

Table 1. Proteins identified by MS and bioinformatics

Protein name	Spot ^{a)}	Acc. No. ^{b)}	Identification mode ^{c)}	Mascot score ^{d)}	Intensity coverage (%) ^{e)}	Sequence coverage (%) ^{f)}	Peptide matches ^{g)}	Mw (kDa) ^{h)}	pI ⁱ⁾	Time point (h) ^{j)}
Acidic leucine-rich nuclear phosphoprotein 32 family member A	80	P39687	PMF	99	48	38	7	29	3.5	
Actin, cytoplasmic 1	56	P60709	PMF			22	6	42	5.7	↓ 24
Actin, cytoplasmic 1	55	P60709	PMF			50	15	43	5.1	
Actin, cytoplasmic 1	57	P60709	PMF	174	89	41	15 (13)	42	5.9	↓ 24 ↓ 48
Actin, cytoplasmic 1	72	P60709	PMF	78	57	24	7	33	4.4	
Actin, cytoplasmic 1	54	P60709	PMF	143	52	52	18	44	5	↑ 48
Actin, cytoplasmic 1	74	P60709	PMF	98	18	79	9	30	5.1	
Actin, cytoplasmic 1	83	P60709	MS/MS	80				28	5.3	↑ 120
Actin, cytoplasmic 2	95	P63261	PMF	119	92	38	8 (7)	26	5.5	↓ 24
Actin-like protein 3	49	P61158	PMF	254	84	55	22	48	5.6	
Adenosylhomocysteinase	58	P23526	PMF	126	83	23	11	44	6.3	
α-enolase	52	P06733	PMF			49	16	48	6.9	
α-enolase	51	P06733	Match					49	6.8	
Aspartyl-tRNA synthetase	43	P14868	PMF	159	91	25	12 (11)	54	6.7	↑ 24
ATP-dependent RNA helicase DDX39	39	O00148	PMF	107	73	22	10	55	5.4	↑↑ 48 ↑ 120
ATP-dependent DNA helicase 2 subunit 1	15	P12956	PMF	88	56	17	10 (9)	75	6.7	↑ 48
ATP-dependent DNA helicase 2 subunit 2	11	P13010	PMF	190	78	31	22 (19)	92	5.5	
ATP synthase β chain	44	P06576	PMF			47	18	50	4.7	
Bifunctional purine biosynthesis protein PURH	23	P31939	PMF	129	65	29	16	68	6.7	
Cofilin-1	105	P23528	PMF, MS/MS	63	56	39	5	19	6.6	
Coronin-1A	33	P31146	PMF	81	43	28	9	60	6.5	↑↑ 16
Coronin-1A	34	P31146	PMF	149	46	36	16 (15)	60	6.6	↓↓ 48 ↓↓ 72 ↓↓ 120
Deoxyuridine 5'-triphosphate nucleotidohydrolase	103	P33316	Match					20	5.7	↓ 2 ↓↓ 16
Dihydrolipoyl dehydrogenase	36	P09622	PMF, MS/MS	126	45	15	9 (6)	56	6.9	↑↑ 16
DJ-1 protein	102	Q99497	PMF, MS/MS	54	36	31	7 (4)	23	6.3	↓ 16 ↓ 24 ↓↓ 72

DNA replication licensing factor MCM7	6	P33993	PMF			12	6	115	6.5	
Elongation factor 2	10	P13639	Match					111	6.9	
Elongation factor 2	9	P13639	PMF			13	8	111	6.9	↑ 24 ↓ 120
Elongation factor 2	8	P13639	Match					111	6.8	
Elongation factor 2	7	P13639	Match					111	6.8	↓ 2
Endoplasmic precursor	2	P14625	PMF	285	84	41	43 (37)	113	4.3	
F-actin capping protein β subunit	76	P47756	PMF	103	46	38	10	31	5.5	
Fructose-bisphosphate aldolase C	62	P09972	PMF	165	70	49	12	40	6.9	↓↓ 16
Fumarate hydratase	53	P07954	PMF	100	100	21	6	46	7.1	
Glutathione S-transferase P	94	P09211	PMF	121	32	62	12 (11)	24	5.4	↓ 16
Glutathione S-transferase P	93	P09211	PMF, MS/MS	85	52	49	7	25	5.1	↑ 120
Glycyl-tRNA synthetase	12	P41250	PMF			16	8	83	6.2	
Growth factor receptor-bound protein 2	97	P62993	PMF	129	83	38	10 (9)	26	6	↓ 16 ↓ 72
GTP-binding nuclear protein Ran	100	P62826	PMF	95	52	45	7	24	7	↑ 24 ↓ 72
Heat shock cognate 71 kDa protein	13	P11142	PMF			18	10	76	5.2	
Heat shock protein 75 kDa	16	Q12931	PMF	207	76	38	25 (23)	79	6.7	
Heat shock protein HSP 90-α	3	P07900	PMF, MS/MS	134	62	32	13	95	4.7	
Heat shock protein HSP 90-β	3	P08238	PMF, MS/MS	321	77	36	14 (13)	95	4.7	
Heat-shock protein β-1	96	P04792	PMF	80	100	23	4	25	5.5	
Heat-shock protein β-1	88	P04792	PMF	168	96	54	11 (10)	27	6.2	↓ 16
Heat shock 70kD protein 9B	14	Q8N1C8	PMF			17	9	76	5.4	
60 kDa heat shock protein	26	P10809	PMF		83	43	17	64	5.1	
60 kDa heat shock protein	25	P10809	PMF	94	31	27	14	64	5	↑ 12
Heterogeneous nuclear ribonucleoprotein A2/B1	70	P22626	Match					34	9.1	↓ 120
Heterogeneous nuclear ribonucleoprotein H	47	P31943	PMF	96	76	29	8	52	6	
Heterogeneous nuclear ribonucleoprotein H	46	P31943	PMF	155	66	46	15	52	5.9	↑ 24
Heterogeneous nuclear ribonucleoprotein K	24	P61978	PMF	140	79	33	14	65	5	↑ 48
Inosine-5'-monophosphate dehydrogenase 2	35	P12268	PMF	68	21	29	10	59	6.8	↑ 16
Interleukin-25	110	Q969H8	PMF	70	46	27	4	15	6.7	↑↑ 120
Isocitrate dehydrogenase [NAD] subunit α	61	P50213	PMF	138	84	31	13 (11)	38	5.9	
L-lactate dehydrogenase B chain	67	P07195	PMF, MS/MS	46	21	19	6	35	5.7	↓ 16
Lamin-B1	17	P20700	PMF	68	16	30	11	75	4.9	↑↑ 48 ↑↑ 72 ↑ 120

Lamin-B1	18	P20700	PMF	120	47	29	14 (13)	72	5	↓↓ 16
Maleate dehydrogenase, cytoplasmic	69	P40925	PMF	83	85	22	6	36	6.8	↓ 48
Maleate dehydrogenase, mitochondrial	78	P40926	PMF	240	86	51	15	33	8.3	
MHC class II antigen (fragment)	99	Q860I9	PMF	64	11	73	5	25	7	
Neutral α -glucosidase AB	5	Q14697	PMF	297	97	40	29 (27)	110	5.9	
Nucleophosmin	63	P06748	PMF	65	62	31	9 (6)	37	4.2	
Nucleoside diphosphate kinase A	104	P15531	PMF		83	57	11	19	5.9	↓↓ 16
Peptidyl-prolyl cis-trans isomerase A	108	P62937	PMF	120	68	59	11	16	7.1	↓ 2 ↑↑ 24
Peptidyl-prolyl cis-trans isomerase A	109	P62937	Match					16	7.6	
Peroxiredoxin-1	101	Q06830	PMF	144	59	71	10	23	7.4	↑ 16 ↑↑ 48
Peroxiredoxin-4	84	Q13162	PMF	89	40	51	8	27	5.6	↓ 24
Phosphoglycerate kinase 1	60	P00558	Match					45	7.5	↑ 16
Phosphoglycerate mutase 1	87	P18669	PMF	193	97	51	12	28	6.9	↓↓ 48 ↓↓ 72 ↓↓ 120
Phosphoglycerate mutase 1	86	P18669	PMF	107	52	44	8	29	6.6	
Phosphoglycerate mutase 1	85	P18669	PMF	254	55	70	19	28	6.1	↑ 16
Plastin-2	20	P13796	PMF	210	80	34	21 (19)	69	5	
Plastin-2	21	P13796	PMF	69	50	12	9	71	5.1	↓ 16
Prohibitin	82	P35232	PMF	229	96	34	13	29	5.1	
Proteasome activator complex subunit 1	77	Q06323	PMF	107	46	37	9	30	5.7	↓ 16
Proteasome activator complex subunit 2	75	Q9UL46	PMF	141	64	46	12	31	5.2	↓ 16
Proteasome subunit α type 2	98	P25787	Match					25	6.9	↓ 48
Proteasome subunit α type 3	81	P25788	PMF	116	60	38	9	29	5	
Protein disulfide-isomerase A3	32	P30101	PMF			40	16	57	5.7	
Protein disulfide-isomerase A3	31	P30101	PMF	176	65	45	20	58	5.6	↑ 12
Rab GDD dissociation Inhibitor β	50	P50395	PMF	198	94	34	18	48	6.4	↑ 72
Rho GDP-dissociation inhibitor 1	91	P52565	Match					26	4.6	
Rho GDP-dissociation inhibitor 2	92	P52566	PMF, MS/MS	83	6	25	3	25	4.9	
RuvB-like 1	42	Q9Y265	PMF, MS/MS	60	25	25	8	53	6.6	↓↓ 48
RuvB-like 1	41	Q9Y265	PMF	152	62	35	12	54	6.5	↑↑ 16
RuvB-like 2	45	Q9Y230	PMF			29	12	50	5.4	
Septin-2	59	Q15019	PMF	130	80	34	12	43	6.5	
Spermidine synthase	73	P19623	PMF	89	6	19	7 (6)	34	5.1	↑ 120
Spliceosome RNA helicase BAT1	38	Q13838	PMF, MS/MS	102	66	24	9	54	5.4	↑↑ 48 ↑ 72

Stathmin	107	P16949	Match					18	5.7	↓ 2 ↓↓ 72
Stress-induced-phosphoprotein 1	23	P31948	PMF	73	26	21	14	68	6.7	
Succinate dehydrogenase [ubiquinone] flavoprotein subunit	19	P31040	PMF	112	92	17	8	72	6.6	
Superoxide dismutase [Cu-Zn]	106	P00441	Match					19	5.7	↓↓ 16
T-complex protein 1 subunit α	28	P17987	PMF			31	14	64	6	
T-complex protein 1 subunit ε	27	P48643	PMF	124	60	38	19	64	5.4	↑ 72
T-complex protein 1 subunit γ	22	P49368	PMF	196	85	36	18 (16)	68	6.4	
T-complex protein 1 subunit τ	30	P50990	PMF	190	85	37	19 (17)	62	5.4	
T-complex protein 1 subunit ζ	29	P40227	PMF	188	85	29	14 (13)	65	6.7	
Transitional endoplasmic reticulum ATPase	4	P55072	Match					100	5	↓ 48
Triosephosphate isomerase	90	P60174	Match					27	6.9	
Triosephosphate isomerase	89	P60174	Match					27	6.7	↑ 2
Tubulin α	37	P05209	PMF	138	48	48	18 (15)	50	5.3	
Tryptophanyl-tRNA synthetase	40	P23381	PMF			22	8	56	6.1	↓ 16
Tyrosine-protein kinase BTK	66	Q06187	PMF			23	10	39	6.9	
Ubiquinol-cytochrome-c reductase complex core protein I	48	P31930	PMF	116	71	28		48	5.4	↑ 2
Voltage-dependent anion-selective channel protein 1	79	P21796	PMF	149	54	52	11	32	9	↓ 12
3-hydroxyacyl-CoA dehydrogenase type-2	99	Q99714	PMF	152	62	77	20	25	7	
14-3-3 protein ε	71	P62258	PMF, MS/MS	69	28	36	9	31	4	
26S proteasome non-ATPase regulatory subunit 14	68	O00487	PMF	74	45	30	7 (6)	35	6.3	
60S acidic ribosomal protein P0	65	P05388	PMF, MS/MS	158	64	10		36	6.1	↑ 9 ↑ 16
60S acidic ribosomal protein P0	64	P05388	PMF	156	54	33	13	36	5.5	
150 kDa oxygen-regulated protein	1	Q9Y4L1	PMF	109	40	28	22	150	5	

- Spot numbers refer to those in Fig. 1
- Accession number in UniProt database
- Proteins were identified by peptide mass fingerprinting (PMF), by fragment ion analysis (MS/MS), by matching to other lymphocyte 2-DE databases (Match) or by both PMF and fragment ion analysis as a combined search (PMF, MS/MS).
- MASCOT score indicates the confidence of the protein identification
- MS-peak intensity coverage of matched peptides

- f) Amino acid coverage of matched peptides
- g) Number of peptides used for identification. If there are many forms of the same peptide, then the total number of different peptides assigned to the protein is in brackets.
- h) Observed Mw
- i) Observed pI
- j) Time point(s) in hours for differential protein expression. The ↑ arrow indicates that the protein is up-regulated from two- to fourfold, whereas the ↓ arrow indicates that the protein is down-regulated. The double arrow indicates that the protein is more than fourfold up- or down-regulated.