

## The Protein Profile of the Human Immature T-cell Line CCRF-CEM

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**Abstract.** *The human immature T-cell line CCRF-CEM is widely used for all kinds of in vitro studies in biochemistry, biology, toxicology and medicine. Knowledge about protein expression is limited and no comprehensive study on the proteome of this cell type has been reported to date. Proteomics technologies were applied in order to analyse the proteins of the CEM cell line. The proteins were separated by two-dimensional (2-D) gel electrophoresis and analysed by MALDI-MS and MALDI-MS-MS following in-gel digestion with trypsin and, finally, protein identification was carried out by peptide mass fingerprint (PMF) and post source decay (PSD), respectively. Approximately 4,500 spots, excised from four 2-D gels, were analysed. The analysis resulted in the identification of about 1,150 proteins, the products of 451 different genes. The majority of the identified proteins were enzymes, regulatory proteins and transporters, while leukocyte markers and oncogenes were also included. The CCRF-CEM cell database today represents one of the largest 2-D databases for eukaryotic proteomes, forming the basis for future expressional studies at the protein level.*

Improved technologies, which involve robotic systems, automated mass spectra acquisition and protein identification, now allow us to create comprehensive protein maps and so introduce analytical tools and databases which may be used for further experimental procedures. Proteome

analysis of a biological sample such as a cell line can provide a clear image of the dynamics, the origin and the potential uses of the studied material, and hence can drive experimental approaches to new fields. In this regard, proteomic analysis, which combines two-dimensional (2-D) electrophoresis and mass spectrometry, finds a wide application in biological and biomedical sciences (1). The advent of proteomics technologies allows the generation of protein profiling and the construction of 2-D protein databases, from which derive information in a high-throughput mode about the state of the products of a genome, as well as changes related to these products, resulting from disorders or the effect of external factors (2-4). Such studies usually consist of two steps; analysis of a protein mixture by 2-D electrophoresis and identification of the proteins by mass spectrometry (MS) or other analytical methods (3, 5). 2-D protein databases are also useful tools in the quantification of differences in the protein levels caused by various diseases, providing information on the protein identity and abundance. The major objective of protein screening of tissue in healthy and diseased states is the detection of drug targets and the establishment of diagnostic markers (6, 7).

It is well known that immortalized malignant haematopoietic cell lines are widely used for the characterization and functional analysis of a large number of genes and proteins. These cell lines have become increasingly important tools in evaluating biological effects of newly developed inhibitory drugs, capable of interfering with critical signalling pathways or with altered proteins or transcripts resulting from the primary genetic changes. In past works of ours, by the application of the above proteomics technologies, we have constructed the 2-D protein database for the human HeLa cell line, including 297 different gene products (8).

The CCRF-CEM cell line is a T lymphoblastoid cell line derived from the peripheral blood buffy coat of a 4-year-old female with acute lymphoblastic leukaemia (9, 10). Two p53

*Abbreviations:* PMF, Peptide mass fingerprint; PSD, post source decay.

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mutations were described in that cell line, resulting in a prolonged half-life (approximately 12 h) of the mutant p53 compared to the wild-type, while the produced mutant p53 protein is fully functional (11, 12). Apart from the expression of mutant p53, CEM cells have the ability to express MDR-1, FAS and Bcl-2, as well as MT (13-15).

Studies indicate that the multidrug resistance phenotype, also expressed here in CEM, seems to associate with the overexpression of proteins which lead to decreased drug accumulation within human tumour cells (10). Thus, in cancer research, the specific cell line is extensively used as a model, investigating the anticancer drug action as well as the mechanisms of the regulation of the anticancer drug resistance (16, 17). Apparently CEM cells are well documented and used in numerous biochemical, biological and toxicological studies, facts that suggest that the specific cell line is an important cellular model for the study of carcinogenesis and in anticancer research (14, 18, 19). However, information on their proteome is limited. This study reports the construction of the 2-D protein database for the CCRF-CEM cell line, including 451 different gene products, forming one of the largest 2-D protein databases for eukaryotic proteomes to date.

## Materials and Methods

**Materials and reagents.** Immobilized pH-gradient (IPG) strips and IPG buffers were purchased from Biorad Laboratories (Hercules, CA, USA). Acrylamide/piperazine-di-acrylamide (PDA) solution (37.5:1, w/v) was purchased from Biosolve Ltd. (Valkenswaard, The Netherlands) and the other reagents for the polyacrylamide gel preparation from BioRad CHAPS was obtained from Roche Diagnostics (Mannheim, Germany), urea from AppliChem (Darmstadt, Germany), thiourea from Fluka (Buchs, Switzerland), 1, 4-dithioerythritol (DTE) and EDTA from Merck (Darmstadt, Germany). Except for CHAPS, which was kept at 23°C, the other reagents were kept at 4°C.

**Culture media.** The cell culture medium RPMI 1640 was used, supplemented with 10% heat-inactivated foetal bovine serum (FBS, Invitrogen Life Tech., Paisley, England), 100 U/ml penicillin, 100 µg/ml streptomycin, 2mM L-glutamine and 20 mM HEPES buffer (culture medium) (all derived from Biochrom, Berlin, Germany).

**Cell cultures.** The CCRF-CEM human immature T-cell line was obtained from the ECACC (Salisbury, UK). Cells ( $3 \times 10^5$  cells/ml) were cultured in culture medium at 37°C in a humidified atmosphere of 5% CO<sub>2</sub> in air. For each experiment, exponentially grown cells were harvested and resuspended ( $1 \times 10^6$  cells/ml) in fresh culture medium every three days.

**Two-dimensional gel electrophoresis.** CEM cells ( $40 \times 10^6$  cells) were washed twice with normal saline and resuspended in 0.5 ml of Urea buffer, consisting of 20 mM Tris, 7 M urea, 2 M thiourea, 4% CHAPS, 10 mM 1,4-dithioerythritol, 1 mM EDTA and a mixture of protease inhibitors [1 mM PMSF and 1 tablet complete™

(Roche Diagnostics) per 50 ml of suspension buffer] and phosphatase inhibitors (0.2 mM Na<sub>2</sub>VO<sub>3</sub> and 1 mM NaF). The suspension was left at room temperature for 1 h and centrifuged at 14000 x g for 60 min. The protein content in the supernatant was determined by the Coomassie blue method (20).

Additionally, the protein content was precisely quantitated using the EXPERION Automated Electrophoresis Station in combination with the Protein 260 Analysis Kit™ (Biorad), according to the manufacturer's instructions, and normalized protein quantity was used for 2-D gel electrophoresis.

2-D gel electrophoresis was performed as reported (3, 8). Samples of 1.0 mg total protein were applied on immobilized pH 4–7 non-linear and 3–10 non-linear gradient strips in sample cups at their basic and acidic ends. Focusing started at 250 V for 30 min and the voltage was gradually increased to 6000 V at 3 V/min and remained constant for a further 18 h. The second-dimensional separation was performed in 12% SDS-polyacrylamide gels (180 x 200x1.5 mm), running at 50 mA per gel in an PROTEAN apparatus (Biorad). After fixation with 50% methanol, containing 10% acetic acid for 2 h, the gels were stained overnight with colloidal Coomassie blue (Novex, San Diego, CA, USA), washed twice with H<sub>2</sub>O and scanned in a densitometer (GS-800 Calibrated Densitometer, Biorad).

**Peptide mass fingerprint (PMF) and post source decay (PSD).** Peptide analysis and protein identification were performed as previously described (21). Spots were automatically detected by Melanie 4.02 software on the Coomassie blue-stained gel, excised by the Proteiner SPII (Bruker Daltonics, Bremen, Germany), destained with 30% acetonitrile in 50 mM ammonium bicarbonate and dried in a speed vacuum concentrator (MaxiDry Plus, Heto, Allerød, Denmark). Each dried gel piece was rehydrated with 5 µl of 1 mM ammonium bicarbonate, containing 50 ng trypsin (Roche Diagnostics) and left for 16 h at room temperature. Twenty µl of 50% acetonitrile, containing 0.3% trifluoroacetic acid, were added to each gel piece and incubated for 15 min with constant shaking. The peptide mixture (1.5 µl) was simultaneously applied with 1 µl of matrix solution, consisting of 0.025% α-cyano-4-hydroxycinnamic acid (Sigma), standard peptides des-Arg-bradykinin (Sigma, 904.4681 Da) and adrenocorticotrophic hormone fragment 18-39 (Sigma, 2465.1989 Da) in 65% ethanol, 35% acetonitrile and 0.03% trifluoroacetic acid. Samples were analyzed for PMF with MALDI-MS in a time-of-flight mass spectrometer (Ultraflex, Bruker Daltonics). Matching peptide and protein searches were performed automatically, as described by Berndt *et al.* (21). Each spectrum was interpreted by the Mascot Software (Matrix Sciences Ltd., London, UK). For peptide identification, the monoisotopic masses were used and a mass tolerance of 0.0025% (25ppm) was allowed. Unmatched peptides or peptides with up to one miscleavage site were not considered. The peptide masses were compared with the theoretical peptide masses of all available proteins from all species using SWISS-PROT, IPI and MSDB databases. The probability score identified by the software was used as the criterion of the identification. Samples not identified by PMF (probability significance of  $p < 0.05$ ) were automatically selected for post source decay (PSD) MS-MS analysis with MALDI-MS-MS. The peptide masses chosen for PSD-MS-MS analysis had a signal intensity of >600 counts and were excluded from the trypsin autodigest, matrix and keratin peaks. The resulting PSD spectra were also interpreted by the Mascot Software and Mascot probability-based scores of

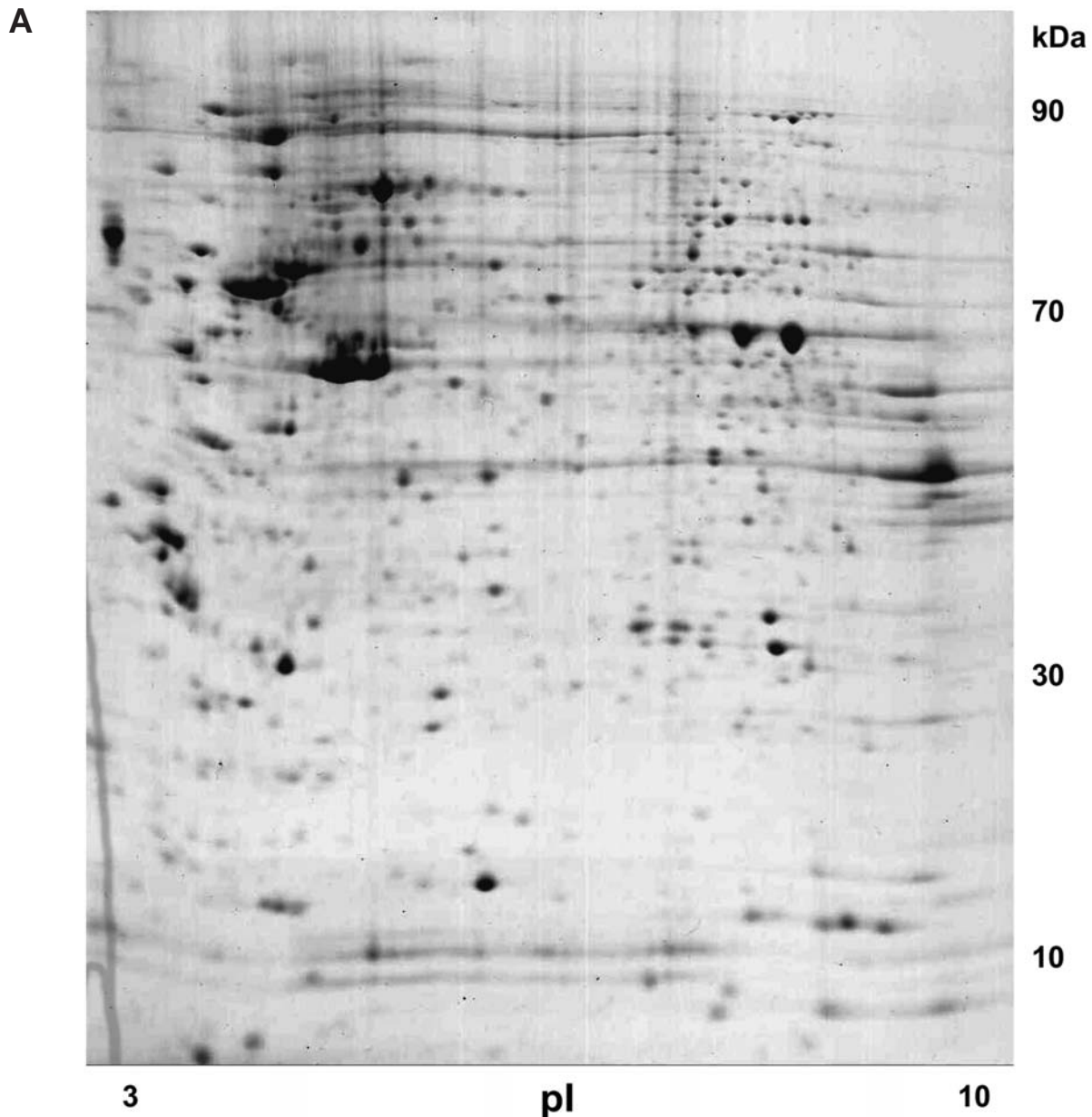


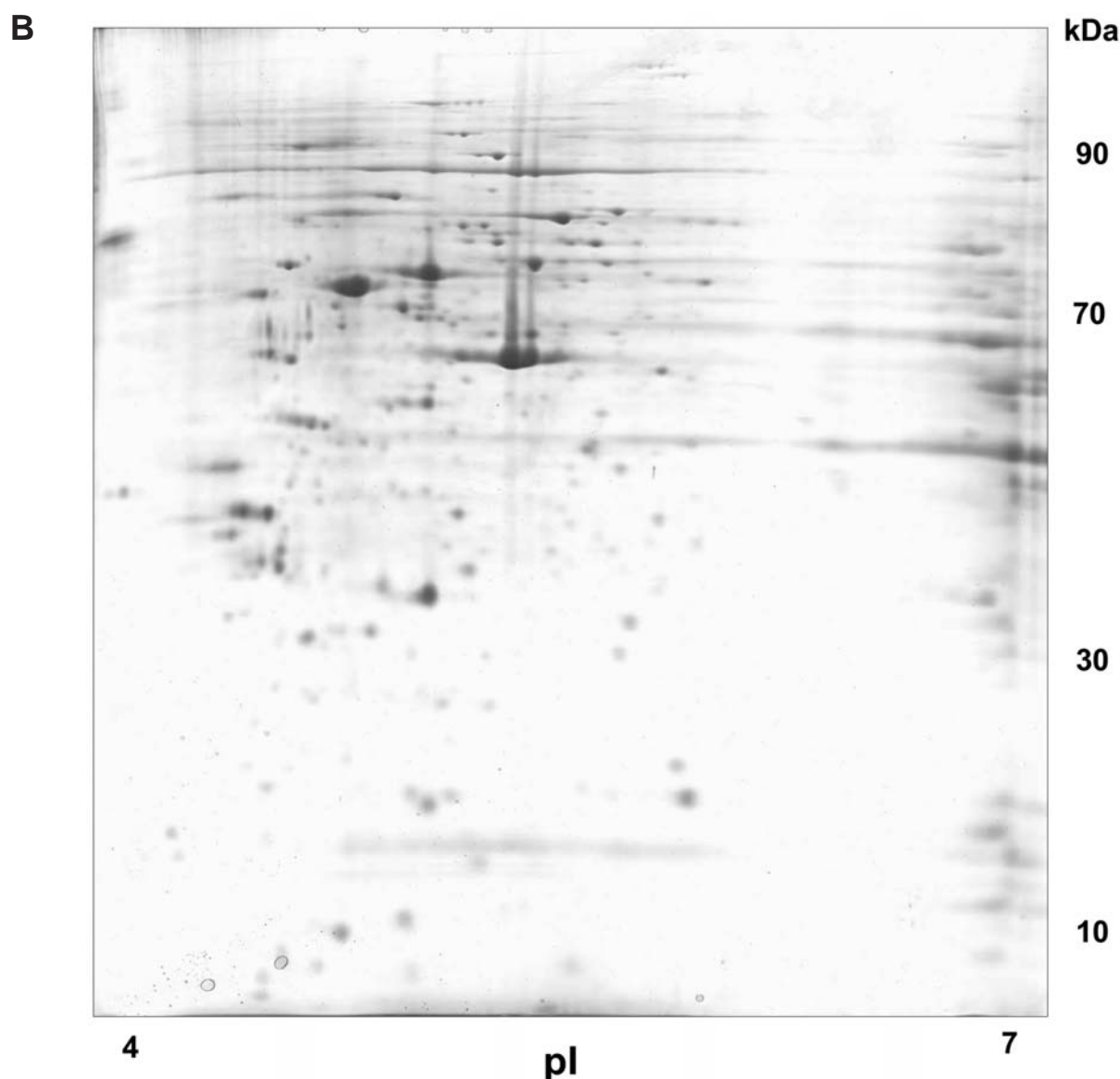
Figure 1. Two-dimensional gel analysis of total protein extract from the CCRF-CEM cells. Proteins were extracted and separated on IPG strip, followed by a 12% SDS-polyacrylamide gel, as described in Materials and Methods. The gels were stained with Coomassie blue. A: separation on IPG strip pH 3-10 non-linear, B: separation on IPG strip pH 4-7 non-linear.

$p < 0.02$  were considered significant. The identified proteins were automatically annotated on the gel image by the Proteinscape software (Bruker).

## Results

**Two-dimensional database.** The protein extract (1 mg) from the immature human T-cell line CCRF-CEM was separated by 2-D electrophoresis on narrow and broad pH range IPG strips and protein spots were visualized following staining

with colloidal Coomassie blue. Figure 1A and 1B show representative examples of the CEM cells proteins separated on a pH 3–10 non-linear (NL) and pH 4–7 NL IPG gel, respectively. Six pH 3–10 and four pH 4–7 IPG gels were analysed and a mean of 1008 spots per gel were detected using the 2-D ImageMaster software. About 4,500 spots were excised from two pH 3–10 and from two pH 4–7 gels and further analysed for protein identification following in-gel digestion with trypsin. Individual samples were analysed for PMF with MALDI-MS in a time-of-flight mass spectrometer

Figure 1. *continued*

and proteins were identified by the peptide mass matching, performed automatically as previously described (21). Samples not identified by PMF were automatically selected for PSD-MS-MS analysis with MALDI-MS-MS. The resulting PSD spectra were interpreted by the Mascot Software. The introduction of internal peptide standards to correct the measured peptide masses allowed the use of very narrow windows of mass tolerance (0.0025%), increasing the confidence of identification, as well as the total identification rate up to 85%. By that procedure, a total of 451 different gene products were identified, of which 380 were identified only in pH 3-10 gels and 71 were identified only in pH 4-7 gels. (Figures 3 and 4).

In Table I, the SWISS-PROT accession numbers are listed as well as the abbreviated and full names of the proteins, the theoretical Mr and pI values, as well as data from the mass spectrometry analysis, *i.e.* the numbers of matching peptides and the probability that the identification is random. As shown in that Table, the listed proteins were identified by 3 up to 42 matching peptides. Nine proteins were identified by 3 matching peptides and 23 proteins were matched by 4 peptides. The majority of the proteins were matched by 5 up to 12 peptides. One protein was identified by 41 peptides (P55072) and one by 42 peptides (Q13813). Respectively, the probability scores varied up to 359 for the lymphocyte cytosolic protein L-plastin (P13796).





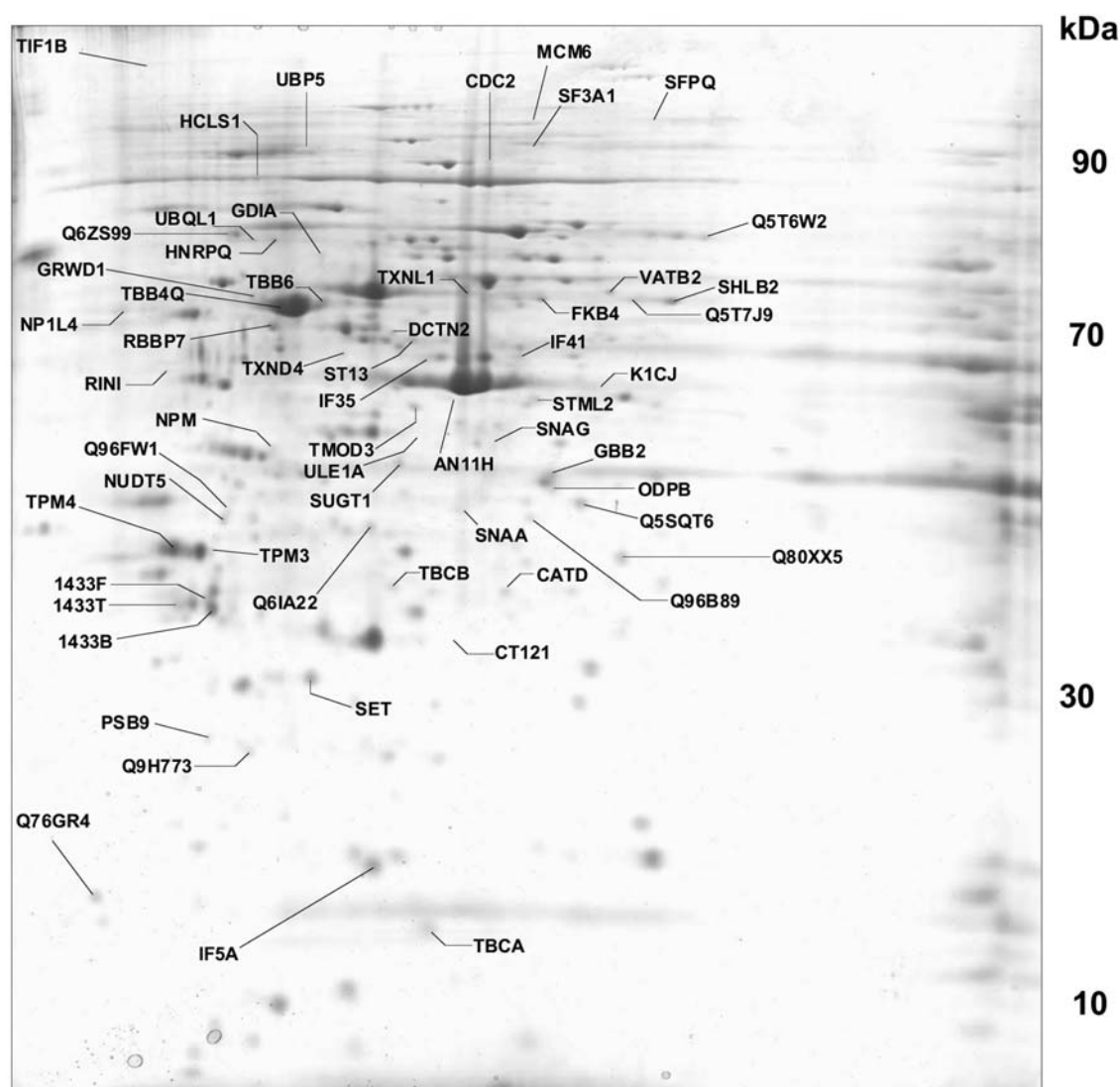


Figure 3. Spot identification of the Figure 1B gel, analysed by PMF and/or PSD-MS-MS. Only proteins exclusively identified in that pH range strip appear on the annotated gel image. The names of the represented proteins are listed in Table I.

proteasome-related proteins (20 proteins), DNA- and RNA-binding or associated proteins (54 proteins), proteins involved in signal transduction pathways (about 16), transport, transcription, translation *etc.* About 17 hypothetical or unknown gene products and many others were detected, for which to date there was no indication about their existence at the protein level. Figure 5 presents proteins distributed according to their function.

## Discussion

Proteomic analysis, which combines 2-D electrophoresis and MS analysis, has a wide application in biological and medical sciences, mainly for protein screening in cells and

tissues obtained from healthy and diseased states and, furthermore, for the discovery of novel diagnostic markers, pathways *etc.* (22, 23). The human immature T-cell line, CCRF-CEM, is known to be extensively used as a model, in numerous biochemical, biological and toxicological studies, while in cancer research it is used in the investigation of anticancer drug action and the mechanisms of regulation of anticancer drug resistance (10, 13, 15, 24, 25).

A major goal of this study was the generation of a comprehensive CCRF-CEM cell 2-D protein database that can be used for further proteomic investigations, forming the background for work on protein expression. That 2-D protein data base consists of 451 different gene products and represents one of the largest 2-D databases for human

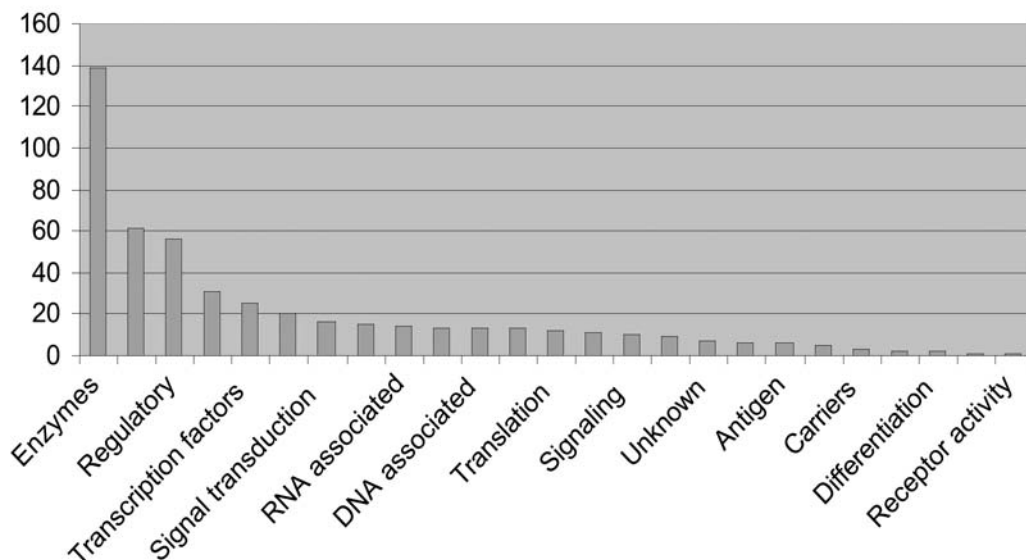


Figure 4. Function of the human immature T-cell line proteins. The proteins identified in this study were classified into functional groups. The annotated function for each protein is given in Table I.

cell proteomes. This became possible primarily by the use of the internal peptide standards which allowed the use of narrow windows of mass tolerance (0.0025%), thus increasing the confidence of identification by the PMF and, secondly, by the automated processing of the unidentified proteins on the PSD mode of the mass spectrometer (21). By that procedure, the identification was based on 4 or more (up to 42) matching peptides and the probability of a random identity assignment was usually lower than  $10^{-5}$ .

Several protein classes with several members of the individual pathways and cascades, signalling, cytoskeleton, proteasome, antioxidant, chaperone, nucleic acid binding and metabolism-related, were defined. Moreover, a series of hypothetical proteins and unknown/unspecified function proteins were identified, described only at the nucleic acid level. These findings, in correlation with the use of CEM cells as a model for anticancer drug treatment, suggest the importance of the represented 2-D map to the relevant experimental procedures.

Recent studies indicate that the CEM cell line has an immature T-cell phenotype expressing CD3, CD4, CD5 and CD7 (8, 9, 26). Consistent with that, we have identified 4 proteins (P27797, P24666, P13796 and P06702) expressed in T-cells including L-plastin, as well as 8 members of HLA antigens. L-plastin (P13796), a T-cell specific actin-bundling protein, stabilizes the actin filament structures which are crucial for the migration of T lymphocytes and for the interface between antigen-presenting cells and T lymphocytes (27). Additionally, in the identified proteins is included cofilin (P23528), which enhances actin polymerization and, as previously reported, collaborates

with L-plastin for the regulation of the dynamic rearrangements of the actin cytoskeleton, which are crucial for the function T lymphocytes. (28).

Recent studies have demonstrated that c-Myc provides protection against p53-mediated apoptosis and that multiple p53 target genes are down-regulated when c-Myc is present, suggesting that elevated levels of Myc counteract p53 activity in human tumor cells that lack ARF. This mechanism could help explain the c-Myc deregulation frequently found in cancer. (29, 30). As mentioned above, the CEM cell line derived from a child with acute lymphoblastic leukaemia and the specific cell line expresses a mutant form of p53. In relation to that, our 2-D database includes 4 proteins (NDKB, NDRG1, FUBP1 and RUVB1) related to myc expression, by which FUBP1 regulates myc expression by binding to a single-stranded far-upstream element (FUSE) upstream of the myc promoter and thus can act both as activator and repressor of transcription, which is in agreement with recent observations indicating that that haematological malignancies are characterized by fusion genes (31). Furthermore, the presented 2-D database includes a number of gene products related with oncogenesis and malignant transformation. This group contains 2 proteins related with *juc* (CRKL and SHUJUN). CRKL (P46109) may mediate the transduction of intracellular signals activating the RAS and JUN kinase signalling pathways, being also a substrate of the BCR-ABL tyrosine kinase. It is interesting that in CEM cells we identified the protein NPM (P06748), a NF-kappaB-binding protein, which is related to cell organization and biogenesis (32). NPM is

Table I. Proteins from the human immature T-cell line CCRF-CEM were extracted and separated by 2-D electrophoresis, as described in Materials and Methods. The proteins were identified by PMF and/or PSD, following in-gel digestion with trypsin. The spots representing the identified proteins are indicated in Figures 2 and 3 and are designated with their abbreviated names or the SWISS-PROT accession numbers or the accession numbers of the other databases. The theoretical Mr and pI values, the matching peptides and the probability of a random identification (Score), as well the annotated subcellular location and function are listed. Score is  $-10 \log(P)$ , where P is the probability that the observed match is a random event (MASCOT, <http://www.matrixscience.com>). Score >53 indicate  $p < 0.05$ .

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
O00217	NUIM_HUMAN	NUIM	NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3)	24202	6.27	53	4 of 26	Enzyme	
O00299	CLIC1_HUMAN	CLIC1	Chloride intracellular channel protein 1 (Nuclear chloride ion channel 27) (NCC27)	27116	4.82	217	14 of 25	Ion channel	Nuclear
O00303	IF35_HUMAN	IF35	Eukaryotic translation initiation factor 3 subunit 5 (eIF-3 epsilon) (eIF3 p47 subunit)	37654	5.12	62	7 of 27	RNA associated	Ribosome
O00625	PIR_HUMAN	PIR	Pirin	32207	6.92	53	4 of 24	Transcription	Nuclear
O14579	COPE_HUMAN	COPE	Coatome epsilon subunit (Epsilon-coat protein) (Epsilon-COP)	34351	4.8	56	7 of 18	Regulatory	Cytoplasmic
O14602	IF1AY_HUMAN	IF1AY	Eukaryotic translation initiation factor 1A, Y-chromosomal (eIF-1A Y isoform) (eIF-4C)	16415	4.84	53	5 of 38	Translation	
O14818	PSA7_HUMAN	PSA7	Proteasome subunit alpha type 7 (EC 3.4.25.1) (Proteasome subunit RC6-1) (Proteasome subunit XAPC7)	28040	8.73	53	5 of 21	Regulatory, enzyme	Cytoplasmic
O14979	O14979_HUMAN	O14979	JKTBP2 (Heterogeneous nuclear ribonucleoprotein D-like) (HNRPDL protein)	46580	9.98	56	7 of 25		
O14992	O14992_HUMAN	O14992	HS24/P52	53132	8.3	69	11 of 51		
O15463	O15463_HUMAN	O15463	PTPL1-associated RhoGAP	143613	6.72	58	6 of 10		
O43175	SERA_HUMAN	SERA	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) (3-PGDH)	57224	6.7	147	18 of 71	Enzyme	
O43396	TXNL1_HUMAN	TXNL1	Thioredoxin-like protein 1 (32 kDa thioredoxin-related protein)	32629	4.58	164	13 of 23	Enzyme, transport	Cytoplasmic
O43684	BUB3_HUMAN	BUB3	Mitotic checkpoint protein BUB3	37587	6.84	103	12 of 43		Nuclear
O43707	ACTN4_HUMAN	ACTN4	Alpha-actinin 4 (Non-muscle alpha-actinin 4) (F-actin cross linking protein)	105244	5.12	54	10 of 71	Structural	Nuclear
O60234	GLMG_HUMAN	GLMG	Glia maturation factor gamma (GMF-gamma)	16961	4.9	56	4 of 9	Signaling, cell growth	
O60361	NDK8_HUMAN	NDK8	Putative nucleoside diphosphate kinase (EC 2.7.4.6) (NDK) (NDP kinase)	15690	8.83	54	5 of 26	Enzyme	
O60506	HNRPO_HUMAN	HNRPO	Heterogeneous nuclear ribonucleoprotein Q (hnRNP Q) (hnRNP-Q)	69817	8.88	100	14 of 52		
O60814	H2BK_HUMAN	H2BK	Histone H2B K (HIRA-interacting protein 1)	13750	11	66	6 of 27		Nuclear
O75083	WDR1_HUMAN	WDR1	WD-repeat protein 1 (Actin interacting protein 1) (AIP1) (NORI-1)	66836	6.64	225	21 of 44		
O75347	TBCA_HUMAN	TBCA	Tubulin-specific chaperone A (Tubulin-folding cofactor A) (CFA) (TCP1-chaperonin cofactor A)	12772	4.94	58	5 of 17	Chaperone	
O75489	NUGM_HUMAN	NUGM	NADH-ubiquinone oxidoreductase 30 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-30KD) (CI-30KD)	30242	7.8	70	9 of 34	Enzyme	Mitochondrial
O75642	IF1AH_HUMAN	IF1AH	Putative eukaryotic translation initiation factor 1A (eIF-1A) (eIF-4C)	16433	4.73	60	6 of 38		
O75792	RNHL_HUMAN	RNHL	Ribonuclease HI large subunit (EC 3.1.26.4) (RNase HI large subunit) (RNase H(35))	33715	4.88	83	9 of 46	Enzyme	
O75832	PSD10_HUMAN	PSD10	26S proteasome non-ATPase regulatory subunit 10 (26S proteasome regulatory subunit p28) (Gankyrin)	24697	6.03	59	7 of 40	Regulatory	

continued



Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
O75874	IDHC_HUMAN	IDHC	Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1.1.1.42) (Oxalosuccinate decarboxylase)	46914	7	110	11 of 27	Enzyme	Cytoplasmic
O75947	ATP5H_HUMAN	ATP5H	ATP synthase D chain, mitochondrial (EC 3.6.3.14) (My032 protein)	18405	4.94	72	5 of 13	Enzyme	
O76003	TXNL2_HUMAN	TXNL2	Thioredoxin-like protein 2 (PKC-interacting cousin of thioredoxin) (PKC-theta-interacting protein)	37693	5.09	54	4 of 19	Regulatory	Cytoplasmic
O95336	6PGL_HUMAN	6PGL	6-phosphogluconolactonase (EC 3.1.1.31) (6PGL)	27814	5.95	76	7 of 28	Enzyme	
O95433	AHSA1_HUMAN	AHSA1	Activator of 90 kDa heat shock protein ATPase homolog 1 (AHA1) (p38) (HSPC322)	38421	5.22	109	9 of 23	Co-chaperone	Cytosolic
O95861	BPNT1_HUMAN	BPNT1	3'(2'),5'-bisphosphate nucleotidase 1 (EC 3.1.3.7) (Bisphosphate 3'-nucleotidase 1)	33713	5.41	83	9 of 36	Enzyme	
O95881	TLP19_HUMAN	TLP19	Thioredoxin-like protein p19 precursor (Endoplasmic reticulum protein ERp19) (UNQ713/PRO1376)	19364	5.1	67	6 of 33		
O96019	ACL6A_HUMAN	ACL6A	Actin-like protein 6A (53 kDa BRG1-associated factor A) (Actin-related protein Baf53a)	47943	5.3	64	6 of 35	Transcription	Nuclear
P00338	LDHA_HUMAN	LDHA	L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH muscle subunit) (LDH-M)	36819	8.45	111	18 of 77	Enzyme	Cytoplasmic
P00367	DHE3_HUMAN	DHE3	Glutamate dehydrogenase 1, mitochondrial precursor (EC 1.4.1.3) (GDH)	61701	7.91	169	23 of 64	Enzyme	Mitochondrial
P00491	PNPH_HUMAN	PNPH	Purine nucleoside phosphorylase (EC 2.4.2.1) (Inosine phosphorylase) (PNP)	32355	6.95	86	14 of 62	Enzyme	
P00505	AATM_HUMAN	AATM	Aspartate aminotransferase, mitochondrial precursor (EC 2.6.1.1) (Transaminase A)	47844	9.38	66	6 of 39	Enzyme	Mitochondrial
P00558	PGK1_HUMAN	PGK1	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protein 2) (PRP 2) (OK/SW-cl.110)	44854	8.27	171	16 of 37	Enzyme	Cytoplasmic
P00813	ADA_HUMAN	ADA	Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	40892	5.8	144	16 of 40	Enzyme	
P01889	1B07_HUMAN	1B07	HLA class I histocompatibility antigen, B-7 alpha chain precursor (MHC class I antigen B*7)	40777	5.65	62	6 of 47	Receptor activity	Membrane
P04040	CATA_HUMAN	CATA	Catalase (EC 1.11.1.6)	59815	7.41	103	13 of 43	Enzyme	Peroxisomal
P04075	ALDOA_HUMAN	ALDOA	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (Lung cancer antigen NY-LU-1)	39720	8.2	130	17 of 74	Enzyme	
P04083	ANXA1_HUMAN	ANXA1	Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindin 9) (P35)	38787	7.04	116	14 of 61	Binding, exocytosis	
P04350	TBB4_HUMAN	TBB4	Tubulin beta-4 chain (Tubulin 5 beta) (Tubulin beta-4)	50055	4.54	170	23 of 50	Structural	Microtubules
P04406	G3P2_HUMAN	G3P2	Glyceraldehyde-3-phosphate dehydrogenase, liver (EC 1.2.1.12) (GAPDH)	36070	8.73	115	17 of 76	Enzyme	Cytoplasmic
P04818	TYSY_HUMAN	TYSY	Thymidylate synthase (EC 2.1.1.45) (TS) (TSase) (OK/SW-cl.29)	35585	6.6	60	6 of 38	Enzyme	
P04908	H2AM_HUMAN	H2AM	Histone H2A.m (H2A/m)	14032	11.66	58	4 of 15		
P05388	RLA0_HUMAN	RLA0	60S acidic ribosomal protein P0 (L10E)	34422	5.77	67	6 of 21	Translation, RNA binding	Ribosomal

*continued*

Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
P06493	CDC2_HUMAN	CDC2	Cell division control protein 2 homolog (EC 2.7.1.37) (p34 protein kinase) (Cyclin-dependent)	34130	8.75	53	3 of 10	Enzyme	Nuclear
P06576	ATPB_HUMAN	ATPB	ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)	56524	5.07	127	24 of 85	Enzyme	Mito-chondrial
P06702	S10A9_HUMAN	S10A9	Calgranulin B (Migration inhibitory factor-related protein 14) (MRP-14) (P14) (Leukocyte L1 complex heavy chain)	13290	6.08	60	4 of 36	Signal transduction, cell-cell signaling	Cytoplasmic
P06733	ENOA_HUMAN	ENOA	Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	47350	7.46	184	17 of 25	Enzyme	Cytoplasmic
P06748	NPM_HUMAN	NPM	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Numatrin) (Nucleolar protein NO38)	32725	4.39	61	7 of 11	RNA binding, transcription,	Nuclear, nucleolus
P06753	TPM3_HUMAN	TPM3	Tropomyosin alpha 3 chain (Tropomyosin 3) (Tropomyosin gamma) (hTM5)	32855	4.38	56	8 of 39	Structural	Cytoskeletal
P06899	H2BR_HUMAN	H2BR	Histone H2B.r (H2B/r) (H2B.1)	13764	11	84	7 of 24	DNA associated, transcription	Nuclear
P07195	LDHB_HUMAN	LDHB	L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH heart subunit) (LDH-H)	36769	5.93	142	11 of 19	Enzyme	Cytoplasmic
P07237	PDIA1_HUMAN	PDIA1	Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-hydroxylase beta subunit) (Cellular thyroid hormone binding protein) (p55)	57479	4.49	347	27 of 39	Enzyme	Endoplasmic reticulum
P07339	CATD_HUMAN	CATD	Cathepsin D precursor (EC 3.4.23.5)	45036	6.5	62	8 of 23	Enzyme	Lysosomal
P07355	ANXA2_HUMAN	ANXA2	Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (Chromobindin 8) (p36)	38676	7.91	139	12 of 26	Binding	Membrane
P07437	TBB2_HUMAN	TBB2	Tubulin beta-2 chain (OK/SW-cl.56)	50095	4.52	293	32 of 50	Structural	Cytoplasmic
P07737	PROF1_HUMAN	PROF1	Profilin-1 (Profilin I)	15084	8.46	115	13 of 62	Structural	
P07741	APT_HUMAN	APT	Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT)	19477	5.7	96	12 of 32	Enzyme	
P07900	HS90A_HUMAN	HS90A	Heat shock protein HSP 90-alpha (HSP 86)	84888	4.66	265	35 of 69	Chaperone	Cytoplasmic
P07910	HNRPC_HUMAN	HNRPC	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1 / hnRNP C2)	33724	4.69	80	9 of 21	RNA splicing	Nuclear
P07954	FUMH_HUMAN	FUMH	Fumarate hydratase, mitochondrial precursor (EC 4.2.1.2) (Fumarase)	54773	9.17	111	13 of 44	Enzyme	Mito-chondrial and cytoplasmic
P08107	HSP71_HUMAN	HSP71	Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2)	70294	5.31	145	16 of 31	Chaperone	
P08133	ANXA6_HUMAN	ANXA6	Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III) (Chromobindin 20)	76036	5.28	68	14 of 67	Regulatory, transport, binding	Cytoplasmic, nuclear
P08238	HS90B_HUMAN	HS90B	Heat shock protein HSP 90-beta (HSP 84) (HSP 90)	83423	4.68	178	26 of 69	Chaperone	
P08670	VIME_HUMAN	VIME	Vimentin	53545	4.77	245	25 of 39		
P08758	ANXA5_HUMAN	ANXA5	Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I) (CBP-I) (Placental anticoagulant protein I)	35840	4.66	74	11 of 72		
P08865	RSSA_HUMAN	RSSA	40S ribosomal protein SA (p40)	32816	4.51	128	14 of 52	Structural	Cytoplasmic

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Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
P09104	ENOG_HUMAN	ENOG	(34/67 kDa laminin receptor) (Colon carcinoma laminin-binding) Gamma enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase)	47450	4.65	200	20 of 38	Enzyme	Cytoplasmic
P09211	GSTP1_HUMAN	GSTP1	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1)	23438	5.3	170	11 of 18	Enzyme	
P09382		LEG1	Galectin-1 (Beta-galactoside-binding lectin L-14-I) (Lactose-binding lectin 1) (S-Lac lectin)	14917	5.15	75	5 of 16		
P09429	HMG1_HUMAN	HMG1	High mobility group protein 1 (HMG-1) (High mobility group protein B1)	24918	5.42	107	10 of 24		
P09622	DLDH_HUMAN	DLDH	Dihydrolipoyl dehydrogenase, mitochondrial precursor (EC 1.8.1.4) (Dihydrolipoamide dehydrogenase) (Glycine cleavage system L protein)	54150	8.6	66	13 of 64	Enzyme	Mito-chondrial
P09651	ROA1_HUMAN	ROA1	Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein)	38805	9.56	123	13 of 50		Nuclear
P10644	KAP0_HUMAN	KAP0	cAMP-dependent protein kinase type I-alpha regulatory subunit (Tissue-specific extinguisher-1)	43183	5	60	9 of 59		
P10768	ESTD_HUMAN	ESTD	Esterase D (EC 3.1.1.1)	31955	7.02	88	9 of 32	Enzyme	Cytoplasmic vesicles
P10809	CH60_HUMAN	CH60	60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (He	61187	5.55	185	24 of 51		Cytoplasmic
P11021	GRP78_HUMAN	GRP78	78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein)	72402	4.8	308	32 of 59	Binding	Endoplasmic reticulum
P11142	HSP7C_HUMAN	HSP7C	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)	71082	5.16	295	35 of 69	Chaperone	Cytoplasmic, nuclear
P11177	ODPB_HUMAN	ODPB	Pyruvate dehydrogenase E1 component beta subunit, mitochondrial precursor (EC 1.2.4.1) (PD	39536	6.63	55	7 of 22	Enzyme	Mitochondrial
P11310	ACADM_HUMAN	ACADM	Acyl-CoA dehydrogenase, medium-chain specific, mitochondrial precursor (EC 1.3.99.3) (MCAD)	47014	8.51	95	10 of 30	Enzyme	Mitochondrial
P11413	G6PD_HUMAN	G6PD	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD)	59553	6.88	164	20 of 65	Enzyme	
P11586	C1TC_HUMAN	C1TC	C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) [Includes: Methylenetetrahydrofolate dehydrogenase)	102048	7.32	70	12 of 44	Enzyme	Cytoplasmic
P12004	PCNA_HUMAN	PCNA	Proliferating cell nuclear antigen (PCNA) (Cyclin)	29092	4.31	128	11 of 22	Cell cycle	Nuclear
P12268	IMD2_HUMAN	IMD2	Inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP dehydrogenase 2) (IMPDH-II)	56225	6.9	162	19 of 60	Enzyme	
P13010	KU86_HUMAN	KU86	ATP-dependent DNA helicase II, 80 kDa subunit (Lupus Ku autoantigen protein p86) (Ku86) (Ku80)	83091	5.58	57	9 of 53	DNA binding, DNA recombination	Nuclear
P13489	RINI_HUMAN	RINI	Placental ribonuclease inhibitor (Ribonuclease/angiogenin inhibitor) (RAI) (Ribonuclease/angiogenin inhibitor)	51634	4.44	76	9 of 43	RNA associated	Cyto-plasmic
P13639	EF2_HUMAN	EF2	Elongation factor 2 (EF-2)	96115	6.82	133	23 of 60	RNA associated, translation	Ribo-somal
P13645	K1CJ_HUMAN	K1CJ	Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	59710	4.87	71	7 of 19	Structural	Cytoskeleton

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Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
P13667	PDIA4_HUMAN	PDIA4	Protein disulfide-isomerase A4 precursor (EC 5.3.4.1) (Protein ERp-72) (ERp72)	73229	4.7	104	18 of 70	Enzyme	Endoplasmic reticulum
P13693	TCTP_HUMAN	TCTP	Translationally controlled tumor protein (TCTP) (p23) (Histamine-releasing factor) (HRF)	19696	4.57	72	6 of 12	Cell life, cell survival	Cytoplasmic
P13796	PLSL_HUMAN	PLSL	L-plastin (Lymphocyte cytosolic protein 1) (LCP-1) (LC64P)	70815	4.96	359	31 of 38	Binding	Cytoplasmic
P13804	ETFA_HUMAN	ETFA	Electron transfer flavoprotein alpha-subunit, mitochondrial precursor (Alpha-ETF)	35399	8.57	88	7 of 38	Transport	Mitochondrial
P14317			Hematopoietic lineage cell specific protein (Hematopoietic cell-specific LYN substrate 1)	54079	4.45	60	8 of 39		
P14550	AK1A1_HUMAN	AK1A1	Alcohol dehydrogenase [NADP+] (EC 1.1.1.2) (Aldehyde reductase)	36760	6.79	97	9 of 30	Enzyme	Cytosolic
P14618	KPYM_HUMAN	KPYM	(Aldo-keto reductase family1 member A1) Pyruvate kinase, isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase muscle isozyme)	58339	7.94	144	18 of 62	Enzyme	Cytosolic
P14625	ENPL_HUMAN	ENPL	Endoplasmic precursor (94 kDa glucose-regulated protein) (GRP94) (gp96 homolog) (Tumor rejection antigen 1)	92696	4.48	198	27 of 44		Endoplasmic reticulum
P14866	HNRPL_HUMAN	HNRPL	Heterogeneous nuclear ribonucleoprotein L (hnRNP L) (P/OKcl.14)	60719	7.13	140	19 of 52	Structural	Nuclear
P15311	EZRI_HUMAN	EZRI	Ezrin (p81) (Cytovillin) (Villin 2)	69338	6.17	92	15 of 47	Structural	Membrane
P15531	NDKA_HUMAN	NDKA	Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A) (NDP kinase A) (Tumor metastatic inhibition factor nm23)	17308	6.11	90	8 of 41	Enzyme	Nuclear, cytoplasmic
P16949	STMN1_HUMAN	STMN1	Stathmin (Phosphoprotein p19) (pp19) (Oncoprotein 18) (Op18) (Leukemia-associated phosphoprotein p18)	17160	5.8	80	10 of 56	Signal transduction, cell growth	Cytoplasmic
P17174	AATC_HUMAN	AATC	Aspartate aminotransferase, cytoplasmic (EC 2.6.1.1) (Transaminase A) (Glutamate oxaloacetate transaminase-1)	46116	6.6	115	15 of 52	Enzyme	Cytoplasmic
P17980	PRS6A_HUMAN	PRS6A	26S protease regulatory subunit 6A (TAT-binding protein 1) (TBP-1) (Proteasome subunit P50)	49457	4.87	181	21 of 32	Transcription	Cytoplasmic, nuclear
P17987	TCPA_HUMAN	TCPA	T-complex protein 1, alpha subunit (TCP-1-alpha) (CCT-alpha)	60818	5.96	74	7 of 28	Structural	Cytoplasmic
P18465	1B57_HUMAN	1B57	HLA class I histocompatibility antigen, B-57 alpha chain precursor (MHC class I antigen B*57)	40541	6.25	54	7 of 47	Antigen	Membrane
P18669	PGAM1_HUMAN	PGAM1	Phosphoglycerate mutase 1 (EC 5.4.2.1) (EC 5.4.2.4) (EC 3.1.3.13) (Phosphoglycerate mutase isozyme B)	28768	7.22	126	14 of 69	Enzyme	Cytosolic
P19105	MLRM_HUMAN	MLRM	Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC)	19707	4.4	93	5 of 6	Regulatory	
P19338	NUCL_HUMAN	NUCL	Nucleolin (Protein C23)	76224	4.31	141	18 of 51	Transcription	Nuclear
P19623			Spermidine synthase (EC 2.5.1.16) (Putrescine aminopropyltransferase) (SPDSY)	34372	5.17	84	7 of 22		
P20073	ANXA7_HUMAN	ANXA7	Annexin A7 (Annexin VII) (Synexin) (OK/SW-cl.95)	52990	5.32	58	8 of 50	Binding	Membrane
P20618	PSB1_HUMAN	PSB1	Proteasome subunit beta type 1 (EC 3.4.25.1) (Proteasome component C5) (Macropain subunit C5)	26700	8.29	67	6 of 19	Regulatory, enzyme	Cytoplasmic, nuclear
P20700	LAM1_HUMAN	LAM1	Lamin B1	66521	4.82	293	33 of 46	Structural	Nuclear membrane
P21281	VATB2_HUMAN	VATB2	Vacuolar ATP synthase subunit B, brain isoform (EC 3.6.3.14) (V-ATPase B2 subunit) (Vacuolar proton pump B isoform 2)	56807	5.55	79	7 of 15	Enzyme, transport	Endo-membrane

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Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
P21333	FLNA_HUMAN	FLNA	Filamin A (Alpha-filamin) (Filamin 1) (Endothelial actin-binding protein) (Actin-binding protein 280)	283322	6	68	18 of 47	Signal transducer	Cytoplasmic, cytoskeletal
P21399	IREB1_HUMAN	IREB1	Iron-responsive element binding protein 1 (IRE-BP 1) (Iron regulatory protein 1) (IRP1) (Ferritin repressor protein) (Aconitate hydratase) (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase)	98849	6.2	98	18 of 46	Binding	Cytoplasmic
P21796	VDAC1_HUMAN	VDAC1	Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1)	30736	8.89	111	9 of 28	Transport	Mitochondrial and membranous
P22061	PIMT_HUMAN	PIMT	Protein-L-isoaspartate(D-aspartate) O-methyltransferase (EC 2.1.1.77) (Protein-beta-aspartate methyltransferase)	24674	7.25	56	4 of 21	Enzyme	Cytoplasmic
P22234	PUR6_HUMAN	PUR6	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase)]	47659	7.26	72	7 of 22	Enzyme	
P22314	UBE1_HUMAN	UBE1	Ubiquitin-activating enzyme E1 (A1S9 protein)	118857	5.5	176	22 of 54	Enzyme	
P22392	NDKB_HUMAN	NDKB	Nucleoside diphosphate kinase B (EC 2.7.4.6) (NDK B) (NDP kinase B) (nm23-H2) (C-myc purine-binding transcription factor PUF)	17400	8.69	99	8 of 26	Enzyme, transcription	Nuclear
P22626	ROA2_HUMAN	ROA2	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2 / hnRNP B1)	37463	9.26	142	17 of 74	Transcription	Nuclear, cytoplasmic
P23246	SFPQ_HUMAN	SFPQ	Splicing factor, proline-and glutamine-rich (Polypyrimidine tract-binding protein-associated splicing factor)	76215	9.95	55	6 of 37	RNA associated	Nuclear
P23258	TBG1_HUMAN	TBG1	Tubulin gamma-1 chain (Gamma-1 tubulin) (Gamma-tubulin complex component 1) (GCP-1)	51479	6.06	93	10 of 33	Structural, binding	Centrosome, microtubule
P23381	SYW_HUMAN	SYW	Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase) (TrpRS) (IFP53) (hWRS)	53473	6.15	54	5 of 24	Enzyme, cell proliferation, translation	Cytoplasmic
P23526	SAHH_HUMAN	SAHH	Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase)	48124	6.29	106	10 of 25	Enzyme	Cytoplasmic
P23527	H2BN_HUMAN	H2BN	Histone H2B.n (H2B/n) (H2B.2)	13766	11	84	7 of 24	DNA binding	Nuclear
P23528	COF1_HUMAN	COF1	Cofilin, non-muscle isoform (Cofilin-1) (18 kDa phosphoprotein) (p18)	18587	8.29	118	11 of 39	Signal transduction, structural	Nuclear
P24666	PPAC_HUMAN	PPAC	Low molecular weight phosphotyrosine protein phosphatase (EC 3.1.3.48) (LMW-PTP) (Low molecular weight cytosolic acid phosphatase)	18355	6.73	87	8 of 40	Enzyme	Membranous
P25705	ATPA_HUMAN	ATPA	ATP synthase alpha chain, mitochondrial precursor (EC 3.6.3.14)	59827	9.56	97	14 of 51	Enzyme, transporter	Mitochondrial
P25786	PSA1_HUMAN	PSA1	Proteasome subunit alpha type 1 (EC 3.4.25.1) (Proteasome component C2) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome nu chain) (30 kDa prosomal protein) (PROS-30)	P25786	6.2	63	8 of 42	Regulatory, enzyme, RNA binding	Cytoplasmic, nuclear
P25787	PSA2_HUMAN	PSA2	Proteasome subunit alpha type 2 (EC 3.4.25.1) (Proteasome component C3) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3)	25767	7.7	55	5 of 32	Regulatory, enzyme	Cytoplasmic, nuclear

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Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
P25788	PSA3_HUMAN	PSA3	Proteasome subunit alpha type 3 (EC 3.4.25.1) (Proteasome component C8) (Macropain subunit alpha type 3)	28512	4.97	76	8 of 37	Regulatory, enzyme	Cytoplasmic, nuclear
P26038	MOES_HUMAN	MOES	Moesin (Membrane-organizing extension spike protein)	67760	6.32	89	12 of 37	Structural	Membranic, cytoskeletal
P26583	HMG2_HUMAN	HMG2	High mobility group protein 2 (HMG-2)	24058	8.04	95	10 of 32	Transcription, DNA associated	Nuclear
P26641	EF1G_HUMAN	EF1G	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) (PRO1608)	50298	6.64	57	10 of 74	Translation	Nuclear
P27348	1433T_HUMAN	1433T	14-3-3 protein tau (14-3-3 protein theta) (14-3-3 protein T-cell) (HS1 protein)	28031	4.41	85	7 of 14	Enzyme	Cytoplasmic
P27797	CRTC_HUMAN	CRTC	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERp60) (grp60)	48282	4.04	114	9 of 18	DNA binding, transcription	Endoplasmic reticulum
P28001	H2AA_HUMAN	H2AA	Histone H2A.a (H2A/a) (H2A.2)	13995	11.66	58	4 of 15	DNA binding	Nucleosome
P28062	PSB8_HUMAN	PSB8	Proteasome subunit beta type 8 precursor (EC 3.4.25.1) (Proteasome component C13) (Macropain subunit C13)	30676	7.83	53	4 of 23	Regulatory, enzyme	Cytoplasmic, nuclear
P28065	PSB9_HUMAN	PSB9	Proteasome subunit beta type 9 precursor (EC 3.4.25.1) (Proteasome chain 7)	23363	4.66	57	7 of 15	Regulatory, enzyme	Cytoplasmic, nuclear
P28066	PSA5_HUMAN	PSA5	Proteasome subunit alpha type 5 (EC 3.4.25.1) (Proteasome zeta chain)	26565	4.45	106	8 of 17	Regulatory, enzyme	Cytoplasmic, nuclear
P28331	NUAM_HUMAN	NUAM	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3)	80490	6.11	72	10 of 34	Enzyme	Mitochondrial
P28838	AMPL_HUMAN	AMPL	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase)	53005	6.72	130	16 of 51	Enzyme	Cytoplasmic
P29401	TKT_HUMAN	TKT	Transketolase (EC 2.2.1.1) (TK)	68518	7.73	105	15 of 56	Enzyme	Cytoplasmic, nuclear
P29692	EF1D_HUMAN	EF1D	Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4)	31085	4.63	119	14 of 36	Translation	
P30040	ERP29_HUMAN	ERP29	Endoplasmic reticulum protein ERp29 precursor (ERp31) (ERp28)	28993	7.5	72	8 of 28	Transport	Endoplasmic reticulum
P30041	PRDX6_HUMAN	PRDX6	Peroxiredoxin 6 (EC 1.11.1.-) (Antioxidant protein 2) (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase A2)	25002	6.29	118	12 of 65	Enzyme	Cytoplasmic, lysosomal
P30048	PRDX3_HUMAN	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial precursor (EC 1.11.1.-) (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (MERS protein homolog) (HBC189) (PRX III)	27693	8.9	58	7 of 46	Enzyme	Mitochondrial
P30084	ECHM_HUMAN	ECHM	Enoyl-CoA hydratase, mitochondrial precursor (EC 4.2.1.17) (Short chain enoyl-CoA hydratase)	31807	8.19	71	6 of 21	Enzyme	Mitochondrial
P30086	PEBP_HUMAN	PEBP	Phosphatidylethanolamine-binding protein (PEBP) (Prostatic binding protein) (HCNPpp) (Neuropolypeptide h3)	21026	7.65	74	7 of 44	Binding	Cytoplasmic
P30101	PDIA3_HUMAN	PDIA3	Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-60) (ERp60)	57145	6.28	221	22 of 43	Enzyme	Endoplasmic reticulum
P30153	2AAA_HUMAN	2AAA	Serine/threonine protein phosphatase 2A, 65 kDa regulatory subunit A, alpha isoform (PP2A, subunit A, PR65-alpha isoform) (PP2A, subunit A, R1-alpha isoform) (Medium tumor antigen-associated 61 kDa protein)	65092	4.8	123	12 of 38	Regulatory	Cytosolic, nuclear, mitochondrial

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Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
P30460	1B08_HUMAN	1B08	HLA class I histocompatibility antigen, B-8 alpha chain precursor (MHC class I antigen B*8)	40647	5.44	76	7 of 47	Antigen	Membranic
P30520	PURA2_HUMAN	PURA2	Adenylosuccinate synthetase 2 (EC 6.3.4.4) (IMP--aspartate ligase 2) (AdSS 2) (AMPSase 2)	50464	6.52	53	5 of 39	Enzyme	Cytoplasmic
P31146	COR1A_HUMAN	COR1A	Coronin-1A (Coronin-like protein p57) (Coronin-like protein A) (CLIPINA) (Tryptophan aspartate-containing coat protein)	51678	6.67	101	15 of 65	Structural	Cytoplasmic
P31150	GDIA_HUMAN	GDIA	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (GDI-1) (XAP-4) (Oligophrenin 2)	51177	4.75	84	8 of 21	Signaling, transport, regulatory	Cytoplasmic
P31153	METK_HUMAN	METK	S-adenosylmethionine synthetase gamma form (EC 2.5.1.6) (Methionine adenosyltransferase) (AdoMet synthetase) (MAT-II)	43661	6	57	8 of 44	Enzyme	
P31930	UQCR1_HUMAN	UQCR1	Ubiquinol-cytochrome-c reductase complex core protein I, mitochondrial precursor (EC 1.10.2.2.)	53269	6.32	174	16 of 25	Enzyme	Mitochondrial membrane
P31939	PUR9_HUMAN	PUR9	Bifunctional purine biosynthesis protein PURH (OK/SW-cl.86) [Includes: Phosphoribosylamino-phosphoribosylaminoimidazole-carboxamide formyltransferase)	65088	6.7	225	26 of 67	Enzyme	Cytoplasmic
P31943	HNRH1_HUMAN	HNRH1	Heterogeneous nuclear ribonucleoprotein H (hnRNP H)	49352	6.25	120	12 of 35	RNA binding	Nuclear;
P31946	1433B_HUMAN	1433B	14-3-3 protein beta/alpha (Protein kinase C inhibitor protein-1) (KCIP-1) (Protein 1054)	28047	4.47	76	10 of 26	Enzyme, regulatory, signaling	nucleoplasm Cytoplasmic
P31948	STIP1_HUMAN	STIP1	Stress-induced-phosphoprotein 1 (STI1) (Hsc70/Hsp90-organizing protein) (Hop) (Transformation-sensitive protein IEF SSP 3521)	63226	6.78	175	29 of 78	Chaperone	Nuclear, Golgi
P32119	PRDX2_HUMAN	PRDX2	Peroxiredoxin 2 (EC 1.11.1.-) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	22049	5.75	94	8 of 35	Enzyme	Cytoplasmic
P33316	DUT_HUMAN	DUT	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial precursor (EC 3.6.1.23) (dUTPase)	26974	10.01	89	9 of 33	Enzyme	Nuclear, Mitochondrial
P33778	H2BF_HUMAN	H2BF	Histone H2B.f (H2B/f) (H2B.1)	13810	11	84	7 of 24	DNA binding, structural, transcription	Nuclear
P33993	MCM7_HUMAN	MCM7	DNA replication licensing factor MCM7 (CDC47 homolog) (P1.1-MCM3)	81883	6.38	59	12 of 61	Cell cycle control, DNA binding	Nuclear
P34897	GLYM_HUMAN	GLYM	Serine hydroxymethyltransferase, mitochondrial precursor (EC 2.1.2.1) (Serine methylase) (Glycine hydroxymethyltransferase)	56413	8.67	53	7 of 35	Enzyme	Mitochondrial
P34932	HSP74_HUMAN	HSP74	Heat shock 70 kDa protein 4 (Heat shock 70-related protein APG-2) (HSP70RY)	95095	4.9	301	37 of 58	Chaperone	Cytoplasmic
P35232	P35232	P35232	Prohibitin	29842	5.46	135	9 of 17	Transcription, cell proliferation	Cytoplasmic

*continued*

Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
P35998	PRS7_HUMAN	PRS7	26S protease regulatory subunit 7 (MSS1 protein)	48871	5.65	56	8 of 35	Chaperone	Cytoplasmic
P36551	HEM6_HUMAN	HEM6	Coproporphyrinogen III oxidase, mitochondrial precursor (EC 1.3.3.3) (Coproporphyrinogenase) (Coprogen oxidase) (COX)	50175	9.7	64	10 of 38	Enzyme	Mitochondrial
P36957	ODO2_HUMAN	ODO2	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial precursor (EC 2.3.1.61) (Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2) (E2K)	48640	9.8	76	8 of 38	Enzyme	Mitochondrial
P37802	TAGL2_HUMAN	TAGL2	Transgelin-2 (SM22-alpha homolog)	22548	8.45	79	10 of 57	Transcription	Cytoplasmic
P37837	TALDO_HUMAN	TALDO	Transaldolase (EC 2.2.1.2)	37687	6.8	86	13 of 51	Enzyme	
P38117	ETFB_HUMAN	ETFB	Electron transfer flavoprotein beta-subunit (Beta-ETF)	28054	8.31	59	6 of 23	Transport, carrier	
P38646	GRP75_HUMAN	GRP75	Stress-70 protein, mitochondrial precursor (75 kDa glucose regulated protein) (GRP 75)	73919	6.01	298	35 of 59	Chaperone, regulatory, transcription	Mitochondrial
P38919	DDX48_HUMAN	DDX48	Probable ATP-dependent helicase DDX48 (DEAD-box protein 48) (Eukaryotic initiation factor 4A-like NUK-34) (Nuclear matrix protein 265) (hNMP 265) (Eukaryotic translation initiation factor 4A isoform 3)	46871	6.3	60	8 of 38	Regulatory	Nuclear
P39687	AN32A_HUMAN	AN32A	Acidic leucine-rich nuclear phosphoprotein 32 family member A (Potent heat-stable protein phosphatase 2A inhibitor I1PP2A)	28682	3.72	71	8 of 44	Signaling	Nuclear, cytoplasmic
P40121	CAPG_HUMAN	CAPG	Macrophage capping protein (Actin-regulatory protein CAP-G)	38778	6.18	53	5 of 10		
P40227	TCPZ_HUMAN	TCPZ	T-complex protein 1, zeta subunit (TCP-1-zeta) (CCT-zeta) (CCT-zeta-1) (Tcp20) (HTR3)	58312	6.65	86	14 of 52	Chaperone	Cytoplasmic
P40925	MDHC_HUMAN	MDHC	Malate dehydrogenase, cytoplasmic (EC 1.1.1.37)	36500	7.45	79	9 of 38	Enzyme	Cytoplasmic
P41250	SYG_HUMAN	SYG	Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS)	83140	6.7	64	9 of 42	Enzyme	Cytoplasmic
P43243	MATR3_HUMAN	MATR3	Matrin 3	95077	6.19	64	10 of 39	Structural	Nuclear
P43487	RANG_HUMAN	RANG	Ran-specific GTPase-activating protein (Ran binding protein 1) (RanBP1)	23466	4.96	77	7 of 18	Regulatory	
P43686	PRS6B_HUMAN	PRS6B	26S protease regulatory subunit 6B (MIP224) (MB67 interacting protein) (TAT-binding protein-7)	47450	4.84	65	10 of 62	Chaperone	Cytoplasmic
P45880	VDAC2_HUMAN	VDAC2	Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2) (Outer mitochondrial membrane protein porin 2)	38638	6.76	91	10 of 48	Transport	Mitochondrial
P45974	UBP5_HUMAN	UBP5	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.1.2.15) (Ubiquitin thiolesterase 5) (Ubiquitin-specific processing protease 5)	96637	4.65	66	9 of 28	Enzyme	Lysosomic
P46109	CRKL_HUMAN	CRKL	Crk-like protein	33869	6.73	53	4 of 19	Signal transduction	Structural
P47756	CAPZB_HUMAN	CAPZB	F-actin capping protein beta subunit (CapZ beta)	31484	5.23	157	13 of 22		
P47813	IF1AX_HUMAN	IF1AX	Eukaryotic translation initiation factor 1A, X-chromosomal (eIF-1A X isoform) (eIF-4C)	16433	4.84	72	7 of 38	Translation	

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Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
P48637	GSHB_HUMAN	GSHB	Glutathione synthetase (EC 6.3.2.3) (Glutathione synthase) (GSH synthetase) (GSH-S)	52523	5.73	71	6 of 15	Enzyme	
P48643	TCPE_HUMAN	TCPE	T-complex protein 1, epsilon subunit (TCP-1-epsilon) (CCT-epsilon)	60088	5.34	136	21 of 47	Chaperone	Cytoplasmic, cytosolic
P48735	IDHP_HUMAN	IDHP	Isocitrate dehydrogenase [NADP], mitochondrial precursor (EC 1.1.1.42)	51333	8.95	106	11 of 55	Enzyme	Mitochondrial
P49368	TCPG_HUMAN	TCPG	T-complex protein 1, gamma subunit (TCP-1-gamma) (CCT-gamma)	60934	6.44	108	15 of 49	Chaperone	Cytoplasmic
P49411	EFTU_HUMAN	EFTU	Elongation factor Tu, mitochondrial precursor (EF-Tu) (P43)	49852	7.68	122	14 of 52	Regulatory, transcription	Mito-chondrial
P49448	DHE4_HUMAN	DHE4	Glutamate dehydrogenase 2, mitochondrial precursor (EC 1.4.1.3) (GDH)	61737	8.67	107	18 of 64	Enzyme	Mitochondrial
P49721	PSB2_HUMAN	PSB2	Proteasome subunit beta type 2 (EC 3.4.25.1) (Proteasome component C7-I) (Macropain subunit C7-I) (Multicatalytic endopeptidase complex subunit C7-I)	22836	6.6	56	7 of 28	Regulatory, enzyme	Cytoplasmic, nuclear
P49748	ACADV_HUMAN	ACADV	Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial precursor (EC 1.3.99.-) (VLCAD)	70744	9.1	55	7 of 36	Enzyme	Mitochondrial membrane
P49773	HINT1_HUMAN	HINT1	Histidine triad nucleotide-binding protein 1 (Adenosine 5'-monophosphoramidase) (Protein kinase C inhibitor 1) (Protein kinase C-interacting protein 1) (PKCI-1)	13671	6.5	71	7 of 24	Signal transduction	Cyto-plasmic and nuclear
P49915	GUAA_HUMAN	GUAA	GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (Glutamine amidotransferase) (GMP synthetase)	77408	6.86	206	24 of 59	Enzyme	Cytoplasmic
P50213	IDH3A_HUMAN	IDH3A	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor (EC 1.1.1.41)	40022	6.93	78	8 of 13	Enzyme	Mitochondrial
P50395	GDIB_HUMAN	GDIB	Rab GDP dissociation inhibitor beta (Rab GDI beta) (GDI-2)	51087	6.39	131	20 of 74	Regulatory	
P50502	ST13_HUMAN	ST13	Hsc70-interacting protein (Hip) (Putative tumor suppressor ST13) (Progesterone receptor-associated p48 protein)	41476	4.92	77	6 of 24	Binding	Cytoplasmic
P50990	TCPQ_HUMAN	TCPQ	T-complex protein 1, theta subunit (TCP-1-theta) (CCT-theta)	60021	5.3	53	6 of 43	Chaperone	Cytoplasmic
P50991	TCPD_HUMAN	TCPD	T-complex protein 1, delta subunit (TCP-1-delta) (CCT-delta) (Stimulator of TAR RNA bindin)	58400	7.94	68	9 of 33	Chaperone	Cytoplasmic
P50995	ANX11_HUMAN	ANX11	Annexin A11 (Annexin XI) (Calcyclin-associated annexin 50) (CAP-50) (56 kDa autoantigen)	54697	7.77	82	15 of 75	Binding	Cytoplasmic, nuclear
P51570	GALK1_HUMAN	GALK1	Galactokinase (EC 2.7.1.6) (Galactose kinase)	42701	6.42	87	10 of 45	Enzyme	Cytoplasmic
P51665	PSD7_HUMAN	PSD7	26S proteasome non-ATPase regulatory subunit 7 (26S proteasome regulatory subunit rpn8) (26S proteasome regulatory subunit S12) (Proteasome subunit p40) (Mov34 protein homolog)	37025	6.3	72	12 of 30	Regulatory	Cytoplasmic
P51991	ROA3_HUMAN	ROA3	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	39798	9.31	53	5 of 19	RNA associated	Intracellular, nucleus
P52565	GDIR_HUMAN	GDIR	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)	23249	4.74	98	8 of 18	Signal transduction	Cytoplasmic

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Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
P52566	GDIS_HUMAN	GDIS	Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI)	23030	4.84	161	15 of 38	Signal transduction	Cytoplasmic
P52597	HNRPF_HUMAN	HNRPF	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1)	45853	5.31	66	5 of 22	RNA associated	Nuclear, nucleoplasm
P52907	CAZA1_HUMAN	CAZA1	F-actin capping protein alpha-1 subunit (CapZ alpha-1)	33073	5.42	119	8 of 16	Structural	Cytoskeletal
P53582	AMPM1_HUMAN	AMPM1	Methionine aminopeptidase 1 (EC 3.4.11.18) (MetAP 1) (MAP 1) (Peptidase M 1)	43215	6.9	63	11 of 42	Enzyme	Cytosolic
P54577	SYYC_HUMAN	SYYC	Tyrosyl-tRNA synthetase, cytoplasmic (EC 6.1.1.1) (Tyrosyl-tRNA ligase) (TyrRS)	59012	6.7	58	8 of 22	Enzyme	Cytoplasmic
P54652	HSP72_HUMAN	HSP72	Heat shock-related 70 kDa protein 2 (Heat shock 70 kDa protein 2)	70262	5.42	54	8 of 33	Chaperone	
P54725	RD23A_HUMAN	RD23A	UV excision repair protein RAD 23 homolog A (hHR23A)	39641	4.24	53	7 of 44	DNA associated	Nuclear
P54753	EPHB3_HUMAN	EPHB3	Ephrin type-B receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor HEK-2)	110287	5.8	64	6 of 24	Signal transduction	Membrane
P54920	SNAA_HUMAN	SNAA	Alpha-soluble NSF attachment protein (SNAP-alpha) (N-ethylmaleimide-sensitive factor attachment protein, alpha)	33681	5.02	64	5 of 11	Transport carrier	Golgi apparatus
P55072	TERA_HUMAN	TERA	Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg(2+)-ATPase p97 subunit)	89818	4.89	345	41 of 59	Chaperone	Nuclear, cytoplasmic
P55263	ADK_HUMAN	ADK	Adenosine kinase (EC 2.7.1.20) (AK) (Adenosine 5'-phosphotransferase)	40918	6.67	122	11 of 27	Enzyme	
P55735	SEC13_HUMAN	SEC13	SEC13-related protein (SEC13-like protein 1)	35900	5.16	62	4 of 7		
P55795	HNRH2_HUMAN	HNRH2	Heterogeneous nuclear ribonucleoprotein H' (hnRNP H') (FTP-3)	49517	6.25	55	12 of 78	RNA associated	Nuclear; nucleoplasm
P55809	SCOT_HUMAN	SCOT	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial precursor (EC 2.8.3.5)	56578	7.52	55	9 of 31	Enzyme	Mitochondrial
P56537	IF6_HUMAN	IF6	Eukaryotic translation initiation factor 6 (eIF-6) (B4 integrin interactor) (CAB) (P57053)	27095	4.31	72	5 of 16	Translation	Cytoplasmic and nuclear
P57053	H2BS_HUMAN	H2BS	Histone H2B.s (H2B/s)	13804	11.05	71	6 of 24	DNA associated, transcription	Nuclear
P57737	CORO7_HUMAN	CORO7	Coronin 7 (70 kDa WD-repeat tumor rejection antigen homolog)	101595	5.55	70	7 of 14		
P58876	H2BB_HUMAN	H2BB	Histone H2B.b (H2B/b) (H2B.1 B) (HIRA-interacting protein 2)	13796	11	84	7 of 24	DNA associated, transcription	Nuclear
P60174	TPIS_HUMAN	TPIS	Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase)	26806	6.91	128	13 of 51	Enzyme	
P60660	MYL6_HUMAN	MYL6	Myosin light polypeptide 6 (Myosin light chain alkali 3) (Myosin light chain 3) (MLC-3) (LC17)	16799	4.4	58	8 of 32	Regulatory	
P60709	ACTB_HUMAN	ACTB	Actin, cytoplasmic 1 (Beta-actin)	42051	5.15	131	19 of 78	Structural	Cytoplasmic
P60842	IF41_HUMAN	IF41	Eukaryotic initiation factor 4A-I (eIF4A-I) (eIF-4A-I)	46352	5.12	53	5 of 20	RNA associated	Ribosomic
P60891	PRPS1_HUMAN	PRPS1	Ribose-phosphate pyrophosphokinase I (EC 2.7.6.1) (Phosphoribosyl pyrophosphate synthetase I) (PRS-I) (PPRibP)	34703	6.6	63	9 of 30	Enzyme	

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Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
P60900	PSA6_HUMAN	PSA6	Proteasome subunit alpha type 6 (EC 3.4.25.1) (Proteasome iota chain)	27837	6.74	69	9 of 60	Regulatory, enzyme	Cytoplasmic
P61086	UBC1_HUMAN	UBC1	Ubiquitin-conjugating enzyme E2-25 kDa (EC 6.3.2.19) (Ubiquitin-protein ligase) (Ubiquitin carrier protein) (E2(25K)) (Huntingtin interacting protein 2) (HIP-2)	22275	5.2	72	5 of 18	Enzyme	Cytoplasmic
P61088	UBE2N_HUMAN	UBE2N	Ubiquitin-conjugating enzyme E2 N (EC 6.3.2.19) (Ubiquitin-protein ligase N) (Ubiquitin carrier protein N)	17184	6.53	76	7 of 37	Enzyme, regulatory	Mitochondrial
P61158	ARP3_HUMAN	ARP3	Actin-like protein 3 (Actin-related protein 3)	47797	5.69	84	12 of 55	Structural	Cytoskeletal
P61163	ACTZ_HUMAN	ACTZ	Alpha-centractin (Centractin) (Centrosome-associated actin homolog) (Actin-RPV) (ARP1)	42614	6.2	116	11 of 30	Structural	Cytoplasmic
P61962	AN11H_HUMAN	AN11H	WD-repeat protein An11 homolog	39528	5.21	66	5 of 12	RNA associated	Cytoplasmic
P61978	HNRPK_HUMAN	HNRPK	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein)	51229	5.18	184	22 of 48		Cytoplasmic
P61981	1433G_HUMAN	1433G	14-3-3 protein gamma (Protein kinase C inhibitor protein-1) (KCIP-1)	28324	4.52	69	13 of 75	Regulatory	Cytoplasmic
P62158	CALM_HUMAN	CALM	Calmodulin (CaM)	16695	3.84	69	6 of 30	Enzyme, regulatory, signaling	Cytoplasmic
P62195	PRS8_HUMAN	PRS8	26S protease regulatory subunit 8 (Proteasome subunit p45) (p45/SUG) (Proteasome 26S subunit ATPase 5) (Thyroid hormone receptor interacting protein 1) (TRIP1)	45626	7.8	63	12 of 38	Chaperone	Cytoplasmic and nuclear
P62258	1433E_HUMAN	1433E	14-3-3 protein epsilon (14-3-3E)	29326	4.36	149	14 of 24	Regulatory, signaling	Cytoplasmic
P62333	PRS10_HUMAN	PRS10	26S protease regulatory subunit S10B (Proteasome subunit p42) (Proteasome 26S subunit ATPase 6 )	44430	7.56	81	11 of 30	Chaperone	Cytoplasmic, nuclear
P62736	ACTA_HUMAN	ACTA	Actin, aortic smooth muscle (Alpha-actin 2)	42380	5.05	53	10 of 78	Structural	Cytoplasmic
P62807	H2BA_HUMAN	H2BA	Histone H2B.a/g/h/k/l (H2B.1 A) (H2B/a) (H2B/g) (H2B/h) (H2B/k) (H2B/l)	13766	11	84	7 of 24	DNA associated, transcription	Nuclear
P62826	RAN_HUMAN	RAN	GTP-binding nuclear protein Ran (GTPase Ran) (Ras-like protein TC4) (Androgen receptor-associated protein 24)	24578	7.59	106	9 of 33	Regulatory, DNA associated	Nuclear, cytoplasmic
P62873	GBB1_HUMAN	GBB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 1 (Transducin beta chain 1)	37377	5.6	63	8 of 36	Regulatory	Membrane
P62879	GBB2_HUMAN	GBB2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 2 (Transducin beta chain 2)	38048	5.85	53	6 of 22	Signaling	
P62937	PPIA_HUMAN	PPIA	Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin A)	18097	7.97	80	9 of 57	Enzyme	Cytoplasmic
P62993	GRB2_HUMAN	GRB2	Growth factor receptor-bound protein 2 (GRB2 adapter protein) (SH2/SH3 adapter GRB2)	25304	6.25	106	11 of 44	Regulatory, signaling	Membranic
P63104	1433Z_HUMAN	1433Z	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein-1) (KCIP-1)	27898	4.43	111	10 of 16	Regulatory	Cytoplasmic
P63241	IF5A_HUMAN	IF5A	Eukaryotic translation initiation factor 5A (eIF-5A) (eIF-4D) (Rev-binding factor)	16918	4.86	57	5 of 15	RNA associated	Nuclear
P63244	GBLP_HUMAN	GBLP	Guanine nucleotide-binding protein beta subunit 2-like 1 (Guanine nucleotide-binding protein beta subunit-like protein 12.3)	35510	7.76	136	13 of 47	Signaling	Membrane
P63261	ACTG_HUMAN	ACTG	Actin, cytoplasmic 2 (Gamma-actin)	42107	5.16	131	19 of 78	Structural	Cytoplasmic

*continued*

Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
P63267	ACTH_HUMAN	ACTH	Actin, gamma-enteric smooth muscle (Smooth muscle gamma actin) (Alpha-actin 3)	42248	5.16	53	10 of 78	Structural	Cytoplasmic
P67809	YBOX1_HUMAN	YBOX1	Nuclease sensitive element binding protein 1 (Y box binding protein-1) (Y-box transcription factor)	35902	10.31	60	7 of 32	Regulatory, transcription	Nuclear
P67936	TPM4_HUMAN	TPM4	Tropomyosin alpha 4 chain (Tropomyosin 4) (TM30p1)	28487	4.36	107	10 of 34	Structural	Cytoskeletal
P68032	ACTC_HUMAN	ACTC	Actin, alpha cardiac (Alpha-cardiac actin)	42334	5.05	61	11 of 78	Structural	Cytoplasmic
P68104	EF1A1_HUMAN	EF1A1	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor 1 A-1) (eEF1A-1)	50451	9.5	71	6 of 27	RNA associated	Cytoplasmic
P68133	ACTS_HUMAN	ACTS	Actin, alpha skeletal muscle (Alpha-actin 1)	42365	5.05	60	11 of 78	Structural	Cytoplasmic
P68363	TBAK_HUMAN	TBAK	Tubulin alpha-ubiquitous chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1)	50803	4.7	218	23 of 43	Structural	
P68366	TBA1_HUMAN	TBA1	Tubulin alpha-1 chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha)	50633	4.69	185	21 of 43	Structural	
P68371	TBBX_HUMAN	TBBX	Tubulin beta-? chain (Tubulin beta-2 chain)	50255	4.52	259	23 of 33	Structural	
P69892	HBG2_HUMAN	HBG2	Hemoglobin gamma-2 chain (Hemoglobin gamma-G chain) (Hb F Ggamma)	16042	7.23	53	4 of 37	Transport, carrier	Cytoplasmic
P69893	TBB1_CRIGR	TBB1	Tubulin beta-1 chain (Beta-tubulin isotype I) (Class I beta tubulin)	49671	4.6	185	16 of 42	Structural	
P78371	TCPB_HUMAN	TCPB	T-complex protein 1, beta subunit (TCP-1-beta) (CCT-beta)	57663	6.42	160	23 of 74	Chaperone	Cytoplasmic
P78406	RAE1L_HUMAN	RAE1L	mRNA-associated protein mrnp 41 (Rae1 protein homolog)	41569	7.9	67	10 of 56	RNA associated, Transport	Nuclear, cytoplasmic
P99024	TBB5_MOUSE	TBB5	Tubulin beta-5 chain	49671	4.6	210	22 of 46	Structural	
Q00610	CLH1_HUMAN	CLH1	Clathrin heavy chain 1 (CLH-17)	193129	5.42	68	6 of 12	Structural	Cytoplasmic
Q01105	SET_HUMAN	SET	SET protein (Phosphatase 2A inhibitor I2PP2A) (I-2PP2A) (Template activating factor I) (TAF-I)	33468	3.95	79	6 of 15	Regulatory, DNA associated, transcription	Cytoplasmic, nuclear
Q02790	FKBP4_HUMAN	FKBP4	FK506-binding protein 4 (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (p59 protein) (HSP binding immunophilin) (HBI) (FKBP52 protein) (52 kDa FK506 binding protein) (FKBP59)	51926	5.11	173	15 of 26	Chaperone, enzyme, regulatory	Nuclear, cytoplasmic
Q03252	LAM2_HUMAN	LAM2	Lamin B2	67761	5.02	137	16 of 31	Structural	Nuclear membrane
Q04726	TLE3_HUMAN	TLE3	Transducin-like enhancer protein 3 (ESG3)	84162	7.2	53	6 of 19	Signal transduction	Nuclear
Q04760	LGUL_HUMAN	LGUL	Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I)	20803	5.08	69	5 of 12	Enzyme	
Q04837	SSB_HUMAN	SSB	Single-stranded DNA-binding protein, mitochondrial precursor (Mt-SSB) (MtSSB) (PWP1-interactive protein 17)	17249	10.04	89	8 of 40	Regulatory	Mitochondrial
Q04917	1433F_HUMAN	1433F	14-3-3 protein eta (Protein AS1)	28241	4.47	54	5 of 11	Regulatory	
Q05639	EF1A2_HUMAN	EF1A2	Elongation factor 1-alpha 2 (EF-1-alpha-2) (Elongation factor 1 A-2) (eEF1A-2) (Statin S1)	50780	9.5	53	6 of 42	Regulatory, RNA associated	Nuclear
Q06323	PSME1_HUMAN	PSME1	Proteasome activator complex subunit 1 (Proteasome activator 28-alpha subunit) (PA28alpha)	28876	5.83	65	5 of 9	Chaperone	

*continued*



Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
Q06830	PRDX1_HUMAN	PRDX1	Peroxisredoxin 1 (EC 1.11.1.-) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2) (Proliferation-associated protein PAG) (Natural killer cell enhancing factor A) (NKEF-A)	22324	8.31	134	13 of 57	Enzyme	Cytoplasmic
Q07000	1C15_HUMAN	1C15	HLA class I histocompatibility antigen, Cw-15 alpha chain precursor (MHC class I antigen Cw*15)	41293	6.29	62	6 of 47	Antigen	
Q07021	MA32_HUMAN	MA32	Complement component 1, Q subcomponent binding protein, mitochondrial precursor (Glycoprotein gC1qBP)	31741	4.47	56	7 of 41		Mitochondrial
Q08752	PPID_HUMAN	PPID	40 kDa peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin-40) (CYP-40)	41006	7.24	62	9 of 59	Enzyme	Cytoplasmic
Q09028	RBBP4_HUMAN	RBBP4	Chromatin assembly factor 1 subunit C (CAF-1 subunit C) (Chromatin assembly factor I p48 subunit) (CAF-I 48 kDa subunit) (CAF-Ip48) (Retinoblastoma binding protein p48) (Retinoblastoma-binding protein 4) (RBBP-4)	47911	4.5	110	12 of 30	Regulatory, cell cycle	Nuclear
Q13162	PRDX4_HUMAN	PRDX4	Peroxisredoxin 4 (EC 1.11.1.-) (Prx-IV) (Thioredoxin peroxidase AO372)	30748	6.24	65	5 of 33	Enzyme	Cytoplasmic
Q13182	Q13182_HUMAN	Q13182	Myosin regulatory light chain MRCL2 (Nonmuscle myosin light chain 2)	19823	4.44	53	5 of 24		
Q13263	TIF1B_HUMAN	TIF1B	Transcription intermediary factor 1-beta (TIF1-beta) (Tripartite motif protein 28) (Nuclear corepressor KAP-1)	90261	5.55	55	8 of 27	Transcription	Nuclear
Q13283	G3BP_HUMAN	G3BP	Ras-GTPase-activating protein binding protein 1 (GAP SH3-domain binding protein 1) (G3BP-1)	52189	5.21	73	6 of 28	Enzyme	Cytoplasmic, nucleus
Q13347	IF32_HUMAN	IF32	Eukaryotic translation initiation factor 3 subunit 2 (eIF-3 beta) (eIF3 p36) (eIF3i)	36877	5.38	143	9 of 13	Translation, RNA binding	Ribosomal
Q13409	DYI2_HUMAN	DYI2	Dynein intermediate chain 2, cytosolic (DH IC-2) (Cytoplasmic dynein intermediate chain 2)	71811	4.85	58	8 of 46	Structural	Cytoskeletal
Q13509	TBB3_HUMAN	TBB3	Tubulin beta-3 chain (Tubulin beta-III) (Tubulin beta-4)	50856	4.57	149	17 of 33	Structural	Cytoskeletal
Q13561	DCTN2_HUMAN	DCTN2	Dynactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide) (p50 dynamitin)	44186	4.86	117	11 of 27	Structural, transport	Cytoplasmic, membranous
Q13748	TBA2_HUMAN	TBA2	Tubulin alpha-2 chain (Alpha-tubulin 2)	50611	4.74	154	18 of 43	Structural	Cytoskeletal
Q13813	SPTA2_HUMAN	SPTA2	Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II spectrin)	285150	5.01	272	42 of 54	Structural	Cytoskeletal
Q13838	UAP56_HUMAN	UAP56	Probable ATP-dependent RNA helicase p47 (HLA-B associated transcript-1)	49416	5.38	65	9 of 44	RNA binding	Nuclear
Q14103	HNRPD_HUMAN	HNRPD	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1)	38581	8.01	55	5 of 26	RNA binding	Nuclear
Q14141	SEPT6_HUMAN	SEPT6	Septin 6	50084	6.65	70	10 of 47	Unknown	Nuclear
Q14257	RCN2_HUMAN	RCN2	Reticulocalbin 2 precursor (Calcium-binding protein ERC-55) (E6-binding protein) (E6BP)	36910	4.01	58	6 of 26	Structural, binding	Endoplasmic reticulum
Q14566	MCM6_HUMAN	MCM6	DNA replication licensing factor MCM6 (P105MCM)	93800	5.09	77	13 of 42	Regulatory	Nuclear

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Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
Q14697	GANAB_HUMAN	GANAB	Neutral alpha-glucosidase AB precursor (EC 3.2.1.84) (Glucosidase II alpha subunit)	107262	6.06	136	23 of 65	Enzyme	Endoplasmic reticulum and Golgi
Q15019	SEPT2_HUMAN	SEPT2	Septin 2 (NEDD5 protein homolog)	41487	6.1	67	7 of 46	Structural, cytokinesis	Endoplasmic reticulum Cytoplasmic
Q15084	PDIA6_HUMAN	PDIA6	Protein disulfide-isomerase A6 precursor (EC 5.3.4.1) (Protein disulfide isomerase P5)	48490	4.7	142	14 of 48	Enzyme	
Q15102	PA1B3_HUMAN	PA1B3	Platelet-activating factor acetylhydrolase IB gamma subunit (EC 3.1.1.47) (PAF acetylhydrolase 29 kDa subunit) (PAF-AH 29 kDa subunit)	25832	6.84	54	6 of 48	Enzyme	
Q15181	IPYR_HUMAN	IPYR	Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-hydrolase) (PPase)	33095	5.64	216	16 of 21	Enzyme	Nuclear
Q15185	TEBP_HUMAN	TEBP	Telomerase-binding protein p23 (Hsp90 co-chaperone) (Progesterone receptor complex p23)	18970	4.11	58	7 of 50	Enzyme, signal transduction	
Q15365	PCBP1_HUMAN	PCBP1	Poly(rC)-binding protein 1 (Alpha-CP1) (hnRNP-E1) (Nucleic acid binding protein SUB2.3)	37987	7.11	75	9 of 39	RNA binding	
Q15435	Q15435_HUMAN	Q15435	Yeast sds22 homolog (Protein phosphatase-1 regulatory subunit 7 alpha1)	41652	4.55	53	9 of 57	Regulatory	Cytoplasmic, nuclear
Q15459	SF3A1_HUMAN	SF3A1	Splicing factor 3 subunit 1 (Spliceosome associated protein 114) (SAP 114) (SF3a120)	88887	4.88	55	4 of 11	RNA associated	Nuclear
Q15691	MARE1_HUMAN	MARE1	Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1)	30020	4.76	112	7 of 12	Structural	Microtubule
Q15907	RB11B_HUMAN	RB11B	Ras-related protein Rab-11B (GTP-binding protein YPT3)	24489	5.6	76	8 of 36	Enzyme	Cytoplasmic
Q16555	DPYL2_HUMAN	DPYL2	Dihydropyrimidinase related protein-2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2)	62710	6.33	151	17 of 43	Enzyme, signal transduction	
Q16576	RBBP7_HUMAN	RBBP7	Histone acetyltransferase type B subunit 2 (Retinoblastoma binding protein P46) (Retinoblastoma-binding protein 7)	48132	4.68	137	12 of 20	Regulatory	
Q16658	FSCN1_HUMAN	FSCN1	Fascin (Singed-like protein) (55 kDa actin bundling protein) (p55)	54992	7.26	70	9 of 36	Structural, cell cycle	Cytoskeletal
Q16778	H2BQ_HUMAN	H2BQ	Histone H2B.q (H2B/q) (H2B-GL105)	13780	11	84	7 of 24	DNA binding	Nuclear
Q16822	PPCKM_HUMAN	PPCKM	Phosphoenolpyruvate carboxykinase, mitochondrial precursor [GTP] (EC 4.1.1.32)	71446	7.65	55	7 of 37	Enzyme	Mitochondrial
Q16836	HCDH_HUMAN	HCDH	Short chain 3-hydroxyacyl-CoA dehydrogenase, mitochondrial precursor (EC 1.1.1.35) (HCDH)	34312	9.41	61	5 of 23	Enzyme	Mitochondrial
Q16891	IMMT_HUMAN	IMMT	Mitochondrial inner membrane protein (Mitofilin) (p87/89)	84025	6.43	61	9 of 67	Unknown	Mitochondrial
Q29865	1C18_HUMAN	1C18	HLA class I histocompatibility antigen, Cw-18 alpha chain precursor (MHC class I antigen Cw*18)	41363	6.6	62	6 of 47	Antigen	Membran
Q29940	1B59_HUMAN	1B59	HLA class I histocompatibility antigen, B-59 alpha chain precursor (MHC class I antigen B*59)	40844	6.25	54	5 of 47	Antigen	Membran
Q29963	1C06_HUMAN	1C06	HLA class I histocompatibility antigen, Cw-6 alpha chain precursor (MHC class I antigen Cw-6 alpha chain)	41399	5.86	62	6 of 47	Antigen	Membran
Q5QNW6	Q5QNW6_HUMAN	Q5QNW6	Histone 2, H2bf	13911	11	53	5 of 18	Chaperone	Cytoplasmic
Q5SP17	Q5SP17_HUMAN	Q5SP17	Heat shock 70kDa protein 1A	70280	5.31	53	8 of 38		

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Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
Q5SQT6	Q5SQT6_HUMAN	Q5SQT6	Pyrophosphatase (Inorganic)	20254	4.87	101	9 of 21	Enzyme	Cytoplasmic
Q5T154	PRDX1_HUMAN	PRDX1	Peroxioredoxin 1(EC 1.11.1.15) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2) (Proliferation-associated protein) (PAG) (Natural killer cell enhancing factor A) (NKEF-A)	10726	4.63	55	4 of 19	Enzyme, cell cycle	Cytoplasmic
Q5T450	Q5T450_HUMAN	Q5T450	Uroporphyrinogen decarboxylase (Fragment)	25526	4.97	53	5 of 28	Enzyme	
Q5T6W2	Q5T6W2_HUMAN	Q5T6W2	Heterogeneous nuclear ribonucleoprotein K (Fragment)	42008	5.23	53	5 of 14	Nucleic acid binding	
Q5T6W5	Q5T6W5_HUMAN	Q5T6W5	Heterogeneous nuclear ribonucleoprotein K	47755	5.28	53	5 of 14	Nucleic acid binding	
Q5T7J9	Q5T7J9_HUMAN	Q5T7J9	OTTHUMP00000016847	48088	5.7	57	5 of 13		
Q5U4P6	Q5U4P6_HUMAN	Q5U4P6	KHSRP protein	73307	8.01	80	13 of 62		
Q5VXV6	Q5VXV6_HUMAN	Q5VXV6	Spectrin, alpha, non-erythrocytic 1 (Alpha-fodrin)	285716	5.02	56	23 of 64	Binding	
Q5VYZ0	Q5VYZ0_HUMAN	Q5VYZ0	PTPL1-associated RhoGAP 1 (PARG1)	143513	6.72	58	6 of 10	Signaling	
Q5W9H6	Q5W9H6_MERUN	Q5W9H6_MERUN	Beta-actin	41736	5.2	83	12 of 22	Structural	Cytoplasmic
Q68CQ5	Q68CQ5_HUMAN	Q68CQ5	Hypothetical protein DKFZp781N1372	48652	7.95	77	8 of 27	Enzyme	
Q6DC98	Q6DC98_HUMAN	Q6DC98	LMNB1 protein (Fragment)	38288	5.12	68	9 of 40	Structural	
Q6FHU0	Q6FHU0_HUMAN	Q6FHU0	Proteasome subunit beta type (EC 3.4.25.1) (Fragment)	30019	5.62	53	5 of 23	Regulatory, enzyme	Cytoplasmic, nuclear
Q6IA22	Q6IA22_HUMAN	Q6IA22	REC14 protein	33727	5.12	77	7 of 18		
Q6IAI0	Q6IAI0_HUMAN	Q6IAI0	HSPC117 protein	55684	7.42	75	11 of 28		
Q6IBS0	Q6IBS0_HUMAN	Q6IBS0	PTK9L protein	39779	6.85	61	7 of 36		
Q6IPB3	Q6IPB3_HUMAN	Q6IPB3	RANBP1 protein	21502	6.52	53	7 of 37		
Q6IPB4	Q6IPB4_HUMAN	Q6IPB4	Hypothetical protein	22217	5.03	53	7 of 37		
Q6NTA2	Q6NTA2_HUMAN	Q6NTA2	HNRPL protein	60822	7.12	58	7 of 26	RNA binding	Nuclear
Q6NWQ3	Q6NWQ3_HUMAN	Q6NWQ3	H2B histone family, member E	14079	11.08	56	7 of 33	DNA binding	Nuclear
Q6PD71	Q6PD71_HUMAN	Q6PD71	Hypothetical protein	73333	9.1	53	9 of 27		
Q6PJT4	Q6PJT4_HUMAN	Q6PJT4	MSN protein (Fragment)	38916	9.91	73	8 of 21	Binding	Cytoplasmic, cytoskeletal
Q6PKI6	Q6PKI6_HUMAN	Q6PKI6	NSEP1 protein (Fragment)	29356	10.75	56	7 of 30	Transcription, DNA binding	Nuclear
Q6SPF2	Q6SPF2_HUMAN	Q6SPF2	CARG binding factor	33364	8.33	65	7 of 25	Nucleic acid binding, mRNA splicing	
Q6UXN9	Q6UXN9_HUMAN	Q6UXN9	WD40 protein	35455	7.79	53	7 of 43		
Q6ZNK5	Q6ZNK5_HUMAN	Q6ZNK5	FLJ00293 protein (Fragment)	93672	9.18	97	17 of 69		
Q6ZS99			Hypothetical protein FLJ45706	65979	4.17	53	7 of 29		
Q6ZSW6			Hypothetical protein FLJ45159	15154	8.83	55	5 of 21		
Q71U36	TBA3_HUMAN	TBA3	Tubulin alpha-3 chain (Alpha-tubulin 3) (Tubulin B-alpha-1)	50787	4.7	185	24 of 68	Structural	Cytoskeletal
Q71V99	Q71V99_HUMAN	Q71V99	Cyclophilin	18130	8.08	70	7 of 28	Transporter	Cytoplasmic
Q76GR4	Q76GR4_HUMAN	Q76GR4	Ligase I, DNA, ATP-dependent (Fragment)	4733	4.63	60	3 of 14	Enzyme	

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Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
Q7KZ74	Q7KZ74_HUMAN	Q7KZ74	A+U-rich element RNA binding factor	30336	8.99	67	7 of 25	Nucleic acid binding, mRNA splicing	
Q7KZ75	Q7KZ75_HUMAN	Q7KZ75	HnRNP JKTBP protein (JKTBP1)	33739	7.41	64	7 of 25	Nucleic acid binding, mRNA splicing	
Q7Z3B4	NUP54_HUMAN	NUP54	Nucleoporin p54 (54 kDa nucleoporin)	55515	7.03	79	11 of 28	Transport	Nuclear
Q7Z4X4	Q7Z4X4_HUMAN	Q7Z4X4	G protein beta subunit-like protein	33626	5.68	77	7 of 18	Unknown/unspecified	
Q7Z5Z4	Q7Z5Z4_HUMAN	Q7Z5Z4	SHUJUN-1	17046	3.95	62	5 of 24		
Q86SF8	Q86SF8_HUMAN	Q86SF8	Full-length cDNA clone CS0DI085YM22 of Placenta of <i>Homo sapiens</i> (human)	32374	4.69	53	5 of 9		
Q86SF8	Q86SF8_HUMAN	Q86SF8	Full-length cDNA clone CS0DI085YM22 of Placenta of <i>Homo sapiens</i> (human) (Full-length cDNA clone CS0DG007YK20 of B cells (Ramos cell line) of <i>Homo sapiens</i> ) (HNRPC protein)	32374	4.69	62	8 of 28	Nucleic acid binding, mRNA splicing	
Q86U12	Q86U12_HUMAN	Q86U12	Full-length cDNA clone CS0CAP007YF18 of Thymus of <i>Homo sapiens</i> (human)	49669	5.08	60	7 of 21	Chaperone	Cytoplasmic
Q8IWW8	Q8IWW8_HUMAN	Q8IWW8	Alcohol dehydrogenase 8	50731	7.84	54	7 of 25	Enzyme	Nuclear, cytoplasmic
Q8IWX1	Q8IWX1_HUMAN	Q8IWX1	3'-5' RNA exonuclease	86537	7.86	78	10 of 28	RNA binding	
Q8IYS1	Q8IYS1_HUMAN	Q8IYS1	ACY1L2 protein (Fragment)	51330	6.09	56	5 of 13	Unknown/unspecified	
Q8N257	H2BX_HUMAN	H2BX	Histone H2B type 12	13768	11	84	7 of 24	DNA associated	Nuclear
Q8TCS8	Q8TCS8_HUMAN	Q8TCS8	Polynucleotide phosphorylase-like protein (EC 2.7.7.8) (Polyribonucleotide nucleotidyltransferase 1)	86509	7.86	78	10 of 28	Enzyme, RNA binding	
Q8WU19	Q8WU19_HUMAN	Q8WU19	K-ALPHA-1 protein	37707	4.62	53	8 of 66	Structural	Cytoskeletal
Q8WVX0	Q8WVX0_HUMAN	Q8WVX0	ECH1 protein	36077	8.36	60	7 of 37	Enzyme	Mitochondrial
Q8WXX5	DNJC9_HUMAN	DNJC9	DnaJ homolog subfamily C member 9 (DnaJ protein SB73)	30062	5.38	54	3 of 8	Chaperone	Cytoplasmic
Q8WYJ6	SEPT1_HUMAN	SEPT1	Septin 1 (LARP) (Serologically defined breast cancer antigen NY-BR-24)	42400	5.54	62	6 of 49	Enzyme, cell cycle	Nuclear, cytoskeletal
Q92597	NDRG1_HUMAN	NDRG1	NDRG1 protein (N-myc downstream regulated gene 1 protein) (Differentiation-related gene 1 protein) (DRG1)	43263	5.67	60	5 of 39	Signaling, cell cycle, differentiation	Cytosolic
Q92598	HS105_HUMAN	HS105	Heat-shock protein 105 kDa (Heat shock 110 kDa protein) (Antigen NY-CO-25)	97716	5.04	83	12 of 32	Chaperone, regulatory	Cytoplasmic
Q92688	AN32B_HUMAN	AN32B	Acidic leucine-rich nuclear phosphoprotein 32 family member B (PHAPI2 protein) (Silver-stainable protein SSP29 Acidic protein rich in leucines)	28941	3.67	59	6 of 25	Signal transduction, cell cycle, differentiation	Nuclear
Q92945	FUBP2_HUMAN	FUBP2	Far upstream element binding protein 2 (FUSE binding protein 2) (KH type splicing regulatory protein)	73063	8.05	66	7 of 33	Regulatory, RNA associated	Nuclear
Q93079	H2BJ_HUMAN	H2BJ	Histone H2B.j (H2B/j)	13752	11	78	7 of 28	DNA binding	Nuclear

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Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
Q96AE4	FUBP1_HUMAN	FUBP1	Far upstream element binding protein 1 (FUSE binding protein 1) (FBP)	67602	7.71	57	7 of 23	Transcription	Nuclear
Q96AT9	RPE_HUMAN	RPE	(DNA helicase V) (HDH V)	25139	5.29	54	3 of 9	Enzyme	
Q96B89	Q96B89_HUMAN	Q96B89	Ribulose-phosphate 3-epimerase (EC 5.1.3.1) (Ribulose-5-phosphate-3-epimerase) (HUSY-17)	33535	5.28	53	4 of 6		
Q96CF4	Q96CF4_HUMAN	Q96CF4	Chromosome 17 open reading frame 25	8643	11	56	4 of 18	DNA binding	Nuclear
Q96EZ9	Q96EZ9_HUMAN	Q96EZ9	HIST1H2BJ protein	36135	8.12	60	7 of 37	Enzyme	Mitochondrial
Q96FW1	OTUB1_HUMAN	OTUB1	ECH1 protein	31492	4.58	72	6 of 19	Regulatory	Mitochondrial
Q96GD0	PLPP_HUMAN	PLPP	Ubiquitin thiolesterase protein OTUB1 (EC 3.4.-.-) (Otubain 1) (OTU domain-containing ubiquitin aldehyde-binding protein 1)	32077	6.51	60	5 of 33	Enzyme	
Q96IM0	Q96IM0_HUMAN	Q96IM0	Pyridoxal phosphate phosphatase (EC 3.1.3.-)	46026	10.03	56	7 of 25	Nucleic acid binding	
Q96IU4	C1IB_HUMAN	C1IB	HNRPDL protein (Fragment)	22346	5.9	67	8 of 29		Cytoplasmic and nuclear
Q96PI1	SPRR4_HUMAN	SPRR4	CCG1-interacting factor B	9186	10.39	53	4 of 32	Structural	Cytoplasmic
Q96RI5	Q96RI5_HUMAN	Q96RI5	Small proline-rich protein 4	72772	6.94	107	17 of 69	Structural	Cytoplasmic
Q96RI6	Q96RI6_HUMAN	Q96RI6	Unconventional myosin 1G methionine form (Fragment)	72740	6.94	107	17 of 69	Structural	Cytoplasmic
Q96S43	Q96S43_HUMAN	Q96S43	Unconventional myosin 1G valine form (Fragment)	27345	8.99	68	7 of 25	Nucleic acid binding, mRNA splicing	
Q96T05	Q96T05_HUMAN	Q96T05	JKTBP1delta6	56647	8.62	72	8 of 28		
Q99426	TBCB_HUMAN	TBCB	Hypothetical protein FLJ14531	27593	4.78	55	4 of 7	Structural	Cytoskeletal
Q99714	HCD2_HUMAN	HCD2	Tubulin-specific chaperone B (Tubulin folding cofactor B) (Cytoskeleton-associated protein 1)	27134	7.94	60	7 of 33	Enzyme	Mitochondrial
Q99733	NP1L4_HUMAN	NP1L4	3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH) (Endoplasmic reticulum-associated amyloid beta-peptide binding protein)	42967	4.32	69	5 of 18	chaperone	Nuclear
Q99747	SNAG_HUMAN	SNAG	Nucleosome assembly protein 1-like 4 (Nucleosome assembly protein 2) (NAP2)	35066	5.07	53	3 of 8	Structural	Membrane
Q99798	ACON_HUMAN	ACON	Gamma-soluble NSF attachment protein (SNAP-gamma) (N-ethylmaleimide-sensitive factor attachment protein)	86113	7.65	107	17 of 60	Enzyme	Mitochondrial
Q99829	CPNE1_HUMAN	CPNE1	Aconitate hydratase, mitochondrial precursor (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase)	59648	5.62	80	8 of 22	Transporter	Cytosolic
Q99832	TCPH_HUMAN	TCPH	Copine I	59842	7.73	85	12 of 45	chaperone	Cytoplasmic
Q99867	TBB4Q_HUMAN	TBB4Q	T-complex protein 1, eta subunit (TCP-1-eta) (CCT-eta) (HIV-1 Nef interacting protein)	48916	4.91	54	10 of 50	Structural	Microtubules
Q99880	H2BC_HUMAN	H2BC	Tubulin beta-4q chain	13812	11	84	7 of 24	DNA binding	Nuclear
Q9BQ67	GRWD1_HUMAN	GRWD1	Histone H2B.c (H2B/c)	49787	4.56	93	11 of 32	unknown/unspecified	Nuclear, nucleolar
Q9BQE3	TBA6_HUMAN	TBA6	Glutamate-rich WD-repeat protein 1	50547	4.73	127	19 of 77	Structural	Cytoplasm
Q9BS26	TXND4_HUMAN	TXND4	Tubulin alpha-6 chain (Alpha-tubulin 6)	47340	4.9	111	9 of 19	Regulatory	Endoplasmic reticulum
			Thioredoxin domain containing protein 4 precursor (Endoplasmic reticulum protein ERp44)						

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Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
Q9BT78	CSN4_HUMAN	CSN4	COP9 signalosome complex subunit 4 (Signalosome subunit 4) (SGN4) (JAB1-containing signalosome subunit 4)	46269	5.5	94	10 of 34	Regulatory	Nuclear and cytoplasmic
Q9BTX7	CT121_HUMAN	CT121	Protein C20orf121	31802	8.27	53	3 of 14	Transport	Microtubules
Q9BUF5	TBB6_HUMAN	TBB6	Tubulin beta-6 chain	50281	4.51	57	9 of 33	Structural	
Q9BWD1	THIC_HUMAN	THIC	Acetyl-CoA acetyltransferase, cytosolic (EC 2.3.1.9) (Cytosolic acetoacetyl-CoA thiolase) (Acetyl CoA transferase-like protein)	41351	6.5	76	8 of 26	Enzyme	
Q9BWL4	Q9BWL4_HUMAN	Q9BWL4	Hypothetical protein HSPC117	55722	7.23	75	11 of 28	Enzyme, regulatory	Cytoplasmic, nuclear
Q9BWZ9	Q9BWZ9_HUMAN	Q9BWZ9	Proteasome (Prosome, macropain) subunit, beta type, 2	Q9BWZ96.6	56	56	6 of 32		
Q9GZS3	Q9GZS3_HUMAN	Q9GZS3	Hypothetical protein FLJ21101 (G protein beta subunit-like protein) (Meiotic recombination protein REC14)	33730	5.12	77	7 of 18		
Q9H3J8	Q9H3J8_HUMAN	Q9H3J8	My027 protein (Chromosome 17 open reading frame 25)	33553	5.28	53	4 of 6	Enzyme	Nuclear, cytoplasmic
Q9H3X0	Q9H3X0_HUMAN	Q9H3X0	Hypothetical protein DKFZp761L1216	31816	6.16	56	5 of 16		
Q9H596	DUS21_HUMAN	DUS21	Dual specificity protein phosphatase 21 (EC 3.1.3.48) (EC 3.1.3.16) (Low molecular weight dual specificity phosphatase 21)	21628	9.06	53	3 of 11		
Q9H773	Q9H773_HUMAN	Q9H773	Hypothetical protein FLJ21190 (RS21C6) (CDA03) (XTP3-transactivated protein A) (XTP3TPA protein)	18783	4.67	55	6 of 47	Enzyme	Mitochondrial
Q9HB71	CYBP_HUMAN	CYBP	Calcyclin-binding protein (CacyBP) (hCacyBP) (Siah-interacting protein) (S100A6-binding protein)	26307	8.59	81	7 of 24		
Q9HC37	MCCC2_HUMAN	MCCC2	Hypothetical protein	33569	5.28	53	4 of 6		
Q9HCC0	MCCC2_HUMAN	MCCC2	Methylcrotonyl-CoA carboxylase beta chain, mitochondrial precursor (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 2)	61807	7.75	55	7 of 28	Enzyme	Cytoplasmic
Q9NR46	SHLB2_HUMAN	SHLB2	SH3 domain GRB2-like protein B2 (Endophilin B2) (PP578)	44174	5.78	65	5 of 21	Regulatory	
Q9NRH3	TBG2_HUMAN	TBG2	Tubulin gamma-2 chain (Gamma-2 tubulin)	51401	5.59	66	8 of 33	Structural	
Q9NS69	TOM22_HUMAN	TOM22	Mitochondrial import receptor subunit TOM22 homolog (Translocase of outer membrane 22 kDa subunit homolog)	15511	3.99	55	4 of 58	Transport	Mitochondrial
Q9NSD9	SYFB_HUMAN	SYFB	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--tRNA ligase beta chain) (PheRS) (HSPC173)	66130	6.4	69	8 of 32	Enzyme	Cytoplasmic
Q9NY65	TBA8_HUMAN	TBA8	Tubulin alpha-8 chain (Alpha-tubulin 8)	50745	4.7	109	15 of 50	Structural	Microtubules
Q9NYL9	TMOD3_HUMAN	TMOD3	Tropomodulin-3 (Ubiquitous tropomodulin) (U-Tmod)	39741	4.83	127	10 of 23	Struclural	Cytoplasmic
Q9P037	Q9P037_HUMAN	Q9P037	HSPC117	55631	7.09	65	10 of 28	Enzyme	Cytoplasmic
Q9P0J3	Q9P0J3_HUMAN	Q9P0J3	Putative 55 kDa protein	55481	7.41	64	10 of 28		
Q9UBE0	ULE1A_HUMAN	ULE1A	Ubiquitin-like 1 activating enzyme E1A (SUMO-1 activating enzyme subunit 1)	38881	4.93	53	3 of 10		
Q9UDG1	Q9UDG1_HUMAN	Q9UDG1	FRUCTOSYLLYSINE-specific binding protein (Fragments)	3318	3.79	53	3 of 29	DNA binding	Nuclear
Q9UE88	Q9UE88_HUMAN	Q9UE88	Histone H2B.1 (Fragment)	11324	10.76	60	5 of 18		
Q9UFN0	Q9UFN0	Q9UFN0	NipSnap3A protein (NipSnap4) (Target for <i>Salmonella</i> secreted protein C) (TassC) (HSPC299)	28562	9.55	74	6 of 36	Regulatory	
Q9UG16	Q9UG16_HUMAN	Q9UG16	Hypothetical protein DKFZp564P0562 (Fragment)	152450	5.23	60	18 of 64		

*continued*

Table I. *continued*

Accession number	Protein name	Protein symbol	Protein description	MW	pI	Mascot score	Peptides matched	Function	Subcellular localization
Q9UGV6	HMG1X_HUMAN	HMG1X	High mobility group protein 1-like 10 (HMG-1L10)	24374	7.55	70	7 of 24	DNA binding	Nuclear
Q9UHD8	SEPT9_HUMAN	SEPT9	Septin 9 (MLL septin-like fusion protein) (MLL septin-like fusion protein MSF-A) (Ovarian/Breast septin)	65613	9.46	61	9 of 73	Cytokinesis	Membran
Q9UHU6	Q9UHU6_HUMAN	Q9UHU6	PRO1578	9618	11.4	55	4 of 27		
Q9UJZ1	STML2_HUMAN	STML2	Stomatin-like protein 2 (SLP-2) (EPB72-like 2) (HSPC108)	38624	7.5	64	5 of 16	Regulatory, transport	Membran
Q9UKK9	NUDT5_HUMAN	NUDT5	ADP-sugar pyrophosphatase (EC 3.6.1.13) (EC 3.6.1.-) (Nucleoside diphosphate-linked moiety X motif 5) (YSA1H) (HSPC115)	24597	4.59	53	4 of 14	Enzyme	
Q9UL46	PSME2_HUMAN	PSME2	Proteasome activator complex subunit 2 (Proteasome activator 28-beta subunit) (PA28beta)	27384	5.26	114	12 of 62	Chaperone	Cytoplasmic
Q9UMS4	PRP19_HUMAN	PRP19	PRP19/PSO4 homolog (Nuclear matrix protein 200) (hPso4)	55602	6.6	53	5 of 44	DNA binding	Nuclear
Q9UMX0	UBQL1_HUMAN	UBQL1	Ubiquilin 1 (Protein linking IAP with cytoskeleton-1) (PLIC-1) (hPLIC-1)	62479	4.76	101	15 of 40	Regulatory	Nuclear, cytoplasmic
Q9UQ80	PA2G4_HUMAN	PA2G4	Proliferation-associated protein 2G4 (Cell cycle protein p38-2G4 homolog) (hG4-1)	44101	6.52	75	11 of 69	Cell cycle	Nuclear
Q9Y230	RUVB2_HUMAN	RUVB2	RuvB-like 2 (EC 3.6.1.-) (48-kDa TATA box-binding protein-interacting protein) (48-kDa TBP-interacting protein)	51295	5.32	52	5 of 17	DNA associated	Nuclear
Q9Y265	RUVB1_HUMAN	RUVB1	RuvB-like 1 (EC 3.6.1.-) (49-kDa TATA box-binding protein-interacting protein) (49 kDa TBP-interacting protein)	50538	6.37	127	16 of 52	Enzyme, transcription, DNA associated	Nuclear
Q9Y277	VDAC3_HUMAN	VDAC3	Voltage-dependent anion-selective channel protein 3 (VDAC-3) (hVDAC3) (Outer mitochondrial membrane protein porin 3)	30981	8.9	76	5 of 28	Transport	Mitochondrial
Q9Y2Z0	SUGT1_HUMAN	SUGT1	Suppressor of G2 allele of SKP1 homolog (Sgt1) (Putative 40-6-3 protein)	38065	4.8	90	7 of 16	Regulatory, DNA associated	Nuclear
Q9Y3F4	STRAP_HUMAN	STRAP	Serine-threonine kinase receptor-associated protein (UNR-interacting protein) (WD-40 repeat protein PT-WD)	38756	4.75	78	10 of 63	RNA binding, translation	
Q9Y3F5	Q9Y3F5_HUMAN	Q9Y3F5	A6 related protein (Hypothetical protein DKFZp434O0516) (Twinfilin-like protein) (PTK9L protein)	39751	6.85	61	7 of 36	Unknown	Unknown
Q9Y3I0	Q9Y3I0_HUMAN	Q9Y3I0	Hypothetical protein HSPC117 (DJ149A16.6 protein) (Novel protein HSPC117)	55688	7.23	75	11 of 28	Unknown	Unknown
Q9Y490	TLN1_HUMAN	TLN1	Talin 1	271716	5.85	71	20 of 54	Structural	Cytoskeletal
Q9Y4L1	OXR_P_HUMAN	OXR_P	150 kDa oxygen-regulated protein precursor (Orp150) (Hypoxia up-regulated 1)	111494	4.88	157	14 of 18	Chaperone	Endoplasmic reticulum
Q9Y512	SAM50_HUMAN	SAM50	SAM50-like protein CGI-51	51962	6.5	82	9 of 36		Mitochondrial
Q9Y617	SERC_HUMAN	SERC	Phosphoserine aminotransferase (EC 2.6.1.52) (PSAT)	40795	7.77	55	8 of 39	Enzyme, cell cycle	

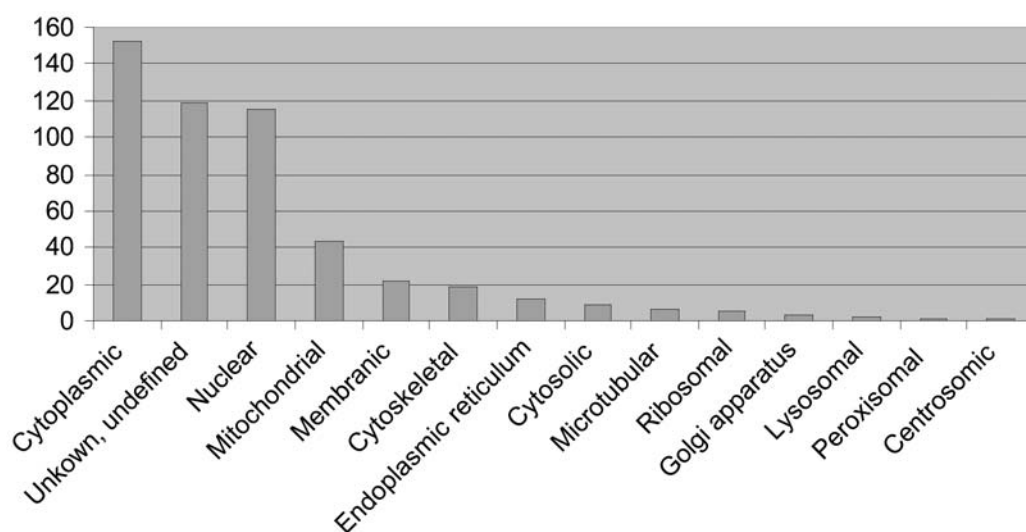


Figure 5. Subcellular location of human immature T-cell line proteins. The proteins of Table I were sorted according to their location. The annotated location for each protein is given in Table I.

considered to be a protooncogene because, as previous studies showed, NPM is involved in a form of non-Hodgkin's lymphoma through a chromosomal translocation [t(2;5)(p23;q35)] that complicates NPM1 and ALK, while in a form of acute promyelocytic leukaemia, the chromosomal translocation t(5;17)(q32;q11) involves NPM1 and RARA (33, 34). Additionally, NPM participates in the t(3;5)(q25.1;q34) chromosomal translocation, the product of which, a NPM1-MLF1 fusion protein, is responsible for myelodysplastic syndrome (MDS), which progresses to acute myeloid leukaemia (AML) (35). Finally, we identified SEPT6 (Q14141), found to be related to acute myeloid leukaemia and acute monocytic leukaemia (36), SET (Q01105) which is related to oncogenesis and apoptosis (37, 38), C1IB (Q96IU4) which interacts with TAF1 (39) and IMDH2 (P12268), which is found to be related to the myeloid cell maturation and the development of malignancies and the growth progression of some tumors (40, 41).

In summary, in our present study we constructed a 2-D database for the human immature T-cell line CCRF-CEM. This database comprises 451 different gene products, resulting from MALDI-MS and MALDI-MS-MS analysis of approximately 4,500 spots taken from four 2-D-gels, representing today one of the largest 2-D databases for human and eukaryotic proteomes. In this 2-D database, 17 hypothetical or unknown gene products were included, while for 119 out of the identified proteins, no subcellular localization had been previously annotated. The represented 2-D database will form a useful tool in the study of carcinogenesis and for anticancer research employing the CCRF-CEM cell line as a model.

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