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## Mass Spectrometry-Based Proteomics Analysis of the Matrix Microenvironment in Pluripotent Stem Cell Culture

Christopher Hughes, *The University of Western Ontario*

Supervisor: Dr. Gilles Lajoie, *The University of Western Ontario*

A thesis submitted in partial fulfillment of the requirements for the Doctor of Philosophy degree in Biochemistry

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# **Mass Spectrometry-Based Proteomics Analysis of the Matrix Microenvironment in Pluripotent Stem Cell Culture**

(Spine title: Proteomics of Human Stem Cell Derived Matrices)

(Thesis format: Integrated-Article)

by

Christopher S. Hughes

Graduate Program in Biochemistry

A thesis submitted in partial fulfillment  
of the requirements for the degree of  
Doctor of Philosophy

The School of Graduate and Postdoctoral Studies  
The University of Western Ontario  
London, Ontario, Canada

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THE UNIVERSITY OF WESTERN ONTARIO  
SCHOOL OF GRADUATE AND POSTDOCTORAL STUDIES

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entitled:

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## Abstract

The stem cell microenvironment contains soluble factors, support cells, and components of the extracellular matrix (ECM) that combine to effect cellular behavior. Mass spectrometry based proteomics offers the opportunity to directly assay components of extracellular microenvironments, thereby providing a sensitive means for obtaining insight into the stem cell niche. In this study we present the generation and analysis of human embryonic stem cell (hESC) and human induced pluripotent stem cell (hiPSC) matrix microenvironments using an MS-based proteomics approach.

One of the primary limitations in the proteomics analysis of hESCs and hiPSCs is the reproducible generation of sufficient cell numbers amenable to experimentation. In Chapter 2 we develop reliable methods for the maintenance and proliferation of hESCs in metabolic labeling medium for use in stable isotope labeling with amino acids in cell culture (SILAC) experiments. Previously, the application of SILAC with hESCs was hindered by the use of medium insufficient for their reproducible culture and the problematic conversion of isotopically labeled arginine to proline. To address these issues, we demonstrate the culture of hESCs, hiPSCs, and mouse ESCs in SILAC conditions using a serum-replacement mixture and alternatively in defined medium. In these optimized conditions we show that the problematic conversion of arginine to proline can be eliminated through the simple addition of exogenous proline to the culture medium.

Within the *in vitro* microenvironment, the ECM plays a significant role in the maintenance and regulation of hESCs and hiPSCs. In order to better understand the



communication between hESCs and hiPSCs and the extracellular matrix, we focused our investigation on this portion of the microenvironment. To facilitate the proteomic analysis of complex ECM mixtures, in Chapter 3 we describe methods for the fractionation and MS-based proteomics analysis of these matrices. Application to a variety of cell-derived and recombinant growth matrices demonstrates not only the effectiveness of our methods, but also the utility of directly assaying matrices used in hESC culture for the determination of factors beneficial for the maintenance of self-renewal and pluripotency.

Through combination of the SILAC growth (Chapter 2) and matrix analysis (Chapter 3) methods, the protein compositions of conditioned matrices from multiple pluripotent stem cell lines are determined (Chapter 4). Within these matrices, numerous antagonists of core pluripotency pathways are identified, such as soluble frizzled related protein (sFRP) 1 and 2. In Chapter 5 we focus on characterizing the functions of sFRP1 and sFRP2 in hESC self-renewal and pluripotency. Taken together, the work presented here illustrates the utility of assaying interactions between stem cells and their matrix microenvironment for the determination of pathways involved in the regulation of the pluripotent phenotype.

**Key Words:** human embryonic stem cells, microenvironment, mass spectrometry, proteomics, extracellular matrix, protein digestion, peptide sequencing, pluripotency, differentiation, induced pluripotent stem cell

## Co-Authorship Statement

### Chapter 1

Hughes, C.S.\*, Nuhn, A.\*, Postovit, L.M., Lajoie, G.A.. (2011) "Proteomics of Human Embryonic Stem Cells". *Proteomics*. 11;4:675 – 690

CSH and AN contributed equally to this manuscript. Both authors along with GL and LMP were involved in the generation of concepts to be presented and the drafting and revisions of the manuscript. All authors contributed to revisions and discussion of concepts.

Hughes, C.S., Ma, B., Lajoie, G.A.. (2010) "De Novo Sequencing Methods in Proteomics". *Methods in Molecular Biology*. 604:105 - 121

CSH wrote the complete initial draft of the manuscript. Generation and discussion of concepts as well as revisions were completed by all authors.

### Chapter 2

Bendall, S.C.\*, Hughes, C.S.\*, Stewart, M.H., Doble, B., Bhatia, M., Lajoie, G.A.. (2008) "Prevention of Amino Acid Conversion in SILAC Experiments with Embryonic Stem Cells". *Molecular and Cellular Proteomics*. 7:1587 – 1597

SCB and CSH contributed equally to this manuscript. SCB and CSH were involved in experimental design, data interpretation, and manuscript preparation. The remaining authors were involved with aspects of experimental design, manuscript revision, and discussion of concepts.

### **Chapter 3**

Hughes, C.S., Postovit, L.M., Lajoie, G.A.. (2010) “Matrigel: A Complex Protein Mixture Required for Optimal Growth of Cell Culture”. *Proteomics*. 10;9:1886 – 1890

CSH designed and performed experiments, interpreted data, and prepared the manuscript. Revisions were completed by all authors, as well as generation and discussion of concepts.

Hughes, C.S., Radan, L., Betts, D., Postovit, L.M., Lajoie, G.A.. (2011) “Proteomic Analysis of Extracellular Matrices used in Stem Cell Culture”. *Proteomics*. 11;20:3983 – 3991

CSH designed and performed experiments, interpreted data, and prepared the manuscript. LR also contributed to experimental work. All authors were involved in revisions of the manuscript and the generation and discussion of concepts.

### **Chapters 4 & 5 & 6**

Hughes, C.S., Radan, L., Stanford, W., Betts, D., Postovit, L.M., Lajoie, G.A.. (2012) “Mass Spectrometry-Based Proteomics Analysis of the Matrix Microenvironment in Pluripotent Stem Cell Culture”. (In Preparation)

CSH designed and performed experiments, interpreted data, and prepared the manuscript. LR also contributed to experimental design as well as work. All other authors were involved with manuscript revisions as well as generation and discussion of concepts. WS donated iPSC lines used in the experiments.

## Dedication

I would like to dedicate this firstly to my family for always being supportive of my endeavors and especially of my never-ending schooling. You have always been there when I have needed you and for that you will always have my appreciation. You have given me everything I have needed to become who I am today, for which I hope one day I can repay you.

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### **Appendix II**

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## List of Abbreviations

1D SDS PAGE	one dimensional sodium dodecyl sulfate polyacrylamide gel electrophoresis
2D SDS PAGE	two dimensional sodium dodecyl sulfate polyacrylamide gel electrophoresis
7AAD	7-amino-actinomycin D
AA	amino acid
Ab	antibody
ABC	ammonium bicarbonate
ACN	acetonitrile
AFP	alpha-feto protein
ANOVA	analysis of variation
AS	ammonium sulfate
BME	beta mercaptoethanol
BMP	bone morphogenetic protein
BSA	bovine serum albumin
CapLC	capillary liquid chromatography
cDNA	complementary DNA
CDX	caudal type homeobox 2
CFU	colony forming unit
CID	collisional induced dissociation
CM	conditioned media
CMTX	conditioned matrix
CMV	cytomegalovirus
CTGF	connective tissue growth factor
DDA	data directed analysis
DMEM	Dulbecco's modified Eagle minimal essential medium
DMSO	dimethyl sulfoxide
DNA	deoxyribonucleic acid
DKK	dickkopf



DTT	dithiothreitol
EB	embroid body
EC	embryonal carcinoma
ECD	electron capture dissociation
ECL	enhanced chemiluminescence
ECM	extracellular matrix
EDTA	ethylenediaminetetraacetic acid
EGF	epidermal growth factor
ESC	embryonic stem cell
ESI	electrospray ionization
ETD	electron transfer dissociation
FA	formic acid
FACS	fluorescence activated cell sorting
FBS	fetal bovine serum
FGF	fibroblast growth factor
FGFR	fibroblast growth factor receptor
GAPDH	glyceraldehyde-3-phosphate dehydrogenase
GATA	gata-binding protein
GeLC	gel enhanced liquid chromatography
GFP	green fluorescent protein
GFR	growth factor reduced
GO	gene ontology
GSC	goosecoid
HARV	high aspect ratio vessel
hdF	hESC derived fibroblast
HDGF	hepatoma derived growth factor
HEK	human embryonic kidney
HGF	hepatocyte growth factor
hESC	human embryonic stem cell

hiPSC	human induced pluripotent stem cell
HPLC	high performance liquid chromatography
HRP	horse radish peroxidase
HSC	hematopoietic stem cell
ICAT	isotope-coded affinity tag
ICC	immunocytochemical
ICM	inner cell mass
ICR	ion cyclotron resonance
IE	iterative exclusion
IE-LC MS/MS	iterative exclusion liquid chromatography tandem mass spectrometry
IEF	isoelectric focusing
IGF	insulin-like growth factor
IGF1R	type 1 insulin-like growth factor receptor
IGFBP	insulin-like growth factor binding protein
IPI	International Protein Index
iPSC	induced pluripotent stem cell
ISCI	International Stem Cell Initiative
iTRAQ	isotope tags for relative and absolute quantification
Klf	Kruppel-like factor
KOSR	knockout serum replacement
LC	liquid chromatography
LC MS/MS	liquid chromatography tandem mass spectrometry
Lefty	left-right determination factor
LIF	leukemia inhibitory factor
LIT	linear ion trap
LOD	limit of detection
m/z	mass to charge ratio
MALDI	matrix assisted laser desorption ionization
MEF	mouse embryonic fibroblast

mESC	mouse embryonic stem cell
MIXL1	mix paired homeobox-like 1
MS	mass spectrometry
MS/MS	tandem mass spectrometry
MudPIT	multidimensional protein identification technology
MW	molecular weight
Myc	myelocytomatosis
NaOH	sodium hydroxide
NEAA	non-essential amino acids
NH <sub>4</sub> OH	ammonium hydroxide
NGF	nerve growth factor
N-GFR	non-growth factor reduced
Oct	octamer
ORF	open-reading frame
PAX	paired-box protein
PCR	polymerase chain reaction
Pkl	peak list
PDGF	platelet derived growth factor
PEDF	pigment epithelium derived factor
PI	propidium iodide
PLGS	protein lynx global server
PMSF	phenylmethylsulphonylfluoride
PTM	post-translational modification
PVDF	polyvinylidene fluoride
Q	quadrupole
QToF	quadrupole time of flight
RGD	Arg-Gly-Asp
RNA	ribonucleic acid
RPLPO	ribosomal protein, large, PO

RPM	revolutions per minute
RPMI	Roswell Park Memorial Institute medium
RT	retention time
RTK	receptor tyrosine kinase
RT-PCR	real-time polymerase chain reaction
SAX	strong anion exchange
SCX	strong cation exchange
SD	standard deviation
SDS	sodium dodecyl sulfate
SEM	standard error of the mean
SF	serum free
sFRP	soluble frizzed related protein
shRNA	short hairpin RNA
SILAC	stable isotope labeling with amino acids in cell culture
SOX	SRY (sex-determining region Y)-box
SPARC	secreted protein acidic and rich in cysteine
SSEA	stage specific embryonic antigen
TBST	tris buffered saline with tween
TGF	transforming growth factor
TIC	total ion chromatograph
TMT	tandem mass tags
ToF	time of flight
Tris	tris(hydroxymethyl) aminomethane
UniProt	Universal Protein Resource
UPLC	ultra performance liquid chromatography
VEGF	vascular endothelial growth factor
WB	western blot
WT	wild type

Ala	(A)	alanine
Arg	(R)	arginine
Asn	(N)	asparagine
Asp	(D)	aspartic acid
Cys	(C)	cysteine
Gln	(Q)	glutamine
Glu	(E)	glutamic acid
Gly	(G)	glycine
His	(H)	histidine
Ile	(I)	isoleucine
Leu	(L)	leucine
Lys	(K)	lysine
Met	(M)	methionine
Phe	(F)	phenylalanine
Pro	(P)	proline
Ser	(S)	serine
Thr	(T)	threonine
Trp	(W)	tryptophan
Tyr	(Y)	tyrosine
Val	(V)	valine

# Chapter 1

## Introduction

### 1.0 Pluripotency and Stem Cells

Stem cells are broadly defined by two primary characteristics: (i) the ability to self-renew, generating daughter cells equal to the parent and (ii) the unique capacity to differentiate into an array of cellular sub-types. Stem cells can provide valuable insight into human development and disease, have exciting potential in regenerative medicine, and can be used as models for drug discovery and toxicity analyses (reviewed in [1]). These properties have prompted the initiation of numerous research studies using stem cells as a model system with the goal of potentially unlocking the molecular mechanisms behind the regulation of the stem cell phenotype.

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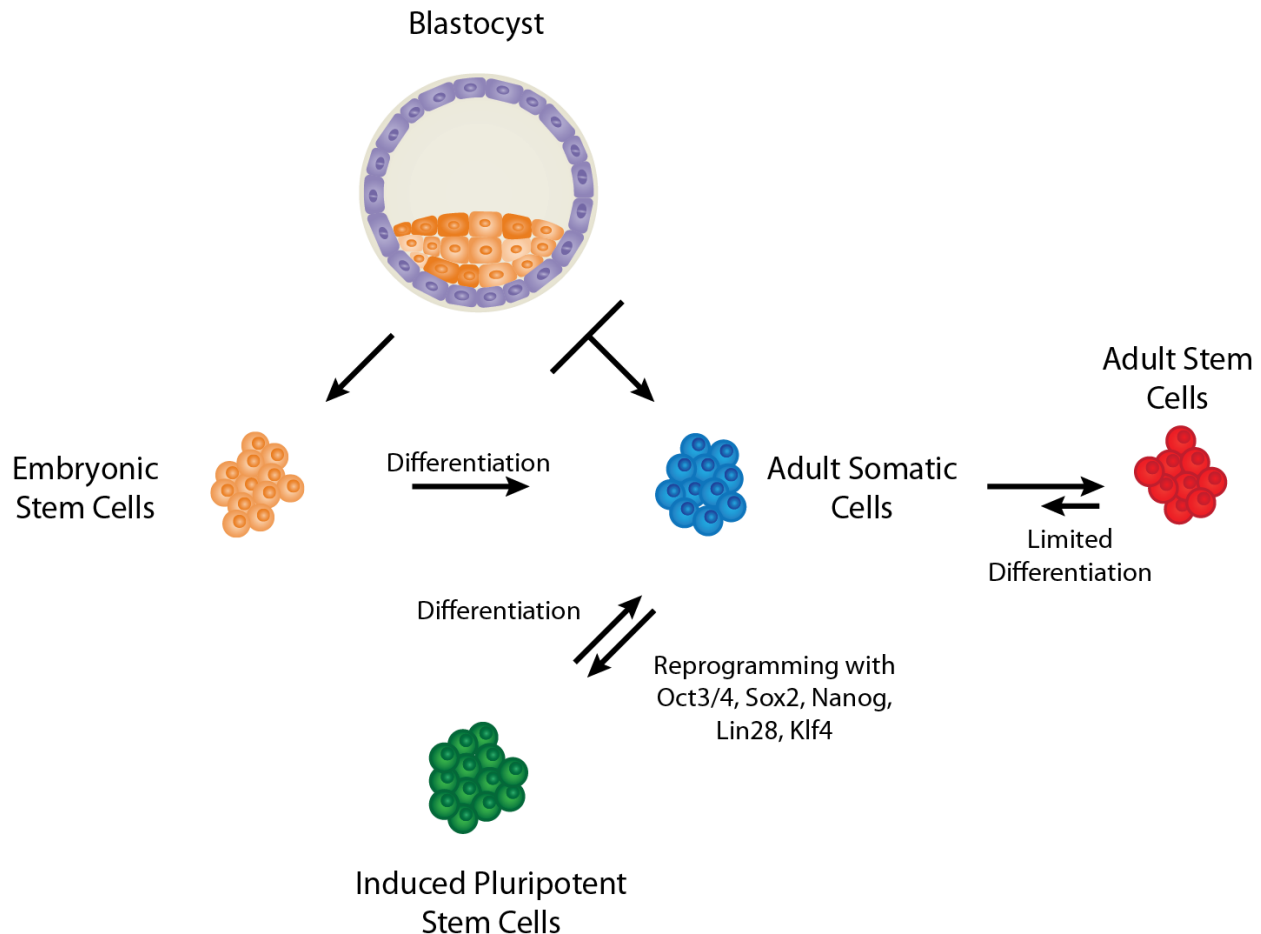
Hughes, C.S.\*, Nuhn, A.\*, Postovit, L.M., Lajoie, G.A.. (2011) "Proteomics of Human Embryonic Stem Cells". *Proteomics*. 11;4:675 – 690

Hughes, C.S., Ma, B., Lajoie, G.A.. (2010) "De Novo Sequencing Methods in Proteomics". *Methods in Molecular Biology*. 604:105 - 121

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Stem cells can be further characterized by their differentiation capabilities and tissue-type of origin. A variety of cell and tissue types can give rise to cells of varying developmental potential. In mammals, pioneering work with teratocarcinomas established the presence of an undifferentiated cell type within these germ-line tumors (reviewed in [2]). These embryonal carcinoma (EC) cells were later cultured in a pluripotent state *in vitro* [3]. EC cells were later observed to have the capacity to differentiate *in vitro* through the formation of embryoid bodies (EB) [4]. Similar work *in vivo* demonstrated the ability of EC cells to generate chimeras and populate the germline in mice [5]. Together these findings suggested the similarity of EC cells to those that populate the inner cell mass (ICM) and contributed towards the discovery of embryonic stem cells (ESC).

Utilizing many of the findings gained from the study of EC cells, the derivation of ESCs from mice was demonstrated by Evans and Martin [6, 7]. ESCs are classified as being pluripotent, meaning they have the ability to differentiate into derivatives of the three primary germ layers (Figure 1.1). *In vitro*, pluripotency is conventionally demonstrated using an EB formation assay as previously mentioned for EC cells. These EBs can be assayed for the presence of markers delineating the three primary germ layers as indicators of differentiation capacity. More stringent tests of pluripotency are carried out *in vivo* using teratoma, chimera, or tetraploid complementation assays. Using a chimera assay to illustrate the ability to contribute to the germ line of injected mice, the *in vivo* pluripotency of mESCs was later demonstrated [8, 9].



**Figure 1.1. Derivation and distinction between stem cell types.** Embryonic stem cells are the pluripotent derivatives of the inner cell mass of the blastocyst. Embryonic stem cells can be differentiated into any of the cells comprising the three primary germ layers. Adult somatic cells will contain tissue-specific populations of adult stem cells that are considered multipotent. Adult somatic cells derived from normal development can be reprogrammed using different combinations of transcription factors to generate induced pluripotent cells. These stem cells are also considered pluripotent and can mimic the differentiation capabilities of their embryonic counterparts. It is currently unknown whether embryonic and induced pluripotent cells are truly equivalent.



Soon after the work in mouse, derivation of pluripotent stem cells from the ICM of blastocyst stage embryos was demonstrated in humans (Figure 1.1) [10]. These hESCs shared the key properties of mESCs in that they could multiply indefinitely and generate cells of the three primary germ layers. Pluripotency could be assayed *in vitro* and *in vivo* using EB and teratoma formation respectively, but due to ethical concerns chimera and tetraploid complementation assays could not be undertaken. Since this time, alternative methods for the derivation of hESCs have been demonstrated, such as from biopsied blastomeres [11, 12].

Comparisons of mouse and human ESC lines have revealed several defining characteristics for each cell type. Identification of an undifferentiated colony is typically performed through the examination of intracellular and cell surface markers. mESCs and hESCs are both known to have strong expression for the nuclear cell markers Oct3/4 and Nanog [13]. On the cell surface, mESCs can be identified by the stage-specific embryonic antigen marker – 1 (SSEA-1) and the absence of SSEA-3 and -4. In hESCs, SSEA-3 and -4 mark undifferentiated cells whereas SSEA-1 is only present on those that have differentiated. Additional differences are observed when examining culture conditions for mESCs and hESCs. mESCs can be maintained in an undifferentiated and pluripotent state on a minimal matrix with supplementation of leukemic inhibitor factor (LIF) and bone morphogenic protein (BMP), whereas hESCs cannot [14, 15]. hESCs are typically grown on a layer of mitotically inactivated mouse feeder (MEF) cells in media supplemented with fibroblast growth factor 2 (FGF2 or basic FGF) [10]. Recent work has suggested that hESCs share several properties with mouse epiblast derived stem cells, whereas mESCs are indicative of a more naïve state

of the ICM [16, 17]. These findings have recently been advanced by the generation of naïve hESCs that share many of the defining properties of mESCs *in vitro* [18].

In contrast to embryonic, adult stem cells (ASC) are classified as being multipotent, meaning they can typically only generate differentiated cells that are a sub-type specific for the lineage to which they already belong (Figure 1.1). In addition to their limited differentiation capacity, ASCs are also have limited self-renewal capacity in culture, making their study difficult. Adult stem cells are thought to act as reservoirs of multipotent progenitors serving to regenerate cellular sub-types residing within specific tissues. This was originally validated in pioneering work with hematopoietic stem cells by Till and McCulloch where it was demonstrated that bone marrow cells could give rise to different types of blood cells [19, 20]. Since this time ASCs have been identified from heart, lung, skin, fat, and liver tissues (reviewed in [21]).

## **1.1 Inducing Pluripotency in Somatic Cells**

The ability to reprogram somatic cells to induced pluripotent stem cells (iPSC) was first demonstrated in mice by Takahashi and Yamanaka [22]. The retroviral introduction of *POU5F1* (herein referred to as Oct3/4), *Nanog*, *Sox 2*, and *c-Myc* into mouse fibroblasts generated cells that shared the characteristic morphology of embryonic stem cells (Figure 1.1). However, due to deficiencies in their developmental potential, they were not classified as pluripotent. Reprogrammed fibroblasts that had the developmental potential of ESCs and were germline competent were later demonstrated in mouse [23, 24]. Shortly after the demonstration of mouse iPSCs, human fibroblasts were

reprogrammed by using different combinations of Oct3/4, Nanog, Sox 2, c-Myc, Lin28, and Klf4 [25-27]. These hiPSCs shared similar gene expression patterns and *in vitro* differentiation capabilities to their ESC counterparts.

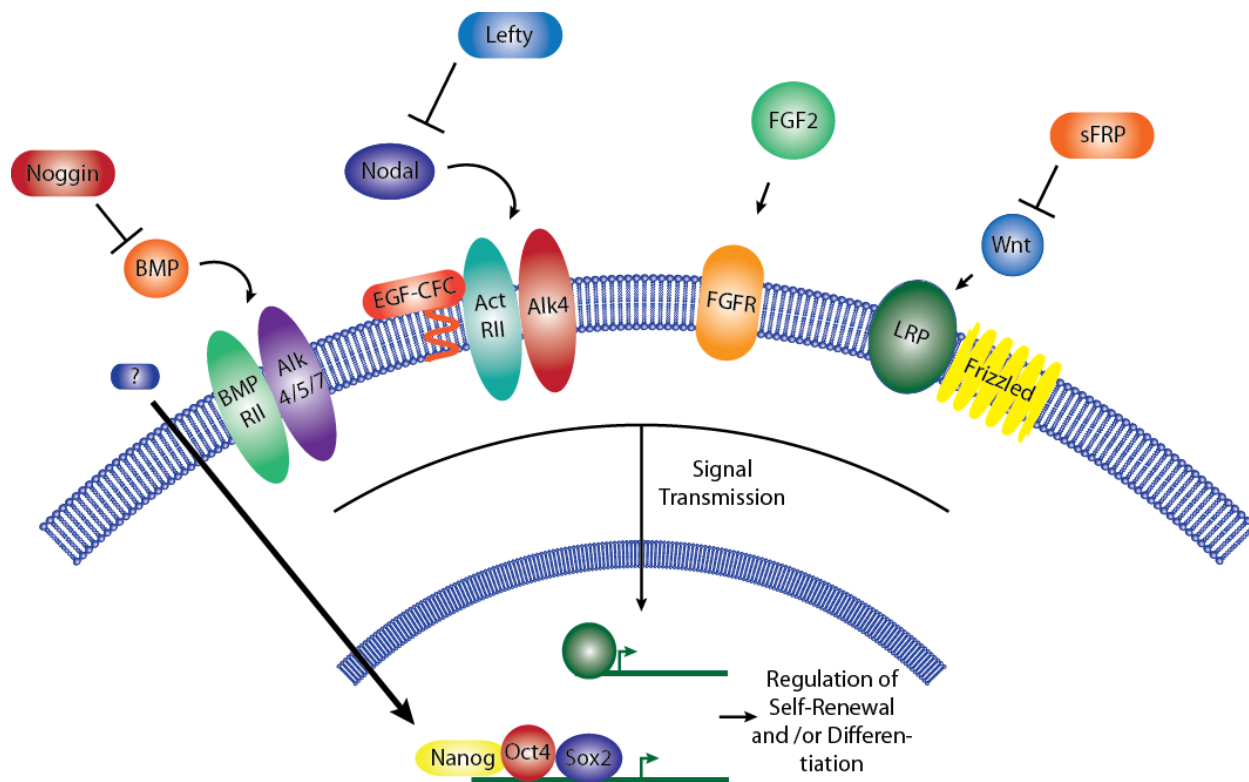
Since these original discoveries, research on the reprogramming factors and methods for transgene introduction have been extensive (reviewed in [28]). Currently, the only factor that is verified to be absolutely essential for reprogramming is Oct3/4. Removal of unnecessary reprogramming factors, such as c-Myc, is deemed necessary for reducing the potential tumorigenicity of iPSCs to facilitate their use in therapeutic applications. Alternative methods for transgene introduction that have been demonstrated include: retroviral, adenoviral, lentiviral, Epstein-Barr Virus, piggyBAC transposase, recombinant protein, and synthetic RNA [28]. The main focus of these alternative methods is the generation of 'footprint' free iPSCs that do not contain any exogenous genetic material resulting from methods used for transgene expression. Using methods such as recombinant proteins and synthetic RNAs, fibroblasts can be efficiently reprogrammed to generate iPSCs free of exogenous genetic material [28].

The observation that somatic cells can be reprogrammed to an embryonic-like state was a groundbreaking step forward in the stem cell field. The ability to generate embryonic-like cells in the lab side-stepped many of the ethical concerns surrounding stem cell research, and brought the prospect of cell-based therapeutics closer to reality. Tissue specific material could now be generated using a patient's own cells, overcoming immunocompatibility concerns. However, the risk of tumor formation in humans has to be eliminated before any significant *in vivo* studies can be carried out. In addition to any

potential clinical applications, these cells also provide new avenues for the study of stem cells and significantly increase the accessibility to this research area. However, due to limited information on the equivalency of induced pluripotent and embryonic stem cells, iPSCs are currently not yet recognized as a suitable replacement for hESCs in research.

## **1.2 Genomic and Proteomic Characterization of hESCs**

Since the establishment of the first hESC line in 1998 by Thomson *et al.*, a significant amount of research on hESC biology has been published [10]. In an effort to better characterize this cell type, many of these studies employed large screens directed at the identification of genes that regulate the pluripotent state [29-36]. Comparisons of gene expression patterns between hESCs, other pluripotent cells, or their differentiated derivatives, have led to the identification of growth and transcription factors that are hallmarks of hESC pluripotency, such as Oct 3/4, Nanog, and Sox 2 (Figure 1.2) [29, 32, 34-42]. The largest of these screens was undertaken by the International Stem Cell Initiative (ISCI). This group undertook characterization of 59 different hESC lines using a variety of analysis methods to identify hallmarks of pluripotency that are cell line independent [13, 43]. When global gene expression patterns were compared with that of the core pluripotency factor Nanog, a positive correlation was observed for many known hESC markers, such as Oct4, Nodal, LIN28, and DNMT3B. The findings of this global analysis led to the discovery of a set of genes that exhibited minimal variance across hESC lines that can be used as true markers of pluripotency. However, with the



**Figure 1.2. Regulation of human embryonic stem cell self-renewal and pluripotency.** The pathways shown represent those believed to play the most significant roles in the regulation of hESCs *in vitro* based on current knowledge. FGF and Activin/Nodal pathways are key regulators required for maintenance of an undifferentiated state and as such is commonly supplemented into culture medium. BMP signaling is known to promote mESC maintenance but induces hESC differentiation. Canonical Wnt signaling has been shown to promote both differentiation and the maintenance of pluripotency. Oct4/Sox2/Nanog are critical for hESC pluripotency, however little is known about their regulation outside of the nucleus or cell itself. The bulk of the knowledge concerning these key pathways has been derived from comparative genomic and proteomic screens of differentiated and undifferentiated stem cells.

rapid generation of new hESC and hiPSC lines, reconciling heterogeneity across populations remains a challenge, especially in proteomics (reviewed in [44]).

Since proteins are the effectors of cellular processes, it is important to investigate how stem cells are regulated by changes at the protein level in addition to genomic analyses. Post-translational modifications (PTM), such as phosphorylation, may influence the activity of pivotal proteins, and this information can only be determined by studying the proteome. The importance of the analysis of the proteome is further emphasized by the fact that changes in RNA abundance do not always correspond to those in their respective proteins. This discordance is the result of post-transcriptional factors, such as stability of mRNA and the rates of translation and protein degradation [45-49]. Discordance between RNA and protein abundance has been observed in the analysis of stem cell populations [45-49]. In one of the first studies to analyze both mRNA and protein abundance levels in stem cells, Fathi *et al.* utilized mass spectrometry (MS)-based proteomics and qRT-PCR genomics approaches to characterize differences between hESCs and EBs [50]. When the proteomic and genomic data were compared there was minimal correlation between the two sets. These findings highlight the necessity for complementary genomic and proteomic analyses in order to fully validate observations made when studying hESC populations.

Technological advances in protein and peptide fractionation techniques, mass spectrometers, and quantitative methods have greatly increased the capacity to analyze and extract biological information from complex cellular samples. With recent advances in the ability to proliferate hESCs to numbers amenable to proteomic experiments, there

have been a surge of proteomic studies looking at hESCs (reviewed in [51-53]). Initial efforts focused on the analysis of the cellular proteomes of hESCs using 2D-SDS-PAGE methods coupled with MS for protein identification [50, 54]. However, these studies were limited in the depth of proteome coverage due to the use of methods that hindered the detection of low abundance proteins. Since this time, multiple large-scale analyses of the proteomes of hESCs and hiPSCs have been completed through utilization of high-resolution MS platforms coupled to multi-dimensional fractionation chromatography [55-57]. Although these studies provide valuable resources, in order to extract greater biological significance from their data and facilitate comparative analysis of hESCs with their differentiated counterparts, researchers have turned to quantitative proteomic methods [58-63]. Quantitative studies have also been applied to the direct analysis of the hESC phosphoproteome during maintenance and differentiation [64-67]. The results of these studies have provided valuable information on the dynamic state of the proteome in hESCs. Collectively, the genomic and proteomic studies that have been completed on hESCs to date have revealed and characterized many of the intracellular pathways currently considered to be critical for pluripotency (Figure 1.2).

### **1.3 Mass Spectrometry-based Proteomics**

The goal of proteomics is to study the entire protein complement of cells or tissues. This not only encompasses the quantitative and qualitative analysis of protein abundance and turnover, but also their PTMs. Reaching this goal has conventionally relied upon technologies such as two-dimensional gel electrophoresis and western blotting. However, these methods offer limited information on a global proteome scale.

Although techniques for obtaining high-resolution and throughput genomic data sets have been available for some time, methods for the acquisition of complementary proteome data have lagged behind.

*1.3.1 Mass Spectrometry-based Proteomics* - In the field of proteomics, MS has become a central technology for the analysis of protein and peptide samples. This is due to the ability of MS instrumentation to rapidly acquire high quality spectra for thousands of peptides from a single sample injection. MS-based proteomics experiments are typically done in a 'bottom-up' approach, in which proteins are enzymatically digested to peptides prior to fractionation and analysis. Analysis of these complex peptide mixtures can yield high resolution and sensitivity data on the protein composition of a sample of interest. Greater instrument capabilities and new software advancements have resulted in the emergence of "top-down" experiments, in which intact proteins are analyzed (reviewed in [68, 69]). Until very recently, top-down experiments had not been amenable to large-scale analyses [70].

*1.3.2 Mass Spectrometry of Proteins and Peptides* - A typical MS analysis takes place in three steps. First, the mass of the intact peptide ions entering an MS in a given time window is measured. In the second step, specific precursor ions are selected in the first mass analyzer (e.g., Quadrupole 1), typically based on their relative abundance to one another, and fragmented in a collision cell (Quadrupole 2). The mass, or more accurately the mass-to-charge ratio ( $m/z$ ), of each fragment ion is detected in a second mass analyzer (e.g., Time of Flight, Linear Ion Trap, Orbitrap, Ion Cyclotron Resonance cell), for each of the previously selected precursors. This type of experiment is referred



to as a tandem MS, or MS/MS analysis. Detailed investigation of the product ion masses within an MS/MS spectrum provides information on the sequence of the peptide selected for fragmentation and, by inference, identification of the protein to which it belongs.

Early forms of MS were not amenable to the analysis of protein samples. Ionization techniques such as electron and chemical ionization would cause high levels of in-source fragmentation for biomolecules. The development of soft ionization techniques, such as matrix-assisted laser desorption ionization (MALDI) and electrospray ionization (ESI), revolutionized the analysis of biomolecules by MS [71-73]. Both of these ionization types are classified as 'soft' techniques because there is little in-source fragmentation of the ionized species, such that the mass of the intact molecular ion can be measured. ESI and MALDI sources can be interfaced to a variety of mass analyzers and instrument architectures compatible with proteomics experiments. The most frequently used designs in proteomics are hybrid instruments that contain a combination of mass analyzers, such as: time of flight (TOF) [74, 75], quadrupole (Q), ion trap (LIT) [76], Fourier transform ion cyclotron resonance (FT-ICR) [77], and Orbitrap [78]. All of these platforms have advantages and disadvantages, for a comprehensive review of instruments types and their characteristics see ([76, 79]).

*1.3.3 Proteomic Analysis of Complex Mixtures* - Even with advancements in instrument scan speed, mass spectrometers can only detect a limited number of ions in a given period of time. To spread the components of an injected sample across a wider time window, chromatographic methods of separation are used prior to MS (Figure 1.3). The

conventional method of fractionation utilized prior to MS analysis is separation with a reversed phase (RP) column that partitions based on the hydrophobic character of the sample components. It is becoming increasingly common for researchers to employ a secondary orthogonal fractionation method prior to RP, such as strong cation exchange (SCX) or 1D-SDS-PAGE. The decrease in fraction complexity and complementary nature of these methods aids in providing an increase in depth of proteome coverage [80, 81]. One distinct advantage of ESI is its compatibility with a number of these on-line separation techniques employed prior to MS analysis.

*1.3.4 Peptide Identification from Mass Spectra* - In order to obtain information on the amino acid series of ions that enter the MS, sequence ions can be generated through fragmentation of the peptide parent ion in an MS collision cell. Each peptide ion dissociates in one place along the backbone so that the difference in mass between the resulting fragment ions potentially corresponds to the mass of an amino acid (reviewed in [82]). The most common form of fragmentation found in MS instrumentation is collision induced dissociation (CID) [83-85]. In CID, peptide ions are induced to fragment through collisions with inert gas molecules. Aside from CID, electron capture (ECD) and electron transfer dissociation (ETD) have been implemented in more recent mass spectrometers [86-88]. The combination of CID and ETD is now available on instrument platforms such as Orbitrap and qFT-ICR mass spectrometers. This allows for the acquisition of spectra from the same sample using two fragmentation techniques generating complementary series of fragment ions [89].

The identification of peptides from fragment ion data relies on spectral interpretation software (Figure 1.3). Conventional search engines perform comparisons between observed and theoretical peptide spectra from an *in silico* digest of a sequence database (reviewed in [90]). Search engines will score peptide matches based on a variety of metrics designed to generate a score representative of the quality of match between the observed and theoretical spectra [90, 91]. However, there has been a recent emergence in software designed to search peptide spectra against a database of previously acquired MS/MS experimental spectra identification [92]. These search engines offer greater sensitivity and speed, but are limited by the content of the experimental spectral databases.

An alternative to the previously mentioned database-dependent approaches are *de novo* methods that make use of computerized methods for determining the sequences of peptides directly from MS/MS spectra [93]. *De novo* methods use the knowledge of the fragmentation methods employed in the MS and basic search parameters input by the user to rebuild the peptide ion series [94-101]. *De novo* sequencing approaches hold a lot of potential due to their ability to identify previously unknown peptide sequences and post-translational modifications. However, utilizing a combination of multiple search engine strategies has been shown to be beneficial to achieving greater depth of coverage in proteomics experiments [102-104].

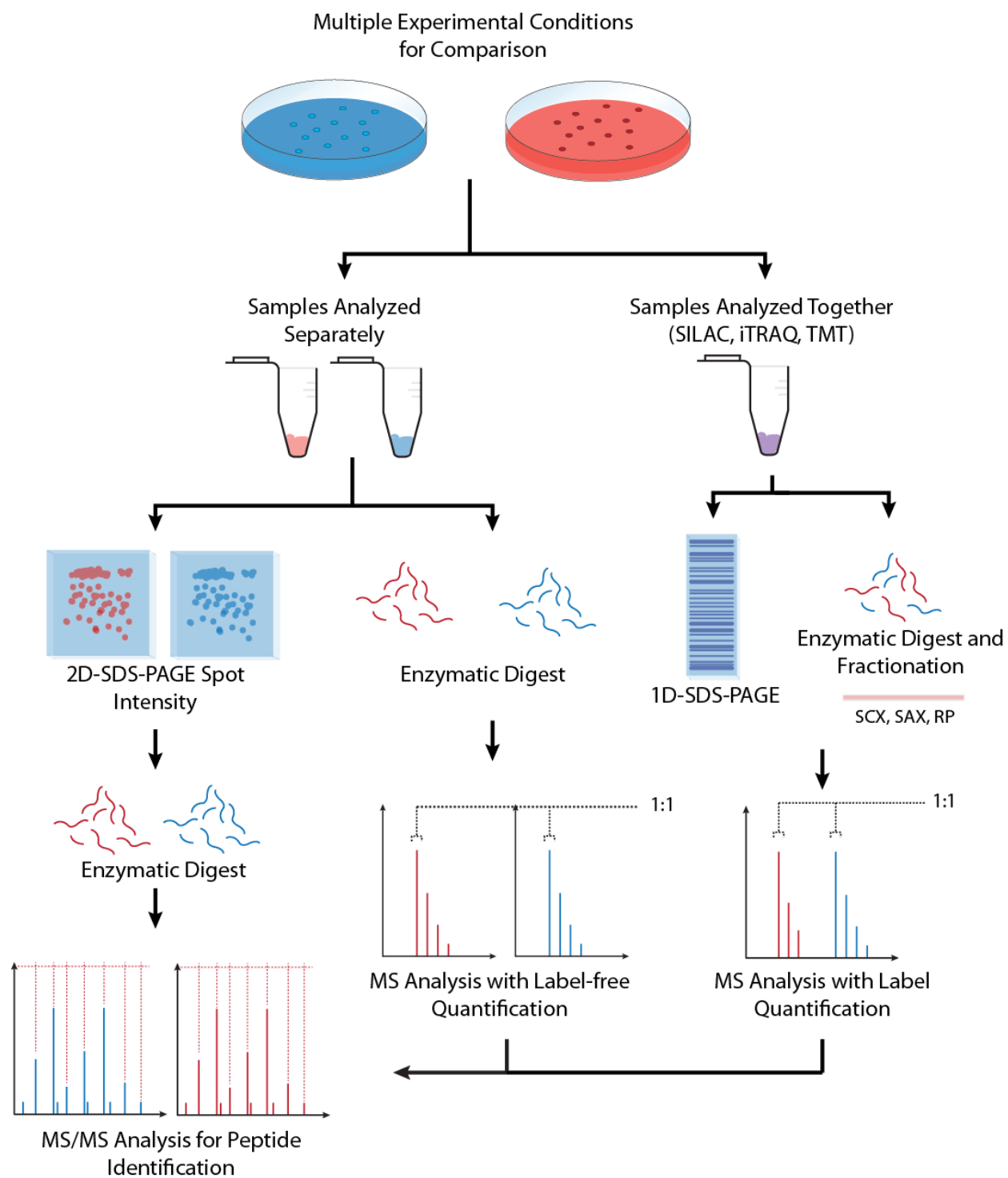
*1.3.5 Quantitative Proteomics* - To increase the biological significance of their data, quantitative proteomic strategies are frequently used to compare different cellular states or conditions (Figure 1.3). Mass spectrometers are not strictly quantitative, so

quantitative labeling is often used; however, label-free techniques are becoming increasingly popular (reviewed in [105, 106]). Application of the quantitative label can be done at the protein or peptide level, prior to analysis on the MS (Figure 1.3).

Reagents that are applied at the peptide level normally target primary amines to obtain complete sample coverage. In methods such as isobaric tags for relative and absolute quantification (iTRAQ) and tandem mass tags (TMT), samples are tagged following proteolytic digestion [107] (Figure 1.3). Peptides in different experimental conditions can be distinguished and quantified in MS/MS spectra based on the label applied. Dimethyl labeling approaches for peptide tagging have also been employed successfully, with the added advantage of minimal reagent expense [108, 109].

The most common alternatives to peptide tagging approaches are based on metabolic incorporation of isotopically labeled amino acids. One such isotopic labeling method, termed stable isotope labeling with amino acids in cell culture (SILAC) involves metabolic incorporation of  $^{13}\text{C}$  and  $^{15}\text{N}$  containing amino acids into a cell's proteome [110, 111]. Other methods based on metabolic incorporation of  $^{15}\text{N}$  have been widely applied both *in vitro* and *in vivo* [112]. Both methods rely on the depletion of native versions of the targeted amino acids or elements and re-supplementation of isotopically labeled versions that can be incorporated into newly synthesized proteins. Metabolic incorporation can also be achieved through the feeding of labeled populations of cells to higher organisms [113]. In all mentioned metabolic approaches, differentially labeled samples are mixed at a defined ratio, and the relative abundance of proteins can be compared quantitatively based on the relative intensities of the peptide forms in MS

**Figure 1.3. Conventional methods used in proteomics analysis of *in vitro* cell populations.** Comparison of multiple experimental conditions can be performed separately or together. Separate sample analysis is conventionally done using 2D-SDS-PAGE fractionation followed by quantification of spot intensity on the gel. Spots that exhibit changes in intensity can be extracted from the gel and subjected to enzymatic digestion and subsequent identification through MS analysis. Alternatively, separate samples can be quantified in a label-free manner based on peptide abundance in the mass spectrum. When an isotopic label is used, samples from separate experimental conditions can be combined for analysis. When metabolic labeling with SILAC is used samples can be combined prior to fractionation and digestion. Alternatively, if iTRAQ or TMT approaches are used samples must remain separate until after enzymatic digestion and labeling. In both cases, peptides are analyzed and quantified in the mass spectrometer in a single analysis. For SILAC, quantification is completed at the MS level, whereas iTRAQ and TMT are performed in the MS/MS spectrum.



spectra. Isotopic labeling using any of the previously mentioned methods offer powerful tools for researchers to directly compare minute changes between cellular states over time (Figure 1.3).

#### **1.4 *In Vitro* Culture of hESCs**

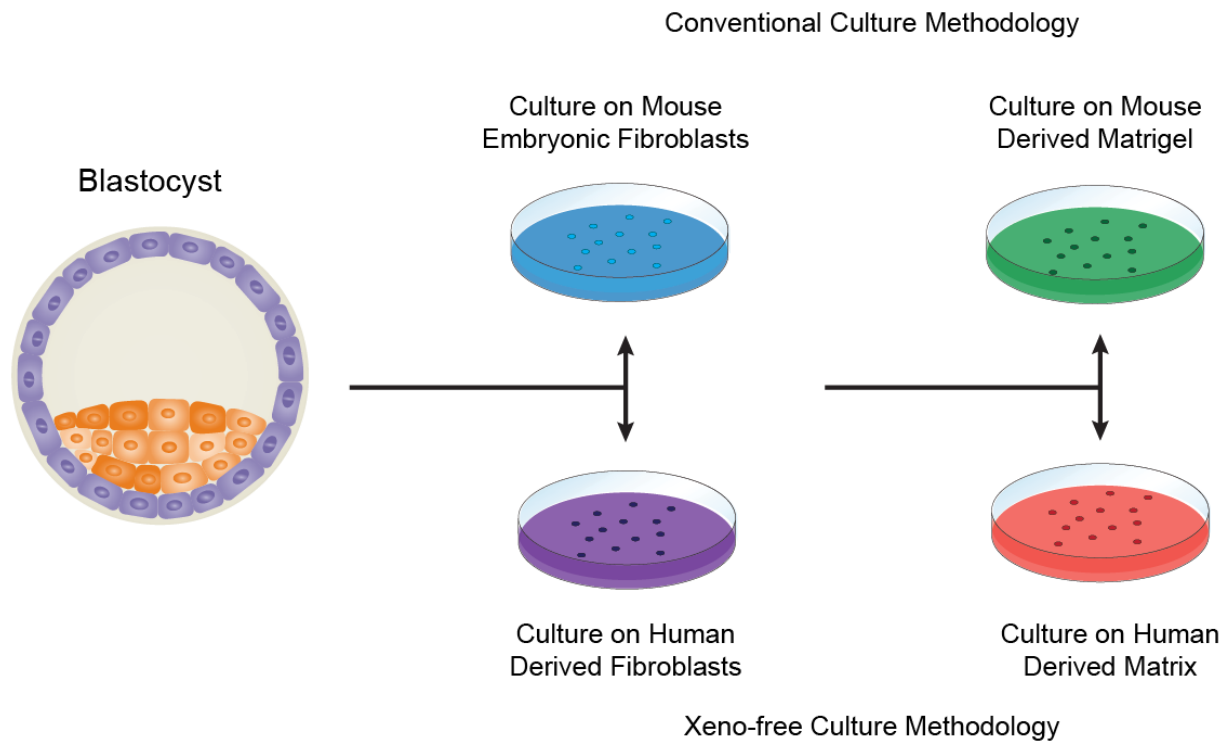
Many experiments and therapeutic applications of hESCs require the cells to be pluripotent and free of non-human contamination. A major limitation to the use of hESCs in medical research is that they can undergo spontaneous differentiation in culture if proper conditions for retaining pluripotency are not maintained. At present, there is limited information about which culture conditions effectively maintain differentiated hESCs *in vitro*, and this restricts the amount of suitable material that can be generated for analysis [114-116]. One reason for this is that many advances in culture conditions for mouse embryonic stem cells are not applicable to hESCs [117].

Since the correct mixture of factors that maintains hESC pluripotency is unknown, hESCs are often derived on a feeder layer of MEF cells (Figure 1.4). This layer provides a growth substrate and secretes various growth factors, cytokines, and adhesion related proteins that promote pluripotency [118, 119]. Other human fibroblasts have also been shown to be supportive of sustained pluripotent hESC growth [120-124]. Due to the potential variability that culture on feeder layers presents and the risk of xeno-transmission from non-human sources, there has been a shift in the field to feeder-free growth of hESCs on defined matrices (Figure 1.4). A significant step forward in hESC culture methods was the discovery by Xu *et al.* that hESCs can be maintained on a layer of basement membrane matrix called Matrigel<sup>TM</sup>, in medium

that has been conditioned by irradiated MEFs (MEF-CM) [125]. Matrigel™™, which is extracted from Englebreth-Holm-Swarm tumors in mice, is a complex mixture of extracellular matrix (ECM) proteins that is composed primarily of laminin, collagen-IV, and enactin [126-128]. Matrigel™ has proven to be effective as a growth matrix for a wide variety of hESC lines using a variety of media formulations [129]. However, concerns regarding the composition and complexity of Matrigel™ and its suitability in research applications have been raised [126, 128, 130-132]. To overcome these limitations, a variety of ECM proteins or synthetic matrices have been evaluated for their ability to support hESC proliferation [133-148].

In parallel to matrix development, there have been numerous advances towards the generation of defined culture medium for hESC growth [149, 150]. All formulations contain growth factors designed to promote the maintenance of pluripotent hESCs, such as bFGF and Activin. In order to elucidate factors essential for the maintenance of hESCs, analyses of the secretomes of supportive feeder layers have been performed [151-154]. Factors supportive of the maintenance of hESC pluripotency, such as pigment epithelium derived factor (PEDF), have been identified through examination of these datasets. It was later demonstrated that PEDF can maintain undifferentiated hESCs without the addition of other exogenous supplements [155]. Other factors, such as Activin A and TGF- $\beta$ 1, were also identified in screens of conditioned media, both of which have been shown to promote the feeder-independent growth of hESCs in the absence of pre-conditioning with MEF layers [115, 156, 157]. Although these screens provide valuable information on extracellular regulation of hESC fate *in vitro*, our





**Figure 1.4. Derivation and culture of human embryonic stem cells.** hESCs derived from the inner cell mass of the blastocyst are conventionally cultured on a layer of mouse embryonic fibroblast feeder cells in medium supplemented with FGF2. Alternatively, hESCs can be derived in xeno-free conditions by culturing them on human derived feeders, such as foreskin fibroblasts. hESCs derived in either condition can be passaged to feeder-free conditions where a culture matrix is substituted as the growth surface. The most commonly employed matrix is Matrigel™ in combination with culture media that has been conditioned on a mouse or human feeder-cell layer. If xeno-free conditions are desired, human cell-derived or recombinant protein matrices can be substituted and used in combination with defined culture medium.

understanding of how these pathways exact this control, alone or in combination, remains inadequate.

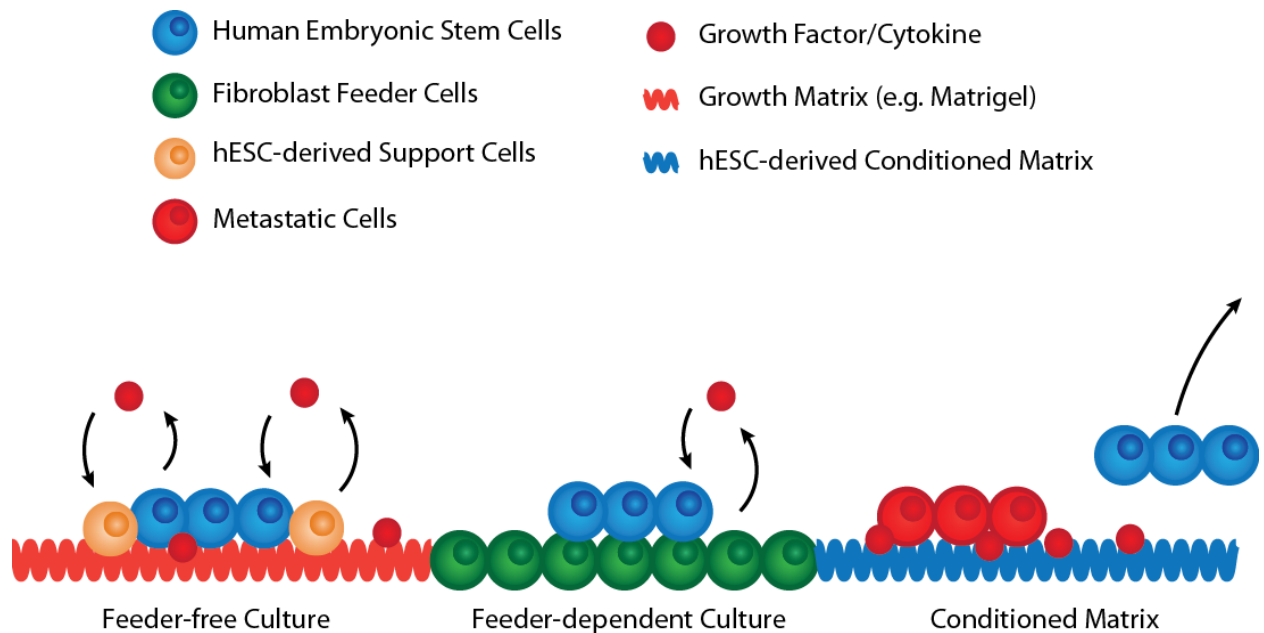
### **1.5 *In Vitro* Microenvironment and hESC Cell Fate**

Based on advances in our knowledge regarding the optimal conditions for hESC culture *in vitro*, it is clear that extracellular processes are critical for maintaining the delicate balance between self-renewal and differentiation. Control over these extracellular processes is governed by a dynamic interplay between the various contributors to the microenvironment. This supportive environment is often referred to as the 'niche' and consists of a combination of accessory support cells, extracellular structure, and autocrine/paracrine signals (Figure 1.5). In stem cells, the concept of the niche was first defined for the hematopoietic system in mammals [158]. Additional evidence from *Drosophila* and *C. elegans* contributed to the development of the understanding of the stem cell niche (reviewed in [159, 160]). Research in mouse has contributed to the bulk of our current insight into the stem cell niche in mammalian systems. An example of this is recent work where the ability of mESCs to interact to form local microenvironments within single colonies that regulate cell-fate decisions dependent on the presence or absence of exogenous factors was demonstrated [161]. Studies such as these provide detailed insight into niche control of stem cells *in vitro*.

Studies directed at the analysis of the hESC niche have been limited due to the complexity its analysis presents. However, as illustrated by the intricate requirements for efficient proliferation *in vitro*, proteomic characterization of the microenvironment

from human stem cells should be a fruitful source of information. The necessity for supplementation of multiple exogenous factors illustrates the dynamic array of extracellular processes that combine to create a suitable hESC niche *in vitro*. Recent work using a global proteomics approach has demonstrated the valuable data that can yield from analysis of this soluble environment [162]. In addition to the components supplemented or secreted into the microenvironment, in this study it was observed that hESCs generate fibroblast cells supportive of self-renewal [162]. From proteomic analysis comparing the secretome of MEF feeders and hESCs, a novel mechanism was proposed wherein the supportive fibroblast cells responded to FGF supplementation to secrete factors that aided in the prevention of cellular differentiation [163, 164]. Although this was not the first global analysis of the hESC secretome, it generated the greatest depth of coverage leading to the identification of numerous stem cell regulatory proteins in the extracellular space.

In order to obtain a complete understanding of the hESC *in vitro* microenvironment, analysis of components other than soluble media components is required. Although numerous studies have focused on analysis of the soluble portion of the microenvironment, the interactions between hESCs and ECM in the niche is poorly understood. The ECM is known to provide structural support for processes such as cell attachment and migration. Moreover, it is widely postulated that the ECM interacts with an array of growth factors, acting to provide sustained release or co-factors required for activation (reviewed in [165]). The complex matrix requirements for the efficient culture of hESCs *in vitro* emphasize the importance of the ECM and the necessity for analysis of this contributor to the niche. Moreover, it was recently observed that metastatic cells



**Figure 1.5. Maintenance of human embryonic stem cells in a dynamic microenvironment.** Cultures maintained on Matrigel™ have been observed to contain hESC-derived cells that support stem cell maintenance through paracrine signaling pathways. On mouse or human fibroblast layers, maintenance of pluripotency is maintained through paracrine signaling with the feeder cells. Alternatively, on Matrigel™ or other matrices, hESCs can be maintained in medium that contains supportive factors secreted from feeder cells during conditioning. Many studies have focused on analysis of factors secreted during conditioning to elucidate hESC supportive pathways. Recent work has demonstrated the ability of hESC conditioned matrices to reprogram metastatic cells. This observation highlights the potential importance of the interactions between hESCs and the growth matrix used *in vitro*. However, few studies have focused on the elucidation of these interactions or the identification of hESC-derived factors in conditioned matrix.

could be 'reprogrammed' to a state that resembled their non-metastatic counterparts following exposure to an hESC conditioned matrix [166]. This observation was dependent on contact with the matrix portion of the microenvironment, and was not observed after exposure to hESC conditioned medium [167]. Studies such as these illustrate the potentially complex interactions between hESCs and the ECM *in vitro*. However, this area of the hESC microenvironment remains poorly understood as a result of the difficulty analysis of the ECM and its interactions presents.

## **1.6 Thesis Objective**

With the potential wealth of information that can be extracted from the analysis of the hESC microenvironment, studies directed at the large-scale analysis of this dynamic environment needs to be undertaken. Critical to these studies will be the development of efficient methods for the analysis of the in-solution and matrix portions of the microenvironment. Moreover, integration of data obtained through the analysis of secreted factors with that of other supportive components of the microenvironment will be paramount for a more comprehensive understanding hESC regulation *in vitro*. With the recent observation that matrix deposited factors have the potential to reprogram metastatic melanoma cells, the ECM component of the hESC microenvironment necessitates further analysis [168]. To this end, one of the goals of this thesis will be directed at creating proteomic methods to facilitate the analysis of hESC and hiPSC conditioned matrices, as well as functional validation of identified candidates of interest.

In working towards these objectives we first develop methods for the efficient growth of hESCs in conditions amenable to SILAC experimentation *in vitro* (Chapter 2). We demonstrate that mouse and human ESCs can be maintained in an undifferentiated and pluripotent state in medium containing isotopically labeled arginine and lysine. We also extend this protocol to the feeder-free growth of hESCs and hiPSCs in SILAC medium that is completely defined. For both of these media formulations, we are able to overcome conversion of isotopically labeled arginine into proline, a typical occurrence in SILAC experiments. Application of these culture methods facilitated the expansion of labeled hESCs for further proteomic experimentation.

In order to extract information on the composition of hESC-derived matrices, proteomic methods directed at the fractionation and analysis of complex ECM-like mixtures were required. To this end, we developed methods aimed at the analysis of the complex ECM Matrigel™ (Chapter 3). By employing a range of fractionation and digestion protocols we demonstrate the complex proteomic profile of Matrigel™. Following this, we applied these methods to other cell-derived and recombinant matrix mixtures commonly used in hESC culture. These analyses revealed commonalities between matrices used in hESC culture. Based on the proteomics data, fibronectin was found to be enriched in all of the cell-derived hESC supportive matrices. To validate the ability of our proteomics approach to identify components critical for the maintenance of hESCs *in vitro*, we exhibit the maintenance of an undifferentiated and pluripotent state for cells grown on fibronectin as a sole matrix support.

After validation of our culture (Chapter 2) and matrix analysis methods (Chapter 3), we applied these conditions to the characterization of hESC and hiPSC conditioned matrices (Chapter 4). From our proteomics screen, we identify over 80 extracellular proteins in matrix conditioned by hESCs and hiPSCs. Comparative analyses with published stem cell secretome datasets aided in the identification of hESC regulatory proteins from our dataset. Based on the ability of the hESC-derived CMTX to enhance the maintenance of an undifferentiated state, we carry out functional validation of candidates identified in the CMTX to determine their roles in hESC pluripotency (Chapter 5). Focusing on the candidate soluble frizzled-related protein 1 & 2 (sFRP) proteins, we utilize a combination of approaches to elucidate their effects on hESC behavior. Taken together, our improved culture methods, matrix analysis protocols, and detailed composition of hESC derived matrices provide an effective toolbox for obtaining a more comprehensive understanding of how this dynamic cell type is regulated *in vitro*.

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## Chapter 2

### Development and Optimization of Growth Conditions for SILAC Experiments in Pluripotent Stem Cells

#### 2.1 Introduction

Large scale identification of proteins using mass spectrometry (MS)-based proteomics has been made possible by recent advances in instrumentation, separation sciences, and bioinformatics [1]. However, the generation of increasingly long lists of proteins now confronts researchers with the more challenging problem of determining the biological significance of particular proteins. For this reason, quantitative proteomic strategies can now be used in order to extract more meaningful information from their datasets. By comparing multiple samples and different conditions vs controls, it is often possible to discern proteins that are altered in a given set of experimental or biological conditions from the thousands that are identified [2].

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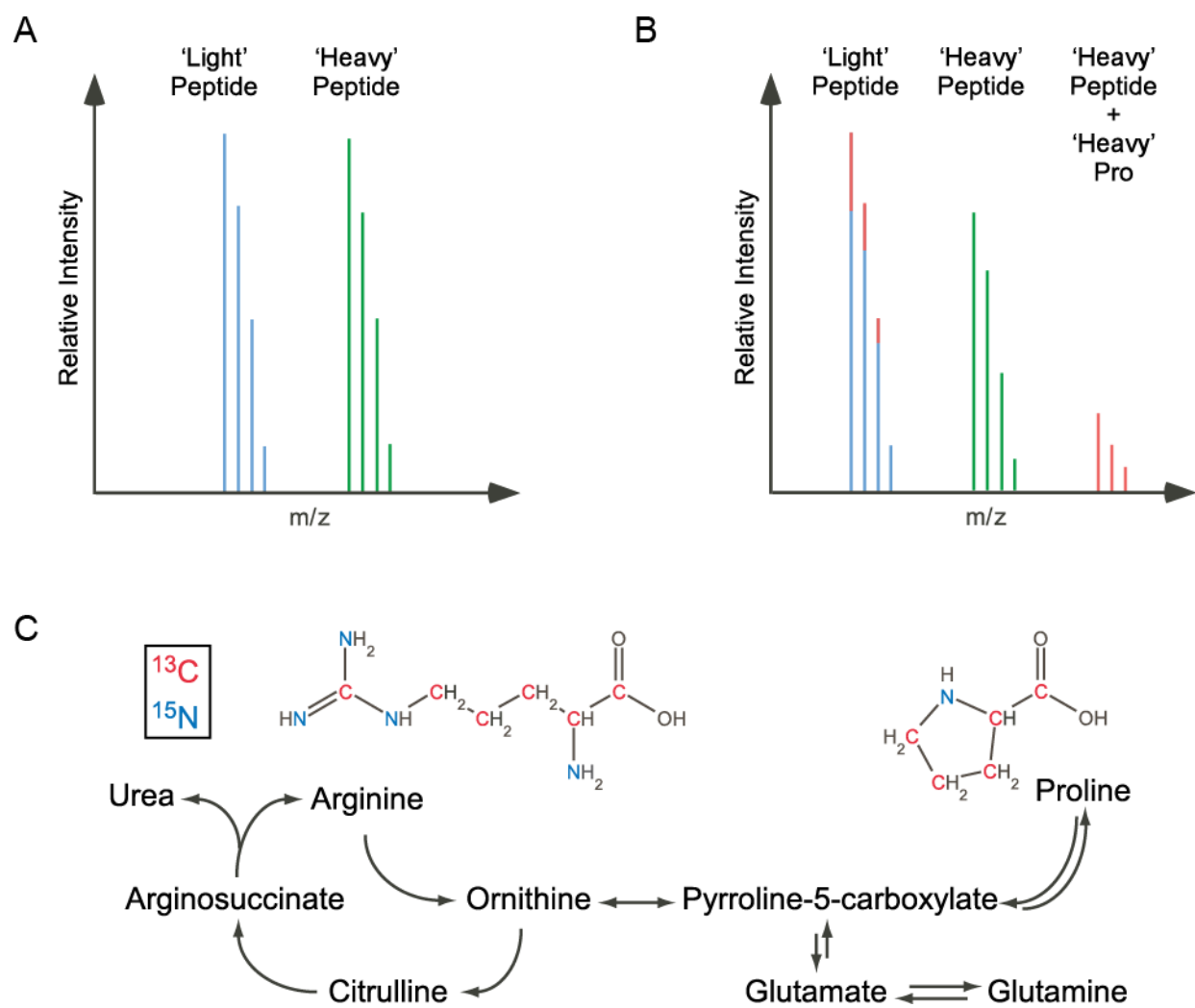
Bendall, S.C.\*, Hughes, C.S.\*, Stewart, M.H., Doble, B., Bhatia, M., Lajoie, G.A.. (2008) "Prevention of Amino Acid Conversion in SILAC Experiments with Embryonic Stem Cells". *Molecular and Cellular Proteomics*. 7:1587 – 1597

\*Denotes equal author contribution



In MS-based proteomics, quantitative strategies typically involve the use of stable isotopic reagents to generate 'heavy' and 'light' samples, which retain their chemical identity and can then be differentiated and directly compared by MS analysis. While chemical labeling methods such as ICAT have demonstrated widespread applicability [1], metabolic incorporation strategies such as stable isotope labeling with amino acids in cell culture (SILAC) are becoming more common for cell types that can be grown for extensive periods of time *in vitro*. Though there are numerous advantages for using SILAC based methods, compared to chemical labeling, a major drawback is the unintended metabolic inter-conversion of isotopic amino acids in the labeling process, generating artifacts affecting the quantification. This is a particular problem with arginine which is a metabolic precursor for proline biosynthesis (Figure 2.1). In general, large scale SILAC experiments use both arginine and lysine to obtain labeling of all possible tryptic peptides thereby maximizing quantitative coverage of all potential peptides in a given experiment.

Several studies using SILAC have described the problematic conversion of isotopically labeled arginine to labeled proline in cells [3-7] (Figure 2.1) which results in an underestimation of the abundance of 'heavy' tryptic peptides containing proline in a relative quantification experiment. This is of particular concern since ~50% of all tryptic peptides between 700 and 6000 Da in the international protein index (IPI) human database contains at least one proline. Moreover, in a recent study it was reported that ~30-40% of all observable proline containing peptides exhibited some level of conversion from heavy arginine [7]. Besides acting to skew the relative abundance observed, conversion of 'heavy' arginine to 'heavy' proline also further complicates the



**Figure 2.1. Metabolic conversion of isotope-coded arginine to proline in SILAC experiments.** The unpredictable conversion of isotopic arginine to proline creates inaccuracy in SILAC based quantitative proteomic experiments. (A) A conceptual mass spectra of a non-proline containing peptide ion from a 1:1 mixture of 'light' and 'heavy' labeled samples. Here the expected 'light' and 'heavy' peptide ions have an equivalent signal. (B) A spectra from a proline containing peptide where arginine to proline conversion has occurred in the same 1:1 mixture. The resulting heavy proline peptide signal (red) has been subtracted from the expected 'heavy' peptide ion signal. (C) Metabolic pathway outlining the inter-conversion of arginine and proline. Isotope-coded arginine with carbon 13 (red) and nitrogen 15 (green) that when used as a synthetic precursor increases the expected mass of proline.

mass spectrometry data by increasing the number of peptide ion peaks. One proposed strategy to minimize this problem is the reduction of the arginine concentration in the SILAC media rendering it metabolically unfavorable as a precursor for proline synthesis [8]. While this does reduce the conversion, it does not prevent it completely [3]. The other is to avoid the use of arginine altogether or by removing the ability to perform arginine catabolism [3, 9, 10]. Finally, alternative corrections can be done mathematically, post-analysis, but these are inaccurate and do not solve the problem of increased peptide ion complexity [4, 11-14].

While reducing the concentration of available arginine in SILAC labeling media was a simple method for preventing its conversion to proline, this approach would be problematic for particular cells types like those with rapid cellular metabolism [15]. Moreover, certain sensitive cell types, such as human embryonic stem cells (hESCs) die or differentiate under restrictive metabolic conditions [7, 16]. To this end, Vanhoof et al. [7] sought to compensate for arginine to proline conversion in SILAC experiments by advocating the use of isotopically labeled arginine ( $^{15}\text{N}_4$  Arg) in 'light' SILAC media as well as ( $^{15}\text{N}_4$   $^{13}\text{C}_6$  Arg) in the 'heavy' media. With the assumption that arginine to proline conversion would be the same under both conditions, the monoisotopic peak of 'light' and 'heavy' proline containing peptide ions could be compared to correctly determine relative abundance, as both would be reduced proportionately. This method does provide a solution but it further complicates the procedure by generating additional converted proline peptide ions in the MS spectra and by adding the cost of expensive isotopic reagents. Also, there is no guarantee that the rate of arginine to proline conversion will be the same when comparing different cell types or treatments. Adding

to these difficulties is the fact that SILAC labeling of both hESCs [7] and ESCs from the mouse (mESC) [17] required the use of mouse embryonic fibroblast (MEF) feeder cells which precludes the attainment of high cell numbers necessary for large scale, SILAC-based proteomic applications [8, 18-21]. Faced with these challenges, we sought a simple solution, for arginine to proline conversion in SILAC experiments that would be compatible with a robust hESC culture protocol free of feeder cells.

In this chapter, we demonstrate that by supplementing SILAC media with standard L-proline, the conversion of isotope coded arginine to labeled proline can be prevented. In addition, when providing sufficient amounts of arginine, no back conversion from the increased proline supplement was observed. When proline supplementation of SILAC media was adapted to both mouse and human ESC culture reagents complete labeling with isotope-coded lysine and arginine can be routinely achieved using standard procedures in the absence of feeder cells without compromising the ESC phenotype. We then extend our approach to demonstrate the growth of hESC and hiPSC lines in SILAC conditions using fully-defined, serum-free growth medium.

## 2.2 Results

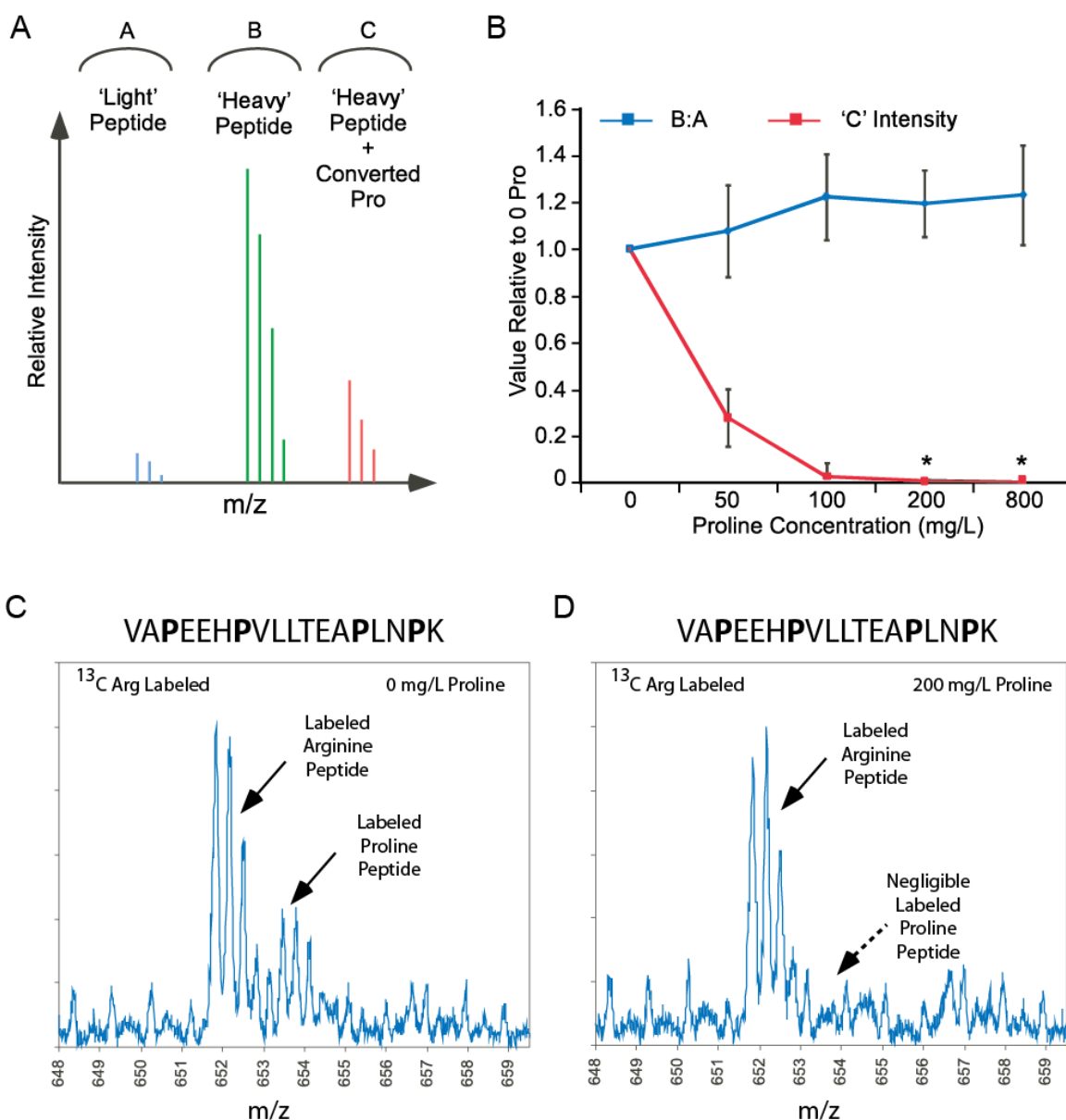
In mammalian cells, the metabolism of arginine and proline are related and each can serve as precursors for one another through slightly different, but related pathways (Figure 2.1 C, reviewed in [22]). In a related pathway, both glutamate and glutamine can be precursors for arginine biosynthesis and products of arginine metabolism (Figure 2.1 C). However, only artifacts of proline synthesis from isotopic arginine have been reported in SILAC experiments. This observation raised the question of availability of amino acids *in vitro* cell culture media, particularly in SILAC formulations, since previous *in vivo* mammalian studies have demonstrated that the inter-conversion of amino acids in this pathway (Figure 2.1 C) is primarily dependent on their bioavailability [23]. Since L-proline is a non-essential amino acid, its concentration in the two main basal media used in standard SILAC experiments, RPMI and DMEM, is only 20 and 0 mg/L, respectively. At the same time, the typical concentration of arginine, a metabolic precursor of proline (Figure 1B), is 200 and 84 mg/L, respectively. Based on this we surmised that the arginine to proline conversion artifacts in SILAC experiments were a direct result of the low or absent concentration of proline in standard SILAC labeling formulations.

*2.2.1 - Proline availability effects on isotopic arginine conversion to proline.* In standard DMEM based SILAC media, in the absence of proline supplement, cells readily convert isotopic arginine to proline, which is then incorporated into newly synthesized proteins. This conversion divides the MS signal of the 'heavy' proline containing peptide in a complex fashion, resulting in false relative abundance values when compared to an

equal amount of 'light' sample (Figure 2.1 A-B). To eliminate this artifact in arginine-based SILAC procedures, we investigated whether increased L-proline supplementation could prevent the conversion in a concentration dependent manner.

Equal amounts of cell lysates extracted from HeLa cells cultured in SILAC media ( $^{13}\text{C}_6$  Arg) containing 0 – 800 mg/L proline were digested with trypsin and subjected to LC-MS/MS analysis. Detected proline conversion peptides were used to build a list of peptide candidates for quantification. By using +2 or +3 charge states, the selection of the peptide candidates was based on whether they were observed in all samples, the number of proline residues, the extent of conversion observed, and whether the sequence contained arginine. Based on the triplicate analysis of all lysates, a list of thirteen peptide candidates was chosen and quantified across the 0 – 800 mg/L proline concentrations.

Throughout the titration of L-proline in SILAC media signals of the converted proline containing peptides were monitored (Figure 2.2 A-B). In addition, the ratio of 'heavy' labeled Arg peptide to light peptide was measured in order to detect whether a decrease in the converted proline peptide signal resulted in a subsequent increase in the expected 'heavy' peptide (Figure 2.2 A-B). Within the set of peptide candidates proline conversion consumed an average of 28% of the monoisotopic signal of the 'heavy' arginine peptide in the 0 mg/L proline sample (standard SILAC media) [5]. As the proline concentration was increased to 50, 100, and 200mg/L the monoisotopic 'heavy' proline peak occupied 9%, 3%, and 2%, respectively. However, within this list of proline containing peptides no peaks corresponding to a converted proline could be



### Figure 2.2. Titration of proline during SILAC labeling with isotope coded arginine.

Candidate proline containing tryptic peptides were monitored in whole cell extracts in <sup>13</sup>C6 arginine samples with 0-800 mg/L L-proline. (A) A conceptual mass spectra indicating the possible peptide ion peaks observed in the arginine labeling experiment. Both the ratio of labeled to unlabeled peptide as well as relative intensity of converted proline peptide ion were monitored in the experiment across 0 – 800 mg/L proline (B) where \* indicates no converted proline peptide ions were detectable from background. (C) A mass spectrum from 0 mg/L proline sample representing the peptide VAPEEHPVLLTEAPLNPK at m/z 652 demonstrating a prevalent converted proline peak at +1.7 m/z from the expected peptide ion. (D) Mass spectrum from the 200 mg/L proline sample depicting the same peptide ion as in (C) and the converted proline ion is notably absent.

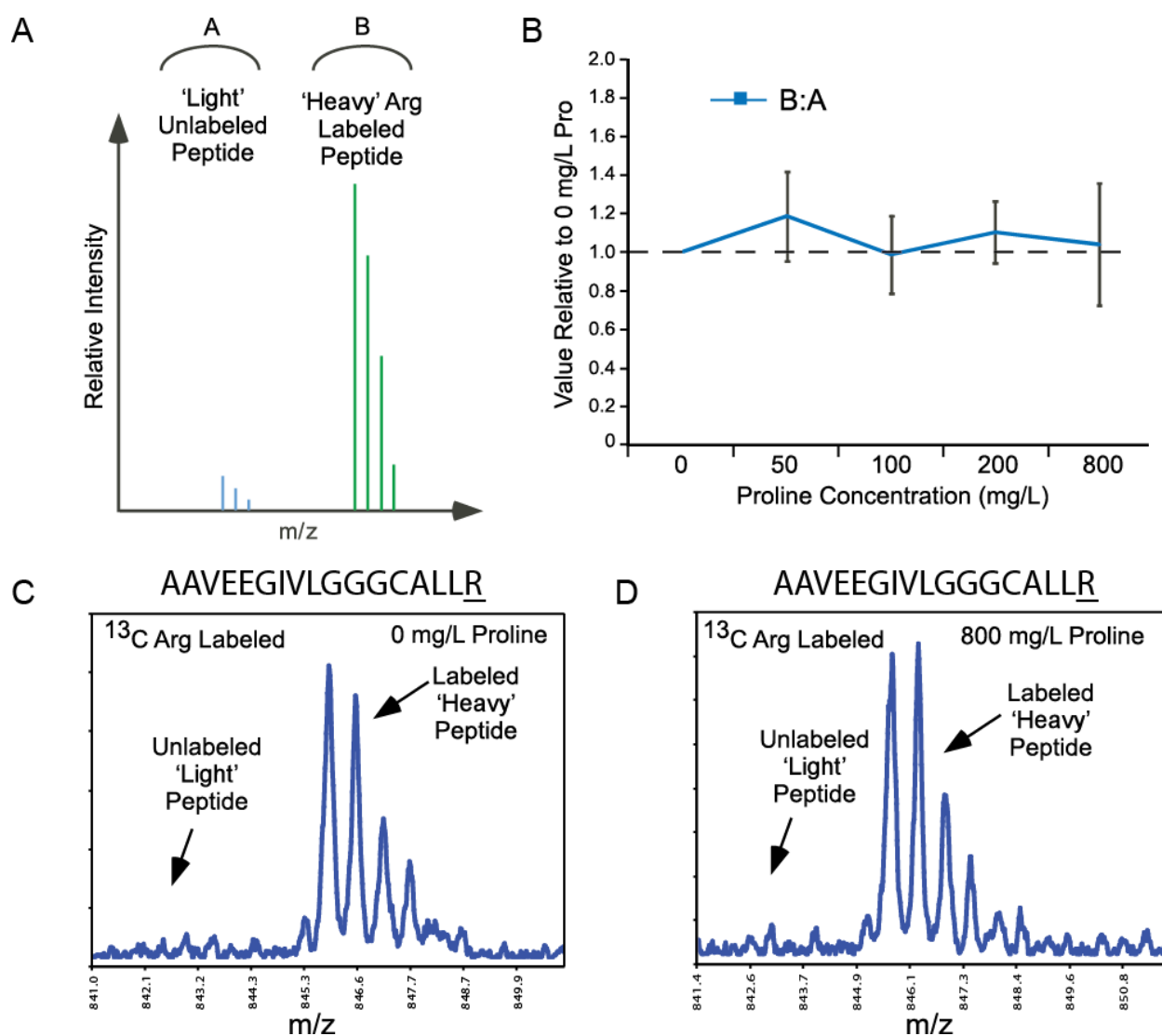
detected in the MS spectrum beyond 100 mg/L of proline. As such, the 2% of total signal seen at 200 mg/L of proline was a result of un-subtracted background in the MS spectrum where there was low signal-to-noise. Moreover, maximum relative signal of 'heavy' arginine labeled peptide (~20% increase vs 0 mg/L Pro) was seen at 200 mg/L and beyond (Figure 2.2 B). Consequently, even in some of the worst cases of proline conversion (Figure 2.2 C) no proline conversion could be observed in cells supplemented with 200 mg/L of proline or greater (Figure 2.2 D). Taken together, these data not only demonstrate that supplementation of standard SILAC media can eliminate the proline conversion, but also return the "lost signal" to the expected peak within the 'heavy' SILAC sample. Most surprisingly, this critical improvement in arginine-based SILAC methods can be achieved by supplementing cell culture media with as little as 200 mg/L of L-proline.

*2.2.2 - Proline availability effects on isotopic arginine labeling.* One concern with supplementing an arginine-based SILAC experiment with proline is that, by a similar biosynthetic mechanism (Figure 2.1 C), the excess proline might be a precursor for arginine synthesis thereby decreasing the efficiency of labeling by the isotope-coded arginine provided. While proline is known to be one of the main substrates in the formation of citrulline, a direct precursor for arginine biosynthesis, it has been demonstrated that this process is only favorable when there is a lack of available arginine [23, 24]. Moreover, to date, the presence of other citrulline precursors, such as glutamine in standard SILAC media, has had no reported detrimental effect on SILAC procedures.



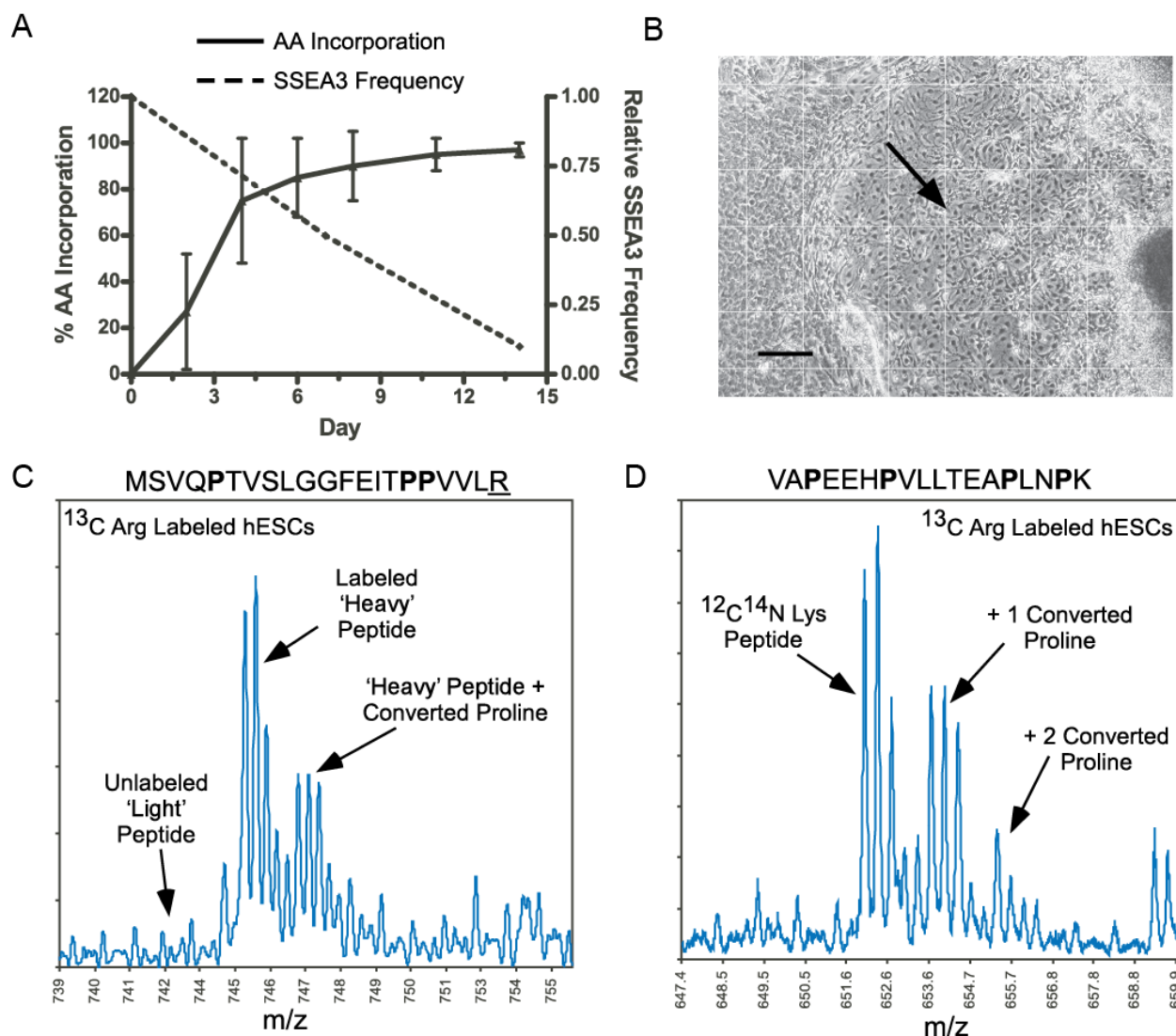
To prevent back conversion of proline into arginine and to increase the media's compatibility with nutritionally sensitive cell types like ESCs [7], we re-supplemented the DMEM-based SILAC media with its standard complement of isotope-coded arginine (0.398 mM). This was in direct contrast to the reported reduction of the concentration of isotope-coded arginine in order to prevent its availability for conversion to proline [5, 8]. At the endpoint in the same proline titration experiments we monitored the 'heavy' arginine labeling efficiency by tracking the ratio of 'heavy' to 'light' peptides which contained arginine (Figure 2.3 A). To minimize proline conversion artifacts that would interfere with these calculations, we avoided peptides with proline in their sequence.

In comparison to 0 mg/L proline (standard SILAC media), the average relative peak area for the 50 – 800 mg/L proline samples exhibited only slight deviations, but overall remained unchanged (Figure 2.3 B). Larger deviations were only observed for peptides with lower signal-to-noise ratios and did not have a noticeable trend as a function of proline concentration. None of the arginine peptides examined in the 0 mg/L proline sample (Figure 2.3 C) or even in samples that were supplemented with 800 mg/L of proline (Figure 2.3 D) exhibited an increase in unlabeled 'light' peptide signal. These data provide evidence that our SILAC media formulation (standard arginine in combination with proline supplementation) is effective in minimizing arginine to proline conversion artifacts without compromising the efficiency of isotope-coded arginine labeling. Thus, in the cell types examined here, an arginine concentration of 0.398 mM, even in the presence of high exogenous proline (up to 800 mg/L), is sufficient to prevent observable proline to arginine back conversion that would interfere with SILAC labeling efficiency.



**Figure 2.3. Isotope coded arginine labeling efficiency across the titration of proline.** Candidate arginine containing tryptic peptides lacking proline were monitored in whole cell extracts in <sup>13</sup>C6 arginine samples with 0-800 mg/L L-proline. (A) A conceptual mass spectra indicating the possible peptide ion peaks observed in the arginine labeling experiment. The peak area ratio between the 'heavy' and 'light' arginine monoisotopic peaks was monitored across the 0 - 800 mg/L proline samples and plotted relative to 0 mg/L proline (B). (C) A mass spectrum representing the peptide AAVEEGIVLGGGCALLR at m/z 845 from the 0mg/L proline sample. (D) Mass spectra of the same peptide ion in the 800 mg/L proline sample demonstrating no compromise in the isotope-coded arginine labeling efficiency or proline to arginine back-conversion. Isotopic amino acids are underlined.

*2.2.3 - Adaptation of SILAC labeling to feeder-free hESC culture.* In order to perform a wide variety of large-scale SILAC-based proteomic experiments with hESCs the ability to generate large numbers of labeled cells has to be achieved. It became clear that SILAC methods compatible with feeder-cell free culture systems would be necessary to attain these high cell numbers (reviewed in [16]). In an attempt to extend standard SILAC labeling procedures to feeder-free hESC culture we confirmed incompatibilities previously highlighted using a feeder-cell based culture system [7]. Using standard SILAC media with  $^{13}\text{C}_6$  arginine and supplemented with 36 ng/mL basic fibroblast growth factor (bFGF) [25], hESC cultures achieved maximum levels of isotope-coded arginine incorporation after only 2 passages or after more than 12 days under SILAC culture conditions (Figure 2.4 A). By day 15 in SILAC media, hESCs had reached 96.5% average efficiency in isotope coded amino acid labeling. However, in the same period of time the hESCs rapidly differentiated as demonstrated by the loss of SSEA3 expression (Figure 2.4 A), a marker of pluripotent stem cells. We also observed the loss of defined hESC undifferentiated colony structure and tight cell morphology indicating the presence of differentiated cell types (Figure 2.4 B). Moreover, manual inspection of the MS data showed that the conversion of arginine to proline was exacerbated in these cells. While it was clear that arginine incorporation was complete in day 14 samples the proline converted peptide ions were prevalent (Figure 2.4 C). In some extreme cases, converted proline peptide ions consumed greater than 50% of the expected peptide ion signal (Figure 2.4 D). The instability of the hESC phenotype combined with the pronounced arginine to proline conversion artifacts indicated that the



**Figure 2.4. Labeling feeder cell free hESCs in standard SILAC media.** hESCs culture on Matrigel™ were grown in standard SILAC media ( $^{13}\text{C}_6$  Arg, dialyzed FBS, 0 mg/L proline) for two weeks. Arginine incorporation, conversion to proline, and hESC phenotype were monitored. (A) The relative SSEA3 frequency and percent heavy arginine incorporation over the SILAC labeling time-course. (B) Differentiated phenotype of hESC after 14 days in standard SILAC media as observed by light microscopy. Scale bars equal 250  $\mu\text{m}$ . (C) A mass spectrum of heavy arginine peptide ion MSVQPTVSLGGFEITPPVLR at 745 m/z. Indicated are the prominent converted proline peptide ion shifted +1.7 m/z, and the absence of the unlabeled ‘light’ arginine peptide ion corresponding to the high level of isotopic amino acid incorporation. (D) A mass spectrum of the peptide ion VAPEEHPVLLTEAPLNPK at 652 m/z. Indicated are the peptide ions shifted +1.7 m/z and +3.4 m/z corresponding to the incorporation of 1 and 2 converted ‘heavy’ proline and consuming more than half of the expected peptide ion intensity. Isotopic amino acids are underlined.

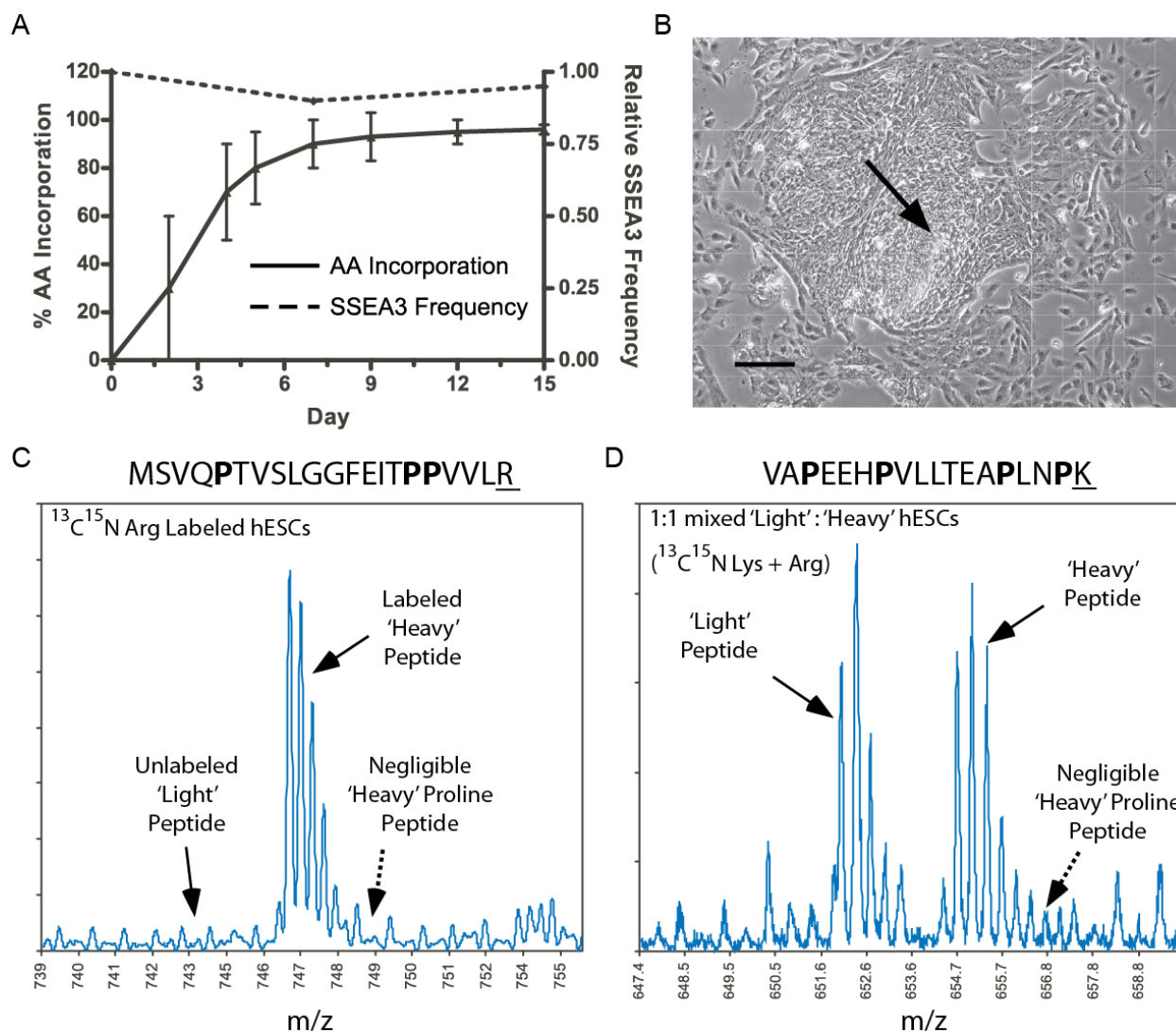
standard SILAC media formulation was not a suitable protocol to adapt to feeder-cell free hESC culture.

There are two main factors responsible for the incompatibility of standard SILAC media with hESC culture, the first being the dialyzed fetal bovine serum (FBS) and the second, the limited growth factor microenvironment (problems reviewed in [16]). To address these issues we revisited the original development of feeder-cell free hESC culture protocols [26]. Xu and co-workers formulated a DMEM based hESC media using a serum replacement reagent [27] that is now commercially available as knockout serum replacement (KOSR – Invitrogen). The hESC media was then pre-conditioned on MEF cell feeder layers to supply the appropriate complement of signaling molecules and growth factors to maintain hESC homeostasis. This method has since become the most widely adopted form of feeder-cell free hESC culture. Coincidentally, the KOSR formulation contains no free lysine or arginine, making it compatible with most popular SILAC applications. Moreover, as we demonstrate to be important here, KOSR contributes 800 mg/L of proline when used at 20% (v/v) in hESC media [27].

A hESC SILAC media with 20% KOSR and  $^{13}\text{C}$   $^{15}\text{N}$  arginine and lysine was formulated taking into account the SILAC compatibility of the media (see experimental methods). The hESC SILAC media was then pre-conditioned on irradiated MEFs according to previously established protocols [26]. The resulting media, when supplemented with 8 ng/mL of bFGF, allowed hESCs to incorporate the isotope coded amino acids at the same rate as observed with standard SILAC media where after 2 passages and more than 12 days in SILAC culture hESC had reached their maximum levels of incorporation

(Figure 2.5 A). Consistent with the preliminary proline titration data, there was no difficulty encountered in isotopic amino acid labeling since the cells were on average 96.1% labeled by day 14. Moreover, in the new media formulation the cells were now able to maintain SSEA3 expression (Figure 2.5 A) and continue to form tight, undifferentiated colony structures (Figure 2.5 B). Inspection of the MS spectra (Figure 2.5 C) of the hESC lysates labeled using the new formulation demonstrated the same level of isotopic amino acid incorporation as standard SILAC media when examining the same peptides (Figure 2.4 C). Additionally, for the same peptide there was no longer any arginine to proline conversion artifacts observed (Figure 2.5 C), even when examining peptides with the highest proportion of converted proline peptide ions (Figure 2.5 D vs 2.4 D). Consequently, when a 14 day SILAC labeled ( $^{13}\text{C}$   $^{15}\text{N}$  Arg and Lys) hESC extract was mixed 1:1 with a 'light' hESC lysate, equivalent levels of the expected 'light' and 'heavy' peptides are observed even in sequences most susceptible to proline conversion artifacts (Figure 2.5 D). These observations clearly demonstrate that combining KOSR as an alternative serum supplement with both a SILAC compatible hESC media formulation and pre-conditioning on feeder cells offers a reliable solution for large-scale hESC applications in quantitative proteomic without compromising data quality.

*2.2.4 - SILAC procedures with feeder-free mESC cultures.* Recently, a landmark analysis of mESCs using a SILAC approach was reported by Graumann *et al.* in which a total of 5111 proteins were identified [17]. However, this study was also routed in a feeder-cell based culture system which, by the authors own admission, contributed to contamination in the analysis. To circumvent this issue these authors performed a

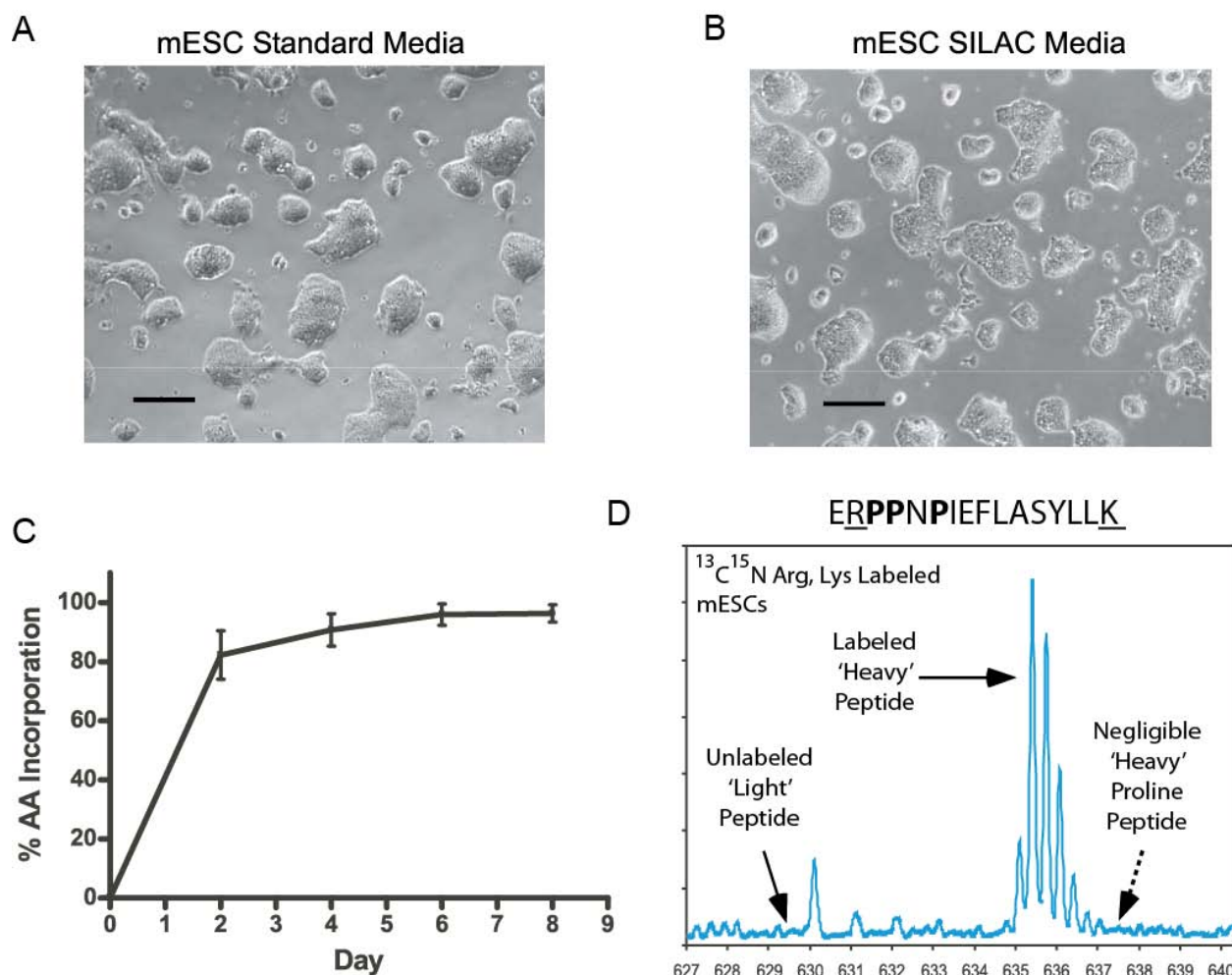


**Figure 2.5. Labeling feeder cell free hESCs in conditioned SILAC media with KOSR.** hESCs cultured on Matrigel™ were grown in MEF conditioned ESC optimized SILAC media ( $^{13}\text{C}^{15}\text{N}$  Arg and Lys, 20% KOSR providing 800 mg/L L-proline) for two weeks. Amino acid incorporation, conversion of arginine to proline, and hESC phenotype were monitored. (A) The relative SSEA3 frequency and percent heavy amino acid incorporation over the SILAC labeling time-course. (B) Undifferentiated phenotype maintained by hESCs after more than 15 days in optimized SILAC media as observed by light microscopy. Scale bars equal 250  $\mu\text{m}$ . (C) A mass spectrum of heavy arginine peptide ion MSVQPTVSLGGFEITPPVLR at  $\sim 747$  m/z. Indicated are the absence of both a converted proline peptide ion and the unlabeled 'light' arginine peptide ion. The absent 'light' peptide ion at 743 m/z also indicates no back-conversion of proline to unlabeled arginine. (D) A mass spectrum of the 1:1 mixed labeled and unlabeled hESC lysates showing 'light' and 'heavy' peptide ion VAPEEHPVLLTEAPLNPK at  $\sim 652$  m/z and 655 m/z. The prominent converted proline peptide ions are now almost undetectable and do not effect the observed 1:1 ratio. Isotopic amino acids are underlined.

cumbersome transition from feeder cell to feeder cell free culture during the labeling process. As these authors noted, the use of dialyzed FBS, prescribed in standard SILAC media [28], made feeder cell independent culture of mESCs difficult. Moreover, having to culture mESCs on feeder layers and/or transition those to feeder cell independent conditions could negatively impact both the scalability of this procedure and the integrity of the mESC phenotype. Because KOSR was originally designed and used as an alternative to FBS for the culture of mESCs [27] we hypothesize that the formulation that we successfully applied to hESCs could also be used in creating a protocol to perform SILAC on completely feeder-cell independent mESC cultures.

Therefore a mESC SILAC media containing 15% KOSR was formulated [27] and the media supplemented with 1000 U/mL of leukemia inhibitory factor (LIF) prior to addition to feeder cell free mESC cultures. After 4 passages in our mESC SILAC media the pluripotent culture morphology was indiscernible from those mESCs cultured under standard conditions (Figure 2.6 A-B). After the same period of time mESCs also achieved maximum incorporation of isotopic amino acids ( $^{13}\text{C}$   $^{15}\text{N}$  Arg and Lys) (Figure 2.6 C) with an average labeling of 96.3%. Moreover, visual inspection of SILAC labeled mESC MS spectra demonstrates similar results as observed with hESCs samples where there is no compromise with levels of isotopic arginine incorporation and no detectable incidence of proline conversion artifacts even in peptide ions with multiple proline residues in the sequence (Figure 2.6 D). In accordance with the observations in the hESC system, the application of a KOSR based SILAC media to a feeder-cell free mouse ESC culture, now provides a robust protocol for routine, large-scale quantitative proteomic experiments using SILAC in mESCs as well.





**Figure 2.6. Labeling feeder cell free mESCs in conditioned SILAC media with KOSR.** mESCs cultured on gelatin were grown in ESC optimized SILAC media (<sup>13</sup>C <sup>15</sup>N Arg and Lys, 15% KOSR providing 600 mg/L L-proline) for 4 passages (8 days). Amino acid incorporation, conversion of arginine to proline, and mESC phenotype were monitored. The undifferentiated phenotype of mESCs grown under standard feeder cell free conditions (A) compared to those grown in optimized SILAC media for 8 days (B) as observed by light microscopy. Scale bars equal 250  $\mu$ m. (C) The average heavy Lys and Arg incorporation over the SILAC labeling time-course. (D) A mass spectrum of peptide ERPPNPIEFLASYLLK at 635.6 m/z from mESCs in ESC optimized SILAC media. The 'heavy' Lys and Arg peptide ion is prominent while the unlabeled 'light' peptide or converted 'heavy' proline peptide ions are absent. The absent 'light' peptide ion at m/z 633 also indicates no back-conversion of proline to unlabeled arginine. Isotopic amino acids are underlined.

*2.2.5 - SILAC of hESCs and hiPSCs in Defined Conditions.* With the recent demonstration that somatic cells can be reprogrammed to generate pluripotent cells, a significant increase in the number of studies employing these induced pluripotent stem cells (iPSC) have been carried out [29]. The clinical potential of human iPSCs (hiPSC) necessitates the need for their culture in defined, xeno-free conditions. As such, a variety of formulations have recently become commercially available [30], many of which can be paired with xeno-free growth matrices. However, very few of these alternatives offer the tested stability and universality of MEF-CM combined with the basement matrix Matrigel™™.

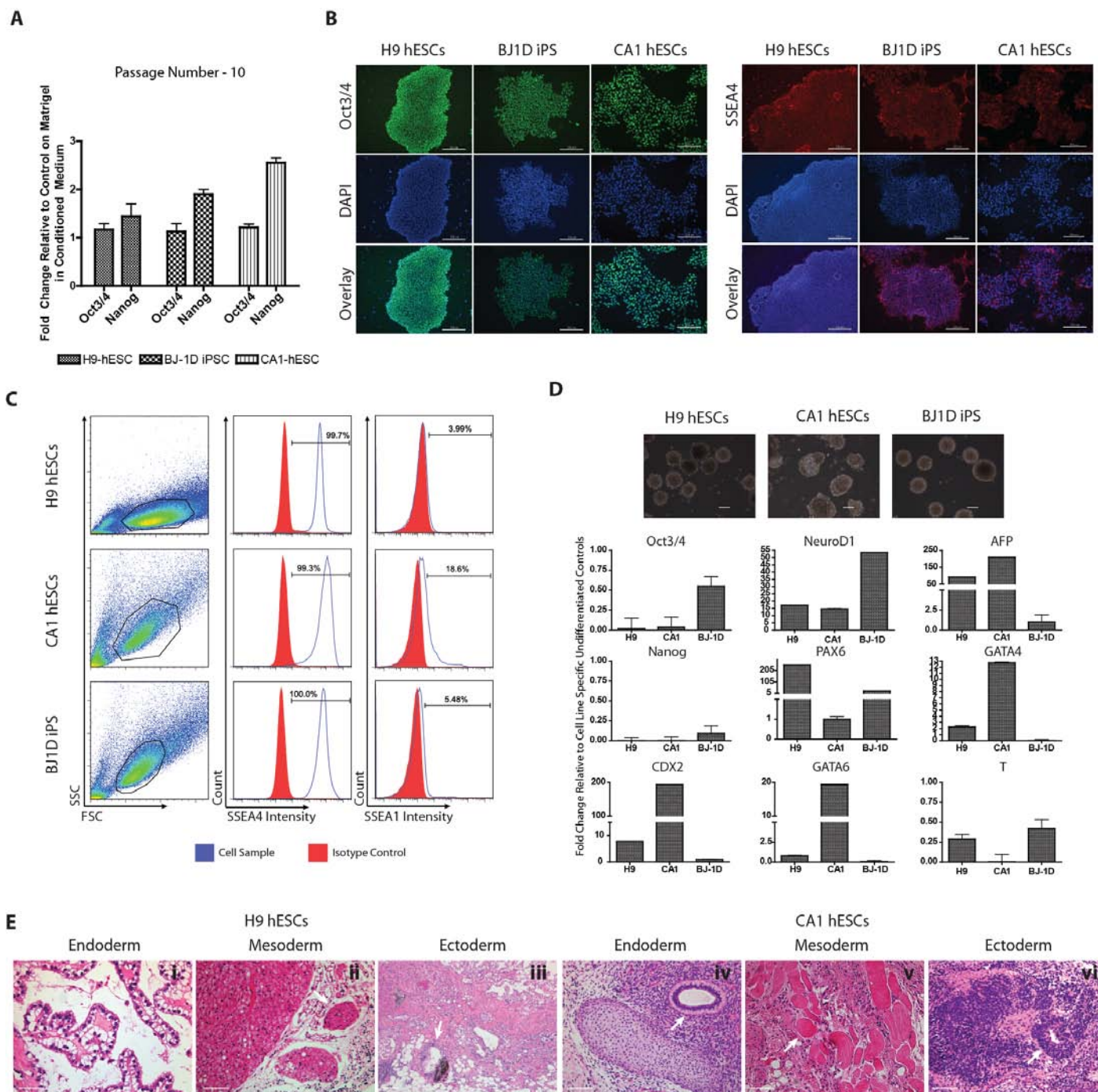
Our previously discussed methods for performing SILAC in human and mouse ESCs utilizes an undefined KOSR-based medium. Since this medium requires pre-conditioning on MEF feeder layers, it is xenogenic and undefined in nature. Coupled with this is the potential for contamination with unlabeled amino acids as a result of conditioning. Although proteomic analyses have attempted to profile the MEF derived contribution to MEF-CM, the composition can vary significantly from batch to batch [31-33]. In order to perform SILAC in any cell system, the ability to control culture medium components is essential. Development of a defined culture medium amenable to SILAC experimentation in hESCs and hiPSCs would be a significant development for proteomics researchers.

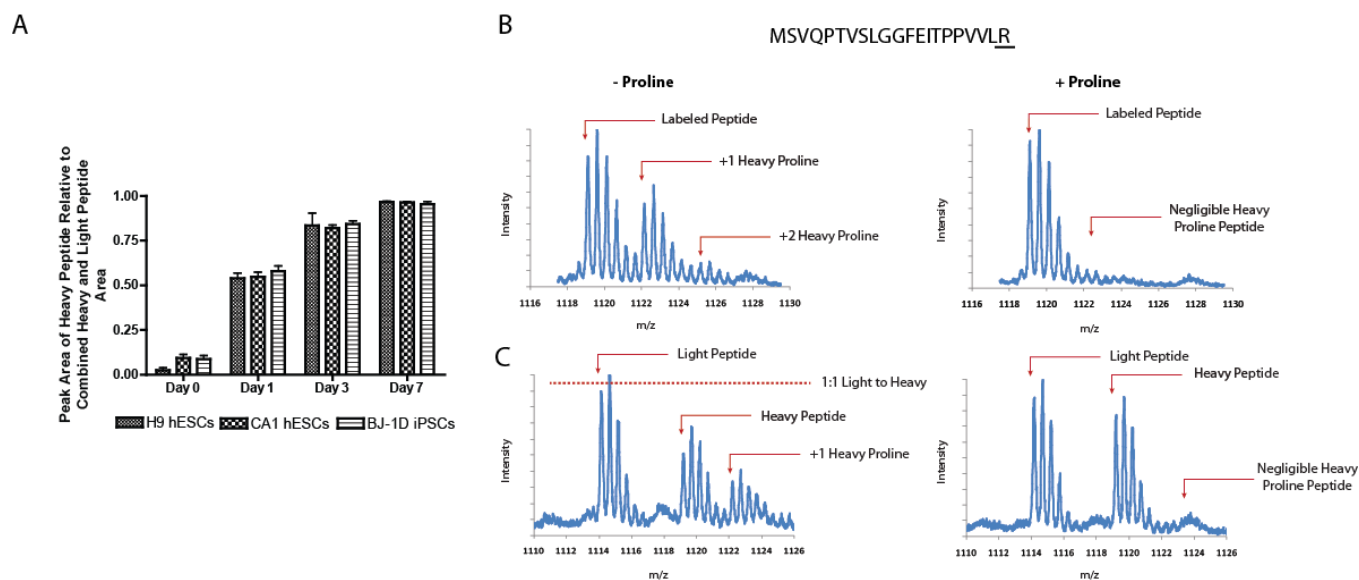
Based on this, we have adapted a commercially available, fully-defined, serum-free medium formulation for performing SILAC in hESCs and hiPSCs [34]. After 10 passages in SILAC medium (>60 days), H9, CA1, and BJ-1D stem cell lines maintained

expression for Oct3/4 and Nanog as indicated by RT-PCR (Figure 2.7 A). All of the tested stem cell lines also retained Oct3/4 and SSEA4 marker expression as visualized using immunofluorescence (Figure 2.7 B). Marker expression was further validated using flow cytometry for SSEA4 and SSEA1 in all cell lines (Figure 2.7 C). After the induction of differentiation *in vitro* using embryoid body assays, all cell lines exhibited increased expression of markers characteristic of each of the three primary germ layers (Figure 2.7 D). Additionally, H9 and CA1 hESCs also retained the ability to differentiate *in vivo* as observed using a teratoma assay. Taken together, these data indicate that extended culture in StemPro-based SILAC medium is capable of maintaining hESC and hiPSC lines in an undifferentiated and pluripotent state.

To test the compatibility of the defined medium for SILAC experimentation, we monitored incorporation of isotopically labeled versions of arginine and lysine. Examining multiple peptides revealed that >96% incorporation can be achieved after just 7 days in defined medium supplemented with isotopically labeled arginine and lysine (Figure 2.8 A). By examining the amino acid composition of the defined culture medium we determined that there was no significant source of L-proline. When cells were grown in defined medium containing no exogenous L-proline, significant conversion from arginine can be observed (Figure 2.8 B). After the addition of 800mg/L of L-proline, there is no longer any signal observable for the isotopically labeled proline containing peptide (Figure 2.8 C). Analysis of 1:1 mixed light and heavy lysates reveals that the addition of L-proline in defined medium restores the previously skewed expected peptide abundance ratio (Figure 2.8 B-C). These observations validate our previous data for SILAC experiments performed in KOSR-based medium.

**Figure 2.7. Labeling feeder cell free hESCs and hiPSCs in defined serum-free SILAC media.** H9, CA1, and BJ-1D were maintained in StemPro SILAC medium with  $^{13}\text{C}$ ,  $^{15}\text{N}$  Arg and Lys, as well as 800mg/L of L-Proline. Following 10 passages, each cell line was assayed for conventional markers of an undifferentiated state. (A) Each cell line maintained strong expression for the markers Oct3/4 and Nanog as determined by RT-PCR. Data is relative to specific matched cell line controls on Matrigel™ in MEF-CM. Error bars represent SD, n=3 (B) Immunocytochemistry data demonstrate expression of Oct3/4 and SSEA4 in all cultures. Scale bars indicate 250um. (C) Flow cytometry data for all cell lines assaying SSEA4 and SSEA1 expression, n=3. All lines maintained strong signal for SSEA4 with minimal SSEA1. Viability was determined using 7-AAD staining. Populations were gated based on 7-AAD exclusion. (D) Embryoid bodies were generated using cells grown in SILAC medium. Phase contrast images showing representative embryoid bodies for each cell line. Scale bars represent 250um. Graphs below show RT-PCR analysis for the markers of pluripotency (Oct3/4, Nanog), trophoblast (CDX2), ectoderm (NeuroD1, PAX6), endoderm (GATA6, GATA4, alpha-fetoprotein), mesoderm (T). Values are fold change relative to cell line specific undifferentiated controls. Error bars represent SD, n=2. RT-PCR assays in both (A) and (D) use RPLPO as a positive control. (E) In vivo analysis of pluripotency. Representative tissues from the three primary germ layers are displayed. Endoderm : gut epithelium (i), columnar epithelium (iv), Mesoderm: muscle tissue (ii, v), cartilage (iv), Ectoderm: neural epithelium (iii), neural-like tissue (vi). Arrows denote structures of interest. Scale bars represent 100um.





**Figure 2.8. Efficient isotopic label incorporation achieved through the use of defined SILAC medium.** hESCs and hiPSCs were grown for a period of 7 days in StemPro SILAC medium containing  $^{13}\text{C}$ ,  $^{15}\text{N}$  arginine and lysine. (A) H9, CA1, and BJ-1D stem cells were harvested at 0,1,3, and 7 days following application of StemPro SILAC medium. Label incorporation was obtained by comparing peak areas for combined scans of light and heavy peptides. A total of 5 peptides were compared in each cell line. (B-C) H9 stem cells grown in the presence and absence of L-proline were tryptically digested and analyzed by MS. Analysis of the proline containing peptide MSVQPTVSLGGFEITPPVLR revealed a significant heavy proline amino acid signal in the absence of exogenous L-proline. The resulting skew in expected peptide ratio from a 1:1 mixture of light and heavy cell lysate can be seen in (C). Following the addition of L-proline, negligible signal for the heavy proline containing peptide remains and the expected peptide ratio is restored in (C). Isotopically labeled amino acids are underlined.

## 2.3 Discussion

Most SILAC procedures take a reductionist approach in controlling amino acid content in cell culture to achieve the desired labeling outcome. These include the use of dialyzed FBS, reduced concentration or total removal of many amino acids (i.e. Arg and Pro), and overall culture conditions optimized using immortalized tissue culture. We believed these methodological aspects preclude the extension of SILAC procedures to ESCs and were at the heart of amino acid conversion artifacts seen using the general labeling procedure. In this chapter, we demonstrate that through supplementation of isotope-coded arginine based SILAC experiments with as little as 200 mg/L of L-proline, isotopic arginine to proline conversion artifacts can be virtually eliminated in a variety of cell types. In addition, using KOSR which provides 800 mg/L of L-proline at 20% as a serum supplement in lysine and arginine based SILAC experiments instead of dialyzed FBS creates a robust media formulation for completely feeder-cell free SILAC experiments using ESCs from both the mouse and the human. We also tested the compatibility of a fully-defined, serum-free medium for use in SILAC experiments with hESCs and hiPSCs. With this medium we were able to maintain all hESC and hiPSC lines tested for an extended period in an undifferentiated and pluripotent state. Moreover, with the addition of L-proline at a concentration of 800mg/L to the medium, we could successfully eliminate conversion from isotopically labeled arginine.

Based on the cellular pathways of proline and arginine metabolism, the addition of proline is an obvious solution to the conversion issue, however the concern has always been the potential back conversion to arginine which would interfere with isotope-coded

arginine labeling [8]. Some studies, such as the recent one using SILAC in mESCs stress that all reagents were prepared without proline for this very reason [17]. To our knowledge, no study to date has demonstrated that the presence of proline actually induces significant back conversion to arginine in a concentration dependent manner during a SILAC procedure. In fact, we demonstrate here that between 0 and 800 mg/L proline that there is no significant change detectable in the labeling of cells with isotope-coded arginine.

Proline is a preferred precursor for arginine biosynthesis in neonates *in vivo* just as arginine is for proline. However it has been clearly demonstrated in a number of studies that the *de novo* biosynthesis of either arginine or proline using the other as a precursor is most strongly influenced by their bioavailability [23, 24, 35]. In other words, if there is sufficient free proline present to maintain cellular homeostasis the endogenous production of proline will not be favored, regardless of the concentration of its available precursors. The same statement can be made in the opposite direction for arginine. With respect to energy and metabolism this observation makes sense as it would be the most efficient. Even though a diminished arginine concentration may be sufficient in certain cell types, it has been reported that this is not completely efficient at preventing proline conversion artifacts [3, 8]. Our study suggests that this was due to the absence of proline in the standard SILAC media formulation. While the inter-conversion of proline and arginine may still exist in cells labeled with isotope-coded arginine using our media formulation, we were unable to detect it with any level of significance. More importantly, our strategy of supplying additional or high concentrations of amino acids



appears to be more effective at eliminating the problem and makes our strategy the most applicable to biologically important *in vitro* cell types like embryonic stem cells.

This work however, is limited in the number of cell lines and peptides tested. Recent research from two groups has expanded this analysis to include a variety of cell lines and thousands of peptides [36, 37]. Comparing the log<sub>2</sub> ratios of peptides and proteins from 293T cells harvested under conventional SILAC conditions or those where proline is supplemented, Lossner *et al.* observed a shift in the expected peptide ratio only in the absence of exogenous proline supplementation. Marcilla *et al.* were able to virtually abolish arginine conversion by supplementing with as little as 300 mg/L of proline [37]. They also observed that there was no back conversion to arginine after proline supplementation as has been suggested previously [38], further validating our results. Both of these studies indicated no negative effects on cell viability as a result of proline addition.

We have illustrated the ability to eliminate conversion of isotopically labeled arginine to proline when performing SILAC experiments in ESCs. Through the supplementation of as little as 200mg/L of L-proline, conversion can be eliminated to undetectable levels. We also demonstrated the growth and maintenance of hESC and hiPSC lines in fully defined SILAC medium. Since our publication other groups have demonstrated large-scale characterization of hESCs using our methods [39]. Although the ability to perform SILAC in defined conditions is a significant step for hESCs and hiPSCs, extension of this work to a xeno-free medium is desirable.

## 2.4 Experimental Methods

*2.4.1 SILAC media formulations* - All SILAC media formulations and labeling procedures were modified from previously described protocols [5, 28]. With the exception of the defined SILAC medium, all SILAC labeling experiments used embryonic stem cell qualified Dulbecco's Modified Eagle's Medium (DMEM – 4500mg/L glucose, with Na pyruvate, and no L-glutamine) that was custom ordered without lysine or arginine (Specialty Media – Millipore). Before use, media was re-supplemented with 2.5 mM L-glutamine (Invitrogen), 0.798 mM isotope-coded L-lysine ( $^{13}\text{C}_6$   $^{15}\text{N}_2$ ), and 0.398 mM isotope-coded L-arginine (either  $^{13}\text{C}_6$  or  $^{13}\text{C}_6$   $^{15}\text{N}_4$ ). In the case of 'light' media, standard L-lysine and L-arginine were used. The DMEM for ESC cell culture was supplemented with 0.1 mM 2-mercaptoethanol, 1% non-essential amino acids (NEAA - Invitrogen), and 20% or 15% Knockout Serum Replacement (KOSR - Invitrogen) reagent for hESC or mESC culture, respectively. Note that ESC media with 1% NEAA will have 11.5 mg/L proline while KOSR at 20% and 15% (v/v) will contribute an additional 800 and 600 mg/L of L-proline, respectively [27]. For HeLa cell culture the DMEM was supplemented with 10% (v/v) dialyzed fetal bovine serum (FBS), 1% (v/v) penicillin-streptomycin (both Invitrogen), and 0 to 800 mg/L of L-proline (Sigma). All media were filter sterilized at 0.2  $\mu\text{M}$ .

*2.4.2 SILAC labeling of human and mouse ESCs and iPSCs* - For SILAC labeling of both hESC, hiPSC, and mESC cultures measures were taken to remove all non-isotopic Arg and Lys from the system. All cells were washed with either PBS or DMEM lacking Arg and Lys prior to exposure to SILAC media. Any reagents requiring dilution with

DMEM were prepared in DMEM lacking Arg and Lys as well. hESC lines H1 and H9 [40] were maintained in feeder-free culture on 1:15 Matrigel<sup>TM</sup> (BD Biosciences) coated plates. hESC SILAC media was supplemented with 4 ng/mL basic fibroblast growth factor (bFGF – Invitrogen) and pre-conditioned on irradiated mouse embryonic fibroblasts (MEFs) according to previously established protocols [26]. The MEF conditioned hESC SILAC media was further supplemented with 8 ng/ml bFGF prior to addition to hESC cultures and changed daily. Cells were passaged every 5-7 days through dissociation with 200 U/mL collagenase IV (Invitrogen). hESCs were cultured for two passages (> 12 days) in SILAC media to achieve maximum isotopic amino acid incorporation. Analysis of hESC culture integrity and expression of pluripotent cell surface markers was performed as previously described [41]. E14K mESC cultures from 129Ola mice were also maintained in the absence of feeder cells on 0.1%(v/v) gelatin (Sigma) coated plates as previously described [42]. mESC SILAC media was supplemented with 1000 units/ml leukemia inhibitory factor (LIF – ESGROW, Millipore) prior to addition to cultures. Cells were passaged 1:3 every 2 days through dissociation in 0.25% trypsin, 2.21 mM EDTA (Wisent). mESCs were cultured for 4 passages (> 8 days) in SILAC media to achieve maximum isotopic amino acid incorporation.

For SILAC experiments in defined medium, hESC (H9, CA1) and hiPSC (BJ-1D) cell lines were grown in feeder-free conditions on 1:30 Matrigel<sup>TM</sup> (BD Biosciences). The CA1 hESC line used in all experiments was obtained from Dr. Cheryle Séguin of The University of Western Ontario [43, 44]. The hiPSC line BJ-1D was derived by reprogramming using retroviral transduction of BJ fibroblasts with the Yamanaka factors

essentially as we have previously described [45] and validated as pluripotent using in vitro and in vivo differentiation assays and expression profiling (unpublished results). Custom DMEM/F12-glutamax that contained no L-arginine or L-lysine was ordered from Invitrogen. SILAC medium was prepared using the StemPro hESC Media system with our custom DMEM/F12 (Invitrogen) according to manufacturer instructions. [ $^{13}\text{C}_6$ ,  $^{15}\text{N}_4$ ] – L-arginine and [ $^{13}\text{C}_6$ ,  $^{15}\text{N}_2$ ] – L-lysine (Cambridge Isotope Laboratories, Andover, MA) were supplemented into the SILAC medium at 71.42mg/L and 80mg/L respectively. Unlabeled L-proline was added to the SILAC medium at a final concentration of 800mg/L. Culture medium was changed daily and cells were passaged every 4-5 days by manual dissection and harvesting of colonies.

Embryoid bodies (EB) were generated using Aggrewell 400Ex plates (StemCell Technologies, Vancouver, Canada). Briefly,  $2 \times 10^6$  hESCs were harvested enzymatically using Accutase (Invitrogen) from Matrigel<sup>TM</sup> coated plates. Cells were reconstituted in Aggrewell medium supplemented with Rock inhibitor (Y-27632, Sigma-Aldrich, St. Louis, MO) at a final concentration of 10 $\mu\text{M}$ . After plating in Aggrewell dishes, EBs were grown for 48 hours at 37°C prior to transfer to ultra-low adherence tissue culture dishes (Corning, Lowell, MA). After 15 days of culture, EB RNA was harvested using Trizol extraction according to the manufacturer's instructions (Invitrogen). EBs were assayed for expression of CDX2, alpha-feto protein (AFP), GATA-6, GATA-4, Oct3/4, PAX-6, T-brachyury, Nanog, and Neurogenic differentiation 1 (NeuroD1) using TaqMan primer probe sets (Invitrogen). Assay information can be found in Appendix Table 1.15. All EB assays were performed in biological and technical duplicate for each cell line and condition.

*2.4.3 Preparation and digestion of cell samples* - To monitor isotopic amino acid incorporation and conversion trypsin digests were prepared from whole cell lysates for LC-MS analysis. Cell culture media was removed and cells were washed with PBS. Cells were then mechanically removed from the plate, lysed by dissociation in 8M urea and 50 mM ammonium bicarbonate, and frozen at -80°C. The protein content was determined by Bradford assay and, where indicated, 'light' and 'heavy' isotopic samples were mixed 1:1 based on total protein concentration prior to digestion. For trypsin digestion, samples were reduced with 10 mM DTT, alkylated with 30 mM iodoacetamide, diluted 1:4 with 50 mM NH<sub>4</sub>CO<sub>3</sub> and treated with modified trypsin (1:25 enzyme/substrate ratio - Promega) at 37°C overnight. The resulting tryptic peptides were extracted using a 1-mL C<sub>18</sub> solid phase extraction cartridge (Waters), eluted with 50% (v/v) ACN, 0.1% (v/v) formic acid (FA) to remove urea and salts and were re-concentrated in a vacuum centrifuge. Dried fractions were reconstituted in 10% FA for LC-MS/MS analysis.

*2.4.4 Liquid chromatography tandem mass spectrometry (LC-MS/MS) analysis* - Between 1.0 and 0.5 µg of each original sample was injected on a NanoAcquity UPLC (Waters) equipped with a 15cm x 75µm C18 reverse phase column employing a 90-minute LC gradient (5-40% ACN, 0.1% FA) and detected in a data-dependent acquisition (DDA) mode by tandem MS (Q-ToF Ultima - Waters). The MS was directed to use the following DDA parameters: survey scan range 400-1800 m/z, 1 s scan, 1-4 precursors selected based on charge state (+2, +3 and +4 ions). MS/MS fragmentation was then performed on the ions using the charge state collision energy profile function.

*2.4.5 Analysis of isotopic amino acid labeling and conversion* - Data analysis for all samples was performed in PEAKS 5.3 software (Bioinformatic Solutions Inc., Waterloo, Canada) [46, 47]. After import into PEAKS, MS/MS spectra from raw data files were refined using the following settings: merge spectra – true (100ppm mass tolerance, 60 second retention time tolerance), correct precursor mass – true, determine precursor charge state – true (minimum charge +2, maximum charge +5), spectral quality filter – true (0.65 threshold), centroid, deisotope, and deconvolute – true. Resulting MS/MS spectra were then *de novo* sequenced using the following parameters: parent monoisotopic mass tolerance – 100ppm, fragment monoisotopic mass tolerance – 0.15 daltons, enzyme specificity –Trypsin, fixed modifications – carbamidomethylation and +10 daltons on Arginine and +8 daltons on Lysine for SILAC, variable modifications – oxidized methionine. After *de novo* analysis, data were searched against the UniProt sequence database (Human taxonomy specified, 20236 total entries) using the following parameters: parent monoisotopic mass tolerance – 100ppm, fragment monoisotopic mass tolerance – 0.15 daltons, , enzyme specificity –Trypsin, fixed modifications – carbamidomethylation and +10 daltons on Arginine and +8 daltons on Lysine for SILAC, variable modifications – oxidized methionine, estimate false-discovery rate – true. Identified peptides were chosen randomly to be investigated manually using MassLynx 4.1. The peak area was determined by integration using the built-in algorithm in MassLynx 4.1 to output peak area values. Peak area of the monoisotopic ions were used for comparison and determination of quantitative ratios of peptide candidates.

*2.4.6 Titration of proline* - HeLa cells were passaged twice at a ratio of 1:8 in SILAC media containing the indicated amount of L-proline to ensure maximum incorporation of the isotopic arginine label (either  $^{13}\text{C}_6$  or  $^{13}\text{C}_6$   $^{15}\text{N}_4$  Arg). SILAC media was changed every 3 days, or as needed based on phenol red indicator. Whole cell lysates were digested and subject to LC-MS/MS in the initial sample analysis. Both potential and confirmed (by MS/MS) proline containing peptides resulting from the conversion of isotopic arginine were noted. All samples were then re-run in triplicate using the “include only” function to target previously detected/suspected proline containing peptides across all samples. The candidate list of proline containing peptides was then used to follow the conversion of arginine to proline over varying proline supplement concentrations. Peptides containing labeled proline derived from isotope-coded arginine were confirmed by MS/MS in the 0 and 50 mg/L proline samples. Thirteen proline converted peptides observed in the replicate analysis and confirmed by MS/MS were used to monitor isotopic arginine to proline conversion in these experiments. These were: VAPEEHPVLLTEAPINPK, LILPGELAK, PMFIVNTNVPR, NTGIICTIGPASR, MSVQPTVSLGGFEITPPVLR, PPYTVVYFPVRGR, YSSLVPIEK, AVFPSLVGRPR, VAPEEHPVLLTEAPINPK, SSGPYGGGGQYFAKPR, QYPKVPR, LAVNMVPFPR, and SSRAGLQFPVGR.

To investigate the possible back conversion of proline to arginine, a similar process was repeated except the arginine containing peptide candidates did not have a proline in their sequence, so that proline conversion could not interfere with arginine incorporation calculations. Based on replicate analysis, those peptides used for arginine incorporation that were consistently observed and confirmed MS/MS were: STELLIR,

AGTGVDNVDLEAATR, VIGSGCNLDSAR, TIAQDYGVLKADEGISFR,  
GKVKVGVDGFGR, and GITINAAHVEYSTAAR.

*2.4.7 SILAC Label Incorporation* - In order to monitor isotope-coded amino acid incorporation and determine the optimum times for SILAC adaptation a list of both Lys and Arg containing candidate peptides for both human and mouse ESCs was generated. Incorporation was obtained by comparing peak areas from combined scans of light and heavy peptides. Those candidate peptides that were consistently identified by MS/MS across all samples during the labeling time course were: NLPQYVSNELLEEAHSVFGQVER, IHFPLATYAPVISA EK,  
SLQDIIAILGMDELSEEDKLTVSR, LISWYDNEFGYSNR, GVDEVTIVNILTNR,  
SSGPTSLFAVTVAPPGAR, ALMLQGVDLLADAVAVTMGPK,  
EVAFAQFGSDLDAATQQLSR, LLEDGEDFN LGDALDSSNSMQTIQK,  
EKPYFFIPEEYTFIQNVPLEDR, VGKDELFALEQSCAQVVLQAANER,  
GFGFVTYATVEEVDAAMNARPHK, VVLAYEPVWAIGTGK, and YPIEHGIITNWDDMEK  
for hESCs; and KATGPPVSELITK, ALLFVPR, GLFIIDDK, YQAVTATLEEK,  
ALMLQGVDLLADAVAVTMGPK, SGETEDTFIADLVVGLCTGQIK, MVNHFIAEFK,  
IGYPAPNFK, IAIYELLFK, ALYETELADARR, SLMDEVVKATSR,  
ERPPNPIEFLASYLLK, TKVHAELADVLTEAVVDSILAIR for mESCs.

For hESCs and hiPSCs grown in defined SILAC medium, label incorporation was monitored for 7 days after exposure to heavy medium. Incorporation was determined through examination of the following peptides: HQGVMVGMGQKDSYVGDEA QSKR,  
HLEINPDHPIVETLR, HVFGESDELIGQK, IHEGCEEPATHNALAK,



GVVDESDIPLNLSR, FQSSHPTDITSLDQYVER, SNYNFEKPFLLWLAR,  
ISEQFTAMFR, VIHDNFGIVEGLMTTVHAITATQK, HSQFIGYPITLYLEKER,  
VILHLKEDQTEYLEERR, MTDQEAIQDLWQWRK.

*2.4.8 Real-time PCR* – RNA was purified using Trizol reagent according to the manufacturer's instructions (Invitrogen) or with the 5 Prime PerfectPure RNA Extraction Kit (5 Prime, Gaithersburg, MD). After NanoDrop quantification, 1µg of cDNA was synthesized using the High Capacity cDNA Reverse Transcription Kit with RNase inhibitor (Invitrogen). Real-time PCR was performed using the TaqMan® Universal PCR Master Mix (Invitrogen). Samples were incubated at 50°C for 2 minutes followed by 10 minutes at 95°C. Samples were then amplified at 95°C for 15 seconds followed by 1 minute at 58°C for 46 cycles. All samples were normalized to RPLPO as a positive control. All primers were obtained from Invitrogen and assay information can be found in Appendix Table 1.15. Each biological replicate was run in triplicate for every marker assayed. All reagents were used according to the manufacturer's instructions.

*2.4.9 Immunofluorescence* – After 10 passages in SILAC medium, H9, CA1, and BJ-1D cells were plated in 6-well dishes coated with Matrigel™™. After 4 days of culture, cells were rinsed and fixed with 4% para-formaldehyde containing 20 mM sucrose. Prior to staining, cells were blocked using the Dako Serum Free Protein Block solution (Dako, Cambridgeshire, UK). Oct-4 (clone 10H11.2), SSEA-4 (clone MC-813-70), and SSEA-1 (clone MC-480) primary antibodies were obtained from Millipore (Billerica, MA). Cells for Oct-4 labeling were permeabilized using a 0.1% Triton X-100 solution prior to blocking. Cells were labeled with primary antibodies for Oct-4 or SSEA-4 as

undifferentiated markers and SSEA-1 for differentiated cells all at concentrations concentrations of 2 µg/mL for 60 minutes at room temperature. Secondary Alexa-fluor 488 goat anti-mouse IgG and Alexa-fluor 568 goat anti-mouse IgM were obtained from Invitrogen (Carlsbad, CA). Secondary antibodies were probed at concentrations of 1 µg/mL for 60 minutes at room temperature. All products were used according to manufacturer's instructions.

*2.4.10 Flow Cytometry* – All reagents and probes for flow cytometry were obtained from eBiosciences (San Diego, CA) unless noted otherwise. Cells were enzymatically harvested using Accutase (Invitrogen) to obtain a single cell suspension. After centrifugation, cell pellets were resuspended in 5% FBS in PBS. Alexa-488 conjugated SSEA-4 and Alexa-647 conjugated SSEA1 were diluted into the cell mixture according to the manufacturer's instructions. Negative control samples contained respective isotype controls for the primary antibodies used. Solutions were incubated for 2 hours and analyzed using an Accuri C6 (BD Biosciences) flow cytometer after rinsing to remove unbound antibody. Populations were gated according to forward and side scatter patterns with filtering for viable cells using 7-aminoactinomycin D staining. Data were analyzed using FlowJo software (Tree Star, Ashland, OR).

*2.4.11 Teratoma Formation and Histological Analysis* – All animal protocols used here have been approved by the University of Western Ontario Council on Animal Care. Nude (Crl:NU-Foxn1<sup>nu</sup>; Charles River) mice were injected in the flank subcutaneously with H9 or CA1 hESCs grown for >10 passages in StemPro SILAC medium. Prior to injection, hESCs were rinsed with PBS, trypsinized, and counted

using trypan blue exclusion. Approximately  $1 \times 10^6$  cells based on live cell counts were resuspended in a 50:50 DMEM:Matrigel™™ mixture totaling 100 $\mu$ L in volume. Injections were performed on each side of three separate mice for each treatment (n=3). Teratomas were allowed to form for 6 – 8 weeks. Teratomas were removed, fixed and embedded in paraffin. Sections were taken from three areas spaced evenly through the tissue and tissue types were defined with hematoxylin and eosin staining.

*2.4.12 Statistical Analysis* – Statistical analyses were performed using GraphPad Prism software. Results are expressed as SD or SEM as indicated in figure legends. Statistical significance was determined using unpaired Students T-tests. Differences were reported as follows: \*  $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$ .

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## Chapter 3

# Proteomic Analysis of Complex Matrices used in Human Embryonic Stem Cell Culture

### 3.1 Introduction

The *in vivo* and *in vitro* extracellular matrix (ECM) is known to play an important role in numerous decisions that direct cell fate and behavior [1-4]. Typical ECM mixtures include combinations of laminins, collagens, glycoproteins, and proteoglycans [5, 6]. However, the constituents of the ECM differ greatly between tissue types. *In vitro*, the main function of the extracellular matrix is to support cell growth and maintenance. For example, the ECM provides physical support for cells whilst maintaining cellular polarization and tissue morphology. Moreover, the ECM is a reservoir for cell signals as it contains specific carbohydrates, proteins, nutrients and growth factors that can direct cellular processes and behavior. An example ECM component being laminin, which cells sense via integrin receptors. Such interactions between cells and laminin have been shown to affect a variety of biological functions, such as cell growth, morphology, differentiation, and migration in a cell-specific manner [7].

This chapter contains excerpts with permission from the following papers:

Hughes, C.S., Postovit, L.M., Lajoie, G.A.. (2010) "Matrigel: A Complex Protein Mixture Required for Optimal Growth of Cell Culture". *Proteomics*. 10;9:1886 – 1890

Hughes, C.S., Radan, L., Betts, D., Postovit, L.M., Lajoie, G.A.. (2011) "Proteomic Analysis of Extracellular Matrices used in Stem Cell Culture". *Proteomics*. 11;20:3983 – 3991

*In vitro*, protein matrices are commonly used when cell proliferation is not favorable on chemically treated tissue culture plastic. Depending on the cellular system of interest, these matrices can consist of a range of components. The most widely utilized example of this is the basement-membrane matrix commercialized as Matrigel™ [8, 9]. Matrigel™ is an assortment of extracellular matrix proteins that have been extracted from Englebreth-Holm-Swarm tumors in mice [8-10]. Matrigel™, which primarily consists of laminin, collagen IV, and enactin, is considered to be a reconstituted basement membrane preparation. Previous research studies have emphasized the need for caution when drawing conclusions based on changes in cellular activity when using Matrigel™ [11]. This recommendation was based on the detection of several growth factors in standard Matrigel™ through the use of immunoassays; these included bFGF, EGF, IGF-1, TGF-β, PDGF, and NGF [11]. Growth factor reduced (GFR) is a version of Matrigel™ that has been modified to reduce the abundance levels of these growth factors [11].

One important application of Matrigel™ is its use for the growth of human embryonic stem cells (hESC). In contrast to mouse ESC culture, hESCs cannot be maintained in an undifferentiated and pluripotent state on gelatin. Thus, Matrigel™ is conventionally used as a substitute for gelatin in feeder-free hESC culture. Unfortunately, the derivation of Matrigel™ from mouse tissue makes it undesirable for the growth of hESCs that can be potentially applied in therapeutic treatments [12, 13]. A variety of alternative ECM proteins or culture systems have been evaluated for their ability to support hESC proliferation [14-28]. In combination or individually, some of these promote the pluripotent growth of undifferentiated hESCs in 2D, 3D, and suspension



culture [16, 29]. Cell-derived matrices generated from human fibroblasts have also been shown to promote pluripotent hESC growth, but the supportive constituents of such preparations are largely unknown or proprietary [30-35]. While most of the previously noted matrices have been shown to support the maintenance of self-renewal and pluripotency in hESCs, none have proven as effective as Matrigel™ [36].

The lack of a defined xeno-free growth matrix remains a significant limitation for the potential extension of hESCs to therapeutic applications [17, 37, 38]. It would be of tremendous value if support proteins that enhance the *in vitro* culture of hESCs could be identified. The development of a defined matrix for hESC growth is currently limited by our understanding of the ECM proteins that regulate hESC attachment and proliferation. Although it has been the subject of a number of studies, there is still a lack of understanding of how ESCs interact with the surrounding ECM *in vitro* and *in vivo* [39-45]. Proteomic analysis of supportive matrices could help elucidate components that promote hESC growth, analogous to the characterization of conditioned medium from supportive fibroblast feeder layers for the identification of soluble regulatory cytokines [46-50].

A major obstacle that examination of these matrices presents is the significant challenge in proteomic analysis due to the complex nature of the samples. ECM mixtures typically consist of large amounts of high molecular weight protein and a variety of low abundance species. Identification of these low abundance proteins can only be obtained by extensive fractionation prior to liquid chromatography (LC) mass spectrometry (MS) analysis [51, 52]. The two most common methods used in

proteomics are fractionation with one dimensional SDS-PAGE at the protein level or, after digestion with trypsin, by ion exchange chromatography at the peptide level. These fractionation steps are typically followed by further separation on a reversed-phase column prior to MS analysis [53]. It has recently been shown that some fractionation protocols prior to LC-MS are in fact complementary [46, 54].

In this chapter we utilize a combination of fractionation and digestion protocols for the analysis of complex ECM samples to attempt to identify hESC supportive proteins. We show that Matrigel™ contains an array of proteins in addition to those known to be directly involved in the structural basis of the basement matrix. This is accomplished by utilizing an in-depth proteomic approach that employs ammonium sulfate precipitation and a dynamic iterative exclusion MS (IE-MS) strategy to detect low abundance components [46]. Using a combination of strong anion and cation exchange as well as SDS-PAGE methods [46, 55], we analyze CellStart, StemXVivo, BridgeECM, and HumanBME, four previously uncharacterized ECM matrices. We also analyze a matrix deposited by irradiated mouse embryonic feeder layers (MEF-CMTX) after maintenance on gelatin for 7 days. After MEF lysis, the remaining matrix has been shown to promote the undifferentiated growth of pluripotent hESCs [56]. By comparing the proteins identified from these samples, we identify fibronectin as a primary component of nearly all the matrix samples, suggesting its importance in the promotion of hESC maintenance and pluripotency. To validate this observation, H9 and CA1 hESCs were cultured in mTeSR1 medium on fibronectin as the sole matrix component.

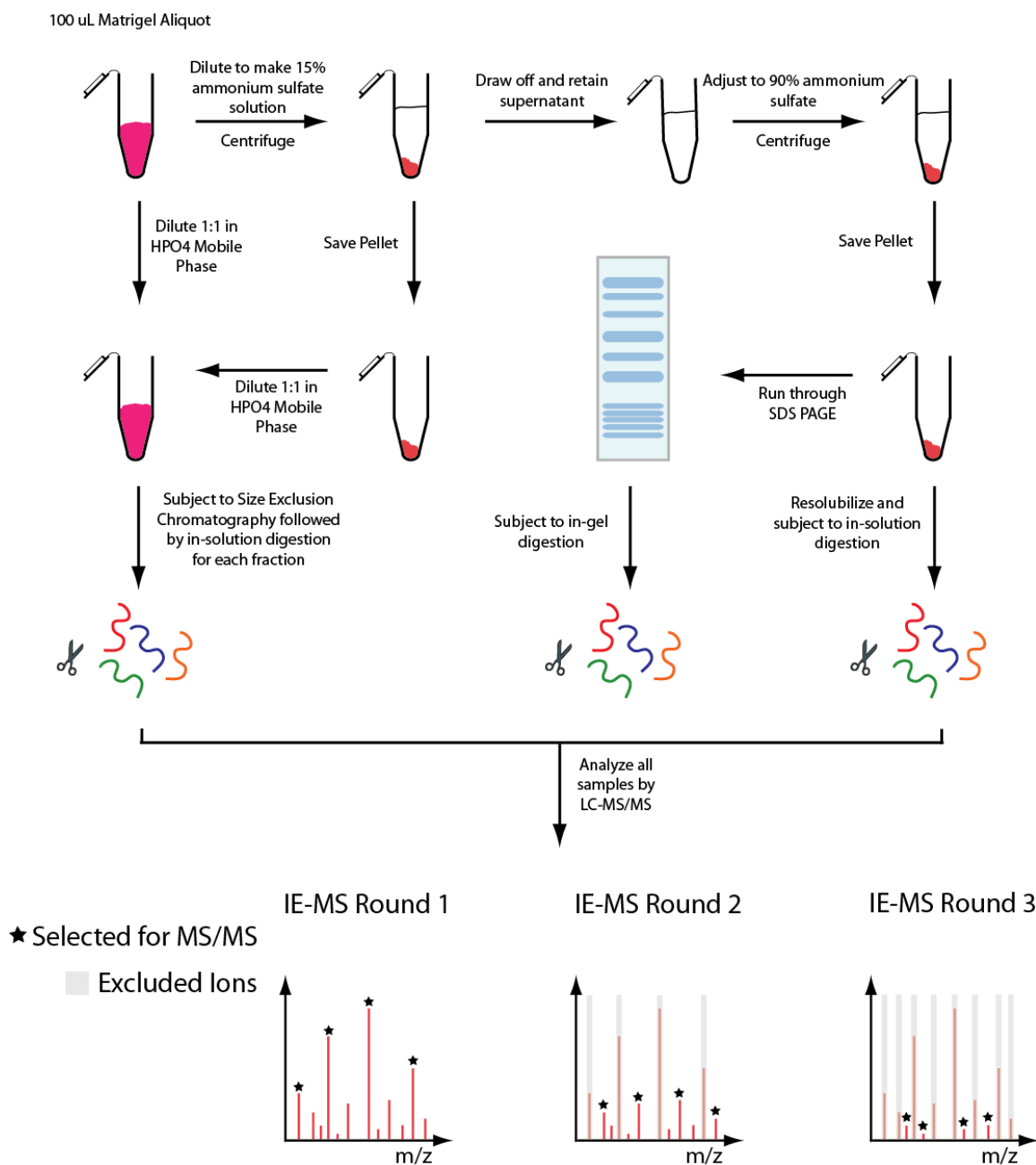
## 3.2 Results

*3.2.1 Fractionation of Matrigel.* Matrigel™ is known to be highly enriched in laminin, collagen, and enactin. Previously published research that revealed the presence of multiple active growth factors in Matrigel™ was based upon detection using immunoassays that are not amenable to a more global analysis of protein composition [11]. Comprehensive analysis of Matrigel™ using MS-based proteomics could potentially reveal the presence of other growth factors and cytokines. The main protein components of Matrigel™, laminin (800,000 Da), collagen IV (540,000 Da), and enactin (158,000 Da) are all significantly larger than the average size of most protein growth factors (<~45,000Da). To facilitate identification of these low abundance factors, fractionation that depletes the abundant high molecular weight (MW) components of Matrigel™ is critical.

Using size exclusion chromatography (SEC) to fractionate Matrigel™ samples, we were unable to obtain effective separation. We observed a large peak early due to the more rapid elution of large proteins from both the standard (N-GFR) and GFR Matrigel™. SEC runs were repeated for 3 technical replicates and typically resulted in ~15 fractions dependent on the elution profile of the sample. Analysis of each SEC fraction with one dimensional SDS-PAGE (1D-SDS-Gel) resulted in gels with very poor resolution, and showed minute amounts of low molecular weight proteins, as determined by Coomassie blue staining. Nevertheless fractions resulting from SEC runs were digested in-solution with trypsin prior to analysis by LC-MS.

Due to the limited separation and loading capacity provided by 1D-SDS-Gels, and the poor resolution of SEC, we adapted a two step ammonium sulfate (AS) precipitation protocol to fractionate both N-GFR and GFR Matrigel™ (Figure 3.1). AS precipitation is not commonly used in proteomics, but has been used for the depletion of N-GFR Matrigel™ to generate the GFR variety [11]. The two step procedure utilized here precipitates protein from Matrigel™ at 15% and 90% AS (w/v). Treatment of Matrigel™ with 15% AS gave a precipitate that was further fractionated by SEC prior to in-solution trypsin digestion. The supernatants from the 15% AS step were further adjusted to 90% AS. The resulting pellets were reconstituted in 8M urea and separated on a 1D-SDS-Gel. These gels contained visible amounts of low molecular weight proteins after staining that were then digested with trypsin and subjected to IE-MS analysis.

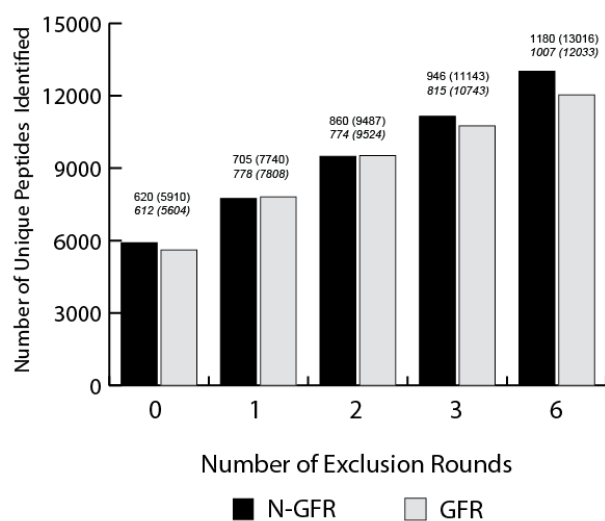
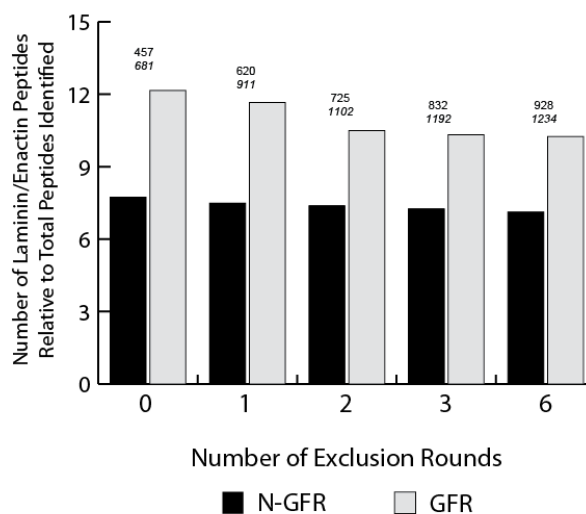
*3.2.2 LC-MS Analysis of Fractionated Matrigel.* LC-MS analysis of the SEC fractions from N-GFR Matrigel™ resulted in identification of 1117 unique peptides. The same analysis on GFR Matrigel™ SEC fractions resulted in the identification of 1521 unique peptides (Figure 3.2 C). The overlap between the two datasets indicates (~20% common) significant differences between the two types of Matrigel™ based on unique peptide identifications. LC-MS analysis of the pellets from 90% AS precipitation after 1D-SDS-Gel fractionation resulted in the identification of 5465 unique peptides for N-GFR and 5080 from GFR (Figure 3.2 C). Combination of SEC and AS precipitation datasets resulted in an increase in the total number of unique peptide identifications to 5910 for N-GFR and 5604 for GFR Matrigel™. Of these peptides, only 457 were matched to laminin/enactin from N-GFR Matrigel™, and 681 from GFR.



**Figure 3.1. Schematic of experimental preparation of N-GFR and GFR Matrigel samples for proteomic analysis.** Aliquots of Matrigel were subject to fractionation with SEC without prior precipitation using AS methods. The pellets of Matrigel aliquots that were precipitated with 15% AS were also subjected to SEC fractionation prior to in-solution digestion with trypsin and LC-MS analysis. The retained supernatant from 15% AS precipitation was further adjusted to 90% AS. Following centrifugation, the resubilized pellet was subject to in-solution digestion with trypsin or further fractionation using a 1D-SDS-Gel. All samples were analyzed using a combination of LC-MS and IE-MS approaches to maximize the depth of sample coverage.

Even with utilization of SEC and AS precipitation coupled with 1D-SDS-Gels, there was still a considerable dynamic range in each fraction to address. To address this, we employed IE analysis to facilitate identification of low-abundance peptide species in the MS as demonstrated previously [11]. IE-MS analysis of the SEC fractions resulted in an increase in the number of unique peptides identified in N-GFR and GFR Matrigel™ to 2588 and 3781 respectively after 4 exclusion rounds (Figure 3.2 B). Six rounds of IE-MS analysis of the fractions resulting from 1D-SDS-Gel separation of the reconstituted pellets from 90% AS precipitation resulted in an increase in unique peptides identified to 11955 and 10368 for N-GFR and GFR Matrigel™ respectively (Figure 3.2 B). Combination of the IE-MS datasets from the SEC and AS methods resulted in an increase in the total number of unique peptides identified to 13016 in N-GFR Matrigel™, corresponding to 1180 proteins (Appendix Table 1.1 – 1.2). Combination of the data for GFR Matrigel™ increased the total number of identifications to 12033 for peptides and 1007 for proteins. These values represent an approximate 2-fold increase in the number of proteins identified through the use of IE-MS with samples from all fractionation types (Figure 3.2 A).

Through the combination of the data from N-GFR and GFR Matrigel™, we can generate a comprehensive dataset. Combination of the SEC datasets from N-GFR and GFR Matrigel™ resulted in the identification 5288 peptides and 452 unique proteins (Figure 3.2 C). Combination of the AS precipitation data resulted in 16995 peptide and 1343 protein identifications (Figure 3.2 C). Of the peptide hits, 748 were assigned to laminin/enactin for samples from SEC fractionation and 1046 for the samples from AS precipitation. These results illustrate the utility of the AS precipitation protocol for the

**A Total Unique Peptide Identifications****B Laminin/Enactin Peptide Identifications****C Total Unique Peptide Identifications**

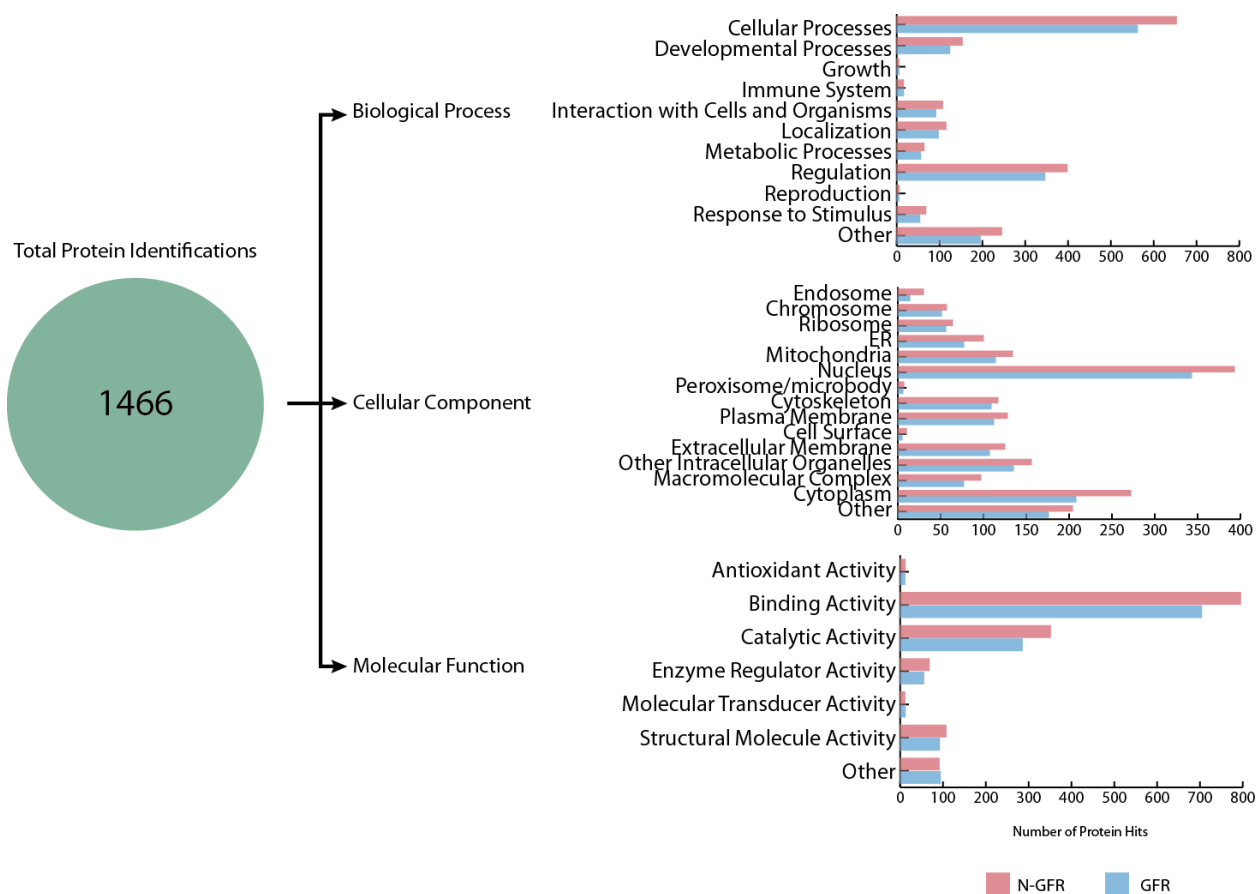
	SEC		AS Precipitation		Combined	
	LC-MS	IE-MS	LC-MS	IE-MS	LC-MS	IE-MS
<b>N-GFR</b>	1117	2588	5465	11955	5910	13016
<b>GFR</b>	1521	3781	5080	10368	5604	12033
<b>Combined</b>	2184	5288	7835	16995	8529	19063

**Figure 3.2. Iterative exclusion analysis of Matrigel samples.** Samples of N-GFR and GFR Matrigel were fractionated using either SEC or AS precipitation coupled with 1D-SDS-Gel methods prior to IE-MS analysis. All LC-MS data files were searched using PEAKS 5.3 software as described in the Methods. (A) Total numbers of unique peptides identified in each round of IE-MS analysis. The number of peptide hits is given above each set of exclusion bars in the format protein# (peptide#) with N-GFR values in normal font and GFR in italics. Values represent total identifications following the combination of SEC and AS datasets. (B) Relative number of laminin/enactin peptides to the total number of identifications as assigned by PEAKS 5.3 across 6 exclusion rounds. As before, total numbers are found above with GFR in italics. (C) Lists the total numbers of peptide identifications found using conventional LC-MS analysis compared with IE-MS for SEC or AS fractionation of N-GFR and GFR Matrigel. LC-MS represents a single injection for each sample, whereas IE-MS represents multiple injections with exclusion lists applied during data acquisition.

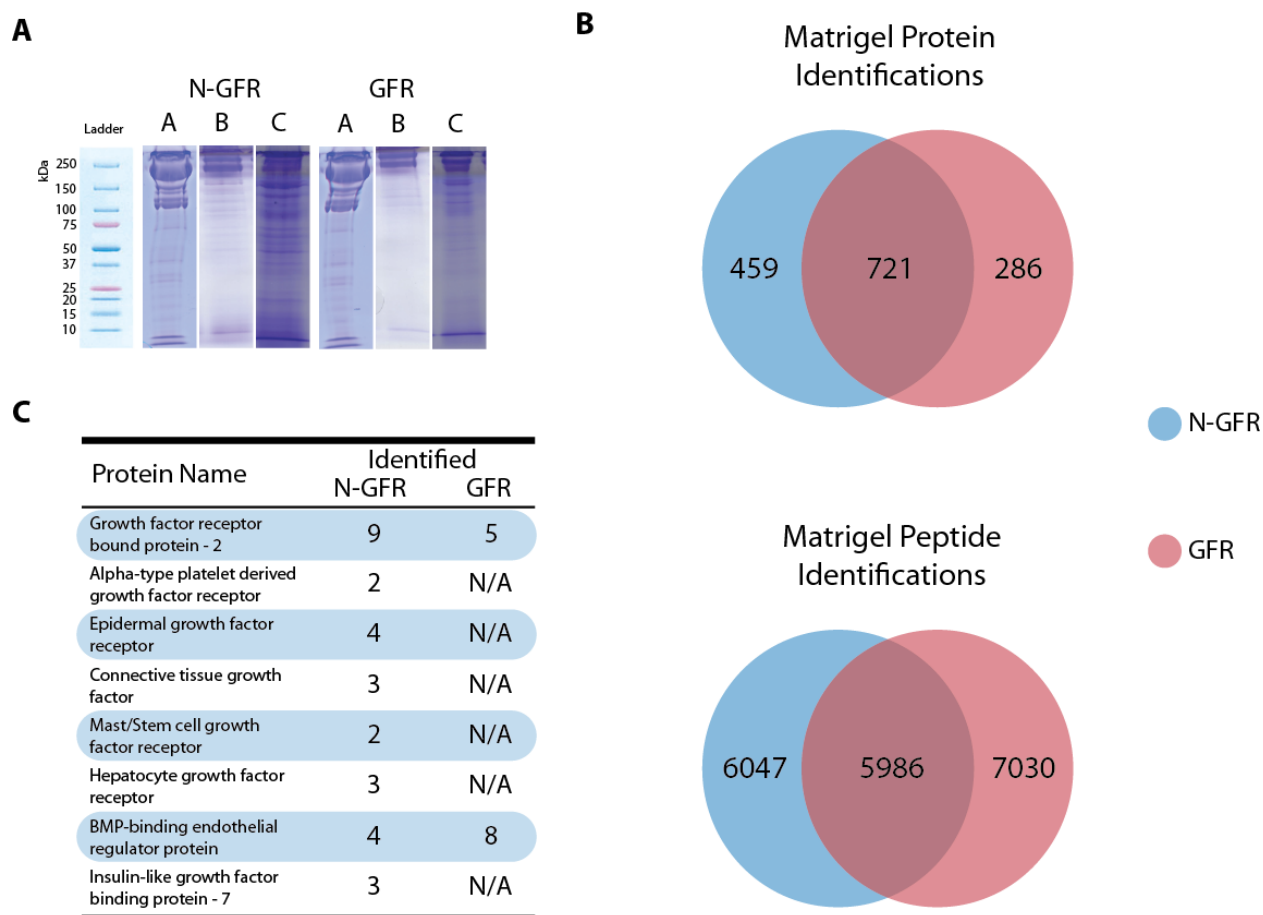
depletion of high-MW components in comparison with SEC in order to facilitate the identification of other proteins in Matrigel™. Combining the data from all Matrigel™ batches and fractionation protocols, we identified a total of 19063 unique peptides and 1466 unique proteins from 280 LC-MS datafiles (Figure 3.3). Gene ontology analysis of the N-GFR and GFR Matrigel™ datasets revealed the presence of numerous intracellular proteins in both formulations (Figure 3.3). Taken together, these data indicate the significant complexity at the protein level for both N-GFR and GFR Matrigel™.

*3.2.3 Comparative Analysis of N-GFR and GFR Matrigel.* GFR is a variant of N-GFR Matrigel™ that has decreased levels of the growth factors and other low molecular weight proteins [11]. This is achieved using an AS precipitation protocol which we have adapted to facilitate analysis of all Matrigel™ samples tested in this study (Figure 3.4 A). Comparison of N-GFR and GFR Matrigel™ revealed that there are at least 721 proteins in common between the two preparations (Figure 3.4 B). N-GFR and GFR Matrigel™ yielded an additional 459 and 286 protein identifications specific to each dataset. Primary structural proteins common between the two types of Matrigel™ such as laminin, nidogen, and fibronectin were more abundant in GFR based on unique peptide number. In N-GFR proteins secondary to the main structural components of Matrigel™, such as SPARC and transferrin were more abundant. Interestingly, a variety of growth factors and their associated pathway members were identified in N-GFR that were not in GFR Matrigel™ (Figure 3.4 C).





**Figure 3.3. Comprehensive proteomics dataset from the analysis of N-GFR and GFR Matrigel.** The number in the green circle on the left represents the total number of protein identifications obtained following the analysis of the combined N-GFR and GFR Matrigel datasets. Identifications were made using PEAKS 5.3 software. Protein identifiers from the list of N-GFR and GFR proteins were mapped to Gene Ontology terms using STRAP software. The three graphs represent Biological Process, Cellular Component, and Molecular Function ontology groupings. The number of mapped annotations for each term for N-GFR can be found in red and for GFR in blue. The wide range of terms that the identifiers mapped to indicates the complexity and range of cellular localizations present for the proteins found in either variety of Matrigel.

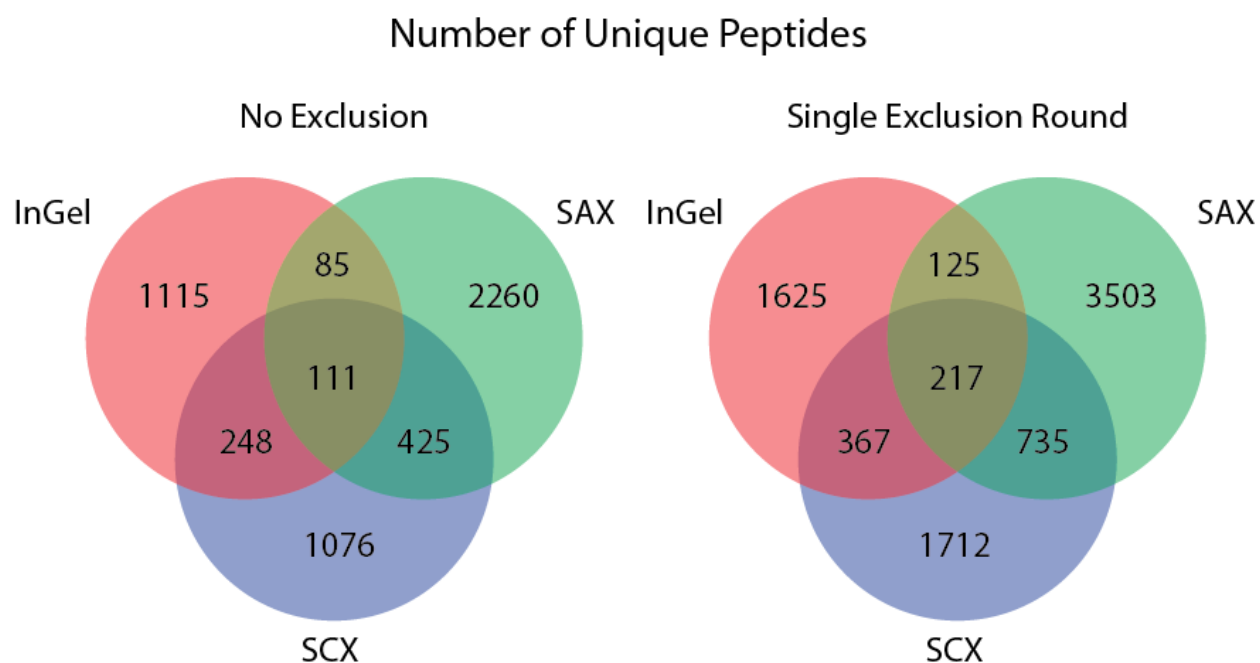


**Figure 3.4. Comparative analysis of N-GFR and GFR Matrigel.** (A) Representative lanes from N-GFR and GFR Matrigel samples that were subject to electrophoresis on 1D-SDS gels. Lane A is neat Matrigel directly as it comes from the manufacturer. Lane B is the pellet that remains after precipitation using a solution of 15% ammonium sulfate precipitation. Lane C is the supernatant after precipitation with 90% ammonium sulfate. Following AS precipitation, a significant increase in protein staining can be seen in the low-MW range in 1D-SDS-Gels of N-GFR and GFR Matrigel samples. (B) Venn diagram illustrating the number of protein and peptide identifications for N-GFR (blue) and GFR (red) Matrigel. Numbers represent total numbers of identifications from data generated by employing IE-MS analysis of Matrigel samples prepared using SEC and AS precipitation fractionation protocols. Data files were analyzed using PEAKS 5.3 software as discussed in the Methods. (C) Table of growth factor and associated binding proteins found in N-GFR or GFR Matrigel. Values in the N-GFR and GFR columns represent the number of unique peptide identifications in each matrix as determined by PEAKS 5.3 software. If the protein was not found, it is denoted by “N/A”.

*3.2.4 Fractionation of Alternative hESC Supportive Matrices.* Adaptation of the AS protocol to the analysis of the HumanBME proved straightforward due to the similar protein abundance profile it shares with Matrigel™. Fractionation of CellStart with the AS protocol proved difficult due to the increased abundance of high-MW protein in this matrix compared with Matrigel™. Due to the limited amount of material we could obtain for MEF-CMTX, BridgeECM, and StemXVivo matrices, we were unable to apply the AS protocol. The limited utility of the AS protocol for the analysis of these matrices highlights the primary shortcoming of this method: the requirement for a large amount of sample due to the high potential for protein loss during the procedure.

In order to overcome the dynamic range of abundance and detect low abundance proteins in these new matrices, we employed a combination of conventional proteomic fractionation and digestion techniques. By utilizing an in-solution digestion protocol coupled to fractionation on strong cation and anion exchange chromatography columns, we could overcome loading constraints caused by lane bleeding on 1D-SDS-Gels to facilitate detection of low-abundance proteins. However, 1D-SDS-Gel fractionation proved applicable to HumanBME, StemXVivo, BridgeECM, and MEF-CMTX, but could not be used for the CellStart matrix due to lane bleeding problems caused by the large abundance of high-MW proteins.

Optimization of the fractionation methods on a HeLa whole cell lysate revealed that numerous peptide identifications were isolated to a single method (Figure 3.5). We also observed that the number of unique peptides identified could be increased by employing IE-MS analysis as described previously [46]. Comparison of the peptides identified for

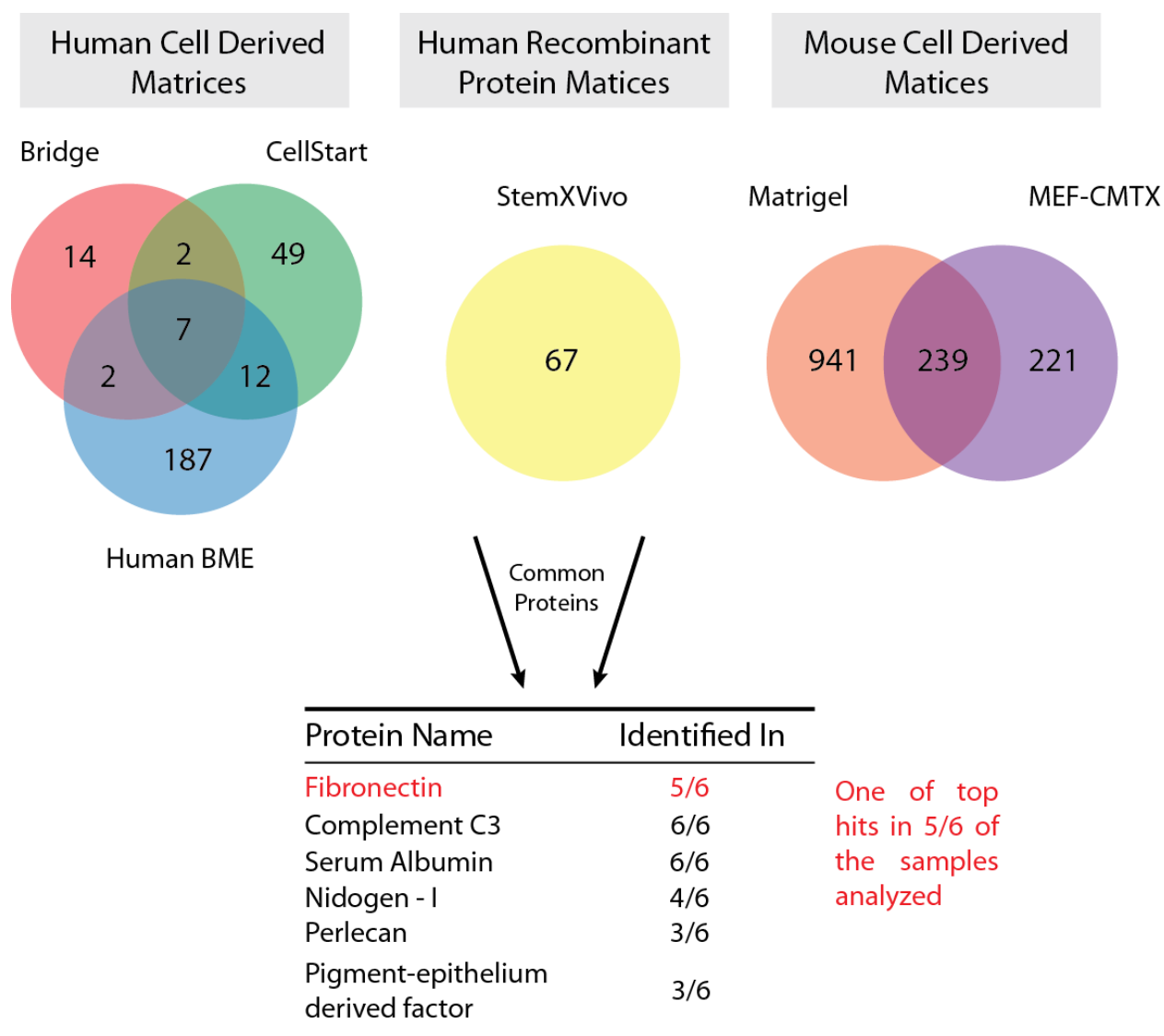


**Figure 3.5. Comparison of methods used to fractionate a complex HeLa cell lysate.** Following enzymatic digestion using trypsin with an in-solution protocol, samples were fractionated using SCX or SAX with a pH gradient elution. Alternatively, cell lysate was separated using a 1D-SDS-Gel and subsequently digested using trypsin with an in-gel protocol. Samples were analyzed by MS with (Single Exclusion Round) or without (No Exclusion) IE-MS. Numbers represent the number of unique peptides identified in the combined fractions for each sample following analysis in PEAKS 5.3 software. Score thresholds were set to ensure an FDR<1% in all datasets.

the three primary fractionation methods tested (SDS-PAGE, SCX, and SAX), revealed that there was only a 2.0% overlap prior to iterative exclusion, and 2.6% after IE-MS analysis (Figure 3.5). This indicates that the differences in identifications are a result of the fractionation methods, as IE analysis will limit changes due to under-sampling of ions in the MS. These results prompted us to employ a combination of in-solution digestion followed by SCX, SAX, or SDS-PAGE fractionation and analysis using IE-MS.

*3.2.5 Analysis of Alternative hESC Supportive Matrices.* Using SAX and SCX fractionation with pH elution, a total of 70 proteins were identified in the CellStart matrix (Figure 3.6, Appendix Table 1.3). From these LC-MS analyses, the two most abundant proteins were fibronectin and serum albumin, representing >60% of all unique peptide identifications. These two high abundance proteins were likely the cause of the difficulties in the 1D-SDS-Gel method, where increasing the gel load resulted in their overloading. The other proteins identified represented a mix of intra and extracellular proteins, the majority of which were identified in Matrigel™.

Fractionation of HumanBME with SAX, SCX, and SDS-PAGE methods yielded 208 protein identifications (Figure 3.6, Appendix Table 1.4). From the analysis we observed that HumanBME is primarily composed of fibronectin, nidogen-1, and alpha-2, gamma-1, and beta-2 laminin isoforms based on the number of unique peptides identified. Other proteins identified included vitronectin, biglycan, insulin-like growth factor – 2, transforming growth factor beta 2, and growth receptor bound protein 2 (Grb2). Comparing the composition of HumanBME with that of Matrigel™ based on protein identifiers indicates a significant similarity between the two matrices. Although the



**Figure 3.6. Comparison of the most abundant components of the ECM samples tested.** Each sample was fractionated using either SCX or SAX chromatography, or 1D-SDS-Gel separation. Fractions were analyzed using IE-MS for a single exclusion round. Numbers in each circle represent the total number of protein identifications for the labeled matrix following the combination of data from all fractionation methods. Protein lists for CellStart, Human BME, StemXVivo, BridgeECM, and MEF-CMTX were generated and compared using PEAKS 5.3 software. Identification numbers include proteins that were matched with 2 unique peptides and had scores above the 1% FDR threshold. Six proteins commonly found at high abundances across the ECM samples are listed in the lower table. Of the proteins identified, fibronectin was an abundant component of 5 of the 6 matrices.

HumanBME dataset appears less complex based the total number of proteins identified when compared with Matrigel™, only a single exclusion round of IE-MS for was performed for the analysis.

Fractionation of StemXVivo with SCX, SAX, and SDS-PAGE methods resulted in a total of 67 unique proteins (Figure 3.6, Appendix Table 1.5). StemXVivo is primarily composed of nidogen-1 and vitronectin. These two proteins comprised >50% of the total unique peptides identified from analysis of StemXVivo. In addition to the primary components identified, a variety of other intra and extracellular proteins were also found, such as syndecan-2, multiple isoforms of actin, and pigment epithelium derived factor (PEDF). A search of unidentified spectra from the StemXVivo dataset against the entire UniProt database (not species restricted, Appendix Table 1.6) yielded numerous non-human peptides, such as 24 for bovine albumin. StemXVivo is marketed as a mixture of recombinant proteins, so the presence of non-human proteins is somewhat surprising.

After fractionation of the MEF-CMTX layer with SAX, SCX, and SDS-PAGE, a total of 460 proteins were identified (Figure 3.6, Appendix Table 1.7). As this matrix is generated through the lysis of mouse feeder cells, the increase in complexity as indicated by the number of proteins identified is not surprising. However, the primary constituents, fibronectin and perlecan, are both classified as extracellular based on gene ontology. The data for MEF-CMTX correlates well with a previous LC-MS analysis of a matrix generated through the lysis of human foreskin fibroblasts [30]. Although the analysis of matrix composition completed by Meng *et al.* was only to a minimal depth,

the majority of proteins identified in their matrices are present in MEF-CMTX based on comparison with our data.

Fractionation of the BridgeECM matrix with SAX, SCX, and SDS-PAGE resulted in 25 protein identifications (Figure 3.6, Appendix Table 1.8). BridgeECM matrix is primarily composed of albumin, comprising 45 of the total 142 identified unique peptides. The matrix also contained the fibronectin, retinol-binding protein 4, plasminogen activator inhibitor 1, and SPARC. Gene ontology analysis of the proteins found in BridgeECM and the other cell-derived ECMs indicates the presence of a range of cellular localization assignments, and a variety of non-ECM proteins (Figure 3.7).

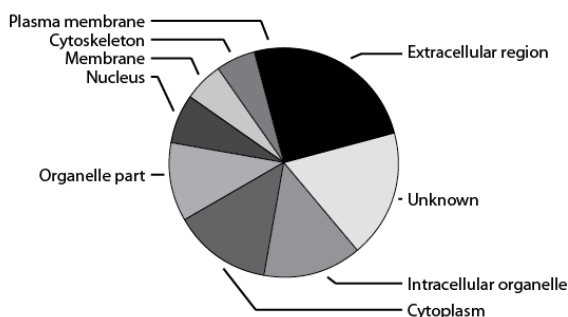
*3.2.6 hESC Growth on a Defined Fibronectin Surface.* Of the ECM samples analyzed, CellStart, BridgeECM, and StemXVivo are marketed as products for the maintenance of hESCs [35, 56]. CellStart and BridgeECM are sold as humanized growth matrices, and StemXVivo as a defined recombinant protein mixture for hESC growth. We were able to maintain H9 hESCs that retained expression of Oct4 and Nanog on CellStart, StemXVivo, and MEF-CMTX matrices using mTeSR1 medium for a maximum of 5 passages (Figure 3.8 A). We were, however, unable to maintain H9 hESCs on BridgeECM or HumanBME matrices for >1 passage using mTeSR1. Despite the limited ability of these matrices to promote hESC growth with mTeSR1, we decided to investigate the viability of a defined matrix based upon the abundant components identified in the matrices analyzed.

Upon comparative examination of the matrix datasets, we observed that fibronectin is a primary component of the all of the cell-derived matrices (Figure 3.6). Based on

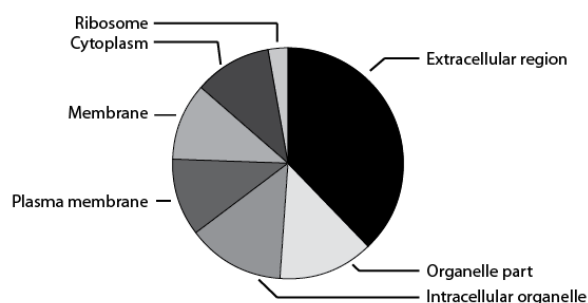


## Gene Ontology - Cellular Component

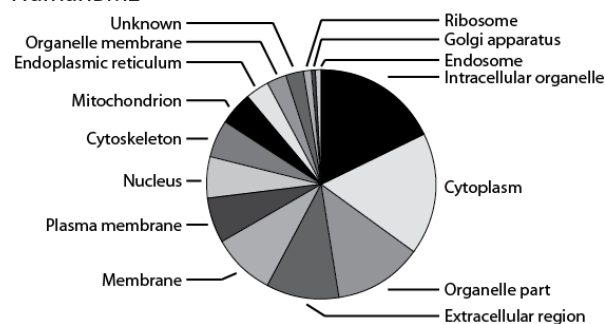
## CellStart



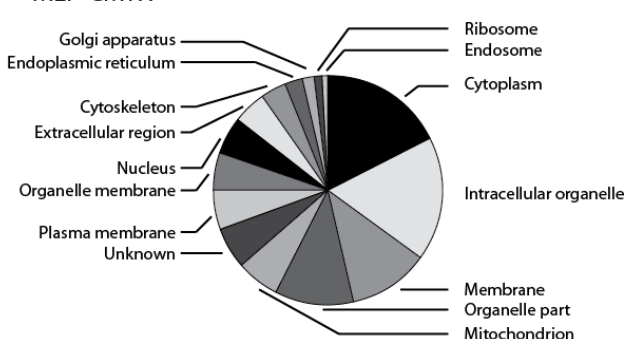
## BridgeECM



## HumanBME

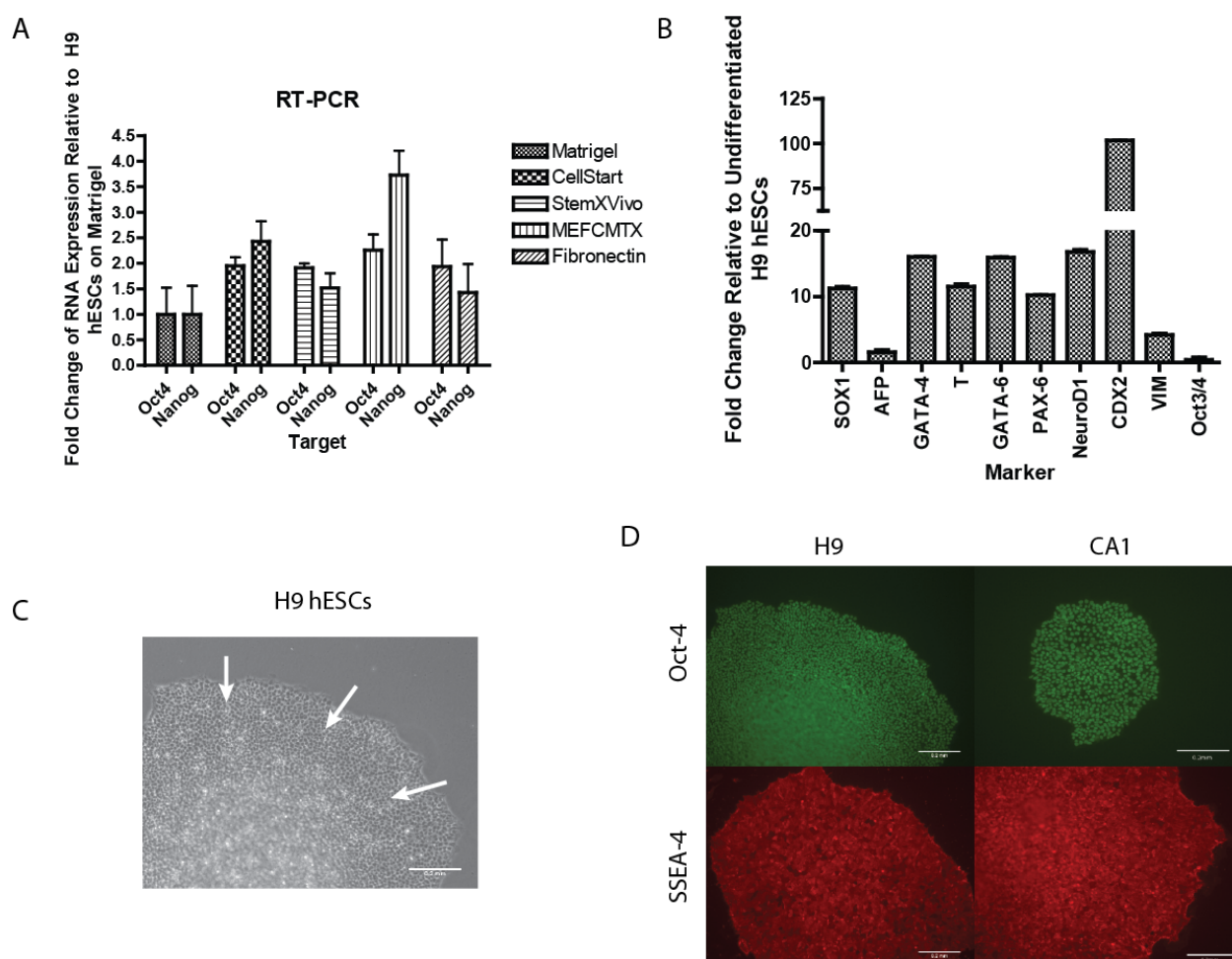


## MEF-CMTX



**Figure 3.7. Gene ontology analysis of the cell-derived matrices tested.** Analysis was done using Scaffold 3.0 software to search protein identifiers against the NCBI Entrez Gene knowledgebase. Protein identifiers were generated using IE-MS analysis of fractionated matrices. With the exception of BridgeECM, all of the matrices tested share similar cellular component profiles with Matrigel (Figure 3.3) and are composed of numerous intracellular proteins. Complete protein identification datasets can be found in the Appendix.

previous evidence that hESCs can be maintained on a combination of collagen IV, laminin, fibronectin, and vitronectin with TeSR1 [17] or on fibronectin alone with defined medium [18, 37], we evaluated a defined system that utilized a combination of fibronectin and mTeSR1. After 10 and 5 passages on fibronectin coated plates, H9 and CA1 hESCs retained typical colony morphology and strong staining for both Oct4 and SSEA-4 markers (Figure 3.8 C-D). For CA1 hESCs, cell growth was not as robust on fibronectin as with H9's, making it difficult to retain a stable culture free of differentiation and amenable to expansion. On other matrices, as well as fibronectin, H9 hESCs retained high levels of Oct4 and Nanog transcript as evidenced by RT-PCR data when compared with hESCs grown on Matrigel™ (Figure 3.8 A). Embryoid bodies generated from H9 cells displayed strong signal for markers of endoderm, ectoderm, and mesoderm lineages in comparison to undifferentiated hESCs grown on fibronectin (Figure 3.8 B). Taken together, these results indicate the ability of fibronectin to sustain H9 hESC self-renewal and pluripotency *in vitro*.



**Figure 3.8. hESC growth characteristics on fibronectin.** H9 and CA1 hESCs were grown on fibronectin for a period of 10 or 5 passages and analyzed for markers of an undifferentiated phenotype. (A) Shows fold change values for Oct4 and Nanog expression in H9 hESCs relative to those grown on Matrigel™ based on RT-PCR analysis. (B) RT-PCR data for embryoid body markers and the pluripotency marker Oct3/4. Values are shown as fold change for embryoid bodies relative to undifferentiated hESCs grown on fibronectin using GAPDH as a control. In both (A) and (B), error bars represent SD, n=3. (C) Phase contrast image illustrating colony morphology during growth on fibronectin coated plates for H9 hESCs. White arrows indicate areas for point of reference to observe undifferentiated cells. (D) Shows immunofluorescence pictures from H9 and CA1 hESCs grown on fibronectin coated plates for 10 or 5 passages respectively. Immunofluorescence was done directly in 24-well fibronectin coated dishes for the markers Oct3/4 and SSEA-4. Scale bars represent 0.2mm on all images.

### 3.3 Discussion

An often overlooked aspect in stem cell culture systems is the composition of the ECM. The primary matrix currently in use continues to be Matrigel™ in the absence of an acceptable alternative that is supportive of a wide range of hESC lines and media formulations. Exactly how Matrigel™ helps stem cells remain in an undifferentiated state remains poorly understood. With the rising demand for xeno-free hESC products, the development of a suitable defined growth matrix is of paramount importance. A contributing factor to the recent developments of defined culture media for hESC growth were data yielded from the analyses of conditioned medium from supportive feeder-cell layers [46-48, 50, 57]. Analogous to the analysis of conditioned medium, characterization of the components of cell-derived matrices could potentially aid in the development of defined surfaces for hESC culture. However, proteomic analysis of complex ECM mixtures is difficult due to the abundance profiles of the common constituents. Here, we demonstrate the development and optimization of methods for the fractionation and analysis of complex ECM mixtures to aid in the identification of hESC supportive matrix components.

In the analysis of Matrigel™, SEC fractionation proved to be of limited utility, even when used in combination with IE-MS. A significant number of the unique peptides identified were assigned to laminin/enactin, the primary components of Matrigel™. AS precipitation in combination with 1D-SDS-Gel fractionation facilitated the identification of a large number of peptides outside of those belonging to laminin and enactin. Gene ontology analysis of the Matrigel™ dataset indicates the presence of numerous cellular

proteins that were either cytoplasmic or nuclear in origin. This implies that although structurally important proteins such as laminin constitute the bulk of what is being extracted from the EHS sarcoma cells, there are also numerous intracellular proteins present. Depletion of low molecular weight components using AS precipitation to create GFR Matrigel™ results in the enrichment of laminin/enactin peptides in comparison to N-GFR. However, the lack of specificity for this method means that numerous other matrix components are lost, as shown through analysis of the supernatant obtained after 15% AS precipitation. This lack of reproducibility combined with limitations in the MS approach due to dynamic range constraints likely contributed to the identification of proteins apparently unique to GFR Matrigel™. As GFR is derived from N-GFR Matrigel™, the identification of proteins unique to GFR Matrigel™ is unexpected. Further proteomic analysis of Matrigel™ using the SAX and SCX methods utilized on the other matrices tested would potentially reconcile these differences by obtaining greater depth of coverage. However, differences between N-GFR and GFR are potentially derived from batch-to-batch variability of Matrigel™ that cannot be addressed in the proteomics approach.

As noted above, Matrigel™ was previously reported to contain specific growth factors [11]. With the optimized proteomics protocol used here we identified several growth and transcription factors such as Grb2 and connective tissue growth factor (CTGF). However, the growth and transcription factors represent only a small fraction of the proteins identified in the analysis of the matrix. We identified numerous proteins directly related to binding and signaling of growth factors. Other ECM proteins identified in this study, fibronectin [58], collagen type IV [59], follistatin [60], and thrombospondin [61],

have been proposed to interact with members TGF- $\beta$  superfamily. The presumed functions of these interactions are to enhance activity and stability of these cytokines in culture. Examples of these ECM interactions have been found to be involved in a variety of pathways, such as fibronectin and vitronectin binding to hepatocyte growth factor receptors leading to enhanced cell migration [62]. Fibronectin type-III domains have also been shown to be involved with vascular endothelial growth factor (VEGF) signaling [63]. Similar interactions have also been demonstrated for a variety of other growth factors [64-67].

The in-depth proteomic analysis of Matrigel™ presented in this study reveals a complex and intricate mixture consisting of numerous structural, growth factors and their binding partners, as well as several other proteins of roles that are not clear in cell culture. We speculate that many of these of proteins play a role in the self-renewal of stem cells when cultured in the presence of Matrigel™. Our analysis of Matrigel™ revealed that it was primarily composed of laminin, collagen, enactin, and fibronectin. Of these, laminin, nidogen-1, and different collagen isoforms have all been shown to be beneficial for hESC maintenance [17, 23, 24, 68-71]. It is perhaps not surprising then that Matrigel™ is the gold standard for the maintenance of a wide array of hESC lines, as it contains most of the proteins shown to promote hESC growth when used individually. However, as a result of the significant depth of coverage we were able to obtain with the use of AS-IE-MS methods, this study also suggests that it will be challenging to replace Matrigel™ in a variety of cell culture and experimental assays due to its complexity.

To complement the Matrigel™ data and facilitate the identification of hESC supportive proteins, we sought to compare matrix components from a variety of cell-culture matrices. Employing a combination of SCX, SAX, and 1D-SDS-Gel approaches, we analyzed other cell-derived and commercial matrices used in hESC culture. Upon inspection of CellStart, StemXVivo, BridgeECM, HumanBME, MEF-CMTX, and Matrigel™ proteomic data, the complexity of these protein mixtures becomes apparent. Based on the number of proteins identified StemXVivo, BridgeECM, and CellStart are more defined matrices in comparison with HumanBME, MEF-CMTX, and Matrigel™. However, based on the proteomics data presented here, none of these matrices are fully defined. Although CellStart and StemXVivo are marketed as such, the number of proteins found indicates they are not as well defined as suggested by the manufacturers.

With the exception of StemXVivo, fibronectin was found to be highly abundant in all of the matrices analyzed. StemXVivo is manufactured as a recombinant protein mixture, and based on our analysis is primarily composed of vitronectin. Vitronectin has previously been shown to sustain hESC pluripotency and survival [15, 19]. This is highlighted in our study by the ability of StemXVivo to promote the growth of H9 hESCs that retain expression of markers indicative of an undifferentiated state (Figure 3.7 A). It has previously been shown that fibronectin and vitronectin both bind integrins that support hESC adhesion [15, 72]. Recent research into synthetic growth surfaces has revealed that integrin RGD and heparin binding peptides promote attachment and proliferation of hESCs [25-28, 73]. These studies suggest that integrin binding by the primary proteins present in ECM mixtures regulate attachment and proliferation.

Undifferentiated hESCs are known to express the fibronectin-specific integrin receptor  $\alpha_5\beta_1$  [18], thus supporting the observation of fibronectin as an effective growth matrix. However, it is likely that other proteins detected in these matrices are also of importance for the growth of a wide range of hESC lines, such as is the case with culture on Matrigel™ or MEFs. This is highlighted by the identification of other proteins like serum albumin and PEDF in several of the matrices analyzed. FBS, of which serum albumin is a primary component, has previously been used as a growth matrix for hESCs [74]. Moreover, PEDF has recently been shown to be beneficial for the feeder-free maintenance of hESCs [75].

Here, we have illustrated the utility of employing different and complementary fractionation methods for the analysis of complex ECM samples in order to elucidate factors essential for hESC survival. Our proteomics analysis reveals the ubiquity of fibronectin in the majority of commonly available matrices. It is noteworthy that none of the matrices tested, including fibronectin, were able to promote and maintain the growth of hESCs with the same efficiency and stability of Matrigel™ when using mTeSR1 medium. H9 and CA1 hESCs differentiated and proliferated poorly after 15 and 5 passages on fibronectin respectively. This indicates that while a defined matrix consisting of a sole component, such as fibronectin is suitable for hESC growth, long-term maintenance and expansion requires a mixture of supportive components in the matrix, medium, or both. Revealing these components through characterization of hESC supportive matrices is a valuable tool for elucidating factors that can have a positive effect on the maintenance of pluripotency.





### 3.4 Methods

*3.4.1 Cell culture and harvest* – H9 (passage 26) and CA1 (passage 27) hESCs were maintained on hESC Qualified Geltrex (Invitrogen, Carlsbad, CA) before passage on to fibronectin coated plates (Millipore, Billerica, MA or BD Biosciences, Franklin Lake, NJ). H9 cells were obtained from WiCell (Wisconsin). The CA1 hESC line used in all experiments was obtained from Dr. Cheryle Séguin of The University of Western Ontario [76, 77]. For all fibronectin experiments conventional 6 well dishes were used. Geltrex, StemXVivo, and BridgeECM were used according to the manufacturer's instructions. CellStart was used as a 25X solution instead of the manufacturer recommended 50X. Cells were maintained in mTeSR1 medium (StemCell Technologies, Vancouver, Canada) on all matrices. Cells were passaged mechanically to minimize variability from enzymatic methods.

Embryoid bodies were generated using the RCCS-2SC 3D bioreactor (Synthecon, Houston, TX) with 2 x10 mL high aspect ratio vessels (HARV). Briefly,  $\sim 2 \times 10^6$  hESCs were harvested from fibronectin coated plates. The equivalent of  $\sim 1 \times 10^6$  hESCs were re-suspended in 8 mL of EB medium containing Knockout DMEM/F12, 20% KOSR (Invitrogen), 2 mM L-glutamine, 0.1 mM  $\beta$ -mercaptoethanol, and 1% non-essential amino acids. The remaining 2 mL was added using syringes to ensure the removal of air bubbles from the vessels. Vessels were left in a 37°C incubator with a rotation rate of 8 rpm. Once EBs had formed (typically after 3-4 days), they were transferred to ultra-low adherence cell culture dishes and grown for a period of 21 days. Cells were then harvested and assayed by RT-PCR for the differentiation markers CDX2, alpha-feto

protein (AFP), GATA-6, GATA-4, Sox-1, PAX-6, T-brachyury, Vimentin, and Neurogenic differentiation 1 (NeuroD1) using TaqMan primer probe sets (Appendix Table 1.15).

*3.4.2 Extracellular matrix analysis* – Human Cultrex basement membrane extract from Trevigen (Gaithersburg, MD), BridgeECM (GlobalStem, Rockville, MD), and CellStart matrix from Invitrogen (Carlsbad, CA) were assayed for protein content using a Bradford assay (data not shown). StemXVivo (R&D Systems, Minneapolis, MN) and BridgeECM were concentrated from their stock solutions using 3 kDa centrifugal filters and reconstituted in 8M Urea and 100mM ammonium bicarbonate (ABC). Lysed MEF matrix was generated by plating of 250,000 irradiated CF-1 cells in each well of a 6-well plate coated with 0.1% gelatin. After 7 days the cells were lysed using a 20 mM NH<sub>4</sub>OH solution. MEF-matrix layers were harvested using a solution of 8 M urea and 100 mM ABC. All matrix samples were analyzed using in-solution digestion followed by fractionation on SCX and SAX columns with pH elution. All samples were also fractionated with 1D-SDS-PAGE and prepared with an in-gel digestion as described earlier. Each fractionation method was run using iterative exclusion as a single technical replicate for each matrix analyzed, for a total of 2 injections per sample.

*3.4.3 Matrigel Preparation* - Two separate lots of growth factor reduced Matrigel™ (A1105 & A3105, CAT# 356234, BD Biosciences, Mississauga, Canada), and one lot of standard Matrigel™ (A3873, CAT# 356230) were aliquoted into 100 µl fractions and stored at -80°C until use. The stock solution of Matrigel™ is at a concentration of ~10 mg/mL based on manufacturer specifications. Protein concentration was assessed with the Bradford assay.

*3.4.4 Reduced Matrigel by Precipitation* - Individual aliquots of standard and GFR Matrigel™ were precipitated using a 15% AS solution as described previously [11]. While the previous study employed a 20% AS solution, we found the 15% AS solution provided a precipitation that resulted in a greater removal of low molecular weight components as deduced from SDS gels analysis. Aliquots were diluted 1:1 using a 30% saturated AS solution to give a final concentration of 15%. Mixtures were left at 4°C for 60 minutes before centrifuging at 12000 g for 15 minutes. The supernatant was drawn into a new tube and brought to 90% AS saturation to precipitate any remaining protein. Solutions were centrifuged for 15 minutes at 12000g and the pellet was reconstituted in 100 mM NH<sub>4</sub>CO<sub>3</sub>. The reconstituted pellet was then subjected to an in-solution digestion with trypsin, or in-gel following 1D-SDS PAGE [46, 78].

*3.4.5 Size Exclusion Chromatography* – 500 µg equivalents of Matrigel™ (as determined by the Bradford assay), as well as pellets from the 15% AS precipitation were run through an off-line size exclusion system. A BioSep-SEC-S2000 column (Phenomenex) fitted with a Security Guard pre-column (Phenomenex) with a phosphate buffer (BioShop Canada Inc.)(0.5 M, pH 7.0) mobile phase was used for separation. The sample was injected manually to an Agilent 1100 HPLC system (Agilent Technologies Inc.) system that provided flow (1 ml/min) as well as detection at 210 nm and 280 nm using a diode array detector.

*3.4.6 In-solution trypsin digestion* – Matrix samples were reduced with 10 mM dithiothreitol (DTT) for 60 minutes. Samples were then alkylated with 40 mM iodoacetamide (IAA) for 60 minutes. The reactions were quenched through the addition

of DTT and left to incubate for another 60 minutes. Samples were then diluted 1/6 in 50 mM ABC. Trypsin (Promega, Madison, WI) at a concentration of 1  $\mu$ g enzyme to 25  $\mu$ g of total protein was added to the mixtures and left to incubate for 24 hours at 37°C. The next day, digests were acidified using neat trifluoroacetic acid and desalted on C18 cartridges (CAT# 2001, Applied Separations, Lehigh Valley, PA). After elution with 50% acetonitrile, samples were evaporated using a SpeedVac. Prior to loading on an SCX column, dried samples were reconstituted in 0.5% formic acid at a pH of ~2. Samples for SAX analysis were reconstituted in 0.5% NaOH at a pH of ~12.

*3.4.7 In-gel trypsin digestion* – 40  $\mu$ g of each matrix was diluted in Laemmli buffer. After heating, matrix samples were loaded in each of two lanes on a 12% SDS-Gel. The gel was stained with Coomassie blue and the gel lanes were divided into 12 fractions based on visual assessment of protein concentration. Gel cubes in each fraction were destained using 20% acetonitrile (ACN) in 1M ABC. Proteins were reduced using 10 mM DTT for 60 minutes, followed by alkylation with 100 mM IAA for 60 minutes. Digestion was carried out using trypsin at a 1/25 ratio overnight in a 37°C water bath. Fractions were extracted the next day using 10% formic acid, sonication, and a final ACN step. Each fraction was dried using a SpeedVac and reconstituted in 10% formic acid prior to injection on to the MS.

*3.4.8 Column preparation* – Columns were packed in 360 O.D. x 200 I.D. capillaries (PolyMicro Technologies, Phoenix, AZ) using a conventional pressure bomb (Next Advance, Averill Park, NY). Frits were prepared by mixing 75  $\mu$ L of potassium silicate with 25  $\mu$ L of formamide, vortexing for 1 minute and rapidly inserting and removing the

capillary end from the resulting mixture. Capillary frits were dried and hardened in a 100°C oven for 2 hours. Capillaries were then rinsed with forward and reverse flow of methanol using the pressure bomb at 200 psi. Prior to packing, capillaries were rinsed for 30 minutes with 0.5% formic acid for SCX and 0.5% NaOH for SAX columns. PolySULFOETHYL A SCX beads (5 µm, 300Å, CAT# PLBMSE0503) were purchased from PolyLC (Columbia, MD) and reconstituted in 10 mM citric acid. SAX beads were purchased from Varian Inc. (10 µm, 1000Å, CAT# PL1451-2102, Palo Alto, CA) and reconstituted in 10 mM NH<sub>4</sub>OH. SCX and SAX columns were packed to a length of ~3 cm for all experiments. All packing was done at a pressure of 200 psi until the desired column length was obtained, then pressurized to 1000 psi to complete packing. Packed columns were rinsed with solvents for conditioning as recommended by the manufacturer.

*3.4.9 Peptide Fractionation* – Peptides were fractionated with SCX and SAX columns using a CapLC system (Waters, Milford, MA) with a flow rate of 2 µL/min. Mobile phase A was composed of 10mM citric acid at a pH of ~2.3, mobile phase B was pH 11.4 10 mM NH<sub>4</sub>OH, and mobile phase C was 500 mM ammonium acetate. Mobile phases were all prepared fresh prior to fractionation to ensure the stability of pH from run to run. Fractionation with pH was carried out using a 120 minute gradient from pH 2 to 12 for SCX, and 12 to 2 for SAX. Salt fractionation was carried using the following steps: 0 mM, 7.5 mM, 15 mM, 30 mM, 45 mM, 60 mM, 75 mM, 90 mM, 105 mM, 120 mM, 150 mM, 300 mM, 500 mM ammonium acetate over 120 minutes. Each fraction was collected offline in a volume of 20 µL. Fractions were dried using a SpeedVac, and reconstituted in 10% formic acid prior to injection on the MS.

*3.4.10 MS Data Acquisition* – Fractions were injected and separated using a nanoAcquity system (Waters, Milford, MA) equipped with a 25 cm x 75  $\mu$ m I.D. C18 column. Fractions were separated using a 1 to 40% ACN gradient over 90 minutes at a flow rate of 300 nL/min. MS analysis was done on a Q-ToF Ultima (Micromass/Waters) using data-dependent acquisition with selection of the four top precursor masses per survey scan. Survey scans were set at 1s, and MS/MS acquisition set at 1s or 6000 cps TIC cut-off. Exclusion lists were generated using in-house software that automatically adds 0.7amu to the precursor masses selected in previous runs and outputs a file also containing retention time information. Each fraction was analyzed for a single exclusion round (2 injections total), adjusting the injection volume dependent on signal intensity in the previous run. In analyses of Matrigel™, each fraction was injected a total of 7 times (6 exclusion rounds).

*3.4.11 MS Data analysis* – Data analysis for all matrices tested was performed in PEAKS 5.3 software (Bioinformatic Solutions Inc., Waterloo, Canada) [79, 80]. After import into PEAKS, MS/MS spectra from raw data files were refined using the following settings: merge spectra – true (100 ppm mass tolerance, 60 second retention time tolerance), correct precursor mass – true, determine precursor charge state – true (minimum charge +2, maximum charge +5), spectral quality filter – true (0.65 threshold), centroid, deisotope, and deconvolute – true. Resulting MS/MS spectra were then *de novo* sequenced using the following parameters: parent monoisotopic mass tolerance – 100ppm, fragment monoisotopic mass tolerance – 0.15 daltons, enzyme specificity – semi-Trypsin, fixed modifications – carbamidomethylation, variable modifications – N-terminal acetylation and oxidized methionine. After *de novo* analysis, data were

searched against the UniProt sequence database (Human taxonomy specified, 20236 total entries or Mouse taxonomy specified, 16376 total entries) using the following parameters: parent monoisotopic mass tolerance – 100 ppm, fragment monoisotopic mass tolerance – 0.15 daltons, enzyme specificity – semi-Trypsin, fixed modifications – carbamidomethylation, variable modifications – N-terminal acetylation and oxidized methionine, estimate false-discovery rate – true.

*3.4.12 Protein identification* – Resultant protein identification data from the database search were processed using PEAKS 5.3 software [81]. Identifications were filtered by assigned score to give a <1.0% false-discovery rate for peptide-spectral matches based on estimation from a decoy-fusion method of database search. Identified proteins were also required to be matched by >2 unique peptides. Proteins that contained similar peptides and could not be differentiated based on MS/MS analysis alone were grouped to satisfy the principles of parsimony. For all matrices analyzed, keratin hits were manually removed from the final datasets.

*3.4.13 Real-time PCR* – RNA was purified using Trizol reagent according to the manufacturer's instructions (Invitrogen) or with the 5 Prime PerfectPure RNA Extraction Kit (5 Prime, Gaithersburg, MD). After NanoDrop quantification, 1 µg of cDNA was synthesized using the High Capacity cDNA Reverse Transcription Kit with RNase inhibitor (Invitrogen). Real-time PCR was performed using the TaqMan® Universal PCR Master Mix (Invitrogen). Samples were incubated at 50°C for 2 minutes followed by 10 minutes at 95°C. Samples were then amplified at 95°C for 15 seconds followed by 1 minute at 58°C for 46 cycles. All samples were normalized to large ribosomal



protein RPLPO as a positive control. All primers were obtained from Invitrogen and assay information can be found in Appendix Table 1.15. Each biological replicate was run in triplicate for every marker assayed. All reagents were used according to the manufacturer's instructions.

*3.4.14 Immunofluorescence* – Passage 10 H9 and 5 CA1 hESCs grown on fibronectin were plated in wells of a 24-well dish coated with the same matrix. After 4 days of culture in mTeSR1 medium cells were rinsed and fixed with 4% para-formaldehyde containing 20 mM sucrose. Prior to staining, cells were blocked using the Dako Serum Free Protein Block solution (Dako, Cambridgeshire, UK). Oct-4 (clone 10H11.2), SSEA-4 (clone MC-813-70), and SSEA-1 (clone MC-480) primary antibodies were obtained from Millipore (Billerica, MA). Cells for Oct-4 labeling were permeabilized using a 0.1% Triton X-100 solution prior to blocking. Cells were labeled with primary antibodies for Oct-4 or SSEA-4 as undifferentiated markers and SSEA-1 for differentiated cells all at concentrations of 2 µg/mL for 60 minutes at room temperature. Secondary Alexa-fluor 488 goat anti-mouse IgG and Alexa-fluor 568 goat anti-mouse IgM were obtained from Invitrogen (Carlsbad, CA). Secondary antibodies were probed at concentrations of 1 µg/mL for 60 minutes at room temperature. All products were used according to manufacturer's instructions.

### 3.4 References

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## Chapter 4

### Proteomic Analysis of the Human Embryonic Stem Cell Depositome

#### 4.1 Introduction

The ECM is a complex network of structural proteins and glycosaminoglycans that function to support cells through the regulation of processes such as adhesion and growth factor signaling [1]. It is not surprising that the generation of a well-defined matrix supportive of these processes in the complex hESC microenvironment has been difficult. Although gelatin is sufficient for the maintenance of mESCs in the presence of specific growth factors, hESCs cannot be propagated in the same conditions. Currently, in the absence of a suitable alternative, Matrigel™ remains the matrix of choice for hESC culture *in vitro*. However, the complex nature of Matrigel™ has been demonstrated previously in this thesis (Chapter 3), and has been described by others who have revealed that it contains numerous growth factors and signaling proteins [2]. Although recent studies have revealed that a variety of defined matrices support the growth of hESCs, few of these can maintain a wide array of stem cell lines and as such are typically not used in place of Matrigel™ [3]. The universality of Matrigel™ indicates that current defined matrices are lacking in critical components required to generate a supportive hESC microenvironment.

This chapter contains excerpts from the following paper:

Hughes, C.S., Radan, L., Stanford, W., Postovit, L.M., Lajoie, G.A.. (2012) "Proteomics Analysis of the Human Embryonic Stem Cell Depositome". (In Preparation)

Because of the challenge proteomic examination of the ECM presents, the majority of studies that have analyzed the hESC microenvironment have focused on support cells and paracrine signaling pathways. The desire to generate well-defined conditions for hESC culture *in vitro* has prompted these investigations into the factors critical for the maintenance of stem cells. Proteomic studies have focused on the analysis of media conditioned by hESC supportive feeder cell layers to elucidate pathways important for maintaining the balance between self-renewal and differentiation [4-9]. These analyses were important contributors to our current knowledge of how hESCs are regulated in the extracellular space by pathways in the soluble portion of the microenvironment. However, there is still a lack of information of how the ECM modulates hESC behavior *in vitro* through interactions with both the cells themselves and the soluble cytokines present in the extracellular milieu.

Given the common underlying plasticity of stem and cancer cells, recent studies have established the ability of embryonic microenvironments to alter the tumorigenic properties of cancer cells (reviewed in [10]). Building on these findings, it was later observed that metastatic melanoma cells could be 'reprogrammed' to a more benign melanocyte phenotype following exposure to a matrix microenvironment generated from hESCs [11]. Importantly, this effect was found to be dependent on the exposure of metastatic cells to the conditioned matrix, and was not observed after treatment with hESC conditioned medium. It was later found that the left-right determination (Lefty) proteins that were deposited in the matrix by hESCs were effectors of the cellular change observed in metastatic cells [12]. The Lefty proteins are antagonists of TGF- $\beta$  signaling that act directly on Nodal protein. Differences in the methylation status and

microRNA profiles for genes and pathways directly related to Lefty/Nodal signaling in metastatic cells on conditioned matrix have recently been observed [13]. Subsequent work with conditioned matrix utilizing mESCs implicated the bone morphogenic protein (BMP) 4 antagonist Gremlin as a primary regulator of the observed changes in metastatic cells [14]. Collectively, these studies were all biased by a targeted analysis of potential effectors of metastatic cells. A comprehensive proteomic analysis of the matrix microenvironment could potentially reveal other factors involved in metastatic cell reprogramming. Furthermore, proteomic analysis of the conditioned matrix could reveal factors important in the regulation of hESC and human induced pluripotent stem cell (hiPSC) pluripotency by the microenvironment *in vitro*.

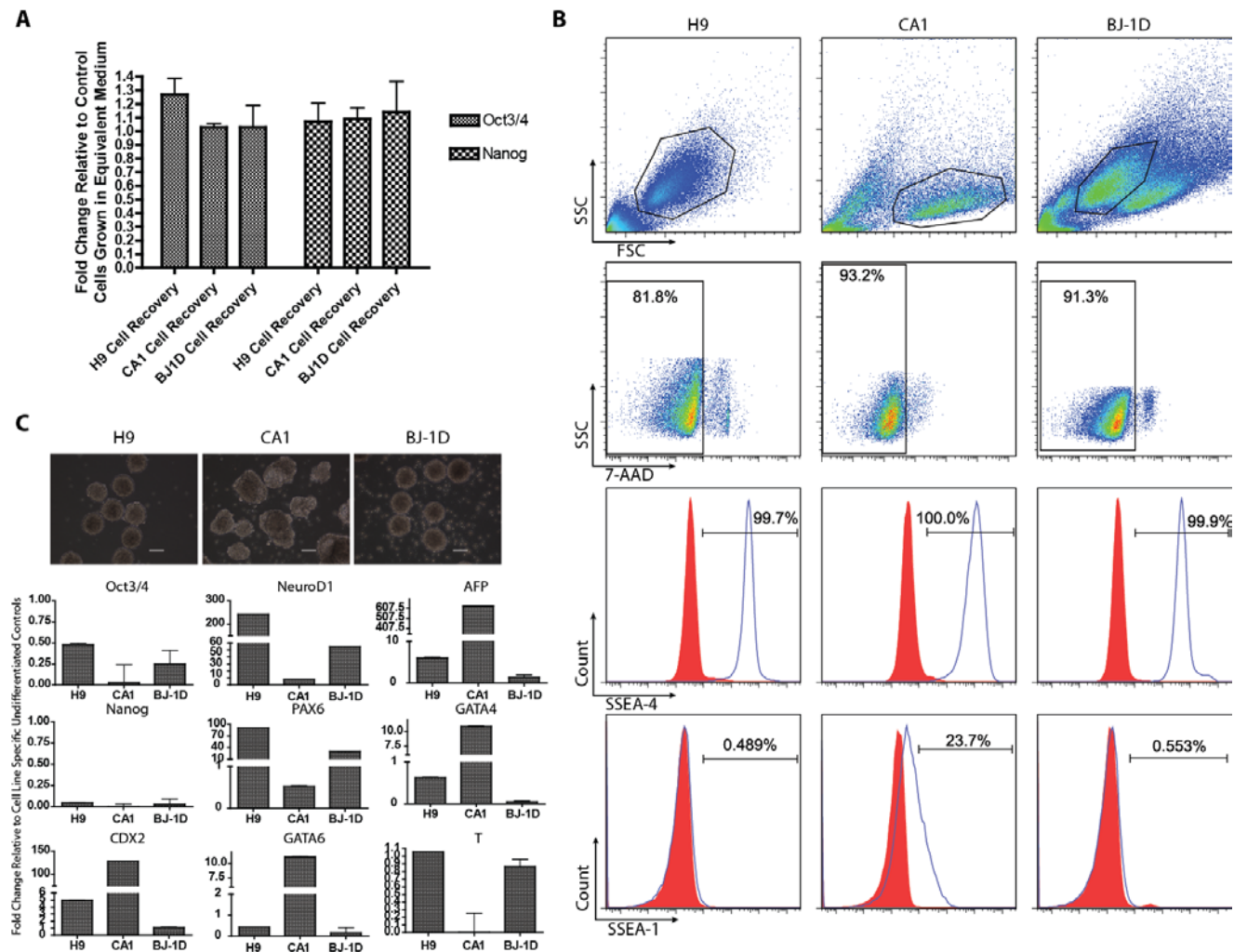
To this end, we have employed a mass spectrometry (MS)-based proteomics screen to identify proteins deposited by hESCs and hiPSCs grown on Matrigel™ *in vitro*. To investigate the hESC-derived matrix, we utilize a metabolic labeling technique known as stable isotope labeling with amino acids in cell culture (SILAC) [15]. SILAC facilitates the identification of hESC-derived proteins in the presence of significant background protein complexity from Matrigel™. Additionally, in order to minimize intracellular protein contamination in our analysis, we have developed methods that remove the requirement for cell lysis to generate CMTX. From proteomic analysis of H9, CA1, and BJ-1D pluripotent stem cell lines, we identify a total of 621, 1355, and 1350 unique proteins respectively. This work represents the first analysis of a stem cell conditioned matrix and resulted in the identification of at least one new microenvironmental contributor responsible for the regulation of hESCs and hiPSCs.



## 4.2 Results

*4.2.1 Proteomic Analysis of Pluripotent Stem Cell Derived CMTX.* To determine factors being deposited by hESCs during growth on Matrigel™, we employed a global MS-based proteomics approach to screen CMTX. Previous studies that have illustrated the effects of CMTX on metastatic cells have employed an NH<sub>4</sub>OH cellular lysis protocol to remove hESCs from Matrigel™. Lysis of cells on the matrix could potentially confound our analysis by releasing high abundance intracellular proteins. To limit the potential for intracellular protein contamination in the CMTX resulting from lysis, we developed a protocol based on Matrigel™ de-polymerization to remove intact cells from the matrix. With this method, the vast majority of the hESCs that were removed remained intact and viable as indicated by 7-AAD staining in flow cytometry (Figure 4.1 B). Moreover, the removal of cell-lysis from the protocol permitted analysis of the undifferentiated state and differentiation capacity of the cells that deposited the matrix (Figure 4.1 A, C).

After cell removal and concentration of the CMTX solution, a combination of strong cation and anion exchange (SCX, SAX), and 1D-Gel methods was employed for fractionation of the complex ECM-like mixture with iterative exclusion MS analysis as discussed previously (Chapter 3). MS analysis of these samples illustrated the limited ability of our assay to determine hESC-derived proteins in our list of identifications (Figure 4.2 A – B). This limitation is directly the result of performing the CMTX experiments on Matrigel™. Since the mixture that gets analyzed by MS represents a mixture of hESC-derived and Matrigel™ proteins, identification specificity is reliant on non-homology between human and mouse proteins. However, by searching the

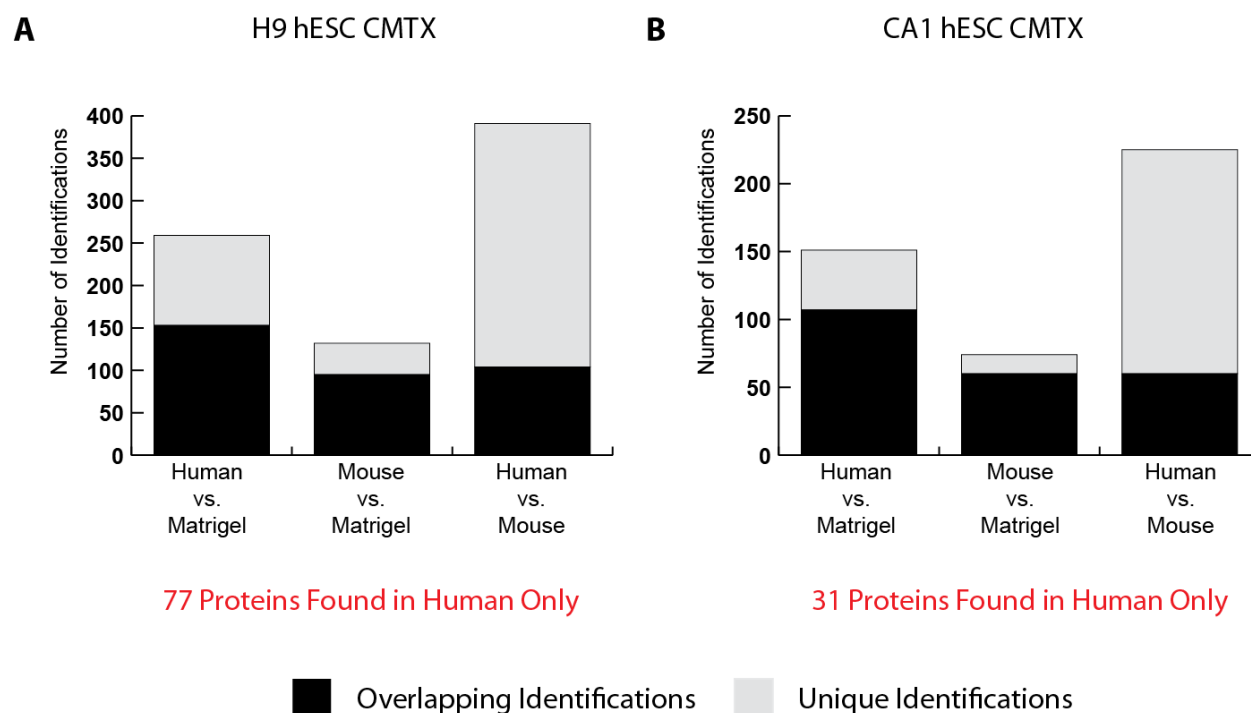


### Figure 4.1. Cell viability and pluripotency during generation and harvest of CMTX.

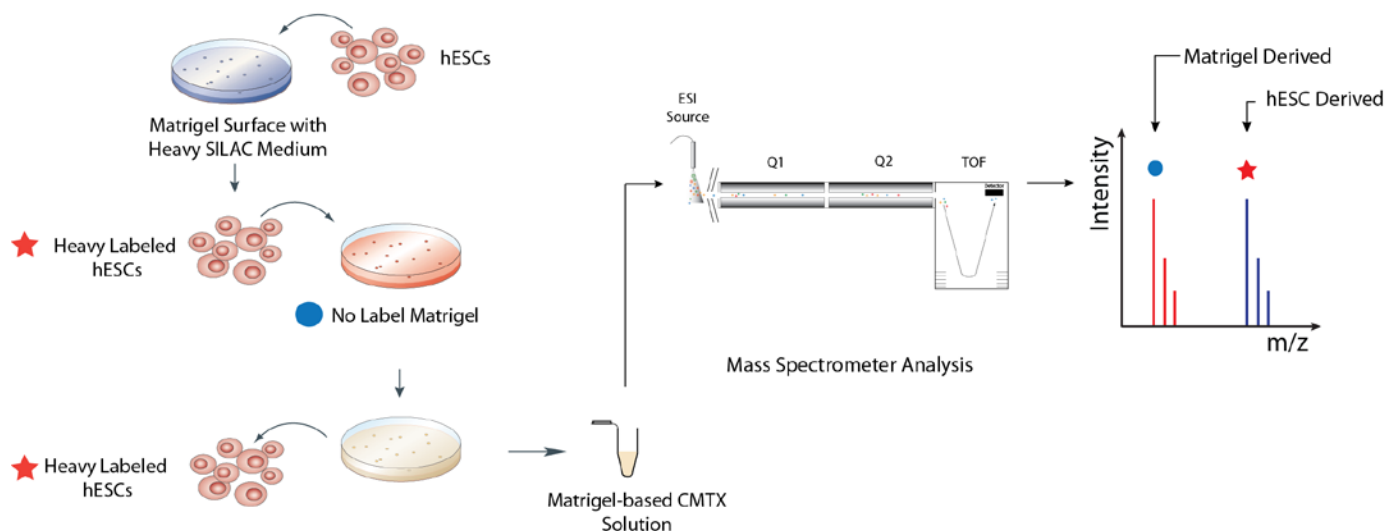
H9 and CA1 hESCs as well as BJ-1D iPSCs were used to generate CMTX. Following harvesting using our cell recovery method that eliminates cell lysis, remaining cells were assayed for viability and markers of pluripotency. (A) RT-PCR analysis of harvested cells for the markers Oct3/4 and Nanog. Values are relative to undifferentiated cells grown in feeder-free conditions not exposed to the CMTX harvesting methods. Error bars represent SD,  $n=3$ . (B) Flow cytometry analysis of cells harvested from CMTX. Cells were assayed for SSEA4 and SSEA1. Viability was determined using 7-AAD staining. (C) Cells harvested from CMTX were used to generate embryoid bodies. Following 14 days in culture, embryoid bodies were harvested and assayed for markers of pluripotency (Oct3/4, Nanog), trophoblast (CDX2), ectoderm (NeuroD1, PAX6), endoderm (GATA6, GATA4, alpha-fetoprotein), and mesoderm (T). Error bars represent SD,  $n=2$ . Values are fold change relative to undifferentiated cells. Phase contrast images of embryoid bodies are provided above. Scale bars represent 250 $\mu$ m. In both (A) and (C), RPLPO is used as a positive control.

data set against a concatenated human and mouse sequence database, we observe that few proteins are identified as belonging to a single species (Figure 4.2 A - B). Many of the identified proteins have also been found in Matrigel™ in our previous proteomic analysis (Figure 4.2 A - B). Taken together, these complications severely limit the specificity and sensitivity of the proteomic analysis. To overcome these challenges, we employed a metabolic labeling approach known as SILAC that we have previously optimized for application in hESCs and hiPSCs (Chapter 2). Using this approach, hESCs and hiPSCs would be fully labeled with 'heavy' arginine and lysine prior to being plated for CMTX generation (Figure 4.3). In this approach, proteins that were deposited during CMTX generation will carry a heavy label and can be distinguished on the MS from Matrigel™ contaminants.

With this protocol, we analyzed CMTX from H9 and CA1 hESCs, as well as BJ-1D hiPSCs. MS analysis yielded a total of 621, 1355, and 1350 labeled proteins identified for H9, CA1, and BJ-1D cell lines respectively (Figure 4.4 A, Appendix Tables 1.9 - 1.11). Comparison of protein identifiers between the cell lines indicates a ~30% overlap between the three datasets (Figure 4.4 A). The gain in the number of proteins in the CA1 and BJ-1D stem cell lines is due to their decreased stability in the StemPro SILAC medium. We observed an increase in cell death and subsequent lysis during general growth of the CA1 and BJ-1D cell lines compared with H9 in StemPro SILAC medium resulting in the identification of additional intracellular proteins. Gene ontology analysis revealed that in the dataset corresponding to each cell line there are proteins representative of several cellular components present. This suggests that a variable



**Figure 4.2. Proteomic analysis of unlabeled hESC derived CMTX.** H9 (A) and CA1 (B) hESC CMTX generated using unlabeled cells was analyzed using an MS-based proteomics approach. Data were searched simultaneously against a concatenated database containing all Mouse and Human protein sequences available in UniProt. Human vs. Matrigel represents the overlap between proteins identified as Human derived in CMTX by PEAKS 5.3 compared with those found in Matrigel (Chapter 3). Mouse vs. Matrigel represents the overlap between proteins identified as Mouse derived in CMTX by PEAKS 5.3 compared with those found in Matrigel. Human vs. Mouse represents the overlap within the CMTX dataset between proteins specified as Human or Mouse derived by PEAKS 5.3. To facilitate inter-species comparisons, protein descriptions were used in all cases. Comparisons were done manually. Overlapping identifications are denoted by a solid black box, and those that are unique by a grey box. For both H9 and CA1 derived CMTX, n=1.



**Figure 4.3. Proteomic analysis of CMTX from hESCs cultured in SILAC medium.** H9 and CA1 hESCs, and BJ-1D iPSCs are grown in defined SILAC medium containing [ $^{13}\text{C}_6$ ,  $^{15}\text{N}_4$ ] - arginine and [ $^{13}\text{C}_6$ ,  $^{15}\text{N}_2$ ] - lysine optimized previously (Chapter 2). After culture for a sufficient amount of time to obtain complete labeling, cells are passaged to culture dishes pre-coated with Matrigel. After 4-5 days of culture on Matrigel in medium containing the heavy isotopic labels, cells are removed using a protocol that does not induce lysis of the cells (see Methods). The remaining conditioned matrix layer is rinsed and harvested. The conditioned matrix solution is then enzymatically digested and fractionated using protocols optimized previously (Chapter 3). Mass spectrometry analysis of the conditioned matrix generated using labeled hESCs permits identification of human proteins. Peptides derived from hESCs will carry an isotopic label and will display a resultant mass shift in the MS, whereas those previously present in Matrigel will not have this difference.

amount of cell lysis is occurring during growth or harvest of the CMTX for all the cell lines.

To limit the contaminants from cell lysis, the dataset was filtered using the “extracellular” and “cell surface” cellular component gene ontology terms. Filtering reduced the number of proteins identified in each dataset to 71, 100, and 95 labeled proteins for H9, CA1, and BJ-1D respectively (Figure 4.4 A, Appendix Tables 1.12 – 1.14). However, the data still contained numerous intracellular proteins (histones, mitochondrial, and cytoskeleton associated). This is primarily the result of the limited specificity of the gene ontology assignments. The overlap between the three individual CMTX datasets is ~35% based on protein identifiers after gene ontology filtering. However, coverage between biological replicates of the same cell line using the identical fractionation methods overlap a minimum of 71% across the samples in the experiment. The reproducibility between biological replicates from single stem cell lines illustrates the consistency of not only the proteomics method, but of the CMTX assay itself.

The hESC and hiPSC CMTX proteomics data indicate that numerous cell line specific factors were deposited based on comparisons between the protein lists. When comparing core ECM proteins, isoforms of fibronectin and laminins, and heparan sulfate proteoglycan linked proteins were present at similar abundance levels based on the number of unique peptides in CMTX from H9 and BJ-1D cell lines. However, BJ-1D CMTX was enriched in matrix remodeling factors, such as matrix metalloproteinase-14 and -15. On the other hand, CMTX derived from CA1 hESCs was found to contain multiple collagen and laminin isoforms not identified in the matrices from the other stem

cell lines. Low abundance factors such as soluble frizzled related protein (sFRP) 1 and 2, and Lefty A and B were identified in CMTX from all cell lines. Interestingly, connective tissue growth factor (CTGF) was identified in CMTX from both hESC lines, but not in that from BJ-1D hiPSCs. In addition, other low abundance factors such as Cerberus and fibroblast growth factor-15 were only identified in CA1 CMTX.

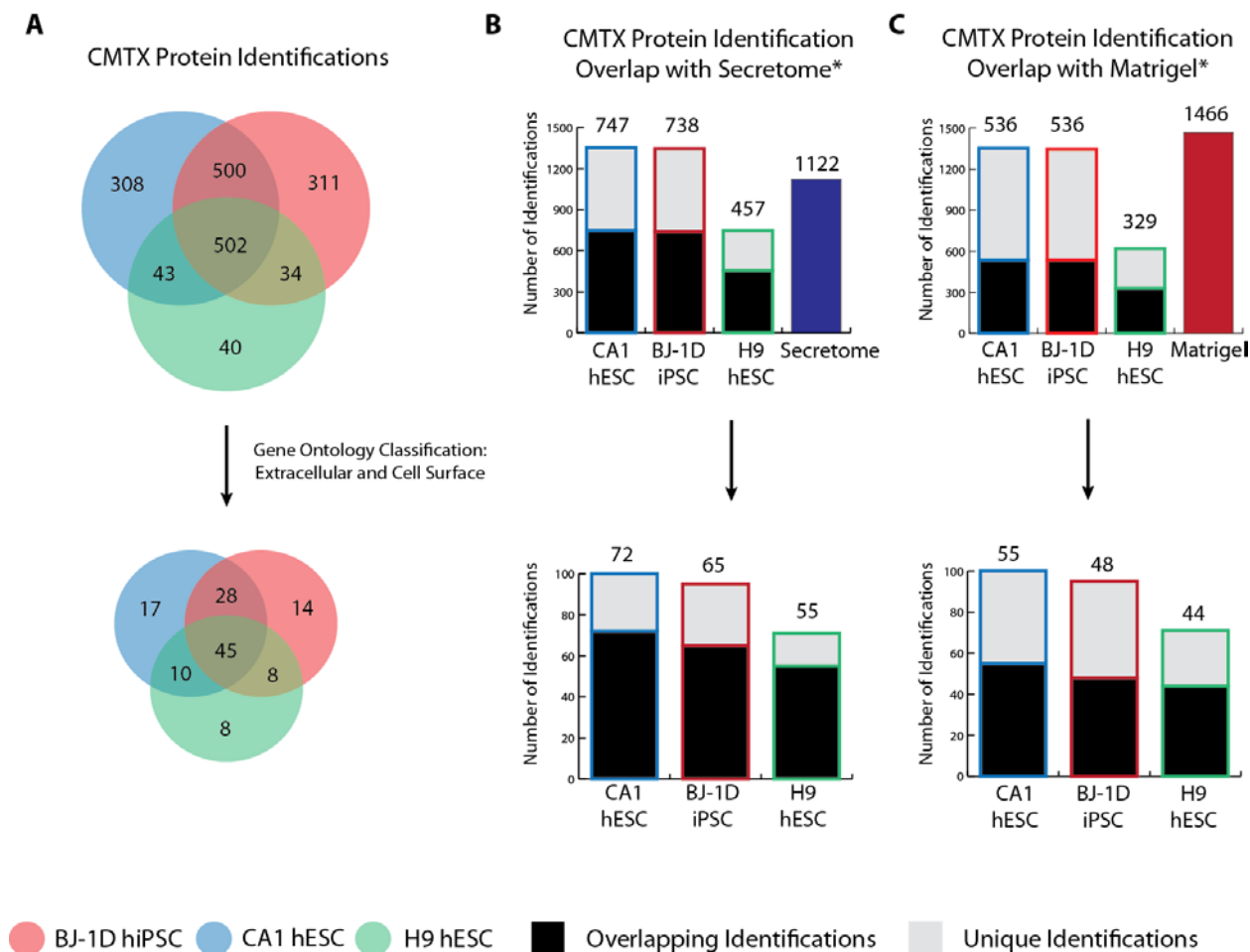
*4.2.2 Secretome Analysis of the hESC Microenvironment.* To further validate and enrich for candidates in the CMTX data, a comparison was performed with a previously published proteomics screen of the H9 hESC secretome obtained from the analysis of hESC conditioned medium [6]. We performed a re-analysis of the H9 hESC secretome raw dataset in the same software (PEAKS 5.3) used to process the CMTX data, to facilitate comparison and minimize variability from protein assignments or identifiers. Comparison with the H9 hESC secretome protein identifiers revealed a 73%, 55%, and 54% overlap between the unfiltered and 77%, 72%, and 68% for the filtered H9, CA1, and BJ-1D CMTX datasets (Figure 4.4 B). These data indicate that although there was a significant variability in the cellular localization of proteins in the unfiltered dataset, this distribution is not unexpected since proteins in the secretome and CMTX datasets share similar profiles. Comparison with the Matrigel™ dataset previously acquired (Chapter 3) revealed that 53%, 40%, and 40% of proteins for H9, CA1, and BJ-1D cell lines are identified in both matrices prior to filtering (Figure 4.4 C). Gene ontology filtered datasets share 62%, 55%, and 50% of proteins with Matrigel™ for H9, CA1, and BJ-1D cell lines. These data illustrate the necessity for SILAC when performing this analysis because many of the proteins found in the CMTX are also found in Matrigel™.

Furthermore, it highlights the ability of this methodology to enhance the sensitivity of our analysis by increasing the confidence in the identification of hESC-derived proteins.

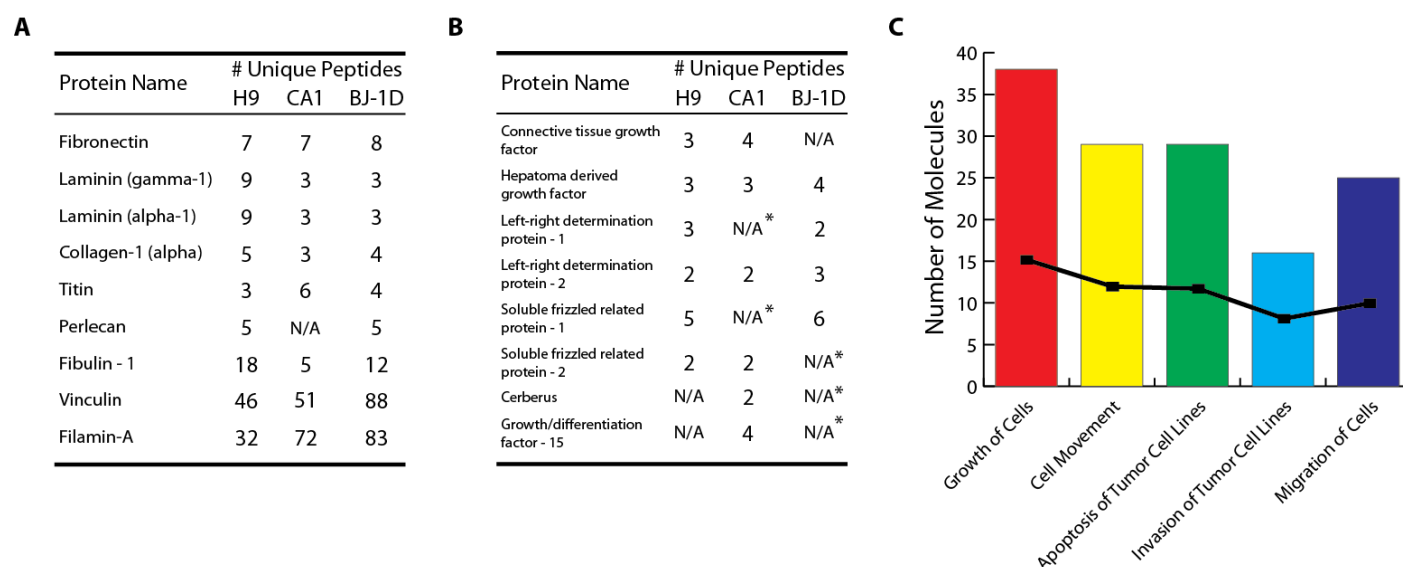
*4.2.3 Factors Identified in Stem Cell Derived CMTX.* As mentioned previously, investigation of the CMTX dataset revealed the presence of numerous hESC and hiPSC regulatory proteins. In order to enrich for hESC and hiPSC derived proteins that are facilitating the maintenance of an undifferentiated state on CMTX, we opted to focus on only those classified as extracellular or cell surface by gene ontology. Not surprisingly, within this filtered dataset we find many core ECM proteins that are also present in Matrigel™ (Figure 4.5 A). The presence of hESC and hiPSC-derived labeled versions of these proteins indicates that the stem cells are generating a self-supporting matrix microenvironment *in vitro*. Further investigation of the filtered CMTX dataset revealed the presence of numerous factors with potential roles in hESC and hiPSC pluripotency (Figure 4.5 B). Other identified factors, such as hepatoma derived (HDGF) and connective tissue growth factor (CTGF) are of particular interest due to their relevance in cancer cell systems, as well as the known interactions of CTGF with the ECM [16-18]. Interestingly, after pathway analysis of the filtered datasets we observe a significant enrichment for molecules involved in cell motility as well as apoptosis or invasion of cancer cells (Figure 4.5 C).

Also of interest in the list of hESC proteins identified are the potential extracellular regulators of hESCs (Figure 4.5 B). The soluble frizzled related proteins (sFRP) 1 and 2 are inhibitors of canonical Wnt signaling [19]. Wnt signaling has been observed to





**Figure 4.4. Proteomic analysis of SILAC hESC and hiPSC derived CMTX.** (A) CMTX from H9 and CA1 hESCs, as well as BJ-1D hiPSCs was analyzed in biological triplicate using an MS-based proteomics protocol. Data files were analyzed using PEAKS 5.3 software. Numbers within the Venn diagrams represent the total number of protein identifications found in each matrix for the specific overlap. Data sets were also filtered using gene ontology classification for cellular component based on the terms “extracellular” and “cell surface”. These values are represented in the lower diagram. (B) CMTX identifications were further compared with a secretome data set acquired through proteomic analysis of hESC conditioned medium. (C) Each data set was individually compared with that previously acquired for Matrigel (Chapter 3). Overlapping identifications are denoted by a black box, and unique identifications are found in grey. The total number of overlapping identifications can be found at the top of the bar in text. All comparisons were done manually based upon protein identifiers. In the case of Matrigel data, protein descriptions were used for comparison as identifiers are species specific. Gene ontology filtered data were compared against entire Matrigel or Secretome data sets. The rightmost bar in the top graphs of (B) and (C) represent total identifications found in Matrigel respectively and the Secretome. \* - datasets can be found in reference 6 and Chapter 3.



**Figure 4.5. Proteins and pathways identified in CMTX from hESCs and hiPSCs.** CMTX was analyzed using an IE-MS proteomics based approach. Proteins were identified using PEAKS 5.3 software. (A) Represents a subset of the core ECM proteins found in CMTX that were also identified in the previous proteomics analysis of Matrigel (Chapter 3). In the case of collagen, the top isoform was chosen. (B) Represents growth factors and proteins known to regulate core hESC pluripotency pathways found in CMTX. \* - indicates when a protein was identified as a single peptide hit. Only proteins with 2 unique peptides are retained, such that these single peptide hits are lost in the final dataset. (C) Pathway analysis performed using Ingenuity Systems Software. The top biological functions identified in all three cell lines were related to cellular movement, growth, and death or invasion of tumor cell lines. Number of molecules denotes the number of candidate proteins identified as being involved with that function found in our dataset. Black boxes represent the  $-\log(p\text{-value})$  for the probability of identifying these pathways as being enriched in our dataset by chance.

contribute to the regulation of both mESCs and hESCs [20]. Extracellular antagonists of Activin/Nodal signaling, left-right determination factors (Lefty) A and B, are also found in the CMTX [21]. Since the Lefty proteins were previously implicated as being involved in the reprogramming of metastatic cells with CMTX, their identification provides additional validation of our proteomics approach [12]. We also identify Cerberus in the CMTX, a regulator of both TGF- $\beta$  and bone morphogenic protein (BMP) signaling. Previous studies directed at the analysis of hESC-derived CMTX have focused on antagonism of the BMP pathway using Gremlin, a protein which shares significant overlap in functionality with Cerberus [14, 21]. The presence of these factors is not surprising since several have previously been identified in screens of MEF and hESC conditioned medium [6]. However, their identification in the CMTX indicates that the ECM is potentially playing a role in their activity.

### 4.3 Discussion

A thorough knowledge of the processes that control the maintenance of pluripotency or differentiation to lineage specific cell types will be critical as hESC research moves toward the clinic. Central to this goal is comprehensive characterization of the extracellular processes governing regulation of hESCs and hiPSCs in their niche. Proteomic analysis of conditioned medium has aided in the development of an understanding of signaling pathways present in the microenvironment. However, few studies have examined the direct interactions of hESCs with the matrix portion of the microenvironment. Utilizing cell culture and proteomics methods developed earlier, we report the characterization of matrices conditioned by hESCs as well as hiPSCs.

The presence of core ECM components in CMTX, such as isoforms of fibronectin, collagen, and laminin illustrates that hESCs and hiPSCs generate a self-supportive niche for attachment and proliferation. All three of these matrix proteins have been shown to promote the growth of hESCs when used as the sole growth support [3, 22-25]. These core proteins regulate critical cellular processes such as cell attachment through integrin binding. Integrin interactions are capable of mediating signal transduction responses similar to those triggered by soluble ligands [26, 27]. Therefore, hESCs potentially utilize these interactions to regulate a diverse array of cellular functions. The presence of these core ECM proteins in the matrix likely promotes these interactions, and explains why matrices that contain them in combination are better at facilitating hESC and hiPSC growth, such as is the case with Matrigel™ [3, 28].

The identification of multiple growth factors and their binding partners in CMTX highlights another potential function for these core fibrous ECM proteins in the matrix. The ECM has been proposed to contribute to the regulation of growth factor signaling in the microenvironment (reviewed in [1]). Central to this function is the presence of specialized domains designed to bind growth factors like VEGF, EGF, HGF, and PDGF on proteins such as fibronectin and laminin. Furthermore, fibronectin has been observed to contribute to TGF- $\beta$  signaling through interaction with latent-TGF- $\beta$  binding proteins [29, 30]. Binding between growth factors and these glycoproteins can also be mediated by interactions with heparan sulfate, a molecule that has been shown to regulate the self-renewal of hESCs [1, 31]. In addition to core ECM proteins, the CMTX also contains an array of binding proteins involved in pathways such as IGF, BMP, and EGF signaling. These binding partners can complement interactions with glycoproteins such as fibronectin. The result of these interactions potentially implicates the ECM in the direction of cellular processes through binding and sequestering of growth factors.

The importance of controlling the activity and concentration of growth factors present in the microenvironment is critical for maintenance of the hESC and hiPSC state. Three key pathways from which we identified regulatory proteins in the CMTX are Wnt, TGF- $\beta$  through Activin/Nodal, and BMP signaling. The sFRP1 and sFRP2 proteins are thought to regulate canonical Wnt signaling through direct binding to the Wnt proteins, although their role in hESCs remains unclear (reviewed in [32]). Wnt signaling through the canonical pathway has been shown to be important in the maintenance of mESC and hESC self-renewal and pluripotency [20]. Lefty A and B are known to regulate TGF- $\beta$  signaling through antagonism of the activating protein Nodal [33]. TGF- $\beta$  activation

through Activin/Nodal signaling is one of the core pathways critical for the maintenance of self-renewal and pluripotency of hESCs [21]. The Lefty proteins were also identified in the original CMTX work involving metastatic cells as a potential regulator of the observed phenotype, acting through hESC-derived matrix deposition [12]. Inhibition of BMP mediated activation of TGF $\beta$  signaling also promotes the maintenance of hESC pluripotency. BMP activates SMAD1/5/8 mediated TGF- $\beta$  pathways that have been implicated in the differentiation of hESCs [21]. Cerberus is an inhibitor of BMP mediated activation that acts through antagonism of BMP-4 [34, 35]. Interestingly, Cerberus has also been shown to inhibit Nodal as well as Wnt signaling pathways [35, 36].

The identification of sFRP1 and sFRP2 as well as the Lefty A and Lefty B proteins further validates the ability of our CMTX proteomic analysis to identify potential regulators of hESC fate. Aside from their activity in the regulation of core hESC pluripotency pathways, both sFRP and Lefty proteins are known to be matrix deposited [37, 38]. Taken together, the findings of this study highlight the ability of MS-based proteomics screening of CMTX to determine *in vitro* effectors of hESC control involving the ECM microenvironment.

## 4.4 Methods

*4.4.1 Cell culture and harvest* – H9 (passage 26) and CA1 (passage 20) hESCs, and BJ-1D (passage 65) iPSCs were maintained on CF-1 irradiated mouse embryonic fibroblast (MEF) feeder layers (GlobalStem, Rockville, MD) using media composed of knockout DMEM/F12, 20% knockout serum replacement, 1% non-essential amino acids, 2mM glutamine (CellGro, Manassas, VA), 0.1 mM 2-mercaptoethanol (Fisher, Toronto, ON), and 4 ng/mL of basic fibroblast growth factor. All media reagents were obtained from Invitrogen unless noted otherwise. H9 cells were obtained from WiCell (WISC, Wisconsin). The CA1 hESC line used in all experiments was obtained from Dr. Cheryle Séguin of The University of Western Ontario [39, 40]. The hiPSC line BJ-1D was derived by reprogramming using retroviral transduction of BJ fibroblasts with the Yamanaka factors essentially as we have previously described [41] and validated as pluripotent using in vitro and in vivo differentiation assays and expression profiling (unpublished results). Cells were passaged mechanically in all experiments and for general maintenance.

For SILAC experiments, hESC and hiPSC cell lines were grown in feeder-free conditions on Matrigel™ (BD Biosciences, Franklin Lake, NJ). Custom DMEM/F12-glutamax that contained no L-arginine or L-lysine was ordered from Invitrogen. SILAC medium was prepared using the StemPro hESC Media system with our custom DMEM/F12 (Invitrogen) according to manufacturer instructions. [ $^{13}\text{C}_6$ ,  $^{15}\text{N}_4$ ] – L-arginine and [ $^{13}\text{C}_6$ ,  $^{15}\text{N}_2$ ] – L-lysine (Cambridge Isotope Laboratories, Andover, MA) were

supplemented into the SILAC medium at 90mg/L and 92mg/L respectively. Unlabeled L-proline was added to the SILAC medium at a final concentration of 800 mg/L [42].

Embryoid bodies (EB) were generated using Aggrewell 400Ex plates (StemCell Technologies, Vancouver, Canada). Briefly,  $2 \times 10^6$  hESCs were harvested enzymatically using Accutase (Invitrogen) from Matrigel™ coated plates. Cells were reconstituted in Aggrewell medium supplemented with Rock inhibitor (Y-27632, Sigma-Aldrich, St. Louis, MO) at a final concentration of 10  $\mu$ M. After plating in Aggrewell dishes, EBs were grown for 48 hours at 37°C prior to transfer to ultra-low adherence tissue culture dishes (Corning, Lowell, MA). After 15 days of culture, EB RNA was harvested using Trizol extraction according to the manufacturer's instructions (Invitrogen). EBs were assayed for expression of CDX2, alpha-feto protein (AFP), GATA-6, GATA-4, Oct3/4, PAX-6, T-brachyury, Nanog, and Neurogenic differentiation 1 (NeuroD1) using TaqMan primer probe sets (Invitrogen). Details of this assay can be found in Appendix Table 1.15. All EB assays were performed in biological and technical duplicate for each cell line and each condition.

*4.4.2 Generation and Harvest of Conditioned Matrix* – H9, CA1, or BJ-1D stem cells were grown in feeder-free conditions on Matrigel™ in heavy-isotope containing SILAC medium for 7 days prior to passaging to plates for CMTX preparation. SILAC labeled stem cells were permitted to grow for a period of 5 days on Matrigel™ in SILAC medium for generation of CMTX. Wells were then rinsed thoroughly with PBS to ensure removal of medium components and cells removed from the Matrigel™ layer using Cell Recovery Solution according to the manufacturer's instructions (BD Biosciences). The



remaining CMTX layer was incubated in a solution containing 8 M urea, 100 mM ammonium bicarbonate (ABC), and 1 M NaCl for 24 hours at 4°C. After the removal of stem cells by spinning, the cell recovery solution was combined with the urea solution and concentrated using high-capacity C18 cartridges (Phenomenex, Torrance, CA). Eluted components were dried using a SpeedVac and reconstituted in 8 M urea with 100 mM ABC for analysis by 1D-SDS-PAGE, strong cation exchange (SCX), or strong anion exchange (SAX) fractionation. CMTX was analyzed in technical duplicate and biological triplicate for each cell line.

*4.4.3 In-solution trypsin digestion* – Matrix samples were reduced with 10 mM dithiothreitol (DTT) for 60 minutes. Samples were then alkylated with 40 mM iodoacetamide (IAA) for 60 minutes. The reactions were quenched through the addition of DTT and left to incubate for another 60 minutes. Samples were then diluted 1/6 in 50 mM ABC. Trypsin (Promega, Madison, WI) at a concentration of 1 µg enzyme to 25 µg of total protein was added to the mixtures and left to incubate for 24 hours at 37°C. The next day, digests were acidified using neat trifluoroacetic acid and desalted on C18 cartridges (Phenomenex, Torrance, CA). After elution with 50% acetonitrile, samples were evaporated using a SpeedVac. Dried samples were reconstituted in 0.5% formic acid at a pH of ~2 prior to loading on an SCX column. Samples for SAX analysis were reconstituted in 0.5% NaOH at a pH of ~12.

*4.4.4 Column preparation* – Columns were packed in 360 O.D. x 200 I.D. capillaries (PolyMicro Technologies, Phoenix, AZ) using a conventional pressure bomb (Next Advance, Averill Park, NY). Frits were prepared by mixing 75 µL of potassium silicate

with 25  $\mu\text{L}$  of formamide, vortexing for 1 minute and rapidly inserting and removing the capillary end from the resulting mixture. Capillary frits were dried in a  $100^{\circ}\text{C}$  oven for 2 hours. Capillaries were then rinsed with forward and reverse flow of methanol using the pressure bomb at 200 psi. Prior to packing, capillaries were rinsed for 30 minutes with 0.5% formic acid or 0.5% NaOH for SCX and SAX respectively. PolySULFOETHYL A SCX beads (5  $\mu\text{M}$ , 300 $\text{\AA}$ , CAT# PLBMSE0503) were purchased from PolyLC (Columbia, MD) and reconstituted in 50% MeOH. SAX beads were purchased from Varian Inc. (10 $\mu\text{m}$ , 1000 $\text{\AA}$ , CAT# PL1451-2102, Palo Alto, CA) and used in the vendor supplied buffer. SCX and SAX columns were packed to a length of 3 cm for all experiments. All packing was done at a pressure of 200 psi until the desired column length was obtained, then pressurized to 1000 psi to complete packing. Packed columns were rinsed with solvents for conditioning as recommended by the manufacturer.

*4.4.5 Peptide Fractionation* – Peptides were fractionated off of SCX and SAX columns using a CapLC system (Waters, Milford, MA) with a flow rate of 2  $\mu\text{L}/\text{min}$ . Mobile phase A was composed of 20 mM citric acid at a pH of  $\sim 2.3$ , mobile phase B was pH 11.4 20 mM  $\text{NH}_4\text{OH}$ . Mobile phases were all prepared fresh prior to fractionation to ensure the stability of pH from run to run. Fractionation with pH was carried out using a 120 minute gradient from pH 2 to 12 for SCX, and 12 to 2 for SAX. Each fraction was collected offline at a volume of 20  $\mu\text{L}$ . Fractions were dried using a SpeedVac, and reconstituted in 10% formic acid prior to injection on the MS.

*4.4.6 In-gel trypsin digestion* – 60 µg of conditioned matrix was diluted in Laemmli buffer. Matrix samples were loaded in each of two lanes on a 10% SDS-Gel. After staining of the gel with Coomassie blue, gel lanes were divided into fractions based on visual assessment of protein concentration. Gel cubes in each fraction were destained using 20% acetonitrile (ACN) in 1 M ABC. Proteins were reduced using 10 mM DTT for 60 minutes, followed by alkylation with 100mM IAA for 60 minutes. Digestions were carried out using trypsin at a 1/25 ratio overnight in a 37°C water bath. Fractions were extracted the next day using 10% formic acid and ACN with sonication. Each fraction was dried using a SpeedVac and reconstituted in 10% formic acid prior to injection on the MS.

*4.4.7 MS analysis* – Fractions were injected and separated using a nanoAcquity system (Waters, Milford, MA) equipped with a 25 cm x 75 µm I.D. C18 column. Fractions were separated using a 1 to 40% ACN gradient over 150 minutes at a flow rate of 300 nL/min. MS analysis was done on a Q-ToF Ultima (Micromass/Waters) using data-dependent acquisition with selection of the four top precursor masses per survey scan. Survey scans were set at 1 s, and MS/MS acquisition set at 1 s or 8000 cps TIC cut-off. Exclusion lists were generated using in-house software that automatically adds 0.7 amu to the precursor masses selected in previous runs and outputs a file also containing retention time information. Each fraction was analyzed for a four exclusion rounds (5 injections total), adjusting the injection volume dependent on signal intensity in the MS survey scan.

*4.4.8 Proteomic Data analysis* – Data analysis for all samples was performed in PEAKS 5.3 software (Bioinformatics Solutions Inc., Waterloo, Canada) [43, 44]. After import into PEAKS, MS/MS spectra from raw data files were refined using the following settings: merge spectra – true (100 ppm mass tolerance, 60 second retention time tolerance), correct precursor mass – true, determine precursor charge state – true (minimum charge +2, maximum charge +5), spectral quality filter – true (0.65 threshold), centroid, deisotope, and deconvolute – true. Resulting MS/MS spectra were then *de novo* sequenced using the following parameters: parent monoisotopic mass tolerance – 100ppm, fragment monoisotopic mass tolerance – 0.15 daltons, enzyme specificity – semi-Trypsin, fixed modifications – carbamidomethylation and +10 daltons on Arginine and +8 daltons on Lysine for SILAC, variable modifications – N-terminal acetylation and oxidized methionine. After *de novo* analysis, data were searched against the UniProt sequence database (Human taxonomy specified, 20236 total entries) using the following parameters: parent monoisotopic mass tolerance – 100 ppm, fragment monoisotopic mass tolerance – 0.15 daltons, enzyme specificity – semi-Trypsin, fixed modifications – carbamidomethylation and +10 daltons on Arginine and +8 daltons on Lysine for SILAC, variable modifications – N-terminal acetylation and oxidized methionine, estimate false-discovery rate – true.

Resultant protein identification data from the database search were further processed using PEAKS 5.3 software. Proteins were filtered by assigned score to give a <1.0% false-discovery rate for peptide-spectral matches based on estimation from a decoy-fusion method of database search. Identified proteins were also required to be derived by >2 unique peptides. Proteins that contained similar peptides and could not be

differentiated based on MS/MS analysis alone were grouped to satisfy the principles of parsimony. For all matrices analyzed, keratin hits were manually removed from the final datasets. Gene ontology analysis was performed using STRAP software (CPC Tools).

*4.4.9 Real-time PCR* – RNA was purified using Trizol reagent according to the manufacturer's instructions (Invitrogen) with the following modification: precipitated RNA pellets in isopropanol were centrifuged for 60 minutes at 12000 g at room temperature. After NanoDrop quantification, 1 µg of cDNA was synthesized using the High Capacity cDNA Reverse Transcription Kit with RNase inhibitor (Invitrogen). Real-time PCR was performed using the TaqMan® Universal PCR Master Mix (Invitrogen). Samples were incubated at 50°C for 2 minutes followed by 10 minutes at 95°C. DNA was then amplified at 95°C for 15 seconds followed by 1 minute at 58°C for 46 cycles. All samples were normalized to the large ribosomal protein RPLPO as a positive control. All primers were obtained from Invitrogen and details of the assay can be found in Appendix Table 1.15. Each biological replicate was run in triplicate for every marker assayed. All reagents were used according to the manufacturer's instructions.

*4.4.10 Flow Cytometry* – All reagents and probes for flow cytometry were obtained from eBiosciences (San Diego, CA) unless noted otherwise. Cells were enzymatically harvested using Accutase (Invitrogen) to obtain a single cell suspension. After centrifugation, cell pellets were resuspended in 5% FBS in PBS. Alexa-488 conjugated SSEA-4 and Alexa-647 conjugated SSEA1 were diluted into the cell mixture according to the manufacturer's instructions. Negative control samples contained respective isotype controls for the primary antibodies used. Solutions were incubated for 2 hours

and analyzed using an Accuri C6 (BD Biosciences) flow cytometer after rinsing to remove unbound antibody. Populations were gated according to forward and side scatter patterns with filtering for viable cells using 7-aminoactinomycin D staining. Data was analyzed using FlowJo software (Tree Star, Ashland, OR).

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## Chapter 5

### Functional Characterization of hESC-Derived CMTX

#### 5.1 Introduction

The two defining characteristics of human embryonic stem cells (hESC), self-renewal and pluripotency, are maintained by a delicate balance of intracellular and extracellular signaling processes. Extracellular regulation is primarily the result of changes in the microenvironment surrounding the cells during growth *in vitro* or *in vivo*. hESCs interact with this 'niche' through support cells, extracellular matrix (ECM) components, and autocrine/paracrine signaling (reviewed in [1-3]). Modulation of any of these supportive elements individually or in combination has been used extensively to alter hESC behavior [1-3]. For example, exogenous growth factor supplementation is used to facilitate the maintenance of hESCs as well as to induce their differentiation. Moreover, recent studies have illustrated that hESC self-renewal and differentiation can be altered through modulation of the properties of the ECM using synthetic mimics, highlighting its importance in the microenvironment (reviewed in [4]).

This chapter contains excerpts from the following paper:

Hughes, C.S., Radan, L., Stanford, W., Betts, D., Postovit, L.M., Lajoie, G.A.. (2012) "Proteomics Analysis of the Human Embryonic Stem Cell Depositome". (In Preparation)

A number of proteomics studies have been conducted to determine factors secreted by feeder layers in an attempt to elucidate proteins and pathways essential for hESC survival [5-8]. Currently only one of these studies has identified members of the soluble frizzled related protein (sFRP) family [9]. As part of our proteomics investigation into the components of CMTX, we identified sFRP1 and 2 across multiple cell lines. The sFRP family of proteins has been shown to regulate canonical Wnt signaling through direct binding to the secreted Wnt cytokines [10]. Central to this role is the direct interaction of sFRP1 and sFRP2 with Wnt3a [11]. The Wnt family is a group of secreted glycoproteins consisting of 19 members that contain 22 - 24 conserved cysteine residues (reviewed in [12]). Wnt signaling plays a prominent role during development and its aberrant regulation plays a role in multiple disease phenotypes (reviewed in [13]).

In humans, the sFRP family is made up of 5 members, sFRP1 – 5 [14]. The sFRPs were originally discovered due to their shared sequence similarity with the frizzled receptors that are directly involved with Wnt signaling [15, 16]. This family now constitutes the largest group of Wnt antagonists [17]. Structurally, the sFRP proteins contain two distinctive domains, an N-terminal cysteine rich domain (CRD) and a C-terminal netrin-like domain [18]. The CRD contains ten conserved cysteine residues and shares a significant similarity with the extracellular domain of the frizzled receptors [19]. The C-terminal netrin domain is postulated to confer heparin binding properties [18, 20, 21]. The primary interest in the sFRPs however, stems from the properties of the N-terminal CRD, that because of the sequence homology with the frizzled receptors,

has been proposed to bind Wnt proteins. This ability to bind Wnt proteins has subsequently been verified and intensely studied since that time (reviewed in [17]).

The sFRP family of proteins have been shown to encompass a diverse profile of expression patterns and context dependent interactions in a variety of tissues and cellular systems (reviewed in [22]). However, although sFRPs family members are known to be important during embryonic development, very little is known about their role in the regulation of ESCs [22]. This is surprising when it is considered that Wnt signaling has been shown to be involved in the direct regulation of the pluripotent state of ESCs (reviewed in [23]). Furthermore, in a recent study comparing 59 different hESC lines a positive correlation between Nanog and sFRP2 gene expression was observed [24]. In addition, sFRP2 was identified as a potential target for Nanog in CHIP on CHIP analyses of hESCs [25]. Taken together, these findings indicate that sFRP family members are potentially playing a vital role in hESC pluripotency.

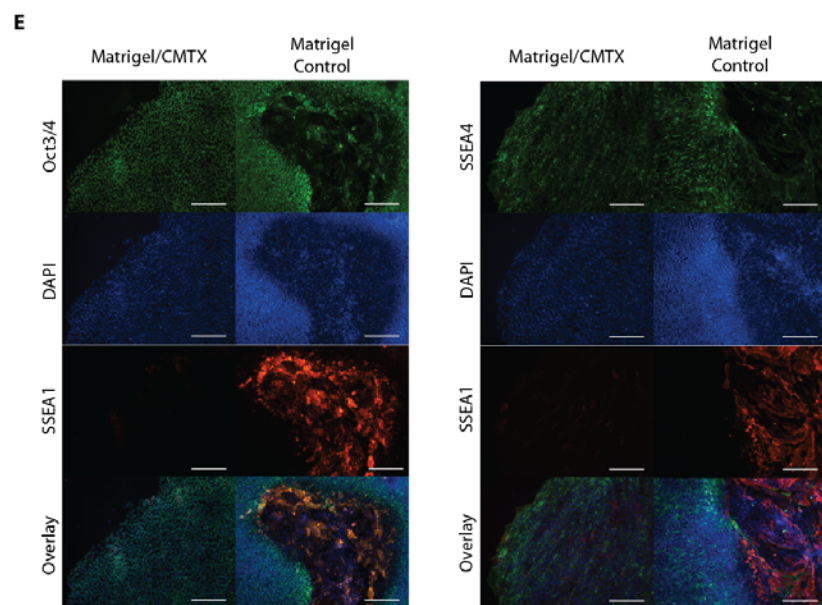
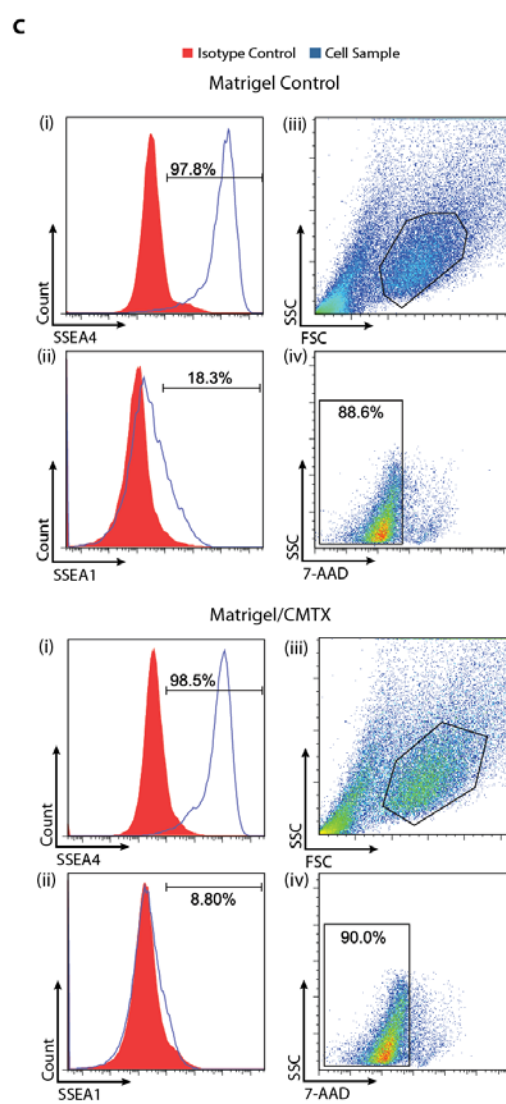
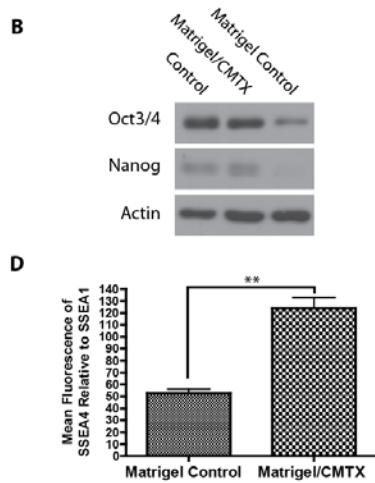
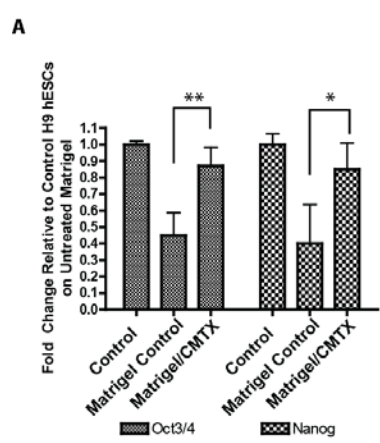
Here we investigate the ability of hESC conditioned matrix (CMTX) to enhance the maintenance of undifferentiated stem cells. To identify and characterize factors potentially responsible for this effect, we utilize the data generated in our proteomics screen of CMTX (Chapter 4) to validate the role of sFRP1 and sFRP2. A combination of techniques is used to characterize the role of the sFRP candidates in the regulation of hESC pluripotency *in vitro*. Additionally, utilizing a metastatic melanoma cell line we demonstrate the effects of exogenous supplementation of sFRP1 and sFRP2. This work represents the first investigation of the hESC and hiPSC matrix microenvironment.

## 5.2 Results

*5.2.1 hESC Derived Matrix for the Maintenance of an Undifferentiated State.* The ability of embryonic microenvironments to suppress the tumorigenic phenotype has been previously illustrated in a number of developmental and cellular systems (reviewed in [26]). However, a limited number of studies have focused on reprogramming stem cells with these same microenvironments. Analogous to metastatic cells, embryonic stem cells can direct cellular changes in response to cues from their microenvironment. With the recent observation that a hESC-derived matrix microenvironment could modulate the behavior of metastatic cells [27], we sought determine what effect exposure would have on the stem cell phenotype. To this end, we monitored changes in the gene and protein expression of hESCs grown on CMTX in the absence of exogenous growth factor supplementation. In this way, matrix dependent changes in hESC behavior could be monitored without interference from soluble factors present in MEF-CM.

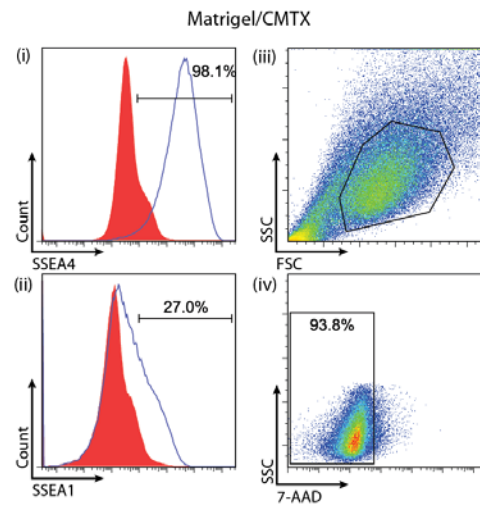
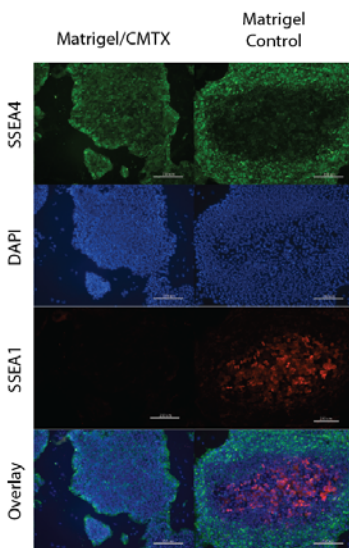
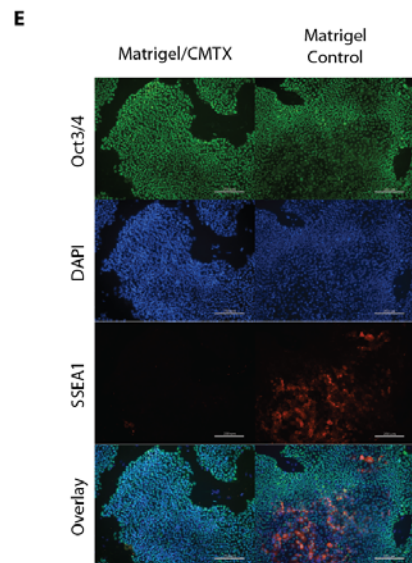
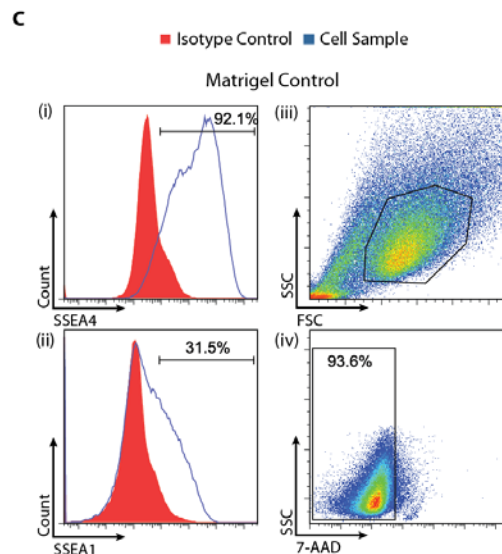
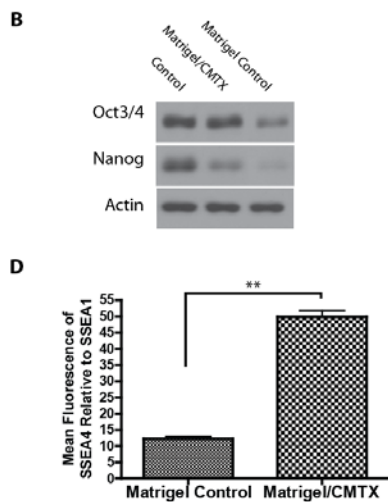
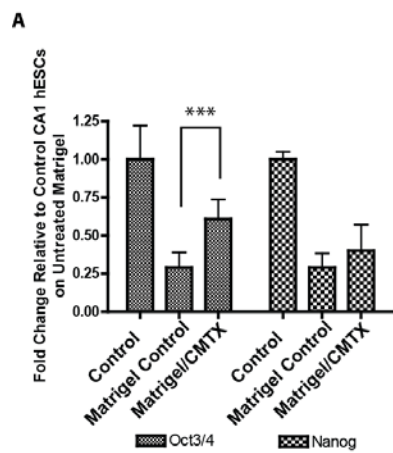
After 4 days of culture in medium that contained no exogenous bFGF (embryoid body medium, EB medium), a decrease in Oct3/4 and Nanog gene and protein expression was observed for H9 hESCs grown on control Matrigel™ and CMTX. However, the reduction in expression was significantly smaller in H9 hESCs grown on CMTX when compared with control cells (Figure 5.1 A-B). A similar trend was observed when H9 hESCs were measured using flow cytometry for SSEA4 and SSEA1 fluorescence. H9 hESCs induced to differentiate on CMTX exhibited an increase in SSEA4 mean fluorescence intensity relative to SSEA1 when compared with control cells (Figure 5.1 C-D). When cultures were examined by immunofluorescence, pockets of SSEA1

**Figure 5.1. hESC generated CMTX enhances the maintenance of an undifferentiated state in H9 cells when compared to those grown on Matrigel™.** Matrigel™/CMTX was generated by growing H9 hESCs on Matrigel™ for 4 days. Following cell removal, fresh H9 hESCs were plated on the CMTX layers. Control Matrigel™ was generated by treating normal Matrigel™ with the cell removal procedure prior to the plating of fresh hESCs as discussed in the Methods. Cells in both conditions were fed with medium not containing bFGF for 4 days. Control samples are hESCs grown on normal Matrigel™ in MEF-CM. (A) RT-PCR data for H9 hESCs cultured on control Matrigel™ and Matrigel™/CMTX. Values represent fold change of Oct3/4 or Nanog expression relative to control hESCs cultured under standard conditions. RPLPO was used as an internal control for both samples. Error bars represent SEM, n=3. (B) Western blot for Oct3/4 and Nanog in H9 hESCs grown on CMTX. Actin is shown as a control. (C) Flow cytometry data for H9 hESCs grown on CMTX. For each sample, plot (i) shows SSEA4 fluorescence (blue) relative to a matched isotype control (solid red), (ii) shows SSEA1 fluorescence relative to isotype control, (iii) scatter plot with the gated cell population shown, (iv) scatter plot with the viable cell population gated. Percentages denote fraction of cells within the gates shown. (D) Results from flow cytometry analysis of H9 hESCs grown on CMTX for the markers SSEA4 and SSEA1. Values represent mean fluorescence intensity of SSEA4 relative to SSEA1 for Matrigel™ Control or Matrigel™/CMTX samples. Values are derived from the data in (C). Error bars represent SEM, n=3. (D) Immunocytochemistry for H9 hESCs grown on Control Matrigel™ or Matrigel™/CMTX. Cells were stained with Oct3/4, SSEA4, DAPI, and SSEA1. Scale bars represent 250um.



**Figure 5.2. hESC generated CMTX enhances the maintenance of an undifferentiated state in CA1 cells when compared to those grown on Matrigel™.** Matrigel™/CMTX was generated by growing CA1 hESCs on Matrigel™ for 4 days. Following cell removal, fresh CA1 hESCs were plated on the CMTX layers. Control Matrigel™ was generated by treating normal Matrigel™ with the cell removal procedure prior to the plating of fresh hESCs as discussed in the Methods. Cells in both conditions were fed with medium not containing bFGF for 4 days. Control samples are hESCs grown on normal Matrigel™ in MEF-CM. (A) RT-PCR data for CA1 hESCs cultured on control Matrigel™ and Matrigel™/CMTX. Values represent fold change of Oct3/4 or Nanog expression relative to control hESCs cultured under standard conditions. RPLPO was used as an internal control for both samples. Error bars represent SEM, n=3. (B) Western blot for Oct3/4 and Nanog in CA1 hESCs grown on CMTX. Actin is shown as a control. (C) Flow cytometry data for CA1 hESCs grown on CMTX. For each sample, plot (i) shows SSEA4 fluorescence (blue) relative to a matched isotype control (solid red), (ii) shows SSEA1 fluorescence relative to isotype control, (iii) scatter plot with the gated cell population shown, (iv) scatter plot with the viable cell population gated. Percentages denote fraction of cells within the gates shown. (D) Results from flow cytometry analysis of CA1 hESCs grown on CMTX for the markers SSEA4 and SSEA1. Values represent mean fluorescence intensity of SSEA4 relative to SSEA1 for Matrigel™ Control or Matrigel™/CMTX samples. Values are derived from the data in (C). Error bars represent SEM, n=3. (E) Immunocytochemistry for CA1 hESCs grown on Control Matrigel™ or Matrigel™/CMTX. Cells were stained with Oct3/4, SSEA4, DAPI, and SSEA1. Scale bars represent 250um.





positive cells could be observed in control cells, indicating differentiation (Figure 5.1 E). SSEA1 positive colonies were observed with a reduced frequency in cells cultured on CMTX. Subsequent analysis of a second hESC line, CA1, revealed similar trends (Figure 5.2 A-E). Taken together, these data indicate that CMTX promotes the preservation of an undifferentiated state and hESCs secrete factors into the matrix that are beneficial for their own maintenance.

*5.2.2 Generation and Testing of an Artificial CMTX.* To functionally validate the proteomics method for profiling the CMTX to identify hESC regulatory proteins, we investigated the roles of sFRP1, sFRP2, Lefty A, and Gremlin further. These proteins were selected on the basis of their suspected roles in hESC regulation as well as their previous implications in CMTX studies involving metastatic cells [27-29]. Moreover, these proteins were not identified in Matrigel™ itself, making their functional validation possible in a CMTX assay that utilizes this matrix without background interference. To determine the potential roles of these candidates in the CMTX, we repeated the hESC CMTX experiments utilizing two separate platforms for analysis.

We first sought to determine if supplementation of recombinant proteins to the matrix, in the absence of conditioning prior to hESC plating, could enhance the maintenance of an undifferentiated state. Recombinant versions of sFRP1 and sFRP2, Lefty A, and Gremlin were supplemented into Matrigel™ at a maximum concentration of 5µg/mL prior to gelation. To ensure maximal recombinant protein incorporation into the matrix, undiluted Matrigel™ was used in all assays to coat culture dishes. The Matrigel™™ layer was then treated with the lysis-free cell removal process (see Chapter 4) prior to

hESC plating to ensure reproducibility with the previous experiments. In H9 hESCs, supplementation with any of the selected proteins did not significantly enhance the expression of the markers of pluripotency Oct3/4 and Nanog (Figure 5.3 A). Alone or in combination, none of the proteins were able to fully replicate the effect observed on CMTX. Similar trends are seen in the CA1 hESC line, where individually or in combination, the matrix supplemented proteins are unable to promote maintenance of an undifferentiated state (Figure 5.3 C). In immunoblotting for Oct3/4 and Nanog we observe analogous changes in Oct3/4 and Nanog protein abundance in both H9 and CA1 hESCs (Figure 5.3 E). These data suggest that sFRP1, sFRP2, Gremlin, and Lefty A are unable to replicate the effects observed on hESC-derived CMTX. However, previous studies have shown that recombinant proteins are not as effective as their equivalent hESC-derived versions [27].

Antibody blocking experiments were performed to further investigate the potential role of the sFRP and Lefty proteins in the CMTX. CMTX was generated by growing H9 or CA1 hESCs on Matrigel™ as before. After cell removal, CMTX was treated with antibodies specific for sFRP1, sFRP2, or Lefty A candidates, individually or in combination, to generate a 'knockdown' CMTX. Unbound antibody was removed by washing and fresh hESCs were plated and grown in EB medium. In this way, sFRP or Lefty proteins that had been deposited in the CMTX during hESC growth would no longer be available for interaction with the newly plated cells. Monitoring changes in gene expression and protein abundance of Oct3/4 and Nanog revealed that none of the antibody treatments promoted a reduction in the maintenance of an undifferentiated state of H9 hESCs when compared with a secondary antibody control (Figure 5.3 B, F). Assay of the CA1

**Figure 5.3. Characteristics of hESCs on recombinant and knockdown CMTX.** Recombinant CMTX was generated by supplementing Matrigel™ with recombinant versions of sFRP1, sFRP2, Lefty, or Gremlin alone or in combination. Knockdown CMTX was made by incubating hESC-derived CMTX with antibodies specific for sFRP1, sFRP2, or Lefty A and Lefty B prior to plating of fresh hESCs. (A) Oct3/4 and Nanog expression in H9 hESCs grown on Recombinant CMTX as determined by RT-PCR. Values represent fold change relative to hESCs grown on Control Matrigel™ (treated with the cell removal process, but not supplemented with recombinant protein). Error bars indicate SD, n=3. (B) Oct3/4 and Nanog expression in H9 hESCs grown on Knockdown CMTX as determined by RT-PCR. Values represent fold change relative to hESCs grown on Matrigel™/CMTX (hESC-derived CMTX treated with the cell removal process, not treated with antibody). Error bars represent SD, n=3. Secondary denotes CMTX treated with a secondary antibody as a control (C) Oct3/4 and Nanog expression in CA1 hESCs on Recombinant CMTX. Error bars indicate SD, n=5. (D) CA1 hESCs on Knockdown CMTX. Error bars indicate SD, n=4. All RT-PCR experiments used RPLPO as an internal control for each sample. (E) Western blots for Oct3/4 and Nanog in H9 and CA1 hESCs grown on Recombinant CMTX. Actin is shown as a control. (F) Western blots for Oct3/4 and Nanog in H9 and CA1 hESCs grown on Knockdown CMTX. Actin is shown as a control.



hESC line revealed identical trends to the H9 cell line (Figure 5.3 D, F). Taken together, these experiments indicate that the sFRP and Lefty proteins do not solely modulate the state of hESCs on the CMTX. This suggests that there are other factors potentially acting to enhance undifferentiated hESC maintenance on CMTX. However, it is also possible that the antibodies utilized are potentially unable to block the function of the selected proteins, or are unable to bind if the target is localized in the matrix.

*5.2.3 Roles of sFRP Proteins in hESC Pluripotency.* Canonical Wnt signaling is a critical pathway with characterized roles during development as well as in ESCs themselves (reviewed in [12]). However, the regulation of hESC pluripotency through Wnt signaling is poorly understood, specifically how the pathway is controlled in the extracellular space. The sFRP family of proteins are known Wnt antagonists whose differential expression has been shown to have significant effects in a variety of cell types and pathological conditions (reviewed in [17]). Interactions between the sFRPs and hESCs and the resultant effects on self-renewal or differentiation are inadequately characterized. Given the importance of Wnt signaling in developmental processes, we chose to investigate the role of the sFRP1 and sFRP2 in the maintenance and regulation of hESC pluripotency.

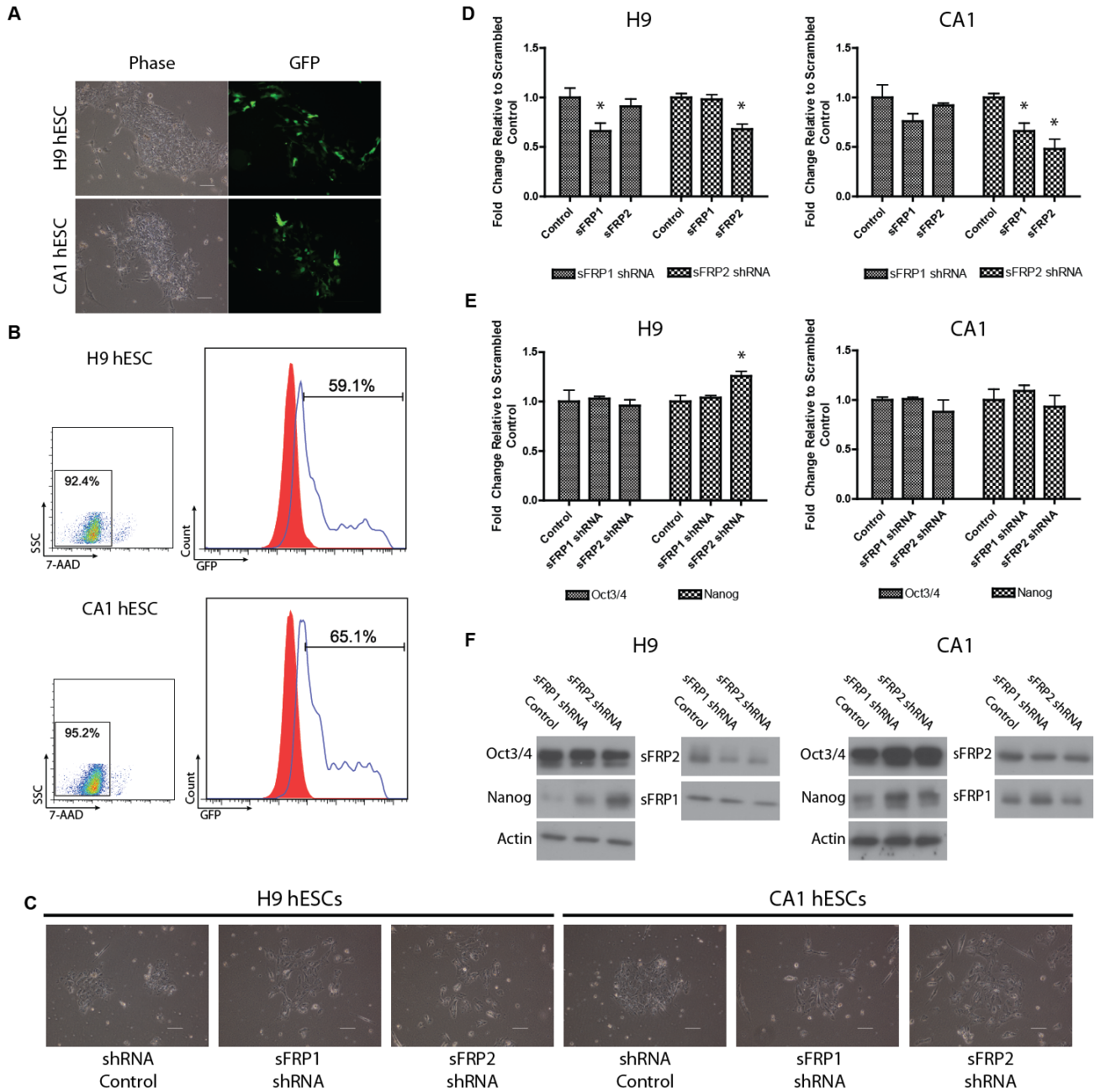
To measure the effect of sFRP1 and sFRP2 on hESC behavior, we employed shRNA mediated knockdowns of each target gene. Initially we attempted to utilize the tetracycline inducible vector, pTRIPZ (Open Biosystems). An inducible system was chosen to permit generation of a homogenous population of undifferentiated cells should our shRNA promote differentiation. We successfully generated stable lines in

HEK293 cells and subsequently verified sFRP1 and sFRP2 knockdown. However, after production of stable H9 and CA1 hESC lines, we were unable to induce shRNA or reporter gene expression using doxycycline in any of the clones tested. Since the puromycin resistance and shRNA genes are on separate promoters, the effect we observe is potentially the result of promoter silencing, a common occurrence in hESCs [30]. To overcome this problem, we utilized a separate tetracycline inducible vector system known as pSUPERIOR. Along with the tetracycline repressor vector, pTetRnls, pSUPERIOR had previously been used to generate stable inducible Oct3/4 shRNA expressing cell lines [31]. However, although we were able to successfully generate stable H9 and CA1 lines, the cells grew poorly under dual-antibiotic selection and were prone to differentiation.

Because of these difficulties, we decided to employ a transient expression of our shRNAs in hESCs. Transient knockdown of gene expression in hESCs is challenging due to the poor efficiency of transfection of these cells. Using cationic lipid based transfection of H9 and CA1 hESCs we were able to achieve >60% efficiency based on GFP reporter expression (Figure 5.4 A-B). Expression of the shRNA constructs could be maintained by transfection on multiple days during experimentation as we did not observe a global reduction in viability as a result of the protocol (Figure 5.4 B). However, when examining colonies that contained small numbers of cells in conditions containing sFRP1 and sFRP2 shRNAs (<10 total cells), we observed a significant reduction in viability in both H9 and CA1 hESCs compared with controls (Figure 5.4 C). Using transient expression of our shRNA constructs, we were only able to obtain ~30% knockdown for both sFRP1 and sFRP2 based on gene expression in H9 and CA1

**Figure 5.4. shRNA mediated knockdown of sFRP1 and sFRP2 expression.** sFRP1 and sFRP2 expression were individually knocked down in H9 and CA1 hESCs using pSUPERIOR plasmid containing shRNA constructs against target transcripts. (A) Phase contrast and fluorescence images of H9 and CA1 hESC colonies transfected with pSUPERIOR plasmid expressing GFP and a scrambled shRNA control. Scale bars represent 250um. (B) Efficiency of transfection using flow cytometry detection of GFP positive cells after treatment. Smaller plots show viability using 7-AAD staining. N=2 for both cell lines. (C) Phase contrast images demonstrating the poor viability of small hESC colonies following transfection compared with scrambled control hESC lines. Scale bars represent 250um. (D) Knockdown of sFRP1 and sFRP2 expression in H9 and CA1 hESCs as measured by RT-PCR. Values are fold change relative to control samples transfected with a scrambled shRNA. Error bars depict SD, n=3. (E) Oct3/4 and Nanog expression in knockdown cells as determined by RT-PCR. Error bars show SD, n=3. For all RT-PCR experiments RPLPO is used as an internal sample control. (F) Immunoblot for Oct3/4, Nanog, sFRP1, and sFRP2 in knockdown and control H9 and CA1 hESCs. Actin is shown as a control for both cell lines.



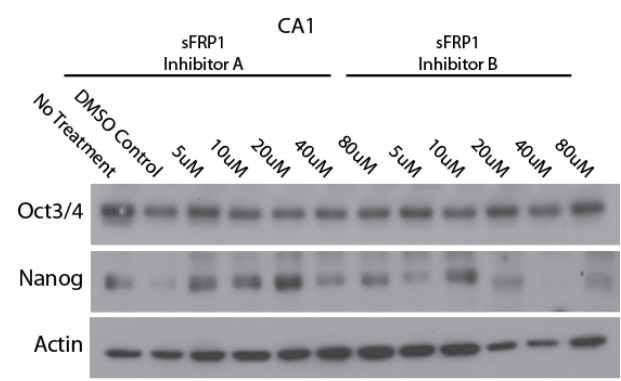
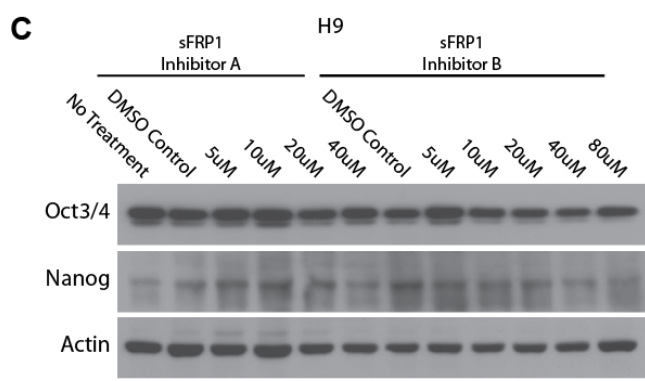
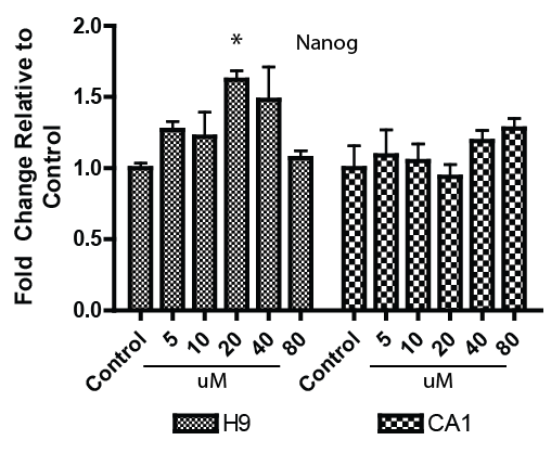
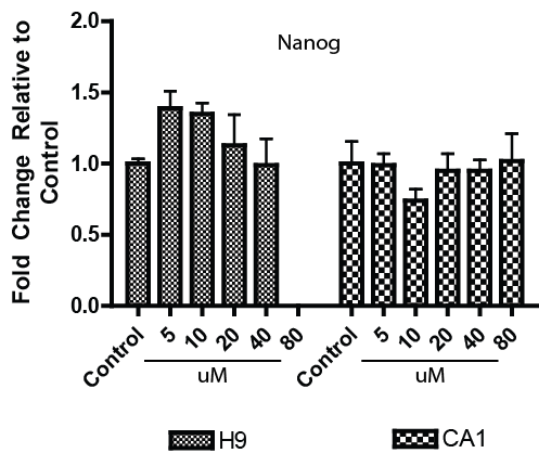
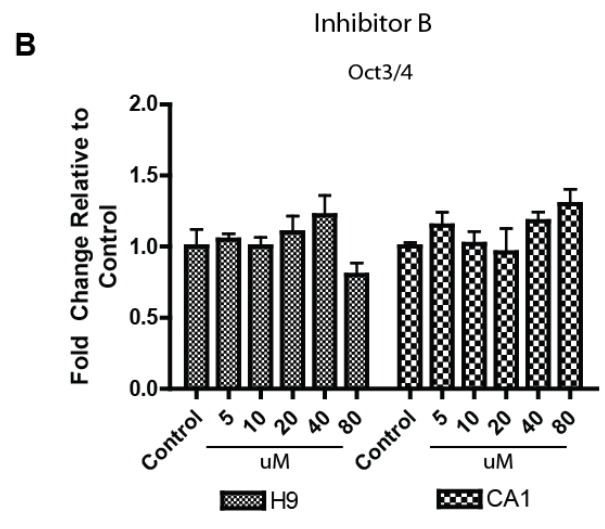
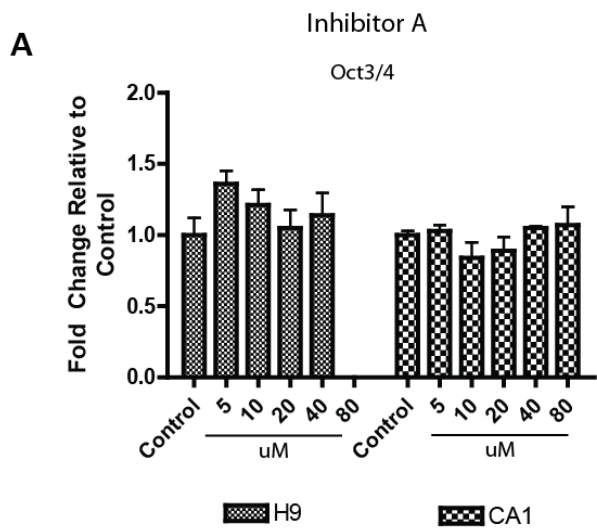


hESCs (Figure 5.4 D). To test the effects of these knockdowns on hESC behavior, H9 and CA1 cells were grown in MEF-CM for 4 days post-transfection. In hESCs containing sFRP1 or sFRP2 shRNA expressing plasmids grown in MEF-CM, we observed no significant change in Oct3/4 and Nanog at both the transcript and protein level (Figure 5.4 E-F). Taken together, these data suggest that sFRP1 and sFRP2 are unable, on their own, to modulate pluripotency marker expression in MEF-CM. However, the effectiveness of the shRNA treatment is potentially confounded by the limited extent of knockdown achieved.

Although we obtained a knockdown of gene expression for sFRP1 and 2 in the hESC lines tested, we observed that the protein level remained relatively unchanged compared with control cells (Figure 5.4 F). To effect sFRP signaling at the protein level, we utilized two separate small molecule inhibitors specific for sFRP1 (herein referred to as sFRP1 Inhibitor A and sFRP1 Inhibitor B) [32]. When H9 or CA1 hESCs grown in MEF-CM were supplemented with either inhibitor, we observed only minor alterations in Oct3/4 and Nanog expression that were not significant at the transcript level (Figure 5.5 A-B). Additionally, we observed no differences based on immunoblot data, indicating that the changes observed at the transcript level were not biologically significant (Figure 5.5 C). Taken together, these results suggest that inhibition of sFRP1 cannot, on its own, promote the changes in the expression of genes directly involved in the maintenance of the stem cell phenotype in MEF-CM.

To test whether inhibition of sFRP1 by small molecule inhibitors has an effect on the differentiation of hESCs, we supplemented multiple concentrations of either inhibitor in

**Figure 5.5. hESCs in MEF-CM supplemented with sFRP1 inhibitors.** H9 and CA1 hESCs were grown in MEF-CM that was supplemented with small molecule inhibitors of sFRP1. Oct3/4 and Nanog expression were assayed by RT-PCR following 4 days of culture in the presence of supplementation. (A) Fold change of Oct3/4 and Nanog expression relative to control for H9 and CA1 hESCs grown in MEF-CM supplemented with sFRP1 inhibitor A. (B) Fold change of Oct3/4 and Nanog expression relative to control for H9 and CA1 hESCs grown in MEF-CM supplemented with sFRP1 inhibitor B. Error bars represent SD, n=3. All RT-PCR experiments used RPLPO as an internal control. (C) Western blots depicting Oct3/4 and Nanog protein expression for H9 and CA1 hESCs grown in MEF-CM supplemented with sFRP1 inhibitors. Actin is shown as a control.

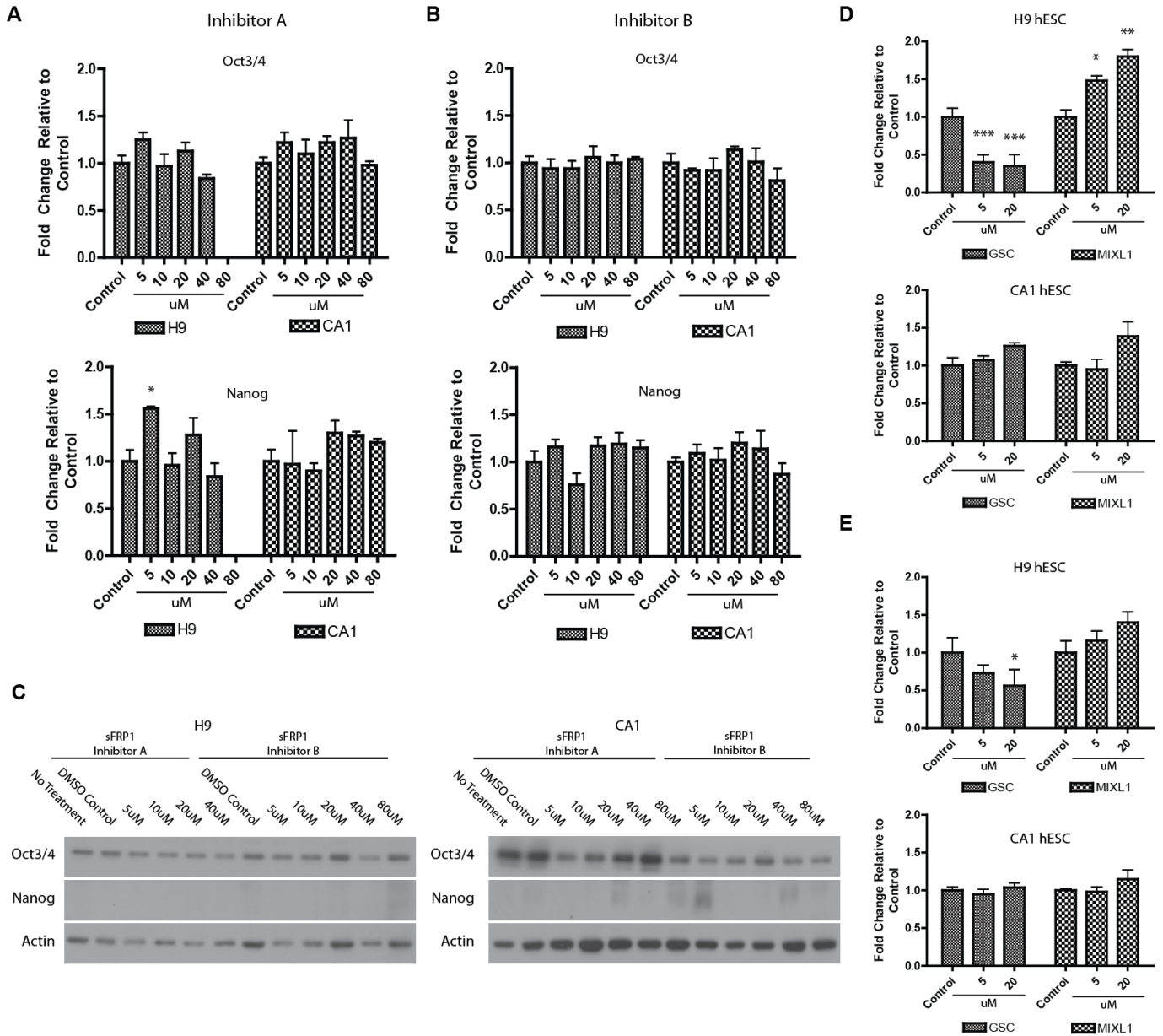


EB medium. Similar to the observed effect in MEF-CM, neither sFRP1 inhibitor was able to alter the expression of Oct3/4 or Nanog in H9 or CA1 hESCs (Figure 5.6 A-B). Analogous to MEF-CM, no observable changes were seen in immunoblots for Oct3/4 and Nanog (Figure 5.6 C). However, due to the poor abundance of Nanog following differentiation based on immunoblots, correlation of gene expression and protein abundance data is challenging.

Since Wnt signaling is known to be involved in the induction of mesendoderm, we examined whether hESCs grown in EB medium supplemented with sFRP1 inhibitors would display an induction of this lineage type [33]. As indicators of mesendoderm, we monitored Goosecoid (GSC) [34] and Mix paired-like homeobox 1 (MIXL1) [35] expression. We observed a significant decrease in GSC expression and subsequent increase in MIXL1 in H9 hESCs grown in the presence of sFRP1 inhibitor A in EB medium (Figure 5.6 D). We observe a similar trend for H9 hESCs grown in the presence of sFRP1 inhibitor B; although significance is not reached in the case of MIXL1 (Figure 5.6 E). We observe no significant change in GSC or MIXL1 expression in CA1 hESCs grown in the presence of either sFRP1 inhibitor in EB medium (Figure 5.6 D).

In order to maximize the knockdown in sFRP1 and sFRP2 activity, we combined transient transfection of the hESCs with small molecule inhibition in both MEF-CM and EB medium. Similar to the previous results in MEF-CM and EB medium supplemented with either sFRP1 inhibitor, we observed no significant changes Oct3/4 in transcript or protein abundance in sFRP1 and sFRP2 shRNA expressing hESCs (Figure 5.7 A-D).

**Figure 5.6. hESCs in embryoid body medium supplemented with sFRP1 inhibitors.** H9 and CA1 hESCs were grown in EB medium that was supplemented with small molecule inhibitors of sFRP1. Oct3/4 and Nanog expression were assayed by RT-PCR following 4 days of culture in the presence of supplementation. (A) Fold change of Oct3/4 and Nanog expression relative to control for H9 and CA1 hESCs grown in EB medium supplemented with sFRP1 inhibitor A. (B) Fold change of Oct3/4 and Nanog expression relative to control for H9 and CA1 hESCs grown in EB medium supplemented with sFRP1 inhibitor B. Error bars represent SD, n=3. (C) Western blots depicting Oct3/4 and Nanog protein expression for H9 and CA1 hESCs grown in embryoid body medium supplemented with sFRP1 inhibitors. Actin is shown as a control. (D) Goosecoid and MIXL1 expression as indicators of mesendoderm induction for H9 and CA1 hESCs grown in the presence of sFRP1 inhibitor A. (E) Goosecoid and MIXL1 expression as indicators of mesendoderm induction for H9 and CA1 hESCs grown in the presence of sFRP1 inhibitor B. Significance was determined through comparison with embryoid body controls. Error bars represent SD, n=3. All RT-PCR experiments used RPLPO as an internal control.



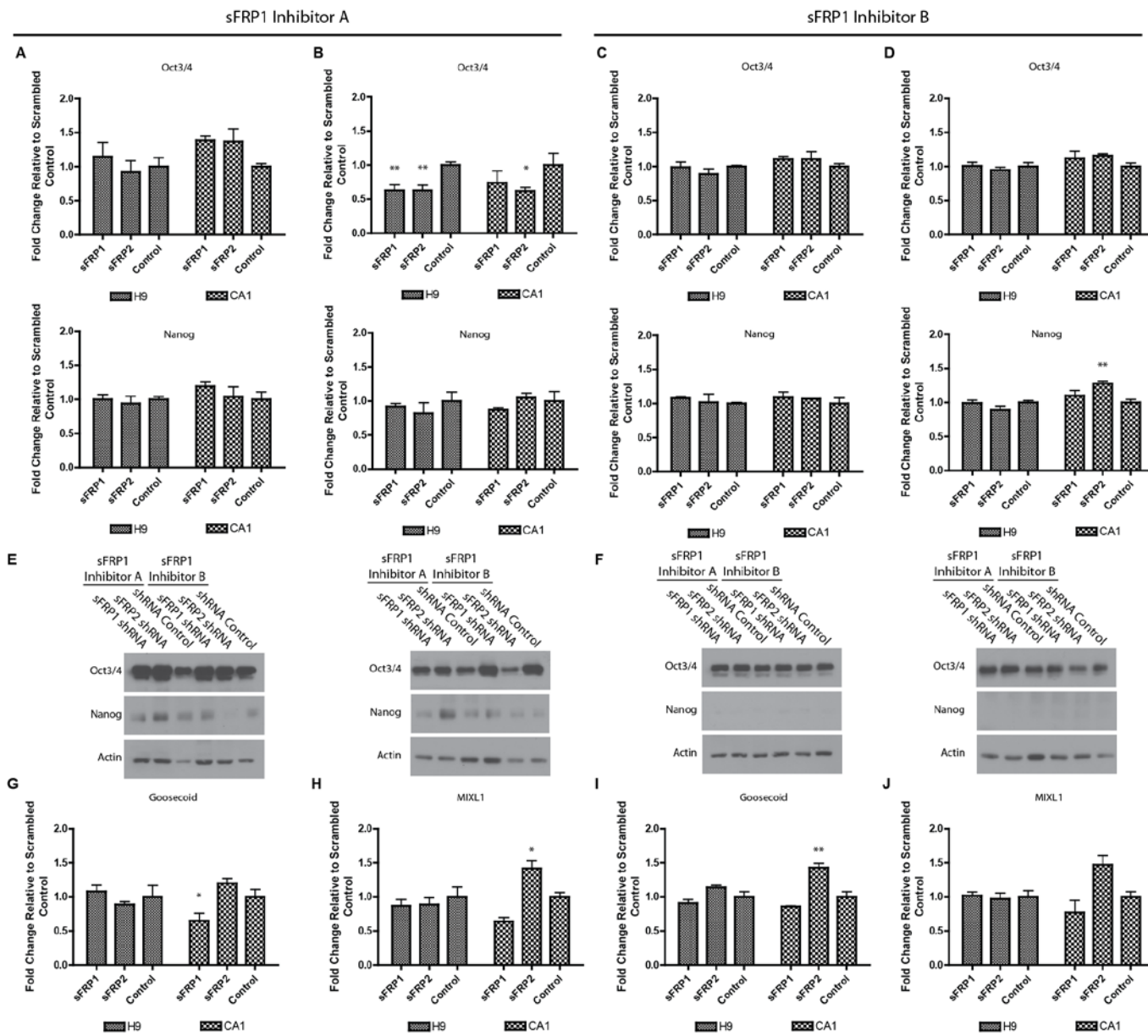
Examination of hESCs grown in EB medium supplemented with sFRP1 inhibitor A or B revealed significant increases in GSC and MIXL1 expression in the sFRP2 knockdown CA1 lines (Figure 5.7 G-J). No significant changes were observed in the H9 hESC line in the presence of either inhibitor (Figure 5.7 G-J). Taken together, these results suggest that modulation of sFRP using sFRP1 inhibitors or shRNA knockdowns are unable to direct changes in hESCs in MEF-CM.

To further examine the potential effects of sFRP1 and sFRP2 on hESCs, we supplemented recombinant versions of these proteins in MEF-CM and EB medium. Since the sFRP family is known to regulate Wnt signaling, and sFRP1 and sFRP2 act directly on Wnt3a, we decided to investigate what role this pathway plays in hESCs [11]. Direct supplementation of Wnt3a in either MEF-CM or EB medium proved beneficial for the maintenance of Oct3/4 and Nanog expression (Figure 5.8 A - C). Supplementation with Wnt3a in EB medium also induced the expression of GSC in H9 and CA1 hESCs (Figure 5.8 D). MIXL1 expression was also significantly upregulated in CA1 hESCs grown in the presence of Wnt3a (Figure 5.8 E).

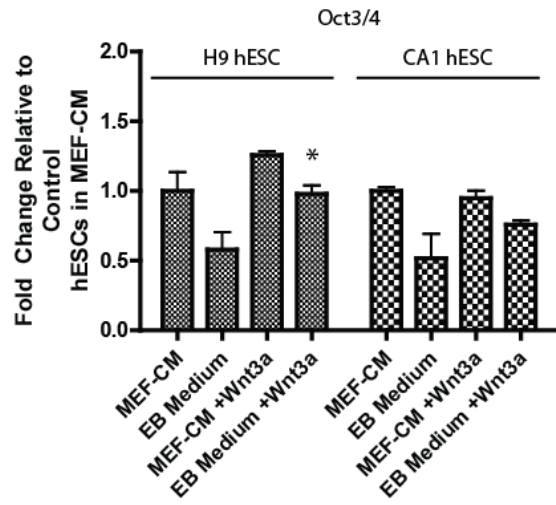
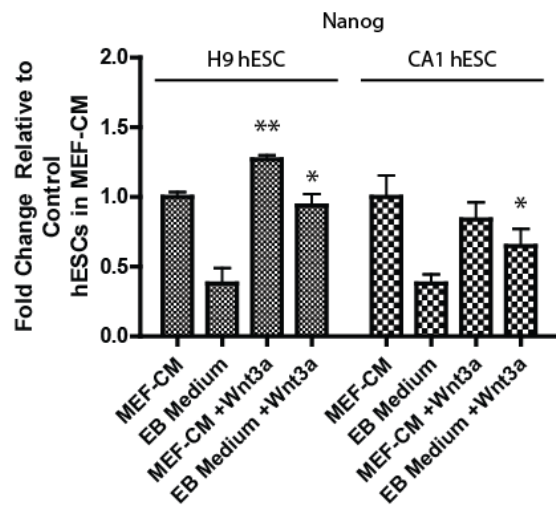
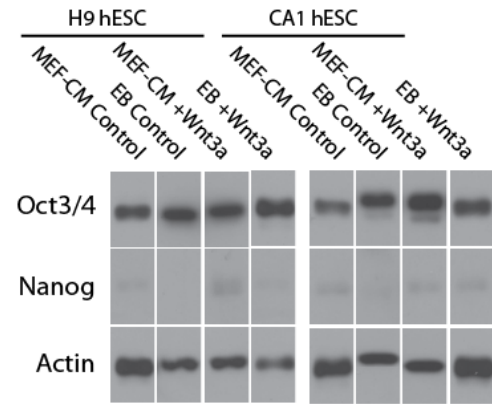
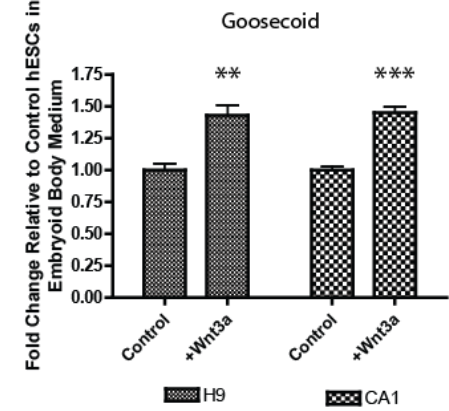
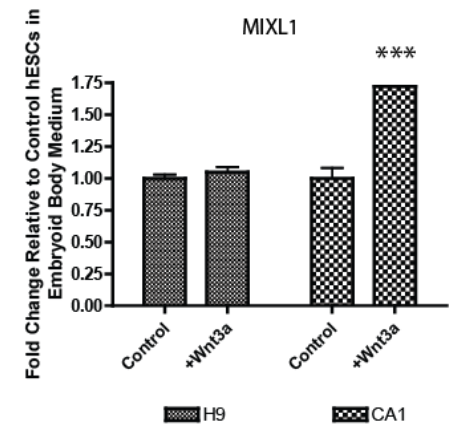
When H9 and CA1 hESCs were supplemented with recombinant sFRP1, sFRP2, and Wnt3a in MEF-CM, we observed that no significant changes were present at both the transcript and protein level (Figure 5.9 A, C, E). However, in EB medium, we observed a significant increase in Nanog expression when sFRP1 or sFRP2 were supplemented in combination with Wnt3a (Figure 5.9 D, F). In CA1 hESCs, we also observed an increase in Oct3/4 expression in the presence of Wnt3a and sFRP1 or sFRP2 (Figure 5.9 B, F). Unfortunately, the low-abundance of Nanog in differentiated hESCs



**Figure 5.7. hESCs with combined exposure to sFRP1 inhibitors and shRNA mediated knockdowns.** H9 and CA1 hESCs transfected with shRNA expressing vectors against sFRP1, sFRP2, or scrambled control were grown in MEF-CM or embryoid body medium that was supplemented with small molecule inhibitors of sFRP1. Oct3/4 and Nanog expression were assayed by RT-PCR following 4 days of culture in the presence of supplementation. (A) Fold change of Oct3/4 and Nanog expression relative to control for H9 and CA1 hESCs grown in MEF-CM supplemented with sFRP1 inhibitor A. Error bars represent SD, n=3. (B) Fold change of Oct3/4 and Nanog expression relative to control for H9 and CA1 hESCs grown in embryoid body medium supplemented with sFRP1 inhibitor A. Error bars represent SD, n=3. (C) Fold change of Oct3/4 and Nanog expression relative to control for H9 and CA1 hESCs grown in MEF-CM supplemented with sFRP1 inhibitor B. Error bars represent SD, n=3. (D) Fold change of Oct3/4 and Nanog expression relative to control for H9 and CA1 hESCs grown in embryoid body medium supplemented with sFRP1 inhibitor B. Error bars represent SD, n=3. (E) Western blots for Oct3/4 and Nanog in H9 and CA1 hESCs transfected with shRNA expressing vectors grown in MEF-CM supplemented with sFRP1 inhibitors. Actin is shown as an internal control. (F) Western blots for Oct3/4 and Nanog in H9 and CA1 hESCs transfected with shRNA expressing vectors grown in embryoid body medium supplemented with sFRP1 inhibitors. Actin is shown as an internal control. (G-J) Fold change of Goosecoid and MIXL1 expression relative to control for H9 and CA1 hESCs grown in embryoid body medium supplemented with sFRP1 inhibitor A (G-H) or sFRP1 inhibitor B (I-J). Error bars represent SD, n=3. All RT-PCR experiments used RPLPO as an internal control.



**Figure 5.8. hESCs in MEF-CM and embryoid body medium with recombinant Wnt3a supplementation.** H9 and CA1 hESCs were grown in MEF-CM or embryoid body medium that was supplemented with recombinant Wnt3a. Oct3/4 and Nanog expression were assayed by RT-PCR following 4 days of culture in the presence of supplementation. (A) Fold change of Oct3/4 expression relative to control for H9 and CA1 hESCs grown in MEF-CM or EB medium supplemented with recombinant Wnt3a at 100ng/mL. Error bars represent SD, n=3. (B) Fold change of Nanog expression relative to control for H9 and CA1 hESCs grown in MEF-CM or EB medium supplemented with recombinant Wnt3a at 100ng/mL. Error bars represent SD, n=3. (C) Western blots for Oct3/4 and Nanog in H9 and CA1 hESCs grown in the presence or absence of 100 ng/mL of Wnt3a. Actin is shown as a control. (D) Fold change of Goosecoid expression relative to control for H9 and CA1 hESCs grown in embryoid body medium supplemented with recombinant Wnt3a, at 100ng/mL. Significance was determined through comparison with the appropriate EB medium control. Error bars represent SD, n=3. (E) Fold change of Goosecoid expression relative to control for H9 and CA1 hESCs grown in embryoid body medium supplemented with recombinant Wnt3a, at 100ng/mL. Significance was determined through comparison with the appropriate EB medium control. Error bars represent SD, n=3. All RT-PCR experiments use RPLPO as an internal control.

**A****B****C****D****E**

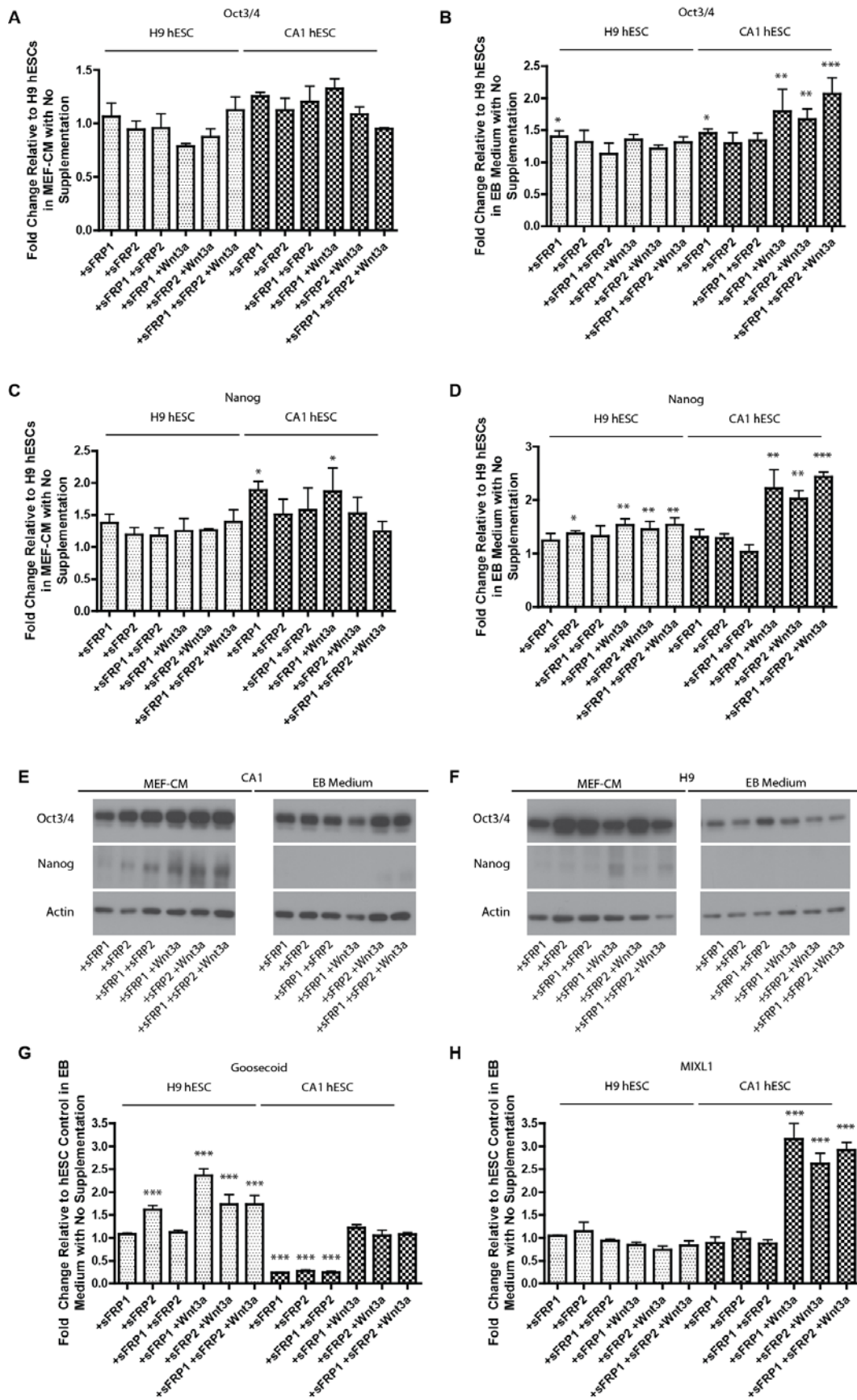
confounded the validation of gene expression results at the protein level (Figure 5.9 E-F). Examination of GSC expression revealed significant increases in H9 hESCs in the presence of Wnt3a and sFRP1 or sFRP2 (Figure 5.9 G). GSC could be reduced through the addition of sFRP1 and sFRP2 in CA1 hESCs (Figure 5.9 G). However, this reduction could be reversed through the addition of Wnt3a (Figure 5.9 G). In CA1 hESCs we also observed a significant induction in MIXL1 expression in the presence of Wnt3a, sFRP1, and sFRP2 (Figure 5.8 H). These data indicate that sFRP1 and sFRP2 proteins are able to act on hESCs during differentiation on their own or through interaction with Wnt3a dependent on the growth factor composition of the microenvironment.

*5.2.4 Effect of sFRP Expression in Metastatic Melanoma Cells.* sFRP1 and sFRP2 have multiple convergent and divergent roles in metastatic cell types (reviewed in [10]). To examine the effects of sFRP1 and sFRP2 expression we utilized a metastatic melanoma cell line (C8161) that was previously employed to demonstrate the reprogramming ability of hESC-derived CMTX [27, 36]. Expression of sFRP2 was found to be minimal in C8161 cells when compared with hESCs and HEK293 lines (Figure 5.10 A). Interestingly, sFRP1 expression was similar to H9 hESCs based on RT-PCR data (Figure 5.10 A). Since sFRP2 expression was found to be low, we transfected the C8161 cells with a vector containing the sFRP2 open-reading frame (ORF) under the control of a constitutive promoter. After 48 hours post-transfection, C8161s transfected with the sFRP2 ORF had a significant decrease in total cell number compared to control cells transfected with the same vector without the sFRP2 ORF (Figure 5.10 B). After selection with puromycin, no cells were able to form stable cell

lines from those transfected with the sFRP2 ORF, whereas numerous clones were derived from the control plate (Figure 5.10 B). However, validation of sFRP2 expression in C8161 cells was difficult due to the inability to harvest cellular RNA and protein as a result of cell death.

To further assess the effects of sFRP1 and sFRP2 on the C8161s we carried out an anchorage independent growth assay. C8161 cells that had been supplemented with 200 ng/mL of sFRP1 and sFRP2 for 4 and 7 days were seeded into soft-agar and permitted to form colonies for 14 days. Cells exposed to sFRP1 and sFRP2 had a significant increase in colony formation relative to control, whereas those exposed to sFRP2 had a significant decrease (Figure 5.10 C). Although the sFRP2 supplemented wells displayed colonies, they tended to be smaller than those found in the sFRP1 or control wells (Figure 5.10 D). Taken together, these data indicate divergent roles for sFRP1 and sFRP2 in metastatic C8161 cells.

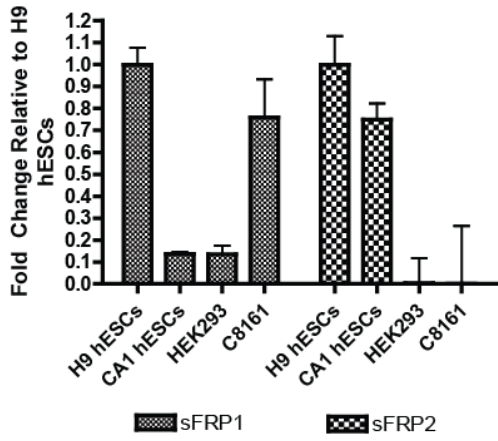
**Figure 5.9. hESCs in MEF-CM and embryoid body medium with recombinant protein supplementation.** H9 and CA1 hESCs were grown in MEF-CM or embryoid body medium that was supplemented with recombinant versions of sFRP1, sFRP2, and Wnt3a. Oct3/4 and Nanog expression were assayed by RT-PCR following 4 days of culture in the presence of supplementation. (A) Fold change of Oct3/4 expression relative to control for H9 and CA1 hESCs grown in MEF-CM medium supplemented with recombinant sFRP1, sFRP2, and Wnt3a, each at 100ng/mL. (B) Fold change of Oct3/4 expression relative to control for H9 and CA1 hESCs grown in embryoid body medium supplemented with recombinant sFRP1, sFRP2, and Wnt3a, each at 100ng/mL. (C) Fold change of Nanog expression relative to control for H9 and CA1 hESCs grown in MEF-CM medium supplemented with recombinant sFRP1, sFRP2, and Wnt3a, each at 100ng/mL. (D) Fold change of Nanog expression relative to control for H9 and CA1 hESCs grown in embryoid body medium supplemented with recombinant sFRP1, sFRP2, and Wnt3a, each at 100ng/mL. Significance was determined through comparison with the appropriate MEF-CM or EB medium control. Error bars represent SD, n=3. (E-F) Western blots depicting Oct3/4 and Nanog protein expression for all experiments. Actin is shown as a control. (G-H) Goosecoid and MIXL1 expression as indicators of mesendoderm induction for H9 and CA1 hESCs grown in embryoid body medium supplemented with recombinant sFRP1, sFRP2, and Wnt3a, each at 100ng/mL. Significance was determined by comparison with MEF-CM and EB medium controls. All RT-PCR experiments use RPLPO as an internal control.



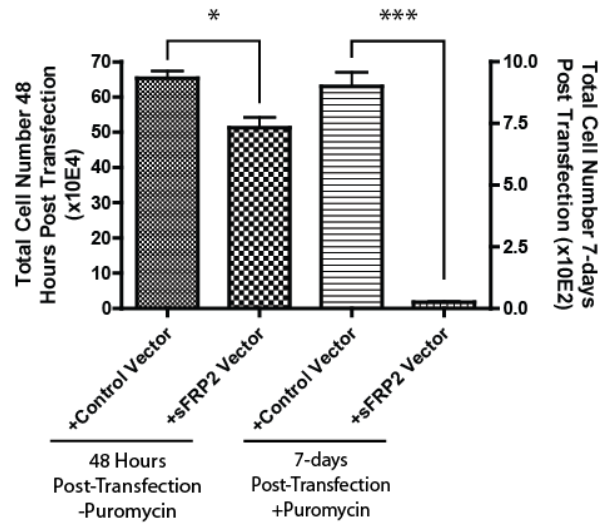


**Figure 5.10. Metastatic melanoma cell line characteristics following sFRP1 and sFRP2 modulation.** C8161 metastatic melanoma cells were grown in the presence or absence of recombinant sFRP1 and sFRP2 or transfected with the sFRP2 open-reading frame under the control of a constitutive promoter. (A) Expression of sFRP1 and sFRP2 in H9 and CA1 hESCs, HEK293, and C8161 cells as determined by RT-PCR. RT-PCR values are fold change relative to H9 hESCs using RPLPO as an internal control. Error bars represent SEM, n=2. (B) C8161 cells were transfected with either a vector containing the sFRP2 open-reading frame or with the same vector containing no insert. Cells were counted 48 hours post transfection and 7-days following the addition of puromycin to assess survival. Error bars represent SD, n=3. (C) C8161 cells grown in the presence or absence of 200 ng/mL of sFRP1 and sFRP2 for 4 or 7 days were tested for anchorage independent growth using a soft-agar assay. Pictures were taken after 7 days, colonies were allowed to form for a total of 14 days prior to counting. Error bars represent SD, n=3. Significance was determined relative to control for all treatments.

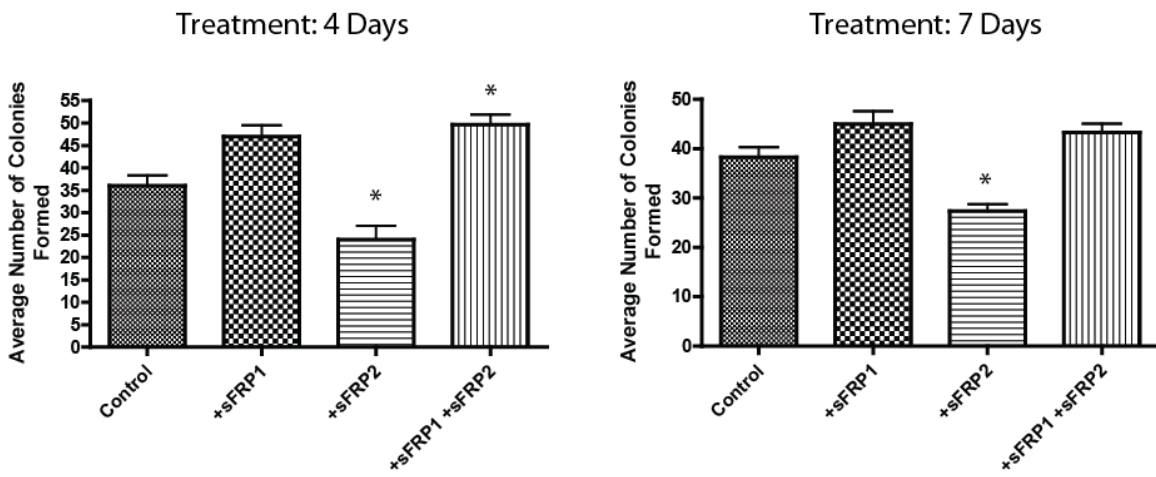
**A**



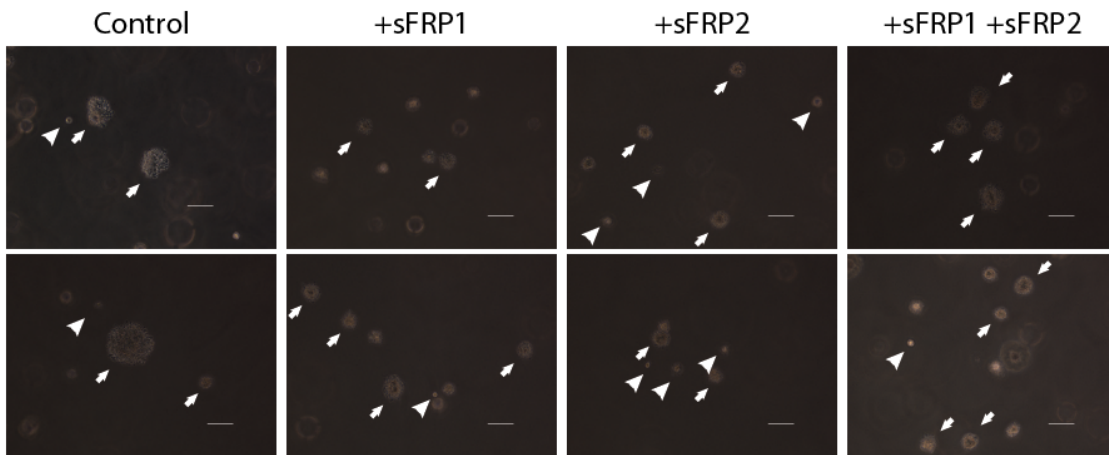
**B**



**C**



**D**



### 5.3 Discussion

The interactions between hESCs and their soluble microenvironment are essential for control over pathways related to self-renewal and differentiation. Cytokines involved in the regulation of these core pathways are often associated with other factors in the microenvironment that aid in the management of their activity or stability. Many of these co-factors can be bound to, or present in the ECM. As such, the study of the interactions between hESCs and the ECM represents a potentially rich source of information regarding regulation of core pluripotency pathways. Highlighting this is the recent observation that hESC-derived matrix microenvironments can reprogram metastatic melanoma cells [27, 36]. Bioactive factors deposited by hESCs during growth are able to direct cell-fate through activity in extracellular pathways within the microenvironment [27]. However, currently there are few studies that aim to investigate the interactions of hESCs with the ECM mediated by protein deposition in the extracellular space.

Based on our work, growth on CMTX in the absence of bFGF promotes the maintenance of an undifferentiated state in hESCs. This indicates that hESCs are depositing factors in the CMTX that serve to regulate the stem cell state. To investigate this finding further and to validate the ability of our MS-based proteomics screen to identify hESC regulatory factors in the matrix, we targeted sFRP1 and sFRP2 for functional analysis. sFRP1 and sFRP2 are thought to regulate canonical Wnt signaling through direct binding to the soluble Wnt cytokines or their cognate membrane receptors (reviewed in [23]). However, the role of sFRP1 and sFRP2 in hESCs remains

unclear. By utilizing a combination of methods, we analyzed the roles of these Wnt regulators in hESCs.

Using shRNA mediated inhibition of sFRP1 and 2 we observed no significant change in Oct3/4 and Nanog in MEF-CM. Similar trends can be observed in the sFRP1 inhibitor data, where neither inhibitor is able to direct a significant change in pluripotency marker expression at both the transcript and protein level. When shRNA mediated knockdown of expression sFRP1 or sFRP2 is combined with the sFRP1 inhibitors, we observe no significant change in Oct3/4 and Nanog expression at the transcript and protein level. Taken together, these findings indicate that sFRP1 and sFRP2 are not able to direct a significant change in hESCs grown in the complex growth factor microenvironment provided by MEF-CM. However, these findings are limited by the lack of positive control for the small molecule inhibitor due to the poor transfectability coupled with the low activity of the canonical Wnt pathway in hESCs.

To determine whether sFRP1 or sFRP2 were acting through Wnt signaling activated by Wnt3a, we investigated their effects when supplemented exogenously. Previous studies have demonstrated that Wnt signaling in ESCs functions in an 'activation' type model [37, 38]. In this model, Wnt signaling induced by Wnt3a promotes hESC survival and proliferation, but also differentiation to mesendoderm, dependent on the culture conditions. However, there is discordance in the literature regarding the activity of Wnt signaling in hESCs, where activation of canonical signaling through Wnt3a is believed to prevent differentiation, referred to as the 'maintenance' model [39]. Based on our observations Wnt3a functions in the 'activation' model to promote stem cell fate

determination. Supplementation of exogenous Wnt3a promotes hESC survival and proliferation, as well as differentiation dependent on the growth factor conditions. Addition of recombinant sFRP1 and sFRP2 in combination with Wnt3a were able to induce pluripotency marker expression, but only in EB medium in the absence of other exogenous growth factors. When supplemented into Matrigel™ matrix to generate an artificial CMTX, both sFRP1 and sFRP2 could not induce maintenance of an undifferentiated state of hESCs. These data suggest that sFRP1 and sFRP2 are not required for the maintenance of hESC pluripotency in the presence of other growth factors, such as in MEF-CM. However, based on the observation that sFRP1 and sFRP2 can regulate the expression of GSC and MIXL1, they are potentially acting to regulate Wnt induced formation of mesendoderm in differentiating hESCs.

These findings are in agreement with the current 'activation' type model suggested for Wnt regulation in hESCs and recent data regarding the cooperative action of the Wnt, FGF, and Activin/Nodal pathways [37]. Wnt activation in hESCs grown in the presence of a supportive growth factor environment can help promote survival and proliferation [39]. However, in MEF-CM Wnt signaling is not required for the maintenance of self-renewal or pluripotency, and cannot direct a cellular change in the presence of strong activation of the core stem cell Activin/Nodal and FGF signaling pathways [40]. In the absence of growth factor supplementation, activation of Wnt signaling promotes differentiation to mesendoderm, a process that can potentially be regulated by sFRP1 and sFRP2.

Due to the biphasic mode of activity for sFRPs as well as Wnt signaling, the ability of sFRP1 or sFRP2 to regulate hESC behavior is potentially dependent on the dynamic balance between the interacting partners [20, 41]. The recombinant protein concentrations tested in our assay may not have been optimal for sFRP activity in the presence of other Wnt regulatory proteins. Previous studies that have attempted to study the effects of sFRP supplementation on hESCs have required the use of non-physiological amounts of recombinant protein to observe a minor effect [42, 43]. The interactions between sFRP proteins and Wnt ligands may also require facilitation through binding with the ECM, as indicated by the identification of sFRP1 and sFRP2 in the CMTX. sFRP action is known to be regulated by heparin mediated binding to Wnt as well as to the ECM [20, 44]. These interacting factors may cooperate to promote hESC fate determination through regulation of Wnt ligand availability. In other cell types, the sFRP proteins have been reported to antagonize, but also augment canonical Wnt signaling [11, 45]. In the metastatic C8161 cell line we observed that sFRP1 promoted and sFRP2 inhibited their malignant potential based on colony formation in a soft-agar assay. In addition, overexpression of sFRP2 prompted a significant decrease in viable cell number. These findings are not surprising given the divergent roles for sFRP1 and sFRP2 in a variety of pathological conditions (reviewed in [17, 22]). However, based on the limited effects of sFRP1 and sFRP2 on hESC state, it is likely that other factors are combining to contribute to the dynamic regulation of the core pluripotency pathways *in vitro*.

## 5.4 Methods

*5.4.1 Cell culture and harvest* – H9 (passage 26) and CA1 (passage 20) hESCs were maintained on CF-1 irradiated mouse embryonic fibroblast (MEF) feeder layers (GlobalStem, Rockville, MD) using media composed of knockout DMEM/F12, 20% knockout serum replacement, 1% non-essential amino acids, 2 mM glutamine (CellGro, Manassas, VA), 0.1 mM 2-mercaptoethanol (Fisher, Toronto, ON), and 4 ng/mL of basic fibroblast growth factor. For feeder-free growth, conventional hESC medium that was conditioned on a layer of mouse embryonic fibroblast feeders (MEF-CM) was used with Matrigel™ (BD Biosciences, Franklin Lake, NJ) coated plates. Medium used for the induction of differentiation in CMTX experiments uses the same recipe as conventional hESC media for growth on MEF feeders as outlined above, minus basic FGF. All media reagents were obtained from Invitrogen unless noted otherwise. H9 cells were obtained from WiCell (WISC, Wisconsin). The CA1 hESC line used in all experiments was obtained from Dr. Cheryle Séguin of The University of Western Ontario [46, 47]. The hiPSC line BJ-1D was derived by reprogramming using retroviral transduction of BJ fibroblasts with the Yamanaka factors essentially as we have previously described [48] and validated as pluripotent using in vitro and in vivo differentiation assays and expression profiling (unpublished results). Cells were passaged mechanically in all experiments and for general maintenance.

Embryoid bodies (EB) were generated using Aggrewell 400Ex plates (StemCell Technologies, Vancouver, Canada). Briefly,  $2 \times 10^6$  hESCs were harvested

enzymatically using Accutase (Invitrogen) from Matrigel™ coated plates. Cells were reconstituted in Aggrewell medium supplemented with Rock inhibitor (Y-27632, Sigma-Aldrich, St. Louis, MO) at a final concentration of 10  $\mu$ M. After plating in Aggrewell dishes, EBs were grown for 48 hours at 37°C prior to transfer to ultra-low adherence tissue culture dishes (Corning, Lowell, MA). After 15 days of culture, EB RNA was harvested using Trizol extraction according to the manufacturer's instructions (Invitrogen). EBs were assayed for expression of CDX2, alpha-feto protein (AFP), GATA-6, GATA-4, Oct3/4, PAX-6, T-brachyury, Nanog, and Neurogenic differentiation 1 (NeuroD1) using TaqMan primer probe sets (Invitrogen). Assay information can be found in Appendix Table 1.15. All EB assays were performed in biological and technical duplicate for each cell line and condition.

*5.4.2 sFRP Knockdown and Inhibition* - sFRP2 and sFRP1 shRNA knockdown cell lines were generated using the pSUPERIOR.neo + GFP vector (Oligoengine, Seattle, USA). shRNA sequences were obtained using the shRNA design tool from Ambion. Oligos were designed to contain 5' XhoI and 3' HindIII restriction enzyme sites. All oligos were synthesized by Invitrogen unless otherwise noted. Oligos were ligated into pSUPERIOR.neo + GFP vector that was previously digested with XhoI and HindIII (New England Biolabs, Ontario, Canada) and transformed into TOP10 chemically competent *E. coli* (Invitrogen). Transformed clones were selected based on ampicillin resistance and plasmid purified using a PureLink HiPure Midi-prep kit (Invitrogen). shRNA effectiveness was tested in HEK293 cells stably transfected with the pCAGTetRnls vector (Addgene.org). After transfection with pSUPERIOR, HEK293 cells were maintained in RPMI + 10% FBS containing 700 ng/mL puromycin and 700  $\mu$ g/mL G418.



shRNA efficiency was determined after 4 days of induction using 1 µg/mL of doxycycline. Sequences for the shRNA constructs found to give the greatest decrease in specific gene expression were selected for use in hESCs. Selected shRNA sequences can be found in Appendix Table 1.16.

hESC lines were transiently transfected with GeneIn reagent (GlobalStem, Rockville, MD). H9 (p30) and CA1 (p22) hESCs were plated at ~80% confluence 24 hours prior to transfection. GeneIn reagents (1:1 mixing ratio) were combined with 4 µg of vector and supplemented into MEF-CM. hESCs were incubated in the media-transfection reagent mixture for 24 hours, followed by a second treatment for a further 24 hours. In cases where differentiation was induced, the second transfection was performed in hESC media –bFGF. Transfection efficiency was determined using flow cytometry based on detection of the GFP reported on the pSUPERIOR vector.

Inhibition of sFRP-1 was carried out using two separate small molecules obtained from Calbiochem (EMD Biosciences, Darmstadt, Germany) [32]. Inhibitors were supplemented at concentrations of 5, 10, 20, 40, and 80 µM in MEF-CM or medium that contained no bFGF. Controls were supplemented with the maximum amount of DMSO used in the experiments with inhibitors present. hESCs were grown in the presence of inhibitor for a period of 4 days during which medium was changed daily.

*5.4.3 Generation of Conditioned Matrix* – H9 or CA1 stem cells were grown in feeder-free conditions on Matrigel™ in MEF-CM. Stem cells were permitted to grow for a period of 5 days on Matrigel™ for generation of CMTX. Wells were then rinsed thoroughly with PBS to ensure removal of medium components and cells removed from

the Matrigel™ layer using Cell Recovery Solution according to the manufacturer's instructions (BD Biosciences). Fresh hESCs were plated on the after rinsing of the matrix layer. After 24h of culture, hESCs were induced to differentiate through feeding with conventional hESC media –bFGF. Control experiments were prepared using regular Matrigel™ that had not been conditioned but had been treated with the cell removal process.

In antibody blocking CMTX experiments, antibodies were obtained as follows: sFRP2 (Origene, Rockville, MD), sFRP1, Lefty 1, 2 (Epitomics, Burlingame, CA). Anti-rabbit IgG secondary antibody was used as a control. After cell removal from the conditioned Matrigel™, layers were rinsed with 1:1000 dilutions of manufacturer antibody stocks in 1% bovine albumin in PBS. Matrices were incubated for 2 hours at 37°C. After incubation, layers were rinsed multiple times with PBS prior to plating of fresh hESCs. In supplementation CMTX experiments, recombinant sFRP1, sFRP2, Lefty A or B, or Gremlin were added to Matrigel™ prior to polymerization at a concentration of 5 µg/mL. After incubation at 37°C for 1 hour, matrices were treated with the cell removal process and rinsed prior to playing of fresh hESCs. Recombinant sFRP1 & 2, Lefty A, and Gremlin proteins were obtained from R&D Systems (Minneapolis, MN). Recombinant Lefty B was obtained from Sigma (St. Louis, MO). In all cases, cells were fed daily with hESC media –bFGF for 3 days prior to harvest.

*5.4.4 Metastatic Melanoma Cell Experimentation* – C8161 cells (described in [49]) were cultured in RPMI containing 10% FBS (Invitrogen). In anchorage independent growth assays, C8161 cells were maintained in the presence or absence of 200ng/mL of

sFRP1 and sFRP2 for 4 – 7 days. At each time point, cells were harvested by trypsinization and counted. Soft-agar experiments were performed by resuspending 9,000 cells in a mixture of RPMI/10% FBS + 0.35% agarose. This mixture was plated onto a previously prepared layer of RPMI/10% FBS + 0.5% agarose in single well of a 6-well dish. Cells in soft-agar were fed every 3 days. Colonies were allowed to form for 14 days after plating. Colonies were counted after staining with 0.005% crystal violet in PBS. Soft-agar assays were performed in triplicate for each time point and condition tested.

C8161 transfections were carried out using GenEln Reagent (GlobalStem). For each transfection, 2 µg of total DNA was diluted in 200 µL of OptiMEM with 3 µL of each GenEln reagent. Approximately 10,000 C8161 cells were plated in a single well of a 6-well dish 24 hours prior to transfection. Cells were transfected with the pCMV-IRES-GFP-Puro (Origene, Rockville, MD) vector with or without the sFRP2 open reading frame (Origene). Transfection efficiency was monitored using GFP expression. Cells were selected using 700 ng/mL of puromycin 48 hours after transfection. Total viable cells were counted using trypan blue exclusion 48 hours and 7-days post transfection. Experiments were repeated in triplicate for each treatment.

*5.4.5 Real-time PCR* – RNA was purified using Trizol reagent according to the manufacturer's instructions (Invitrogen) with the following modification: precipitated RNA pellets in isopropanol were centrifuged for 60 minutes at 12000 g at room temperature. After NanoDrop quantification, 1 µg of cDNA was synthesized using the High Capacity cDNA Reverse Transcription Kit with RNase inhibitor (Invitrogen). Real-time PCR was

performed using the TaqMan® Universal PCR Master Mix (Invitrogen). Samples were incubated at 50°C for 2 minutes followed by 10 minutes at 95°C. Samples were then amplified at 95°C for 15 seconds followed by 1 minute at 58°C for 46 cycles. All samples were normalized to the large ribosomal protein RPLPO as a positive control. All primers were obtained from Invitrogen and assay information can be found in Appendix Table 1.15. Each biological replicate was run in triplicate for every marker assayed. All reagents were used according to the manufacturer's instructions.

*5.4.6 Immunofluorescence* – Immunofluorescence was performed as described previously [50]. Briefly, cells were rinsed and fixed with 4% para-formaldehyde containing 20 mM sucrose. Fixed cells were permeabilized using 0.1% Triton-X100. Prior to staining, cells were blocked using the Dako Serum Free Protein Block solution (Dako, Cambridgeshire, UK). Oct-4 (clone 10H11.2), SSEA-4 (clone MC-813-70), and SSEA-1 (clone MC-480) primary antibodies were obtained from Millipore (Billerica, MA). Cells for Oct-4 labeling were permeabilized using a 0.1% Triton X-100 solution prior to blocking. Cells were labeled with primary antibodies for Oct-4 or SSEA-4 as undifferentiated markers and SSEA-1 for differentiated cells all at concentrations concentrations of 2 µg/mL for 60 minutes at room temperature. Secondary Alexa-fluor 488 goat anti-mouse IgG and Alexa-fluor 568 goat anti-mouse IgM were obtained from Invitrogen (Carlsbad, CA). Secondary antibodies were probed at concentrations of 1 µg/mL for 60 minutes at room temperature. All products were used according to manufacturer's instructions.

*5.4.7 Flow Cytometry* – All reagents and probes for flow cytometry were obtained from eBiosciences (San Diego, CA) unless noted otherwise. Cells were enzymatically harvested using Accutase (Invitrogen) to obtain a single cell suspension. After centrifugation, cell pellets were resuspended in 5% FBS in PBS. Alexa-488 conjugated SSEA-4 and Alexa-647 conjugated SSEA1 were diluted into the cell mixture according to the manufacturer's instructions. Negative control samples contained respective isotype controls for the primary antibodies used. Solutions were incubated for 2 hours and analyzed using an Accuri C6 (BD Biosciences) flow cytometer after rinsing to remove unbound antibody. Populations were gated according to forward and side scatter patterns with filtering for viable cells using 7-aminoactinomycin D staining. Data was analyzed using FlowJo software (Tree Star, Ashland, OR).

*5.4.8 Immunoblotting* – Harvested cell pellets were reconstituted in mammalian protein extraction reagent containing protease inhibitor cocktail (Thermo Fisher, Toronto, Canada). 20 µg of protein based on Bradford assay was run on an 8% SDS-Gel. Proteins were transferred to a PVDF membrane (Millipore) and incubated in 5% milk overnight at 4°C. After rinsing in TBS containing 0.1% Tween-20, membranes were incubated for 4 hours with primary antibodies. Oct3/4, Nanog, sFRP1, and sFRP2 antibodies were obtained from Epitomics (Burlingame, CA). β-Actin antibody was obtained from Santa Cruz Biotech (Santa Cruz, CA). After rinsing, membranes were incubated with specific HRP-conjugated secondary antibodies for 1 hour. Blots were developed using Pierce ECL reagent and CL-Xposure film (Thermo).

*5.4.9 Statistical Analysis* – Statistical analyses were performed using GraphPad Prism software. Results are expressed as SD or SEM as indicated in figure legends. Statistical significance was determined using one-way ANOVA with Tukey post-hoc analysis. When only two samples were being compared, unpaired Students T-tests were applied. Differences were reported as follows: \*  $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$ .

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## Chapter 6

### Discussion

#### 6.1 Summary of Accomplishments

It is clear that the microenvironment plays a critical role in the regulation of hESC fate. Central to the potential application of hESCs in therapeutic applications are advances in controlled methods for modulating the pluripotent state. Paramount for development is increasing our knowledge of the processes eliciting control in this dynamic environment. To obtain a complete understanding of the *in vitro* stem cell niche, analysis of soluble and ECM contributors to this environment is necessary. Due to the complex requirements for the *in vitro* maintenance of hESCs, direct analysis of the ECM presents a significant challenge. To this end, we have developed proteomic methodologies for the direct study of the ECM portion of the microenvironment (Chapters 2 – 3). Additionally, we have demonstrated the application of these methods to the analysis of this complex environment, and in doing so have elucidated novel factors involved in hESC regulation (Chapters 4-5).

This chapter contains excerpts from the following paper:

Hughes, C.S., Radan, L., Stanford, W., Betts, D., Postovit, L.M., Lajoie, G.. (2012) "Mass Spectrometry-Based Proteomics Analysis of the Matrix Microenvironment in Pluripotent Stem Cell Culture". (In Preparation)

The complexity of Matrigel™ necessitates the use of quantitative proteomics techniques to study the ECM portion of the microenvironment. To this end, we have developed conditions for the application of the metabolic labeling approach, SILAC, to hESCs (Chapter 2). This new protocol eliminates conversion of isotopically labeled arginine amino acids to proline derivatives and represents a significant increase in simplicity and reduction in cost when compared with alternative methods for addressing this conversion. We also further extend our SILAC approach to a defined hESC media formulation. This defined alternative offers an attractive platform for the study of the microenvironment free of contaminating contributions from MEF feeder layers present in conditioned medium. Furthermore, the extension of this defined medium to the growth of hiPSCs presents new opportunities for the quantitative study of stem cell biology.

A secondary challenge for the analysis of the ECM portion of the microenvironment is the protein complexity of these matrices. MS-based proteomics studies consistently struggle to identify the low-abundance components of complex mixtures in the face of a large dynamic range of protein concentration. This is further complicated with ECM mixtures due to their propensity to polymerize when not chilled. Although our quantitative SILAC strategy would enable distinction between hESC and Matrigel derived proteins, the presence of candidates derived from both sources significantly increases the complexity of the CMTX solution. In order to facilitate the detection of low abundance hESC derived proteins, we have shown the benefits of using a combination of conventional proteomics techniques (Chapter 3). Upon application for the analysis of Matrigel and other cell-derived matrices, we successfully achieve significant depth of coverage in these complex samples. Furthermore, we illustrated the utility of analyzing

matrices used in stem cell culture for the elucidation of components critical for the maintenance of hESC pluripotency.

Finally, through application of the SILAC (Chapter 2) and ECM analysis methodologies (Chapter 3), we obtained a proteomic profile of a matrix layer preconditioned by hESCs (Chapter 4). We then reconcile proteomic datasets from the soluble and ECM portions of the microenvironment previously obtained. Investigation of the CMTX revealed that hESCs generate a self-sustaining niche rich in supportive factors found in Matrigel, as well as in conditioned medium. Functional validation of candidate factors illustrates the complexity of hESC-ECM interactions (Chapter 5). Taken together, these studies will aid in the development of tools for studying the complex interactions between hESCs and their microenvironment.

## **6.2 The hESC Niche and the ECM**

One of the primary goals of research focused on the microenvironment is to elucidate all the processes involved in the control of hESC fate. The ability to control if a stem cell self-renews or differentiates is critical to the potential therapeutic application of hESCs. Parallel to this need is the ability to direct lineage specific differentiation to generate pure populations of tissue-specific cell types. Currently, hESC differentiation is directed through the use of cocktails of exogenously supplemented growth factors (reviewed in [1]). Depending on the desired cell type, multiple differing cocktails can be required dependent on the time point of the differentiation protocol [2]. Which factors are supplemented is conventionally determined through large screens of proteins involved in pathways that are known to be critical for the regulation of pluripotency. However,

many of these generated protocols struggle to produce pure populations of tissue-specific cell types. This shortcoming stems from an incomplete understanding of all of the processes contributing to hESC control within the *in vitro* microenvironment. As we have shown in this thesis, these processes can potentially be governed by interactions of hESCs or cytokines with the ECM.

### 6.2.1 Wnt Signaling in the Microenvironment

There are three primary pathways that are activated upon binding of Wnt ligands to their cognate receptors (For a review of Wnt signaling, see [3, 4]). The canonical pathway involves interaction of Wnt ligands at the cell surface with Frizzled (Fz)/low-density lipoprotein receptor-related protein (LRP) complexes. In the absence of Wnt, cytoplasmic  $\beta$ -catenin is associated with a complex containing Axin and Adenomatous Polyposis Coli (APC). This complex facilitates the phosphorylation of  $\beta$ -catenin by glycogen synthase kinase 3- $\beta$  (GSK-3 $\beta$ ) resulting in its subsequent degradation. Upon binding of Wnt ligands, phosphorylation of  $\beta$ -catenin is inhibited allowing it to translocate to the nucleus where it regulates gene expression through interaction with lymphoid enhancer factor (LEF)/T-cell factor (TCF) transcription factors.

In the extracellular space, Wnt proteins are relatively insoluble due to the presence of a palmitoyl lipid modification. This modification has been shown to be important for the secretion, activity, and solubility of Wnt proteins as well as for their interactions with binding partners [5]. In the extracellular space Wnt signaling is antagonized through interactions with a variety of inhibitors (reviewed in [6]). The two main groups are the soluble frizzled related proteins (sFRP) and the Dickkopf (Dkk) family. Dkk proteins are

believed to inhibit canonical Wnt signaling through interaction with the LRP receptors [6]. The sFRP family is thought to bind directly to the Wnt ligands themselves, leading to a diverse array of potential roles for these proteins other than antagonism. This is emphasized by the multiple divergent roles for the sFRP family members in a variety of pathological conditions (reviewed in [7, 8]).

In mouse ESCs, activation of the canonical Wnt pathway is understood to promote the maintenance of self-renewal and pluripotency (reviewed in [9]). In human ESCs, the picture is less clear, and contrasting roles for canonical Wnt signaling have been suggested [10, 11]. However, recent data has garnered support for a model of Wnt signaling activation that supports stem cell fate determination [12, 13]. Activation of canonical Wnt signaling enhances hESC growth and survival in an undifferentiated state, as well as their differentiation. However, aberrant regulation of the canonical pathway is thought to be involved in diseases such as cancer [3]. Therefore, control over the activity of Wnt ligands in the extracellular space is potentially critical for the proper maintenance of the ES cell phenotype.

From our analysis it remains unclear what role the sFRP proteins play in the regulation of Wnt signaling in the extracellular space and the resultant changes in hESC phenotype (Chapter 5). shRNA mediated knockdown of sFRP1 or 2 gene expression or direct inhibition of sFRP1 protein using a small molecule inhibitor results in no change in expression for Oct3/4 and Nanog, hallmarks of pluripotency. Based on our findings with direct supplementation of soluble recombinant Wnt3a, it is clear that Wnt3a promotes stem cell fate determination dependent on the growth factor microenvironment. sFRP1

and sFRP2 are unable to inhibit Wnt3a induced changes when supplemented in MEF-CM. These data are potentially confounded by the presence of numerous other Wnt regulatory proteins in both hESC conditioned medium [14] and in the CMTX (Chapter 4-5), such as Cerberus. The reduction of sFRP activity through small molecule inhibition or shRNA knockdown is potentially compensated for by these other regulatory proteins or increased activity of additional sFRP family members. The effects of direct supplementation of sFRP1 and sFRP2 are also potentially reduced in this way, where other proteins can restore the proper balance of Wnt activity. The complexity and cross-talk in signaling pathways present in the microenvironment suggests that a combination of factors act on hESCs. This is highlighted by the results of our proteomics screen where other antagonists of core pluripotency pathways were identified.

### *6.2.2 TGF- $\beta$ Signaling in the Microenvironment*

In the MS-based proteomics screen of CMTX we identified factors implicated in the regulation of TGF- $\beta$  pathways, specifically Lefty 1 and 2 and Cerberus proteins (Chapter 4). The TGF- $\beta$  superfamily of proteins consists of over 30 members, including Activins, Nodal, and bone morphogenic proteins (BMP). TGF- $\beta$  family members are directly involved in processes such as cell growth and apoptosis. Furthermore, this family has been implicated as playing a prominent role during embryonic development in processes such as gastrulation and patterning (reviewed in [15]). TGF- $\beta$  signaling primarily operates via transmission of extracellular signals through complexes of type-I (activin receptor-like kinases, e.g. ALK4, ALK7) and type-II (activin receptor IIB,

ActRIIB) transmembrane receptors and their associated co-factors (e.g. Cripto). These signals are translated to phosphorylation events in different complexes of Smad proteins that in turn regulate target gene expression in the nucleus (reviewed in [15]).

TGF- $\beta$  signaling is mediated through interactions between soluble factors in the microenvironment. The Lefty proteins are extracellular antagonists of TGF- $\beta$  signaling that act through inhibition of the embryonic morphogen Nodal [16]. Regulation of Nodal activity through inhibition by Lefty has been shown to be critical for proper development during embryogenesis [16]. In hESCs, activation of the Smad2/3 branch of the TGF- $\beta$  pathway mediated by Nodal or Activin is known to be one of the core processes critical for the maintenance of self-renewal and pluripotency [17, 18]. Defined media such as E8 and the defined SILAC medium employed here contain exogenous Activin or Nodal to facilitate the maintenance of undifferentiated hESCs [19, 20]. Activin has also been found in MEF conditioned medium screened using MS-based proteomics [14, 21]. Inhibition of Lefty proteins has been shown to promote maintenance of undifferentiated hESCs; however, correct differentiation of these cells is impaired [22]. Interestingly however, inhibition of Nodal using Lefty does not induce differentiation of hESCs [18]. Moreover, induction of Lefty has been observed to be important for exit from the pluripotent state in embryoid body formation assays [23]. Taken together, these findings indicate that Lefty functions to maintain a balance of Nodal induced TGF- $\beta$  initiation in hESCs.

Detection of Lefty isoforms in CMTX illustrates that hESCs are secreting factors to generate a matrix microenvironment designed to regulate extracellular signaling



involving soluble factors. Although the direct supplementation of recombinant Lefty was not able to enhance the maintenance of an undifferentiated state in hESCs induced to differentiate, regulation of Nodal signaling by Lefty in the microenvironment has previously been observed to be facilitated through interactions with the ECM [24]. In *Xenopus* embryos, the interaction of Lefty with ECM linked heparan sulfate proteoglycans has been observed to facilitate control over Nodal signaling [24]. The ECM enhances the stability, transport, and effective range of the Lefty and Nodal proteins [24]. These effects aid in the generation of morphogen gradients important for proper development. Similar processes in the microenvironment potentially contribute to maintenance of a 'primed' hESC state, wherein control over differentiation is enhanced by interactions between Lefty and Nodal facilitated by the ECM.

The ability of Lefty containing CMTX to enhance maintenance of an undifferentiated state is potentially acting through pathways alternative to Nodal induced TGF- $\beta$  activation. The positive effects of Nodal signaling on hESCs are well established [17, 18]. However, exogenous supplementation with Lefty does not induce differentiation of hESCs [18]. Expression of Nodal and Lefty proteins are known to be rapidly decreased following the induction of differentiation [25]. The presence of Lefty in the CMTX and the absence of hESC derived Nodal following differentiation potentially confer an enhancement in the maintenance of undifferentiated cells through other TGF- $\beta$  pathways. BMP signaling through Smad 1/5/8 is observed to be increased specifically in differentiated hESCs [25]. Moreover, BMP signaling induced by the extracellular cytokine BMP-4 is known to induce differentiation of hESCs, and its inhibition using antagonists such as Noggin to block differentiation [26, 27]. Lefty has been observed to

inhibit BMP-4 induced TGF- $\beta$  activation by blocking the phosphorylation of Smad proteins in P19 embryonal carcinoma cells [28]. In our CMTX experiments, Lefty may be acting on BMP-4 induced TGF- $\beta$  signaling and thereby inhibiting differentiation resulting from activation of this pathway. This is highlighted by the presence of other factors in the CMTX that inhibit Nodal/BMP signaling, such as Cerberus.

### *6.2.3 New View of the hESC Microenvironment*

Using the assays presented here we observed the ability of the CMTX, containing regulators of the Wnt and TGF- $\beta$  pathways, to alter the behavior of hESCs in the microenvironment. However, in our recombinant and antibody blocking CMTX experiments, both of these pathways were monitored individually and neither was able to fully recapitulate the positive effect observed for hESCs on CMTX. The microenvironment is considered to be an effector of cellular change acting through a dynamic balance resulting from an array of contributors. As such, it is likely that the core pathways we have investigated here function together in the CMTX to generate the observed effect. Indeed, multiple levels of cross-talk have been suggested amongst the FGF/TGF- $\beta$ /Wnt pathways [13, 29]. In hESCs, the maintenance of self-renewal and pluripotency is controlled by the co-operative activity of these three core pathways. The addition of the ECM to this model adds an additional layer of complexity, wherein proteins bound to the matrix can act to regulate individual pathways, the effects of which are subsequently potentiated through cross-talk with others. Given the known roles of the ECM in the contribution to the generation of morphogen gradients in other

developmental systems, it is not hard to envision a similar activity regulating pluripotency in the hESC niche.

### **6.3 Development of ECM Environments for hESCs**

The ECM is one of the core elements governing cellular changes in the microenvironment. Not only can the ECM regulate cell growth, attachment, and movement, but in hESC culture can affect processes such as differentiation. The beneficial effects of the ECM are further highlighted by the positive outcome observed when *in vivo* injections directed at teratoma formation are performed using hESCs diluted in Matrigel™ [30]. The proposed mechanism for the enhancement observed in the presence of Matrigel™ is related to the reduction of apoptosis through interactions with the ECM and the potential for Matrigel to induce growth factor stimulation [30]. The xenogenic nature of Matrigel inhibits its use with injections or otherwise in potential therapeutic strategies. Developing an understanding of the processes and factors regulated by the components of Matrigel, or other hESC supportive matrices will aid in the generation of xeno-free matrices for use *in vitro* or *in vivo*.

Using the techniques presented in this thesis, analysis of the diverse range of matrices available for hESC culture will assist in the development of ECM supports suitable for a wide range of hESCs. Using MS-based proteomics we demonstrate the utility of determining the composition of cell-derived and recombinant growth matrices used in hESC culture (Chapter 3). From these studies we were able to elucidate factors directly related to the enhancement of hESC growth in *in vitro* culture. Moreover, using the methods developed and optimized here to facilitate the analysis of hESC-derived

matrices, we were able to characterize a novel self-supportive matrix microenvironment generated by the stem cells during growth *in vitro*. The findings of these works will have a direct application towards obtaining a comprehensive understanding of hESC interactions within the microenvironment. Perhaps more importantly however, the information contained in this thesis can be used to aid in the development of biomaterials designed to mimic the ECM.

In recent years, as a direct result of the potential for the application of stem cells in therapeutic applications, numerous biomaterials have been tested for their viability for the maintenance of hESCs (reviewed in [31]). Natural materials such as collagen, hyaluronic acid, and alginate have all shown promise for the control of self-renewal or differentiation of stem cells [32-34]. Synthetic materials such as PLGA and PEG have also been utilized to control the properties of stem cells *in vitro* (reviewed in [35]). Pioneering work from the Langer group was one of the first studies to analyze hESC-ECM interactions on a large-scale using synthetic polymer based arrays [36, 37]. Utilizing different combinations of acrylate, diacrylate, dimethacrylate, and triacrylate monomers, they profile over 1700 ECM interactions in a single array. In recent years, nano-scale array platforms that utilize conventional DNA spotting technology have facilitated the analysis of a wide range of biomaterials for their effect on stem cell maintenance and differentiation [38-42]. The designs of polymers or bioactive materials to be screened are typically done in a discovery type fashion, or through mimicry of known cell-ECM interactions. Elucidating core ECM factors present in cell-derived matrices can potentially aid in directing these array-based screens. By focusing on

matrices known to be beneficial for stem cell maintenance, factors identified in our proteomics screen can be used to generate biomaterials tailored for hESCs.

Aside from the ability to regulate the activity of these matrices through modulation of properties such as stiffness, size, and shape, other physical modifications can be made to promote the desired experimental outcome [35]. The addition of bioactive growth factors directly to the polymerized matrix has been used to modulate the self-renewal and differentiation of hESCs [43, 44]. Controlling the availability of these growth factors can be regulated through the addition of compounds such as heparan sulfate to the matrix [35]. Based on the findings presented here, the presence of multiple soluble growth factor binding and regulatory proteins in the matrix can regulate the differentiation of stem cells. By determining the pathways that are potentially regulated by candidate proteins identified in the CMTX, our proteomic analyses can aid in the development of biomaterials that mimic the necessary binding or cytokine requirements. Furthermore, investigating components of hESC-derived matrix microenvironments as we have attempted to do here can be completed on defined matrices instead of Matrigel. The ability to control the deposition and release of bioactive growth factors from the matrix through the use of synthetic alternatives will permit direct validation of deposited factors. Together, these complementary studies would be beneficial for determining ECM-associated regulatory proteins that can be combined with biomaterials to control pathways related to self-renewal and differentiation.

## 6.4 Studying hESCs using Quantitative Proteomics

With the increase in research focused on ESCs, the number of developmentally related cell types that can be successfully cultured *in vitro* is rising. It is clear that comparison of pluripotent or multipotent progenitor cells with differentiated sub-types can provide valuable information on stem cell regulation. The application of high-throughput genomic technologies in these areas has already resulted in advancement in our understanding of stem cells. However, global screening using proteomics methods has lagged behind, partially due to the difficulty in achieving cell quantities amenable to these experiments. This is particularly difficult for hESCs due to their strict culture requirements.

Application of metabolic labeling approaches such as SILAC opens new avenues for performing comparative analyses of multipotent and differentiated cell types. Utilization of our SILAC protocol provides researchers with the tools necessary to acquire the quantities of cells required, in a reproducible fashion, for proteomics experiments. Currently there is only one other example of a defined hESC culture medium amenable to SILAC experimentation presented in the literature [45]. However, as the efficiency of methods for the *in vitro* culture of hESCs continues to increase, so too will the development of enhanced media for their culture. This is highlighted by recent work from the Thomson lab where they systematically tested individual medium components to assess their necessity for the maintenance of hESCs and hiPSCs [20]. They demonstrated that the SCs could be maintained for extended periods in media containing just eight ingredients, referred to as E8 (insulin, selenium, transferrin,

l-ascorbic acid, FGF2 and TGF- $\beta$  (or Nodal) in DMEM/F12). E8 has the added benefit of being serum-free, offering an attractive platform for the analysis of conditioned media from hESCs grown in feeder-free conditions. As we have demonstrated here (Chapter 2), the adaption of chemically defined culture media such as E8 to SILAC experimentation can be achieved simply by modulating the amino acid composition, even for metabolically sensitive cell types such as hESCs.

Outside of direct comparisons of pluripotent and differentiated cell types, quantitative proteomics methods like SILAC offer many other attractive research avenues in the study of hESC biology. An emerging area where quantitative mass spectrometry approaches have a direct application is in the analysis of global protein turnover in hESCs. The metabolic incorporation of the SILAC label permits time-dependent analysis of protein synthesis and degradation rates, analogous to a pulse-chase style experiment [46]. Currently there are no examples of the direct analysis of protein turnover on a global scale in mouse or human ESCs. The most comprehensive proteomics studies of hESCs and hiPSCs to date have focused on measuring abundance snapshots [47]. Recent work from the Selbach lab has demonstrated the utility of measuring protein and mRNA degradation rates to obtain a picture of global cell regulation as a function of turnover [48].

It is not hard to envision the potential applications for SILAC derived turnover measurements in hESCs or their niches. Direct examination of the pathways that feed into the maintenance of homeostasis through modulation of the synthesis and degradation of proteins on a global scale can potentially clarify the mechanisms

governing pluripotency of hESCs and preservation of a state primed for differentiation. Furthermore, metabolic labeling with SILAC can be used to unlock the potential mechanisms that regulate the switch from a primed state to differentiation in stem cell populations. When coupled with established methods for measuring mRNA turnover [49], or high-resolution screens of global translation rates using ribosome density profiling [50], the potential acquisition of a global measurement of hESC control makes the application of SILAC protocols such as those developed here (Chapter 2) an attractive platform in stem cell research. Additionally, coupling these quantitative proteomics analysis platforms to investigation of hESC niches offers the opportunity to monitor temporal signaling patterns as indicated by differential protein levels in conditioned media or matrices.

## **6.5 Future Applications in Stem Cell Research**

### *6.5.1 Niches from other stem cells*

The hESC niche represents a dynamic environment that is critical for control over decisions concerning cell fate and its analysis is crucial for a complete understanding of pluripotency. However, the recent expansion of research involving adult stem cells (ASC) offers new opportunities for studies directed at investigation of the microenvironment. Furthermore, the rapid expansion of derived induced pluripotent stem (iPS) cells from a variety of tissue and disease types offers interesting new avenues for study of the microenvironment. The analysis of CMTX completed here (Chapter 4) was performed on a single iPS cell line. Our findings indicate significant similarity between the hESC and iPS cell derived matrices analyzed. However, due to



the distinct differences between iPS lines dependent on their derivation method or parental cell origin [51, 52] (reviewed in [53]), expansion of our analysis to include other lines is desirable.

The application of quantitative proteomic methodologies such as those developed here (Chapter 2) also offer interesting avenues for continuing exploratory studies in stem cell niches *in vitro*. The induction of pluripotency in iPS cells is known to take upwards of 30 days following transgene expression in culture [54]. Quantitative changes of protein turnover during reprogramming coupled with temporal examination of secreted factors in the niche would provide valuable insight into processes contributing to the induction of pluripotency. The assessment of expression patterns during reprogramming of candidate proteins identified in this thesis (Chapter 4) could reveal valuable information on factors such as the sFRP, Cerberus, and Lefty proteins. With the previous knowledge that these proteins function at the crossroads of the undifferentiated and differentiated state, their examination during reprogramming could reveal distinct expression patterns that contribute to pluripotency. Additionally, these trends can be compared to data generated in this and other studies of the microenvironment to characterize their correlation to known roles in hESCs.

#### *6.5.2 Addressing heterogeneity in stem cell cultures*

Two of the core components of the microenvironment are the ECM support and paracrine/autocrine signaling regulated by soluble factors. In the hESC niche this can be expanded to include accessory or support cells that contribute to processes involved with both of the previously mentioned core components. In two-dimensional adherent

cultures *in vitro* hESCs tend to grow as tight aggregates. hESCs are refractory to passaging or maintenance as single cells. Within these cell clusters, recent work has observed the ability of hESCs to generate colony specific niches that contain signaling gradients that effect core pluripotency pathways [55]. These findings suggest that a level of cellular heterogeneity exists within hESC cultures and even within specific colonies. The non-homogeneous nature of stem cell culture has been noted before in the literature [56-60]. This variability can be the result of differences in cell cycle progression as well as spontaneous differentiation. Even in a wholly undifferentiated population, differences in core pluripotency genes such as Nanog have been observed [61]. Considering the ability of the microenvironment to elicit changes in cell behavior, differences in hESC colony specific niches can potentially be a significant contributor to this heterogeneity. By collecting data that represents an average of a heterogeneous population, the potential sensitivity of the results is limited as changes represented in a sub-type of cells will be diluted. Therefore, developing methods directed at monitoring hESC characteristics at a single-cell level are critical for in-depth microenvironment analysis.

Recent developments in methods for single-cell monitoring of global processes such as transcription and translation offer new avenues for stem cell research (reviewed in [62, 63]). Furthermore, with the development of methods for high-throughput analysis of matrices using spotted arrays (see Section 5.3), single-cell analysis of the hESC niche is now potentially viable. As such, studies directed at single-cell analysis of behavior patterns in hESC niches have been presented [55]. The work presented here offers potential extensions for modeling of single-cells in hESC niches. Using factors

identified in our proteomic characterizations of matrices (Chapter 3 – 4) in combination with micropatterning techniques for generating ECM arrays, the activity of single cells within colonies in response to seeded gradients of deposited factors could be assayed. Arrays such as these can potentially reveal the specific regulatory mechanisms of factors identified in our analysis of CMTX, such as the sFRP and Lefty proteins. The expression of Lefty B has previously been observed to change dependent on hESC colony size, indicating the potentially dynamic nature of these inhibitors [55]. Furthermore, the established gradient signaling mechanisms of both the Wnt and Nodal pathways in development indicate that a similar process may be occurring *in vitro* in the hESC niche. The ability to perform directed screens based off of factors identified in our study coupled with high-resolution single-cell data acquisition offers an attractive platform for addressing key questions concerning the hESC microenvironment.

## 6.6 References

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## Appendix I

### Supporting Datasets and Information for the Analysis of the Pluripotent Stem Cell Depositome

**Table A1.1 N-GFR Matrigel Protein Identifications.** List of all proteins identified in N-GFR Matrigel (non-growth factor reduced) with corresponding accession, description, PEAKS score, unique peptide numbers, and coverage (in %).

Accession	Description	Score	Coverage (%)	#Unique
P19137 LAMA1_MOUSE	Laminin subunit alpha-1 OS=M	548.72	73	299
P02469 LAMB1_MOUSE	Laminin subunit beta-1 OS=M	534.59	81	232
P10493 NID1_MOUSE	Nidogen-1 OS=Mus musculus	506.09	91	199
P02468 LAMC1_MOUSE	Laminin subunit gamma-1 OS	521.29	88	198
Q8VDD5 MYH9_MOUSE	Myosin-9 OS=Mus musculus	445.87	74	117
Q05793 PGBM_MOUSE	Basement membrane-specific	426.69	56	115
P16546 SPTA2_MOUSE	Spectrin alpha chain, brain OS	399.37	77	113
P07724 ALBU_MOUSE	Serum albumin OS=Mus mus	394.86	93	79
P20029 GRP78_MOUSE	78 kDa glucose-regulated pro	418.33	86	78
P19324 SERPH_MOUSE	Serpin H1 OS=Mus musculus	385.85	87	77
P63038 CH60_MOUSE	60 kDa heat shock protein, mi	380.07	92	74
P01027 CO3_MOUSE	Complement C3 OS=Mus mus	330.22	67	67
P07214 SPRC_MOUSE	SPARC OS=Mus musculus G	395.48	80	66
P20152 VIME_MOUSE	Vimentin OS=Mus musculus	390.87	96	66
P09103 PDIA1_MOUSE	Protein disulfide-isomerase O	372.59	93	66
Q80X90 FLNB_MOUSE	Filamin-B OS=Mus musculus	322.12	52	59
Q62261 SPTB2_MOUSE	Spectrin beta chain, brain 1 O	307.59	61	59
Q9QXS1 PLEC_MOUSE	Plectin OS=Mus musculus GN	255.85	52	58
P63017 HSP7C_MOUSE	Heat shock cognate 71 kDa p	415.5	89	56
Q3UQ28 PXDN_MOUSE	Peroxidasin homolog OS=Mus	364.3	72	56
Q01853 TERA_MOUSE	Transitional endoplasmic retic	333.88	72	55
P27773 PDIA3_MOUSE	Protein disulfide-isomerase A3	333.85	80	54
Q9JHU4 DYHC1_MOUSE	Cytoplasmic dynein 1 heavy c	282.97	49	54
P14733 LMNB1_MOUSE	Lamin-B1 OS=Mus musculus	373.76	86	52
Q6P5E4 UGGG1_MOUSE	UDP-glucose:glycoprotein glu	325.06	61	52
Q92111 TRFE_MOUSE	Serotransferrin OS=Mus musc	335.58	78	50
Q9D0E1 HNRPM_MOUSE	Heterogeneous nuclear ribonu	305.06	83	50
Q61838 A2M_MOUSE	Alpha-2-macroglobulin OS=M	319.31	66	46
A2ARV4 LRP2_MOUSE	Low-density lipoprotein recept	253.95	51	46
P48678 LMNA_MOUSE	Prelamin-A/C OS=Mus muscu	311.51	74	45
P08113 ENPL_MOUSE	Endoplasmic reticulum chaper	284.57	64	44
Q8VIJ6 SFPQ_MOUSE	Splicing factor, proline- and gl	311.2	69	43
Q9R0B9 PLOD2_MOUSE	Procollagen-lysine,2-oxoglutar	302.4	71	43
Q64727 VINC_MOUSE	Vinculin OS=Mus musculus G	290.92	81	43
P38647 GRP75_MOUSE	Stress-70 protein, mitochondri	317.3	74	42
Q8K310 MATR3_MOUSE	Matrin-3 OS=Mus musculus G	310.31	65	40
Q61879 MYH10_MOUSE	Myosin-10 OS=Mus musculus	328.74	54	39
P26039 TLN1_MOUSE	Talin-1 OS=Mus musculus GN	216.74	48	39
Q8CGC7 SYEP_MOUSE	Bifunctional aminoacyl-tRNA s	283.42	51	38
P14211 CALR_MOUSE	Calreticulin OS=Mus musculus	300.3	91	37
P08003 PDIA4_MOUSE	Protein disulfide-isomerase A4	285.22	69	37
Q68FD5 CLH_MOUSE	Clathrin heavy chain 1 OS=M	244.47	51	37
P11276 FINC_MOUSE	Fibronectin OS=Mus musculus	298.28	37	36
P13020 GELS_MOUSE	Gelsolin OS=Mus musculus G	277.29	59	35
P16858 G3P_MOUSE	Glyceraldehyde-3-phosphate d	323.25	84	33
P62806 H4_MOUSE	Histone H4 OS=Mus musculus	247.47	82	33
Q922R8 PDIA6_MOUSE	Protein disulfide-isomerase A6	328.41	80	32
O08677 KNG1_MOUSE	Kininogen-1 OS=Mus musculu	310.69	53	32
P56480 ATPB_MOUSE	ATP synthase subunit beta, m	287.08	86	31
Q99PV0 PRP8_MOUSE	Pre-mRNA-processing-splicing	247.66	40	31
Q6PDQ2 CHD4_MOUSE	Chromodomain-helicase-DNA	241.84	43	31
P09405 NUCL_MOUSE	Nucleolin OS=Mus musculus	266.11	69	30
P06909 CFAH_MOUSE	Complement factor H OS=Mus	263.83	41	30
P10126 EF1A1_MOUSE	Elongation factor 1-alpha 1 OS	252.38	71	29



P08032	SPTA1_MOUSE	Spectrin alpha chain, erythrocyte	249.83	39	29
O70133	DHX9_MOUSE	ATP-dependent RNA helicase X	229.17	42	29
O88569	ROA2_MOUSE	Heterogeneous nuclear ribonucleoprotein	297.94	78	28
Q8K0E8	FIBB_MOUSE	Fibrinogen beta chain OS=Mus musculus	315.58	74	27
P08249	MDHM_MOUSE	Malate dehydrogenase, mitochondrial	307.82	77	27
Q8BTM8	FLNA_MOUSE	Filamin-A OS=Mus musculus	240.2	31	27
P17742	PPIA_MOUSE	Peptidyl-prolyl cis-trans isomerase	294.46	83	26
P52480	KPYM_MOUSE	Pyruvate kinase isozymes M1/M2	254.26	59	26
Q8VCM7	FIBG_MOUSE	Fibrinogen gamma chain OS=Mus musculus	289.26	72	25
Q03265	ATPA_MOUSE	ATP synthase subunit alpha, mitochondrial	280.6	75	25
P29341	PABP1_MOUSE	Polyadenylate-binding protein 1	265.8	59	25
Q91W90	TXND5_MOUSE	Thioredoxin domain-containing protein	276.26	78	24
O08795	GLU2B_MOUSE	Glucosidase 2 subunit beta OS=Mus musculus	265.43	59	24
Q9D8E6	RL4_MOUSE	60S ribosomal protein L4 OS=Mus musculus	243.16	59	24
P29533	VCAM1_MOUSE	Vascular cell adhesion protein 1	228.91	54	24
P05202	AATM_MOUSE	Aspartate aminotransferase, mitochondrial	223.94	67	24
Q99PL5	RRBP1_MOUSE	Ribosome-binding protein 1 OS=Mus musculus	202.39	28	24
P11499	HS90B_MOUSE	Heat shock protein HSP 90-beta class B	294.42	69	23
O88322	NID2_MOUSE	Nidogen-2 OS=Mus musculus	271.23	40	23
P21614	VTDB_MOUSE	Vitamin D-binding protein OS=Mus musculus	257.96	67	22
Q9R0E2	PLOD1_MOUSE	Procollagen-lysine,2-oxoglutarate 5-oxylase	243.69	48	22
P39061	COIA1_MOUSE	Collagen alpha-1(XVIII) chain	228.75	34	22
Q61001	LAMA5_MOUSE	Laminin subunit alpha-5 OS=Mus musculus	227.53	28	22
Q91W39	NCOA5_MOUSE	Nuclear receptor coactivator 5	216.62	47	22
P47911	RL6_MOUSE	60S ribosomal protein L6 OS=Mus musculus	215.87	67	22
P20108	PRDX3_MOUSE	Thioredoxin-dependent peroxidoreductase 3	273.48	86	21
Q8R326	PSPC1_MOUSE	Paraspeckle component 1 OS=Mus musculus	223.02	53	21
Q9JKR6	HYOU1_MOUSE	Hypoxia up-regulated protein 1	219.62	50	21
P14206	RSSA_MOUSE	40S ribosomal protein SA OS=Mus musculus	272.53	71	20
Q01405	SC23A_MOUSE	Protein transport protein Sec23A	270.64	62	20
Q9WTP6	KAD2_MOUSE	Adenylate kinase 2, mitochondrial	247.36	80	20
P01942	HBA_MOUSE	Hemoglobin subunit alpha OS=Mus musculus	243.8	100	20
P61979	HNRPK_MOUSE	Heterogeneous nuclear ribonucleoprotein K	242.52	71	20
P58252	EF2_MOUSE	Elongation factor 2 OS=Mus musculus	241.7	45	20
Q9D8N0	EF1G_MOUSE	Elongation factor 1-gamma OS=Mus musculus	227.23	62	20
Q00623	APOA1_MOUSE	Apolipoprotein A-I OS=Mus musculus	223.26	73	20
Q99K48	NONO_MOUSE	Non-POU domain-containing protein 1	216.7	65	20
Q3U1J4	DDB1_MOUSE	DNA damage-binding protein 1	214.68	34	20
Q8BU30	SYIC_MOUSE	Isoleucyl-tRNA synthetase, cytoplasmic	208.43	39	20
P62259	1433E_MOUSE	14-3-3 protein epsilon OS=Mus musculus	279.64	87	19
P17225	PTBP1_MOUSE	Polypyrimidine tract-binding protein 1	273.25	71	19
P02088	HBB1_MOUSE	Hemoglobin subunit beta-1 OS=Mus musculus	269.07	83	19
Q91X72	HEMO_MOUSE	Hemopexin OS=Mus musculus	242.73	60	19
Q8VDJ3	VIGLN_MOUSE	Vigilin OS=Mus musculus GNAS	208	28	19
P57759	ERP29_MOUSE	Endoplasmic reticulum resident protein 29	244.39	68	18
Q9Z247	FKBP9_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP9	230.77	51	18
Q9DC23	DJC10_MOUSE	DnaJ homolog subfamily C member 10	217.63	56	18
Q61595	KTN1_MOUSE	Kinectin OS=Mus musculus	209.35	42	18
Q9EQK5	MVP_MOUSE	Major vault protein OS=Mus musculus	182.04	42	18
Q9CU62	SMC1A_MOUSE	Structural maintenance of chromosomes 1A	176.97	30	18
Q7TPR4	ACTN1_MOUSE	Alpha-actinin-1 OS=Mus musculus	318.99	62	17
Q61292	LAMB2_MOUSE	Laminin subunit beta-2 OS=Mus musculus	218.1	25	17
P62301	RS13_MOUSE	40S ribosomal protein S13 OS=Mus musculus	209.86	44	17
P62908	RS3_MOUSE	40S ribosomal protein S3 OS=Mus musculus	191.2	70	17
P61982	1433G_MOUSE	14-3-3 protein gamma OS=Mus musculus	270.33	96	16

Q61937 NPM_MOUSE	Nucleophosmin OS=Mus mus	224.16	63	16
Q9Z1Q9 SYVC_MOUSE	Valyl-tRNA synthetase OS=Mu	216.69	31	16
Q9CZU6 CISY_MOUSE	Citrate synthase, mitochondria	198.63	42	16
Q64433 CH10_MOUSE	10 kDa heat shock protein, mi	197.06	85	16
P25444 RS2_MOUSE	40S ribosomal protein S2 OS=	193.63	72	16
P29758 OAT_MOUSE	Ornithine aminotransferase, m	192.73	46	16
Q9WTM5 RUVB2_MOUSE	RuvB-like 2 OS=Mus musculu	164.84	51	16
A2ASS6 TITIN_MOUSE	Titin OS=Mus musculus GN=7	70.94	6	16
Q9Z2X1 HNRPF_MOUSE	Heterogeneous nuclear ribonu	249.84	70	15
P27659 RL3_MOUSE	60S ribosomal protein L3 OS=	237.73	63	15
P23780 BGAL_MOUSE	Beta-galactosidase OS=Mus r	229.32	45	15
Q9WV54 ASAH1_MOUSE	Acid ceramidase OS=Mus mu	224.05	46	15
P57776 EF1D_MOUSE	Elongation factor 1-delta OS=	223.25	76	15
Q8R3Q6 CCD58_MOUSE	Coiled-coil domain-containing	212.39	81	15
Q922B2 SYDC_MOUSE	Aspartyl-tRNA synthetase, cyt	207.71	50	15
O08810 U5S1_MOUSE	116 kDa U5 small nuclear ribo	205.25	31	15
O08749 DLDH_MOUSE	Dihydrolipoyl dehydrogenase,	204.92	62	15
P61358 RL27_MOUSE	60S ribosomal protein L27 OS	191.92	53	15
P53026 RL10A_MOUSE	60S ribosomal protein L10a O	188.98	43	15
Q9Z1Z0 USO1_MOUSE	General vesicular transport fa	100.33	43	15
O35643 AP1B1_MOUSE	AP-1 complex subunit beta-1 (	248.1	50	14
Q9D1M4 MCA3_MOUSE	Eukaryotic translation elongati	230.67	84	14
Q9DBG5 PLIN3_MOUSE	Perilipin-3 OS=Mus musculus	222.6	73	14
P62962 PROF1_MOUSE	Profilin-1 OS=Mus musculus C	222.4	86	14
P97496 SMRC1_MOUSE	SWI/SNF complex subunit SM	219.45	54	14
Q61207 SAP_MOUSE	Sulfated glycoprotein 1 OS=M	215.05	51	14
Q3UPH1 PRRC1_MOUSE	Protein PRRC1 OS=Mus mus	209.4	55	14
Q587J6 LITD1_MOUSE	LINE-1 type transposase dom	206.2	42	14
P40142 TKT_MOUSE	Transketolase OS=Mus musc	205.43	39	14
P62918 RL8_MOUSE	60S ribosomal protein L8 OS=	202.4	70	14
P62082 RS7_MOUSE	40S ribosomal protein S7 OS=	192.4	63	14
Q91VM5 RBMXL_MOUSE	Heterogeneous nuclear ribonu	184.22	51	14
P29699 FETUA_MOUSE	Alpha-2-HS-glycoprotein OS=	286.43	69	13
P62843 RS15_MOUSE	40S ribosomal protein S15 OS	240.01	82	13
P07901 HS90A_MOUSE	Heat shock protein HSP 90- $\alpha$	230.89	57	13
Q3THW5 H2AV_MOUSE	Histone H2A.V OS=Mus musc	222.74	79	13
P12970 RL7A_MOUSE	60S ribosomal protein L7a OS	218.32	50	13
Q61576 FKB10_MOUSE	Peptidyl-prolyl cis-trans isome	211.94	50	13
Q99JR5 TINAL_MOUSE	Tubulointerstitial nephritis anti	211.76	47	13
P24369 PPIB_MOUSE	Peptidyl-prolyl cis-trans isome	207.16	63	13
Q9CYZ2 TPD54_MOUSE	Tumor protein D54 OS=Mus n	204.5	71	13
Q8BG05 ROA3_MOUSE	Heterogeneous nuclear ribonu	197.34	36	13
Q9DBJ1 PGAM1_MOUSE	Phosphoglycerate mutase 1 C	191.64	72	13
Q8BP92 RCN2_MOUSE	Reticulocalbin-2 OS=Mus mus	169.45	66	13
Q62376 RU17_MOUSE	U1 small nuclear ribonucleopr	169	31	13
P62270 RS18_MOUSE	40S ribosomal protein S18 OS	152.31	62	13
P63101 1433Z_MOUSE	14-3-3 protein zeta/delta OS=	278.83	85	12
Q9CQU0 TXD12_MOUSE	Thioredoxin domain-containing	237.42	85	12
Q9D1Q6 ERP44_MOUSE	Endoplasmic reticulum reside	227.11	72	12
P31001 DESM_MOUSE	Desmin OS=Mus musculus G	224.21	54	12
P62317 SMD2_MOUSE	Small nuclear ribonucleoprote	213.65	72	12
Q8BWT1 THIM_MOUSE	3-ketoacyl-CoA thiolase, mitoc	212.23	64	12
P18242 CATD_MOUSE	Cathepsin D OS=Mus muscul	198.86	54	12
Q3V1T4 P3H1_MOUSE	Prolyl 3-hydroxylase 1 OS=Mu	197.25	34	12
Q9CXW3 CYBP_MOUSE	Calcyclin-binding protein OS=	197.07	54	12

Q8BH97 RCN3_MOUSE	Reticulocalbin-3 OS=Mus mus	186.96	63	12
P62754 RS6_MOUSE	40S ribosomal protein S6 OS=	181.51	41	12
Q99J14 PSMD6_MOUSE	26S proteasome non-ATPase	171.19	60	12
Q9CSN1 SNW1_MOUSE	SNW domain-containing prote	163.32	40	12
Q8BJ71 NUP93_MOUSE	Nuclear pore complex protein	160.84	57	12
P80316 TCPE_MOUSE	T-complex protein 1 subunit e	155.97	52	12
Q8BH61 F13A_MOUSE	Coagulation factor XIII A chain	142.51	22	12
P57780 ACTN4_MOUSE	Alpha-actinin-4 OS=Mus musc	261.83	52	11
P49312 ROA1_MOUSE	Heterogeneous nuclear ribonu	225.25	60	11
O35658 C1QBP_MOUSE	Complement component 1 Q s	225.2	64	11
O89086 RBM3_MOUSE	Putative RNA-binding protein	209.29	80	11
Q99020 ROAA_MOUSE	Heterogeneous nuclear ribonu	209.03	46	11
Q9EQH3 VPS35_MOUSE	Vacuolar protein sorting-assoc	195.32	37	11
P31230 AIMP1_MOUSE	Aminoacyl tRNA synthase con	191.2	59	11
Q9JKF1 IQGA1_MOUSE	Ras GTPase-activating-like pr	188.25	29	11
Q9WVA4 TAGL2_MOUSE	Transgelin-2 OS=Mus muscul	187.6	60	11
Q922Q8 LRC59_MOUSE	Leucine-rich repeat-containing	187.54	44	11
Q9Z2N8 ACL6A_MOUSE	Actin-like protein 6A OS=Mus	186.72	46	11
Q60716 P4HA2_MOUSE	Prolyl 4-hydroxylase subunit a	186.15	47	11
P97351 RS3A_MOUSE	40S ribosomal protein S3a OS	178.15	46	11
P06151 LDHA_MOUSE	L-lactate dehydrogenase A ch	177.41	40	11
Q9CPR4 RL17_MOUSE	60S ribosomal protein L17 OS	170.26	49	11
Q8C854 MYEF2_MOUSE	Myelin expression factor 2 OS	170.12	38	11
P20918 PLMN_MOUSE	Plasminogen OS=Mus muscul	167.79	28	11
Q9EPU0 RENT1_MOUSE	Regulator of nonsense transcr	164.61	26	11
P63085 MK01_MOUSE	Mitogen-activated protein kina	161.4	45	11
Q8BMS1 ECHA_MOUSE	Trifunctional enzyme subunit a	149.87	44	11
P32067 LA_MOUSE	Lupus La protein homolog OS	147.52	51	11
Q9QZQ1 AFAD_MOUSE	Afadin OS=Mus musculus GN	133.07	17	11
Q60902 EP15R_MOUSE	Epidermal growth factor recep	125.71	29	11
P26443 DHE3_MOUSE	Glutamate dehydrogenase 1, t	118.4	31	11
P68254 1433T_MOUSE	14-3-3 protein theta OS=Mus	251.79	82	10
O35887 CALU_MOUSE	Calumenin OS=Mus musculus	217.5	82	10
P62307 RUXF_MOUSE	Small nuclear ribonucleoprote	209.92	99	10
Q8VHX6 FLNC_MOUSE	Filamin-C OS=Mus musculus	188.92	25	10
Q8CG70 P3H3_MOUSE	Prolyl 3-hydroxylase 3 OS=M	187.37	39	10
O08547 SC22B_MOUSE	Vesicle-trafficking protein SEC	185.45	60	10
Q02257 PLAK_MOUSE	Junction plakoglobin OS=Mus	182.85	37	10
P62264 RS14_MOUSE	40S ribosomal protein S14 OS	182.34	72	10
Q9R0E1 PLOD3_MOUSE	Procollagen-lysine,2-oxoglutar	179.05	31	10
P16675 PPGB_MOUSE	Lysosomal protective protein C	176.42	24	10
P07356 ANXA2_MOUSE	Annexin A2 OS=Mus musculu	170.13	43	10
Q99KI0 ACON_MOUSE	Aconitate hydratase, mitochor	169.72	28	10
Q9Z204 HNRPC_MOUSE	Heterogeneous nuclear ribonu	169.56	36	10
P60122 RUVB1_MOUSE	RuvB-like 1 OS=Mus musculu	153.17	41	10
Q60864 STIP1_MOUSE	Stress-induced-phosphoprotei	151.8	29	10
P23249 MOV10_MOUSE	Putative helicase MOV-10 OS	149.84	19	10
P70699 LYAG_MOUSE	Lysosomal alpha-glucosidase	143.05	19	10
Q8BX10 PGAM5_MOUSE	Serine/threonine-protein phos	138.1	55	10
Q8R1Q8 DC1L1_MOUSE	Cytoplasmic dynein 1 light inte	137.93	41	10
P35700 PRDX1_MOUSE	Peroxiredoxin-1 OS=Mus mus	137.09	59	10
Q6PDM2 SRSF1_MOUSE	Serine/arginine-rich splicing fa	135.94	47	10
O08585 CLCA_MOUSE	Clathrin light chain A OS=Mus	127.56	22	10
Q8R4X3 RBM12_MOUSE	RNA-binding protein 12 OS=M	123.46	14	10
P62204 CALM_MOUSE	Calmodulin OS=Mus musculu	233.23	99	9

P62315 SMD1_MOUSE	Small nuclear ribonucleoprote	214.63	81	9
Q8R2Z5 VWA1_MOUSE	von Willebrand factor A doma	191.31	53	9
Q9CQ92 FIS1_MOUSE	Mitochondrial fission 1 protein	190.05	75	9
Q9CQF3 CPSF5_MOUSE	Cleavage and polyadenylation	189.59	62	9
P36552 HEM6_MOUSE	Coproporphyrinogen-III oxidas	185.7	47	9
P56959 FUS_MOUSE	RNA-binding protein FUS OS=	184.78	27	9
Q62167 DDX3X_MOUSE	ATP-dependent RNA helicase	182.47	46	9
Q9WTX5 SKP1_MOUSE	S-phase kinase-associated pr	178.41	66	9
P60335 PCBP1_MOUSE	Poly(rC)-binding protein 1 OS=	176.4	54	9
Q8R081 HNRPL_MOUSE	Heterogeneous nuclear ribonu	174.18	34	9
Q60715 P4HA1_MOUSE	Prolyl 4-hydroxylase subunit a	173.86	35	9
Q99KN9 EPN4_MOUSE	Clathrin interactor 1 OS=Mus	170.43	22	9
P47963 RL13_MOUSE	60S ribosomal protein L13 OS	169.23	44	9
P46412 GPX3_MOUSE	Glutathione peroxidase 3 OS=	169.14	41	9
Q9R0U0 SRS10_MOUSE	Serine/arginine-rich splicing fa	169	24	9
Q9WU78 PDC6L_MOUSE	Programmed cell death 6-inter	166.5	30	9
P99029 PRDX5_MOUSE	Peroxiredoxin-5, mitochondria	164.98	43	9
P48036 ANXA5_MOUSE	Annexin A5 OS=Mus musculu	162.59	50	9
Q61147 CERU_MOUSE	Ceruloplasmin OS=Mus musc	161.4	21	9
Q9CYR0 SSBP_MOUSE	Single-stranded DNA-binding	158.75	56	9
Q60749 KHDR1_MOUSE	KH domain-containing, RNA-b	157.57	53	9
Q60597 ODO1_MOUSE	2-oxoglutarate dehydrogenase	155	30	9
Q6ZQI3 MLEC_MOUSE	Malectin OS=Mus musculus G	153.92	42	9
Q8C0C7 SYFA_MOUSE	Phenylalanyl-tRNA synthetase	149.8	30	9
Q3U0V1 FUBP2_MOUSE	Far upstream element-binding	148.22	26	9
Q91YN9 BAG2_MOUSE	BAG family molecular chaper	147.76	59	9
Q501J6 DDX17_MOUSE	Probable ATP-dependent RNA	147.43	26	9
Q7TMK9 HNRPQ_MOUSE	Heterogeneous nuclear ribonu	145.1	23	9
Q60631 GRB2_MOUSE	Growth factor receptor-bound	137.42	52	9
Q6NZJ6 IF4G1_MOUSE	Eukaryotic translation initiat	131.75	15	9
Q9Z110 P5CS_MOUSE	Delta-1-pyrroline-5-carboxylat	129.88	20	9
Q61656 DDX5_MOUSE	Probable ATP-dependent RNA	126.9	23	9
Q9R1C7 PR40A_MOUSE	Pre-mRNA-processing factor 4	120.39	15	9
P24270 CATA_MOUSE	Catalase OS=Mus musculus C	120.12	37	9
Q9Z0X1 AIFM1_MOUSE	Apoptosis-inducing factor 1, m	115.55	23	9
Q9Z1D1 EIF3G_MOUSE	Eukaryotic translation initiat	111.96	20	9
Q61696 HS71A_MOUSE	Heat shock 70 kDa protein 1A	273.85	61	8
Q01768 NDKB_MOUSE	Nucleoside diphosphate kinas	236.67	72	8
P07759 SPA3K_MOUSE	Serine protease inhibitor A3K	225.39	54	8
P15532 NDKA_MOUSE	Nucleoside diphosphate kinas	215.23	74	8
P61924 COPZ1_MOUSE	Coatomer subunit zeta-1 OS=	206.86	77	8
Q9CPT4 CS010_MOUSE	UPF0556 protein C19orf10 ho	199.77	49	8
Q60605 MYL6_MOUSE	Myosin light polypeptide 6 OS	198.17	67	8
Q9D3D9 ATPD_MOUSE	ATP synthase subunit delta, m	196.56	64	8
P16045 LEG1_MOUSE	Galectin-1 OS=Mus musculus	193.94	77	8
Q8BL97 SRSF7_MOUSE	Serine/arginine-rich splicing fa	192.06	39	8
Q9DB20 ATPO_MOUSE	ATP synthase subunit O, mito	186.39	55	8
Q9JIQ3 DBLOH_MOUSE	Diablo homolog, mitochondria	179.04	58	8
Q9QXT0 CNPY2_MOUSE	Protein canopy homolog 2 OS	176.77	66	8
P17751 TPIS_MOUSE	Triosephosphate isomerase C	171.23	53	8
Q61584 FXR1_MOUSE	Fragile X mental retardation s	170.2	36	8
Q9JHJ0 TMOD3_MOUSE	Tropomodulin-3 OS=Mus mus	169.13	45	8
Q3TCN2 PLBL2_MOUSE	Putative phospholipase B-like	168.8	30	8
P62983 RS27A_MOUSE	Ubiquitin-40S ribosomal prote	168.18	67	8
P63276 RS17_MOUSE	40S ribosomal protein S17 OS	167.5	50	8

Q08879 FBLN1_MOUSE	Fibulin-1 OS=Mus musculus	159.57	35	8
Q61171 PRDX2_MOUSE	Peroxiredoxin-2 OS=Mus mus	157.72	63	8
P28656 NP1L1_MOUSE	Nucleosome assembly protein	156.32	42	8
Q9D2G2 ODO2_MOUSE	Dihydrolipoyllysine-residue su	150.86	34	8
P62858 RS28_MOUSE	40S ribosomal protein S28 OS	148.94	61	8
Q99PT1 GDIR1_MOUSE	Rho GDP-dissociation inhibitor	148.52	41	8
P08228 SODC_MOUSE	Superoxide dismutase [Cu-Zn]	144.71	44	8
Q06890 CLUS_MOUSE	Clusterin OS=Mus musculus	143.09	33	8
P21107 TPM3_MOUSE	Tropomyosin alpha-3 chain O	141.88	43	8
Q9D0I9 SYRC_MOUSE	Arginyl-tRNA synthetase, cyto	135.72	20	8
Q9D338 RM19_MOUSE	39S ribosomal protein L19, mi	135.71	37	8
P10605 CATB_MOUSE	Cathepsin B OS=Mus musculu	134.87	25	8
P70372 ELAV1_MOUSE	ELAV-like protein 1 OS=Mus r	134.43	31	8
Q9CX56 PSMD8_MOUSE	26S proteasome non-ATPase	131.98	42	8
Q61646 HPT_MOUSE	Haptoglobin OS=Mus musculu	131.2	38	8
P55302 AMRP_MOUSE	Alpha-2-macroglobulin recept	130.45	24	8
Q8BGD9 IF4B_MOUSE	Eukaryotic translation initiat	127.26	31	8
O70493 SNX12_MOUSE	Sorting nexin-12 OS=Mus mu	120.16	53	8
P39447 ZO1_MOUSE	Tight junction protein ZO-1 OS	117.3	21	8
Q61464 ZN638_MOUSE	Zinc finger protein 638 OS=M	116.1	17	8
Q6ZWN5 RS9_MOUSE	40S ribosomal protein S9 OS=	114.88	41	8
Q6NV83 SR140_MOUSE	U2 snRNP-associated SURP	108.89	17	8
Q8CGK3 LONM_MOUSE	Lon protease homolog, mitoch	95.66	31	8
P17156 HSP72_MOUSE	Heat shock-related 70 kDa pro	297.25	50	7
Q00898 A1AT5_MOUSE	Alpha-1-antitrypsin 1-5 OS=M	244.08	56	7
Q9CQV8 1433B_MOUSE	14-3-3 protein beta/alpha OS=	231.61	80	7
Q03734 SPA3M_MOUSE	Serine protease inhibitor A3M	231.04	68	7
Q91WP6 SPA3N_MOUSE	Serine protease inhibitor A3N	210.64	50	7
P28665 MUG1_MOUSE	Murinoglobulin-1 OS=Mus mu	191.6	27	7
P63242 IF5A1_MOUSE	Eukaryotic translation initiat	183.7	60	7
P62830 RL23_MOUSE	60S ribosomal protein L23 OS	183.07	79	7
P21619 LMNB2_MOUSE	Lamin-B2 OS=Mus musculus	181.24	41	7
P29788 VTNC_MOUSE	Vitronectin OS=Mus musculus	179.24	35	7
Q9QUR7 PIN1_MOUSE	Peptidyl-prolyl cis-trans isome	177.79	75	7
P62996 TRA2B_MOUSE	Transformer-2 protein homolo	176.31	45	7
P58022 LOXL2_MOUSE	Lysyl oxidase homolog 2 OS=	173.8	38	7
Q62093 SRSF2_MOUSE	Serine/arginine-rich splicing fa	172.65	50	7
P83877 TXN4A_MOUSE	Thioredoxin-like protein 4A OS	171.32	77	7
Q9D0W5 PPIL1_MOUSE	Peptidyl-prolyl cis-trans isome	165.4	55	7
Q9Z2U0 PSA7_MOUSE	Proteasome subunit alpha typ	163.82	48	7
Q9CQR2 RS21_MOUSE	40S ribosomal protein S21 OS	159.77	66	7
P35564 CALX_MOUSE	Calnexin OS=Mus musculus	159.57	34	7
Q9Z2U1 PSA5_MOUSE	Proteasome subunit alpha typ	158.72	56	7
P61458 PHS_MOUSE	Pterin-4-alpha-carbinolamine	157.62	58	7
Q9CQL1 MGNR_MOUSE	Protein mago nashi homolog	155.58	58	7
P61327 MGN_MOUSE	Protein mago nashi homolog	155.58	58	7
P35980 RL18_MOUSE	60S ribosomal protein L18 OS	147.12	46	7
Q8R4R6 NUP53_MOUSE	Nucleoporin NUP53 OS=Mus	142.03	45	7
P70670 NACAM_MOUSE	Nascent polypeptide-associate	141.54	18	7
Q8VDM4 PSMD2_MOUSE	26S proteasome non-ATPase	139.68	36	7
P03975 IGEB_MOUSE	IgE-binding protein OS=Mus r	138.53	20	7
Q9CXI5 MANF_MOUSE	Mesencephalic astrocyte-deriv	138.06	51	7
P08905 LYZ2_MOUSE	Lysozyme C-2 OS=Mus musc	135.63	61	7
Q04447 KCRB_MOUSE	Creatine kinase B-type OS=M	134.76	40	7
O09061 PSB1_MOUSE	Proteasome subunit beta type	133.9	54	7

Q9D6Z1 NOP56_MOUSE	Nucleolar protein 56 OS=Mus	133.24	32	7
Q62189 SNRPA_MOUSE	U1 small nuclear ribonucleopr	130.42	32	7
P84089 ERH_MOUSE	Enhancer of rudimentary hom	129.86	38	7
Q9QZH3 PPIE_MOUSE	Peptidyl-prolyl cis-trans isome	129.57	49	7
Q6ZQ38 CAND1_MOUSE	Cullin-associated NEDD8-diss	126.99	22	7
P14148 RL7_MOUSE	60S ribosomal protein L7 OS=	118.82	27	7
P30416 FKBP4_MOUSE	Peptidyl-prolyl cis-trans isome	117.11	22	7
Q03173 ENAH_MOUSE	Protein enabled homolog OS=	116.98	15	7
P17427 AP2A2_MOUSE	AP-2 complex subunit alpha-2	116.16	21	7
Q91WJ8 FUBP1_MOUSE	Far upstream element-binding	114.06	17	7
Q9CZX8 RS19_MOUSE	40S ribosomal protein S19 OS	108.86	37	7
Q8R180 ERO1A_MOUSE	ERO1-like protein alpha OS=M	107.75	26	7
P09411 PGK1_MOUSE	Phosphoglycerate kinase 1 OS	105.87	34	7
Q3UPL0 SC31A_MOUSE	Protein transport protein Sec3	99.98	15	7
Q8BX70 VP13C_MOUSE	Vacuolar protein sorting-assoc	92.49	8	7
P22599 A1AT2_MOUSE	Alpha-1-antitrypsin 1-2 OS=M	267.66	71	6
Q9QZQ8 H2AY_MOUSE	Core histone macro-H2A.1 OS	202.82	47	6
P62305 RUXE_MOUSE	Small nuclear ribonucleoprote	191.04	77	6
P62897 CYC_MOUSE	Cytochrome c, somatic OS=M	189.27	63	6
Q6IRU2 TPM4_MOUSE	Tropomyosin alpha-4 chain O	169.6	75	6
Q8CDN6 TXNL1_MOUSE	Thioredoxin-like protein 1 OS=	166.23	57	6
Q6PDG5 SMRC2_MOUSE	SWI/SNF complex subunit SM	160.75	36	6
Q7M6Y3 PICA_MOUSE	Phosphatidylinositol-binding c	160.26	21	6
P40124 CAP1_MOUSE	Adenylyl cyclase-associated p	157.78	33	6
P16110 LEG3_MOUSE	Galectin-3 OS=Mus musculus	157.13	26	6
Q921F2 TADBP_MOUSE	TAR DNA-binding protein 43 O	155.04	28	6
Q9CXZ1 NDUS4_MOUSE	NADH dehydrogenase [ubiquin	154.95	51	6
Q9CWZ3 RBM8A_MOUSE	RNA-binding protein 8A OS=M	152.18	53	6
O55135 IF6_MOUSE	Eukaryotic translation initiatio	151.91	34	6
P99028 QCR6_MOUSE	Cytochrome b-c1 complex sut	147.81	61	6
P11404 FABPH_MOUSE	Fatty acid-binding protein, hea	145.61	65	6
Q9D967 MGDP1_MOUSE	Magnesium-dependent phosph	139.1	54	6
P97807 FUMH_MOUSE	Fumarate hydratase, mitochor	138.43	31	6
P56391 CX6B1_MOUSE	Cytochrome c oxidase subunit	136.35	63	6
P28798 GRN_MOUSE	Granulins OS=Mus musculus	135.27	41	6
Q76MZ3 2AAA_MOUSE	Serine/threonine-protein phos	134.5	33	6
Q9D0F9 PGM1_MOUSE	Phosphoglucomutase-1 OS=M	130.29	30	6
Q9CVB6 ARPC2_MOUSE	Actin-related protein 2/3 comp	127.56	49	6
P47962 RL5_MOUSE	60S ribosomal protein L5 OS=	126.81	25	6
P06728 APOA4_MOUSE	Apolipoprotein A-IV OS=Mus r	125.6	32	6
Q68FL6 SYMC_MOUSE	Methionyl-tRNA synthetase, c	125.23	35	6
Q6NVF9 CPSF6_MOUSE	Cleavage and polyadenylation	125.21	23	6
O55128 SAP18_MOUSE	Histone deacetylase complex	124.82	48	6
Q61704 ITIH3_MOUSE	Inter-alpha-trypsin inhibitor he	123.95	40	6
P47738 ALDH2_MOUSE	Aldehyde dehydrogenase, mit	122.02	19	6
Q8BND5 QSOX1_MOUSE	Sulfhydryl oxidase 1 OS=Mus	121.41	22	6
P62911 RL32_MOUSE	60S ribosomal protein L32 OS	119.51	45	6
O35206 COFA1_MOUSE	Collagen alpha-1(XV) chain O	118.93	12	6
Q9D620 RFIP1_MOUSE	Rab11 family-interacting prote	118.52	39	6
P14131 RS16_MOUSE	40S ribosomal protein S16 OS	115.94	42	6
P26369 U2AF2_MOUSE	Splicing factor U2AF 65 kDa s	113.64	18	6
Q6Y7W8 PERQ2_MOUSE	PERQ amino acid-rich with G	113.33	11	6
P08226 APOE_MOUSE	Apolipoprotein E OS=Mus mu	110.83	43	6
P62702 RS4X_MOUSE	40S ribosomal protein S4, X is	107.6	37	6
P62751 RL23A_MOUSE	60S ribosomal protein L23a O	106.34	33	6

P97311 MCM6_MOUSE	DNA replication licensing factor	105.9	32	6
Q9CPP6 NDUA5_MOUSE	NADH dehydrogenase [ubiquinol	102.93	60	6
Q8K297 GT251_MOUSE	Procollagen galactosyltransferase	102.73	24	6
O88477 IF2B1_MOUSE	Insulin-like growth factor 2 mRNA	102.59	27	6
Q9CQE1 NPS3A_MOUSE	Protein NipSnap homolog 3A	99.65	31	6
Q91VA6 PDIP2_MOUSE	Polymerase delta-interacting protein	97.93	30	6
Q8C8U0 LIPB1_MOUSE	Liprin-beta-1 OS=Mus musculus	97.25	38	6
Q08943 SSRP1_MOUSE	FACT complex subunit SSRP1	95.91	18	6
Q8VEK3 HNRPU_MOUSE	Heterogeneous nuclear ribonucleoprotein	94.26	13	6
P04186 CFAB_MOUSE	Complement factor B OS=Mus musculus	93.37	19	6
Q99ME9 NOG1_MOUSE	Nucleolar GTP-binding protein	92.9	19	6
Q99K30 ES8L2_MOUSE	Epidermal growth factor receptor	89.96	28	6
P17182 ENOA_MOUSE	Alpha-enolase OS=Mus musculus	85.55	28	6
Q8VDP4 K1967_MOUSE	Protein KIAA1967 homolog OS=Mus musculus	85.25	15	6
Q8C7E9 CSTFT_MOUSE	Cleavage stimulation factor subunit	81.11	31	6
O54724 PTRF_MOUSE	Polymerase I and transcript release factor	75.87	30	6
Q61830 MRC1_MOUSE	Macrophage mannose receptor	74.94	15	6
P27661 H2AX_MOUSE	Histone H2A.x OS=Mus musculus	298.05	80	5
P68033 ACTC_MOUSE	Actin, alpha cardiac muscle 1	288.9	79	5
P99024 TBB5_MOUSE	Tubulin beta-5 chain OS=Mus musculus	276.71	72	5
Q64475 H2B1B_MOUSE	Histone H2B type 1-B OS=Mus musculus	230.53	69	5
Q6ZWY9 H2B1C_MOUSE	Histone H2B type 1-C/E/G OS=Mus musculus	230.53	69	5
P10853 H2B1F_MOUSE	Histone H2B type 1-F/J/L OS=Mus musculus	230.53	69	5
Q64478 H2B1H_MOUSE	Histone H2B type 1-H OS=Mus musculus	230.53	69	5
P10854 H2B1M_MOUSE	Histone H2B type 1-M OS=Mus musculus	230.53	69	5
Q8CGP2 H2B1P_MOUSE	Histone H2B type 1-P OS=Mus musculus	230.53	69	5
Q64525 H2B2B_MOUSE	Histone H2B type 2-B OS=Mus musculus	230.53	69	5
O35737 HNRH1_MOUSE	Heterogeneous nuclear ribonucleoprotein	209.95	45	5
P62960 YBOX1_MOUSE	Nuclease-sensitive element-binding protein	179.02	48	5
Q9EPJ9 ARFG1_MOUSE	ADP-ribosylation factor GTPase	157.19	43	5
Q99KR7 PPIF_MOUSE	Peptidyl-prolyl cis-trans isomerase	149.63	50	5
P23506 PIMT_MOUSE	Protein-L-isoaspartate(D-aspartate) methyltransferase	147.94	48	5
P01837 IGKC_MOUSE	Ig kappa chain C region OS=Mus musculus	146.11	68	5
P01872 IGHM_MOUSE	Ig mu chain C region secreted	145.64	18	5
P01873 MUCM_MOUSE	Ig mu chain C region membrane	145.64	17	5
P61089 UBE2N_MOUSE	Ubiquitin-conjugating enzyme	145.42	68	5
P62320 SMD3_MOUSE	Small nuclear ribonucleoprotein	145.08	69	5
P62492 RB11A_MOUSE	Ras-related protein Rab-11A	144.29	38	5
Q9WVA2 TIM8A_MOUSE	Mitochondrial import inner membrane	142.52	82	5
Q91WK2 EIF3H_MOUSE	Eukaryotic translation initiation factor	142.35	42	5
Q8K2C9 HACD3_MOUSE	3-hydroxyacyl-CoA dehydratase	142.17	27	5
Q923G2 RPAB3_MOUSE	DNA-directed RNA polymerase	141.08	47	5
Q62523 ZYX_MOUSE	Zyxin OS=Mus musculus GN=	139.77	33	5
Q6P5E6 GGA2_MOUSE	ADP-ribosylation factor-binding protein	139.48	39	5
P62242 RS8_MOUSE	40S ribosomal protein S8 OS=Mus musculus	137.35	32	5
P23198 CBX3_MOUSE	Chromobox protein homolog 3	137.04	32	5
O88696 CLPP_MOUSE	Putative ATP-dependent Clp protease	136.87	50	5
O70325 GPX41_MOUSE	Phospholipid hydroperoxide glutathione	131.66	32	5
Q9WV98 TIM9_MOUSE	Mitochondrial import inner membrane	131.61	74	5
Q8BKC5 IPO5_MOUSE	Importin-5 OS=Mus musculus	131.18	50	5
P14115 RL27A_MOUSE	60S ribosomal protein L27a OS=Mus musculus	130.47	39	5
Q9CYL5 GAPR1_MOUSE	Golgi-associated plant pathogenesis	130.25	61	5
Q61990 PCBP2_MOUSE	Poly(rC)-binding protein 2 OS=Mus musculus	129.95	42	5
P80317 TCPZ_MOUSE	T-complex protein 1 subunit zeta	129.84	38	5
P68037 UB2L3_MOUSE	Ubiquitin-conjugating enzyme	129.59	64	5

P98078 DAB2_MOUSE	Disabled homolog 2 OS=Mus	129.02	16	5
P18760 COF1_MOUSE	Cofilin-1 OS=Mus musculus G	128.27	57	5
P68510 1433F_MOUSE	14-3-3 protein eta OS=Mus m	127.7	63	5
Q9WV55 VAPA_MOUSE	Vesicle-associated membrane	127.6	46	5
P49722 PSA2_MOUSE	Proteasome subunit alpha typ	125.75	34	5
Q9QYJ0 DNJA2_MOUSE	DnaJ homolog subfamily A me	125.55	44	5
P84099 RL19_MOUSE	60S ribosomal protein L19 OS	124.59	26	5
Q61233 PLSL_MOUSE	Plastin-2 OS=Mus musculus G	124.26	26	5
Q3TXS7 PSMD1_MOUSE	26S proteasome non-ATPase	123.94	21	5
P14824 ANXA6_MOUSE	Annexin A6 OS=Mus musculu	123.83	23	5
Q6DFW4 NOP58_MOUSE	Nucleolar protein 58 OS=Mus	123.27	38	5
Q8K2B3 DHSA_MOUSE	Succinate dehydrogenase [ub	121.47	28	5
P52196 THTR_MOUSE	Thiosulfate sulfurtransferase C	120.95	31	5
Q61545 EWS_MOUSE	RNA-binding protein EWS OS	120.79	20	5
Q9CQF9 PCYOX_MOUSE	Prenylcysteine oxidase OS=M	120.7	30	5
Q60668 HNRPD_MOUSE	Heterogeneous nuclear ribonu	120.36	32	5
Q8C0E2 VP26B_MOUSE	Vacuolar protein sorting-assoc	119.49	38	5
Q9CZM2 RL15_MOUSE	60S ribosomal protein L15 OS	119.27	36	5
Q8BP40 PPA6_MOUSE	Lysophosphatidic acid phosph	119.24	29	5
Q8QZT1 THIL_MOUSE	Acetyl-CoA acetyltransferase,	117.51	25	5
Q6GU68 ISLR_MOUSE	Immunoglobulin superfamily c	117	25	5
Q61166 MARE1_MOUSE	Microtubule-associated protein	116.89	35	5
P68040 GBLP_MOUSE	Guanine nucleotide-binding pr	116.23	32	5
Q8CG71 P3H2_MOUSE	Prolyl 3-hydroxylase 2 OS=MU	116.03	25	5
P80314 TCPB_MOUSE	T-complex protein 1 subunit b	114.83	21	5
Q99KJ8 DCTN2_MOUSE	Dynactin subunit 2 OS=Mus m	110.29	21	5
Q02819 NUCB1_MOUSE	Nucleobindin-1 OS=Mus musc	110.19	28	5
Q9JJ18 RL38_MOUSE	60S ribosomal protein L38 OS	109.1	37	5
Q8BIQ5 CSTF2_MOUSE	Cleavage stimulation factor su	108.24	39	5
P01868 IGHG1_MOUSE	Ig gamma-1 chain C region se	107.77	23	5
P01869 IGH1M_MOUSE	Ig gamma-1 chain C region, m	107.77	19	5
Q9D6R2 IDH3A_MOUSE	Isocitrate dehydrogenase [NA	106.01	31	5
P01864 GCAB_MOUSE	Ig gamma-2A chain C region s	105.64	25	5
Q9DBH5 LMAN2_MOUSE	Vesicular integral-membrane	105.5	16	5
P60843 IF4A1_MOUSE	Eukaryotic initiation factor 4A-	104.88	39	5
P60867 RS20_MOUSE	40S ribosomal protein S20 OS	103.56	36	5
Q9CXF4 TBC15_MOUSE	TBC1 domain family member	103.27	20	5
Q05117 PPA5_MOUSE	Tartrate-resistant acid phosph	102.8	25	5
Q8K2C7 OS9_MOUSE	Protein OS-9 OS=Mus muscu	101.23	21	5
Q61768 KINH_MOUSE	Kinesin-1 heavy chain OS=MU	101.04	18	5
Q9CR09 UFC1_MOUSE	Ubiquitin-fold modifier-conjuga	100.86	29	5
P53994 RAB2A_MOUSE	Ras-related protein Rab-2A O	100.6	35	5
Q9CQA3 DHSB_MOUSE	Succinate dehydrogenase [ub	98.53	48	5
Q8BTV2 CPSF7_MOUSE	Cleavage and polyadenylation	95.34	25	5
Q9CQE8 CN166_MOUSE	UPF0568 protein C14orf166 h	94.34	43	5
Q9DCW4 ETFB_MOUSE	Electron transfer flavoprotein s	93.52	24	5
P26516 PSD7_MOUSE	26S proteasome non-ATPase	92.26	29	5
O35593 PSDE_MOUSE	26S proteasome non-ATPase	91.81	35	5
P14685 PSMD3_MOUSE	26S proteasome non-ATPase	89.43	17	5
P28653 PGS1_MOUSE	Biglycan OS=Mus musculus G	89.11	18	5
Q921X9 PDIA5_MOUSE	Protein disulfide-isomerase A5	89.11	25	5
P09671 SODM_MOUSE	Superoxide dismutase [Mn], m	88.39	43	5
Q9D1M0 SEC13_MOUSE	Protein SEC13 homolog OS=M	86.18	47	5
Q5XJY5 COPD_MOUSE	Coatomer subunit delta OS=M	84.37	20	5
Q8CGF7 TCRG1_MOUSE	Transcription elongation regul	83.91	11	5



P62281	RS11_MOUSE	40S ribosomal protein S11 OS=	81.73	22	5
P15508	SPTB1_MOUSE	Spectrin beta chain, erythrocy	80.59	12	5
P12023	A4_MOUSE	Amyloid beta A4 protein OS=M	62.12	18	5
Q80UW8	RPAB1_MOUSE	DNA-directed RNA polymeras	61.88	40	5
O88685	PRS6A_MOUSE	26S protease regulatory subu	57.92	25	5
A2AAJ9	OBSCN_MOUSE	Obscurin OS=Mus musculus C	26.01	4	5
Q8BFZ3	ACTBL_MOUSE	Beta-actin-like protein 2 OS=M	267.16	65	4
O08638	MYH11_MOUSE	Myosin-11 OS=Mus musculus	214.94	29	4
Q3THE2	ML12B_MOUSE	Myosin regulatory light chain 1	192.28	77	4
P85094	ISC2A_MOUSE	Isochorismatase domain-conta	179.06	63	4
Q6URW6	MYH14_MOUSE	Myosin-14 OS=Mus musculus	171.93	23	4
Q9QZM0	UBQL2_MOUSE	Ubiquilin-2 OS=Mus musculus	160.23	18	4
O08807	PRDX4_MOUSE	Peroxiredoxin-4 OS=Mus mus	153.87	40	4
P84078	ARF1_MOUSE	ADP-ribosylation factor 1 OS=	152.99	58	4
P61205	ARF3_MOUSE	ADP-ribosylation factor 3 OS=	152.99	58	4
Q64213	SF01_MOUSE	Splicing factor 1 OS=Mus mus	145.58	13	4
Q08369	GATA4_MOUSE	Transcription factor GATA-4 C	144.96	18	4
Q9DB15	RM12_MOUSE	39S ribosomal protein L12, mi	141.47	66	4
P84104	SRSF3_MOUSE	Serine/arginine-rich splicing fa	139.23	36	4
P09542	MYL3_MOUSE	Myosin light chain 3 OS=Mus	137.71	36	4
P62748	HPCL1_MOUSE	Hippocalcin-like protein 1 OS=	137.1	52	4
Q9D1B9	RM28_MOUSE	39S ribosomal protein L28, mi	133.83	48	4
Q9QUM9	PSA6_MOUSE	Proteasome subunit alpha typ	131.26	21	4
P99027	RLA2_MOUSE	60S acidic ribosomal protein F	130.62	63	4
Q80UM7	MOGS_MOUSE	Mannosyl-oligosaccharide glu	130.11	22	4
Q9DBR0	AKAP8_MOUSE	A-kinase anchor protein 8 OS=	129.59	34	4
O70251	EF1B_MOUSE	Elongation factor 1-beta OS=M	129.02	32	4
Q64010	CRK_MOUSE	Adapter molecule crk OS=Mus	128.1	26	4
Q9DBG6	RPN2_MOUSE	Dolichyl-diphosphooligosaccha	125.84	18	4
Q3UZ39	LRRF1_MOUSE	Leucine-rich repeat flightless-i	124.96	19	4
P62075	TIM13_MOUSE	Mitochondrial import inner me	124.46	54	4
Q99LT0	DPY30_MOUSE	Protein dpy-30 homolog OS=M	123.87	83	4
Q9R099	TBL2_MOUSE	Transducin beta-like protein 2	123.17	18	4
Q3V1L4	5NTC_MOUSE	Cytosolic purine 5'-nucleotida	123.14	18	4
Q9Z2D8	MBD3_MOUSE	Methyl-CpG-binding domain p	122.12	30	4
P43274	H14_MOUSE	Histone H1.4 OS=Mus muscu	119.7	37	4
P63323	RS12_MOUSE	40S ribosomal protein S12 OS=	118.78	36	4
P59708	PM14_MOUSE	Pre-mRNA branch site protein	117.18	44	4
O55029	COPB2_MOUSE	Coatomer subunit beta' OS=M	116.91	18	4
Q9CYD3	CRTAP_MOUSE	Cartilage-associated protein C	116.23	31	4
Q9WVK4	EHD1_MOUSE	EH domain-containing protein	115.68	17	4
P62309	RUXG_MOUSE	Small nuclear ribonucleoprote	115.17	83	4
P30412	PPIC_MOUSE	Peptidyl-prolyl cis-trans isome	114.97	34	4
P97371	PSME1_MOUSE	Proteasome activator complex	114.85	29	4
O09167	RL21_MOUSE	60S ribosomal protein L21 OS=	112.76	38	4
Q9CZU3	SK2L2_MOUSE	Superkiller viralicidic activity 2	112.67	22	4
Q8CIE6	COPA_MOUSE	Coatomer subunit alpha OS=M	111.18	16	4
O35900	LSM2_MOUSE	U6 snRNA-associated Sm-like	111.13	62	4
P62267	RS23_MOUSE	40S ribosomal protein S23 OS=	111.05	64	4
Q8QZY1	EIF3L_MOUSE	Eukaryotic translation initiator	110.88	15	4
Q7TPV4	MBB1A_MOUSE	Myb-binding protein 1A OS=M	110.37	19	4
P45878	FKBP2_MOUSE	Peptidyl-prolyl cis-trans isome	109.14	68	4
P14869	RLA0_MOUSE	60S acidic ribosomal protein F	109.08	24	4
P97493	THIOM_MOUSE	Thioredoxin, mitochondrial OS=	108.77	51	4
Q9DAR7	DCPS_MOUSE	Scavenger mRNA-decapping	108.34	43	4

P51410 RL9_MOUSE	60S ribosomal protein L9 OS=M	108.33	37	4
Q5SUC9 SCO1_MOUSE	Protein SCO1 homolog, mitoc	107.84	37	4
Q9ERK4 XPO2_MOUSE	Exportin-2 OS=Mus musculus	106.79	18	4
Q99JB2 STML2_MOUSE	Stomatin-like protein 2 OS=M	106.55	33	4
Q99P88 NU155_MOUSE	Nuclear pore complex protein	106.13	25	4
O88653 LTOR3_MOUSE	Ragulator complex protein LA	105.85	50	4
P08122 CO4A2_MOUSE	Collagen alpha-2(IV) chain OS	104.41	11	4
Q9Z0R4 ITSN1_MOUSE	Intersectin-1 OS=Mus muscul	104.23	13	4
Q9CR57 RL14_MOUSE	60S ribosomal protein L14 OS	104.03	27	4
Q9QX47 SON_MOUSE	Protein SON OS=Mus muscul	103.93	13	4
Q8R1B4 EIF3C_MOUSE	Eukaryotic translation initiat	103.41	18	4
P05064 ALDOA_MOUSE	Fructose-bisphosphate aldolase	103.26	21	4
Q9DAW9 CNN3_MOUSE	Calponin-3 OS=Mus musculus	103.23	25	4
Q6ZWY3 RS27L_MOUSE	40S ribosomal protein S27-like	102.88	39	4
Q9JJH1 RNAS4_MOUSE	Ribonuclease 4 OS=Mus mus	102.87	36	4
B2RY56 RBM25_MOUSE	RNA-binding protein 25 OS=M	102.76	16	4
P46938 YAP1_MOUSE	Yorkie homolog OS=Mus mus	102.71	37	4
Q8BP67 RL24_MOUSE	60S ribosomal protein L24 OS	102.26	19	4
P25206 MCM3_MOUSE	DNA replication licensing fact	100.52	17	4
P70318 TIAR_MOUSE	Nucleolysin TIAR OS=Mus m	99.09	26	4
Q61733 RT31_MOUSE	28S ribosomal protein S31, m	97.62	19	4
Q9WTP7 KAD3_MOUSE	GTP:AMP phosphotransferase	96.96	33	4
Q9WUK2 IF4H_MOUSE	Eukaryotic translation initiat	95.49	22	4
P81117 NUCB2_MOUSE	Nucleobindin-2 OS=Mus musc	93.85	27	4
Q3UQN2 FCHO2_MOUSE	FCH domain only protein 2 OS	93.43	8	4
P61759 PFD3_MOUSE	Prefoldin subunit 3 OS=Mus m	93.36	24	4
Q6ZQL4 WDR43_MOUSE	WD repeat-containing protein	93.31	15	4
Q9QXC1 FETUB_MOUSE	Fetuin-B OS=Mus musculus G	92.2	26	4
O54962 BAF_MOUSE	Barrier-to-autointegration fact	91.84	51	4
Q9R1P0 PSA4_MOUSE	Proteasome subunit alpha typ	91.52	28	4
Q9R0N0 GALK1_MOUSE	Galactokinase OS=Mus musc	90.6	20	4
O08788 DCTN1_MOUSE	Dynactin subunit 1 OS=Mus m	90.59	24	4
P62073 TIM10_MOUSE	Mitochondrial import inner me	88.1	50	4
Q8VE22 RT23_MOUSE	28S ribosomal protein S23, m	87.88	47	4
P62869 ELOB_MOUSE	Transcription elongation factor	87.83	34	4
Q8BG32 PSD11_MOUSE	26S proteasome non-ATPase	86.82	25	4
P18572 BASI_MOUSE	Basigin OS=Mus musculus G	86.81	15	4
Q07813 BAX_MOUSE	Apoptosis regulator BAX OS=	86.37	28	4
Q8BI84 MIA3_MOUSE	Melanoma inhibitory activity pr	85.77	15	4
Q8CJ69 BMPER_MOUSE	BMP-binding endothelial regul	85.61	8	4
Q9JII6 AK1A1_MOUSE	Alcohol dehydrogenase [NAD]	83.12	17	4
Q9D2M8 UB2V2_MOUSE	Ubiquitin-conjugating enzyme	82.5	30	4
Q9CZY3 UB2V1_MOUSE	Ubiquitin-conjugating enzyme	82.5	24	4
P63158 HMGB1_MOUSE	High mobility group protein B1	82.49	30	4
Q9QZD9 EIF3I_MOUSE	Eukaryotic translation initiat	81.23	15	4
Q8BHN3 GANAB_MOUSE	Neutral alpha-glucosidase AB	80.52	17	4
Q01279 EGFR_MOUSE	Epidermal growth factor recep	80.35	8	4
P0C6F1 DYH2_MOUSE	Dynein heavy chain 2, axonen	79.82	5	4
Q64012 RALY_MOUSE	RNA-binding protein Raly OS=	79.36	24	4
P51150 RAB7A_MOUSE	Ras-related protein Rab-7a OS	78.31	27	4
Q9Z1Y4 TRIP6_MOUSE	Thyroid receptor-interacting pr	78.28	18	4
P54728 RD23B_MOUSE	UV excision repair protein RA	76.89	16	4
P62852 RS25_MOUSE	40S ribosomal protein S25 OS	74.95	36	4
Q6NWW9 FND3B_MOUSE	Fibronectin type III domain-co	74.33	7	4
P45376 ALDR_MOUSE	Aldose reductase OS=Mus m	74.17	17	4

Q921M3 SF3B3_MOUSE	Splicing factor 3B subunit 3 OS=Mus musculus	73.92	10	4
Q99LC5 ETF_A_MOUSE	Electron transfer flavoprotein subunit A OS=Mus musculus	70.88	19	4
P23116 EIF3A_MOUSE	Eukaryotic translation initiation factor 3 subunit A OS=Mus musculus	69.55	12	4
P62245 RS15A_MOUSE	40S ribosomal protein S15a OS=Mus musculus	69.42	32	4
Q8BMF4 ODP2_MOUSE	Dihydrodipicolyllysine-residue aminopeptidase OS=Mus musculus	69.37	15	4
Q8VHN8 SDOS_MOUSE	Protein syndesmosis OS=Mus musculus	68.74	32	4
Q60675 LAMA2_MOUSE	Laminin subunit alpha-2 OS=Mus musculus	67.04	13	4
Q91VD9 NDUS1_MOUSE	NADH-ubiquinone oxidoreductase subunit 1 OS=Mus musculus	65.74	15	4
Q9Z0R6 ITSN2_MOUSE	Intersectin-2 OS=Mus musculus	54.58	14	4
Q6NS46 RRP5_MOUSE	Protein RRP5 homolog OS=Mus musculus	53.84	7	4
Q91YU8 SSF1_MOUSE	Suppressor of SWI4 1 homolog OS=Mus musculus	51.26	20	4
Q91ZX7 LRP1_MOUSE	Pro-low-density lipoprotein receptor OS=Mus musculus	49.22	6	4
Q62407 SPEG_MOUSE	Striated muscle-specific serine/threonine phosphatase OS=Mus musculus	43.9	4	4
Q6GSS7 H2A2A_MOUSE	Histone H2A type 2-A OS=Mus musculus	299.33	88	3
P16627 HS71L_MOUSE	Heat shock 70 kDa protein 1-like OS=Mus musculus	245.91	63	3
P84228 H32_MOUSE	Histone H3.2 OS=Mus musculus	225.13	78	3
Q60972 RBBP4_MOUSE	Histone-binding protein RBBP4 OS=Mus musculus	181.84	37	3
O08583 THOC4_MOUSE	THO complex subunit 4 OS=Mus musculus	177.44	55	3
Q9R0B6 LAMC3_MOUSE	Laminin subunit gamma-3 OS=Mus musculus	157.72	12	3
Q8VEA4 MIA40_MOUSE	Mitochondrial intermembrane protein MIA40 OS=Mus musculus	147.38	32	3
Q61029 LAP2B_MOUSE	Lamina-associated polypeptide 2B OS=Mus musculus	141.23	28	3
Q9DBG9 TX1B3_MOUSE	Tax1-binding protein 3 OS=Mus musculus	127.96	47	3
P61971 NTF2_MOUSE	Nuclear transport factor 2 OS=Mus musculus	124.44	57	3
Q8VDM6 HNRL1_MOUSE	Heterogeneous nuclear ribonucleoprotein L1 OS=Mus musculus	122.56	29	3
Q60973 RBBP7_MOUSE	Histone-binding protein RBBP7 OS=Mus musculus	121.86	28	3
Q8BFY9 TNPO1_MOUSE	Transportin-1 OS=Mus musculus	121.11	35	3
P24452 CAPG_MOUSE	Macrophage-capping protein OS=Mus musculus	116.32	21	3
P70296 PEBP1_MOUSE	Phosphatidylethanolamine-binding protein 1 OS=Mus musculus	115.57	33	3
Q5SFM8 RBM27_MOUSE	RNA-binding protein 27 OS=Mus musculus	114.99	14	3
Q99P27 PG12B_MOUSE	Group XIIb secretory phospholipase A2 OS=Mus musculus	114.95	42	3
P05201 AATC_MOUSE	Aspartate aminotransferase, cytosolic OS=Mus musculus	112.61	17	3
O88630 GOSR1_MOUSE	Golgi SNAP receptor complex subunit 1 OS=Mus musculus	112.52	26	3
Q9DCJ5 NDUA8_MOUSE	NADH dehydrogenase [ubiquinone] subunit 8 OS=Mus musculus	111.93	23	3
Q91ZW3 SMCA5_MOUSE	SWI/SNF-related matrix-associated actin-dependent nuclear corepressor OS=Mus musculus	110.71	20	3
Q9CXW4 RL11_MOUSE	60S ribosomal protein L11 OS=Mus musculus	109.24	20	3
Q99KE1 MAOM_MOUSE	NAD-dependent malic enzyme OS=Mus musculus	109.22	18	3
P24472 GSTA4_MOUSE	Glutathione S-transferase A4 OS=Mus musculus	108.91	30	3
Q6ZWW7 RL35_MOUSE	60S ribosomal protein L35 OS=Mus musculus	108.47	22	3
Q9EQU5 SET_MOUSE	Protein SET OS=Mus musculus	108.04	22	3
Q61581 IBP7_MOUSE	Insulin-like growth factor-binding protein 7 OS=Mus musculus	107.86	31	3
Q9D7V9 NAAA_MOUSE	N-acyl ethanolamine-hydrolyzing lipase OS=Mus musculus	106.78	16	3
P51660 DHB4_MOUSE	Peroxisomal multifunctional enzyme OS=Mus musculus	106.33	11	3
O55057 PDE6D_MOUSE	Retinal rod rhodopsin-sensitive phosphodiesterase OS=Mus musculus	106.28	29	3
P12787 COX5A_MOUSE	Cytochrome c oxidase subunit 5a OS=Mus musculus	105.87	70	3
Q61247 A2AP_MOUSE	Alpha-2-antiplasmin OS=Mus musculus	105.7	15	3
Q920A5 RISC_MOUSE	Retinoid-inducible serine carboxylase OS=Mus musculus	105.45	13	3
P62849 RS24_MOUSE	40S ribosomal protein S24 OS=Mus musculus	105.44	29	3
P12265 BGLR_MOUSE	Beta-glucuronidase OS=Mus musculus	103.8	9	3
P29391 FRIL1_MOUSE	Ferritin light chain 1 OS=Mus musculus	103.19	31	3
Q08093 CNN2_MOUSE	Calponin-2 OS=Mus musculus	103.04	21	3
Q91VC3 IF4A3_MOUSE	Eukaryotic initiation factor 4A-3 OS=Mus musculus	102.5	27	3
P70168 IMB1_MOUSE	Importin subunit beta-1 OS=Mus musculus	102.1	9	3
P11438 LAMP1_MOUSE	Lysosome-associated membrane protein 1 OS=Mus musculus	101.69	27	3
P35979 RL12_MOUSE	60S ribosomal protein L12 OS=Mus musculus	101.62	42	3
Q9CY16 RT28_MOUSE	28S ribosomal protein S28, mouse OS=Mus musculus	100.73	29	3

Q80UY2 KCMF1_MOUSE	E3 ubiquitin-protein ligase KC	99.9	16	3
Q9ES28 ARHG7_MOUSE	Rho guanine nucleotide excha	99.82	13	3
P97429 ANXA4_MOUSE	Annexin A4 OS=Mus musculu	99.76	29	3
Q3TKT4 SMCA4_MOUSE	Transcription activator BRG1	99.26	8	3
Q8VH51 RBM39_MOUSE	RNA-binding protein 39 OS=M	98.83	16	3
Q61823 PDCD4_MOUSE	Programmed cell death protei	98.32	23	3
Q8BGS0 MAK16_MOUSE	Protein MAK16 homolog OS=	98.24	24	3
P08074 CBR2_MOUSE	Carbonyl reductase [NADPH]	97.51	26	3
Q61703 ITIH2_MOUSE	Inter-alpha-trypsin inhibitor he	97.11	15	3
Q9D8U8 SNX5_MOUSE	Sorting nexin-5 OS=Mus musc	96.46	18	3
P63028 TCTP_MOUSE	Translationally-controlled tumo	95.69	28	3
P63325 RS10_MOUSE	40S ribosomal protein S10 OS	95.03	31	3
Q9Z0H3 SNF5_MOUSE	SWI/SNF-related matrix-assoc	94.48	21	3
P00920 CAH2_MOUSE	Carbonic anhydrase 2 OS=MU	92.49	16	3
Q9CR68 UCRI_MOUSE	Cytochrome b-c1 complex sub	92.31	35	3
Q9CPX7 RT16_MOUSE	28S ribosomal protein S16, m	92.02	29	3
P97390 VPS45_MOUSE	Vacuolar protein sorting-assoc	91.87	12	3
Q922Y1 UBXN1_MOUSE	UBX domain-containing protei	91.79	26	3
Q6ZQ88 KDM1A_MOUSE	Lysine-specific histone demetf	90.79	7	3
P24547 IMDH2_MOUSE	Inosine-5'-monophosphate de	90.54	18	3
Q9R0X4 ACOT9_MOUSE	Acyl-coenzyme A thioesterase	90.19	24	3
P29416 HEXA_MOUSE	Beta-hexosaminidase subunit	90.14	18	3
Q8BYK6 YTHD3_MOUSE	YTH domain family protein 3 O	89.41	16	3
Q9R1P3 PSB2_MOUSE	Proteasome subunit beta type	89.33	28	3
P99026 PSB4_MOUSE	Proteasome subunit beta type	89.03	26	3
P46467 VPS4B_MOUSE	Vacuolar protein sorting-assoc	88.96	20	3
P62821 RAB1A_MOUSE	Ras-related protein Rab-1A O	88.86	38	3
Q60649 CLPB_MOUSE	Caseinolytic peptidase B prote	88.36	10	3
Q6ZPY7 KDM3B_MOUSE	Lysine-specific demethylase 3	87.93	12	3
P07146 TRY2_MOUSE	Anionic trypsin-2 OS=Mus mu	87.92	19	3
Q7TN75 PEG10_MOUSE	Retrotransposon-derived prote	87.76	17	3
P04117 FABP4_MOUSE	Fatty acid-binding protein, adip	87.65	27	3
Q9QYS9 QKI_MOUSE	Protein quaking OS=Mus mus	87.43	29	3
P19536 COX5B_MOUSE	Cytochrome c oxidase subunit	87.3	30	3
Q8VE88 F1142_MOUSE	Protein FAM114A2 OS=Mus r	87	35	3
Q9Z0P5 TWF2_MOUSE	Twinfilin-2 OS=Mus musculus	86.77	10	3
Q9CQ40 RM49_MOUSE	39S ribosomal protein L49, mi	86.41	22	3
Q9EQS3 MYCBP_MOUSE	C-Myc-binding protein OS=MU	86.21	58	3
P42932 TCPQ_MOUSE	T-complex protein 1 subunit th	86.11	18	3
Q921G8 GCP2_MOUSE	Gamma-tubulin complex comp	86.02	26	3
Q8R010 AIMP2_MOUSE	Aminoacyl tRNA synthase con	85.74	26	3
Q06138 CAB39_MOUSE	Calcium-binding protein 39 OS	84.6	12	3
Q922V4 PLRG1_MOUSE	Pleiotropic regulator 1 OS=MU	83.77	8	3
Q9D0F3 LMAN1_MOUSE	Protein ERGIC-53 OS=Mus m	83.65	10	3
Q9CPV4 GLOD4_MOUSE	Glyoxalase domain-containing	83.52	22	3
Q64511 TOP2B_MOUSE	DNA topoisomerase 2-beta O	82.94	6	3
P46935 NEDD4_MOUSE	E3 ubiquitin-protein ligase NE	82.54	20	3
Q3U7R1 ESYT1_MOUSE	Extended synaptotagmin-1 OS	82.33	12	3
Q9JMA1 UBP14_MOUSE	Ubiquitin carboxyl-terminal hyd	82.27	16	3
Q69ZA1 CDK13_MOUSE	Cyclin-dependent kinase 13 O	82.26	11	3
Q3U9G9 LBR_MOUSE	Lamin-B receptor OS=Mus mu	82.19	10	3
O88544 CSN4_MOUSE	COP9 signalosome complex s	82.02	31	3
Q3UKC1 TAXB1_MOUSE	Tax1-binding protein 1 homolo	81.85	22	3
A2AGT5 CKAP5_MOUSE	Cytoskeleton-associated prote	80.73	11	3
Q9DBY8 NVL_MOUSE	Nuclear valosin-containing pro	80.32	10	3

Q9DBG7 SRPR_MOUSE	Signal recognition particle rec	79.88	10	3
Q8VC70 RBMS2_MOUSE	RNA-binding motif, single-str	78.67	30	3
Q921F4 HNRL_MOUSE	Heterogeneous nuclear ribonu	78.49	13	3
P01029 CO4B_MOUSE	Complement C4-B OS=Mus m	77.2	10	3
Q9CZ44 NSF1C_MOUSE	NSFL1 cofactor p47 OS=Mus	76.88	12	3
P61961 UFM1_MOUSE	Ubiquitin-fold modifier 1 OS=M	75.89	69	3
P41105 RL28_MOUSE	60S ribosomal protein L28 OS	75.18	29	3
Q6ZWW3 RL10_MOUSE	60S ribosomal protein L10 OS	75.07	19	3
O55023 IMPA1_MOUSE	Inositol monophosphatase 1 C	75.02	28	3
Q9D1K7 CT027_MOUSE	UPF0687 protein C2orf27 ho	74.68	25	3
P62827 RAN_MOUSE	GTP-binding nuclear protein R	74.63	17	3
Q7TQH0 ATX2L_MOUSE	Ataxin-2-like protein OS=Mus	74.44	8	3
Q9QXV1 CBX8_MOUSE	Chromobox protein homolog 8	74.42	9	3
Q80WJ7 LYRIC_MOUSE	Protein LYRIC OS=Mus musc	74.26	24	3
Q3V4B5 COMD6_MOUSE	COMM domain-containing pro	73.82	47	3
Q9CQP2 TPPC2_MOUSE	Trafficking protein particle con	73.21	35	3
Q99J99 THTM_MOUSE	3-mercaptopyruvate sulfurtran	73.12	14	3
P62900 RL31_MOUSE	60S ribosomal protein L31 OS	72.65	40	3
P59325 IF5_MOUSE	Eukaryotic translation initiat	72.42	12	3
P61965 WDR5_MOUSE	WD repeat-containing protein	71.65	16	3
Q8BX22 SALL4_MOUSE	Sal-like protein 4 OS=Mus mu	71.53	11	3
O88508 DNM3A_MOUSE	DNA (cytosine-5)-methyltrans	71.08	7	3
Q6PB66 LPPRC_MOUSE	Leucine-rich PPR motif-contai	70.76	6	3
Q9CR00 PSMD9_MOUSE	26S proteasome non-ATPase	70.41	22	3
Q9CR21 ACPM_MOUSE	Acyl carrier protein, mitochond	70.38	14	3
Q6PGN1 F132B_MOUSE	Protein FAM132B OS=Mus m	69.87	9	3
Q8BL66 EEA1_MOUSE	Early endosome antigen 1 OS	69.47	8	3
Q9Z1N2 ORC1_MOUSE	Origin recognition complex su	68.93	9	3
Q8C5Q4 GRSF1_MOUSE	G-rich sequence factor 1 OS=	68.88	20	3
Q61263 SOAT1_MOUSE	Sterol O-acyltransferase 1 OS	68.41	43	3
Q9R087 GPC6_MOUSE	Glypican-6 OS=Mus musculus	67.47	21	3
P63168 DYL1_MOUSE	Dynein light chain 1, cytoplas	67.42	48	3
Q80U93 NU214_MOUSE	Nuclear pore complex protein	67.23	10	3
Q9WUU7 CATZ_MOUSE	Cathepsin Z OS=Mus muscul	65.2	25	3
Q9CZG9 PDZ11_MOUSE	PDZ domain-containing protei	64.59	65	3
O35604 NPC1_MOUSE	Niemann-Pick C1 protein OS=	64.28	8	3
P11983 TCPA_MOUSE	T-complex protein 1 subunit a	63.34	13	3
Q9Z1N5 DX39B_MOUSE	Spliceosome RNA helicase D	62.3	16	3
Q9D6J6 NDUV2_MOUSE	NADH dehydrogenase [ubiqui	61.76	24	3
Q80W00 PP1RA_MOUSE	Serine/threonine-protein phos	60.53	17	3
P80318 TCPG_MOUSE	T-complex protein 1 subunit g	59.81	38	3
P54775 PRS6B_MOUSE	26S protease regulatory subun	59.62	8	3
Q9CQM9 GLRX3_MOUSE	Glutaredoxin-3 OS=Mus musc	59.13	16	3
P14901 HMOX1_MOUSE	Heme oxygenase 1 OS=Mus m	58.37	19	3
Q8BMJ2 SYLC_MOUSE	Leucyl-tRNA synthetase, cyto	58	8	3
P29268 CTGF_MOUSE	Connective tissue growth facto	57.19	13	3
Q6P5F9 XPO1_MOUSE	Exportin-1 OS=Mus musculus	57.04	7	3
Q9CR98 F136A_MOUSE	Protein FAM136A OS=Mus m	56.87	25	3
Q9DCD5 TJAP1_MOUSE	Tight junction-associated prote	54.46	5	3
P83940 ELOC_MOUSE	Transcription elongation facto	53.8	44	3
Q9JJ28 FLII_MOUSE	Protein flightless-1 homolog C	53.33	10	3
Q63870 CO7A1_MOUSE	Collagen alpha-1(VII) chain O	48.67	11	3
Q80T85 DCAF5_MOUSE	DDB1- and CUL4-associated	47.52	10	3
P70336 ROCK2_MOUSE	Rho-associated protein kinase	47.44	7	3
Q99KW3 TARA_MOUSE	TRIO and F-actin-binding prot	43.34	8	3

P16056 MET_MOUSE	Hepatocyte growth factor rece	42.77	9	3
Q6QIY3 SCNAA_MOUSE	Sodium channel protein type 1	41.52	6	3
Q9CW03 SMC3_MOUSE	Structural maintenance of chr	40.92	12	3
Q8BJ37 TYDP1_MOUSE	Tyrosyl-DNA phosphodiestera	40.08	12	3
Q6ZWQ0 SYNE2_MOUSE	Nesprin-2 OS=Mus musculus	37.4	7	3
O88700 BLM_MOUSE	Bloom syndrome protein homo	36.33	8	3
Q6NZC7 S23IP_MOUSE	SEC23-interacting protein OS	34.81	6	3
Q6PDK2 MLL2_MOUSE	Histone-lysine N-methyltransfe	34.74	3	3
A2A7S8 K1522_MOUSE	Uncharacterized protein KIAA	34	7	3
Q9QXZ0 MACF1_MOUSE	Microtubule-actin cross-linking	33.73	4	3
Q924A2 CIC_MOUSE	Protein capicua homolog OS=	33.17	4	3
Q99PJ1 PCD15_MOUSE	Protocadherin-15 OS=Mus mu	32.93	5	3
Q6R5N8 TLR13_MOUSE	Toll-like receptor 13 OS=Mus	32.86	13	3
Q9CXA2 PRCM_MOUSE	Probable proline racemase OS	30.3	8	3
B2RX88 CSPP1_MOUSE	Centrosome and spindle pole	30.26	8	3
Q6PGL7 FAM21_MOUSE	WASH complex subunit FAM2	30.03	8	3
Q8BLN6 UNC80_MOUSE	Protein unc-80 homolog OS=M	29.79	8	3
B9EKI3 TMF1_MOUSE	TATA element modulatory fac	29.2	7	3
A2AAE1 K1109_MOUSE	Uncharacterized protein KIAA	27.33	7	3
Q766D5 B4GN4_MOUSE	N-acetyl-beta-glucosaminyl-gly	26.91	9	3
Q3UHU5 K0802_MOUSE	Uncharacterized protein KIAA	26.9	4	3
Q80TY5 VP13B_MOUSE	Vacuolar protein sorting-assoc	26.69	4	3
Q6GQT6 SCAP_MOUSE	Sterol regulatory element-bind	26.49	9	3
Q9R244 TRPC2_MOUSE	Short transient receptor poten	25.77	8	3
A2ARZ3 FSIP2_MOUSE	Fibrous sheath-interacting pro	25.37	5	3
O88491 NSD1_MOUSE	Histone-lysine N-methyltransfe	24.67	4	3
Q4VK74 IL28A_MOUSE	Interleukin-28A OS=Mus musc	24.52	13	3
Q8CGK6 IL28B_MOUSE	Interleukin-28B OS=Mus musc	24.52	13	3
P06800 PTPRC_MOUSE	Receptor-type tyrosine-protein	21.91	7	3
P63260 ACTG_MOUSE	Actin, cytoplasmic 2 OS=Mus	354.61	86	2
Q64522 H2A2B_MOUSE	Histone H2A type 2-B OS=Mus	301.18	90	2
P07758 A1AT1_MOUSE	Alpha-1-antitrypsin 1-1 OS=M	257.13	61	2
P68372 TBB2C_MOUSE	Tubulin beta-2C chain OS=Mus	256.34	65	2
Q7TMM9 TBB2A_MOUSE	Tubulin beta-2A chain OS=Mus	245.26	60	2
Q9CWF2 TBB2B_MOUSE	Tubulin beta-2B chain OS=Mus	245.26	60	2
Q64524 H2B2E_MOUSE	Histone H2B type 2-E OS=Mus	212.55	72	2
Q922F4 TBB6_MOUSE	Tubulin beta-6 chain OS=Mus	210.98	45	2
P70333 HNRH2_MOUSE	Heterogeneous nuclear ribonu	178.13	29	2
Q9CQ19 MYL9_MOUSE	Myosin regulatory light polype	176.32	81	2
P63163 RSMN_MOUSE	Small nuclear ribonucleoprote	165.88	50	2
Q9JKB3 DBPA_MOUSE	DNA-binding protein A OS=M	149.05	29	2
P26040 EZRI_MOUSE	Ezrin OS=Mus musculus GN=	133.84	17	2
P35550 FBRL_MOUSE	rRNA 2'-O-methyltransferase	131.03	30	2
P26043 RADI_MOUSE	Radixin OS=Mus musculus G	130.02	22	2
Q6PFR5 TRA2A_MOUSE	Transformer-2 protein homolo	125.44	26	2
Q6P1F6 2ABA_MOUSE	Serine/threonine-protein phos	122.58	30	2
P35278 RAB5C_MOUSE	Ras-related protein Rab-5C O	121.99	25	2
Q62241 RU1C_MOUSE	U1 small nuclear ribonucleopr	118.52	40	2
P01644 KV5AB_MOUSE	Ig kappa chain V-V region HP	117.47	47	2
P26041 MOES_MOUSE	Moesin OS=Mus musculus G	115.89	25	2
P97461 RS5_MOUSE	40S ribosomal protein S5 OS=	111.9	50	2
P97290 IC1_MOUSE	Plasma protease C1 inhibitor	110.09	15	2
Q60590 A1AG1_MOUSE	Alpha-1-acid glycoprotein 1 O	109.67	38	2
Q9CQN1 TRAP1_MOUSE	Heat shock protein 75 kDa, m	106.44	15	2
Q9R1P1 PSB3_MOUSE	Proteasome subunit beta type	101.53	27	2

Q921H8 THIKA_MOUSE	3-ketoacyl-CoA thiolase A, pe	101.43	25	2
Q99JX3 GORS2_MOUSE	Golgi reassembly-stacking pro	100.57	17	2
Q62426 CYTB_MOUSE	Cystatin-B OS=Mus musculus	100.39	33	2
Q9ESB3 HRG_MOUSE	Histidine-rich glycoprotein OS=	97.47	10	2
Q9CS42 PRPS2_MOUSE	Ribose-phosphate pyrophosph	97.36	25	2
P26883 FKB1A_MOUSE	Peptidyl-prolyl cis-trans isome	97.14	25	2
Q9ET22 DPP2_MOUSE	Dipeptidyl peptidase 2 OS=Mu	96.81	14	2
Q9ES46 PARVB_MOUSE	Beta-parvin OS=Mus musculu	96.59	11	2
Q9JJV2 PROF2_MOUSE	Profilin-2 OS=Mus musculus C	96.56	32	2
P97379 G3BP2_MOUSE	Ras GTPase-activating protei	95.87	15	2
Q9DCH4 EIF3F_MOUSE	Eukaryotic translation initiat	95.71	16	2
Q511X5 IASPP_MOUSE	RelA-associated inhibitor OS=	93.77	17	2
Q9DCD6 GBRAP_MOUSE	Gamma-aminobutyric acid rec	93.28	32	2
P47955 RLA1_MOUSE	60S acidic ribosomal protein F	92.16	42	2
P10639 THIO_MOUSE	Thioredoxin OS=Mus musculu	91.4	21	2
O88968 TCO2_MOUSE	Transcobalamin-2 OS=Mus m	91.23	12	2
P70663 SPRL1_MOUSE	SPARC-like protein 1 OS=Mus	90.96	10	2
Q8BHD7 ROD1_MOUSE	Regulator of differentiation 1 C	90.78	21	2
Q61510 TRI25_MOUSE	E3 ubiquitin/ISG15 ligase TRII	89.97	12	2
Q9Z1B5 MD2L1_MOUSE	Mitotic spindle assembly chec	89.56	24	2
Q8CI43 MYL6B_MOUSE	Myosin light chain 6B OS=Mus	88.95	25	2
O35744 CH3L3_MOUSE	Chitinase-3-like protein 3 OS=	88.68	18	2
Q8BRG8 TM209_MOUSE	Transmembrane protein 209 C	88.01	12	2
Q04857 CO6A1_MOUSE	Collagen alpha-1(VI) chain OS	86.6	8	2
Q7TPD3 ROBO2_MOUSE	Roundabout homolog 2 OS=M	86.24	9	2
P26618 PGFRA_MOUSE	Alpha-type platelet-derived gro	86.16	20	2
P62196 PRS8_MOUSE	26S protease regulatory subu	85.38	16	2
P04919 B3AT_MOUSE	Band 3 anion transport protei	85.3	9	2
Q6NZN0 RBM26_MOUSE	RNA-binding protein 26 OS=M	84.87	10	2
Q64324 STXB2_MOUSE	Syntaxin-binding protein 2 OS	84.53	12	2
Q8K183 PDXK_MOUSE	Pyridoxal kinase OS=Mus mus	83.89	14	2
Q6ZWM4 NAA38_MOUSE	N-alpha-acetyltransferase 38,	83.77	34	2
Q9WVJ2 PSD13_MOUSE	26S proteasome non-ATPase	83.47	18	2
P60824 CIRBP_MOUSE	Cold-inducible RNA-binding pr	83.03	36	2
Q9CQT2 RBM7_MOUSE	RNA-binding protein 7 OS=M	83.02	14	2
P97360 ETV6_MOUSE	Transcription factor ETV6 OS=	82.86	12	2
Q8BSQ9 PB1_MOUSE	Protein polybromo-1 OS=Mus	82.61	9	2
P67984 RL22_MOUSE	60S ribosomal protein L22 OS	82.26	20	2
P22892 AP1G1_MOUSE	AP-1 complex subunit gamma	82.25	15	2
P62855 RS26_MOUSE	40S ribosomal protein S26 OS	82.11	39	2
Q6A065 CE170_MOUSE	Centrosomal protein of 170 kD	82.04	8	2
Q91YD3 DCP1A_MOUSE	mRNA-decapping enzyme 1A	80.74	9	2
P51885 LUM_MOUSE	Lumican OS=Mus musculus C	80.71	24	2
Q9CSU0 RPR1B_MOUSE	Regulation of nuclear pre-mR	80.64	15	2
O35114 SCRB2_MOUSE	Lysosome membrane protein	80.59	9	2
Q8BKG3 PTK7_MOUSE	Inactive tyrosine-protein kinas	80.26	10	2
P97425 ECP2_MOUSE	Eosinophil cationic protein 2 C	80.11	38	2
Q9Z1Z2 STRAP_MOUSE	Serine-threonine kinase recep	80.08	24	2
Q9Z175 LOXL3_MOUSE	Lysyl oxidase homolog 3 OS=	79.56	4	2
Q69ZQ2 ISY1_MOUSE	Pre-mRNA-splicing factor ISY	78.99	19	2
Q9Z0M5 LICH_MOUSE	Lysosomal acid lipase/cholest	78.41	29	2
Q6A4J8 UBP7_MOUSE	Ubiquitin carboxyl-terminal h	78.11	7	2
P02463 CO4A1_MOUSE	Collagen alpha-1(IV) chain OS	77.9	9	2
P10649 GSTM1_MOUSE	Glutathione S-transferase Mu	77.56	19	2
Q80W21 GSTM7_MOUSE	Glutathione S-transferase Mu	77.56	32	2

P15626 GSTM2_MOUSE	Glutathione S-transferase Mu	77.56	18	2
Q8CHU3 EPN2_MOUSE	Epsin-2 OS=Mus musculus G	77.46	10	2
P97855 G3BP1_MOUSE	Ras GTPase-activating protein	77.44	16	2
Q8K221 ARFP2_MOUSE	Arfaptin-2 OS=Mus musculus	77.15	24	2
O35841 API5_MOUSE	Apoptosis inhibitor 5 OS=Mus	76.97	14	2
P01887 B2MG_MOUSE	Beta-2-microglobulin OS=Mus	76.51	29	2
Q3UIA2 RHG17_MOUSE	Rho GTPase-activating protein	76.47	11	2
P17047 LAMP2_MOUSE	Lysosome-associated membr	76.26	10	2
Q9DCT8 CRIP2_MOUSE	Cysteine-rich protein 2 OS=M	76.03	35	2
O35207 CDKA1_MOUSE	Cyclin-dependent kinase 2-as	75.84	20	2
P54823 DDX6_MOUSE	Probable ATP-dependent RNA	75.65	13	2
A2ASQ1 AGRIN_MOUSE	Agrin OS=Mus musculus GN=	75.62	8	2
O08709 PRDX6_MOUSE	Peroxiredoxin-6 OS=Mus mus	75.59	14	2
P26231 CTNA1_MOUSE	Catenin alpha-1 OS=Mus mus	75.57	15	2
Q9QZ23 NFU1_MOUSE	NFU1 iron-sulfur cluster scaff	75.47	16	2
Q920B9 SP16H_MOUSE	FACT complex subunit SPT16	75.44	11	2
Q9WU28 PFD5_MOUSE	Prefoldin subunit 5 OS=Mus m	75.37	29	2
Q69ZW3 EHBP1_MOUSE	EH domain-binding protein 1 O	75.32	4	2
Q60692 PSB6_MOUSE	Proteasome subunit beta type	74.74	16	2
Q91VR2 ATPG_MOUSE	ATP synthase subunit gamma	74.65	25	2
Q9Z2Y8 PROSC_MOUSE	Proline synthase co-transcribe	74.53	19	2
Q60737 CSK21_MOUSE	Casein kinase II subunit alpha	74.48	17	2
Q9QUI0 RHOA_MOUSE	Transforming protein RhoA OS	74.2	20	2
O55234 PSB5_MOUSE	Proteasome subunit beta type	74.17	16	2
Q9D8C6 MED11_MOUSE	Mediator of RNA polymerase	74.11	23	2
Q01730 RSU1_MOUSE	Ras suppressor protein 1 OS=	73.76	24	2
P10518 HEM2_MOUSE	Delta-aminolevulinic acid dehy	73.27	13	2
O08740 RPB11_MOUSE	DNA-directed RNA polymeras	73.26	47	2
Q99KV1 DJB11_MOUSE	DnaJ homolog subfamily B me	73.11	19	2
Q78HU3 F125A_MOUSE	Multivesicular body subunit 12	73.1	15	2
Q9D8W5 PSD12_MOUSE	26S proteasome non-ATPase	73.01	13	2
P06745 G6PI_MOUSE	Glucose-6-phosphate isomera	72.55	10	2
Q62419 SH3G1_MOUSE	Endophilin-A2 OS=Mus muscu	72.42	30	2
Q3UPF5 ZCCHV_MOUSE	Zinc finger CCCH-type antivira	72.3	12	2
P35441 TSP1_MOUSE	Thrombospondin-1 OS=Mus m	71.94	13	2
O70435 PSA3_MOUSE	Proteasome subunit alpha typ	71.91	14	2
Q91VY9 ZN622_MOUSE	Zinc finger protein 622 OS=M	71.75	12	2
Q9JJY4 DDX20_MOUSE	Probable ATP-dependent RNA	71.52	22	2
Q91ZA3 PCCA_MOUSE	Propionyl-CoA carboxylase alp	71.5	11	2
Q9JHW2 NIT2_MOUSE	Omega-amidase NIT2 OS=M	70.81	18	2
P06683 CO9_MOUSE	Complement component C9 C	70.71	13	2
P21460 CYTC_MOUSE	Cystatin-C OS=Mus musculus	70.4	20	2
Q6ZQ58 LARP1_MOUSE	La-related protein 1 OS=Mus	70.39	10	2
Q9CQ75 NDUA2_MOUSE	NADH dehydrogenase [ubiqui	70.08	24	2
O35459 ECH1_MOUSE	Delta(3,5)-Delta(2,4)-dienoyl-C	69.16	18	2
Q9JII5 DAZP1_MOUSE	DAZ-associated protein 1 OS=	68.92	15	2
Q8VDT9 RM50_MOUSE	39S ribosomal protein L50, mi	68.59	44	2
P47941 CRKL_MOUSE	Crk-like protein OS=Mus mus	68.58	15	2
Q5RKR3 ISLR2_MOUSE	Immunoglobulin superfamily c	68.47	16	2
Q9D883 U2AF1_MOUSE	Splicing factor U2AF 35 kDa s	68.36	32	2
Q9ESP1 SDF2L_MOUSE	Stromal cell-derived factor 2-li	67.99	24	2
Q923D2 BLVRB_MOUSE	Flavin reductase OS=Mus mu	67.58	18	2
Q8BX90 FND3A_MOUSE	Fibronectin type-III domain-co	67.34	8	2
Q8BIW1 PRUNE_MOUSE	Protein prune homolog OS=M	67.18	7	2
Q9Z2I0 LETM1_MOUSE	LETM1 and EF-hand domain-	67	9	2



Q9ERE7 MESD_MOUSE	LDLR chaperone MESD OS=M	66.71	17	2
Q9CPY7 AMPL_MOUSE	Cytosol aminopeptidase OS=M	65.46	16	2
P13634 CAH1_MOUSE	Carbonic anhydrase 1 OS=Mu	65.02	8	2
Q9R1P4 PSA1_MOUSE	Proteasome subunit alpha typ	64.79	24	2
Q91Z31 PTBP2_MOUSE	Polypyrimidine tract-binding pr	64.7	18	2
P53996 CNBP_MOUSE	Cellular nucleic acid-binding p	64.63	13	2
P10107 ANXA1_MOUSE	Annexin A1 OS=Mus musculu	64.25	11	2
P80313 TCPH_MOUSE	T-complex protein 1 subunit e	64.06	9	2
P19157 GSTP1_MOUSE	Glutathione S-transferase P 1	63.76	15	2
Q923D4 SF3B5_MOUSE	Splicing factor 3B subunit 5 O	63.72	33	2
Q9DCT2 NDUS3_MOUSE	NADH dehydrogenase [ubiquin	63.55	26	2
Q8CCS6 PABP2_MOUSE	Polyadenylate-binding protein	63.08	11	2
P39054 DYN2_MOUSE	Dynamin-2 OS=Mus musculus	63.07	8	2
Q80X50 UBP2L_MOUSE	Ubiquitin-associated protein 2	62.83	12	2
O88531 PPT1_MOUSE	Palmitoyl-protein thioesterase	62.02	8	2
Q9CWP6 MSPD2_MOUSE	Motile sperm domain-containin	61.36	8	2
Q9R0L7 AKP8L_MOUSE	A-kinase anchor protein 8-like	60.88	6	2
Q9DBT5 AMPD2_MOUSE	AMP deaminase 2 OS=Mus m	60.77	13	2
Q91W69 EPN3_MOUSE	Epsin-3 OS=Mus musculus G	60.37	5	2
P19253 RL13A_MOUSE	60S ribosomal protein L13a O	60.35	19	2
O35857 TIM44_MOUSE	Mitochondrial import inner me	60.22	12	2
Q6ZWX6 IF2A_MOUSE	Eukaryotic translation initiator	60.12	9	2
O35166 GOSR2_MOUSE	Golgi SNAP receptor complex	60.01	24	2
O55013 TPPC3_MOUSE	Trafficking protein particle con	59.05	14	2
P70335 ROCK1_MOUSE	Rho-associated protein kinase	59	8	2
O70439 STX7_MOUSE	Syntaxin-7 OS=Mus musculus	58.91	21	2
Q91YW3 DNJC3_MOUSE	DnaJ homolog subfamily C me	58.85	6	2
Q9Z108 STAU1_MOUSE	Double-stranded RNA-binding	58.73	5	2
Q9JLV6 PNKP_MOUSE	Bifunctional polynucleotide ph	58.49	10	2
P47757 CAPZB_MOUSE	F-actin-capping protein subun	57.36	25	2
Q9WTR2 M3K6_MOUSE	Mitogen-activated protein kina	57.36	3	2
Q62296 TEAD4_MOUSE	Transcriptional enhancer facto	57.16	12	2
Q8C170 MYO9A_MOUSE	Myosin-IXa OS=Mus musculu	57.04	4	2
P19096 FAS_MOUSE	Fatty acid synthase OS=Mus r	56.94	6	2
Q9CXY6 ILF2_MOUSE	Interleukin enhancer-binding f	56.84	11	2
Q7TQ95 LNP_MOUSE	Protein lunapark OS=Mus mu	56.79	14	2
Q8CCK0 H2AW_MOUSE	Core histone macro-H2A.2 OS	56.69	20	2
Q8QZY9 SF3B4_MOUSE	Splicing factor 3B subunit 4 O	56.55	17	2
Q61702 ITI1_MOUSE	Inter-alpha-trypsin inhibitor he	56.44	7	2
P63037 DNJA1_MOUSE	DnaJ homolog subfamily A me	56.28	18	2
P80315 TCPD_MOUSE	T-complex protein 1 subunit d	56	11	2
P15306 TRBM_MOUSE	Thrombomodulin OS=Mus mu	55.83	12	2
Q8CGR5 KLK14_MOUSE	Kallikrein-14 OS=Mus muscul	55.64	13	2
P61211 ARL1_MOUSE	ADP-ribosylation factor-like pr	55.52	9	2
O70400 PDLI1_MOUSE	PDZ and LIM domain protein	55.42	24	2
P56565 S10A1_MOUSE	Protein S100-A1 OS=Mus mu	55.32	38	2
Q9CYI4 LUC7L_MOUSE	Putative RNA-binding protein	55.29	9	2
Q61598 GDIB_MOUSE	Rab GDP dissociation inhibito	55.15	12	2
P35951 LDLR_MOUSE	Low-density lipoprotein recept	55.07	9	2
Q9Z0J0 NPC2_MOUSE	Epididymal secretory protein E	55.07	12	2
P19221 THRB_MOUSE	Prothrombin OS=Mus muscul	54.98	8	2
Q8R3C6 RBM19_MOUSE	Probable RNA-binding protein	54.96	11	2
P62889 RL30_MOUSE	60S ribosomal protein L30 OS	54.55	16	2
Q7TT37 ELP1_MOUSE	Elongator complex protein 1 C	54.52	8	2
P34022 RANG_MOUSE	Ran-specific GTPase-activator	54.33	29	2

Q9Z2L6 MINP1_MOUSE	Multiple inositol polyphosphate	53.85	11	2
Q9D945 LLPH_MOUSE	Protein LLP homolog OS=Mus	53.66	37	2
P70460 VASP_MOUSE	Vasodilator-stimulated phosph	53.54	23	2
Q8K1J6 TRNT1_MOUSE	CCA tRNA nucleotidyltransfer	53.46	18	2
P47753 CAZA1_MOUSE	F-actin-capping protein subun	52.82	10	2
Q00PI9 HNRL2_MOUSE	Heterogeneous nuclear ribonu	52.71	7	2
Q8CH25 SLTM_MOUSE	SAFB-like transcription modul	52.65	6	2
Q8BRF7 SCFD1_MOUSE	Sec1 family domain-containin	52.61	14	2
P23953 ESTN_MOUSE	Liver carboxylesterase N OS=	52.28	6	2
Q9CPW4 ARPC5_MOUSE	Actin-related protein 2/3 comp	52.22	21	2
Q569Z6 TR150_MOUSE	Thyroid hormone receptor-ass	52.02	4	2
Q148V7 K1468_MOUSE	LisH domain and HEAT repea	51.88	15	2
Q91VZ6 SMAP1_MOUSE	Stromal membrane-associated	51.54	13	2
Q9EPU4 CPSF1_MOUSE	Cleavage and polyadenylation	51.23	3	2
P32921 SYWC_MOUSE	Tryptophanyl-tRNA synthetase	51.1	11	2
Q62318 TIF1B_MOUSE	Transcription intermediary fac	50.94	8	2
Q8BL99 DOP1_MOUSE	Protein dopey-1 OS=Mus mus	50.82	5	2
P21126 UBL4A_MOUSE	Ubiquitin-like protein 4A OS=M	50.79	27	2
Q8K4M5 COMD1_MOUSE	COMM domain-containing pro	50.73	16	2
O08715 AKAP1_MOUSE	A-kinase anchor protein 1, mit	50.43	5	2
O88543 CSN3_MOUSE	COP9 signalosome complex s	50.16	19	2
Q9WTQ5 AKA12_MOUSE	A-kinase anchor protein 12 OS	49.83	8	2
O88958 GNP11_MOUSE	Glucosamine-6-phosphate iso	49.58	21	2
P09528 FRIH_MOUSE	Ferritin heavy chain OS=Mus	48.67	12	2
Q9CWK8 SNX2_MOUSE	Sorting nexin-2 OS=Mus musc	48.6	13	2
Q9ERU9 RBP2_MOUSE	E3 SUMO-protein ligase RanB	47.93	5	2
Q07456 AMBP_MOUSE	Protein AMBP OS=Mus musc	46.96	6	2
P05532 KIT_MOUSE	Mast/stem cell growth factor r	46.9	8	2
Q9D5V5 CUL5_MOUSE	Cullin-5 OS=Mus musculus G	46.6	13	2
Q8BNJ6 NETO2_MOUSE	Neuropilin and tolloid-like prot	46.6	10	2
Q6P3D0 NUD16_MOUSE	U8 snoRNA-decapping enzym	46.36	16	2
Q6ZWR6 SYNE1_MOUSE	Nesprin-1 OS=Mus musculus	46.01	4	2
Q8CG48 SMC2_MOUSE	Structural maintenance of chr	45.84	6	2
Q8BMK4 CKAP4_MOUSE	Cytoskeleton-associated prote	45.28	16	2
Q6PE15 ABHDA_MOUSE	Abhydrolase domain-containin	44.99	17	2
O70591 PFD2_MOUSE	Prefoldin subunit 2 OS=Mus n	44.78	27	2
Q8VHK9 DHX36_MOUSE	Probable ATP-dependent RNA	44.73	5	2
P70288 HDAC2_MOUSE	Histone deacetylase 2 OS=Mu	44.49	13	2
O09106 HDAC1_MOUSE	Histone deacetylase 1 OS=Mu	44.49	8	2
Q8BTS4 NUP54_MOUSE	Nuclear pore complex protein	44.27	10	2
Q05D44 IF2P_MOUSE	Eukaryotic translation initiat	43.78	11	2
Q9D1R9 RL34_MOUSE	60S ribosomal protein L34 OS	43.66	15	2
P47964 RL36_MOUSE	60S ribosomal protein L36 OS	42.33	12	2
Q61329 ZFXH3_MOUSE	Zinc finger homeobox protein	41.92	5	2
Q99LI8 HGS_MOUSE	Hepatocyte growth factor-regu	41.86	11	2
Q9CPN8 IF2B3_MOUSE	Insulin-like growth factor 2 mR	41.86	7	2
Q91YT0 NDUV1_MOUSE	NADH dehydrogenase [ubiqui	41.39	9	2
Q8R311 CTGE5_MOUSE	Cutaneous T-cell lymphoma-a	41.3	6	2
Q61599 GDIR2_MOUSE	Rho GDP-dissociation inhibito	40.99	16	2
Q8BYC4 GPR20_MOUSE	G-protein coupled receptor 20	40.87	13	2
Q99MY8 ASH1L_MOUSE	Probable histone-lysine N-met	39.28	5	2
Q9Z1P6 NDUA7_MOUSE	NADH dehydrogenase [ubiqui	38.74	34	2
Q62504 MINT_MOUSE	Msx2-interacting protein OS=M	38.6	6	2
Q91Z58 CF132_MOUSE	Uncharacterized protein C6orf	38.28	5	2
Q60952 CP250_MOUSE	Centrosome-associated prote	38.05	5	2

Q9JKP5 MBNL1_MOUSE	Muscleblind-like protein 1 OS=	37.89	5	2
Q8C181 MBNL2_MOUSE	Muscleblind-like protein 2 OS=	37.89	5	2
Q9CX34 SUGT1_MOUSE	Suppressor of G2 allele of SK	37.85	8	2
Q8JZM7 CDC73_MOUSE	Parafibromin OS=Mus muscu	37.15	4	2
Q80TC6 ZSWM5_MOUSE	Zinc finger SWIM domain-con	37	6	2
Q9QYC0 ADDA_MOUSE	Alpha-adducin OS=Mus musc	36.46	5	2
Q8BPY9 FIGL1_MOUSE	Fidgetin-like protein 1 OS=Mu	35.84	6	2
Q8R105 VP37C_MOUSE	Vacuolar protein sorting-assoc	35.71	25	2
Q14AX6 CDK12_MOUSE	Cyclin-dependent kinase 12 O	35.38	4	2
Q6ZQA0 NBEL2_MOUSE	Neurobeachin-like protein 2 O	34.98	3	2
P11369 POL2_MOUSE	Retrovirus-related Pol polypro	34.9	5	2
Q8BH31 MFSD8_MOUSE	Major facilitator superfamily d	34.85	5	2
Q04750 TOP1_MOUSE	DNA topoisomerase 1 OS=Mu	34.45	11	2
Q571H0 NPA1P_MOUSE	Nucleolar pre-ribosomal-assoc	34.37	4	2
Q9JK83 PAR6B_MOUSE	Partitioning defective 6 homolo	34.28	17	2
Q91Z10 CELR3_MOUSE	Cadherin EGF LAG seven-pas	33.62	6	2
Q61390 TCPW_MOUSE	T-complex protein 1 subunit z	33.6	24	2
Q8BGQ7 SYAC_MOUSE	Alanyl-tRNA synthetase, cytop	33.42	8	2
Q69ZH9 RHG23_MOUSE	Rho GTPase-activating protein	33.16	3	2
P49718 MCM5_MOUSE	DNA replication licensing fact	33.11	6	2
Q69ZN7 MYOF_MOUSE	Myoferlin OS=Mus musculus	32.75	6	2
Q9WTS6 TEN3_MOUSE	Teneurin-3 OS=Mus musculus	32.67	4	2
P98200 AT8A2_MOUSE	Probable phospholipid-transpo	32.61	9	2
O35071 KIF1C_MOUSE	Kinesin-like protein KIF1C OS	32.57	8	2
Q8BLX7 COGA1_MOUSE	Collagen alpha-1(XVI) chain C	32.23	7	2
P48725 PCNT_MOUSE	Pericentrin OS=Mus musculus	32.23	5	2
Q61245 COBA1_MOUSE	Collagen alpha-1(XI) chain OS	31.75	6	2
Q9QZ09 PHTF1_MOUSE	Putative homeodomain transcr	31.6	15	2
Q8CH77 NAV1_MOUSE	Neuron navigator 1 OS=Mus r	31.46	6	2
O35161 CELR1_MOUSE	Cadherin EGF LAG seven-pas	31.22	7	2
Q5QNQ9 CORA1_MOUSE	Collagen alpha-1(XXVII) chair	31.2	5	2
Q30D77 COOA1_MOUSE	Collagen alpha-1(XXIV) chain	30.6	8	2
Q9Z1X4 ILF3_MOUSE	Interleukin enhancer-binding f	30.52	3	2
Q3URV1 BROM1_MOUSE	Protein broad-minded OS=Mu	30.52	6	2
Q9Z2U2 ZN292_MOUSE	Zinc finger protein 292 OS=Mu	30.51	2	2
Q3V1M1 IGS10_MOUSE	Immunoglobulin superfamily r	30.43	7	2
Q9ERR7 SEP15_MOUSE	15 kDa selenoprotein OS=Mus	30.42	23	2
Q8VCW8 ACSF2_MOUSE	Acyl-CoA synthetase family m	30.34	9	2
Q8BGA5 KRR1_MOUSE	KRR1 small subunit processo	30.25	8	2
Q8BWT5 DIP2A_MOUSE	Disco-interacting protein 2 hor	30.17	4	2
Q9JH14 S13A1_MOUSE	Solute carrier family 13 memb	29.98	15	2
P17710 HXX1_MOUSE	Hexokinase-1 OS=Mus muscu	29.84	5	2
Q80YF9 RHG33_MOUSE	Rho GTPase-activating protein	29.76	5	2
Q6AW69 CGNL1_MOUSE	Cingulin-like protein 1 OS=Mu	29.54	8	2
Q91WC3 ACSL6_MOUSE	Long-chain-fatty-acid--CoA lig	29.1	11	2
Q0GGX2 ZN541_MOUSE	Zinc finger protein 541 OS=Mu	29.07	9	2
P14873 MAP1B_MOUSE	Microtubule-associated protein	29.05	3	2
Q91XQ0 DYH8_MOUSE	Dynein heavy chain 8, axonen	28.88	2	2
Q811P8 RHG32_MOUSE	Rho GTPase-activating protein	28.64	2	2
Q8BRB7 MYST4_MOUSE	Histone acetyltransferase MY	28.53	4	2
Q5SSE9 ABCAD_MOUSE	ATP-binding cassette sub-fam	28.36	4	2
Q3UNW5 TF2L1_MOUSE	Transcription factor CP2-like p	28.33	9	2
Q9JLN9 MTOR_MOUSE	Serine/threonine-protein kinas	28.02	5	2
Q8C8R3 ANK2_MOUSE	Ankyrin-2 OS=Mus musculus	27.89	5	2
Q69ZR2 HECD1_MOUSE	E3 ubiquitin-protein ligase HE	27.85	6	2

Q8CGE9 RGS12_MOUSE	Regulator of G-protein signaling	27.55	8	2
Q8BN57 CC033_MOUSE	Uncharacterized protein C3orf	27.51	17	2
Q80YV3 TRRAP_MOUSE	Transformation/transcription co	27.46	7	2
Q61941 NNTM_MOUSE	NAD(P) transhydrogenase, mi	27.45	16	2
Q91YD6 VILL_MOUSE	Villin-like protein OS=Mus mus	27.43	5	2
P11881 ITPR1_MOUSE	Inositol 1,4,5-trisphosphate re	27.36	7	2
Q3UHK3 GREB1_MOUSE	Protein GREB1 OS=Mus mus	27.29	7	2
Q80WE4 KI20B_MOUSE	Kinesin-like protein KIF20B O	27.16	3	2
P58749 TM6S1_MOUSE	Transmembrane 6 superfamily	27.15	12	2
Q812E0 CPEB2_MOUSE	Cytoplasmic polyadenylation e	27	11	2
Q571C7 BDP1_MOUSE	Transcription factor TFIIIB cor	26.97	4	2
P54276 MSH6_MOUSE	DNA mismatch repair protein	26.93	7	2
P14719 ILRL1_MOUSE	Interleukin-1 receptor-like 1 O	26.87	6	2
Q60584 FBXW2_MOUSE	F-box/WD repeat-containing p	26.72	9	2
Q0VF58 COJA1_MOUSE	Collagen alpha-1(XIX) chain C	26.52	4	2
Q61290 CAC1E_MOUSE	Voltage-dependent R-type cal	26.47	4	2
P53995 APC1_MOUSE	Anaphase-promoting complex	26.44	6	2
Q9JHJ3 NCUG1_MOUSE	Lysosomal protein NCU-G1 O	26.39	11	2
Q8R554 OTU7A_MOUSE	OTU domain-containing protei	26.36	6	2
P31938 MP2K1_MOUSE	Dual specificity mitogen-activa	26.34	18	2
O88737 BSN_MOUSE	Protein bassoon OS=Mus mus	26.32	6	2
P70227 ITPR3_MOUSE	Inositol 1,4,5-trisphosphate re	26.31	3	2
Q45VK7 DYHC2_MOUSE	Cytoplasmic dynein 2 heavy c	26.3	7	2
Q3U108 ARI5A_MOUSE	AT-rich interactive domain-cor	25.88	3	2
Q3UVY5 CN135_MOUSE	Pecanex-like protein C14orf13	25.81	4	2
Q9R016 BIR1E_MOUSE	Baculoviral IAP repeat-contain	25.69	6	2
Q8JZM8 MUC4_MOUSE	Mucin-4 OS=Mus musculus G	25.62	5	2
A2RSQ0 DEN5B_MOUSE	DENN domain-containing prot	25.55	12	2
Q9Z351 KCNQ2_MOUSE	Potassium voltage-gated char	25.49	5	2
Q9ESK9 RBCC1_MOUSE	RB1-inducible coiled-coil prote	25.35	5	2
Q9CW46 RAVR1_MOUSE	Ribonucleoprotein PTB-bindin	25.22	10	2
Q9JMG7 HDGR3_MOUSE	Hepatoma-derived growth fact	25.17	6	2
Q8C0P7 ZN451_MOUSE	Zinc finger protein 451 OS=M	25.05	8	2
Q9QYT7 PIGQ_MOUSE	Phosphatidylinositol N-acetyl	24.96	12	2
Q68FH0 PKP4_MOUSE	Plakophilin-4 OS=Mus muscul	24.79	5	2
Q8CG73 FTM_MOUSE	Protein fantom OS=Mus musc	24.77	6	2
Q8BLG0 PHF20_MOUSE	PHD finger protein 20 OS=M	24.69	6	2
C4P6S0 SHTAP_MOUSE	Sperm head and tail associate	24.58	2	2
Q69ZC8 K1704_MOUSE	Uncharacterized protein KIAA	24.49	12	2
Q8CJ27 ASPM_MOUSE	Abnormal spindle-like microce	24.17	5	2
O70481 UBR1_MOUSE	E3 ubiquitin-protein ligase UB	24.17	5	2
P35546 RET_MOUSE	Proto-oncogene tyrosine-prote	23.92	3	2
P16283 B3A3_MOUSE	Anion exchange protein 3 OS-	23.68	3	2
Q2EY15 PRTG_MOUSE	Protogenin OS=Mus musculus	23.6	2	2
Q80VM7 ANR24_MOUSE	Ankyrin repeat domain-contain	23.57	11	2
Q4QRL3 CC88B_MOUSE	Coiled-coil domain-containing	23.41	8	2
A2APU8 C114B_MOUSE	Transmembrane protein C9orf	23.41	7	2
Q9WU42 NCOR2_MOUSE	Nuclear receptor corepressor	23.33	6	2
Q3UH53 SDK1_MOUSE	Protein sidekick-1 OS=Mus m	23.02	5	2
Q91V27 MELPH_MOUSE	Melanophilin OS=Mus muscul	21.77	9	2
Q69ZX6 MOR2A_MOUSE	MORC family CW-type zinc fir	21.43	5	2
Q9Z0J4 NOS1_MOUSE	Nitric oxide synthase, brain O	21.29	7	2
Q6PAJ1 BCR_MOUSE	Breakpoint cluster region prote	21.12	6	2
Q9Z0E1 CB065_MOUSE	Uncharacterized protein C2orf	20.12	3	2
Q69ZU6 THS7A_MOUSE	Thrombospondin type-1 doma	20.03	6	2

**Table A1.2 GFR Matrigel Protein Identifications.** List of all proteins identified in GFR Matrigel (growth factor reduced) with corresponding accession, description, PEAKS score, unique peptide numbers, and coverage (in %).

Accession	Description	Score	Coverage (%)	#Unique
P19137 LAMA1_MOUSE	Laminin subunit alpha-1 OS=Mus	628.63	84	416
P10493 NID1_MOUSE	Nidogen-1 OS=Mus musculus G	578.16	94	306
P02469 LAMB1_MOUSE	Laminin subunit beta-1 OS=Mus	567.28	80	267
P02468 LAMC1_MOUSE	Laminin subunit gamma-1 OS=M	569.94	87	245
Q05793 PGBM_MOUSE	Basement membrane-specific he	501.41	67	159
Q8VDD5 MYH9_MOUSE	Myosin-9 OS=Mus musculus GN	450.04	81	108
P16546 SPTA2_MOUSE	Spectrin alpha chain, brain OS=M	368.54	76	103
P20152 VIME_MOUSE	Vimentin OS=Mus musculus GN	420.08	97	90
Q9QXS1 PLEC_MOUSE	Plectin OS=Mus musculus GN=F	289.16	66	79
P01027 CO3_MOUSE	Complement C3 OS=Mus muscu	345.76	72	78
Q9JHU4 DYHC1_MOUSE	Cytoplasmic dynein 1 heavy cha	295.63	60	76
P19324 SERPH_MOUSE	Serpin H1 OS=Mus musculus G	392.76	87	73
P63038 CH60_MOUSE	60 kDa heat shock protein, mitoc	377.09	91	67
P20029 GRP78_MOUSE	78 kDa glucose-regulated protei	393.79	80	66
Q3UQ28 PXDN_MOUSE	Peroxidasin homolog OS=Mus m	366.86	71	63
Q62261 SPTB2_MOUSE	Spectrin beta chain, brain 1 OS=	292.18	64	58
P14733 LMNB1_MOUSE	Lamin-B1 OS=Mus musculus GN	381.83	92	55
P07724 ALBU_MOUSE	Serum albumin OS=Mus muscul	381.35	88	55
Q8VIJ6 SFPQ_MOUSE	Splicing factor, proline- and gluta	342.28	75	55
Q9D0E1 HNRPM_MOUSE	Heterogeneous nuclear ribonucle	315.82	88	53
P63017 HSP7C_MOUSE	Heat shock cognate 71 kDa prot	408.96	92	49
P09103 PDIA1_MOUSE	Protein disulfide-isomerase OS=	337.38	93	49
Q80X90 FLNB_MOUSE	Filamin-B OS=Mus musculus GN	279.12	52	49
P48678 LMNA_MOUSE	Prelamin-A/C OS=Mus musculus	314.07	83	46
Q01853 TERA_MOUSE	Transitional endoplasmic reticul	315.18	67	44
O88322 NID2_MOUSE	Nidogen-2 OS=Mus musculus G	312.75	57	44
Q68FD5 CLH_MOUSE	Clathrin heavy chain 1 OS=Mus	268.36	67	43
Q61879 MYH10_MOUSE	Myosin-10 OS=Mus musculus G	326.98	66	41
Q8K310 MATR3_MOUSE	Matrin-3 OS=Mus musculus GN=	312.04	67	40
Q8CGC7 SYEP_MOUSE	Bifunctional aminoacyl-tRNA syn	307.57	70	40
P29341 PABP1_MOUSE	Polyadenylate-binding protein 1	304.55	71	40
P26039 TLN1_MOUSE	Talin-1 OS=Mus musculus GN=	259.38	56	40
Q64727 VINC_MOUSE	Vinculin OS=Mus musculus GN=	253.67	67	38
Q8K0E8 FIBB_MOUSE	Fibrinogen beta chain OS=Mus r	294.75	72	37
P16858 G3P_MOUSE	Glyceraldehyde-3-phosphate def	332.58	87	36
P38647 GRP75_MOUSE	Stress-70 protein, mitochondrial	285.7	78	36
O88569 ROA2_MOUSE	Heterogeneous nuclear ribonucle	330.65	69	35
P11276 FINC_MOUSE	Fibronectin OS=Mus musculus G	250.45	36	35
Q03265 ATPA_MOUSE	ATP synthase subunit alpha, mit	292.18	80	32
Q61001 LAMA5_MOUSE	Laminin subunit alpha-5 OS=Mus	263.25	38	32
Q9D8E6 RL4_MOUSE	60S ribosomal protein L4 OS=M	259.07	69	32
P56480 ATPB_MOUSE	ATP synthase subunit beta, mito	311.5	79	31
P27773 PDIA3_MOUSE	Protein disulfide-isomerase A3 C	254.3	68	30
Q92111 TRFE_MOUSE	Serotransferrin OS=Mus muscul	259.15	54	29
Q99K48 NONO_MOUSE	Non-POU domain-containing oct	248.34	73	28
Q61595 KTN1_MOUSE	Kinectin OS=Mus musculus GN=	225.51	51	28
O08677 KNG1_MOUSE	Kininogen-1 OS=Mus musculus	321.8	58	27
Q8BTM8 FLNA_MOUSE	Filamin-A OS=Mus musculus GN	214.25	31	27
Q8VCM7 FIBG_MOUSE	Fibrinogen gamma chain OS=M	305.52	62	26
Q922R8 PDIA6_MOUSE	Protein disulfide-isomerase A6 C	289.63	89	26
P14211 CALR_MOUSE	Calreticulin OS=Mus musculus G	283.76	84	26
P08249 MDHM_MOUSE	Malate dehydrogenase, mitochor	274.69	81	26
P08032 SPTA1_MOUSE	Spectrin alpha chain, erythrocyte	227.32	45	25
A2ASS6 TITIN_MOUSE	Titin OS=Mus musculus GN=Ttn	79.26	8	25

Q61838 A2M_MOUSE	Alpha-2-macroglobulin OS=Mus	237.43	39	24
Q9EQK5 MVP_MOUSE	Major vault protein OS=Mus mus	234.07	65	24
P58252 EF2_MOUSE	Elongation factor 2 OS=Mus mus	210.56	45	24
P52480 KPYM_MOUSE	Pyruvate kinase isozymes M1/M	263.15	73	23
Q9R0B9 PLOD2_MOUSE	Procollagen-lysine,2-oxoglutarate	225.37	52	23
Q9CSN1 SNW1_MOUSE	SNW domain-containing protein	223.7	74	23
P08113 ENPL_MOUSE	Endoplasmic reticulum protein OS=Mus musculus	210.35	44	23
P07214 SPRC_MOUSE	SPARC OS=Mus musculus GN	328.36	86	22
P61979 HNRPK_MOUSE	Heterogeneous nuclear ribonucle	275.26	78	22
Q6P5E4 UGGG1_MOUSE	UDP-glucose:glycoprotein glucosyl	245.58	46	22
Q8R326 PSPC1_MOUSE	Paraspeckle component 1 OS=M	237.26	72	22
O70133 DHX9_MOUSE	ATP-dependent RNA helicase A	231.54	39	22
Q9Z1Q9 SYVC_MOUSE	Valyl-tRNA synthetase OS=Mus	229.3	50	22
Q9R0E2 PLOD1_MOUSE	Procollagen-lysine,2-oxoglutarate	220.66	47	22
Q60902 EP15R_MOUSE	Epidermal growth factor receptor	204.53	57	22
P11499 HS90B_MOUSE	Heat shock protein HSP 90-beta	287.33	77	21
Q01405 SC23A_MOUSE	Protein transport protein Sec23A	253.94	51	21
P06909 CFAH_MOUSE	Complement factor H OS=Mus n	239.29	42	21
Q61576 FKB10_MOUSE	Peptidyl-prolyl cis-trans isomeras	231.43	70	21
Q8BU30 SYIC_MOUSE	Isoleucyl-tRNA synthetase, cytop	226.03	53	21
Q9DC23 DJC10_MOUSE	DnaJ homolog subfamily C mem	216.46	43	21
P57776 EF1D_MOUSE	Elongation factor 1-delta OS=M	245.75	59	20
P12970 RL7A_MOUSE	60S ribosomal protein L7a OS=M	234.46	65	20
P10126 EF1A1_MOUSE	Elongation factor 1-alpha 1 OS=	230.27	64	20
P62908 RS3_MOUSE	40S ribosomal protein S3 OS=M	227.08	74	20
P28665 MUG1_MOUSE	Murinoglobulin-1 OS=Mus muscu	225.66	42	20
O08810 U5S1_MOUSE	116 kDa U5 small nuclear ribonu	215.23	50	20
Q99PV0 PRP8_MOUSE	Pre-mRNA-processing-splicing f	205.05	44	20
Q80U93 NU214_MOUSE	Nuclear pore complex protein Nu	202.82	37	20
P25444 RS2_MOUSE	40S ribosomal protein S2 OS=M	248.19	74	19
P27659 RL3_MOUSE	60S ribosomal protein L3 OS=M	243.55	75	19
Q8BG05 ROA3_MOUSE	Heterogeneous nuclear ribonucle	239.4	56	19
P21614 VTDB_MOUSE	Vitamin D-binding protein OS=M	219.5	80	19
Q91X72 HEMO_MOUSE	Hemopexin OS=Mus musculus C	214.76	47	19
P47911 RL6_MOUSE	60S ribosomal protein L6 OS=M	213.42	63	19
P62806 H4_MOUSE	Histone H4 OS=Mus musculus C	211.8	89	19
Q8BMS1 ECHA_MOUSE	Trifunctional enzyme subunit alp	176.45	57	19
P17742 PPIA_MOUSE	Peptidyl-prolyl cis-trans isomeras	262.45	87	18
Q91W90 TXND5_MOUSE	Thioredoxin domain-containing p	243.31	72	18
Q60716 P4HA2_MOUSE	Prolyl 4-hydroxylase subunit alph	235.78	74	18
Q9Z247 FKBP9_MOUSE	Peptidyl-prolyl cis-trans isomeras	230.13	59	18
O08795 GLU2B_MOUSE	Glucosidase 2 subunit beta OS=	212.02	42	18
Q7TQH0 ATX2L_MOUSE	Ataxin-2-like protein OS=Mus mu	183.98	33	18
P56959 FUS_MOUSE	RNA-binding protein FUS OS=M	217.44	44	17
P06151 LDHA_MOUSE	L-lactate dehydrogenase A chain	214.78	58	17
Q3V1T4 P3H1_MOUSE	Prolyl 3-hydroxylase 1 OS=Mus	202.57	41	17
Q60749 KHDR1_MOUSE	KH domain-containing, RNA-bind	167.03	64	17
Q99P88 NU155_MOUSE	Nuclear pore complex protein Nu	144.18	51	17
O35643 AP1B1_MOUSE	AP-1 complex subunit beta-1 OS	251.4	56	16
P14206 RSSA_MOUSE	40S ribosomal protein SA OS=M	236.01	65	16
P17225 PTBP1_MOUSE	Polypyrimidine tract-binding prote	233.6	69	16
P21619 LMNB2_MOUSE	Lamin-B2 OS=Mus musculus GN	226.76	68	16
P80316 TCPE_MOUSE	T-complex protein 1 subunit eps	212.14	72	16
Q06890 CLUS_MOUSE	Clusterin OS=Mus musculus GN	208.92	61	16
Q60715 P4HA1_MOUSE	Prolyl 4-hydroxylase subunit alph	202.55	48	16

Q91VM5 RBMXL_MOUSE	Heterogeneous nuclear ribonucle	191.2	49	16
P62918 RL8_MOUSE	60S ribosomal protein L8 OS=M	187.04	45	16
Q8R0W0 EPIPL_MOUSE	Epiplakin OS=Mus musculus GN	138.44	22	16
P29699 FETUA_MOUSE	Alpha-2-HS-glycoprotein OS=Mu	254.26	78	15
Q9Z2X1 HNRPF_MOUSE	Heterogeneous nuclear ribonucle	246.37	73	15
Q99JR5 TINAL_MOUSE	Tubulointerstitial nephritis antige	221.83	49	15
Q61292 LAMB2_MOUSE	Laminin subunit beta-2 OS=Mus	199.43	33	15
P97496 SMRC1_MOUSE	SWI/SNF complex subunit SMA	199	54	15
P53026 RL10A_MOUSE	60S ribosomal protein L10a OS=	197.71	50	15
Q3U0V1 FUBP2_MOUSE	Far upstream element-binding pr	196.1	40	15
Q9EPU0 RENT1_MOUSE	Regulator of nonsense transcript	194.67	50	15
Q99020 ROAA_MOUSE	Heterogeneous nuclear ribonucle	194.01	53	15
Q00623 APOA1_MOUSE	Apolipoprotein A-I OS=Mus mus	189.43	80	15
Q9Z110 P5CS_MOUSE	Delta-1-pyrroline-5-carboxylate s	184.08	42	15
Q8BMJ2 SYLC_MOUSE	Leucyl-tRNA synthetase, cytopla	168.22	35	15
P19096 FAS_MOUSE	Fatty acid synthase OS=Mus mu	143.77	33	15
P98078 DAB2_MOUSE	Disabled homolog 2 OS=Mus mu	236.55	36	14
P31001 DESM_MOUSE	Desmin OS=Mus musculus GN=	235.27	63	14
P57759 ERP29_MOUSE	Endoplasmic reticulum resident p	221.56	70	14
Q9WV54 ASAH1_MOUSE	Acid ceramidase OS=Mus musc	221.17	61	14
P39061 COIA1_MOUSE	Collagen alpha-1(XVIII) chain OS	199.06	32	14
Q9WU78 PDC6L_MOUSE	Programmed cell death 6-interac	198.76	35	14
P62301 RS13_MOUSE	40S ribosomal protein S13 OS=M	197.1	54	14
Q9D0I9 SYRC_MOUSE	Arginyl-tRNA synthetase, cytopla	187.49	60	14
Q68FL6 SYMC_MOUSE	Methionyl-tRNA synthetase, cyto	184.53	54	14
Q8K2B3 DHSA_MOUSE	Succinate dehydrogenase [ubiqu	184.26	53	14
P24270 CATA_MOUSE	Catalase OS=Mus musculus GN	179.58	44	14
Q3TXS7 PSMD1_MOUSE	26S proteasome non-ATPase re	178.57	55	14
P09405 NUCL_MOUSE	Nucleolin OS=Mus musculus GN	176.22	62	14
P02088 HBB1_MOUSE	Hemoglobin subunit beta-1 OS=	221.35	88	13
Q9DB20 ATPO_MOUSE	ATP synthase subunit O, mitoch	215.62	78	13
Q08879 FBLN1_MOUSE	Fibulin-1 OS=Mus musculus GN	209.08	50	13
P61358 RL27_MOUSE	60S ribosomal protein L27 OS=M	196.06	59	13
P42567 EPS15_MOUSE	Epidermal growth factor receptor	185.33	48	13
Q9JKR6 HYOU1_MOUSE	Hypoxia up-regulated protein 1 C	179.9	43	13
Q8BH97 RCN3_MOUSE	Reticulocalbin-3 OS=Mus muscu	172.07	54	13
Q8BHN3 GANAB_MOUSE	Neutral alpha-glucosidase AB OS	167.31	56	13
Q9R0E1 PLOD3_MOUSE	Procollagen-lysine,2-oxoglutarate	160.58	42	13
Q99PL5 RRBP1_MOUSE	Ribosome-binding protein 1 OS=	157.4	19	13
P62270 RS18_MOUSE	40S ribosomal protein S18 OS=M	157.37	65	13
Q8K297 GT251_MOUSE	Procollagen galactosyltransferas	144.08	55	13
P49312 ROA1_MOUSE	Heterogeneous nuclear ribonucle	238.04	68	12
P62843 RS15_MOUSE	40S ribosomal protein S15 OS=M	233.43	83	12
Q8CG70 P3H3_MOUSE	Prolyl 3-hydroxylase 3 OS=Mus r	191.34	51	12
Q8R081 HNRPL_MOUSE	Heterogeneous nuclear ribonucle	188.9	38	12
Q8C0E2 VP26B_MOUSE	Vacuolar protein sorting-associat	184.32	63	12
Q501J6 DDX17_MOUSE	Probable ATP-dependent RNA h	166.08	31	12
Q9D8N0 EF1G_MOUSE	Elongation factor 1-gamma OS=	162.74	43	12
Q61545 EWS_MOUSE	RNA-binding protein EWS OS=M	162.55	32	12
P63085 MK01_MOUSE	Mitogen-activated protein kinase	162.49	58	12
Q35887 CALU_MOUSE	Calumenin OS=Mus musculus G	161.42	57	12
P10605 CATB_MOUSE	Cathepsin B OS=Mus musculus	147	38	12
Q8BH61 F13A_MOUSE	Coagulation factor XIII A chain C	127.1	24	12
P07901 HS90A_MOUSE	Heat shock protein HSP 90-alpha	244.17	53	11
P62259 1433E_MOUSE	14-3-3 protein epsilon OS=Mus r	224.63	87	11



Q9CQU0 TXD12_MOUSE	Thioredoxin domain-containing p	204.43	78	11
P31230 AIMP1_MOUSE	Aminoacyl tRNA synthase comp	195.67	57	11
Q3UPH1 PRRC1_MOUSE	Protein PRRC1 OS=Mus muscu	191.79	45	11
Q9CPR4 RL17_MOUSE	60S ribosomal protein L17 OS=N	185.15	61	11
Q91W39 NCOA5_MOUSE	Nuclear receptor coactivator 5 O	170.94	51	11
Q9Z204 HNRPC_MOUSE	Heterogeneous nuclear ribonucle	169.11	48	11
Q64433 CH10_MOUSE	10 kDa heat shock protein, mitoc	167.21	74	11
P97461 RS5_MOUSE	40S ribosomal protein S5 OS=M	158.99	80	11
Q8CIE6 COPA_MOUSE	Coatomer subunit alpha OS=Mus	158.19	44	11
Q7TPV4 MBB1A_MOUSE	Myb-binding protein 1A OS=Mus	153.13	42	11
P80313 TCPH_MOUSE	T-complex protein 1 subunit eta	142.58	47	11
Q9Z1Z0 USO1_MOUSE	General vesicular transport facto	104.98	49	11
P63101 1433Z_MOUSE	14-3-3 protein zeta/delta OS=M	238.87	73	10
Q60605 MYL6_MOUSE	Myosin light polypeptide 6 OS=M	201.05	88	10
P01942 HBA_MOUSE	Hemoglobin subunit alpha OS=M	197.41	92	10
Q8BP92 RCN2_MOUSE	Reticulocalbin-2 OS=Mus muscu	190.72	67	10
P13020 GELS_MOUSE	Gelsolin OS=Mus musculus GN=	187.12	40	10
P62830 RL23_MOUSE	60S ribosomal protein L23 OS=N	185.19	74	10
P62317 SMD2_MOUSE	Small nuclear ribonucleoprotein	184.64	72	10
Q3THW5 H2AV_MOUSE	Histone H2A.V OS=Mus muscult	184.51	90	10
P0C0S6 H2AZ_MOUSE	Histone H2A.Z OS=Mus muscult	184.51	84	10
Q76MZ3 2AAA_MOUSE	Serine/threonine-protein phosph	168.96	71	10
P09411 PGK1_MOUSE	Phosphoglycerate kinase 1 OS=	168.15	48	10
Q64478 H2B1H_MOUSE	Histone H2B type 1-H OS=Mus r	165.46	59	10
Q64525 H2B2B_MOUSE	Histone H2B type 2-B OS=Mus r	165.46	60	10
Q64475 H2B1B_MOUSE	Histone H2B type 1-B OS=Mus r	165.46	54	10
Q6ZWY9 H2B1C_MOUSE	Histone H2B type 1-C/E/G OS=N	165.46	54	10
P10853 H2B1F_MOUSE	Histone H2B type 1-F/J/L OS=M	165.46	54	10
Q8CGP1 H2B1K_MOUSE	Histone H2B type 1-K OS=Mus r	165.46	54	10
P10854 H2B1M_MOUSE	Histone H2B type 1-M OS=Mus r	165.46	54	10
Q9WTM5 RUVB2_MOUSE	RuvB-like 2 OS=Mus musculus	163.48	37	10
Q9CQF3 CPSF5_MOUSE	Cleavage and polyadenylation sp	162.33	72	10
P29533 VCAM1_MOUSE	Vascular cell adhesion protein 1	147.87	26	10
P40142 TKT_MOUSE	Transketolase OS=Mus musculu	147.23	41	10
Q8BFY9 TNPO1_MOUSE	Transportin-1 OS=Mus musculus	145.26	51	10
Q8C854 MYEF2_MOUSE	Myelin expression factor 2 OS=N	140.81	29	10
Q9D6R2 IDH3A_MOUSE	Isocitrate dehydrogenase [NAD]	140.48	36	10
Q3UPL0 SC31A_MOUSE	Protein transport protein Sec31A	136.87	18	10
Q9CU62 SMC1A_MOUSE	Structural maintenance of chrom	131.66	19	10
Q91VD9 NDUS1_MOUSE	NADH-ubiquinone oxidoreductas	130.52	30	10
A2AN08 UBR4_MOUSE	E3 ubiquitin-protein ligase UBR4	130.21	14	10
O08788 DCTN1_MOUSE	Dynactin subunit 1 OS=Mus mus	123.77	28	10
P39447 ZO1_MOUSE	Tight junction protein ZO-1 OS=N	122.52	12	10
Q7TPR4 ACTN1_MOUSE	Alpha-actinin-1 OS=Mus muscul	231.84	61	9
P62962 PROF1_MOUSE	Profilin-1 OS=Mus musculus GN	213.75	98	9
P61982 1433G_MOUSE	14-3-3 protein gamma OS=Mus	205.68	68	9
Q8R2Z5 VWA1_MOUSE	von Willebrand factor A domain-	190.66	45	9
P16045 LEG1_MOUSE	Galectin-1 OS=Mus musculus G	186.91	84	9
P63276 RS17_MOUSE	40S ribosomal protein S17 OS=N	185.97	70	9
P17182 ENOA_MOUSE	Alpha-enolase OS=Mus muscult	182.71	71	9
Q8R4R6 NUP53_MOUSE	Nucleoporin NUP53 OS=Mus m	182.35	63	9
P62754 RS6_MOUSE	40S ribosomal protein S6 OS=M	174.7	40	9
Q922Q8 LRC59_MOUSE	Leucine-rich repeat-containing p	173.54	34	9
Q8BJ71 NUP93_MOUSE	Nuclear pore complex protein Nu	173.53	60	9
P17751 TPIS_MOUSE	Triosephosphate isomerase OS=	172.68	57	9

Q91VA6 PDIP2_MOUSE	Polymerase delta-interacting pro	170.25	53	9
P35980 RL18_MOUSE	60S ribosomal protein L18 OS=M	169.27	45	9
Q8BWT1 THIM_MOUSE	3-ketoacyl-CoA thiolase, mitoch	162.73	50	9
P47963 RL13_MOUSE	60S ribosomal protein L13 OS=M	162.64	50	9
Q8R3Q6 CCD58_MOUSE	Coiled-coil domain-containing pr	161.95	77	9
P80314 TCPB_MOUSE	T-complex protein 1 subunit beta	161.92	49	9
P09542 MYL3_MOUSE	Myosin light chain 3 OS=Mus mu	160.79	77	9
Q61937 NPM_MOUSE	Nucleophosmin OS=Mus muscu	155.24	52	9
P35564 CALX_MOUSE	Calnexin OS=Mus musculus GN	153.24	34	9
P62264 RS14_MOUSE	40S ribosomal protein S14 OS=M	142.15	68	9
P08003 PDIA4_MOUSE	Protein disulfide-isomerase A4 C	141.22	32	9
P60122 RUVB1_MOUSE	RuvB-like 1 OS=Mus musculus C	138.76	43	9
P80318 TCPG_MOUSE	T-complex protein 1 subunit gamma	138.39	39	9
P42932 TCPQ_MOUSE	T-complex protein 1 subunit theta	136.09	20	9
Q6P5F9 XPO1_MOUSE	Exportin-1 OS=Mus musculus G	134.69	21	9
P80315 TCPD_MOUSE	T-complex protein 1 subunit delta	130.63	66	9
Q60864 STIP1_MOUSE	Stress-induced-phosphoprotein 1	127.75	38	9
P14148 RL7_MOUSE	60S ribosomal protein L7 OS=M	127.72	54	9
P97807 FUMH_MOUSE	Fumarate hydratase, mitochondr	127.56	31	9
Q6Y7W8 PERQ2_MOUSE	PERQ amino acid-rich with GYF	120.16	19	9
P15508 SPTB1_MOUSE	Spectrin beta chain, erythrocyte	117.5	25	9
A2ASQ1 AGRIN_MOUSE	Agrin OS=Mus musculus GN=Ag	95.72	15	9
Q9QZQ1 AFAD_MOUSE	Afadin OS=Mus musculus GN=M	95.68	12	9
P07759 SPA3K_MOUSE	Serine protease inhibitor A3K OS	232.17	69	8
Q921F2 TADBP_MOUSE	TAR DNA-binding protein 43 OS	184.85	33	8
Q8BMF4 ODP2_MOUSE	Dihydrolipoyllysine-residue acety	181.28	23	8
Q64213 SF01_MOUSE	Splicing factor 1 OS=Mus muscu	177.48	38	8
P56391 CX6B1_MOUSE	Cytochrome c oxidase subunit 6	164.45	76	8
Q61584 FXR1_MOUSE	Fragile X mental retardation synd	162.87	33	8
P47941 CRKL_MOUSE	Crk-like protein OS=Mus muscul	162.46	38	8
Q9D1M0 SEC13_MOUSE	Protein SEC13 homolog OS=Mus	162.4	53	8
Q9D1Q6 ERP44_MOUSE	Endoplasmic reticulum resident p	157.31	52	8
Q91WJ8 FUBP1_MOUSE	Far upstream element-binding pr	156.44	22	8
Q8CJ69 BMPER_MOUSE	BMP-binding endothelial regulato	149.26	26	8
Q61656 DDX5_MOUSE	Probable ATP-dependent RNA h	147.46	28	8
P03975 IGEB_MOUSE	IgE-binding protein OS=Mus mus	145.94	22	8
P54775 PRS6B_MOUSE	26S protease regulatory subunit	145.91	61	8
Q9QZD9 EIF3I_MOUSE	Eukaryotic translation initiation fa	145.41	58	8
P62858 RS28_MOUSE	40S ribosomal protein S28 OS=M	144.16	61	8
Q99MD9 NASP_MOUSE	Nuclear autoantigenic sperm pro	141.9	38	8
P62082 RS7_MOUSE	40S ribosomal protein S7 OS=M	136.64	44	8
P84089 ERH_MOUSE	Enhancer of rudimentary homolo	136.12	62	8
Q02819 NUCB1_MOUSE	Nucleobindin-1 OS=Mus muscul	135.8	36	8
Q9CYR0 SSBP_MOUSE	Single-stranded DNA-binding pro	135.27	55	8
Q8QZT1 THIL_MOUSE	Acetyl-CoA acetyltransferase, mi	134.28	35	8
P58022 LOXL2_MOUSE	Lysyl oxidase homolog 2 OS=Mus	130.35	32	8
P62702 RS4X_MOUSE	40S ribosomal protein S4, X isof	128.4	42	8
Q80X50 UBP2L_MOUSE	Ubiquitin-associated protein 2-lik	120.98	12	8
Q9Z0R4 ITSN1_MOUSE	Intersectin-1 OS=Mus musculus	113.86	21	8
Q9QXZ0 MACF1_MOUSE	Microtubule-actin cross-linking fa	87.91	10	8
P70670 NACAM_MOUSE	Nascent polypeptide-associated	74.36	15	8
Q8BFZ3 ACTBL_MOUSE	Beta-actin-like protein 2 OS=Mus	245.03	90	7
Q3THE2 ML12B_MOUSE	Myosin regulatory light chain 12E	219.34	86	7
P57780 ACTN4_MOUSE	Alpha-actinin-4 OS=Mus muscul	207.71	43	7
O35658 C1QBP_MOUSE	Complement component 1 Q sub	194.88	49	7

P20108 PRDX3_MOUSE	Thioredoxin-dependent peroxide	192.15	66	7
Q9CYZ2 TPD54_MOUSE	Tumor protein D54 OS=Mus mus	187.91	71	7
P62204 CALM_MOUSE	Calmodulin OS=Mus musculus C	181	92	7
P29788 VTNC_MOUSE	Vitronectin OS=Mus musculus G	172.36	40	7
Q8BL97 SRSF7_MOUSE	Serine/arginine-rich splicing fact	160.71	52	7
P62242 RS8_MOUSE	40S ribosomal protein S8 OS=M	160.65	37	7
P14115 RL27A_MOUSE	60S ribosomal protein L27a OS=	158.67	59	7
Q9R0U0 SRS10_MOUSE	Serine/arginine-rich splicing fact	154.71	50	7
Q8R1Q8 DC1L1_MOUSE	Cytoplasmic dynein 1 light interm	154.07	32	7
Q9D0W5 PPIL1_MOUSE	Peptidyl-prolyl cis-trans isomeras	146.53	52	7
Q9D1M4 MCA3_MOUSE	Eukaryotic translation elongation	145.93	81	7
P46412 GPX3_MOUSE	Glutathione peroxidase 3 OS=M	139.92	46	7
Q61207 SAP_MOUSE	Sulfated glycoprotein 1 OS=Mus	137.18	24	7
Q9CPT4 CS010_MOUSE	UPF0556 protein C19orf10 homol	136.72	66	7
Q9JKF1 IQGA1_MOUSE	Ras GTPase-activating-like prote	134.51	29	7
P97351 RS3A_MOUSE	40S ribosomal protein S3a OS=M	131.15	35	7
P47962 RL5_MOUSE	60S ribosomal protein L5 OS=M	129.5	35	7
Q922B2 SYDC_MOUSE	Aspartyl-tRNA synthetase, cytop	126.34	19	7
O08585 CLCA_MOUSE	Clathrin light chain A OS=Mus m	125.67	28	7
P14131 RS16_MOUSE	40S ribosomal protein S16 OS=M	124.48	49	7
P20918 PLMN_MOUSE	Plasminogen OS=Mus musculus	122.47	29	7
Q9WVK4 EHD1_MOUSE	EH domain-containing protein 1	121.32	47	7
Q60597 ODO1_MOUSE	2-oxoglutarate dehydrogenase, r	120.05	22	7
Q9CQN1 TRAP1_MOUSE	Heat shock protein 75 kDa, mito	117.9	57	7
P23116 EIF3A_MOUSE	Eukaryotic translation initiation fa	117.34	19	7
P61965 WDR5_MOUSE	WD repeat-containing protein 5	115.35	41	7
P68040 GBLP_MOUSE	Guanine nucleotide-binding prote	108.25	35	7
Q8VDP4 K1967_MOUSE	Protein KIAA1967 homolog OS=	86.8	12	7
Q9R1C7 PR40A_MOUSE	Pre-mRNA-processing factor 40	84.49	16	7
A2ARV4 LRP2_MOUSE	Low-density lipoprotein receptor-	83.4	14	7
P68033 ACTC_MOUSE	Actin, alpha cardiac muscle 1 OS	297.4	82	6
P68254 1433T_MOUSE	14-3-3 protein theta OS=Mus mu	191.19	67	6
Q61029 LAP2B_MOUSE	Lamina-associated polypeptide 2	167.55	32	6
Q9CQR2 RS21_MOUSE	40S ribosomal protein S21 OS=M	163.47	63	6
Q62523 ZYX_MOUSE	Zyxin OS=Mus musculus GN=Zy	156.93	32	6
O89086 RBM3_MOUSE	Putative RNA-binding protein 3 C	156.82	84	6
O08583 THOC4_MOUSE	THO complex subunit 4 OS=Mus	156.48	52	6
Q9DB15 RM12_MOUSE	39S ribosomal protein L12, mito	150.59	58	6
P16110 LEG3_MOUSE	Galectin-3 OS=Mus musculus G	146.21	25	6
Q6IRU2 TPM4_MOUSE	Tropomyosin alpha-4 chain OS=	145.92	72	6
P24369 PPIB_MOUSE	Peptidyl-prolyl cis-trans isomeras	142.75	61	6
P18760 COF1_MOUSE	Cofilin-1 OS=Mus musculus GN=	140.58	44	6
O70251 EF1B_MOUSE	Elongation factor 1-beta OS=Mus	139.33	33	6
P84099 RL19_MOUSE	60S ribosomal protein L19 OS=M	131.61	37	6
P47738 ALDH2_MOUSE	Aldehyde dehydrogenase, mitoch	130.38	23	6
Q8VDM4 PSMD2_MOUSE	26S proteasome non-ATPase re	130.05	47	6
P62996 TRA2B_MOUSE	Transformer-2 protein homolog b	129.59	36	6
Q9CZU3 SK2L2_MOUSE	Superkiller viralicidic activity 2-lik	128.24	36	6
P60335 PCBP1_MOUSE	Poly(rC)-binding protein 1 OS=M	126.85	41	6
Q9QZM0 UBQL2_MOUSE	Ubiquilin-2 OS=Mus musculus G	125.92	19	6
Q9CZM2 RL15_MOUSE	60S ribosomal protein L15 OS=M	125.6	43	6
P18242 CATD_MOUSE	Cathepsin D OS=Mus musculus	124.75	36	6
P19536 COX5B_MOUSE	Cytochrome c oxidase subunit 5	124.52	81	6
P35700 PRDX1_MOUSE	Peroxiredoxin-1 OS=Mus muscu	122.67	52	6
P26443 DHE3_MOUSE	Glutamate dehydrogenase 1, mi	122.19	18	6

B2RY56 RBM25_MOUSE	RNA-binding protein 25 OS=Mus	121.82	16	6
Q9R0N0 GALK1_MOUSE	Galactokinase OS=Mus musculu	119.87	32	6
Q9DBG5 PLIN3_MOUSE	Perilipin-3 OS=Mus musculus G	117.38	29	6
P08228 SODC_MOUSE	Superoxide dismutase [Cu-Zn] C	116.16	44	6
Q9CYA6 ZCHC8_MOUSE	Zinc finger CCHC domain-contai	116.06	28	6
P02463 CO4A1_MOUSE	Collagen alpha-1(IV) chain OS=M	113.52	25	6
Q9WVA4 TAGL2_MOUSE	Transgelin-2 OS=Mus musculus	112.12	48	6
Q8K2C9 HACD3_MOUSE	3-hydroxyacyl-CoA dehydratase	112.08	47	6
Q8R1B4 EIF3C_MOUSE	Eukaryotic translation initiation fa	105.56	16	6
Q8BX22 SALL4_MOUSE	Sal-like protein 4 OS=Mus musc	100.89	18	6
Q61646 HPT_MOUSE	Haptoglobin OS=Mus musculus	100.85	36	6
P36552 HEM6_MOUSE	Coproporphyrinogen-III oxidase,	100.71	26	6
Q60675 LAMA2_MOUSE	Laminin subunit alpha-2 OS=Mus	99.81	21	6
Q99KI0 ACON_MOUSE	Aconitate hydratase, mitochondr	97.86	21	6
Q8CGK3 LONM_MOUSE	Lon protease homolog, mitochor	97.43	24	6
Q6ZWN5 RS9_MOUSE	40S ribosomal protein S9 OS=M	79.64	34	6
Q6PDK2 MLL2_MOUSE	Histone-lysine N-methyltransfera	38.25	9	6
P99024 TBB5_MOUSE	Tubulin beta-5 chain OS=Mus m	308.45	75	5
P22599 A1AT2_MOUSE	Alpha-1-antitrypsin 1-2 OS=Mus	197.39	51	5
Q01768 NDKB_MOUSE	Nucleoside diphosphate kinase B	184.91	79	5
Q9CQV8 1433B_MOUSE	14-3-3 protein beta/alpha OS=M	174.06	65	5
Q9DBG3 AP2B1_MOUSE	AP-2 complex subunit beta OS=	173.99	30	5
Q9CQ92 FIS1_MOUSE	Mitochondrial fission 1 protein O	159.79	67	5
P62315 SMD1_MOUSE	Small nuclear ribonucleoprotein	154.51	50	5
Q9QZQ8 H2AY_MOUSE	Core histone macro-H2A.1 OS=M	151.84	51	5
Q61171 PRDX2_MOUSE	Peroxiredoxin-2 OS=Mus muscu	147.28	55	5
Q8BIQ5 CSTF2_MOUSE	Cleavage stimulation factor subu	145.22	40	5
Q9QYJ0 DNJA2_MOUSE	DnaJ homolog subfamily A mem	144.03	48	5
P62983 RS27A_MOUSE	Ubiquitin-40S ribosomal protein	142.44	51	5
Q9Z2D8 MBD3_MOUSE	Methyl-CpG-binding domain prot	140.79	49	5
Q61147 CERU_MOUSE	Ceruloplasmin OS=Mus musculu	135.87	20	5
Q6PDG5 SMRC2_MOUSE	SWI/SNF complex subunit SMA	135.55	35	5
Q99KV1 DJB11_MOUSE	DnaJ homolog subfamily B mem	130.5	43	5
P07356 ANXA2_MOUSE	Annexin A2 OS=Mus musculus C	129.89	42	5
Q8BKC5 IPO5_MOUSE	Importin-5 OS=Mus musculus G	126.81	36	5
P28798 GRN_MOUSE	Granulins OS=Mus musculus GN	126.15	27	5
Q5SFM8 RBM27_MOUSE	RNA-binding protein 27 OS=Mus	125.54	30	5
O35206 COFA1_MOUSE	Collagen alpha-1(XV) chain OS=	125.53	14	5
Q8VEK3 HNRPU_MOUSE	Heterogeneous nuclear ribonucle	124.81	23	5
Q9WTP6 KAD2_MOUSE	Adenylate kinase 2, mitochondria	122.92	46	5
P59708 PM14_MOUSE	Pre-mRNA branch site protein p	122.52	42	5
P63323 RS12_MOUSE	40S ribosomal protein S12 OS=M	121.74	39	5
Q9DCJ5 NDUA8_MOUSE	NADH dehydrogenase [ubiquino	119.56	49	5
P70372 ELAV1_MOUSE	ELAV-like protein 1 OS=Mus mu	119.23	37	5
P70168 IMB1_MOUSE	Importin subunit beta-1 OS=Mus	117.19	28	5
P16675 PPGB_MOUSE	Lysosomal protective protein OS	115.23	15	5
Q91VC3 IF4A3_MOUSE	Eukaryotic initiation factor 4A-III	114.73	30	5
Q9CPP6 NDUA5_MOUSE	NADH dehydrogenase [ubiquino	113.59	59	5
P23780 BGAL_MOUSE	Beta-galactosidase OS=Mus mu	112.54	23	5
Q8BTV2 CPSF7_MOUSE	Cleavage and polyadenylation sp	112.13	28	5
Q9QUR7 PIN1_MOUSE	Peptidyl-prolyl cis-trans isomera	112.03	57	5
Q5XJY5 COPD_MOUSE	Coatomer subunit delta OS=Mus	110.78	30	5
Q99JB2 STML2_MOUSE	Stomatin-like protein 2 OS=Mus	107.75	58	5
P63163 RSMN_MOUSE	Small nuclear ribonucleoprotein-	106.13	53	5
P27048 R SMB_MOUSE	Small nuclear ribonucleoprotein-	106.13	42	5

P35979 RL12_MOUSE	60S ribosomal protein L12 OS=M	104.43	39	5
P61161 ARP2_MOUSE	Actin-related protein 2 OS=Mus	104.22	45	5
Q6ZQ38 CAND1_MOUSE	Cullin-associated NEDD8-dissoc	102.51	23	5
Q80YR5 SAFB2_MOUSE	Scaffold attachment factor B2 OS	101.78	10	5
P41105 RL28_MOUSE	60S ribosomal protein L28 OS=M	101.76	30	5
Q61164 CTCF_MOUSE	Transcriptional repressor CTCF	101.23	31	5
Q6NVF9 CPSF6_MOUSE	Cleavage and polyadenylation sp	98.57	18	5
Q60631 GRB2_MOUSE	Growth factor receptor-bound pr	97.96	30	5
P81117 NUCB2_MOUSE	Nucleobindin-2 OS=Mus muscul	97.27	35	5
P01887 B2MG_MOUSE	Beta-2-microglobulin OS=Mus m	96.82	40	5
Q6NZJ6 IF4G1_MOUSE	Eukaryotic translation initiation fa	94.61	9	5
P07146 TRY2_MOUSE	Anionic trypsin-2 OS=Mus musc	93.95	33	5
P17427 AP2A2_MOUSE	AP-2 complex subunit alpha-2 O	93.87	18	5
Q62318 TIF1B_MOUSE	Transcription intermediary factor	93.2	19	5
Q8BX70 VP13C_MOUSE	Vacuolar protein sorting-associat	91.94	8	5
Q99KN9 EPN4_MOUSE	Clathrin interactor 1 OS=Mus mu	91.69	21	5
Q9DCH4 EIF3F_MOUSE	Eukaryotic translation initiation fa	90.42	34	5
P26369 U2AF2_MOUSE	Splicing factor U2AF 65 kDa sub	89.38	24	5
Q921M4 GOGA2_MOUSE	Golgin subfamily A member 2 OS	88.85	18	5
Q9JIF7 COPB_MOUSE	Coatomer subunit beta OS=Mus	79.81	17	5
Q9EQH3 VPS35_MOUSE	Vacuolar protein sorting-associat	77.21	19	5
Q60865 CAPR1_MOUSE	Caprin-1 OS=Mus musculus GN	76.84	15	5
P62281 RS11_MOUSE	40S ribosomal protein S11 OS=M	75.98	34	5
Q8BYA0 TBCD_MOUSE	Tubulin-specific chaperone D OS	75.81	30	5
P62192 PRS4_MOUSE	26S protease regulatory subunit	72.86	18	5
Q91ZU6 DYST_MOUSE	Dystonin OS=Mus musculus GN	59.7	6	5
B2RX14 TUT4_MOUSE	Terminal uridylyltransferase 4 OS	47.93	9	5
Q8BYK6 YTHD3_MOUSE	YTH domain family protein 3 OS	47.63	13	5
P27661 H2AX_MOUSE	Histone H2A.x OS=Mus muscult	244.51	77	4
Q61696 HS71A_MOUSE	Heat shock 70 kDa protein 1A O	225.55	69	4
P17879 HS71B_MOUSE	Heat shock 70 kDa protein 1B O	225.55	70	4
O08638 MYH11_MOUSE	Myosin-11 OS=Mus musculus G	193.41	35	4
Q00898 A1AT5_MOUSE	Alpha-1-antitrypsin 1-5 OS=Mus	187.58	40	4
Q62167 DDX3X_MOUSE	ATP-dependent RNA helicase D	185.97	62	4
Q02257 PLAK_MOUSE	Junction plakoglobin OS=Mus m	141.54	40	4
Q99JX3 GORS2_MOUSE	Golgi reassembly-stacking prote	131.66	36	4
Q9D6Z1 NOP56_MOUSE	Nucleolar protein 56 OS=Mus m	131.47	23	4
Q9WTX5 SKP1_MOUSE	S-phase kinase-associated prote	127.34	28	4
Q9Z175 LOXL3_MOUSE	Lysyl oxidase homolog 3 OS=MU	126.2	14	4
Q9D3D9 ATPD_MOUSE	ATP synthase subunit delta, mitc	125.78	64	4
Q9CX56 PSMD8_MOUSE	26S proteasome non-ATPase re	123.85	31	4
Q9CQT2 RBM7_MOUSE	RNA-binding protein 7 OS=Mus	123.77	42	4
Q99LC5 ETFA_MOUSE	Electron transfer flavoprotein sub	122.83	39	4
Q8CG71 P3H2_MOUSE	Prolyl 3-hydroxylase 2 OS=Mus	122.13	27	4
P62307 RUXF_MOUSE	Small nuclear ribonucleoprotein	121.18	60	4
P08122 CO4A2_MOUSE	Collagen alpha-2(IV) chain OS=M	119.75	18	4
P01837 IGKC_MOUSE	Ig kappa chain C region OS=Mus	118.81	42	4
O55029 COPB2_MOUSE	Coatomer subunit beta' OS=Mus	118.73	29	4
Q8VDJ3 VIGLN_MOUSE	Vigilin OS=Mus musculus GN=H	118.34	16	4
Q61704 ITIH3_MOUSE	Inter-alpha-trypsin inhibitor heavy	117.12	16	4
Q9EPJ9 ARFG1_MOUSE	ADP-ribosylation factor GTPase-	115.62	21	4
Q9EPU4 CPSF1_MOUSE	Cleavage and polyadenylation sp	115.05	21	4
Q8VHX6 FLNC_MOUSE	Filamin-C OS=Mus musculus GN	114.76	10	4
O88968 TCO2_MOUSE	Transcobalamin-2 OS=Mus mus	114.39	36	4
P32261 ANT3_MOUSE	Antithrombin-III OS=Mus muscul	112.82	37	4

P62897 CYC_MOUSE	Cytochrome c, somatic OS=Mus	112.2	47	4
Q9D0F9 PGM1_MOUSE	Phosphoglucomutase-1 OS=Mus	111.21	20	4
P80317 TCPZ_MOUSE	T-complex protein 1 subunit zeta	111.11	21	4
Q9JHJ0 TMOD3_MOUSE	Tropomodulin-3 OS=Mus muscu	109.41	32	4
P51410 RL9_MOUSE	60S ribosomal protein L9 OS=M	109.2	47	4
O08749 DLDH_MOUSE	Dihydrolipoyl dehydrogenase, mi	108.8	29	4
Q9JLV5 CUL3_MOUSE	Cullin-3 OS=Mus musculus GN=	108.1	20	4
Q08369 GATA4_MOUSE	Transcription factor GATA-4 OS=	107.3	35	4
Q8C0C7 SYFA_MOUSE	Phenylalanyl-tRNA synthetase al	107.25	30	4
Q8BX10 PGAM5_MOUSE	Serine/threonine-protein phosph	106.16	22	4
Q9D1B9 RM28_MOUSE	39S ribosomal protein L28, mitoc	106.04	39	4
Q9CR57 RL14_MOUSE	60S ribosomal protein L14 OS=N	105.64	28	4
P40124 CAP1_MOUSE	Adenylyl cyclase-associated prot	105.1	19	4
Q6NZN0 RBM26_MOUSE	RNA-binding protein 26 OS=Mus	103.31	13	4
Q3U7R1 ESYT1_MOUSE	Extended synaptotagmin-1 OS=M	102.59	30	4
O09167 RL21_MOUSE	60S ribosomal protein L21 OS=N	101.91	41	4
P01864 GCAB_MOUSE	Ig gamma-2A chain C region sec	99.17	35	4
P97927 LAMA4_MOUSE	Laminin subunit alpha-4 OS=Mus	99.06	12	4
P60867 RS20_MOUSE	40S ribosomal protein S20 OS=N	98.94	29	4
P61924 COPZ1_MOUSE	Coatomer subunit zeta-1 OS=M	98.59	52	4
Q8BTS4 NUP54_MOUSE	Nuclear pore complex protein Nu	96.43	18	4
Q9DBJ1 PGAM1_MOUSE	Phosphoglycerate mutase 1 OS=	94.45	19	4
P05064 ALDOA_MOUSE	Fructose-bisphosphate aldolase	94.27	21	4
Q04447 KCRB_MOUSE	Creatine kinase B-type OS=Mus	93.86	22	4
P62855 RS26_MOUSE	40S ribosomal protein S26 OS=N	93.07	32	4
P21107 TPM3_MOUSE	Tropomyosin alpha-3 chain OS=	93.01	23	4
Q9CQL1 MGNR_MOUSE	Protein mago nashi homolog 1-r	92.09	64	4
P61327 MGN_MOUSE	Protein mago nashi homolog OS	92.09	64	4
Q00PI9 HNRL2_MOUSE	Heterogeneous nuclear ribonucle	91.8	23	4
Q91WK2 EIF3H_MOUSE	Eukaryotic translation initiation fa	91.09	27	4
Q8C5Q4 GRSF1_MOUSE	G-rich sequence factor 1 OS=M	90.98	22	4
P61458 PHS_MOUSE	Pterin-4-alpha-carbinolamine del	90.06	44	4
Q9Z2W0 DNPEP_MOUSE	Aspartyl aminopeptidase OS=M	89.81	23	4
Q9WVG6 CARM1_MOUSE	Histone-arginine methyltransfera	89.1	17	4
P99029 PRDX5_MOUSE	Peroxiredoxin-5, mitochondrial C	87.21	24	4
Q62093 SRSF2_MOUSE	Serine/arginine-rich splicing fact	85.94	32	4
Q6PDAQ CHD4_MOUSE	Chromodomain-helicase-DNA-bi	85.9	13	4
P62267 RS23_MOUSE	40S ribosomal protein S23 OS=N	84.59	51	4
Q6ZQI3 MLEC_MOUSE	Malectin OS=Mus musculus GN=	84.3	36	4
Q9Z1D1 EIF3G_MOUSE	Eukaryotic translation initiation fa	84.07	10	4
Q07417 ACADS_MOUSE	Short-chain specific acyl-CoA de	83.73	17	4
Q8BH74 NU107_MOUSE	Nuclear pore complex protein Nu	83.48	20	4
Q6NV83 SR140_MOUSE	U2 snRNP-associated SURP md	81.53	15	4
Q9CWE0 FA54B_MOUSE	Protein FAM54B OS=Mus muscu	80.94	27	4
P01898 HA10_MOUSE	H-2 class I histocompatibility anti	80.38	20	4
Q9JJF3 NO66_MOUSE	Lysine-specific demethylase NO	80.04	15	4
Q62189 SNRPA_MOUSE	U1 small nuclear ribonucleoprote	79.57	18	4
Q8BGQ7 SYAC_MOUSE	Alanyl-tRNA synthetase, cytoplas	79.19	11	4
P11404 FABPH_MOUSE	Fatty acid-binding protein, heart	77.86	41	4
P28656 NP1L1_MOUSE	Nucleosome assembly protein 1-	77.2	17	4
Q8R4X3 RBM12_MOUSE	RNA-binding protein 12 OS=Mus	77.13	14	4
P19253 RL13A_MOUSE	60S ribosomal protein L13a OS=	76.89	25	4
O88685 PRS6A_MOUSE	26S protease regulatory subunit	72.54	26	4
P30416 FKBP4_MOUSE	Peptidyl-prolyl cis-trans isomer	71.67	18	4
Q61464 ZN638_MOUSE	Zinc finger protein 638 OS=Mus	66.84	9	4

P62852 RS25_MOUSE	40S ribosomal protein S25 OS=M	65.93	42	4
Q9D0F3 LMAN1_MOUSE	Protein ERGIC-53 OS=Mus mus	63.66	7	4
Q9CW46 RAVR1_MOUSE	Ribonucleoprotein PTB-binding	53.82	20	4
Q8BTI8 SRRM2_MOUSE	Serine/arginine repetitive matrix	53.64	6	4
A2AAJ9 OBSCN_MOUSE	Obscurin OS=Mus musculus GN	49.59	7	4
Q6NZC7 S23IP_MOUSE	SEC23-interacting protein OS=M	47.32	13	4
Q63870 CO7A1_MOUSE	Collagen alpha-1(VII) chain OS=	45.39	13	4
Q8BKX6 SMG1_MOUSE	Serine/threonine-protein kinase	43.86	6	4
Q69Z38 PEAK1_MOUSE	Pseudopodium-enriched atypica	42.38	4	4
Q8BLN6 UNC80_MOUSE	Protein unc-80 homolog OS=Mus	33.16	11	4
P68372 TBB2C_MOUSE	Tubulin beta-2C chain OS=Mus	293.24	76	3
P17156 HSP72_MOUSE	Heat shock-related 70 kDa prote	274.47	53	3
Q922F4 TBB6_MOUSE	Tubulin beta-6 chain OS=Mus m	243.61	68	3
Q8R1M2 H2AJ_MOUSE	Histone H2A.J OS=Mus musculu	232.45	76	3
Q03734 SPA3M_MOUSE	Serine protease inhibitor A3M OS	224.13	62	3
P16627 HS71L_MOUSE	Heat shock 70 kDa protein 1-like	209.77	54	3
Q9R0B6 LAMC3_MOUSE	Laminin subunit gamma-3 OS=M	201.59	23	3
Q91WP6 SPA3N_MOUSE	Serine protease inhibitor A3N OS	176.74	47	3
P70333 HNRH2_MOUSE	Heterogeneous nuclear ribonucle	176.34	32	3
Q8R010 AIMP2_MOUSE	Aminoacyl tRNA synthase comp	142.86	48	3
Q61033 LAP2A_MOUSE	Lamina-associated polypeptide 2	142.83	28	3
P15532 NDKA_MOUSE	Nucleoside diphosphate kinase A	140.62	61	3
P84228 H32_MOUSE	Histone H3.2 OS=Mus musculus	140.31	81	3
O08807 PRDX4_MOUSE	Peroxiredoxin-4 OS=Mus muscu	127.14	37	3
Q923G2 RPAB3_MOUSE	DNA-directed RNA polymerases	124.51	37	3
Q6DFW4 NOP58_MOUSE	Nucleolar protein 58 OS=Mus m	122.6	34	3
Q9WV55 VAPA_MOUSE	Vesicle-associated membrane p	122.18	29	3
P62196 PRS8_MOUSE	26S protease regulatory subunit	115.88	33	3
P84104 SRSF3_MOUSE	Serine/arginine-rich splicing fact	114.67	33	3
Q7M6Y3 PICA_MOUSE	Phosphatidylinositol-binding clath	114.26	22	3
Q9QXT0 CNPY2_MOUSE	Protein canopy homolog 2 OS=M	113.92	26	3
P12787 COX5A_MOUSE	Cytochrome c oxidase subunit 5	113.87	66	3
Q9CR68 UCRI_MOUSE	Cytochrome b-c1 complex subur	109.02	41	3
Q9JJ18 RL38_MOUSE	60S ribosomal protein L38 OS=M	108.21	57	3
P62320 SMD3_MOUSE	Small nuclear ribonucleoprotein	105.51	36	3
Q8K4L0 DDX54_MOUSE	ATP-dependent RNA helicase D	105.45	18	3
P99028 QCR6_MOUSE	Cytochrome b-c1 complex subur	105.09	66	3
Q99JX4 EIF3M_MOUSE	Eukaryotic translation initiation fa	104.91	45	3
Q921H8 THIKA_MOUSE	3-ketoacyl-CoA thiolase A, perox	104.91	11	3
Q9DCT8 CRIP2_MOUSE	Cysteine-rich protein 2 OS=Mus	104.25	24	3
P63242 IF5A1_MOUSE	Eukaryotic translation initiation fa	103.75	69	3
Q69ZA1 CDK13_MOUSE	Cyclin-dependent kinase 13 OS=	103.51	12	3
P62821 RAB1A_MOUSE	Ras-related protein Rab-1A OS=	101.93	37	3
P46938 YAP1_MOUSE	Yorkie homolog OS=Mus muscu	101.48	26	3
P62075 TIM13_MOUSE	Mitochondrial import inner memb	101.22	57	3
Q8BP67 RL24_MOUSE	60S ribosomal protein L24 OS=M	100.87	26	3
Q3TCN2 PLBL2_MOUSE	Putative phospholipase B-like 2	100.78	22	3
Q8VDM6 HNRL1_MOUSE	Heterogeneous nuclear ribonucle	99.82	25	3
Q6ZWV7 RL35_MOUSE	60S ribosomal protein L35 OS=M	98.56	27	3
Q9QX47 SON_MOUSE	Protein SON OS=Mus musculus	97.42	17	3
Q9R0L7 AKP8L_MOUSE	A-kinase anchor protein 8-like O	96.95	30	3
P23198 CBX3_MOUSE	Chromobox protein homolog 3 C	96.8	32	3
O88630 GOSR1_MOUSE	Golgi SNAP receptor complex m	96.36	14	3
Q3UIA2 RHG17_MOUSE	Rho GTPase-activating protein 1	95.21	27	3
P70318 TIAR_MOUSE	Nucleolysin TIAR OS=Mus musc	93.44	10	3

Q9ESB3 HRG_MOUSE	Histidine-rich glycoprotein OS=M	93.38	23	3
Q9CYD3 CRTAP_MOUSE	Cartilage-associated protein OS=	93.18	16	3
P46935 NEDD4_MOUSE	E3 ubiquitin-protein ligase NEDD	93.03	19	3
Q9DC61 MPPA_MOUSE	Mitochondrial-processing peptida	92.32	26	3
Q9R0I7 YLPM1_MOUSE	YLP motif-containing protein 1 O	91.61	13	3
P56399 UBP5_MOUSE	Ubiquitin carboxyl-terminal hydro	91.43	31	3
P26231 CTNA1_MOUSE	Catenin alpha-1 OS=Mus muscu	90.91	22	3
O88477 IF2B1_MOUSE	Insulin-like growth factor 2 mRN	90.65	16	3
Q9CYL5 GAPR1_MOUSE	Golgi-associated plant pathogen	90.52	34	3
Q8VC70 RBMS2_MOUSE	RNA-binding motif, single-strand	90.27	23	3
P62849 RS24_MOUSE	40S ribosomal protein S24 OS=M	90.26	44	3
P05202 AATM_MOUSE	Aspartate aminotransferase, mito	89.84	17	3
P68510 1433F_MOUSE	14-3-3 protein eta OS=Mus mus	89.59	51	3
P62827 RAN_MOUSE	GTP-binding nuclear protein Ran	88.18	17	3
P04186 CFAB_MOUSE	Complement factor B OS=Mus m	88.15	9	3
P70335 ROCK1_MOUSE	Rho-associated protein kinase 1	87.37	9	3
Q64010 CRK_MOUSE	Adapter molecule crk OS=Mus m	87.25	26	3
Q9D824 FIP1_MOUSE	Pre-mRNA 3'-end-processing fac	86.98	13	3
Q64737 PUR2_MOUSE	Trifunctional purine biosynthetic	86.81	14	3
P62309 RUXG_MOUSE	Small nuclear ribonucleoprotein	86.46	33	3
P30412 PPIC_MOUSE	Peptidyl-prolyl cis-trans isomer	86.31	34	3
Q9DCT2 NDUS3_MOUSE	NADH dehydrogenase [ubiquino	86.01	25	3
Q9CZ13 QCR1_MOUSE	Cytochrome b-c1 complex subun	85.07	18	3
Q63850 NUP62_MOUSE	Nuclear pore glycoprotein p62 O	85	11	3
Q8R0F3 SUMF1_MOUSE	Sulfatase-modifying factor 1 OS=	84.76	10	3
Q7TSC1 PRC2A_MOUSE	Protein PRRC2A OS=Mus muscu	84.41	12	3
P62960 YBOX1_MOUSE	Nuclease-sensitive element-bind	84.26	29	3
Q9JJH1 RNAS4_MOUSE	Ribonuclease 4 OS=Mus muscu	83.51	57	3
Q02053 UBA1_MOUSE	Ubiquitin-like modifier-activating	82.99	18	3
Q99KJ8 DCTN2_MOUSE	Dynactin subunit 2 OS=Mus mus	82.91	16	3
Q8QZY1 EIF3L_MOUSE	Eukaryotic translation initiation fa	82.54	15	3
O08547 SC22B_MOUSE	Vesicle-trafficking protein SEC22	81.07	20	3
Q9CXF4 TBC15_MOUSE	TBC1 domain family member 15	80.43	11	3
Q99JI4 PSMD6_MOUSE	26S proteasome non-ATPase re	78.02	34	3
P25206 MCM3_MOUSE	DNA replication licensing factor	77.85	12	3
Q3U2P1 SC24A_MOUSE	Protein transport protein Sec24A	76.92	10	3
Q9Z2I8 SUCB2_MOUSE	Succinyl-CoA ligase [GDP-formin	76.36	15	3
Q8BSQ9 PB1_MOUSE	Protein polybromo-1 OS=Mus m	76.31	11	3
Q9JJY4 DDX20_MOUSE	Probable ATP-dependent RNA h	76.04	10	3
Q99PU8 DHX30_MOUSE	Putative ATP-dependent RNA he	75.5	14	3
Q61753 SERA_MOUSE	D-3-phosphoglycerate dehydroge	75.46	8	3
P21126 UBL4A_MOUSE	Ubiquitin-like protein 4A OS=Mus	75.08	29	3
Q6ZWV3 IRL10_MOUSE	60S ribosomal protein L10 OS=M	75.02	22	3
Q8C7E9 CSTFT_MOUSE	Cleavage stimulation factor subu	74.97	56	3
P14685 PSMD3_MOUSE	26S proteasome non-ATPase re	74.42	17	3
O54774 AP3D1_MOUSE	AP-3 complex subunit delta-1 OS	74.23	11	3
Q9CZX8 RS19_MOUSE	40S ribosomal protein S19 OS=M	73.41	19	3
Q6ZQH8 NU188_MOUSE	Nucleoporin NUP188 homolog C	72.13	8	3
Q8K0V4 CNOT3_MOUSE	CCR4-NOT transcription comple	72.11	9	3
Q9D8W5 PSD12_MOUSE	26S proteasome non-ATPase re	71.65	22	3
Q9D6J6 NDUV2_MOUSE	NADH dehydrogenase [ubiquino	69.31	21	3
Q8CGR5 KLK14_MOUSE	Kallikrein-14 OS=Mus musculus	68.68	19	3
Q922D8 C1TC_MOUSE	C-1-tetrahydrofolate synthase, cy	68.32	6	3
Q8BJZ4 RT35_MOUSE	28S ribosomal protein S35, mito	67.61	25	3
Q9CQA3 DHSB_MOUSE	Succinate dehydrogenase [ubiqu	67.39	22	3



Q9ERU9 RBP2_MOUSE	E3 SUMO-protein ligase RanBP2	66.14	5	3
Q80W00 PP1RA_MOUSE	Serine/threonine-protein phosphatase 1A	65.76	20	3
Q3UQN2 FCHO2_MOUSE	FCH domain only protein 2 OS=Mus musculus	65.28	8	3
P46735 MYO1B_MOUSE	Myosin-Ib OS=Mus musculus GN=	64.08	16	3
P62869 ELOB_MOUSE	Transcription elongation factor B	63.71	25	3
Q61768 KINH_MOUSE	Kinesin-1 heavy chain OS=Mus musculus	62.2	14	3
Q05186 RCN1_MOUSE	Reticulocalbin-1 OS=Mus musculus	61.69	17	3
P62911 RL32_MOUSE	60S ribosomal protein L32 OS=Mus musculus	61.32	33	3
Q921G8 GCP2_MOUSE	Gamma-tubulin complex component 2	59.65	8	3
Q60737 CSK21_MOUSE	Casein kinase II subunit alpha OS=Mus musculus	58.98	25	3
Q62425 NDUA4_MOUSE	NADH dehydrogenase [ubiquinone] subunit 4	58.48	52	3
P08226 APOE_MOUSE	Apolipoprotein E OS=Mus musculus	56.71	14	3
Q7TMK9 HNRPQ_MOUSE	Heterogeneous nuclear ribonucleoprotein Q	55.71	10	3
Q8JZQ9 EIF3B_MOUSE	Eukaryotic translation initiation factor 3B	54.55	9	3
Q8R180 ERO1A_MOUSE	ERO1-like protein alpha OS=Mus musculus	54.17	9	3
P70336 ROCK2_MOUSE	Rho-associated protein kinase 2	53.06	22	3
Q8BHP7 OLM2A_MOUSE	Olfactomedin-like protein 2A OS=Mus musculus	52.24	5	3
Q80YT7 MYOME_MOUSE	Myomegalin OS=Mus musculus	50.3	6	3
P39054 DYN2_MOUSE	Dynammin-2 OS=Mus musculus GN=	48.76	16	3
Q921G7 ETFD_MOUSE	Electron transfer flavoprotein-ubiquinone reductase	45.85	15	3
Q8R4U0 STAB2_MOUSE	Stabilin-2 OS=Mus musculus GN=	44.73	5	3
Q6PE13 PRRT3_MOUSE	Proline-rich transmembrane protein 3	44.01	16	3
Q2UY11 COSA1_MOUSE	Collagen alpha-1(XXVIII) chain OS=Mus musculus	43.61	6	3
Q6ZWR6 SYNE1_MOUSE	Nesprin-1 OS=Mus musculus GN=	41.9	7	3
Q8C0S4 TT21A_MOUSE	Tetratricopeptide repeat protein 21A	41.45	10	3
P58871 TB182_MOUSE	182 kDa tankyrase-1-binding protein	40.05	7	3
Q9DBT5 AMPD2_MOUSE	AMP deaminase 2 OS=Mus musculus	38.76	4	3
Q8BRH4 MLL3_MOUSE	Histone-lysine N-methyltransferase 3	38.58	3	3
Q9WU60 ATR_N_MOUSE	Attractin OS=Mus musculus GN=	37.9	4	3
O88700 BLM_MOUSE	Bloom syndrome protein homolog	36.94	7	3
Q8CC88 K0564_MOUSE	Uncharacterized protein KIAA0564	36.03	7	3
Q99KW3 TARA_MOUSE	TRIO and F-actin-binding protein	35.79	5	3
Q60750 EPHA1_MOUSE	Ephrin type-A receptor 1 OS=Mus musculus	35.56	7	3
P14404 EVI1_MOUSE	MDS1 and EVI1 complex locus protein	35.51	5	3
Q8R3Y8 I2BP1_MOUSE	Interferon regulatory factor 2-binding protein 1	35.49	14	3
A2A884 ZEP3_MOUSE	Transcription factor HIVEP3 OS=Mus musculus	35.11	4	3
O88799 ZAN_MOUSE	Zonadhesin OS=Mus musculus GN=	34.79	6	3
Q64331 MYO6_MOUSE	Myosin-VI OS=Mus musculus GN=	33.61	13	3
Q70FJ1 AKAP9_MOUSE	A-kinase anchor protein 9 OS=Mus musculus	32.52	8	3
O88935 SYN1_MOUSE	Synapsin-1 OS=Mus musculus GN=	31.79	6	3
Q3TLH4 PRC2C_MOUSE	Protein PRRC2C OS=Mus musculus	31.21	4	3
Q80TL7 MON2_MOUSE	Protein MON2 homolog OS=Mus musculus	30.86	6	3
Q8BUV3 GEPH_MOUSE	Gephyrin OS=Mus musculus GN=	30.01	12	3
Q9WTS5 TEN2_MOUSE	Teneurin-2 OS=Mus musculus GN=	29.3	10	3
Q8CIQ7 DOCK3_MOUSE	Dedicator of cytokinesis protein 3	29.23	9	3
Q62059 CSPG2_MOUSE	Versican core protein OS=Mus musculus	29.06	2	3
Q99MZ6 MYO7B_MOUSE	Myosin-VIIb OS=Mus musculus GN=	28.57	15	3
A2AJ76 HMCN2_MOUSE	Hemicentin-2 OS=Mus musculus	27.44	3	3
Q9Z0W3 NU160_MOUSE	Nuclear pore complex protein NU160	27.33	14	3
Q6ZQ93 UBP34_MOUSE	Ubiquitin carboxyl-terminal hydrolase B34	26.94	7	3
Q8C115 PKHH2_MOUSE	Pleckstrin homology domain-containing protein 2	25.61	8	3
O88737 BSN_MOUSE	Protein bassoon OS=Mus musculus	24.57	7	3
Q8R4Y4 STAB1_MOUSE	Stabilin-1 OS=Mus musculus GN=	24.53	7	3
P63260 ACTG_MOUSE	Actin, cytoplasmic 2 OS=Mus musculus	320.19	81	2
Q64523 H2A2C_MOUSE	Histone H2A type 2-C OS=Mus musculus	225.53	81	2

Q6GSS7 H2A2A_MOUSE	Histone H2A type 2-A OS=Mus r	225.53	75	2
O35737 HNRH1_MOUSE	Heterogeneous nuclear ribonucle	200.41	36	2
P68368 TBA4A_MOUSE	Tubulin alpha-4A chain OS=Mus	200.31	69	2
Q6URW6 MYH14_MOUSE	Myosin-14 OS=Mus musculus G	167.87	32	2
P84084 ARF5_MOUSE	ADP-ribosylation factor 5 OS=M	151.3	48	2
Q5SX39 MYH4_MOUSE	Myosin-4 OS=Mus musculus GN	141.44	23	2
P61205 ARF3_MOUSE	ADP-ribosylation factor 3 OS=M	140.45	60	2
P84078 ARF1_MOUSE	ADP-ribosylation factor 1 OS=M	140.45	56	2
P61750 ARF4_MOUSE	ADP-ribosylation factor 4 OS=M	139.9	46	2
Q91Z83 MYH7_MOUSE	Myosin-7 OS=Mus musculus GN	126.27	19	2
Q62241 RU1C_MOUSE	U1 small nuclear ribonucleoprote	120.71	33	2
P13541 MYH3_MOUSE	Myosin-3 OS=Mus musculus GN	119.13	16	2
Q9CZU6 CISY_MOUSE	Citrate synthase, mitochondrial C	111.29	36	2
Q99LT0 DPY30_MOUSE	Protein dpy-30 homolog OS=Mus	110.44	45	2
Q60668 HNRPD_MOUSE	Heterogeneous nuclear ribonucle	110.12	17	2
P26040 EZRI_MOUSE	Ezrin OS=Mus musculus GN=Ez	108.86	11	2
Q9ES28 ARHG7_MOUSE	Rho guanine nucleotide exchang	103.72	18	2
Q9DBR0 AKAP8_MOUSE	A-kinase anchor protein 8 OS=M	102.68	30	2
P21550 ENOB_MOUSE	Beta-enolase OS=Mus musculus	102.22	42	2
Q71LX4 TLN2_MOUSE	Talin-2 OS=Mus musculus GN=	101.27	15	2
O35593 PSDE_MOUSE	26S proteasome non-ATPase re	98.43	30	2
Q9JIQ3 DBLOH_MOUSE	Diablo homolog, mitochondrial C	97.61	22	2
Q9CXW3 CYBP_MOUSE	Calcyclin-binding protein OS=M	97.32	24	2
P01644 KV5AB_MOUSE	Ig kappa chain V-V region HP R	96.08	51	2
P01645 KV5AC_MOUSE	Ig kappa chain V-V region HP 93	96.08	51	2
Q8BGS0 MAK16_MOUSE	Protein MAK16 homolog OS=M	95.36	27	2
P26043 RADI_MOUSE	Radixin OS=Mus musculus GN=	95.27	16	2
P17183 ENOG_MOUSE	Gamma-enolase OS=Mus musc	94.51	49	2
Q60710 SAMH1_MOUSE	SAM domain and HD domain-co	93.34	23	2
Q6P1F6 2ABA_MOUSE	Serine/threonine-protein phosph	93.13	33	2
Q9CWZ3 RBM8A_MOUSE	RNA-binding protein 8A OS=Mus	92.05	26	2
Q8R105 VP37C_MOUSE	Vacuolar protein sorting-associat	91.68	24	2
P51660 DHB4_MOUSE	Peroxisomal multifunctional enzy	90.69	7	2
O70325 GPX41_MOUSE	Phospholipid hydroperoxide gluta	89.86	19	2
P35922 FMR1_MOUSE	Fragile X mental retardation prot	89.72	19	2
Q91VR2 ATPG_MOUSE	ATP synthase subunit gamma, n	89.66	13	2
Q9CXW4 RL11_MOUSE	60S ribosomal protein L11 OS=N	89.42	17	2
P10639 THIO_MOUSE	Thioredoxin OS=Mus musculus C	88.05	47	2
Q8VDV3 R3GEF_MOUSE	Guanine nucleotide exchange fa	87.69	21	2
Q9CQF9 PCYOX_MOUSE	Preylcysteine oxidase OS=Mus	86.94	19	2
Q8BGD9 IF4B_MOUSE	Eukaryotic translation initiation fa	86.82	20	2
P61971 NTF2_MOUSE	Nuclear transport factor 2 OS=M	86.8	32	2
P48962 ADT1_MOUSE	ADP/ATP translocase 1 OS=Mus	86.62	29	2
Q9QZH3 PPIE_MOUSE	Peptidyl-prolyl cis-trans isomer	86.47	26	2
Q61733 RT31_MOUSE	28S ribosomal protein S31, mito	86.07	18	2
P67778 PHB_MOUSE	Prohibitin OS=Mus musculus GN	85.99	31	2
Q80UY2 KCMF1_MOUSE	E3 ubiquitin-protein ligase KCMF	85.6	34	2
Q9R099 TBL2_MOUSE	Transducin beta-like protein 2 O	85.11	31	2
Q9DCX2 ATP5H_MOUSE	ATP synthase subunit d, mitoch	84.95	15	2
Q91YD3 DCP1A_MOUSE	mRNA-decapping enzyme 1A OS	84.92	6	2
Q6ZWX6 IF2A_MOUSE	Eukaryotic translation initiation fa	83.58	13	2
Q8R0G9 NU133_MOUSE	Nuclear pore complex protein Nu	83.05	12	2
Q9JJV2 PROF2_MOUSE	Profilin-2 OS=Mus musculus GN	82.6	28	2
P63325 RS10_MOUSE	40S ribosomal protein S10 OS=N	82.56	10	2
Q9ERK4 XPO2_MOUSE	Exportin-2 OS=Mus musculus G	82.54	17	2

Q9D620 RFIP1_MOUSE	Rab11 family-interacting protein	82.51	26	2
P54071 IDHP_MOUSE	Isocitrate dehydrogenase [NADP	81.51	8	2
P97371 PSME1_MOUSE	Proteasome activator complex s	81.37	27	2
P11983 TCPA_MOUSE	T-complex protein 1 subunit alph	81.29	15	2
Q5SUF2 LC7L3_MOUSE	Luc7-like protein 3 OS=Mus mus	80.99	13	2
P61963 DCAF7_MOUSE	DDB1- and CUL4-associated fac	80.62	31	2
P61211 ARL1_MOUSE	ADP-ribosylation factor-like prote	80.03	27	2
Q9R1Z8 VINEX_MOUSE	Vinexin OS=Mus musculus GN=	80.02	14	2
P26516 PSD7_MOUSE	26S proteasome non-ATPase re	79.54	14	2
Q9DBG9 TX1B3_MOUSE	Tax1-binding protein 3 OS=Mus	78.73	43	2
P26883 FKB1A_MOUSE	Peptidyl-prolyl cis-trans isomeras	78.72	34	2
Q61990 PCBP2_MOUSE	Poly(rC)-binding protein 2 OS=M	78.55	22	2
Q9CY57 FOP_MOUSE	Friend of PRMT1 protein OS=M	77.41	25	2
Q8C8U0 LIPB1_MOUSE	Liprin-beta-1 OS=Mus musculus	77.35	10	2
P62835 RAP1A_MOUSE	Ras-related protein Rap-1A OS=	77.17	13	2
Q99J16 RAP1B_MOUSE	Ras-related protein Rap-1b OS=	77.17	13	2
Q99LF4 RTCB_MOUSE	tRNA-splicing ligase RtcB homol	77.06	12	2
Q9CXI5 MANF_MOUSE	Mesencephalic astrocyte-derived	76.98	13	2
P63168 DYL1_MOUSE	Dynein light chain 1, cytoplasmic	76.6	35	2
Q8C5L3 CNOT2_MOUSE	CCR4-NOT transcription comple	75.71	13	2
P01868 IGHG1_MOUSE	Ig gamma-1 chain C region secr	75.09	19	2
P01869 IGH1M_MOUSE	Ig gamma-1 chain C region, mer	75.09	16	2
Q80UM7 MOGS_MOUSE	Mannosyl-oligosaccharide glucos	74.72	8	2
P14901 HMOX1_MOUSE	Heme oxygenase 1 OS=Mus mu	74.63	40	2
P42227 STAT3_MOUSE	Signal transducer and activator d	74.54	19	2
Q9Z0H3 SNF5_MOUSE	SWI/SNF-related matrix-associa	74.19	15	2
P70365 NCOA1_MOUSE	Nuclear receptor coactivator 1 O	73.53	15	2
P47955 RLA1_MOUSE	60S acidic ribosomal protein P1	72.92	37	2
P99027 RLA2_MOUSE	60S acidic ribosomal protein P2	72.78	30	2
Q9Z0X1 AIFM1_MOUSE	Apoptosis-inducing factor 1, mito	72.22	10	2
P63037 DNJA1_MOUSE	DnaJ homolog subfamily A mem	71.92	38	2
Q7TQC7 GPTC2_MOUSE	G patch domain-containing prote	71.08	11	2
Q8R0S2 IQEC1_MOUSE	IQ motif and SEC7 domain-conta	70.66	12	2
O35207 CDKA1_MOUSE	Cyclin-dependent kinase 2-assoc	70.32	20	2
P43274 H14_MOUSE	Histone H1.4 OS=Mus musculus	70.04	22	2
Q9QXC1 FETUB_MOUSE	Fetuin-B OS=Mus musculus GN=	69.89	11	2
P70663 SPRL1_MOUSE	SPARC-like protein 1 OS=Mus n	69.73	4	2
Q8R0J7 VP37B_MOUSE	Vacuolar protein sorting-associa	69.64	22	2
Q91VC4 PLVAP_MOUSE	Plasmalemma vesicle-associate	69.64	14	2
Q9QZE5 COPG_MOUSE	Coatomer subunit gamma OS=M	69.47	15	2
Q80UW2 FBX2_MOUSE	F-box only protein 2 OS=Mus mu	69.44	14	2
Q9Z1Y4 TRIP6_MOUSE	Thyroid receptor-interacting prote	68.81	14	2
Q9D554 SF3A3_MOUSE	Splicing factor 3A subunit 3 OS=	68.44	12	2
P49717 MCM4_MOUSE	DNA replication licensing factor M	68.17	10	2
P62334 PRS10_MOUSE	26S protease regulatory subunit	67.7	23	2
Q99PT1 GDIR1_MOUSE	Rho GDP-dissociation inhibitor 1	67.44	18	2
Q04857 CO6A1_MOUSE	Collagen alpha-1(VI) chain OS=M	67.17	7	2
Q3TKT4 SMCA4_MOUSE	Transcription activator BRG1 OS	65.58	11	2
Q9DCW4 ETFB_MOUSE	Electron transfer flavoprotein su	65.47	9	2
P28653 PGS1_MOUSE	Biglycan OS=Mus musculus GN=	65.22	8	2
P97360 ETV6_MOUSE	Transcription factor ETV6 OS=M	65.13	6	2
Q9DCT5 SDF2_MOUSE	Stromal cell-derived factor 2 OS=	64.76	18	2
Q99NG0 ARIP4_MOUSE	Helicase ARIP4 OS=Mus muscu	64.35	4	2
Q91YN9 BAG2_MOUSE	BAG family molecular chaperone	64.27	29	2
Q8BMP6 GCP60_MOUSE	Golgi resident protein GCP60 OS	64.12	13	2

Q99K28 ARFG2_MOUSE	ADP-ribosylation factor GTPase-	63.52	6	2
P67984 RL22_MOUSE	60S ribosomal protein L22 OS=M	63.41	19	2
P83877 TXN4A_MOUSE	Thioredoxin-like protein 4A OS=I	62.35	26	2
Q78YZ6 SCOC_MOUSE	Short coiled-coil protein OS=Mus	62.26	30	2
Q9JII5 DAZP1_MOUSE	DAZ-associated protein 1 OS=M	62.03	19	2
P28658 ATX10_MOUSE	Ataxin-10 OS=Mus musculus GN	62	6	2
P16125 LDHB_MOUSE	L-lactate dehydrogenase B chain	61.36	24	2
Q9CT10 RANB3_MOUSE	Ran-binding protein 3 OS=Mus r	61.25	4	2
Q921N6 DDX27_MOUSE	Probable ATP-dependent RNA h	61.05	7	2
Q62376 RU17_MOUSE	U1 small nuclear ribonucleoprote	60.8	13	2
Q3UJB9 EDC4_MOUSE	Enhancer of mRNA-decapping p	60.77	11	2
Q8BFR5 EFTU_MOUSE	Elongation factor Tu, mitochondr	60.42	18	2
Q8JZN5 ACAD9_MOUSE	Acyl-CoA dehydrogenase family	58.91	18	2
P62748 HPCL1_MOUSE	Hippocalcin-like protein 1 OS=M	57.74	17	2
P26638 SYSC_MOUSE	Seryl-tRNA synthetase, cytoplas	57.45	18	2
Q06335 APLP2_MOUSE	Amyloid-like protein 2 OS=Mus r	57.27	11	2
Q925F2 ESAM_MOUSE	Endothelial cell-selective adhesi	56.91	12	2
P01872 IGHM_MOUSE	Ig mu chain C region secreted fo	56.77	6	2
P01873 MUCM_MOUSE	Ig mu chain C region membrane	56.77	6	2
Q920Q4 VPS16_MOUSE	Vacuolar protein sorting-associat	56.71	6	2
P97452 BOP1_MOUSE	Ribosome biogenesis protein BC	56.65	12	2
Q9CXY6 ILF2_MOUSE	Interleukin enhancer-binding fact	56.64	11	2
Q3TW96 UAP1L_MOUSE	UDP-N-acetylhexosamine pyrop	56.56	12	2
Q8R317 UBQL1_MOUSE	Ubiquilin-1 OS=Mus musculus G	56.49	22	2
P53995 APC1_MOUSE	Anaphase-promoting complex su	55.99	6	2
Q64012 RALY_MOUSE	RNA-binding protein Raly OS=M	55.47	7	2
Q8CCS6 PABP2_MOUSE	Polyadenylate-binding protein 2	55.34	11	2
P34884 MIF_MOUSE	Macrophage migration inhibitory	55.3	28	2
O54941 SMCE1_MOUSE	SWI/SNF-related matrix-associa	55.22	8	2
P29758 OAT_MOUSE	Ornithine aminotransferase, mito	54.74	7	2
P18572 BASI_MOUSE	Basigin OS=Mus musculus GN=	54.49	12	2
Q99KR7 PPIF_MOUSE	Peptidyl-prolyl cis-trans isomeras	54.09	16	2
Q8BI84 MIA3_MOUSE	Melanoma inhibitory activity prote	53.97	4	2
Q99N92 RM27_MOUSE	39S ribosomal protein L27, mitoc	53.9	17	2
P62814 VATB2_MOUSE	V-type proton ATPase subunit B,	53.54	13	2
P40646 SOX7_MOUSE	Transcription factor SOX-7 OS=I	53.49	17	2
P60766 CDC42_MOUSE	Cell division control protein 42 ho	53.08	10	2
O35286 DHX15_MOUSE	Putative pre-mRNA-splicing facto	52.9	8	2
Q99K30 ES8L2_MOUSE	Epidermal growth factor receptor	52.7	14	2
Q9CW03 SMC3_MOUSE	Structural maintenance of chrom	52.28	6	2
O35864 CSN5_MOUSE	COP9 signalosome complex sub	52.05	20	2
Q60972 RBBP4_MOUSE	Histone-binding protein RBBP4 C	51.91	13	2
P01867 IGG2B_MOUSE	Ig gamma-2B chain C region OS	51.91	6	2
Q8BGA5 KRR1_MOUSE	KRR1 small subunit processome	51.9	16	2
Q64324 STXB2_MOUSE	Syntaxin-binding protein 2 OS=M	51.85	17	2
Q8BMK4 CKAP4_MOUSE	Cytoskeleton-associated protein	51.81	7	2
P46471 PRS7_MOUSE	26S protease regulatory subunit	51.55	13	2
Q9WUU7 CATZ_MOUSE	Cathepsin Z OS=Mus musculus	51.49	12	2
Q3UPH7 ARH40_MOUSE	Rho guanine nucleotide exchang	50.93	11	2
Q8BYC4 GPR20_MOUSE	G-protein coupled receptor 20 O	50.69	19	2
O35218 CPSF2_MOUSE	Cleavage and polyadenylation sp	50.31	18	2
Q8BPM0 DAAM1_MOUSE	Disheveled-associated activator	50.02	11	2
Q8VCW8 ACSF2_MOUSE	Acyl-CoA synthetase family mem	49.9	15	2
Q9WUM5 SUCA_MOUSE	Succinyl-CoA ligase [GDP-formin	49.64	12	2
Q9WTR2 M3K6_MOUSE	Mitogen-activated protein kinase	49.27	6	2

Q6A0A9 F120A_MOUSE	Constitutive coactivator of PPAR	49.24	5	2
Q8C0T5 SI1L1_MOUSE	Signal-induced proliferation-assc	49.08	7	2
Q9D1A2 CNBP2_MOUSE	Cytosolic non-specific dipeptidas	48.79	12	2
O55201 SPT5H_MOUSE	Transcription elongation factor S	48.38	12	2
Q921M3 SF3B3_MOUSE	Splicing factor 3B subunit 3 OS=	47.94	8	2
Q8CDN6 TXNL1_MOUSE	Thioredoxin-like protein 1 OS=M	47.36	28	2
Q8VHN7 GPR98_MOUSE	G-protein coupled receptor 98 O	47.22	3	2
P37889 FBLN2_MOUSE	Fibulin-2 OS=Mus musculus GN	47.03	8	2
Q8CGF7 TCRG1_MOUSE	Transcription elongation regulatc	46.76	8	2
Q61510 TRI25_MOUSE	E3 ubiquitin/ISG15 ligase TRIM2	46.03	6	2
Q8VD65 PI3R4_MOUSE	Phosphoinositide 3-kinase regula	45.7	9	2
Q8CH18 CCAR1_MOUSE	Cell division cycle and apoptosis	45.46	3	2
Q6A4J8 UBP7_MOUSE	Ubiquitin carboxyl-terminal hydro	45.28	13	2
Q9CXZ1 NDUS4_MOUSE	NADH dehydrogenase [ubiquinol	45.15	19	2
P24547 IMDH2_MOUSE	Inosine-5'-monophosphate dehy	44.07	10	2
Q9EP97 SENP3_MOUSE	Sentrin-specific protease 3 OS=M	43.8	8	2
O88783 FA5_MOUSE	Coagulation factor V OS=Mus m	43.75	5	2
Q8K4Z5 SF3A1_MOUSE	Splicing factor 3A subunit 1 OS=	43.58	5	2
O55057 PDE6D_MOUSE	Retinal rod rhodopsin-sensitive d	43.32	21	2
O88543 CSN3_MOUSE	COP9 signalosome complex sub	43.24	16	2
Q9WTQ5 AKA12_MOUSE	A-kinase anchor protein 12 OS=	43.17	3	2
Q8VE97 SRSF4_MOUSE	Serine/arginine-rich splicing fact	42.77	10	2
O35465 FKBP8_MOUSE	Peptidyl-prolyl cis-trans isomeras	42.75	14	2
Q8C419 GP158_MOUSE	Probable G-protein coupled rece	42.71	10	2
P97379 G3BP2_MOUSE	Ras GTPase-activating protein-b	42.53	9	2
Q61425 HCDH_MOUSE	Hydroxyacyl-coenzyme A dehydr	42.22	20	2
Q9Z0R6 ITSN2_MOUSE	Intersectin-2 OS=Mus musculus	42.1	10	2
Q8C9B9 DIDO1_MOUSE	Death-inducer obliterator 1 OS=M	41.39	5	2
Q8BU51 BPIL3_MOUSE	Bactericidal/permeability-increas	40.62	14	2
P97479 MYO7A_MOUSE	Myosin-VIIa OS=Mus musculus	39.51	9	2
Q91YT0 NDUV1_MOUSE	NADH dehydrogenase [ubiquinol	39.51	14	2
Q08943 SSRP1_MOUSE	FACT complex subunit SSRP1 C	38.94	14	2
A2AAE1 K1109_MOUSE	Uncharacterized protein KIAA110	38.91	6	2
P70390 SHOX2_MOUSE	Short stature homeobox protein	38.86	8	2
O88444 ADCY1_MOUSE	Adenylate cyclase type 1 OS=M	38.61	12	2
P48725 PCNT_MOUSE	Pericentrin OS=Mus musculus G	38.53	11	2
Q9D7N3 RT09_MOUSE	28S ribosomal protein S9, mitoch	38.32	13	2
Q64430 ATP7A_MOUSE	Copper-transporting ATPase 1 C	38.3	11	2
Q99PP2 ZN318_MOUSE	Zinc finger protein 318 (Fragmer	37.87	5	2
P84091 AP2M1_MOUSE	AP-2 complex subunit mu OS=M	37.8	14	2
Q8CGN4 BCOR_MOUSE	BCL-6 corepressor OS=Mus mu	37.77	4	2
Q9DC33 HM20A_MOUSE	High mobility group protein 20A C	37.72	10	2
P97384 ANX11_MOUSE	Annexin A11 OS=Mus musculus	37.56	4	2
P11531 DMD_MOUSE	Dystrophin OS=Mus musculus G	37.56	9	2
Q5SF07 IF2B2_MOUSE	Insulin-like growth factor 2 mRN	37.18	12	2
Q01320 TOP2A_MOUSE	DNA topoisomerase 2-alpha OS=	37.16	8	2
P08121 CO3A1_MOUSE	Collagen alpha-1(III) chain OS=N	37.05	9	2
Q69ZU6 THS7A_MOUSE	Thrombospondin type-1 domain-	36.94	6	2
Q9QZ09 PHTF1_MOUSE	Putative homeodomain transcrip	36.62	7	2
P52734 FGD1_MOUSE	FYVE, RhoGEF and PH domain-	36.61	4	2
Q91YW3 DNJC3_MOUSE	DnaJ homolog subfamily C mem	36.34	4	2
Q8CFE4 SCYL2_MOUSE	SCY1-like protein 2 OS=Mus mu	36.23	6	2
Q4QY64 ATAD5_MOUSE	ATPase family AAA domain-cont	35.76	7	2
Q8R0L9 TADA3_MOUSE	Transcriptional adapter 3 OS=M	35.73	14	2
O35954 PITM1_MOUSE	Membrane-associated phosphat	35.43	11	2

Q6PGN1 F132B_MOUSE	Protein FAM132B OS=Mus mus	35.41	8	2
Q9Z329 ITPR2_MOUSE	Inositol 1,4,5-trisphosphate rece	35.37	10	2
P54320 ELN_MOUSE	Elastin OS=Mus musculus GN=	35.17	20	2
Q9Z108 STAU1_MOUSE	Double-stranded RNA-binding pr	34.73	23	2
O88491 NSD1_MOUSE	Histone-lysine N-methyltransfera	34.66	9	2
Q3UFQ8 LR16B_MOUSE	Leucine-rich repeat-containing p	34.6	8	2
Q6PHB0 I20RA_MOUSE	Interleukin-20 receptor subunit a	34.47	4	2
Q9DCC4 P5CR3_MOUSE	Proline-5-carboxylate reductas	34.09	15	2
O54724 PTRF_MOUSE	Polymerase I and transcript relea	33.88	8	2
O88705 HCN3_MOUSE	Potassium/sodium hyperpolariza	33.88	11	2
Q61290 CAC1E_MOUSE	Voltage-dependent R-type calciu	33.64	7	2
Q6ZQ88 KDM1A_MOUSE	Lysine-specific histone demethyl	33.6	11	2
Q61702 ITIH1_MOUSE	Inter-alpha-trypsin inhibitor heav	33.31	8	2
Q6P4S8 INT1_MOUSE	Integrator complex subunit 1 OS	33.25	8	2
Q8BN57 CC033_MOUSE	Uncharacterized protein C3orf33	33.07	11	2
Q3UHK3 GREB1_MOUSE	Protein GREB1 OS=Mus muscul	33.07	5	2
Q91VR5 DDX1_MOUSE	ATP-dependent RNA helicase D	32.87	15	2
Q6ZWQ0 SYNE2_MOUSE	Nesprin-2 OS=Mus musculus GN	32.74	8	2
O35071 KIF1C_MOUSE	Kinesin-like protein KIF1C OS=M	32.69	12	2
Q922B9 SSFA2_MOUSE	Sperm-specific antigen 2 homold	32.01	9	2
A8C756 THADA_MOUSE	Thyroid adenoma-associated pro	31.65	6	2
P0C5E4 PTPRQ_MOUSE	Phosphatidylinositol phosphatas	31.6	4	2
Q5DTT2 PSD1_MOUSE	PH and SEC7 domain-containing	31.4	8	2
Q6QIY3 SCNAA_MOUSE	Sodium channel protein type 10	31.28	8	2
Q0VGM9 RTEL1_MOUSE	Regulator of telomere elongation	31.22	5	2
Q8CH25 SLTM_MOUSE	SAFB-like transcription modulato	31.21	3	2
P55012 S12A2_MOUSE	Solute carrier family 12 member	31.03	10	2
Q8BXR5 NALCN_MOUSE	Sodium leak channel non-selecti	30.84	7	2
A1L3T7 FA65C_MOUSE	Protein FAM65C OS=Mus muscu	30.82	9	2
Q8VE73 CUL7_MOUSE	Cullin-7 OS=Mus musculus GN=	30.65	7	2
Q8C0P7 ZN451_MOUSE	Zinc finger protein 451 OS=Mus	30.59	8	2
Q2EG98 PK1L3_MOUSE	Polycystic kidney disease protein	30.59	7	2
P13705 MSH3_MOUSE	DNA mismatch repair protein Ms	30.41	7	2
Q3URY6 ARMC2_MOUSE	Armadillo repeat-containing prote	30.02	11	2
P46737 BRCC3_MOUSE	Lys-63-specific deubiquitinase B	29.91	9	2
P97311 MCM6_MOUSE	DNA replication licensing factor	29.82	11	2
Q8C267 SETB2_MOUSE	Histone-lysine N-methyltransfera	29.53	7	2
A7L9Z8 AT2C2_MOUSE	Calcium-transporting ATPase typ	29.51	10	2
Q4G0F8 UBN1_MOUSE	Ubinuclein-1 OS=Mus musculus	29.46	9	2
A2BH40 ARI1A_MOUSE	AT-rich interactive domain-conta	29.41	6	2
Q80WQ9 ZBED4_MOUSE	Zinc finger BED domain-containi	29.14	11	2
Q9JJN0 POLH_MOUSE	DNA polymerase eta OS=Mus m	29.05	9	2
P49582 ACHA7_MOUSE	Neuronal acetylcholine receptor	28.31	3	2
Q8C0R9 YG015_MOUSE	Leucine-rich repeat and death do	28.02	8	2
Q8JZR4 EAA5_MOUSE	Excitatory amino acid transport	27.86	13	2
Q80TS3 LPHN3_MOUSE	Latrophilin-3 OS=Mus musculus	27.7	4	2
Q61037 TSC2_MOUSE	Tuberin OS=Mus musculus GN=	27.63	8	2
Q14BI7 TDRD9_MOUSE	Putative ATP-dependent RNA he	27.57	10	2
P04187 GRAB_MOUSE	Granzyme B(G,H) OS=Mus mus	27.37	20	2
Q91YU6 LZTS2_MOUSE	Leucine zipper putative tumor su	27.34	11	2
Q01815 CAC1C_MOUSE	Voltage-dependent L-type calciu	27.26	13	2
Q8C120 SH3R3_MOUSE	SH3 domain-containing RING fin	27.05	5	2
Q09XV5 CHD8_MOUSE	Chromodomain-helicase-DNA-bi	27.02	9	2
P59997 KDM2A_MOUSE	Lysine-specific demethylase 2A	27.01	8	2
P55937 GOGA3_MOUSE	Golgin subfamily A member 3 OS	27	8	2

Q8BG67 EFR3A_MOUSE	Protein EFR3 homolog A OS=Mu	26.89	11	2
Q6R5N8 TLR13_MOUSE	Toll-like receptor 13 OS=Mus mu	26.88	7	2
Q9QZS7 NPHN_MOUSE	Nephrin OS=Mus musculus GN=	26.87	5	2
P48356 LEPR_MOUSE	Leptin receptor OS=Mus muscul	26.62	8	2
Q9WV34 MPP2_MOUSE	MAGUK p55 subfamily member	26.62	4	2
Q6P1C6 LRIG3_MOUSE	Leucine-rich repeats and immun	26.43	7	2
P11247 PERM_MOUSE	Myeloperoxidase OS=Mus musc	26.16	14	2
Q61493 DPOLZ_MOUSE	DNA polymerase zeta catalytic s	26.14	8	2
A2ARZ3 FSIP2_MOUSE	Fibrous sheath-interacting protei	26.03	5	2
P97714 ADA1D_MOUSE	Alpha-1D adrenergic receptor OS	26.02	9	2
Q9D415 DLGP1_MOUSE	Disks large-associated protein 1	25.97	6	2
Q6IQX7 CHSS2_MOUSE	Chondroitin sulfate synthase 2 O	25.97	9	2
P57080 UBP25_MOUSE	Ubiquitin carboxyl-terminal hydro	25.95	7	2
Q8CHY3 DYM_MOUSE	Dymeclin OS=Mus musculus GN	25.91	7	2
B2RQE8 RHG42_MOUSE	Rho GTPase-activating protein 4	25.9	6	2
Q9D168 INT12_MOUSE	Integrator complex subunit 12 O	25.79	10	2
P51557 STAR_MOUSE	Steroidogenic acute regulatory p	25.79	13	2
Q9D2K4 IQCH_MOUSE	IQ domain-containing protein H O	25.76	6	2
Q7TSH4 CP110_MOUSE	Centrosomal protein CP110 OS=	25.63	2	2
Q9Z1S0 BUB1B_MOUSE	Mitotic checkpoint serine/threonin	25.45	8	2
Q9QXL2 KIF21A_MOUSE	Kinesin-like protein KIF21A OS=	25.35	9	2
Q9QXL1 KIF21B_MOUSE	Kinesin-like protein KIF21B OS=	25.33	5	2
Q921C3 BRWD1_MOUSE	Bromodomain and WD repeat-co	25.28	4	2
P58742 AAAS_MOUSE	Aladin OS=Mus musculus GN=A	25.27	8	2
Q3TEI4 CO039_MOUSE	Uncharacterized protein C15orf3	25.22	10	2
Q7TSH7 KCNF1_MOUSE	Potassium voltage-gated channe	24.92	13	2
Q3ZT31 SNX25_MOUSE	Sorting nexin-25 OS=Mus muscu	24.89	13	2
Q8CJ12 GPR64_MOUSE	G-protein coupled receptor 64 O	24.82	6	2
Q6PIX5 RHDF1_MOUSE	Inactive rhomboid protein 1 OS=	24.8	13	2
Q9QXH4 ITAX_MOUSE	Integrin alpha-X OS=Mus muscu	24.77	10	2
Q8K0L0 ASB2_MOUSE	Ankyrin repeat and SOCS box pr	24.35	3	2
Q80T85 DCAF5_MOUSE	DDB1- and CUL4-associated fac	24.16	6	2
P70327 TBX6_MOUSE	T-box transcription factor TBX6 O	24.04	9	2
Q60603 KCNH1_MOUSE	Potassium voltage-gated channe	24	4	2
Q62388 ATM_MOUSE	Serine-protein kinase ATM OS=M	23.89	10	2
Q9JHW4 SELB_MOUSE	Selenocysteine-specific elongatio	23.85	17	2
Q6PR54 RIF1_MOUSE	Telomere-associated protein RIF	23.75	7	2
P59808 SASH1_MOUSE	SAM and SH3 domain-containing	23.72	6	2
P0CW70 D19L2_MOUSE	Protein dpy-19 homolog 2 OS=M	23.51	13	2
Q8C8R3 ANK2_MOUSE	Ankyrin-2 OS=Mus musculus GN	23.41	6	2
P53349 M3K1_MOUSE	Mitogen-activated protein kinase	23.32	5	2
Q9R155 S26A4_MOUSE	Pendrin OS=Mus musculus GN=	23.04	8	2
Q00519 XDH_MOUSE	Xanthine dehydrogenase/oxidase	22.92	7	2
C8YR32 LOXH1_MOUSE	Lipoxygenase homology domain	22.87	5	2
P97303 BACH2_MOUSE	Transcription regulator protein B	22.77	3	2
Q8BNJ2 ATS4_MOUSE	A disintegrin and metalloprotein	22.72	5	2
A7M7C7 SKOR2_MOUSE	SKI family transcriptional corepre	21.59	4	2
O88196 TTC3_MOUSE	E3 ubiquitin-protein ligase TTC3	21.07	6	2
Q8CI32 BAG5_MOUSE	BAG family molecular chaperone	20.8	11	2

**Table A1.3 Cell Start Protein Identifications.** List of all proteins identified in Cell Start growth matrix with corresponding accession, description, PEAKS score, unique peptide numbers, and coverage (in %).



Accession	Description	Score	Coverage (%)	#Unique
P02768 ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=ALBU	740.91	92	508
P02751 FINC_HUMAN	Fibronectin OS=Homo sapiens GN=FN1	590.06	67	213
P01023 A2MG_HUMAN	Alpha-2-macroglobulin OS=Homo sapiens	355.02	44	37
P02790 HEMO_HUMAN	Hemopexin OS=Homo sapiens GN=HPX	379.25	68	34
P43652 AFAM_HUMAN	Afamin OS=Homo sapiens GN=AFM PE=	308.01	62	25
P00738 HPT_HUMAN	Haptoglobin OS=Homo sapiens GN=HP	398.12	67	23
P02675 FIBB_HUMAN	Fibrinogen beta chain OS=Homo sapiens	300.96	64	22
P02671 FIBA_HUMAN	Fibrinogen alpha chain OS=Homo sapiens	239.94	35	18
P02679 FIBG_HUMAN	Fibrinogen gamma chain OS=Homo sapiens	253.11	53	17
P02765 FETUA_HUMAN	Alpha-2-HS-glycoprotein OS=Homo sapiens	253.45	62	16
P02749 APOH_HUMAN	Beta-2-glycoprotein 1 OS=Homo sapiens	250.57	59	13
P04217 A1BG_HUMAN	Alpha-1B-glycoprotein OS=Homo sapiens	246.04	39	12
P02652 APOA2_HUMAN	Apolipoprotein A-II OS=Homo sapiens GN=	234.22	73	10
P02766 TTHY_HUMAN	Transthyretin OS=Homo sapiens GN=TTF	225.45	68	10
P08253 MMP2_HUMAN	72 kDa type IV collagenase OS=Homo sapiens	197.89	32	8
Q96PD5 PGRP2_HUMAN	N-acetylmuramoyl-L-alanine amidase OS=	179.89	27	6
P01871 IGHM_HUMAN	Ig mu chain C region OS=Homo sapiens	169.57	36	6
P01834 IGKC_HUMAN	Ig kappa chain C region OS=Homo sapiens	189.08	78	5
P10909 CLUS_HUMAN	Clusterin OS=Homo sapiens GN=CLU PE=	180.73	35	5
Q8WZ42 TITIN_HUMAN	Titin OS=Homo sapiens GN=TTN PE=1 S	50.51	2	5
P01876 IGHA1_HUMAN	Ig alpha-1 chain C region OS=Homo sapiens	151.25	22	4
P69905 HBA_HUMAN	Hemoglobin subunit alpha OS=Homo sapiens	138.46	49	4
P02760 AMBP_HUMAN	Protein AMBP OS=Homo sapiens GN=AM	112.1	18	4
P00450 CERU_HUMAN	Ceruloplasmin OS=Homo sapiens GN=CF	103.12	8	4
P68871 HBB_HUMAN	Hemoglobin subunit beta OS=Homo sapiens	176.25	48	3
P01860 IGHG3_HUMAN	Ig gamma-3 chain C region OS=Homo sapiens	166.83	34	3
P01024 CO3_HUMAN	Complement C3 OS=Homo sapiens GN=	146.6	19	3
P35030 TRY3_HUMAN	Trypsin-3 OS=Homo sapiens GN=PRSS3	145.59	13	3
P0CG05 LAC2_HUMAN	Ig lambda-2 chain C regions OS=Homo sapiens	136.88	68	3
P0CG06 LAC3_HUMAN	Ig lambda-3 chain C regions OS=Homo sapiens	136.88	68	3
B9A064 IGLL5_HUMAN	Immunoglobulin lambda-like polypeptide 5	136.88	28	3
P0CG04 LAC1_HUMAN	Ig lambda-1 chain C regions OS=Homo sapiens	136.88	42	3
P05155 IC1_HUMAN	Plasma protease C1 inhibitor OS=Homo sapiens	129.22	19	3
P0C0L4 CO4A_HUMAN	Complement C4-A OS=Homo sapiens GN=	113.65	23	3
P0C0L5 CO4B_HUMAN	Complement C4-B OS=Homo sapiens GN=	113.65	23	3
P02763 A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 OS=Homo sapiens	110.28	46	3
P02647 APOA1_HUMAN	Apolipoprotein A-I OS=Homo sapiens GN=	88.02	12	3
P02771 FETA_HUMAN	Alpha-fetoprotein OS=Homo sapiens GN=	69.2	4	3
P35556 FBN2_HUMAN	Fibrillin-2 OS=Homo sapiens GN=FBN2	45.74	5	3
Q2PPJ7 RGPA2_HUMAN	Ral GTPase-activating protein subunit alpha	38.22	2	3
P20929 NEBU_HUMAN	Nebulin OS=Homo sapiens GN=NEB PE=	37.95	3	3
O15018 PDZD2_HUMAN	PDZ domain-containing protein 2 OS=Homo sapiens	32.88	3	3
P07477 TRY1_HUMAN	Trypsin-1 OS=Homo sapiens GN=PRSS1	143.81	26	2
Q16610 ECM1_HUMAN	Extracellular matrix protein 1 OS=Homo sapiens	103.56	35	2
P02774 VTDB_HUMAN	Vitamin D-binding protein OS=Homo sapiens	83.32	31	2
O14647 CHD2_HUMAN	Chromodomain-helicase-DNA-binding protein	43.46	4	2
Q9UNH5 CC14A_HUMAN	Dual specificity protein phosphatase CDC	43.19	6	2
Q9Y6W5 WASF2_HUMAN	Wiskott-Aldrich syndrome protein family member	38.65	2	2
P24821 TENA_HUMAN	Tenascin OS=Homo sapiens GN=TNC PE=	36.58	3	2
Q3L8U1 CHD9_HUMAN	Chromodomain-helicase-DNA-binding protein	35.78	2	2
Q96KC8 DNJC1_HUMAN	DnaJ homolog subfamily C member 1 OS=	35.29	12	2
Q95IE3 2B1C_HUMAN	HLA class II histocompatibility antigen, DR	32.1	10	2
P01911 2B1F_HUMAN	HLA class II histocompatibility antigen, DR	32.1	8	2
Q29974 2B1G_HUMAN	HLA class II histocompatibility antigen, DR	32.1	8	2

P04229 2B11_HUMAN	HLA class II histocompatibility antigen, DR	32.1	5	2
P01912 2B13_HUMAN	HLA class II histocompatibility antigen, DR	32.1	5	2
P20039 2B1B_HUMAN	HLA class II histocompatibility antigen, DR	32.1	5	2
Q5Y7A7 2B1D_HUMAN	HLA class II histocompatibility antigen, DR	32.1	5	2
Q9GIY3 2B1E_HUMAN	HLA class II histocompatibility antigen, DR	32.1	5	2
Q30154 DRB5_HUMAN	HLA class II histocompatibility antigen, DR	32.1	5	2
Q14517 FAT1_HUMAN	Protocadherin Fat 1 OS=Homo sapiens G	31.9	3	2
Q9Y4H2 IRS2_HUMAN	Insulin receptor substrate 2 OS=Homo sa	30.26	5	2
Q7L4P6 BEND5_HUMAN	BEN domain-containing protein 5 OS=Hor	30.07	8	2
O15083 ERC2_HUMAN	ERC protein 2 OS=Homo sapiens GN=ER	29.66	3	2
Q07075 AMPE_HUMAN	Glutamyl aminopeptidase OS=Homo sapi	29.26	3	2
O00555 CAC1A_HUMAN	Voltage-dependent P/Q-type calcium char	29.06	3	2
Q07869 PPARA_HUMAN	Peroxisome proliferator-activated recepto	28.92	2	2
Q15262 PTPRK_HUMAN	Receptor-type tyrosine-protein phosphata	28.88	5	2
Q96T88 UHRF1_HUMAN	E3 ubiquitin-protein ligase UHRF1 OS=Hc	28.46	3	2
Q2M329 CCD96_HUMAN	Coiled-coil domain-containing protein 96 C	27.76	3	2

**Table A1.4 Human BME Protein Identifications.** List of all proteins identified in Human BME growth matrix with corresponding accession, description, PEAKS score, unique peptide numbers, and coverage (in %).

Accession	Description	Score	Coverage (%)	#Unique
P02751 FINC_HUMAN	Fibronectin OS=Homo sapiens G	341.22	45	102
P24043 LAMA2_HUMAN	Laminin subunit alpha-2 OS=Hoi	304.77	30	66
P55268 LAMB2_HUMAN	Laminin subunit beta-2 OS=Hom	283.73	35	46
Q05707 COEA1_HUMAN	Collagen alpha-1(XIV) chain OS=	264.19	41	46
P01023 A2MG_HUMAN	Alpha-2-macroglobulin OS=Hom	289	38	45
P11047 LAMC1_HUMAN	Laminin subunit gamma-1 OS=H	279.33	39	43
P98160 PGBM_HUMAN	Basement membrane-specific he	258.87	19	42
P08670 VIME_HUMAN	Vimentin OS=Homo sapiens GN	258.73	73	37
O15230 LAMA5_HUMAN	Laminin subunit alpha-5 OS=Hoi	253.7	16	34
P07942 LAMB1_HUMAN	Laminin subunit beta-1 OS=Hom	238.75	24	27
P14543 NID1_HUMAN	Nidogen-1 OS=Homo sapiens G	237.82	30	27
P12111 CO6A3_HUMAN	Collagen alpha-3(VI) chain OS=I	226.55	19	27
Q16363 LAMA4_HUMAN	Laminin subunit alpha-4 OS=Hoi	224.5	27	25
P01024 CO3_HUMAN	Complement C3 OS=Homo sapi	205.4	23	24
P11021 GRP78_HUMAN	78 kDa glucose-regulated protei	235.26	46	23
P14625 ENPL_HUMAN	Endoplasmin OS=Homo sapiens	215.43	38	22
O43707 ACTN4_HUMAN	Alpha-actinin-4 OS=Homo sapie	281.68	56	21
P02545 LMNA_HUMAN	Prelamin-A/C OS=Homo sapiens	213.42	47	21
P02768 ALBU_HUMAN	Serum albumin OS=Homo sapie	200.8	42	21
P12814 ACTN1_HUMAN	Alpha-actinin-1 OS=Homo sapie	269.31	58	20
P07237 PDIA1_HUMAN	Protein disulfide-isomerase OS=	206.6	45	19
Q13813 SPTA2_HUMAN	Spectrin alpha chain, brain OS=I	186.17	21	17
P02671 FIBA_HUMAN	Fibrinogen alpha chain OS=Hom	172.58	26	16
P23142 FBLN1_HUMAN	Fibulin-1 OS=Homo sapiens GN	200.91	25	15
Q15084 PDIA6_HUMAN	Protein disulfide-isomerase A6 C	197.7	42	15
P18206 VINC_HUMAN	Vinculin OS=Homo sapiens GN=	183.25	27	14
O75369 FLNB_HUMAN	Filamin-B OS=Homo sapiens GN	175.11	14	14
P02675 FIBB_HUMAN	Fibrinogen beta chain OS=Homc	169.47	42	14
P01243 CSH_HUMAN	Chorionic somatomammotropin	222.66	69	13
P11277 SPTB1_HUMAN	Spectrin beta chain, erythrocyte	181.32	19	13
P04083 ANXA1_HUMAN	Annexin A1 OS=Homo sapiens C	178.26	42	13
P08603 CFAH_HUMAN	Complement factor H OS=Homc	177.55	19	13
P10809 CH60_HUMAN	60 kDa heat shock protein, mito	176.8	45	13
P32119 PRDX2_HUMAN	Peroxiredoxin-2 OS=Homo sapie	183.65	38	12
P07355 ANXA2_HUMAN	Annexin A2 OS=Homo sapiens C	177.18	44	12
P02679 FIBG_HUMAN	Fibrinogen gamma chain OS=Ho	189.08	38	11
P30101 PDIA3_HUMAN	Protein disulfide-isomerase A3 C	155.47	33	11
Q15582 BGH3_HUMAN	Transforming growth factor-beta	154.17	36	11
P69905 HBA_HUMAN	Hemoglobin subunit alpha OS=H	180.04	64	10
P06576 ATPB_HUMAN	ATP synthase subunit beta, mito	174.82	34	10
P49748 ACADV_HUMAN	Very long-chain specific acyl-Co	174.26	26	10
P21980 TGM2_HUMAN	Protein-glutamine gamma-glutar	161.7	24	10
P35579 MYH9_HUMAN	Myosin-9 OS=Homo sapiens GN	158.65	15	10
Q03252 LMNB2_HUMAN	Lamin-B2 OS=Homo sapiens GI	155.23	25	10
P51884 LUM_HUMAN	Lumican OS=Homo sapiens GN	140.59	34	10
P50454 SERPH_HUMAN	Serpin H1 OS=Homo sapiens GI	180.83	33	9
P21333 FLNA_HUMAN	Filamin-A OS=Homo sapiens GI	154.91	13	9
Q14112 NID2_HUMAN	Nidogen-2 OS=Homo sapiens G	146.91	12	9
P39059 COFA1_HUMAN	Collagen alpha-1(XV) chain OS=	163.68	18	8
Q9Y6N6 LAMC3_HUMAN	Laminin subunit gamma-3 OS=H	158.79	17	8
P14314 GLU2B_HUMAN	Glucosidase 2 subunit beta OS=	148.61	31	8
P60660 MYL6_HUMAN	Myosin light polypeptide 6 OS=H	145.14	75	8
P20700 LMNB1_HUMAN	Lamin-B1 OS=Homo sapiens GI	144.74	26	8
P55072 TERA_HUMAN	Transitional endoplasmic reticulu	142.86	15	8

P10909	CLUS_HUMAN	Clusterin OS=Homo sapiens GN	137.86	25	8
P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial	145.13	27	7
P36957	ODO2_HUMAN	Dihydrolipoylysine-residue succi	135.47	22	7
P00747	PLMN_HUMAN	Plasminogen OS=Homo sapiens	133.52	10	7
P02549	SPTA1_HUMAN	Spectrin alpha chain, erythrocyte	131.8	8	7
P30048	PRDX3_HUMAN	Thioredoxin-dependent peroxide	121.33	29	7
P00488	F13A_HUMAN	Coagulation factor XIII A chain C	116.64	18	7
P01857	IGHG1_HUMAN	Ig gamma-1 chain C region OS=	186.51	53	6
P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa prot	184	28	6
P68871	HBB_HUMAN	Hemoglobin subunit beta OS=Ho	167.04	48	6
P04792	HSPB1_HUMAN	Heat shock protein beta-1 OS=H	151.58	36	6
P20774	MIME_HUMAN	Mimecan OS=Homo sapiens GN	135.79	34	6
P08758	ANXA5_HUMAN	Annexin A5 OS=Homo sapiens C	132.3	23	6
P21810	PGS1_HUMAN	Biglycan OS=Homo sapiens GN	132.24	22	6
P62805	H4_HUMAN	Histone H4 OS=Homo sapiens C	130.91	41	6
P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerat	129.29	42	6
P02647	APOA1_HUMAN	Apolipoprotein A-I OS=Homo sa	127.95	25	6
P04004	VTNC_HUMAN	Vitronectin OS=Homo sapiens C	127.76	16	6
P07585	PGS2_HUMAN	Decorin OS=Homo sapiens GN=	124	16	6
P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mi	122.42	21	6
P06396	GELS_HUMAN	Gelsolin OS=Homo sapiens GN=	119.73	13	6
Q12805	FBLN3_HUMAN	EGF-containing fibulin-like extrac	116.62	19	6
P63104	1433Z_HUMAN	14-3-3 protein zeta/delta OS=Ho	116.55	47	6
P63267	ACTH_HUMAN	Actin, gamma-enteric smooth m	194.38	40	5
P62736	ACTA_HUMAN	Actin, aortic smooth muscle OS=	194.38	40	5
P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 O	194.38	40	5
P68133	ACTS_HUMAN	Actin, alpha skeletal muscle OS=	194.38	40	5
Q9NYU2	UGGG1_HUMAN	UDP-glucose:glycoprotein glucos	135.54	7	5
P39060	COIA1_HUMAN	Collagen alpha-1(XVIII) chain O	130.82	12	5
P51888	PRELP_HUMAN	Prolargin OS=Homo sapiens GN	127.01	14	5
P17661	DESM_HUMAN	Desmin OS=Homo sapiens GN=	126.75	25	5
P80303	NUCB2_HUMAN	Nucleobindin-2 OS=Homo sapie	124.47	28	5
P09211	GSTP1_HUMAN	Glutathione S-transferase P OS=	120.59	33	5
P25705	ATPA_HUMAN	ATP synthase subunit alpha, mit	114.16	18	5
P02748	CO9_HUMAN	Complement component C9 OS=	106.89	13	5
P0C0L4	CO4A_HUMAN	Complement C4-A OS=Homo sa	102.47	7	5
P0C0L5	CO4B_HUMAN	Complement C4-B OS=Homo sa	102.47	7	5
P35749	MYH11_HUMAN	Myosin-11 OS=Homo sapiens G	102.39	8	5
Q9NR28	DBLOH_HUMAN	Diablo homolog, mitochondrial C	101.43	24	5
P35555	FBN1_HUMAN	Fibrillin-1 OS=Homo sapiens GN	97.14	4	5
P07954	FUMH_HUMAN	Fumarate hydratase, mitochondri	89.86	17	5
Q01082	SPTB2_HUMAN	Spectrin beta chain, brain 1 OS=	87.78	6	5
P02765	FETUA_HUMAN	Alpha-2-HS-glycoprotein OS=Ho	80.75	25	5
P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta	140.06	19	4
P40926	MDHM_HUMAN	Malate dehydrogenase, mitochol	132.99	30	4
Q06830	PRDX1_HUMAN	Peroxiredoxin-1 OS=Homo sapi	121.31	29	4
P24534	EF1B_HUMAN	Elongation factor 1-beta OS=Ho	119.55	30	4
Q13162	PRDX4_HUMAN	Peroxiredoxin-4 OS=Homo sapi	116.87	21	4
P13667	PDIA4_HUMAN	Protein disulfide-isomerase A4 C	110.55	11	4
Q14257	RCN2_HUMAN	Reticulocalbin-2 OS=Homo sapi	108.08	25	4
Q96HE7	ERO1A_HUMAN	ERO1-like protein alpha OS=Ho	106.34	13	4
P07737	PROF1_HUMAN	Profilin-1 OS=Homo sapiens GN	102.52	45	4
Q9BS26	ERP44_HUMAN	Endoplasmic reticulum resident	97.38	14	4
Q9UBS4	DJB11_HUMAN	DnaJ homolog subfamily B mem	96.49	14	4
Q9UIJ7	KAD3_HUMAN	GTP:AMP phosphotransferase,	93.16	21	4

Q07954	LRP1_HUMAN	Prolow-density lipoprotein recept	90.68	3	4
Q15008	PSMD6_HUMAN	26S proteasome non-ATPase re	87.94	14	4
P30041	PRDX6_HUMAN	Peroxioredoxin-6 OS=Homo sapi	85.61	29	4
P00450	CERU_HUMAN	Ceruloplasmin OS=Homo sapien	83.68	8	4
P30044	PRDX5_HUMAN	Peroxioredoxin-5, mitochondrial C	82.93	28	4
P24821	TENA_HUMAN	Tenascin OS=Homo sapiens GN	54.92	6	4
Q8IZT6	ASPM_HUMAN	Abnormal spindle-like microceph	44.64	5	4
P54652	HSP72_HUMAN	Heat shock-related 70 kDa prote	162.58	23	3
Q00887	PSG9_HUMAN	Pregnancy-specific beta-1-glyco	162.56	24	3
P34931	HS71L_HUMAN	Heat shock 70 kDa protein 1-like	129.92	20	3
P04040	CATA_HUMAN	Catalase OS=Homo sapiens GN	112.92	21	3
P62258	1433E_HUMAN	14-3-3 protein epsilon OS=Homo	108.22	16	3
P61604	CH10_HUMAN	10 kDa heat shock protein, mitoc	108.04	35	3
P01834	IGKC_HUMAN	Ig kappa chain C region OS=Homo	106.98	56	3
Q08380	LG3BP_HUMAN	Galectin-3-binding protein OS=H	100.86	8	3
P07437	TBB5_HUMAN	Tubulin beta chain OS=Homo sa	93.94	9	3
P09525	ANXA4_HUMAN	Annexin A4 OS=Homo sapiens G	92.2	15	3
Q9Y490	TLN1_HUMAN	Talin-1 OS=Homo sapiens GN=	90.4	2	3
Q09666	AHNK_HUMAN	Neuroblast differentiation-associ	89.83	3	3
Q9BQE3	TBA1C_HUMAN	Tubulin alpha-1C chain OS=Homo	88	9	3
P35232	PHB_HUMAN	Prohibitin OS=Homo sapiens GN	85.74	15	3
P09382	LEG1_HUMAN	Galectin-1 OS=Homo sapiens G	85.61	30	3
P27797	CALR_HUMAN	Calreticulin OS=Homo sapiens C	83.22	19	3
P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 OS=	81.94	13	3
Q5VTE0	EF1A3_HUMAN	Putative elongation factor 1-alph	81.94	13	3
Q12874	SF3A3_HUMAN	Splicing factor 3A subunit 3 OS=	81.59	12	3
P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate del	78.53	16	3
P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucle	77.15	12	3
Q10567	AP1B1_HUMAN	AP-1 complex subunit beta-1 OS	77.02	9	3
P20936	RASA1_HUMAN	Ras GTPase-activating protein 1	76.73	5	3
P01031	CO5_HUMAN	Complement C5 OS=Homo sapi	74.8	5	3
P54819	KAD2_HUMAN	Adenylate kinase 2, mitochondria	72.1	26	3
P07910	HNRPC_HUMAN	Heterogeneous nuclear ribonucle	71.44	23	3
Q13561	DCTN2_HUMAN	Dynactin subunit 2 OS=Homo sa	68.74	13	3
Q01518	CAP1_HUMAN	Adenylyl cyclase-associated prot	67.94	9	3
P60709	ACTB_HUMAN	Actin, cytoplasmic 1 OS=Homo s	216.5	44	2
P63261	ACTG_HUMAN	Actin, cytoplasmic 2 OS=Homo s	214.32	44	2
P01860	IGHG3_HUMAN	Ig gamma-3 chain C region OS=	175.52	51	2
P69892	HBG2_HUMAN	Hemoglobin subunit gamma-2 O	173.02	61	2
P69891	HBG1_HUMAN	Hemoglobin subunit gamma-1 O	170.8	61	2
P11465	PSG2_HUMAN	Pregnancy-specific beta-1-glyco	137.96	21	2
P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha	131.12	23	2
P25815	S100P_HUMAN	Protein S100-P OS=Homo sapie	91.58	39	2
P63220	RS21_HUMAN	40S ribosomal protein S21 OS=H	90.01	30	2
P04206	KV307_HUMAN	Ig kappa chain V-III region GOL	89.85	45	2
P01620	KV302_HUMAN	Ig kappa chain V-III region SIE C	89.85	31	2
P01622	KV304_HUMAN	Ig kappa chain V-III region Ti OS	89.85	31	2
P01623	KV305_HUMAN	Ig kappa chain V-III region WOL	89.85	31	2
P18135	KV312_HUMAN	Ig kappa chain V-III region HAH	89.85	26	2
P18136	KV313_HUMAN	Ig kappa chain V-III region HIC C	89.85	26	2
P15311	EZRI_HUMAN	Ezrin OS=Homo sapiens GN=EZ	88.03	9	2
P23396	RS3_HUMAN	40S ribosomal protein S3 OS=H	85.87	11	2
P01019	ANGT_HUMAN	Angiotensinogen OS=Homo sap	85.07	12	2
P42126	ECI1_HUMAN	Enoyl-CoA delta isomerase 1, m	83.5	15	2
P01009	A1AT_HUMAN	Alpha-1-antitrypsin OS=Homo sa	82	9	2

P98095	FBLN2_HUMAN	Fibulin-2 OS=Homo sapiens GN	80.14	2	2
P01593	KV101_HUMAN	Ig kappa chain V-I region AG OS	79.95	31	2
P31949	S10AB_HUMAN	Protein S100-A11 OS=Homo sa	78.4	34	2
P62993	GRB2_HUMAN	Growth factor receptor-bound pr	76.56	11	2
Q6NZI2	PTRF_HUMAN	Polymerase I and transcript relea	76.06	10	2
P01617	KV204_HUMAN	Ig kappa chain V-II region TEW	75.38	29	2
P06309	KV205_HUMAN	Ig kappa chain V-II region GM60	75.38	19	2
P23528	COF1_HUMAN	Cofilin-1 OS=Homo sapiens GN	75.06	14	2
Q15149	PLEC_HUMAN	Plectin OS=Homo sapiens GN=f	72.18	7	2
P01766	HV305_HUMAN	Ig heavy chain V-III region BRO	71.59	25	2
P51659	DHB4_HUMAN	Peroxisomal multifunctional enzy	69.47	6	2
P19404	NDUV2_HUMAN	NADH dehydrogenase [ubiquino	68.9	9	2
P30049	ATPD_HUMAN	ATP synthase subunit delta, mitc	68.54	14	2
P05160	F13B_HUMAN	Coagulation factor XIII B chain C	68.43	4	2
Q13219	PAPP1_HUMAN	Pappalysin-1 OS=Homo sapiens	67.72	3	2
Q04837	SSBP_HUMAN	Single-stranded DNA-binding pro	65.41	18	2
P46109	CRKL_HUMAN	Crk-like protein OS=Homo sapie	65.25	11	2
P01042	KNG1_HUMAN	Kininogen-1 OS=Homo sapiens	64.19	3	2
Q08830	FGL1_HUMAN	Fibrinogen-like protein 1 OS=Ho	64.04	11	2
P07339	CATD_HUMAN	Cathepsin D OS=Homo sapiens	63.2	6	2
Q81VN8	RPESP_HUMAN	RPE-spondin OS=Homo sapiens	62.23	9	2
P04843	RPN1_HUMAN	Dolichyl-diphosphooligosacchari	61.45	4	2
Q16787	LAMA3_HUMAN	Laminin subunit alpha-3 OS=Ho	61.2	2	2
O43852	CALU_HUMAN	Calumenin OS=Homo sapiens G	58.94	17	2
Q15293	RCN1_HUMAN	Reticulocalbin-1 OS=Homo sapi	57.79	8	2
P30040	ERP29_HUMAN	Endoplasmic reticulum resident	57.42	21	2
P11940	PABP1_HUMAN	Polyadenylate-binding protein 1	52.1	5	2
Q9H361	PABP3_HUMAN	Polyadenylate-binding protein 3	52.1	6	2
P78371	TCPB_HUMAN	T-complex protein 1 subunit beta	49.77	9	2
P10412	H14_HUMAN	Histone H1.4 OS=Homo sapiens	46.66	13	2
Q14571	ITPR2_HUMAN	Inositol 1,4,5-trisphosphate rece	35.19	1	2
Q9P2P6	STAR9_HUMAN	StAR-related lipid transfer protei	31.91	2	2
Q9P2D1	CHD7_HUMAN	Chromodomain-helicase-DNA-bi	31.53	1	2
Q7Z2Z1	TICRR_HUMAN	Treslin OS=Homo sapiens GN=f	30.44	2	2
Q5TZA2	CROCC_HUMAN	Rootletin OS=Homo sapiens GN	30.02	4	2
Q03001	DYST_HUMAN	Dystonin OS=Homo sapiens GN	29.73	2	2
Q9P2F8	SI1L2_HUMAN	Signal-induced proliferation-assc	29.63	3	2
Q8WZ42	TITIN_HUMAN	Titin OS=Homo sapiens GN=TT	29.6	2	2
Q4LDE5	SVEP1_HUMAN	Sushi, von Willebrand factor type	28.41	1	2
Q81VF2	AHNK2_HUMAN	Protein AHNAK2 OS=Homo sap	26.15	1	2
Q9NW75	GPCC2_HUMAN	G patch domain-containing prote	25.7	12	2
P07478	TRY2_HUMAN	Trypsin-2 OS=Homo sapiens GN	25.63	10	2
Q8IVL0	NAV3_HUMAN	Neuron navigator 3 OS=Homo s	25.51	2	2
Q9NU22	MDN1_HUMAN	Midasin OS=Homo sapiens GN=f	24.63	2	2

**Table A1.5 StemXVivo Protein Identifications.** List of all proteins identified in StemXVivo growth matrix with corresponding accession, description, PEAKS score, unique peptide numbers, and coverage (in %).



Accession	Description	Score	Coverage (%)	#Unique
P04004 VTNC_HUMAN	Vitronectin OS=Homo sapiens GN	388.02	71	115
P14543 NID1_HUMAN	Nidogen-1 OS=Homo sapiens GN	412.42	53	109
P34741 SDC2_HUMAN	Syndecan-2 OS=Homo sapiens GI	239.36	43	22
P11142 HSP7C_HUMAN	Heat shock cognate 71 kDa protein	219.5	32	11
P02768 ALBU_HUMAN	Serum albumin OS=Homo sapiens	176.5	13	11
P26641 EF1G_HUMAN	Elongation factor 1-gamma OS=Ho	176.44	33	8
P34932 HSP74_HUMAN	Heat shock 70 kDa protein 4 OS=H	187.57	19	7
O94985 CSTN1_HUMAN	Calsyntenin-1 OS=Homo sapiens G	129.26	10	6
P01024 CO3_HUMAN	Complement C3 OS=Homo sapien	141.05	11	5
P07900 HS90A_HUMAN	Heat shock protein HSP 90-alpha	196.22	24	4
P63261 ACTG_HUMAN	Actin, cytoplasmic 2 OS=Homo sa	146.59	30	4
P60709 ACTB_HUMAN	Actin, cytoplasmic 1 OS=Homo sa	146.59	27	4
P14618 KPYM_HUMAN	Pyruvate kinase isozymes M1/M2	140.5	21	4
P01023 A2MG_HUMAN	Alpha-2-macroglobulin OS=Homo	133.62	12	4
P23142 FBLN1_HUMAN	Fibulin-1 OS=Homo sapiens GN=F	118.99	6	4
P04083 ANXA1_HUMAN	Annexin A1 OS=Homo sapiens GN	118.41	11	4
P08238 HS90B_HUMAN	Heat shock protein HSP 90-beta C	199.68	28	3
Q9BQE3 TBA1C_HUMAN	Tubulin alpha-1C chain OS=Homo	121.93	20	3
P68363 TBA1B_HUMAN	Tubulin alpha-1B chain OS=Homo	121.93	20	3
P23396 RS3_HUMAN	40S ribosomal protein S3 OS=Hon	119.7	20	3
Q5VTE0 EF1A3_HUMAN	Putative elongation factor 1-alpha-	109.9	15	3
P68104 EF1A1_HUMAN	Elongation factor 1-alpha 1 OS=Hc	109.9	11	3
P00450 CERU_HUMAN	Ceruloplasmin OS=Homo sapiens	100.07	6	3
Q16543 CDC37_HUMAN	Hsp90 co-chaperone Cdc37 OS=H	90.9	19	3
P0C0L4 CO4A_HUMAN	Complement C4-A OS=Homo sapi	77.95	5	3
P0C0L5 CO4B_HUMAN	Complement C4-B OS=Homo sapi	77.95	5	3
Q9Y623 MYH4_HUMAN	Myosin-4 OS=Homo sapiens GN=I	67.15	4	3
P08865 RSSA_HUMAN	40S ribosomal protein SA OS=Hon	112.46	10	2
P19823 ITI2_HUMAN	Inter-alpha-trypsin inhibitor heavy c	102.91	7	2
P67809 YBOX1_HUMAN	Nuclease-sensitive element-bindin	101.59	20	2
P02656 APOC3_HUMAN	Apolipoprotein C-III OS=Homo sap	98.62	16	2
P62263 RS14_HUMAN	40S ribosomal protein S14 OS=Ho	98.35	16	2
P02647 APOA1_HUMAN	Apolipoprotein A-I OS=Homo sapie	96.73	21	2
P01031 CO5_HUMAN	Complement C5 OS=Homo sapien	95.88	4	2
Q66LE6 2ABD_HUMAN	Serine/threonine-protein phosphat	94.37	9	2
P63151 2ABA_HUMAN	Serine/threonine-protein phosphat	94.37	11	2
P33778 H2B1B_HUMAN	Histone H2B type 1-B OS=Homo s	94.29	19	2
P62807 H2B1C_HUMAN	Histone H2B type 1-C/E/F/G/I OS=	94.29	19	2
P58876 H2B1D_HUMAN	Histone H2B type 1-D OS=Homo s	94.29	19	2
Q93079 H2B1H_HUMAN	Histone H2B type 1-H OS=Homo s	94.29	19	2
P06899 H2B1J_HUMAN	Histone H2B type 1-J OS=Homo s	94.29	19	2
O60814 H2B1K_HUMAN	Histone H2B type 1-K OS=Homo s	94.29	19	2
Q99880 H2B1L_HUMAN	Histone H2B type 1-L OS=Homo s	94.29	19	2
Q99879 H2B1M_HUMAN	Histone H2B type 1-M OS=Homo s	94.29	19	2
Q99877 H2B1N_HUMAN	Histone H2B type 1-N OS=Homo s	94.29	19	2
P23527 H2B1O_HUMAN	Histone H2B type 1-O OS=Homo s	94.29	19	2
Q16778 H2B2E_HUMAN	Histone H2B type 2-E OS=Homo s	94.29	19	2
Q5QNW6 H2B2F_HUMAN	Histone H2B type 2-F OS=Homo s	94.29	19	2
Q8N257 H2B3B_HUMAN	Histone H2B type 3-B OS=Homo s	94.29	19	2
P57053 H2BFS_HUMAN	Histone H2B type F-S OS=Homo s	94.29	19	2
P53621 COPA_HUMAN	Coatomer subunit alpha OS=Homo	91.65	6	2
P36955 PEDF_HUMAN	Pigment epithelium-derived factor	89.1	6	2
P60842 IF4A1_HUMAN	Eukaryotic initiation factor 4A-I OS	83.3	7	2
P53396 ACLY_HUMAN	ATP-citrate synthase OS=Homo sa	82.41	6	2

P31749	AKT1_HUMAN	RAC-alpha serine/threonine-protein	82.32	12	2
P68871	HBB_HUMAN	Hemoglobin subunit beta OS=Homo	78.59	25	2
P55072	TERA_HUMAN	Transitional endoplasmic reticulum	76.98	4	2
P46782	RS5_HUMAN	40S ribosomal protein S5 OS=Homo	76.59	11	2
O00506	STK25_HUMAN	Serine/threonine-protein kinase 25	75.38	9	2
P78371	TCPB_HUMAN	T-complex protein 1 subunit beta C	74.84	8	2
P05388	RLA0_HUMAN	60S acidic ribosomal protein P0 OS=	74.81	15	2
Q8NHW5	RLA0L_HUMAN	60S acidic ribosomal protein P0-lik	74.81	11	2
P62269	RS18_HUMAN	40S ribosomal protein S18 OS=Homo	69.34	20	2
P62826	RAN_HUMAN	GTP-binding nuclear protein Ran C	68.52	27	2
P81605	DCD_HUMAN	Dermcidin OS=Homo sapiens GN=	59.42	13	2
O15169	AXIN1_HUMAN	Axin-1 OS=Homo sapiens GN=AX	47.22	3	2
P05546	HEP2_HUMAN	Heparin cofactor 2 OS=Homo sapi	37.09	4	2

**Table A1.6 StemXVivo Protein Identifications (not species restricted).** List of all proteins identified in StemXVivo growth matrix when searched against the entire UniProt database (not species restricted) with corresponding accession, description, PEAKS score, unique peptide numbers, and coverage (in %).

Accession	Description	Score	Coverage (%)	#Unique
Q7SIH1 A2MG_BOVIN	Alpha-2-macroglobulin OS=Bos tau	291.83	37	41
P15497 APOA1_BOVIN	Apolipoprotein A-I OS=Bos taurus G	286.69	75	32
Q2UVX4 CO3_BOVIN	Complement C3 OS=Bos taurus GN	253.94	33	29
P02769 ALBU_BOVIN	Serum albumin OS=Bos taurus GN=	297.68	67	22
P50448 F12AI_BOVIN	Factor XIIa inhibitor OS=Bos taurus	203.22	39	16
P02081 HBBF_BOVIN	Hemoglobin fetal subunit beta OS=B	201.32	66	14
P33433 HRG_BOVIN	Histidine-rich glycoprotein (Fragmer	196.95	28	10
Q3T052 ITIH4_BOVIN	Inter-alpha-trypsin inhibitor heavy ch	177.34	17	8
Q32PJ2 APOA4_BOVIN	Apolipoprotein A-IV OS=Bos taurus	136.8	28	8
P01030 CO4_BOVIN	Complement C4 (Fragments) OS=B	172.36	16	7
P80109 PHLD_BOVIN	Phosphatidylinositol-glycan-specific	141.5	10	6
P17697 CLUS_BOVIN	Clusterin OS=Bos taurus GN=CLU	122.97	15	6
Q32KY0 APOD_BOVIN	Apolipoprotein D OS=Bos taurus GN	110.26	27	6
P34955 A1AT_BOVIN	Alpha-1-antitrypsin OS=Bos tau	151.74	23	5
P56652 ITIH3_BOVIN	Inter-alpha-trypsin inhibitor heavy ch	123.99	9	5
P12763 FETUA_BOVIN	Alpha-2-HS-glycoprotein OS=Bos ta	148.64	25	4
P01044 KNG1_BOVIN	Kininogen-1 OS=Bos taurus GN=KN	176.7	21	3
Q3MHN5 VTDB_BOVIN	Vitamin D-binding protein OS=Bos t	103.11	12	3
P01045 KNG2_BOVIN	Kininogen-2 OS=Bos taurus GN=KN	170.41	19	2
Q3SZ57 FETA_BOVIN	Alpha-fetoprotein OS=Bos taurus G	116.63	8	2
P00735 THRB_BOVIN	Prothrombin OS=Bos taurus GN=F2	98.14	7	2
Q29443 TRFE_BOVIN	Serotransferrin OS=Bos taurus GN=	90.11	5	2
P81644 APOA2_BOVIN	Apolipoprotein A-II OS=Bos taurus C	80.49	26	2
Q32PF2 ACLY_BOVIN	ATP-citrate synthase OS=Bos tauru	77.96	7	2
Q3MHN2 CO9_BOVIN	Complement component C9 OS=Bc	71.57	6	2
Q03247 APOE_BOVIN	Apolipoprotein E OS=Bos taurus GN	57.34	8	2

**Table A1.7 MEF-CMTX Protein Identifications.** List of all proteins identified in MEF-CMTX (mouse embryonic fibroblast conditioned matrix) with corresponding accession, description, PEAKS score, unique peptide numbers, and coverage (in %).

Accession	Description	Score	Coverage (%)	#Unique
P11276 FINC_MOUSE	Fibronectin OS=Mus musculus GN	581.48	74	357
Q05793 PGBM_MOUSE	Basement membrane-specific hep	439.44	49	109
P37889 FBLN2_MOUSE	Fibulin-2 OS=Mus musculus GN=F	355.86	44	53
Q61554 FBN1_MOUSE	Fibrillin-1 OS=Mus musculus GN=F	365.34	34	51
P20152 VIME_MOUSE	Vimentin OS=Mus musculus GN=V	360.59	79	51
P35441 TSP1_MOUSE	Thrombospondin-1 OS=Mus musc	349.48	54	45
Q8VDD5 MYH9_MOUSE	Myosin-9 OS=Mus musculus GN=M	350.89	51	38
P56480 ATPB_MOUSE	ATP synthase subunit beta, mitoch	314.42	75	28
P11087 CO1A1_MOUSE	Collagen alpha-1(I) chain OS=Mus	282.08	47	26
Q60847 COCA1_MOUSE	Collagen alpha-1(XII) chain OS=M	253.63	28	26
P16858 G3P_MOUSE	Glyceraldehyde-3-phosphate dehyd	319.04	72	24
P19324 SERPH_MOUSE	Serpin H1 OS=Mus musculus GN=S	295.98	75	24
Q80YX1 TENA_MOUSE	Tenascin OS=Mus musculus GN=T	307.73	27	22
P08113 ENPL_MOUSE	Endoplasmin OS=Mus musculus G	275.18	49	21
P48036 ANXA5_MOUSE	Annexin A5 OS=Mus musculus GN	246.52	45	20
P27773 PDIA3_MOUSE	Protein disulfide-isomerase A3 OS	240.13	59	20
P48678 LMNA_MOUSE	Prelamin-A/C OS=Mus musculus C	202.89	41	19
P08249 MDHM_MOUSE	Malate dehydrogenase, mitochond	277.85	64	18
P20029 GRP78_MOUSE	78 kDa glucose-regulated protein C	258.38	48	18
Q60932 VDAC1_MOUSE	Voltage-dependent anion-selective	245.44	61	18
P09103 PDIA1_MOUSE	Protein disulfide-isomerase OS=M	242.36	55	18
P62806 H4_MOUSE	Histone H4 OS=Mus musculus GN	214.42	54	18
Q99K41 EMIL1_MOUSE	EMILIN-1 OS=Mus musculus GN=E	267.68	48	17
P10107 ANXA1_MOUSE	Annexin A1 OS=Mus musculus GN	248.47	62	17
Q68FD5 CLH_MOUSE	Clathrin heavy chain 1 OS=Mus m	215.3	36	17
Q61879 MYH10_MOUSE	Myosin-10 OS=Mus musculus GN=M	276.25	42	16
P07356 ANXA2_MOUSE	Annexin A2 OS=Mus musculus GN	267.91	65	16
P10126 EF1A1_MOUSE	Elongation factor 1-alpha 1 OS=M	231.29	49	16
Q9JHU4 DYHC1_MOUSE	Cytoplasmic dynein 1 heavy chain	198.4	26	16
P01027 CO3_MOUSE	Complement C3 OS=Mus musculu	191.3	29	16
Q99LC5 ETFA_MOUSE	Electron transfer flavoprotein subu	254.74	57	15
P67778 PHB_MOUSE	Prohibitin OS=Mus musculus GN=	243.64	79	15
Q99JR5 TINAL_MOUSE	Tubulointerstitial nephritis antigen-	242	47	15
P17742 PPIA_MOUSE	Peptidyl-prolyl cis-trans isomerase	233.89	59	15
P19783 COX41_MOUSE	Cytochrome c oxidase subunit 4 is	227.74	47	15
Q01149 CO1A2_MOUSE	Collagen alpha-2(I) chain OS=Mus	223.78	39	15
Q8BTM8 FLNA_MOUSE	Filamin-A OS=Mus musculus GN=F	203.11	22	15
O35129 PHB2_MOUSE	Prohibitin-2 OS=Mus musculus GN	224.33	67	14
Q9WTI7 MYO1C_MOUSE	Myosin-Ic OS=Mus musculus GN=M	210.49	41	14
P52480 KPYM_MOUSE	Pyruvate kinase isozymes M1/M2 C	188.48	56	14
Q9QXS1 PLEC_MOUSE	Plectin OS=Mus musculus GN=Ple	172.22	25	14
O88322 NID2_MOUSE	Nidogen-2 OS=Mus musculus GN=N	248.24	20	13
Q9DCN2 NB5R3_MOUSE	NADH-cytochrome b5 reductase 3	245.19	52	13
Q9DBJ1 PGAM1_MOUSE	Phosphoglycerate mutase 1 OS=M	227.39	68	13
Q9DCX2 ATP5H_MOUSE	ATP synthase subunit d, mitochon	224.83	76	13
P07724 ALBU_MOUSE	Serum albumin OS=Mus musculus	188.34	34	13
Q03265 ATPA_MOUSE	ATP synthase subunit alpha, mitoc	247.63	56	12
P22777 PAI1_MOUSE	Plasminogen activator inhibitor 1 C	233.08	64	12
Q8BMK4 CKAP4_MOUSE	Cytoskeleton-associated protein 4	227.44	45	12
P06151 LDHA_MOUSE	L-lactate dehydrogenase A chain C	222.32	49	12
P09055 ITB1_MOUSE	Integrin beta-1 OS=Mus musculus	221.29	30	12
O88207 CO5A1_MOUSE	Collagen alpha-1(V) chain OS=Mus	184.56	35	12
P37804 TAGL_MOUSE	Transgelin OS=Mus musculus GN=T	181.07	76	12
P63038 CH60_MOUSE	60 kDa heat shock protein, mitoch	243.31	53	11

P51655 GPC4_MOUSE	Glypican-4 OS=Mus musculus GN=	218.62	40	11
P17182 ENOA_MOUSE	Alpha-enolase OS=Mus musculus	207.07	59	11
P26039 TLN1_MOUSE	Talin-1 OS=Mus musculus GN=Tr	198.41	30	11
P17751 TPIS_MOUSE	Triosephosphate isomerase OS=M	196.62	53	11
Q8CG19 LTBP1_MOUSE	Latent-transforming growth factor b	185.33	17	11
Q8BMS1 ECHA_MOUSE	Trifunctional enzyme subunit alpha	212.35	39	10
P35564 CALX_MOUSE	Calnexin OS=Mus musculus GN=C	205.29	42	10
Q80X90 FLNB_MOUSE	Filamin-B OS=Mus musculus GN=	180.59	24	10
P35700 PRDX1_MOUSE	Peroxiredoxin-1 OS=Mus musculus	142.73	57	10
P01942 HBA_MOUSE	Hemoglobin subunit alpha OS=Mus	127.01	70	10
Q9D6X6 PRS23_MOUSE	Serine protease 23 OS=Mus musc	228.51	41	9
P16045 LEG1_MOUSE	Galectin-1 OS=Mus musculus GN=	200.58	65	9
Q61703 ITIH2_MOUSE	Inter-alpha-trypsin inhibitor heavy c	193.6	22	9
P14069 S10A6_MOUSE	Protein S100-A6 OS=Mus musculu	184.59	75	9
P38647 GRP75_MOUSE	Stress-70 protein, mitochondrial O	173.67	33	9
Q9D1D4 TMEDA_MOUSE	Transmembrane emp24 domain-co	163.9	34	9
P63017 HSP7C_MOUSE	Heat shock cognate 71 kDa proteir	216.39	36	8
P62962 PROF1_MOUSE	Profilin-1 OS=Mus musculus GN=F	184.52	64	8
P58252 EF2_MOUSE	Elongation factor 2 OS=Mus musc	179.44	31	8
O08756 HCD2_MOUSE	3-hydroxyacyl-CoA dehydrogenase	174.7	52	8
P49817 CAV1_MOUSE	Caveolin-1 OS=Mus musculus GN=	173.56	56	8
P42208 SEPT2_MOUSE	Septin-2 OS=Mus musculus GN=S	173.24	43	8
P99029 PRDX5_MOUSE	Peroxiredoxin-5, mitochondrial OS-	168.5	51	8
P05064 ALDOA_MOUSE	Fructose-bisphosphate aldolase A	160.07	38	8
P08121 CO3A1_MOUSE	Collagen alpha-1(III) chain OS=M	159.6	20	8
P24369 PPIB_MOUSE	Peptidyl-prolyl cis-trans isomerase	156.06	61	8
P32261 ANT3_MOUSE	Antithrombin-III OS=Mus musculus	155.97	40	8
Q60605 MYL6_MOUSE	Myosin light polypeptide 6 OS=Mus	197.87	74	7
P61982 1433G_MOUSE	14-3-3 protein gamma OS=Mus m	197.21	48	7
P48962 ADT1_MOUSE	ADP/ATP translocase 1 OS=Mus r	195.35	53	7
P63101 1433Z_MOUSE	14-3-3 protein zeta/delta OS=Mus	187.73	45	7
P62259 1433E_MOUSE	14-3-3 protein epsilon OS=Mus m	186.09	49	7
Q02257 PLAK_MOUSE	Junction plakoglobin OS=Mus mus	182.94	36	7
Q9DB77 QCR2_MOUSE	Cytochrome b-c1 complex subunit	181.77	34	7
Q62009 POSTN_MOUSE	Periostin OS=Mus musculus GN=F	169.26	33	7
Q9DBG6 RPN2_MOUSE	Dolichyl-diphosphooligosaccharide	167.93	18	7
Q99P72 RTN4_MOUSE	Reticulon-4 OS=Mus musculus GN	162.74	12	7
Q3V1M1 IGS10_MOUSE	Immunoglobulin superfamily memb	160.41	22	7
Q64433 CH10_MOUSE	10 kDa heat shock protein, mitoch	158.56	53	7
P14211 CALR_MOUSE	Calreticulin OS=Mus musculus GN	156.64	41	7
P47738 ALDH2_MOUSE	Aldehyde dehydrogenase, mitoch	152.71	28	7
Q9CPT4 CS010_MOUSE	UPF0556 protein C19orf10 homold	151.83	50	7
P01831 THY1_MOUSE	Thy-1 membrane glycoprotein OS=	150.21	32	7
P30999 CTND1_MOUSE	Catenin delta-1 OS=Mus musculus	132.85	34	7
Q00623 APOA1_MOUSE	Apolipoprotein A-I OS=Mus muscu	111.33	14	7
P29699 FETUA_MOUSE	Alpha-2-HS-glycoprotein OS=Mus	93.03	12	7
P99024 TBB5_MOUSE	Tubulin beta-5 chain OS=Mus mus	300.34	70	6
Q922R8 PDIA6_MOUSE	Protein disulfide-isomerase A6 OS-	177.82	28	6
P14206 RSSA_MOUSE	40S ribosomal protein SA OS=Mus	172.96	37	6
O54724 PTRF_MOUSE	Polymerase I and transcript release	165.27	41	6
Q9CQ60 PGL_MOUSE	6-phosphogluconolactonase OS=M	163.4	58	6
Q9D6R2 IDH3A_MOUSE	Isocitrate dehydrogenase [NAD] su	162.7	32	6
P16546 SPTA2_MOUSE	Spectrin alpha chain, brain OS=M	154.23	30	6
Q64523 H2A2C_MOUSE	Histone H2A type 2-C OS=Mus mu	153.48	63	6
Q6GSS7 H2A2A_MOUSE	Histone H2A type 2-A OS=Mus mu	153.48	62	6

P18760 COF1_MOUSE	Cofilin-1 OS=Mus musculus GN=C	149.72	51	6
P19221 THRB_MOUSE	Prothrombin OS=Mus musculus G	142.61	23	6
Q3U7R1 ESYT1_MOUSE	Extended synaptotagmin-1 OS=M	142.07	21	6
Q99JB2 STML2_MOUSE	Stomatin-like protein 2 OS=Mus m	140.46	36	6
P51150 RAB7A_MOUSE	Ras-related protein Rab-7a OS=M	140.24	36	6
Q61704 ITIH3_MOUSE	Inter-alpha-trypsin inhibitor heavy c	134.96	7	6
Q6GQT1 A2MP_MOUSE	Alpha-2-macroglobulin-P OS=Mus	133.24	10	6
Q9R0Q3 TMED2_MOUSE	Transmembrane emp24 domain-co	120.8	43	6
Q9Z0G4 WISP2_MOUSE	WNT1-inducible-signaling pathway	95.85	14	6
Q7TPR4 ACTN1_MOUSE	Alpha-actinin-1 OS=Mus musculus	209.95	29	5
Q9CPQ3 TOM22_MOUSE	Mitochondrial import receptor subu	162.06	73	5
Q64449 MRC2_MOUSE	C-type mannose receptor 2 OS=M	161.05	28	5
P97429 ANXA4_MOUSE	Annexin A4 OS=Mus musculus GN	160.41	25	5
Q9D051 ODPB_MOUSE	Pyruvate dehydrogenase E1 comp	158.08	31	5
Q6IRU2 TPM4_MOUSE	Tropomyosin alpha-4 chain OS=M	152.53	35	5
Q9WV54 ASAH1_MOUSE	Acid ceramidase OS=Mus muscul	151.8	36	5
Q9CQQ7 AT5F1_MOUSE	ATP synthase subunit b, mitochon	151.39	42	5
Q9CPQ8 ATP5L_MOUSE	ATP synthase subunit g, mitochon	148.8	43	5
Q9DB20 ATPO_MOUSE	ATP synthase subunit O, mitochon	145.36	55	5
Q9DCS9 NDUBA_MOUSE	NADH dehydrogenase [ubiquinone	144.59	40	5
Q91V41 RAB14_MOUSE	Ras-related protein Rab-14 OS=M	144.13	34	5
P63242 IF5A1_MOUSE	Eukaryotic translation initiation fact	141.88	52	5
Q8QZT1 THIL_MOUSE	Acetyl-CoA acetyltransferase, mito	139.92	25	5
P12787 COX5A_MOUSE	Cytochrome c oxidase subunit 5A,	137.05	52	5
Q9R0Y5 KAD1_MOUSE	Adenylate kinase isoenzyme 1 OS=	134.64	50	5
P62908 RS3_MOUSE	40S ribosomal protein S3 OS=Mus	134.44	25	5
P08207 S10AA_MOUSE	Protein S100-A10 OS=Mus muscu	132.92	49	5
P16460 ASSY_MOUSE	Argininosuccinate synthase OS=M	132.88	32	5
P62492 RB11A_MOUSE	Ras-related protein Rab-11A OS=M	132.84	26	5
P46638 RB11B_MOUSE	Ras-related protein Rab-11B OS=M	132.84	26	5
P57776 EF1D_MOUSE	Elongation factor 1-delta OS=Mus	132.4	20	5
P14602 HSPB1_MOUSE	Heat shock protein beta-1 OS=Mus	131.71	58	5
Q9DCW4 ETFB_MOUSE	Electron transfer flavoprotein subu	130.32	26	5
P29758 OAT_MOUSE	Ornithine aminotransferase, mitoch	127.65	28	5
Q08879 FBLN1_MOUSE	Fibulin-1 OS=Mus musculus GN=F	126.94	7	5
P57759 ERP29_MOUSE	Endoplasmic reticulum resident pro	126.22	30	5
Q3THE2 ML12B_MOUSE	Myosin regulatory light chain 12B C	123.64	31	5
O08807 PRDX4_MOUSE	Peroxiredoxin-4 OS=Mus musculus	120.68	36	5
P56395 CYB5_MOUSE	Cytochrome b5 OS=Mus musculus	114.04	25	5
Q02248 CTNB1_MOUSE	Catenin beta-1 OS=Mus musculus	113.49	17	5
O08709 PRDX6_MOUSE	Peroxiredoxin-6 OS=Mus musculus	113.38	33	5
P01029 CO4B_MOUSE	Complement C4-B OS=Mus muscu	109.12	23	5
P11688 ITA5_MOUSE	Integrin alpha-5 OS=Mus musculus	108.93	5	5
Q8VDP6 CDIPT_MOUSE	CDP-diacylglycerol--inositol 3-phos	107.11	26	5
P62301 RS13_MOUSE	40S ribosomal protein S13 OS=MU	101.37	32	5
Q922F4 TBB6_MOUSE	Tubulin beta-6 chain OS=Mus mus	247.93	55	4
P57780 ACTN4_MOUSE	Alpha-actinin-4 OS=Mus musculus	193	30	4
O08638 MYH11_MOUSE	Myosin-11 OS=Mus musculus GN=	182.1	37	4
P97298 PEDF_MOUSE	Pigment epithelium-derived factor	161.86	29	4
P00405 COX2_MOUSE	Cytochrome c oxidase subunit 2 O	160.13	33	4
P05202 AATM_MOUSE	Aspartate aminotransferase, mitoc	157.02	47	4
Q9R001 ATS5_MOUSE	A disintegrin and metalloproteinase	155.55	22	4
P68254 1433T_MOUSE	14-3-3 protein theta OS=Mus musc	153.89	38	4
Q64727 VINC_MOUSE	Vinculin OS=Mus musculus GN=V	148.88	39	4
Q9JKR6 HYOU1_MOUSE	Hypoxia up-regulated protein 1 OS	147.92	24	4



P09411 PGK1_MOUSE	Phosphoglycerate kinase 1 OS=Mus musculus GN=	146.68	35	4
P53994 RAB2A_MOUSE	Ras-related protein Rab-2A OS=Mus musculus GN=	145.57	42	4
Q9WVA4 TAGL2_MOUSE	Transgelin-2 OS=Mus musculus GN=	145.29	31	4
Q62186 SSRD_MOUSE	Translocon-associated protein subunit 1 OS=Mus musculus GN=	142.72	45	4
P34884 MIF_MOUSE	Macrophage migration inhibitory factor OS=Mus musculus GN=	141.34	46	4
Q6URW6 MYH14_MOUSE	Myosin-14 OS=Mus musculus GN=	141.17	24	4
O35639 ANXA3_MOUSE	Annexin A3 OS=Mus musculus GN=	138.36	36	4
Q8CGP2 H2B1P_MOUSE	Histone H2B type 1-P OS=Mus musculus GN=	136.6	46	4
Q64475 H2B1B_MOUSE	Histone H2B type 1-B OS=Mus musculus GN=	136.6	37	4
Q6ZWY9 H2B1C_MOUSE	Histone H2B type 1-C/E/G OS=Mus musculus GN=	136.6	37	4
P10853 H2B1F_MOUSE	Histone H2B type 1-F/J/L OS=Mus musculus GN=	136.6	37	4
Q64478 H2B1H_MOUSE	Histone H2B type 1-H OS=Mus musculus GN=	136.6	37	4
Q8CGP1 H2B1K_MOUSE	Histone H2B type 1-K OS=Mus musculus GN=	136.6	37	4
P10854 H2B1M_MOUSE	Histone H2B type 1-M OS=Mus musculus GN=	136.6	37	4
Q64525 H2B2B_MOUSE	Histone H2B type 2-B OS=Mus musculus GN=	136.6	37	4
P07214 SPRC_MOUSE	SPARC OS=Mus musculus GN=	135.04	24	4
P43406 ITAV_MOUSE	Integrin alpha-V OS=Mus musculus GN=	132.86	14	4
Q61171 PRDX2_MOUSE	Peroxiredoxin-2 OS=Mus musculus GN=	129.18	27	4
Q64310 SURF4_MOUSE	Surfeit locus protein 4 OS=Mus musculus GN=	127.56	22	4
Q9DBL1 ACDSB_MOUSE	Short/branched chain specific acyl-CoA oxidase OS=Mus musculus GN=	127.15	47	4
Q9DCT2 NDUS3_MOUSE	NADH dehydrogenase [ubiquinone] subunit 3 OS=Mus musculus GN=	125.81	13	4
Q9CXE7 TMED5_MOUSE	Transmembrane emp24 domain-containing protein 5 OS=Mus musculus GN=	124.12	21	4
O08992 SDCB1_MOUSE	Syntenin-1 OS=Mus musculus GN=	124.04	27	4
P97315 CSR1_MOUSE	Cysteine and glycine-rich protein 1 OS=Mus musculus GN=	123.53	46	4
P14148 RL7_MOUSE	60S ribosomal protein L7 OS=Mus musculus GN=	117.96	31	4
Q9D6U8 F162A_MOUSE	Protein FAM162A OS=Mus musculus GN=	117.11	51	4
P0CG50 UBC_MOUSE	Polyubiquitin-C OS=Mus musculus GN=	115.44	22	4
P0CG49 UBB_MOUSE	Polyubiquitin-B OS=Mus musculus GN=	115.44	40	4
P62983 RS27A_MOUSE	Ubiquitin-40S ribosomal protein S2 OS=Mus musculus GN=	115.44	37	4
P62984 RL40_MOUSE	Ubiquitin-60S ribosomal protein L4 OS=Mus musculus GN=	115.44	27	4
Q99J16 RAP1B_MOUSE	Ras-related protein Rap-1b OS=Mus musculus GN=	114.9	34	4
P62835 RAP1A_MOUSE	Ras-related protein Rap-1A OS=Mus musculus GN=	114.9	26	4
O54962 BAF_MOUSE	Barrier-to-autointegration factor OS=Mus musculus GN=	111.12	55	4
P10605 CATB_MOUSE	Cathepsin B OS=Mus musculus GN=	111.07	30	4
Q9D2G2 ODO2_MOUSE	Dihydrolypoyllysine-residue succinyl-CoA synthetase OS=Mus musculus GN=	110.35	35	4
Q9CZU6 CISY_MOUSE	Citrate synthase, mitochondrial OS=Mus musculus GN=	108.32	21	4
Q8BH95 ECHM_MOUSE	Enoyl-CoA hydratase, mitochondrial OS=Mus musculus GN=	106.09	20	4
Q9WTP7 KAD3_MOUSE	GTP:AMP phosphotransferase, mitochondrial OS=Mus musculus GN=	105.03	21	4
P15532 NDKA_MOUSE	Nucleoside diphosphate kinase A (cytosolic) OS=Mus musculus GN=	104.98	43	4
Q9CQ92 FIS1_MOUSE	Mitochondrial fission 1 protein OS=Mus musculus GN=	103.52	39	4
P56135 ATPK_MOUSE	ATP synthase subunit f, mitochondrial OS=Mus musculus GN=	103.42	36	4
O88783 FA5_MOUSE	Coagulation factor V OS=Mus musculus GN=	102.44	10	4
Q60715 P4HA1_MOUSE	Prolyl 4-hydroxylase subunit alpha OS=Mus musculus GN=	101.08	16	4
Q9CRB9 CHCH3_MOUSE	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3 OS=Mus musculus GN=	99.03	33	4
Q9R0P5 DEST_MOUSE	Dextrin OS=Mus musculus GN=	97.52	29	4
Q99PT1 GDIR1_MOUSE	Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=	93.01	28	4
Q7TMF3 NDUAC_MOUSE	NADH dehydrogenase [ubiquinone] subunit 6 OS=Mus musculus GN=	88.86	28	4
Q07235 GDN_MOUSE	Glia-derived nexin OS=Mus musculus GN=	86.54	22	4
O09131 GSTO1_MOUSE	Glutathione S-transferase omega-1 OS=Mus musculus GN=	74.84	26	4
P51863 VA0D1_MOUSE	V-type proton ATPase subunit d 1 OS=Mus musculus GN=	72.57	13	4
Q8BFZ3 ACTBL_MOUSE	Beta-actin-like protein 2 OS=Mus musculus GN=	276.89	69	3
P62874 GBB1_MOUSE	Guanine nucleotide-binding protein beta-1 OS=Mus musculus GN=	174.49	34	3
Q9CQV8 1433B_MOUSE	14-3-3 protein beta/alpha OS=Mus musculus GN=	155.48	30	3
P62821 RAB1A_MOUSE	Ras-related protein Rab-1A OS=Mus musculus GN=	146.8	59	3
P84084 ARF5_MOUSE	ADP-ribosylation factor 5 OS=Mus musculus GN=	146.56	71	3

Q9JKF1 IQGA1_MOUSE	Ras GTPase-activating-like protein	135.47	23	3
P19157 GSTP1_MOUSE	Glutathione S-transferase P 1 OS=	134.43	38	3
P10493 NID1_MOUSE	Nidogen-1 OS=Mus musculus GN=	132.54	19	3
P50543 S10AB_MOUSE	Protein S100-A11 OS=Mus muscu	131.95	78	3
Q60930 VDAC2_MOUSE	Voltage-dependent anion-selective	130.73	18	3
Q8VDN2 AT1A1_MOUSE	Sodium/potassium-transporting AT	128.81	28	3
P62880 GBB2_MOUSE	Guanine nucleotide-binding protein	127.98	29	3
Q08093 CNN2_MOUSE	Calponin-2 OS=Mus musculus GN	126.29	18	3
P68510 1433F_MOUSE	14-3-3 protein eta OS=Mus muscu	123.73	53	3
P61620 S61A1_MOUSE	Protein transport protein Sec61 su	122.41	23	3
Q9CYN9 RENK_MOUSE	Renin receptor OS=Mus musculus	121.99	19	3
Q8BMF4 ODP2_MOUSE	Dihydrolipoyllysine-residue acetyltr	119.27	15	3
Q9CXD9 LRC17_MOUSE	Leucine-rich repeat-containing prot	118.67	19	3
Q9WVJ2 PSD13_MOUSE	26S proteasome non-ATPase regu	117.63	32	3
Q8VEM8 MPCP_MOUSE	Phosphate carrier protein, mitoch	117.42	21	3
P19096 FAS_MOUSE	Fatty acid synthase OS=Mus musc	116.59	10	3
O54734 OST48_MOUSE	Dolichyl-diphosphooligosaccharide	116.1	13	3
P27090 TGFB2_MOUSE	Transforming growth factor beta-2	115.87	14	3
P61027 RAB10_MOUSE	Ras-related protein Rab-10 OS=M	115.87	32	3
P17225 PTBP1_MOUSE	Polypyrimidine tract-binding protein	114.52	17	3
P25444 RS2_MOUSE	40S ribosomal protein S2 OS=Mus	114.32	18	3
Q01730 RSU1_MOUSE	Ras suppressor protein 1 OS=Mus	114.21	43	3
P10833 RRAS_MOUSE	Ras-related protein R-Ras OS=M	113.73	30	3
P70168 IMB1_MOUSE	Importin subunit beta-1 OS=Mus m	113.34	14	3
Q0GNC1 INF2_MOUSE	Inverted formin-2 OS=Mus musculi	112.8	15	3
Q9R087 GPC6_MOUSE	Glypican-6 OS=Mus musculus GN=	112.77	24	3
Q9CQ22 LTOR1_MOUSE	Ragulator complex protein LAMTO	111.96	35	3
P60867 RS20_MOUSE	40S ribosomal protein S20 OS=M	111.21	23	3
Q923D2 BLVRB_MOUSE	Flavin reductase OS=Mus musculi	110.61	23	3
P47911 RL6_MOUSE	60S ribosomal protein L6 OS=Mus	110.19	25	3
Q9Z1Q5 CLIC1_MOUSE	Chloride intracellular channel prote	109.84	36	3
P20108 PRDX3_MOUSE	Thioredoxin-dependent peroxide re	109.36	20	3
P19536 COX5B_MOUSE	Cytochrome c oxidase subunit 5B,	109.24	30	3
P15626 GSTM2_MOUSE	Glutathione S-transferase Mu 2 OS	108.99	43	3
P63323 RS12_MOUSE	40S ribosomal protein S12 OS=M	108.86	41	3
Q91YQ5 RPN1_MOUSE	Dolichyl-diphosphooligosaccharide	108.44	16	3
Q61469 LPP1_MOUSE	Lipid phosphate phosphohydrolase	107.49	25	3
P14869 RLA0_MOUSE	60S acidic ribosomal protein P0 OS	107.32	21	3
Q9WU78 PDC6L_MOUSE	Programmed cell death 6-interactin	106.72	24	3
P99028 QCR6_MOUSE	Cytochrome b-c1 complex subunit	106.2	63	3
P63024 VAMP3_MOUSE	Vesicle-associated membrane prot	106.02	46	3
P28653 PGS1_MOUSE	Biglycan OS=Mus musculus GN=B	105.83	27	3
Q8BH04 PCKGM_MOUSE	Phosphoenolpyruvate carboxykina	104.74	19	3
P35279 RAB6A_MOUSE	Ras-related protein Rab-6A OS=M	104.23	39	3
P35762 CD81_MOUSE	CD81 antigen OS=Mus musculus C	104.22	29	3
Q62465 VAT1_MOUSE	Synaptic vesicle membrane proteir	103.84	15	3
Q8R2G6 CCD80_MOUSE	Coiled-coil domain-containing prote	103.31	10	3
Q9CQH3 NDUB5_MOUSE	NADH dehydrogenase [ubiquinone	102.14	15	3
P30412 PPIC_MOUSE	Peptidyl-prolyl cis-trans isomerase	101.39	19	3
P14131 RS16_MOUSE	40S ribosomal protein S16 OS=M	99.66	27	3
P60843 IF4A1_MOUSE	Eukaryotic initiation factor 4A-I OS=	99.53	18	3
P62827 RAN_MOUSE	GTP-binding nuclear protein Ran C	98.85	16	3
P62270 RS18_MOUSE	40S ribosomal protein S18 OS=M	98.16	30	3
P09671 SODM_MOUSE	Superoxide dismutase [Mn], mitoch	96.59	21	3
P62264 RS14_MOUSE	40S ribosomal protein S14 OS=M	95.11	17	3

O70456 1433S_MOUSE	14-3-3 protein sigma OS=Mus mus	94.96	19	3
P62082 RS7_MOUSE	40S ribosomal protein S7 OS=Mus	94.49	26	3
P21614 VTDB_MOUSE	Vitamin D-binding protein OS=Mus	92.81	21	3
P80317 TCPZ_MOUSE	T-complex protein 1 subunit zeta C	92.62	16	3
Q9DAW9 CNN3_MOUSE	Calponin-3 OS=Mus musculus GN	91.81	23	3
P62702 RS4X_MOUSE	40S ribosomal protein S4, X isofor	91.05	15	3
P07091 S10A4_MOUSE	Protein S100-A4 OS=Mus musculu	91.04	26	3
O55143 AT2A2_MOUSE	Sarcoplasmic/endoplasmic reticulu	89.83	12	3
Q8K3J1 NDUS8_MOUSE	NADH dehydrogenase [ubiquinone	88.76	15	3
Q9EP69 SAC1_MOUSE	Phosphatidylinositide phosphatase	88.42	10	3
Q9R0P3 ESTD_MOUSE	S-formylglutathione hydrolase OS=	85.32	19	3
P61622 ITA11_MOUSE	Integrin alpha-11 OS=Mus muscult	85.14	14	3
Q9ERS2 NDUAD_MOUSE	NADH dehydrogenase [ubiquinone	84.05	21	3
Q06185 ATP5I_MOUSE	ATP synthase subunit e, mitochond	82.61	42	3
Q9QXS6 DREB_MOUSE	Drebrin OS=Mus musculus GN=Dk	81.93	10	3
Q9CQS8 SC61B_MOUSE	Protein transport protein Sec61 sub	80.5	38	3
P97449 AMPN_MOUSE	Aminopeptidase N OS=Mus muscul	80.24	6	3
Q8R5J9 PRAF3_MOUSE	PRA1 family protein 3 OS=Mus mu	78.42	16	3
Q9QUI0 RHOA_MOUSE	Transforming protein RhoA OS=M	78.31	33	3
Q99KF1 TMED9_MOUSE	Transmembrane emp24 domain-co	77.07	16	3
Q8R2Q8 BST2_MOUSE	Bone marrow stromal antigen 2 OS	74.79	12	3
P08228 SODC_MOUSE	Superoxide dismutase [Cu-Zn] OS-	74.13	21	3
Q6PHZ2 KCC2D_MOUSE	Calcium/calmodulin-dependent pro	72.44	14	3
Q9CQW9 IFM3_MOUSE	Interferon-induced transmembrane	70.3	9	3
Q791V5 MTCH2_MOUSE	Mitochondrial carrier homolog 2 OS	62	17	3
Q07456 AMBP_MOUSE	Protein AMBP OS=Mus musculus	57.51	6	3
Q8BFZ9 ERLN2_MOUSE	Erlin-2 OS=Mus musculus GN=Erlin	55.84	21	3
Q61838 A2M_MOUSE	Alpha-2-macroglobulin OS=Mus m	53.7	20	3
P48722 HS74L_MOUSE	Heat shock 70 kDa protein 4L OS=	45.77	5	3
A2ASS6 TITIN_MOUSE	Titin OS=Mus musculus GN=Ttn P	40.13	3	3
P63260 ACTG_MOUSE	Actin, cytoplasmic 2 OS=Mus mus	363.12	92	2
P62737 ACTA_MOUSE	Actin, aortic smooth muscle OS=M	315.47	81	2
P63268 ACTH_MOUSE	Actin, gamma-enteric smooth mus	315.47	81	2
Q7TMM9 TBB2A_MOUSE	Tubulin beta-2A chain OS=Mus mu	280.71	63	2
P02088 HBB1_MOUSE	Hemoglobin subunit beta-1 OS=M	177.89	50	2
P61750 ARF4_MOUSE	ADP-ribosylation factor 4 OS=Mus	165.61	57	2
P51881 ADT2_MOUSE	ADP/ATP translocase 2 OS=Mus r	163.06	35	2
P61205 ARF3_MOUSE	ADP-ribosylation factor 3 OS=Mus	155.84	65	2
P84078 ARF1_MOUSE	ADP-ribosylation factor 1 OS=Mus	155.84	60	2
P21107 TPM3_MOUSE	Tropomyosin alpha-3 chain OS=M	148.08	33	2
P58771 TPM1_MOUSE	Tropomyosin alpha-1 chain OS=M	146.22	36	2
P08752 GNAI2_MOUSE	Guanine nucleotide-binding protein	136.24	33	2
P02104 HBE_MOUSE	Hemoglobin subunit epsilon-Y2 OS	133.34	27	2
P84244 H33_MOUSE	Histone H3.3 OS=Mus musculus G	130.48	54	2
Q03350 TSP2_MOUSE	Thrombospondin-2 OS=Mus musc	128.66	23	2
P35278 RAB5C_MOUSE	Ras-related protein Rab-5C OS=M	126.58	35	2
Q9D1G1 RAB1B_MOUSE	Ras-related protein Rab-1B OS=M	122.28	49	2
O35459 ECH1_MOUSE	Delta(3,5)-Delta(2,4)-dienoyl-CoA i	119.25	23	2
Q91V61 SFXN3_MOUSE	Sideroflexin-3 OS=Mus musculus C	117.24	45	2
P61021 RAB5B_MOUSE	Ras-related protein Rab-5B OS=M	114.26	22	2
Q01853 TERA_MOUSE	Transitional endoplasmic reticulum	112.67	19	2
Q9JK53 PRELP_MOUSE	Prolargin OS=Mus musculus GN=F	111.9	14	2
Q60931 VDAC3_MOUSE	Voltage-dependent anion-selective	109.35	22	2
Q8BMD8 SCMC1_MOUSE	Calcium-binding mitochondrial carr	105.08	16	2
P85094 ISC2A_MOUSE	Isochorismatase domain-containing	104.94	31	2

Q6ZQI3 MLEC_MOUSE	Malectin OS=Mus musculus GN=M	103.42	22	2
P62830 RL23_MOUSE	60S ribosomal protein L23 OS=M	102.63	34	2
P39876 TIMP3_MOUSE	Metalloproteinase inhibitor 3 OS=M	102.58	11	2
Q9CQM2 ERD22_MOUSE	ER lumen protein retaining recepto	101.35	15	2
P68040 GBLP_MOUSE	Guanine nucleotide-binding protein	101.13	20	2
P62196 PRS8_MOUSE	26S protease regulatory subunit 8	100.68	29	2
Q9CQ65 MTAP_MOUSE	S-methyl-5'-thioadenosine phospho	98.09	13	2
Q9CQN1 TRAP1_MOUSE	Heat shock protein 75 kDa, mitoch	97.72	10	2
Q9DB05 SNAA_MOUSE	Alpha-soluble NSF attachment pro	97.66	14	2
O70251 EF1B_MOUSE	Elongation factor 1-beta OS=Mus r	97.03	16	2
Q78IK2 USMG5_MOUSE	Up-regulated during skeletal muscl	96.61	43	2
O08547 SC22B_MOUSE	Vesicle-trafficking protein SEC22b	96.39	26	2
Q9DCJ5 NDUA8_MOUSE	NADH dehydrogenase [ubiquinone	96.35	40	2
Q9CYR0 SSBP_MOUSE	Single-stranded DNA-binding prote	95.48	18	2
O35640 ANXA8_MOUSE	Annexin A8 OS=Mus musculus GN	95.41	18	2
O88456 CPNS1_MOUSE	Calpain small subunit 1 OS=Mus m	94.89	30	2
O35682 MYADM_MOUSE	Myeloid-associated differentiation r	94.64	10	2
Q9CR62 M2OM_MOUSE	Mitochondrial 2-oxoglutarate/malat	94.6	11	2
P58022 LOXL2_MOUSE	Lysyl oxidase homolog 2 OS=Mus	94.52	6	2
Q9CY50 SSRA_MOUSE	Translocon-associated protein sub	93.99	20	2
Q9CXI5 MANF_MOUSE	Mesencephalic astrocyte-derived n	93.77	36	2
Q62425 NDUA4_MOUSE	NADH dehydrogenase [ubiquinone	93.05	27	2
Q9R118 HTRA1_MOUSE	Serine protease HTRA1 OS=Mus r	93.04	9	2
Q61937 NPM_MOUSE	Nucleophosmin OS=Mus musculus	92.11	32	2
P09535 IGF2_MOUSE	Insulin-like growth factor II OS=M	91.89	23	2
Q9CYL5 GAPR1_MOUSE	Golgi-associated plant pathogenes	91.45	17	2
P27659 RL3_MOUSE	60S ribosomal protein L3 OS=Mus	90.38	14	2
Q9D8E6 RL4_MOUSE	60S ribosomal protein L4 OS=Mus	89.83	15	2
Q9QXT0 CNPY2_MOUSE	Protein canopy homolog 2 OS=M	88.9	23	2
P13020 GELS_MOUSE	Gelsolin OS=Mus musculus GN=G	88.48	18	2
P17710 HXK1_MOUSE	Hexokinase-1 OS=Mus musculus	88.14	6	2
Q8K482 EMIL2_MOUSE	EMILIN-2 OS=Mus musculus GN=	86.29	8	2
Q9D0S9 HINT2_MOUSE	Histidine triad nucleotide-binding p	86.18	31	2
P62245 RS15A_MOUSE	40S ribosomal protein S15a OS=M	86.18	34	2
P51174 ACADL_MOUSE	Long-chain specific acyl-CoA dehy	85.46	21	2
P62849 RS24_MOUSE	40S ribosomal protein S24 OS=M	84.93	20	2
Q99KV1 DJB11_MOUSE	DnaJ homolog subfamily B membe	84.65	11	2
P62843 RS15_MOUSE	40S ribosomal protein S15 OS=M	83.57	15	2
Q91VR2 ATPG_MOUSE	ATP synthase subunit gamma, mit	83.44	7	2
P06745 G6PI_MOUSE	Glucose-6-phosphate isomerase C	83.39	9	2
Q8BIJ6 SYIM_MOUSE	Isoleucyl-tRNA synthetase, mitoch	82.88	10	2
P67984 RL22_MOUSE	60S ribosomal protein L22 OS=M	82.75	27	2
P97807 FUMH_MOUSE	Fumarate hydratase, mitochondrial	82.72	26	2
P36536 SAR1A_MOUSE	GTP-binding protein SAR1a OS=M	82.69	16	2
Q9CQE8 CN166_MOUSE	UPF0568 protein C14orf166 homo	82.45	19	2
Q8BG05 ROA3_MOUSE	Heterogeneous nuclear ribonucleo	81.66	10	2
Q9CQA3 DHSB_MOUSE	Succinate dehydrogenase [ubiquin	80.72	9	2
P61804 DAD1_MOUSE	Dolichyl-diphosphooligosaccharide	80.15	19	2
Q9CQZ6 NDUB3_MOUSE	NADH dehydrogenase [ubiquinone	80.01	27	2
Q99KIO ACON_MOUSE	Aconitate hydratase, mitochondrial	79.04	10	2
Q921X9 PDIA5_MOUSE	Protein disulfide-isomerase A5 OS	78.78	16	2
Q64133 AOFA_MOUSE	Amine oxidase [flavin-containing] A	78.48	10	2
Q99L13 3HIDH_MOUSE	3-hydroxyisobutyrate dehydrogena	77.24	9	2
Q9CR68 UCRI_MOUSE	Cytochrome b-c1 complex subunit	77.2	24	2
P29391 FRIL1_MOUSE	Ferritin light chain 1 OS=Mus musc	76.87	21	2

Q9CXW4 RL11_MOUSE	60S ribosomal protein L11 OS=Mus musculus	76.66	15	2
Q9D8N0 EF1G_MOUSE	Elongation factor 1-gamma OS=Mus musculus	76.14	11	2
Q9JM76 ARPC3_MOUSE	Actin-related protein 2/3 complex subunit 3 OS=Mus musculus	75.8	13	2
Q9CPP6 NDUA5_MOUSE	NADH dehydrogenase [ubiquinone] subunit 5 OS=Mus musculus	75.54	25	2
Q9CQR4 ACO13_MOUSE	Acyl-coenzyme A thioesterase 13 OS=Mus musculus	75.28	43	2
P10404 ENV1_MOUSE	MLV-related proviral Env polyprotein OS=Mus musculus	75.22	11	2
P11370 ENV2_MOUSE	Retrovirus-related Env polyprotein OS=Mus musculus	75.22	2	2
P61022 CHP1_MOUSE	Calcium-binding protein p22 OS=Mus musculus	75.13	11	2
Q61207 SAP_MOUSE	Sulfated glycoprotein 1 OS=Mus musculus	74.74	10	2
O88569 ROA2_MOUSE	Heterogeneous nuclear ribonucleoprotein A2 OS=Mus musculus	74.13	20	2
Q61702 ITIH1_MOUSE	Inter-alpha-trypsin inhibitor heavy chain 1 OS=Mus musculus	73.75	4	2
Q9Z2I9 SUCB1_MOUSE	Succinyl-CoA ligase [ADP-forming] subunit beta OS=Mus musculus	72.79	12	2
P28301 LYOX_MOUSE	Protein-lysine 6-oxidase OS=Mus musculus	72.7	8	2
P46935 NEDD4_MOUSE	E3 ubiquitin-protein ligase NEDD4 OS=Mus musculus	72.13	9	2
Q8K4L4 POF1B_MOUSE	Protein POF1B OS=Mus musculus	70.24	5	2
P23927 CRYAB_MOUSE	Alpha-crystallin B chain OS=Mus musculus	70.2	18	2
Q8BKG3 PTK7_MOUSE	Inactive tyrosine-protein kinase 7 OS=Mus musculus	68.51	5	2
Q9DAS9 GBG12_MOUSE	Guanine nucleotide-binding protein gamma-12 OS=Mus musculus	67.59	22	2
Q61425 HCDH_MOUSE	Hydroxyacyl-coenzyme A dehydrogenase OS=Mus musculus	67.29	14	2
P63085 MK01_MOUSE	Mitogen-activated protein kinase 1 OS=Mus musculus	66.66	20	2
Q63844 MK03_MOUSE	Mitogen-activated protein kinase 3 OS=Mus musculus	66.66	10	2
Q2PZL6 FAT4_MOUSE	Protocadherin Fat 4 OS=Mus musculus	65.7	4	2
O09111 NDUBB_MOUSE	NADH dehydrogenase [ubiquinone] subunit beta OS=Mus musculus	65.07	13	2
Q8R2Y8 PTH2_MOUSE	Peptidyl-tRNA hydrolase 2, mitochondrial OS=Mus musculus	64.81	20	2
Q60692 PSB6_MOUSE	Proteasome subunit beta type-6 OS=Mus musculus	64.69	9	2
P63001 RAC1_MOUSE	Ras-related C3 botulinum toxin substrate 1 OS=Mus musculus	64.06	20	2
Q9CZY3 UB2V1_MOUSE	Ubiquitin-conjugating enzyme E2 variant 1 OS=Mus musculus	63.86	35	2
Q9CPR4 RL17_MOUSE	60S ribosomal protein L17 OS=Mus musculus	63.81	9	2
Q9CZD3 SYG_MOUSE	Glycyl-tRNA synthetase OS=Mus musculus	63.72	6	2
Q3UIU2 NDUB6_MOUSE	NADH dehydrogenase [ubiquinone] subunit beta OS=Mus musculus	63.65	13	2
Q9CZW5 TOM70_MOUSE	Mitochondrial import receptor subunit TOM70 OS=Mus musculus	63.56	11	2
P12032 TIMP1_MOUSE	Metalloproteinase inhibitor 1 OS=Mus musculus	63.55	11	2
Q9JHR7 IDE_MOUSE	Insulin-degrading enzyme OS=Mus musculus	63.22	6	2
Q920A5 RISC_MOUSE	Retinoid-inducible serine carboxypeptidase OS=Mus musculus	62.58	11	2
P55002 MFAP2_MOUSE	Microfibrillar-associated protein 2 OS=Mus musculus	61.8	9	2
P08905 LYZ2_MOUSE	Lysozyme C-2 OS=Mus musculus	61.51	16	2
Q9D1M7 FKB11_MOUSE	Peptidyl-prolyl cis-trans isomerase 11 OS=Mus musculus	61.33	10	2
Q9QUM9 PSA6_MOUSE	Proteasome subunit alpha type-6 OS=Mus musculus	60.75	14	2
P47754 CAZA2_MOUSE	F-actin-capping protein subunit alpha OS=Mus musculus	59.89	13	2
P59999 ARPC4_MOUSE	Actin-related protein 2/3 complex subunit 4 OS=Mus musculus	59.63	18	2
P00493 HPRT_MOUSE	Hypoxanthine-guanine phosphoribosyltransferase OS=Mus musculus	59.29	17	2
Q99M71 EPDR1_MOUSE	Mammalian ependymin-related protein OS=Mus musculus	58.98	9	2
Q61941 NNTM_MOUSE	NAD(P) transhydrogenase, mitochondrial OS=Mus musculus	54.41	4	2
Q9CZ13 QCR1_MOUSE	Cytochrome b-c1 complex subunit 1 OS=Mus musculus	53.81	7	2
Q07813 BAX_MOUSE	Apoptosis regulator BAX OS=Mus musculus	52.34	12	2
O08999 LTBP2_MOUSE	Latent-transforming growth factor binding protein 2 OS=Mus musculus	50.49	4	2
Q9QZE5 COPG_MOUSE	Coatomer subunit gamma OS=Mus musculus	50.39	6	2
O35166 GOSR2_MOUSE	Golgi SNAP receptor complex member 2 OS=Mus musculus	44.67	13	2
Q04857 CO6A1_MOUSE	Collagen alpha-1(VI) chain OS=Mus musculus	44.59	6	2
Q52KG5 KIF26A_MOUSE	Kinesin-like protein KIF26A OS=Mus musculus	43.45	4	2
P62331 ARF6_MOUSE	ADP-ribosylation factor 6 OS=Mus musculus	40.97	21	2
Q62315 JARD2_MOUSE	Protein Jumonji OS=Mus musculus	40.51	3	2
Q6GQT0 CC14A_MOUSE	Dual specificity protein phosphatase 14 OS=Mus musculus	39.51	2	2
Q5GIG6 TNI3K_MOUSE	Serine/threonine-protein kinase TNI3 OS=Mus musculus	38.89	4	2
P80315 TCPD_MOUSE	T-complex protein 1 subunit delta OS=Mus musculus	38.75	10	2

Q9CQE1 NPS3A_MOUSE	Protein NipSnap homolog 3A OS=M	37.78	17	2
P28741 KIF3A_MOUSE	Kinesin-like protein KIF3A OS=Mus	37.2	9	2
Q8BQM9 MD12L_MOUSE	Mediator of RNA polymerase II tran	36.65	3	2
Q8R0P8 ABHD8_MOUSE	Abhydrolase domain-containing pro	36.05	5	2
Q99LP6 GRPE1_MOUSE	GrpE protein homolog 1, mitochon	35.76	9	2
Q9ET54 PALLD_MOUSE	Palladin OS=Mus musculus GN=P	35.55	4	2
P26041 MOES_MOUSE	Moesin OS=Mus musculus GN=Ms	34.74	7	2
Q9QYX7 PCLO_MOUSE	Protein piccolo OS=Mus musculus	32.29	4	2
Q3V0M2 LRC36_MOUSE	Leucine-rich repeat-containing prot	32.25	3	2
P49025 CTRO_MOUSE	Citron Rho-interacting kinase OS=	31.72	3	2
P97433 RGNEF_MOUSE	Rho-guanine nucleotide exchange	31.29	3	2
Q8BV57 SRCRL_MOUSE	Scavenger receptor cysteine-rich d	30.76	2	2
Q9JKY5 HIP1R_MOUSE	Huntingtin-interacting protein 1-rela	30.61	3	2
Q8BXR9 OSBL6_MOUSE	Oxysterol-binding protein-related p	30.55	2	2
P58545 BTBD3_MOUSE	BTB/POZ domain-containing prote	29.84	3	2
Q6A026 PDS5A_MOUSE	Sister chromatid cohesion protein P	29.42	4	2
A2AAJ9 OBSCN_MOUSE	Obscurin OS=Mus musculus GN=C	29	2	2
Q7TN37 TRPM4_MOUSE	Transient receptor potential cation	29	5	2
Q99MZ6 MYO7B_MOUSE	Myosin-VIIb OS=Mus musculus GN	28.07	9	2
Q9D0K0 TBCD7_MOUSE	TBC1 domain family member 7 OS	27.8	4	2
Q8K4G1 LTBP4_MOUSE	Latent-transforming growth factor b	27.49	2	2

**Table A1.8 Bridge ECM Protein Identifications.** List of all proteins identified in Bridge ECM with corresponding accession, description, PEAKS score, unique peptide numbers, and coverage (in %).

Accession	Description	Score	Coverage (%)	#Unique
P02768 ALBU_HUMAN	Serum albumin OS=Homo sapiens	380.41	61	45
P01308 INS_HUMAN	Insulin OS=Homo sapiens GN=INS	246.91	55	11
P01008 ANT3_HUMAN	Antithrombin-III OS=Homo sapiens	203.89	42	10
P02753 RET4_HUMAN	Retinol-binding protein 4 OS=Homo	242.54	42	7
P02774 VTDB_HUMAN	Vitamin D-binding protein OS=Hom	240.19	40	7
P02647 APOA1_HUMAN	Apolipoprotein A-I OS=Homo sapien	186.29	39	4
Q16270 IBP7_HUMAN	Insulin-like growth factor-binding pro	158.22	38	4
P05121 PAI1_HUMAN	Plasminogen activator inhibitor 1 OS	156.04	33	4
P02751 FINC_HUMAN	Fibronectin OS=Homo sapiens GN=	154.81	14	4
Q15582 BGH3_HUMAN	Transforming growth factor-beta-ind	153.91	27	4
P61769 B2MG_HUMAN	Beta-2-microglobulin OS=Homo sap	139.26	59	4
P09486 SPRC_HUMAN	SPARC OS=Homo sapiens GN=SP	180.39	41	3
P01024 CO3_HUMAN	Complement C3 OS=Homo sapiens	162.77	16	3
P69905 HBA_HUMAN	Hemoglobin subunit alpha OS=Hom	159.17	53	3
P06727 APOA4_HUMAN	Apolipoprotein A-IV OS=Homo sapie	151.78	20	3
P08697 A2AP_HUMAN	Alpha-2-antiplasmin OS=Homo sapi	145.85	21	3
P02656 APOC3_HUMAN	Apolipoprotein C-III OS=Homo sapie	138.57	25	3
Q15063 POSTN_HUMAN	Periostin OS=Homo sapiens GN=PC	127.09	23	3
P01861 IGHG4_HUMAN	Ig gamma-4 chain C region OS=Hor	105.87	25	3
P01859 IGHG2_HUMAN	Ig gamma-2 chain C region OS=Hor	105.87	27	3
P01857 IGHG1_HUMAN	Ig gamma-1 chain C region OS=Hor	105.87	28	3
P0C0L4 CO4A_HUMAN	Complement C4-A OS=Homo sapie	126.79	17	2
P0C0L5 CO4B_HUMAN	Complement C4-B OS=Homo sapie	126.79	17	2
P05546 HEP2_HUMAN	Heparin cofactor 2 OS=Homo sapie	95.37	2	2
Q9UNH5 CC14A_HUMAN	Dual specificity protein phosphatase	44.58	8	2



**Table A1.9 H9 hESC CMTX Protein Identifications.** List of all proteins identified in CMTX from H9 hESCs with corresponding accession, description, PEAKS score, unique peptide numbers, and coverage (in %).

Accession	Description	Score	Coverage (%)	#Unique
P18206 VINC_HUMAN	Vinculin OS=Homo sapiens GN=VCL PE	336.02	71	46
P49327 FAS_HUMAN	Fatty acid synthase OS=Homo sapiens G	335.58	49	39
P55072 TERA_HUMAN	Transitional endoplasmic reticulum ATPa	309.23	62	34
P04406 G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogen	363.29	78	32
Q13813 SPTA2_HUMAN	Spectrin alpha chain, brain OS=Homo sa	310.79	58	32
P21333 FLNA_HUMAN	Filamin-A OS=Homo sapiens GN=FLNA	302.94	40	32
P02649 APOE_HUMAN	Apolipoprotein E OS=Homo sapiens GN=	308.11	90	28
P62258 1433E_HUMAN	14-3-3 protein epsilon OS=Homo sapiens	320.22	72	26
P35579 MYH9_HUMAN	Myosin-9 OS=Homo sapiens GN=MYH9	300.44	56	25
P14625 ENPL_HUMAN	Endoplasmic reticulum protein OS=Homo sapiens GN=HS	284.56	64	24
P13639 EF2_HUMAN	Elongation factor 2 OS=Homo sapiens G	274.58	61	24
P53396 ACLY_HUMAN	ATP-citrate synthase OS=Homo sapiens	293.82	59	23
P07900 HS90A_HUMAN	Heat shock protein HSP 90-alpha OS=H	389.97	83	22
P07195 LDHB_HUMAN	L-lactate dehydrogenase B chain OS=Hc	303.38	72	21
P08670 VIME_HUMAN	Vimentin OS=Homo sapiens GN=VIM PE	265.5	66	21
P14618 KPYM_HUMAN	Pyruvate kinase isozymes M1/M2 OS=H	290.21	81	20
P04075 ALDOA_HUMAN	Fructose-bisphosphate aldolase A OS=H	262.37	69	20
P08238 HS90B_HUMAN	Heat shock protein HSP 90-beta OS=Ho	413.63	89	19
O75874 IDHC_HUMAN	Isocitrate dehydrogenase [NADP] cytopl	321.85	75	19
P30041 PRDX6_HUMAN	Peroxiredoxin-6 OS=Homo sapiens GN=	245.25	76	19
P63104 1433Z_HUMAN	14-3-3 protein zeta/delta OS=Homo sapi	304.18	84	18
P00338 LDHA_HUMAN	L-lactate dehydrogenase A chain OS=Hc	289.55	58	18
P13010 XRCC5_HUMAN	X-ray repair cross-complementing protei	251.16	66	18
P23142 FBLN1_HUMAN	Fibulin-1 OS=Homo sapiens GN=FBLN1	246.74	42	18
P62805 H4_HUMAN	Histone H4 OS=Homo sapiens GN=HIST	236.13	58	18
P68104 EF1A1_HUMAN	Elongation factor 1-alpha 1 OS=Homo sa	301.38	64	17
Q5VTE0 EF1A3_HUMAN	Putative elongation factor 1-alpha-like 3	301.38	62	17
P50454 SERPH_HUMAN	Serpin H1 OS=Homo sapiens GN=SERP	284.9	79	17
P07355 ANXA2_HUMAN	Annexin A2 OS=Homo sapiens GN=ANX	282.38	75	17
P06733 ENOA_HUMAN	Alpha-enolase OS=Homo sapiens GN=E	271.08	71	17
P08758 ANXA5_HUMAN	Annexin A5 OS=Homo sapiens GN=ANX	267.87	71	17
Q9HB71 CYBP_HUMAN	Calcyclin-binding protein OS=Homo sapi	247.66	80	17
P35580 MYH10_HUMAN	Myosin-10 OS=Homo sapiens GN=MYH	291.87	55	16
P62195 PRS8_HUMAN	26S protease regulatory subunit 8 OS=H	268.24	71	16
P29401 TKT_HUMAN	Transketolase OS=Homo sapiens GN=T	267.48	58	16
Q01995 TAGL_HUMAN	Transgelin OS=Homo sapiens GN=TAG	255.39	91	16
O75369 FLNB_HUMAN	Filamin-B OS=Homo sapiens GN=FLNB	249.62	37	16
P61247 RS3A_HUMAN	40S ribosomal protein S3a OS=Homo sa	247.05	65	16
P12956 XRCC6_HUMAN	X-ray repair cross-complementing protei	241.39	58	16
Q99623 PHB2_HUMAN	Prohibitin-2 OS=Homo sapiens GN=PHE	236.99	66	16
P63261 ACTG_HUMAN	Actin, cytoplasmic 2 OS=Homo sapiens	411.37	89	15
P12814 ACTN1_HUMAN	Alpha-actinin-1 OS=Homo sapiens GN=	288.91	71	15
P19338 NUCL_HUMAN	Nucleolin OS=Homo sapiens GN=NCL F	283.04	74	15
P22314 UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme	275.66	50	15
P11021 GRP78_HUMAN	78 kDa glucose-regulated protein OS=Hc	263.96	54	15
P05455 LA_HUMAN	Lupus La protein OS=Homo sapiens GN	262.72	65	14
Q01105 SET_HUMAN	Protein SET OS=Homo sapiens GN=SE	253.98	53	14
P49321 NASP_HUMAN	Nuclear autoantigenic sperm protein OS	238.83	57	14
P31939 PUR9_HUMAN	Bifunctional purine biosynthesis protein F	227.41	52	14
Q92626 PXDN_HUMAN	Peroxidasin homolog OS=Homo sapiens	224.22	34	14
P46777 RL5_HUMAN	60S ribosomal protein L5 OS=Homo sap	216.48	56	14
P60174 TPIS_HUMAN	Triosephosphate isomerase OS=Homo s	247.24	68	13
P62424 RL7A_HUMAN	60S ribosomal protein L7a OS=Homo sa	245.96	73	13
P28074 PSB5_HUMAN	Proteasome subunit beta type-5 OS=Hor	239.92	48	13

P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A OS=	238.61	74	13
P23396	RS3_HUMAN	40S ribosomal protein S3 OS=Homo sap	214.29	71	13
Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB OS=Homo	194.72	37	13
P29692	EF1D_HUMAN	Elongation factor 1-delta OS=Homo sapi	191.68	63	13
P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein OS=	285.01	63	12
P12268	IMDH2_HUMAN	Inosine-5'-monophosphate dehydrogena	248.93	62	12
P15311	EZRI_HUMAN	Ezrin OS=Homo sapiens GN=EZR PE=1	242.92	65	12
Q15008	PSMD6_HUMAN	26S proteasome non-ATPase regulatory	225.22	59	12
P62906	RL10A_HUMAN	60S ribosomal protein L10a OS=Homo s	220.28	51	12
Q01518	CAP1_HUMAN	Adenylyl cyclase-associated protein 1 OS	219.12	64	12
P10909	CLUS_HUMAN	Clusterin OS=Homo sapiens GN=CLU P	218.1	47	12
P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 OS	211.9	45	12
P78371	TCPB_HUMAN	T-complex protein 1 subunit beta OS=Hc	206.5	63	12
P50990	TCPQ_HUMAN	T-complex protein 1 subunit theta OS=H	197.99	61	12
P62269	RS18_HUMAN	40S ribosomal protein S18 OS=Homo sa	180.58	65	12
Q9BWD1	THIC_HUMAN	Acetyl-CoA acetyltransferase, cytosolic C	171.83	57	12
O14818	PSA7_HUMAN	Proteasome subunit alpha type-7 OS=Hc	283.39	78	11
P51665	PSD7_HUMAN	26S proteasome non-ATPase regulatory	262.72	63	11
P34932	HSP74_HUMAN	Heat shock 70 kDa protein 4 OS=Homo	258.03	61	11
P05067	A4_HUMAN	Amyloid beta A4 protein OS=Homo sapi	245.23	42	11
P06748	NPM_HUMAN	Nucleophosmin OS=Homo sapiens GN=	244.29	58	11
Q9BT78	CSN4_HUMAN	COP9 signalosome complex subunit 4 O	228.48	65	11
Q15019	SEPT2_HUMAN	Septin-2 OS=Homo sapiens GN=SEPT2	227.76	68	11
P62277	RS13_HUMAN	40S ribosomal protein S13 OS=Homo sa	210.38	60	11
O00231	PSD11_HUMAN	26S proteasome non-ATPase regulatory	208.69	45	11
P33993	MCM7_HUMAN	DNA replication licensing factor MCM7 C	197.51	53	11
Q14152	EIF3A_HUMAN	Eukaryotic translation initiation factor 3 s	193.07	29	11
P31948	STIP1_HUMAN	Stress-induced-phosphoprotein 1 OS=Hc	189.36	47	11
Q01082	SPTB2_HUMAN	Spectrin beta chain, brain 1 OS=Homo s	187.11	24	11
P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 OS=Hom	187.11	44	11
O43175	SERA_HUMAN	D-3-phosphoglycerate dehydrogenase O	226.38	46	10
P08865	RSSA_HUMAN	40S ribosomal protein SA OS=Homo sap	217.03	50	10
P62333	PRS10_HUMAN	26S protease regulatory subunit 10B OS	204.95	63	10
P35998	PRS7_HUMAN	26S protease regulatory subunit 7 OS=H	193.65	49	10
P52209	6PGD_HUMAN	6-phosphogluconate dehydrogenase, de	183.14	45	10
P05388	RLA0_HUMAN	60S acidic ribosomal protein P0 OS=Hor	177.82	48	10
P49368	TCPG_HUMAN	T-complex protein 1 subunit gamma OS=	158.53	31	10
P61254	RL26_HUMAN	60S ribosomal protein L26 OS=Homo sa	145.76	63	10
P07437	TBB5_HUMAN	Tubulin beta chain OS=Homo sapiens G	349.97	77	9
P09211	GSTP1_HUMAN	Glutathione S-transferase P OS=Homo s	238.92	68	9
P27348	1433T_HUMAN	14-3-3 protein theta OS=Homo sapiens C	231.58	77	9
P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein	228.4	68	9
Q04917	1433F_HUMAN	14-3-3 protein eta OS=Homo sapiens GN	220.77	63	9
Q9Y490	TLN1_HUMAN	Talin-1 OS=Homo sapiens GN=TLN1 PE	212.9	47	9
P04792	HSPB1_HUMAN	Heat shock protein beta-1 OS=Homo sap	205.19	68	9
P62826	RAN_HUMAN	GTP-binding nuclear protein Ran OS=Hc	205.06	54	9
Q9H9Z2	LN28A_HUMAN	Protein lin-28 homolog A OS=Homo sapi	202.17	54	9
Q08431	MFGM_HUMAN	Lactadherin OS=Homo sapiens GN=MFG	201.22	32	9
P11047	LAMC1_HUMAN	Laminin subunit gamma-1 OS=Homo sa	190.38	26	9
P17980	PRS6A_HUMAN	26S protease regulatory subunit 6A OS=	180.2	57	9
P25391	LAMA1_HUMAN	Laminin subunit alpha-1 OS=Homo sapi	175.98	19	9
P26641	EF1G_HUMAN	Elongation factor 1-gamma OS=Homo s	157.43	36	9
P61160	ARP2_HUMAN	Actin-related protein 2 OS=Homo sapien	154.07	43	9
Q9Y617	SERC_HUMAN	Phosphoserine aminotransferase OS=Hc	129.68	38	9
O43707	ACTN4_HUMAN	Alpha-actinin-4 OS=Homo sapiens GN=	286.21	68	8

P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain OS=Homo s	271.24	69	8
P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 OS=Hc	233.19	60	8
P31946	1433B_HUMAN	14-3-3 protein beta/alpha OS=Homo sap	228.19	62	8
P07737	PROF1_HUMAN	Profilin-1 OS=Homo sapiens GN=PFN1	220.45	69	8
P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoprotein	207.89	56	8
Q92598	HS105_HUMAN	Heat shock protein 105 kDa OS=Homo s	207.71	44	8
P60900	PSA6_HUMAN	Proteasome subunit alpha type-6 OS=Hc	202.72	53	8
Q9Y224	CN166_HUMAN	UPF0568 protein C14orf166 OS=Homo s	197.1	45	8
P62314	SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1 C	188.31	65	8
Q9Y265	RUVB1_HUMAN	RuvB-like 1 OS=Homo sapiens GN=RUV	188.12	62	8
Q9Y4L1	HYOU1_HUMAN	Hypoxia up-regulated protein 1 OS=Hom	185.61	39	8
Q9Y266	NUDC_HUMAN	Nuclear migration protein nudC OS=Hom	180.71	58	8
P20618	PSB1_HUMAN	Proteasome subunit beta type-1 OS=Hor	178.86	51	8
Q9P289	MST4_HUMAN	Serine/threonine-protein kinase MST4 O	172.08	30	8
P07942	LAMB1_HUMAN	Laminin subunit beta-1 OS=Homo sapien	163.14	32	8
P62249	RS16_HUMAN	40S ribosomal protein S16 OS=Homo sa	162	46	8
Q12906	ILF3_HUMAN	Interleukin enhancer-binding factor 3 OS	158.13	32	8
P40227	TCPZ_HUMAN	T-complex protein 1 subunit zeta OS=Hc	157.28	40	8
Q15907	RB11B_HUMAN	Ras-related protein Rab-11B OS=Homo	134.75	48	8
Q99613	EIF3C_HUMAN	Eukaryotic translation initiation factor 3 s	106.16	16	8
Q00610	CLH1_HUMAN	Clathrin heavy chain 1 OS=Homo sapien	262.2	47	7
P12277	KCRB_HUMAN	Creatine kinase B-type OS=Homo sapien	228.22	54	7
P32119	PRDX2_HUMAN	Peroxiredoxin-2 OS=Homo sapiens GN=	197.38	69	7
Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6 OS=Hom	193.64	44	7
P22234	PUR6_HUMAN	Multifunctional protein ADE2 OS=Homo s	190.82	46	7
P43686	PRS6B_HUMAN	26S protease regulatory subunit 6B OS=	189.68	56	7
P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-ri	188.3	44	7
P26038	MOES_HUMAN	Moesin OS=Homo sapiens GN=MSN PE	187.8	51	7
O60664	PLIN3_HUMAN	Perilipin-3 OS=Homo sapiens GN=PLIN3	185.14	41	7
O43809	CPSF5_HUMAN	Cleavage and polyadenylation specificity	179.4	46	7
P25789	PSA4_HUMAN	Proteasome subunit alpha type-4 OS=Hc	173.83	42	7
Q9UUK9	NUDT5_HUMAN	ADP-sugar pyrophosphatase OS=Homo	169.15	35	7
Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-contain	168.24	35	7
P37837	TALDO_HUMAN	Transaldolase OS=Homo sapiens GN=T	160.44	39	7
P14543	NID1_HUMAN	Nidogen-1 OS=Homo sapiens GN=NID1	159.74	40	7
P11940	PABP1_HUMAN	Polyadenylate-binding protein 1 OS=Hor	158.35	42	7
Q02790	FKBP4_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP	157.52	34	7
P62081	RS7_HUMAN	40S ribosomal protein S7 OS=Homo sap	157.04	39	7
P09661	RU2A_HUMAN	U2 small nuclear ribonucleoprotein A' OS	156.58	28	7
P02751	FINC_HUMAN	Fibronectin OS=Homo sapiens GN=FN1	155.38	19	7
P39019	RS19_HUMAN	40S ribosomal protein S19 OS=Homo sa	150.74	68	7
Q99832	TCPH_HUMAN	T-complex protein 1 subunit eta OS=Hor	149.16	45	7
Q9Y230	RUVB2_HUMAN	RuvB-like 2 OS=Homo sapiens GN=RUV	146.97	29	7
Q9Y310	RTCB_HUMAN	tRNA-splicing ligase RtcB homolog OS=	143.49	34	7
P25786	PSA1_HUMAN	Proteasome subunit alpha type-1 OS=Hc	141.46	35	7
P54577	SYYC_HUMAN	Tyrosyl-tRNA synthetase, cytoplasmic O	141.08	46	7
O15144	ARPC2_HUMAN	Actin-related protein 2/3 complex subuni	139.1	40	7
P09486	SPRC_HUMAN	SPARC OS=Homo sapiens GN=SPARC	135.89	24	7
P06753	TPM3_HUMAN	Tropomyosin alpha-3 chain OS=Homo s	293.76	60	6
P07910	HNRPC_HUMAN	Heterogeneous nuclear ribonucleoprotein	214.86	53	6
P61981	1433G_HUMAN	14-3-3 protein gamma OS=Homo sapien	213.26	63	6
P28066	PSA5_HUMAN	Proteasome subunit alpha type-5 OS=Hc	207.13	60	6
P02792	FRIL_HUMAN	Ferritin light chain OS=Homo sapiens GN	203.6	51	6
Q13162	PRDX4_HUMAN	Peroxiredoxin-4 OS=Homo sapiens GN=	199.84	52	6
Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase OS=H	195.71	58	6

P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 OS=Homo sa	192.74	61	6
P35241	RADI_HUMAN	Radixin OS=Homo sapiens GN=RDX PE	188.72	44	6
P09972	ALDOC_HUMAN	Fructose-bisphosphate aldolase C OS=H	188.17	62	6
P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform OS=	187.43	51	6
P48643	TCPE_HUMAN	T-complex protein 1 subunit epsilon OS=	183.95	72	6
P25398	RS12_HUMAN	40S ribosomal protein S12 OS=Homo sa	182.76	80	6
O00299	CLIC1_HUMAN	Chloride intracellular channel protein 1 C	179.56	51	6
Q99598	TSNAX_HUMAN	Translin-associated protein X OS=Homo	178.92	57	6
P50991	TCPD_HUMAN	T-complex protein 1 subunit delta OS=H	177.82	49	6
P67809	YBOX1_HUMAN	Nuclease-sensitive element-binding prot	176.18	38	6
Q06830	PRDX1_HUMAN	Peroxiredoxin-1 OS=Homo sapiens GN=	175.86	54	6
Q16851	UGPA_HUMAN	UTP--glucose-1-phosphate uridylyltransf	173.41	43	6
Q99536	VAT1_HUMAN	Synaptic vesicle membrane protein VAT1	172.83	66	6
P62750	RL23A_HUMAN	60S ribosomal protein L23a OS=Homo s	170.76	50	6
P49720	PSB3_HUMAN	Proteasome subunit beta type-3 OS=Hor	169.9	67	6
P23528	COF1_HUMAN	Cofilin-1 OS=Homo sapiens GN=CFL1 F	166.71	57	6
Q961Z0	PAWR_HUMAN	PRKC apoptosis WT1 regulator protein C	164.92	46	6
P25205	MCM3_HUMAN	DNA replication licensing factor MCM3 C	163.19	32	6
P62888	RL30_HUMAN	60S ribosomal protein L30 OS=Homo sa	161.64	66	6
Q13561	DCTN2_HUMAN	Dynactin subunit 2 OS=Homo sapiens G	160.54	46	6
P08708	RS17_HUMAN	40S ribosomal protein S17 OS=Homo sa	158.26	65	6
P13797	PLST_HUMAN	Plastin-3 OS=Homo sapiens GN=PLS3 F	158.08	34	6
P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondria	158	56	6
P61604	CH10_HUMAN	10 kDa heat shock protein, mitochondria	157.8	76	6
P37802	TAGL2_HUMAN	Transgelin-2 OS=Homo sapiens GN=TA	154.49	46	6
P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGA	153.32	36	6
P62987	RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 OS=	151.42	73	6
P0CG48	UBC_HUMAN	Polyubiquitin-C OS=Homo sapiens GN=U	151.42	44	6
P62979	RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a OS	151.42	50	6
P0CG47	UBB_HUMAN	Polyubiquitin-B OS=Homo sapiens GN=U	151.42	82	6
P11586	C1TC_HUMAN	C-1-tetrahydrofolate synthase, cytoplasm	150.42	36	6
P62263	RS14_HUMAN	40S ribosomal protein S14 OS=Homo sa	146.9	46	6
Q9Y295	DRG1_HUMAN	Developmentally-regulated GTP-binding	146.21	40	6
Q9P2J5	SYLC_HUMAN	Leucyl-tRNA synthetase, cytoplasmic OS	144.85	31	6
P27816	MAP4_HUMAN	Microtubule-associated protein 4 OS=Ho	139.1	35	6
P52788	SPSY_HUMAN	Spermine synthase OS=Homo sapiens C	133.44	36	6
P62851	RS25_HUMAN	40S ribosomal protein S25 OS=Homo sa	133.38	39	6
Q92945	FUBP2_HUMAN	Far upstream element-binding protein 2	132.08	31	6
Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 OS=	131.3	16	6
P14314	GLU2B_HUMAN	Glucosidase 2 subunit beta OS=Homo s	131.01	23	6
P17987	TCPA_HUMAN	T-complex protein 1 subunit alpha OS=H	124.66	35	6
P84243	H33_HUMAN	Histone H3.3 OS=Homo sapiens GN=H3	118.62	47	6
P68431	H31_HUMAN	Histone H3.1 OS=Homo sapiens GN=HI	118.62	50	6
Q71DI3	H32_HUMAN	Histone H3.2 OS=Homo sapiens GN=HI	118.62	50	6
Q16695	H31T_HUMAN	Histone H3.1t OS=Homo sapiens GN=H	118.62	50	6
P18077	RL35A_HUMAN	60S ribosomal protein L35a OS=Homo s	105.88	44	6
P09493	TPM1_HUMAN	Tropomyosin alpha-1 chain OS=Homo s	288.32	69	5
P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein	278.47	57	5
P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 OS=Homo s	245.89	85	5
P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-I OS=Hom	216.02	60	5
P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta OS=	209.42	58	5
O60506	HNRPQ_HUMAN	Heterogeneous nuclear ribonucleoprotein	197.27	41	5
Q16181	SEPT7_HUMAN	Septin-7 OS=Homo sapiens GN=SEPT7	185.8	60	5
P09429	HMGB1_HUMAN	High mobility group protein B1 OS=Hom	172.39	46	5
P61289	PSME3_HUMAN	Proteasome activator complex subunit 3	172.33	56	5

P06744 G6PI_HUMAN	Glucose-6-phosphate isomerase OS=Homo sapiens GN=G6P	166.32	31	5
P51149 RAB7A_HUMAN	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A	164.95	35	5
P55209 NP1L1_HUMAN	Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NP1L1	163.61	35	5
Q13263 TIF1B_HUMAN	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TIF1B	163.39	27	5
P08133 ANXA6_HUMAN	Annexin A6 OS=Homo sapiens GN=ANXA6	159.78	38	5
Q8NC51 PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=PAIRB	158.06	53	5
P23526 SAHH_HUMAN	Adenosylhomocysteinase OS=Homo sapiens GN=SAHH	157.63	40	5
P08195 4F2_HUMAN	4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=4F2	157.23	28	5
P61353 RL27_HUMAN	60S ribosomal protein L27 OS=Homo sapiens GN=RL27	156.91	68	5
P02794 FRIH_HUMAN	Ferritin heavy chain OS=Homo sapiens GN=FRIH	155.21	45	5
P09874 PARP1_HUMAN	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1	153.6	24	5
P37108 SRP14_HUMAN	Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14	153.37	71	5
Q7L2H7 EIF3M_HUMAN	Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M	153.35	35	5
Q8N474 SFRP1_HUMAN	Secreted frizzled-related protein 1 OS=Homo sapiens GN=SFRP1	152.97	46	5
Q14566 MCM6_HUMAN	DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6	152.81	35	5
Q15717 ELAV1_HUMAN	ELAV-like protein 1 OS=Homo sapiens GN=ELAV1	152.1	33	5
P39060 COIA1_HUMAN	Collagen alpha-1(XVIII) chain OS=Homo sapiens GN=COIA1	151.31	31	5
P17174 AATC_HUMAN	Aspartate aminotransferase, cytoplasmic OS=Homo sapiens GN=AATC	149.96	37	5
O75347 TBCA_HUMAN	Tubulin-specific chaperone A OS=Homo sapiens GN=TBCA	149.6	69	5
P30050 RL12_HUMAN	60S ribosomal protein L12 OS=Homo sapiens GN=RL12	149.08	46	5
P62316 SMD2_HUMAN	Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SMD2	149.08	61	5
P50502 F10A1_HUMAN	Hsc70-interacting protein OS=Homo sapiens GN=F10A1	148.29	48	5
P63244 GBLP_HUMAN	Guanine nucleotide-binding protein subunit gamma-1 OS=Homo sapiens GN=GBLP	145.32	30	5
P15880 RS2_HUMAN	40S ribosomal protein S2 OS=Homo sapiens GN=RS2	144.24	40	5
P43487 RANG_HUMAN	Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANG	143.31	33	5
P63162 RSMN_HUMAN	Small nuclear ribonucleoprotein-associated protein OS=Homo sapiens GN=RSMN	141.93	45	5
P14678 RSMB_HUMAN	Small nuclear ribonucleoprotein-associated protein OS=Homo sapiens GN=RSMB	141.93	40	5
Q9Y2Z0 SUGT1_HUMAN	Suppressor of G2 allele of SKP1 homolog OS=Homo sapiens GN=SUGT1	139.32	30	5
P16949 STMN1_HUMAN	Stathmin OS=Homo sapiens GN=STMN1	139.17	38	5
P49721 PSB2_HUMAN	Proteasome subunit beta type-2 OS=Homo sapiens GN=PSB2	136.22	38	5
Q15691 MARE1_HUMAN	Microtubule-associated protein RP/EB family class 1 member 1 OS=Homo sapiens GN=MARE1	136.04	26	5
P78417 GSTO1_HUMAN	Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1	133.58	33	5
P62244 RS15A_HUMAN	40S ribosomal protein S15a OS=Homo sapiens GN=RS15A	132.41	48	5
P61758 PFD3_HUMAN	Prefoldin subunit 3 OS=Homo sapiens GN=PFD3	132.03	52	5
O43399 TPD54_HUMAN	Tumor protein D54 OS=Homo sapiens GN=TPD54	131.62	50	5
P46926 GNPI1_HUMAN	Glucosamine-6-phosphate isomerase 1 OS=Homo sapiens GN=GNPI1	130.85	39	5
P00491 PNPH_HUMAN	Purine nucleoside phosphorylase OS=Homo sapiens GN=PNPH	129.66	35	5
Q05682 CALD1_HUMAN	Caldesmon OS=Homo sapiens GN=CALD1	129.12	23	5
P50914 RL14_HUMAN	60S ribosomal protein L14 OS=Homo sapiens GN=RL14	128.61	50	5
P35232 PHB_HUMAN	Prohibitin OS=Homo sapiens GN=PHB	126.96	45	5
Q02878 RL6_HUMAN	60S ribosomal protein L6 OS=Homo sapiens GN=RL6	124.55	44	5
P59998 ARPC4_HUMAN	Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4	122.31	31	5
P14868 SYDC_HUMAN	Aspartyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=SYDC	121.1	19	5
Q9P2E9 RRBP1_HUMAN	Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1	120.34	17	5
P98160 PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan OS=Homo sapiens GN=PGBM	118.87	9	5
P49736 MCM2_HUMAN	DNA replication licensing factor MCM2 OS=Homo sapiens GN=MCM2	118.52	28	5
P13667 PDIA4_HUMAN	Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4	118.29	21	5
Q8N163 K1967_HUMAN	Protein KIAA1967 OS=Homo sapiens GN=K1967	117.88	27	5
O43242 PSMD3_HUMAN	26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3	116.46	30	5
P82979 SARNP_HUMAN	SAP domain-containing ribonucleoprotein OS=Homo sapiens GN=SARNP	112.71	42	5
P62899 RL31_HUMAN	60S ribosomal protein L31 OS=Homo sapiens GN=RL31	110.06	49	5
P30044 PRDX5_HUMAN	Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5	105.91	49	5
P46781 RS9_HUMAN	40S ribosomal protein S9 OS=Homo sapiens GN=RS9	105.12	45	5
Q14914 PTGR1_HUMAN	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1	102	17	5
Q9UHD8 SEPT9_HUMAN	Septin-9 OS=Homo sapiens GN=SEPT9	96.07	12	5

Q9BYT8 NEUL_HUMAN	Neurolysin, mitochondrial OS=Homo sap	89.07	16	5
Q562R1 ACTBL_HUMAN	Beta-actin-like protein 2 OS=Homo sapie	283.36	65	4
P15531 NDKA_HUMAN	Nucleoside diphosphate kinase A OS=H	209.18	81	4
P84077 ARF1_HUMAN	ADP-ribosylation factor 1 OS=Homo sap	198.78	68	4
P61204 ARF3_HUMAN	ADP-ribosylation factor 3 OS=Homo sap	198.78	67	4
P61158 ARP3_HUMAN	Actin-related protein 3 OS=Homo sapien	186.94	55	4
A6NL28 TPM3L_HUMAN	Putative tropomyosin alpha-3 chain-like p	177.37	30	4
P06493 CDK1_HUMAN	Cyclin-dependent kinase 1 OS=Homo sa	176.85	45	4
P62917 RL8_HUMAN	60S ribosomal protein L8 OS=Homo sap	163.71	49	4
P98095 FBLN2_HUMAN	Fibulin-2 OS=Homo sapiens GN=FBLN2	161.78	22	4
Q9NTK5 OLA1_HUMAN	Obg-like ATPase 1 OS=Homo sapiens G	160.13	39	4
P05198 IF2A_HUMAN	Eukaryotic translation initiation factor 2 s	158.5	55	4
P14324 FPPS_HUMAN	Farnesyl pyrophosphate synthase OS=H	156.36	43	4
P46778 RL21_HUMAN	60S ribosomal protein L21 OS=Homo sa	155.43	37	4
Q12904 AIMP1_HUMAN	Aminoacyl tRNA synthase complex-inter	154.01	35	4
P54687 BCAT1_HUMAN	Branched-chain-amino-acid aminotransfe	148.58	35	4
Q13310 PABP4_HUMAN	Polyadenylate-binding protein 4 OS=Hon	148.03	38	4
Q15365 PCBP1_HUMAN	Poly(rC)-binding protein 1 OS=Homo sap	147.77	42	4
P62841 RS15_HUMAN	40S ribosomal protein S15 OS=Homo sa	146.2	57	4
Q96FW1 OTUB1_HUMAN	Ubiquitin thioesterase OTUB1 OS=Hom	145.27	56	4
P62191 PRS4_HUMAN	26S protease regulatory subunit 4 OS=H	144.04	49	4
P40925 MDHC_HUMAN	Malate dehydrogenase, cytoplasmic OS=	143.7	36	4
P18621 RL17_HUMAN	60S ribosomal protein L17 OS=Homo sa	142.87	36	4
P46783 RS10_HUMAN	40S ribosomal protein S10 OS=Homo sa	140.61	65	4
P62847 RS24_HUMAN	40S ribosomal protein S24 OS=Homo sa	139.36	47	4
P62158 CALM_HUMAN	Calmodulin OS=Homo sapiens GN=CAL	139.12	42	4
P07339 CATD_HUMAN	Cathepsin D OS=Homo sapiens GN=CT	138.13	35	4
Q9UHV9 PFD2_HUMAN	Prefoldin subunit 2 OS=Homo sapiens G	137.32	49	4
P12429 ANXA3_HUMAN	Annexin A3 OS=Homo sapiens GN=ANX	136.03	25	4
P40926 MDHM_HUMAN	Malate dehydrogenase, mitochondrial OS	134.76	52	4
Q14974 IMB1_HUMAN	Importin subunit beta-1 OS=Homo sapie	133.4	21	4
O00487 PSDE_HUMAN	26S proteasome non-ATPase regulatory	132	59	4
P16401 H15_HUMAN	Histone H1.5 OS=Homo sapiens GN=HI	130.92	55	4
Q15366 PCBP2_HUMAN	Poly(rC)-binding protein 2 OS=Homo sap	129.35	30	4
P62913 RL11_HUMAN	60S ribosomal protein L11 OS=Homo sa	126.26	26	4
P33991 MCM4_HUMAN	DNA replication licensing factor MCM4 C	124.89	21	4
Q86VP6 CAND1_HUMAN	Cullin-associated NEDD8-dissociated pr	122.03	21	4
Q01581 HMCS1_HUMAN	Hydroxymethylglutaryl-CoA synthase, cy	120.32	39	4
P00492 HPRT_HUMAN	Hypoxanthine-guanine phosphoribosyltra	119.62	31	4
Q15631 TSN_HUMAN	Translin OS=Homo sapiens GN=TSN PE	119.35	37	4
P23381 SYWC_HUMAN	Tryptophanyl-tRNA synthetase, cytoplast	119.1	26	4
Q71UI9 H2AV_HUMAN	Histone H2A.V OS=Homo sapiens GN=H	118.48	40	4
O75821 EIF3G_HUMAN	Eukaryotic translation initiation factor 3 s	118.24	30	4
O15145 ARPC3_HUMAN	Actin-related protein 2/3 complex subuni	118.05	26	4
O14974 MYPT1_HUMAN	Protein phosphatase 1 regulatory subuni	117.1	32	4
P25788 PSA3_HUMAN	Proteasome subunit alpha type-3 OS=H	116.52	20	4
P39023 RL3_HUMAN	60S ribosomal protein L3 OS=Homo sap	115.31	24	4
P27797 CALR_HUMAN	Calreticulin OS=Homo sapiens GN=CAL	114.84	24	4
P22102 PUR2_HUMAN	Trifunctional purine biosynthetic protein a	114.26	37	4
P26373 RL13_HUMAN	60S ribosomal protein L13 OS=Homo sa	109.44	27	4
Q7L5N1 CSN6_HUMAN	COP9 signalosome complex subunit 6 O	108.68	25	4
O76003 GLRX3_HUMAN	Glutaredoxin-3 OS=Homo sapiens GN=C	107.36	59	4
Q09666 AHNK_HUMAN	Neuroblast differentiation-associated pro	107.34	12	4
P49755 TMEDA_HUMAN	Transmembrane emp24 domain-containi	106.72	28	4
P24539 AT5F1_HUMAN	ATP synthase subunit b, mitochondrial C	103.2	26	4

Q16643 DREB_HUMAN	Drebrin OS=Homo sapiens GN=DBN1 P	102.08	22	4
O43324 MCA3_HUMAN	Eukaryotic translation elongation factor 1	100.42	66	4
P13798 ACPH_HUMAN	Acylamino-acid-releasing enzyme OS=H	99.27	9	4
Q9NZL4 HPBP1_HUMAN	Hsp70-binding protein 1 OS=Homo sapi	89.62	36	4
Q16555 DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 OS	87.34	21	4
Q9Y376 CAB39_HUMAN	Calcium-binding protein 39 OS=Homo sa	70.45	25	4
Q13509 TBB3_HUMAN	Tubulin beta-3 chain OS=Homo sapiens	299.53	62	3
P62807 H2B1C_HUMAN	Histone H2B type 1-C/E/F/G/I OS=Homoc	219.86	70	3
O60814 H2B1K_HUMAN	Histone H2B type 1-K OS=Homo sapiens	219.86	70	3
P05141 ADT2_HUMAN	ADP/ATP translocase 2 OS=Homo sapien	179.31	58	3
Q9NZI8 IF2B1_HUMAN	Insulin-like growth factor 2 mRNA-bindin	170.99	45	3
O75610 LFTY1_HUMAN	Left-right determination factor 1 OS=Hon	170.03	45	3
Q13765 NACA_HUMAN	Nascent polypeptide-associated complex	165.46	37	3
P60660 MYL6_HUMAN	Myosin light polypeptide 6 OS=Homo sap	159.68	56	3
P61163 ACTZ_HUMAN	Alpha-centractin OS=Homo sapiens GN=	156.76	51	3
O43390 HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein	156.46	38	3
O14744 ANM5_HUMAN	Protein arginine N-methyltransferase 5 C	146.45	37	3
P04216 THY1_HUMAN	Thy-1 membrane glycoprotein OS=Homoc	143.96	50	3
Q13126 MTAP_HUMAN	S-methyl-5'-thioadenosine phosphorylas	133.09	47	3
P46782 RS5_HUMAN	40S ribosomal protein S5 OS=Homo sap	130.54	50	3
Q07020 RL18_HUMAN	60S ribosomal protein L18 OS=Homo sa	130.02	40	3
Q14444 CAPR1_HUMAN	Caprin-1 OS=Homo sapiens GN=CAPRI	127.48	26	3
Q06323 PSME1_HUMAN	Proteasome activator complex subunit 1	126.52	42	3
Q07021 C1QBP_HUMAN	Complement component 1 Q subcompo	126.18	25	3
Q15056 IF4H_HUMAN	Eukaryotic translation initiation factor 4H	125.33	34	3
P49903 SPS1_HUMAN	Selenide, water dikinase 1 OS=Homo sa	123.68	30	3
P52907 CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 C	123.21	22	3
Q15417 CNN3_HUMAN	Calponin-3 OS=Homo sapiens GN=CNN	122.16	28	3
P62873 GBB1_HUMAN	Guanine nucleotide-binding protein G(I)/G	121.55	19	3
P60866 RS20_HUMAN	40S ribosomal protein S20 OS=Homo sa	121.54	37	3
P51858 HDGF_HUMAN	Hepatoma-derived growth factor OS=Ho	120.58	45	3
P39687 AN32A_HUMAN	Acidic leucine-rich nuclear phosphoprote	119.87	42	3
P30086 PEBP1_HUMAN	Phosphatidylethanolamine-binding protei	117.71	26	3
Q9UL46 PSME2_HUMAN	Proteasome activator complex subunit 2	117.63	54	3
P31153 METK2_HUMAN	S-adenosylmethionine synthase isoform	116.44	37	3
P16422 EPCAM_HUMAN	Epithelial cell adhesion molecule OS=Ho	116.32	42	3
P30040 ERP29_HUMAN	Endoplasmic reticulum resident protein 2	114.65	35	3
P38159 HNRPG_HUMAN	Heterogeneous nuclear ribonucleoprotein	113.99	37	3
O43776 SYNC_HUMAN	Asparaginyl-tRNA synthetase, cytoplasm	113.91	17	3
O15372 EIF3H_HUMAN	Eukaryotic translation initiation factor 3 s	113.73	34	3
P55060 XPO2_HUMAN	Exportin-2 OS=Homo sapiens GN=CSE1	113.11	28	3
P07741 APT_HUMAN	Adenine phosphoribosyltransferase OS=	112.81	26	3
P68400 CSK21_HUMAN	Casein kinase II subunit alpha OS=Homoc	112.49	23	3
P07814 SYEP_HUMAN	Bifunctional aminoacyl-tRNA synthetase	111.68	17	3
P61088 UBE2N_HUMAN	Ubiquitin-conjugating enzyme E2 N OS=	111.56	36	3
O75487 GPC4_HUMAN	Glypican-4 OS=Homo sapiens GN=GPC	108.65	22	3
Q9NYL9 TMOD3_HUMAN	Tropomodulin-3 OS=Homo sapiens GN=	105.91	36	3
Q96AE4 FUBP1_HUMAN	Far upstream element-binding protein 1 C	105.87	27	3
Q13868 EXOS2_HUMAN	Exosome complex component RRP4 OS	105.36	31	3
P23352 KALM_HUMAN	Anosmin-1 OS=Homo sapiens GN=KAL	104.99	23	3
P28072 PSB6_HUMAN	Proteasome subunit beta type-6 OS=Hor	104.25	13	3
P07093 GDN_HUMAN	Glia-derived nexin OS=Homo sapiens G	103.16	30	3
Q9BUL8 PDC10_HUMAN	Programmed cell death protein 10 OS=H	103.14	30	3
Q9Y262 EIF3L_HUMAN	Eukaryotic translation initiation factor 3 s	102.46	23	3
Q9NVA2 SEP11_HUMAN	Septin-11 OS=Homo sapiens GN=SEPT	101.76	16	3



Q99439 CNN2_HUMAN	Calponin-2 OS=Homo sapiens GN=CNN	101.4	35	3
Q86V81 THOC4_HUMAN	THO complex subunit 4 OS=Homo sapie	100.47	20	3
P19367 HXK1_HUMAN	Hexokinase-1 OS=Homo sapiens GN=H	99.53	25	3
O43143 DHX15_HUMAN	Putative pre-mRNA-splicing factor ATP-c	98.45	16	3
Q9NZL9 MAT2B_HUMAN	Methionine adenosyltransferase 2 subun	96.34	20	3
Q15785 TOM34_HUMAN	Mitochondrial import receptor subunit TC	95.81	30	3
O15347 HMGB3_HUMAN	High mobility group protein B3 OS=Homo	94.94	30	3
P35613 BASI_HUMAN	Basigin OS=Homo sapiens GN=BSG PE	94.46	21	3
O60701 UGDH_HUMAN	UDP-glucose 6-dehydrogenase OS=Horo	94.26	15	3
P36404 ARL2_HUMAN	ADP-ribosylation factor-like protein 2 OS	94.05	18	3
Q13283 G3BP1_HUMAN	Ras GTPase-activating protein-binding p	93.52	30	3
P62280 RS11_HUMAN	40S ribosomal protein S11 OS=Homo sa	92.73	26	3
P49588 SYAC_HUMAN	Alanyl-tRNA synthetase, cytoplasmic OS	92.24	23	3
Q92820 GGH_HUMAN	Gamma-glutamyl hydrolase OS=Homo s	91.51	14	3
P54709 AT1B3_HUMAN	Sodium/potassium-transporting ATPase	90.93	13	3
P52272 HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein	90.72	29	3
P39656 OST48_HUMAN	Dolichyl-diphosphooligosaccharide--prot	90.22	12	3
P29279 CTGF_HUMAN	Connective tissue growth factor OS=Horo	89.8	26	3
O43852 CALU_HUMAN	Calumenin OS=Homo sapiens GN=CAL	89.45	34	3
Q8WZ42 TITIN_HUMAN	Titin OS=Homo sapiens GN=TTN PE=1	88.5	10	3
Q9UNM6 PSD13_HUMAN	26S proteasome non-ATPase regulatory	87.85	29	3
P26640 SYVC_HUMAN	Valyl-tRNA synthetase OS=Homo sapier	87.67	6	3
Q8WUD1 RAB2B_HUMAN	Ras-related protein Rab-2B OS=Homo s	86.44	37	3
P12109 CO6A1_HUMAN	Collagen alpha-1(VI) chain OS=Homo sa	86.44	11	3
P11717 MPRI_HUMAN	Cation-independent mannose-6-phospha	85.96	10	3
O00625 PIR_HUMAN	Pirin OS=Homo sapiens GN=PIR PE=1	85.62	11	3
O15067 PUR4_HUMAN	Phosphoribosylformylglycinamide synth	85.19	14	3
P00505 AATM_HUMAN	Aspartate aminotransferase, mitochondr	84.18	24	3
P48556 PSMD8_HUMAN	26S proteasome non-ATPase regulatory	83.86	19	3
P28070 PSB4_HUMAN	Proteasome subunit beta type-4 OS=Horo	81.96	20	3
P30566 PUR8_HUMAN	Adenylosuccinate lyase OS=Homo sapie	81.94	14	3
P55786 PSA_HUMAN	Puromycin-sensitive aminopeptidase OS	81.73	17	3
O00232 PSD12_HUMAN	26S proteasome non-ATPase regulatory	80.72	28	3
Q00688 FKBP3_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP	78.08	20	3
Q16543 CDC37_HUMAN	Hsp90 co-chaperone Cdc37 OS=Homo s	77.65	12	3
Q01469 FABP5_HUMAN	Fatty acid-binding protein, epidermal OS	77.1	30	3
Q15233 NONO_HUMAN	Non-POU domain-containing octamer-bi	76.95	20	3
O43237 DC1L2_HUMAN	Cytoplasmic dynein 1 light intermediate c	76.74	15	3
Q13838 DX39B_HUMAN	Spliceosome RNA helicase DDX39B OS	76.23	14	3
O00148 DX39A_HUMAN	ATP-dependent RNA helicase DDX39A	76.23	12	3
O75822 EIF3J_HUMAN	Eukaryotic translation initiation factor 3 s	74.95	27	3
P60953 CDC42_HUMAN	Cell division control protein 42 homolog	74.69	16	3
O00303 EIF3F_HUMAN	Eukaryotic translation initiation factor 3 s	73.8	21	3
P13984 T2FB_HUMAN	General transcription factor IIF subunit 2	73.22	21	3
P33992 MCM5_HUMAN	DNA replication licensing factor MCM5 C	71.25	19	3
Q92769 HDAC2_HUMAN	Histone deacetylase 2 OS=Homo sapien	70.35	17	3
P12270 TPR_HUMAN	Nucleoprotein TPR OS=Homo sapiens G	69.44	11	3
A6NDG6 PGP_HUMAN	Phosphoglycolate phosphatase OS=Horo	64.58	13	3
Q7Z4W1 DCXR_HUMAN	L-xylulose reductase OS=Homo sapiens	63.74	18	3
Q58FF7 H90B3_HUMAN	Putative heat shock protein HSP 90-beta	351.09	74	2
Q9BYX7 ACTBM_HUMAN	Putative beta-actin-like protein 3 OS=Ho	242.61	54	2
P19105 ML12A_HUMAN	Myosin regulatory light chain 12A OS=Ho	184.34	72	2
O14950 ML12B_HUMAN	Myosin regulatory light chain 12B OS=Ho	184.34	72	2
O00292 LFTY2_HUMAN	Left-right determination factor 2 OS=Horo	176.3	53	2
P63241 IF5A1_HUMAN	Eukaryotic translation initiation factor 5A-	163.75	50	2

P13929 ENOB_HUMAN	Beta-enolase OS=Homo sapiens GN=EN	157.2	53	2
P21796 VDAC1_HUMAN	Voltage-dependent anion-selective chan	146.33	35	2
P20042 IF2B_HUMAN	Eukaryotic translation initiation factor 2 s	138.9	61	2
A6NK07 IF2BL_HUMAN	Eukaryotic translation initiation factor 2 s	138.9	54	2
P60983 GMFB_HUMAN	Glia maturation factor beta OS=Homo sa	132.25	51	2
P62136 PP1A_HUMAN	Serine/threonine-protein phosphatase Pf	123.53	30	2
P50453 SPB9_HUMAN	Serpin B9 OS=Homo sapiens GN=SERP	123.16	28	2
Q13200 PSMD2_HUMAN	26S proteasome non-ATPase regulatory	122.62	29	2
P62829 RL23_HUMAN	60S ribosomal protein L23 OS=Homo sa	120.57	59	2
P60891 PRPS1_HUMAN	Ribose-phosphate pyrophosphokinase 1	120.08	43	2
P68402 PA1B2_HUMAN	Platelet-activating factor acetylhydrolase	119.43	46	2
P20290 BTF3_HUMAN	Transcription factor BTF3 OS=Homo sap	119.35	50	2
P61026 RAB10_HUMAN	Ras-related protein Rab-10 OS=Homo s	119.09	32	2
Q9Y3B4 PM14_HUMAN	Pre-mRNA branch site protein p14 OS=H	116.79	29	2
P35268 RL22_HUMAN	60S ribosomal protein L22 OS=Homo sa	116.54	27	2
O43765 SGTA_HUMAN	Small glutamine-rich tetratricopeptide rep	115.19	22	2
Q92688 AN32B_HUMAN	Acidic leucine-rich nuclear phosphoprote	114.51	26	2
Q5VYJ4 RUEL1_HUMAN	Putative small nuclear ribonucleoprotein	113.85	48	2
P62304 RUXE_HUMAN	Small nuclear ribonucleoprotein E OS=H	113.85	48	2
P62241 RS8_HUMAN	40S ribosomal protein S8 OS=Homo sap	112.85	33	2
Q99729 ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein	112.38	22	2
P20339 RAB5A_HUMAN	Ras-related protein Rab-5A OS=Homo s	110.79	32	2
P25705 ATPA_HUMAN	ATP synthase subunit alpha, mitochondr	110.15	42	2
P31943 HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein	109.47	21	2
P24534 EF1B_HUMAN	Elongation factor 1-beta OS=Homo sapi	107.85	31	2
Q12905 ILF2_HUMAN	Interleukin enhancer-binding factor 2 OS	107.42	21	2
Q92522 H1X_HUMAN	Histone H1x OS=Homo sapiens GN=H1	106.49	34	2
P30048 PRDX3_HUMAN	Thioredoxin-dependent peroxide reducta	106.1	32	2
Q14103 HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein	104.99	19	2
Q15046 SYK_HUMAN	Lysyl-tRNA synthetase OS=Homo sapien	103.8	19	2
O00151 PDLI1_HUMAN	PDZ and LIM domain protein 1 OS=Hom	103.42	39	2
P61020 RAB5B_HUMAN	Ras-related protein Rab-5B OS=Homo s	103.21	33	2
O00264 PGRC1_HUMAN	Membrane-associated progesterone rec	102.86	26	2
O15116 LSM1_HUMAN	U6 snRNA-associated Sm-like protein LS	101.19	25	2
P06576 ATPB_HUMAN	ATP synthase subunit beta, mitochondria	100.8	33	2
Q9UBT2 SAE2_HUMAN	SUMO-activating enzyme subunit 2 OS=	100.15	15	2
P55327 TPD52_HUMAN	Tumor protein D52 OS=Homo sapiens G	99.57	21	2
Q07866 KLC1_HUMAN	Kinesin light chain 1 OS=Homo sapiens	99.17	19	2
Q04760 LGUL_HUMAN	Lactoylglutathione lyase OS=Homo sapi	98.72	23	2
P53367 ARFP1_HUMAN	Arfaptin-1 OS=Homo sapiens GN=ARFIP	98.07	26	2
O15212 PFD6_HUMAN	Prefoldin subunit 6 OS=Homo sapiens G	97.95	43	2
P09936 UCHL1_HUMAN	Ubiquitin carboxyl-terminal hydrolase iso	97.81	19	2
Q99873 ANM1_HUMAN	Protein arginine N-methyltransferase 1 C	97.08	16	2
P41091 IF2G_HUMAN	Eukaryotic translation initiation factor 2 s	97.06	22	2
Q2VIR3 IF2GL_HUMAN	Eukaryotic translation initiation factor 2 s	97.06	17	2
P13861 KAP2_HUMAN	cAMP-dependent protein kinase type II-a	95.1	23	2
P51571 SSRD_HUMAN	Translocon-associated protein subunit de	94.78	39	2
P21741 MK_HUMAN	Midkine OS=Homo sapiens GN=MDK PE	94.22	34	2
Q96CT7 CC124_HUMAN	Coiled-coil domain-containing protein 12	93.73	21	2
Q13576 IQGA2_HUMAN	Ras GTPase-activating-like protein IQGA	92.82	12	2
Q92890 UFD1_HUMAN	Ubiquitin fusion degradation protein 1 ho	92.65	27	2
Q9BZZ5 API5_HUMAN	Apoptosis inhibitor 5 OS=Homo sapiens	92.58	16	2
O95433 AHSA1_HUMAN	Activator of 90 kDa heat shock protein A	92.26	36	2
Q15818 NPTX1_HUMAN	Neuronal pentraxin-1 OS=Homo sapiens	91.91	18	2
O15355 PPM1G_HUMAN	Protein phosphatase 1G OS=Homo sapi	91.32	14	2

P23284	PIIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PIIB	91.23	50	2
P48047	ATPO_HUMAN	ATP synthase subunit O, mitochondrial COX5B OS=Homo sapiens GN=ATPO	90.81	57	2
Q00341	VIGLN_HUMAN	Vigilin OS=Homo sapiens GN=HDLBP1 OS=Homo sapiens GN=VIGLN	90.4	18	2
Q99426	TBCB_HUMAN	Tubulin-folding cofactor B OS=Homo sapiens GN=TBCB	90.35	34	2
O14745	NHRF1_HUMAN	Na(+)/H(+) exchange regulatory cofactor 1 OS=Homo sapiens GN=NHRF1	89.18	20	2
P53621	COPA_HUMAN	Coatomer subunit alpha OS=Homo sapiens GN=COPA	89	13	2
Q8WVM8	SCFD1_HUMAN	Sec1 family domain-containing protein 1 OS=Homo sapiens GN=SCFD1	88.71	9	2
Q93009	UBP7_HUMAN	Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens GN=UBP7	87.4	11	2
P19784	CSK22_HUMAN	Casein kinase II subunit alpha' OS=Homo sapiens GN=CSK22	87	21	2
P52565	GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=GDIR1	86.8	23	2
P25325	THTM_HUMAN	3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=THTM	86.75	23	2
P48444	COPD_HUMAN	Coatomer subunit delta OS=Homo sapiens GN=COPD	86.37	17	2
P31350	RIR2_HUMAN	Ribonucleoside-diphosphate reductase subunit beta OS=Homo sapiens GN=RIR2	86.12	18	2
P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB	85.76	25	2
P47914	RL29_HUMAN	60S ribosomal protein L29 OS=Homo sapiens GN=RL29	85.69	28	2
Q96HF1	SFRP2_HUMAN	Secreted frizzled-related protein 2 OS=Homo sapiens GN=SFRP2	85.64	18	2
P46776	RL27A_HUMAN	60S ribosomal protein L27a OS=Homo sapiens GN=RL27A	85.06	45	2
P83731	RL24_HUMAN	60S ribosomal protein L24 OS=Homo sapiens GN=RL24	84.82	43	2
P46109	CRKL_HUMAN	Crk-like protein OS=Homo sapiens GN=CRKL	84.45	10	2
Q13347	EIF3I_HUMAN	Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I	84.43	36	2
Q13557	KCC2D_HUMAN	Calcium/calmodulin-dependent protein kinase II gamma OS=Homo sapiens GN=KCC2D	84.24	22	2
Q93008	USP9X_HUMAN	Probable ubiquitin carboxyl-terminal hydrolase 9 OS=Homo sapiens GN=USP9X	83.52	6	2
P31689	DNJA1_HUMAN	DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNJA1	83.1	17	2
P62753	RS6_HUMAN	40S ribosomal protein S6 OS=Homo sapiens GN=RS6	83.1	20	2
O75477	ERLN1_HUMAN	Erlin-1 OS=Homo sapiens GN=ERLIN1 OS=Homo sapiens GN=ERLN1	83.03	21	2
P48681	NEST_HUMAN	Nestin OS=Homo sapiens GN=NES PE=1 OS=Homo sapiens GN=NEST	82.69	7	2
Q15293	RCN1_HUMAN	Reticulocalbin-1 OS=Homo sapiens GN=RCN1	82.52	15	2
Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9	82.38	12	2
P61201	CSN2_HUMAN	COP9 signalosome complex subunit 2 OS=Homo sapiens GN=CSN2	82.3	30	2
P07237	PDIA1_HUMAN	Protein disulfide-isomerase OS=Homo sapiens GN=PDIA1	82.12	23	2
Q99460	PSMD1_HUMAN	26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1	81.85	15	2
P23921	RIR1_HUMAN	Ribonucleoside-diphosphate reductase subunit alpha OS=Homo sapiens GN=RIR1	81.2	12	2
P20700	LMNB1_HUMAN	Lamin-B1 OS=Homo sapiens GN=LMNB1	81.12	16	2
Q9NR31	SAR1A_HUMAN	GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A	81.06	31	2
Q9Y4Z0	LSM4_HUMAN	U6 snRNA-associated Sm-like protein LSm4 OS=Homo sapiens GN=LSM4	80.17	24	2
Q9UKM9	RALY_HUMAN	RNA-binding protein Raly OS=Homo sapiens GN=RALY	80.15	23	2
Q13442	HAP28_HUMAN	28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens GN=HAP28	79.27	18	2
P54578	UBP14_HUMAN	Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=UBP14	77.51	12	2
P10155	RO60_HUMAN	60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=RO60	77.36	14	2
P62318	SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SMD3	77.19	30	2
P05937	CALB1_HUMAN	Calbindin OS=Homo sapiens GN=CALB1	76.96	30	2
P31949	S10AB_HUMAN	Protein S100-A11 OS=Homo sapiens GN=S100A11	76.5	66	2
P83916	CBX1_HUMAN	Chromobox protein homolog 1 OS=Homo sapiens GN=CBX1	76.14	18	2
O60925	PFD1_HUMAN	Prefoldin subunit 1 OS=Homo sapiens GN=PFD1	76.11	17	2
P62857	RS28_HUMAN	40S ribosomal protein S28 OS=Homo sapiens GN=RS28	76.11	64	2
Q9BPX5	ARP5L_HUMAN	Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARP5L	75.98	46	2
Q53GQ0	DHB12_HUMAN	Estradiol 17-beta-dehydrogenase 12 OS=Homo sapiens GN=DHB12	75.89	26	2
P63220	RS21_HUMAN	40S ribosomal protein S21 OS=Homo sapiens GN=RS21	75.76	23	2
Q14166	TTL12_HUMAN	Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens GN=TTL12	75.74	12	2
P18065	IBP2_HUMAN	Insulin-like growth factor-binding protein 2 OS=Homo sapiens GN=IBP2	75.65	26	2
O14776	TCRG1_HUMAN	Transcription elongation regulator 1 OS=Homo sapiens GN=TCRG1	75.28	11	2
P30419	NMT1_HUMAN	Glycylpeptide N-tetradecanoyltransferase OS=Homo sapiens GN=NMT1	74.95	13	2
Q04837	SSBP_HUMAN	Single-stranded DNA-binding protein, mitochondrial OS=Homo sapiens GN=SSBP	74.91	40	2
P61803	DAD1_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase OS=Homo sapiens GN=DAD1	74.36	19	2
P35606	COPB2_HUMAN	Coatomer subunit beta' OS=Homo sapiens GN=COPB2	73.93	9	2

Q71UM5 RS27L_HUMAN	40S ribosomal protein S27-like OS=Homo sapiens	73.48	25	2
P42677 RS27_HUMAN	40S ribosomal protein S27 OS=Homo sapiens	73.48	25	2
P09012 SNRPA_HUMAN	U1 small nuclear ribonucleoprotein A OS=Homo sapiens	72.57	17	2
Q9H9Q2 CSN7B_HUMAN	COP9 signalosome complex subunit 7b OS=Homo sapiens	72.26	18	2
P51572 BAP31_HUMAN	B-cell receptor-associated protein 31 OS=Homo sapiens	72.21	26	2
Q9NR45 SIAS_HUMAN	Sialic acid synthase OS=Homo sapiens	71.88	22	2
P14174 MIF_HUMAN	Macrophage migration inhibitory factor OS=Homo sapiens	71.14	21	2
P35249 RFC4_HUMAN	Replication factor C subunit 4 OS=Homo sapiens	71.04	19	2
Q09028 RBBP4_HUMAN	Histone-binding protein RBBP4 OS=Homo sapiens	70.9	13	2
P54136 SYRC_HUMAN	Arginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens	70.83	10	2
O75531 BAF_HUMAN	Barrier-to-autointegration factor OS=Homo sapiens	70.71	35	2
Q9UNZ2 NSF1C_HUMAN	NSFL1 cofactor p47 OS=Homo sapiens	69.71	19	2
Q96SM3 CPXM1_HUMAN	Probable carboxypeptidase X1 OS=Homo sapiens	69.31	18	2
Q9Y5K8 VATD_HUMAN	V-type proton ATPase subunit D OS=Homo sapiens	69.29	32	2
Q14257 RCN2_HUMAN	Reticulocalbin-2 OS=Homo sapiens GN=RCN2	68.29	21	2
O00410 IPO5_HUMAN	Importin-5 OS=Homo sapiens GN=IPO5	68.23	13	2
O95218 ZRAB2_HUMAN	Zinc finger Ran-binding domain-containing protein 2 OS=Homo sapiens	67.78	14	2
P08243 ASNS_HUMAN	Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens	67.46	10	2
P12830 CADH1_HUMAN	Cadherin-1 OS=Homo sapiens GN=CDH1	67.27	10	2
P18124 RL7_HUMAN	60S ribosomal protein L7 OS=Homo sapiens	67.2	16	2
P12081 SYHC_HUMAN	Histidyl-tRNA synthetase, cytoplasmic OS=Homo sapiens	66.96	18	2
Q07157 ZO1_HUMAN	Tight junction protein ZO-1 OS=Homo sapiens	66.86	11	2
P36578 RL4_HUMAN	60S ribosomal protein L4 OS=Homo sapiens	66.42	19	2
P29762 RABP1_HUMAN	Cellular retinoic acid-binding protein 1 OS=Homo sapiens	65.26	28	2
Q9UBW8 CSN7A_HUMAN	COP9 signalosome complex subunit 7a OS=Homo sapiens	65.1	29	2
Q96K17 BT3L4_HUMAN	Transcription factor BTF3 homolog 4 OS=Homo sapiens	65.06	22	2
Q92896 GSLG1_HUMAN	Golgi apparatus protein 1 OS=Homo sapiens	64.9	11	2
Q9BVK6 TMED9_HUMAN	Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens	64.33	17	2
Q96S86 HPLN3_HUMAN	Hyaluronan and proteoglycan link protein 3 OS=Homo sapiens	63.53	27	2
P35221 CTNA1_HUMAN	Catenin alpha-1 OS=Homo sapiens GN=CTNA1	63.32	7	2
Q15758 AAAT_HUMAN	Neutral amino acid transporter B(0) OS=Homo sapiens	61.89	14	2
Q14980 NUMA1_HUMAN	Nuclear mitotic apparatus protein 1 OS=Homo sapiens	61.85	11	2
Q13098 CSN1_HUMAN	COP9 signalosome complex subunit 1 OS=Homo sapiens	61.49	9	2
Q96QK1 VPS35_HUMAN	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens	60.93	20	2
P04843 RPN1_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase OS=Homo sapiens	60.23	13	2
Q9Y5K5 UCHL5_HUMAN	Ubiquitin carboxyl-terminal hydrolase isoform 5 OS=Homo sapiens	60.2	15	2
Q92922 SMRC1_HUMAN	SWI/SNF complex subunit SMARCC1 OS=Homo sapiens	58.63	13	2
Q9Y624 JAM1_HUMAN	Junctional adhesion molecule A OS=Homo sapiens	58.15	14	2
Q92841 DDX17_HUMAN	Probable ATP-dependent RNA helicase OS=Homo sapiens	58.1	17	2
P17844 DDX5_HUMAN	Probable ATP-dependent RNA helicase OS=Homo sapiens	58.1	16	2
Q9Y5K6 CD2AP_HUMAN	CD2-associated protein OS=Homo sapiens	58.01	12	2
Q13243 SRSF5_HUMAN	Serine/arginine-rich splicing factor 5 OS=Homo sapiens	57.91	18	2
P20810 ICAL_HUMAN	Calpastatin OS=Homo sapiens GN=CAS	57.44	12	2
P46060 RAGP1_HUMAN	Ran GTPase-activating protein 1 OS=Homo sapiens	56.23	11	2
P19623 SPEE_HUMAN	Spermidine synthase OS=Homo sapiens	55.93	17	2
Q99614 TTC1_HUMAN	Tetratricopeptide repeat protein 1 OS=Homo sapiens	55.64	21	2
P09960 LKHA4_HUMAN	Leukotriene A-4 hydrolase OS=Homo sapiens	55.24	6	2
P62861 RS30_HUMAN	40S ribosomal protein S30 OS=Homo sapiens	54.98	34	2
Q96PK2 MACF4_HUMAN	Microtubule-actin cross-linking factor 1, isoform 2 OS=Homo sapiens	52.81	11	2
P10768 ESTD_HUMAN	S-formylglutathione hydrolase OS=Homo sapiens	52.37	10	2
P07203 GPX1_HUMAN	Glutathione peroxidase 1 OS=Homo sapiens	52.1	12	2
Q96P16 RPR1A_HUMAN	Regulation of nuclear pre-mRNA domain protein 1 OS=Homo sapiens	51.91	20	2
Q9BVC6 TM109_HUMAN	Transmembrane protein 109 OS=Homo sapiens	51.87	39	2
Q9UPG8 PLAL2_HUMAN	Zinc finger protein PLAGL2 OS=Homo sapiens	51.33	10	2
Q99615 DNJC7_HUMAN	DnaJ homolog subfamily C member 7 OS=Homo sapiens	50.77	10	2

O94985 CSTN1_HUMAN	Calsyntenin-1 OS=Homo sapiens GN=C	50.13	6	2
Q9H4M9 EHD1_HUMAN	EH domain-containing protein 1 OS=H	49.9	16	2
P11413 G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase	49	22	2
Q9H0I2 CP048_HUMAN	Uncharacterized protein C16orf48 OS=H	46.14	22	2
P06756 ITAV_HUMAN	Integrin alpha-V OS=Homo sapiens GN=	45.34	7	2
O15078 CE290_HUMAN	Centrosomal protein of 290 kDa OS=Hor	45.23	13	2
P02768 ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=	44.59	24	2
Q13043 STK4_HUMAN	Serine/threonine-protein kinase 4 OS=H	44.22	21	2
P40763 STAT3_HUMAN	Signal transducer and activator of transc	43.51	5	2
Q8NE01 CNNM3_HUMAN	Metal transporter CNNM3 OS=Homo sap	42.32	21	2
P45974 UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5 C	41.68	9	2
P49454 CENPF_HUMAN	Centromere protein F OS=Homo sapiens	41.67	10	2
Q08752 PPID_HUMAN	Peptidyl-prolyl cis-trans isomerase D OS	41.04	16	2
P10586 PTPRF_HUMAN	Receptor-type tyrosine-protein phosphat	39.02	8	2
Q9BXP5 SRRT_HUMAN	Serrate RNA effector molecule homolog	38.84	16	2
P63000 RAC1_HUMAN	Ras-related C3 botulinum toxin substrate	37.18	17	2
Q7L4E1 FA73B_HUMAN	Protein FAM73B OS=Homo sapiens GN=	36.38	15	2

**Table A1.10 CA1 hESC CMTX Protein Identifications.** List of all proteins identified in CMTX from CA1 hESCs with corresponding accession, description, PEAKS score, unique peptide numbers, and coverage (in %).

Accession	Description	Score	Coverage (%)	#Unique	
P21333	FLNA_HUMAN	Filamin-A OS=Homo sapiens GN=FLNA	348.93	55	72
P49327	FAS_HUMAN	Fatty acid synthase OS=Homo sapiens	346.52	58	67
Q13813	SPTA2_HUMAN	Spectrin alpha chain, brain OS=Homo s	328.54	61	63
O75369	FLNB_HUMAN	Filamin-B OS=Homo sapiens GN=FLNB	333.1	56	55
P13639	EF2_HUMAN	Elongation factor 2 OS=Homo sapiens	340.62	73	53
P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrog	333.99	91	52
P18206	VINC_HUMAN	Vinculin OS=Homo sapiens GN=VCL P	329.26	76	51
P29401	TKT_HUMAN	Transketolase OS=Homo sapiens GN=	331.75	78	46
P14618	KPYM_HUMAN	Pyruvate kinase isozymes M1/M2 OS=H	332.22	90	44
Q01995	TAGL_HUMAN	Transgelin OS=Homo sapiens GN=TAG	307.02	95	41
P35580	MYH10_HUMAN	Myosin-10 OS=Homo sapiens GN=MYH	306.82	57	38
Q01082	SPTB2_HUMAN	Spectrin beta chain, brain 1 OS=Homo	296.14	61	38
P30041	PRDX6_HUMAN	Peroxioredoxin-6 OS=Homo sapiens GN	292.67	93	38
P06733	ENOA_HUMAN	Alpha-enolase OS=Homo sapiens GN=	301.35	88	37
P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATP	275.21	62	36
P35579	MYH9_HUMAN	Myosin-9 OS=Homo sapiens GN=MYH9	314.85	63	35
P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A OS=	311.67	82	33
P07355	ANXA2_HUMAN	Annexin A2 OS=Homo sapiens GN=AN	303.45	91	33
P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 OS=Homo s	315.8	76	32
P62258	1433E_HUMAN	14-3-3 protein epsilon OS=Homo sapie	302.7	87	32
Q06830	PRDX1_HUMAN	Peroxioredoxin-1 OS=Homo sapiens GN	299.56	88	31
P53396	ACLY_HUMAN	ATP-citrate synthase OS=Homo sapien	270.95	69	31
O75874	IDHC_HUMAN	Isocitrate dehydrogenase [NADP] cytop	294.86	76	30
P07195	LDHB_HUMAN	L-lactate dehydrogenase B chain OS=H	292.67	73	30
P60174	TPIS_HUMAN	Triosephosphate isomerase OS=Homo	279.5	96	30
P08758	ANXA5_HUMAN	Annexin A5 OS=Homo sapiens GN=AN	271.34	70	30
P12814	ACTN1_HUMAN	Alpha-actinin-1 OS=Homo sapiens GN=	315.82	71	28
P63104	1433Z_HUMAN	14-3-3 protein zeta/delta OS=Homo sap	308.88	83	27
P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein OS	282.81	66	27
P07737	PROF1_HUMAN	Profilin-1 OS=Homo sapiens GN=PFN1	273.18	97	26
P62805	H4_HUMAN	Histone H4 OS=Homo sapiens GN=HIS	261.7	63	26
Q14315	FLNC_HUMAN	Filamin-C OS=Homo sapiens GN=FLNC	259.7	42	26
P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondri	257.33	75	26
P50454	SERP_HUMAN	Serpin H1 OS=Homo sapiens GN=SER	284.13	73	25
P00338	LDHA_HUMAN	L-lactate dehydrogenase A chain OS=H	282.93	81	25
P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha OS=H	321.76	60	24
O43707	ACTN4_HUMAN	Alpha-actinin-4 OS=Homo sapiens GN=	316.9	69	24
P23528	COF1_HUMAN	Cofilin-1 OS=Homo sapiens GN=CFL1	282.49	93	24
P05455	LA_HUMAN	Lupus La protein OS=Homo sapiens G	262.62	72	24
P31939	PUR9_HUMAN	Bifunctional purine biosynthesis protein	254.56	72	24
P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain OS=Homo s	319.2	95	23
P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A O	254.93	93	23
P61247	RS3A_HUMAN	40S ribosomal protein S3a OS=Homo s	240.82	77	23
P50990	TCPQ_HUMAN	T-complex protein 1 subunit theta OS=H	229.91	58	23
P02794	FRIH_HUMAN	Ferritin heavy chain OS=Homo sapiens	221.88	77	23
Q9Y490	TLN1_HUMAN	Talin-1 OS=Homo sapiens GN=TLN1 P	215.08	50	23
Q14914	PTGR1_HUMAN	Prostaglandin reductase 1 OS=Homo s	261.73	69	22
P37802	TAGL2_HUMAN	Transgelin-2 OS=Homo sapiens GN=T	245.46	97	22
P14625	ENPL_HUMAN	Endoplasmin OS=Homo sapiens GN=H	241.99	47	22
P02649	APOE_HUMAN	Apolipoprotein E OS=Homo sapiens G	240.53	71	22
Q9Y617	SERC_HUMAN	Phosphoserine aminotransferase OS=H	222.4	67	22
P27348	1433T_HUMAN	14-3-3 protein theta OS=Homo sapiens	300.35	76	21
P09211	GSTP1_HUMAN	Glutathione S-transferase P OS=Homo	279.58	92	21
Q04917	1433F_HUMAN	14-3-3 protein eta OS=Homo sapiens G	273.6	77	21
P12956	XRCC6_HUMAN	X-ray repair cross-complementing prote	251.79	61	21

P08133	ANXA6_HUMAN	Annexin A6 OS=Homo sapiens GN=AN	238.21	55	21
P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 OS=Hor	229.71	60	21
P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprote	268.74	90	20
P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme	253.05	57	20
P23396	RS3_HUMAN	40S ribosomal protein S3 OS=Homo sa	251.58	85	20
P26038	MOES_HUMAN	Moesin OS=Homo sapiens GN=MSN P	231.03	52	20
P39019	RS19_HUMAN	40S ribosomal protein S19 OS=Homo s	213.37	81	20
P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 OS=Homo	291.45	94	19
Q00610	CLH1_HUMAN	Clathrin heavy chain 1 OS=Homo sapie	262.75	47	19
P52209	6PGD_HUMAN	6-phosphogluconate dehydrogenase, d	252.13	74	19
P25398	RS12_HUMAN	40S ribosomal protein S12 OS=Homo s	250.95	92	19
P08670	VIME_HUMAN	Vimentin OS=Homo sapiens GN=VIM F	247.55	59	19
P13010	XRCC5_HUMAN	X-ray repair cross-complementing prote	247.19	66	19
P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondr	246.2	72	19
Q99832	TCPH_HUMAN	T-complex protein 1 subunit eta OS=Hc	241.03	68	19
P48643	TCPE_HUMAN	T-complex protein 1 subunit epsilon OS	239.83	79	19
Q01469	FABP5_HUMAN	Fatty acid-binding protein, epidermal OS	260.11	90	18
P04083	ANXA1_HUMAN	Annexin A1 OS=Homo sapiens GN=AN	248.02	68	18
P02792	FRIL_HUMAN	Ferritin light chain OS=Homo sapiens G	247.82	73	18
P78371	TCPB_HUMAN	T-complex protein 1 subunit beta OS=H	239.24	67	18
P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 OS=Homo s	236.01	73	18
P37837	TALDO_HUMAN	Transaldolase OS=Homo sapiens GN=	234.66	59	18
P22234	PUR6_HUMAN	Multifunctional protein ADE2 OS=Homc	233.69	64	18
O00231	PSD11_HUMAN	26S proteasome non-ATPase regulator	226.15	67	18
P62333	PRS10_HUMAN	26S protease regulatory subunit 10B OS	217.59	62	18
P49368	TCPG_HUMAN	T-complex protein 1 subunit gamma OS	214.46	57	18
Q14152	EIF3A_HUMAN	Eukaryotic translation initiation factor 3	209.47	34	18
P84243	H33_HUMAN	Histone H3.3 OS=Homo sapiens GN=H	175.68	66	18
P63241	IF5A1_HUMAN	Eukaryotic translation initiation factor 5A	255.86	87	17
P40926	MDHM_HUMAN	Malate dehydrogenase, mitochondrial C	252.14	77	17
P15311	EZRI_HUMAN	Ezrin OS=Homo sapiens GN=EZR PE=	245.75	62	17
O00299	CLIC1_HUMAN	Chloride intracellular channel protein 1	242.59	92	17
P34932	HSP74_HUMAN	Heat shock 70 kDa protein 4 OS=Homc	240.68	44	17
P46777	RL5_HUMAN	60S ribosomal protein L5 OS=Homo sa	239.17	61	17
P62195	PRS8_HUMAN	26S protease regulatory subunit 8 OS=	238.18	66	17
P11021	GRP78_HUMAN	78 kDa glucose-regulated protein OS=H	236.37	54	17
P62826	RAN_HUMAN	GTP-binding nuclear protein Ran OS=H	236	68	17
P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQG	226.51	50	17
P11586	C1TC_HUMAN	C-1-tetrahydrofolate synthase, cytoplas	222.32	50	17
Q9P2E9	RRBP1_HUMAN	Ribosome-binding protein 1 OS=Homo	203.88	25	17
P62081	RS7_HUMAN	40S ribosomal protein S7 OS=Homo sa	201.56	65	17
P62269	RS18_HUMAN	40S ribosomal protein S18 OS=Homo s	194.93	70	17
P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta OS	276.43	74	16
P61981	1433G_HUMAN	14-3-3 protein gamma OS=Homo sapie	258.46	86	16
P19338	NUCL_HUMAN	Nucleolin OS=Homo sapiens GN=NCL	252	64	16
P51665	PSD7_HUMAN	26S proteasome non-ATPase regulator	244.25	69	16
P09936	UCHL1_HUMAN	Ubiquitin carboxyl-terminal hydrolase is	239.85	83	16
P62424	RL7A_HUMAN	60S ribosomal protein L7a OS=Homo s	234.48	62	16
P09874	PARP1_HUMAN	Poly [ADP-ribose] polymerase 1 OS=Hc	232.46	43	16
P32119	PRDX2_HUMAN	Peroxiredoxin-2 OS=Homo sapiens GN	231.95	57	16
P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochonc	231.84	71	16
P28074	PSB5_HUMAN	Proteasome subunit beta type-5 OS=Hc	230.33	59	16
O00410	IPO5_HUMAN	Importin-5 OS=Homo sapiens GN=IPO5	225.82	44	16
Q99497	PARK7_HUMAN	Protein DJ-1 OS=Homo sapiens GN=P/	225.33	84	16
P04792	HSPB1_HUMAN	Heat shock protein beta-1 OS=Homo sa	224.97	68	16
P31948	STIP1_HUMAN	Stress-induced-phosphoprotein 1 OS=H	224.9	47	16



Q96KP4 CNDP2_HUMAN	Cytosolic non-specific dipeptidase OS=	216.01	45	16
P35232 PHB_HUMAN	Prohibitin OS=Homo sapiens GN=PHB	215.51	82	16
P61604 CH10_HUMAN	10 kDa heat shock protein, mitochondri	200.28	83	16
P12277 KCRB_HUMAN	Creatine kinase B-type OS=Homo sapie	231.14	69	15
P61978 HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprote	230.93	58	15
Q9Y224 CN166_HUMAN	UPF0568 protein C14orf166 OS=Homo	227.23	89	15
P20618 PSB1_HUMAN	Proteasome subunit beta type-1 OS=Ho	226.83	73	15
O60664 PLIN3_HUMAN	Perilipin-3 OS=Homo sapiens GN=PLIN	225.59	69	15
P63244 GBLP_HUMAN	Guanine nucleotide-binding protein sub	225.36	67	15
P35998 PRS7_HUMAN	26S protease regulatory subunit 7 OS=	221.78	59	15
P12429 ANXA3_HUMAN	Annexin A3 OS=Homo sapiens GN=AN	220.33	71	15
P06744 G6PI_HUMAN	Glucose-6-phosphate isomerase OS=H	219.01	44	15
P07910 HNRPC_HUMAN	Heterogeneous nuclear ribonucleoprote	210.07	58	15
P62316 SMD2_HUMAN	Small nuclear ribonucleoprotein Sm D2	204.96	69	15
Q9Y230 RUVB2_HUMAN	RuvB-like 2 OS=Homo sapiens GN=RU	199.09	41	15
P08238 HS90B_HUMAN	Heat shock protein HSP 90-beta OS=H	322.53	65	14
P31946 1433B_HUMAN	14-3-3 protein beta/alpha OS=Homo sa	273.43	78	14
P22626 ROA2_HUMAN	Heterogeneous nuclear ribonucleoprote	245.9	60	14
O43175 SERA_HUMAN	D-3-phosphoglycerate dehydrogenase	239.46	69	14
Q9HB71 CYBP_HUMAN	Calcyclin-binding protein OS=Homo sap	236.91	71	14
P06748 NPM_HUMAN	Nucleophosmin OS=Homo sapiens GN=	223.88	69	14
P23246 SFPQ_HUMAN	Splicing factor, proline- and glutamine-r	206.38	47	14
P60900 PSA6_HUMAN	Proteasome subunit alpha type-6 OS=H	205.63	56	14
Q04760 LGUL_HUMAN	Lactoylglutathione lyase OS=Homo sap	200.5	55	14
P52272 HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprote	199.66	69	14
P30044 PRDX5_HUMAN	Peroxisredoxin-5, mitochondrial OS=Hor	198.85	79	14
Q01518 CAP1_HUMAN	Adenylyl cyclase-associated protein 1 C	197.81	63	14
P62263 RS14_HUMAN	40S ribosomal protein S14 OS=Homo s	197.37	56	14
Q7KZF4 SND1_HUMAN	Staphylococcal nuclease domain-conta	195.29	38	14
P62280 RS11_HUMAN	40S ribosomal protein S11 OS=Homo s	193.73	63	14
P46781 RS9_HUMAN	40S ribosomal protein S9 OS=Homo sa	174.48	42	14
P00441 SODC_HUMAN	Superoxide dismutase [Cu-Zn] OS=Hor	238.57	94	13
P26641 EF1G_HUMAN	Elongation factor 1-gamma OS=Homo s	218.09	45	13
P40227 TCPZ_HUMAN	T-complex protein 1 subunit zeta OS=H	216.61	51	13
O75347 TBCA_HUMAN	Tubulin-specific chaperone A OS=Hom	214.46	80	13
Q9H9Z2 LN28A_HUMAN	Protein lin-28 homolog A OS=Homo sap	212.11	61	13
P25789 PSA4_HUMAN	Proteasome subunit alpha type-4 OS=H	211.26	61	13
Q15631 TSN_HUMAN	Translin OS=Homo sapiens GN=TSN P	210.85	49	13
P62906 RL10A_HUMAN	60S ribosomal protein L10a OS=Homo	208.71	41	13
Q01581 HMCS1_HUMAN	Hydroxymethylglutaryl-CoA synthase, c	207.81	58	13
P13796 PLSL_HUMAN	Plastin-2 OS=Homo sapiens GN=LCP1	205.66	48	13
P54577 SYYC_HUMAN	Tyrosyl-tRNA synthetase, cytoplasmic C	203.19	55	13
O15067 PUR4_HUMAN	Phosphoribosylformylglycinamide syn	203.17	36	13
Q14019 COTL1_HUMAN	Coactosin-like protein OS=Homo sapie	195.2	61	13
P58107 EPIPL_HUMAN	Epiplakin OS=Homo sapiens GN=EPPH	162.59	25	13
O14818 PSA7_HUMAN	Proteasome subunit alpha type-7 OS=H	250.18	88	12
P09972 ALDOC_HUMAN	Fructose-bisphosphate aldolase C OS=	244.1	74	12
P50453 SPB9_HUMAN	Serpin B9 OS=Homo sapiens GN=SER	224.88	58	12
O75531 BAF_HUMAN	Barrier-to-autointegration factor OS=Ho	218.95	76	12
A8MW06 TMSL3_HUMAN	Thymosin beta-4-like protein 3 OS=Hor	213.97	89	12
P62328 TYB4_HUMAN	Thymosin beta-4 OS=Homo sapiens GI	213.97	89	12
P62277 RS13_HUMAN	40S ribosomal protein S13 OS=Homo s	210.57	61	12
Q9UL46 PSME2_HUMAN	Proteasome activator complex subunit 2	205.93	79	12
Q15008 PSMD6_HUMAN	26S proteasome non-ATPase regulator	201.47	41	12
Q99623 PHB2_HUMAN	Prohibitin-2 OS=Homo sapiens GN=PH	200.27	56	12
Q15056 IF4H_HUMAN	Eukaryotic translation initiation factor 4H	199.77	86	12

Q05682	CALD1_HUMAN	Caldesmon OS=Homo sapiens GN=CA	199.43	38	12
P23284	PIIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B OS	197.78	58	12
P29692	EF1D_HUMAN	Elongation factor 1-delta OS=Homo sap	197.36	46	12
P49321	NASP_HUMAN	Nuclear autoantigenic sperm protein OS	196.07	45	12
P78417	GSTO1_HUMAN	Glutathione S-transferase omega-1 OS	195.01	44	12
Q13200	PSMD2_HUMAN	26S proteasome non-ATPase regulator	188.9	53	12
P17980	PRS6A_HUMAN	26S protease regulatory subunit 6A OS	182.86	53	12
O15144	ARPC2_HUMAN	Actin-related protein 2/3 complex subur	181.92	52	12
P61353	RL27_HUMAN	60S ribosomal protein L27 OS=Homo s	180.7	60	12
Q02878	RL6_HUMAN	60S ribosomal protein L6 OS=Homo sa	172.46	38	12
Q15907	RB11B_HUMAN	Ras-related protein Rab-11B OS=Homoc	172.3	68	12
P42704	LPPRC_HUMAN	Leucine-rich PPR motif-containing prote	141.1	30	12
P30153	2AAA_HUMAN	Serine/threonine-protein phosphatase 2	249.96	67	11
P07741	APT_HUMAN	Adenine phosphoribosyltransferase OS	220.09	90	11
Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6 OS=Hor	218.87	67	11
P05387	RLA2_HUMAN	60S acidic ribosomal protein P2 OS=Hc	205.56	83	11
P28066	PSA5_HUMAN	Proteasome subunit alpha type-5 OS=H	204.62	72	11
P62158	CALM_HUMAN	Calmodulin OS=Homo sapiens GN=CA	201.81	59	11
P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding prote	201.55	68	11
Q92598	HS105_HUMAN	Heat shock protein 105 kDa OS=Homo	197.04	34	11
P40925	MDHC_HUMAN	Malate dehydrogenase, cytoplasmic OS	196.66	57	11
Q15691	MARE1_HUMAN	Microtubule-associated protein RP/EB f	196.23	44	11
P25786	PSA1_HUMAN	Proteasome subunit alpha type-1 OS=H	190.99	65	11
P17174	AATC_HUMAN	Aspartate aminotransferase, cytoplasm	190.75	49	11
P43487	RANG_HUMAN	Ran-specific GTPase-activating protein	189.74	64	11
Q9BWD1	THIC_HUMAN	Acetyl-CoA acetyltransferase, cytosolic	186.62	61	11
P26639	SYTC_HUMAN	Threonyl-tRNA synthetase, cytoplasmic	183.97	41	11
Q04837	SSBP_HUMAN	Single-stranded DNA-binding protein, m	179.68	72	11
P46782	RS5_HUMAN	40S ribosomal protein S5 OS=Homo sa	179.5	57	11
P48681	NEST_HUMAN	Nestin OS=Homo sapiens GN=NES PE	178.4	18	11
P18621	RL17_HUMAN	60S ribosomal protein L17 OS=Homo s	174.85	61	11
P07093	GDN_HUMAN	Glia-derived nexin OS=Homo sapiens G	174.5	52	11
P60903	S10AA_HUMAN	Protein S100-A10 OS=Homo sapiens G	173.03	80	11
P18124	RL7_HUMAN	60S ribosomal protein L7 OS=Homo sa	172.34	59	11
P62760	VISL1_HUMAN	Visinin-like protein 1 OS=Homo sapiens	171.01	69	11
O15145	ARPC3_HUMAN	Actin-related protein 2/3 complex subur	163	49	11
P07814	SYEP_HUMAN	Bifunctional aminoacyl-tRNA synthetase	161.29	23	11
P09493	TPM1_HUMAN	Tropomyosin alpha-1 chain OS=Homo s	304.36	90	10
P06753	TPM3_HUMAN	Tropomyosin alpha-3 chain OS=Homo s	299.42	81	10
P31947	1433S_HUMAN	14-3-3 protein sigma OS=Homo sapien	222.04	87	10
P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform OS	221.74	68	10
Q96FW1	OTUB1_HUMAN	Ubiquitin thioesterase OTUB1 OS=Hom	214.87	47	10
Q9Y696	CLIC4_HUMAN	Chloride intracellular channel protein 4	211.06	76	10
Q9NZI8	IF2B1_HUMAN	Insulin-like growth factor 2 mRNA-bindin	203.41	43	10
P63220	RS21_HUMAN	40S ribosomal protein S21 OS=Homo s	202.13	71	10
Q13907	IDI1_HUMAN	Isopentenyl-diphosphate Delta-isomera	201.96	59	10
O95336	6PGL_HUMAN	6-phosphogluconolactonase OS=Homo	201.05	77	10
P27695	APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase	200.37	61	10
P30084	ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial OS	199.04	68	10
Q7L2H7	EIF3M_HUMAN	Eukaryotic translation initiation factor 3	198.27	71	10
P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 O	197.36	54	10
Q16851	UGPA_HUMAN	UTP--glucose-1-phosphate uridylyltrans	196.5	38	10
Q9Y265	RUVB1_HUMAN	RuvB-like 1 OS=Homo sapiens GN=RU	191.5	54	10
P62829	RL23_HUMAN	60S ribosomal protein L23 OS=Homo s	191.41	69	10
P30040	ERP29_HUMAN	Endoplasmic reticulum resident protein	190.48	56	10
P22102	PUR2_HUMAN	Trifunctional purine biosynthetic protein	189.59	42	10

P22061	PIMT_HUMAN	Protein-L-isoaspartate(D-aspartate) O-r	188.54	70	10
P50991	TCPD_HUMAN	T-complex protein 1 subunit delta OS=H	188.22	42	10
P24539	AT5F1_HUMAN	ATP synthase subunit b, mitochondrial	187.12	48	10
O00151	PDLI1_HUMAN	PDZ and LIM domain protein 1 OS=Hor	184.55	42	10
O43242	PSMD3_HUMAN	26S proteasome non-ATPase regulator	181.74	44	10
P48047	ATPO_HUMAN	ATP synthase subunit O, mitochondrial	181.19	72	10
P15559	NQO1_HUMAN	NAD(P)H dehydrogenase [quinone] 1 C	177.1	56	10
P62249	RS16_HUMAN	40S ribosomal protein S16 OS=Homo s	174.88	66	10
Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprote	174.67	28	10
P51149	RAB7A_HUMAN	Ras-related protein Rab-7a OS=Homo s	174.17	56	10
Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB OS=Homo	174	28	10
Q07020	RL18_HUMAN	60S ribosomal protein L18 OS=Homo s	172.96	48	10
P62750	RL23A_HUMAN	60S ribosomal protein L23a OS=Homo	172.53	61	10
P63173	RL38_HUMAN	60S ribosomal protein L38 OS=Homo s	168.34	61	10
P53634	CATC_HUMAN	Dipeptidyl peptidase 1 OS=Homo sapie	165.77	31	10
P07237	PDIA1_HUMAN	Protein disulfide-isomerase OS=Homo s	165.08	39	10
P49755	TMEDA_HUMAN	Transmembrane emp24 domain-containi	164.65	48	10
P27816	MAP4_HUMAN	Microtubule-associated protein 4 OS=H	162.42	27	10
P17987	TCPA_HUMAN	T-complex protein 1 subunit alpha OS=	160.58	48	10
P26373	RL13_HUMAN	60S ribosomal protein L13 OS=Homo s	144.94	37	10
Q9GZZ1	NAA50_HUMAN	N-alpha-acetyltransferase 50, NatE cata	132.28	55	10
P12829	MYL4_HUMAN	Myosin light chain 4 OS=Homo sapiens	209.03	63	9
P09429	HMGB1_HUMAN	High mobility group protein B1 OS=Hon	205.41	61	9
P13797	PLST_HUMAN	Plastin-3 OS=Homo sapiens GN=PLS3	201.43	57	9
P49588	SYAC_HUMAN	Alanyl-tRNA synthetase, cytoplasmic O	197.17	52	9
P12268	IMDH2_HUMAN	Inosine-5'-monophosphate dehydrogen	194.48	37	9
P16401	H15_HUMAN	Histone H1.5 OS=Homo sapiens GN=H	193.64	58	9
P15880	RS2_HUMAN	40S ribosomal protein S2 OS=Homo sa	188.02	65	9
P09960	LKHA4_HUMAN	Leukotriene A-4 hydrolase OS=Homo s	186.75	46	9
P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta OS	185.32	64	9
P00491	PNPH_HUMAN	Purine nucleoside phosphorylase OS=H	185.17	48	9
P14324	FPPS_HUMAN	Farnesyl pyrophosphate synthase OS=	183.31	48	9
Q9UNM6	PSD13_HUMAN	26S proteasome non-ATPase regulator	182.21	55	9
P49720	PSB3_HUMAN	Proteasome subunit beta type-3 OS=Ho	181.6	64	9
P12004	PCNA_HUMAN	Proliferating cell nuclear antigen OS=Ho	180.66	59	9
P09382	LEG1_HUMAN	Galectin-1 OS=Homo sapiens GN=LGA	177.62	74	9
Q15404	RSU1_HUMAN	Ras suppressor protein 1 OS=Homo sa	174.31	68	9
P07108	ACBP_HUMAN	Acyl-CoA-binding protein OS=Homo sa	173.46	85	9
P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial OS=Ho	171.62	31	9
Q99536	VAT1_HUMAN	Synaptic vesicle membrane protein VAT	170.64	52	9
P43686	PRS6B_HUMAN	26S protease regulatory subunit 6B OS	169.89	27	9
P62244	RS15A_HUMAN	40S ribosomal protein S15a OS=Homo	167.74	76	9
P09661	RU2A_HUMAN	U2 small nuclear ribonucleoprotein A' C	166.35	54	9
P14678	RSMB_HUMAN	Small nuclear ribonucleoprotein-associ	165.31	71	9
P63162	RSMN_HUMAN	Small nuclear ribonucleoprotein-associ	165.31	58	9
P60866	RS20_HUMAN	40S ribosomal protein S20 OS=Homo s	164.06	54	9
Q9Y295	DRG1_HUMAN	Developmentally-regulated GTP-binding	155.66	48	9
Q5T7N2	LITD1_HUMAN	LINE-1 type transposase domain-conta	154.94	32	9
P00505	AATM_HUMAN	Aspartate aminotransferase, mitochond	153.16	33	9
Q8N163	K1967_HUMAN	Protein KIAA1967 OS=Homo sapiens G	150.4	22	9
P41250	SYG_HUMAN	Glycyl-tRNA synthetase OS=Homo sap	147.43	20	9
P18077	RL35A_HUMAN	60S ribosomal protein L35a OS=Homo	133.07	30	9
P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-I OS=Hor	226.95	48	8
A6NL28	TPM3L_HUMAN	Putative tropomyosin alpha-3 chain-like	208.17	50	8
P61758	PFD3_HUMAN	Prefoldin subunit 3 OS=Homo sapiens	199.6	68	8
Q01105	SET_HUMAN	Protein SET OS=Homo sapiens GN=SE	195.99	62	8

P54819	KAD2_HUMAN	Adenylate kinase 2, mitochondrial OS=H	185.35	69	8
P08865	RSSA_HUMAN	40S ribosomal protein SA OS=Homo sa	182.55	38	8
Q13185	CBX3_HUMAN	Chromobox protein homolog 3 OS=Hor	182.55	55	8
P60983	GMFB_HUMAN	Glia maturation factor beta OS=Homo s	180.6	61	8
P49903	SPS1_HUMAN	Selenide, water dikinase 1 OS=Homo s	180.22	53	8
P06493	CDK1_HUMAN	Cyclin-dependent kinase 1 OS=Homo s	179.88	62	8
P46783	RS10_HUMAN	40S ribosomal protein S10 OS=Homo s	179.6	57	8
P60981	DEST_HUMAN	Dextrin OS=Homo sapiens GN=DSTN I	179.56	53	8
Q9Y310	RTCB_HUMAN	tRNA-splicing ligase RtcB homolog OS=	178.44	61	8
P31949	S10AB_HUMAN	Protein S100-A11 OS=Homo sapiens G	177.92	90	8
Q08J23	NSUN2_HUMAN	tRNA (cytosine(34)-C(5))-methyltransfe	177.48	41	8
Q99714	HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type	174.35	54	8
O43809	CPSF5_HUMAN	Cleavage and polyadenylation specificit	173.5	61	8
P61289	PSME3_HUMAN	Proteasome activator complex subunit 3	172.4	56	8
P16152	CBR1_HUMAN	Carbonyl reductase [NADPH] 1 OS=Ho	170.91	57	8
P62888	RL30_HUMAN	60S ribosomal protein L30 OS=Homo s	170.01	73	8
P60953	CDC42_HUMAN	Cell division control protein 42 homolog	169.87	53	8
Q13838	DX39B_HUMAN	Spliceosome RNA helicase DDX39B OS=	168.78	32	8
Q14566	MCM6_HUMAN	DNA replication licensing factor MCM6	168.26	18	8
P62241	RS8_HUMAN	40S ribosomal protein S8 OS=Homo sa	166.8	57	8
P14550	AK1A1_HUMAN	Alcohol dehydrogenase [NADP+] OS=H	166.66	44	8
Q9NR30	DDX21_HUMAN	Nucleolar RNA helicase 2 OS=Homo sa	165.94	33	8
P61158	ARP3_HUMAN	Actin-related protein 3 OS=Homo sapie	165.63	31	8
P35268	RL22_HUMAN	60S ribosomal protein L22 OS=Homo s	164.76	71	8
O60701	UGDH_HUMAN	UDP-glucose 6-dehydrogenase OS=Ho	164.38	26	8
P25788	PSA3_HUMAN	Proteasome subunit alpha type-3 OS=H	164.07	49	8
O43765	SGTA_HUMAN	Small glutamine-rich tetratricopeptide re	163.55	43	8
P10909	CLUS_HUMAN	Clusterin OS=Homo sapiens GN=CLU I	161.11	26	8
Q9BT78	CSN4_HUMAN	COP9 signalosome complex subunit 4 C	161	44	8
Q15233	NONO_HUMAN	Non-POU domain-containing octamer-b	159.68	58	8
P30048	PRDX3_HUMAN	Thioredoxin-dependent peroxide reduct	158.44	42	8
P16949	STMN1_HUMAN	Stathmin OS=Homo sapiens GN=STMN	158.27	46	8
Q09666	AHNK_HUMAN	Neuroblast differentiation-associated pr	156.33	19	8
P35573	GDE_HUMAN	Glycogen debranching enzyme OS=Ho	155.97	22	8
Q9H9Q2	CSN7B_HUMAN	COP9 signalosome complex subunit 7b	155.47	46	8
Q9Y266	NUDC_HUMAN	Nuclear migration protein nudC OS=Ho	154.8	39	8
Q9P2J5	SYLC_HUMAN	Leucyl-tRNA synthetase, cytoplasmic O	154.16	25	8
P06454	PTMA_HUMAN	Prothymosin alpha OS=Homo sapiens C	153.41	62	8
P14868	SYDC_HUMAN	Aspartyl-tRNA synthetase, cytoplasmic	150.83	26	8
Q16181	SEPT7_HUMAN	Septin-7 OS=Homo sapiens GN=SEPT	149.87	45	8
Q07955	SRSF1_HUMAN	Serine/arginine-rich splicing factor 1 OS	147.48	47	8
P82979	SARNP_HUMAN	SAP domain-containing ribonucleoprote	146.35	57	8
P49721	PSB2_HUMAN	Proteasome subunit beta type-2 OS=Ho	145.15	36	8
Q9P258	RCC2_HUMAN	Protein RCC2 OS=Homo sapiens GN=f	140.96	34	8
P62851	RS25_HUMAN	40S ribosomal protein S25 OS=Homo s	138.86	38	8
Q15019	SEPT2_HUMAN	Septin-2 OS=Homo sapiens GN=SEPT	138.5	29	8
Q9UBE0	SAE1_HUMAN	SUMO-activating enzyme subunit 1 OS=	129.01	39	8
Q15075	EEA1_HUMAN	Early endosome antigen 1 OS=Homo s	118.81	15	8
P07437	TBB5_HUMAN	Tubulin beta chain OS=Homo sapiens C	336.6	82	7
P22392	NDKB_HUMAN	Nucleoside diphosphate kinase B OS=H	246.77	92	7
P84077	ARF1_HUMAN	ADP-ribosylation factor 1 OS=Homo sa	211.12	85	7
P61204	ARF3_HUMAN	ADP-ribosylation factor 3 OS=Homo sa	211.12	80	7
Q16555	DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 C	197.25	55	7
P55209	NP1L1_HUMAN	Nucleosome assembly protein 1-like 1 C	196.55	34	7
P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 OS=H	193.66	47	7
P60660	MYL6_HUMAN	Myosin light polypeptide 6 OS=Homo sa	188.78	68	7

P23526	SAHH_HUMAN	Adenosylhomocysteinase OS=Homo sa	185.35	45	7
Q99439	CNN2_HUMAN	Calponin-2 OS=Homo sapiens GN=CN	184.61	47	7
Q15181	IPYR_HUMAN	Inorganic pyrophosphatase OS=Homo s	181.03	55	7
P02751	FINC_HUMAN	Fibronectin OS=Homo sapiens GN=FN	180.55	15	7
P30050	RL12_HUMAN	60S ribosomal protein L12 OS=Homo s	178.97	61	7
Q14195	DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 C	178.97	41	7
Q12906	ILF3_HUMAN	Interleukin enhancer-binding factor 3 O	178.57	40	7
P07602	SAP_HUMAN	Proactivator polypeptide OS=Homo sap	174.69	49	7
P36405	ARL3_HUMAN	ADP-ribosylation factor-like protein 3 O	174.54	77	7
P27797	CALR_HUMAN	Calreticulin OS=Homo sapiens GN=CA	174.41	33	7
P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1	173.63	42	7
P45974	UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5	173.14	24	7
P68036	UB2L3_HUMAN	Ubiquitin-conjugating enzyme E2 L3 OS	172.83	68	7
Q92499	DDX1_HUMAN	ATP-dependent RNA helicase DDX1 O	171.05	35	7
Q15942	ZYX_HUMAN	Zyxin OS=Homo sapiens GN=ZYX PE=	170.75	29	7
Q71UI9	H2AV_HUMAN	Histone H2A.V OS=Homo sapiens GN=	168.63	56	7
P0C0S5	H2AZ_HUMAN	Histone H2A.Z OS=Homo sapiens GN=	168.63	56	7
P62753	RS6_HUMAN	40S ribosomal protein S6 OS=Homo sa	168.53	34	7
P53999	TCP4_HUMAN	Activated RNA polymerase II transcripti	168.38	51	7
Q13126	MTAP_HUMAN	S-methyl-5'-thioadenosine phosphorylas	167.58	48	7
P61106	RAB14_HUMAN	Ras-related protein Rab-14 OS=Homo s	166.8	52	7
P20290	BTF3_HUMAN	Transcription factor BTF3 OS=Homo sa	166.72	66	7
Q9Y2B0	CNPY2_HUMAN	Protein canopy homolog 2 OS=Homo s	166.64	60	7
P37108	SRP14_HUMAN	Signal recognition particle 14 kDa prote	166.3	43	7
P50502	F10A1_HUMAN	Hsc70-interacting protein OS=Homo sa	165.92	33	7
P05067	A4_HUMAN	Amyloid beta A4 protein OS=Homo sap	165.88	26	7
P33176	KINH_HUMAN	Kinesin-1 heavy chain OS=Homo sapie	164.98	43	7
Q9H4A6	GOLP3_HUMAN	Golgi phosphoprotein 3 OS=Homo sapi	164.79	39	7
Q92626	PXDN_HUMAN	Peroxidasin homolog OS=Homo sapien	164.48	19	7
Q12904	AIMP1_HUMAN	Aminoacyl tRNA synthase complex-inte	164.32	38	7
Q9Y3F4	STRAP_HUMAN	Serine-threonine kinase receptor-assoc	163.17	37	7
P62841	RS15_HUMAN	40S ribosomal protein S15 OS=Homo s	161.77	51	7
P24534	EF1B_HUMAN	Elongation factor 1-beta OS=Homo sap	161.67	39	7
Q13263	TIF1B_HUMAN	Transcription intermediary factor 1-beta	159.97	28	7
P61019	RAB2A_HUMAN	Ras-related protein Rab-2A OS=Homo	159.04	41	7
P63279	UBC9_HUMAN	SUMO-conjugating enzyme UBC9 OS=	158.47	32	7
Q15843	NEDD8_HUMAN	NEDD8 OS=Homo sapiens GN=NEDD8	157.58	62	7
P61088	UBE2N_HUMAN	Ubiquitin-conjugating enzyme E2 N OS=	156.94	68	7
Q02790	FKBP4_HUMAN	Peptidyl-prolyl cis-trans isomerase FKB	156.86	31	7
P46926	GNP11_HUMAN	Glucosamine-6-phosphate isomerase 1	156.83	42	7
Q9HC38	GLOD4_HUMAN	Glyoxalase domain-containing protein 4	156.2	36	7
P30046	DOPD_HUMAN	D-dopachrome decarboxylase OS=Hon	155.11	56	7
Q9Y2Z0	SUGT1_HUMAN	Suppressor of G2 allele of SKP1 homol	154.77	47	7
Q13557	KCC2D_HUMAN	Calcium/calmodulin-dependent protein	154.3	42	7
Q9H3K6	BOLA2_HUMAN	BolA-like protein 2 OS=Homo sapiens C	153.94	72	7
Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A OS=H	153.93	17	7
Q02543	RL18A_HUMAN	60S ribosomal protein L18a OS=Homo	153.88	47	7
P08708	RS17_HUMAN	40S ribosomal protein S17 OS=Homo s	153.64	76	7
O00232	PSD12_HUMAN	26S proteasome non-ATPase regulator	153.09	39	7
P59998	ARPC4_HUMAN	Actin-related protein 2/3 complex subur	152.93	62	7
O75489	NDUS3_HUMAN	NADH dehydrogenase [ubiquinone] iron	152.91	50	7
P43243	MATR3_HUMAN	Matrin-3 OS=Homo sapiens GN=MATR	152.12	29	7
P32969	RL9_HUMAN	60S ribosomal protein L9 OS=Homo sa	151.38	58	7
P46778	RL21_HUMAN	60S ribosomal protein L21 OS=Homo s	151.07	40	7
P05937	CALB1_HUMAN	Calbindin OS=Homo sapiens GN=CALB	150.86	45	7
Q15149	PLEC_HUMAN	Plectin OS=Homo sapiens GN=PLEC F	149.19	18	7

Q5VYK3 ECM29_HUMAN	Proteasome-associated protein ECM29	149.05	37	7
Q9BYT8 NEUL_HUMAN	Neurolysin, mitochondrial OS=Homo sa	148.81	24	7
Q9NZL4 HPBP1_HUMAN	Hsp70-binding protein 1 OS=Homo sap	148.69	33	7
Q16658 FSCN1_HUMAN	Fascin OS=Homo sapiens GN=FSCN1	148.66	32	7
P55145 MANF_HUMAN	Mesencephalic astrocyte-derived neuro	148.56	54	7
P36578 RL4_HUMAN	60S ribosomal protein L4 OS=Homo sa	146.26	23	7
P62633 CNBP_HUMAN	Cellular nucleic acid-binding protein OS	146.06	53	7
Q13283 G3BP1_HUMAN	Ras GTPase-activating protein-binding	145.21	27	7
P55769 NH2L1_HUMAN	NHP2-like protein 1 OS=Homo sapiens	144.72	41	7
P61081 UBC12_HUMAN	NEDD8-conjugating enzyme Ubc12 OS	144.21	44	7
P62857 RS28_HUMAN	40S ribosomal protein S28 OS=Homo s	143.07	57	7
P63000 RAC1_HUMAN	Ras-related C3 botulinum toxin substrat	142.95	35	7
Q86VP6 CAND1_HUMAN	Cullin-associated NEDD8-dissociated p	141.54	17	7
Q9NP97 DLRB1_HUMAN	Dynein light chain roadblock-type 1 OS:	139.12	91	7
Q92616 GCN1L_HUMAN	Translational activator GCN1 OS=Homo	138.81	17	7
P27635 RL10_HUMAN	60S ribosomal protein L10 OS=Homo s	138.37	31	7
P25205 MCM3_HUMAN	DNA replication licensing factor MCM3	137.11	38	7
Q15370 ELOB_HUMAN	Transcription elongation factor B polype	136.92	49	7
P48556 PSMD8_HUMAN	26S proteasome non-ATPase regulator	129.8	35	7
O75947 ATP5H_HUMAN	ATP synthase subunit d, mitochondrial	125.39	55	7
P52701 MSH6_HUMAN	DNA mismatch repair protein Msh6 OS:	125.36	15	7
O43324 MCA3_HUMAN	Eukaryotic translation elongation factor	117.5	40	7
Q9BXJ9 NAA15_HUMAN	N-alpha-acetyltransferase 15, NatA aux	117.3	13	7
P12270 TPR_HUMAN	Nucleoprotein TPR OS=Homo sapiens	117	12	7
P62136 PP1A_HUMAN	Serine/threonine-protein phosphatase F	243.73	62	6
Q9BUF5 TBB6_HUMAN	Tubulin beta-6 chain OS=Homo sapiens	236.14	78	6
P15531 NDKA_HUMAN	Nucleoside diphosphate kinase A OS=H	234.26	72	6
Q06323 PSME1_HUMAN	Proteasome activator complex subunit 1	180.47	65	6
P21291 CSRP1_HUMAN	Cysteine and glycine-rich protein 1 OS=	177.09	65	6
Q15121 PEA15_HUMAN	Astrocytic phosphoprotein PEA-15 OS=	173.78	88	6
P36404 ARL2_HUMAN	ADP-ribosylation factor-like protein 2 O	172.92	53	6
P52292 IMA2_HUMAN	Importin subunit alpha-2 OS=Homo sap	172.76	37	6
P21796 VDAC1_HUMAN	Voltage-dependent anion-selective cha	168.48	43	6
Q9Y333 LSM2_HUMAN	U6 snRNA-associated Sm-like protein L	168.45	86	6
O60610 DIAP1_HUMAN	Protein diaphanous homolog 1 OS=Hor	168.43	26	6
Q99598 TSNAX_HUMAN	Translin-associated protein X OS=Hom	167.99	57	6
Q9Y262 EIF3L_HUMAN	Eukaryotic translation initiation factor 3	167.96	35	6
Q96FQ6 S10AG_HUMAN	Protein S100-A16 OS=Homo sapiens G	165.62	56	6
P04632 CPNS1_HUMAN	Calpain small subunit 1 OS=Homo sapi	164.99	63	6
Q14103 HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprote	164.86	45	6
Q15365 PCBP1_HUMAN	Poly(rC)-binding protein 1 OS=Homo sa	164.63	64	6
P20700 LMNB1_HUMAN	Lamin-B1 OS=Homo sapiens GN=LMN	163.92	33	6
P35221 CTNA1_HUMAN	Catenin alpha-1 OS=Homo sapiens GN	162.63	41	6
Q9UBQ7 GRHPR_HUMAN	Glyoxylate reductase/hydroxypyruvate r	162.59	41	6
P13073 COX41_HUMAN	Cytochrome c oxidase subunit 4 isoform	161.11	62	6
P63313 TYB10_HUMAN	Thymosin beta-10 OS=Homo sapiens G	159.97	82	6
Q99471 PFD5_HUMAN	Prefoldin subunit 5 OS=Homo sapiens	155.84	60	6
Q16643 DREB_HUMAN	Drebrin OS=Homo sapiens GN=DBN1	155.38	24	6
Q9Y3B8 ORN_HUMAN	Oligoribonuclease, mitochondrial OS=H	155.01	45	6
P62913 RL11_HUMAN	60S ribosomal protein L11 OS=Homo s	154.16	30	6
Q9UKK9 NUDT5_HUMAN	ADP-sugar pyrophosphatase OS=Homo	151.76	36	6
Q8WW12 PCNP_HUMAN	PEST proteolytic signal-containing nucl	151.72	57	6
P29762 RABP1_HUMAN	Cellular retinoic acid-binding protein 1 C	150.66	53	6
P84103 SRSF3_HUMAN	Serine/arginine-rich splicing factor 3 OS	150.21	46	6
O14737 PDCD5_HUMAN	Programmed cell death protein 5 OS=H	148.72	51	6
P33993 MCM7_HUMAN	DNA replication licensing factor MCM7	148.56	30	6

P11177	ODPB_HUMAN	Pyruvate dehydrogenase E1 componen	147.9	45	6
P05388	RLA0_HUMAN	60S acidic ribosomal protein P0 OS=Hc	147.46	30	6
Q9NTK5	OLA1_HUMAN	Obg-like ATPase 1 OS=Homo sapiens	147.09	32	6
P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein	145.35	46	6
P49736	MCM2_HUMAN	DNA replication licensing factor MCM2	145.31	36	6
P62917	RL8_HUMAN	60S ribosomal protein L8 OS=Homo sa	144.43	38	6
P13667	PDIA4_HUMAN	Protein disulfide-isomerase A4 OS=Hor	143.85	16	6
Q9Y4L1	HYOU1_HUMAN	Hypoxia up-regulated protein 1 OS=Hor	143.53	25	6
Q12765	SCRN1_HUMAN	Secernin-1 OS=Homo sapiens GN=SCI	143.3	26	6
P00492	HPRT_HUMAN	Hypoxanthine-guanine phosphoribosylti	143.03	31	6
Q9Y5K6	CD2AP_HUMAN	CD2-associated protein OS=Homo sapi	142.91	23	6
O00244	ATOX1_HUMAN	Copper transport protein ATOX1 OS=H	142.36	78	6
P13693	TCTP_HUMAN	Translationally-controlled tumor protein	141.86	40	6
O14579	COPE_HUMAN	Coatomer subunit epsilon OS=Homo sa	140.79	39	6
P49915	GUAA_HUMAN	GMP synthase [glutamine-hydrolyzing] c	140.65	31	6
O15372	EIF3H_HUMAN	Eukaryotic translation initiation factor 3	140.43	38	6
P02545	LMNA_HUMAN	Prelamin-A/C OS=Homo sapiens GN=L	139.03	22	6
O15347	HMGB3_HUMAN	High mobility group protein B3 OS=Hon	138.78	36	6
P49773	HINT1_HUMAN	Histidine triad nucleotide-binding protei	138.55	44	6
P47985	UCRI_HUMAN	Cytochrome b-c1 complex subunit Ries	138.07	50	6
P50914	RL14_HUMAN	60S ribosomal protein L14 OS=Homo s	137.31	41	6
P33991	MCM4_HUMAN	DNA replication licensing factor MCM4	136.27	29	6
Q92945	FUBP2_HUMAN	Far upstream element-binding protein 2	136.11	21	6
P62899	RL31_HUMAN	60S ribosomal protein L31 OS=Homo s	134.45	49	6
O75223	GGCT_HUMAN	Gamma-glutamylcyclotransferase OS=h	134.27	70	6
P54578	UBP14_HUMAN	Ubiquitin carboxyl-terminal hydrolase 14	134.27	27	6
P07686	HEXB_HUMAN	Beta-hexosaminidase subunit beta OS=	133.34	21	6
P07942	LAMB1_HUMAN	Laminin subunit beta-1 OS=Homo sapie	132.97	23	6
P24666	PPAC_HUMAN	Low molecular weight phosphotyrosine	132.04	51	6
P54136	SYRC_HUMAN	Arginyl-tRNA synthetase, cytoplasmic C	131.23	21	6
P07339	CATD_HUMAN	Cathepsin D OS=Homo sapiens GN=C	129.38	24	6
P09525	ANXA4_HUMAN	Annexin A4 OS=Homo sapiens GN=AN	127.84	40	6
Q93009	UBP7_HUMAN	Ubiquitin carboxyl-terminal hydrolase 7	127.06	15	6
P27144	KAD4_HUMAN	Adenylate kinase isoenzyme 4, mitocho	126.67	32	6
O95671	ASML_HUMAN	N-acetylserotonin O-methyltransferase-	126.58	32	6
O76003	GLRX3_HUMAN	Glutaredoxin-3 OS=Homo sapiens GN=	126.53	43	6
P20674	COX5A_HUMAN	Cytochrome c oxidase subunit 5A, mito	126.09	43	6
P09669	COX6C_HUMAN	Cytochrome c oxidase subunit 6C OS=H	124.52	61	6
Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 OS	124.05	17	6
Q6PKG0	LARP1_HUMAN	La-related protein 1 OS=Homo sapiens	123.34	17	6
Q9NUP9	LIN7C_HUMAN	Protein lin-7 homolog C OS=Homo sapi	122.09	44	6
P46779	RL28_HUMAN	60S ribosomal protein L28 OS=Homo s	121.53	42	6
A0MZ66	SHOT1_HUMAN	Shootin-1 OS=Homo sapiens GN=KIAA	119.09	16	6
P46821	MAP1B_HUMAN	Microtubule-associated protein 1B OS=	117.05	12	6
P62312	LSM6_HUMAN	U6 snRNA-associated Sm-like protein L	112.24	46	6
P14174	MIF_HUMAN	Macrophage migration inhibitory factor c	107.42	21	6
Q14978	NOLC1_HUMAN	Nucleolar and coiled-body phosphoprot	99.59	20	6
O43491	E41L2_HUMAN	Band 4.1-like protein 2 OS=Homo sapie	97.88	13	6
Q8WZ42	TITIN_HUMAN	Titin OS=Homo sapiens GN=TTN PE=1	73.43	6	6
Q9H0U4	RAB1B_HUMAN	Ras-related protein Rab-1B OS=Homo	192.63	70	5
Q13765	NACA_HUMAN	Nascent polypeptide-associated comple	181.13	45	5
Q13310	PABP4_HUMAN	Polyadenylate-binding protein 4 OS=Hc	178.55	39	5
O60506	HNRPQ_HUMAN	Heterogeneous nuclear ribonucleoprote	176.7	37	5
Q92841	DDX17_HUMAN	Probable ATP-dependent RNA helicase	175.85	36	5
Q99733	NP1L4_HUMAN	Nucleosome assembly protein 1-like 4 c	162.28	31	5
P83916	CBX1_HUMAN	Chromobox protein homolog 1 OS=Hor	160.03	36	5

O43399	TPD54_HUMAN	Tumor protein D54 OS=Homo sapiens	158.98	63	5
P13804	ETFA_HUMAN	Electron transfer flavoprotein subunit al	158.63	42	5
P46060	RAGP1_HUMAN	Ran GTPase-activating protein 1 OS=H	158.3	59	5
O00429	DNM1L_HUMAN	Dynamin-1-like protein OS=Homo sapie	156.28	41	5
Q9Y5L4	TIM13_HUMAN	Mitochondrial import inner membrane tr	156	79	5
P22087	FBRL_HUMAN	rRNA 2'-O-methyltransferase fibrillarin C	155.35	45	5
Q9BUT1	BDH2_HUMAN	3-hydroxybutyrate dehydrogenase type	154.27	50	5
Q15185	TEBP_HUMAN	Prostaglandin E synthase 3 OS=Homo	153.53	63	5
O75348	VATG1_HUMAN	V-type proton ATPase subunit G 1 OS=	152.94	43	5
P62314	SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1	150.93	54	5
P36969	GPX4_HUMAN	Phospholipid hydroperoxide glutathione	150.71	42	5
P61970	NTF2_HUMAN	Nuclear transport factor 2 OS=Homo sa	150.68	81	5
P61160	ARP2_HUMAN	Actin-related protein 2 OS=Homo sapie	150.56	37	5
P52565	GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 OS=H	148.99	41	5
Q14444	CAPR1_HUMAN	Caprin-1 OS=Homo sapiens GN=CAPR	148.85	24	5
P28072	PSB6_HUMAN	Proteasome subunit beta type-6 OS=Ho	148.75	60	5
P05198	IF2A_HUMAN	Eukaryotic translation initiation factor 2	148.23	40	5
P17096	HMGA1_HUMAN	High mobility group protein HMG-I/HMG	146.09	71	5
Q15785	TOM34_HUMAN	Mitochondrial import receptor subunit T	144.63	38	5
P55327	TPD52_HUMAN	Tumor protein D52 OS=Homo sapiens	143.28	45	5
A6NDG6	PGP_HUMAN	Phosphoglycolate phosphatase OS=Ho	143.21	51	5
P43246	MSH2_HUMAN	DNA mismatch repair protein Msh2 OS=	142.84	23	5
P54920	SNAA_HUMAN	Alpha-soluble NSF attachment protein C	142.08	43	5
P56537	IF6_HUMAN	Eukaryotic translation initiation factor 6	141.86	45	5
P08590	MYL3_HUMAN	Myosin light chain 3 OS=Homo sapiens	141.71	54	5
P28838	AMPL_HUMAN	Cytosol aminopeptidase OS=Homo sap	141.63	19	5
Q13619	CUL4A_HUMAN	Cullin-4A OS=Homo sapiens GN=CUL4	141.56	22	5
Q6GMV3	CB079_HUMAN	Uncharacterized protein C2orf79 OS=H	140.53	47	5
P35520	CBS_HUMAN	Cystathionine beta-synthase OS=Homo	139.65	30	5
P04818	TYSY_HUMAN	Thymidylate synthase OS=Homo sapier	137.73	42	5
P10599	THIO_HUMAN	Thioredoxin OS=Homo sapiens GN=TX	137.64	55	5
P62304	RUXE_HUMAN	Small nuclear ribonucleoprotein E OS=	137.16	73	5
Q13616	CUL1_HUMAN	Cullin-1 OS=Homo sapiens GN=CUL1	136.98	27	5
Q07021	C1QBP_HUMAN	Complement component 1 Q subcompo	136.76	26	5
P28070	PSB4_HUMAN	Proteasome subunit beta type-4 OS=Ho	136.62	39	5
Q15046	SYK_HUMAN	Lysyl-tRNA synthetase OS=Homo sapie	136.46	19	5
Q13011	ECH1_HUMAN	Delta(3,5)-Delta(2,4)-dienoyl-CoA isom	135.78	26	5
P42766	RL35_HUMAN	60S ribosomal protein L35 OS=Homo s	135.76	31	5
Q9BRX8	CJ058_HUMAN	UPF0765 protein C10orf58 OS=Homo s	135.53	57	5
Q9UHV9	PFD2_HUMAN	Prefoldin subunit 2 OS=Homo sapiens	135.52	63	5
Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1	135.35	31	5
P30520	PURA2_HUMAN	Adenylosuccinate synthetase isozyme 2	134.92	25	5
P26196	DDX6_HUMAN	Probable ATP-dependent RNA helicase	134.91	32	5
Q9UBQ5	EIF3K_HUMAN	Eukaryotic translation initiation factor 3	134.67	38	5
Q99622	C10_HUMAN	Protein C10 OS=Homo sapiens GN=C1	134.51	48	5
Q15417	CNN3_HUMAN	Calponin-3 OS=Homo sapiens GN=CN	133.86	29	5
P63208	SKP1_HUMAN	S-phase kinase-associated protein 1 O	133.12	34	5
P30566	PUR8_HUMAN	Adenylosuccinate lyase OS=Homo sapi	132.58	24	5
Q08257	QOR_HUMAN	Quinone oxidoreductase OS=Homo sap	131.97	36	5
Q9NZJ9	NUDT4_HUMAN	Diphosphoinositol polyphosphate phosph	131.71	53	5
Q9H910	HN1L_HUMAN	Hematological and neurological express	131.22	41	5
Q9Y4Z0	LSM4_HUMAN	U6 snRNA-associated Sm-like protein L	130.73	55	5
Q99873	ANM1_HUMAN	Protein arginine N-methyltransferase 1	128.61	20	5
Q13868	EXOS2_HUMAN	Exosome complex component RRP4 O	128.58	36	5
P23381	SYWC_HUMAN	Tryptophanyl-tRNA synthetase, cytoplas	128.08	36	5
Q9Y5Y2	NUBP2_HUMAN	Cytosolic Fe-S cluster assembly factor I	127.96	46	5



Q53GQ0	DHB12_HUMAN	Estradiol 17-beta-dehydrogenase 12 OS=Homo sapiens GN=DHB12	126.82	29	5
P36542	ATPG_HUMAN	ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATPG	126.11	20	5
P51571	SSRD_HUMAN	Translocon-associated protein subunit c OS=Homo sapiens GN=SSRD	125.65	36	5
P23142	FBLN1_HUMAN	Fibulin-1 OS=Homo sapiens GN=FBLN1	125.2	10	5
P36871	PGM1_HUMAN	Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1	125.04	25	5
P42574	CASP3_HUMAN	Caspase-3 OS=Homo sapiens GN=CASP3	124.36	34	5
Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1	124.13	22	5
O00233	PSMD9_HUMAN	26S proteasome non-ATPase regulator OS=Homo sapiens GN=PSMD9	122.79	24	5
O75083	WDR1_HUMAN	WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1	122.74	27	5
P17858	K6PL_HUMAN	6-phosphofructokinase, liver type OS=Homo sapiens GN=K6PL	122.52	29	5
P56385	ATP5I_HUMAN	ATP synthase subunit e, mitochondrial OS=Homo sapiens GN=ATP5I	121.73	62	5
P48739	PIPNB_HUMAN	Phosphatidylinositol transfer protein beta OS=Homo sapiens GN=PIPNB	121.53	33	5
Q02952	AKA12_HUMAN	A-kinase anchor protein 12 OS=Homo sapiens GN=AKA12	121.52	17	5
P19623	SPEE_HUMAN	Spermidine synthase OS=Homo sapiens GN=SPEE	121.36	31	5
P23193	TCEA1_HUMAN	Transcription elongation factor A protein 1 OS=Homo sapiens GN=TCEA1	121.15	34	5
P14735	IDE_HUMAN	Insulin-degrading enzyme OS=Homo sapiens GN=IDE	120.41	18	5
P49419	AL7A1_HUMAN	Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=AL7A1	120.33	22	5
P33316	DUT_HUMAN	Deoxyuridine 5'-triphosphate nucleotidyl transferase OS=Homo sapiens GN=DUT	120.29	33	5
P83731	RL24_HUMAN	60S ribosomal protein L24 OS=Homo sapiens GN=RL24	120.2	38	5
P61221	ABCE1_HUMAN	ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1	119.89	26	5
Q07866	KLC1_HUMAN	Kinesin light chain 1 OS=Homo sapiens GN=KLC1	119.79	24	5
P62310	LSM3_HUMAN	U6 snRNA-associated Sm-like protein L3 OS=Homo sapiens GN=LSM3	119.72	71	5
Q9BUL8	PDC10_HUMAN	Programmed cell death protein 10 OS=Homo sapiens GN=PDC10	119.72	29	5
O76094	SRP72_HUMAN	Signal recognition particle 72 kDa protein OS=Homo sapiens GN=SRP72	119.34	31	5
Q00341	VIGLN_HUMAN	Vigilin OS=Homo sapiens GN=HDLBP1	119.28	21	5
P62306	RUXF_HUMAN	Small nuclear ribonucleoprotein F OS=Homo sapiens GN=RUXF	117.29	58	5
Q9NR31	SAR1A_HUMAN	GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A	117.12	25	5
P20340	RAB6A_HUMAN	Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A	117.06	39	5
P49458	SRP09_HUMAN	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP09	116.38	57	5
O15143	ARC1B_HUMAN	Actin-related protein 2/3 complex subunit 1 OS=Homo sapiens GN=ARC1B	116.24	29	5
Q96C36	P5CR2_HUMAN	Proline-5-carboxylate reductase 2 OS=Homo sapiens GN=P5CR2	115.93	32	5
P48061	SDF1_HUMAN	Stromal cell-derived factor 1 OS=Homo sapiens GN=SDF1	115.65	42	5
P35249	RFC4_HUMAN	Replication factor C subunit 4 OS=Homo sapiens GN=RFC4	115.58	22	5
Q8NFF5	FAD1_HUMAN	FAD synthase OS=Homo sapiens GN=FAD1	115.43	27	5
Q9BPW8	NIPS1_HUMAN	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPS1	114.5	26	5
Q13242	SRSF9_HUMAN	Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9	114.01	34	5
Q16543	CDC37_HUMAN	Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37	113.75	27	5
Q15102	PA1B3_HUMAN	Platelet-activating factor acetylhydrolase 1B OS=Homo sapiens GN=PA1B3	113.18	35	5
Q14203	DCTN1_HUMAN	Dynactin subunit 1 OS=Homo sapiens GN=DCTN1	112.77	27	5
P49591	SYSC_HUMAN	Seryl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=SYSC	112.66	24	5
P06730	IF4E_HUMAN	Eukaryotic translation initiation factor 4E OS=Homo sapiens GN=IF4E	108.68	20	5
P08243	ASNS_HUMAN	Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens GN=ASNS	108.57	19	5
P13798	ACPH_HUMAN	Acylamino-acid-releasing enzyme OS=Homo sapiens GN=ACPH	108.49	12	5
P41091	IF2G_HUMAN	Eukaryotic translation initiation factor 2 OS=Homo sapiens GN=IF2G	108.11	31	5
P07203	GPX1_HUMAN	Glutathione peroxidase 1 OS=Homo sapiens GN=GPX1	107.71	36	5
P55786	PSA_HUMAN	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=PSA	102.38	12	5
Q9UIJ7	KAD3_HUMAN	GTP:AMP phosphotransferase, mitochondrial OS=Homo sapiens GN=KAD3	99.68	24	5
O60925	PFD1_HUMAN	Prefoldin subunit 1 OS=Homo sapiens GN=PFD1	99.18	38	5
Q9UKM9	RALY_HUMAN	RNA-binding protein Raly OS=Homo sapiens GN=RALY	97.85	32	5
P35612	ADDB_HUMAN	Beta-adducin OS=Homo sapiens GN=ADDB	97.71	21	5
Q15459	SF3A1_HUMAN	Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1	94.15	13	5
Q9BVK6	TMED9_HUMAN	Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens GN=TMED9	92.8	26	5
Q13509	TBB3_HUMAN	Tubulin beta-3 chain OS=Homo sapiens GN=TBB3	295.38	75	4
P62140	PP1B_HUMAN	Serine/threonine-protein phosphatase PP1B OS=Homo sapiens GN=PP1B	226.21	49	4
P16403	H12_HUMAN	Histone H1.2 OS=Homo sapiens GN=H12	216.11	54	4
Q99877	H2B1N_HUMAN	Histone H2B type 1-N OS=Homo sapiens GN=H2B1N	197.21	66	4

P62807	H2B1C_HUMAN	Histone H2B type 1-C/E/F/G/I OS=Hom	197.21	57	4
P58876	H2B1D_HUMAN	Histone H2B type 1-D OS=Homo sapie	197.21	57	4
Q93079	H2B1H_HUMAN	Histone H2B type 1-H OS=Homo sapie	197.21	57	4
O60814	H2B1K_HUMAN	Histone H2B type 1-K OS=Homo sapie	197.21	57	4
Q99879	H2B1M_HUMAN	Histone H2B type 1-M OS=Homo sapie	197.21	57	4
Q5QNW6	H2B2F_HUMAN	Histone H2B type 2-F OS=Homo sapie	197.21	57	4
P57053	H2BFS_HUMAN	Histone H2B type F-S OS=Homo sapie	197.21	52	4
P18085	ARF4_HUMAN	ADP-ribosylation factor 4 OS=Homo sa	187.48	81	4
P35241	RADI_HUMAN	Radixin OS=Homo sapiens GN=RDX P	179.37	32	4
Q13162	PRDX4_HUMAN	Peroxioredoxin-4 OS=Homo sapiens GN	179	38	4
Q96FJ2	DYL2_HUMAN	Dynein light chain 2, cytoplasmic OS=H	174.74	65	4
P31943	HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprote	159.81	38	4
P26583	HMGB2_HUMAN	High mobility group protein B2 OS=Hon	157.67	33	4
P38919	IF4A3_HUMAN	Eukaryotic initiation factor 4A-III OS=Hc	157.14	33	4
O00425	IF2B3_HUMAN	Insulin-like growth factor 2 mRNA-bindin	155.79	30	4
P39687	AN32A_HUMAN	Acidic leucine-rich nuclear phosphoprot	154.16	31	4
Q9NUQ9	FA49B_HUMAN	Protein FAM49B OS=Homo sapiens GN	151.38	41	4
Q15436	SC23A_HUMAN	Protein transport protein Sec23A OS=H	149.19	27	4
P31153	METK2_HUMAN	S-adenosylmethionine synthase isoform	147.82	32	4
P43490	NAMPT_HUMAN	Nicotinamide phosphoribosyltransferase	146.85	54	4
P30085	KCY_HUMAN	UMP-CMP kinase OS=Homo sapiens G	146.6	44	4
P09455	RET1_HUMAN	Retinol-binding protein 1 OS=Homo sap	146.33	44	4
Q99729	ROAA_HUMAN	Heterogeneous nuclear ribonucleoprote	145.1	36	4
P38159	HNRPG_HUMAN	Heterogeneous nuclear ribonucleoprote	144.1	46	4
Q15366	PCBP2_HUMAN	Poly(rC)-binding protein 2 OS=Homo sa	143.12	51	4
Q9NWU2	CT011_HUMAN	Protein C20orf11 OS=Homo sapiens G	141.57	48	4
Q9ULZ3	ASC_HUMAN	Apoptosis-associated speck-like protein	141.54	40	4
P62847	RS24_HUMAN	40S ribosomal protein S24 OS=Homo s	138.89	44	4
P61923	COPZ1_HUMAN	Coatomer subunit zeta-1 OS=Homo sap	138.84	40	4
Q9UI30	TR112_HUMAN	tRNA methyltransferase 112 homolog C	137.88	56	4
P49411	EFTU_HUMAN	Elongation factor Tu, mitochondrial OS=	136.06	23	4
Q9BRA2	TXD17_HUMAN	Thioredoxin domain-containing protein	135.66	43	4
Q9UBQ0	VPS29_HUMAN	Vacuolar protein sorting-associated pro	135.66	45	4
P34897	GLYM_HUMAN	Serine hydroxymethyltransferase, mitoc	135.37	23	4
P05386	RLA1_HUMAN	60S acidic ribosomal protein P1 OS=Hc	135.35	66	4
P04216	THY1_HUMAN	Thy-1 membrane glycoprotein OS=Hom	134.55	30	4
O75608	LYPA1_HUMAN	Acyl-protein thioesterase 1 OS=Homo s	134.27	37	4
P13716	HEM2_HUMAN	Delta-aminolevulinic acid dehydratase C	133.85	38	4
P62834	RAP1A_HUMAN	Ras-related protein Rap-1A OS=Homo	133.82	27	4
P61224	RAP1B_HUMAN	Ras-related protein Rap-1b OS=Homo	133.82	27	4
P08579	RU2B_HUMAN	U2 small nuclear ribonucleoprotein B" C	133.69	30	4
Q9BS26	ERP44_HUMAN	Endoplasmic reticulum resident protein	133.02	33	4
P55010	IF5_HUMAN	Eukaryotic translation initiation factor 5	132.77	34	4
Q96AG4	LRC59_HUMAN	Leucine-rich repeat-containing protein 5	131.75	33	4
Q16629	SRSF7_HUMAN	Serine/arginine-rich splicing factor 7 OS	131.7	20	4
Q9UGI8	TES_HUMAN	Testin OS=Homo sapiens GN=TES PE	131.58	17	4
Q9Y3B4	PM14_HUMAN	Pre-mRNA branch site protein p14 OS=	131.55	42	4
Q9BZZ5	API5_HUMAN	Apoptosis inhibitor 5 OS=Homo sapiens	130.78	34	4
P41567	EIF1_HUMAN	Eukaryotic translation initiation factor 1	130.36	63	4
Q9NY33	DPP3_HUMAN	Dipeptidyl peptidase 3 OS=Homo sapie	130.1	23	4
Q00688	FKBP3_HUMAN	Peptidyl-prolyl cis-trans isomerase FKB	129.99	38	4
Q8NBS9	TXND5_HUMAN	Thioredoxin domain-containing protein	129.86	21	4
Q8IXM2	BAP18_HUMAN	Chromatin complexes subunit BAP18 C	129.54	44	4
P61026	RAB10_HUMAN	Ras-related protein Rab-10 OS=Homo	129	52	4
Q9ULC4	MCTS1_HUMAN	Malignant T cell-amplified sequence 1 C	128.22	51	4
P84090	ERH_HUMAN	Enhancer of rudimentary homolog OS=	127.9	53	4

Q96IZ0 PAWR_HUMAN	PRKC apoptosis WT1 regulator protein	127.53	34	4
Q9UBT2 SAE2_HUMAN	SUMO-activating enzyme subunit 2 OS=	127.48	23	4
Q7L1Q6 BZW1_HUMAN	Basic leucine zipper and W2 domain-co	127.41	23	4
P36639 8ODP_HUMAN	7,8-dihydro-8-oxoguanine triphosphatas	127.23	29	4
P13489 RINI_HUMAN	Ribonuclease inhibitor OS=Homo sapie	126.94	15	4
Q9C005 DPY30_HUMAN	Protein dpy-30 homolog OS=Homo sap	126.61	65	4
Q13158 FADD_HUMAN	Protein FADD OS=Homo sapiens GN=f	126.59	50	4
P11216 PYGB_HUMAN	Glycogen phosphorylase, brain form OS	126.5	16	4
P41208 CETN2_HUMAN	Centrin-2 OS=Homo sapiens GN=CETN	125.68	42	4
Q07666 KHDR1_HUMAN	KH domain-containing, RNA-binding, si	125.54	41	4
Q13347 EIF3I_HUMAN	Eukaryotic translation initiation factor 3	125.45	34	4
Q7L5N1 CSN6_HUMAN	COP9 signalosome complex subunit 6 C	124.89	42	4
Q99584 S10AD_HUMAN	Protein S100-A13 OS=Homo sapiens G	124.64	71	4
P67809 YBOX1_HUMAN	Nuclease-sensitive element-binding pro	124.46	35	4
P11766 ADHX_HUMAN	Alcohol dehydrogenase class-3 OS=Ho	124.39	15	4
P62942 FKB1A_HUMAN	Peptidyl-prolyl cis-trans isomerase FKB	124.26	56	4
P35237 SPB6_HUMAN	Serpin B6 OS=Homo sapiens GN=SER	124.21	25	4
O14745 NHRF1_HUMAN	Na(+)/H(+) exchange regulatory cofacto	124.14	24	4
Q96CT7 CC124_HUMAN	Coiled-coil domain-containing protein 12	123.93	35	4
O14979 HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprote	123.03	19	4
Q9GZT3 SLIRP_HUMAN	SRA stem-loop-interacting RNA-binding	122.52	59	4
O75340 PDCD6_HUMAN	Programmed cell death protein 6 OS=H	122.24	21	4
Q9Y6A5 TACC3_HUMAN	Transforming acidic coiled-coil-containir	120.35	16	4
O95456 PSMG1_HUMAN	Proteasome assembly chaperone 1 OS	120.27	43	4
O00264 PGRC1_HUMAN	Membrane-associated progesterone rec	120.06	29	4
P46776 RL27A_HUMAN	60S ribosomal protein L27a OS=Homo	119.89	43	4
P10768 ESTD_HUMAN	S-formylglutathione hydrolase OS=Hom	118.79	32	4
O75964 ATP5L_HUMAN	ATP synthase subunit g, mitochondrial	118.21	48	4
O95816 BAG2_HUMAN	BAG family molecular chaperone regula	117.96	28	4
Q8TCD5 NT5C_HUMAN	5'(3')-deoxyribonucleotidase, cytosolic t	117.95	38	4
P35244 RFA3_HUMAN	Replication protein A 14 kDa subunit O	117.26	51	4
P15121 ALDR_HUMAN	Aldose reductase OS=Homo sapiens G	116.57	32	4
Q12905 ILF2_HUMAN	Interleukin enhancer-binding factor 2 O	116.36	26	4
O75368 SH3L1_HUMAN	SH3 domain-binding glutamic acid-rich-	116.19	61	4
P61326 MGN_HUMAN	Protein mago nashi homolog OS=Homc	115.68	32	4
Q96A72 MGN2_HUMAN	Protein mago nashi homolog 2 OS=Hor	115.68	32	4
Q9P2M7 CING_HUMAN	Cingulin OS=Homo sapiens GN=CGN F	115.57	14	4
P51659 DHB4_HUMAN	Peroxisomal multifunctional enzyme typ	115.3	23	4
Q92520 FAM3C_HUMAN	Protein FAM3C OS=Homo sapiens GN:	114.77	33	4
Q8N1G4 LRC47_HUMAN	Leucine-rich repeat-containing protein 4	114.53	22	4
P10606 COX5B_HUMAN	Cytochrome c oxidase subunit 5B, mito	113.36	59	4
P51991 ROA3_HUMAN	Heterogeneous nuclear ribonucleoprote	112.56	33	4
Q8NC51 PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-t	112.55	32	4
P12830 CADH1_HUMAN	Cadherin-1 OS=Homo sapiens GN=CD	112.39	9	4
O95372 LYPA2_HUMAN	Acyl-protein thioesterase 2 OS=Homo s	111.76	40	4
P35613 BASI_HUMAN	Basigin OS=Homo sapiens GN=BSG P	110.96	20	4
Q8IZQ5 SELH_HUMAN	Selenoprotein H OS=Homo sapiens GN	110.76	30	4
O00743 PPP6_HUMAN	Serine/threonine-protein phosphatase 6	110.46	21	4
O43252 PAPS1_HUMAN	Bifunctional 3'-phosphoadenosine 5'-ph	109.93	16	4
P38606 VATA_HUMAN	V-type proton ATPase catalytic subunit	109.75	21	4
P12081 SYHC_HUMAN	Histidyl-tRNA synthetase, cytoplasmic C	108.91	18	4
P33992 MCM5_HUMAN	DNA replication licensing factor MCM5	108.62	18	4
P48449 ERG7_HUMAN	Lanosterol synthase OS=Homo sapiens	107.72	15	4
Q9NX63 CHCH3_HUMAN	Coiled-coil-helix-coiled-coil-helix domair	107.59	22	4
O00303 EIF3F_HUMAN	Eukaryotic translation initiation factor 3	106.68	25	4
Q8IYD1 ERF3B_HUMAN	Eukaryotic peptide chain release factor	106.49	24	4

O75475 PSIP1_HUMAN	PC4 and SFRS1-interacting protein OS	105.59	22	4
Q92522 H1X_HUMAN	Histone H1x OS=Homo sapiens GN=H1	103.64	42	4
Q8IXM3 RM41_HUMAN	39S ribosomal protein L41, mitochondri	103.23	41	4
Q8N8S7 ENAH_HUMAN	Protein enabled homolog OS=Homo sa	103.14	20	4
Q92896 GSLG1_HUMAN	Golgi apparatus protein 1 OS=Homo sa	103.11	12	4
P40429 RL13A_HUMAN	60S ribosomal protein L13a OS=Homo	102.57	26	4
Q9H0D6 XRN2_HUMAN	5'-3' exoribonuclease 2 OS=Homo sapi	102.57	13	4
Q9NSD9 SYFB_HUMAN	Phenylalanyl-tRNA synthetase beta cha	102.47	10	4
P14314 GLU2B_HUMAN	Glucosidase 2 subunit beta OS=Homo	102.28	16	4
Q86V81 THOC4_HUMAN	THO complex subunit 4 OS=Homo sapi	102.08	28	4
Q99988 GDF15_HUMAN	Growth/differentiation factor 15 OS=Ho	101.63	27	4
O14618 CCS_HUMAN	Copper chaperone for superoxide dism	101.48	16	4
Q08752 PPID_HUMAN	Peptidyl-prolyl cis-trans isomerase D OS	101.47	24	4
P26640 SYVC_HUMAN	Valyl-tRNA synthetase OS=Homo sapi	101.13	17	4
Q9BRG1 VPS25_HUMAN	Vacuolar protein-sorting-associated pro	100.97	30	4
Q13561 DCTN2_HUMAN	Dynactin subunit 2 OS=Homo sapiens	100.02	26	4
P47914 RL29_HUMAN	60S ribosomal protein L29 OS=Homo s	98.91	21	4
Q9BVG4 CX026_HUMAN	UPF0368 protein Cxorf26 OS=Homo sa	98.87	24	4
P31689 DNJA1_HUMAN	DnaJ homolog subfamily A member 1 C	98.39	16	4
O15355 PPM1G_HUMAN	Protein phosphatase 1G OS=Homo sap	98.26	20	4
P63165 SUMO1_HUMAN	Small ubiquitin-related modifier 1 OS=H	98.05	57	4
Q99417 MYCBP_HUMAN	C-Myc-binding protein OS=Homo sapi	97.87	58	4
P46379 BAG6_HUMAN	Large proline-rich protein BAG6 OS=H	97.72	11	4
P29279 CTGF_HUMAN	Connective tissue growth factor OS=H	93.72	15	4
Q14008 CKAP5_HUMAN	Cytoskeleton-associated protein 5 OS=	93.41	14	4
P62993 GRB2_HUMAN	Growth factor receptor-bound protein 2	93.17	29	4
Q9Y3U8 RL36_HUMAN	60S ribosomal protein L36 OS=Homo s	91.98	31	4
Q07065 CKAP4_HUMAN	Cytoskeleton-associated protein 4 OS=	91.64	21	4
P47897 SYQ_HUMAN	Glutaminyl-tRNA synthetase OS=Homo	90.69	27	4
P62070 RRAS2_HUMAN	Ras-related protein R-Ras2 OS=Homo	90.49	33	4
Q9UHD8 SEPT9_HUMAN	Septin-9 OS=Homo sapiens GN=SEPT	90.49	22	4
P04181 OAT_HUMAN	Ornithine aminotransferase, mitochondr	90.38	24	4
P46939 UTRO_HUMAN	Utrophin OS=Homo sapiens GN=UTRN	88.37	9	4
Q9Y376 CAB39_HUMAN	Calcium-binding protein 39 OS=Homo s	86.83	20	4
Q4VC31 CCD58_HUMAN	Coiled-coil domain-containing protein 5	86.34	27	4
Q99436 PSB7_HUMAN	Proteasome subunit beta type-7 OS=H	86.09	34	4
P61313 RL15_HUMAN	60S ribosomal protein L15 OS=Homo s	83.42	11	4
Q9UDR5 AASS_HUMAN	Alpha-aminoadipic semialdehyde syntha	81.96	10	4
P22307 NLTP_HUMAN	Non-specific lipid-transfer protein OS=H	81.42	11	4
Q9BRF8 CPPED_HUMAN	Calcineurin-like phosphoesterase doma	81.31	37	4
P02452 CO1A1_HUMAN	Collagen alpha-1(I) chain OS=Homo sa	76.55	28	4
Q15369 ELOC_HUMAN	Transcription elongation factor B polype	75.23	45	4
P49189 AL9A1_HUMAN	4-trimethylaminobutyraldehyde dehydro	73.78	12	4
P40616 ARL1_HUMAN	ADP-ribosylation factor-like protein 1 OS	67.07	42	4
P09496 CLCA_HUMAN	Clathrin light chain A OS=Homo sapien	57.3	19	4
Q7L7L0 H2A3_HUMAN	Histone H2A type 3 OS=Homo sapiens	220.39	68	3
P04908 H2A1B_HUMAN	Histone H2A type 1-B/E OS=Homo sap	220.39	63	3
P10412 H14_HUMAN	Histone H1.4 OS=Homo sapiens GN=H	216.2	69	3
P61586 RHOA_HUMAN	Transforming protein RhoA OS=Homo s	207.08	68	3
P19105 ML12A_HUMAN	Myosin regulatory light chain 12A OS=H	198.03	57	3
O14950 ML12B_HUMAN	Myosin regulatory light chain 12B OS=H	198.03	56	3
Q02539 H11_HUMAN	Histone H1.1 OS=Homo sapiens GN=H	186.73	48	3
P84085 ARF5_HUMAN	ADP-ribosylation factor 5 OS=Homo sa	185.14	69	3
P35749 MYH11_HUMAN	Myosin-11 OS=Homo sapiens GN=MYH	179.32	39	3
P05141 ADT2_HUMAN	ADP/ATP translocase 2 OS=Homo sap	178.45	48	3
P63167 DYL1_HUMAN	Dynein light chain 1, cytoplasmic OS=H	173.27	65	3

O00571	DDX3X_HUMAN	ATP-dependent RNA helicase DDX3X	170.74	30	3
P61254	RL26_HUMAN	60S ribosomal protein L26 OS=Homo s	153.08	52	3
P62873	GBB1_HUMAN	Guanine nucleotide-binding protein G(I)	149.03	29	3
P17844	DDX5_HUMAN	Probable ATP-dependent RNA helicase	147.94	22	3
Q92688	AN32B_HUMAN	Acidic leucine-rich nuclear phosphoprot	145.49	39	3
Q12931	TRAP1_HUMAN	Heat shock protein 75 kDa, mitochondri	139.38	23	3
P48735	IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitoc	137.56	22	3
Q9P1F3	CF115_HUMAN	Costars family protein C6orf115 OS=Ho	134.83	64	3
P42677	RS27_HUMAN	40S ribosomal protein S27 OS=Homo s	134.49	40	3
Q93062	RBPMS_HUMAN	RNA-binding protein with multiple splici	134.46	39	3
Q9NX02	NALP2_HUMAN	NACHT, LRR and PYD domains-contain	133.77	24	3
Q16836	HCDH_HUMAN	Hydroxyacyl-coenzyme A dehydrogenas	133.68	48	3
Q71UM5	RS27L_HUMAN	40S ribosomal protein S27-like OS=Hor	133.64	40	3
P80723	BASP1_HUMAN	Brain acid soluble protein 1 OS=Homo s	130.23	48	3
P47755	CAZA2_HUMAN	F-actin-capping protein subunit alpha-2	129.41	23	3
P68402	PA1B2_HUMAN	Platelet-activating factor acetylhydrolas	129.2	44	3
Q9NZL9	MAT2B_HUMAN	Methionine adenosyltransferase 2 subu	128.96	42	3
Q13526	PIN1_HUMAN	Peptidyl-prolyl cis-trans isomerase NIM	128.58	48	3
P51148	RAB5C_HUMAN	Ras-related protein Rab-5C OS=Homo	128.3	39	3
P11047	LAMC1_HUMAN	Laminin subunit gamma-1 OS=Homo sa	128.29	12	3
Q9H3R5	CENPH_HUMAN	Centromere protein H OS=Homo sapien	126.82	49	3
P47813	IF1AX_HUMAN	Eukaryotic translation initiation factor 1A	126.09	45	3
O14602	IF1AY_HUMAN	Eukaryotic translation initiation factor 1A	126.09	45	3
Q96IX5	USMG5_HUMAN	Up-regulated during skeletal muscle gro	125.63	47	3
Q13151	ROA0_HUMAN	Heterogeneous nuclear ribonucleoprote	125.54	29	3
O75607	NPM3_HUMAN	Nucleoplasmin-3 OS=Homo sapiens GN	124.93	29	3
Q99613	EIF3C_HUMAN	Eukaryotic translation initiation factor 3	124.89	26	3
Q9NYL9	TMOD3_HUMAN	Tropomodulin-3 OS=Homo sapiens GN	124.12	26	3
O75390	CISY_HUMAN	Citrate synthase, mitochondrial OS=Hor	123.78	18	3
Q9P289	MST4_HUMAN	Serine/threonine-protein kinase MST4	123.44	28	3
P62854	RS26_HUMAN	40S ribosomal protein S26 OS=Homo s	123.28	42	3
P17812	PYRG1_HUMAN	CTP synthase 1 OS=Homo sapiens GN	123.12	21	3
P54687	BCAT1_HUMAN	Branched-chain-amino-acid aminotrans	123	26	3
P52434	RPAB3_HUMAN	DNA-directed RNA polymerases I, II, an	122.62	25	3
Q8WUM4	PDC6I_HUMAN	Programmed cell death 6-interacting pro	122.37	23	3
Q9BY32	ITPA_HUMAN	Inosine triphosphate pyrophosphatase	120.89	35	3
Q96AC1	FERM2_HUMAN	Fermitin family homolog 2 OS=Homo sa	119.86	22	3
O43396	TXNL1_HUMAN	Thioredoxin-like protein 1 OS=Homo sa	119.7	40	3
Q9Y3C6	PPIL1_HUMAN	Peptidyl-prolyl cis-trans isomerase-like	119.47	31	3
Q9UQE7	SMC3_HUMAN	Structural maintenance of chromosome	118.55	22	3
Q00796	DHSO_HUMAN	Sorbitol dehydrogenase OS=Homo sap	118.03	25	3
P62877	RBX1_HUMAN	E3 ubiquitin-protein ligase RBX1 OS=H	117.05	33	3
P04080	CYTB_HUMAN	Cystatin-B OS=Homo sapiens GN=CST	116.74	65	3
O60869	EDF1_HUMAN	Endothelial differentiation-related factor	116.26	43	3
Q9H773	DCTP1_HUMAN	dCTP pyrophosphatase 1 OS=Homo sa	116.15	39	3
Q9UQ80	PA2G4_HUMAN	Proliferation-associated protein 2G4 OS	115.83	22	3
Q13618	CUL3_HUMAN	Cullin-3 OS=Homo sapiens GN=CUL3	115.72	15	3
P04179	SODM_HUMAN	Superoxide dismutase [Mn], mitochondri	115.24	25	3
P16083	NQO2_HUMAN	Ribosylidihydronicotinamide dehydroger	114.81	30	3
O00273	DFFA_HUMAN	DNA fragmentation factor subunit alpha	114.55	35	3
Q96DE0	NUD16_HUMAN	U8 snoRNA-decapping enzyme OS=Ho	114.52	56	3
Q9P000	COMD9_HUMAN	COMM domain-containing protein 9 OS	114.3	31	3
Q9UIL1	SCOC_HUMAN	Short coiled-coil protein OS=Homo sapi	113.32	29	3
Q9NQP4	PFD4_HUMAN	Prefoldin subunit 4 OS=Homo sapiens	113.22	38	3
P23919	KTHY_HUMAN	Thymidylate kinase OS=Homo sapiens	112.9	33	3
P61201	CSN2_HUMAN	COP9 signalosome complex subunit 2	112.11	32	3

Q15717 ELAV1_HUMAN	ELAV-like protein 1 OS=Homo sapiens	112.02	20	3
Q86UP2 KTN1_HUMAN	Kinectin OS=Homo sapiens GN=KTN1	111.99	11	3
Q8TEA8 DTD1_HUMAN	D-tyrosyl-tRNA(Tyr) deacylase 1 OS=H	111.97	32	3
Q6ZRY4 RBPS2_HUMAN	RNA-binding protein with multiple splicing	111.74	32	3
O43143 DHX15_HUMAN	Putative pre-mRNA-splicing factor ATP-	111.74	21	3
P62910 RL32_HUMAN	60S ribosomal protein L32 OS=Homo s	111.73	45	3
Q9NR45 SIAS_HUMAN	Sialic acid synthase OS=Homo sapiens	111.51	20	3
P62266 RS23_HUMAN	40S ribosomal protein S23 OS=Homo s	111.48	16	3
P32321 DCTD_HUMAN	Deoxycytidylate deaminase OS=Homo	111.13	20	3
P35080 PROF2_HUMAN	Profilin-2 OS=Homo sapiens GN=PFN2	110.75	57	3
O14773 TPP1_HUMAN	Tripeptidyl-peptidase 1 OS=Homo sapi	110.66	31	3
P45880 VDAC2_HUMAN	Voltage-dependent anion-selective cha	110.22	22	3
P29966 MARCS_HUMAN	Myristoylated alanine-rich C-kinase sub	109.99	14	3
P39023 RL3_HUMAN	60S ribosomal protein L3 OS=Homo sa	109.82	15	3
P98095 FBLN2_HUMAN	Fibulin-2 OS=Homo sapiens GN=FBLN	109.77	12	3
P06737 PYGL_HUMAN	Glycogen phosphorylase, liver form OS	109.33	13	3
Q16527 CSR2_HUMAN	Cysteine and glycine-rich protein 2 OS=	108.45	25	3
Q9NRV9 HEBP1_HUMAN	Heme-binding protein 1 OS=Homo sapi	108.16	46	3
O14880 MGST3_HUMAN	Microsomal glutathione S-transferase 3	108.14	26	3
P14923 PLAK_HUMAN	Junction plakoglobin OS=Homo sapiens	107.99	21	3
P62318 SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3	107.82	37	3
P46087 NOP2_HUMAN	Putative ribosomal RNA methyltransfera	107.14	13	3
Q969H8 CS010_HUMAN	UPF0556 protein C19orf10 OS=Homo s	106.3	21	3
P29373 RABP2_HUMAN	Cellular retinoic acid-binding protein 2 C	106.07	51	3
Q9Y5J9 TIM8B_HUMAN	Mitochondrial import inner membrane tr	105.86	52	3
O75190 DNJB6_HUMAN	DnaJ homolog subfamily B member 6 C	105.52	18	3
Q86X76 NIT1_HUMAN	Nitrilase homolog 1 OS=Homo sapiens	105.47	13	3
P60228 EIF3E_HUMAN	Eukaryotic translation initiation factor 3	105.39	24	3
P41223 BUD31_HUMAN	Protein BUD31 homolog OS=Homo sap	105.37	38	3
P52789 HXK2_HUMAN	Hexokinase-2 OS=Homo sapiens GN=H	104.68	18	3
O75663 TIPRL_HUMAN	TIP41-like protein OS=Homo sapiens G	104.43	24	3
Q8TBC4 UBA3_HUMAN	NEDD8-activating enzyme E1 catalytic	104.42	18	3
Q96P16 RPR1A_HUMAN	Regulation of nuclear pre-mRNA domai	104.32	28	3
P30626 SORCN_HUMAN	Sorcin OS=Homo sapiens GN=SRI PE-	104.25	30	3
O43805 SSNA1_HUMAN	Sjogren syndrome nuclear autoantigen	104.04	21	3
P11279 LAMP1_HUMAN	Lysosome-associated membrane glycop	103.74	14	3
O75821 EIF3G_HUMAN	Eukaryotic translation initiation factor 3	103.54	22	3
P51911 CNN1_HUMAN	Calponin-1 OS=Homo sapiens GN=CN	103.35	22	3
Q14974 IMB1_HUMAN	Importin subunit beta-1 OS=Homo sapi	102.69	14	3
Q15363 TMED2_HUMAN	Transmembrane emp24 domain-containi	102.61	30	3
Q9Y5K5 UCHL5_HUMAN	Ubiquitin carboxyl-terminal hydrolase is	102.46	19	3
O75391 SPAG7_HUMAN	Sperm-associated antigen 7 OS=Homo	102.31	27	3
Q7L190 DPPA4_HUMAN	Developmental pluripotency-associated	102.08	25	3
Q56VL3 OCAD2_HUMAN	OCIA domain-containing protein 2 OS=	101.96	24	3
Q8NCW5 AIBP_HUMAN	Apolipoprotein A-I-binding protein OS=H	101.91	36	3
Q16795 NDUA9_HUMAN	NADH dehydrogenase [ubiquinone] 1 a	101.49	20	3
Q9Y5J7 TIM9_HUMAN	Mitochondrial import inner membrane tr	101.22	45	3
Q9NPJ3 ACO13_HUMAN	Acyl-coenzyme A thioesterase 13 OS=H	100.73	22	3
O00622 CYR61_HUMAN	Protein CYR61 OS=Homo sapiens GN=	100.58	16	3
Q8WU90 ZC3HF_HUMAN	Zinc finger CCCH domain-containing pr	100.56	18	3
Q2Q1W2 LIN41_HUMAN	Tripartite motif-containing protein 71 OS	100.38	9	3
Q14157 UBP2L_HUMAN	Ubiquitin-associated protein 2-like OS=	100.19	7	3
Q92979 NEP1_HUMAN	Ribosomal RNA small subunit methyltra	99.69	34	3
Q9UBW8 CSN7A_HUMAN	COP9 signalosome complex subunit 7a	99.23	18	3
Q6P2Q9 PRP8_HUMAN	Pre-mRNA-processing-splicing factor 8	99.16	16	3
Q08431 MFGM_HUMAN	Lactadherin OS=Homo sapiens GN=MF	98.91	12	3

P09012 SNRPA_HUMAN	U1 small nuclear ribonucleoprotein A O	98.54	21	3
O60762 DPM1_HUMAN	Dolichol-phosphate mannosyltransferase	97.75	39	3
P54886 P5CS_HUMAN	Delta-1-pyrroline-5-carboxylate synthase	97.38	13	3
P78330 SERB_HUMAN	Phosphoserine phosphatase OS=Homo sapiens	97.17	29	3
Q14683 SMC1A_HUMAN	Structural maintenance of chromosome	96.89	13	3
P10620 MGST1_HUMAN	Microsomal glutathione S-transferase 1	96.84	30	3
Q9H444 CHM4B_HUMAN	Charged multivesicular body protein 4b	96.69	24	3
P51970 NDUA8_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha	96.5	23	3
P35659 DEK_HUMAN	Protein DEK OS=Homo sapiens GN=DEK	96.28	18	3
P49023 PAXI_HUMAN	Paxillin OS=Homo sapiens GN=PAXN	96.09	11	3
Q16891 IMMT_HUMAN	Mitochondrial inner membrane protein 1	95.78	11	3
Q8NBT2 SPC24_HUMAN	Kinetochore protein Spc24 OS=Homo sapiens	95.76	34	3
P19388 RPAB1_HUMAN	DNA-directed RNA polymerases I, II, and III	95.69	25	3
Q8WWM7 ATX2L_HUMAN	Ataxin-2-like protein OS=Homo sapiens	95.21	13	3
P51858 HDGF_HUMAN	Hepatoma-derived growth factor OS=Homo sapiens	94.92	26	3
Q96CN7 ISOC1_HUMAN	Isochorismatase domain-containing protein	94.28	29	3
P98179 RBM3_HUMAN	Putative RNA-binding protein 3 OS=Homo sapiens	93.74	42	3
O14974 MYPT1_HUMAN	Protein phosphatase 1 regulatory subunit 1	93.67	16	3
P67812 SC11A_HUMAN	Signal peptidase complex catalytic subunit	93.53	26	3
Q01860 PO5F1_HUMAN	POU domain, class 5, transcription factor	93.19	14	3
O15212 PFD6_HUMAN	Prefoldin subunit 6 OS=Homo sapiens	93.17	53	3
P60468 SC61B_HUMAN	Protein transport protein Sec61 subunit beta	93.17	49	3
O43447 PIIH_HUMAN	Peptidyl-prolyl cis-trans isomerase H OS=Homo sapiens	93.05	24	3
Q15637 SF01_HUMAN	Splicing factor 1 OS=Homo sapiens GN=SF01	92.68	9	3
P61011 SRP54_HUMAN	Signal recognition particle 54 kDa protein	92.52	18	3
P35637 FUS_HUMAN	RNA-binding protein FUS OS=Homo sapiens	92.41	25	3
P21741 MK_HUMAN	Midkine OS=Homo sapiens GN=MDK	92.16	23	3
Q9UHD1 CHRD1_HUMAN	Cysteine and histidine-rich domain-containing protein	92.01	18	3
Q9NRN7 ADPPT_HUMAN	L-aminoadipate-semialdehyde dehydrogenase	91.89	18	3
Q8WXX5 DNJC9_HUMAN	DnaJ homolog subfamily C member 9 C	91.37	17	3
P11413 G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase	91.14	10	3
Q9HAV7 GRPE1_HUMAN	GrpE protein homolog 1, mitochondrial	90.4	27	3
Q9NQW7 XPP1_HUMAN	Xaa-Pro aminopeptidase 1 OS=Homo sapiens	89.9	11	3
O15230 LAMA5_HUMAN	Laminin subunit alpha-5 OS=Homo sapiens	88.56	7	3
P53618 COPB_HUMAN	Coatomer subunit beta OS=Homo sapiens	88.36	12	3
Q9H7C9 CK067_HUMAN	UPF0366 protein C11orf67 OS=Homo sapiens	88.3	50	3
Q14498 RBM39_HUMAN	RNA-binding protein 39 OS=Homo sapiens	88.2	16	3
Q9BWJ5 SF3B5_HUMAN	Splicing factor 3B subunit 5 OS=Homo sapiens	87.94	59	3
O14561 ACPM_HUMAN	Acyl carrier protein, mitochondrial OS=Homo sapiens	87.93	34	3
O00487 PSDE_HUMAN	26S proteasome non-ATPase regulator	87.85	39	3
Q9UJ70 NAGK_HUMAN	N-acetyl-D-glucosamine kinase OS=Homo sapiens	87.78	27	3
Q13867 BLMH_HUMAN	Bleomycin hydrolase OS=Homo sapiens	87.64	11	3
P11441 UBL4A_HUMAN	Ubiquitin-like protein 4A OS=Homo sapiens	87.52	23	3
P05556 ITB1_HUMAN	Integrin beta-1 OS=Homo sapiens GN=ITB1	87.25	10	3
Q9BYD1 RM13_HUMAN	39S ribosomal protein L13, mitochondrial	86.76	34	3
Q53GG5 PDLI3_HUMAN	PDZ and LIM domain protein 3 OS=Homo sapiens	86.38	13	3
Q9UNE7 CHIP_HUMAN	E3 ubiquitin-protein ligase CHIP OS=Homo sapiens	86.31	19	3
Q9NQ48 LZTL1_HUMAN	Leucine zipper transcription factor-like protein	86.21	22	3
Q02750 MP2K1_HUMAN	Dual specificity mitogen-activated protein kinase	85.56	13	3
Q14980 NUMA1_HUMAN	Nuclear mitotic apparatus protein 1 OS=Homo sapiens	85.56	12	3
Q9NYU2 UGGG1_HUMAN	UDP-glucose:glycoprotein glucosyltransferase	85.38	8	3
O00483 NDUA4_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha	84.09	37	3
P61599 NAA20_HUMAN	N-alpha-acetyltransferase 20, NatB catalytic	83.25	17	3
O15305 PMM2_HUMAN	Phosphomannomutase 2 OS=Homo sapiens	82.68	14	3
Q8WVJ2 NUDC2_HUMAN	NudC domain-containing protein 2 OS=Homo sapiens	82.57	19	3
P82930 RT34_HUMAN	28S ribosomal protein S34, mitochondrial	82.32	31	3

Q9P0J0 NDUAD_HUMAN	NADH dehydrogenase [ubiquinone] 1 a	81.88	19	3
P00918 CAH2_HUMAN	Carbonic anhydrase 2 OS=Homo sapie	81.64	24	3
P61457 PHS_HUMAN	Pterin-4-alpha-carbinolamine dehydrata	81.29	49	3
Q9NX24 NHP2_HUMAN	H/ACA ribonucleoprotein complex subu	80.98	19	3
O75935 DCTN3_HUMAN	Dynactin subunit 3 OS=Homo sapiens C	80.82	16	3
O43776 SYNC_HUMAN	Asparaginyl-tRNA synthetase, cytoplasi	78.81	12	3
Q9BV57 MTND_HUMAN	1,2-dihydroxy-3-keto-5-methylthiopente	78.58	31	3
O14776 TCRG1_HUMAN	Transcription elongation regulator 1 OS	78.46	8	3
O60716 CTND1_HUMAN	Catenin delta-1 OS=Homo sapiens GN=	78.31	13	3
Q32P28 P3H1_HUMAN	Prolyl 3-hydroxylase 1 OS=Homo sapie	77.96	8	3
O94760 DDAH1_HUMAN	N(G),N(G)-dimethylarginine dimethylam	77.81	13	3
O00762 UBE2C_HUMAN	Ubiquitin-conjugating enzyme E2 C OS=	77.44	22	3
P62861 RS30_HUMAN	40S ribosomal protein S30 OS=Homo s	76.48	20	3
P39060 COIA1_HUMAN	Collagen alpha-1(XVIII) chain OS=Hom	75.9	14	3
O60613 SEP15_HUMAN	15 kDa selenoprotein OS=Homo sapier	75.78	22	3
O14744 ANM5_HUMAN	Protein arginine N-methyltransferase 5	75.63	15	3
Q96HQ2 C2AIL_HUMAN	CDKN2AIP N-terminal-like protein OS=	75.18	24	3
Q12841 FSTL1_HUMAN	Follistatin-related protein 1 OS=Homo s	74.92	23	3
P36543 VATE1_HUMAN	V-type proton ATPase subunit E 1 OS=	73.98	16	3
O60256 KPRB_HUMAN	Phosphoribosyl pyrophosphate synthas	73.54	22	3
O75937 DNJC8_HUMAN	DnaJ homolog subfamily C member 8 C	73.14	29	3
Q7LBC6 KDM3B_HUMAN	Lysine-specific demethylase 3B OS=Ho	72.5	12	3
Q9NPE3 NOP10_HUMAN	H/ACA ribonucleoprotein complex subu	72.2	62	3
P62253 UB2G1_HUMAN	Ubiquitin-conjugating enzyme E2 G1 O	71.77	15	3
Q8NFU3 TSTD1_HUMAN	Thiosulfate sulfurtransferase/rhodanese	69.82	21	3
Q9BR76 COR1B_HUMAN	Coronin-1B OS=Homo sapiens GN=CC	69.77	10	3
Q9Y547 HSB11_HUMAN	Heat shock protein beta-11 OS=Homo s	67.64	49	3
Q8WUW1 BRK1_HUMAN	Protein BRICK1 OS=Homo sapiens GN	67.4	37	3
Q00325 MPCP_HUMAN	Phosphate carrier protein, mitochondria	66.68	17	3
Q13564 ULA1_HUMAN	NEDD8-activating enzyme E1 regulator	62.1	11	3
Q5T0N5 FBP1L_HUMAN	Formin-binding protein 1-like OS=Homc	61.49	16	3
Q8NF91 SYNE1_HUMAN	Nesprin-1 OS=Homo sapiens GN=SYN	61.01	6	3
P52788 SPSY_HUMAN	Spermine synthase OS=Homo sapiens	59.64	17	3
P49916 DNLI3_HUMAN	DNA ligase 3 OS=Homo sapiens GN=L	59.01	5	3
P84098 RL19_HUMAN	60S ribosomal protein L19 OS=Homo s	58.49	24	3
P54727 RD23B_HUMAN	UV excision repair protein RAD23 homc	54.59	15	3
O14949 QCR8_HUMAN	Cytochrome b-c1 complex subunit 8 OS	50.95	39	3
P24043 LAMA2_HUMAN	Laminin subunit alpha-2 OS=Homo sap	36.38	8	3
Q5T5P2 SKT_HUMAN	Sickle tail protein homolog OS=Homo s	36.23	9	3
Q9UMZ3 PTPRQ_HUMAN	Phosphatidylinositol phosphatase PTPF	36.05	5	3
Q9BVA1 TBB2B_HUMAN	Tubulin beta-2B chain OS=Homo sapie	330.95	80	2
Q13885 TBB2A_HUMAN	Tubulin beta-2A chain OS=Homo sapie	329.55	80	2
P04350 TBB4_HUMAN	Tubulin beta-4 chain OS=Homo sapiens	302.6	76	2
P07951 TPM2_HUMAN	Tropomyosin beta chain OS=Homo sap	286.14	58	2
Q9BQE3 TBA1C_HUMAN	Tubulin alpha-1C chain OS=Homo sapi	275.14	76	2
P62979 RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a C	249.3	73	2
P36873 PP1G_HUMAN	Serine/threonine-protein phosphatase F	230.3	53	2
P16402 H13_HUMAN	Histone H1.3 OS=Homo sapiens GN=H	208.58	66	2
P11940 PABP1_HUMAN	Polyadenylate-binding protein 1 OS=Ho	197.97	41	2
Q99867 TBB4Q_HUMAN	Putative tubulin beta-4q chain OS=Hom	195.25	59	2
P08134 RHOC_HUMAN	Rho-related GTP-binding protein RhoC	192.52	59	2
A6NKZ8 YI016_HUMAN	Putative tubulin beta chain-like protein	188.29	48	2
Q14240 IF4A2_HUMAN	Eukaryotic initiation factor 4A-II OS=Ho	180.35	35	2
P30154 2AAB_HUMAN	Serine/threonine-protein phosphatase 2	178.49	55	2
Q9H4B7 TBB1_HUMAN	Tubulin beta-1 chain OS=Homo sapiens	172.85	30	2
P12235 ADT1_HUMAN	ADP/ATP translocase 1 OS=Homo sap	168.81	39	2



O43390 HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprote	149.02	26	2
O00292 LFTY2_HUMAN	Left-right determination factor 2 OS=Ho	135.99	34	2
Q16576 RBBP7_HUMAN	Histone-binding protein RBBP7 OS=Ho	132.75	30	2
P62191 PRS4_HUMAN	26S protease regulatory subunit 4 OS=	125.52	41	2
P61020 RAB5B_HUMAN	Ras-related protein Rab-5B OS=Homo	123.52	35	2
P61077 UB2D3_HUMAN	Ubiquitin-conjugating enzyme E2 D3 OS	123.06	31	2
Q96RU2 UBP28_HUMAN	Ubiquitin carboxyl-terminal hydrolase 28	122.59	12	2
P62879 GBB2_HUMAN	Guanine nucleotide-binding protein G(I)	119.57	27	2
Q13404 UB2V1_HUMAN	Ubiquitin-conjugating enzyme E2 varian	117.06	39	2
Q15819 UB2V2_HUMAN	Ubiquitin-conjugating enzyme E2 varian	116.9	45	2
O00764 PDXK_HUMAN	Pyridoxal kinase OS=Homo sapiens GN	116.49	35	2
Q09028 RBBP4_HUMAN	Histone-binding protein RBBP4 OS=Ho	115.76	16	2
P20339 RAB5A_HUMAN	Ras-related protein Rab-5A OS=Homo	115.52	26	2
P61163 ACTZ_HUMAN	Alpha-centractin OS=Homo sapiens GN	114.53	26	2
O96008 TOM40_HUMAN	Mitochondrial import receptor subunit T	110.41	33	2
O60763 USO1_HUMAN	General vesicular transport factor p115	109.9	23	2
Q9NVD7 PARVA_HUMAN	Alpha-parvin OS=Homo sapiens GN=P	109.79	26	2
P49902 5NTC_HUMAN	Cytosolic purine 5'-nucleotidase OS=Hc	108.62	29	2
P18859 ATP5J_HUMAN	ATP synthase-coupling factor 6, mitoch	107.86	41	2
Q9NXH9 TRM1_HUMAN	N(2),N(2)-dimethylguanosine tRNA met	106.8	24	2
P31942 HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprote	106.42	37	2
Q14166 TTL12_HUMAN	Tubulin--tyrosine ligase-like protein 12 C	106.11	26	2
P62330 ARF6_HUMAN	ADP-ribosylation factor 6 OS=Homo sa	105.77	18	2
P63172 DYLT1_HUMAN	Dynein light chain Tctex-type 1 OS=Hor	104.88	51	2
Q9NUG6 PDRG1_HUMAN	p53 and DNA damage-regulated protein	104.32	23	2
O60502 NCOAT_HUMAN	Bifunctional protein NCOAT OS=Homo	102.68	21	2
P48507 GSH0_HUMAN	Glutamate--cysteine ligase regulatory su	102.5	24	2
O95983 MBD3_HUMAN	Methyl-CpG-binding domain protein 3 C	102.05	18	2
Q9H2U2 IPYR2_HUMAN	Inorganic pyrophosphatase 2, mitochon	102.01	20	2
Q9UBI1 COMD3_HUMAN	COMM domain-containing protein 3 OS	101.68	31	2
P51153 RAB13_HUMAN	Ras-related protein Rab-13 OS=Homo	101.47	26	2
Q86Y39 NDUAB_HUMAN	NADH dehydrogenase [ubiquinone] 1 a	101.07	32	2
P43034 LIS1_HUMAN	Platelet-activating factor acetylhydrolas	100.5	23	2
Q9NRX4 PHP14_HUMAN	14 kDa phosphohistidine phosphatase C	100.38	42	2
P32322 P5CR1_HUMAN	Proline-5-carboxylate reductase 1, mi	100.32	20	2
P55957 BID_HUMAN	BH3-interacting domain death agonist C	100.01	38	2
Q9N2T2 OGFR_HUMAN	Opioid growth factor receptor OS=Homo	99.66	18	2
P55036 PSMD4_HUMAN	26S proteasome non-ATPase regulator	99.41	19	2
P80294 MT1H_HUMAN	Metallothionein-1H OS=Homo sapiens	99.38	66	2
P47895 AL1A3_HUMAN	Aldehyde dehydrogenase family 1 mem	99.32	19	2
P14543 NID1_HUMAN	Nidogen-1 OS=Homo sapiens GN=NID	99.03	9	2
Q9UJZ1 STML2_HUMAN	Stomatin-like protein 2 OS=Homo sapie	98.98	29	2
Q9Y3C4 TPRKB_HUMAN	TP53RK-binding protein OS=Homo sap	98.86	31	2
Q9H4G4 GAPR1_HUMAN	Golgi-associated plant pathogenesis-re	98.79	34	2
Q13418 ILK_HUMAN	Integrin-linked protein kinase OS=Homo	98.7	18	2
Q9Y2V2 CHSP1_HUMAN	Calcium-regulated heat stable protein 1	98.48	44	2
Q15024 EXOS7_HUMAN	Exosome complex component RRP42 C	98.12	25	2
P50995 ANX11_HUMAN	Annexin A11 OS=Homo sapiens GN=A	98.04	18	2
P07919 QCR6_HUMAN	Cytochrome b-c1 complex subunit 6, mi	97.86	60	2
P49006 MRP_HUMAN	MARCKS-related protein OS=Homo sa	97.19	29	2
Q92769 HDAC2_HUMAN	Histone deacetylase 2 OS=Homo sapie	97.1	15	2
Q9H299 SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-	97.09	31	2
Q6DKJ4 NXN_HUMAN	Nucleoredoxin OS=Homo sapiens GN=	96.92	17	2
O43488 ARK72_HUMAN	Aflatoxin B1 aldehyde reductase memb	96.74	22	2
O43852 CALU_HUMAN	Calumenin OS=Homo sapiens GN=CAL	96.52	16	2
Q9Y3Y2 CHTOP_HUMAN	Chromatin target of PRMT1 protein OS	96.03	27	2

Q9UK76 HN1_HUMAN	Hematological and neurological express	95.88	32	2
P14854 CX6B1_HUMAN	Cytochrome c oxidase subunit 6B1 OS=	95.77	40	2
P61966 AP1S1_HUMAN	AP-1 complex subunit sigma-1A OS=Ho	95.37	28	2
Q9UBK9 UXT_HUMAN	Protein UXT OS=Homo sapiens GN=U	95.24	35	2
A0AVT1 UBA6_HUMAN	Ubiquitin-like modifier-activating enzyme	94.73	18	2
Q9UBP6 TRMB_HUMAN	tRNA (guanine-N(7)-)-methyltransferase	94.63	17	2
Q9P0S9 TM14C_HUMAN	Transmembrane protein 14C OS=Homo	94.07	62	2
Q15427 SF3B4_HUMAN	Splicing factor 3B subunit 4 OS=Homo	93.81	26	2
P35250 RFC2_HUMAN	Replication factor C subunit 2 OS=Hom	93.74	12	2
Q9UBC3 DNM3B_HUMAN	DNA (cytosine-5)-methyltransferase 3B	93.71	9	2
P06132 DCUP_HUMAN	Uroporphyrinogen decarboxylase OS=H	93.6	24	2
O60888 CUTA_HUMAN	Protein CutA OS=Homo sapiens GN=C	93.52	36	2
Q16540 RM23_HUMAN	39S ribosomal protein L23, mitochondri	93.41	31	2
P42167 LAP2B_HUMAN	Lamina-associated polypeptide 2, isofo	92.93	20	2
P42166 LAP2A_HUMAN	Lamina-associated polypeptide 2, isofo	92.93	14	2
O14907 TX1B3_HUMAN	Tax1-binding protein 3 OS=Homo sapie	92.73	31	2
O43237 DC1L2_HUMAN	Cytoplasmic dynein 1 light intermediate	92.59	21	2
Q13232 NDK3_HUMAN	Nucleoside diphosphate kinase 3 OS=H	92	40	2
Q9H993 CF211_HUMAN	UPF0364 protein C6orf211 OS=Homo s	91.98	13	2
O95232 LC7L3_HUMAN	Luc7-like protein 3 OS=Homo sapiens C	91.9	18	2
Q9NXG2 THUM1_HUMAN	THUMP domain-containing protein 1 OS	91.29	18	2
Q12849 GRSF1_HUMAN	G-rich sequence factor 1 OS=Homo sap	90.84	26	2
O75688 PPM1B_HUMAN	Protein phosphatase 1B OS=Homo sap	89.87	10	2
Q04323 UBXN1_HUMAN	UBX domain-containing protein 1 OS=H	89.79	32	2
P14406 CX7A2_HUMAN	Cytochrome c oxidase subunit 7A2, mit	89.65	39	2
Q9H6S3 ES8L2_HUMAN	Epidermal growth factor receptor kinase	89.64	14	2
Q9BSD7 NTPCR_HUMAN	Cancer-related nucleoside-triphospha	89.21	24	2
P41214 EIF2D_HUMAN	Eukaryotic translation initiation factor 2I	89.15	20	2
A6NDU8 CE051_HUMAN	UPF0600 protein C5orf51 OS=Homo sa	88.97	15	2
Q14061 COX17_HUMAN	Cytochrome c oxidase copper chaperon	88.94	48	2
Q9NYL4 FKB11_HUMAN	Peptidyl-prolyl cis-trans isomerase FKB	88.82	15	2
P19387 RPB3_HUMAN	DNA-directed RNA polymerase II subur	88.77	20	2
Q96GK7 FAH2A_HUMAN	Fumarylacetoacetate hydrolase domain	88.33	13	2
Q15642 CIP4_HUMAN	Cdc42-interacting protein 4 OS=Homo s	88.04	16	2
Q9BT73 PSMG3_HUMAN	Proteasome assembly chaperone 3 OS	88.01	23	2
Q9Y5B9 SP16H_HUMAN	FACT complex subunit SPT16 OS=Hor	87.4	7	2
P56134 ATPK_HUMAN	ATP synthase subunit f, mitochondrial C	87.36	26	2
P62273 RS29_HUMAN	40S ribosomal protein S29 OS=Homo s	87.36	48	2
P10619 PPGB_HUMAN	Lysosomal protective protein OS=Homo	87.22	10	2
O60518 RNBP6_HUMAN	Ran-binding protein 6 OS=Homo sapier	87.07	7	2
Q9Y3D6 FIS1_HUMAN	Mitochondrial fission 1 protein OS=Hom	86.95	28	2
Q9HBM1 SPC25_HUMAN	Kinetochore protein Spc25 OS=Homo s	86.86	21	2
P19367 HXK1_HUMAN	Hexokinase-1 OS=Homo sapiens GN=H	86.41	8	2
Q96EK6 GNA1_HUMAN	Glucosamine 6-phosphate N-acetyltran	86.41	18	2
Q9H4M9 EHD1_HUMAN	EH domain-containing protein 1 OS=Ho	86.24	15	2
P15374 UCHL3_HUMAN	Ubiquitin carboxyl-terminal hydrolase is	86.23	37	2
O95813 CER1_HUMAN	Cerberus OS=Homo sapiens GN=CER	86.12	21	2
P40937 RFC5_HUMAN	Replication factor C subunit 5 OS=Hom	86.1	25	2
P55039 DRG2_HUMAN	Developmentally-regulated GTP-binding	86.02	14	2
P20338 RAB4A_HUMAN	Ras-related protein Rab-4A OS=Homo	85.98	35	2
Q15293 RCN1_HUMAN	Reticulocalbin-1 OS=Homo sapiens GN	85.72	24	2
A2VDF0 FUCM_HUMAN	Fucose mutarotase OS=Homo sapiens	85.71	26	2
P23588 IF4B_HUMAN	Eukaryotic translation initiation factor 4E	85.61	17	2
Q7Z2W9 RM21_HUMAN	39S ribosomal protein L21, mitochondri	85.6	27	2
Q92905 CSN5_HUMAN	COP9 signalosome complex subunit 5 C	85.48	19	2
Q7RTV0 PHF5A_HUMAN	PHD finger-like domain-containing prote	85.47	32	2

Q16774 KGUA_HUMAN	Guanylate kinase OS=Homo sapiens G	84.97	12	2
O60783 RT14_HUMAN	28S ribosomal protein S14, mitochondri	84.75	27	2
Q04637 IF4G1_HUMAN	Eukaryotic translation initiation factor 4	84.69	9	2
Q05209 PTN12_HUMAN	Tyrosine-protein phosphatase non-rece	84.65	16	2
Q9H2J4 PDCL3_HUMAN	Phosducin-like protein 3 OS=Homo sap	84.64	29	2
O60884 DNJA2_HUMAN	DnaJ homolog subfamily A member 2 C	84.63	18	2
P67870 CSK2B_HUMAN	Casein kinase II subunit beta OS=Homo	84.56	9	2
Q9ULV4 COR1C_HUMAN	Coronin-1C OS=Homo sapiens GN=CC	84.23	22	2
P49643 PRI2_HUMAN	DNA primase large subunit OS=Homo s	84.03	17	2
Q7Z2Z2 ETUD1_HUMAN	Elongation factor Tu GTP-binding doma	83.91	11	2
Q9BW83 IFT27_HUMAN	Intraflagellar transport protein 27 homol	83.84	17	2
Q13951 PEBB_HUMAN	Core-binding factor subunit beta OS=H	83.76	23	2
Q8WTX7 GATL3_HUMAN	GATS-like protein 3 OS=Homo sapiens	83.64	20	2
P00568 KAD1_HUMAN	Adenylate kinase isoenzyme 1 OS=Hor	83.62	14	2
Q96H20 SNF8_HUMAN	Vacuolar-sorting protein SNF8 OS=Hor	83.59	16	2
P54105 ICLN_HUMAN	Methylosome subunit pICln OS=Homo s	83.25	11	2
Q9NR28 DBLOH_HUMAN	Diablo homolog, mitochondrial OS=Hor	83.12	25	2
Q9NS69 TOM22_HUMAN	Mitochondrial import receptor subunit T	83.03	37	2
Q9BX68 HINT2_HUMAN	Histidine triad nucleotide-binding protei	82.54	34	2
O43617 TPPC3_HUMAN	Trafficking protein particle complex sub	82.46	34	2
P46109 CRKL_HUMAN	Crk-like protein OS=Homo sapiens GN=	82.28	12	2
O15116 LSM1_HUMAN	U6 snRNA-associated Sm-like protein L	82.24	31	2
P15927 RFA2_HUMAN	Replication protein A 32 kDa subunit O	82.12	33	2
P09486 SPRC_HUMAN	SPARC OS=Homo sapiens GN=SPARC	82.12	10	2
O95373 IPO7_HUMAN	Importin-7 OS=Homo sapiens GN=IPO	81.84	8	2
Q16186 ADRM1_HUMAN	Proteasomal ubiquitin receptor ADRM1	81.75	13	2
Q13442 HAP28_HUMAN	28 kDa heat- and acid-stable phosphop	81.62	24	2
P48444 COPD_HUMAN	Coatomer subunit delta OS=Homo sapi	81.29	12	2
O75380 NDUS6_HUMAN	NADH dehydrogenase [ubiquinone] iron	81.2	27	2
A8MWD9 RUXGL_HUMAN	Small nuclear ribonucleoprotein G-like p	81.11	37	2
P62308 RUXG_HUMAN	Small nuclear ribonucleoprotein G OS=	81.11	17	2
Q96HE7 ERO1A_HUMAN	ERO1-like protein alpha OS=Homo sap	81.11	15	2
P55854 SUMO3_HUMAN	Small ubiquitin-related modifier 3 OS=H	80.97	24	2
P30049 ATPD_HUMAN	ATP synthase subunit delta, mitochond	80.77	27	2
Q9UKY7 CDV3_HUMAN	Protein CDV3 homolog OS=Homo sapi	80.75	16	2
Q3LXA3 DHAK_HUMAN	Bifunctional ATP-dependent dihydroxya	80.72	25	2
P29218 IMPA1_HUMAN	Inositol monophosphatase 1 OS=Homo	80.63	8	2
P61803 DAD1_HUMAN	Dolichyl-diphosphooligosaccharide--pro	80.51	34	2
O96000 NDUBA_HUMAN	NADH dehydrogenase [ubiquinone] 1 b	80.43	27	2
Q9Y5S9 RBM8A_HUMAN	RNA-binding protein 8A OS=Homo sap	80.42	21	2
Q15833 STXB2_HUMAN	Syntaxin-binding protein 2 OS=Homo s	80.37	19	2
Q99447 PCY2_HUMAN	Ethanolamine-phosphate cytidyltransf	80.21	23	2
Q96C90 PP14B_HUMAN	Protein phosphatase 1 regulatory subur	80.1	59	2
P15954 COX7C_HUMAN	Cytochrome c oxidase subunit 7C, mito	79.92	41	2
P35611 ADDA_HUMAN	Alpha-adducin OS=Homo sapiens GN=	79.78	16	2
P52758 UK114_HUMAN	Ribonuclease UK114 OS=Homo sapien	79.42	31	2
O95793 STAU1_HUMAN	Double-stranded RNA-binding protein S	79.38	16	2
Q01081 U2AF1_HUMAN	Splicing factor U2AF 35 kDa subunit O	79.3	11	2
P00390 GSHR_HUMAN	Glutathione reductase, mitochondrial O	79.25	9	2
Q8N0X7 SPG20_HUMAN	Spartin OS=Homo sapiens GN=SPG20	79.24	5	2
Q86SZ2 TPC6B_HUMAN	Trafficking protein particle complex sub	79.01	17	2
O75431 MTX2_HUMAN	Metaxin-2 OS=Homo sapiens GN=MTX	78.94	13	2
P49589 SYCC_HUMAN	Cysteinyl-tRNA synthetase, cytoplasmic	78.77	17	2
Q9H944 MED20_HUMAN	Mediator of RNA polymerase II transcrip	78.61	21	2
Q9Y285 SYFA_HUMAN	Phenylalanyl-tRNA synthetase alpha ch	78.51	13	2
P78344 IF4G2_HUMAN	Eukaryotic translation initiation factor 4	78.49	10	2

P07311 ACYP1_HUMAN	Acylphosphatase-1 OS=Homo sapiens	78.49	23	2
Q9UQ35 SRRM2_HUMAN	Serine/arginine repetitive matrix protein	78.46	9	2
P25391 LAMA1_HUMAN	Laminin subunit alpha-1 OS=Homo sap	78.39	9	2
Q9Y6M9 NDUB9_HUMAN	NADH dehydrogenase [ubiquinone] 1 b	78.27	18	2
Q06481 APLP2_HUMAN	Amyloid-like protein 2 OS=Homo sapier	78	11	2
Q9ULA0 DNPEP_HUMAN	Aspartyl aminopeptidase OS=Homo sap	77.95	17	2
Q9UNH7 SNX6_HUMAN	Sorting nexin-6 OS=Homo sapiens GN=	77.94	19	2
P04439 1A03_HUMAN	HLA class I histocompatibility antigen, A	77.85	18	2
P56192 SYMC_HUMAN	Methionyl-tRNA synthetase, cytoplasmic	77.47	8	2
P61086 UBE2K_HUMAN	Ubiquitin-conjugating enzyme E2 K OS=	77.36	39	2
O60841 IF2P_HUMAN	Eukaryotic translation initiation factor 5B	77.17	13	2
Q5TDH0 DDI2_HUMAN	Protein DDI1 homolog 2 OS=Homo sap	77.15	6	2
P52815 RM12_HUMAN	39S ribosomal protein L12, mitochondri	76.8	21	2
Q92572 AP3S1_HUMAN	AP-3 complex subunit sigma-1 OS=Hor	76.56	10	2
O00170 AIP_HUMAN	AH receptor-interacting protein OS=Hor	76.24	25	2
Q9NTX5 ECHD1_HUMAN	Enoyl-CoA hydratase domain-containing	76.14	15	2
Q9Y3D9 RT23_HUMAN	28S ribosomal protein S23, mitochondri	76.04	18	2
P53365 ARFP2_HUMAN	Arfaptin-2 OS=Homo sapiens GN=ARF	75.97	14	2
A6NK07 IF2BL_HUMAN	Eukaryotic translation initiation factor 2	75.91	13	2
P20042 IF2B_HUMAN	Eukaryotic translation initiation factor 2	75.91	13	2
P10155 RO60_HUMAN	60 kDa SS-A/Ro ribonucleoprotein OS=	75.88	11	2
P55060 XPO2_HUMAN	Exportin-2 OS=Homo sapiens GN=CSE	75.51	13	2
Q14CX7 NAA25_HUMAN	N-alpha-acetyltransferase 25, NatB aux	75.31	9	2
Q13148 TADBP_HUMAN	TAR DNA-binding protein 43 OS=Homoc	74.94	14	2
Q96SM3 CPXM1_HUMAN	Probable carboxypeptidase X1 OS=Hor	74.86	10	2
Q99426 TBCB_HUMAN	Tubulin-folding cofactor B OS=Homo sa	74.55	9	2
Q92890 UFD1_HUMAN	Ubiquitin fusion degradation protein 1 h	74.47	14	2
P37268 FDFT_HUMAN	Squalene synthase OS=Homo sapiens	74.35	15	2
Q9UMY4 SNX12_HUMAN	Sorting nexin-12 OS=Homo sapiens GN	74.31	17	2
Q9UL25 RAB21_HUMAN	Ras-related protein Rab-21 OS=Homo	74.11	28	2
Q9NPH2 INO1_HUMAN	Inositol-3-phosphate synthase 1 OS=Ho	73.91	8	2
Q16706 MA2A1_HUMAN	Alpha-mannosidase 2 OS=Homo sapier	73.43	9	2
Q9UJC5 SH3L2_HUMAN	SH3 domain-binding glutamic acid-rich-	73.32	25	2
Q02978 M2OM_HUMAN	Mitochondrial 2-oxoglutarate/malate car	73.19	21	2
Q9Y3B7 RM11_HUMAN	39S ribosomal protein L11, mitochondri	73.04	46	2
Q9BU89 DOHH_HUMAN	Deoxyhypusine hydroxylase OS=Homo	73.02	18	2
P11233 RALA_HUMAN	Ras-related protein Ral-A OS=Homo sa	72.88	22	2
O00625 PIR_HUMAN	Pirin OS=Homo sapiens GN=PIR PE=1	72.82	16	2
Q9UHB9 SRP68_HUMAN	Signal recognition particle 68 kDa prote	72.49	11	2
Q99543 DNJC2_HUMAN	DnaJ homolog subfamily C member 2 C	72.4	12	2
P63272 SPT4H_HUMAN	Transcription elongation factor SPT4 O	72.32	21	2
Q9H8S9 MOL1B_HUMAN	Mps one binder kinase activator-like 1B	72.25	19	2
Q7L9L4 MOL1A_HUMAN	Mps one binder kinase activator-like 1A	72.25	14	2
Q9UBV8 PEF1_HUMAN	Peflin OS=Homo sapiens GN=PEF1 PE	72.06	11	2
Q9NV35 NUD15_HUMAN	Probable 7,8-dihydro-8-oxoguanine triph	71.94	7	2
Q5TZA2 CROCC_HUMAN	Rootletin OS=Homo sapiens GN=CROCC	71.86	9	2
Q14671 PUM1_HUMAN	Pumilio homolog 1 OS=Homo sapiens C	71.78	5	2
Q5SSJ5 HP1B3_HUMAN	Heterochromatin protein 1-binding prote	71.74	12	2
Q96HR9 REEP6_HUMAN	Receptor expression-enhancing protein	71.42	29	2
P01116 RASK_HUMAN	GTPase KRas OS=Homo sapiens GN=	70.95	17	2
P01111 RASN_HUMAN	GTPase NRas OS=Homo sapiens GN=	70.95	17	2
Q9NVA2 SEP11_HUMAN	Septin-11 OS=Homo sapiens GN=SEP	70.48	17	2
Q8TDP1 RNH2C_HUMAN	Ribonuclease H2 subunit C OS=Homo	70.4	15	2
Q9UH65 SWP70_HUMAN	Switch-associated protein 70 OS=Homoc	70.06	12	2
Q13153 PAK1_HUMAN	Serine/threonine-protein kinase PAK 1	69.67	6	2
P56747 CLD6_HUMAN	Claudin-6 OS=Homo sapiens GN=CLD	69.55	13	2

Q6IQ22 RAB12_HUMAN	Ras-related protein Rab-12 OS=Homo	69.4	13	2
Q7Z4H3 HDDC2_HUMAN	HD domain-containing protein 2 OS=Hc	69.3	22	2
O00629 IMA4_HUMAN	Importin subunit alpha-4 OS=Homo sap	69.15	8	2
Q8NC69 KCTD6_HUMAN	BTB/POZ domain-containing protein KC	68.94	19	2
Q8IZ83 A16A1_HUMAN	Aldehyde dehydrogenase family 16 mer	68.93	12	2
P29083 T2EA_HUMAN	General transcription factor IIE subunit	68.87	11	2
Q9Y6E0 STK24_HUMAN	Serine/threonine-protein kinase 24 OS=	68.56	15	2
P23378 GCSP_HUMAN	Glycine dehydrogenase [decarboxylatin	68.21	4	2
Q5TFE4 NT5D1_HUMAN	5'-nucleotidase domain-containing prote	68.2	11	2
Q9UKF6 CPSF3_HUMAN	Cleavage and polyadenylation specificit	67.53	8	2
O95218 ZRB2_HUMAN	Zinc finger Ran-binding domain-contain	67.15	9	2
P04183 KITH_HUMAN	Thymidine kinase, cytosolic OS=Homo	66.94	14	2
Q16718 NDUA5_HUMAN	NADH dehydrogenase [ubiquinone] 1 a	66.93	30	2
P60510 PP4C_HUMAN	Serine/threonine-protein phosphatase 4	66.73	10	2
P61225 RAP2B_HUMAN	Ras-related protein Rap-2b OS=Homo	66.56	21	2
Q03426 KIME_HUMAN	Mevalonate kinase OS=Homo sapiens	66.39	13	2
O00154 BACH_HUMAN	Cytosolic acyl coenzyme A thioester hyd	66.35	22	2
O95235 KIF20A_HUMAN	Kinesin-like protein KIF20A OS=Homo	65.81	13	2
Q14011 CIRBP_HUMAN	Cold-inducible RNA-binding protein OS=	65.66	22	2
O43583 DENR_HUMAN	Density-regulated protein OS=Homo sa	65.64	19	2
P20585 MSH3_HUMAN	DNA mismatch repair protein Msh3 OS=	65.59	17	2
Q8N5K1 CISD2_HUMAN	CDGSH iron-sulfur domain-containing p	65.57	34	2
P52888 THOP1_HUMAN	Thimet oligopeptidase OS=Homo sapie	65.26	4	2
Q9GZQ8 MLP3B_HUMAN	Microtubule-associated proteins 1A/1B	65.03	23	2
A6NCE7 MP3B2_HUMAN	Microtubule-associated proteins 1A/1B	65.03	23	2
O75534 CSDE1_HUMAN	Cold shock domain-containing protein E	65.03	9	2
Q9BZL1 UBL5_HUMAN	Ubiquitin-like protein 5 OS=Homo sapie	64.94	25	2
O14925 TIM23_HUMAN	Mitochondrial import inner membrane tr	64.93	13	2
Q5SRD1 TI23B_HUMAN	Putative mitochondrial import inner mer	64.93	11	2
Q9Y3B2 EXOS1_HUMAN	Exosome complex component CSL4 OS=	64.87	13	2
Q13636 RAB31_HUMAN	Ras-related protein Rab-31 OS=Homo	64.3	19	2
P05204 HMG2_HUMAN	Non-histone chromosomal protein HMG	64.24	56	2
P56377 AP1S2_HUMAN	AP-1 complex subunit sigma-2 OS=Hor	64.03	17	2
P61960 UFM1_HUMAN	Ubiquitin-fold modifier 1 OS=Homo sap	63.89	27	2
P18065 IBP2_HUMAN	Insulin-like growth factor-binding proteir	63.87	8	2
Q9BRJ7 SDOS_HUMAN	Protein syndesmos OS=Homo sapiens	63.48	17	2
O00217 NDUS8_HUMAN	NADH dehydrogenase [ubiquinone] iron	63.33	18	2
Q96QK1 VPS35_HUMAN	Vacuolar protein sorting-associated pro	63.32	13	2
Q13155 AIMP2_HUMAN	Aminoacyl tRNA synthase complex-inte	63.04	10	2
Q07812 BAX_HUMAN	Apoptosis regulator BAX OS=Homo sap	62.59	19	2
P52732 KIF11_HUMAN	Kinesin-like protein KIF11 OS=Homo sa	62.44	5	2
O00115 DNS2A_HUMAN	Deoxyribonuclease-2-alpha OS=Homo	61.62	7	2
P49406 RM19_HUMAN	39S ribosomal protein L19, mitochondri	61.61	11	2
Q9H9J2 RM44_HUMAN	39S ribosomal protein L44, mitochondri	61.5	10	2
P49756 RBM25_HUMAN	RNA-binding protein 25 OS=Homo sapi	61.38	3	2
Q6NVY1 HIBCH_HUMAN	3-hydroxyisobutyryl-CoA hydrolase, mit	61.25	11	2
P19404 NDUV2_HUMAN	NADH dehydrogenase [ubiquinone] flav	61.16	16	2
Q96BM9 ARL8A_HUMAN	ADP-ribosylation factor-like protein 8A	61.03	15	2
Q9NVJ2 ARL8B_HUMAN	ADP-ribosylation factor-like protein 8B	61.03	15	2
O75251 NDUS7_HUMAN	NADH dehydrogenase [ubiquinone] iron	60.96	8	2
Q9Y2R0 CCD56_HUMAN	Coiled-coil domain-containing protein 5	60.9	27	2
O94826 TOM70_HUMAN	Mitochondrial import receptor subunit T	59.92	9	2
P14927 QCR7_HUMAN	Cytochrome b-c1 complex subunit 7 OS	59.92	27	2
P63098 CANB1_HUMAN	Calcineurin subunit B type 1 OS=Homo	59.79	11	2
P14866 HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprote	58.35	12	2
P21281 VATB2_HUMAN	V-type proton ATPase subunit B, brain	58.26	10	2

Q02218 ODO1_HUMAN	2-oxoglutarate dehydrogenase, mitoch	58.05	8	2
Q9Y2Q9 RT28_HUMAN	28S ribosomal protein S28, mitochondri	57.96	13	2
P31930 QCR1_HUMAN	Cytochrome b-c1 complex subunit 1, mi	57.88	13	2
P56556 NDUA6_HUMAN	NADH dehydrogenase [ubiquinone] 1 a	57.21	31	2
O43678 NDUA2_HUMAN	NADH dehydrogenase [ubiquinone] 1 a	57.14	20	2
Q96K17 BT3L4_HUMAN	Transcription factor BTF3 homolog 4 O	56.73	33	2
O43865 SAHH2_HUMAN	Putative adenosylhomocysteinase 2 OS	56.61	16	2
Q9Y530 CF130_HUMAN	Uncharacterized protein C6orf130 OS=	56.26	26	2
O15498 YKT6_HUMAN	Synaptobrevin homolog YKT6 OS=Homo	55.34	10	2
Q14677 EPN4_HUMAN	Clathrin interactor 1 OS=Homo sapiens	55.24	6	2
Q92747 ARC1A_HUMAN	Actin-related protein 2/3 complex subur	54.89	26	2
Q99661 KIF2C_HUMAN	Kinesin-like protein KIF2C OS=Homo s	54.64	11	2
Q9NVM6 DJC17_HUMAN	DnaJ homolog subfamily C member 17	54.21	22	2
O75718 CRTAP_HUMAN	Cartilage-associated protein OS=Homo	53.78	6	2
Q02880 TOP2B_HUMAN	DNA topoisomerase 2-beta OS=Homo s	53.64	5	2
Q13428 TCOF_HUMAN	Treacle protein OS=Homo sapiens GN=	52.99	13	2
Q8WZA0 LZIC_HUMAN	Protein LZIC OS=Homo sapiens GN=L	52.68	23	2
Q9H7Z7 PGES2_HUMAN	Prostaglandin E synthase 2 OS=Homo	52.65	12	2
O95881 TXD12_HUMAN	Thioredoxin domain-containing protein	51.81	14	2
P61513 RL37A_HUMAN	60S ribosomal protein L37a OS=Homo	51.22	28	2
P56381 ATP5E_HUMAN	ATP synthase subunit epsilon, mitochor	51.1	53	2
O75438 NDUB1_HUMAN	NADH dehydrogenase [ubiquinone] 1 b	51.05	48	2
Q7Z4W1 DCXR_HUMAN	L-xylulose reductase OS=Homo sapien	50.8	14	2
Q9UPG8 PLAL2_HUMAN	Zinc finger protein PLAGL2 OS=Homo	50.6	3	2
Q8TE73 DYH5_HUMAN	Dynein heavy chain 5, axonemal OS=H	50.53	7	2
O00754 MA2B1_HUMAN	Lysosomal alpha-mannosidase OS=Ho	50.45	5	2
O75822 EIF3J_HUMAN	Eukaryotic translation initiation factor 3	50.25	9	2
Q9BYN0 SRXN1_HUMAN	Sulfiredoxin-1 OS=Homo sapiens GN=	49.96	61	2
Q96HF1 SFRP2_HUMAN	Secreted frizzled-related protein 2 OS=	48.73	8	2
O15484 CAN5_HUMAN	Calpain-5 OS=Homo sapiens GN=CAP	48.49	4	2
P49207 RL34_HUMAN	60S ribosomal protein L34 OS=Homo s	48.49	13	2
Q9NYF8 BCLF1_HUMAN	Bcl-2-associated transcription factor 1 C	48.31	5	2
P38117 ETFB_HUMAN	Electron transfer flavoprotein subunit be	47.14	20	2
Q8WVB6 CTF18_HUMAN	Chromosome transmission fidelity prote	46.84	8	2
P61916 NPC2_HUMAN	Epididymal secretory protein E1 OS=Hc	46.16	28	2
Q8IUR0 TPPC5_HUMAN	Trafficking protein particle complex sub	44.87	27	2
Q86UW8 HPLN4_HUMAN	Hyaluronan and proteoglycan link prote	42.29	10	2
P09038 FGF2_HUMAN	Heparin-binding growth factor 2 OS=Ho	41.24	15	2
Q9Y5Z4 HEBP2_HUMAN	Heme-binding protein 2 OS=Homo sapi	40.86	16	2
P06703 S10A6_HUMAN	Protein S100-A6 OS=Homo sapiens GN	40.68	17	2
Q9NRC6 SPTN5_HUMAN	Spectrin beta chain, brain 4 OS=Homo	39.95	8	2
Q6IQ55 TTBK2_HUMAN	Tau-tubulin kinase 2 OS=Homo sapiens	39.21	7	2
P49454 CENPF_HUMAN	Centromere protein F OS=Homo sapien	39.1	4	2
Q8IVF4 DYH10_HUMAN	Dynein heavy chain 10, axonemal OS=	38.62	6	2
Q5JWR5 DOP1_HUMAN	Protein dopey-1 OS=Homo sapiens GN	38.37	7	2
Q8NE71 ABCF1_HUMAN	ATP-binding cassette sub-family F mem	38.26	6	2
Q14669 TRIPC_HUMAN	Probable E3 ubiquitin-protein ligase TR	38.23	8	2
Q9BXM0 PRAX_HUMAN	Periaxin OS=Homo sapiens GN=PRX F	38.04	9	2
Q7Z5P9 MUC19_HUMAN	Mucin-19 OS=Homo sapiens GN=MUC	37.93	6	2
Q9HB07 MYG1_HUMAN	UPF0160 protein MYG1, mitochondrial	37.63	10	2
Q9Y4W2 LAS1L_HUMAN	Protein LAS1 homolog OS=Homo sapie	36.25	9	2
P20929 NEBU_HUMAN	Nebulin OS=Homo sapiens GN=NEB P	36.01	5	2
Q86TB3 ALPK2_HUMAN	Alpha-protein kinase 2 OS=Homo sapie	35.61	6	2
O75179 ANR17_HUMAN	Ankyrin repeat domain-containing prote	35.5	4	2
Q4G0P3 HYDIN_HUMAN	Hydrocephalus-inducing protein homold	34.73	3	2
Q8N6I1 EID2_HUMAN	EP300-interacting inhibitor of differentia	33.82	14	2

O14815 CAN9_HUMAN	Calpain-9 OS=Homo sapiens GN=CAP	33.32	7	2
Q07157 ZO1_HUMAN	Tight junction protein ZO-1 OS=Homo s	33.22	8	2
P08123 CO1A2_HUMAN	Collagen alpha-2(I) chain OS=Homo sa	33.2	26	2
Q5K651 SAMD9_HUMAN	Sterile alpha motif domain-containing p	31.36	3	2
Q17RW2 COOA1_HUMAN	Collagen alpha-1(XXIV) chain OS=Hom	30.94	9	2
O75145 LIPA3_HUMAN	Liprin-alpha-3 OS=Homo sapiens GN=f	30.5	4	2
Q07954 LRP1_HUMAN	Prolow-density lipoprotein receptor-rela	29.94	6	2
Q96FE5 LIGO1_HUMAN	Leucine-rich repeat and immunoglobulin	29.17	12	2
Q9H6A0 DEN2D_HUMAN	DENN domain-containing protein 2D OS	28.18	14	2
Q8IXJ9 ASXL1_HUMAN	Putative Polycomb group protein ASXL	27.93	8	2
Q70EL4 UBP43_HUMAN	Ubiquitin carboxyl-terminal hydrolase 43	27.56	7	2
P49761 CLK3_HUMAN	Dual specificity protein kinase CLK3 OS	27.5	5	2

**Table A1.11 BJ-1D hiPSC CMTX Protein Identifications.** List of all proteins identified in CMTX from BJ-1D hiPSCs with corresponding accession, description, PEAKS score, unique peptide numbers, and coverage (in %).



Accession	Description	Score	Coverage (%)	#Unique
Q13813 SPTA2_HUMAN	Spectrin alpha chain, brain OS=Homo sap	415.57	69	88
P18206 VINC_HUMAN	Vinculin OS=Homo sapiens GN=VCL PE=	406.76	75	88
P21333 FLNA_HUMAN	Filamin-A OS=Homo sapiens GN=FLNA P	420.58	60	83
P49327 FAS_HUMAN	Fatty acid synthase OS=Homo sapiens GN	404.62	54	77
P04406 G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogena	393.33	80	59
P08670 VIME_HUMAN	Vimentin OS=Homo sapiens GN=VIM PE=	376.46	88	57
P13639 EF2_HUMAN	Elongation factor 2 OS=Homo sapiens GN	376.7	74	56
P14618 KPYM_HUMAN	Pyruvate kinase isozymes M1/M2 OS=Hor	388.34	84	55
P06733 ENOA_HUMAN	Alpha-enolase OS=Homo sapiens GN=EN	378.09	91	53
P55072 TERA_HUMAN	Transitional endoplasmic reticulum ATPas	320.9	66	48
Q01082 SPTB2_HUMAN	Spectrin beta chain, brain 1 OS=Homo sap	340.04	53	47
P29401 TKT_HUMAN	Transketolase OS=Homo sapiens GN=TK	341.77	71	46
P35579 MYH9_HUMAN	Myosin-9 OS=Homo sapiens GN=MYH9 P	359.17	55	43
P68104 EF1A1_HUMAN	Elongation factor 1-alpha 1 OS=Homo sap	382.81	83	41
P04075 ALDOA_HUMAN	Fructose-bisphosphate aldolase A OS=Ho	363.24	90	40
P07737 PROF1_HUMAN	Profilin-1 OS=Homo sapiens GN=PFN1 PE	331.51	97	40
P18669 PGAM1_HUMAN	Phosphoglycerate mutase 1 OS=Homo sa	327.03	87	36
P35580 MYH10_HUMAN	Myosin-10 OS=Homo sapiens GN=MYH10	346.9	57	35
P78371 TCPB_HUMAN	T-complex protein 1 subunit beta OS=Hom	336.45	73	34
P46940 IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP	291.2	45	34
P60174 TPIS_HUMAN	Triosephosphate isomerase OS=Homo sa	321.71	95	33
P62805 H4_HUMAN	Histone H4 OS=Homo sapiens GN=HIST1	297.26	62	33
P50454 SERPH_HUMAN	Serpin H1 OS=Homo sapiens GN=SERPIN	335.1	84	32
Q01995 TAGL_HUMAN	Transgelin OS=Homo sapiens GN=TAGLN	303.06	85	32
Q14152 EIF3A_HUMAN	Eukaryotic translation initiation factor 3 sub	272.93	40	32
P30101 PDIA3_HUMAN	Protein disulfide-isomerase A3 OS=Homo	266.77	59	32
P12814 ACTN1_HUMAN	Alpha-actinin-1 OS=Homo sapiens GN=AC	366.51	67	31
P22626 ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins	315.99	68	31
P00558 PGK1_HUMAN	Phosphoglycerate kinase 1 OS=Homo sap	304.57	86	31
P61978 HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein	290.36	61	31
O75874 IDHC_HUMAN	Isocitrate dehydrogenase [NADP] cytoplas	327.63	82	30
P07355 ANXA2_HUMAN	Annexin A2 OS=Homo sapiens GN=ANXA	315.97	72	30
P53396 ACLY_HUMAN	ATP-citrate synthase OS=Homo sapiens G	293.91	42	30
P12956 XRCC6_HUMAN	X-ray repair cross-complementing protein 6	290.56	63	30
P07814 SYEP_HUMAN	Bifunctional aminoacyl-tRNA synthetase O	283.37	42	30
P50395 GDIB_HUMAN	Rab GDP dissociation inhibitor beta OS=H	323.5	73	29
Q06830 PRDX1_HUMAN	Peroxiredoxin-1 OS=Homo sapiens GN=P	312.03	81	29
P05455 LA_HUMAN	Lupus La protein OS=Homo sapiens GN=	308.2	74	29
P48643 TCPE_HUMAN	T-complex protein 1 subunit epsilon OS=H	283.95	73	29
P62937 PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A OS=H	279.13	81	28
Q00610 CLH1_HUMAN	Clathrin heavy chain 1 OS=Homo sapiens	346.23	61	27
P13010 XRCC5_HUMAN	X-ray repair cross-complementing protein 5	301.23	64	27
P30041 PRDX6_HUMAN	Peroxiredoxin-6 OS=Homo sapiens GN=P	297.01	85	27
P26038 MOES_HUMAN	Moesin OS=Homo sapiens GN=MSN PE=	289.19	70	27
P50990 TCPQ_HUMAN	T-complex protein 1 subunit theta OS=Hor	261.43	57	27
P14625 ENPL_HUMAN	Endoplasmin OS=Homo sapiens GN=HSP	257.85	45	27
P08238 HS90B_HUMAN	Heat shock protein HSP 90-beta OS=Hom	381.28	73	26

P23528 COF1_HUMAN	Cofilin-1 OS=Homo sapiens GN=CFL1 PE	351.29	93	26
P62328 TYB4_HUMAN	Thymosin beta-4 OS=Homo sapiens GN=	311.08	93	26
O75369 FLNB_HUMAN	Filamin-B OS=Homo sapiens GN=FLNB P	275.65	31	26
P34932 HSP74_HUMAN	Heat shock 70 kDa protein 4 OS=Homo sa	270.13	55	26
P52272 HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein	265.99	81	26
Q86UP2 KTN1_HUMAN	Kinectin OS=Homo sapiens GN=KTN1 PE	259.22	43	26
O43707 ACTN4_HUMAN	Alpha-actinin-4 OS=Homo sapiens GN=AC	340.07	62	25
P40926 MDHM_HUMAN	Malate dehydrogenase, mitochondrial OS=	321.36	87	25
Q99832 TCPH_HUMAN	T-complex protein 1 subunit eta OS=Homc	297.49	76	25
P23246 SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich	281.88	51	25
P49368 TCPG_HUMAN	T-complex protein 1 subunit gamma OS=H	262.99	61	25
P62258 1433E_HUMAN	14-3-3 protein epsilon OS=Homo sapiens	316.26	73	24
P62158 CALM_HUMAN	Calmodulin OS=Homo sapiens GN=CALM	288.06	73	24
P00338 LDHA_HUMAN	L-lactate dehydrogenase A chain OS=Hom	272.17	80	24
O00231 PSD11_HUMAN	26S proteasome non-ATPase regulatory s	270.46	60	24
P61604 CH10_HUMAN	10 kDa heat shock protein, mitochondrial C	264.25	97	24
P11586 C1TC_HUMAN	C-1-tetrahydrofolate synthase, cytoplasmic	261.8	48	24
P11142 HSP7C_HUMAN	Heat shock cognate 71 kDa protein OS=H	343.82	71	23
P09211 GSTP1_HUMAN	Glutathione S-transferase P OS=Homo sa	311.37	67	23
P63104 1433Z_HUMAN	14-3-3 protein zeta/delta OS=Homo sapier	309.6	75	23
Q14315 FLNC_HUMAN	Filamin-C OS=Homo sapiens GN=FLNC P	269.23	28	23
P11021 GRP78_HUMAN	78 kDa glucose-regulated protein OS=Hon	268.24	55	23
Q9P2E9 RRBP1_HUMAN	Ribosome-binding protein 1 OS=Homo sap	264.54	35	23
P49321 NASP_HUMAN	Nuclear autoantigenic sperm protein OS=H	264.04	52	23
P08758 ANXA5_HUMAN	Annexin A5 OS=Homo sapiens GN=ANXA	263.47	61	23
P10809 CH60_HUMAN	60 kDa heat shock protein, mitochondrial C	254.47	72	23
Q9P2J5 SYLC_HUMAN	Leucyl-tRNA synthetase, cytoplasmic OS=	249.98	34	23
P27816 MAP4_HUMAN	Microtubule-associated protein 4 OS=Hom	246.38	48	23
P06748 NPM_HUMAN	Nucleophosmin OS=Homo sapiens GN=N	297.11	57	22
P04083 ANXA1_HUMAN	Annexin A1 OS=Homo sapiens GN=ANXA	293.21	82	22
O60664 PLIN3_HUMAN	Perilipin-3 OS=Homo sapiens GN=PLIN3 f	286.02	68	22
P07195 LDHB_HUMAN	L-lactate dehydrogenase B chain OS=Hon	280.74	70	22
P19338 NUCL_HUMAN	Nucleolin OS=Homo sapiens GN=NCL PE	279.66	70	22
P37802 TAGL2_HUMAN	Transgelin-2 OS=Homo sapiens GN=TAG	265.75	90	22
P23396 RS3_HUMAN	40S ribosomal protein S3 OS=Homo sapie	264.34	79	22
P25398 RS12_HUMAN	40S ribosomal protein S12 OS=Homo sapi	255.07	87	22
P61247 RS3A_HUMAN	40S ribosomal protein S3a OS=Homo sapi	237.12	67	22
Q00839 HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein	235.34	38	22
P67936 TPM4_HUMAN	Tropomyosin alpha-4 chain OS=Homo sap	337.21	92	21
Q01469 FABP5_HUMAN	Fatty acid-binding protein, epidermal OS=H	310.82	91	21
P52209 6PGD_HUMAN	6-phosphogluconate dehydrogenase, decd	302.27	67	21
P22314 UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1	287.66	52	21
P15311 EZRI_HUMAN	Ezrin OS=Homo sapiens GN=EZR PE=1 S	275.31	62	21
P08133 ANXA6_HUMAN	Annexin A6 OS=Homo sapiens GN=ANXA	263.46	54	21
P06744 G6PI_HUMAN	Glucose-6-phosphate isomerase OS=Hom	260.96	53	21
Q9UQE7 SMC3_HUMAN	Structural maintenance of chromosomes p	246.91	43	21
Q9Y617 SERC_HUMAN	Phosphoserine aminotransferase OS=Hon	235	63	21

Q13263 TIF1B_HUMAN	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TIF1B PE=1	229.1	41	21
P07900 HS90A_HUMAN	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90A PE=1	354.61	61	20
P25205 MCM3_HUMAN	DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1	241	43	20
P22102 PUR2_HUMAN	Trifunctional purine biosynthetic protein ad OS=Homo sapiens GN=PUR2 PE=1	236.14	44	20
P43243 MATR3_HUMAN	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1	234.49	38	20
P27348 1433T_HUMAN	14-3-3 protein theta OS=Homo sapiens GN=1433T PE=1	294.62	80	19
P09936 UCHL1_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme 1 OS=Homo sapiens GN=UCHL1 PE=1	288.93	72	19
P62826 RAN_HUMAN	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1	265.32	67	19
P62333 PRS10_HUMAN	26S protease regulatory subunit 10B OS=Homo sapiens GN=PRS10 PE=1	253.46	62	19
Q05682 CALD1_HUMAN	Caldesmon OS=Homo sapiens GN=CALD1 PE=1	247.38	42	19
P31948 STIP1_HUMAN	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1	245.14	54	19
Q14566 MCM6_HUMAN	DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1	232.1	40	19
P07237 PDIA1_HUMAN	Protein disulfide-isomerase OS=Homo sapiens GN=PDIA1 PE=1	223.79	52	19
P36578 RL4_HUMAN	60S ribosomal protein L4 OS=Homo sapiens GN=RL4 PE=1	196.33	53	19
O43175 SERA_HUMAN	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=SERA PE=1	270.54	53	18
P40227 TCPZ_HUMAN	T-complex protein 1 subunit zeta OS=Homo sapiens GN=TCPZ PE=1	265.84	67	18
P33993 MCM7_HUMAN	DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1	260.76	58	18
P28074 PSB5_HUMAN	Proteasome subunit beta type-5 OS=Homo sapiens GN=PSB5 PE=1	245.18	59	18
Q15691 MARE1_HUMAN	Microtubule-associated protein RP/EB family class 1A OS=Homo sapiens GN=MARE1 PE=1	238.96	62	18
P62081 RS7_HUMAN	40S ribosomal protein S7 OS=Homo sapiens GN=RS7 PE=1	197.73	68	18
P12270 TPR_HUMAN	Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1	196.85	25	18
P07910 HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C OS=Homo sapiens GN=HNRPC PE=1	261.66	66	17
P05387 RLA2_HUMAN	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RLA2 PE=1	260.83	84	17
P61981 1433G_HUMAN	14-3-3 protein gamma OS=Homo sapiens GN=1433G PE=1	253.74	81	17
P32119 PRDX2_HUMAN	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1	249.71	42	17
Q99623 PHB2_HUMAN	Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1	241.91	71	17
Q16851 UGPA_HUMAN	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGPA PE=1	240.68	59	17
P17174 AATC_HUMAN	Aspartate aminotransferase, cytoplasmic class 2 OS=Homo sapiens GN=AATC PE=1	239.08	62	17
P31939 PUR9_HUMAN	Bifunctional purine biosynthesis protein PUR9 OS=Homo sapiens GN=PUR9 PE=1	235.43	46	17
P63244 GBLP_HUMAN	Guanine nucleotide-binding protein subunit gamma-1 OS=Homo sapiens GN=GBLP PE=1	234.94	62	17
P39019 RS19_HUMAN	40S ribosomal protein S19 OS=Homo sapiens GN=RS19 PE=1	227.91	77	17
P62277 RS13_HUMAN	40S ribosomal protein S13 OS=Homo sapiens GN=RS13 PE=1	216.5	60	17
Q9Y4L1 HYOU1_HUMAN	Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1	215.56	43	17
P48681 NEST_HUMAN	Nestin OS=Homo sapiens GN=NES PE=1	208.5	26	17
O00232 PSD12_HUMAN	26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSD12 PE=1	197.18	41	17
O75347 TBCA_HUMAN	Tubulin-specific chaperone A OS=Homo sapiens GN=TBCA PE=1	252.01	79	16
P09874 PARP1_HUMAN	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1	250.38	39	16
Q9HB71 CYBP_HUMAN	Calcyclin-binding protein OS=Homo sapiens GN=CYPB PE=1	245.55	75	16
Q9BWD1 THIC_HUMAN	Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=THIC PE=1	237.68	63	16
Q15008 PSMD6_HUMAN	26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1	232.3	62	16
Q96KP4 CNDP2_HUMAN	Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1	224.69	47	16
P05556 ITB1_HUMAN	Integrin beta-1 OS=Homo sapiens GN=ITCB PE=1	223.84	34	16
Q08211 DHX9_HUMAN	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1	213.57	33	16
P54136 SYRC_HUMAN	Arginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=SYRC PE=1	182	37	16
P02794 FRIH_HUMAN	Ferritin heavy chain OS=Homo sapiens GN=FRIH PE=1	181.41	64	16
P62701 RS4X_HUMAN	40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RS4X PE=1	178.24	63	16
P35221 CTNA1_HUMAN	Catenin alpha-1 OS=Homo sapiens GN=CTNA1 PE=1	271.34	55	15

P26599 PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 OS=	259.33	46	15
P62195 PRS8_HUMAN	26S protease regulatory subunit 8 OS=Ho	257.2	70	15
P02792 FRIL_HUMAN	Ferritin light chain OS=Homo sapiens GN=	256.12	69	15
P09972 ALDOC_HUMAN	Fructose-bisphosphate aldolase C OS=Ho	253.88	72	15
Q15084 PDIA6_HUMAN	Protein disulfide-isomerase A6 OS=Homo	244.61	60	15
Q16658 FSCN1_HUMAN	Fascin OS=Homo sapiens GN=FSCN1 PE	238.45	51	15
P31949 S10AB_HUMAN	Protein S100-A11 OS=Homo sapiens GN=	232.54	89	15
P25705 ATPA_HUMAN	ATP synthase subunit alpha, mitochondria	227.18	46	15
Q92499 DDX1_HUMAN	ATP-dependent RNA helicase DDX1 OS=	225.41	50	15
P29692 EF1D_HUMAN	Elongation factor 1-delta OS=Homo sapier	224.66	70	15
P30044 PRDX5_HUMAN	Peroxiredoxin-5, mitochondrial OS=Homo	222.4	72	15
Q9BXP5 SRRT_HUMAN	Serrate RNA effector molecule homolog O	220.57	40	15
P08865 RSSA_HUMAN	40S ribosomal protein SA OS=Homo sapie	220.51	64	15
P17980 PRS6A_HUMAN	26S protease regulatory subunit 6A OS=H	218.83	59	15
P62316 SMD2_HUMAN	Small nuclear ribonucleoprotein Sm D2 OS	215.67	87	15
Q01581 HMCS1_HUMAN	Hydroxymethylglutaryl-CoA synthase, cyto	215.52	46	15
O43242 PSMD3_HUMAN	26S proteasome non-ATPase regulatory s	214.44	43	15
Q8NC51 PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-bind	206.55	56	15
P33991 MCM4_HUMAN	DNA replication licensing factor MCM4 OS	206.07	39	15
P10599 THIO_HUMAN	Thioredoxin OS=Homo sapiens GN=TXN F	201.64	78	15
P02649 APOE_HUMAN	Apolipoprotein E OS=Homo sapiens GN=A	192.7	65	15
P10909 CLUS_HUMAN	Clusterin OS=Homo sapiens GN=CLU PE-	190.18	30	15
Q12906 ILF3_HUMAN	Interleukin enhancer-binding factor 3 OS=	182.82	23	15
P07437 TBB5_HUMAN	Tubulin beta chain OS=Homo sapiens GN-	436.88	80	14
P12268 IMDH2_HUMAN	Inosine-5'-monophosphate dehydrogenase	255.92	46	14
P63220 RS21_HUMAN	40S ribosomal protein S21 OS=Homo sapi	250.13	84	14
Q9NZI8 IF2B1_HUMAN	Insulin-like growth factor 2 mRNA-binding	249.44	38	14
P13796 PLSL_HUMAN	Plastin-2 OS=Homo sapiens GN=LCP1 PE	239.04	50	14
Q99497 PARK7_HUMAN	Protein DJ-1 OS=Homo sapiens GN=PAR	233.87	65	14
P27695 APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase O	232.53	49	14
P22234 PUR6_HUMAN	Multifunctional protein ADE2 OS=Homo sa	226.99	58	14
P43686 PRS6B_HUMAN	26S protease regulatory subunit 6B OS=H	226.07	53	14
P62424 RL7A_HUMAN	60S ribosomal protein L7a OS=Homo sapi	223.33	47	14
Q9H9Z2 LN28A_HUMAN	Protein lin-28 homolog A OS=Homo sapier	219.49	56	14
P37837 TALDO_HUMAN	Transaldolase OS=Homo sapiens GN=TAL	205.72	54	14
P47897 SYQ_HUMAN	Glutamyl-tRNA synthetase OS=Homo sa	204.3	38	14
P78417 GSTO1_HUMAN	Glutathione S-transferase omega-1 OS=H	200.85	49	14
P11717 MPRI_HUMAN	Cation-independent mannose-6-phosphate	198.8	14	14
P41250 SYG_HUMAN	Glycyl-tRNA synthetase OS=Homo sapien	196.4	37	14
Q02878 RL6_HUMAN	60S ribosomal protein L6 OS=Homo sapie	189.81	50	14
P62269 RS18_HUMAN	40S ribosomal protein S18 OS=Homo sapi	182.87	73	14
P18124 RL7_HUMAN	60S ribosomal protein L7 OS=Homo sapie	172.62	58	14
P60842 IF4A1_HUMAN	Eukaryotic initiation factor 4A-I OS=Homo	272.09	70	13
Q04917 1433F_HUMAN	14-3-3 protein eta OS=Homo sapiens GN=	272.01	78	13
P30086 PEBP1_HUMAN	Phosphatidylethanolamine-binding protein	237.8	79	13
Q9Y265 RUVB1_HUMAN	RuvB-like 1 OS=Homo sapiens GN=RUVB	236.18	66	13
P18084 ITB5_HUMAN	Integrin beta-5 OS=Homo sapiens GN=ITC	235.94	44	13

P23526 SAHH_HUMAN	Adenosylhomocysteinase OS=Homo sapie	234.94	57	13
Q9UNM6 PSD13_HUMAN	26S proteasome non-ATPase regulatory s	234.76	63	13
P25789 PSA4_HUMAN	Proteasome subunit alpha type-4 OS=Hon	229.68	68	13
P16152 CBR1_HUMAN	Carbonyl reductase [NADPH] 1 OS=Homo	226.77	69	13
Q14103 HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein	225.83	52	13
P50991 TCPD_HUMAN	T-complex protein 1 subunit delta OS=Hor	225.14	44	13
P07108 ACBP_HUMAN	Acyl-CoA-binding protein OS=Homo sapie	219.18	90	13
P17987 TCPA_HUMAN	T-complex protein 1 subunit alpha OS=Ho	213.66	48	13
P16401 H15_HUMAN	Histone H1.5 OS=Homo sapiens GN=HIS	211.69	52	13
P43487 RANG_HUMAN	Ran-specific GTPase-activating protein OS	205.19	75	13
Q92626 PXDN_HUMAN	Peroxidasin homolog OS=Homo sapiens G	198.67	21	13
P14174 MIF_HUMAN	Macrophage migration inhibitory factor OS	195.3	79	13
Q9BQG0 MBB1A_HUMAN	Myb-binding protein 1A OS=Homo sapiens	182.01	25	13
P09493 TPM1_HUMAN	Tropomyosin alpha-1 chain OS=Homo sap	324.63	87	12
P09651 ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein	308.23	68	12
O14818 PSA7_HUMAN	Proteasome subunit alpha type-7 OS=Hon	266.6	79	12
P22392 NDKB_HUMAN	Nucleoside diphosphate kinase B OS=Hor	255.67	93	12
P80723 BASP1_HUMAN	Brain acid soluble protein 1 OS=Homo sap	243.12	71	12
Q99536 VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1	237.69	51	12
P35998 PRS7_HUMAN	26S protease regulatory subunit 7 OS=Hor	223.13	43	12
P60900 PSA6_HUMAN	Proteasome subunit alpha type-6 OS=Hon	216.15	49	12
P49756 RBM25_HUMAN	RNA-binding protein 25 OS=Homo sapiens	214.61	31	12
P00491 PNPH_HUMAN	Purine nucleoside phosphorylase OS=Hon	207.86	60	12
P46777 RL5_HUMAN	60S ribosomal protein L5 OS=Homo sapie	206.63	56	12
P62888 RL30_HUMAN	60S ribosomal protein L30 OS=Homo sapi	201.88	86	12
O00299 CLIC1_HUMAN	Chloride intracellular channel protein 1 OS	201.7	56	12
P62263 RS14_HUMAN	40S ribosomal protein S14 OS=Homo sapi	201.49	42	12
Q00341 VIGLN_HUMAN	Vigilin OS=Homo sapiens GN=HDLBP PE	201.21	37	12
Q8N163 K1967_HUMAN	Protein KIAA1967 OS=Homo sapiens GN=	199.82	28	12
P49773 HINT1_HUMAN	Histidine triad nucleotide-binding protein 1	198.96	87	12
P53621 COPA_HUMAN	Coatomer subunit alpha OS=Homo sapien	197.87	23	12
Q01518 CAP1_HUMAN	Adenylyl cyclase-associated protein 1 OS=	193.62	42	12
Q15233 NONO_HUMAN	Non-POU domain-containing octamer-bind	192.37	35	12
Q9Y224 CN166_HUMAN	UPF0568 protein C14orf166 OS=Homo sa	191.72	52	12
P00505 AATM_HUMAN	Aspartate aminotransferase, mitochondrial	189.9	44	12
P26641 EF1G_HUMAN	Elongation factor 1-gamma OS=Homo sap	186.2	23	12
P23142 FBLN1_HUMAN	Fibulin-1 OS=Homo sapiens GN=FBLN1 F	164.33	26	12
P46781 RS9_HUMAN	40S ribosomal protein S9 OS=Homo sapie	156.63	41	12
P54577 SYYC_HUMAN	Tyrosyl-tRNA synthetase, cytoplasmic OS=	156.42	41	12
P00441 SODC_HUMAN	Superoxide dismutase [Cu-Zn] OS=Homo	248.33	75	11
Q01105 SET_HUMAN	Protein SET OS=Homo sapiens GN=SET	245.06	41	11
Q9UHB9 SRP68_HUMAN	Signal recognition particle 68 kDa protein C	241.29	45	11
P20618 PSB1_HUMAN	Proteasome subunit beta type-1 OS=Homo	227.06	60	11
P53999 TCP4_HUMAN	Activated RNA polymerase II transcriptiona	226.58	76	11
Q9UBC3 DNM3B_HUMAN	DNA (cytosine-5)-methyltransferase 3B OS	225.72	35	11
O75531 BAF_HUMAN	Barrier-to-autointegration factor OS=Homo	224.18	78	11
P16949 STMN1_HUMAN	Stathmin OS=Homo sapiens GN=STMN1	221.6	56	11

O60506 HNRPQ_HUMAN	Heterogeneous nuclear ribonucleoprotein	221.25	53	11
P63313 TYB10_HUMAN	Thymosin beta-10 OS=Homo sapiens GN=	220.92	84	11
Q14697 GANAB_HUMAN	Neutral alpha-glucosidase AB OS=Homo s	220.41	30	11
Q16555 DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 OS=	208.62	48	11
P14868 SYDC_HUMAN	Aspartyl-tRNA synthetase, cytoplasmic OS	208.43	39	11
P14866 HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein	198.09	40	11
P17096 HMGA1_HUMAN	High mobility group protein HMG-I/HMG-Y	196.9	82	11
P08708 RS17_HUMAN	40S ribosomal protein S17 OS=Homo sapi	195.24	73	11
P38646 GRP75_HUMAN	Stress-70 protein, mitochondrial OS=Homo	193.13	37	11
P41091 IF2G_HUMAN	Eukaryotic translation initiation factor 2 sub	191.66	50	11
P23284 PIIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B OS=H	189.48	45	11
P60866 RS20_HUMAN	40S ribosomal protein S20 OS=Homo sapi	188.77	50	11
Q7KZF4 SND1_HUMAN	Staphylococcal nuclease domain-containin	187.48	28	11
Q02790 FKBP4_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP4	186.94	35	11
P46783 RS10_HUMAN	40S ribosomal protein S10 OS=Homo sapi	186.53	58	11
P13693 TCTP_HUMAN	Translationally-controlled tumor protein OS	182.69	74	11
P62829 RL23_HUMAN	60S ribosomal protein L23 OS=Homo sapi	182.08	60	11
Q14019 COTL1_HUMAN	Coactosin-like protein OS=Homo sapiens	178.96	65	11
P62280 RS11_HUMAN	40S ribosomal protein S11 OS=Homo sapi	171.23	73	11
A0MZ66 SHOT1_HUMAN	Shootin-1 OS=Homo sapiens GN=KIAA15	168.93	37	11
P02545 LMNA_HUMAN	Prelamin-A/C OS=Homo sapiens GN=LMN	154.33	22	11
P13797 PLST_HUMAN	Plastin-3 OS=Homo sapiens GN=PLS3 PE	241.79	51	10
A6NL28 TPM3L_HUMAN	Putative tropomyosin alpha-3 chain-like pro	237.92	47	10
P61158 ARP3_HUMAN	Actin-related protein 3 OS=Homo sapiens	213.13	49	10
P42166 LAP2A_HUMAN	Lamina-associated polypeptide 2, isoform	211.37	35	10
Q04760 LGUL_HUMAN	Lactoylglutathione lyase OS=Homo sapien	209.72	63	10
P19367 HXK1_HUMAN	Hexokinase-1 OS=Homo sapiens GN=HK	208.28	28	10
Q9Y262 EIF3L_HUMAN	Eukaryotic translation initiation factor 3 sub	206.56	35	10
O00429 DNM1L_HUMAN	Dynamin-1-like protein OS=Homo sapiens	206.48	49	10
P60981 DEST_HUMAN	Dextrin OS=Homo sapiens GN=DSTN PE=	205.47	47	10
Q9NR30 DDX21_HUMAN	Nucleolar RNA helicase 2 OS=Homo sapie	204.61	33	10
P51991 ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein	203.9	43	10
O95336 6PGL_HUMAN	6-phosphogluconolactonase OS=Homo sa	202.04	59	10
P04792 HSPB1_HUMAN	Heat shock protein beta-1 OS=Homo sapie	199.56	66	10
Q9UHV9 PFD2_HUMAN	Prefoldin subunit 2 OS=Homo sapiens GN	196.4	82	10
P07093 GDN_HUMAN	Glia-derived nexin OS=Homo sapiens GN=	195.88	49	10
P56192 SYMC_HUMAN	Methionyl-tRNA synthetase, cytoplasmic O	195.28	26	10
Q15843 NEDD8_HUMAN	NEDD8 OS=Homo sapiens GN=NEDD8 P	192.98	59	10
P35613 BASI_HUMAN	Basigin OS=Homo sapiens GN=BSG PE=	191.53	32	10
Q9BXJ9 NAA15_HUMAN	N-alpha-acetyltransferase 15, NatA auxilia	188.31	32	10
P12429 ANXA3_HUMAN	Annexin A3 OS=Homo sapiens GN=ANXA	187.54	46	10
Q08J23 NSUN2_HUMAN	tRNA (cytosine(34)-C(5))-methyltransferas	184.54	34	10
Q8NBS9 TXND5_HUMAN	Thioredoxin domain-containing protein 5 C	180.98	36	10
P31942 HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein	179.33	39	10
P54819 KAD2_HUMAN	Adenylate kinase 2, mitochondrial OS=Hor	177.28	66	10
Q9BT78 CSN4_HUMAN	COP9 signalosome complex subunit 4 OS=	174.7	46	10
O60701 UGDH_HUMAN	UDP-glucose 6-dehydrogenase OS=Homo	173.53	29	10

Q7Z478 DHX29_HUMAN	ATP-dependent RNA helicase DHX29 OS=Homo sapiens GN=DHX29 PE=	168.63	23	10
Q9Y624 JAM1_HUMAN	Junctional adhesion molecule A OS=Homo sapiens GN=JAM1 PE=	160.72	31	10
P07339 CATD_HUMAN	Cathepsin D OS=Homo sapiens GN=CATD PE=	160.67	35	10
P27635 RL10_HUMAN	60S ribosomal protein L10 OS=Homo sapiens GN=RL10 PE=	159.37	35	10
O14776 TCRG1_HUMAN	Transcription elongation regulator 1 OS=Homo sapiens GN=TCRG1 PE=	158.41	21	10
P49591 SYSC_HUMAN	Seryl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=SYSC PE=	148.36	36	10
P06753 TPM3_HUMAN	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=	328.7	86	9
P31946 1433B_HUMAN	14-3-3 protein beta/alpha OS=Homo sapiens GN=1433B PE=	231.54	59	9
P35241 RADI_HUMAN	Radixin OS=Homo sapiens GN=RDX PE=	226.95	57	9
Q06323 PSME1_HUMAN	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=	224.08	59	9
P12277 KCRB_HUMAN	Creatine kinase B-type OS=Homo sapiens GN=KCRB PE=	215.57	64	9
P60660 MYL6_HUMAN	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=	213.37	76	9
Q99729 ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A OS=Homo sapiens GN=ROAA PE=	203.41	42	9
Q15365 PCBP1_HUMAN	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=	201.77	59	9
Q9Y310 RTCB_HUMAN	tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=	198.78	42	9
P30084 ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHM PE=	197.31	47	9
O76003 GLRX3_HUMAN	Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=	193.53	54	9
P14550 AK1A1_HUMAN	Alcohol dehydrogenase [NADP+] OS=Homo sapiens GN=AK1A1 PE=	189.89	51	9
Q07955 SRSF1_HUMAN	Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=	188.29	62	9
P61289 PSME3_HUMAN	Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=	187.73	48	9
Q9UL46 PSME2_HUMAN	Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=	187.62	53	9
Q13618 CUL3_HUMAN	Cullin-3 OS=Homo sapiens GN=CUL3 PE=	186.78	47	9
Q14195 DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYL3 PE=	183	30	9
Q15417 CNN3_HUMAN	Calponin-3 OS=Homo sapiens GN=CNN3 PE=	182.31	31	9
P30040 ERP29_HUMAN	Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=	182.2	42	9
O14737 PDCD5_HUMAN	Programmed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=	181.55	56	9
P15880 RS2_HUMAN	40S ribosomal protein S2 OS=Homo sapiens GN=RS2 PE=	178.29	36	9
P29966 MARCS_HUMAN	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCS PE=	175.91	34	9
Q9Y230 RUVB2_HUMAN	RuvB-like 2 OS=Homo sapiens GN=RUVB2 PE=	175.67	39	9
Q9BZZ5 API5_HUMAN	Apoptosis inhibitor 5 OS=Homo sapiens GN=API5 PE=	175.1	36	9
P34897 GLYM_HUMAN	Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=GLYM PE=	172.74	26	9
P62249 RS16_HUMAN	40S ribosomal protein S16 OS=Homo sapiens GN=RS16 PE=	172.1	45	9
Q9NTJ3 SMC4_HUMAN	Structural maintenance of chromosomes protein 4 OS=Homo sapiens GN=SMC4 PE=	171.69	19	9
P25786 PSA1_HUMAN	Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSA1 PE=	169.93	46	9
O76094 SRP72_HUMAN	Signal recognition particle 72 kDa protein OS=Homo sapiens GN=SRP72 PE=	168.49	35	9
O60502 NCOAT_HUMAN	Bifunctional protein NCOAT OS=Homo sapiens GN=NCOAT PE=	166.84	25	9
Q8N8S7 ENAH_HUMAN	Protein enabled homolog OS=Homo sapiens GN=ENAH PE=	164.96	31	9
Q9Y5X3 SNX5_HUMAN	Sorting nexin-5 OS=Homo sapiens GN=SNX5 PE=	163.57	34	9
P62750 RL23A_HUMAN	60S ribosomal protein L23a OS=Homo sapiens GN=RL23A PE=	156.73	54	9
Q9NY33 DPP3_HUMAN	Dipeptidyl peptidase 3 OS=Homo sapiens GN=DPP3 PE=	154.57	24	9
P49915 GUAA_HUMAN	GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GUAA PE=	151.81	18	9
P61088 UBE2N_HUMAN	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=	149.84	61	9
P50453 SPB9_HUMAN	Serpin B9 OS=Homo sapiens GN=SERPINF1 PE=	139.99	36	9
P78347 GTF2I_HUMAN	General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=	117.84	21	9
P06454 PTMA_HUMAN	Prothymosin alpha OS=Homo sapiens GN=PTMA PE=	202.36	44	8
P09429 HMGB1_HUMAN	High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=	197.6	53	8
P68036 UB2L3_HUMAN	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UB2L3 PE=	195.56	73	8

Q99439 CNN2_HUMAN	Calponin-2 OS=Homo sapiens GN=CNN2	194.23	38	8
P51665 PSD7_HUMAN	26S proteasome non-ATPase regulatory s	190.42	48	8
P62191 PRS4_HUMAN	26S protease regulatory subunit 4 OS=Ho	185.03	43	8
P49736 MCM2_HUMAN	DNA replication licensing factor MCM2 OS	180.21	25	8
P06737 PYGL_HUMAN	Glycogen phosphorylase, liver form OS=H	179.54	27	8
P07741 APT_HUMAN	Adenine phosphoribosyltransferase OS=H	179.19	68	8
P63173 RL38_HUMAN	60S ribosomal protein L38 OS=Homo sapi	178.86	57	8
Q13126 MTAP_HUMAN	S-methyl-5'-thioadenosine phosphorylase	178.21	35	8
P22061 PIMT_HUMAN	Protein-L-isoaspartate(D-aspartate) O-met	178.09	63	8
Q9Y696 CLIC4_HUMAN	Chloride intracellular channel protein 4 OS	177.26	66	8
O00244 ATOX1_HUMAN	Copper transport protein ATOX1 OS=Hom	174.55	76	8
P27797 CALR_HUMAN	Calreticulin OS=Homo sapiens GN=CALR	172.97	46	8
P50552 VASP_HUMAN	Vasodilator-stimulated phosphoprotein OS	172.41	42	8
P62244 RS15A_HUMAN	40S ribosomal protein S15a OS=Homo sa	172.26	72	8
P23381 SYWC_HUMAN	Tryptophanyl-tRNA synthetase, cytoplasmic	172.23	46	8
Q15019 SEPT2_HUMAN	Septin-2 OS=Homo sapiens GN=SEPT2 P	169.9	46	8
P17844 DDX5_HUMAN	Probable ATP-dependent RNA helicase D	168.46	35	8
Q9Y266 NUDC_HUMAN	Nuclear migration protein nudC OS=Homo	167.43	45	8
Q13561 DCTN2_HUMAN	Dynactin subunit 2 OS=Homo sapiens GN	166.59	32	8
Q7L2H7 EIF3M_HUMAN	Eukaryotic translation initiation factor 3 sub	164.07	41	8
P62913 RL11_HUMAN	60S ribosomal protein L11 OS=Homo sapi	163.63	44	8
Q9UKK9 NUDT5_HUMAN	ADP-sugar pyrophosphatase OS=Homo sa	163.22	30	8
P62633 CNBP_HUMAN	Cellular nucleic acid-binding protein OS=H	161.71	31	8
Q9Y6G9 DC1L1_HUMAN	Cytoplasmic dynein 1 light intermediate ch	161.68	36	8
Q9UKM9 RALY_HUMAN	RNA-binding protein Raly OS=Homo sapie	160.61	32	8
P60903 S10AA_HUMAN	Protein S100-A10 OS=Homo sapiens GN=	160.34	58	8
P62241 RS8_HUMAN	40S ribosomal protein S8 OS=Homo sapie	159	51	8
Q9H910 HN1L_HUMAN	Hematological and neurological expressed	158.93	60	8
O15347 HMGB3_HUMAN	High mobility group protein B3 OS=Homo s	158.66	51	8
P48444 COPD_HUMAN	Coatomer subunit delta OS=Homo sapiens	156.83	22	8
P23921 RIR1_HUMAN	Ribonucleoside-diphosphate reductase lar	155.77	27	8
P35268 RL22_HUMAN	60S ribosomal protein L22 OS=Homo sapi	155.7	51	8
Q96AE4 FUBP1_HUMAN	Far upstream element-binding protein 1 OS	155.34	35	8
P18621 RL17_HUMAN	60S ribosomal protein L17 OS=Homo sapi	155.25	44	8
P31153 METK2_HUMAN	S-adenosylmethionine synthase isoform ty	155.08	22	8
P39023 RL3_HUMAN	60S ribosomal protein L3 OS=Homo sapie	155	37	8
Q99471 PFD5_HUMAN	Prefoldin subunit 5 OS=Homo sapiens GN	152.78	68	8
Q99459 CDC5L_HUMAN	Cell division cycle 5-like protein OS=Homo	152.12	30	8
O15372 EIF3H_HUMAN	Eukaryotic translation initiation factor 3 sub	149.94	36	8
P13667 PDIA4_HUMAN	Protein disulfide-isomerase A4 OS=Homo	148.57	22	8
Q9P258 RCC2_HUMAN	Protein RCC2 OS=Homo sapiens GN=RCC	147.38	34	8
P60228 EIF3E_HUMAN	Eukaryotic translation initiation factor 3 sub	147.21	25	8
Q9GZZ1 NAA50_HUMAN	N-alpha-acetyltransferase 50, NatE catalyt	145.55	53	8
P02751 FINC_HUMAN	Fibronectin OS=Homo sapiens GN=FN1 P	139.94	9	8
P62851 RS25_HUMAN	40S ribosomal protein S25 OS=Homo sapi	139.67	50	8
Q14683 SMC1A_HUMAN	Structural maintenance of chromosomes p	137.71	16	8
P14678 RSMB_HUMAN	Small nuclear ribonucleoprotein-associated	137.1	55	8



P78344 IF4G2_HUMAN	Eukaryotic translation initiation factor 4 gar	136.91	19	8
Q09666 AHNK_HUMAN	Neuroblast differentiation-associated prote	136.7	9	8
Q6PKG0 LARP1_HUMAN	La-related protein 1 OS=Homo sapiens GN	136.3	26	8
P53634 CATC_HUMAN	Dipeptidyl peptidase 1 OS=Homo sapiens	136.19	24	8
P56385 ATP5I_HUMAN	ATP synthase subunit e, mitochondrial OS	133.41	71	8
P62899 RL31_HUMAN	60S ribosomal protein L31 OS=Homo sapi	132.46	43	8
O43491 E41L2_HUMAN	Band 4.1-like protein 2 OS=Homo sapiens	130.34	24	8
Q15907 RB11B_HUMAN	Ras-related protein Rab-11B OS=Homo sa	127.85	39	8
P23193 TCEA1_HUMAN	Transcription elongation factor A protein 1	125.98	42	8
P27144 KAD4_HUMAN	Adenylate kinase isoenzyme 4, mitochon	122.02	51	8
Q6FI13 H2A2A_HUMAN	Histone H2A type 2-A OS=Homo sapiens	272.39	84	7
Q16777 H2A2C_HUMAN	Histone H2A type 2-C OS=Homo sapiens	272.39	77	7
P15531 NDKA_HUMAN	Nucleoside diphosphate kinase A OS=Hor	243.59	73	7
O00571 DDX3X_HUMAN	ATP-dependent RNA helicase DDX3X OS	209.3	54	7
P25787 PSA2_HUMAN	Proteasome subunit alpha type-2 OS=Hom	208.64	56	7
P28066 PSA5_HUMAN	Proteasome subunit alpha type-5 OS=Hom	207.79	55	7
P20290 BTF3_HUMAN	Transcription factor BTF3 OS=Homo sapie	190.87	67	7
Q92598 HS105_HUMAN	Heat shock protein 105 kDa OS=Homo sa	187.69	29	7
Q16181 SEPT7_HUMAN	Septin-7 OS=Homo sapiens GN=SEPT7 P	185.01	46	7
P06493 CDK1_HUMAN	Cyclin-dependent kinase 1 OS=Homo sapi	184.69	40	7
P50502 F10A1_HUMAN	Hsc70-interacting protein OS=Homo sapie	181.9	27	7
P26196 DDX6_HUMAN	Probable ATP-dependent RNA helicase D	180.68	37	7
O43809 CPSF5_HUMAN	Cleavage and polyadenylation specificity fa	180.06	60	7
Q15185 TEBP_HUMAN	Prostaglandin E synthase 3 OS=Homo sap	179.35	54	7
P54578 UBP14_HUMAN	Ubiquitin carboxyl-terminal hydrolase 14 O	178.35	40	7
Q13765 NACA_HUMAN	Nascent polypeptide-associated complex s	177.65	30	7
P32969 RL9_HUMAN	60S ribosomal protein L9 OS=Homo sapie	175.75	52	7
Q92945 FUBP2_HUMAN	Far upstream element-binding protein 2 OS	175.63	24	7
Q99460 PSMD1_HUMAN	26S proteasome non-ATPase regulatory s	175.02	27	7
O75368 SH3L1_HUMAN	SH3 domain-binding glutamic acid-rich-like	171.67	71	7
P11216 PYGB_HUMAN	Glycogen phosphorylase, brain form OS=H	170.16	17	7
Q15046 SYK_HUMAN	Lysyl-tRNA synthetase OS=Homo sapiens	169.41	26	7
Q96P16 RPR1A_HUMAN	Regulation of nuclear pre-mRNA domain-c	168.28	47	7
Q9NP97 DLRB1_HUMAN	Dynein light chain roadblock-type 1 OS=Hc	167.74	90	7
Q04837 SSBP_HUMAN	Single-stranded DNA-binding protein, mito	166.94	62	7
P49903 SPS1_HUMAN	Selenide, water dikinase 1 OS=Homo sapi	165.04	39	7
P49588 SYAC_HUMAN	Alanyl-tRNA synthetase, cytoplasmic OS=H	163.95	25	7
P33992 MCM5_HUMAN	DNA replication licensing factor MCM5 OS	162.73	28	7
Q16543 CDC37_HUMAN	Hsp90 co-chaperone Cdc37 OS=Homo sa	160.96	32	7
P61758 PFD3_HUMAN	Prefoldin subunit 3 OS=Homo sapiens GN	160.86	64	7
O43399 TPD54_HUMAN	Tumor protein D54 OS=Homo sapiens GN	160.49	41	7
P30520 PURA2_HUMAN	Adenylosuccinate synthetase isozyme 2 O	160.19	26	7
P62753 RS6_HUMAN	40S ribosomal protein S6 OS=Homo sapie	159.71	37	7
Q00688 FKBP3_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP3	158.13	44	7
Q9Y295 DRG1_HUMAN	Developmentally-regulated GTP-binding pr	157.98	37	7
Q08752 PPID_HUMAN	Peptidyl-prolyl cis-trans isomerase D OS=H	156.48	37	7
Q9UK76 HN1_HUMAN	Hematological and neurological expressed	155.3	54	7

O95347 SMC2_HUMAN	Structural maintenance of chromosomes p	154.66	21	7
P63279 UBC9_HUMAN	SUMO-conjugating enzyme UBC9 OS=Ho	154.41	28	7
P36405 ARL3_HUMAN	ADP-ribosylation factor-like protein 3 OS=H	153.13	62	7
P05198 IF2A_HUMAN	Eukaryotic translation initiation factor 2 sub	152.12	33	7
P61586 RHOA_HUMAN	Transforming protein RhoA OS=Homo sap	151.4	50	7
Q07065 CKAP4_HUMAN	Cytoskeleton-associated protein 4 OS=Ho	151.13	24	7
Q9Y3F4 STRAP_HUMAN	Serine-threonine kinase receptor-associat	150.82	44	7
Q15121 PEA15_HUMAN	Astrocytic phosphoprotein PEA-15 OS=Ho	149.34	71	7
Q9C005 DPY30_HUMAN	Protein dpy-30 homolog OS=Homo sapien	148.58	57	7
O00273 DFFA_HUMAN	DNA fragmentation factor subunit alpha OS	148.43	47	7
P62760 VISL1_HUMAN	Visinin-like protein 1 OS=Homo sapiens G	147.75	59	7
P37108 SRP14_HUMAN	Signal recognition particle 14 kDa protein C	147.44	44	7
Q9HC38 GLOD4_HUMAN	Glyoxalase domain-containing protein 4 OS	147.33	39	7
P12081 SYHC_HUMAN	Histidyl-tRNA synthetase, cytoplasmic OS=	147.27	28	7
P54727 RD23B_HUMAN	UV excision repair protein RAD23 homolog	144.2	22	7
Q15717 ELAV1_HUMAN	ELAV-like protein 1 OS=Homo sapiens GN	143.63	32	7
P04843 RPN1_HUMAN	Dolichyl-diphosphooligosaccharide--proteir	142.15	20	7
Q15404 RSU1_HUMAN	Ras suppressor protein 1 OS=Homo sapie	141.75	34	7
Q14204 DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 OS=H	141.6	13	7
P46926 GNPI1_HUMAN	Glucosamine-6-phosphate isomerase 1 OS	141.14	40	7
P06132 DCUP_HUMAN	Uroporphyrinogen decarboxylase OS=Hon	140.74	45	7
P62857 RS28_HUMAN	40S ribosomal protein S28 OS=Homo sapi	140.12	86	7
Q14980 NUMA1_HUMAN	Nuclear mitotic apparatus protein 1 OS=Ho	139.98	17	7
P52701 MSH6_HUMAN	DNA mismatch repair protein Msh6 OS=Ho	137.38	14	7
P50914 RL14_HUMAN	60S ribosomal protein L14 OS=Homo sapi	135.86	33	7
Q9H0D6 XRN2_HUMAN	5'-3' exoribonuclease 2 OS=Homo sapiens	133.65	20	7
P09661 RU2A_HUMAN	U2 small nuclear ribonucleoprotein A' OS=	132.84	37	7
P23588 IF4B_HUMAN	Eukaryotic translation initiation factor 4B O	132.64	15	7
P48556 PSMD8_HUMAN	26S proteasome non-ATPase regulatory s	129.93	32	7
P35249 RFC4_HUMAN	Replication factor C subunit 4 OS=Homo s	127.73	31	7
P14314 GLU2B_HUMAN	Glucosidase 2 subunit beta OS=Homo sap	127.34	19	7
P15927 RFA2_HUMAN	Replication protein A 32 kDa subunit OS=H	126.98	33	7
P08243 ASNS_HUMAN	Asparagine synthetase [glutamine-hydrolyz	125.23	17	7
Q9UHD8 SEPT9_HUMAN	Septin-9 OS=Homo sapiens GN=SEPT9 P	124.38	26	7
P61254 RL26_HUMAN	60S ribosomal protein L26 OS=Homo sapi	123.1	39	7
Q5T0N5 FBP1L_HUMAN	Formin-binding protein 1-like OS=Homo sa	123.01	19	7
P62312 LSM6_HUMAN	U6 snRNA-associated Sm-like protein LSm	119.5	91	7
Q15370 ELOB_HUMAN	Transcription elongation factor B polypepti	117.43	37	7
P48061 SDF1_HUMAN	Stromal cell-derived factor 1 OS=Homo sa	116.68	44	7
P61353 RL27_HUMAN	60S ribosomal protein L27 OS=Homo sapi	114.35	61	7
P50570 DYN2_HUMAN	Dynamamin-2 OS=Homo sapiens GN=DNM2	114.2	17	7
P18077 RL35A_HUMAN	60S ribosomal protein L35a OS=Homo sap	98.79	30	7
P40222 TXLNA_HUMAN	Alpha-taxilin OS=Homo sapiens GN=TXLN	84.34	21	7
Q9BUF5 TBB6_HUMAN	Tubulin beta-6 chain OS=Homo sapiens G	262.48	62	6
P55209 NP1L1_HUMAN	Nucleosome assembly protein 1-like 1 OS=	199.97	34	6
P61204 ARF3_HUMAN	ADP-ribosylation factor 3 OS=Homo sapie	196.38	77	6
P84077 ARF1_HUMAN	ADP-ribosylation factor 1 OS=Homo sapie	196.38	72	6

Q92841 DDX17_HUMAN	Probable ATP-dependent RNA helicase D	192.35	29	6
P06576 ATPB_HUMAN	ATP synthase subunit beta, mitochondrial	190.16	37	6
P67809 YBOX1_HUMAN	Nuclease-sensitive element-binding protein	190.09	44	6
O00487 PSDE_HUMAN	26S proteasome non-ATPase regulatory s	181.88	54	6
Q9Y5J9 TIM8B_HUMAN	Mitochondrial import inner membrane trans	180.61	65	6
P30566 PUR8_HUMAN	Adenylosuccinate lyase OS=Homo sapiens	180.24	47	6
O00425 IF2B3_HUMAN	Insulin-like growth factor 2 mRNA-binding	177.95	36	6
P30046 DOPD_HUMAN	D-dopachrome decarboxylase OS=Homo s	177.9	67	6
P60983 GMFB_HUMAN	Glia maturation factor beta OS=Homo sapi	174.53	58	6
Q9Y333 LSM2_HUMAN	U6 snRNA-associated Sm-like protein LS	174.34	81	6
P49720 PSB3_HUMAN	Proteasome subunit beta type-3 OS=Homo	172.88	57	6
P30050 RL12_HUMAN	60S ribosomal protein L12 OS=Homo sapi	169.81	59	6
P14324 FPPS_HUMAN	Farnesyl pyrophosphate synthase OS=Hor	169.63	31	6
P35520 CBS_HUMAN	Cystathionine beta-synthase OS=Homo sa	167.32	37	6
P33176 KINH_HUMAN	Kinesin-1 heavy chain OS=Homo sapiens	166.59	17	6
Q12905 ILF2_HUMAN	Interleukin enhancer-binding factor 2 OS=I	166.12	24	6
P62318 SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3 OS	162.13	67	6
Q15056 IF4H_HUMAN	Eukaryotic translation initiation factor 4H O	159.32	50	6
O95372 LYPA2_HUMAN	Acyl-protein thioesterase 2 OS=Homo sap	154.42	51	6
O00303 EIF3F_HUMAN	Eukaryotic translation initiation factor 3 sub	153.11	48	6
Q8WVM8 SCFD1_HUMAN	Sec1 family domain-containing protein 1 O	152.53	24	6
O14979 HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein	152.45	23	6
O95816 BAG2_HUMAN	BAG family molecular chaperone regulator	152.41	30	6
Q71UI9 H2AV_HUMAN	Histone H2A.V OS=Homo sapiens GN=H2	151.34	31	6
P0C0S5 H2AZ_HUMAN	Histone H2A.Z OS=Homo sapiens GN=H2	151.34	31	6
P31350 RIR2_HUMAN	Ribonucleoside-diphosphate reductase su	150.92	25	6
P45974 UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5 OS	150.74	25	6
P55265 DSRAD_HUMAN	Double-stranded RNA-specific adenosine	150.64	19	6
P05388 RLA0_HUMAN	60S acidic ribosomal protein P0 OS=Homo	150.45	36	6
P55769 NH2L1_HUMAN	NHP2-like protein 1 OS=Homo sapiens GN	150.36	55	6
O60264 SMCA5_HUMAN	SWI/SNF-related matrix-associated actin-c	148.81	17	6
P20700 LMNB1_HUMAN	Lamin-B1 OS=Homo sapiens GN=LMNB1	148.41	28	6
Q5T7N2 LITD1_HUMAN	LINE-1 type transposase domain-containin	147.44	19	6
O15212 PFD6_HUMAN	Prefoldin subunit 6 OS=Homo sapiens GN	146.76	75	6
Q96AG4 LRC59_HUMAN	Leucine-rich repeat-containing protein 59 C	146	42	6
O75223 GGCT_HUMAN	Gamma-glutamylcyclotransferase OS=Hor	144.87	36	6
O15067 PUR4_HUMAN	Phosphoribosylformylglycinamide syntha	144.82	25	6
P22413 ENPP1_HUMAN	Ectonucleotide pyrophosphatase/phospho	140.99	18	6
P47756 CAPZB_HUMAN	F-actin-capping protein subunit beta OS=H	139.26	33	6
Q13283 G3BP1_HUMAN	Ras GTPase-activating protein-binding pro	138.61	22	6
P49411 EFTU_HUMAN	Elongation factor Tu, mitochondrial OS=Ho	138.54	28	6
Q13616 CUL1_HUMAN	Cullin-1 OS=Homo sapiens GN=CUL1 PE-	137.46	27	6
P62841 RS15_HUMAN	40S ribosomal protein S15 OS=Homo sapi	136.41	57	6
O43143 DHX15_HUMAN	Putative pre-mRNA-splicing factor ATP-de	136.26	22	6
Q9NZL4 HPBP1_HUMAN	Hsp70-binding protein 1 OS=Homo sapien	136.07	29	6
Q8N474 SFRP1_HUMAN	Secreted frizzled-related protein 1 OS=Hor	135.61	26	6
P84090 ERH_HUMAN	Enhancer of rudimentary homolog OS=Hor	135.37	38	6

O15145 ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3	132.65	38	6
Q8N0X7 SPG20_HUMAN	Spartin OS=Homo sapiens GN=SPG20 PE	130.8	22	6
Q86V81 THOC4_HUMAN	THO complex subunit 4 OS=Homo sapiens	130.58	44	6
P59998 ARPC4_HUMAN	Actin-related protein 2/3 complex subunit 4	128.79	55	6
O14974 MYPT1_HUMAN	Protein phosphatase 1 regulatory subunit 1	128.79	21	6
P26373 RL13_HUMAN	60S ribosomal protein L13 OS=Homo sapi	128.59	32	6
P51659 DHB4_HUMAN	Peroxisomal multifunctional enzyme type 2	128.3	24	6
Q8IVW6 ARI3B_HUMAN	AT-rich interactive domain-containing prote	127.95	32	6
O75489 NDUS3_HUMAN	NADH dehydrogenase [ubiquinone] iron-su	127.71	26	6
Q13085 ACACA_HUMAN	Acetyl-CoA carboxylase 1 OS=Homo sapien	127.4	13	6
P30153 2AAA_HUMAN	Serine/threonine-protein phosphatase 2A	127.29	24	6
Q8IZQ5 SELH_HUMAN	Selenoprotein H OS=Homo sapiens GN=S	127.24	39	6
P48047 ATPO_HUMAN	ATP synthase subunit O, mitochondrial OS	127.13	41	6
P25788 PSA3_HUMAN	Proteasome subunit alpha type-3 OS=Hom	126.49	25	6
O75947 ATP5H_HUMAN	ATP synthase subunit d, mitochondrial OS	125.19	45	6
Q15369 ELOC_HUMAN	Transcription elongation factor B polypepti	123.91	41	6
Q9UKV3 ACINU_HUMAN	Apoptotic chromatin condensation inducer	121.49	12	6
Q9UBE0 SAE1_HUMAN	SUMO-activating enzyme subunit 1 OS=Ho	120.57	32	6
Q16891 IMMT_HUMAN	Mitochondrial inner membrane protein OS=	120.48	12	6
Q9Y2X3 NOP58_HUMAN	Nucleolar protein 58 OS=Homo sapiens G	114.23	25	6
P15121 ALDR_HUMAN	Aldose reductase OS=Homo sapiens GN=	112.92	39	6
P55145 MANF_HUMAN	Mesencephalic astrocyte-derived neurotro	112.85	47	6
P06730 IF4E_HUMAN	Eukaryotic translation initiation factor 4E O	110.98	28	6
P62273 RS29_HUMAN	40S ribosomal protein S29 OS=Homo sapi	109.59	52	6
P61081 UBC12_HUMAN	NEDD8-conjugating enzyme Ubc12 OS=H	109.41	37	6
P99999 CYC_HUMAN	Cytochrome c OS=Homo sapiens GN=CYC	101.03	28	6
P28340 DPOD1_HUMAN	DNA polymerase delta catalytic subunit OS	99.12	12	6
P09669 COX6C_HUMAN	Cytochrome c oxidase subunit 6C OS=Hor	88.88	49	6
Q93077 H2A1C_HUMAN	Histone H2A type 1-C OS=Homo sapiens	262.76	75	5
P31947 1433S_HUMAN	14-3-3 protein sigma OS=Homo sapiens G	189.81	56	5
Q15366 PCBP2_HUMAN	Poly(rC)-binding protein 2 OS=Homo sapie	177.41	42	5
Q8N1G4 LRC47_HUMAN	Leucine-rich repeat-containing protein 47	172.96	34	5
Q9P289 MST4_HUMAN	Serine/threonine-protein kinase MST4 OS=	163.93	32	5
Q9P1F3 CF115_HUMAN	Costars family protein C6orf115 OS=Hom	163.39	80	5
Q9UBQ7 GRHPR_HUMAN	Glyoxylate reductase/hydroxypyruvate red	158.58	28	5
Q13151 ROA0_HUMAN	Heterogeneous nuclear ribonucleoprotein	158.36	38	5
P11388 TOP2A_HUMAN	DNA topoisomerase 2-alpha OS=Homo sa	157.26	18	5
Q13907 IDI1_HUMAN	Isopentenyl-diphosphate Delta-isomerase	156.78	45	5
P11279 LAMP1_HUMAN	Lysosome-associated membrane glycopro	156.01	37	5
P20962 PTMS_HUMAN	Parathyrosin OS=Homo sapiens GN=PTM	155.16	24	5
P24534 EF1B_HUMAN	Elongation factor 1-beta OS=Homo sapien	154.83	44	5
P26583 HMGB2_HUMAN	High mobility group protein B2 OS=Homo	153.44	52	5
Q9Y2B0 CNPY2_HUMAN	Protein canopy homolog 2 OS=Homo sapi	152.97	58	5
Q16643 DREB_HUMAN	Drebrin OS=Homo sapiens GN=DBN1 PE=	152.54	21	5
Q99598 TSNAX_HUMAN	Translin-associated protein X OS=Homo s	149.52	36	5
Q07020 RL18_HUMAN	60S ribosomal protein L18 OS=Homo sapi	149.43	31	5
Q9NTK5 OLA1_HUMAN	Obg-like ATPase 1 OS=Homo sapiens GN	148.08	29	5

P52565 GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=GDIR1 PE=1	147.64	38	5
Q15942 ZYX_HUMAN	Zyxin OS=Homo sapiens GN=ZYX PE=1	147.47	17	5
P62314 SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SMD1 PE=1	146.59	56	5
Q15181 IPYR_HUMAN	Inorganic pyrophosphatase OS=Homo sapiens GN=IPYR PE=1	145.07	34	5
Q9UQ80 PA2G4_HUMAN	Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1	143.18	26	5
Q14166 TTL12_HUMAN	Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens GN=TTL12 PE=1	142.77	22	5
P38159 HNRPG_HUMAN	Heterogeneous nuclear ribonucleoprotein G OS=Homo sapiens GN=HNRPG PE=1	142.73	40	5
P62993 GRB2_HUMAN	Growth factor receptor-bound protein 2 OS=Homo sapiens GN=GRB2 PE=1	142.24	33	5
Q4V328 GRAP1_HUMAN	GRIP1-associated protein 1 OS=Homo sapiens GN=GRAP1 PE=1	142.03	20	5
O75475 PSIP1_HUMAN	PC4 and SFRS1-interacting protein OS=Homo sapiens GN=PSIP1 PE=1	141.93	23	5
P05067 A4_HUMAN	Amyloid beta A4 protein OS=Homo sapiens GN=A4 PE=1	140.83	19	5
Q9P2M7 CING_HUMAN	Cingulin OS=Homo sapiens GN=CGN PE=1	140.29	18	5
Q9H9Q2 CSN7B_HUMAN	COP9 signalosome complex subunit 7b OS=Homo sapiens GN=CSN7B PE=1	139.8	37	5
P29762 RABP1_HUMAN	Cellular retinoic acid-binding protein 1 OS=Homo sapiens GN=RABP1 PE=1	139.76	53	5
O60256 KPRB_HUMAN	Phosphoribosyl pyrophosphate synthase-alpha OS=Homo sapiens GN=KPRB PE=1	139.74	30	5
P40121 CAPG_HUMAN	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1	139.14	25	5
Q99613 EIF3C_HUMAN	Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3C PE=1	137.87	15	5
P47813 IF1AX_HUMAN	Eukaryotic translation initiation factor 1A, X OS=Homo sapiens GN=IF1AX PE=1	137.72	36	5
O14602 IF1AY_HUMAN	Eukaryotic translation initiation factor 1A, Y OS=Homo sapiens GN=IF1AY PE=1	137.72	36	5
P36871 PGM1_HUMAN	Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1	137.46	20	5
O43776 SYNC_HUMAN	Asparaginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=SYNC PE=1	136.71	16	5
P55327 TPD52_HUMAN	Tumor protein D52 OS=Homo sapiens GN=TPD52 PE=1	136.6	41	5
P62847 RS24_HUMAN	40S ribosomal protein S24 OS=Homo sapiens GN=RS24 PE=1	135.34	30	5
O60220 TIM8A_HUMAN	Mitochondrial import inner membrane translocator subunit 8A OS=Homo sapiens GN=TIM8A PE=1	134.53	44	5
Q6IBS0 TWF2_HUMAN	Twinfilin-2 OS=Homo sapiens GN=TWF2 PE=1	134.5	28	5
P54709 AT1B3_HUMAN	Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=AT1B3 PE=1	134.47	41	5
Q8N1F7 NUP93_HUMAN	Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1	134.36	18	5
Q9NYL9 TMOD3_HUMAN	Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1	134.17	25	5
O00151 PDLI1_HUMAN	PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLI1 PE=1	134.16	30	5
P83731 RL24_HUMAN	60S ribosomal protein L24 OS=Homo sapiens GN=RL24 PE=1	133.95	22	5
P83916 CBX1_HUMAN	Chromobox protein homolog 1 OS=Homo sapiens GN=CBX1 PE=1	133.15	36	5
Q9BPW8 NIPS1_HUMAN	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPS1 PE=1	132.84	36	5
P14854 CX6B1_HUMAN	Cytochrome c oxidase subunit 6B1 OS=Homo sapiens GN=CX6B1 PE=1	132.84	50	5
P28072 PSB6_HUMAN	Proteasome subunit beta type-6 OS=Homo sapiens GN=PSB6 PE=1	131.74	31	5
Q9Y3B8 ORN_HUMAN	Oligoribonuclease, mitochondrial OS=Homo sapiens GN=ORN PE=1	131.32	39	5
P35080 PROF2_HUMAN	Profilin-2 OS=Homo sapiens GN=PFN2 PE=1	131.06	54	5
Q9BUL8 PDC10_HUMAN	Programmed cell death protein 10 OS=Homo sapiens GN=PDC10 PE=1	130.56	49	5
Q99417 MYCBP_HUMAN	C-Myc-binding protein OS=Homo sapiens GN=MYCBP PE=1	130.13	46	5
P49458 SRP09_HUMAN	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP09 PE=1	129.82	63	5
Q9Y2V2 CHSP1_HUMAN	Calcium-regulated heat stable protein 1 OS=Homo sapiens GN=CHSP1 PE=1	129.71	35	5
P35611 ADDA_HUMAN	Alpha-adducin OS=Homo sapiens GN=ADDA PE=1	128.57	15	5
Q13098 CSN1_HUMAN	COP9 signalosome complex subunit 1 OS=Homo sapiens GN=CSN1 PE=1	128.2	22	5
Q93062 RBPMS_HUMAN	RNA-binding protein with multiple splicing OS=Homo sapiens GN=RBPMS PE=1	127.94	42	5
P28070 PSB4_HUMAN	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSB4 PE=1	127.88	29	5
P21796 VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1	127.14	27	5
Q7L190 DPPA4_HUMAN	Developmental pluripotency-associated protein 4 OS=Homo sapiens GN=DPPA4 PE=1	127.02	34	5
Q15637 SF01_HUMAN	Splicing factor 1 OS=Homo sapiens GN=SF01 PE=1	126.72	14	5

Q9UGI8 TES_HUMAN	Testin OS=Homo sapiens GN=TES PE=1	125.18	20	5
P55010 IF5_HUMAN	Eukaryotic translation initiation factor 5 OS=Homo sapiens GN=IF5 PE=1	124.23	22	5
Q9Y4Z0 LSM4_HUMAN	U6 snRNA-associated Sm-like protein LSM4 OS=Homo sapiens GN=LSM4 PE=1	124.15	45	5
P61916 NPC2_HUMAN	Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=1	124	48	5
P62942 FKBP1A_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1	123.45	64	5
Q93009 UBP7_HUMAN	Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens GN=UBP7 PE=1	122.55	12	5
P33316 DUT_HUMAN	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS=Homo sapiens GN=DUT PE=1	121.34	30	5
P32321 DCTD_HUMAN	Deoxycytidylate deaminase OS=Homo sapiens GN=DCTD PE=1	121.14	42	5
Q13242 SRSF9_HUMAN	Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1	120.63	38	5
P63165 SUMO1_HUMAN	Small ubiquitin-related modifier 1 OS=Homo sapiens GN=SUMO1 PE=1	119.88	50	5
O43795 MYO1B_HUMAN	Myosin-Ib OS=Homo sapiens GN=MYO1B PE=1	119.86	15	5
P51114 FXR1_HUMAN	Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1	119.51	12	5
P26639 SYTC_HUMAN	Threonyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=SYTC PE=1	119.35	17	5
Q9NVP1 DDX18_HUMAN	ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=DDX18 PE=1	118.06	19	5
P36404 ARL2_HUMAN	ADP-ribosylation factor-like protein 2 OS=Homo sapiens GN=ARL2 PE=1	117.48	30	5
P24539 AT5F1_HUMAN	ATP synthase subunit b, mitochondrial OS=Homo sapiens GN=AT5F1 PE=1	115.66	30	5
P45973 CBX5_HUMAN	Chromobox protein homolog 5 OS=Homo sapiens GN=CBX5 PE=1	115.4	43	5
Q9P0J0 NDUAD_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subunit OS=Homo sapiens GN=NDUAD PE=1	114.53	31	5
P17677 NEUM_HUMAN	Neuromodulin OS=Homo sapiens GN=GAU1 PE=1	114.53	26	5
Q9BRP8 WIBG_HUMAN	Partner of Y14 and mago OS=Homo sapiens GN=WIBG PE=1	114.21	24	5
O95865 DDAH2_HUMAN	N(G),N(G)-dimethylarginine dimethylaminohydrolase OS=Homo sapiens GN=DDAH2 PE=1	112.71	26	5
Q14847 LASP1_HUMAN	LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1	111.79	29	5
Q92878 RAD50_HUMAN	DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1	109.33	10	5
Q9BQ04 RBM4B_HUMAN	RNA-binding protein 4B OS=Homo sapiens GN=RBM4B PE=1	109.23	17	5
Q9BWF3 RBM4_HUMAN	RNA-binding protein 4 OS=Homo sapiens GN=RBM4 PE=1	109.23	16	5
Q15020 SART3_HUMAN	Squamous cell carcinoma antigen recognition cluster protein 3 OS=Homo sapiens GN=SART3 PE=1	109.09	16	5
Q9UBQ0 VPS29_HUMAN	Vacuolar protein sorting-associated protein 29 OS=Homo sapiens GN=VPS29 PE=1	108.11	32	5
P39748 FEN1_HUMAN	Flap endonuclease 1 OS=Homo sapiens GN=FEN1 PE=1	106.17	26	5
O43447 PPIH_HUMAN	Peptidyl-prolyl cis-trans isomerase H OS=Homo sapiens GN=PPIH PE=1	103.73	40	5
P82979 SARNP_HUMAN	SAP domain-containing ribonucleoprotein OS=Homo sapiens GN=SARNP PE=1	103.56	29	5
Q15075 EEA1_HUMAN	Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1	101.05	9	5
Q9BVG4 CX026_HUMAN	UPF0368 protein Cxorf26 OS=Homo sapiens GN=CX026 PE=1	100.76	31	5
P20674 COX5A_HUMAN	Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1	100.34	37	5
Q99436 PSB7_HUMAN	Proteasome subunit beta type-7 OS=Homo sapiens GN=PSB7 PE=1	97.33	24	5
O75643 U520_HUMAN	U5 small nuclear ribonucleoprotein 200 kDa OS=Homo sapiens GN=U520 PE=1	95.25	4	5
P78330 SERB_HUMAN	Phosphoserine phosphatase OS=Homo sapiens GN=SERB PE=1	95.03	24	5
P55957 BID_HUMAN	BH3-interacting domain death agonist OS=Homo sapiens GN=BID PE=1	94.65	33	5
Q14978 NOLC1_HUMAN	Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens GN=NOLC1 PE=1	92.44	22	5
P11413 G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1	92.21	13	5
Q96PY5 FMNL2_HUMAN	Formin-like protein 2 OS=Homo sapiens GN=FMNL2 PE=1	88.46	9	5
P98160 PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan OS=Homo sapiens GN=PGBM PE=1	84.39	4	5
P61326 MGN_HUMAN	Protein mago nashi homolog OS=Homo sapiens GN=MGN PE=1	83.83	40	5
Q96A72 MGN2_HUMAN	Protein mago nashi homolog 2 OS=Homo sapiens GN=MGN2 PE=1	83.83	39	5
P29373 RABP2_HUMAN	Cellular retinoic acid-binding protein 2 OS=Homo sapiens GN=RABP2 PE=1	83.11	61	5
Q9NPE3 NOP10_HUMAN	H/ACA ribonucleoprotein complex subunit OS=Homo sapiens GN=NOP10 PE=1	78.6	70	5
Q4VC31 CCD58_HUMAN	Coiled-coil domain-containing protein 58 OS=Homo sapiens GN=CCD58 PE=1	77.49	47	5
P19388 RPAB1_HUMAN	DNA-directed RNA polymerases I, II, and III OS=Homo sapiens GN=RPAB1 PE=1	71.27	23	5

P63241 IF5A1_HUMAN	Eukaryotic translation initiation factor 5A-1	286.42	81	4
P11940 PABP1_HUMAN	Polyadenylate-binding protein 1 OS=Homo	242.19	43	4
P08107 HSP71_HUMAN	Heat shock 70 kDa protein 1A/1B OS=Homo	217.74	44	4
P62140 PP1B_HUMAN	Serine/threonine-protein phosphatase PP1	195.3	47	4
P31943 HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein	184.88	44	4
Q06210 GFPT1_HUMAN	Glucosamine--fructose-6-phosphate aminotransferase (cytosolic) OS=Homo sapiens GN=GFPT1	175.37	28	4
P41567 EIF1_HUMAN	Eukaryotic translation initiation factor 1 OS=Homo sapiens GN=EIF1	164.11	79	4
P04216 THY1_HUMAN	Thy-1 membrane glycoprotein OS=Homo sapiens GN=THY1	154.44	25	4
Q9UI30 TR112_HUMAN	tRNA methyltransferase 112 homolog OS=Homo sapiens GN=TR112	153.69	42	4
Q8IXM2 BAP18_HUMAN	Chromatin complexes subunit BAP18 OS=Homo sapiens GN=BAP18	149.65	54	4
Q13185 CBX3_HUMAN	Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3	148.56	39	4
P51858 HDGF_HUMAN	Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF	148.24	49	4
P43246 MSH2_HUMAN	DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2	147.07	20	4
Q9H3K6 BOLA2_HUMAN	BolA-like protein 2 OS=Homo sapiens GN=BOLA2	144.1	43	4
Q16630 CPSF6_HUMAN	Cleavage and polyadenylation specificity factor 6 OS=Homo sapiens GN=CPSF6	143.95	20	4
Q13347 EIF3I_HUMAN	Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I	143.07	18	4
P17812 PYRG1_HUMAN	CTP synthase 1 OS=Homo sapiens GN=PYRG1	139.55	21	4
Q9NQT4 EXOS5_HUMAN	Exosome complex component RRP46 OS=Homo sapiens GN=EXOS5	139.28	33	4
P84103 SRSF3_HUMAN	Serine/arginine-rich splicing factor 3 OS=Homo sapiens GN=SRSF3	138.96	30	4
P61970 NTF2_HUMAN	Nuclear transport factor 2 OS=Homo sapiens GN=NTF2	138.45	69	4
P52907 CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAZA1	138.21	31	4
P36969 GPX4_HUMAN	Phospholipid hydroperoxide glutathione peroxidase 4 OS=Homo sapiens GN=GPX4	138.12	29	4
Q9Y2Z0 SUGT1_HUMAN	Suppressor of G2 allele of SKP1 homolog OS=Homo sapiens GN=SUGT1	136.71	24	4
Q9BRA2 TXD17_HUMAN	Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXD17	136.32	42	4
P62917 RL8_HUMAN	60S ribosomal protein L8 OS=Homo sapiens GN=RL8	136.01	24	4
Q15029 U5S1_HUMAN	116 kDa U5 small nuclear ribonucleoprotein OS=Homo sapiens GN=U5S1	135.96	12	4
Q14444 CAPR1_HUMAN	Caprin-1 OS=Homo sapiens GN=CAPRIN1	135.89	24	4
O75607 NPM3_HUMAN	Nucleoplasm-3 OS=Homo sapiens GN=NPM3	135.26	41	4
O43765 SGTA_HUMAN	Small glutamine-rich tetratricopeptide repeat-containing protein OS=Homo sapiens GN=SGTA	135.11	23	4
P11177 ODPB_HUMAN	Pyruvate dehydrogenase E1 component subunit beta OS=Homo sapiens GN=ODPB	134.41	16	4
Q9NRX4 PHP14_HUMAN	14 kDa phosphohistidine phosphatase OS=Homo sapiens GN=PHP14	131.26	56	4
Q13619 CUL4A_HUMAN	Cullin-4A OS=Homo sapiens GN=CUL4A	131.24	21	4
Q9Y3B4 PM14_HUMAN	Pre-mRNA branch site protein p14 OS=Homo sapiens GN=PM14	129.85	35	4
P35232 PHB_HUMAN	Prohibitin OS=Homo sapiens GN=PHB	126.82	37	4
P30048 PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase 3 OS=Homo sapiens GN=PRDX3	125.71	36	4
P62306 RUXF_HUMAN	Small nuclear ribonucleoprotein F OS=Homo sapiens GN=RUXF	124.69	56	4
Q9Y5L4 TIM13_HUMAN	Mitochondrial import inner membrane translocator subunit TIM13 OS=Homo sapiens GN=TIM13	124.68	54	4
P00492 HPRT_HUMAN	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT	124.39	25	4
O75348 VATG1_HUMAN	V-type proton ATPase subunit G 1 OS=Homo sapiens GN=VATG1	124.33	42	4
Q9NPH2 INO1_HUMAN	Inositol-3-phosphate synthase 1 OS=Homo sapiens GN=INO1	123.91	17	4
P36639 8ODP_HUMAN	7,8-dihydro-8-oxoguanine triphosphatase OS=Homo sapiens GN=8ODP	123.84	19	4
P10606 COX5B_HUMAN	Cytochrome c oxidase subunit 5B, mitochondrial OS=Homo sapiens GN=COX5B	123.61	60	4
O00622 CYR61_HUMAN	Protein CYR61 OS=Homo sapiens GN=CYR61	122.93	20	4
Q5VYJ4 RUEL1_HUMAN	Putative small nuclear ribonucleoprotein p0 OS=Homo sapiens GN=RUEL1	122.73	62	4
P62304 RUXE_HUMAN	Small nuclear ribonucleoprotein E OS=Homo sapiens GN=RUXE	122.73	62	4
Q9UNZ2 NSF1C_HUMAN	NSFL1 cofactor p47 OS=Homo sapiens GN=NSF1C	122.61	35	4
P12004 PCNA_HUMAN	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA	121.45	20	4

Q9UNH7 SNX6_HUMAN	Sorting nexin-6 OS=Homo sapiens GN=SN	120.33	18	4
Q9BQI0 AIF1L_HUMAN	Allograft inflammatory factor 1-like OS=Ho	119.91	38	4
Q96AC1 FERM2_HUMAN	Fermitin family homolog 2 OS=Homo sapie	119.84	15	4
P35244 RFA3_HUMAN	Replication protein A 14 kDa subunit OS=H	119.22	40	4
Q92896 GSLG1_HUMAN	Golgi apparatus protein 1 OS=Homo sapie	118.67	9	4
Q8WUM4 PDC6I_HUMAN	Programmed cell death 6-interacting prote	118.37	19	4
Q9NUQ9 FA49B_HUMAN	Protein FAM49B OS=Homo sapiens GN=F	118.02	19	4
P07203 GPX1_HUMAN	Glutathione peroxidase 1 OS=Homo sapie	117.92	34	4
Q13158 FADD_HUMAN	Protein FADD OS=Homo sapiens GN=FAI	117.5	53	4
O60888 CUTA_HUMAN	Protein CutA OS=Homo sapiens GN=CUT	117.22	43	4
Q13442 HAP28_HUMAN	28 kDa heat- and acid-stable phosphoprot	116.43	24	4
Q14011 CIRBP_HUMAN	Cold-inducible RNA-binding protein OS=H	116.32	43	4
P09525 ANXA4_HUMAN	Annexin A4 OS=Homo sapiens GN=ANXA	116.04	31	4
Q9H299 SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-like	115.58	52	4
P31930 QCR1_HUMAN	Cytochrome b-c1 complex subunit 1, mitoc	115	23	4
Q9Y371 SHLB1_HUMAN	Endophilin-B1 OS=Homo sapiens GN=SH	114.92	11	4
Q96SM3 CPXM1_HUMAN	Probable carboxypeptidase X1 OS=Homo	114.6	17	4
P14735 IDE_HUMAN	Insulin-degrading enzyme OS=Homo sapie	114.59	14	4
P46779 RL28_HUMAN	60S ribosomal protein L28 OS=Homo sapi	114.42	28	4
Q99873 ANM1_HUMAN	Protein arginine N-methyltransferase 1 OS	114.31	18	4
Q07666 KHDR1_HUMAN	KH domain-containing, RNA-binding, signa	114.08	27	4
Q9H444 CHM4B_HUMAN	Charged multivesicular body protein 4b OS	113.93	43	4
P40937 RFC5_HUMAN	Replication factor C subunit 5 OS=Homo s	113.69	22	4
Q14CX7 NAA25_HUMAN	N-alpha-acetyltransferase 25, NatB auxilia	113.62	12	4
P39687 AN32A_HUMAN	Acidic leucine-rich nuclear phosphoprotein	113.27	31	4
Q15257 PTPA_HUMAN	Serine/threonine-protein phosphatase 2A a	112.87	24	4
Q99584 S10AD_HUMAN	Protein S100-A13 OS=Homo sapiens GN=	112.84	45	4
P42285 SK2L2_HUMAN	Superkiller viralicidic activity 2-like 2 OS=H	112.73	17	4
P30626 SORCN_HUMAN	Sorcin OS=Homo sapiens GN=SRI PE=1	112.51	22	4
Q99961 SH3G1_HUMAN	Endophilin-A2 OS=Homo sapiens GN=SH	112.33	16	4
Q9H1E3 NUCKS_HUMAN	Nuclear ubiquitous casein and cyclin-depe	111.79	27	4
P63208 SKP1_HUMAN	S-phase kinase-associated protein 1 OS=H	111.35	27	4
P09382 LEG1_HUMAN	Galectin-1 OS=Homo sapiens GN=LGALS	110.41	39	4
Q9ULC4 MCTS1_HUMAN	Malignant T cell-amplified sequence 1 OS=	109.93	38	4
O75821 EIF3G_HUMAN	Eukaryotic translation initiation factor 3 sub	109.22	21	4
Q8WWY3 PRP31_HUMAN	U4/U6 small nuclear ribonucleoprotein Prp	109.11	33	4
P24666 PPAC_HUMAN	Low molecular weight phosphotyrosine pro	108.01	22	4
P35637 FUS_HUMAN	RNA-binding protein FUS OS=Homo sapie	107.92	29	4
O60925 PFD1_HUMAN	Prefoldin subunit 1 OS=Homo sapiens GN	107.79	24	4
P52788 SPSY_HUMAN	Spermine synthase OS=Homo sapiens GN	107.68	23	4
O75312 ZPR1_HUMAN	Zinc finger protein ZPR1 OS=Homo sapier	107.14	19	4
O75955 FLOT1_HUMAN	Flotillin-1 OS=Homo sapiens GN=FLOT1 F	106.47	26	4
Q9Y285 SYFA_HUMAN	Phenylalanyl-tRNA synthetase alpha chain	105.83	18	4
P05937 CALB1_HUMAN	Calbindin OS=Homo sapiens GN=CALB1	104.54	31	4
P35606 COPB2_HUMAN	Coatomer subunit beta' OS=Homo sapiens	104.41	6	4
P09455 RET1_HUMAN	Retinol-binding protein 1 OS=Homo sapier	104.33	51	4
P55786 PSA_HUMAN	Puromycin-sensitive aminopeptidase OS=H	104.15	7	4



Q07866 KLC1_HUMAN	Kinesin light chain 1 OS=Homo sapiens GN=KLC1	102.84	18	4
P51149 RAB7A_HUMAN	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A	102.73	36	4
P05204 HMGN2_HUMAN	Non-histone chromosomal protein HMG-17 OS=Homo sapiens GN=HMGN2	102.58	51	4
Q9Y376 CAB39_HUMAN	Calcium-binding protein 39 OS=Homo sapiens GN=CAB39	102.37	23	4
O43324 MCA3_HUMAN	Eukaryotic translation elongation factor 1 epsilon OS=Homo sapiens GN=MCA3	102.05	39	4
Q13308 PTK7_HUMAN	Inactive tyrosine-protein kinase 7 OS=Homo sapiens GN=PTK7	101.96	9	4
P12830 CADH1_HUMAN	Cadherin-1 OS=Homo sapiens GN=CDH1	101.75	7	4
P40429 RL13A_HUMAN	60S ribosomal protein L13a OS=Homo sapiens GN=RL13A	101.69	29	4
O43252 PAPS1_HUMAN	Bifunctional 3'-phosphoadenosine 5'-phosphatase OS=Homo sapiens GN=PAPS1	101.48	19	4
P63000 RAC1_HUMAN	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1	100.68	26	4
P19623 SPEE_HUMAN	Spermidine synthase OS=Homo sapiens GN=SPEE	100.49	24	4
Q9GZT3 SLIRP_HUMAN	SRA stem-loop-interacting RNA-binding protein OS=Homo sapiens GN=SLIRP	100.31	55	4
Q9BYT8 NEUL_HUMAN	Neurolysin, mitochondrial OS=Homo sapiens GN=NEUL	99.07	13	4
Q9NSD9 SYFB_HUMAN	Phenylalanyl-tRNA synthetase beta chain OS=Homo sapiens GN=SYFB	98.12	11	4
P51148 RAB5C_HUMAN	Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C	97.15	31	4
Q9BS26 ERP44_HUMAN	Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44	95.98	16	4
P61086 UBE2K_HUMAN	Ubiquitin-conjugating enzyme E2 K OS=Homo sapiens GN=UBE2K	95.94	36	4
Q99426 TBCB_HUMAN	Tubulin-folding cofactor B OS=Homo sapiens GN=TBCB	95.64	16	4
Q02543 RL18A_HUMAN	60S ribosomal protein L18a OS=Homo sapiens GN=RL18A	94.95	29	4
A6NDG6 PGP_HUMAN	Phosphoglycolate phosphatase OS=Homo sapiens GN=PGP	94.5	15	4
A8MWD9 RUXGL_HUMAN	Small nuclear ribonucleoprotein G-like protein OS=Homo sapiens GN=RUXGL	94.4	26	4
P62308 RUXG_HUMAN	Small nuclear ribonucleoprotein G OS=Homo sapiens GN=RUXG	94.4	26	4
Q32P28 P3H1_HUMAN	Prolyl 3-hydroxylase 1 OS=Homo sapiens GN=P3H1	94.24	7	4
Q969H8 CS010_HUMAN	UPF0556 protein C19orf10 OS=Homo sapiens GN=CS010	93.93	26	4
Q14203 DCTN1_HUMAN	Dynactin subunit 1 OS=Homo sapiens GN=DCTN1	91.52	11	4
Q9UKY7 CDV3_HUMAN	Protein CDV3 homolog OS=Homo sapiens GN=CDV3	90.41	19	4
P25325 THTM_HUMAN	3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=THTM	88.59	24	4
O00154 BACH_HUMAN	Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=BACH	86.47	12	4
Q03701 CEBPZ_HUMAN	CCAAT/enhancer-binding protein zeta OS=Homo sapiens GN=CEBPZ	83.82	8	4
Q5TZA2 CROCC_HUMAN	Rootletin OS=Homo sapiens GN=CROCC	83.36	7	4
Q9Y2S6 CCD72_HUMAN	Coiled-coil domain-containing protein 72 OS=Homo sapiens GN=CCD72	83.29	36	4
P36542 ATPG_HUMAN	ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATPG	83.27	27	4
P38117 ETFB_HUMAN	Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB	82.51	29	4
P13073 COX41_HUMAN	Cytochrome c oxidase subunit 4 isoform 1 OS=Homo sapiens GN=COX41	81.1	32	4
P61221 ABCE1_HUMAN	ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1	73.47	15	4
Q8WWM7 ATX2L_HUMAN	Ataxin-2-like protein OS=Homo sapiens GN=ATX2L	73.05	7	4
Q13435 SF3B2_HUMAN	Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2	71.02	8	4
Q04637 IF4G1_HUMAN	Eukaryotic translation initiation factor 4 gamma OS=Homo sapiens GN=IF4G1	68.82	6	4
Q96PK6 RBM14_HUMAN	RNA-binding protein 14 OS=Homo sapiens GN=RBM14	68.35	10	4
Q86X55 CARM1_HUMAN	Histone-arginine methyltransferase CARM1 OS=Homo sapiens GN=CARM1	58.7	16	4
Q8TDI0 CHD5_HUMAN	Chromodomain-helicase-DNA-binding protein 5 OS=Homo sapiens GN=CHD5	57.07	6	4
Q9HCM1 CL035_HUMAN	Uncharacterized protein C12orf35 OS=Homo sapiens GN=CL035	56.46	5	4
P35659 DEK_HUMAN	Protein DEK OS=Homo sapiens GN=DEK	52.16	11	4
Q8WZ42 TITIN_HUMAN	Titin OS=Homo sapiens GN=TTN PE=1 SV=1	50.28	4	4
Q8IZC6 CORA1_HUMAN	Collagen alpha-1(XXVII) chain OS=Homo sapiens GN=CORA1	46.19	10	4
Q13509 TBB3_HUMAN	Tubulin beta-3 chain OS=Homo sapiens GN=TBB3	328.66	65	3
P16403 H12_HUMAN	Histone H1.2 OS=Homo sapiens GN=HIST1H2B	246.08	54	3

P19105 ML12A_HUMAN	Myosin regulatory light chain 12A OS=Homo sapiens GN=ML12A	218.29	64	3
O14950 ML12B_HUMAN	Myosin regulatory light chain 12B OS=Homo sapiens GN=ML12B	218.29	63	3
P62136 PP1A_HUMAN	Serine/threonine-protein phosphatase PP1A OS=Homo sapiens GN=PP1A	214.64	50	3
P36873 PP1G_HUMAN	Serine/threonine-protein phosphatase PP1G OS=Homo sapiens GN=PP1G	207.58	51	3
P80297 MT1X_HUMAN	Metallothionein-1X OS=Homo sapiens GN=MT1X	173.44	93	3
O00292 LFTY2_HUMAN	Left-right determination factor 2 OS=Homo sapiens GN=LFTY2	171.99	39	3
Q13526 PIN1_HUMAN	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens GN=PIN1	157.53	56	3
P84085 ARF5_HUMAN	ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5	155.55	56	3
Q9Y6M1 IF2B2_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens GN=IF2B2	152.9	22	3
P13804 ETFA_HUMAN	Electron transfer flavoprotein subunit alpha OS=Homo sapiens GN=ETFA	145.32	53	3
Q9BUT1 BDH2_HUMAN	3-hydroxybutyrate dehydrogenase type 2 OS=Homo sapiens GN=BDH2	138.72	40	3
P22087 FBRL_HUMAN	rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBRL	138.49	42	3
P61163 ACTZ_HUMAN	Alpha-centractin OS=Homo sapiens GN=ACTZ	138.07	57	3
P42677 RS27_HUMAN	40S ribosomal protein S27 OS=Homo sapiens GN=RS27	137.93	40	3
Q5VTR2 BRE1A_HUMAN	E3 ubiquitin-protein ligase BRE1A OS=Homo sapiens GN=BRE1A	136.26	19	3
Q6GMV3 CB079_HUMAN	Uncharacterized protein C2orf79 OS=Homo sapiens GN=CB079	135.56	52	3
Q16629 SRSF7_HUMAN	Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7	135.25	20	3
P12829 MYL4_HUMAN	Myosin light chain 4 OS=Homo sapiens GN=MYL4	135.23	70	3
O43768 ENSA_HUMAN	Alpha-endosulfine OS=Homo sapiens GN=ENSA	133.61	69	3
P14923 PLAK_HUMAN	Junction plakoglobin OS=Homo sapiens GN=PLAK	132.84	17	3
Q9BX68 HINT2_HUMAN	Histidine triad nucleotide-binding protein 2 OS=Homo sapiens GN=HINT2	132.21	40	3
P04080 CYTB_HUMAN	Cystatin-B OS=Homo sapiens GN=CSTB	130.76	55	3
Q92769 HDAC2_HUMAN	Histone deacetylase 2 OS=Homo sapiens GN=HDAC2	129.78	22	3
Q15437 SC23B_HUMAN	Protein transport protein Sec23B OS=Homo sapiens GN=SC23B	129.03	16	3
Q9BQ52 RNZ2_HUMAN	Zinc phosphodiesterase ELAC protein 2 OS=Homo sapiens GN=RNZ2	128.98	14	3
P48735 IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDHP	128.95	25	3
P62873 GBB1_HUMAN	Guanine nucleotide-binding protein G(I)/G(S) subunit beta-1 OS=Homo sapiens GN=GBB1	128.14	17	3
P46782 RS5_HUMAN	40S ribosomal protein S5 OS=Homo sapiens GN=RS5	128.04	30	3
P49006 MRP_HUMAN	MARCKS-related protein OS=Homo sapiens GN=MRP	127.99	28	3
Q9Y3C6 PPIL1_HUMAN	Peptidyl-prolyl cis-trans isomerase-like 1 OS=Homo sapiens GN=PPIL1	127.31	39	3
Q7L1Q6 BZW1_HUMAN	Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1	126.41	28	3
P54920 SNAA_HUMAN	Alpha-soluble NSF attachment protein OS=Homo sapiens GN=SNAA	126.36	25	3
O76021 RL1D1_HUMAN	Ribosomal L1 domain-containing protein 1 OS=Homo sapiens GN=RL1D1	125.66	32	3
Q6P2Q9 PRP8_HUMAN	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRP8	124.22	15	3
Q9NPJ3 ACO13_HUMAN	Acyl-coenzyme A thioesterase 13 OS=Homo sapiens GN=ACO13	124.06	21	3
Q96PU8 QKI_HUMAN	Protein quaking OS=Homo sapiens GN=QKI	122.86	48	3
Q9H0A0 NAT10_HUMAN	N-acetyltransferase 10 OS=Homo sapiens GN=NAT10	122.86	14	3
Q15833 STXB2_HUMAN	Syntaxin-binding protein 2 OS=Homo sapiens GN=STXB2	122.7	20	3
P10768 ESTD_HUMAN	S-formylglutathione hydrolase OS=Homo sapiens GN=ESTD	122.62	29	3
O00264 PGRC1_HUMAN	Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRC1	122.35	36	3
Q12996 CSTF3_HUMAN	Cleavage stimulation factor subunit 3 OS=Homo sapiens GN=CSTF3	121.58	17	3
Q99733 NP1L4_HUMAN	Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NP1L4	120.55	26	3
P19784 CSK22_HUMAN	Casein kinase II subunit alpha' OS=Homo sapiens GN=CSK22	120.09	22	3
P11172 PYR5_HUMAN	Uridine 5'-monophosphate synthase OS=Homo sapiens GN=PYR5	119.61	34	3
P62854 RS26_HUMAN	40S ribosomal protein S26 OS=Homo sapiens GN=RS26	118.32	31	3
O00567 NOP56_HUMAN	Nucleolar protein 56 OS=Homo sapiens GN=NOP56	118.13	20	3
A6NDU8 CE051_HUMAN	UPF0600 protein C5orf51 OS=Homo sapiens GN=CE051	116.57	50	3

P05386 RLA1_HUMAN	60S acidic ribosomal protein P1 OS=Homo	115.59	49	3
O43278 SPIT1_HUMAN	Kunitz-type protease inhibitor 1 OS=Homo	115.29	7	3
P46776 RL27A_HUMAN	60S ribosomal protein L27a OS=Homo sap	114.98	39	3
Q9NRN7 ADPPT_HUMAN	L-aminoadipate-semialdehyde dehydrogen	114.55	21	3
Q15555 MARE2_HUMAN	Microtubule-associated protein RP/EB fam	114.43	29	3
P0CG34 TB15A_HUMAN	Thymosin beta-15A OS=Homo sapiens GN	113.57	36	3
P0CG35 TB15B_HUMAN	Thymosin beta-15B OS=Homo sapiens GN	113.57	36	3
Q9H0U4 RAB1B_HUMAN	Ras-related protein Rab-1B OS=Homo sap	113.53	31	3
Q92928 RAB1C_HUMAN	Putative Ras-related protein Rab-1C OS=H	113.53	30	3
P16422 EPCAM_HUMAN	Epithelial cell adhesion molecule OS=Homo	113.42	10	3
P46109 CRKL_HUMAN	Crk-like protein OS=Homo sapiens GN=CF	111.98	17	3
Q08431 MFGM_HUMAN	Lactadherin OS=Homo sapiens GN=MFGM	111.36	14	3
Q12874 SF3A3_HUMAN	Splicing factor 3A subunit 3 OS=Homo sap	110.95	13	3
Q961Z0 PAWR_HUMAN	PRKC apoptosis WT1 regulator protein OS	110.95	25	3
Q9Y6E2 BZW2_HUMAN	Basic leucine zipper and W2 domain-conta	110.32	16	3
O00764 PDXK_HUMAN	Pyridoxal kinase OS=Homo sapiens GN=F	110.13	23	3
P52888 THOP1_HUMAN	Thimet oligopeptidase OS=Homo sapiens	110.12	15	3
O75494 SRS10_HUMAN	Serine/arginine-rich splicing factor 10 OS=	109.44	30	3
P49589 SYCC_HUMAN	CysteinyI-tRNA synthetase, cytoplasmic O	108.74	12	3
O75340 PDCD6_HUMAN	Programmed cell death protein 6 OS=Homo	108.64	26	3
Q13451 FKBP5_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP5	108.23	13	3
Q01081 U2AF1_HUMAN	Splicing factor U2AF 35 kDa subunit OS=H	108.04	17	3
Q71UM5 RS27L_HUMAN	40S ribosomal protein S27-like OS=Homo	107.95	40	3
P54687 BCAT1_HUMAN	Branched-chain-amino-acid aminotransfer	107.36	18	3
P40925 MDHC_HUMAN	Malate dehydrogenase, cytoplasmic OS=H	106.84	24	3
Q9NV70 EXOC1_HUMAN	Exocyst complex component 1 OS=Homo	106.75	18	3
P62906 RL10A_HUMAN	60S ribosomal protein L10a OS=Homo sap	106.18	31	3
Q9H4M9 EHD1_HUMAN	EH domain-containing protein 1 OS=Homo	104.8	25	3
Q9NZL9 MAT2B_HUMAN	Methionine adenosyltransferase 2 subunit	104.76	24	3
P04179 SODM_HUMAN	Superoxide dismutase [Mn], mitochondrial	104.75	17	3
P09960 LKHA4_HUMAN	Leukotriene A-4 hydrolase OS=Homo sapi	104.56	9	3
Q15785 TOM34_HUMAN	Mitochondrial import receptor subunit TOM	104.54	24	3
P23919 KTHY_HUMAN	Thymidylate kinase OS=Homo sapiens GN	104.02	25	3
P42766 RL35_HUMAN	60S ribosomal protein L35 OS=Homo sapi	103.1	39	3
P52434 RPAB3_HUMAN	DNA-directed RNA polymerases I, II, and I	102.78	21	3
O75608 LYPA1_HUMAN	Acyl-protein thioesterase 1 OS=Homo sap	102.13	27	3
Q86U42 PABP2_HUMAN	Polyadenylate-binding protein 2 OS=Homo	102.09	22	3
Q14677 EPN4_HUMAN	Clathrin interactor 1 OS=Homo sapiens GN	102.05	17	3
Q9Y5Z4 HEBP2_HUMAN	Heme-binding protein 2 OS=Homo sapiens	101.95	20	3
Q96K17 BT3L4_HUMAN	Transcription factor BTF3 homolog 4 OS=H	101.61	36	3
Q9UMY4 SNX12_HUMAN	Sorting nexin-12 OS=Homo sapiens GN=S	101.15	40	3
P61201 CSN2_HUMAN	COP9 signalosome complex subunit 2 OS=	100.4	21	3
P58546 MTPN_HUMAN	Myotrophin OS=Homo sapiens GN=MTPN	100.02	25	3
O43805 SSNA1_HUMAN	Sjogren syndrome nuclear autoantigen 1	99.99	28	3
O60841 IF2P_HUMAN	Eukaryotic translation initiation factor 5B O	99.32	12	3
P49023 PAXI_HUMAN	Paxillin OS=Homo sapiens GN=PXN PE=1	98.54	14	3
Q9Y6Y8 S23IP_HUMAN	SEC23-interacting protein OS=Homo sapi	98.24	13	3

Q96CT7 CC124_HUMAN	Coiled-coil domain-containing protein 124	97.64	26	3
P51511 MMP15_HUMAN	Matrix metalloproteinase-15 OS=Homo sapiens	97.07	8	3
Q8NFU3 TSTD1_HUMAN	Thiosulfate sulfurtransferase/rhodanese-like	96.82	31	3
O75330 HMMR_HUMAN	Hyaluronan mediated motility receptor OS=	96.74	24	3
Q9Y2W1 TR150_HUMAN	Thyroid hormone receptor-associated protei	96.6	12	3
O75400 PR40A_HUMAN	Pre-mRNA-processing factor 40 homolog A	96.29	7	3
Q9H0S4 DDX47_HUMAN	Probable ATP-dependent RNA helicase D	96.18	25	3
P62861 RS30_HUMAN	40S ribosomal protein S30 OS=Homo sapi	96.07	34	3
Q5T6F2 UBAP2_HUMAN	Ubiquitin-associated protein 2 OS=Homo s	95.19	7	3
Q16186 ADRM1_HUMAN	Proteasomal ubiquitin receptor ADRM1 OS	95.01	11	3
P49902 5NTC_HUMAN	Cytosolic purine 5'-nucleotidase OS=Hom	94.73	15	3
P49721 PSB2_HUMAN	Proteasome subunit beta type-2 OS=Hom	94.17	19	3
P53367 ARFP1_HUMAN	Arfaptin-1 OS=Homo sapiens GN=ARFIP1	94.01	14	3
Q05086 UBE3A_HUMAN	Ubiquitin-protein ligase E3A OS=Homo sa	93.97	11	3
Q9H9A6 LRC40_HUMAN	Leucine-rich repeat-containing protein 40	93.81	10	3
O60869 EDF1_HUMAN	Endothelial differentiation-related factor 1	93.76	41	3
Q9UQ35 SRRM2_HUMAN	Serine/arginine repetitive matrix protein 2	93.59	11	3
Q15435 PP1R7_HUMAN	Protein phosphatase 1 regulatory subunit 7	93.13	23	3
P27694 RFA1_HUMAN	Replication protein A 70 kDa DNA-binding	93.02	15	3
P08579 RU2B_HUMAN	U2 small nuclear ribonucleoprotein B'' OS=	93.01	28	3
P38606 VATA_HUMAN	V-type proton ATPase catalytic subunit A	92.51	9	3
Q96TA1 NIBL1_HUMAN	Niban-like protein 1 OS=Homo sapiens GN	92.31	10	3
Q9NQP4 PFD4_HUMAN	Prefoldin subunit 4 OS=Homo sapiens GN	91.87	22	3
P49419 AL7A1_HUMAN	Alpha-aminoacidic semialdehyde dehydrog	91.7	11	3
Q8WVJ2 NUDC2_HUMAN	NudC domain-containing protein 2 OS=Ho	91.06	19	3
Q9BY32 ITPA_HUMAN	Inosine triphosphate pyrophosphatase OS	90.55	28	3
Q13895 BYST_HUMAN	Bystin OS=Homo sapiens GN=BYSL PE=	90.54	5	3
Q9NZD2 GLTP_HUMAN	Glycolipid transfer protein OS=Homo sapie	90.2	17	3
Q7L014 DDX46_HUMAN	Probable ATP-dependent RNA helicase D	90.09	11	3
Q14914 PTGR1_HUMAN	Prostaglandin reductase 1 OS=Homo sapi	89.81	16	3
P13489 RINI_HUMAN	Ribonuclease inhibitor OS=Homo sapiens	89.8	14	3
Q15393 SF3B3_HUMAN	Splicing factor 3B subunit 3 OS=Homo sa	89.75	7	3
Q8WW12 PCNP_HUMAN	PEST proteolytic signal-containing nuclear	89.66	15	3
Q8IXM3 RM41_HUMAN	39S ribosomal protein L41, mitochondrial	89.42	36	3
Q16527 CSR2_HUMAN	Cysteine and glycine-rich protein 2 OS=Ho	89.24	13	3
P20042 IF2B_HUMAN	Eukaryotic translation initiation factor 2 sub	88.58	25	3
A6NK07 IF2BL_HUMAN	Eukaryotic translation initiation factor 2 sub	88.58	20	3
Q99622 C10_HUMAN	Protein C10 OS=Homo sapiens GN=C10o	88.42	48	3
Q96RU2 UBP28_HUMAN	Ubiquitin carboxyl-terminal hydrolase 28 O	88.14	13	3
O15514 RPB4_HUMAN	DNA-directed RNA polymerase II subunit F	88.11	37	3
O60341 KDM1A_HUMAN	Lysine-specific histone demethylase 1A OS	88.07	11	3
Q8IX90 SKA3_HUMAN	Spindle and kinetochore-associated protei	87.95	10	3
P62266 RS23_HUMAN	40S ribosomal protein S23 OS=Homo sapi	87.56	23	3
O60716 CTND1_HUMAN	Catenin delta-1 OS=Homo sapiens GN=C	87.52	16	3
Q56VL3 OCAD2_HUMAN	OCIA domain-containing protein 2 OS=Ho	87.45	42	3
O75822 EIF3J_HUMAN	Eukaryotic translation initiation factor 3 sub	87.24	20	3
P18859 ATP5J_HUMAN	ATP synthase-coupling factor 6, mitochond	87.1	31	3

Q9Y5K6 CD2AP_HUMAN	CD2-associated protein OS=Homo sapiens	87.04	15	3
O60749 SNX2_HUMAN	Sorting nexin-2 OS=Homo sapiens GN=SN	86.95	13	3
Q92522 H1X_HUMAN	Histone H1x OS=Homo sapiens GN=H1FX	86.88	31	3
P49643 PRI2_HUMAN	DNA primase large subunit OS=Homo sap	86.84	9	3
Q16204 CCDC6_HUMAN	Coiled-coil domain-containing protein 6 OS	86.7	14	3
Q9UII2 ATIF1_HUMAN	ATPase inhibitor, mitochondrial OS=Homo	86.28	25	3
Q9BTE3 MCMBP_HUMAN	Mini-chromosome maintenance complex-b	86.04	9	3
Q8WUW1 BRK1_HUMAN	Protein BRICK1 OS=Homo sapiens GN=C	85.16	40	3
O00159 MYO1C_HUMAN	Myosin-Ic OS=Homo sapiens GN=MYO1C	84.93	6	3
Q96G03 PGM2_HUMAN	Phosphoglucomutase-2 OS=Homo sapien	84.79	17	3
O60306 AQR_HUMAN	Intron-binding protein aquarius OS=Homo	84.76	9	3
Q15642 CIP4_HUMAN	Cdc42-interacting protein 4 OS=Homo sap	84.55	14	3
O94760 DDAH1_HUMAN	N(G),N(G)-dimethylarginine dimethylamino	83.98	32	3
P11047 LAMC1_HUMAN	Laminin subunit gamma-1 OS=Homo sapie	83.87	6	3
O43264 ZW10_HUMAN	Centromere/kinetochore protein zw10 hom	83.24	12	3
Q9UMS4 PRP19_HUMAN	Pre-mRNA-processing factor 19 OS=Homo	82.92	10	3
Q8N6M0 OTU6B_HUMAN	OTU domain-containing protein 6B OS=Ho	82.7	25	3
Q15293 RCN1_HUMAN	Reticulocalbin-1 OS=Homo sapiens GN=R	82.62	16	3
Q92917 GPKOW_HUMAN	G patch domain and KOW motifs-containir	82.51	18	3
Q8NCW5 AIBP_HUMAN	Apolipoprotein A-I-binding protein OS=Hor	82.16	14	3
Q86XP3 DDX42_HUMAN	ATP-dependent RNA helicase DDX42 OS-	82.1	13	3
Q14008 CKAP5_HUMAN	Cytoskeleton-associated protein 5 OS=Ho	81.36	9	3
O14618 CCS_HUMAN	Copper chaperone for superoxide dismuta	80.6	25	3
O43865 SAHH2_HUMAN	Putative adenosylhomocysteinase 2 OS=H	79.39	16	3
P07311 ACYP1_HUMAN	Acylphosphatase-1 OS=Homo sapiens GN	78.94	35	3
Q9HB07 MYG1_HUMAN	UPF0160 protein MYG1, mitochondrial OS	78.78	12	3
Q15102 PA1B3_HUMAN	Platelet-activating factor acetylhydrolase I	77.77	11	3
Q52LJ0 FA98B_HUMAN	Protein FAM98B OS=Homo sapiens GN=F	77.62	12	3
O60832 DKC1_HUMAN	H/ACA ribonucleoprotein complex subunit	77.26	18	3
Q13868 EXOS2_HUMAN	Exosome complex component RRP4 OS=	77.13	30	3
Q14061 COX17_HUMAN	Cytochrome c oxidase copper chaperone C	77.09	75	3
Q9NQ48 LZTL1_HUMAN	Leucine zipper transcription factor-like prot	76.86	9	3
Q8IIV08 PLD3_HUMAN	Phospholipase D3 OS=Homo sapiens GN-	76.83	12	3
P09496 CLCA_HUMAN	Clathrin light chain A OS=Homo sapiens G	76.59	11	3
P10155 RO60_HUMAN	60 kDa SS-A/Ro ribonucleoprotein OS=Ho	74	12	3
P62330 ARF6_HUMAN	ADP-ribosylation factor 6 OS=Homo sapie	72.99	18	3
Q9Y3U8 RL36_HUMAN	60S ribosomal protein L36 OS=Homo sapi	72.72	29	3
O43237 DC1L2_HUMAN	Cytoplasmic dynein 1 light intermediate ch	72.09	9	3
Q9Y2Q9 RT28_HUMAN	28S ribosomal protein S28, mitochondrial C	71.69	31	3
P35237 SPB6_HUMAN	Serpin B6 OS=Homo sapiens GN=SERPIN	71.25	19	3
Q9BWJ5 SF3B5_HUMAN	Splicing factor 3B subunit 5 OS=Homo sap	71.1	41	3
O95239 KIF4A_HUMAN	Chromosome-associated kinesin KIF4A OS	70.97	6	3
P30419 NMT1_HUMAN	Glycylpeptide N-tetradecanoyltransferase	70.75	11	3
Q9Y3D9 RT23_HUMAN	28S ribosomal protein S23, mitochondrial C	70.5	17	3
Q7LBC6 KDM3B_HUMAN	Lysine-specific demethylase 3B OS=Homo	70.24	3	3
O00762 UBE2C_HUMAN	Ubiquitin-conjugating enzyme E2 C OS=Ho	69.93	36	3
Q14157 UBP2L_HUMAN	Ubiquitin-associated protein 2-like OS=Hor	69.67	8	3

Q92879 CELF1_HUMAN	CUGBP Elav-like family member 1 OS=Ho	68.9	8	3
Q9NQW7 XPP1_HUMAN	Xaa-Pro aminopeptidase 1 OS=Homo sap	68.7	9	3
Q5TFE4 NT5D1_HUMAN	5'-nucleotidase domain-containing protein	68.33	8	3
Q86V88 MGDP1_HUMAN	Magnesium-dependent phosphatase 1 OS	67.49	27	3
P07686 HEXB_HUMAN	Beta-hexosaminidase subunit beta OS=Ho	67.18	12	3
O94973 AP2A2_HUMAN	AP-2 complex subunit alpha-2 OS=Homo s	67.1	12	3
P62253 UB2G1_HUMAN	Ubiquitin-conjugating enzyme E2 G1 OS=H	66.99	11	3
P24752 THIL_HUMAN	Acetyl-CoA acetyltransferase, mitochondria	66.66	16	3
Q9Y4C1 KDM3A_HUMAN	Lysine-specific demethylase 3A OS=Homo	65.93	7	3
Q9C0C9 UBE2O_HUMAN	Ubiquitin-conjugating enzyme E2 O OS=Ho	64.65	11	3
P47985 UCRI_HUMAN	Cytochrome b-c1 complex subunit Rieske,	64.15	20	3
P0C7P4 UCRIL_HUMAN	Putative cytochrome b-c1 complex subunit	64.15	19	3
O00115 DNS2A_HUMAN	Deoxyribonuclease-2-alpha OS=Homo sap	63.14	9	3
P10253 LYAG_HUMAN	Lysosomal alpha-glucosidase OS=Homo s	62.42	8	3
P16083 NQO2_HUMAN	Ribosyldihyronicotinamide dehydrogenas	61.65	18	3
Q9UHD1 CHRD1_HUMAN	Cysteine and histidine-rich domain-contain	61.41	15	3
Q92485 ASM3B_HUMAN	Acid sphingomyelinase-like phosphodieste	60.83	9	3
Q6DKJ4 NXN_HUMAN	Nucleoredoxin OS=Homo sapiens GN=NX	60.58	13	3
Q8NE71 ABCF1_HUMAN	ATP-binding cassette sub-family F membe	56.4	8	3
Q9HAV7 GRPE1_HUMAN	GrpE protein homolog 1, mitochondrial OS	56.04	28	3
Q9H1B7 I2BPL_HUMAN	Interferon regulatory factor 2-binding prote	54.33	11	3
Q01970 PLCB3_HUMAN	1-phosphatidylinositol-4,5-bisphosphate ph	46.82	5	3
P36406 TRI23_HUMAN	E3 ubiquitin-protein ligase TRIM23 OS=Ho	42.95	13	3
Q5U5R9 HECD2_HUMAN	Probable E3 ubiquitin-protein ligase HECT	40.01	5	3
P25391 LAMA1_HUMAN	Laminin subunit alpha-1 OS=Homo sapien	35.67	5	3
P68371 TBB2C_HUMAN	Tubulin beta-2C chain OS=Homo sapiens	424.6	82	2
P63261 ACTG_HUMAN	Actin, cytoplasmic 2 OS=Homo sapiens GI	415.2	86	2
Q9BVA1 TBB2B_HUMAN	Tubulin beta-2B chain OS=Homo sapiens	407.9	80	2
P04350 TBB4_HUMAN	Tubulin beta-4 chain OS=Homo sapiens G	389.06	76	2
Q9BQE3 TBA1C_HUMAN	Tubulin alpha-1C chain OS=Homo sapiens	327.76	74	2
P62979 RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a OS=	291.21	63	2
P0CG48 UBC_HUMAN	Polyubiquitin-C OS=Homo sapiens GN=UE	279.3	75	2
P0CG47 UBB_HUMAN	Polyubiquitin-B OS=Homo sapiens GN=UE	279.3	93	2
P35749 MYH11_HUMAN	Myosin-11 OS=Homo sapiens GN=MYH11	207.27	34	2
Q8TAA3 PSA7L_HUMAN	Proteasome subunit alpha type-7-like OS=	205.77	54	2
Q13310 PABP4_HUMAN	Polyadenylate-binding protein 4 OS=Homo	201.17	41	2
P68431 H31_HUMAN	Histone H3.1 OS=Homo sapiens GN=HIS	182.91	72	2
Q71DI3 H32_HUMAN	Histone H3.2 OS=Homo sapiens GN=HIS	182.91	72	2
P13929 ENOB_HUMAN	Beta-enolase OS=Homo sapiens GN=ENC	176.46	51	2
P56545 CTBP2_HUMAN	C-terminal-binding protein 2 OS=Homo sap	174.47	37	2
Q13162 PRDX4_HUMAN	Peroxiredoxin-4 OS=Homo sapiens GN=P	157.8	25	2
P63167 DYL1_HUMAN	Dynein light chain 1, cytoplasmic OS=Hom	157.64	61	2
O75610 LFTY1_HUMAN	Left-right determination factor 1 OS=Homo	157.28	31	2
Q13363 CTBP1_HUMAN	C-terminal-binding protein 1 OS=Homo sap	153.58	32	2
Q96FJ2 DYL2_HUMAN	Dynein light chain 2, cytoplasmic OS=Hom	152.48	40	2
O43390 HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein	147.99	24	2
P52597 HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein	136.85	27	2

Q15436 SC23A_HUMAN	Protein transport protein Sec23A OS=Hom	133.71	12	2
P38919 IF4A3_HUMAN	Eukaryotic initiation factor 4A-III OS=Hom	132.82	26	2
Q13404 UB2V1_HUMAN	Ubiquitin-conjugating enzyme E2 variant 1	130.6	50	2
Q96FW1 OTUB1_HUMAN	Ubiquitin thioesterase OTUB1 OS=Homo s	127.92	17	2
P18085 ARF4_HUMAN	ADP-ribosylation factor 4 OS=Homo sapie	127.46	48	2
O60282 KIF5C_HUMAN	Kinesin heavy chain isoform 5C OS=Hom	125.8	14	2
P46778 RL21_HUMAN	60S ribosomal protein L21 OS=Homo sapi	125.05	35	2
Q15819 UB2V2_HUMAN	Ubiquitin-conjugating enzyme E2 variant 2	124.61	44	2
Q9ULZ3 ASC_HUMAN	Apoptosis-associated speck-like protein co	124.37	32	2
P04899 GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) su	121.44	24	2
P61160 ARP2_HUMAN	Actin-related protein 2 OS=Homo sapiens	121.32	14	2
Q9Y6E0 STK24_HUMAN	Serine/threonine-protein kinase 24 OS=Ho	119.76	26	2
Q96C90 PP14B_HUMAN	Protein phosphatase 1 regulatory subunit 1	118.44	48	2
Q13155 AIMP2_HUMAN	Aminoacyl tRNA synthase complex-interac	116.73	33	2
Q9UHY1 NRBP_HUMAN	Nuclear receptor-binding protein OS=Hom	113.38	14	2
P62910 RL32_HUMAN	60S ribosomal protein L32 OS=Homo sapi	111.91	24	2
P61077 UB2D3_HUMAN	Ubiquitin-conjugating enzyme E2 D3 OS=H	109.06	35	2
Q9P287 BCCIP_HUMAN	BRCA2 and CDKN1A-interacting protein C	108.56	17	2
Q9BSD7 NTPCR_HUMAN	Cancer-related nucleoside-triphosphatase	108.32	45	2
Q9UJQ4 SALL4_HUMAN	Sal-like protein 4 OS=Homo sapiens GN=s	106.89	21	2
O14579 COPE_HUMAN	Coatomer subunit epsilon OS=Homo sapie	105.69	23	2
P09234 RU1C_HUMAN	U1 small nuclear ribonucleoprotein C OS=	105.67	19	2
P68402 PA1B2_HUMAN	Platelet-activating factor acetylhydrolase IB	104.35	17	2
P48739 PIPNB_HUMAN	Phosphatidylinositol transfer protein beta is	102.3	22	2
Q96IX5 USMG5_HUMAN	Up-regulated during skeletal muscle growth	101.49	45	2
Q9H6R4 NOL6_HUMAN	Nucleolar protein 6 OS=Homo sapiens GN	101.44	6	2
O43598 RCL_HUMAN	Deoxyribonucleoside 5'-monophosphate N	101.42	26	2
Q9BRG1 VPS25_HUMAN	Vacuolar protein-sorting-associated protei	101.28	14	2
Q8WXF1 PSPC1_HUMAN	Paraspeckle component 1 OS=Homo sapi	99.71	22	2
P67775 PP2AA_HUMAN	Serine/threonine-protein phosphatase 2A c	99.63	16	2
Q07021 C1QBP_HUMAN	Complement component 1 Q subcompone	98.8	15	2
Q99567 NUP88_HUMAN	Nuclear pore complex protein Nup88 OS=	98.75	14	2
Q13177 PAK2_HUMAN	Serine/threonine-protein kinase PAK 2 OS	97.58	21	2
Q92922 SMRC1_HUMAN	SWI/SNF complex subunit SMARCC1 OS=	97.06	8	2
Q8NBT2 SPC24_HUMAN	Kinetochore protein Spc24 OS=Homo sap	96.91	24	2
P15954 COX7C_HUMAN	Cytochrome c oxidase subunit 7C, mitoch	96.87	52	2
Q9BPX5 ARP5L_HUMAN	Actin-related protein 2/3 complex subunit 5	96.72	27	2
P47755 CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 OS	96.54	20	2
Q9UIL1 SCOC_HUMAN	Short coiled-coil protein OS=Homo sapiens	96.47	32	2
P63151 2ABA_HUMAN	Serine/threonine-protein phosphatase 2A s	95.89	24	2
Q5JWF2 GNAS1_HUMAN	Guanine nucleotide-binding protein G(s) su	95.78	9	2
Q9UJZ1 STML2_HUMAN	Stomatin-like protein 2 OS=Homo sapiens	94.74	23	2
O95989 NUDT3_HUMAN	Diphosphoinositol polyphosphate phospho	94.72	18	2
Q12904 AIMP1_HUMAN	Aminoacyl tRNA synthase complex-interac	94.7	15	2
Q8IUD2 RB6I2_HUMAN	ELKS/Rab6-interacting/CAST family mem	94.12	20	2
P04632 CPNS1_HUMAN	Calpain small subunit 1 OS=Homo sapiens	93.86	18	2
Q14766 LTBP1_HUMAN	Latent-transforming growth factor beta-bin	93.84	6	2

Q15631 TSN_HUMAN	Translin OS=Homo sapiens GN=TSN PE=	93.49	25	2
Q15397 K0020_HUMAN	Pumilio domain-containing protein KIAA00	93.09	18	2
Q3KQU3 MA7D1_HUMAN	MAP7 domain-containing protein 1 OS=Ho	92.59	15	2
Q8TEA8 DTD1_HUMAN	D-tyrosyl-tRNA(Tyr) deacylase 1 OS=Hom	90.6	25	2
P60953 CDC42_HUMAN	Cell division control protein 42 homolog OS	90.45	28	2
Q9UBI6 GBG12_HUMAN	Guanine nucleotide-binding protein G(I)/G	90.45	36	2
Q9Y263 PLAP_HUMAN	Phospholipase A-2-activating protein OS=	90.34	11	2
O75934 SPF27_HUMAN	Pre-mRNA-splicing factor SPF27 OS=Hom	89.59	18	2
P08195 4F2_HUMAN	4F2 cell-surface antigen heavy chain OS=	89.5	8	2
P50281 MMP14_HUMAN	Matrix metalloproteinase-14 OS=Homo sap	89.06	10	2
P68400 CSK21_HUMAN	Casein kinase II subunit alpha OS=Homo s	88.78	19	2
Q02952 AKA12_HUMAN	A-kinase anchor protein 12 OS=Homo sap	88.6	11	2
O15042 SR140_HUMAN	U2 snRNP-associated SURP motif-contain	87.91	11	2
Q8NDC0 MISSL_HUMAN	MAPK-interacting and spindle-stabilizing p	87.78	12	2
P07919 QCR6_HUMAN	Cytochrome b-c1 complex subunit 6, mitoc	87.64	27	2
O00499 BIN1_HUMAN	Myc box-dependent-interacting protein 1 C	87.42	24	2
Q5TAP6 UT14C_HUMAN	U3 small nucleolar RNA-associated proteir	87.38	10	2
Q15276 RABE1_HUMAN	Rab GTPase-binding effector protein 1 OS	86.97	9	2
Q04323 UBXN1_HUMAN	UBX domain-containing protein 1 OS=Hon	86.92	16	2
Q9NV35 NUD15_HUMAN	Probable 7,8-dihydro-8-oxoguanine triphos	86.9	13	2
O75152 ZC11A_HUMAN	Zinc finger CCCH domain-containing prote	86.73	10	2
Q9Y5A9 YTHD2_HUMAN	YTH domain family protein 2 OS=Homo sa	86.69	8	2
O75391 SPAG7_HUMAN	Sperm-associated antigen 7 OS=Homo sa	86.47	27	2
P09012 SNRPA_HUMAN	U1 small nuclear ribonucleoprotein A OS=	86.26	11	2
P42574 CASP3_HUMAN	Caspase-3 OS=Homo sapiens GN=CASP3	85.84	18	2
Q13011 ECH1_HUMAN	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomera	85.79	15	2
P00568 KAD1_HUMAN	Adenylate kinase isoenzyme 1 OS=Homo	85.73	13	2
Q9Y520 PRC2C_HUMAN	Protein PRRC2C OS=Homo sapiens GN=	85.45	7	2
Q9NR19 ACSA_HUMAN	Acetyl-coenzyme A synthetase, cytoplasm	85.41	7	2
P21291 CSR1_HUMAN	Cysteine and glycine-rich protein 1 OS=Ho	85.25	25	2
O60258 FGF17_HUMAN	Fibroblast growth factor 17 OS=Homo sap	85.07	21	2
O75390 CISY_HUMAN	Citrate synthase, mitochondrial OS=Homo	84.95	14	2
Q9NR28 DBLOH_HUMAN	Diablo homolog, mitochondrial OS=Homo s	84.46	13	2
Q7Z2W4 ZCCHV_HUMAN	Zinc finger CCCH-type antiviral protein 1 C	83.81	4	2
Q9BUJ2 HNRL1_HUMAN	Heterogeneous nuclear ribonucleoprotein	83.64	7	2
Q969V3 NCLN_HUMAN	Nicalin OS=Homo sapiens GN=NCLN PE=	83.57	13	2
Q14181 DPOA2_HUMAN	DNA polymerase alpha subunit B OS=Hon	83.52	9	2
Q13148 TADBP_HUMAN	TAR DNA-binding protein 43 OS=Homo sa	82.87	14	2
Q9UBT2 SAE2_HUMAN	SUMO-activating enzyme subunit 2 OS=Ho	82.82	14	2
O95218 ZRAB2_HUMAN	Zinc finger Ran-binding domain-containing	82.24	13	2
Q5SSJ5 HP1B3_HUMAN	Heterochromatin protein 1-binding protein	82.15	18	2
P09132 SRP19_HUMAN	Signal recognition particle 19 kDa protein C	81.87	32	2
Q9NRF8 PYRG2_HUMAN	CTP synthase 2 OS=Homo sapiens GN=C	81.59	8	2
Q9Y3E1 HDGR3_HUMAN	Hepatoma-derived growth factor-related pr	81.54	18	2
O00233 PSMD9_HUMAN	26S proteasome non-ATPase regulatory s	81.3	13	2
P00390 GSHR_HUMAN	Glutathione reductase, mitochondrial OS=	81.01	14	2
P62875 RPAB5_HUMAN	DNA-directed RNA polymerases I, II, and I	80.88	30	2



P61956 SUMO2_HUMAN	Small ubiquitin-related modifier 2 OS=Homo sapiens	80.85	43	2
Q9UJC3 HOOK1_HUMAN	Protein Hook homolog 1 OS=Homo sapiens	80.74	8	2
Q9NVA2 SEP11_HUMAN	Septin-11 OS=Homo sapiens GN=SEPT11	80.42	13	2
Q15007 FL2D_HUMAN	Pre-mRNA-splicing regulator WTAP OS=Homo sapiens	80.32	18	2
O43290 SNUT1_HUMAN	U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens	80.28	15	2
P41227 NAA10_HUMAN	N-alpha-acetyltransferase 10, NatA catalytic subunit OS=Homo sapiens	80.28	21	2
Q15126 PMVK_HUMAN	Phosphomevalonate kinase OS=Homo sapiens	80.19	20	2
A6NIZ1 RP1BL_HUMAN	Ras-related protein Rap-1b-like protein OS=Homo sapiens	79.86	22	2
P61224 RAP1B_HUMAN	Ras-related protein Rap-1b OS=Homo sapiens	79.86	17	2
P62834 RAP1A_HUMAN	Ras-related protein Rap-1A OS=Homo sapiens	79.86	8	2
P56134 ATPK_HUMAN	ATP synthase subunit f, mitochondrial OS=Homo sapiens	79.85	26	2
Q7Z739 YTHD3_HUMAN	YTH domain family protein 3 OS=Homo sapiens	79.7	7	2
Q9UBW8 CSN7A_HUMAN	COP9 signalosome complex subunit 7a OS=Homo sapiens	79.56	17	2
P51571 SSRD_HUMAN	Translocon-associated protein subunit delta OS=Homo sapiens	79.5	23	2
Q15363 TMED2_HUMAN	Transmembrane emp24 domain-containing protein 2 OS=Homo sapiens	79.08	9	2
Q9P210 CPSF2_HUMAN	Cleavage and polyadenylation specificity factor 2 OS=Homo sapiens	79	13	2
Q9H3R5 CENPH_HUMAN	Centromere protein H OS=Homo sapiens	78.83	17	2
O95793 STAU1_HUMAN	Double-stranded RNA-binding protein Staufen 1 OS=Homo sapiens	78.65	6	2
Q93034 CUL5_HUMAN	Cullin-5 OS=Homo sapiens GN=CUL5 PE=1	78.64	12	2
Q13464 ROCK1_HUMAN	Rho-associated protein kinase 1 OS=Homo sapiens	77.86	5	2
Q16706 MA2A1_HUMAN	Alpha-mannosidase 2 OS=Homo sapiens	77.77	4	2
Q14738 2A5D_HUMAN	Serine/threonine-protein phosphatase 2A subunit delta OS=Homo sapiens	77.77	11	2
P55263 ADK_HUMAN	Adenosine kinase OS=Homo sapiens GN=ADK	77.29	9	2
P18065 IBP2_HUMAN	Insulin-like growth factor-binding protein 2 OS=Homo sapiens	77.23	27	2
P62310 LSM3_HUMAN	U6 snRNA-associated Sm-like protein LSM3 OS=Homo sapiens	77.04	34	2
O60885 BRD4_HUMAN	Bromodomain-containing protein 4 OS=Homo sapiens	76.79	9	2
P55039 DRG2_HUMAN	Developmentally-regulated GTP-binding protein 2 OS=Homo sapiens	76.74	20	2
P31483 TIA1_HUMAN	Nucleolysin TIA-1 isoform p40 OS=Homo sapiens	76.61	9	2
Q9P0K7 RAI14_HUMAN	Ankycorbin OS=Homo sapiens GN=RAI14	76.54	9	2
Q9NQG5 RPR1B_HUMAN	Regulation of nuclear pre-mRNA domain-containing protein 1 OS=Homo sapiens	76.47	23	2
O75190 DNJB6_HUMAN	DnaJ homolog subfamily B member 6 OS=Homo sapiens	76.03	8	2
Q86YP4 P66A_HUMAN	Transcriptional repressor p66-alpha OS=Homo sapiens	75.65	12	2
P67870 CSK2B_HUMAN	Casein kinase II subunit beta OS=Homo sapiens	75.58	13	2
Q9H223 EHD4_HUMAN	EH domain-containing protein 4 OS=Homo sapiens	75.44	9	2
Q9UJC5 SH3L2_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 2 OS=Homo sapiens	75.06	25	2
O60346 PHLP1_HUMAN	PH domain leucine-rich repeat-containing protein 1 OS=Homo sapiens	74.43	9	2
Q9NR45 SIAS_HUMAN	Sialic acid synthase OS=Homo sapiens GN=SIAS	74.15	15	2
Q9BV57 MTND_HUMAN	1,2-dihydroxy-3-keto-5-methylthiopentene-2-lyase OS=Homo sapiens	74.05	15	2
Q9NUP9 LIN7C_HUMAN	Protein lin-7 homolog C OS=Homo sapiens	74.02	36	2
O43678 NDUA2_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subunit OS=Homo sapiens	73.91	32	2
P60510 PP4C_HUMAN	Serine/threonine-protein phosphatase 4 catalytic subunit OS=Homo sapiens	73.7	16	2
Q01780 EXOSX_HUMAN	Exosome component 10 OS=Homo sapiens	73.54	6	2
Q9Y5S9 RBM8A_HUMAN	RNA-binding protein 8A OS=Homo sapiens	72.87	25	2
Q12765 SCRN1_HUMAN	Secernin-1 OS=Homo sapiens GN=SCRN1	72.58	7	2
Q9UNF1 MAGD2_HUMAN	Melanoma-associated antigen D2 OS=Homo sapiens	72.46	11	2
Q00796 DHSO_HUMAN	Sorbitol dehydrogenase OS=Homo sapiens	72.11	15	2
Q99829 CPNE1_HUMAN	Copine-1 OS=Homo sapiens GN=CPNE1	71.96	12	2

Q95456 PSMG1_HUMAN	Proteasome assembly chaperone 1 OS=H	71.94	20	2
P30837 AL1B1_HUMAN	Aldehyde dehydrogenase X, mitochondrial	71.86	7	2
Q08257 QOR_HUMAN	Quinone oxidoreductase OS=Homo sapien	71.79	17	2
Q9NQ88 TIGAR_HUMAN	Probable fructose-2,6-bisphosphatase TIG	71.65	7	2
Q9HCD5 NCOA5_HUMAN	Nuclear receptor coactivator 5 OS=Homo s	71.43	7	2
Q9C0C2 TB182_HUMAN	182 kDa tankyrase-1-binding protein OS=H	71.43	9	2
Q96QK1 VPS35_HUMAN	Vacuolar protein sorting-associated protei	71.43	10	2
O60613 SEP15_HUMAN	15 kDa selenoprotein OS=Homo sapiens C	71.28	23	2
O00754 MA2B1_HUMAN	Lysosomal alpha-mannosidase OS=Homo	70.84	4	2
O75937 DNJC8_HUMAN	DnaJ homolog subfamily C member 8 OS=	70.81	20	2
Q13867 BLMH_HUMAN	Bleomycin hydrolase OS=Homo sapiens G	70.58	15	2
Q92979 NEP1_HUMAN	Ribosomal RNA small subunit methyltransf	70.53	17	2
P22307 NLTP_HUMAN	Non-specific lipid-transfer protein OS=Horr	69.7	9	2
Q16718 NDUA5_HUMAN	NADH dehydrogenase [ubiquinone] 1 alph	69.22	38	2
P55036 PSMD4_HUMAN	26S proteasome non-ATPase regulatory s	69.05	15	2
Q71RC2 LARP4_HUMAN	La-related protein 4 OS=Homo sapiens GN	68.92	5	2
Q9Y6M9 NDUB9_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta	68.86	13	2
Q9BW83 IFT27_HUMAN	Intraflagellar transport protein 27 homolog	68.69	13	2
Q99661 KIF2C_HUMAN	Kinesin-like protein KIF2C OS=Homo sapi	68.2	6	2
Q02818 NUCB1_HUMAN	Nucleobindin-1 OS=Homo sapiens GN=NU	68.14	13	2
P52292 IMA2_HUMAN	Importin subunit alpha-2 OS=Homo sapien	67.93	8	2
Q9NUQ6 SPS2L_HUMAN	SPATS2-like protein OS=Homo sapiens G	67.55	6	2
Q9H4A6 GOLP3_HUMAN	Golgi phosphoprotein 3 OS=Homo sapiens	67.46	13	2
Q9UHX1 PUF60_HUMAN	Poly(U)-binding-splicing factor PUF60 OS=	67.43	24	2
Q9H074 PAIP1_HUMAN	Polyadenylate-binding protein-interacting p	67.38	10	2
Q9ULV4 COR1C_HUMAN	Coronin-1C OS=Homo sapiens GN=CORC	67.35	12	2
O00471 EXOC5_HUMAN	Exocyst complex component 5 OS=Homo	67.21	3	2
Q9NPJ6 MED4_HUMAN	Mediator of RNA polymerase II transcrip	67.18	22	2
Q14155 ARHG7_HUMAN	Rho guanine nucleotide exchange factor 7	67.04	9	2
P42704 LPPRC_HUMAN	Leucine-rich PPR motif-containing protein,	67	10	2
O95232 LC7L3_HUMAN	Luc7-like protein 3 OS=Homo sapiens GN=	66.75	8	2
Q9NR31 SAR1A_HUMAN	GTP-binding protein SAR1a OS=Homo sa	66.74	21	2
Q9Y6B6 SAR1B_HUMAN	GTP-binding protein SAR1b OS=Homo sa	66.74	17	2
Q13596 SNX1_HUMAN	Sorting nexin-1 OS=Homo sapiens GN=SN	66.53	11	2
Q96MW1 CCD43_HUMAN	Coiled-coil domain-containing protein 43 C	66.27	18	2
Q9Y2R0 CCD56_HUMAN	Coiled-coil domain-containing protein 56 C	65.91	21	2
Q9P0V9 SEP10_HUMAN	Septin-10 OS=Homo sapiens GN=SEPT10	65.67	7	2
Q8WVB6 CTF18_HUMAN	Chromosome transmission fidelity protein	65.6	8	2
P12955 PEPD_HUMAN	Xaa-Pro dipeptidase OS=Homo sapiens G	65.51	4	2
Q12849 GRSF1_HUMAN	G-rich sequence factor 1 OS=Homo sapien	65.37	13	2
Q13492 PICAL_HUMAN	Phosphatidylinositol-binding clathrin assem	65.24	10	2
Q96C01 F136A_HUMAN	Protein FAM136A OS=Homo sapiens GN=	64.59	14	2
Q9BU89 DOHH_HUMAN	Deoxyhypusine hydroxylase OS=Homo sa	64.54	14	2
Q9NX63 CHCH3_HUMAN	Coiled-coil-helix-coiled-coil-helix domain-co	64.42	21	2
O14929 HAT1_HUMAN	Histone acetyltransferase type B catalytic s	64.35	13	2
Q03426 KIME_HUMAN	Mevalonate kinase OS=Homo sapiens GN	64.12	7	2
P08473 NEP_HUMAN	Neprilysin OS=Homo sapiens GN=MME P	64.01	3	2

Q15750 TAB1_HUMAN	TGF-beta-activated kinase 1 and MAP3K7	63.83	7	2
P62070 RRAS2_HUMAN	Ras-related protein R-Ras2 OS=Homo sap	63.79	18	2
P61960 UFM1_HUMAN	Ubiquitin-fold modifier 1 OS=Homo sapien	63.63	35	2
P49755 TMEDA_HUMAN	Transmembrane emp24 domain-containing	63.6	13	2
Q12841 FSTL1_HUMAN	Follistatin-related protein 1 OS=Homo sapi	63.48	7	2
Q13153 PAK1_HUMAN	Serine/threonine-protein kinase PAK 1 OS	63.03	14	2
Q08379 GOGA2_HUMAN	Golgin subfamily A member 2 OS=Homo s	62.85	6	2
Q13564 JLA1_HUMAN	NEDD8-activating enzyme E1 regulatory s	62.68	6	2
P19525 E2AK2_HUMAN	Interferon-induced, double-stranded RNA-	62.6	5	2
P54886 P5CS_HUMAN	Delta-1-pyrroline-5-carboxylate synthase C	62.58	9	2
Q9NX40 OCAD1_HUMAN	OCIA domain-containing protein 1 OS=Ho	61.98	11	2
Q8N983 RM43_HUMAN	39S ribosomal protein L43, mitochondrial C	61.98	20	2
P32322 P5CR1_HUMAN	Pyrroline-5-carboxylate reductase 1, mitoc	61.29	14	2
P51003 PAPOA_HUMAN	Poly(A) polymerase alpha OS=Homo sapie	60.84	7	2
Q9NRJ5 PAPOB_HUMAN	Poly(A) polymerase beta OS=Homo sapier	60.84	6	2
Q07960 RHG01_HUMAN	Rho GTPase-activating protein 1 OS=Hom	60.52	12	2
Q13428 TCOF_HUMAN	Treacle protein OS=Homo sapiens GN=TC	60.45	7	2
Q8I283 A16A1_HUMAN	Aldehyde dehydrogenase family 16 membe	60.3	8	2
P56537 IF6_HUMAN	Eukaryotic translation initiation factor 6 OS	60.12	18	2
P21281 VATB2_HUMAN	V-type proton ATPase subunit B, brain iso	59.64	12	2
Q96P48 ARAP1_HUMAN	Arf-GAP with Rho-GAP domain, ANK repe	59.42	6	2
Q9NX58 LYAR_HUMAN	Cell growth-regulating nucleolar protein OS	59.29	13	2
O00217 NDUS8_HUMAN	NADH dehydrogenase [ubiquinone] iron-su	58.56	13	2
P46060 RAGP1_HUMAN	Ran GTPase-activating protein 1 OS=Hom	58.21	16	2
Q9BXF3 CECR2_HUMAN	Cat eye syndrome critical region protein 2	58	5	2
A6NHR9 SMHD1_HUMAN	Structural maintenance of chromosomes fl	57.73	5	2
Q96RE7 NACC1_HUMAN	Nucleus accumbens-associated protein 1 C	57.73	7	2
Q9BRP1 PDD2L_HUMAN	Programmed cell death protein 2-like OS=	57.11	12	2
Q14498 RBM39_HUMAN	RNA-binding protein 39 OS=Homo sapiens	56.94	6	2
Q05519 SRS11_HUMAN	Serine/arginine-rich splicing factor 11 OS=	56.7	15	2
P19404 NDUV2_HUMAN	NADH dehydrogenase [ubiquinone] flavop	56.23	17	2
O75251 NDUS7_HUMAN	NADH dehydrogenase [ubiquinone] iron-su	56.15	8	2
Q9BZL1 UBL5_HUMAN	Ubiquitin-like protein 5 OS=Homo sapiens	55.86	25	2
Q00059 TFAM_HUMAN	Transcription factor A, mitochondrial OS=H	55.73	16	2
P35612 ADDB_HUMAN	Beta-adducin OS=Homo sapiens GN=ADD	54.77	15	2
Q9Y5K5 UCHL5_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozy	54.46	8	2
Q9UPT5 EXOC7_HUMAN	Exocyst complex component 7 OS=Homo	54.28	4	2
P19387 RPB3_HUMAN	DNA-directed RNA polymerase II subunit F	54.09	12	2
P60468 SC61B_HUMAN	Protein transport protein Sec61 subunit be	53.55	36	2
O00479 HMGN4_HUMAN	High mobility group nucleosome-binding d	53.51	33	2
P45880 VDAC2_HUMAN	Voltage-dependent anion-selective channe	53.49	7	2
Q9UHY7 ENOPH_HUMAN	Enolase-phosphatase E1 OS=Homo sapie	53.36	13	2
P46939 UTRO_HUMAN	Utrophin OS=Homo sapiens GN=UTRN P	53.05	4	2
Q86X76 NIT1_HUMAN	Nitrilase homolog 1 OS=Homo sapiens GN	52.26	14	2
Q92520 FAM3C_HUMAN	Protein FAM3C OS=Homo sapiens GN=F/	51.99	15	2
P21912 DHSD_HUMAN	Succinate dehydrogenase [ubiquinone] iro	51.74	7	2
P20936 RASA1_HUMAN	Ras GTPase-activating protein 1 OS=Hom	51.56	4	2

Q9H3S7 PTN23_HUMAN	Tyrosine-protein phosphatase non-recepto	51.35	5	2
P52732 KIF11_HUMAN	Kinesin-like protein KIF11 OS=Homo sapien	51.09	4	2
Q9H4B8 DPEP3_HUMAN	Dipeptidase 3 OS=Homo sapiens GN=DPEP3	50.87	7	2
Q9N9Y1 CHCH8_HUMAN	Coiled-coil-helix-coiled-coil-helix domain-co	50.55	48	2
Q15545 TAF7_HUMAN	Transcription initiation factor TFIID subunit	50.54	9	2
P35968 VGFR2_HUMAN	Vascular endothelial growth factor recepto	50.16	3	2
Q96A26 F162A_HUMAN	Protein FAM162A OS=Homo sapiens GN=FAM162A	49.71	20	2
P61513 RL37A_HUMAN	60S ribosomal protein L37a OS=Homo sapien	49.06	39	2
Q9Y530 CF130_HUMAN	Uncharacterized protein C6orf130 OS=Homo	48.84	21	2
Q14690 RRP5_HUMAN	Protein RRP5 homolog OS=Homo sapiens GN=RRP5	48.67	3	2
Q9UIJ7 KAD3_HUMAN	GTP:AMP phosphotransferase, mitochond	48.44	19	2
Q9Y2W2 WBP11_HUMAN	WW domain-binding protein 11 OS=Homo	48.14	4	2
Q7L4E1 FA73B_HUMAN	Protein FAM73B OS=Homo sapiens GN=FAM73B	47.7	5	2
Q13416 ORC2_HUMAN	Origin recognition complex subunit 2 OS=H	47.54	7	2
Q15388 TOM20_HUMAN	Mitochondrial import receptor subunit TOM	47.43	24	2
P49792 RBP2_HUMAN	E3 SUMO-protein ligase RanBP2 OS=Homo	47.42	6	2
P20585 MSH3_HUMAN	DNA mismatch repair protein Msh3 OS=Homo	47.22	10	2
O94906 PRP6_HUMAN	Pre-mRNA-processing factor 6 OS=Homo	47.09	8	2
P46013 KI67_HUMAN	Antigen KI-67 OS=Homo sapiens GN=MKI67	46.36	5	2
O15144 ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2	46.29	22	2
P46821 MAP1B_HUMAN	Microtubule-associated protein 1B OS=Homo	45.98	3	2
Q9Y6A5 TACC3_HUMAN	Transforming acidic coiled-coil-containing p	45.75	6	2
Q9UPG8 PLAL2_HUMAN	Zinc finger protein PLAGL2 OS=Homo sapien	45.47	3	2
Q9UK45 LSM7_HUMAN	U6 snRNA-associated Sm-like protein LSMD	44.9	22	2
Q9Y2R5 RT17_HUMAN	28S ribosomal protein S17, mitochondrial	44.81	20	2
P43490 NAMPT_HUMAN	Nicotinamide phosphoribosyltransferase O	43.41	12	2
Q9NY12 GAR1_HUMAN	H/ACA ribonucleoprotein complex subunit	42.8	20	2
Q9Y4F1 FARP1_HUMAN	FERM, RhoGEF and pleckstrin domain-co	42.61	5	2
P49207 RL34_HUMAN	60S ribosomal protein L34 OS=Homo sapien	42.29	13	2
Q9P2P6 STAR9_HUMAN	StAR-related lipid transfer protein 9 OS=H	42.21	4	2
O95139 NDUB6_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta	41.56	21	2
O00562 PITM1_HUMAN	Membrane-associated phosphatidylinositol	41.45	5	2
O75155 CAND2_HUMAN	Cullin-associated NEDD8-dissociated prote	41	7	2
P82933 RT09_HUMAN	28S ribosomal protein S9, mitochondrial	39.74	8	2
A8MVX0 ARG33_HUMAN	Rho guanine nucleotide exchange factor 3	39.66	7	2
P60891 PRPS1_HUMAN	Ribose-phosphate pyrophosphokinase 1 C	38.75	9	2
P11908 PRPS2_HUMAN	Ribose-phosphate pyrophosphokinase 2 C	38.75	9	2
P20929 NEBU_HUMAN	Nebulin OS=Homo sapiens GN=NEB PE=	38.67	2	2
Q8NHP8 PLBL2_HUMAN	Putative phospholipase B-like 2 OS=Homo	38.66	13	2
P61599 NAA20_HUMAN	N-alpha-acetyltransferase 20, NatB catalyt	38.53	20	2
Q9Y618 NCOR2_HUMAN	Nuclear receptor corepressor 2 OS=Homo	38.36	3	2
Q8NF91 SYNE1_HUMAN	Nesprin-1 OS=Homo sapiens GN=SYNE1	38.27	6	2
Q92833 JARD2_HUMAN	Protein Jumonji OS=Homo sapiens GN=JARD2	37.86	7	2
P20930 FILA_HUMAN	Filaggrin OS=Homo sapiens GN=FLG PE=	37.59	2	2
Q6Q759 SPG17_HUMAN	Sperm-associated antigen 17 OS=Homo sapien	37.51	3	2
Q0VF96 CGNL1_HUMAN	Cingulin-like protein 1 OS=Homo sapiens	37.38	8	2
Q99541 PLIN2_HUMAN	Perilipin-2 OS=Homo sapiens GN=PLIN2	36.46	14	2

Q81WZ3 ANKH1_HUMAN	Ankyrin repeat and KH domain-containing	36.02	5	2
Q9NRV9 HEBP1_HUMAN	Heme-binding protein 1 OS=Homo sapiens	35.77	11	2
Q15027 ACAP1_HUMAN	Arf-GAP with coiled-coil, ANK repeat and F	35.73	5	2
Q5JPE7 NOMO2_HUMAN	Nodal modulator 2 OS=Homo sapiens GN=	35.63	3	2
O60488 ACSL4_HUMAN	Long-chain-fatty-acid--CoA ligase 4 OS=H	35.57	8	2
O95613 PCNT_HUMAN	Pericentrin OS=Homo sapiens GN=PCNT	35.1	3	2
O43157 PLXB1_HUMAN	Plexin-B1 OS=Homo sapiens GN=PLXNB	34.97	4	2
O00555 CAC1A_HUMAN	Voltage-dependent P/Q-type calcium chan	33.97	3	2
Q9Y566 SHAN1_HUMAN	SH3 and multiple ankyrin repeat domains p	33.87	4	2
Q9H2Z4 NKX24_HUMAN	Homeobox protein Nkx-2.4 OS=Homo sap	32.67	8	2
Q702N8 XIRP1_HUMAN	Xin actin-binding repeat-containing protein	32.65	3	2
Q92630 DYRK2_HUMAN	Dual specificity tyrosine-phosphorylation-re	32.04	4	2
O95935 TBX18_HUMAN	T-box transcription factor TBX18 OS=Hom	31.95	5	2
Q13490 BIRC2_HUMAN	Baculoviral IAP repeat-containing protein 2	31.77	7	2
O14802 RPC1_HUMAN	DNA-directed RNA polymerase III subunit	31.77	4	2
Q7Z317 ZN572_HUMAN	Zinc finger protein 572 OS=Homo sapiens	31.45	4	2
Q7L2E3 DHX30_HUMAN	Putative ATP-dependent RNA helicase DH	31.4	8	2
Q9NRS4 TMPS4_HUMAN	Transmembrane protease serine 4 OS=Ho	31.25	8	2
P31689 DNJA1_HUMAN	DnaJ homolog subfamily A member 1 OS=	30.78	13	2
Q9UJU5 FOXD3_HUMAN	Forkhead box protein D3 OS=Homo sapie	30.14	10	2
Q15543 TAF13_HUMAN	Transcription initiation factor TFIID subunit	29.7	22	2
Q8N9L9 ACOT4_HUMAN	Acyl-coenzyme A thioesterase 4 OS=Hom	29.08	5	2
Q13206 DDX10_HUMAN	Probable ATP-dependent RNA helicase D	28.86	7	2
Q5JRC9 FA47A_HUMAN	Protein FAM47A OS=Homo sapiens GN=F	28.76	4	2
Q9NYF0 DACT1_HUMAN	Dapper homolog 1 OS=Homo sapiens GN=	28.41	6	2
Q8N302 AGGF1_HUMAN	Angiogenic factor with G patch and FHA d	28.11	5	2
Q9Y485 DMXL1_HUMAN	DmX-like protein 1 OS=Homo sapiens GN=	28.08	2	2
Q6ZQQ6 WDR87_HUMAN	WD repeat-containing protein 87 OS=Hom	27.55	5	2
Q96A46 MFRN2_HUMAN	Mitoferrin-2 OS=Homo sapiens GN=SLC2	27.52	11	2
Q9C0G0 ZN407_HUMAN	Zinc finger protein 407 OS=Homo sapiens	27.46	4	2
Q96M20 CT152_HUMAN	Uncharacterized protein C20orf152 OS=H	26.88	6	2
Q9NRL3 STRN4_HUMAN	Striatin-4 OS=Homo sapiens GN=STRN4	26.4	6	2
Q96PK2 MACF4_HUMAN	Microtubule-actin cross-linking factor 1, iso	26.39	6	2
Q92616 GCN1L_HUMAN	Translational activator GCN1 OS=Homo sa	25.57	5	2

**Table A1.12 H9 hESC Extracellular and Cell Surface Protein Identifications.** List of all proteins identified in CMTX from H9 hESCs that are classified as 'extracellular' or 'cell surface' by cellular component gene ontology. Corresponding accession, description, unique peptide numbers are shown.

UniProt ID	Name	# Unique Peptides
P18206	Vinculin	46
P21333	Filamin-A	32
P02649	Apolipoprotein E	28
P04075	Fructose-bisphosphate aldolase A	20
P23142	Fibulin-1	18
P62805	Histone H4	18
P07355	Annexin A2	17
P11021	78 kDa glucose-regulated protein	15
P12814	Alpha-actinin-1	15
Q92626	Peroxidasin homolog	14
P62937	Peptidyl-prolyl cis-trans isomerase A	13
P11142	Heat shock cognate 71 kDa protein	12
P10909	Clusterin	12
P05067	Amyloid beta A4 protein	11
P04792	Heat shock protein beta-1	9
Q9Y490	Talin-1	9
P11047	Laminin subunit gamma-1	9
P25391	Laminin subunit alpha-1	9
P07942	Laminin subunit beta-1	8
O43707	Alpha-actinin-4	8
Q92598	Heat shock protein 105 kDa	8
P02751	Fibronectin	7
P54577	Tyrosyl-tRNA synthetase, cytoplasmic	7
P09486	SPARC	7
P10809	60 kDa heat shock protein, mitochondrial	6
P67809	Nuclease-sensitive element-binding protein 1	6
P84243	Histone H3.3	6
P68431	Histone H3.1	6
Q71DI3	Histone H3.2	6
P09429	High mobility group protein B1	5
Q8N474	Secreted frizzled-related protein 1	5
P50395	Rab GDP dissociation inhibitor beta	5
P08195	4F2 cell-surface antigen heavy chain	5
P06744	Glucose-6-phosphate isomerase	5
P98160	Basement membrane-specific heparan sulfate proteoglycan c	5
P39060	Collagen alpha-1(XVIII) chain	5
P62158	Calmodulin	4
P98095	Fibulin-2	4
Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional	4
P07339	Cathepsin D	4
P27797	Calreticulin	4
P11717	Cation-independent mannose-6-phosphate receptor	3
O75487	Glypican-4	3
P23352	Anosmin-1	3
P07093	Glia-derived nexin	3
P29279	Connective tissue growth factor	3
O75610	Left-right determination factor 1	3
P52907	F-actin-capping protein subunit alpha-1	3
P51858	Hepatoma-derived growth factor	3
P38159	Heterogeneous nuclear ribonucleoprotein G	3
Q92820	Gamma-glutamyl hydrolase	3
O43852	Calumenin	3
Q8WZ42	Titin	3
P12109	Collagen alpha-1(VI) chain	3

P07237	Protein disulfide-isomerase	2
P14174	Macrophage migration inhibitory factor	2
O00264	Membrane-associated progesterone receptor component 1	2
P06576	ATP synthase subunit beta, mitochondrial	2
P54578	Ubiquitin carboxyl-terminal hydrolase 14	2
O15078	Centrosomal protein of 290 kDa	2
Q15046	Lysyl-tRNA synthetase	2
Q00341	Vigilin	2
Q96HF1	Secreted frizzled-related protein 2	2
Q9BYX7	Putative beta-actin-like protein 3	2
O00292	Left-right determination factor 2	2
P50453	Serpin B9	2
P21741	Midkine	2
P53621	Coatomer subunit alpha	2
P18065	Insulin-like growth factor-binding protein 2	2
Q96S86	Hyaluronan and proteoglycan link protein 3	2
P02768	Serum albumin	2



**Table A1.13 CA1 hESC Extracellular and Cell Surface Protein Identifications.** List of all proteins identified in CMTX from CA1 hESCs that are classified as 'extracellular' or 'cell surface' by cellular component gene ontology. Corresponding accession, description, unique peptide numbers are shown.

UniProt ID	Name	# Unique Peptides
P21333	Filamin-A	72
P18206	Vinculin	51
P04075	Fructose-bisphosphate aldolase A	33
P07355	Annexin A2	33
P12814	Alpha-actinin-1	28
P11142	Heat shock cognate 71 kDa protein	27
P10809	60 kDa heat shock protein, mitochondrial	26
P62805	Histone H4	26
O43707	Alpha-actinin-4	24
Q9Y490	Talin-1	23
P62937	Peptidyl-prolyl cis-trans isomerase A	23
P02649	Apolipoprotein E	22
P06576	ATP synthase subunit beta, mitochondrial	19
P84243	Histone H3.3	18
P11021	78 kDa glucose-regulated protein	17
P50395	Rab GDP dissociation inhibitor beta	16
P04792	Heat shock protein beta-1	16
P06744	Glucose-6-phosphate isomerase	15
P00441	Superoxide dismutase [Cu-Zn]	13
P54577	Tyrosyl-tRNA synthetase, cytoplasmic	13
P50453	Serpin B9	12
P62328	Thymosin beta-4	12
P62158	Calmodulin	11
P07093	Glia-derived nexin	11
Q92598	Heat shock protein 105 kDa	11
P07237	Protein disulfide-isomerase	10
Q9Y696	Chloride intracellular channel protein 4	10
Q00839	Heterogeneous nuclear ribonucleoprotein U	10
P31947	14-3-3 protein sigma	10
P09429	High mobility group protein B1	9
P38646	Stress-70 protein, mitochondrial	9
P09382	Galectin-1	9
P10909	Clusterin	8
P05067	Amyloid beta A4 protein	7
P02751	Fibronectin	7
P07602	Proactivator polypeptide	7
P27797	Calreticulin	7
P52907	F-actin-capping protein subunit alpha-1	7
Q92626	Peroxidasin homolog	7
Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional p	7
P55145	Mesencephalic astrocyte-derived neurotrophic factor	7
P14174	Macrophage migration inhibitory factor	6
P54578	Ubiquitin carboxyl-terminal hydrolase 14	6
P07942	Laminin subunit beta-1	6
P13693	Translationally-controlled tumor protein	6
P07339	Cathepsin D	6
Q8WZ42	Titin	6
P14735	Insulin-degrading enzyme	5
Q15046	Lysyl-tRNA synthetase	5
Q00341	Vigilin	5
P10599	Thioredoxin	5
Q9BRX8	Redox-regulatory protein PAMM	5
P23142	Fibulin-1	5
O75083	WD repeat-containing protein 1	5

P48061	Stromal cell-derived factor 1	5
O00264	Membrane-associated progesterone receptor component 1	4
P29279	Connective tissue growth factor	4
P02452	Collagen alpha-1(I) chain	4
P26583	High mobility group protein B2	4
P38159	Heterogeneous nuclear ribonucleoprotein G	4
P13489	Ribonuclease inhibitor	4
Q99584	Protein S100-A13	4
P67809	Nuclease-sensitive element-binding protein 1	4
P15121	Aldose reductase	4
Q92520	Protein FAM3C	4
Q99988	Growth/differentiation factor 15	4
P05556	Integrin beta-1	3
P47755	F-actin-capping protein subunit alpha-2	3
P11047	Laminin subunit gamma-1	3
Q9UQE7	Structural maintenance of chromosomes protein 3	3
Q00796	Sorbitol dehydrogenase	3
P98095	Fibulin-2	3
Q9NRV9	Heme-binding protein 1	3
Q969H8	UPF0556 protein C19orf10	3
Q8NCW5	Apolipoprotein A-I-binding protein	3
O00622	Protein CYR61	3
P51858	Hepatoma-derived growth factor	3
P21741	Midkine	3
O15230	Laminin subunit alpha-5	3
Q32P28	Prolyl 3-hydroxylase 1	3
P39060	Collagen alpha-1(XVIII) chain	3
Q12841	Follistatin-related protein 1	3
P24043	Laminin subunit alpha-2	3
P11233	Ras-related protein Ral-A	2
O75145	Liprin-alpha-3	2
Q96HF1	Secreted frizzled-related protein 2	2
P08123	Collagen alpha-2(I) chain	2
O00292	Left-right determination factor 2	2
Q9H4G4	Golgi-associated plant pathogenesis-related protein 1	2
O43852	Calumenin	2
O95813	Cerberus	2
P09486	SPARC	2
P25391	Laminin subunit alpha-1	2
P18065	Insulin-like growth factor-binding protein 2	2
O75718	Cartilage-associated protein	2
P61916	Epididymal secretory protein E1	2
Q86UW8	Hyaluronan and proteoglycan link protein 4	2
P09038	Heparin-binding growth factor 2	2
Q7Z5P9	Mucin-19	2
Q17RW2	Collagen alpha-1(XXIV) chain	2

**Table A1.14 BJ-1D hiPSC Extracellular and Cell Surface Protein Identifications.**

List of all proteins identified in CMTX from BJ-1D hiPSCs that are classified as 'extracellular' or 'cell surface' by cellular component gene ontology. Corresponding accession, description, unique peptide numbers are shown.

Uniprot ID	Name	# Unique Peptides
P18206	Vinculin	88
P21333	Filamin-A	83
P04075	Fructose-bisphosphate aldolase A	40
P62805	Histone H4	33
P12814	Alpha-actinin-1	31
P07355	Annexin A2	30
P50395	Rab GDP dissociation inhibitor beta	29
P62937	Peptidyl-prolyl cis-trans isomerase A	28
P62328	Thymosin beta-4	26
O43707	Alpha-actinin-4	25
P62158	Calmodulin	24
P10809	60 kDa heat shock protein, mitochondrial	23
P11142	Heat shock cognate 71 kDa protein	23
P11021	78 kDa glucose-regulated protein	23
Q00839	Heterogeneous nuclear ribonucleoprotein U	22
P06744	Glucose-6-phosphate isomerase	21
Q9UQE7	Structural maintenance of chromosomes protein 3	21
P07237	Protein disulfide-isomerase	19
P05556	Integrin beta-1	16
P10599	Thioredoxin	15
P02649	Apolipoprotein E	15
P10909	Clusterin	15
P11717	Cation-independent mannose-6-phosphate receptor	14
Q92626	Peroxidasin homolog	13
P14174	Macrophage migration inhibitory factor	13
Q00341	Vigilin	12
P53621	Coatomer subunit alpha	12
P23142	Fibulin-1	12
P54577	Tyrosyl-tRNA synthetase, cytoplasmic	12
P00441	Superoxide dismutase [Cu-Zn]	11
P13693	Translationally-controlled tumor protein	11
P38646	Stress-70 protein, mitochondrial	11
P07093	Glia-derived nexin	10
P07339	Cathepsin D	10
P04792	Heat shock protein beta-1	10
P50453	Serpin B9	9
P27797	Calreticulin	8
P02751	Fibronectin	8
P09429	High mobility group protein B1	8
Q9Y696	Chloride intracellular channel protein 4	8
Q15046	Lysyl-tRNA synthetase	7
Q92598	Heat shock protein 105 kDa	7
P48061	Stromal cell-derived factor 1	7
P40222	Alpha-taxilin	7
P54578	Ubiquitin carboxyl-terminal hydrolase 14	7
P67809	Nuclease-sensitive element-binding protein 1	6
P15121	Aldose reductase	6
P55145	Mesencephalic astrocyte-derived neurotrophic factor	6
P22413	Ectonucleotide pyrophosphatase/phosphodiesterase family member 1	6
Q8N474	Secreted frizzled-related protein 1	6
P06576	ATP synthase subunit beta, mitochondrial	6
P98160	Basement membrane-specific heparan sulfate proteoglycan core protein 1	5
P31947	14-3-3 protein sigma	5
P26583	High mobility group protein B2	5

P38159	Heterogeneous nuclear ribonucleoprotein G	5
P61916	Epididymal secretory protein E1	5
P05067	Amyloid beta A4 protein	5
P51858	Hepatoma-derived growth factor	4
P52907	F-actin-capping protein subunit alpha-1	4
O00622	Protein CYR61	4
Q99584	Protein S100-A13	4
P09382	Galectin-1	4
Q32P28	Prolyl 3-hydroxylase 1	4
Q969H8	UPF0556 protein C19orf10	4
Q8WZ42	Titin	4
P14735	Insulin-degrading enzyme	4
P51511	Matrix metalloproteinase-15	3
O00292	Left-right determination factor 2	3
O43278	Kunitz-type protease inhibitor 1	3
P13489	Ribonuclease inhibitor	3
P11047	Laminin subunit gamma-1	3
Q8NCW5	Apolipoprotein A-I-binding protein	3
Q92485	Acid sphingomyelinase-like phosphodiesterase 3b	3
P25391	Laminin subunit alpha-1	3
O00264	Membrane-associated progesterone receptor component 1	3
O75330	Hyaluronan mediated motility receptor	3
Q9UII2	ATPase inhibitor, mitochondrial	3
P50281	Matrix metalloproteinase-14	2
Q99541	Perilipin-2	2
O43157	Plexin-B1	2
P68431	Histone H3.1	2
Q71DI3	Histone H3.2	2
O75610	Left-right determination factor 1	2
P47755	F-actin-capping protein subunit alpha-2	2
Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional protei	2
Q14766	Latent-transforming growth factor beta-binding protein 1	2
O60258	Fibroblast growth factor 17	2
P18065	Insulin-like growth factor-binding protein 2	2
Q00796	Sorbitol dehydrogenase	2
Q02818	Nucleobindin-1	2
Q12841	Follistatin-related protein 1	2
Q92520	Protein FAM3C	2
Q9NRV9	Heme-binding protein 1	2
Q8N302	Angiogenic factor with G patch and FHA domains 1	2
P08195	4F2 cell-surface antigen heavy chain	2

**Table A1.15 Real Time PCR Primer Information.** List of all primers used in real-time PCR experiments in this thesis with corresponding target, assay identification, and NCBI gene reference.

Target	Assay ID	NCBI Gene Reference
SRY (sex determining region Y)-box 1	Hs01057642_s1	NM_005986.2
alpha-fetoprotein	Hs00173490_m1	NM_001134.1
GATA binding protein 4	Hs00171403_m1	NM_002052.3
T, brachyury homolog (mouse)	Hs00610080_m1	NM_003181.2
GATA binding protein 6	Hs00232018_m1	NM_005257.3
paired box 6	Hs01088112_m1	NM_001127612.1
neurogenic differentiation 1	Hs00159598_m1	NM_002500.2
caudal type homeobox 2	Hs01078080_m1	NM_001265.3
Nanog homeobox	Hs02387400_g1	NM_024865.2
Pou class 5 homeobox 1	Hs00742896_s1	NM_203289.3
Secreted frizzled related protein - 1	Hs00610060_m1	NM_003012.4
Secreted frizzled related protein - 2	Hs00293258_m1	NM_003013.2
Wingless-type MMTV Integration Site Family Member 3A	Hs00263977_m1	NM_033131.3
Goosecoid	Hs00418279_m1	NM_173849.2
Mix paired-like homeobox 1	Hs00430824_g1	NM_031944.1



**Table A1.16 shRNA Sequence Information.** List of all short hairpin sequences used in transient knockdown experiments in this thesis with corresponding sequence and oligo name shown.

Oligo sequence (5' to 3')	Oligo name
GATCCGGGCCATTTAGATTAGGAATTCAAGAGATTCCTAATCTAAATGGCCCTTTTTTC	sFRP1 shRNA Top
TCGAGAAAAAAGGGCCATTTAGATTAGGAATCTCTTGAATTCCTAATCTAAATGGCCCG	sFRP1 shRNA Bottom
GATCCGCCACCCGAATCTTGTAGTTCAAGAGACTACAAGATTCGGGTGGGCTTTTTTC	sFRP2 shRNA Top
TCGAGAAAAAAGCCACCCGAATCTTGTAGTCTCTTGAACTACAAGATTCGGGTGGGCG	sFRP2 shRNA Bottom
GATCCGCTTGAACCGCCAGATCTATTCAAGAGATAGATCTGGCGTTCAAGCTTTTTTC	Control Top
TCGAGAAAAAAGCTTGAACCGCCAGATCTATCTCTTGAATAGATCTGGCGTTCAAGCG	Control Bottom

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# Christopher Hughes

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## Education

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**Quantitative Proteomics Workshop Short Course** – ASMS 2009

**FT-ICR Mass Spectrometry Workshop Short Course** – ASMS 2008

## Achievements and Publications

### Publications:

**Hughes, C.S. et al.** (2012) Mass Spectrometry-Based Proteomics Analysis of the Matrix Microenvironment in Pluripotent Stem Cell Culture. (In preparation)

Liu, S. and **Hughes, C.S.** (2011) Recent Advances and Special Considerations for the Analysis of Phosphorylated Peptides by LC-ESI-MS/MS. *Current Anal. Chem.* (accepted - in press)

**Hughes, C.S. et al.** (2011) Proteomic analysis of matrices used in the growth of human embryonic stem cells. *Proteomics* (accepted - in press)

**Hughes, C.S.** and Nuhn, A. *et al.* (2011) Proteomics of human embryonic stem cells. *Proteomics* 11:4, 675-690

**Hughes, C. S. et al.** (2010) Matrigel: A complex protein mixture required for optimal growth of cell culture. *Proteomics* 10:9,1886-1890

**Hughes, C.S. et al.** (2010) De novo sequencing methods in proteomics. *Methods in Mol. Biol.* 604, 105-121

Bendall, S.C., **Hughes, C.S. et al.** (2009) An Enhanced Mass Spectrometry Approach Reveals Human Embryonic Stem Cell Growth Factors in Culture. *Mol. Cell. Proteomics.* 8; 3, 421-432

Bendall, S.C. and **Hughes, C.S.** *et al.* (2008) Prevention of amino acid conversion in SILAC experiments with embryonic stem cells. *Mol. Cell. Prot.* 7:9,1587 - 1597

Wu, J., **Hughes, C.S.** *et al.* (2007) High-throughput cytochrome P450 inhibition assays using laser diode thermal desorption-atmospheric pressure chemical ionization-tandem mass spectrometry. *Anal. Chem.* 79:12, 4657 – 4665

### Presentations:

**Hughes, C.S.** *et al.* (2011) – HUPO 2011 – Analysis of Human Embryonic Stem Cell Depositome (Poster Number – P1346)

**Hughes, C.S.** *et al.* (2011) – ISSCR – Analysis of Human Embryonic Stem Cell Depositome (Poster Number – 2219)

**Hughes, C.S.** *et al.* (2010) – Canadian National Proteomics Network Conference – Analysis of Human Embryonic Stem Cell Depositome (Poster)

**Hughes, C.S.** *et al.* (2010) – HUPO 2010 – Matrigel: A complex mixture required for optimal growth of cell culture (Poster)

**Hughes, C.S.** *et al.* (2010) – HUPO 2010 – Analysis and quantitation of a glycogen synthase kinase-3 knockout embryonic stem cell line to a depth of >3500 proteins (Poster Number)

**Hughes, C.S.** *et al.* (2009) – ASMS 2009 – Analysis and quantitation of a glycogen synthase kinase-3 knockout embryonic stem cell line to a depth of >3500 proteins (Poster)

**Hughes, C.S.** *et al.* (2008) – ASMS 2008 – Prevention of amino acid conversion in SILAC experiments with embryonic stem cells (Oral presentation)

### Awards:

NSERC Canadian Graduate Scholarship – Doctoral (May 2009 – Current)

NSERC Canadian Graduate Scholarship – Masters (May 2008 – May 2009)

NSERC Undergraduate Research Scholarship – (Jan 2006 – May 2006)

USC Excellence in Teaching Award – (2009, 2011)

Young Investigator Award – HUPO 2010

CSMS Student Travel Award – ASMS 2009

### Professional Experience

**Apr. - Sept. 2006**      **Merck Frosst Canada** – Pointe-Claire, QC

I spent a single work term at Merck Frosst working on the drug metabolism team. My main project while at Merck involved testing and validating a new mass spectrometer ion source based on thermal desorption. I was involved in all aspects of the project from sample and instrument preparation, analysis, interpretation, and manuscript authoring. My work at Merck resulted in a publication: Wu, J. (2007) *Anal. Chem.* 79:12, 4657 – 4665.

**Jan. - Apr. 2006**

**Radiant Technologies Inc.** – Burlington, ON

I spent a single work term at Radiant working in the drug purification division. While there I would perform large column (80L) purification and separation of an active drug ingredient from natural sources. I was part of all stages of the process from crude product to purified form. My main duties were running, maintenance, packing of the large columns, and purification post-column.

**Sept. 2004 - Sept. 2005**

**MDS Sciex** – Concord, ON

I spent two work terms in the demo and projects laboratory department. While at MDS, I worked with all types of MDS Sciex mass spectrometry hardware and software as well as on HPLC hardware from a wide range of manufacturers. I completed a project profiling carcinogenic food dyes found in spices from around the world. As well, I completed another project profiling excipients from analgesic drugs in an attempt to identify counterfeit drugs. Both of these reports have been presented at conferences and are frequently used as sales information for instrumentation. I also acted in a support role providing worldwide technical support on Sciex hardware and software.

**Jan. - Apr. 2004**

**Agriculture and Agri-Food Canada** – Harrow, ON

While at Agri-food, I worked in the dry beans division. I studied bean plants under various diseased conditions in an attempt to isolate resistant varieties. Inoculated plants were analyzed visually as well as at the DNA level for changes. A secondary project I was part of involved the results of mechanical damage to seedling growth and maturity.