

# Supporting Information

## **Quantitative Proteomic Analysis of HeLa Cells in Response to Biocompatible Fe<sub>2</sub>C@C Nanoparticles: <sup>16</sup>O/<sup>18</sup>O-Labeled & HPLC-ESI-Orbit-Trap Profiling Approach**

*Murtaza Hasan<sup>a,b</sup>, Ghazala Mustafa<sup>c</sup>, Javed iqbal<sup>d</sup>, Muhammad Ashfaq<sup>a</sup>, Nasir Mahmood<sup>e,f,\*</sup>*

*<sup>a</sup>Department of Biochemistry and Biotechnology, The Islamia University of Bahawalpur, Pakistan*

*<sup>b</sup>Department of Materials Science and Engineering, College of Engineering, Peking University, Beijing, 178001, China.*

*<sup>c</sup>Department of Plant Sciences, Quaid-i-Azam University, Islamabad 45320, Pakistan*

*<sup>d</sup>College of Life Sciences, Shenzhen University, Shenzhen 10590, China*

*<sup>e</sup> School of Engineering, RMIT University, 124 La Trobe Street, 3001 Melbourne, Victoria, Australia*

*<sup>f</sup>Center of Micro-Nano Functional Materials and Devices, School of Energy Science and Engineering, State key Laboratory of Electronic Thin Films and Integrated Devices, University of Electronic Science and Technology of China, Chengdu, 611731, China*

\*Corresponding Author: Nasir Mahmood (PhD.) Email: [nasir.mahmood@rmit.edu.au](mailto:nasir.mahmood@rmit.edu.au) and  
Phone/Fax: +61423669339.

## **Materials and method (SM)**

### **Synthesis of Fe<sub>2</sub>C@C NPs (MS1)**

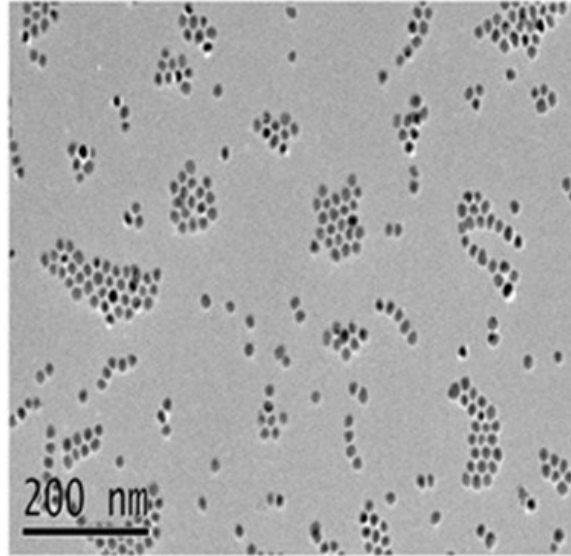
In a typical synthesis of Fe<sub>2</sub>C@C NPs, octadecylamine (14.5 g) and cetrimonium bromide (CTAB, 0.113 g) was heated to 120 °C after degassing under N<sub>2</sub> flow, while later on Fe(CO)<sub>5</sub> (0.5 mL, 3.6 mmol) is injected under a N<sub>2</sub> blanket. Afterwards temperature was raised to 180 °C at 10 °C /min and kept constant for 10 min, and then increased to 350 °C and kept for 10 min before cooling to room temperature. Finally product was washed repeatedly with ethanol and hexane for 6 times and dried under vacuum at 70 °C. The morphological study was carried out using FEI Tecnai T20 transmission electron microscopy (TEM), shown in Figure S1 where homogeneity in size and well dispersions obvious.

### **Surface Coating of Nanoparticles**

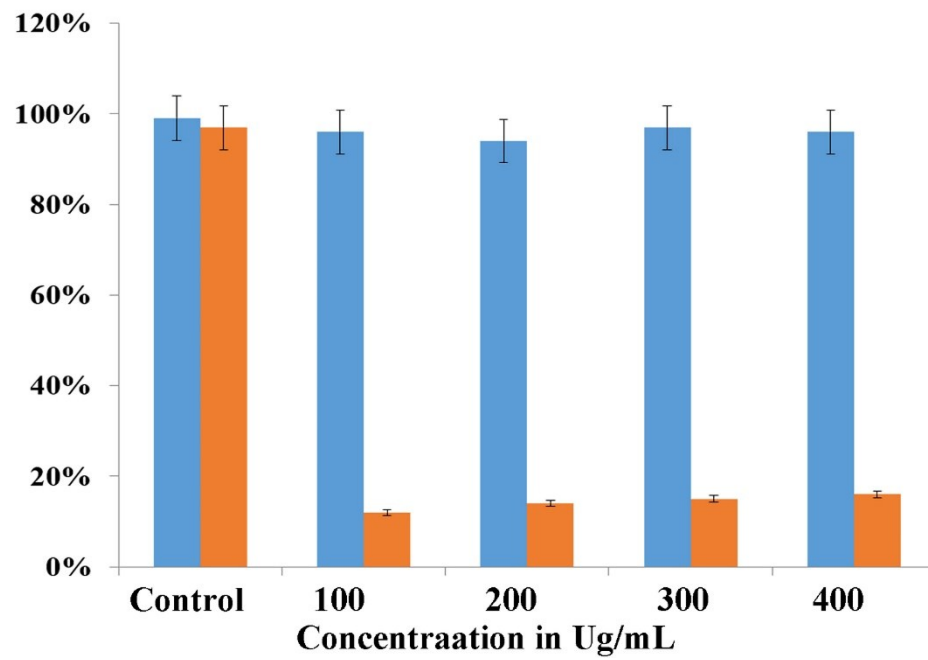
Initially, 0.4 g of protocatechuic acid (PA) was dissolved the mixed solution of 1 mL pyridine and 3 mL toluene. Then the mixture was added drop wise into 100 mL of the toluene containing 100 mg Fe<sub>2</sub>C@C NPs. The Fe<sub>2</sub>C@C NPs were precipitated after addition of PA solution. The precipitate was dissolved in sodium carbonate solution (1%, w/v, 10 mL). Excess ethanol was added to the solution and the product was collected by centrifugation. Finally, the product was washed 6 times repeatedly with water and ethanol.

### ***In-vitro* cytotoxicity of Fe<sub>2</sub>C@C NPs (MS2)**

The MTT assay on HeLa cell was employed to study the cytotoxicity effect of Fe<sub>2</sub>C NPs. The 96-well cell culture plates were used to seed the cells at 5×10<sup>3</sup> cells in each well, which were then incubated overnight at 37 °C under 5% CO<sub>2</sub>. A fresh culture medium with different concentrations of Fe<sub>2</sub>C NPs was used to replace the old one and further incubated for 24 h. The MTT assay studies were carried out after cleansing the cells with Dulbecco's phosphate buffered saline (DPBS). The luminescence microplate reader (Spectra ax M2, Molecular Device, USA) was used to record the OD570 value (Abs.) for each cell-well.



**Fig. S1.** TEM image of  $\text{Fe}_2\text{C}@\text{C}$  NPs and (b) size distribution of  $\text{Fe}_2\text{C}@\text{C}$  NPs.



**Fig. S2.** Cytotoxicity of  $\text{Fe}_2\text{C}@\text{C}$  NPs with and without biocompatible coating in HeLa cell line.

**Table S1.** Expression of total protein in response to Fe<sub>2</sub>C@C NPs.

Protein ID	Description	Symbol	O16/O18 ratio	Molecular Weight	IP	Status	Location	Function
P0CG48	UBC Polyubiquitin-C	UBC	0.21	77,039 DA	5	upregulated	Cytoplasm Nucleus	Activation of protein kinases, and in signaling
P62979	RPS27A Ubiquitin-40S ribosomal protein S27a	RPS27A	0.21	17,965 DA	5	upregulated	Cytoplasm Nucleus	Activation of protein kinases, and in signaling.
P62987	UBA52 Ubiquitin-60S ribosomal protein L40	UBA52	0.21	14,728 DA	5	upregulated	Cytoplasm Nucleus	Activation of protein kinases, and in signaling.
P52209	PGD 6-phosphogluconate dehydrogenase, decarboxylating	PGD	0.31	51872DA	1	upregulated	Cytoplasm	oxidative decarboxylation
Q16881	TXNRD1 Thioredoxin reductase 1, cytoplasmic	TXNRD1	0.33	70,906 DA	2	upregulation	Cytoplasm Nucleus	Formation of cell membrane protrusions
P07355	ANXA2 Annexin A2	ANXA2	0.37	38,604 DA	13	upregulated	Membrane, Extracellular matrix	Calcium-regulated membrane-binding protein
Q15293	RCN1 Reticulocalbin-1	RCN1	0.39	38,890 DA	1	upregulated	Endoplasmic reticulum	Regulate calcium-dependent activities
P63173	RPL38 60S ribosomal protein L38	RPL38	0.39	8,218 DA	1	Upregulated	Ribosomes large sub unit	structural constituent of ribosome
P00338	LDHA L-lactate dehydrogenase A chain	LDHA	0.39	36,689 DA	3	Upregulated	Cytoplasm	Control fermentation process
P42166	TMPO Lamina-associated polypeptide 2, isoform alpha	TMPO	0.4	75,492 DA	2	upregulated	Nucleus	structural organization of the nucleus
P08758	ANXA5 Annexin A5	ANXA5	0.41	35,937 DA	2	upregulated	Cytosole	Anticoagulant protein
P23528	CFL1 Cofilin-1	CFL1	0.42	18 kda	7	upregulated	Protein kinase receptor	No data
P13797	PLS3 Plastin-3	PLS3	0.43	70,811 DA	1	upregulated	Cytoplasm	Regulation of bone development
P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	0.44	57,937 DA	8	Upregulated	Cytoplasm Nucleus	Tumor cell proliferation and survival
P27348	YWHAQ 14-3-3 protein theta	YWHAQ	0.45	27,764 DA	3	upregulated	Cytoplasm	Negatively regulates the kinase activity
O75533	SF3B1 Splicing factor 3B subunit 1	SF3B1	0.47	145,830 DA	2	Upregulated	Nucleus, Spliceosome	splicing of rare class of nuclear pre-mRNA intron.
P18085	ARF4 ADP-ribosylation factor 4	ARF4	0.47	20,511 DA	2	Upregulated	Golgi apparatus	vesicle budding and uncoating within the Golgi apparatus
Q01518	CAP1 Adenylyl cyclase-associated protein 1	CAP1	0.47	51,901 DA	1	upregulated	Cell membrane	Cell polarity
P18669	PGAM1 Phosphoglycerate mutase 1	PGAM1	0.48	28,804 DA	1	Upregulated	Cytoplasm	reduced activity
P10599	TXN Thioredoxin	TXN	0.49	11,737 DA	1	Upregulated	Nucleus cytoplasm	inhibits caspase-3 activity
P29401	TKT Transketolase	TKT	0.49	67,878 DA	6	Upregulated	Cytosol	Activates co-factor
Q9UK76	HN1 Hematological and neurological expressed 1 protein	HN1	0.49	16,015 DA	1	Upregulated	Nucleus	N-terminally processed
P51610	HCFC1 Host cell factor 1	HCFC1	0.49	208,732 DA	1	Upregulated	Cytoplasm Nucleus	Control of the cell cycle
P37802	TAGLN2 Transgelin-2	TAGLN2	0.5	22,391 DA	1	up	extracellular exosome	Differentiation process
P40227	CCT6A T-complex protein 1 subunit zeta	CCT6A	0.5	58,024 DA	1	Up	Cytoplasm	folding of actin and tubulin.
P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	0.5	49,924 DA	5	up	Cytoskeleton	major constituent of microtubules
P49915	GMPS GMP synthase	GMPS	0.51	76,715 DA	2	up	Cytoplasm	cellular processes important for cell division.
P07195	LDHB L-lactate dehydrogenase B chain	LDHB	0.51	36,638 DA	4	up	Cytoplasm	Fermentation process
P49327	FASN Fatty acid synthase	FASN	0.52	273,427 DA	5	Up	Cytoplasm	Carrier protein
P11586	MTHFD1 C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	0.52	101,559 DA	1	up	Cytoplasm	part of One-carbon metabolism
P09211	GSTP1 Glutathione S-transferase P	GSTP1	0.52	23,356 DA	1	up	Cytoplasm, nucleus, mitochondria	prevent neurodegeneration
P62258	YWHAE 14-3-3 protein epsilon	YWHAE	0.52	29,174 DA	3	up	Cytoplasm, Melanosomes	modulation of the activity of the binding partner
P63104	YWHAZ 14-3-3 protein zeta/delta	YWHAZ	0.52	27,745 DA	6	up	Cytoplasm, Melanosomes	modulation of the activity of the binding partner
P51149	RAB7A Ras-related protein Rab-7a	RAB7A	0.52	23,490 DA	2	up	Cytoplasm	Key regulator in endo-lysosomal trafficking.
P17655	CAPN2 Calpain-2 catalytic subunit	CAPN2	0.53	79,995 DA	1	up	Cytoplasm, cell membrane	Calcium-regulated non-lysosomal thiol-protease
O00764	PDXK Pyridoxal kinase	PDXK	0.53	35,102 DA	2	up	Cytoplasm	synthesis of pyridoxal-5-phosphate from vitamin B6.
P06744	GPI Glucose-6-phosphate isomerase	GPI	0.53	63,147 DA	3	up	Cytoplasm	tumor-secreted cytokine and an angiogenic factor
P07900	HSP90AA1 Heat shock protein HSP 90-alpha	HSP90AA1	0.53	84,660 DA	15	up	Cytoplasm, Cell,m melanosomes	cell cycle control and signal transduction
O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	0.53	55,024 DA	1	up	Cytosol nucleoplasm	biosynthesis of glycosaminoglycans
P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	0.54	83,264 DA	16	up	Cytoplasm Melanosomes	control target protein in cell cycle and signal transduction

P53621	COPA Coatomer subunit alpha	COPA	0.54	138,346 DA	1	up	Cytoplasm Golgi bodies	Golgi structural integrity and endocytic recycling
P98082	DAB2 Disabled homolog 2	DAB2	0.55	82,448DA	1	up	Cytoplasm Vesicle membrane	Act as a tumor suppressor
P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	0.56	29,484 DA	1	up	Cytoplasm Nucleus	multicatalytic proteinase complex
Q06830	PRDX1 Peroxiredoxin-1	PRDX1	0.56	22,110 DA	3	up	Cytoplasm Melanosomes	Involved in redox regulation of the cell.
P06733	ENO1 Alpha-enolase	ENO1	0.56	47169DA	8	up	Cytoplasm Cell membrane	Control growth, hypoxia tolerance and allergic responses
P18206	VCL Vinculin	VCL	0.56	123,799 DA	3	up	Cell membrane	cell-matrix adhesion and cell-cell adhesion
P48643	CCT5 T-complex protein 1 subunit epsilon	CCT5	0.56	59,671 DA	3	up	Cytoplasm	in vitro, in the folding of actin and tubulin
P41250	GARS Glycine--tRNA ligase	GARS	0.56	83,166 DA	3	up	Cytoplasm, Mitochondria, Axon	A universal pleiotropic signaling molecule
P53396	ACLY ATP-citrate synthase	ACLY	0.56	120839 DA	3	up	Cytoplasm	Synthesis of cytosolic acetyl-CoA
Q9NR31	SAR1A GTP-binding protein SAR1a	SAR1A	0.56	22,367 DA	1	up	ER and Golgi	Transport from the endoplasmic reticulum to the Golgi apparatus
P04792	HSPB1 Heat shock protein beta-1	HSPB1	0.57	22,783 DA	4	up	Cytoplasm Nucleus	Involved in stress resistance and actin organization
Q14818	PSMA7 Proteasome subunit alpha type-7	PSMA7	0.57	27,887 DA	1	up	Cytoplasm Nucleus	immune response
P62826	RAN GTP-binding nuclear protein Ran	RAN	0.57	24,423 DA	2	up	Nucleus nuclear membrane	Involved in chromatin condensation and control of cell cycle
P15311	EZR Ezrin	EZR	0.57	69,413 DA	4	up	Cytoskeleton Cell membrane	connections cytoskeletal structures to the plasma membrane
P45974	USP5 Ubiquitin carboxyl-terminal hydrolase 5	USP5	0.58	95,786 DA	1	up	Lysosomes	proteasomal recognition
Q99497	PARK7 Protein DJ-1	PARK7	0.58	19,891 DA	1	up	Cytoplasm nucleus Mitochondria	cell protection mechanism against induced metal toxicity
Q15021	NCAPD2 Condensin complex subunit 1	NCAPD2	0.59	157,182 DA	1	up	Cytoplasm Nucleus	Regulatory subunit of the condensin complex
P52907	CAPZA1 F-actin-capping protein subunit alpha-1	CAPZA1	0.59	32,923 DA	1	up	Cytoplasm	F-actin-capping proteins bind in a Ca <sup>2+</sup> -independent
Q9NTK5	OLA1 Obg-like ATPase 1	OLA1	0.59	44,744 DA	1	up	Cytoplasm Nucleus	Hydrolyzes ATP and GTP
Q15691	MAPRE1 Microtubule-associated protein RP/EB family member	MAPRE1	0.59	29,999 DA	1	up	Cytoskeleton	regulates the dynamics of the microtubule cytoskeleton
Q93009	USP7 Ubiquitin carboxyl-terminal hydrolase 7	USP7	0.6	128,302 DA	1	up	Cytoplasm Nucleus	crucial for Treg cell function
P50991	CCT4 T-complex protein 1 subunit delta	CCT4	0.6	57,924 DA	1	up	Cytoplasm, Cytoskeleton	folding of proteins upon ATP hydrolysis
Q71U36	TUBA1A Tubulin alpha-1A chain	TUBA1A	0.6	50,136 DA	6	up	Cytoskeleton	constituent of microtubules
Q92973	TNPO1 Transportin-1	TNPO1	0.6	102,355 DA	1	up	Cytoplasm Nucleus	Nuclear protein import as nuclear transport receptor
P31689	DNAJA1 DnaJ homolog subfamily A member 1	DNAJA1	0.6	44,868 DA	1	up	Cytoplasm, Nucleus ,mitochondria	Promotes apoptosis in response to cellular stress
Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	0.61	59,367 DA	2	up	Cytoplasm	folding of actin and tubulin
P60842	EIF4A1 Eukaryotic initiation factor 4A-I	EIF4A1	0.61	46,154 DA	2	up	Cytoplasm Membrane	scanning for the initiator codon
Q14240	EIF4A2 Eukaryotic initiation factor 4A-II	EIF4A2	0.61	46,402 DA	1	up	Cytosol	required for mRNA binding to ribosome
P00761	Trypsin OS=Sus scrofa PE=1 SV=1	Trypsin	0.62	24,409 DA	7	up	Extracellular space	Preferential cleavage
Q00610	CLTC Clathrin heavy chain 1	CLTC	0.62	191,615 DA	6	up	Cytoplasm Melanosomes	Major protein of the polyhedral coat of coated pits and vesicles
P22392	NME2 Nucleoside diphosphate kinase B	NME2	0.62	17,298 DA	3	up	Cytoplasm Nucleus	synthesis of nucleoside triphosphates other than ATP
P55060	CSE1L Exportin-2	CSE1L	0.62	110,417 DA	4	up	Cytoplasm Nucleus	Cargo of GTP- and GDP between the cytoplasm and nucleus
Q96GG9	DCUN1D1 DCN1-like protein 1	DCUN1D1	0.62	30,124 DA	1	up	Nucleus	facilitating malignant transformation and carcinogenic progression
P07437	TUBB Tubulin beta chain	TUBB	0.63	49,671 DA	12	up	Cytoplasm	It binds two moles of GTP
P68371	TUBB4B Tubulin beta-4B chain	TUBB4B	0.63	49,831 DA	8	up	Cytoplasm	It binds two moles of GTP
Q86VP6	CAND1 Cullin-associated NEDD8-dissociated protein 1	CAND1	0.63	136,376 DA	2	up	Cytoplasm Nucleus	promotes the exchange of the substrate-recognition
P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	0.63	60,344 DA	1	up	Cytoplasm	in vitro, in the folding of actin and tubulin
Q92499	DDX1 ATP-dependent RNA helicase DDX1	DDX1	0.64	82,432 DA	5	up	Cytoplasm Nucleus	play a role in RNA clearance at DNA double-strand breaks
P50990	CCT8 T-complex protein 1 subunit theta	CCT8	0.64	59,621 DA	2	up	Cytoplasm	in vitro, in the folding of actin and tubulin
P61204	ARF3 ADP-ribosylation factor 3	ARF3	0.64	20,601 DA	3	up	Cytoplasm Golgi bodies	Involved in protein trafficking
P84077	ARF1 ADP-ribosylation factor 1	ARF1	0.64	20,697 DA	3	up	Cytoplasm Golgi bodies	Involved in protein trafficking among different compartments.
P84085	ARF5 ADP-ribosylation factor 5	ARF5	0.64	20,530 DA	1	up	Cytoplasm Golgi bodies	Involved in protein trafficking
Q16658	FSCN1 Fascin	FSCN1	0.64	54,530 DA	2	up	Cytoplasm	organization of actin filament bundles

Q13748	TUBA3D Tubulin alpha-3C/D chain	TUBA3D	0.65	49,960 DA	1	up	Cytoplasm	It binds two moles of GTP
P26639	TARS Threonine--tRNA ligase, cytoplasmic	TARS	0.65	83,435 DA	1	up	Cytoplasm	threonine-tRNA ligase activity
Q9HB71	CACYBP Calcyclin-binding protein	CACYBP	0.66	26,210 DA	1	up	Cytoplasm Nucleus	alcium-dependent ubiquitination
O75937	DNAJC8 DnaJ homolog subfamily C member 8	DNAJC8	0.66	29,842 Da	1	up	Cytoplasm Nucleoplasm	RNA splicing
P00558	PGK1 Phosphoglycerate kinase 1	PGK1	0.66	44,615 DA	4	up	Cytoplasm	glycolytic enzyme
P27797	CALR Calreticulin	CALR	0.66	48,142 DA	8	up	Cytoplasm Endoplasmic reticulum	Involved in maternal gene expression regulation
P07737	PFN1 Profilin-1	PFN1	0.66	15,054 DA	3	up	Cytoskeleton	affects the structure of the cytoskeleton
Q53FA3	HSPA1L Heat shock 70kDa protein 1-like variant	HSPA1L	0.67	70404 DA	4	up	Cytosol nucleoplasm	Stress responses
O00629	KPNA4 Importin subunit alpha-4	KPNA4	0.67	57,887 DA	1	up	Cytoplasm nucleus	In vitro, mediates the nuclear import of human cytomegalovirus
P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma cat	PPP1CC	0.68	36,984 DA	2	up	Cytoplasm Nucleus Mitochondria	Control of chromatin structure and cell cycle progression
P62136	PPP1CA Serine/threonine-protein phosphatase PP1-alpha cat	PPP1CA	0.68	37,512 DA	2	up	Cytoplasm Nucleus	chromatin structure and cell cycle progression
P62140	PPP1CB Serine/threonine-protein phosphatase PP1-beta cata	PPP1CB	0.68	37,187 DA	1	up	Cytoplasm Nucleus	control of chromatin structure and cell cycle progression
Q14978	NOLC1 Nucleolar and coiled-body phosphoprotein 1	NOLC1	0.68	73,603 DA	2	up	Cytoplasm Nucleus	maintenance of the fundamental structure of the fibrillar cente
Q14974	KPNB1 Importin subunit beta-1	KPNB1	0.68	97,170 DA	3	up	Cytoplasm Nuclear envelop	Functions in nuclear protein import
P61981	YWHAG 14-3-3 protein gamma	YWHAG	0.68	28,303 DA	3	up	Cytoplasm	Adapter protein implicated in the regulation of a large spectrum
Q16181	SEPT7 Septin-7	7-Sep	0.68	50,680 DA	1	up	Cytoplasm	Involved in cytokinesis
Q9NYU2	UGGT1 UDP-glucose: glycoprotein glucosyltransferase 1	UGGT1	0.69	177,190 DA	1	up	Endoplasmic reticulum	Recognizes glycoproteins with minor folding defects
P20700	LMNB1 Lamin-B1	LMNB1	0.7	66,408 DA	1	up	Nucleus inner membrane	framework for the nuclear envelope
P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	0.7	50,141 DA	10	up	Nucleus cytoplasm	involved importantly in Th1 cytokine production
Q05639	EEF1A2 Elongation factor 1-alpha 2	EEF1A2	0.7	50,470 DA	11	up	Nucleus	promotes Protein synthesis
Q8N1F7	NUP93 Nuclear pore complex protein Nup93	NUP93	0.7	93,488 DA	1	up	Nucleus membrane	Plays a role in the nuclear pore complex
P06753	TPM3 Tropomyosin alpha-3 chain	TPM3	0.7	32,950 DA	1	up	Cytoskeleton	stabilizing cytoskeleton actin filaments.
O14980	XPO1 Exportin-1	XPO1	0.7	123,386 DA	3	up	Nucleus cytoplasm	Mediates the nuclear export of cellular proteins
P60174	TP11 Triosephosphate isomerase	TP11	0.7	30,791 DA	3	up	Cytosol nucleus	Carbohydrate biosynthesis
Q53EL6	PDCD4 Programmed cell death protein 4	PDCD4	0.71	51,735 DA	1	up	Nucleus cytoplasm	Inhibits translation initiation and cap-dependent translation
Q9BUJ2	HNRNPUL1 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL1	0.71	95,739 DA	1	up	Nucleus	Acts as a basic transcriptional regulator
P22234	PAICS Multifunctional protein ADE2	PAICS	0.72	47,079 DA	1	up	Cytosol	Synthesis pathway
Q09028	RBBP4 Histone-binding protein RBBP4	RBBP4	0.73	47,656 DA	1	up	Nucleus	may target chromatin assembly factors
Q9ULV4	CORO1C Coronin-1C	CORO1C	0.73	53,249 DA	3	up	Cytoplasm Cell membrane	May be involved in cytokinesis, motility, and signal transduction
P11142	HSPA8 Heat shock cognate 71 kDa protein	HSPA8	0.73	70,898 DA	16	up	Cytoplasm nucleus cell membrane	Acts as a repressor of transcriptional activation
P55209	NAP1L1 Nucleosome assembly protein 1-like 1	NAP1L1	0.73	45,374 DA	1	up	Nucleus	modulating chromatin formation to regulation of cell proliferation.
P35232	PHB Prohibitin	PHB	0.73	29,804 DA	2	up	Mitochondrial Inner membrane	regulating mitochondrial respiration activity and in aging
O43707	ACTN4 Alpha-actinin-4	ACTN4	0.73	104,854 DA	6	up	Cytoplasm Nucleus	vesicular trafficking via its association with the CART complex
Q6IS14	EIF5A1 Eukaryotic translation initiation factor 5A-1-like	EIF5A1	0.73	16,773 DA	2	up	Cytoplasm Nuclues ER	Involved in actin dynamics and cell cycle progression
Q9GZV4	EIF5A2 Eukaryotic translation initiation factor 5A-2	EIF5A2	0.73	16,793 DA	2	up	Cytoplasm Nuclues ER	Functions as a regulator of apoptosis
P41091	EIF2S3 Eukaryotic translation initiation factor 2 subunit	EIF2S3	0.73	51,109 DA	2	up	Cytoplasm	early steps of protein synthesis by forming a ternary complex
P55072	VCP Transitional endoplasmic reticulum ATPase	VCP	0.74	89,322 DA	5	up	Cytoplasm Nuclues ER	Necessary for the fragmentation of Golgi stacks during mitosis
P30050	RPL12 60S ribosomal protein L12	RPL12	0.74	17,819 DA	1	up	Cytosol	Structural formation of ribosomes
P08107	HSPA1B Heat shock 70 kDa protein 1A/1B	HSPA1B	0.74	70 KD	7	up	Cytoplasm Nucleus	this protein stabilizes existing proteins against aggregation
O15165	C18orf1 Uncharacterized protein C18orf1	C18orf1	0.74	33,900 DA	1	up	Early endosome membrane	plays a role in cell proliferation, differentiation, apoptosis
O95373	IPO7 Importin-7	IPO7	0.75	119,517 DA	1	up	Cytoplasm Nucleus	Functions in nuclear protein import
P14649	MYL6B Myosin light chain 6B	MYL6B	0.76	22,764 DA	1	up	Cytosol	Regulatory light chain of myosin
P60660	MYL6 Myosin light polypeptide 6	MYL6	0.76	16,930 DA	1	up	Cytosol	Regulatory light chain of myosin

P61106	RAB14 Ras-related protein Rab-14	RAB14	0.76	23,897 DA	2	up	Endosome membrane	membrane trafficking between the Golgi complex and endosomes
P46940	IQGAP1 Ras GTPase-activating-like protein IQGAP1	IQGAP1	0.76	189,252 DA	4	up	Cell membrane	promote neurite outgrowth.
P36776	LONP1 Lon protease homolog, mitochondrial	LONP1	0.76	106,489 DA	4	up	Mitochondrial matrix	mediates the selective degradation of misfolded, unassembled
P12956	XRCC6 X-ray repair cross-complementing protein 6	XRCC6	0.76	69,843 DA	1	up	Nucleus Chromosomes	DNA non-homologous end joining
Q92945	KHSRP Far upstream element-binding protein 2	KHSRP	0.77	73,115 DA	5	up	Nucleus Cytoplasm	degradation of inherently unstable mRNAs contain AU-rich element
P21291	CSRP1 Cysteine and glycine-rich protein 1	CSRP1	0.77	20,567 DA	1	up	Nucleus	Could play a role in neuronal development
P12004	PCNA Proliferating cell nuclear antigen	PCNA	0.78	28,769 DA	1	up	Nucleus	involved in error-free pathway and employs recombination mechanisms
P26641	EEF1G Elongation factor 1-gamma	EEF1G	0.78	50,119 DA	8	up	Cytoplasm Nucleus	anchoring the complex to other cellular components
P05026	ATP1B1 Sodium/potassium-transporting ATPase subunit beta-	ATP1B1	0.79	35061 DA	4	up	Cell membrane	Involved in cell adhesion and establishing epithelial cell polarity
P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	0.79	36,053 DA	5	up	Cytoplasm Nucleus	playing a role in glycolysis and nuclear functions
P35637	FUS RNA-binding protein FUS	FUS	0.79	53,426 DA	5	up	Nucleus	May play a role in maintenance of genomic integrity.
Q14828	SCAMP3 Secretory carrier-associated membrane protein 3	SCAMP3	0.79	38,287 DA	1	up	Membrane	Acts as a recycling carrier to the cell surface
Q86V81	ALYREF THO complex subunit 4	ALYREF	0.79	26,888 DA	1	up	Cytoplasm Nucleus	Involved in transcription elongation and genome stability
Q15029	EFTUD2 116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	0.79	109,436 DA	1	up	Nucleus	required for pre-mRNA splicing. Binds GTP.
Q13263	TRIM28 Transcription intermediary factor 1-beta	TRIM28	0.8	88,550 DA	4	up	Nucleus	remodeling and deacetylation (NuRD) complex
P08670	VIM Vimentin	VIM	0.8	53652 DA	16	up	Cytoplasm	Involved with LARP6 in the stabilization of type I collagen mRNAs
Q13765	NACA Nascent polypeptide-associated complex subunit alp	NACA	0.8	23,384 DA	2	up	Cytoplasm Nucleus	Prevents inappropriate targeting of non-secretory polypeptides ER
Q01082	SPTBN1 Spectrin beta chain, non-erythrocytic 1	SPTBN1	0.8	274,609 DA	2	up	Cytoplasm Cytoskeleton	Ca dependent movement of the cytoskeleton at the membrane
P62937	PPIA Peptidyl-prolyl cis-trans isomerase A	PPIA	0.8	18,012 DA	6	up	Cytoplasm	accelerate the folding of proteins
P14314	PRKCSH Glucosidase 2 subunit beta	PRKCSH	0.81	59,425 DA	1	up	Endoplasmic reticulum	Glycan metabolism
Q04637	EIF4G1 Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	0.81	175,491 DA	2	up	Cytoplasm	involved in the recognition of the mRNA cap
P31930	UQCRC1 Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	0.81	52,646 DA	1	up	Mitochondrion inner membrane	It mediate formation of the complex between cytochromes c and c1.
P29692	EEF1D Elongation factor 1-delta	EEF1D	0.81	71,408 DA	4	up	Nucleus	Heat shock protein binding
P13639	EEF2 Elongation factor 2	EEF2	0.81	95,338 DA	11	up	Cytoplasm Nucleus	the mRNA and conformational changes in the ribosome
P30086	PEBP1 Phosphatidylethanolamine-binding protein 1	PEBP1	0.82	21,057 DA	1	up	Cytoplasm	presynaptic cholinergic neurons of the central nervous system
Q13838	DDX39B Spliceosome RNA helicase DDX39B	DDX39B	0.82	48,991 DA	1	up	Cytoplasm Nucleus	Involved in nuclear export of spliced and unspliced mRNA.
P00505	GOT2 Aspartate aminotransferase, mitochondrial	GOT2	0.82	33,811 DA	5	up	Golgi apparatus cell membrane CM	play a role in Golgi membrane trafficking
P30048	PRDX3 Thioredoxin-dependent peroxide reductase, mitochondon	PRDX3	0.82	48,991 DA	1	up	Cytoplasm Nucleus	Involved in nuclear export of spliced and unspliced mRNA
P04083	ANXA1 Annexin A1	ANXA1	0.82	38,714 DA	10	up	Nucleus Cytoplasm membrane	Plays important roles in the innate immune response
Q15459	SF3A1 Splicing factor 3A subunit 1	SF3A1	0.82	88,886 DA	2	up	Nucleus	involved in the assembly of the 'E' complex
Q96AE4	FUBP1 Far upstream element-binding protein 1	FUBP1	0.82	67,560 DA	2	up	Nucleus	act both as activator and repressor of transcription
P63010	AP2B1 AP-2 complex subunit beta	AP2B1	0.83	104553 DA	2	up	Cell membrane	involved in clathrin-dependent endocytosis
O60869	EDF1 Endothelial differentiation-related factor 1	EDF1	0.83	16,369 DA	2	up	Cytoplasm nucleus	cells differentiation, lipid metabolism
P53999	SUB1 Activated RNA polymerase II transcriptional coacti	SUB1	0.83	14,395 DA	1	up	Nucleus	Also binds, in vitro, non-specifically to double-stranded DNA
Q9H4A6	GOLPH3 Golgi phosphoprotein 3	GOLPH3	0.83	33,811 DA	1	up	Mitochondria, Cell membrane, GA	regulation of mitochondrial lipids biosynthesis.
P21333	FLNA Filamin-A	FLNA	0.83	280,739 DA	39	up	Cytoplasm > cytoskeleton	Involved in ciliogenesis
Q92616	GCN1L1 Translational activator GCN1	GCN1L1	0.83	292,758 DA	2	up	Cytoplasm	activity in response to amino acid starvation
Q01105	SET Protein SET	SET	0.84	33,489 DA	7	up	Cytoplasm Nucleus, ER	Multitasking protein, involved in apoptosis, transcription, nucleosome
P19338	NCL Nucleolin	NCL	0.84	76614 DA	9	up	Cytoplasm nucleus	associated with intranuclear chromatin and pre-ribosomal particles
P04843	RPN1 Dolichyl-diphosphooligosaccharide--protein glycosy	RPN1	0.84	68,569 DA	7	up	ER, Melanosomes	Essential subunit of the N-oligosaccharyl transferase
O75369	FLNB Filamin-B	FLNB	0.84	278,164 DA	3	up	Cytoplasm > cytoskeleton	Connects cell membrane constituents to the actin cytoskeleton.
Q14444	CAPRN1 Caprin-1	CAPRN1	0.84	78,366 DA	4	up	Cytosole	translation of mRNAs of proteins involved in synaptic plasticity
P62820	RAB1A Ras-related protein Rab-1A	RAB1A	0.84	22,678 DA	2	uo	Golgi ER, Cytoplasm	regulators of intracellular membrane trafficking

Q9H0U4	RAB1B Ras-related protein Rab-1B	RAB1B	0.84	22,171 DA	2	up	Cytoplasm membrane	Regulators of intracellular membrane trafficking
P62249	RPS16 40S ribosomal protein S16	RPS16	0.84	16,445 DA	1	up	cytosol, membrane ribosomes	structural constituent of ribosome
Q9Y4L1	HYOU1 Hypoxia up-regulated protein 1	HYOU1	0.84	111,335 DA	2	up	Endoplasmic reticulum lumen	pivotal role in cytoprotective cellular mechanisms triggered by $\alpha 2$ deprivation
Q9Y2B0	CNPY2 Protein canopy homolog 2	CNPY2	0.85	20,652 DA	1	up	Endoplasmic reticulum	stabilizing myosin regulatory light chain
P30101	PDIA3 Protein disulfide-isomerase A3	PDIA3	0.85	56,782 DA	7	up	Endoplasmic reticulum Melanosome	Catalyzes the rearrangement of -S-S- bonds in proteins
Q969X5	ERGIC1 Endoplasmic reticulum-Golgi intermediate compartment	ERGIC1	0.85	32,592 DA	1	up	EPR and G A	Possible role in transport between endoplasmic reticulum and Golgi apparatus
P62277	RPS13 40S ribosomal protein S13	RPS13	0.86	17,222 DA	6	up	Cytosol	Structural constituents of ribosomes
Q03135	CAV1 Caveolin-1	CAV1	0.86	20,472 DA	2	up	Golgi Cell membrane	May act as a scaffolding protein within caveolar membranes
Q14697	GANAB Neutral alpha-glucosidase AB	GANAB	0.86	106,874 DA	2	up	ER and Golgi A	This protein is involved in the pathway N-glycan metabolism
P08133	ANXA6 Annexin A6	ANXA6	0.86	75,873 DA	6	up	Cytoplasm melanosomes	May regulate the release of $Ca^{2+}$ from intracellular stores.
Q15149	PLEC Plectin	PLEC	0.86	531,791 DA	10	up	Cytoskeleton cell junction	plays a major role in the maintenance of myofiber integrity
Q12907	LMAN2 Vesicular integral-membrane protein VIP36	LMAN2	0.87	40,229 DA	1	up	Endoplasmic Reti Golgi apparatus	Role as intracellular lectin in the early secretory pathway
P26038	MSN Moesin	MSN	0.87	67,820 DA	2	up	Cytoplasm, Cell membrane	inhibit herpes simplex virus 1 infection at an early stage
P35241	RDX Radixin	RDX	0.87	52,679 DA	2	up	Cytoplasm > cytoskeleton	crucial role in the binding actin filaments to the plasma membrane
P61019	RAB2A Ras-related protein Rab-2A	RAB2A	0.88	23,546 DA	5	up	EPR and G A	protein transport from the endoplasmic reticulum to the Golgi complex
P00966	ASS1 Argininosuccinate synthase	ASS1	0.88	46,530 DA	6	up	Cytosol, Mitochondria Nucleus etc	Is indirectly involved in the control of blood pressure
P60709	ACTB Actin, cytoplasmic 1	ACTB	0.88	41,737 DA	9	up	Cytoplasm Cytoskeleton	involved in various types of cell motility
Q6P2Q9	PRPF8 Pre-mRNA-processing-splicing factor 8	PRPF8	0.88	273,600 DA	1	up	Nucleus	splice sites on pre-mRNA substrates
P23396	RPS3 40S ribosomal protein S3	RPS3	0.88	26,688 DA	6	up	Cytoplasm Nucleus Mitochondria	UV radiation and induces apoptosis by caspase-dependent JNK activation
P35579	MYH9 Myosin-9	MYH9	0.88	226,532 DA	9	up	Cytoplasm, Cytoskeleton	play a role in cytokinesis, cell shape
O00571	DDX3X ATP-dependent RNA helicase DDX3X	DDX3X	0.88	73,243 DA	5	up	Cytoplasm Nucleus Mitochondria	Acts as a cofactor for XPO1-mediated nuclear export
Q00839	HNRNPU Heterogeneous nuclear ribonucleoprotein U	HNRNPU	0.88	90,584 DA	4	up	Cytoplasm nucleus, cell surface	circadian regulation of the core clock component ARNTL/BMAL1
Q14157	UBAP2L Ubiquitin-associated protein 2-like	UBAP2L	0.88	114,535 DA	2	up	PeG protein complex	role in the activity of long-term repopulating hematopoietic stem cells
O00264	PGRMC1 Membrane-associated progesterone receptor component	PGRMC1	0.89	21,671 DA	1	up	EPR melanosome	Receptor for progesterone, heme binding
P08195	SLC3A2 4F2 cell-surface antigen heavy chain	SLC3A2	0.89	67,994 DA	7	up	cell membrane	Required for the function of light chain amino-acid transporters
P15924	DSP Desmoplakin	DSP	0.89	331,774 DA	4	up	Cytoplasm Cemm membrane	Involved in the organization of the desmosomal cadherin-plakoglobin complex
Q15056	EIF4H Eukaryotic translation initiation factor 4H	EIF4H	0.89	27,385 DA	2	up	Cytoplasm	Stimulates the RNA helicase activity of EIF4A in the translation initiation
Q8NC51	SERBP1 Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	0.89	44,965 DA	4	up	Cytoplasm nucleus	regulation of mRNA stability
P62633	CNBP Cellular nucleic acid-binding protein	CNBP	0.89	19,463 DA	1	up	Cytoplasm EPR	Involved in sterol-mediated repression
Q9NVP1	DDX18 ATP-dependent RNA helicase DDX18	DDX18	0.89	75,407 DA	2	up	Nucleus	Probable RNA-dependent helicase
P55854	SUMO3 Small ubiquitin-related modifier 3	SUMO3	0.89	11,637 DA	1	up	Cytoplasm nucleus	Plays a role in the regulation of sumoylation status of SETX
Q6EEV6	SUMO4 Small ubiquitin-related modifier 4	SUMO4	0.89	10,685 DA	1	up	nucleus	activation of E1 complex SAE1-SAE2
P31946	YWHAB 14-3-3 protein beta/alpha	YWHAB	0.89	28,082 DA	3	up	Cytoplasm	blockage of neuronal apoptosis elicited by SRPK2
P67809	YBX1 Nuclease-sensitive element-binding protein 1	YBX1	0.9	35,924 DA	3	up	Cytoplasm Nucleus	role in DNA repair
P07237	P4HB Protein disulfide-isomerase	P4HB	0.9	57,116 DA	11	up	EPR Cell membrane	altering the plasma membrane redox state and enhancing cell migration
P62244	RPS15A 40S ribosomal protein S15a	RPS15A	0.9	14,840 DA	1	up	Cytoplasm membrane	structural constituent of ribosome
P80723	BASP1 Brain acid soluble protein 1	BASP1	0.9	22,693 DA	4	up	Cell membrane	transcription regulatory region DNA binding
Q9BZZ5	API5 Apoptosis inhibitor 5	API5	0.9	59,005 DA	1	up	Cytoplasm Nucleus	Its depletion enhances the cytotoxic action of the chemotherapeutic drug
Q9P035	PTPLAD1 3-hydroxyacyl-CoA dehydratase 3	PTPLAD1	0.9	43,160 DA	2	up	EPR	involved in INSR internalization
P32969	RPL9P9 60S ribosomal protein L9	RPL9P9	0.91	21,863 DA	7	up	Cytoplasm membrane nucleus	structural constituent of ribosome
P51991	HNRNPA3 Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	0.91	39,595 DA	5	up	Nucleus	role in cytoplasmic trafficking of RNA
Q81YD1	GSPT2 Eukaryotic peptide chain release factor GTP-binding	GSPT2	0.91	68,883 DA	1	up	Cytoplasm	play a role in cell cycle progression
Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	0.91	629,101 DA	15	up	Nucleus	May be required for neuronal cell differentiation.



P23284	PPIB Peptidyl-prolyl cis-trans isomerase B	PPIB	0.91	23,743 DA	4	up	EPR melanosome	PPIases accelerate the folding of proteins
Q96A33	CCDC47 Coiled-coil domain-containing protein 47	CCDC47	0.92	55,318 DA	1	up	Membrane	calcium ion binding
A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	0.92	NA	6	up	NO data	No data
P51571	SSR4 Translocon-associated protein subunit delta	SSR4	0.92	18,999 DA	5	up	EPR	regulate the retention of ER resident proteins.
P78347	GTF2I General transcription factor II-I	GTF2I	0.92	112416 DA	5	up	Cytoplasm nucleus	Acts as a coregulator for USF1 by binding independently
P06748	NPM1 Nucleophosmin	NPM1	0.92	32,575 DA	7	up	Cytoplasm Nucleus	Involved in diverse cellular processes such as ribosome biogenesis
P46782	RPS5 40S ribosomal protein S5	RPS5	0.92	22876 DA	2	up	Cytosol,membrane	structural constituent of ribosome
P09429	HMGB1 High mobility group protein B1	HMGB1	0.92	24,894 DA	4	up	Cytoplasm nucleus cell membrane	promotes recruitment of ALD-DNA to endosomes
O75390	CS Citrate synthase, mitochondrial	CS	0.92	51,712 DA	1	up	Mitochondrai matrix	synthesizes isocitrate from oxaloacetate
P17096	HMGA1 High mobility group protein HMGI/HMG-Y	HMGA1	0.92	19,694 DA	1	up	Nucleus Chromosomes	involved in the transcription regulation of genes containing
P11021	HSPA5 78 kDa glucose-regulated protein	HSPA5	0.93	55,010 DA	1	up	Cytoplasm Apical C membrane	Acts as the major transporter of tyrosine in fibroblasts
P22695	UQCRC2 Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	0.93	48,443 DA	1	up	Mitochondrial Inner Membrane	The core protein 2 is required for the assembly of the complex.
P12814	ACTN1 Alpha-actinin-1	ACTN1	0.93	103,058 DA	3	up	Cytoplasm	variety of intracellular structures
P42704	LRPPRC Leucine-rich PPR motif-containing protein, mitocho	LRPPRC	0.94	157,905 DA	10	up	Mitochondria Nucleus	role in RNA metabolism in both nuclei and mitochondria
P26368	U2AF2 Splicing factor U2AF 65 kDa subunit	U2AF2	0.94	53,501 DA	4	up	Nucleus	Required for the export of mRNA out of the nucleus
O60506	SYNCRIP Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	0.94	69,603 DA	8	up	Cytoplasm EPR Nucleus	involved in cytoplasmic vesicle-based mRNA transport
Q12905	ILF2 Interleukin enhancer-binding factor 2	ILF2	0.94	43,062 DA	2	up	Cytoplasm Nucleus	promote the formation of stable DNA-dependent protein kinase
Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	0.94	238,260 DA	2	up	Cytoplasm nucleus chromosome	proper alignment of the mitotic spindle during asymmetric cell division
Q07065	CKAP4 Cytoskeleton-associated protein 4	CKAP4	0.95	66,022 DA	8	up	EPR Cell membrane	anchoring of the endoplasmic reticulum to microtubules.
P62913	RPL11 60S ribosomal protein L11	RPL11	0.95	20,252 DA	1	up	Nucleus	Required for rRNA maturation and formation of the 60S ribosomal subunit
P62873	GNB1 Guanine nucleotide-binding protein G(I)/G(S)/G(T)	GNB1	0.95	37,377 DA	1	up	Cytosol membrane sheath	involved as transducer in various transmembrane signaling systems
P62879	GNB2 Guanine nucleotide-binding protein G(I)/G(S)/G(T)	GNB2	0.95	37,331 DA	1	up	Cytoplasm	involved as transducer in various transmembrane signaling systems
Q9HAV0	GNB4 Guanine nucleotide-binding protein subunit beta-4	GNB4	0.95	37567 DA	1	up	Organelle membrane	involved as transducer in various transmembrane signaling systems
P07954	FH Fumarate hydratase, mitochondrial	FH	0.95	54,637 DA	2	up	Cytoplasm Mitochondria	Acts as a tumor suppressor
P14625	HSP90B1 Endoplasmic	HSP90B1	0.95	92,469 DA	8	up	EPR melanosomes	EPR associated degradation (ERAD). Has ATPase activity
P13667	PDIA4 Protein disulfide-isomerase A4	PDIA4	0.96	72,932 DA	4	up	EPR melanosome	Catalyzes the rearrangement of -S-S- bonds in protein
Q96N66	MBOAT7 Lysophospholipid acyltransferase 7	MBOAT7	0.96	44733 DA	1	up	Membrane	catalyze the reacylation step of the phospholipid remodeling pathway
O75844	ZMPSTE24 CAAX prenyl protease 1 homolog	ZMPSTE24	0.96	54,813 DA	2	up	Membrane of EPR and GA	Proteolytically removes the C-terminal three residues of farnesylated proteins
P23246	SFPQ Splicing factor, proline- and glutamine-rich	SFPQ	0.97	76,149 DA	5	up	Cytoplasm Nucleus	transcriptional repression of circadian target genes, such as PER1
P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	0.97	61,055 DA	15	up	Mitochondria Matrix	May also prevent misfolding and promote the refolding
Q00325	SLC25A3 Phosphate carrier protein, mitochondrial	SLC25A3	0.97	40,095 DA	3	up	Mitochondrai Inner membrane	role regulation of the mitochondrial permeability transition pore
Q01650	SLC7A5 Large neutral amino acids transporter small subunit	SLC7A5	0.98	55,010 Da	1	up	Cytoplasm Cell membrane	Acts as the major transporter of tyrosine in fibroblasts.
P37198	NUP62 Nuclear pore glycoprotein p62	NUP62	0.98	53,255 DA	1	up	Cytoplasm Nucleus	Involved in nucleocytoplasmic transport
Q96GQ7	DDX27 Probable ATP-dependent RNA helicase DDX27	DDX27	0.98	89,835 DA	1	up	Nucleus	Probable ATP-dependent RNA helicase
P38646	HSPA9 Stress-70 protein, mitochondrial	HSPA9	0.98	73,680 DA	14	up	Mitochondria Nucleus	cell proliferation and cellular aging
Q9Y277	VDAC3 Voltage-dependent anion-selective channel protein	VDAC3	0.98	30,659 DA	2	up	Mitochondrial membrane	membrane that allows diffusion of small hydrophilic molecules
P50454	SERPINH1 Serpin H1	SERPINH1	0.98	46,441 DA	6	up	EPR	involved as a chaperone in the biosynthetic pathway of collagen
Q9Y676	MRPS18B 28S ribosomal protein S18b, mitochondrial	MRPS18B	0.99	29,396 DA	1	up	Mitochondrial	structural constituent of ribosome
P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	0.99	35077 DA	5	up	Cytoplasm Nucleus membrane	Promotes migration of breast carcinoma cells by binding to and activating integrins
Q7KZF4	SND1 Staphylococcal nuclease domain-containing protein	SND1	0.99	101,997 DA	2	up	Cytoplasm Nucleus Melanosome	Transcriptional coactivator for the Epstein-Barr virus nuclear antigen 2
Q15084	PDIA6 Protein disulfide-isomerase A6	PDIA6	0.99	48,121 DA	8	up	EPR Cytoplasm	inhibits aggregation of misfolded proteins
P61978	HNRNP K Heterogeneous nuclear ribonucleoprotein K	HNRNP K	1	50,976 DA	14	up	Cytoplasm Nucleus	Induction of apoptosis, but not cell cycle arrest
P01891	HLA-A HLA class I histocompatibility antigen, A-68 alpha	HLA-A	1	40,909 DA	2	up	Membrane	Involved in the presentation of foreign antigens to the immune system.

P01892	HLA-A HLA class I histocompatibility antigen, A-2 alpha	HLA-A	1	40,922 DA	2	up	Membrane	Involved in the presentation of foreign antigens to the immune system.
P04439	HLA-A HLA class I histocompatibility antigen, A-3 alpha	HLA-A	1	40,841 DA	2	up	membrane	nvolved in the presentation of foreign antigens to the immune system
P05534	HLA-A HLA class I histocompatibility antigen, A-24 alpha	HLA-A	1	40,689 DA	2	up	membrane	nvolved in the presentation of foreign antigens to the immune system
P10314	HLA-A HLA class I histocompatibility antigen, A-32 alpha	HLA-A	1	41,048 DA	2	up	membrane	Involved in the presentation of foreign antigens to the immune system.
P16188	HLA-A HLA class I histocompatibility antigen, A-30 alpha	HLA-A	1	40,905 DA	2	up	membrane	Involved in the presentation of foreign antigens to the immune system.
P16189	HLA-A HLA class I histocompatibility antigen, A-31 alpha	HLA-A	1	41,004 DA	2	up	membrane	nvolved in the presentation of foreign antigens to the immune system
P18462	HLA-A HLA class I histocompatibility antigen, A-25 alpha	HLA-A	1	41,218 DA	2	up	membrane	nvolved in the presentation of foreign antigens to the immune system
P30443	HLA-A HLA class I histocompatibility antigen, A-1 alpha	HLA-A	1	40,846 DA	2	up	membrane	Involved in the presentation of foreign antigens to the immune system.
P30453	HLA-A HLA class I histocompatibility antigen, A-34 alpha	HLA-A	1	41,055 DA	2	up	membrane	Involved in the presentation of foreign antigens to the immune system.
P30456	HLA-A HLA class I histocompatibility antigen, A-43 alpha	HLA-A	1	41,033 DA	2	up	membrane	nvolved in the presentation of foreign antigens to the immune system
P30459	HLA-A HLA class I histocompatibility antigen, A-74 alpha	HLA-A	1	40,891 DA	2	up	membrane	nvolved in the presentation of foreign antigens to the immune system
P30512	HLA-A HLA class I histocompatibility antigen, A-29 alpha	HLA-A	1	40,863 DA	2	up	membrane	Involved in the presentation of foreign antigens to the immune system.
Q29960	HLA-C HLA class I histocompatibility antigen, Cw-16 alph	HLA-C	1	40,753 DA	2	up	membrane	Involved in the presentation of foreign antigens to the immune system.
Q95604	HLA-C HLA class I histocompatibility antigen, Cw-17 alph	HLA-C	1	41,238 DA	2	up	membrane	nvolved in the presentation of foreign antigens to the immune system
P05387	RPLP2 60S acidic ribosomal protein P2	RPLP2	1	11,665 DA	4	up	Cytosol Membrane	Plays an important role in the elongation step of protein synthesis.
Q16630	CPSF6 Cleavage and polyadenylation specificity factor su	CPSF6	1	59,210 DA	4	up	Nucleus	Involved in association with NUDT21/CPSF5 in pre-mRNA 3'-end pol
P39656	DDOST Dolichyl-diphosphooligosaccharide--protein glycosy	DDOST	1	50,801 DA	2	up	EPR	This protein is involved in the pathway protein glycosylation
O60488	ACSL4 Long-chain-fatty-acid--CoA ligase 4	ACSL4	1	79,188 DA	1	up	Membrane of Mitochondria EPR	synthesis of cellular lipids, and degradation via beta-oxidation
O95573	ACSL3 Long-chain-fatty-acid--CoA ligase 3	ACSL3	1	80,420 DA	1	up	Membrane of Mitochondria EPR	both synthesis of cellular lipids, and degradation via beta-oxidation
Q13283	G3BP1 Ras GTPase-activating protein-binding protein 1	G3BP1	1.01	52,164 DA	1	up	Cytoplasm Cell membrane Nucleus	May be a regulated effector of stress granule assembly
P45880	VDAC2 Voltage-dependent anion-selective channel protein	VDAC2	1.01	31,567 DA	6	up	Mitochondrial membrane	Allows diffusion of small hydrophilic molecules
Q6YN16	HSDL2 Hydroxysteroid dehydrogenase-like protein 2	HSDL2	1.01	45,395 DA	1	up	Peroxisome	Has apparently no steroid dehydrogenase activity
Q9H7Z7	PTGES2 Prostaglandin E synthase 2	PTGES2	1.02	41,943 DA	2	up	GA membrane	Isomerase that catalyzes the conversion of PGH2 into the more stable p
Q13148	TARDBP TAR DNA-binding protein 43	TARDBP	1.02	44,740 DA	4	up	Nucleus	nvolved in the regulation of CFTR splicing
Q13813	SPTAN1 Spectrin alpha chain, non-erythrocytic 1	SPTAN1	1.02	284,539 DA	2	up	Cytoplasm	calcium-dependent movement of the cytoskeleton at the membrane
Q16836	HADH Hydroxyacyl-coenzyme A dehydrogenase, mitochondria	HADH	1.03	34,294 DA	1	up	Mitochondrian Matrix	mitochondrial beta-oxidation of short chain fatty acids
P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	1.03	49,229 DA	9	up	Nucleus	Inhibits, together with CUGBP1, insulin receptor (IR) pre-mRNA exon
O43390	HNRNPR Heterogeneous nuclear ribonucleoprotein R	HNRNPR	1.04	70,943 DA	6	up	Nucleus Cytoplasm	Play an important role in processing of precursor mRNA in the nucleus
P25705	ATP5A1 ATP synthase subunit alpha, mitochondrial	ATP5A1	1.04	59,751 DA	15	up	Mitochondrial matrix membrane	Mitochondrial membrane ATP synthase
Q07021	C1QBP Complement component 1 Q subcomponent-binding prot	C1QBP	1.04	31,362 DA	7	up	Cytoplasm, Nucleus ,mitochondria cm	Involved in regulation of antiviral response by inhibiting DDX58- and I
Q9Y3C1	NOPI6 Nucleolar protein 16	NOPI6	1.04	21,188 DA	1	up	Nucleus	ribosomal large subunit biogenesis
Q96PK6	RBM14 RNA-binding protein 14	RBM14	1.05	69,492 DA	1	up	Nucleus	transcriptional repressor
P04844	RPN2 Dolichyl-diphosphooligosaccharide--protein glycosy	RPN2	1.05	69,284 DA	7	up	EPR	transfer of a high mannose oligosaccharide from a lipid-linked
P26599	PTBP1 Polypyrimidine tract-binding protein 1	PTBP1	1.05	57,221 DA	11	up	Nucleus	role in pre-mRNA splicing and in the regulation of alternative splicing
P21796	VDAC1 Voltage-dependent anion-selective channel protein	VDAC1	1.05	30,773 DA	6	up	Mitochondrial Membrane Cell membr	responsible for the release of mitochondrial products that triggers apopt
P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	1.05	34,274 DA	8	up	Cytoplasm Nucleus	structural constituent of ribosome
P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	1.05	49,542 DA	1	up	Mitochondria	A-site of ribosomes during protein biosynthesis.
Q15366	PCBP2 Poly(rC)-binding protein 2	PCBP2	1.05	38,580 DA	2	up	Nucleus Cytoplasm	role in initiation of viral RNA replication in concert with the viral prote
P22626	HNRNPA2B1 Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	1.06	37,430 DA	14	up	Cytoplasm Nucleus	Involved in miRNA sorting into exosomes following sumoylation
P09651	HNRNPA1 Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	1.06	38,747 DA	10	up	Cytoplasm Nucleus	play a role in HCV RNA replication
P27824	CANX Calnexin	CANX	1.06	67,568 DA	10	up	EPR membrane	It may act in assisting protein assembly
P62888	RPL30 60S ribosomal protein L30	RPL30	1.06	12,784 DA	3	up	Cytoplasm Nucleus Membrane	structural constituent of ribosome
P16615	ATP2A2 Sarcoplasmic/endoplasmic reticulum calcium ATPase	ATP2A2	1.07	114,757 DA	2	up	EPR SPR	involved in the regulation of the contraction/relaxation cycle

Q14103	HNRNPD Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	1.08	38,434 DA	2	up	cytoplasm Nucleus	involved in the regulation of PER2 translation
Q99729	HNRNPAB Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	1.08	36,225 DA	5	up	Nucleus Cytoplasm	binds to APOB mRNA transcripts around the RNA editing site
P38159	RBMX RNA-binding motif protein, X chromosome	RBMX	1.08	42,332 DA	3	up	Nucleus	Plays also a role in the cytoplasmic TNFR1 trafficking pathways
P17844	DDX5 Probable ATP-dependent RNA helicase DDX5	DDX5	1.09	69,148 DA	5	up	Nucleus	Involved in the alternative regulation of pre-mRNA splicing
Q92841	DDX17 Probable ATP-dependent RNA helicase DDX17	DDX17	1.09	80,272 DA	2	up	Nucleus	mediated mRNA degradation
P34897	SHMT2 Serine hydroxymethyltransferase, mitochondrial	SHMT2	1.09	55,993 DA	2	up	Mitochondria cytoplasm Nucleus	Contributes to the de novo mitochondrial thymidylate biosynthesis
Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	1.1	140,958 DA	8	up	Nucleus Cytoplasm	Unwinds double-stranded DNA and RNA in a 3' to 5' direction
P52597	HNRNPF Heterogeneous nuclear ribonucleoprotein F	HNRNPF	1.1	45,672 DA	7	up	Nucleus	role in the regulation of alternative splicing events
P43243	MATR3 Matrin-3	MATR3	1.1	94,623 DA	3	up	Nucleus Matrix	play a role in transcription or may interact with other nuclear matrix proteins
P31327	CPS1 Carbamoyl-phosphate synthase	CPS1	1.1	164,939 DA	18	up	Mitochondria Nucleus	role in removing excess ammonia from the cell.
O14880	MGST3 Microsomal glutathione S-transferase 3	MGST3	1.1	16,516 DA	2	up	EPR	Also functions as a glutathione peroxidase.
P54709	ATP1B3 Sodium/potassium-transporting ATPase subunit beta-	ATP1B3	1.1	74,176 DA	1	up	Mitochondrial membrane	May have a function in the urea cycle
P61026	RAB10 Ras-related protein Rab-10	RAB10	1.11	22,541 DA	1	up	EPR GA	EPR dynamics, morphology controlling tubulation along microtubules
P02545	LMNA Prelamin-A/C	LMNA	1.11	74,139 DA	8	up	Nucleus	It acts to disrupt mitosis and induce DNA damage
P99999	CYCS Cytochrome c	CYCS	1.11	11,749 DA	1	up	Mitochondrial membrane	activation of caspase-9, which accelerates apoptosis by activating other caspases
Q9BVC6	TMEM109 Transmembrane protein 109	TMEM109	1.11	26,210 DA	1	up	EPR Nuclear membrane	Can form voltage-gated calcium and potassium channels in vitro
P54886	ALDH18A1 Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	1.12	87,302 DA	2	up	Mitochondrial membrane	Biosynthesis of proline, ornithine and arginine
P98179	RBM3 Putative RNA-binding protein 3	RBM3	1.14	17,170 DA	1	up	Cytoplasm Nucleus	enhances protein synthesis at both physiological and mild hypothermic temperatures
P62081	RPS7 40S ribosomal protein S7	RPS7	1.14	22,127 DA	8	up	Cytoplasm	Required for rRNA maturation
O14548	COX7A2L Cytochrome c oxidase subunit 7A-related protein, mitochondrial	COX7A2L	1.14	12,615 DA	1	up	Mitochondrial inner membrane	Involved in the regulation of oxidative phosphorylation and energy metabolism
Q10471	GALNT2 Polypeptide N-acetylgalactosaminyltransferase 2	GALNT2	1.15	64,733 DA	4	up	Golgi Apparatus	involved in immunoglobulin A1 (IgA1) hinge region
O43143	DHX15 Putative pre-mRNA-splicing factor ATP-dependent RN	DHX15	1.15	90,933 DA	1	up	Nucleus	involved in disassembly of spliceosomes after the release of mature mRNA
P31942	HNRNPH3 Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	1.16	36,926 DA	1	up	Nucleus	splicing process and participates in early heat shock-induced splicing activation
O43169	CYB5B Cytochrome b5 type B	CYB5B	1.16	16,332 DA	2	up	Mitochondria membrane	function as an electron carrier for several membrane bound oxygenases
O75643	SNRNP200 U5 small nuclear ribonucleoprotein 200 kDa helicas	SNRNP200	1.16	244,508 DA	2	up	Nucleus	essential step in the assembly of a catalytically active spliceosome
P36957	DLST Dihydropyridyllysine-residue succinyltransferase co	DLST	1.16	48,755 DA	1	up	Mitochondria	Involves in lipamide dehydrogenase
P39748	FEN1 Flap endonuclease 1	FEN1	1.17	42,593 DA	1	up	Nucleus	involved in replication and repair of rDNA and in repairing mitochondrial DNA
Q9NR30	DDX21 Nucleolar RNA helicase 2	DDX21	1.17	87,344 DA	8	up	Nucleus Cytoplasm	Involved in rRNA processing
O14974	PPP1R12A Protein phosphatase 1 regulatory subunit 12A	PPP1R12A	1.17	115,281 DA	1	up	Cytoplasm	involved in dephosphorylation of PLK1
O00159	MYO1C Unconventional myosin-1c	MYO1C	1.18	121,682 DA	2	up	Cytoplasm nucleus	Binds phosphoinositides and links the actin cytoskeleton to cellular membranes
P06576	ATP5B ATP synthase subunit beta, mitochondrial	ATP5B	1.19	56,560 DA	9	up	trtarsubunit beta, mitochondr	Mitochondrial membrane ATP synthase
Q02218	OGDH 2-oxoglutarate dehydrogenase, mitochondrial	OGDH	1.19	115,935 DA	2	up	Mitochondrial matrix	Regulate lipamide dehydrogenase
Q99623	PHB2 Prohibitin-2	PHB2	1.21	33,296 DA	6	up	Cytoplasm Mitochondria Nucleus	Probably involved in regulating mitochondrial respiration activity and in mitochondrial membrane dynamics
P12236	SLC25A6 ADP/ATP translocase 3	SLC25A6	1.22	32,866 DA	7	up	Mitochondria Inner mem	responsible for the release of mitochondrial products that triggers apoptosis
Q9UJS0	SLC25A13 Calcium-binding mitochondrial carrier protein Aral	SLC25A13	1.24	74,176 DA	1	up	Mitochondria Inner mem	May have a function in the urea cycle
P09874	PARP1 Poly	PARP1	1.24	113,084 DA	4	up	Nucleus	Involved in the base excision repair (BER) pathway
P15880	RPS2 40S ribosomal protein S2	RPS2	1.24	31,324 DA	1	up	Cytoplasm membrane nucleus	structural constituent of ribosome
P13804	ETFA Electron transfer flavoprotein subunit alpha, mito	ETFA	1.24	35,080 DA	1	up	Mitochondrial matrix	It transfers the electrons to the main mitochondrial respiratory chain via ubiquinone
Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	1.25	26,923 DA	4	up	Mitochondria	contribute to the neuronal dysfunction associated with Alzheimer disease
Q16563	SYPL1 Synaptophysin-like protein 1	SYPL1	1.27	28,565 DA	1	up	Cytoplasm membrane	transporter activity
Q96AG4	LRRCS9 Leucine-rich repeat-containing protein 59	LRRCS9	1.27	34,930 DA	1	up	EPR Nucleus	Required for nuclear import of FGF1
J3QL51	RPL17-C18ORF32 Protein RPL17-C18ORF32	RPL17-C18ORF32	1.28	21,397 DA	2	up	Cytosol Nucleus	structural constituent of ribosome
P18621	RPL17 60S ribosomal protein L17	RPL17	1.28	21,397 DA	2	up	Cytosol Nucleus	structural constituent of ribosome

Q9BSJ8	ESYT1 Extended synaptotagmin-1	ESYT1	1.29	122,856 DA	3	up	EPR Cell membrane	promotes the formation of appositions between the ER and the cell membrane
P05141	SLC25A5 ADP/ATP translocase 2	SLC25A5	1.3	32,852 DA	8	up	Mitochondria Inner membrane	play a role in chromosome segregation
Q9NVH1	DNAJC11 DnaJ homolog subfamily C member 11	DNAJC11	1.3	63,278 DA	2	up	Mitochondria	Acts as Chaperon
Q9UQ80	PA2G4 Proliferation-associated protein 2G4	PA2G4	1.31	43,787 DA	1	up	Nucleus Cytoplasm	Regulates cell proliferation, differentiation, and survival
P62263	RPS14 40S ribosomal protein S14	RPS14	1.32	16,273 DA	1	up	Cytoplasm Mitochondria Nucleus	structural constituent of ribosome
Q02543	RPL18A 60S ribosomal protein L18a	RPL18A	1.32	20,762 DA	1	up	Cytosol membrane	Structural constituent of ribosome
P34932	HSPA4 Heat shock 70 kDa protein 4	HSPA4	1.33	94,331 DA	1	up	Cytoplasm	ATP binding
Q96EP5	DAZAP1 DAZ-associated protein 1	DAZAP1	1.33	43,383 DA	1	up	Nucleus Cytoplasm	RNA-binding protein, which may be required during spermatogenesis.
P11388	TOP2A DNA topoisomerase 2-alpha	TOP2A	1.35	174,385 DA	1	up	Nucleus Cytoplasm	regulating the period length of ARNTL/BMAL1 transcriptional oscillation
P52272	HNRNPM Heterogeneous nuclear ribonucleoprotein M	HNRNPM	1.35	77,516 DA	1	up	Nucleus	may initiate a series of signaling events leading to tumor necrosis factor production
O14979	HNRPDL Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	1.36	46,438 DA	4	up	Nucleus Cytoplasm	Acts as a transcriptional regulator. Promotes transcription repression.
P57053	H2BFS Histone H2B type F-S	H2BFS	1.37	13,944 DA	4	up	Nucleus cytoplasm	modifications of histones, also called histone code, and nucleosome remodeling
Q5QNW6	HIST2H2BF Histone H2B type 2-F	HIST2H2BF	1.37	13,920 DA	4	up	Nucleus Chromosomes	modifications of histones, also called histone code, and nucleosome remodeling
Q99879	HIST1H2BM Histone H2B type 1-M	HIST1H2BM	1.37	13,989 DA	4	up	Nucleus Chromosomes	modifications of histones, also called histone code, and nucleosome remodeling
Q99880	HIST1H2BL Histone H2B type 1-L	HIST1H2BL	1.37	13,952 DA	4	up	Nucleus Chromosomes	modifications of histones, also called histone code, and nucleosome remodeling
P18754	RCC1 Regulator of chromosome condensation	RCC1	1.37	44,969 DA	1	up	Nucleus Cytoplasm	role in nucleo-cytoplasmic transport, mitosis and nuclear-envelope assembly
P43307	SSR1 Translocon-associated protein subunit alpha	SSR1	1.38	32,235 DA	1	up	EPR	involved in the recycling of the translocation apparatus
Q16629	SRSF7 Serine/arginine-rich splicing factor 7	SRSF7	1.38	27,367 DA	2	up	Nucleus Cytoplasm	Required for pre-mRNA splicing
P61513	RPL37A 60S ribosomal protein L37a	RPL37A	1.39	10,275 DA	1	up	Cytosol Nucleus	structural constituent of ribosome
O75494	SRSF10 Serine/arginine-rich splicing factor 10	SRSF10	1.4	31,301 DA	1	up	Nucleus Cytoplasm	regulation of alternative splicing in neurons, with isoform
Q15393	SF3B3 Splicing factor 3B subunit 3	SF3B3	1.41	135,577 DA	2	up	Nucleus	splicing of rare class of nuclear pre-mRNA intron
Q15233	NONO Non-POU domain-containing octamer-binding protein	NONO	1.45	54,232 DA	2	up	Nucleus	DNA- and RNA binding protein, involved in several nuclear processes
Q8IU66	HIST2H2AB Histone H2A type 2-B	HIST2H2AB	1.46	13,995 DA	2	up	Nucleus chromosomes	modifications of histones, also called histone code, and nucleosome remodeling
P46778	RPL21 60S ribosomal protein L21	RPL21	1.48	18,565 DA	3	up	Cytoplasm Nucleus membrane	structural constituent of ribosome
P02786	TFRC Transferrin receptor protein 1	TFRC	1.49	84,871 DA	5	up	Cell membrane melanosomes	Acts as a receptor for new-world arenaviruses
P16104	H2AFX Histone H2A.x	H2AFX	1.5	15,145 DA	6	downregulated	Nucleus chromosomes	Histones play a central role in transcription regulation, DNA repair, DNA replication, and cell cycle progression
Q96QV6	HIST1H2AA Histone H2A type 1-A	HIST1H2AA	1.5	14,234 DA	6	downregulated	Nucleus chromosomes	modifications of histones, also called histone code, and nucleosome remodeling
P35268	RPL22 60S ribosomal protein L22	RPL22	1.52	14,787 DA	1	downregulated	cytoplasm nucleus	structural constituent of ribosome
P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	1.52	35,503 DA	6	downregulated	Mitochondrial Matrix	Enzyme activity is enhanced by acetylation
P11940	PABPC1 Polyadenylate-binding protein 1	PABPC1	1.54	70,671 DA	2	downregulated	Cytoplasm Nucleus	Involved in cytoplasmic regulatory processes of mRNA metabolism
Q13310	PABPC4 Polyadenylate-binding protein 4	PABPC4	1.54	70,783 DA	2	downregulated	Cytoplasm	involved in cytoplasmic regulatory processes of mRNA metabolism
O15260	SURF4 Surfitei locus protein 4	SURF4	1.57	30,394 DA	1	downregulated	EPR GA	Architecture of the EPR intermediate compartment and of the Golgi apparatus
P62158	CALM3 Calmodulin	CALM3	1.58	16,838 DA	1	downregulated	Cytoplasm	regulates the centrosome cycle and progression through cytokinesis
P62910	RPL32 60S ribosomal protein L32	RPL32	1.63	15,860 DA	1	downregulated	Cytosol membrane	structural constituent of ribosome
P46783	RPS10 40S ribosomal protein S10	RPS10	1.65	18,898 DA	1	downregulated	Cytoplasm Nucleus	Component of the 40S ribosomal subunit.
P05386	RPLP1 60S acidic ribosomal protein P1	RPLP1	1.66	11,514 DA	2	downregulated	Cytoplasm	Plays an important role in the elongation step of protein synthesis
P0C088	HIST1H2AM Histone H2A type 1	HIST1H2AM	1.72	14,091 DA	1	downregulated	Nucleus Chromosomes	modifications of histones, also called histone code, and nucleosome remodeling
Q16777	HIST2H2AC Histone H2A type 2-C	HIST2H2AC	1.72	13,988 DA	1	downregulated	Nucleus Chromosomes	modifications of histones, also called histone code, and nucleosome remodeling
Q9BTM1	H2AFJ Histone H2A.J	H2AFJ	1.72	14,019 DA	1	downregulated	Nucleus Chromosomes	Histones, also called histone code, and nucleosome remodeling.
Q7L7L0	HIST3H2A Histone H2A type 3	HIST3H2A	1.72	14,121 DA	5	downregulated	Nucleus chromosomes	modifications of histones, also called histone code, and nucleosome remodeling
P07602	PSAP Proactivator polypeptide	PSAP	1.73	58,113 DA	1	downregulated	Lysosomes	sequential action of specific hydrolases
P18124	RPL7 60S ribosomal protein L7	RPL7	1.87	29,226 DA	2	downregulated	Cytoplasm Nucleus Membrane	Plays a regulatory role in the translation apparatus; inhibits cell-free translation
O60812	HNRNPCL1 Heterogeneous nuclear ribonucleoprotein C-like 1	HNRNPCL1	1.96	32,142 DA	1	downregulated	Nucleus	May play a role in nucleosome assembly by neutralizing basic proteins

P07910	HNRNPC Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	1.96	33,670 DA	1	downregulated	Nucleus	stability and the level of translation of bound mRNA molecules
P47914	RPL29 60S ribosomal protein L29	RPL29	1.98	17,752 DA	1	downregulated	Cytosol membrane	structural constituent of ribosome
Q02878	RPL6 60S ribosomal protein L6	RPL6	2.15	32,728 DA	2	Downregulated	Cytosol Nucleus	structural constituent of ribosome
P62241	RPS8 40S ribosomal protein S8	RPS8	2.21	24,205 DA	3	Downregulated	Cytoplasm membrane	structural constituent of ribosome
P61604	HSPE1 10 kDa heat shock protein, mitochondrial	HSPE1	2.25	10,932 DA	1	Downregulated	Mitochondrion matrix	suppresses the ATPase activity of the latter
P0C0S5	H2AFZ Histone H2A.Z	H2AFZ	2.47	13,553 DA	4	Downregulated	Nucleus Chromosomes	required for chromosome segregation during cell division
Q71U19	H2AFV Histone H2A.V	H2AFV	2.47	13,509 DA	4	Downregulated	Nucleus Chromosomes	required for chromosome segregation during cell division
P62805	HIST4H4 Histone H4	HIST4H4	3	11,367 DA	5	downregulated	Nucleus Chromosomes	histone code, and nucleosome remodeling
P84243	H3F3B Histone H3.3	H3F3B	3.02	15,328 DA	2	Downregulated	Nucleus Chromosomes	histone code, and nucleosome remodeling
P20674	COX5A Cytochrome c oxidase subunit 5A, mitochondrial	COX5A	6.61	16,762 DA	1	down regulated	Mitochondrial membrane	mitochondrial electron transport.

**Table S2.** Differentially expression of key proteins in response to Fe<sub>2</sub>C@C NPs.

Accession Number	Gene Name	O16/O18 Ratio	Sequence of Unique peptide	Retention Time	Function
P0CG48	UBC	0.21	K.TITLEVEPSDTIENVK*.A	51.5 min	Activation of protein kinases, and in signaling
P62979	RPS27A	0.21	K.TITLEVEPSDTIENVK*.A	51.5 min	Activation of protein kinases, and in signaling.
P62987	UBA52	0.21	K.TITLEVEPSDTIENVK*.A	51.5 min	Activation of protein kinases, and in signaling.
P52209	PGD	0.31	R.LGDLWTLDDITLTDWTKPSLSGVAPLPR*.S	97.6 min	Oxidative decarboxylation
Q16881	TXNRD1	0.33	R.VVGFHVLGPNAGEVTQGFAAALK*.C	74.3 min	Formation of cell membrane protrusions
P07355	ANXA2	0.37	K.GDLEN AFLNLVQCIQNKPLYFADR*.L	117.1 min	Calcium-regulated membrane-binding protein
Q15293	RCN1	0.39	R.IDNDGDGFVTTEELK*.T	38.4 min	Regulate calcium-dependent activities
P63173	RPL38	0.39	R.YLYTLVITDK*.E	50.9 min	Structural constituent of ribosome
P00338	LDHA	0.39	K.DLADELALVDVIEDK*.L	92.6 min	Control fermentation process
P42166	TMPO	0.4	R.QEDKDDLDVTELTNEDLLDQLVK*.Y	84.8 min	Structural organization of the nucleus
P07858	ANXA5	0.41	K.GLGTDEESILTLTSR*.S	90.3 min	Anticoagulant protein
P23528	CFL1	0.42	K.EILVGDVGTVDPPYATFVK*.M	72.4 min	No data
P13797	PLS3	0.43	K.ANDDIIVNWNVR*.T	54.7 min	Regulation of bone development
P14618	PKM	0.44	K.IYVDDGLISLQVK*.Q	62.2 min	Tumor cell proliferation and survival
P27348	YWHAQ	0.45	K.TAFDEAIAELDTLNEDSYK*.	90.8 min	Negatively regulates the kinase activity
P75533	SF3B1	0.47	K.LLVVDDESTLSPEEQK*.E	49.9 min	Splicing of nuclear pre-mRNA intron.
P18085	ARF4	0.47	R.IQEVADELQK*.M	21.4 min	Vesicle budding,uncoating in Golgi apparatus
Q01518	CAP1	0.47	K.AGAAPYVQAFDSSLAGPVAEYLK*.I	117.5 min	Cell polarity
P18669	PGAM1	0.48	R.ALPFWNEEIVPQIK*.E	78.8 min	Reduced activity
P10599	TXN	0.49	K.TAFQEALDAAGDK*.L	41.2 min	Inhibits caspase-3 activity
P29401	TKT	0.49	R.TSRPENAIYNNNEDFQVGQAK*.V	39.6 min	Activates co-factor
Q9UK76	HN1	0.49	R.VLRPPGGGSNFLGFDEPTEQPVR*.K	56.3 min	N-terminally processed
P51610	HCFC1	0.49	R.LGDLWTLDDITLTDWTKPSLSGVAPLPR*.S	99.7 min	Control of the cell cycle
P16104	H2AFX	1.5	R.HLQLAIR*.N	19.5 min	Role in transcription regulation, DNA repair, DNA replication
Q96Qv6	HIST1H2AA	1.5	R.HLQLAIR*.N	19.5 min	Modifications of histones, code, and nucleosome remodeling
P35268	RPL22	1.52	K.ITVTSEVPFSK*.R	37.3 min	Structural constituent of ribosome
P40926	MDH2	1.52	K.VAVLGASGGIGQPLSLLK*.N	85.7 min	Enzyme activity is enhanced by acetylation
P11940	PABPC1	1.54	K.GFGFVCFSSPEEATK*.A	57.5 min	Cytoplasmic regulatory processes of mRNA metabolism
Q13310	PABPC4	1.54	K.GFGFVCFSSPEEATK*.A	57.5 min	Cytoplasmic regulatory processes of mRNA metabolism
O15260	SURF4	1.57	R.LCLISTFLEDGIR*.M	84.2 min	Architecture of the EPR intermediate compartment and of the Golgi
P62158	CALM1	1.58	K.EAFSLFDKDGDTITTK*.E	46.7 min	Regulates the centrosome cycle and progression through cytokinesis
P62910	RPL32	1.63	K.SYCAEIAHNVSCK*.N	22.0 min	Structural constituent of ribosome
P46783	RPS10	1.65	R.IAIYELLFK*.E	79.3 min	Component of the 40S ribosomal subunit.
P05386	RPLP1	1.66	K.ALANVNIGSLICNVGAGGPAPAAEK*.K	76.2 min	Plays an important role in the elongation step of protein synthesis
P0C0S8	HIST1H2AG	1.72	K.VTIAQGGVLPNIQAVLLPK*.K	83.1 min	Modifications of histones code and nucleosome remodeling
Q16777	HIST2H2AC	1.72	K.VTIAQGGVLPNIQAVLLPK*.K	83.1 min	Modifications of histones code and nucleosome remodeling
Q9BTM1	H2AFJ	1.72	K.VTIAQGGVLPNIQAVLLPK*.K	83.1 min	Modification of Histones code and nucleosome remodeling.
Q7L7L0	HIST3H2A	1.72	R.HLQLAIR*.N	19.5 min	Modifications of histone code, and nucleosome remodeling

P07602	PSAP	1.73	K.EIVDSYLPVILDIK*.G	111.9 min	Sequential action of specific hydrolases
P18124	RPL7	1.87	R.IVEPYIAWGYPNLK*.S	40.7 min	Translation apparatus; inhibits cell-free translation of mRNAs
O60812	HNRNPCL1	1.96	R.VFIGNLNTLVVK*.K	58.5 min	Role in nucleosome assembly by neutralizing basic proteins
P07910	HNRNPC	1.96	R.VFIGNLNTLVVK*.K	58.5 min	Stability and the level of translation of bound mRNA molecules
P47914	RPL29	1.98	K.AQAAAPASVPAQPK*.R	17.9 min	Structural constituent of ribosome
P02878	RPL6	2.15	K.QLASGLLLVTGPLVLNR*.V	82.7 min	Structural constituent of ribosome
P62241	RPS8	2.21	R.IIDVVYNASNELVR*.T	50.1 min	Structural constituent of ribosome
P61604	HSPE1	2.25	K.VLQATVVAVGSGSK*.G	25.8 min	Suppresses the ATPase activity of the latter
P0C0S5	H2AFZ	2.47	R.AGLQFPVGR*.I	32.5 min	Required for chromosome segregation during cell division
Q71U19	H2AFV	2.47	R.HLQLAIR*.G	19.5 min	Required for chromosome segregation during cell division
P62805	HIST1H4A	3	R.DNIQGITKPAIR*.R	24.2 min	Histone code, and nucleosome remodeling
P84243	H3F3A	3.02	R.YRPGTVALR*.E	16.6 min	Histone code, and nucleosome remodeling
P20674	COX5A	6.61	K.EIYPYVIQELRPTLNELGISTPEELGLDKV*	114.5 min	Mitochondrial electron transport.