

Spot number	Description	UniProt KB entry	Gene name	Theoretical pI	Theoretical MW	MASCOT protein score	Coverage (%)	Matched/s earched peaks	MSMS	MS/MS score	m/z	z
1	Vinculin	Q64727	VCL	5.77	116586.17	160	23.3	18/28	179QQLTHQEHRR188	57	1305.6350	1
2	Heat shock protein 90, beta (Grp94), member 1	P08113	HSP90B1	4.72	90096.75	214	27.1	22/28	385SILFVPTSAPR395	63	1187.7090	1
3	Gelsolin	P13020	GSN	5.72	83344.38	107	18.1	11/21	176HVVPNEVVVQR166	38	1275.7180	1
4	Gelsolin	P13020	GSN	5.72	83344.38	87	14.2	9/19	176HVVPNEVVVQR166	55	1275.7371	1
5	Glycyl-tRNA synthetase	Q9CZD3	GARS	6.24	81877.77	99	15.6	8/11	309LPFAAAQIGNSFR321	87	1391.7400	1
6	Stress-70 protein, mitochondrial	P38647	HSPA9	5.50	68612.84	274	39.9	22/25	188NAVITVPAYFNDSQR202	88	1694.8590	1
7	Transketolase	P40142	TKT	7.23	67630.48	104	25.0	9/15	111LDNLVAIFDINR122	86	1402.7660	1
8	Calreticulin	P14211	CALR	4.33	46347.39	134	36.3	10/19	25EQFLDGDWNTNR358	87	1451.6730	1
9	T-complex protein 1 subunit alpha	P11983	TCP1	5.82	60448.64	208	30.9	17/26	434EQLAIAEFAR443	54	1147.6190	1
10	Chaperonin containing Tcp1, subunit 5 (epsilon)	P80316	CCT5	5.72	59492.89	210	48.1	18/31	353LGFAGVQVEISFGTTK358	104	1653.8910	1
11	Peptidyl-prolyl cis-trans isomerase FKBP4 (FK506-binding protein 4)	P30416	FKBP4	5.54	51572.38	125	29.5	11/18	235FQIPPHAEELR244	56	1207.6520	1
12	Protein disulfide isomerase associated 4	P09103	PDIA4	4.72	55090.04	210	37.3	18/29	84VDATEESDLAQQYGVRR99	134	1780.8490	1
13	Chaperonin containing Tcp1, subunit 2 (beta)	P80314	CCT2	5.98	57346.04	104	23.6	12/20	377GATQQILDEAER388	93	1330.6630	1
14	RuvB-like protein 2	Q9WMT5	RUVBL2	5.49	50981.32	279	51.0	21/27	429VYSLFDDESRR438	49	1228.6190	1
15	Vimentin	P20152	VIM	5.05	53556.48	180	44.8	17/29	326EMEENFALEAANYQDTIGR344	181	2201.0110	1
16	Vimentin	P20152	VIM	5.05	53556.48	251	48.0	24/34	345LQDEIQNMKEEMAR358	101	1734.8270	1
17	Eukaryotic translation initiation factor 4A1	Q4FZL1	EIF4A1	5.32	46153.93	95	23.9	13/26	147LQMEAPHIVGTGPR161	70	1618.9110	1
18	Vimentin	P20152	VIM	5.05	53556.48	256	50.7	22/31	345LQDEIQNMKEEMAR358	118	1734.8580	1
19	Serine (or cysteine) peptidase inhibitor, clade B, member 6a	Q60854	SERPINB6A	5.53	42598.91	196	40.7	16/20	84TGTQYLLR91	35	951.5470	1
20	Phosphoglycerate kinase 1	P09411	PGK1	8.02	44419.28	156	41.2	13/18	157LGDVYVNDAFGTAAHR171	140	1634.7990	1
21	Fructose-bisphosphate aldolase A	P05064	ALDOA	8.40	39224.74	220	56.3	16/20	88ADDGRPFQVQIK99	83	1342.7170	1
22	Acetyl-Coenzyme A acetyltransferase 2	Q8CAY6	ACAT2	7.16	41297.73	122	31.5	8/13	195AGHFDKEIVPVLVSSR210	120	1753.9611	1
23	Acetyl-Coenzyme A acetyltransferase 2	Q8CAY6	ACAT2	7.16	41297.73	175	40.8	12/17	195AGHFDKEIVPVLVSSR210	145	1753.9580	1
24	Protein phosphatase 1, catalytic subunit, alpha isoform	P62137	PPP1CA	5.94	37408.90	201	39.4	14/19	60LGGDIHQYDILLR73	72	1722.8361	1
25	Annexin A1 (Lipocortin I)	P10107	ANXA1	7.15	38603.11	113	33.5	9/18	114TPAQFDADLR124	41	1262.6021	1
26	Annexin A3	Q35639	ANXA3	5.50	36252.90	219	53.9	18/40	14DYPGFSPSVDAAAIR28	116	1623.7889	1
27	Glyceraldehyde-3-phosphate dehydrogenase	P16858	GAPDH	8.45	35678.82	116	25.5	9/16	308LISWYDNEYGYSNR321	101	1779.8101	1
28	Lactate dehydrogenase A	P06151	LDHA	7.76	36367.34	134	32.5	12/20	213SLNPELGTADADKEQWK228	107	1830.8890	1
29	Annexin A5	P48036	ANXA5	4.82	35752.44	175	34.8	12/15	5GTVTDFPFGDGR16	78	1268.5900	1
30	Esterase D/formylglutathione hydrolase	Q9R0P3	ESD	6.70	31319.58	95	27.7	7/17	65SGYQQAASEHGLVVIAPDTSR86	183	2283.1570	1
31	Voltage-dependent anion channel 1	Q60932	VDAC1	8.55	32351.49	158	39.2	10/16	243YQVDPDACFSAK254	55	1400.6250	1
32	Guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 (Gnb2l1), mRNA	P68040	GNB2L1	7.57	34945.54	178	46.1	11/15	140YTVQDESHSEWVSCVR155	145	1981.8610	1
33	Proteasome (prosome, macropain) subunit, alpha type 1	Q9R1P4	PSMA1	6.00	29546.54	86	24.7	7/8	4NQYDNDVTWVSPQGR18	101	1778.8210	1
34	Glutathione S-transferase omega 1	O09131	GSTO1	6.91	27497.62	105	35.4	9/17	12GSAPPGPVPEGQIR25	92	1361.7330	1
35	Chloride intracellular channel 1	Q9Z1Q5	CLIC1	5.09	26881.63	134	50.6	9/19	209YLSNAYAR216	57	957.4930	1
36	Lectin, galactose binding, soluble 3	Q8C253	LGALS3	8.58	27414.73	120	29.5	10/19	225VAVNDHALLQYNHR238	109	1649.8550	1
37	Methylthioadenosine phosphorylase	Q9CQ65	MTAP	6.78	30930.69	132	31.4	10/13	134GVCHIPMAEPFCPK147	84	1642.7660	1
38	Proteasome subunit alpha type-4	Q9R1P0	PSMA4	7.58	29470.77	86	28.5	6/12	55LLDEVFSEK64	60	1226.6300	1
39	Peroxiredoxin 4	O08807	PRDX4	5.83	26476.01	120	40.1	8/16	190DYGVYLEDGSHTLR203	104	1624.7700	1
40	Peroxiredoxin 6	O08709	PRDX6	5.72	24739.45	230	66.5	13/17	42DFTPVCTTELGR53	72	1395.6610	1
41	triosephosphate isomerase 1	P17751	TPI1	5.56	32191.76	136	41.4	10/23	86DLGATVVVVLGHSESR99	87	1539.7810	1
42	RAN GTPase activating protein 1	P62826	RANGAP1	7.20	24291.91	161	40.3	11/21	61FNWVDTAGQEK71	67	1294.6140	1
43	Superoxide dismutase [Mn], mitochondrial	P09671	SOD2	7.30	22222.14	76	33.0	6/22	54HHAAYVNNLNATEEK68	111	1710.8270	1
44	Peroxiredoxin 1	P35700	PRDX1	8.26	22176.50	201	59.8	14/22	129GLFIIDDKILR140	89	1359.7870	1
45	Peptidyl-prolyl cis-trans isomerase A	P17742	PPIA	7.88	17840.15	147	63.4	11/19	77SIYGEKFEDENFILK91	115	1831.9290	1

Supplementary Table 3

Protein identification by Peptide Mass Fingerprint (PMF). For each identified spot mass spectrometry parameters are reported (average ratio, MW and pI, MASCOT score, protein coverage, n° matched over searched peaks, the sequence of the fragmented peptide and its MS/MS score, mass (m)/charge (z) ratio and charge status (z)), along with recommended protein name and Uniprot Knowledgebase accession number. To confirm identification, a MS/MS spectrum per protein was collected by MALDI ToF/ToF, as acceptance criterium.