

The Proteome Profile of Two Cell Lines and their Xenografts Isolated from a Patient with Clear Cell Sarcoma (Soft Tissue Melanoma)

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Abstract. We report the establishment of two novel clear cell sarcoma (CCS) cell lines (soft tissue melanoma) from a patient and the production of the corresponding xenografts after xenotransplantation of those cells to NOD/SCID mice. As no comprehensive study on the relevant proteomes of this type of cancer has been reported to date, proteomics technologies were applied in a first attempt to analyze the proteins of the two cell lines and their corresponding primary xenografts. Total protein extracts were separated by two dimensional gel electrophoresis (2-DE) and analysed by MALDI-MS and MALDI-MS-MS following in-gel digestion with trypsin. Protein identification was carried out by peptide mass fingerprint (PMF) and post source decay (PSD), respectively. Comparative analysis revealed that 124 proteins were common between the cell lines and the xenografts; 249 proteins were found to be expressed only in the proteome of the cell lines, while 178 proteins were expressed only in the proteome of xenografts. Our results demonstrated that both cell lines and xenografts were positive for vimentin and S100

reported as markers for CCS. After functional analysis, 27 different protein groups were identified in the analysed proteomes, including apoptosis-related proteins, oncogenes and several proteins closely related to TP-53 and NF-κB pathways. Furthermore, the proteins nestin, stem cell growth factor CLC11 and mdr-1, closely related to malignant-melanoma-initiating cells, were found to be expressed in both the cell lines and their corresponding xenografts. Since there are no data concerning protein expression in CCS, this study may contribute to the understanding of the molecular basis of the disease, while the cell lines as well as the developed xenografts may be used as tools for the development of new therapeutic strategies to tackle this rare but fatal malignancy.

Human malignant melanoma is a highly aggressive and drug resistant type of cancer. There are an estimated 132,000 new melanoma skin cancer cases worldwide each year, while in European population death rates from melanoma have been continuously and significantly increasing over time. In Western Europe and in Mediterranean countries, this increase has affected young people (aged 25-50 years) by a magnitude of 3% to 8% per year (1, 2). Nowadays, the incidence of melanoma appears to be on a steady rise throughout the world, mainly due to increased ultraviolet exposure from the sun. In its early stages, malignant melanoma can be successfully cured, but once it has progressed to the metastatic stage, it is extremely difficult to treat and appears resistant to most current therapies (3). Despite many years of intensive laboratory and clinical research, the sole effective cure is surgical dissection of the primary tumor before it achieves a thickness greater than 1 mm (3, 4). Thus, the need to find a melanoma “signature” is critical. What is more important

Abbreviations: PMF, Peptide mass fingerprint; PSD, post source decay; DMEM, Dulbecco's modified Eagle's medium; FCS, fetal calf serum.

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though is to find a proper model to study melanoma and to determine the limitations of such a system.

Clear cell sarcoma of tendons and aponeuroses (CCS), or soft tissue melanoma, is a rare malignant tumor with a poor prognosis described for first time by Enzinger in 1965. This type of malignancy is a rare tumor derived from neural crest cells and usually occurs in tendons and aponeuroses of the extremities of young adults (between 20 and 40 years old). In patients, the tumor is usually found in the distal lower extremities, especially the lower limbs, while there is a high propensity for regional or distant metastases, frequently attached to tendons or aponeuroses (5). It behaves like a high-grade soft tissue sarcoma and is associated with poor overall survival. CCS has been observed to be more prevalent in Caucasians than in African Americans or Asians. The clinical course is difficult to predict as metastases may appear after a quiescent period of time, or may result in a rapid and fatal progression (6).

Because of the melanocytic features that the tumor exhibits, its distinction from malignant melanoma may be difficult. Immunohistochemical studies in most cases show that the neoplastic cells are positive for HMB-45 and react with antibody against S100 protein. Most cases show a reciprocal cytogenetic translocation t(12;22)(q13;q12) that creates a unique chimeric fusion EWSR1/ATF1 gene transcript (7). The beneficial effects of adjuvant chemotherapy and radiotherapy have not been fully evaluated. The disease tends to recur locally and after a protracted clinical course it metastasizes, finally leading to death (6).

In this study we report two novel primaries cell lines established from a patient with CCS and their corresponding primary xenografts after the xenotransplantation of these cells to SCID mice. We applied differential proteomic analysis in order to study the proteomes and elucidate potential differences between the *ex vivo* (cell lines) and the *in vivo* material (xenografts).

Materials and Methods

Patient data. A sample removed from a metastatic lymph node after surgery from a 53-year old male Greek patient used to establish a cell line from which two clones have been developed while at the very low passages. After the surgery, the patient initially received radiotherapy and consequently chemotherapy using a chemotherapeutic schedule that consisted of Farmorubicin (epirubicin; Pfizer Hellas SA), Oncorin (vincristin; Pharmaserv-Lilly, Hellas) and Deticene (dacarbazine; Aventis Pharma, Hellas) but the patient finally died due to the disease a year later and after several metastases had developed. PCR analysis of the primary cell line revealed that this cell line was strongly positive for gp100, positive for trp2, and negative for Melan A, trp1 and tyrosinase.

Materials and reagents. Culture media and fetal calf serum (FCS) were obtained from Invitrogen-GIBCO (Invitrogen Ltd, UK). Six to eight week-old male NOD.CB17-*Prkdc^{scid}*/J mice were obtained from

Jackson labs (Bar Harbor, ME, USA) and maintained under specific pathogen-free flora in the animal facility of the Biomedical Research Foundation of the Academy of Athens until use. All animals were treated according to Greek laws (2015/92) and the instructions of the EU and the European council (86/609 and ETS123, respectively) governing the use and handling of animals in experiments.

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.

Cell cultures and xenografts. In order to establish the initial primary cell line, a piece of the surgically excised lymph node was minced and small tissue fragments were placed in 100-mm plastic culture dishes. Cells were grown in RPMI-1640 medium supplemented with 10% heat-inactivated FCS, 2 mM L-glutamine and antibiotics. After 2 days, most of the tissue fragments had attached to the culture dish, allowing addition of more medium. After 5 days, many small cells with spindle to dendritic shapes were growing out of the tissue fragments. These presumptive tumor cells increased rapidly in number and could be trypsinized and transferred to larger culture vessels within 2 weeks after setting up the culture. The cell line thus obtained was designated GRmel8. After one passage to immunocompromised mice and further subculture, two clones have been identified, designated as UDCCS-1 and WDCCS-1

For the establishment of the two clones the original cell line was inoculated into the two axillary regions of 5 mice at a density of 1×10^6 cells per injection. One tumor was developed which subsequently was subcultured. From the culture of this tumor, two clones (mel8A and mel8B) were isolated that were further expanded and then passed into animals until the fourth passage. These two tumors (termed 4p8A and 4p8B) as well as the two initial clones established were finally analyzed for their proteome.

Two-dimensional gel electrophoresis. Cells in culture (40×10^6) or xenografts (>1 g) were washed 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, Basel, Switzerland) per 50 ml of suspension buffer] and phosphate inhibitors (0.2 mM Na₂VO₃ and 1 mM NaF). The produced mixtures were lysed by sonication at 3×60 s in 35% amplification and the suspension was centrifuged at 14000×g for 30 min. The protein content of the supernatants was determined using an EXPERION Automated Electrophoresis Station in combination with Protein 260 Analysis Kit™ (Biorad) according to the manufacturer's instructions.

2-D Gel electrophoresis was performed as reported previously (8). Total protein (1 mg) was applied on immobilized pH 3-10 non-linear gradient strips in sample cups at their acidic and basic 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 (180×200×1.5 mm), running at 50 mA per gel in a 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 water 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 described elsewhere (9). Spots were automatically detected by Melanie 4.02 software on the Coomassie blue-stained gel, excised by a 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, Allered, Denmark). Each dried gel piece was rehydrated with 5 µl of 1 mM ammonium bicarbonate containing 50 ng trypsin (Roche Diagnostics) and left in the dark overnight at room temperature. Twenty microlitters of 50% acetonitrile, containing 0.3% trifluoroacetic acid were added to each gel 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 II, Bruker Daltonics). Matching peptide and protein searches were performed automatically, as described by Berndt *et al.* (9). 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% (25 ppm) was allowed. Unmatched peptides or peptides with up to one missed cleavage site were not taken into account. 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 or 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 $p < 0.02$ were considered significant. The identified proteins were annotated on the gel image by hand.

Results

The protein extracts from the two cell lines and the corresponding xenografts were separated by 2-DE electrophoresis on IPG strips and the spots were visualized with colloidal Coomassie blue (Figure 1). Two gels for each of the samples (the two cell lines and the corresponding xenografts) were run and analyzed independently by the 2D ImageMaker software. Approximately 1,250 protein spots per gel were detected. All the detected spots were excised from the gels and further analyzed for PMF with MALDI-MS in a time-of-flight mass spectrometer. Protein

identification by the peptide mass matching was performed automatically. Using an internal peptide standard to correct the measured peptide masses we were able to use very narrow windows of mass tolerance (0.0025%) and hence increase the confidence of identification, as well as the total identification rate up to 85%, resulting in the identification of 551 different gene products.

The analysis of the results indicated that the two cell lines expressed a total of 373 different gene products while the xenografts were found to express a total of 302 different gene products (Figure 2). Comparative analysis indicated that 124 proteins were commonly expressed between the cell lines and the xenografts, 249 proteins expressed only in the cell line proteomes, while 178 proteins were expressed only in the xenograft proteomes. Tables I, II and III present the common and the differentially expressed proteins identified, their SwissProt accession numbers, symbol, full name, molecular weight, MASCOT score of the identification, and protein coverage. Twenty mouse proteins including albumin, hemoglobin chains, ferritin and globin were found included in the xenograft proteome, possibly related to the host organism (mouse). The highest score (416) of identification corresponded to the protein desmulin (O15061) belonging to the cell line proteome, the highest score (287) of the xenograft proteome corresponded to mouse transferrin (Q58E69), while of common proteins the human 78 kDa glucose-regulated protein (P11021) was identified with a score of 357. Furthermore, the sex-determining region Y protein (P79181) and the G-gamma-hemoglobin mutant (Q14476) specific for the Greek population were identified in both cell lines and xenograft (Table I) (10, 11).

Subcellular localization. The subcellular localization of the identified proteins was sought in publicly accessible databases (SwissProt and GeneAtlas). Of the proteins identified in the cell lines and the xenografts, 27% and 28% respectively were found to be localized in the cytoplasm, 19% and 24%, respectively, in the nucleus, 18% and 14% respectively, in the mitochondria and 6% and 4% respectively were found to be membrane-related (Figure 3). For 5% of the cell line proteins and 10% of the xenograft proteins, no data were found related to their localization. The subcellular location of each protein is given in Tables I, II and III.

Function. Searching SwissProt and GeneAtlas, 27 different protein functional groups were identified in the proteomes (Figure 4). Enzymes represented the most abundant fraction of the proteome (21% and 18% for the cell line and xenograft proteome, respectively), while no reports were found for the function of 10% of the xenograft and 5% of the cell line proteins. Furthermore, structural proteins, transcription factors, DNA- and RNA-associated proteins were identified. It is interesting that the cell line proteome

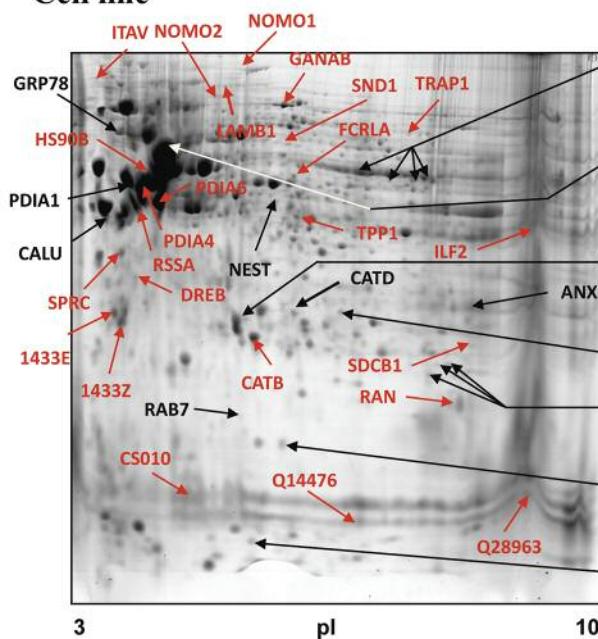
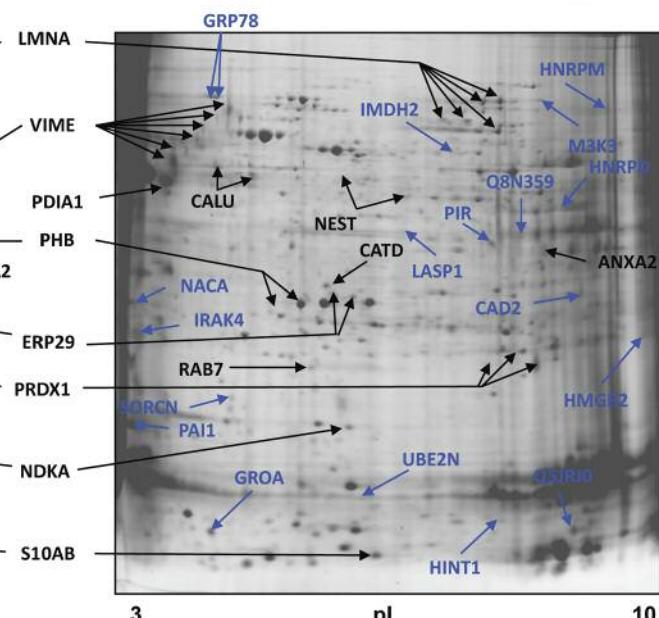
Cell line**Xenograft**

Figure 1. Representative two-dimensional gels of total protein extracts from the CCS cell lines (left) and their corresponding xenografts (right). Proteins were extracted and separated on IPG strip pH 3-10 non-linearly, followed by a 12% SDS-polyacrylamide gel. The gels were stained with Coomassie blue. With red color representative proteins exclusively expressed in the cell lines were marked, with blue color representative proteins exclusively expressed in the xenografts were marked, with black color representative proteins expressed in both cell lines and xenografts. were marked.

includes 31 proteins related to apoptosis and 35 proteins closely related to oncogenesis and cancer. In xenografts, 26 proteins were identified related to apoptosis and 35 proteins were related to cancer. The function of each protein is also given in Tables I, II and III.

Discussion

Clear cell sarcoma of tendons and aponeuroses or soft tissue melanoma is a rare malignant tumor with a poor prognosis, derived from neural crest cells and the tumor is usually found in the distal lower extremities, especially the lower limbs, while there is a high propensity for regional or distant metastases, frequently attached to tendons or aponeuroses (5, 6). In cancer, established cell lines have proven to be potent tools towards the understanding of the biological and molecular characteristics of malignancies and are widely used in terms of making more accurate diagnoses and developing therapeutic strategies. Even more valuable tools towards this target are xenografts representing models of this disease that are more relevant to the clinical situation.

However, only very few CCS cell lines that are well documented have been reported to date (12-16). We herein present the proteome profiles of two newly established CCS cell lines, as well as their two corresponding xenografts. These

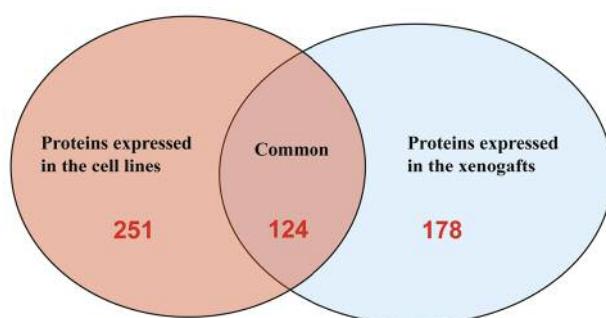


Figure 2. Visualization of the comparative of the identified proteins as shown in Tables I, II and III.

cell lines and their xenografts originated from the same male patient confirmed by the identification of a sex-determining region Y protein (P79181) and of the G-gamma-hemoglobin (Q14476) a specific for the Greek population mutant in both the cell line and in the xenografts proteome (10, 11).

The immunohistochemical profile of CCS of tendons and aponeuroses reveals that cells are highly positive for vimentin (96%), HMB-45 (90%), MITF (71%), S100 (64%), and Melan-A103/Melan-A (50% and 43% respectively) (5, 7). Our results demonstrated that both cell lines and xenografts

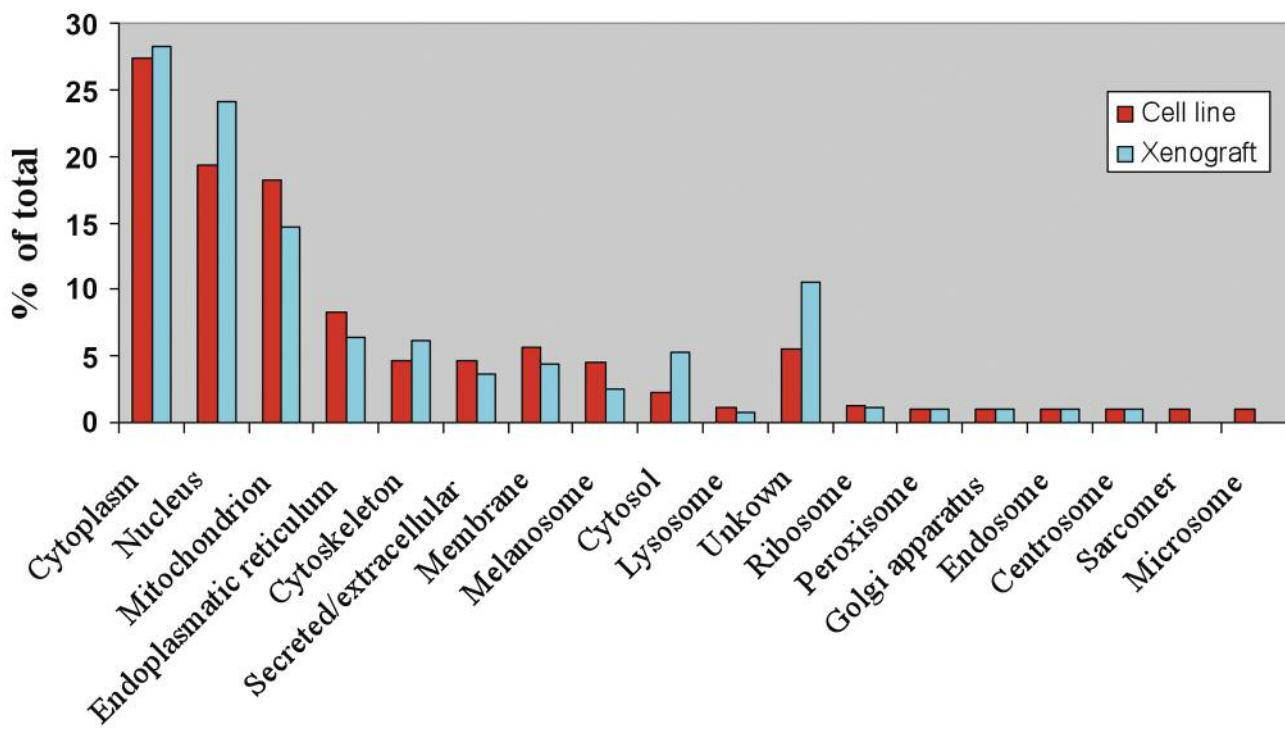


Figure 3. Subcellular localization of the identified protein. The proteins in Tables I, II and III were categorized according to their localization in the cells. Red bars: localization of the cell line proteins, blue bars: localization of the xenograft proteins.

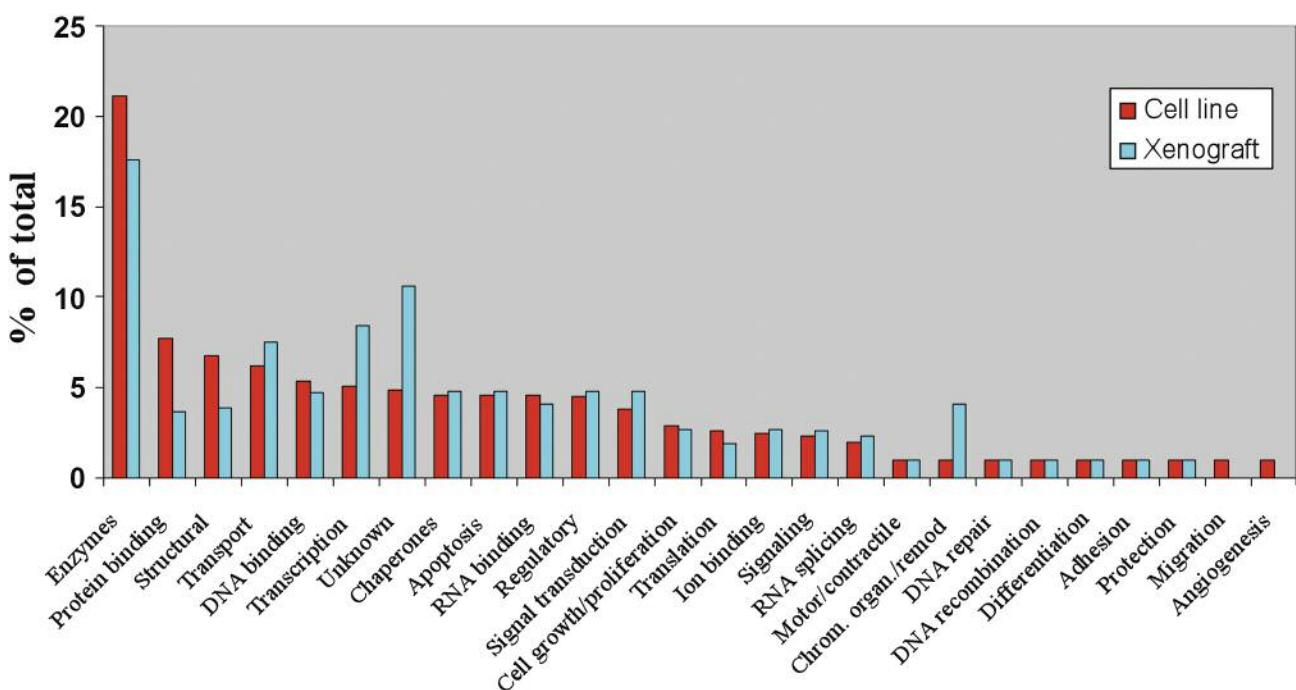


Figure 4. Classification of the identified proteins into functional groups. Protein molecules and their function are given in Tables I, II and III. Red bars: functions of the cell line proteins, blue bars: functions of the xenograft proteins.

were positive for vimentin and S100 (Table I) in accordance with the CCS diagnosis. It was not possible to identify Melan-A in the cell lines nor to the xenografts, which again is in accordance with PCR analysis of the primary cell line, but despite to the absence of Melan-A, we have identified 22 proteins previously reported to be expressed in melanosomes (17). Of these proteins, 13 were found exclusively in the cell line proteomes, while 9 were common to both the xenograft and cell line proteomes. The expression of melanosome-related proteins supports the neural crest origin of CCS, while the differences between the cell lines and the xenografts may reflect different differentiation stages as the appearance of melanosomes has been reported as being related to the maturation stage of the CCS (18). Another protein previously described to be expressed in melanocytes and melanoma and which may be useful for the diagnosis of the melanoma is Fc receptor-like and mucin-like 1 protein (FCRL), also suggested to be a potential target for melanoma immunotherapy (19). Our results indicated that the FCRLa protein (Q7L513) was identified in the cell line proteomes.

Although there are clear differences between *in vitro* (cell line) and *in vivo* (xenograft) melanosome-related proteins, the common proteins might be interesting for further study. Previous reports suggest that many melanoma-associated antigens are recognized by cytotoxic T lymphocytes, thus indicating a possible importance of these proteins in the development of novel therapeutic interventions towards the treatment of that malignancy (20).

Moritake *et al.* (18) reported that C-MYC may be involved in the malignant progression of CCS. Interestingly, among the common proteins identified here are two that are closely related to the C-MYC pathway, namely ENOA/ MBP-1 (P06733) and NDRG1 (Q92597). The first is reported to bind the C-MYC promoter while the second is said to be a downstream target of the N-NYC (21-23). An additional finding towards the central role that C-MYC may play in the progression of the disease is that two more C-MYC related proteins were exclusively identified in xenografts. The hnRNP is reported to be implicated in cellular proliferation with TIAL-1 by a C-MYC dependent pathway and the PAI-1 is a putative up-regulated C-MYC gene.

In an attempt to identify new markers for the disease, Schaefer *et al.* reported the up-regulation of ERBB3 as such a marker (24). Interestingly among the common proteins identified, we identified the proliferation-associated protein 2G4 (PA2G4, Q9UQ80), which has previously been reported to be involved in growth regulation via an ERBB3-regulated signal transduction pathway (25).

An interesting finding regarding the molecular events leading to CCS was the identification of several proteins expressed in both xenografts and cell lines related to the regulation of apoptosis. From these apoptosis-related proteins,

18 were found to be common while 13 were exclusively expressed in the cell lines and 8 in the xenografts. The group of common apoptosis-regulated proteins included 7 heat shock proteins (HSP71, CH60, HSP7C, HSPB1, TRAP1) as well as nucleophosmin (NPM), cathepsin D (CATD), galectin-1 (LEG1), calreticulin (CALR), prohibitin (PHB), the translationally-controlled tumor protein (TCTP) and the tumor metastatic process associated protein (NDKA). In addition to these proteins, in the cell line proteome the HS1-associating protein X-1 (HAX1), a dynamin-like protein (OPA1), the programmed cell death protein 8 (PDCD8), gelsolin (GELS), cathepsin B (CATB), annexin A4 and A5 (ANXA4, ANXA5), the tumor rejection antigen 1 (ENPL) the DNA damage-binding protein 1 (DDB1) and the CDK5 activator-binding protein C53 (CK5P3) were also identified. Exclusively in the xenograft proteomes we have identified thioredoxin (THIO), two thioredoxin-like proteins (TXNL1 and TXND5), cofilin-1 (COF1), clusterin (Q9ERD1), an leucine-rich acidic nuclear protein (AN32A), a protein involved in the ARE/AUBP-mediated modulation of BCL2 mRNA decay during apoptosis (HNRPD), interleukin-17A (IL17) and a TSC22 family protein which protects T-cells from IL2 deprivation-induced apoptosis through the inhibition of FOXO3 transcriptional activity leading to the down-regulation of the pro-apoptotic factor BCL2 (26). Apart the apoptosis-related proteins we identified 5 proteins previously suggested as oncogenes (PDIA1, FUMH, GRP75, IF32, PARK7) and two as antioncogenes (ENOA, NPM) expressed in both cell line and xenograft. Three oncogenes (LEPRE1, SMC3, FKBP4) were found to be expressed only in the cell line, while seven oncogenic proteins (PSD10, F10A1, RAB25, HNRPD, RAB37, PHF2, ITPA) were only found expressed in xenografts. In order to characterize the molecular trail, these findings must be considered together with the evidence that several proteins closely related to TP-53 and NF- κ B pathways have been identified to be commonly and differentially expressed in the studied materials. Furthermore, the differential expression of these proteins in the cell lines and in xenografts is not yet known, the elucidation of their role in CCS needs more study.

Tumour-initiating cells capable of self-renewal and differentiation, which are also responsible for tumour growth, have been identified in human haematological malignancies and solid cancers. If such minority cell populations are associated with tumour progression in human patients, specific targeting of tumour-initiating cells could be a strategy to eradicate types of cancer currently resistant to systemic therapy. Schatton *et al.* (27) and Keshet *et al.* (28) have demonstrated that chemoresistant cells expressing MDR1+ and/or ATP-binding cassette transporter (ABCB5) were capable of inducing regression of melanomas in xenotransplantation models. They advocate the existence of malignant-melanoma-initiating cells (MMIC) that exhibit

stem cell characteristics and increased survival due to a treatment-resistant phenotype. The proteome analysis of the cell lines and their corresponding xenografts revealed some stem cell characteristics. These include the protein nestin (P48681) and the stem cell growth factor CLC11 (Q9Y240) that were found to be expressed in both the proteome of the cell lines and their corresponding xenografts. Nestin is an intermediate filament protein expressed in the cytoplasm of neuroepithelial stem cells, associated also with multiple stem cell populations (29). An increased expression of nestin in malignant melanoma it was previously observed (30), suggesting the participation of a stem cell population in the disease. In accordance with this the expression of nestin in the analysed samples may signify the presence of a nestin-positive undifferentiated subpopulation among the cells, which may further suggest the existence of a MMIC population in both cell lines and xenografts. Furthermore, consistent with the observation that MMIC are chemoresistant, we identified P-glycoprotein class IA (Q28963) in the cell line proteome. The absence of that protein from the xenograft proteome possibly relates to the limited number of MMIC cells in the tumor *in vivo*.

Finally, the major goal of our study was the identification of the differences between the *in vitro* (cell lines) and the corresponding *in vivo* (xenografts) materials used for the cancer studies. The proteomic analysis indicated 249 proteins were found to be expressed only in the cell line proteomes, while 178 proteins were expressed only in the xenograft proteomes. These differentially expressed proteins may be important in the response to treatment in the cell lines and their xenografts and may reflect the disease outcome and metastasis as it was observed in humans (31).

Concluding, we herein present two novel CCS cell lines, their corresponding xenografts and the proteome profiles for them. To date there are no data, at least to our knowledge, concerning the proteome profiling of CCS, thus this study may help in the understanding of the molecular basis of this rare but fatal disease, while the cell lines and the xenografts reported herein may be useful tools in the development of new therapeutic strategies.

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Table I. Common proteins identified in the human CCS cell lines and their corresponding xenografts. Proteins were extracted and separated by 2-D gel 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, SWISS-PROT accession numbers, or the accession numbers of other databases. The theoretical molecular weight, the probability of a random identification (Score), the percentage of the coverage of the protein by the identified peptides, as well as the annotated subcellular location and function are listed. A brief comment on the precise function of each protein is also listed. Score is $-10^{\ast}\log(P)$, where P is the probability that the observed match is a random event (MASCOT, <http://www.matrixscience.com>) ; score >27 indicates $p<0.05$.

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
O14979	HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like (JKTBPI delta6)	137	33	30336.70	Nucleus, cytoplasm	DNA binding, transcription	
O43852	CALU_HUMAN	Calumenin precursor (Crocalbin) (IEF SSP 9302)	138	48	37197.58	Endoplasmic reticulum, secreted, melanosome	Regulatory, transport	Involved in regulation of vitamin K-dependent carboxylation.
075531	BAF_HUMAN	Barrier-to-autointegration factor (Breakpoint cluster region protein 1)	104	64	10280.11	Nucleus, cytoplasm	DNA associated, chromatin organization, remodeling	Plays fundamental roles in nuclear assembly, chromatin organization, gene expression and gonad development.
075934	BCAS2_HUMAN	Breast carcinoma amplified sequence 2 (DNA amplified in mammary carcinoma 1 protein)	136	62	26229.04	Nucleus	RNA binding, structural splicing	Associated with the spliceosome.
075947	ATP5H_HUMAN	ATP synthase D chain, Mitochondrion (EC 3.6.3.14)	123	80	18405.48	Mitochondrion	Enzyme	One of the chains of the nonenzymatic component (CF(0)) of the Mitochondrion ATPase complex.
094760	DDAH1_HUMAN	NG,NG-dimethylarginine dimethylaminohydrolase 1 (EC 3.5.3.18) (Dimethylargininase 1)	57	25	31313.02	Cytosol	Enzyme, signal transduction	Hydrolyzes NG,NG-dimethyl-L-arginine (ADMA) and N(G)-monomethyl-L-arginine (MMA) which act as inhibitors of NOS. Has a role in nitric oxide generation.
P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, Mitochondrion precursor (EC 1.4.1.3) (GDH)	227	55	61701.32	Mitochondrion	Enzyme, signaling	May be involved in learning and memory reactions by increasing the turnover of the excitatory neurotransmitter glutamate.
P00441	SODC_HUMAN	Superoxide dismutase [Cu-Zn] (EC 1.15.1.1)	57	43	16022.95	Cytoplasm	Enzyme	Destroys radicals which are normally produced within the cells.
P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protein 2) (PRP 2)	143	53	44854.24	Cytoplasm	Enzyme	Glycolytic enzyme and a polymerase alpha cofactor protein.

Table I. *continued*

Table I. *continued*

Accession number	Protein symbol	Protein name	Score (%)	Coverage MW	Protein	Subcellular localisation	Function	Brief comment
P02511	CRYAB_HUMAN	Alpha crystallin B chain (Alpha(B)-crystallin) (Rosenthal fiber component)	135	63 20146.42	Cytoplasm, nucleus	Transport, protein binding, anti-apoptosis		May contribute to the transparency and refractive index of the lens.
P02545	LMNA_HUMAN	Lamin-A/C (70 kDa lamin)	349	49 74379.81	Nucleus	Structural, chromatin organization, transcription		Component of the nuclear lamina, which is thought to provide a framework for the nuclear envelope and may interact with chromatin. It is involved in the modulation of TGF-beta1 on collagen production, a marker of mesenchymal differentiation <i>via</i> nuclear phosphatases such as PPP2R3B. Protects cells from the toxic effects of hydrogen peroxide.
P04040	CATA_HUMAN	Catalase (EC 1.11.1.6)	168	37 59815.80	Peroxisome	Enzyme		
P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase)	163	52 39720.44	Cytosol	Enzyme		
P04179	SODM_HUMAN	(Lung cancer antigen NY-LU-1) Superoxide dismutase [Mn], Mitochondrion precursor (EC 1.15.1.1)	89	51 24877.62	Mitochondrion	Enzyme		Destroys radicals. The manganese superoxide dismutase catabolic pathway of activated oxygen species and free radical detoxification, destroying radical which are normally produced within the cells and which are toxic to biological system.
P04181	OAT_HUMAN	Ornithine aminotransferase, mitochondrial precursor (EC 2.6.1.13) (Ornithine--oxo-acid aminotransferase)	150	44 48846.33	Mitochondrion	Enzyme		
P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH)	195	56 36070.42	Cytoplasm	Enzyme, apoptosis		Has glycolytic activity. It is also involved in membrane trafficking in the early secretory pathway. Has a role in cell death/apoptosis.
P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH)	132	47 36070.42	Cytoplasm	Enzyme		It is involved in membrane trafficking.

Table I. *continued*

Table I. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P04792	HSPB1_HUMAN	Heat-shock protein beta-1 (HspB1) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27)	122	44	22825.51	Cytoplasm, cytoskeleton	Chaperone, anti-apoptosis	Involved in stress resistance and actin organization.
P05387	RLA2_HUMAN	60S acidic ribosomal protein P2 (NY-REN-44 antigen) (Renal carcinoma antigen NY-REN-44)	128	93	11657.85	Ribosome	Translation, RNA binding	
P05388	RLAO_HUMAN	60S acidic ribosomal protein P0 (L10E) ATP synthase beta chain, Mitochondrion precursor (EC 3.6.3.14)	145	55	34422.86	Ribosome	Translation, RNA binding	
P06576	ATPB_HUMAN	ATP synthase beta chain, Mitochondrion precursor (EC 3.6.3.14)	181	54	56524.60	Mitochondrion	Enzyme	
P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neuronal enolase) (NNE) (MBP-1) (MPB-1)	214	59	47350.41	Cytoplasm, membrane	Enzyme, transcription, cell growth	
P06748	NPM_HUMAN	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Numatrin) (Nucleolar protein NO38)	115	41	32725.91	Nucleus	Transcription, anti-apoptosis, signal transduction, transport, cell proliferation	
P07237	PDIA1_HUMAN	Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-hydroxylase subunit beta)	64	27	57479.82	Endoplasmic reticulum, melanosome	Enzyme	
P07339	CATD_HUMAN	Cathepsin D precursor (EC 3.4.23.5) (Contains: Cathepsin D light chain; Cathepsin D heavy chain)	141	44	45036.82	Lysosome, melanosome	Enzyme, apoptosis	Acid protease active in intracellular protein breakdown. Involved in the pathogenesis of several diseases such as breast cancer and possibly Alzheimer disease. Involved in proteolytic degradation, cell invasion, and apoptosis. Has a role in promoting cancer cell proliferation and invasion.
P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Lipocortin II)	265	73	38676.86	Secreted, membrane, melanosome	Regulatory, signaling, transport, protein binding,	Calcium-regulated membrane-binding protein whose affinity for calcium

Table I. *continued*

Table I. *continued*

Accession number	Protein symbol	Protein name	Score (%)	Coverage MW	Protein	Subcellular localisation	Function	Brief comment
		(Calpastatin I heavy chain) (Chromobindin-8) (p36)					cell growth	is greatly enhanced by anionic phospholipids. It binds two calcium ions with high affinity. May be involved in heat-stress response.
P07437 P07954	TBB2_HUMAN FUMH_HUMAN	Tubulin beta-2 chain Fumarate hydratase, Mitochondrion precursor (EC 4.2.1.2) (Fumarae)	221 80	56 32	50095.14 54773.23	Cytoplasm Mitochondrion, cytoplasm	Structural Enzyme	Stimulates both the proliferation and differentiation of osteoclasts precursors through production of GM-CSF (granulocyte-macrophage colony-stimulating factor) and TNFSF11, respectively.
P08107	HSP71_HUMAN	Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2)	247	52	70294.14	Nucleus, mitochondrion, endoplasmic reticulum	Chaperone, anti-apoptosis	Acts as a tumor suppressor protein. Antioncogene FH germline mutation associated to early onset uterine and skin leiomyomata and renal cell cancer.
P08559	ODPA_HUMAN	Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial precursor (EC 1.2.4.1)	102	24	43951.87	Mitochondrion	Enzyme	In cooperation with other chaperones, Hsp70s stabilize preexistent proteins against aggregation and mediate the folding of newly translated polypeptides in the cytosol as well as within organelles.
P08670	VIME_HUMAN	Vimentin	330	74	53545.06	Cytoskeleton	Structural	These chaperones participate in all these processes through their ability to recognize nonnative conformations of other proteins. They bind extended peptide segments with a net hydrophobic character exposed by polypeptides during translation and membrane translocation, or following stress-induced damage. Catalyzes the overall conversion of pyruvate.
							Class-III intermediate filaments	in various non-epithelial cells, especially mesenchymal cells. Highly expressed in fibroblasts, some expression in T- and B-lymphocytes, and little or no expression in Burkitt's lymphoma cell lines. Expressed in many hormone-independent mammary carcinoma cell lines.

Table I. *continued*

Table I. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P09211	GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1)	100	60	23438.07	Cytoplasm	Enzyme	Conjugation of reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles. It is a susceptibility factor in squamous-cell carcinoma of the esophagus and in Barrett's esophagus carcinoma. Candidate gene for sensitive detection in plasma or serum of cancer gastric and prostatic, using DNA methylation markers.
P09382	LEGI_HUMAN	Galectin-1 (Beta-galactoside-binding lectin L-14-1) (Lactose-binding lectin 1) (S-Lac lectin 1)	103	70	14917.29	Cytoplasm		May regulate cell apoptosis and cell differentiation. Binds beta-galactoside. Binds CD45, CD3 and CD4. Inhibits CD45 protein phosphatase activity and therefore the dephosphorylation of Lyn kinase. Positive regulation of I-kappaB kinase/NF-kappaB cascade. Regulates tumor angiogenesis.
P09429	HMG1_HUMAN	High mobility group protein 1 (HMG-1) (High mobility group protein B1)	89	34	24918.18	Nucleus	DNA binding, transcription, DNA repair, recombination	Binds preferentially single-stranded DNA and unwinds double stranded DNA. Interacts with TP53 and TP73 (HMGB1-mediated modulation of TP53 and TP73-dependent transactivation) interacting with MSH2, MSH6.
P09936	UCHL1_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (EC 6.-.-.-)	125	66	25150.59	Cytoplasm		Enzyme involved both in the processing of ubiquitin precursors and of ubiquitinated proteins.
P10768	ESTD_HUMAN	S-formylglutathione hydrolase (Esterase D) (EC 3.1.1.1)	77	29	31955.65	Cytoplasm	Enzyme	Serine hydrolase involved in the detoxification of formaldehyde. It is proposed as genetic marker of retinoblastoma.
P10809	CH60_HUMAN	60 kDa heat shock protein, Mitochondrion precursor (Hsp60) (60 kDa chaperonin) (CPN60)	263	60	61187.44	Mitochondrion	Chaperone, regulation of apoptosis	Implicated in mitochondrial protein import and macromolecular assembly. It is involvement in tumorigenesis, functional distinction in pathways involved in senescence.

Table I. *continued*

Table I. *continued*

Accession number	Protein symbol	Protein name	Score (%)	Coverage MW	Subcellular localisation	Function	Brief comment
P11021	GRP78_HUMAN	78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein)	357	53 72402.48	Endoplasmic reticulum, melanosome	Chaperone, signal transduction, anti-apoptosis	Plays a role in facilitating the assembly of multimeric protein complexes inside the ER. Its' expression correlates with histologic differentiation and favorable prognosis in neuroblast tumors. Negative regulation of caspase activity.
P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)	328	62 71082.31	Cytoplasm, melanosome	Chaperone, anti-apoptosis, signal transduction	Chaperone. Isoform 2 may function as an endogenous inhibitory regulator of HSC70 by competing the cochaperones.
P11177	ODPR_HUMAN	Pyruvate dehydrogenase E1 component beta subunit, Mitochondrion precursor (EC 1.2.4.1)	150	51 39536.14	Mitochondrion	Enzyme	Part of a complex that catalyzes the overall conversion of pyruvate to acetyl-CoA and CO ₂ .
P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD)	176	51 59553.12	Cytoplasm	Enzyme	Produces pentose sugars for nucleic acid synthesis and main producer of NADPH reducing power.
P12270	TPR_HUMAN	Nucleoprotein TPR	332	29 265839.71	Nucleus	Transport	Component of the cytoplasmic fibrils of the nuclear pore complex implicated in nuclear protein import. Its N-terminus is involved in activation of oncogenic kinases.
P13645	K1C10_HUMAN	Keratin, type I cytoskeletal 10 (Cyokeratin-10) (CK-10) (Keratin-10) (K10)	121	22 59710.96	Cytoskeleton	Structural	Part of telomere-specific complex, called shelterin. Interaction with POT1 (interaction has previously been implicated in the regulation of telomere length). Chromosomal aberrations involving TPR are a cause of thyroid papillary carcinoma (PACT). Involved in tumorigenic rearrangements with the MET or RAF genes.
P13693	TCTP_HUMAN	Translationally-controlled tumor protein (TCTP)	87	29 19696.62	Cytoskeleton	Ion binding, anti-apoptosis, transport	Involved in calcium binding and microtubule stabilization.

Table I. *continued*

Table I. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
		(Histamine-releasing factor) (HRF)						Found in several healthy and tumoral cells including erythrocytes, hepatocytes, macrophages, platelets, keratinocytes, erythroleukemia cells, gliomas, melanomas, hepatoblastomas, and lymphomas. It cannot be detected in kidney and renal cell carcinoma (RCC).
P13804	ETFA_HUMAN	Electron transfer flavoprotein alpha-subunit, Mitochondrion precursor (Alpha-ETF)	159	50	35399.71	Mitochondrion	Transport, electron transport	The electron transfer flavoprotein serves as a specific electron acceptor for several dehydrogenases.
P14314	GLU2B_HUMAN	Glucosidase II beta subunit precursor (Protein kinase C substrate, 60.1 kDa protein, heavy chain)	134	33	60228.14	Endoplasmic reticulum	Signal transduction	Regulatory subunit of glucosidase II.
P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	184	41	60719.43	Nucleus	RNA binding	Component of the heterogeneous nuclear ribonucleoprotein (hnRNP) complexes.
P15531	NDKA_HUMAN	Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A) (NDP kinase A) (Tumor metastatic process-associated protein) (Metastasis inhibition factor nm23)	156	78	17308.74	Cytoplasm, nucleus	Enzyme, DNA binding, protein binding, regulation of apoptosis	It has a role in the synthesis of nucleoside triphosphates. It was found mutated in aggressive neuroblastoma with a reduced expression in tumor progression to the metastatic phenotype.
P16219	ACADS_HUMAN	Acyl-CoA dehydrogenase, short-chain specific, Mitochondrion precursor (EC 1.3.99.2) (SCAD)	141	50	44610.89	Mitochondrion	Enzyme, electron transport	
P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.1) (EC 5.4.2.4) (EC 3.1.3.13) (Phosphoglycerate mutase 1)	172	55	28768.84	Cytosol	Enzyme	Interconversion of 3- and 2-phosphoglycerate with 2,3-bisphosphoglycerate as the primer of the reaction. Can also catalyze the reaction of EC 5.4.2.4 (synthase) and EC 3.1.3.13 (phosphatase), but with a reduced activity.
P21796	VDAC1_HUMAN	Voltage-dependent	148	69	30736.57	Mitochondrion,	Transport, apoptosis	It serves as a channel for

Table I. *continued*

Table I. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P22626	ROA2_HUMAN	anion-selective channel protein 1 (VDAC-1) (hVDAC1)	146	43	37463.75	Nucleus, cytoplasm	Transport, DNA & RNA binding, RNA splicing	small hydrophilic molecules, involved in cell volume regulation and apoptosis. Involved with pre-mRNA processing. Forms complexes (ribonucleosomes) with at least 20 other different hnRNP and heterogeneous nuclear RNA in the nucleous.
P24666	PPAC_HUMAN	Low molecular weight phosphotyrosine protein phosphatase (EC 3.1.3.48) (LMW-PTP)	85	48	18355.90	Cytoplasm	Enzyme	Acts on tyrosine phosphorylated proteins, low-MW aryl phosphates and natural and synthetic acyl phosphates. Isoform does not possess phosphatase activity. Produces ATP from ADP in the presence of a proton gradient across the membrane. The alpha chain is a regulatory subunit. The proteasome is a multicatalytic proteinase complex which is characterized by its ability to cleave peptides with Arg, Phe, Tyr, Leu, and Glu adjacent to the leaving group at neutral or slightly basic pH. The proteasome has an ATP-dependent proteolytic activity.
P25398 P25705	RS12_HUMAN ATPA_HUMAN	40S ribosomal protein S12 ATP synthase alpha chain, Mitochondrion precursor (EC 3.6.3.14)	69 289	36 58	14727.57 59827.63	Ribosome Mitochondrion	Translation, RNA binding Enzyme	It is a molecular chaperone in the biosynthesis of myeloperoxidase. Promotes folding, oligomeric assembly and quality control in the ER.
P25786	PSA1_HUMAN	Proteasome subunit alpha type 1 (EC 3.4.25.1) (Macropain subunit C2)	93	47	29821.97	Cytoplasm, nucleus	Enzyme	The proteasome is a multicatalytic proteinase complex which is characterized by its ability to cleave peptides with Arg, Phe, Tyr, Leu, and Glu adjacent to the leaving group at neutral or slightly basic pH. The proteasome has an ATP-dependent proteolytic activity.
P27797	CALR_HUMAN	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERp60) (grp60)	201	49	48282.89	Endoplasmic reticulum, cytoplasm, cytosol, secreted, extracellular	Transcription, chaperone, protein binding, regulation of apoptosis, ion binding	Plays an important role in the processing of secretory proteins within the endoplasmic reticulum (ER), by participating in the folding of proteins in the ER. Plays a regulatory role in the
P28331	NUAM_HUMAN	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor (EC 1.6.99.3)	300	52	80490.93	Mitochondrion	Enzyme	
P30040	ERP29_HUMAN	Endoplasmic reticulum protein ERp29 precursor (ERp31) (ERp28)	130	39	29032.18	Endoplasmic reticulum, melanosome	Chaperone, enzyme, transport	
P30041	PRDX6_HUMAN	Peroxiredoxin-6	191	69	25002.19	Cytoplasm, lysosome,	Enzyme	

Table I. *continued*

Table I. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
		(EC 1.11.1.15) (Antioxidant protein 2) (1-Cys peroxiredoxin) (1-Cys PRX)				cytoplasmic vesicles		activation of the transcription factor NF-kappaB. Involved in redox regulation of the cell. Can reduce H ₂ O ₂ and short chain organic, fatty acid, and phospholipid hydroperoxides. May play a role in the regulation of phospholipid turnover as well as in protection against oxidative injury. Fatty acid beta-oxidation enzyme.
P30084	ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial precursor (EC 4.2.1.17) (Short chain enoyl-CoA hydratase Phosphatidyl-lethanolamine-binding protein (HCNPPp) (Prostatic-binding protein) (HCNPPp) (Neuropolyepptide h3)	80	28	31823.30	Mitochondrion	Enzyme	Binds ATP, opioids and phosphatidylethanolamine. Has lower affinity for phosphatidylinositol and phosphatidylcholine. Serine protease inhibitor which inhibits thrombin, neutropepsin and chymotrypsin but not trypsin, tissue type plasminogen activator and elastase. Interacts with ERP27.
P30086	PEBP_HUMAN		86	33	21026.67	Cytoplasm	Signal transduction, protein binding, apoptosis	
P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-60) (ERP60) Alpha-2-macroglobulin receptor-associated protein precursor (Alpha-2-MRAP) (Low density lipoprotein receptor-related protein-associated protein 1)	118	24	57145.90	Endoplasmic reticulum	Chaperone, translation, transport, signal transduction	
P30533	AMRP_HUMAN		194	42	41440.90	Endoplasmic reticulum, cytoplasm, membrane	Chaperone, cell growth, ion binding	Interacts with LRP1/alpha-2-macroglobulin receptor and glycoprotein 330.
P30837	AL1IB1_HUMAN	Aldehyde dehydrogenase X, mitochondrial precursor (EC 1.2.1.3) (ALDH class 2)	171	34	57637.38	Mitochondrion	Enzyme	Involved in the metabolism of corticosteroids, biogenic amines, neurotransmitters, and lipid peroxidation.
P31930	UQCR1_HUMAN	Ubiquinol-cytochrome-c reductase complex core protein I, mitochondrial precursor (Ubiquinol-cytochrome-c reductase complex core	208	48	53269.68	Mitochondrion	Enzyme, electron transport	It is a component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is part of the mitochondrial respiratory chain. This

Table I. *continued*

Table I. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P31937	3HIDH_HUMAN	protein 1) (Core protein I) (Complex III subunit 1)	100	44	35704.91	Mitochondrion	Enzyme	protein may mediate formation of the complex between cytochromes c and c1.
P31942	HNRH3_HUMAN	3-hydroxyisobutyrate dehydrogenase, Mitochondrion precursor (EC 1.1.1.31) (HIBADH)	130	53	36960.10	Nucleus	RNA binding, RNA splicing	Involved in the splicing process and participates in early heat shock-induced splicing arrest. Due to their great structural variations the different isoforms may possess different functions in the splicing reaction.
P31948	STIPI1_HUMAN	Stress-induced-phosphoprotein 1 (STI1) (Hsc70/Hsp90-organizing protein) (Hop)	213	47	63226.64	Cytoplasm, nucleus	Chaperone	Mediates the association of the molecular chaperones HSC70 and HSP90.
P31949	S10AB_HUMAN	Protein S100-A11 (S100 calcium-binding protein A11) (Protein S100C) (Calgizzarin) (MLN 70)	79	56	11846.87	Cytoplasm, nucleus	Signal transduction, ion binding	May be functioning in motility, invasion, and tubulin polymerization (negative regulation of cell proliferation).
P32322	P5CR1_HUMAN	Pyrroline-5-carboxylate reductase 1 (EC 1.5.1.2) (P5CR 1) (P5C reductase 1)	189	54	33567.64	Mitochondrion	Enzyme	
P35232	PHB_HUMAN	Prohibitin	210	72	29842.92	Mitochondrion	Transcription, signal transduction, regulation of apoptosis	Inhibits DNA synthesis. It binds to the Rb protein as well as E2F and this binding was necessary to suppress cell proliferation. It is potential tumor suppressor regulating E2F1 function. An anti-proliferative protein, a regulator of cell-cycle progression and in apoptosis.
P38159	HNRPG_HUMAN	Heterogeneous nuclear ribonucleoprotein G (hnRNP G) (RNA-binding motif protein, X chromosome) (Glycoprotein p43)	108	27	42306.33	Nucleus	RNA binding, RNA splicing	
P38646	GRP75_HUMAN	Stress-70 protein, Mitochondrion precursor (75 kDa glucose-regulated	333	57	73919.88	Mitochondrion	Chaperone, regulatory, transcription	Implicated in the control of cell proliferation and cellular aging. May also act as a chaperone.

Table I. *continued*

Table I. *continued*

Accession number	Protein symbol	Protein name	Score (%)	Coverage	Protein MW	Subcellular localisation	Function	Brief comment
		protein) (GRP75)						Protooncogene, playing a role in the control of cell proliferation, controls centrosome duplication via modulating centrosomal localization of TP53. Interacting HSPD1 through its N-terminal region (involvement in tumorigenesis, functional distinction in pathways involved in senescence), a good candidate target for cancer therapy.
P47756	CAPZB_HUMAN	F-actin capping protein beta subunit (CapZ beta)	95	44	31484.84	Cytoplasm, cytoskeleton	Structural	F-actin-capping proteins bind to the fast growing ends of actin filaments thereby blocking the exchange of subunits at these ends. Component of the ubiquinol-cytochrome c reductase complex.
P47985	UCRL_HUMAN	Ubiquinol-cytochrome c reductase iron-sulfur subunit, Mitochondrion precursor (EC 1.10.2.2)	87	27	29918.48	Mitochondrion	Enzyme, electron transport	Expressed in CNS stem cells. Playing a role in nervous system development and upon terminal neural differentiation, down-regulated and replaced by neurofilaments.
P48681	NEST_HUMAN	Nestin	210	30	177169.96	Cytoskeleton	Structural, transport, differentiation	Promotes the GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis.
P49411	EFTU_HUMAN	Elongation factor Tu, Mitochondrion precursor (EF-Tu) (P43)	209	58	49852.31	Mitochondrion	Translation	
P50213	IDH3A_HUMAN	Isocitrate dehydrogenase [NAD] subunit alpha, Mitochondrion precursor (EC 1.1.1.41)	149	40	40022.24	Mitochondrion	Enzyme	
P50454	SERPH_HUMAN	Serpin H1 [Precursor] (Collagen-binding protein) (Colligin) (47 kDa heat shock protein) (Rheumatoid arthritis-related antigen RA-A47) (Arsenic-transactivated protein 3)	80	38	46525.22	Endoplasmic reticulum	Enzyme, regulatory	Binds specifically to collagen. Could be involved as a chaperone in the biosynthetic pathway of collagen.
P51149	RAB7_HUMAN	Ras-related protein Rab-7	126	49	23759.95	Endosome, lysosome, phagosome, melanosome	Phagocytosis	Involved in late endocytic transport.
P52565	GDIR_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1)	66	34	23249.73	Cytoplasm	Regulatory, signaling, anti-apoptosis	Regulates the GDP/GTP exchange reaction of the Rho proteins by

Table I. *continued*

Table I. continued

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
		(Rho-GDI alpha)						inhibiting the dissociation of GDP from them, and the subsequent binding of GTP to them.
P52907	CAZAI1_HUMAN	F-actin capping protein alpha-1 subunit (CapZ alpha-1)	135	64	33073.39	Cytoplasm, cytoskeleton	Structural	F-actin-capping proteins bind to the fast growing ends of actin filaments thereby blocking the exchange of subunits at these ends.
P55809	SCOT_HUMAN	Succinyl-CoA: 3-ketoacid-coenzyme A transferase 1, Mitochondrion precursor (EC 2.8.3.5) Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase)	82	24	56578.10	Mitochondrion	Enzyme	Key enzyme for ketone body catabolism.
P60174	TPIS_HUMAN		215	72	26806.81		Enzyme	TPI deficiency is an autosomal recessive disorder. It is the most severe clinical disorder of glycolysis. It is associated with neonatal jaundice, chronic hemolytic anemia, progressive neuromuscular dysfunction, cardiomypathy and increased susceptibility to infection.
P60660	MYL6_HUMAN	Myosin light polypeptide 6 (Myosin light chain alkali 3) (Myosin light chain 3) (MLC-3)	131	60	16959.16	Cytoskeleton, cytoplasm	Structural	Regulatory light chain of myosin.
P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin)	185	55	42051.86	Cytoskeleton, cytoskeleton	Structural, motor/contractile	
P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein)	220	47	51229.51	Cytoplasm, nucleus	RNA binding, RNA splicing	Polymerization of globular actin (G-actin) leads to a structural filament (F-actin) in the form of a two-stranded helix.
P62195	PRSS8_HUMAN	26S protease regulatory subunit 8 (Proteasome subunit p45) (p45/SUG) (Proteasome 26S subunit ATPase 5)	164	52	45768.12	Cytoplasm, nucleus	Enzyme, chaperone, transcription, anti-apoptosis	One of the major pre-mRNA-binding proteins. Binds tenaciously to poly(C) sequences. Likely to play a role in the nuclear metabolism of hnRNAs, particularly for pre-mRNAs that contain cytidine-rich sequences. Can also bind poly(C) single-stranded DNA.
P62805	H4_HUMAN	Histone H4	88	53	11229.34	Nucleus	Transcription, DNA binding, chromatin organization, remodeling	It is involved in the ATP-dependent degradation of ubiquitininated proteins, negative regulation of programmed cell death.

Table I. continued

Table I. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPase) (Rotanase) (Cyclophilin A)	113	82	18097.93	Cytoplasm	Enzyme	Accelerate the folding of proteins. Major intracellular receptor for the immunosuppressive agent cyclosporin A, with intrinsic peptidyl-prolyl cis-trans isomerase activity.
P62988	UBIQ_HUMAN	Ubiquitin	110	64	8559.62	Cytoplasm, nucleus	Protein binding, cell cycle, transcription	Protein modifier which can be covalently attached to target lysines either as a monomer or as a lysine-linked polymer. Attachment to proteins as a Lys-48-linked polymer usually leads to their degradation by proteasome.
P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin)	104	36	42107.92	Cytoplasm, cytoskeleton	Structural, motor/contractile	Polymerization of globular actin (G-actin) leads to a structural filament (F-actin) in the form of a two-stranded helix.
P67809	YBOX1_HUMAN	Nuclease sensitive element-binding protein 1 (Y-box binding protein 1) (Y-box transcription factor)	92	42	35902.67	Cytoplasm, nucleus	Transcription, RNA binding	Binds to splice sites in pre-mRNA and regulates splice site selection. Binds and stabilizes cytoplasmic mRNA. Contributes to the regulation of translation by modulating the interaction between the mRNA and eukaryotic initiation factors.
P78371	TCPB_HUMAN	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	246	64	57663.22	Cytoplasm	Chaperone	Molecular chaperone; assist the folding of proteins upon ATP hydrolysis. Known to play a role, <i>in vitro</i> , in the folding of actin and tubulin.
P82650	RT22_HUMAN	Mitochondrion 28S ribosomal protein S22 (S22mt) (MRP-S22)	170	57	41425.46	Mitochondrion	Protein binding	
P84090	ERH_HUMAN	Enhancer of rudimentary homolog	69	46	12422.07		Regulatory, protein binding, cell cycle	May have a role in the cell cycle, playing a role in enhancement of pyrimidine biosynthesis, in cell cycle regulation, and repression of the tissue-specific transcription factor HNF-1 (hepatocyte nuclear factor-1) through binding the coactivator DCoH (dimerization cofactor of HNF1).
Q03252	LMNB2_HUMAN	Lamin-B2	259	52	67761.53	Nucleus	Structural, transcription	Lamins are components of the nuclear lamina, a fibrous layer on

Table I. *continued*

Table I. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
Q04837	SSB_HUMAN	Single-stranded DNA-binding protein, Mitochondrion precursor (Mt-SSB) (MtSSB) (PWP1-interacting protein 17)	123	64	17249.03	Mitochondrion	Regulatory	the nucleoplasmic side of the inner nuclear membrane, which is thought to provide a framework for the nuclear envelope and may also interact with chromatin. Probably involved in mitochondrial DNA replication.
Q05066	SRY_HUMAN	Sex-determining region Y protein (Testis-determining factor)	57	62	10669.46	Nucleus, cytoplasm	Transcription, DNA-binding, protein binding	Transcriptional regulator which control a genetic switch in male development. It is necessary and sufficient for initiating male sex determination by directing the development of supporting cell precursors (pre-Sertoli cells) as Sertoli rather than granulosa cells.
Q06830	PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	165	67	22324.36	Cytoplasm, melanosome	Enzyme	In male adult brain involved in the maintenance of motor functions of dopaminergic neurons. Involved in redox regulation of the cell, playing a role in elimination of peroxides generated during metabolism. Might participate in the signaling cascades of growth factors and tumor necrosis factor-alpha by regulating the intracellular concentrations of H ₂ O ₂ .
Q07955	SFRS1_HUMAN	Splicing factor, arginine/serine-rich 1 (pre-mRNA splicing factor SF2, P33 subunit)	82	40	27710.82	Cytoplasm, nucleus	RNA splicing	Plays a role in preventing exon skipping, ensuring the accuracy of splicing and regulating alternative splicing.
Q12931	TRAP1_HUMAN	(Alternative-splicing factor 1) Heat shock protein 75 kDa, mitochondrial precursor (HSP 75) (Tumor necrosis factor type 1 receptor-associated protein) (TRAP-1)	200	44	80344.80	Mitochondrion	Chaperone	Chaperone that expresses an ATPase activity. Might play a role in protecting mitochondria against damaging stimuli <i>via</i> decrease of reactive oxygen species generation, protecting cells from oxidative stress and apoptosis.

Table I. *continued*

Table I. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
Q13011	ECH1_HUMAN	Delta3,5-delta2,4-dienoyl-CoA isomerase, Mitochondrion precursor (EC 5.3.3.-)	174	57	36135.51	Mitochondrion peroxisome	Enzyme	Isomerization of 3-trans,5-cis-dienoyl-CoA to 2-trans,4-trans-dienoyl-CoA. Fatty acid beta-oxidation cycle; auxiliary isomerization steps.
Q13162	PRDX4_HUMAN	Peroxiredoxin-4 (EC 1.11.1.15) (Prx-IV) (Thioredoxin peroxidase AO372) (Thioredoxin-dependent peroxide veductase A0372)	192	67	30748.90	Cytoplasm	Enzyme	Probably involved in redox regulation of the cell. Regulates the activation of NF-kappa-B in the cytosol by a modulation of I-kappa-B-alpha phosphorylation.
Q13347	IF32_HUMAN	Eukaryotic translation initiation factor 3 subunit 2 (eIF-3 beta) (eIF3 p36) (eIF3i) (TGF-beta receptor-interacting protein 1) (TRIP-1)	71	32	36877.76	Cytoplasm	Translation	Bind to the 40S ribosome and promotes the binding of methionyl-tRNAI and mRNA. Anticancer gene, cadmium-responsive proto-oncogene, binds to TGFBR.
Q14476	Q14476_HUMAN	G-gamma-hemoglobin gene from Greek HPFH mutant, complete cds. (Fragment)	57	44	11089.64		Transport	
Q15293	RCN1_HUMAN	Reticulocalbin-1 precursor	155	50	38866.16	Endoplasmic reticulum	Regulatory, ion binding	
Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 (Alpha-CP1) (hnRNP-E1) (Nucleic acid-binding protein SUB2.3)	119	45	37987.14	Nucleus, cytoplasm	DNA & RNA binding	May regulate calcium-dependent activities in the Endoplasmic reticulum or post-ER compartment.
Q28842	Q28842_RABIT	Interleukin-1 receptor antagonist intracellular form (Fragment)	57	72	7651.91	Extracellular	Immune response, receptor activity	Single-stranded nucleic acid binding protein that binds preferentially to oligo dC.
Q8NB7	SUMF2_HUMAN	Sulfatase-modifying factor 2 precursor (C-alpha-formylglycine-generating enzyme 2)	115	48	33949.87	Endoplasmic reticulum	Enzyme	Seems to lack formyl-glycine generating activity and to be unable to convert newly synthesized inactive sulfatases to their active form by modifying an active site cysteine residue to 3-oxoalanine.
Q92597	NDRG1_HUMAN	NDRG1 protein (N-myc downstream-regulated gene 1 protein) (Differentiation-related gene 1 protein)	90	33	43263.89	Cytoplasm, nucleus, cell membrane	Growth inhibition, protein binding	
Q92945	FUBP2_HUMAN	Far upstream element-binding protein 2 (FUSE-binding protein 2) (KH type splicing regulatory protein)	125	32	73063.05	Nucleus, cytoplasm	RNA splicing, RNA binding	Binds to the dendritic targeting element and may play a role in mRNA trafficking.
Q96KK5	H2A1H_HUMAN	Histone H2A type 1-H (H2A/s)	66	38	13766.79	Nucleus	Transcription, DNA binding, chromatin organization, remodeling	

Table I. *continued*

Table I. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
Q99497	PARK7_HUMAN	Protein DJ-1 (Oncogene DJ1)	95	45	20049.55	Nucleus, cytoplasm	Signal transduction, protection, transcription	Positive regulator of androgen receptor-dependent transcription. Protooncogene, involved in the oxidative stress response found in lung and prostate cancer.
Q99714	HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)	232	88	27003.16	Mitochondrion	Enzyme	Binds intracellular amyloid-beta. It may contribute to the neuronal dysfunction associated with Alzheimer disease.
Q99798	ACON_HUMAN	Aconitate hydratase, Mitochondrion precursor (EC 4.2.1.3) (Citrate hydro-lyase)	273	43	86113.20	Mitochondrion	Enzyme	
Q9HAV7	GRPE1_HUMAN	GtpE protein homolog 1, Mitochondrion precursor (Mt-GtpE#1) (HMGE)	136	53	24492.00	Mitochondrion	Chaperone	Essential component of the PAM complex, required for the translocation of transit peptide-containing proteins from the inner membrane into the Mitochondrion matrix. Essential for the activities of the Hsp 70 system which assists protein folding.
Q9HCN8	SDF2L_HUMAN	Stromal cell-derived factor 2-like protein 1 precursor (SDF2-like protein 1) (PWP1-interacting protein 8)	94	54	23811.74	Endoplasmic reticulum	Unknown	
Q9UBS4	DNJBB_HUMAN	DnaJ homolog subfamily B member 11 precursor (ER-associated dna protein 3) (ErB3)	174	51	40773.73	Endoplasmic reticulum	Chaperone, translation	
Q9UJZ1	STML2_HUMAN	Stomatin-like protein 2 (SLP-2) (EPB72-like 2)	178	59	38624.24	Membrane, cytoplasm, cytoskeleton	Regulatory, transport, signal transduction	Involved in growth regulation by ERBB3-regulated signal transduction pathway.
Q9UQ80	PA2G4_HUMAN	Proliferation-associated protein 133 2G4 (Cell cycle protein p38-2G4 homolog) (hG4-1) (ErB3-binding protein 1)	46	44101.31		Nucleus	Signal transduction, cell proliferation, RNA and DNA binding, transcription	
Q9Y232	CDYL1_HUMAN	Chromodomain Y-like protein (CDY-like)	57	13	66891.13	Nucleus	DNA associated, transcription	Repressor of transcription with histone acetyltransferase activity, chromodomain protein, Y chromosome-like.
Q9Y265	RUVBL1_HUMAN	RuvB-like 1 (EC 3.6.1.-) (49-kDa TATA box-binding protein-interacting protein) (49 kDa TBP-interacting protein)	194	48	50538.44	Nucleus, cytoplasm, membrane	Transcription, protein binding, enzyme, DNA associated, DNA recombination	Possesses single-stranded DNA-stimulated ATPase and ATP-dependent DNA helicase (3' to 5' activity, ATPase/helicase complex is an essential cofactor for oncogenic transformation by c-Myc).

Table II. Proteins identified only in the human CCS cell lines and not in their corresponding xenografts. Proteins were extracted and separated by 2-D gel 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, the SWISS-PROT accession numbers, or the accession numbers of other databases. The theoretical molecular weight, the probability of a random identification (Score), the percentage of the coverage of the protein by the identified peptides, as well as the annotated subcellular location and function are listed. A brief comment on the precise function of each protein is also listed. Score is $-10^{\ast}\log(P)$, where P is the probability that the observed match is a random event (MASCOT, <http://www.matrixscience.com>); score >57 indicates $p<0.05$.

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
Q00165	HAX1_HUMAN	HS1-associating protein X-1 (HAX-1) (HS1-binding protein)	87	52	31601.05	Mitochondrion, endoplasmic reticulum, nucleus	Regulatory, anti-apoptosis, protein binding	Directly associates with HS1, through binding to its N-terminal region. May function in promoting cell survival. May also associate with cortactin/EM1 in non-lymphoid cells.
Q00560	SDCB1_HUMAN	Syntenin-1 (Syndecan binding protein 1) (Melanoma differentiation-associated protein 9)	62	26	32594.98	Membrane, cytosol, endoplasmic reticulum, nucleus, melanosomes	Signaling, regulatory, structural	Seems to function as an adapter protein.
O14773	TPP1_HUMAN	Tripeptidyl-peptidase I precursor (EC 3.4.14.9) (TPP-1) (Tripeptidyl aminopeptidase) (Lysosomal peptidstatin-insensitive protease)	72	14	61703.78	Lysosome, melanosomes	Enzyme	Lysosomal serine protease with tripeptidyl-peptidase I activity. May act as a non-specific lysosomal peptidase which generates tripeptides from the breakdown products produced by lysosomal proteases.
O15061	DMN_HUMAN	Desmulin	416	39	173005.40	Cytoplasm	Structural, protein binding	Mechanical support to the muscle fibers by making a linkage between the extracellular matrix via the dystrophin-associated protein complex (DAPC) and the Z-disk.
O15460	P4HA2_HUMAN	Prolyl 4-hydroxylase alpha-2 subunit precursor (EC 1.14.11.2) (4-PH alpha-2) (Procollagen-proline-2-oxoglutarate-4-dioxygenase subunit alpha-2)	214	46	61262.77	Endoplasmic reticulum	Enzyme	
O43402	CX4NB_HUMAN	Neighbor of COX4	87	46	24213.83	Nucleus, mitochondrion	Unknown/unspecified	
O60313	OPA1_HUMAN	Dynamamin-like 120 kDa protein, mitochondrial precursor	236	33	112158.04	Mitochondrion	Transport, regulation of apoptosis	
O60568	PLOD3_HUMAN	Procollagen-lysine-2-oxoglutarate 5-dioxygenase 3 precursor (EC 1.14.11.4) (Lysyl hydroxylase 3)	384	52	85301.69	Endoplasmic reticulum, membrane	Enzyme	Forms hydroxylysine residues in -Xaa-Lys-Gly- sequences in collagens. These hydroxylysines serve as sites of attachment for carbohydrate units and are essential for the stability of the intermolecular collagen cross-links.
O75083	WDR1_HUMAN	WD-repeat protein 1 (Actin-interacting	58	12	66705.08	Cytoplasm, cytoskeleton	Structural	Induces disassembly of actin filaments in conjunction with

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score (%)	Coverage MW	Subcellular localisation	Function	Brief comment
075390	CLSY_HUMAN	protein 1) (API) (NORI-1) precursor (EC 2.3.3.1)	34	51907.60	Mitochondrion	Enzyme	ADF/cofilin family proteins.
075431	MTX2_HUMAN	Metaxin-2	139	50	Mitochondrion	Transport Enzyme	
075439	MPPB_HUMAN	Mitochondrial processing peptidase beta subunit, mitochondrial precursor (EC 3.4.24.64)	153	44	Mitochondrion	Enzyme	
075608	LYPA1_HUMAN	Acyl-protein thioesterase 1 (EC 3.1.2.-)	70	37	24995.62	Cytoplasm	Enzyme
094905	ERLN2_HUMAN	(Lyso)phosphatase I Erlin-2 Endoplasmic reticulum lipid raft-associated protein 2 (Stomatin-prohibitin-fotilin-HflC/K domain-containing protein 2) (SPFH domain-containing protein 2)	213	59	38043.54	Endoplasmic reticulum	
094925	GLSK_HUMAN	Glutaminase kidney isoform, mitochondrial precursor (EC 3.5.1.2) (GLS)	124	36	74269.22	Mitochondrion	Enzyme
095302	FKBP9_HUMAN	(L-glutamine amidohydrolase) FK506-binding protein 9 precursor (EC 5.2.1.8) (Peptidyl-prolyl-cis-trans isomerase)	223	40	63499.68	Endoplasmic reticulum	Enzyme, ion binding
095571	ETHE1_HUMAN	ETHE1 protein, mitochondrial precursor (EC 3.-.-.-) (Ethylmalonic encephalopathy protein 1)	73	31	28368.30	Cytoplasm, nucleus, mitochondrion	Enzyme
095831	PDCD8_HUMAN	Apoptosis-inducing factor 1, mitochondrial, precursor (EC 1.-.-.-) (Programmed cell death protein 8)	192	48	67144.01	Mitochondrion, nucleus	Enzyme, signal transduction, apoptosis, DNA binding, DNA fragmentation, protein binding
095881	TXD12_HUMAN	Thioredoxin domain-	70	43	19364.64	Endoplasmic reticulum	Enzyme, regulatory

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
O96008	TOM40_HUMAN	containing protein 12 precursor (Thioredoxin-like protein p19) (Endoplasmic reticulum protein ERP19) (ERP18)	87	34	38211.27	Mitochondrion	Chaperone	thiol-disulfide oxidase activity.
P00167	CYB5_HUMAN	Probable mitochondrial import receptor subunit TOM40 homolog (Translocase subunit homolog) Cytochrome b5	68	49	15189.47	Endoplasmic reticulum, cytoplasm Mitochondrion	Enzyme, electron transport	Channel-forming protein essential for import of protein precursors into mitochondria
P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial precursor (EC 1.4.1.3) (GDH)	175	49	61701.32	Mitochondrion	Enzyme	Electron carrier for several membrane bound oxygenases. Involved in learning and memory reactions by increasing the turnover of the excitatory neurotransmitter glutamate
P00505	AATM_HUMAN	Aspartate aminotransferase, mitochondrial precursor (EC 2.6.1.1) (Transaminase A) (Glutamate oxaloacetate transaminase 2, mAspAT, Fatty acid-binding protein, FABP-1)	57	25	47844.42	Mitochondrion, membrane	Enzyme	Facilitates cellular uptake of long-chain free fatty acids (By similarity).
P01011	AACT_HUMAN	Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1-antichymotrypsin His-Pro-less]	168	47	47791.60	Secreted	Protein binding, DNA binding	It can inhibit neutrophil cathepsin G and mast cell chymase, both of which can convert angiotensin-1 to the active angiotensin-2.
P02452	CO1A1_HUMAN	Collagen alpha-1(I) chain precursor Apolipoprotein E precursor (Apo-E)	58	16	139824.95	Secreted, extracellular	Protein binding, structural	
P02649	APOE_HUMAN		225	68	36245.80	Secreted	Signal transduction, metabolism, apoptosis, transport, synaptic transmission	Mediates the binding, internalization, and catabolism of lipoprotein particles.
P05198	IF2A_HUMAN	Eukaryotic translation initiation factor 2 subunit 1 (Eukaryotic translation initiation factor 2 subunit alpha)	216	59	36243.44	Cytoplasm, nucleus	RNA associated	Functions in the early steps of protein synthesis by forming a ternary complex with GTP and initiator tRNA. This complex binds to a 40S ribosomal subunit, followed by mRNA binding to form a 43S preinitiation complex. Junction of the 60S ribosomal subunit to form the 80S initiation complex is preceded by hydrolysis of the GTP bound to eIF-2 and release of an eIF-2-GDP binary complex. In order

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P06396	GELS_HUMAN	Gelsolin precursor (Actin-depolymerizing factor) (ADF) (Brevin) (AGEL)	141	34	86043.34	Cytoplasm, cytoskeleton, secreted	Structural, regulatory, apoptosis	for eIF-2 to recycle and catalyze another round of initiation, the GDP bound to eIF-2 must exchange with GTP by way of a reaction catalyzed by eIF-2B. Calcium-regulated, actin-modulating protein that binds to the plus (or barbed) ends of actin monomers or filaments, preventing monomer exchange (end-blocking or capping). It can promote the assembly of monomers into filaments (nucleation) as well as sever filaments already formed.
P06756	ITAV_HUMAN	Integrin alpha-V precursor (Vitronectin receptor alpha subunit) (CD51 antigen)	59	8	117061.87	Membrane	Receptor, adhesion, communication	The alpha-V integrins are receptors for vitronectin, cytokeratin, fibronectin, fibrinogen, laminin, matrix metalloproteinase-2, osteopontin, osteomodulin, prothrombin, thrombospondin and von Willebrand factor. They recognize the sequence R-G-D in a wide array of ligands. In case of HIV-1 infection, the interaction with extracellular viral Tat protein seems to enhance angiogenesis in Kaposi's sarcoma lesions.
P07195	LDHB_HUMAN	L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH heart subunit)	207	62	36769.21	Cytoplasm	Enzyme	
P07686	HEXB_HUMAN	Beta-hexosaminidase beta chain precursor (EC 3.2.1.52) (N-acetyl-beta-glucosaminidase)	94	22	63327.35	Lysosome	Enzyme	Responsible for the degradation of GM2 gangliosides and a variety of other molecules containing terminal N-acetyl hexosamines, in the brain and other tissues.
P07858	CATB_HUMAN	Cathepsin B precursor (EC 3.4.22.1) (Cathepsin B1) (APP secretase) (APPS)	60	23	38766.20	Lysosome, melanosomes	Enzyme, protein binding, regulation of apoptosis	Participates in intracellular degradation and turnover of proteins. Has also been implicated in tumor invasion and metastasis.
P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (HSP 86)	118	30	84888.80	Cytoplasm, melanosome	Chaperone, apoptosis	Molecular chaperone. Has ATPase activity, negatively regulating mitochondrial cell death. Binding to cells <i>via</i> a high affinity receptor, laminin is thought to
P07942	LAMB1_HUMAN	Laminin beta-1 chain precursor (Laminin B1 chain)	130	16	205178.34	Secreted, extracellular, membrane	Adhesion, differentiation, migration, motility,	

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P07951	TPM2_HUMAN	Tropomyosin beta chain (Tropomyosin 2) (Beta-tropomyosin)	99	34	32944.61	Cytoplasm, sarcomer	Motor/contractile	mediate the attachment, migration and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components. Mediates the attachment, migration and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.
P08133	ANXA6_HUMAN	Annexin A6 (Annexin VI) (Lipocortin V) (P68) (P70) (Protein III) (Chromobindin-20)	247	46	76036.66	Cytoplasm	Regulatory, transport	Binds to actin filaments in muscle and non-muscle cells. Plays a central role, in association with the troponin complex, in the calcium dependent regulation of vertebrate striated muscle contraction. May regulate the release of Ca(2+) from intracellular stores.
P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 84) (HSP 90)	295	45	83423.19	Cytoplasm, melanosome	Chaperone	Molecular chaperone. Has ATPase activity.
P08708	RS17_HUMAN	40S ribosomal protein S17	77	69	15466.37	Cytoplasm	Translation, structural, RNA binding	
P08758	ANXA5_HUMAN	Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I) (CBP-I)	243	75	35840.38	Cytoplasm	Regulatory, transport, anti-apoptosis, signal transduction	Anticoagulant protein that acts as an indirect inhibitor of the thromboplatin-specific complex.
P08865	RSSA_HUMAN	40S ribosomal protein SA (Laminin receptor 1) (34/67 kDa laminin receptor) (p40) (Colon carcinoma laminin-binding protein) (NEMICHD4) (Multidrug resistance-associated protein MGrl-Ag)	112	47	32816.43	Cytoplasm	Signal transduction, translation	Plays a major role in tumor aggressiveness and metastasis.
P09486	SPRC_HUMAN	SPARC precursor	119	27	35465.03	Secreted, extracellular	Signaling, ion binding, cell growth, regulatory, structural	Appears to regulate cell growth through interactions with the extracellular matrix and cytokines.
P09493	TPM1_HUMAN	Tropomyosin 1 alpha chain (Alpha-40)	140	40	32745.70	Cytoplasm, sarcomer	Motor/contractile	Binds to actin filaments in muscle and non-muscle cells. Plays a

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
		tropomyosin)						central role, in association with the troponin complex, in the calcium dependent regulation of vertebrate striated muscle contraction.
P09525	ANXA4_HUMAN	Annexin A4 (Annexin IV) (Lipocortin IV)	257	69	35957.17	Cytoplasm	Regulatory, transport, anti-apoptosis, signal transduction	Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis.
P09622	DLDH_HUMAN	Dihydrolipoyl dehydrogenase, mitochondrial precursor (EC 1.8.1.4)	128	36	54686.14	Mitochondrion	Enzyme	Component of the glycine cleavage system as well as of the alpha-ketoacid dehydrogenase complexes.
P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 (Helix destabilizing protein) (Single-strand RNA-binding protein)	127	35	38805.13	Nucleus, cytoplasm	DNA & RNA binding, RNA splicing	Involved in the packaging of pre-mRNA into hnRNP particles, transport of poly(A) mRNA from the nucleus to the cytoplasm and may modulate splice site selection.
P09936	UCHL1_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (EC 6.-.-.-) (UCH-L1) (Ubiquitin thioesterase L1)	125	66	25150.59	Cytoplasm	Enzyme	Ubiquitin-protein hydrolase involved both in the processing of ubiquitin precursors and of ubiquitinated proteins.
P10253	LYAG_HUMAN	Lysosomal alpha-glucosidase precursor (EC 3.2.1.20) (Acid maltase) (Alpha-glucosidase alfa)	100	16	106126.12	Lysosome	Enzyme	
P11047	LAMC1_HUMAN	Laminin gamma-1 chain precursor (Laminin B2 chain)	267	29	183194.63	Secreted, extracellular, membrane	Adhesion, differentiation, migration, motility, cell proliferation	Binding to cells <i>via</i> a high affinity receptor, laminin is thought to mediate the attachment, migration and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.
P11498	PYC_HUMAN	Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1)	355	44	130292.69	Mitochondrion	Enzyme	Pyruvate carboxylase catalyzes a 2-step reaction, involving the ATP-dependent carboxylation of the covalently attached biotin in the first step and the transfer of the carboxyl group to pyruvate in the second. Catalyzes in a tissue specific manner, the initial reactions of glucose (liver, kidney) and lipid (adipose tissue, liver, brain) synthesis

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P12004	PCNA_HUMAN	Proliferating cell nuclear antigen (Cyclin) (Lipocortin III)	147	55	29092.42	Nucleus	Cell proliferation, DNA binding	from pyruvate.
P12429	ANXA3_HUMAN	Annexin A3 (Annexin III) (Placental anticoagulant protein III) (PAP-III)	73	33	36392.68	Cytoplasm	Signal transduction, transport	Inhibitor of phospholipase A2
P12956	KU70_HUMAN	ATP-dependent DNA helicase II, 70 kDa subunit (EC 3.6.1.-) (Lupus Ku autoantigen protein p70)	217	42	69953.12	Nucleus	Enzyme, DNA binding, DNA repair, DNA recombination	Single stranded DNA-dependent ATP-dependent helicase. Has a role in chromosome translocation.
P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	268	54	96115.27	Cytoplasm	RNA binding, translation	This protein promotes the GTP-dependent translocation of the nascent protein chain from the A-site to the P-site of the ribosome.
P13667	PDIA4_HUMAN	Protein disulfide-isomerase A4 precursor (EC 5.3.4.1) (ERp72)	174	39	73229.10	Endoplasmic reticulum, melanosomes	Protein binding	
P13674	P4HA1_HUMAN	Prolyl 4-hydroxylase alpha-1 subunit precursor (EC 1.14.11.2) (4-PH alpha-1) (Procollagen-proline-2-oxoglutarate-4-dioxygenase subunit alpha-1)	241	52	61296.13	Endoplasmic reticulum	Enzyme	
P14618	KPYM_HUMAN	Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein)	290	55	58339.20	Cytosol	Enzyme	Glycolytic enzyme that catalyzes the transfer of a phosphoryl group from phosphoenolpyruvate (PEP) to ADP, generating ATP.
P14625	ENPL_HUMAN	Endoplasmic precursor (94 kDa glucose-regulated protein) (GRP94) (gp96 homolog)	344	56	92696.45	Endoplasmic reticulum	Transport, ion binding, anti-apoptosis	Molecular chaperone that functions in the processing and transport of secreted proteins.
P14854	CX6B1_HUMAN	(Tumor rejection antigen 1) Cytochrome c oxidase subunit VIb isoform 1 (EC 1.9.3.1) (COX VIb-1)	62	62	10282.76	Mitochondrion	Enzyme, structural, electron transport	Connects the two COX monomers into the physiological dimeric form.
P15311	EZRL_HUMAN	Ezrin (p81) (Cytovillin) (Vilin-2)	83	19	69338.72	Membrane	Structural	Probably involved in connections of major cytoskeletal structures to the plasma membrane.
P17987	TCPA_HUMAN	T-complex protein 1 subunit alpha (TCP-1-alpha) (CCT-alpha)	184	36	60818.77	Cytoplasm	Chaperone	Molecular chaperone; assists the folding of proteins upon ATP hydrolysis. Known to play a role, <i>in vitro</i> , in the folding of actin and tubulin.
P18206	VINC_HUMAN	Vinculin (Metavinculin)	298	40	124160.98	Cytoplasm, cytoskeleton	Adhesion	Involved in cell adhesion. May be involved in the attachment of the actin-based microfilaments to the

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P18859	ATP5J_HUMAN	ATP synthase coupling factor 6, mitochondrial precursor (EC 3.6.3.14) (ATPase subunit F6)	107	50	12579.60	Mitochondrion	Enzyme, transport	plasma membrane. May also play important roles in cell morphology and locomotion.
P19105	MIRM_HUMAN	Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC)	57	39	19707.47	Cytoplasm	Protein binding	This is one of the chains of the nonenzymatic component (CF(0) subunit) of the mitochondrial ATPase complex. F6 seems to be part of the stalk that links CF(0) to CF(1). Also involved in the restoration of oligomycin-sensitive ATPase activity to depleted F1-F0 complexes.
P19338	NUCL_HUMAN	Nucleolin (Protein C23)	211	39	76494.34	Nucleus	Cell growth, RNA binding, angiogenesis Enzyme	
P19367	HXK1_HUMAN	Hexokinase-1 (EC 2.7.1.1) (Hexokinase type I) (HK 1) (Brain form hexokinase)	99	19	103559.58	Mitochondrion		
P20700	LMNB1_HUMAN	Lamin-B1	305	52	66521.69	Nucleus	Structural	Component of the nuclear lamina, a fibrous layer on the nucleoplasmic side of the inner nuclear membrane, which is thought to provide a framework for the nuclear envelope and may also interact with chromatin.
P22392	NDKB_HUMAN	Nucleoside diphosphate kinase B (EC 2.7.4.6) (NDK B) (NDP kinase B) (mm23-H2) (C-myc purin binding transcription factor PUF)	63	57	17400.98	Cytoplasm, nucleus	Enzyme	
P22695	UQCR2_HUMAN	Ubiquinol-cytochrome-c reductase complex core protein 2, mitochondrial precursor (Ubiquinol-cytochrome-c reductase complex core protein 2) (Core protein II) (Complex III subunit 2)	89	42	48583.95	Mitochondrion	Enzyme, electron transport	This is a component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is part of the mitochondrial respiratory chain. The core protein 2 is required for the assembly of the complex.
P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (Polyproline tract-binding protein-associated-splicing factor) (PTB-associated-splicing factor) (PSF)	167	37	76215.67	Nucleus	DNA & RNA binding, RNA splicing	DNA- and RNA binding protein, involved in several nuclear processes.
P23381	SYW_HUMAN	Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase) (TrpRS) (IFP53) (hWRs)	77	27	53473.73	Cytoplasm	Enzyme	

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P23527	H2BN_HUMAN	Histone H2B.n (H2Bn) (H2B.2)	65	41	13766.52	Nucleus	Transcription, DNA binding	
P23786	CPT2_HUMAN	Carnitine O-palmitoyl-transferase II, mitochondrial precursor (EC 2.3.1.21) (CPT II)	80	27	74243.59	Mitochondrion	Enzyme	
P25787	PSA2_HUMAN	Proteasome subunit alpha type 2 (EC 3.4.25.1) (Macropain subunit C3)	95	59	25865.27	Cytoplasm, nucleus	Enzyme	The proteasome is a multicatalytic proteinase complex which is characterized by its ability to cleave peptides with Arg, Phe, Tyr, Leu, and Glu adjacent to the leaving group at neutral or slightly basic pH. The proteasome has an ATP-dependent proteolytic activity. PSMA2 may have a potential regulatory effect on another component(s) of the proteasome complex through tyrosine phosphorylation.
P25788	PSA3_HUMAN	Proteasome subunit alpha type 3 (EC 3.4.25.1) (Macropain subunit C8)	111	36	28512.13	Cytoplasm, nucleus	Enzyme	Multicatalytic proteinase complex which is characterized by its ability to cleave peptides with Arg Phe, Tyr, Leu, and Glu adjacent to the leaving group at neutral or slightly basic pH. The proteasome has an ATP-dependent proteolytic activity.
P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	36	67760.79	Cytoskeleton, cytoplasm	Structural, cell motility		
P27824	CALX_HUMAN	Cahnexin precursor (Major histocompatibility complex class I antigen-binding protein p88)	139	31	67982.02	Endoplasmic reticulum	Ion binding, protein binding, angiogenesis	Calcium-binding protein that interacts with newly synthesized glycoproteins in the endoplasmic reticulum.
P28070	PSB4_HUMAN	Proteasome subunit beta type 4 precursor (EC 3.4.25.1) (Macropain beta chain)	72	50	29230.46	Cytoplasm, nucleus	Enzyme	Multicatalytic proteinase complex which is characterized by its ability to cleave peptides with Arg, Phe, Tyr, Leu, and Glu adjacent to the leaving group at neutral or slightly basic pH. The proteasome has an ATP-dependent proteolytic activity. EF-1-beta and EF-1-delta stimulate the exchange of GDP bound to EF-1-alpha to GTP.
P29692	EF1D_HUMAN	Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4)	62	22	31085.78	Cytoplasm, nucleus	DNA and RNA binding, translation, signal transduction	
P30042	ES1_HUMAN	ES1 protein homolog, mitochondrial precursor (Protein KNP-1) (Protein GT335)	90	45	28466.83	Mitochondrion	Unknown/unspecified	GDP bound to EF-1-alpha to GTP.

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P30740	ILEU_HUMAN	Leukocyte elastase inhibitor (LEI) (Serpin B1) (Monocyte/neutrophil elastase inhibitor)	63	30	42828.74	Cytoplasm	Enzyme, regulatory	Regulates the activity of the neutrophil proteases elastase, cathepsin G, proteinase-3, chymase, chymotrypsin, and kallikrein-3.
P31040	DHSA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor	209	36	73671.67	Mitochondrion	Enzyme	Involved in Carbohydrate metabolism and tricarboxylic acid cycle.
P32322	P5CR1_HUMAN	Pyrroline-5-carboxylate reductase 1 (EC 1.5.1.2)	146	58	33567.64		Enzyme	
P33778	H2BF_HUMAN	Histone H2B _f (H2B _f)	60	47	13810.54	Nucleus	Transcription, DNA binding	
P34897	GLYM_HUMAN	Serine hydroxymethyltransferase, mitochondrial precursor (EC 2.1.2.1) (Serine methylase)	95	25	56413.90	Mitochondrion	Enzyme	Interconversion of serine and glycine.
P34932	HSP74_HUMAN	Heat shock 70 kDa protein 4 (Heat shock 70-related protein APG-2) (HSP70/RY)	139	31	95095.61	Cytoplasm, nucleus	Chaperone	
P36542	ATPG_HUMAN	ATP synthase gamma chain, mitochondrial precursor	73	27	33032.29	Mitochondrion	Enzyme, transport	Produces ATP from ADP. The gamma chain is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex.
P36551	HEM6_HUMAN	Coproporphyrinogen III oxidase, mitochondrial precursor	185	48	50918.27	Mitochondrion	Enzyme	
		(EC 1.3.3.3) (Coproporphyrinogenase)						
P37837	TALDO_HUMAN	Transaldolase (EC 2.2.1.2)	58	17	37687.52	Cytoplasm	Enzyme	The electron transfer flavoprotein serves as a specific electron acceptor for several dehydrogenases, including five acyl-CoA dehydrogenases, glutaryl-CoA and sarcosine dehydrogenase. It transfers the electrons to the main mitochondrial respiratory chain <i>via</i> ETF-ubiquinone oxidoreductase.
P38117	ETFB_HUMAN	Electron transfer flavoprotein beta-subunit (Beta-ETF)	92	31	28054.24	Mitochondrion	Electron transport, carrier	Catalytic subunit of the peripheral V _i complex of vacuolar ATPase. V-ATPase vacuolar ATPase is responsible for acidifying a variety of intracellular compartments in eukaryotic cells.
P38606	VATA1_HUMAN	Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform (EC 3.6.3.14) (V-ATPase subunit A) (Vacuolar proton pump subunit alpha)	118	32	68659.64	Cytoplasm, lysosome	Enzyme, transport	Binds to spliced mRNAs and is involved in non-sense-mediated
P38919	DDX48_HUMAN	Probable ATP-dependent RNA helicase	189	57	47126.29	Nucleus	Translation, RNA binding	

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score (%)	Coverage Protein MW	Subcellular localisation	Function	Brief comment
P39059	COFA1_HUMAN	DDX48 (EC 3.6.1.-) (DEAD box protein 48) Collagen alpha-1(XV) chain precursor [Contains: Endostatin (Endostatin-XV) (Restin) (Related to endostatin)]	72	15 142201.91	Secreted, extracellular	Protein binding, structural	decay of mRNAs containing premature stop codons.
P40925	MDHC_HUMAN	Malate dehydrogenase, cytoplasmic (EC 1.1.1.37)	69	33 36500.06	Cytoplasm	Enzyme	Structural protein that stabilizes microvessels and muscle cells, both in heart and in skeletal muscle. Endostatin potently inhibits angiogenesis.
P40939	ECHA_HUMAN	Trifunctional enzyme alpha subunit, mitochondrial precursor (TP-alpha) (78 kDa gastrin-binding protein)	281	51 83688.15	Mitochondrion	Enzyme	
P41250	SYG_HUMAN	Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine- tRNA ligase) (GlyRS)	115	19 83827.87	Cytoplasm	Enzyme	
P42704	LPPRC_HUMAN	130 kDa leucine- rich protein (LRP 130) (GP130) (Leucine-rich PPR- motif containing protein)	295	41 146306.44	Mitochondrion, nucleus	Transport, RNA binding	
P43243	MATR3_HUMAN	Matrin-3	166	30 95077.99	Nucleus	Protein binding, structural	
P43246	MSH2_HUMAN	DNA mismatch repair protein Msh2 (MutS protein homolog 2)	76	13 105417.97	Nucleus	DNA binding, DNA repair	
P43304	GPDM_HUMAN	Glycerol-3-phosphate dehydrogenase, mitochondrial precursor (EC 1.1.99.5) (GPD-M) (GPDH-M)	377	45 81295.76	Mitochondrion	Enzyme	
P43897	EFTS_HUMAN	Elongation factor Ts, mitochondrial precursor (EF-Ts) (EF-TsMt)	68	31 35710.37	Mitochondrion	RNA associated, translation	Associates with the EF-Tu.GDP complex and induces the exchange of GDP to GTP. It remains bound to the aminoacyl-tRNA.EF-Tu.GTP complex up to the GTP hydrolysis stage on the ribosome.
P45880	VDAC2_HUMAN	Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2) (Outer mitochondrial membrane protein porin 2)	90	38 38638.88	Mitochondrion	Transport	Forms a channel through the mitochondrial outer membrane that allows diffusion of small hydrophilic molecules.
P45954	ACDSB_HUMAN	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial [Precursor] (EC 1.3.99.-, SB CAD)	216	50 47797.42	Mitochondrion	Enzyme	Plays a role in controlling the metabolic flux of valproic acid in the development of toxicity of this agent.

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P45974	UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.1.2.15) (Ubiquitin thioesterase 5) (Ubiquitin-specific-processing protease 5)	141	28	96637.67	Cytoplasm	Enzyme	Cleaves linear and branched multiubiquitin polymers with a marked preference for branched polymers.
P47755	CAZA2_HUMAN	F-actin capping protein alpha-2 subunit (CapZ alpha-2)	146	71	33025.65	Cytoplasm	Structural	F-actin-capping proteins bind in a Ca(2+)-independent manner to the fast growing ends of actin filaments (barbed end) thereby blocking the exchange of subunits at these ends.
P48643	TCPCE_HUMAN	T-complex protein 1 subunit epsilon (TCP-1-epsilon) (CCT-epsilon)	176	46	60088.98	Cytoplasm	Chaperone	Molecular chaperone; assist the folding of proteins upon ATP hydrolysis. Known to play a role, <i>in vitro</i> , in the folding of actin and tubulin.
P48735	IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitochondrial precursor (EC 1.1.1.42) (Oxaloacetate decarboxylase)	85	36	51333.03	Mitochondrion	Enzyme	Plays a role in intermediary metabolism and energy production. It may tightly associate or interact with the pyruvate dehydrogenase complex.
P49368	TCPG_HUMAN	T-complex protein 1 subunit gamma (TCP-1-gamma) (CCT-gamma) (hTRIC5)	123	29	61065.53	Cytoplasm	Chaperone	Molecular chaperone; assist the folding of proteins upon ATP hydrolysis. Known to play a role, <i>in vitro</i> , in the folding of actin and tubulin.
P49419	AL7A1_HUMAN	Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Antiquitin-1)	105	26	55713.57	Mitochondrion	Enzyme	
		Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine -tRNA ligase) (AlaRS)	190	36	107475.50	Cytoplasm	Enzyme	
P49588	SYA_HUMAN	Proteasome subunit beta type 2 (EC 34.25.1) (Macropain subunit C7-I)	74	41	22992.74	Cytoplasm, nucleus	Enzyme	Multicatalytic proteinase complex which is characterized by its ability to cleave peptides with Arg, Phe, Tyr, Leu, and Glu adjacent to the leaving group at neutral or slightly basic pH. The proteasome has an ATP-dependent proteolytic activity. This subunit has a chymotrypsin-like activity.
P49721	PSB2_HUMAN	GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (Glutamine amidotransferase)	144	38	77408.23	Cytoplasm	Enzyme	Involved in the <i>de novo</i> synthesis of guanine nucleotides which are not only essential for DNA and RNA synthesis, but also provide GTP,
P49915	CUAA_HUMAN							

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2)	207	64	51087.05	Cytoplasm		which is involved in a number of cellular processes important for cell division.
P51570	GALK1_HUMAN	Galactokinase (EC 2.7.1.6) (Galactose kinase)	143	39	42701.74	Cytoplasm	Regulates the GDP/GTP exchange reaction of most Rab proteins by inhibiting the dissociation of GDP from them, and the subsequent binding of GTP to them.	
P51665	PSD7_HUMAN	26S proteasome non-ATPase regulatory subunit 7 (26S proteasome regulatory subunit rpn8)	57	32	37059.52	Cytosol	Enzyme	Acts as a regulatory subunit of the 26S proteasome which is involved in the ATP-dependent degradation of ubiquitinated proteins.
P54920	SNAA_HUMAN	Alpha-soluble NSF attachment protein (SNAP-alpha) (SNAP-alpha) (Nethylmaleimide-sensitive factor attachment protein, alpha)	246	74	33681.47	Membrane, Golgi apparatus	Protein binding, transport	Required for vesicular transport between the endoplasmic reticulum and the Golgi apparatus.
P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg(2+)-ATPase p97 subunit (Valosin-containing protein) (VCP)	348	53	89818.93	Cytoplasm, nucleus	Chaperone, structural, transport	Necessary for the fragmentation of Golgi stacks during mitosis and for their reassembly after mitosis. Involved in the formation of the transitional endoplasmic reticulum (TER).
P55735	SEC13_HUMAN	SEC13-related protein (SEC13-like protein 1) (SEC13-like protein 1)	80	35	35900.27	Endoplasmic reticulum	Transport	
P56537	IF6_HUMAN	Eukaryotic translation initiation factor 6 (eIF-6) (B4 integrin interactor) (CAB)	109	58	27095.39	Cytoplasm, Nucleus	RNA associated	Binds to the 60S ribosomal subunit and prevents its association with the 40S ribosomal subunit to form the 80S initiation complex.
P58876	H2BB_HUMAN	Histone H2.B.b (H2B.b) (H2B.1 B) (HIRA-interacting protein 2)	59	41	13796.53	Nucleus		
P60900	PSA6_HUMAN	Proteasome subunit alpha type 6 (EC 3.4.25.1) (Macropain iota chain)	119	38	27837.98	Cytoplasm, nucleus	Transcription, DNA binding	Multicatalytic proteinase complex which is characterized by its ability to cleave peptides with Arg, Phe, Tyr, Leu, and Glu adjacent to the leaving group at neutral or slightly basic pH. The proteasome has an ATP-dependent proteolytic activity.
P61158	ARP3_HUMAN	Actin-like protein 3 (Actin-related protein 3)	172	53	47797.15	Cytoplasm, cytoskeleton	Enzyme	Functions as ATP-binding component of the Arp2/3 complex.
P61326	MGN_HUMAN	Mago nashi protein homolog 14-3-3 protein gamma	102	56	17209.81	Nucleus	Protein binding	
P61981	1433G_HUMAN	(Protein kinase C inhibitor protein 1) (KCP1)	104	47	28324.94	Cytoplasm	Signal transduction, protein binding, differentiation	

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P62158	CALM_HUMAN	Calmodulin (CaM)	58	45	16695.79	Cytoplasm	Ion binding, signaling	Controls a large number of enzymes and other proteins by Ca(2+).
P62333	PRS10_HUMAN	26S protease regulatory subunit S10B (Proteasome 26S subunit ATPase 6)	171	53	44430.21	Cytoplasm, nucleus	Enzyme, chaperone	The 26S protease is involved in the ATP-dependent degradation of ubiquitinated proteins. The regulatory (or ATPase) complex confers ATP dependency and substrate specificity to the 26S complex.
P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2)	140	52	42380.96	Cytoplasm, cytoskeleton	Structural	Involved in various types of cell motility.
P62826	RAN_HUMAN	GTP-binding nuclear protein Ran (GTPase Ran) (Ras-like protein TC4) (Androgen receptor-associated protein 24)	159	44	24578.68	Nucleus, cytoplasm, melanosomes	Transcription, signaling, transport	GTP-binding protein involved in nucleocytoplasmic transport. Required for the import of protein into the nucleus and also for RNA export. Involved in chromatin condensation and control of cell cycle in cancer cells.
P62873	GBB1_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 1 (Transducin beta chain 1)	141	52	38020.27	Membrane	Regulatory	Guanine nucleotide-binding proteins (G proteins) are involved as a modulator or transducer in various transmembrane signalling systems. The beta and gamma chains are required for the GTPase activity, for replacement of GDP by GTP, and for G protein-effector interaction.
P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCP-1)	161	72	27898.79	Cytoplasm, melanosomes	Signaling, protein binding	GTP-binding protein involved in nucleocytoplasmic transport. Required for the import of protein into the nucleus and also for RNA export. Involved in chromatin condensation and control of cell cycle in cancer cells.
P63241	IF5A_HUMAN	Eukaryotic translation initiation factor 5A (eIF-5A) (eIF-4D) (Rev-binding factor)	66	50	16918.45	Nucleus	RNA associated	The precise role of eIF-5A in protein biosynthesis is not known but it functions by promoting the formation of the first peptide bond.
P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain (Troponyosin-4) (TM30p1)	62	44	28487.49	Cytoplasm, sarcomer	Motor/contractile	Binds to actin filaments in muscle and non-muscle cells. Plays a central role, in association with the tropomodulin complex, in the calcium dependent regulation of vertebrate striated muscle contraction.
P68363	TBAK_HUMAN	Tubulin alpha-ubiquitous chain (Alpha-tubulin)	141	41	50803.86	Cytoplasm, cytoskeleton	Structural	Tubulin is the major constituent of microtubules. It binds two moles

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score (%)	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P68371	TBB2C_HUMAN	ubiquitous) (Tubulin K-alpha-1)						of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha-chain.
P82664	RT10_HUMAN	Tubulin beta-2C chain (Tubulin beta-2 chain)	292	63	50255.17	Cytoplasm, cytoskeleton	Structural	Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha-chain. It was detected in melanoma.
P69849	NOMO3_HUMAN	Nodal modulator 3 precursor	98	17	135066.70	Membrane	Protein binding	
P82664	RT10_HUMAN	Mitochondrial 28S ribosomal protein S10 (S10mt) (MRP-S10)	85	32	23099.08	Mitochondrion	Structural, RNA associated	
Q02218	ODO1_HUMAN	2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor (EC 1.2.4.2)	257	39	114600.62	Mitochondrion	Enzyme	
Q02387	Q02387_HUMAN	Alpha-ketoglutarate dehydrogenase Kruppel-associated box (Fragment)	57	73	4880.58		Transcription, DNA binding	
Q02790	FKBP4_HUMAN	FK506-binding protein 4 (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPase) (Rotamase)	180	49	51926.14	Cytoplasm nucleus	Enzyme, protein binding, chaperone	Protooncogene, component of unactivated mammalian steroid receptor complexes that sediment at 8-10 S. May have a rotamase activity and play a role in the intracellular trafficking of hetero-oligomeric forms of steroid hormone receptors.
Q02809	PLOD1_HUMAN	Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1 precursor (EC 1.14.11.4) (Lysyl hydroxylase 1)	276	41	84067.60	Endoplasmic reticulum, membrane	Enzyme	Forms hydroxylysine residues in -Xaa-Lys-Gly- sequences in collagens, serves as sites of attachment for carbohydrate units and are essential for the stability of the intermolecular collagen cross-links.
Q04695	K1C17_HUMAN	Keratin, type I cytoskeletal 17 (Cytokeratin-17) (CK-17) (Keratin-17) (K17) (39.1)	64	29	48230.11	Membrane	Structural	
Q07021	MA32_HUMAN	Complement component 1, Q subcomponent-binding protein, mitochondrial precursor (Glycoprot	75	31	31741.76	Mitochondrion	Protein binding	
Q10713	MPPA_HUMAN	Mitochondrial processing peptidase alpha subunit, mitochondrial precursor (EC 3.4.24.64)	204	37	58728.79	Mitochondrion	Enzyme	

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
Q12905	ILF2_HUMAN	Interleukin enhancer-binding factor 2 (Nuclear factor of activated T-cells 45 kDa)	117	34	43263.27	Nucleus	Transcription, DNA binding	Appears to function predominantly as a heterodimeric complex with ILF3. This complex may regulate transcription of the IL2 gene during T-cell activation. It can also promotes the formation of stable DNA-dependent protein kinase holoenzyme complexes on DNA.
Q12906	ILF3_HUMAN	Interleukin enhancer-binding factor 3 (Nuclear factor of activated T-cells 90 kDa) (NF-AT-90)	82	19	95678.22	Nucleus	Transcription, DNA binding	Subunit of Nuclear Factor of Activated T-cells (NF-AT).
Q13409	DY12_HUMAN	Dynein intermediate chain 2, cytosolic (DH IC-2) (Cyttoplasmic dynein intermediate chain 2)	91	31	71811.26	Cytoplasm, cytoskeleton	Protein binding, structural	May facilitate double-stranded RNA-regulated gene expression at the level of post-transcription. Can act as a translation inhibitory protein which binds to coding sequences of acid beta-glucosidase (GCase) and other mRNAs and functions at the initiation phase of GCase mRNA translation, probably by inhibiting its binding to polyosomes.
Q13813	SPTA2_HUMAN	Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II spectrin) (Fodrin alpha chain)	415	31	285150.47	Cytoplasm, cytoskeleton	Structural	The intermediate chains seem to help dynein bind to dynactin 150 kDa component.
Q14257	RCN2_HUMAN	Reticulocalbin-2 precursor (Calcium-binding protein ERC-55) (E6-binding protein) (E6BP)	169	47	36910.66	Endoplasmic reticulum	Ion binding, protein binding	Seems to be involved in secretion, interacts with calmodulin in a calcium-dependent manner and is thus candidate for the calcium-dependent movement of the cytoskeleton at the membrane.
Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB precursor (EC 3.2.1.84) (Glucosidase II alpha subunit)	307	49	107262.82	Endoplasmic reticulum, Golgi apparatus, melanosome	Enzyme, protein binding	
Q14764	MVP_HUMAN	Major vault protein (MVP) (Lung resistance-related protein)	369	54	99420.00	Cytoplasm, nucleus	Signal transduction, transport	
Q15019	SEPT2_HUMAN	Septin-2 (Protein NEIDD5)	57	34	41689.34	Cytoplasm, nucleus	Protein binding, cytokinesis	Involved in cytokinesis.
Q15029	U5SL_HUMAN	116 kDa U5 small nuclear ribo-nucleoprotein component (U5 snRNP-specific protein, 116 kDa)	346	51	110335.64	Nucleus	RNA splicing	Component of the U5 snRNP complex required for pre-mRNA splicing.
Q15067	ACOX1_HUMAN	Acyl-coenzyme A	92	23	74907.33	Peroxisome	Enzyme	

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score (%)	Coverage	Protein MW	Subcellular localisation	Function	Brief comment
Q15075	EEA1_HUMAN	oxidase 1, peroxisomal (EC 1.3.3.6) (Palmitoyl-CoA oxidase) (AOX) (Endosome-associated protein p162) (Zinc finger FYVE domain-containing protein 2)	98	15	163336.50	Cytoplasm, endosomes	Ion binding, protein binding	Binds phospholipid vesicles containing phosphatidylinositol 3-phosphate and participates in endosomal trafficking.
Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6 precursor (EC 5.3.4.1) (Protein disulfide isomerase P5)	183	57	48490.41	Endoplasmic reticulum, melanosomes	Enzyme	
Q15155	NOMO1_HUMAN	Nodal modulator 1 precursor (pM5)	237	32	135236.80	Membrane	Protein binding	It was detected in melanoma.
Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein)	98	33	54311.32	Nucleus	RNA splicing, DNA and RNA binding	
Q15691	MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1)	77	50	30020.21	Cytoplasm, centrosome	Cell proliferation, protein binding, regulation	
Q16531	DDBB1_HUMAN	DNA damage-binding protein 1 (Damage-specific DNA-binding protein 1) (UV-damaged DNA-binding factor) (DDB p127 subunit)	142	19	128141.79	Cytoplasm, nucleus	DNA binding, protein binding, cell life, regulation of apoptosis	DNA repair Binds to pyrimidine dimers. Required for histone H3 and histone H4 ubiquitination in response to ultraviolet and may be important for subsequent DNA repair.
Q16555	DPYLY2_HUMAN	Dihydropryimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2)	178	55	62710.74	Cytoplasm	Signal transduction, enzyme, development	Involved in neuronal growth cone collapse.
Q16610	ECM1_HUMAN	Extracellular matrix protein 1 precursor (Secretory component p55)	170	50	62231.88	Secreted, extracellular	Signal transition	Positive regulation of I-kappaB kinase/NF-kappaB cascade
Q16643	DREB_HUMAN	Drebrin (Developmentally-regulated brain protein)	81	23	71706.57	Cytoplasm	Structural, protein binding, migration	Might play some role in cell migration, extension of neuronal processes and plasticity of dendrites, respectively.
Q16658	FSCN1_HUMAN	Fascin (Singed-like protein) (55 kDa actin bundling protein) (p55)	244	61	54992.25	Cytoplasm	Structural	Organizes filamentous actin into bundles with a minimum of 4:1:1 actin/fascin ratio. Probably involved in the assembly of actin filament bundles present in microspikes, membrane ruffles, and stress fibers.
Q16718	NUFM_HUMAN	NADH-ubiquinone oxidoreductase 13 kDa-B subunit (EC 1.6.5.3) (EC 1.6.99.3)	178	79	13376.16	Mitochondrion	Electron transport	

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
Q16891	IMMT_HUMAN	Mitochondrial inner membrane protein (Mitofillin) (p87/89) (Cell proliferation-inducing gene 4 protein)	358	48	84025.50	Mitochondrion	Structural, protein binding	Multidrug resistance protein 1, P-glycoprotein 1, CD243 antigen (P08183, MDR1_HUMAN). The P-glycoproteins (Pgp's) are a small family of proteins frequently associated with the multidrug resistance phenotype in drug-selected cell lines.
Q228963	Q228963_PIG	P-glycoprotein class IA (Fragment)	57	49	8052.26	Membrane	Transport, resistance	
Q32P28	Q32P28_HUMAN	Prolyl 3-hydroxylase 1 [Precursor] (EC 1.14.11.7) (LEPRE1 protein)	219	36	79727.40	Endoplasmic reticulum, secreted, extracellular	Cell growth	Negative regulation of cell proliferation. Antioncogene. Basement membrane-associated chondroitin sulfate proteoglycan (CSPG). Has prolyl 3-hydroxylase activity catalyzing the post-translational formation of 3-hydroxyproline in γ -Xaa-Pro-Gly sequences in collagens, especially types IV and V. May be involved in the secretory pathway of cells. Has growth suppressive activity in fibroblasts.
Q38L19	Q38L19_HUMAN	60 kDa heat shock protein, mitochondrial [Precursor] (HSP-60) (Hsp60)	82	32	61345.51	Mitochondrion	Chaperone, regulation of apoptosis	
Q3KQW3	Q3KQW3_HUMAN	Peptidylprolyl isomerase A, isoform 1 (EC 5.2.1.8) (PPase A)	57	35	18228.97	Cytoplasm, nucleus	Enzyme	Implicated in mitochondrial protein import and macromolecular assembly. May facilitate the correct folding of imported proteins. May also prevent misfolding and promote the refolding and proper assembly of unfolded polypeptides generated under stress conditions in the mitochondrial matrix.
Q3UF58	Q3UF58_MOUSE	Catalase (EC 1.11.1.6)	69	26	59945.70	Mitochondrion	PPases accelerate the folding of proteins. It catalyzes the cis-trans isomerization of proline imidic peptide bonds in oligopeptides.	
Q3ZCQ8	Q3ZCQ8_TIM50_HUMAN	Import inner membrane translocase subunit TIM50, mitochondrial precursor	135	29	39849.62	Mitochondrion	Enzyme Transport	

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score (%)	Coverage Protein MW	Subcellular localisation	Function	Brief comment
Q4FJV4	Q4FJV4_MOUSE	Anxal protein (Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830)	358	85	38995.08		mitochondrial inner membrane
Q4KL76	Q4KL76_MOUSE	Heat shock protein 1 (Chaperonin 10) (Bone marrow macrophage cDNA, RIKEN full-length enriched library)	58	48	10955.87		
Q542H1	Q542H1_MOUSE	thymic cells cDNA, RIKEN full-length enriched library, clone:E430021	180	87	18794.61		
Q545F4	Q545F4_MOUSE	ES cells cDNA, RIKEN full-length enriched library, clone:2410043L14 product: heat shock protein 1 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2, isoform b variant [Fragment]	145	58	23056.74	Nucleus	DNA binding
Q59G16	Q59G16_HUMAN	Atpb protein	81	40	34335.80	Ribosome	Translation, structural
Q5FWB6	Q5FWB6_MOUSE	Nodal modulator	176	18	140434.51	Membrane	Protein binding
Q5JPE7	NOMO2_HUMAN	2 precursor (pM5 protein 2) Mitochondrial ribosomal protein L50	97	46	18484.43		It was detected in melanoma.
Q5TTE0	RM50_HUMAN	Lamin A/C	139	42	55842.63	Cytoskeleton	Structural Ion binding
Q5TC18	Q5TC18_HUMAN	ENC-1AS	57	26	38519.20		
Q5URX0	Q5URX0_HUMAN	Putative uncharacterized protein DKFZp686J1643 Calcium-binding mitochondrial carrier protein SCaMC-1	76	11	100036.86	Cytoplasm	
Q6AWC9	Q6AWC9_HUMAN	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial [Precursor]	138	39	53532.40	Mitochondrion	Transport
Q6NUK1	SCMC1_HUMAN	(EC 3.1.2.4)	75	20	43724.50	Mitochondrion	Enzyme
Q6NVY1	HIBCH_HUMAN	ZNF396 protein Myosin regulatory light chain A, smooth muscle homolog	57	12	18922.19	Nucleus	Transcription, DNA binding
Q6PID1	Q6PID1_HUMAN	40S ribosomal protein S12	73	45	19939.54	Cytosol	Ion binding
Q6ZWWQ9	Q6ZWWQ9_MOUSE		89	50	14904.63	Ribosome	Translation, structural

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (p100 co-activator) (100 kDa coactivator)	335	46	102617.76	Cytoplasm, nucleus, melanosomes	Transcription, cell growth	Mediator of second messages in STAT6 pathway. Functions as a bridging factor between STAT6 and the basal transcription factor. Plays a role in PIM1 regulation of MYB activity. Functions as a transcriptional coactivator for the Epstein-Barr virus nuclear antigen 2 (EBNA2).
Q7L513	FCRLA_HUMAN	Fc receptor-like and mucin-like 1 (FREB) (FCRLa)	89	29	39230.53	Secreted, cytoplasm	Differentiation	May be implicated in B-cell differentiation and lymphomagenesis. Expressed in melanoma and melanocytes.
Q8CFX1	G6PE_MOUSE	GDH/6PGL endoplasmic bifunctional protein [Precursor] (Glucose 1-dehydrogenase) (EC 1.1.1.47)	168	40	89424.89	Microsome	Enzyme	
		Prolyl 3-hydroxylase 3 [Precursor] (EC 1.14.11.7) (Leprecan-like protein 2)	209	30	82583.93	Endoplasmic reticulum	Enzyme	Has prolyl 3-hydroxylase activity catalyzing the post-translational formation of 3-hydroxyproline in -Xaa-Pro-Gly-sequences in collagens, especially types IV and V.
Q8IVL6	P3H3_HUMAN	Similar to metallo-beta-lactamase superfamily protein	103	37	31493.04		Enzyme	
Q8IY16	Q8IY16_HUMAN	Theonine synthase-like 1(TSH1)	117	21	84100.47			
Q8IYQ7	THNS1_HUMAN	Thioredoxin domain-containing protein 5 precursor (Thioredoxin-like protein p46)	160	47	48282.92	Endoplasmic reticulum	Enzyme, regulatory	Implicated in a number of cellular events that are regulated during mitosis, including homotypic membrane fusion, spindle pole body function, and ubiquitin-dependent protein degradation.
Q8NBSS9	TXND5_HUMAN	(Endoplasmic reticulum protein ERp46)						Possesses thioredoxin activity.
Q8NFH4	NUP37_HUMAN	Nucleoporin Nup37 (p37)	79	29	37140.21	Nucleus	Transport	Has been shown to reduce insulin disulfide bonds. Also complements protein disulfide-isomerase deficiency in yeast.
Q8TAAQ2	SMRC2_HUMAN	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily C member 2 (SWI/SNF complex 170 kDa subunit (BRG1-associated factor 170)	89	13	133195.90	Nucleus	Transcription, DNA associated	Involved in transcriptional activation and repression of select genes by chromatin remodeling.
Q8TB65	Q8TB65_HUMAN	Cytochrome c oxidase	57	28	16922.75	Mitochondrion	Electron transport, enzyme	

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score (%)	Coverage MW	Subcellular localisation	Function	Brief comment
Q8TC58	PNPT1_HUMAN	subunit Va, (COX5A protein) Polyribonucleotide nucleotidyltransferase 1, mitochondrial precursor (EC 2.7.7.8) (PNPase old-35)	213	44	86509.85	Mitochondrion	Enzyme Involved in mRNA degradation. Hydrolyzes single-stranded polyribonucleotides processively in the 3'- to 5'-direction.
Q922X6	Q922X6_MOUSE	Major vault protein	115	26	96150.28		
Q969H8	CS010_HUMAN	Protein C19orf10 precursor (Stromal cell-derived growth factor SF20) (Interleukin-25) (IL-25)	68	32	18897.36	Secreted	Found expressed in lung carcinoma, breast carcinoma and colon carcinoma cell lines.
Q969S9	EFG2_HUMAN	Elongation factor G2, mitochondrial precursor (mEF-G 2) (Elongation factor G2)	123	25	87401.41	Mitochondrion	Promotes the GTP-dependent translocation of the nascent protein chain from the A-site to the P-site of the ribosome. Accelerate the folding of proteins during protein synthesis.
Q96AY3	FKB10_HUMAN	FK506-binding protein 10 precursor (EC 5.2.1.8) (Peptidyl-l-prolyl cis-trans isomerase)	177	49	64717.38	Endoplasmic reticulum	Enzyme, transport
Q96CG8	CTHR1_HUMAN	Collagen triple helix repeat-containing protein 1 precursor (NMTC1 protein)	65	34	26777.34	Secreted, extracellular	Structural May act as a negative regulator of collagen matrix deposition.
Q96DB5	FA82B_HUMAN	Protein FAM82B	66	28	36013.44		
Q96DV4	RM38_HUMAN	39S ribosomal protein L38, mitochondrial [Precursor]	116	33	41016.52	Unknown/unspecified Mitochondrion	Unknown/unspecified Structural, RNA associated
Q96DZ1	XTP3B_HUMAN	XTP3-transactivated gene B protein precursor (ER lectin)	73	31	55678.60	Endoplasmic reticulum	
Q96ER9	CCD51_HUMAN	Coiled-coil domain-containing protein 51	144	36	42583.02	Membrane	
Q96HC5	Q96HC5_HUMAN	U2 small nuclear RNA auxiliary factor 2 (U2 (RNU2)) small nuclear RNA auxiliary factor 2, isoform CRA_c)	57	21	53429.11	Nucleus	Protein binding, RNA splicing
Q96IR7	HPDL_HUMAN	4-hydroxyphenylpyruvate dioxygenase-like protein (Glyoxalase domain-containing protein 1)	143	60	39703.48	Unknown/unspecified	Unknown/unspecified
Q96J01	THOC3_HUMAN	THO complex subunit 3 (Tho3) (TEX1 homolog)	90	32	39431.09	Nucleus	Regulatory, differentiation
Q96JB5	CK5P3_HUMAN	CDK5 regulatory subunit-associated protein 3 (CDK5 activator-binding protein C53) (HSF-27)	119	23	57227.14		Regulatory, cell proliferation, apoptosis
Q96RP9	EFG1_HUMAN	Elongation factor G1, mito-	69	12	84193.65	Mitochondrion	RNA associated, translation Promotes the GTP-dependent

Table II. *continued*

Table II. continued

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
Q96RQ3	MCCA_HUMAN	CoA carboxylase alpha chain, mitochondrial precursor (mEF-G 1) (Elongation factor G1)	241	48	80895.12	Mitochondrion	Enzyme	translocation of the nascent protein chain from the A-site to the P-site of the ribosome.
Q99747	SNAG_HUMAN	Gamma-soluble NSF attachment protein (SNAP-gamma) (N-ethylmaleimide-sensitive factor attachment protein, gamma)	130	43	35066.47	Membrane, cytosol	Protein binding, transport	Required for vesicular transport between the endoplasmic reticulum and the Golgi apparatus.
Q99832	TCPH_HUMAN	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef interacting protein)	100	25	59842.12	Cytoplasm	Chaperone	Molecular chaperone; assist the folding of proteins upon ATP hydrolysis. Known to play a role, <i>in vitro</i> , in the folding of actin and tubulin.
Q99LL6	Q99LL6_MOUSE	Collal protein (Fragment)	64	31	59224.78	Extracellular	Structural	Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha-chain.
Q9BQE3	TBA1C_HUMAN	Tubulin alpha-6 chain (Alpha-tubulin 6)	73	24	50547.72	Cytoplasm, mitochondria	Inhibits the calcium channel activity	Inhibits the calcium channel activity of ITPR1. May have a role in the control of oxidative protein folding in the endoplasmic reticulum.
Q9BS26	TXND4_HUMAN	Thioredoxin domain-containing protein 4 precursor (Endoplasmic reticulum resident protein ERp44)	189	46	47340.55	Endoplasmic reticulum	Enzyme, regulatory	Required to retain ERO1L and ERO1LB in the endoplasmic reticulum.
Q9BSD0	Q9BSD0_HUMAN	GLUD2 protein	68	34	29386.10		Enzyme	
Q9BT09	CNPY3_HUMAN	Protein canopy homolog 3 [Precursor] (Trinucleotide repeat-containing gene 5 protein) (CTG repeat protein 4a) (Expanded repeat-domain protein CAG/CTG 5)	72	35	31127.80	Secreted		
Q9BXW7	CECR5_HUMAN	Cat eye syndrome critical region protein 5 precursor	95	33	46747.96	Cytoplasm	Unknown/unspecified	

Table II. continued

Table II. *continued*

Accession number	Protein symbol	Protein name	Score (%)	Coverage Protein MW	Subcellular localisation	Function	Brief comment
Q9GZL7 WDR12_HUMAN		WD-repeat protein 12 (YTM1 homolog)	98	36 48190.88	Nucleus	Signaling	
Q9H2U2 IPYR2_HUMAN		Inorganic pyrophosphatase 2, mitochondrial precursor (EC 3.6.1.1) (PPase 2)	87	28 38451.22	Mitochondrion	Enzyme	
Q9HDC9 APMAP_HUMAN		Adipocyte plasma membrane-associated protein (BSCv protein)	160	37 46621.91	Membrane	Differentiation	May play a role in adipocyte differentiation.
Q9NS69 TOM22_HUMAN		Mitochondrial import receptor subunit TOM22 homolog (Translocase of outer membrane 22 kDa subunit homolog) (hTom22)	91	65 15380.74	Mitochondrion	Chaperone	Central receptor component of the translocase of the outer membrane of mitochondria (TOM complex) responsible for the recognition and translocation of cytosolically synthesized mitochondrial preproteins.
Q9NU11 ABHDA_HUMAN		Abhydrolase domain-containing protein 10, mitochondrial [Precursor] (EC 3.4.-.-)	76	32 34252.88	Mitochondrion	Enzyme	
Q9NVA2 SEP11_HUMAN		Septin-11	179	46 49521.26	Cytoplasm, cytoskeleton	Enzyme, protein binding, cytokinesis	Involved in cytokinesis.
Q9NX40 OCAD1_HUMAN		OC1A domain-containing protein 1 (Ovarian carcinoma immunoreactive antigen)	132	33 27779.84	Endosome		
Q9NYU2 UGGG1_HUMAN		UDP-glucose:glycoprotein glucosyltransferase 1 precursor (EC 2.4.1.-) (UDP-glucose ceramide glucosyltransferase-like 1)	107	17 175437.23	Endoplasmic reticulum, Golgi apparatus	Enzyme	Recognizes glycoproteins with minor folding defects.
Q9P0J1 PDPL_HUMAN		[Pyravate dehydrogenase [lipoamid]-] phosphatase 1, mitochondrial precursor	139	53 61585.78	Mitochondrion	Enzyme	
Q9P2R7 SUCB1_HUMAN		Succinyl-CoA ligase [ADP-forming] beta-chain, mitochondrial precursor (EC 6.2.1.5) (Succinyl-CoA synthetase, beta A chain)	100	38 50641.35	Mitochondrion	Enzyme	
Q9UH99 UN84B_HUMAN		Sad1unc-84-like protein 2 (Rab5-interacting protein) (Rab5IP)	93	23 80489.64	Nucleus, endosomes	Unknown/unspecified	
Q9UI30 TR112_HUMAN		TRM112-like protein	59	42 14304.30	Nucleus	Regulatory, RNA splicing, DNA and RNA binding	Plays a role in DNA double-strand break (DSB) repair and pre-mRNA splicing reaction. Binds double-stranded DNA in a sequence-nonspecific manner. Acts as a structural component of the nuclear
Q9UMS4 PRP19_HUMAN		Pre-mRNA splicing factor 19 (PRP19/PSO4 homolog) (Nuclear matrix protein 200) (hPsø4)	142	44 55602.51			

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
Q9UNM6	PSD13_HUMAN	26S proteasome non-ATPase regulatory subunit 13 (26S proteasome regulatory subunit S11)	145	39	43176.24	Cytosol	Enzyme	framework. May also serve as a support for spliceosome binding and activity.
Q9UQE7	SMC3_HUMAN	Structural maintenance of chromosome 3 (Chondroitin sulfate proteoglycan 6) (Chromosome-associated polypeptide hCAP)	125	22	141852.98	Nucleus	Signal transduction, structural, cell cycle	Essential for spliceosome assembly in a oligomerization-dependent manner and might also be important for spliceosome stability. May have E3 ubiquitin ligase activity. The PSO4 complex is required in the DNA interstrand cross-links (ICLs) repair process. Overexpression of PRPF19 might extend the cellular life span by increasing the resistance to stress or by improving the DNA repair capacity of the cells.
Q9Y224	CN166_HUMAN	Protein C14orf166	80	47	28164.75	Nucleus, cytoplasm	Protein binding	Acts as a regulatory subunit of the 26S proteasome which is involved in the ATP-dependent degradation of ubiquitinated proteins.
Q9Y230	RUVB2_HUMAN	RuvB-like 2 (EC 3.6.1.-) (48-kDa TATA box-binding protein-interacting protein) (48 kDa TBP-interacting protein)	224	58	51164.58	Nucleus, cytoplasm, membrane	Transcription, protein binding, enzyme , DNA associated, DNA recombination	Possesses single-stranded DNA stimulated ATPase and ATP-dependent DNA helicase (5' to 3') activity.
Q9Y240	CLC11_HUMAN	C-type lectin domain family 11 member A	84	29	36014.63	Cytoplasm, secreted	Signaling, differentiation	Stimulates the proliferation and differentiation of hematopoietic precursor cells from various lineages.
Q9Y285	SYFA_HUMAN	secreted C-type lectin, p47	145	40	57453.49	Cytoplasm	Enzyme	
		Phenylalanine-tRNA synthetase alpha chain (EC 6.1.1.20) (Phenylalanine-tRNA ligase alpha chain)						
Q9Y2B0	MSAP_HUMAN	MIR-interacting saposin-like protein precursor	209	76	20981.30	Endoplasmic reticulum	Protein binding	
Q9Y4L1	OXRPHUMAN	(Transmembrane protein 4) 150 kDa oxygen-regulated protein precursor (Orp150) (Hypoxia up-regulated 1)	319	51	111494.29	Endoplasmic reticulum	Protein binding, protection	

Table II. *continued*

Table II. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
Q9Y512	SAM50_HUMAN	Sorting and assembly machinery component 50 homolog	162	44	52328.45	Mitochondrion	Structural	May be required for the assembly pathway of mitochondrial outer membrane proteins.
Q9Y680	FKBP7_HUMAN	FK506-binding protein 7 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase)	67	28	30332.25	Endoplasmic reticulum	Enzyme	Accelerate the folding of proteins during protein synthesis.
Q9Y6C2	EMILIN1_HUMAN	EMILIN-1 precursor (Elastin microfibril interface-located protein 1) (Elastin microfibril interfacer 1)	223	34	107940.99	Secreted, extracellular	Cell adhesion, protein binding	Responsible for anchoring smooth muscle cells to elastic fibers, and may be involved not only in the formation of the elastic fiber, but also in the processes that regulate vessel assembly. Has cell adhesive capacity.
P49189	AL9A1_HUMAN	4-trimethylaminobutyraldehyde dehydrogenase (EC 1.2.1.47) (TMABADH)	105	30	54679.32	Cytoplasm	Enzyme	Catalyzes the irreversible oxidation of a broad range of aldehydes.
P62258	I433E_HUMAN	14-3-3 epsilon (14-3-3E)	129	58	29296.48	Cytoplasm, melanosomes	Signaling	
P62879	GBB2_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 2 (Transducin beta chain 2)	106	33	37917.30		Signaling	Guanine nucleotide-binding proteins (G proteins) are involved as a modulator or transducer in various transmembrane signaling systems. The beta and gamma chains are required for the GTPase activity, for replacement of GDP by GTP, and for G protein-effector interaction.
P63244	GBLP_HUMAN	Guanine nucleotide-binding protein beta subunit 2-like 1 (Guanine nucleotide-binding protein)	165	71	35510.73	Cytoplasm	Signaling	Seems to bind protein kinase C acting as an intracellular receptor to anchor the activated PKC to the cytoskeleton.
Q1KMD3HNRL2_HUMAN		Heterogeneous nuclear ribonucleoprotein U-like protein 2 (Scaffold-attachment factor A2) (SAF-A2)	159	41	72891.39	Nucleus		

Table III. Proteins identified only in the xenografts not in the human CCS cell lines. Proteins were extracted and separated by 2-D gel 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, the SWISS-PROT accession numbers, or the accession numbers of other databases. The theoretical molecular weight, the probability of a random identification (Score), the percentage of the coverage of the protein by the identified peptides, as well as the annotated subcellular location and function are listed. A brief comment on the precise function of each protein was also 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 >57 indicate $p<0.05$.

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
O00232	PSD12_HUMAN	26S proteasome non-ATPase regulatory subunit 12 (26S proteasome regulatory subunit p55)	57	18	53138.68	Cytosol	Enzyme, regulatory	Involved in the ATP-dependent degradation of ubiquitinated proteins.
O00233	PSMD9_HUMAN	26S proteasome non-ATPase regulatory subunit 9 (26S proteasome regulatory subunit p27)	99	53	24809.54	Cytoplasm, cytosol, nucleus	Enzyme, regulatory	Involved in the ATP-dependent degradation of ubiquitinated proteins.
O00625	PIR_HUMAN	Pirin	97	39	32207.30	Nucleus	Transcription	Cofactor of the NF1/CTF1 transcriptional activator, binding to NF1/CTF1 and BCL3.
O08692	O08692_MOUSE	Myeloid bactericin (Fl) (Neutrophilic granule protein)	87	42	19661.72	Extracellular		Possible related to host animal (SCID mouse).
O08855	O08855_MOUSE	Apolipoprotein A-I	107	34	30525.61	Extracellular		Possible related to host animal (SCID mouse).
O15511	ARPC5_HUMAN	Actin-related protein 2/3 complex subunit 5 (ARP2/3 complex 16 kDa subunit) (p16-ARC)	63	55	16236.28	Cytoplasm, cytoskeleton	Structural, cell motility	It is involved in regulation of actin polymerization and mediates the formation of branched actin networks.
O43396	TXNL1_HUMAN	Thioredoxin-like protein 1 (32-kDa thioredoxin-related protein)	144	50	32498.84	Cytoplasm	Enzyme, electron transport, signal transduction, apoptosis	
O43819	SCO22_HUMAN	SCO22 protein homolog, mitochondrial precursor	74	31	29962.45	Mitochondrion	Enzyme, transport, ion binding, chaperone	
O43825	B3GT2_HUMAN	Beta-1,3-galactosyltransferase 2 (EC 2.4.1.-) (Beta-1,3-GalTase 2) (Beta3Gal-T2)	57	19	49638.19	Golgi apparatus	Enzyme, signaling	Involved in the biosynthesis of the carbohydrate moieties of glycolipids and glycoproteins.
O60884	DNJA2_HUMAN	Dnal homolog subfamily A member 2 (HTRA-interacting protein 4) (Cell cycle progression restoration gene 3 protein)	85	25	46343.83	Membrane	Chaperone, cell growth/proliferation	Co-chaperone of Hsc70, positive regulation of cell proliferation.
O75176	O75176_HUMAN	KIAA0692 protein (Fragment)	57	9	88198.08	Unknown/unspecified		
O75351	VPS4B_HUMAN	Vacuolar sorting protein 4b (SKD1 protein)	64	19	49442.55	Membrane	Chaperone, transport, transcription	Involved in intracellular protein transport.
O75489	NUGM_HUMAN	NADH-ubiquinone oxidoreductase 30 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3)	83	32	30336.75	Mitochondrion	Enzyme, electron transport	Transfer of electrons from NADH to the respiratory chain.
O75635	SPB7_HUMAN	Serpin B7 (Megsin) (TP55)	61	31	43162.60		Enzyme, regulatory	Served as inhibitor of Lys-specific proteases.

Table III. *continued*

Table III. continued

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
Q75832	PSD10_HUMAN	26S proteasome non-ATPase regulatory subunit 10 (26S proteasome regulatory subunit p28) (Gankyrin)	99	50	24697.49	Cytoplasm	Enzyme, regulatory	Involved in the ATP-dependent degradation of ubiquitinated proteins, protooncogene, playing an important role in the development of hepatocellular carcinomas.
O94844	RHBT1_HUMAN	Rho-related BTB domain-containing protein 1	57	10	80506.56	Cytoplasm, peroxisome	Signaling	
O95347	SMC2_HUMAN	Structural maintenance of chromosome 2-like 1 protein (Chromosome-associated protein E)	57	9	136266.18	Cytoplasm, nucleus	DNA binding, replication, repair	Involved in mitotic chromosome segregation, chromatin organization, remodeling.
O95881	TXD12_HUMAN	Thioredoxin domain-containing protein 12 precursor (EC 1.8.4.2) (Thioredoxin-like protein P19)	68	43	19364.64	Endoplasmic reticulum	Enzyme, electron transport	
P02088	HBB1_MOUSE	Hemoglobin subunit beta-1	173	88	15825.19			Possible related to host animal (SCID mouse).
P02675	FIBB_HUMAN	Fibrinogen beta chain precursor [Contains: Fibrinopeptide B]	68	18	56576.52	Secreted	Regulatory, adhesion	Acts as a cofactor in platelet aggregation, regulates cell adhesion and spreading, displays vasoconstrictor and chemotactic activities.
P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K ₁) (67 kDa cytokeratin)	57	16	66018.01	Cytoskeleton	Structural	
P04908	H2A1B_HUMAN	Histone H2A type 1-B	63	38	14032.94	Nucleus	Transcription, DNA binding	
P05121	PAI1_HUMAN	Plasminogen activator inhibitor 1 precursor (PAI-1) (Endothelial plasminogen activator inhibitor)	57	21	45088.05	Secreted	chromatin organization, remodeling Enzyme	It is involved in the regulation of fibrinolysis. It is a putative up-regulated c-Myc target gene.
P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14)	153	46	56524.60	Mitochondrion	Enzyme, transport	
P06753	TPM3_HUMAN	Tropomyosin alpha-3 chain (Tropomyosin-3)	81	33	32855.76	Cytoplasm, cytoskeleton	Motor/contractile	
P07108	ACBP_HUMAN	(Tropomyosin gamma) (hTM5) Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (DBI) (Endozepine) (EP)	101	84	9906.98	Cytoplasm	Regulatory, transport	
P07737	PROF1_HUMAN	Profilin-1 (Profilin I)	98	59	15084.58	Cytoplasm, mitochondria	Regulatory	Binds to actin and affects the structure of the cytoskeleton.
P08779	K1C16_HUMAN	Keratin, type I cytoskeletal 16 (Cytokeratin-16) (CK-16) (Keratin-16) (K16)	105	37	51447.29	Cytoskeleton	Structural	

Table III. continued

Table III. continued

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P09341	GROA_HUMAN	Growth-regulated protein alpha precursor (CXCL1) (Melanoma growth stimulatory activity) (MGSA) (Neutrophil-activating protein 3)	58	41	11522.31	Secreted	Chemotaxis, signaling, growth regulator	It is potent inducer of senescence in stromal fibroblasts (depending on functional TP53), having a role for cell survival and the malignant transformation of ovarian epithelial cells. Possible therapeutic target as well as a diagnostic marker in ovarian cancer.
P09936	UCHL1_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (EC 6.-.-.-)	113	47	25150.59	Cytoplasm, nucleus	Enzyme, transcription	
P09972	ALDOC_HUMAN	Fructose-bisphosphate aldolase C (EC 4.1.2.13) (Brain-type aldolase)	129	44	39699.35	Cytosol	Enzyme	
P10599	THIO_HUMAN	Thioredoxin (ATL-derived factor) (ADF) (Surface-associated sulphhydryl Protein) (SASP)	87	84	11883.81	Cytoplasm	Enzyme, signal transduction, cell growth/ proliferation, apoptosis	
P10606	COX5B_HUMAN	Cytochrome c oxidase polypeptide Vb, mitochondrial precursor (EC 1.9.3.1)	82	50	13915.03	Mitochondrion	Enzyme, transport	One of the nuclear-coded polypeptide chains of cytochrome c oxidase.
P11310	ACADM_HUMAN	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor (EC 1.3.99.3) (MCAD)	167	42	47014.75	Mitochondrion	Enzyme	
P12035	K2C3_HUMAN	Keratin, type II cytoskeletal 3 (Cytokeratin-3) (CK-3) (Keratin-3) (K3) (65 kDa cytokeratin)	64	12	64635.66	Cytoskeleton	Structural	
P12268	IMDH2_HUMAN	Inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMPDH-II)	232	46	56225.82	Cytoplasm	Enzyme	Involved in the regulation of cell growth, in the development of malignancy and the growth progression of some tumors.
P13535	MYH8_HUMAN	Myosin-8 (Myosin heavy chain, skeletal muscle, perinatal) (MyHC-perinatal)	57	15	223593.86	Cytoplasm	Structural	
P13797	PLST_HUMAN	Plastin-3 (T-plastin)	57	16	70904.29	Cytoplasm	Protein binding	
P14854	CX6B1_HUMAN	Cytochrome c oxidase subunit VIb isoform 1 (EC 1.9.3.1) (COX VIb-1)	108	76	10282.76	Mitochondrion	Enzyme, electron transport	Connects the two COX monomers into the physiological dimeric form.
P14927	QCR7_HUMAN	Ubiquinol-cytochrome c reductase complex 14 kDa protein (EC 1.10.2.2) (Complex III subunit 7)	102	60	13390.94	Mitochondrion	Enzyme, electron transport	

Table III. continued

Table III. continued

Accession number	Protein symbol	Protein name	Score (%)	Coverage Protein MW	Subcellular localisation	Function	Brief comment
P17980	PRS6A_HUMAN	26S protease regulatory subunit 6A (TAF-binding protein 1) (TBP-1) (Proteasome subunit P50)	59	19 49457.56	Cytoplasm, nucleus	Chaperone, transcription	Involved in the ATP-dependent degradation of ubiquitinated proteins.
P19388	RPB5_HUMAN	DNA-directed RNA polymerase II 23 kDa polypeptide (EC 2.7.7.6) (RPB25) (RPB5) (RPABC1) (XA NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) Protein-L-isoadpartate (D-aspartate) O-methyltransferase (EC 2.1.1.77) (Protein-beta-aspartate methyltransferase)	82	34 24709.78	Cytoplasm, nucleus	Enzyme, transcription	
P19404	NUHM_HUMAN	NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) Protein-L-isoadpartate (D-aspartate) O-methyltransferase (EC 2.1.1.77) (Protein-beta-aspartate methyltransferase)	139	58 27659.12	Mitochondrion	Enzyme, electron transport	
P22061	PIMT_HUMAN	Ubiquinol-cytochrome-c reductase complex core protein 2, mitochondrial precursor (Ubiquinol-cytochrome-c reductase complex core protein 2, mitochondrial precursor (Ubiquinol-cytochrome-c reductase complex core protein 2 Core protein II) Coflin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein) (p18) Elongation factor 1-beta (EF-1-beta)	81	40 24674.61	Cytoplasm	Enzyme	Has a role in the repair and/or degradation of damaged proteins.
P22695	UQCR2_HUMAN	Ubiquinol-cytochrome-c reductase complex core protein 2, mitochondrial precursor (Ubiquinol-cytochrome-c reductase complex core protein 2, mitochondrial precursor (Ubiquinol-cytochrome-c reductase complex core protein 2 Core protein II) Coflin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein) (p18) Elongation factor 1-beta (EF-1-beta)	133	40 48583.95	Mitochondrion	Enzyme	Component of the ubiquinol-cytochrome c reductase complex.
P23528	COF1_HUMAN	Coflin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein) (p18)	97	60 18587.70	Nucleus, cytoplasm, cytoskeleton	Structural, anti-apoptosis	
P24534	EF1B_HUMAN	Elongation factor 1-beta (EF-1-beta)	67	24 24788.29	Endoplasmic reticulum	Translation	
P25325	THTM_HUMAN	3-mercaptopropionate sulfurtransferase (EC 2.8.1.2) (MST)	72	19 33311.70	Cytoplasm	Enzyme	
P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial precursor (EC 3.6.3.14) High mobility group protein B2 (High mobility group protein 2) (HMG-2)	91	20 59827.63	Mitochondrion	Enzyme, transport	
P26583	HMGB2_HUMAN	Adenylate kinase isoenzyme 4, mitochondrial (EC 2.7.4.3) (Adenylate kinase 3-like 1)	92	40 24058.75	Nucleus	DNA binding, transcription	Binds preferentially single-stranded DNA and unwinds double stranded DNA. Interacts with TP53, stimulating TP53 binding to DNA containing TP53 consensus site.
P27144	KAD4_HUMAN	Adenylate kinase isoenzyme 4, mitochondrial (EC 2.7.4.3)	61	22 25366.25	Mitochondrion	Enzyme	
P28838	AMPL_HUMAN	Cytosol aminopeptidase	132	36 53005.97	Cytoplasm	Enzyme, ion binding	Involved in processing and

Table III. continued

Table III. continued

Accession number	Protein symbol	Protein name	Score (%)	Coverage MW	Protein	Subcellular localisation	Function	Brief comment
P30085	KCY_HUMAN	(EC 3.4.11.1) (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase)	29	22436.37	Nucleus, cytoplasm			regular turnover of intracellular proteins.
P30533	AMRP_HUMAN	(EC 2.7.4.14) (Cytidylate kinase) (Deoxycytidylyl kinase) (Cytidine monophosphate kinase) Alpha-2-macroglobulin receptor-associated protein precursor (Alpha-2-MRAP) (Low density lipoprotein receptor-related protein-associated protein 1) Sorcin (22 kDa protein) (CP-22) (V19)	42	41440.90	Endoplasmic reticulum, cytoplasm, cell surface	Chaperone, cell proliferation/growth, ion binding	Enzyme	Catalyzes specific phosphoryl transfer. Interacts with LRPI/alpha-2-macroglobulin receptor and glycoprotein 330.
P30626	SORCN_HUMAN		78	36	21947.46	Cytoplasm	Signal transduction, transport	It is associated with the development of multidrug-resistance in leukemia cells.
P31689	DNJA1_HUMAN	Dnaj homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (Dnaj protein homolog 2) Heterogeneous nuclear ribonucleoprotein H (hnRNP H)	103	30	45580.73	Membrane, nucleus	Chaperone, transport	Co-chaperone of Hsc70. Involved in protein import into mitochondria.
P31943	HNRH1_HUMAN	Histone H2B type 1-B (H2B.f) (H2B.f) (H2B.1) Profilin-2 (Profilin II)	145	52	49352.47	Nucleus	RNA binding, RNA splicing	Component of the heterogeneous nuclear ribonucleoprotein (hnRNP) complexes.
P33778	H2B1B_HUMAN	Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9) (K9)	102	57	13810.54	Nucleus	Transcription, DNA binding, chromatin organization, remodeling	
P35080	PROF2_HUMAN	Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9)	60	32	15247.35	Cytoplasm, cytoskeleton	Regulatory	
P35527	KIC9_HUMAN		101	30	62319.99	Cytoskeleton	Structural	
P35908	K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	67	16	66110.50	Cytoskeleton		
P36957	ODO2_HUMAN	Dihydrolipooyl sime-residue succinyltransferase component of 2-oxoglutarate dehydrogenase (EC 2.3.1.61)	113	31	48951.51	Mitochondrion	Protein binding	Part of a complex that catalyzes the overall conversion of 2-oxoglutarate to succinyl-CoA and CO ₂ .
P37802	TAGL2_HUMAN	Transgelin-2 (SM22-alpha homolog)	103	34	22417.20	Nucleus	Transcription	
P39687	AN32A_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member A (Potent heat-stable protein phosphatase 2A inhibitor II/PP2A) (Acidic nuclear phosphoprotein pp32) (Leucine-rich acidic nuclear protein)	91	26	28682.32	Nucleus, cytoplasm	Signaling, transport, protein binding, regulation of apoptosis	Implicated in proliferation, differentiation, caspase-dependent and -independent apoptosis, suppression of transformation.

Table III. continued

Table III. continued

Accession number	Protein symbol	Protein name	Score (%)	Coverage Protein MW	Subcellular localisation	Function	Brief comment
P40926	MDHM_HUMAN	Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37)	177	59 35964.93	Mitochondrion	Enzyme	
P48047	ATPO_HUMAN	ATP synthase O subunit, mitochondrial precursor (EC 3.6.3.14) (Oligomycin sensitivity conferral protein) (OSCP)	64	31 23376.70	Mitochondrion	Enzyme, transport	Part of ATRases.
P49458	SRP09_HUMAN	Signal recognition particle 9 kDa protein (SRP9)	72	60 10088.11	Cytoplasm, endoplasmic reticulum	RNA binding	
P49773	HINT1_HUMAN	Histidine triad nucleotide-binding protein 1 (Adenosine 5'-monophoramidase) (Protein kinase C inhibitor 1)	103	65 13776.10	Cytoplasm, nucleus	Enzyme, signal transduction	
P50502	F10A1_HUMAN	Hsc70-interacting protein (Hip) (Suppression of tumorigenicity protein 13) (Putative tumor suppressor ST13) (Protein FAM10A1)	62	18 41476.54	Cytoplasm	Chaperone, protein folding	Antioncogene, has chaperone activity, it may contribute to the interaction of HSC70 with various target proteins.
P51659	DHB4_HUMAN	Peroxisomal multifunctional enzyme type 2 (MFE-2) (D-bifunctional protein) (DBP) (17-beta-HSD 4) (EC 1.1.1.35)	57	13 79961.43	Peroxisome	Enzyme, transport, protein binding	Bifunctional enzyme acting on the peroxisomal beta-oxidation pathway for fatty acids.
P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	124	34 77618.38	Nucleus	RNA binding, RNA splicing	Pre-mRNA binding protein. Involved in splicing. Acting as a receptor for carinoembryonic antigen in Kupffer cells, it may initiate a series of signaling events leading to tyrosine phosphorylation of proteins and induction of IL-1 alpha, IL-6, IL-10 and tumor necrosis factor alpha cytokines.

Table III. continued

Table III. continued

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P54707	AT12A_HUMAN	Potassium-transporting ATPase alpha chain 2 (EC 3.6.3.10) (Proton pump) (Non-gastric H(+)/K(+) ATPase subunit alpha)	58	11	116680.57	Membrane	Enzyme, transport	
P54819	KAD2_HUMAN	Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP transphosphorylase)	87	39	26557.82	Mitochondrion	Enzyme	Essential for maintenance and cell growth, acting in concert with FADD and caspase-10. It mediates a novel intrinsic apoptotic pathway that may be involved in tumorigenesis.
P55265	DSRAD_HUMAN	Double-stranded RNA-specific adenosine deaminase (EC 3.5.4.-) (DRADA) (136 kDa double-stranded RNA-binding protein)	61	6	137107.27	Cytoplasm, nucleus	Enzyme, RNA associated	DNA modifying enzyme.
P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H' (hnRNP H') (FTP-3)	125	43	49517.39	Nucleus	RNA binding, RNA splicing	
P55854	SUMO3_HUMAN	Small ubiquitin-related modifier 3 precursor (SUMO-3) (Ubiquitin-like protein SMT13A)	61	34	11686.75	Cytoplasm	Regulatory, protein binding	
P57053	H2BFS_HUMAN	Histone H2B type F-S (H2B.s) (H2B/s)	58	46	13804.54	Nucleus	Transcription, DNA binding, chromatin organization, remodeling	
P57735	RAB25_HUMAN	Ras-related protein Rab-25 (CATX-8)	57	29	23595.04	Membrane	Signaling	Regulates the apical recycling and/or transcytotic pathways.
P61088	UBE2N_HUMAN	Ubiquitin-conjugating enzyme E2 N (EC 6.3.2.19) (Ubiquitin-protein ligase N)	95	33	17184.00	Cytoplasm, nucleus	Signaling, regulatory	Protooncogene.
P61604	CH10_HUMAN	10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (CPN10)	86	47	10793.83	Mitochondrion	Chaperone	Positive regulation of NF-kappaB kinase/NF-kappaB cascade, activation of NF-kappaB transcription factor.
P62072	TIM10_HUMAN	Mitochondrial import inner membrane translocase subunit Tim10	57	40	10554.03	Mitochondrion	Enzyme, transport, ion binding	Involved in mitochondrial protein biogenesis.
P62633	CNBP_HUMAN	Cellular nucleic acid-binding protein (CNBP) (Zinc finger protein 9)	97	55	20704.04	Cytoplasm, endoplasmic reticulum, nucleus	Transcription, RNA binding	Single stranded DNA-binding protein involved in sterol-mediated repression.
P62807	H2B1C_HUMAN	Histone H2B type 1-C/E/F/G/I (H2B _{afg/hkl}) (H2B.1A) (H2B/a) (H2B _g) (H2Bh) (H2B/k)	102	60	13679.48	Nucleus	Transcription, DNA binding, chromatin organization, remodeling	

Table III. continued

Table III. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
P62993	GRB2_HUMAN	Growth factor receptor-bound protein 2 (Adapter protein GRB2) (SH2/SH3 adapter GRB2) (Protein Ash)	115	50	25304.48	Cytosol	Signaling, signal transduction, growth factor	Adapter protein that provides a critical link between cell surface growth factor receptors and the Ras signaling pathway. EGFR and PDGFR and other cellular tyrosine phosphorylated proteins receptors to signaling for mitogenesis and cytoskeletal reorganization. Acts as a transcriptional activator.
P82970	NSBP1_HUMAN	Nucleosome-binding protein 1	57	24	31505.90	Nucleus		
Q02818	NUCB1_HUMAN	Nucleobindin-1 precursor (CALNUC)	63	25	53846.33	Golgi apparatus, membrane	Homeostasis, ion binding	Major calcium-binding protein of the Golgi apparatus.
Q13242	SFRS9_HUMAN	Splicing factor, arginine/serine-rich 9 (Pre-mRNA-splicing factor SRp30C) Integrin-linked protein kinase 1 (EC 2.7.11.1) (ILK-1)(59 kDa serine/threonine protein kinase)	116	51	25640.47	Nucleus	RNA splicing	Has a role in constitutive splicing.
Q13418	ILK1_HUMAN	Integrin-linked protein kinase 1 (EC 2.7.11.1) (ILK-1)(59 kDa serine/threonine protein kinase)	57	24	51899.12	Cytoplasm	Enzyme, signal transduction	Acts as a mediator of inside-out integrin signaling. Regulates integrin-mediated signal transduction and cell adhesion, mediate cell architecture.
Q13442	HAP28_HUMAN	28 kDa heat- and acid-stable phosphoprotein (PDGF-associated protein) (PAP) Diacylglycerol kinase zeta (EC 2.7.1.107) (Dihydroceride kinase zeta) (DGK-zeta) (DAG kinase zeta)	105	45	20617.63		Signal transduction, cell growth/proliferation	
Q13574	DGKZ_HUMAN	(DAG kinase zeta) (DGK-zeta) Four and a half LIM domains protein 3 (FHL-3) (Skeletal muscle LIM-protein 2) (SLIM 2)	60	13	12581.84	Cytoplasm, nucleus	Enzyme, signal transduction	
Q13643	FHL3_HUMAN	Nascent polypeptide-associated complex subunit alpha (NAC-alpha) (Alpha-NAC) (Hom s 2.02)	58	10	33208.51		Regulatory, development	
Q13765	NACA_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein)	57	25	23369.71	Cytoplasm, nucleus	Chaperone, transcription, translation	May act as a specific coactivator for JUN, binding to DNA and stabilizing the interaction of JUN homodimers with target gene promoters.
Q14103	HNRPD_HUMAN	Zinc finger protein 160 (Zinc finger protein HZF5) (Fragment)	83	23	38581.37	Nucleus	RNA binding, transcription	Binds to RNA molecules that contain AU-rich elements (AREs). It is target of MYC proto-oncogene mRNA. Involved in the ARE/AUBP-mediated modulation of BCL2 mRNA decay during apoptosis. Controls proliferation with TIAL1 by a MYC-dependent pathway.
Q14589	ZN160_HUMAN	Zinc finger protein 160 (Zinc finger protein HZF5) (Fragment)	57	31	19847.66	Nucleus		Involved in transcriptional regulation.

Table III. *continued*

Table III. continued

Accession number	Protein symbol	Protein name	Score (%)	Coverage MW	Protein name	Score (%)	Coverage MW	Subcellular localisation	Function	Brief comment
Q14696	MESD2_HUMAN	Mesoderm development candidate 2 (NY-REΝ61 antigen)	103	46	26231.37	Endoplasmic reticulum			Chaperone	
Q14828	Q14828_HUMAN	MG44 protein (Fringe)	57	9	43143.21	Nucleus				
Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 (LASP-1) (MLN 50)	105	34	30097.37	Cytoplasm				Important role in the regulation of dynamic actin-based, cytoskeletal activities, cytoskeleton organization and biogenesis.
Q15004	PAF_HUMAN	PCNA-associated factor (p15PAF) (Overexpressed in anaplastic thyroid carcinoma 1) (OEATC-1)	57	40	12093.20	Nucleus, mitochondrion			Protection	Involved in protection of cells from UV-induced cell death.
Q15102	PA1B3_HUMAN	Platelet-activating factor acetylhydrolase IB subunit gamma (EC 3.1.1.47) (PAF acetylhydrolase 29 kDa subunit)	69	36	25832.27	Cytoplasm			Enzyme	
Q15181	IPYR_HUMAN	Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-hydrolase) (PPase)	136	44	33095.33	Cytoplasm			Enzyme	
Q15185	TEBP_HUMAN	Prostaglandin E synthase 3 (EC 5.3.99.3) (Cytosolic prostaglandin E2 synthase) (cPGES)	89	53	18970.53	Cytoplasm			Enzyme, signal transduction, chaperone	Disrupting receptor-mediated transcriptional activation, by promoting disassembly of transcriptional regulatory complexes, telomerase activity.
Q15773	MLF2_HUMAN	Myeloid leukemia factor 2 (Myelodysplasia-myeloid leukemia factor 2)	57	25	28186.23	Cytoplasm, nucleus				Unknown/unspecified
Q16552	IL17_HUMAN	Interleukin-17A precursor (IL-17A) (IL-17) (Cytotoxic T-lymphocyte-associated antigen 8)	57	40	17835.01	Secreted			Signaling, apoptosis	
Q16718	NDUAS5_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 (EC 1.6.5.3) (EC 1.6.99.3)	129	56	13376.16	Mitochondrion			Enzyme	
Q31349	Q31349_BOSIN	Serum albumin (Fragment)	139	34	55486.66					
Q50EX0	TRIM5_GORG	Tripartite motif-containing protein 5 (EC 6.3.2.-) (TRIM5alpha)	59	36	22257.72	Cytoplasm			Enzyme	
Q53G17	Q53G17_HUMAN	NADH dehydrogenase (Ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	57	25	24233.77					

Table III. continued

Table III. *continued*

Accession number	Protein symbol	Protein name	Score (%)	Coverage Protein MW	Subcellular localisation	Function	Brief comment
Q53XZ1	Q53XZ1_HUMAN	Clathrin, light polypeptide (Lca)	60	27	23704.45		
Q58E69	Q58E69_MOUSE	Transferin (17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library)	287	47	78840.54		
Q51ST8	Q51ST8_MACFA	Heterogeneous nuclear ribonucleoprotein C (Fragment)	65	23	29304.61	DNA & RNA binding	
Q51RJ0	Q51RJ0_HUMAN	TSC22 domain family, member 3	68	49	12303.23	Nucleus	Transcription, anti-apoptosis Inhibits anti-CD3 induced NFKB1 nuclear translocation.
Q51VFD6	Q51VFD6_HUMAN	Centrosomal protein 1 (Fragment)	57	21	40837.26		
Q51VF3	PCID2_HUMAN	PCI domain-containing protein 2 (CSN12-like protein)	57	16	46627.04		
Q5QNV8	Q5QNV8_MOUSE	Novel protein	57	18	66275.05		
Q5R975	Q5R975_PONPY	Hypothetical protein DKFZp59G0439	179	48	55355.96	Protein binding, signal transduction	
Q5T6W2	Q5T6W2_HUMAN	Heterogeneous nuclear ribonucleoprotein K (Fragment)	57	16	42008.79		
Q61649	Q61649_MOUSE	Alpha-globin mRNA. (Fragment)	57	68	6212.03		
Q66GS9	CP135_HUMAN	Centrosomal protein of 135 kDa (Cep135 protein) (Centrosomal protein 4) Histone H4 (Fragment)	78	22	133878.36	Centrosome	
Q6FGB8	Q6FGB8_HUMAN	SULT1C2 protein	57	41	11386.40	Nucleus	
Q6PD90	Q6PD90_HUMAN	MHC class I	63	48	11815.89		
Q6T715	Q6T715_HUMAN	antigen (Fragment)	57	26	21061.17		
Q76M58	Q76M58_HUMAN	40S ribosomal protein S12	100	59	14904.63	Ribosome	
Q7L8A9	Q7L8A9_VASH_HUMAN	Vasohibin	57	25	41045.13	Secreted	
						Translation Regulatory	Angiogenesis inhibitor. Acting as an endothelium-derived negative feedback regulator of angiogenesis, having an activity to prevent neointimal formation by inhibiting adventitial angiogenesis, activated by VEGF in endothelial cells.

Table III. *continued*

Table III. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
Q7Z3B4	NUP54_HUMAN	Nucleoporin p54 (54 kDa nucleoporin)	217	35	55515.39	Nucleus	Transport	
Q7Z4D7	Q7Z4D7_HUMAN	MSTP102 (Fragment)	57	56	5953.26			
Q7Z554	Q7Z554_HUMAN	Tropomodulin T cardiac isoform	57	23	27512.60	Nucleus		
Q80WC8	Q80WC8_MOUSE	Hist2h4 protein (Fragment)	57	41	12479.98			
Q80Y35	Q80Y35_MOUSE	Nuclear mitotic apparatus protein 1	57	10	236598.84			
Q811R0	Q811R0_RAT	HOMER1G	67	33	21978.29	Mitochondrion		
Q86Y43	Q86Y43_HUMAN	Putative calcium binding transporter	57	18	49551.48			
Q8BP05	Q8BP05_MOUSE	18 days pregnant adult female placenta and extraembryonic tissue cDNA, RIKEN full-length enriched library, clone:3830418K20 product:apolipoprotein A-I, full insert sequence)	177	43	30596.64	Extracellular		
Q8BP04	Q8BP04_MOUSE	11 days embryo whole body cDNA, RIKEN full-length enriched library, clone: 2700073B15 product: hemoglobin, beta adult major chain, full insert sequence	67	44	15228.86			
Q8BQX4	Q8BQX4_MOUSE	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230353A13)	57	23	29516.82			
Q8C7C7	ALBU_MOUSE	2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:C2002	150	26	67013.48			
Q8C9T9	Q8C9T9_MOUSE	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430108K10 product:hypothetical protein, full insert sequence.[Fragment]	64	22	63889.06			
Q8CGP4	Q8CGP4_MOUSE	Histone protein H1h2aa (Novel H2A histone family (H2a) member)	63	42	14047.86	Nucleus	DNA binding	
Q8IWA7	Q8IWA7_HUMAN	RAB37, member RAS oncogene family, isoform 3	60	31	24268.22	Cytoplasm, nucleus	Signaling	
Q8IZQ5	SE1H_HUMAN	Selenoprotein H	58	41	13512.23			
Q8IZS8	Q8IZS8_HUMAN	Voltage-gated calcium channel alpha(2)delta-3 subunit	57	9	124073.64	Membrane	Transport	Involved in a redox-related process. Subunit of voltage-dependent calcium channels.

Table III. *continued*

Table III. *continued*

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
Q8N1N0 CLC4F_HUMAN	C-type lectin domain family 4 member F (C-type lectin superfamily member 13) (C-type lectin)	57 12 60398.64	Membrane		Receptor			Receptor with an affinity for galactose and fucose.
Q8N359 Q8N359_HUMAN	PHF2 protein (Fragment)	63 19 50869.88	Nucleus		Transcription			Served as transcription factor, protooncogene. Regulates transcription affecting gene expression by influencing chromatin structure.
Q8NBS9 TXND5_HUMAN	Thioredoxin domain-containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum)	157 37 48282.92	Endoplasmic reticulum		Enzyme, electron transport, regulatory, anti-apoptosis			
Q8NC51 PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein (PAIR RNA-binding protein 1) (PAIR-RBP1)	97 26 44995.48	Cytoplasm, nucleus		RNA binding			Involved in the regulation of mRNA stability.
Q92804 RBP56_HUMAN	TATA-binding protein-associated factor 2N (RNA-binding protein 56) (TAFII68) (TAFII68)	65 18 62021.19	Nucleus		Transcription, DNA associated			Has role during transcription initiation at distinct promoters.
Q93077 H2A1C_HUMAN	Histone H2A type 1-C	79 41 13965.90	Nucleus		Transcription, DNA binding, chromatin organization, remodelling			
Q96AE4 FUBP1_HUMAN	Far upstream element-binding protein 1 (FUSE-binding protein 1) (FBP) (DNA helicase V)	194 44 67602.50	Nucleus		Transcription, DNA associated			Activator and repressor of transcription.
Q96D15 RCN3_HUMAN	Reticulocalbin-3 precursor (EF-hand calcium-binding protein RLP49)	76 39 37470.00	Endoplasmic reticulum		Regulatory, ion binding			
Q96IU4 AB14B_HUMAN	Abhydrolase domain-containing protein 14B (EC 3.1.1.1) (CCG1-interacting factor B)	83 38 22445.60	Cytoplasm, nucleus		Enzyme			
Q96K21 ZFY19_HUMAN	Zinc finger FYVE domain-containing protein 19 (MLL partner containing FYVE domain)	85 18 52410.61	Nucleus		Enzyme, transcription			Involved in transcriptional regulation.
Q96QR8 PURB_HUMAN	Transcriptional activator protein Pur-beta (Purine-rich element-binding protein B)	167 51 33260.50	Nucleus		Transcription, DNA binding			Participates in transcriptional and translational regulation.
Q99623 PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (Repressor of estrogen receptor activity)	98 41 33275.92	Nucleus		Transcription			It is a mediator of transcriptional repression by nuclear hormone receptors, negative regulation of transcription.

Table III. *continued*

Table III. continued

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
Q99759	M3K3_HUMAN	Mitogen-activated protein kinase kinase kinase 3 (EC 2.7.11.25) (MAPK/ERK kinase kinase 3)	57	14	71324.52	Cytoplasm, nucleus	Enzyme, signal transduction	Component of a protein kinase signal transduction cascade.
Q99878	H2A1J_HUMAN	Histone H2A type 1-J	60	35	13796.80	Nucleus	Transcription, DNA binding, chromatin organization, remodeling	Positive regulation of I kappaB kinase/NF-kappaB cascade.
Q99K47	Q99K47_MOUSE	Fibrinogen, alpha polypeptide	112	27	61801.21		Signal transduction, protein binding	cooperates with MAP3K7 leading to NF-kappaB activation.
Q99LT4	Q99LT4_MOUSE	Tcf15 protein (Fragment)	59	38	17022.76	Nucleus		
Q9BWJ5	SF3B5_HUMAN	Splicing factor 3B subunit 5 (SF3b5) (Pre-mRNA-splicing factor SF3b 10 kDa subunit)	85	65	10242.83	Cytoskeleton		
Q9BWL4	CV028_HUMAN	UPF0027 protein C22orf28	133	29	55722.03	Mitochondrion		
Q9BXG8	HINT2_HUMAN	Histidine triad nucleotide-binding protein 2 (EC 3.5.5.1) (HINT-2) (HINT-3) (HHT-17 kDa) (PKC ζ -1-related HHT protein)	67	39	17208.26			
Q9BXU0	TEX12_HUMAN	Testis-expressed sequence 12 protein	57	43	14155.21	Cytoplasm	Enzyme	Hydrolyses ITP, regulating ITP concentration in cells.
Q9BY32	ITPA_HUMAN	Inosine triphosphate pyrophosphatase (EC 3.6.1.19) (ITPase) (Inosine triphosphatase) (Putative oncogene protein hcl4-06-p)	71	32	21831.04			
Q9CPX4	Q9CPX4_MOUSE	10 days embryo whole body cDNA, RIKEN full-length enriched library, clone: 2600017112 product: ferritin light chain 1, full insert sequence	175	72	20816.51			
Q9CY06	Q9CY06_MOUSE	13 days embryo liver cDNA, RIKEN full-length enriched library, clone: 25104040P05 product: hemoglobin, beta adult major chain, full insert sequence	110	71	15159.79			
Q9CY10	Q9CY10_MOUSE	13 days embryo liver cDNA, RIKEN full-length enriched library, clone: 2510040B16 product: hemoglobin, beta adult major chain, full insert sequence	67	44	155306.84			
Q9D8U7	DTWD1_MOUSE	DTW domain-containing protein 1	57	20	35282.76	Cytoplasm	Protein binding, anti-apoptosis,	
Q9ERD1	Q9ERD1_RAT	Clusterin (Fragment)	84	36	25200.33		differentiation, proliferation	
Q9H385	Q9H385_HUMAN	PRO2603	57	57	5909.12	Endoplasmic reticulum	Enzyme, regulatory	Folding of proteins
Q9NWM8FKB14_HUMAN		FK506-binding protein	80	40	24270.48			

Table III. continued

Table III. continued

Accession number	Protein symbol	Protein name	Score	Coverage (%)	Protein MW	Subcellular localisation	Function	Brief comment
Q9NWZ3	IRAK4_HUMAN	I4 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPase) Interleukin-1 receptor-associated kinase 4 (EC 2.7.11.1) (IRAK-4) (NY-REN-64 antigen)	57	18	51953.10	Cytosol	Enzyme, signal transduction, transcription	during protein synthesis.
Q9NX63	CHCH3_HUMAN	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3	77	38	26421.33	Mitochondrion		
Q9NXR1	NDE1_HUMAN	Nuclear distribution protein nude homolog 1 (NudE)	57	15	38841.56	Cytoplasm, centrosome	Regulatory	Required for centrosome duplication and formation and function of the mitotic spindle.
Q9NYL9	TIMOD3_HUMAN	Trponomodulin-3 (Ubiquitous tropomodulin)	84	18	39741.36	Cytoplasm, cytoskeleton	Motor/contractile	
Q9UIJ7	KAD3_HUMAN	GTP-AMP phosphotransferase (U-Tmod) mitochondrial (EC 2.7.4.10) (Adenylate kinase 3) (AK3) Zinc finger protein 222	57	27	25418.51	Mitochondrion	Enzyme	
Q9UK12	ZN222_HUMAN	Ubiquilin-1 (Protein linking IAP with cytoskeleton 1) (PLIC-1) (hPLIC-1)	57	19	54265.22	Nucleus	Regulatory, transcription, ion binding	Involved in transcriptional regulation.
Q9UMX0	UBQL1_HUMAN	Microtubule-actin crosslinking factor 1, isoforms 1/2/3/5 (Actin cross-linking family protein)	89	24	62479.44	Cytoplasm, nucleus	Regulatory, apoptosis	
Q9UPN3	MACF1_HUMAN	Centriole associated protein CEP110	66	7	623625.85	Cytoplasm, cytoskeleton	Structural, ion binding	
Q9Y489	Q9Y489_HUMAN	Protein CEP110	61	11	117425.51			
Q9Y5J7	TIM9_HUMAN	Mitochondrial import inner membrane translocase subunit Tim9	70	65	10599.21	Mitochondrion	Enzyme , transport, ion binding	
Q9Y623	MYH4_HUMAN	Myosin-4 (Myosin heavy chain, skeletal muscle, fetal) (Myosin heavy chain IIb) (MyHC-IIb)	57	8	223843.67	Cytoplasm	Structural	

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