05515

- Accession number in UniProt database
- Accession number in GenBank database
- Spot numbers refer to those in Fig. 1
- Time point(s) in hours for differential protein expression. The \uparrow arrow indicates that the protein is up-regulated from two- to fourfold, whereas the \downarrow arrow indicates that the protein is down-regulated. 'Out' indicates differences, which were not reproducible and 'mix' indicates that two proteins were identified from a single spot.
- The double arrow indicates that the gene product is at least fourfold up- or down-regulated. The \leftrightarrow arrow indicates that gene product did not change significantly in terms of expression level.
- F stands for molecular function, P for biological process and C for cellular component.