

Supplemental Table 1. Membrane and membrane-associated proteins identified in AsPC-1 cells. Highlighted proteins were only found in AsPC-1 cells.

Accession #	Protein name	Unique peptides	Total peptides	Mr (KDa)	PI	Peptides identified	Subcellular localization
CH10_HUMAN	10 kDa heat shock protein	2	2	10.9	8.89	VLQATVVAVG SGSK VVLDDKDYFL FR	Mitochondrion
ANXA2_HUMAN	Annexin A2	10	24	38.6	7.57	STVHEILCK STVHEILCK AYTNFDAERD ALNIETAIKT K AYTNFDAERD ALNIETAIK AYTNFDAERD ALNIETAIK GVDEVTIVNI LTNR GVDEVTIVNI LTNR GVDEVTIVNI LTNR GVDEVTIVNI LTNR GVDEVTIVNI LTNR GVDEVTIVNI LTNR TPAQYDASEL KASMK TPAQYDASEL KASMK TPAQYDASEL K GLGTDEDSLI EIICSR GLGTDEDSLI EIICSR GLGTDEDSLI EIICSR GLGTDEDSLI EIICSR GLGTDEDSLI EIICSR GLGTDEDSLI EIICSR TDLEKDIISD TSGDFRK TDLEKDIISD TSGDFRK RAEDGSVIDY ELIDQDAR SYSPYDMLES IR	Plasma membrane
G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase	5	7	36	8.57	LVINGNPITI FQER IISNASCTTN CLAPLAK VIHDNFGIVE GLMTTVHAIT ATQK VIHDNFGIVE GLMTTVHAIT ATQK	Membrane

NPM_HUMAN	Nucleophosmin	2	6	32.6	4.64	GALQNIIPAS TGA AK LISWYDNEFG YSNR LISWYDNEFG YSNR MSVQPTVSLG GFEITPPVVL R MSVQPTVSLG GFEITPPVVL R MSVQPTVSLG GFEITPPVVL R MSVQPTVSLG GFEITPPVVL R MSVQPTVSLG GFEITPPVVL R MTDQEIQDL WQWR	Cytosol
ODPB_HUMAN	Pyruvate dehydrogenase E1 component subunit beta	2	3	39.2	6.2	IMEGPAFNFL DAPAVR IMEGPAFNFL DAPAVR ILEDNSIPQV K	Mitochondrion
ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1	2	3	37.4	8.97	LFIGGLSFET TEESLR LFIGGLSFET TEESLR GFGFVTFDDH DPVDKIVLQK	Nucleus
ETFA_HUMAN	Electron transfer flavoprotein subunit alpha	2	5	35.1	8.62	QSTLVIAEHA NDSLAPITLN TITAATR QSTLVIAEHA NDSLAPITLN TITAATR QSTLVIAEHA NDSLAPITLN TITAATR GLLPEELTPL ILATQK GLLPEELTPL ILATQK	Mitochondrion
ROBO1_HUMAN	Roundabout homolog 1	2	2	180.8	5.7	GARTPKVVKQ GGMNWADLLP PPPAHPPPHS NSEEYNISVD ESYDQEMP GARTPKVVKQ GGMNWADLLP PPPAHPPPHS NSEEYNISVD ESYDQEMP VPKQGGMNWA DLLPPPAHP PPHSNSEEYN ISVDESYDQE MPCPVPP	Membrane
PRDX5_HUMAN	Peroxiredoxin-5	2	5	22	8.85	GVLFQVPGAF TPGCSK GVLFQVPGAF TPGCSK ALNVEPDGTG LTCSLAPNII SQL ALNVEPDGTG LTCSLAPNII SQL ALNVEPDGTG LTCSLAPNII SQL	Mitochondrion

SSRD_HUMAN	Translocon-associated protein subunit delta	2	3	19	5.76	FFDEESYSLL R	Endoplasmic reticulum membrane
						NNEDISIIPP LFTVSVDHR NNEDISIIPP LFTVSVDHR	
HINT2_HUMAN	Histidine triad nucleotide-binding protein 2	2	3	17.2	9.2	ILDKSLPADI LYEDQQCLVF R	Mitochondrion
						ISQAEEEDQQ LLGHLLLVAK ISQAEEEDQQ LLGHLLLVAK	
FIS1_HUMAN	Mitochondrial fission 1 protein	2	4	16.9	8.84	STQFEYAWCL VR	Mitochondrion outer membrane
						GIVLLEELLP K GIVLLEELLP K GIVLLEELLP K	
PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase	4	10	27.7	7.68	PAVTQHAPYF K	Mitochondrion
						QISRDYGVLL EGSGLALR QISRDYGVLL EGSGLALR QISRDYGVLL EGSGLALR DYGVLLEGSG LALR DYGVLLEGSG LALR DYGVLLEGSG LALR DYGVLLEGSG LALR GLFIIDPNGV IK GLFIIDPNGV IK	
CYB5B_HUMAN	Cytochrome b5 type B	2	4	16.3	4.88	FLNEHPGGEE VLLEQAGVDA SESFEDVGHS SDAR FLNEHPGGEE VLLEQAGVDA SESFEDVGHS SDAR QYYIGDIHPS DLKPESGSK QYYIGDIHPS DLKPESGSK	Mitochondrion outer membrane
PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A	2	3	18	7.68	VNPTVFFDIA VDGEPLGR VSFELFADKV PK	Cytoplasm.

DOT1L_HUMAN	Histone-lysine N-methyltransferase	2	2	184.7	9.39	VSFELFADKV PK	Nucleus
						LEKLSGLAAP DY	
						SLPISIPNST VQPNKLPVSI PLASVVLPSR	
ATPO_HUMAN	ATP synthase subunit O	6	11	23.3	9.97	LVRPPVQVYG IEGR	Mitochondrion inner membrane
ATP5H_HUMAN	ATP synthase subunit d, mitochondrial	3	7	18.5	5.21	QNKLEQVEKE LLR	Mitochondrion inner membrane
						VAQILKEPK	
						VAASVLNPYV K	
						FSPLTTNLIN LLAENGR	
						FSPLTTNLIN LLAENGR	
						FSPLTTNLIN LLAENGR	
						FSPLTTNLIN LLAENGR	
						FSPLTTNLIN LLAENGR	
						FSPLTTNLIN LLAENGR	
						GEVPCTVTSA SPLEEATLSE LKTVLK	
RAB1B_HUMAN	Ras-related protein Rab-1B	3	7	22.2	5.55	YGLIPEEFFQ FLYPK	Membrane
						YGLIPEEFFQ FLYPK	
						HVVQSISTQQ EKETIAK	
						VVDNTTAKF ADSLGIPFLE TSAK	
						VVDNTTAKF ADSLGIPFLE TSAK	
						EFADSLGIPF LETSAK	
						EFADSLGIPF LETSAK	
						EFADSLGIPF LETSAK	
RAB7A_HUMAN	Ras-related protein Rab-7a	3	5	23.5	6.39	EAINVEQAFQ TIAR	Intracellular membrane-bound organelle
						EAINVEQAFQ TIAR	
						DPENFPFVVL GNKIDLENR	
						DPENFPFVVL GNKIDLENR	
						DPENFPFVVL GNK	
						EAINVEQAFQ TIAR	

[illegible]

KAD2_HUMAN	Adenylate kinase 2	7	20	26.5	7.67	ICPVETLVEE AIQCAEK	Mitochondrial inner membrane
						ICPVETLVEE AIQCAEK	
						ICPVETLVEE AIQCAEK	
						PSVPAAEPEY PK	
						LAENFCVCHL ATGDMLR	
						LVSDVMVEL IEK	
						LVSDVMVEL IEK	
						LVSDVMVEL IEK	
						LVSDVMVEL IEK	
						LVSDVMVEL IEK	
						NGFLLDGFPR	
						NGFLLDGFPR	
						NGFLLDGFPR	
						NGFLLDGFPR	
						NGFLLDGFPR	
						NGFLLDGFPR	
						LDSVIEFSIP DILLIR	
						LDSVIEFSIP DILLIR	
						LQAYHTQTTP LIEYR	
						LQAYHTQTTP LIEYR	
						GIHSAIDASQ TPDVVFASIL AAFSK	
						GIHSAIDASQ TPDVVFASIL AAFSK	
						GIHSAIDASQ TPDVVFASIL AAFSK	
HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2	6	10	26.9	7.65	GLVAVITGGA SGLGLATAER	Plasma membrane
						GLVAVITGGA SGLGLATAER	
						LVGQGASAVL LDLPNSGGEA QAK	
						LVGQGASAVL LDLPNSGGEA QAK	
						LVGQGASAVL LDLPNSGGEA QAK	
						LGNNCVFAPA DVTSEKDVQT ALALAK	
						VLDVNLMGTF NVIR	
						VLDVNLMGTF NVIR	
						GVIINTASVA AFEGQVGQAA YSASK	

CY1_HUMAN	Cytochrome c1, heme protein	5	10	35.4	9.15	GGIVGMTLPI AR	Mitochondrion inner membrane
						SDLELHPPSY PWSHR	
						SDLELHPPSY PWSHR	
						GLLSSLDHTS IR	
						LFDYFPKPYP NSEAAR	
						AANNGALPPD LSYIVR	
						AANNGALPPD LSYIVR	
						AANNGALPPD LSYIVR	
						AANNGALPPD LSYIVR	
						AANNGALPPD LSYIVR	
D3D2_HUMAN	3,2-trans-enoyl-CoA isomerase	3	13	32.8	8.8	HGGEDYVFSL LTGYCEPPTG VSLR	Mitochondrion inner membrane
						HGGEDYVFSL LTGYCEPPTG VSLR	
						VLVEPDAGAG VAVMK	
						VLVEPDAGAG VAVMK	
						VLVEPDAGAG VAVMK	
						VLVEPDAGAG VAVMK	
						GVILTSDRPG VFSAGLDLTE MCGR	
						GVILTSDRPG VFSAGLDLTE MCGR	
						GVILTSDRPG VFSAGLDLTE MCGR	
						GVILTSDRPG VFSAGLDLTE MCGR	
						DADVQNFVSF ISK	
						DADVQNFVSF ISK	
						DADVQNFVSF ISK	
						DADVQNFVSF ISK	
C1QBP_HUMAN	Complement component 1 Q subcomponent-binding protein	3	8	31.3	4.74	AFVDFLSDEI K	Plasma membrane
						AFVDFLSDEI K	
						VEEQEPELTS TPNFVVEVIK	
						VEEQEPELTS TPNFVVEVIK	
						ALVLDCHYPE DEVGQEDEAE SDIFSIR	

ETHE1_HUMAN	Protein ETHE1	4	11	27.9	6.35	ALVLDCHYPE DEVGQEDEAE SDIFSIR	Mitochondrion
						ALVLDCHYPE DEVGQEDEAE SDIFSIR	
						ALVLDCHYPE DEVGQEDEAE SDIFSIR	
						EAVLIDPVLE TAPR	
						EAVLIDPVLE TAPR	
						EAVLIDPVLE TAPR	
						EAVLIDPVLE TAPR	
						EAVLIDPVLE TAPR	
						LSGAQADLHI EDGDSIR	
						LTLSCFEFVK	
AAAT_HUMAN	Neutral amino acid transporter B(0)	3	5	56.6	5.34	LTLSCFEFVK	Integral to plasma membrane
						IMGNLNLPKP QQIDFAVPAN MR	
						IMGNLNLPKP QQIDFAVPAN MR	
						IMGNLNLPKP QQIDFAVPAN MR	
						SAAINASVGA AGSAENAPSK	
						STEPELIQVK SELPLDPLPV PTEEGNPLLK	
						STEPELIQVK SELPLDPLPV PTEEGNPLLK	
						SELPLDPLPV PTEEGNPLLK	
						SELPLDPLPV PTEEGNPLLK	
MDHM_HUMAN	Malate dehydrogenase	3	5	35.5	8.92	VAVLGASGGI GQPLSLLLK	Mitochondrion inner membrane
						VAVLGASGGI GQPLSLLLK	
						LTLYDIAHTP GVAADLSHIE TK	
						VDFPQDQLTA LTGR	
						VDFPQDQLTA LTGR	
ETFB_HUMAN	Electron transfer flavoprotein subunit beta	4	6	27.8	8.25	LGPLQVAR	Mitochondrion
						LAEKEKVDLV LLGK	
						LAEKEKVDLV LLGK	
						LPAVVTADLR	
						LPAVVTADLR	
SPRE_HUMAN	Sepiapterin reductase	3	6	28	8.25	KIEVIKPGDL GVDLTSK	Cytoplasm
						TLAPLLASLL SPGSVLVLSA R	

						TLAPLLASLL SPGSVLVLSA R VPADLGAEAG LQQLLGALR VPADLGAEAG LQQLLGALR LLINNAGSL GDVSK LLINNAGSL GDVSK		
CPNS1_HUMAN	Calpain small subunit 1	3	4	28.3	5.05	AGGGGGGGGG GGGGGGGGGG GTAMR GGGGGGGGGG GGGGGGGGGT AMRILGGVIS AISEAAAQYN PEPPPPR ILGGVISAIS EAAAQYNPEP PPPR ILGGVISAIS EAAAQYNPEP PPPR	Plasma membrane	
HDHD3_HUMAN	Haloacid dehalogenase-like hydrolase domain- containing protein 3	3	4	28	6.21	LLTWDVKDTL LR	Mitochondrion	
						AHGLEVEPSA LEQGFR AHGLEVEPSA LEQGFR AVGMHSFLVV GPQALDPVVR		
ERP29_HUMAN	Endoplasmic reticulum protein ERp29	2	3	29	6.77	GALPLDTVTF YK	Endoplasmic reticulum lumen	
						SLNILTAFQK SLNILTAFQK		
HYAL3_HUMAN	Hyaluronidase-3	2	2	46.5	8.55	MTTQLGPALV LGVALCLGCG QPLPQVPERP FSVLWNVPSA HCE HLALAAYQIH HSLRPGFAGP AVLDWEEWCP LWA	Lysosome	
1433G_HUMAN	14-3-3 protein gamma	2	2	28.3	4.8	TAFDDAIAEL DTLNEDSYK DSTLIMQLLR	Cytoplasm	
MUC16_HUMAN	Mucin-16	2	2	2351.9		ESHSPALADS ETPKATTQMV ITTTVGDPAP STSMPVHGSS ETTNIK DTAHTTEAMHA SMHTNTAVAN VGTSISGHES QSSVPADSHT SKATSPMG	Integral to membrane	
ACTB_HUMAN	Actin, cytoplasmic 1	13	22	41.7	5.29	DDDIAALVVD NGSGMCK AGFAGDDAPR AGFAGDDAPR AVFPSIVGRP R	Cytoplasm	

						GIVTNWDDME K		
						GIVTNWDDME K		
						IWHHTFYNEL R		
						IWHHTFYNEL R		
						VAPEEHPVLL TEAPLNPK		
						VAPEEHPVLL TEAPLNPK		
						TTGIVMDSGD GVTHTVPIYE GYALPHAILR		
						GYSFTTTAER		
						LCYVALDFEQ EMATAASSSS LEK		
						LCYVALDFEQ EMATAASSSS LEK		
						LCYVALDFEQ EMATAASSSS LEK		
						FEQEMATAAS SSSLEK		
						SYELPDGQVI TIGNER		
						SYELPDGQVI TIGNER		
						DLYANTVLSG GTTMYPGIAD R		
						DLYANTVLSG GTTMYPGIAD R		
						DLYANTVLSG GTTMYPGIAD R		
						QEYDESGPSI VHR		
ACTC_HUMAN	Actin, alpha cardiac muscle 1	2	2	42	5.23	AGFAGDDAPR		Cytoplasm
						AGFAGDDAPR		
						AVFPSIVGRP R		
						YPIEHGIITN WDDMEK		
						IWHHTFYNEL R		
						IWHHTFYNEL R		
						SYELPDGQVI TIGNER		
						SYELPDGQVI TIGNER		
						FRCPETLFQP SFIGMESAGI HETTYNSIMK		
						CDIDIRKDL		
STML2_HUMAN	Stomatin-like protein 2	4	11	38.5	6.87	ILEPGLNILI PVLDR		Membrane
						ILEPGLNILI PVLDR		
						ILEPGLNILI PVLDR		
						ILEPGLNILI PVLDR		
						QAQILASEAE KAEQINQAAG EASAVLAK		

						ILAAALTQHN GDAAASLTVA EQYVSAFSK ILAAALTQHN GDAAASLTVA EQYVSAFSK ILAAALTQHN GDAAASLTVA EQYVSAFSK ILAAALTQHN GDAAASLTVA EQYVSAFSK ILAAALTQHN GDAAASLTVA EQYVSAFSK ILAAALTQHN GDAAASLTVA EQYVSAFSK DSNTILLPSN PGDVTSMVAQ AMGVIYGALTK DSNTILLPSN PGDVTSMVAQ AMGVIYGALTK	
VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog	4	6	41.9	5.88	CLVLTGFGGY DK	Integral to membrane
						CLVLTGFGGY DK LPPLPVTSGM EGAGVVIKVG EGVSDR LPPLPVTSGM EGAGVVIKVG EGVSDR VVTYGKMANLL TGPK AVCGFHLGYL DGEVELVSGV VAR	
SUCB2_HUMAN	Succinyl-CoA ligase [GDP-forming] beta-chain	3	3	46.5	6.15	SCNGPVLVGS PQGGVDIEEV AASNPELIFK	Mitochondrion
						IDATQVEVNP FGETPEGQVV CFDAK ILNNSGLPIT SAIDLEDAK	
QCR2_HUMAN	Cytochrome b-c1 complex subunit 2	3	4	48.4	8.74	LPNGLVIASL ENYSPVSR	Mitochondrion inner membrane
						LPNGLVIASL ENYSPVSR YEDFSNLGTT HLLR AVAFQNPQTH VIENLHAAAY R	
ACADM_HUMAN	Medium-chain specific acyl-CoA dehydrogenase	2	6	46.6	8.61	AFTGFIVEAD TPGIQIGR	Mitochondrion
						AFTGFIVEAD TPGIQIGR AFAGDIANQL ATDAVQILGG NGFNTEYPVE AFAGDIANQL ATDAVQILGG NGFNTEYPVE AFAGDIANQL ATDAVQILGG NGFNTEYPVE AFAGDIANQL ATDAVQILGG NGFNTEYPVE	
HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F	2	5	45.6	5.38	ITGEAFVQFA SQELA EK	Nucleus
						ITGEAFVQFA SQELA EK	

						ATENDIYNFF SPLNPVR ATENDIYNFF SPLNPVR ATENDIYNFF SPLNPVR	
THIL_HUMAN	Acetyl-CoA acetyltransferase	2	6	45.2	8.98	TPIGSFLGSL SLLPATK	Mitochondrion inner membrane
						TPIGSFLGSL SLLPATK IVAFADAAVE PIDFPIAPVY AASMVLK IVAFADAAVE PIDFPIAPVY AASMVLK IVAFADAAVE PIDFPIAPVY AASMVLK IVAFADAAVE PIDFPIAPVY AASMVLK	
PDIA6_HUMAN	Protein disulfide-isomerase A6	2	3	48.1	4.95	TGEAIVDAAL SALR	Endoplasmic reticulum lumen
						TGEAIVDAAL SALR ALDLFSDNAP PPELLEIINE DIAK	
EFTU_HUMAN	Elongation factor Tu	2	5	49.5	7.26	LLDAVDTYIP VPAR LLDAVDTYIP VPAR LLDAVDTYIP VPAR LLDAVDTYIP VPAR	Mitochondrion
						DLEKPFLPV EAVYSVPGR	
CISY_HUMAN	Citrate synthase	2	3	51.7	8.45	ASASSTNLKD ILADLIPK ALGVLAQLIW SR ALGVLAQLIW SR	Mitochondrion
1A25_HUMAN	HLA class I histocompatibility antigen, A-25 alpha chain	2	3	41.2	6.09	FIAVG YVDDT QFVR	Integral to membrane
						AEQWRAYLEG RCVEWLR AEQWRAYLEG RCVEWLR	
IVD_HUMANI	Isovaleryl-CoA dehydrogenase	2	2	46.3	8.45	FLQEHLAPK	Mitochondrion
						LAGGPLGLMQ AVLDHTIPYL HVREAFGQKI GHFQLMQGK	
APMAP_HUMAN	Adipocyte plasma membrane- associated protein	2	4	46.5	5.82	LFENQLVGPE SIAHIGDVMF TGTADGR	Integral to membrane

VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1	12	15	30.8	8.62	LFENQLVGPE SIAHIGDVMF TGTADGR	
						LFENQLVGPE SIAHIGDVMF TGTADGR	
						FPNGVQLSPA EDFVLVAETT MAR	
						FPNGVQLSPA EDFVLVAETT MAR	
						WNTDNTLGTE ITVEDQLAR	Plasma membrane
						GLKLTFDSSF SPNTGKK	
						LTFDSSFSPN TGKK	
						GALVLGYEGW LAGYQMNFET AK	
						GALVLGYEGW LAGYQMNFET AK	
						VTQSNFAVG Y K	
						TDEFQLHTNV NDGTEFGGSI YQK	
						KLETAVNLAW TAGNSNTR	
						YQIDPDACFS AK	
						VNNSSLIGLG YTQTLKPGIK	
						LTLSALLDGK NVNAGGHK	
						LTLSALLDGK	
						LTLSALLDGK	
						LGLGLEFQA	
						LGLGLEFQA	
3HIDH_HUMAN	3-hydroxyisobutyrate dehydrogenase	7	16	35.3	8.38	EFQDAGEQVV SSPADVAEKA DRIITMLPTS	Mitochondrion
						INAIEAYSGA NGILKKV	
						EFQDAGEQVV SSPADVAEKA DRIITMLPTS	
						INAIEAYSGA NGILKKV	
						IITMLPTSIN AIEAYSGANG ILKK	
						IITMLPTSIN AIEAYSGANG ILKK	
						IITMLPTSIN AIEAYSGANG ILK	
						IITMLPTSIN AIEAYSGANG ILK	
						IITMLPTSIN AIEAYSGANG ILK	
						IITMLPTSIN AIEAYSGANG ILK	
						ICNNMLLAIS MIGTAEAMNL GIR	
						ICNNMLLAIS MIGTAEAMNL GIR	
						ICNNMLLAIS MIGTAEAMNL GIR	
						ICNNMLLAIS MIGTAEAMNL GIR	

						ICNNMLLAIS MIGTAEAMNL GIR SPILLGSLAH QIYR SPILLGSLAH QIYR GSLAHQIYR DFSSVFQFLR EEETF	
VDAC2_HUMAN	Voltage-dependent anion-selective channel protein 2	5	7	31.5	7.5	SCSGVEFSTS GSSNTDTGKV TGTLETK TGDFQLHTNV NDGTEFGGSI YQK TGDFQLHTNV NDGTEFGGSI YQK YQLDPTASIS AK VNNSSLIGVG YTQTLRPGVK LTLSALVDGK LTLSALVDGK	Integral to membrane
PHB2_HUMAN	Prohibitin-2	4	9	33.3	9.83	IGGVQQDTIL AEGLHFR IPWFQYPIIY DIR IPWFQYPIIY DIR IVQAEGEAEA AK IYLTADNLVL NLQDESFTR IYLTADNLVL NLQDESFTR IYLTADNLVL NLQDESFTR IYLTADNLVL NLQDESFTR IYLTADNLVL NLQDESFTR	Membrane
ANXA4_HUMAN	Annexin A4	3	6	35.9	5.84	GLGTDEDAII SVLAYR GLGTDEDAII SVLAYR GAGTDEGCLI EILASR GAGTDEGCLI EILASR GAGTDEGCLI EILASR SETSGSFEDA LLAIVK	Cytoplasm
ADT2_HUMAN	ADP/ATP translocase 2	5	11	32.9	9.76	TDAAVSFAKD FLAGGVAAAI SKTAVAPIER TDAAVSFAKD FLAGGVAAAI SK TDAAVSFAKD FLAGGVAAAI SK TDAAVSFAKD FLAGGVAAAI SK TDAAVSFAKD FLAGGVAAAI SK	Integral to membrane

						DFLAGGVAAA ISK	
						DFLAGGVAAA ISK	
						EQGVLSFWRG NLANVIRYFP TQALNF	
						YFPTQALNFA FK	
						YFPTQALNFA FK	
						YFPTQALNFA FK	
SFXN3_HUMAN	Sideroflexin-3	4	8	35.5	9.26	GELPLDINIQ EPR	Integral to membrane
						QLGTAYVSAT TGAVATALGL KSLTKHLPPL	
						QLGTAYVSAT TGAVATALGL K	
						QLGTAYVSAT TGAVATALGL K	
						QLGTAYVSAT TGAVATALGL K	
						FVPFAAVAAA NCINIPLMR	
						FVPFAAVAAA NCINIPLMR	
						FVPFAAVAAA NCINIPLMR	
ECH1_HUMAN	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase	4	10	35.8	8.16	GSSAQEEASG VALGEAPDHS YESLR	Mitochondrion
						CPKPVIAAVH GGCIGGGVDL VTACDIR	
						VIGNQSLVNE LAFTAR	
						VIGNQSLVNE LAFTAR	
						VIGNQSLVNE LAFTAR	
						VFPDKEVMLD AALALAAEIS SK	
						VFPDKEVMLD AALALAAEIS SK	
						VFPDKEVMLD AALALAAEIS SK	
						VFPDKEVMLD AALALAAEIS SK	
						VFPDKEVMLD AALALAAEIS SK	
THTM_HUMAN	3-mercaptopyruvate sulfurtransferase	3	7	33.2	6.13	ALVSAQWVAE ALR	Cytoplasm
						ALVSAQWVAE ALR	
						AGQPLQLLDA SWYLPK	
						AGQPLQLLDA SWYLPK	
						AGQPLQLLDA SWYLPK	
						DGIEPGHIPG TVNIPFTDFL SQEGLEK	
						DGIEPGHIPG TVNIPFTDFL SQEGLEK	

ATPG_HUMAN	ATP synthase subunit gamma	3	6	33	9.23	IYGLGSLALY EK IYGLGSLALY EK GLCGAIHSSI AK ELIEIISGAA ALD ELIEIISGAA ALD ELIEIISGAA ALD	Mitochondrial inner membrane
PHB_HUMAN	Prohibitin	3	5	29.8	5.57	FGLALAVAGG VVNSALYNVD AGHR AAELIANSLA TAGDGLIELR AAELIANSLA TAGDGLIELR AAELIANSLA TAGDGLIELR NITYLPAGQS VLLQLPQ	integral to plasma membrane
NB5R3_HUMAN	NADH-cytochrome b5 reductase 3	3	3	34.2	7.18	LIDREIISHD TR FALPSPQHIL GLPVGQHIYL SAR SVGMIAGGTG ITPMLQVIR	Membrane
BDH_HUMAN	D-beta-hydroxybutyrate dehydrogenase	2	3	38.1	9.1	VSVVEPGNFI AATSLYSPES IQAIAK VSVVEPGNFI AATSLYSPES IQAIAK METYCSSGST DTSPVIDAVT HALTATTPYT	Mitochondrial inner membrane
HCDH_HUMAN	Hydroxyacyl-coenzyme A dehydrogenase	2	4	34.3	8.88	TLSTIATSTD AASVVHSTD L VVEAIVENLK TLSTIATSTD AASVVHSTD L VVEAIVENLK LLVPYLMEAI R LLVPYLMEAI R	Mitochondrion
SUCA_HUMAN	Succinyl-CoA ligase [GDP-forming] subunit alpha	2	5	35	9.01	ISALQSAGVV VSMSPAQLGT TIYKEFEK ISALQSAGVV VSMSPAQLGT TIYKEFEK ISALQSAGVV VSMSPAQLGT TIYKEFEK ISALQSAGVV VSMSPAQLGT TIYK	Mitochondrial inner membrane
LDHA_HUMAN	L-lactate dehydrogenase A chain	3	5	36.7	8.84	ATLKDQLIYN LLKEEQTPQN K	Cytoplasm

						ATLKDQLIYN LLK LLIVSNPVDI LTYVAWK LLIVSNPVDI LTYVAWK LLIVSNPVDI LTYVAWK	
MTCH2_HUMAN	Mitochondrial carrier homolog 2	3	10	33.3	8.25	ADAASQVLLG SGLTILSQPL MYVK ADAASQVLLG SGLTILSQPL MYVK ADAASQVLLG SGLTILSQPL MYVK ADAASQVLLG SGLTILSQPL MYVK ADAASQVLLG SGLTILSQPL MYVK ADAASQVLLG SGLTILSQPL MYVK ADAASQVLLG SGLTILSQPL MYVK QVCQLPGLFS YAQHIASIDG RR VLQHYQESDK GEELGPGNVQ K	Integral to membrane
THTR_HUMAN	Thiosulfate sulfurtransferase	2	3	33.4	6.77	EGHPVTSEPS RPEPAVFK GAVNMPFMDF LTEDGFEKGP EELR GAVNMPFMDF LTEDGFEKGP EELR	Plasma membrane
CO7A1_HUMAN	Collagen alpha-1(VII) chain	2	2	295	5.95	PGVGVPGPS PGPPGVK DSAVILGPPG PRGAK	Basement membrane
ABHDB_HUMAN	Abhydrolase domain-containing protein 11	2	2	34.7	8.85	GGAEPRLPL SYR LIAVDISPVE STGVSHFATY VAAMR	Unknown
SSB_HUMAN	Single-stranded DNA-binding protein	3	5	17.2	9.59	ESETTSLVL ER QVEGKNPVTI FSLATNEMWR QVEGKNPVTI FSLATNEMWR QATTIIADNI IFLSDQTK QATTIIADNI IFLSDQTK	Mitochondrion
ATPB_HUMAN	ATP synthase subunit beta	28	95	56.5	5.26	ETRLVLEVAQ HLGESTVR ETRLVLEVAQ HLGESTVR	Mitochondrial inner membrane

LVLEVAQHLG ESTVR
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TIAMDGTEGL VR
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GQKVLD SGAP IKIPVGPETL GR
VLDSGAPIKI PVGPETLGR
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QFAPIHAEAP EFMEMSVEQE ILVTGIK
QFAPIHAEAP EFMEMSVEQE ILVTGIK
QFAPIHAEAP EFMEMSVEQE ILVTGIK
QFAPIHAEAP EFMEMSVEQE ILVTGIK
QFAPIHAEAP EFMEMSVEQE ILVTGIK
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VVDLLAPYAK
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IGLFGGAGVG K
IGLFGGAGVG K

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EGNDLYHEMI ESGVINLK
VALVYGQMNE PPGAR
VALVYGQMNE PPGAR
VALTGLTVAE YFR
VALTGLTVAE YFR
VALTGLTVAE YFR
DQEGQDVLLF IDNIFR
DQEGQDVLLF IDNIFR
FTQAGSEVSA LLGR
FTQAGSEVSA LLGR
FTQAGSEVSA LLGR
FTQAGSEVSA LLGR
IPSAVGYQPT LATDMGMTMQE R

KGSITSVQAI YVPADDLTDP APATTFAHLD
ATTVLSR
KGSITSVQAI YVPADDLTDP APATTFAHLD
ATTVLSR
GSITSVQAIY VPADDLTDP PATTF AHLDA
TTVLSR
GSITSVQAIY VPADDLTDP PATTF AHLDA
TTVLSR
PAPATTFAHL DATTVLSR
PAPATTFAHL DATTVLSR
AIAELGIYPA VDPLDSTSR
AIAELGIYPA VDPLDSTSR
AIAELGIYPA VDPLDSTSR
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AIAELGIYPA VDPLDSTSR
IMDPNIVGSE HYDVAR
IMDPNIVGSE HYDVAR
PNIVGSEHYD VAR
SLQDIILG MDELSEEDKL TVSR
SLQDIILG MDELSEEDKL TVSR
SLQDIILG MDELSEEDKL TVSR
SLQDIILG MDELSEEDKL TVSR
FLSQPFQVAE VFTGHMGK
FLSQPFQVAE VFTGHMGK
FLSQPFQVAE VFTGHMGK
GFQQILAGEY DHLPEQAFYM VGPIEEAVAK
GFQQILAGEY DHLPEQAFYM VGPIEEAVAK
GFQQILAGEY DHLPEQAFYM VGPIEEAVAK
GFQQILAGEY DHLPEQAFYM VGPIEEAVAK
GFQQILAGEY DHLPEQAFYM VGPIEEAVAK

						GIRPAINVGL SVSR	
						GIRPAINVGL SVSR	
						GIRPAINVGL SVSR	
						EVAFAQFGS DLDAATQQL SR	
						EVAFAQFGS DLDAATQQL SR	
						EVAFAQFGS DLDAATQQL SR	
						EVAFAQFGS DLDAATQQL SR	
						EVAFAQFGS DLDAATQQL SR	
						EVAFAQFGS DLDAATQQL SR	
						EVAFAQFGS DLDAATQQL SR	
						FENAFLSHVV SQHQALLGTI R	
						FENAFLSHVV SQHQALLGTI R	
						ISEQSDAKLK EIVTNFLAGF EA	
						ISEQSDAKLK EIVTNFLAGF EA	
						LKEIVTNFLA GFEA	
						LKEIVTNFLA GFEA	
						LKEIVTNFLA GFEA	
						LKEIVTNFLA GFEA	
						EIVTNFLAGF EA	
GLYM_HUMAN	Serine hydroxymethyltransferase	12	21	56	8.76	GLELIASENF CSR	Mitochondrion
						AALEALGSCL NNKYSEGYPG KR	
						YYGGAEEVDE IELLCQR	
						YYGGAEEVDE IELLCQR	
						ISATSIFFES MPYKLNPK	
						ISATSIFFES MPYKLNPK	
						ISATSIFFES MPYKLNPK	
						ISATSIFFES MPYK	
						TGLIDYNQLA LTAR	
						TGLIDYNQLA LTAR	
						TGLIDYNQLA LTAR	
						TGLIDYNQLA LTAR	
						LIIAGTSAYA R 230lidy	
						AHLLADMAHI SGLVAAK	

						GYSLVSGGTD NHLVLVDLRP K		
						GYSLVSGGTD NHLVLVDLRP K		
						VLELVSITAN KNTCPGDR		
						VLELVSITAN KNTCPGDR		
						VVDFIDEGVN IGLEVK		
						VVDFIDEGVN IGLEVK		
						LQDFKSFLK DSETSQR		
DLDH_HUMAN	Dihydrolipoyl dehydrogenase	7	16	54.1	7.95	ADQPIDADVT VIGSGPGGYV AAIK	Mitochondrion	
						ADQPIDADVT VIGSGPGGYV AAIK		
						ADQPIDADVT VIGSGPGGYV AAIK		
						TVCIEKNETL GGTCLNVGCI PSK		
						TVCIEKNETL GGTCLNVGCI PSK		
						NQVTATKADG GTQVIDTK		
						NLGLEELGIE LDPR		
						NLGLEELGIE LDPR		
						NLGLEELGIE LDPR		
						IPNIYAIGDV VAGPMLAHK		
						IPNIYAIGDV VAGPMLAHK		
						IPNIYAIGDV VAGPMLAHK		
						IPNIYAIGDV VAGPMLAHK		
						IPNIYAIGDV VAGPMLAHK		
						SEEQKKEGI EYK		
						VCHAHPTLSE AFR		
CH60_HUMAN	60 kDa heat shock protein	5	10	61	5.7	ALMLQGVDLL ADAVAVTMGP K	Mitochondrial inner membrane	
						ALMLQGVDLL ADAVAVTMGP K		
						ALMLQGVDLL ADAVAVTMGP K		
						AAVEEGIVLG GGCALLR		
						AAVEEGIVLG GGCALLR		
						CIPALDSLTP ANEDQKIGIE IIKR		
						TALLDAAGVA SLLTTAEVVV TEIPKEEKD		
						TALLDAAGVA SLLTTAEVVV TEIPKEEKD		
						TALLDAAGVA SLLTTAEVVV TEIPKEEK		

QCRI_HUMAN	Cytochrome b-c1 complex subunit 1	6	12	52.6	5.94	TALLDAAGVA SLLTTAEVVV TEIPKEEK	Mitochondrial inner membrane
						TATFAQALQF VPETQVSLLD NGLR	
						TATFAQALQF VPETQVSLLD NGLR	
						AVELLGDIVQ NCSLEDSQIE KER	
						AVELLGDIVQ NCSLEDSQIE KER	
						DVVFNYLHAT AFQGTPLAQA VEGPSENVR	
						DVVFNYLHAT AFQGTPLAQA VEGPSENVR	
						DVVFNYLHAT AFQGTPLAQA VEGPSENVR	
						ADLTEYLSH YKAPR	
						ADLTEYLSH YKAPR	
ECHB_HUMAN	Trifunctional enzyme subunit beta	6	12	51.3	9.45	MVLAAAGGVE HQQLDLAQK	Mitochondrion envelope
						MVLAAAGGVE HQQLDLAQK	
						LCTSATESEV AR	
						TPFLLSGTSY KDLMPHDLAR	
						TPFLLSGTSY KDLMPHDLAR	
						AALTGLLHR	
						AALTGLLHR	
						LAAAFVSRL EQDEYALR	
						LAAAFVSRL EQDEYALR	
						AQDEGLSDV VPFK	
ODO2_HUMAN	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	4	7	48.6	9.01	DFMYVSQDPK DQLLLGPTYA TPK	Plasma membrane
						DFMYVSQDPK DQLLLGPTYA TPK	
						EGGQYGLVAA CAAGGQGHAM IVEAYPK	
						EGGQYGLVAA CAAGGQGHAM IVEAYPK	
						EGGQYGLVAA CAAGGQGHAM IVEAYPK	
						TPAFAESVTE GDVRWEK	
						TPAFAESVTE GDVRWEK	
						LGFMFAFVK	
						ASAFALQEQP VVNAVIDDTT K	

TBA1B_HUMAN	Tubulin alpha-1B chain	4	6	50.1	4.94	ASAFALQEQP VVNAVIDDDTT K ASAFALQEQP VVNAVIDDDTT K AAVEDPRVLL LDL TIGGGDDSFN TFFSETGAGK AVFVDLEPTV IDEVR AVFVDLEPTV IDEVR QLFHPEQLIT GKEDAANNYA R QLFHPEQLIT GKEDAANNYA R LISQIVSSIT ASLR	Microtubule
ALDH2_HUMAN	Aldehyde dehydrogenase	3	7	56.3	6.63	VAEQTPLTAL YVANLIK VAEQTPLTAL YVANLIK VAEQTPLTAL YVANLIK TFVQEDIYDE FVER TFVQEDIYDE FVER ANNSTYGLAA AVFTK ANNSTYGLAA AVFTK	Mitochondrion
CALR_HUMAN	Calreticulin	4	7	48.1	4.29	EPAVYFKEQF LDGDGWTSR EPAVYFKEQF LDGDGWTSR CKDDEFTHLY TLIVRPDNTY EVK CKDDEFTHLY TLIVRPDNTY EVK IDNSQVESGS LEDDWDFLPP KK SGTIFDNFLI TNDEAYAEFF GNETWGVTK SGTIFDNFLI TNDEAYAEFF GNETWGVTK	Cytoplasm
HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K	3	6	50.9	5.39	IILDLISESP IK IILDLISESP IK GSYGDLGGPI ITTQVTIPK GSYGDLGGPI ITTQVTIPK IITITGTQDQ IQNAQYLLQN SVK IITITGTQDQ IQNAQYLLQN SVK	Nucleus
DHE3_HUMAN	Glutamate dehydrogenase 1	3	4	61.4	7.66	AKPYEGSILE ADCDILIPAA SEK IIAEGANGPT TPEADKIFLE R IIAEGANGPT TPEADKIFLE R ISGASEKDIV HSGLAYTMER	Mitochondrion

TBB2C_HUMAN	Tubulin beta-2C chain	3	5	49.8	4.79	SGPFGQIFRP DNFVFGQSGA GNNWAK SGPFGQIFRP DNFVFGQSGA GNNWAK FGQSGAGNNW AK ALTVPELTQQ MFDAK ALTVPELTQQ MFDAK	Microtubule
ENOA_HUMAN	Alpha-enolase	2	2	47.1	7.01	DATNVGDEGG FAPNILENKE GLELLK 2 YISPDQLADL YK	Plasma membrane
KCNK3_HUMAN	Potassium channel subfamily K member 3	2	2	43.5	9.26	NGQAGGGGGG GSAHTT NGQAGGGGGG GSAH	Integral to membrane
PDIA3_HUMAN	Protein disulfide-isomerase A3	4	7	56.7	5.98	SDVLELTDDN FESR TFSHELSDFG LESTAGEIPV VAIR LSKDPNIVIA K ELSDFISYLQ R ELSDFISYLQ R ELSDFISYLQ R ELSDFISYLQ R	Endoplasmic reticulum lumen
PDIA1_HUMAN	Protein disulfide-isomerase	3	3	57.1	4.76	QFLQAAEAID DIPFGITSNS DVFSK HNQLPLVIEF TEQTAPK YKPESEELTA ER	Plasma membrane
GRP75_HUMAN	Stress-70 protein	26	87	73.6	5.87	ASEAIKGAVV GIDLGTTNSC VAVMEGK ASEAIKGAVV GIDLGTTNSC VAVMEGK TTPSVVAFTA DGERLVGMPA KR TTPSVVAFTA DGERLVGMPA KR TTPSVVAFTA DGERLVGMPA KR TTPSVVAFTA DGER TTPSVVAFTA DGER QAVTNPNTF YATKR QAVTNPNTF YATKR QAVTNPNTF YATKR QAVTNPNTF YATKR LYSPSQIGAF VLMK LYSPSQIGAF VLMK	Cell surface mitochondrion

LYSPSQIGAF VLMK
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LYSPSQIGAF VLMK
LYSPSQIGAF VLMK
MKETAENYLG HTAK
NAVITVPAYF NDSQR
NAVITVPAYF NDSQR
NAVITVPAYF NDSQR
NAVITVPAYF NDSQR
NAVITVPAYF NDSQR
QATKDAGQIS GLNVLR
QATKDAGQIS GLNVLR
QATKDAGQIS GLNVLR
DAGQISGLNV LR
DAGQISGLNV LR
DAGQISGLNV LR
VINEPTAAAL AYGLDK
VINEPTAAAL AYGLDK
GVFEVKSTNG DTFLGGEDFD QALLR
GVFEVKSTNG DTFLGGEDFD QALLR
STNGDTFLGG EDFDQALLR
STNGDTFLGG EDFDQALLR
STNGDTFLGG EDFDQALLR
STNGDTFLGG EDFDQALLR
STNGDTFLGG EDFDQALLR
STNGDTFLGG EDFDQALLR
ETGVDLTKDN MALQR
ETGVDLTKDN MALQR
ETGVDLTKDN MALQR
ETGVDLTKDN MALQR
AKCELSVVQ TDINLPYLTM DSSGPK

[illegible]

PPCKM_HUMAN	Phosphoenolpyruvate carboxykinase [GTP]	8	18	70.6	7.56	VEAVNMAEGI IHDTEK VEAVNMAEGI IHDTEK KDSETGENIR QAASSLQQAS LK QAASSLQQAS LKLFEMAYKK QAASSLQQAS LKLFEMAYKK QAASSLQQAS LKLFEMAYKK QAASSLQQAS LK QAASSLQQAS LK	Mitochondrion
						VLSGDLGQLP TGIRDFVEHS AR VLSGDLGQLP TGIRDFVEHS AR LCQPEGIHIC DGTEAENTAT LTLLEQQGLI R LCQPEGIHIC DGTEAENTAT LTLLEQQGLI R GQLGNWMSPA DFQR TMYVLPFSMG PVGSPLSR IGVQLTDSAY VVASMR LGTPVLQALG DGDFVK LGTPVLQALG DGDFVK LGTPVLQALG DGDFVK LGTPVLQALG DGDFVK LGTPVLQALG DGDFVK GVPLVYEAFN WR GVPLVYEAFN WR GVPLVYEAFN WR GVPLVYEAFN WR AIDTTQLFSL PK AIDTTQLFSL PK	
CMC2_HUMAN	Calcium-binding mitochondrial carrier protein Aralar2	7	16	74.1	7.14	YLNIFGESQP NPK YLNIFGESQP NPK IAPLEEGTLP FNLAEAQR IAPLEEGTLP FNLAEAQR IAPLEEGTLP FNLAEAQR	Integral to plasam membrane

Protein	Accession	Length	Score	Mass	Charge	Peptide	Location
HSP71_HUMAN	Heat shock 70 kDa protein 1	6	13	70	5.48	IAPLEEGTLP FNLAEAQR	Cytoplasm
						QKASGDSARP VLLQVAESAY R	
						QKASGDSARP VLLQVAESAY R	
						ASGDSARPVL LQVAESAYR	
						ASGDSARPVL LQVAESAYR	
						ASGDSARPVL LQVAESAYR	
						ASGDSARPVL LQVAESAYR	
						ASGDSARPVL LQVAESAYR	
						FGLGSVAGAV GATAVYPIDL VK	
						FGLGSVAGAV GATAVYPIDL VK	
						GLLPQLLGVA PEK	
						LQVAGEITTG PR	
						TTPSYVAFTD TER	
						AFYPEEISSM VLTK	
						AFYPEEISSM VLTK	
						NAVITVPAYF NDSQR	
						NAVITVPAYF NDSQR	
						NAVITVPAYF NDSQR	
						NAVITVPAYF NDSQR	
						QATKDAGVIA GLNVLR	
						QATKDAGVIA GLNVLR	
						QATKDAGVIA GLNVLR	
GPDM_HUMAN	Glycerol-3-phosphate dehydrogenase	8	15	80.8	7.23	DAGVIAGLVN LR	Mitochondrial inner membrane
						IINEPTAAAI AYGLDR	
						IINEPTAAAI AYGLDR	
						ELEQVCNP II SGLYQGAGGP GPGGFQAQGP K	
						ELEQVCNP II SGLYQGAGGP GPGGFQAQGP K	
						ELEQVCNP II SGLYQGAGGP GPGGFQAQGP K	
						ELEQVCNP II SGLYQGAGGP GPGGFQAQGP K	
						MNLAIALTAA R	
						YGAATANYME VVSLLK	
						YGAATANYME VVSLLK	
						CKDVLTGQEF DVR	
						SMAEDTINAA VK	

						TVGLFLQGGK DWSPTLYIR LVQDYGLESE VAQHLAATYG DK LVQDYGLESE VAQHLAATYG DK TRLAFLNVQA AEEALPR TRLAFLNVQA AEEALPR TRLAFLNVQA AEEALPR TRLAFLNVQA AEEALPR LAFLNVQAAE EALPR LAFLNVQAAE EALPR LAFLNVQAAE EALPR LAFLNVQAAE EALPR LAFLNVQAAE EALPR	
GRP78_HUMAN	78 kDa glucose-regulated protein	7	12	72.3	5.07	TKPYIQVDIG GGQTK	Integral to endoplasmic reticulum
						TFAPEEISAM VLTK TFAPEEISAM VLTK TFAPEEISAM VLTK TFAPEEISAM VLTK VTHAVVTVPA YFNDAQR IEIESFYEGE DFSETLTR IEIESFYEGE DFSETLTR AKFEELNMDL FR AKFEELNMDL FR SQIFSTASDN QPTVTIK DNHLLGTFDL TGIPPAPR	
RIB1_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	5	11	68.5	5.96	VTAEVVLAHL GGGSTSR	Membrane
						VTAEVVLAHL GGGSTSR VTAEVVLAHL GGGSTSR VTAEVVLAHL GGGSTSR ATSFLLALEP ELEAR	

						ATSFLLALEP ELEAR ATSFLLALEP ELEAR ATSFLLALEP ELEAR SEDLLDYGPF R YDYQRQPD SG ISSIR ALTSEIALLQ SR		
ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase	3	5	70.3	8.92	ASNTAEVFFD GVRVPSENVL GEVGSGFK ASNTAEVFFD GVRVPSENVL GEVGSGFK AGLGSGLSLS GLVHPELSR AGLGSGLSLS GLVHPELSR ALVERGGVVT SNPLGF	Mitochondrial inner membrane	
ACSL5_HUMAN	Long-chain-fatty-acid--CoA ligase 5	2	4	75.9	6.49	GAMITHQNIV SNAAAFK GAMITHQNIV SNAAAFK SSLVGVVVPD TDVLPSFAAK SSLVGVVVPD TDVLPSFAAK	Integral to membrane	
ODP2_HUMAN	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	3	5	65.7	7.96	ILVPEGTRDV PLGTPLCIIV EK	Mitochondrion	
TRAP1_HUMAN	Heat shock protein 75 kDa	3	6	80.1	8.3	DVPLGTPLCI IVEK GVETIANDVV SLATK GVETIANDVV SLATK GVETIANDVV SLATK GTITIQDTGI GMTQEELVSN LGTIAR GTITIQDTGI GMTQEELVSN LGTIAR GTITIQDTGI GMTQEELVSN LGTIAR ATDILPKW AQLLQPTLEI NPR AQLLQPTLEI NPR	Mitochondrion	
DHSA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit	2	5	72.6	7.06	VSDSISAQYP VVDHEFDVAVV VGAGGAGLR	Membrane	

						VSDSISAQYP VVDHEFDAVV VGAGGAGLR	
						LGANSLLDLV VFGR	
						LGANSLLDLV VFGR	
						LGANSLLDLV VFGR	
AIFM1_HUMAN	Apoptosis-inducing factor 1	2	3	66.9	9.04	VLIVSEDPPEL PYMRPPLSK	Mitochondrion
						ALGTEVIQLF PEKGNMGK	
						ALGTEVIQLF PEKGNMGK	
ECHA_HUMAN	Trifunctional enzyme subunit alpha	17	46	82.9	9.16	ELHSEFSEVM NEIWASDQIR	Mitochondrial inner membrane.
						TVLGTPEVLL GALPGAGGTQ R	
						TVLGTPEVLL GALPGAGGTQ R	
						TVLGTPEVLL GALPGAGGTQ R	
						TVLGTPEVLL GALPGAGGTQ R	
						TVLGTPEVLL GALPGAGGTQ R	
						TVLGTPEVLL GALPGAGGTQ R	
						MVGVPAAALDM MLTGR	
						MVGVPAAALDM MLTGR	
						MVGVPAAALDM MLTGR	
						MVGVPAAALDM MLTGR	
						MVGVPAAALDM MLTGR	
						MVGVPAAALDM MLTGR	
						MVGVPAAALDM MLTGR	
						MVGVPAAALDM MLTGR	
						MVGVPAAALDM MLTGR	
						MGLVDQLVEP LGPGLKPPEE R	
						MGLVDQLVEP LGPGLKPPEE R	
						MGLVDQLVEP LGPGLKPPEE R	
						TIEYLEEVAI TFAK	
						TIEYLEEVAI TFAK	
						TIEYLEEVAI TFAK	
						TIEYLEEVAI TFAK	
						LTAYAMTIPF VR	
						LTAYAMTIPF VR	
						LTAYAMTIPF VR	
						DSIFSNLTGQ LDYQGFEK	

						DSIFSNLTGQ LDYQGFEK	
						ADMVIEAVFE DLSLK	
						ADMVIEAVFE DLSLK	
						ADMVIEAVFE DLSLK	
						VLKEVEAVIP DHCIFASNTS ALPISEIAAV SK	
						VLKEVEAVIP DHCIFASNTS ALPISEIAAV SK	
						EVEAVIPDHC IFASNTSALP ISEIAAVSK	
						EVEAVIPDHC IFASNTSALP ISEIAAVSK	
						MQLLEIITTE K	
						MQLLEIITTE K	
						CLAPMMSEVI R	
						KLDSLTTSTFG FPVGAATLVD EVGVDVAK	
						KLDSLTTSTFG FPVGAATLVD EVGVDVAK	
						KLDSLTTSTFG FPVGAATLVD EVGVDVAK	
						HVAEDLGKVF GER	
						FGGGNPELLT QMVSK	
						FGGGNPELLT QMVSK	
						DLNSDMDSIL ASLK	
						DLNSDMDSIL ASLK	
						DLNSDMDSIL ASLK	
						DLNSDMDSIL ASLK	
						QFTPCQLLAD HANSPNKK	
NUCL_HUMAN	Nucleolin	6	13	76.6	4.6	QKVEGTEPTT AFNLFVGNLN FNK	Cell cortex
						QKVEGTEPTT AFNLFVGNLN FNK	
						VEGTEPTTAF NLFVGNLNFN K	
						VEGTEPTTAF NLFVGNLNFN K	
						VEGTEPTTAF NLFVGNLNFN K	
						VEGTEPTTAF NLFVGNLNFN K	
						TGISDVFAKN DLA VVDVR	
						NLPYKVTQDE LKEVFEDAAE IR	
						NLPYKVTQDE LKEVFEDAAE IR	
						TLVLSNLSYS ATEETLQEVF EK	
						TLVLSNLSYS ATEETLQEVF EK	
						TLVLSNLSYS ATEETLQEVF EK	

CALX_HUMAN	Calnexin	5	9	67.5	4.47	GLSEDTEET LKESFDGSVR	Integral to membrane
						APVPTGEVYF ADSFDR	
						APVPTGEVYF ADSFDR	
						GTLSGWILSK	
						GTLSGWILSK	
						CESAPGCGVW QRPVIDNPY KGK	
						KIPNPdffED LEPFR	
						KIPNPdffED LEPFR	
						IPNPdffEDL EPFR	
						IPNPdffEDL EPFR	
ACON_HUMAN	Aconitate hydratase	2	3	85.4	7.36	AKDINQEVYN FLATAGAK	Mitochondrion
						NDANPETHAF VTSPEIVTAL AIAGTLK	
						NDANPETHAF VTSPEIVTAL AIAGTLK	
IMMT_HUMAN	Mitochondrial inner membrane protein	2	2	83.6	6.08	LAQQEKQEQV KIESLAK	Integral to membrane
						QTASVTLQAI AAQNAAVQAV NAHSNILK	
						QTASVTLQAI AAQNAAVQAV NAHSNILK	
PDIA4_HUMAN	Protein disulfide-isomerase A4	2	2	72.9	4.96	EVSQPDWTPP PEVTLVLTK	Endoplasmic reticulum (lumen)
						YGIVDYMIEQ SGPPSKEILT LK	
ENPL_HUMAN	Endoplasmin	16	28	92.4	4.76	EGSRTDDEVV QREEEAIQLD GLNASQIR	Endoplasmic reticulum membrane
						EGSRTDDEVV QREEEAIQLD GLNASQIR	
						TDDEVVQREE EAIQLDGLNA SQIR	
						TDDEVVQREE EAIQLDGLNA SQIR	
						ELISNASDAL DKIR	
						ELISNASDAL DKIR	
						LISLTDENAL SGNEELTVK	
						LISLTDENAL SGNEELTVK	
						LISLTDENAL SGNEELTVK	
						LISLTDENAL SGNEELTVK	
						NLLHVTDTGV GMTREELVK	

						SILFVPTSAP R	
						GLFDEYGSK	
						RVFITDDFHD MMPK	
						GVVDSDDLPL NVSR	
						GVVDSDDLPL NVSR	
						FQSSHPTDI TSLDQYVER	
						FQSSHPTDI TSLDQYVER	
						GYEVIYLTEP VDEYCIQALP EFDGKR	
						GYEVIYLTEP VDEYCIQALP EFDGKR	
						EAVEKEFEPL LNWMKDK 625alkd	
						EAVEKEFEPL LNWMKDK	
						EAVEKEFEPL LNWMK	
						LTESPCALVA SQYGWSGNME R	
						LTESPCALVA SQYGWSGNME R	
						AQAYQTGKDI STNYASQK	
						SGYLLPDTK	
						SGYLLPDTK	
ACTN4_HUMAN	Alpha-actinin-4	12	27	104.8	5.27	KDDPVTNLNN AFEVAEK	Extracellular region
						KDDPVTNLNN AFEVAEK	
						KDDPVTNLNN AFEVAEK	
						LASDLLEWIR	
						LASDLLEWIR	
						CQLEINFNTL QTK	
						DYETATLSDI KALIR	
						QLEAIDQLHL EYAK	
						QLEAIDQLHL EYAK	
						QLEAIDQLHL EYAK	
						LSGSNPYTTV TPQIINSKWE K	
						LSGSNPYTTV TPQIINSKWE K	
						QFASQANVVG PWIQTk	
						QFASQANVVG PWIQTk	
						QFASQANVVG PWIQTk	
						QFASQANVVG PWIQTk	

ODO1_HUMAN	2-oxoglutarate dehydrogenase E1 component	8	18	115.9	6.39	QFASQANVVG PWIQTK	Mitochondrial membrane
						VGWEQLLTTI AR	
						VGWEQLLTTI AR	
						VGWEQLLTTI AR	
						VGWEQLLTTI AR	
						TINEVENQIL TR 7	
						TINEVENQIL TR	
						GISQEQMQEF R	
						ETTDTDADQ VIASF	
						MAPYQGPDAV PGALDYKSFS TALYGESDL	
						MAPYQGPDAV PGALDYKSFS TALYGESDL	
						FGLEGCEVLI PALK	
						FGLEGCEVLI PALK	
						FGLEGCEVLI PALK	
GANAB_HUMAN	Neutral alpha-glucosidase AB	6	9	106.8	5.74	VVNAPIFHVN SDDPEAVMYV CK	Endoplasmic reticulum
						VVNAPIFHVN SDDPEAVMYV CK	
						STFHKDVVVD LVCYR	
						YAELLVSQGV VNPQEYEEI SKYDK	
						QILLPFRKPL IIFTPK	
						QILLPFRKPL IIFTPK	
						IEQLSPFPFD LLLK	
						IEQLSPFPFD LLLK	
						IEQLSPFPFD LLLK	
						IEQLSPFPFD LLLK	
						LLDTAFDLDV FKNFS	
						LLDTAFDLDV FK	
						LLDTAFDLDV FK	
						LLDTAFDLDV FK	
GANAB_HUMAN	Neutral alpha-glucosidase AB	6	9	106.8	5.74	SLLLSVNAR	Endoplasmic reticulum
						QYASLTGTQA LPPLFSLGYH QSR	

						HHGPQTLYLP VTLSSIPVFQ R	
						FSFSGNTLVS SSADPEGHFE TPIWIER	
						FSFSGNTLVS SSADPEGHFE TPIWIER	
						VVIIGAGKPA AVVLQTK	
						VVIIGAGKPA AVVLQTK	
						LSFQHDPETS VLVL R	
						LSFQHDPETS VLVL R	
SYIM_HUMAN	Isoleucyl-tRNA synthetase	5	7	113.7	6.78	TALAEAELEY NPEHVSR	Mitochondrion
						TALAEAELEY NPEHVSR	
						AVLEEGTDVV IK	
						TKDEYLINSQ TTEHIVK	
						TVIVHGFTLG EKGEKMSKSL	
						SCQTALVEIL DVIVR	
						SCQTALVEIL DVIVR	
TERA_HUMAN	Transitional endoplasmic reticulum ATPase	4	6	89.3	5.14	GILLYGPPGT GK	Endoplasmic reticulum
						QAAPCVLFFD ELDSIAK	
						QAAPCVLFFD ELDSIAK	
						QAAPCVLFFD ELDSIAK	
						LDQLIYIPLP DEK	
						KSPVAKDVDL EFLAK	
LONM_HUMAN	Lon protease homolog	4	7	106.4	6.01	ILEFIAVSQ L R	Mitochondrion
						ILEFIAVSQ L R	
						VLFICTANVT DTIPEPLRDR	
						LSSDVLTLI K	
						LSSDVLTLI K	
						IVSGEAE SVE VTPENLQDFV GKPVFTVER	
						IVSGEAE SVE VTPENLQDFV GKPVFTVER	
						IVSGEAE SVE VTPENLQDFV GKPVFTVER	
						IVSGEAE SVE VTPENLQDFV GKPVFTVER	
SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1	2	2	101.9	6.74	NLPGLVQEGE PFSEEATLFT K	Cytoplasm
						VLPAQATEYA FAFIQVPQDD DARTDAVDSV	
						VR	

AT1A1_HUMAN	Sodium/potassium-transporting ATPase subunit alpha-1 precursor	2	2	112.8	5.13	GVGIISEGNE TVEDIAAR	Integral to membrane
						LNIPVSQVNP R	
ITB1_HUMAN	Integrin beta-1; Fibronectin receptor subunit beta	3	4	88.4	5.3	IGFGSFVEKT VMPYISTTPA K	Plasma membrane
						IGFGSFVEK	
						IGFGSFVEK	
						SAVTTVVNPK YEGK	
						SAVTTVVNPK YEGK	
HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2	2	3	85.1	4.85	YGGQPLFSEK FPTLWSGAR	Nucleus
						YNVLGAETVL NQMR	
						YNVLGAETVL NQMR	
IMB1_HUMAN	Importin subunit beta-1	3	5	97.1	4.68	MELITILEK	Nucleus envelope
						MELITILEK	
						NEILTAIQG MRKEEPSNNV KLAATNALLN	
						SLEFTKANFD KESER	
						LAATNALLNS LEFTK	
						LAATNALLNS LEFTK	
HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U	2	8	90.5	5.76	SSGPTSLFAV TVAPPGAR	Cell surface
						SSGPTSLFAV TVAPPGAR	
						SSGPTSLFAV TVAPPGAR	
						SSGPTSLFAV TVAPPGAR	
						SSGPTSLFAV TVAPPGAR	
						EKPYFPIPEE YTFIQNVPLE DR	
						EKPYFPIPEE YTFIQNVPLE DR	
S12A1_HUMAN	Solute carrier family 12 member 1	2	2	121.3	7.18	YLGVAICVGA CVVRDATGNM NDTIISGMNC	Integral to membrane
						NGSAACGLGY DFSR	
						ARKGSISDLL YMAWLEILTK NLPPVLLVRG	
						NHKNVLTfYS	

IL4RA_HUMAN	Interleukin-4 receptor alpha chain	2	2	89.6	4.99	MGWLCSGLLF PVSCLVLLQV ASSGNMKVLQ EPTCVSDYMS ISTCEW MGWLCSGLLF PVSCLVLLQV ASSGNMKVLQ EPTCVSDYMS ISTCEW MGWLCSGLLF PVSCLVLLQV ASSGNMKVLQ EPTCVSDYMS ISTCEW MGWLCSGLLF PVSCLVLLQV ASSGNMKVLQ EPTCVSDYMS ISTCEW MGWLCSGLLF PVSCLVLLQV ASSGNMKVLQ EPTCVSDYMS ISTCEW MGWLCSGLLF PVSCLVLLQV ASSGNMKVLQ EPTCVSDYMS ISTCEW MGWLCSGLLF PVSCLVLLQV ASSGNMKVLQ EPTCVSDYMS ISTCEW MGWLCSGLLF PVSCLVLLQV ASSGNMKVLQ EPTCVSDYMS ISTCEW APDPSPGGVP LEAS	Integral to plasma membrane
FRAP_HUMAN	FKBP12-rapamycin complex-associated protein	2	2	288.7	6.73	DASAVSLSES KSSQDSSDYS TSE SGQGDALASG PVETGPMKK	Golgi membrane
LPPRC_HUMAN	Leucine-rich PPR motif-containing protein	15	26	157.8	5.81	AIAAKEKDIQ EESTFSSR LIASYCNVGD IEGASKILGF MK LIASYCNVGD IEGASK LIASYCNVGD IEGASK TKDLPVTEAV FSALVTGHAR TKDLPVTEAV FSALVTGHAR DLPVTEAVFS ALVTGHAR DLPVTEAVFS ALVTGHAR DLPVTEAVFS ALVTGHAR DLPVTEAVFS ALVTGHAR FSALVTGHAR AGDMENAENI LTVMR AGDMENAENI LTVMR	Membrane

						SNTLPISLQS IR	
						TVQLTSSELE STLETLK	
						TVQLTSSELE STLETLK	
						QLILVLCSEE NMQK	
						CVANNQVETL EKLVELTQK	
						CVANNQVETL EKLVELTQK	
						AFAETHIKGF TLNDAANSR	
						RDYLKEAVTT LK	
						MVFINNIALA QIK	
						SVLELIPELN EKEEAYNSLM K	
						SVLELIPELN EKEEAYNSLM K	
						SVLELIPELN EKEEAYNSLM K	
						SVLELIPELN EKEEAYNSLM K	
						SVLELIPELN EKEEAYNSLM K	
FA62A_HUMAN	Extended synaptotagmin-1	3	5	122.8	5.57	ALTLGALTLP LAR	Membrane
						ALTLGALTLP LAR	
						LTPRPTAAEL EEVLQVNSLI QTQK	
						LTPRPTAAEL EEVLQVNSLI QTQK	
						HLSPYATLTV GDSSHK	
HYOU1_HUMAN	Hypoxia up-regulated protein 1	3	5	111.3	5.16	DINTTAQNIM FYDMGSGSTV CTIVTYQMVK	Endoplasmic reticulum
						TKEAGMQPQL	
						DAVVYPILVE FTR	
						DAVVYPILVE FTR	
						DAVVYPILVE FTR	
						LQDLTLRDLE KQER	
KTN1_HUMAN	Kinectin	2	2	156.2	5.52	SVEELLEAE LK	Integral to plasma membrane
						ALKEEIGNVQ LEK	
EDC4_HUMAN	Enhancer of mRNA-decapping protein 4	2	2	151.6	5.55	ASIDIEDATQ HLR	Cytoplasm
						ALQDVQIRFQ PQLNPDVVAP LPTHTAHEDF	
						TFGESRPELG	
						ALQDVQIRFQ PQLNPDVVAP LPTHTAHEDF	
						TFGESRPELG	

CLH1_HUMAN	Clathrin heavy chain 1	7	10	191.5	5.48	ISGETIFVTA PHEATAGIIG VNR GQCDELEINV CNENSLFK NLQNLLILTA IK NLQNLLILTA IK ESYVETELIF ALAK ESYVETELIF ALAK LLYNNVSNFG R LASTLVHLGE YQAAVDGAR LASTLVHLGE YQAAVDGAR QLPLVKPYLR	Plasma membrane
MYOF_HUMAN	Myoferlin	4	5	234.6	5.84	ILVELATFLE K ILVELATFLE K IPANQLAELW LK YPQEKNNGPK VPVELRVNIW LGLSAVEKKF NSFAEG ACGDVLVTAE LILR	Integral to membrane
ITB4_HUMAN	Integrin beta-4	2	3	202	5.74	CSFNGDFVCG QCVCSEGWSG QTCNCSTGSL SDIQPCLREG ED CSFNGDFVCG QCVCSEGWSG QTCNCSTGSL SDIQPCLREG ED LLELQEVDLS LR LLELQEVDLS LR	Plasma membrane
IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1	2	2	189.1	6.08	ILAIGLINEA LDEGDAQK	Plasma membrane
SC16A_HUMAN	Protein transport protein Sec16A	2	2	233.4	5.4	FQPGETLTEI LETPATSEQE AEHQR CESPATTLWA QSELPDFGGN VLLAPAAPAL YVCAKPQPPV VQPPEEAM AGSALPGFAN SPAGSTSVVL VPPAHGTLVP DGNKANHSSH QEDT	Membrane
FLNB_HUMAN	Filamin-B	2	3	278	5.49	SPFTVGVAAP LDLSK VTASGPGLSS YGVPASLPVD FAIDAR VTASGPGLSS YGVPASLPVD FAIDAR	Integral to membrane

PLEC1_HUMAN	Plectin-1	3	4	531.4	5.73	QVKLVNIRND DIADGNPKLT LGLIWTHIL QVKLVNIRND DIADGNPKLT LGLIWTHIL ALQALEELRL QAEEAER APVPASELLA SGVLSR APVPASELLA SGVLSR	Plasam membrane
ZFHX4_HUMAN	Zinc finger homeobox protein 4	2	2	393.5	5.94	LENPADPQLM INPFQLDPAT AAALAPGLGE LSPY CSICNVAYSQ SSTLEIHMRS VLHQTKARAA KLEPSGHV	Nucleus
PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit	2	2	468	6.75	CGAALAGHQL IR CELLHSMVMF MLGKATQMPE	Nucleus
4F2_HUMAN	4F2 cell-surface antigen heavy chain	2	2	57.9	5.2	LLTSFLPAQL LR GQSEDPGSLL SLFR	Integral to membrane
SRP68_HUMAN	Signal recognition particle 68 kDa protein	2	2	70.7	8.75	MAAEKQVPGG GGGGGSGGGG G QVPGGGGGGG SGGGGSGGGG GS	Endoplasmic reticulum
OST48_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	2	2	48.8	5.43	TLVLLDNLNV R VGETAPPNAY TVTDLVEYSI VIQQLSNGK	Integral to membrane
ZZEF1_HUMAN	Zinc finger ZZ-type and EF-hand domain-containing protein 1	2	2	330.8	5.62	CSDMDLCKTC FLGGVKPEGH GDDHEMVNME FTCDHCQGLI IGR QPSKSLRLEE QSAKAVDTDM IILPCLSRPA RCDQATAESN PVTQK	Anaphase-promoting complex
ARI1A_HUMAN	AT-rich interactive domain-containing protein 1A	2	2	241.9	6.24	TPQPSSPMDQ MGKMRPQPYG GTNPYSQQQG PPSGPQQGHG YPGQPYG MRPQPYGGTN PYSQQQGPPS GPQQGHGYPG	Nucleus
IF4G1_HUMAN	Eukaryotic translation initiation factor 4 gamma 1	2	2	175.4	5.27	VQSAAPARPG PAAHVYPAGS QVMMIPSQIS YPASQGAYYI PGQGR	Cytosol

						EFLLGFQFIF ASMQKPEGLP HISDVVLDKA NKTPRLPLDP TRLQGI	
ANPRC_HUMAN	Atrial natriuretic peptide clearance receptor	2	2	59.8	5.93	LAGGTGGGGV GGGGGGAGIG GGR	Integral to membrane
VP13D_HUMAN	Vacuolar protein sorting-associated protein 13D	2	2	491.5	6.15	GGTGGGGVGG GGGGAGIGGG RQER SIPEQANAASV PDSVALESDS VGTYLPGASR VGE	
LAMP1_HUMAN	Lysosome-associated membrane glycoprotein 1	2	3	44.7	9	IGGLTSVITS TVEGVKTEGG VSGFISGLGK TVESITDIRA DIDKK	Integral to plasma membrane
HS90B_HUMAN	Heat shock protein HSP 90-beta	3	3	83.2	4.97	FFLQGIQLNT ILPDARDPAF K FFLQGIQLNT ILPDARDPAF K ADLINNLGTI AK	Cytoplasm
CEAM6_HUMAN	Carcinoembryonic antigen-related cell adhesion molecule 6	3	4	37.2	5.56	GVVDSIDLPL NISR CLELSELAIE DKENYKK HLEINPDHPI VETLR EVLLLAHNLP QNR	Integral to plasma membrane
P5CS_HUMAN	Delta-1-pyrroline-5-carboxylate synthetase	2	4	87.2	6.66	IGYSWYKGER VDGNSLIVGY VIGTQQATPG PAYSGR VDGNSLIVGY VIGTQQATPG PAYSGR VDGNSLIVGY VIGTQQATPG PAYSGR	Mitochondrial inner membrane
VMAT2_HUMAN	Synaptic vesicular amine transporter	2	2	55.7	5.69	SNIPFITVPL SR GPVGLEGLLT TK GPVGLEGLLT TK GTPLTTLLKD PYILIAAGSI CFANMGIAML EPALPIWMME TM GTPLTTLLKD PYILIAAGSI CFANMGIAML EPALPIWMME TM GTPLTTLLKD PYILIAAGSI CFANMGIAML EPALPIWMME TM	Integral to plasma membrane

						IPFAKNIYGL IAPNFGVGFA IGMVDSSMMP IMGYLVDLR IPFAKNIYGL IAPNFGVGFA IGMVDSSMMP IMGYLVDLR	
AOFB_HUMAN	Amine oxidase [flavin- containing] B	2	2	58.7	7.2	CIVYYKEPFW R	Integral to membrane
						IPEDIWQSE PESVDVPAQP ITTFLER	
HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H	2	4	49.2	5.89	STGEAFVQFA SQEIAEK	Nucleus
						STGEAFVQFA SQEIAEK ATENDIYNFF SPLNPVR ATENDIYNFF SPLNPVR	
TBA1A_HUMAN	Tubulin alpha-1A chain	2	3	50.1	4.94	AVFVDLEPTV IDEVR AVFVDLEPTV IDEVR	Microtubule
						QLFHPEQLIT GKEDAANNYA R	
VIME_HUMAN	Vimentin	2	4	53.6	5.06	LLQDSVDFSL ADAINTEFK	Plasma membrane
						ISLPLPNFSS LNL ISLPLPNFSS LNL ISLPLPNFSS LNL	
ACTG_HUMAN	Actin, cytoplasmic 2	14	28	41.8	5.31	EEEIAALVID NGSGMCK EEEIAALVID NGSGMCK EEEIAALVID NGSGMCK AGFAGDDAPR AGFAGDDAPR AGFAGDDAPR AVFPSIVGRP R AVFPSIVGRP R IWHHTFYNEL R IWHHTFYNEL R VAPEEHPVLL TEAPLNPK VAPEEHPVLL TEAPLNPK VAPEEHPVLL TEAPLNPK TTGIVMDSGD GVTHTVPIYE GYALPHAILR TTGIVMDSGD GVTHTVPIYE GYALPHAILR	Cytoplasm

						DLTDYLMK GYSFTTTAER EKLCYVALDF EQEMATAASS SSLEK LCYVALDFEQ EMATAASSSS LEK LCYVALDFEQ EMATAASSSS LEK LCYVALDFEQ EMATAASSSS LEK LCYVALDFEQ EMATAASSSS LEK SYELPDGQVI TIGNER SYELPDGQVI TIGNER CPEALFQPSF LGMESCGIHE TTFNSIMK DLYANTVLSG GTTMYPGIAD R DLYANTVLSG GTTMYPGIAD R EITALAPSTM K	
AATM_HUMAN	Aspartate aminotransferase	4	6	47.4	9.14	SSWWTHVEMG PPDPI LGVTE AFK NLDKEYLP I G GLAEFCK NLDKEYLP I G GLAEFCK FVTVQTISGT GALR TCGFDFTGAV EDISK TCGFDFTGAV EDISK	Plasma membrane
THIK_HUMAN	3-ketoacyl-CoA thiolase	3	4	44.3	8.76	GGFKDTPDE LLSAVMTAVL K GAGAIMARIA QFLSDIPETV PLSTVNR AEELGLPILG VLR AEELGLPILG VLR	Intracellular membrane- bounded organelle
ODPA_HUMAN	Pyruvate dehydrogenase E1 component alpha subunit, somatic form	2	4	43.3	8.35	LEEGPPVTTV LTR EIEDAAQFAT ADPEPPLEEL GYHIYSSDPP FEVR EIEDAAQFAT ADPEPPLEEL GYHIYSSDPP FEVR EIEDAAQFAT ADPEPPLEEL GYHIYSSDPP FEVR	Intracellular membrane- bounded organelle

Protein Name	Accession Number	Molecular Weight (kDa)	pI	Length (aa)	Charge (pKa)	Sequence	Location
TMLH_HUMAN	Trimethyllysine dioxygenase	2	3	49.5	7.64	TLLVDGFYAA EQVLQK	Mitochondrion matrix
DYH9_HUMAN	Dynein heavy chain 9, axonemal	2	2	511.6	5.65	TLLVDGFYAA EQVLQK EDVGECHNHM IGIGPVLNIY PWNK NLNTVFRLMTD AQVADERFLV LINDLLASGE IPDLYSDDDEV ENII VTQIGQKGYL QIEQALEAG AVVLIENLEE SIDPVLGPLL GREVIKKG	Dynein complex
SFRS1_HUMAN	Splicing factor, arginine/serine-rich 1	2	6	27.7	10.37	GGPPFAFVEF EDPRDAEDAV YGR	Cytosome
1433Z_HUMAN	14-3-3 protein zeta/delta	2	3	27.7	4.73	GGGGGGGGGA PR GGGGGGGGGA PR GGGGGGGGGA PR GGGGGGGGGA PR GGGGGGGGGA PR SVTEQGAELS NEERNLLSVA YK SVTEQGAELS NEERNLLSVA YK DICNDVLSLL EK DICNDVLSLL EK	Cytoplasm
CY1_HUMAN	Cytochrome c1, heme protein	2	3	35.4	9.15	SDLELHPPSY PWSHR AANNALPPD LSYIVR AANNALPPD LSYIVR	Integral to membrane
RAB1A_HUMAN	Ras-related protein Rab-1A	3	7	22.7	5.93	VVDYTTAKEF ADSLGIPFLE TSAK VVDYTTAKEF ADSLGIPFLE TSAK EFADSLGIPF LETSAK EFADSLGIPF LETSAK EFADSLGIPF LETSAK EFADSLGIPF LETSAK NATNVEQSFM TMAAEIK	Endoplasmic reticulum.
SODM_HUMAN	Superoxide dismutase [Mn]	2	5	24.7	8.35	DFGSFDKFK AIWNVINWEN VTER AIWNVINWEN VTER	Mitochondrion

						AIWNVINWEN VTER AIWNVINWEN VTER	
RHOA_HUMAN	Transforming protein RhoA precursor	2	3	21.8	5.83	QVELALWDTA GQEDYDR QVELALWDTA GQEDYDR HFCPNVPIIL VGNKK	Plasma membrane
PPRC1_HUMAN	Peroxisome proliferator-activated receptor gamma coactivator-related protein 1	2	2	177.4	6.11	SSSSSSSSSS SSSSSSSSR	Nucleus
LYPA1_HUMAN	Acyl-protein thioesterase 1	2	2	24.7	6.29	SSSSSSSSSS SSSRSR IILGGFSQGG ALSLYTALTQ QK LAGVTALSCW LPLR	Mitochondrion
TEP1_HUMAN	Telomerase protein component 1	2	2	290.2	8.26	ETLEQSQGAH VLALGPLEAS ARAR	Nucleus
TITIN_HUMAN	Titin	16	16	3813.8	6.01	DVKLWERPSM QLLGLFRCEG SVSC SIATVEMVID GAAGQQ LYVEPAAPLG APTY MAHEGALTGV TTDQK LTVKDVTKEQ QGEY NDGGMEENMA TLM NDGGMEENMA TLM SNCTVSVHVS DRIVPPSFIR K EIRPGGNYKM GGDPIPNVK FMSPLEDQTV K CGPGEPAYVD EPVNMSTPAT AENAAGISEP SRAT EGAFYKFRVS AVNIAGIGEP GEV MKVQNLLPDH EYQFRVKA VAAVNEKGRS DPRQLGVPV VLACNAGGPG EPAEVPGETVK YGVSGSDQTL TIKQA	Cytosol
EGFR_HUMAN	Epidermal growth factor receptor precursor	2	3	134.2	6.26	MRPSGTAGAA LLALLAA	Integral to membrane

DPP4_HUMAN	Dipeptidyl peptidase 4	2	3	88.2	5.67	IPLNLQIIR IPLNLQIIR NTDSLSSVTN ATSIQITAP FRPSEPHFTL DGNSFYK FRPSEPHFTL DGNSFYK	Plasma membrane
NSUN2_HUMAN	tRNA (cytosine-5-)- methyltransferase NSUN2	2	2	86.4	6.33	ELPGLKWMPG ITQWK	Cytoplasm
EF2_HUMAN	Elongation factor 2	2	2	95.3	6.41	ILLTQENPFF R TFCQLILDPI FK GGGQIIPTAR R	Cytoplasm
DHX9_HUMAN	ATP-dependent RNA helicase A	2	2	140.9	6.41	YPSPFFVFGE K	Cytoplasm.
SYG_HUMAN	Glycyl-tRNA synthetase	2	2	83.1	6.61	RAGYGAGVGG GYR LPFAAAQIGN SFR	Mitochondrial matrix
DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17	3	3	72.3	3.94	TFFSFPAVVA PFK RGGFGARGGG GLPPKK	Nucleus
KU70_HUMAN	ATP-dependent DNA helicase 2 subunit 1	3	4	69.8	6.23	PKLMQLVDHR GGGGGGGGRS R GGGGGGGGRS R IISSDRDLA VVFYGTEK	Membrane fraction
HS90A_HUMAN	Heat shock protein HSP 90- alpha	2	3	84.6	4.94	NIYVLQELDN PGAK DTGIFLDLMH LK DTGIFLDLMH LK ADLINNLGTI AK	Cytoplasm
AN32B_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member B	2	2	28.8	3.94	GVVDSEDLPL NISR GVVDSEDLPL NISR HLEINPDHSI IETLR HLEINPDHSI IETLR LEFLSLINVG LISVSNL	Nucleus

APOE_HUMAN	Apolipoprotein E	2	3	36.1	5.65	LPNLTHLNLS GNK EGAERGLSAI R EGAERGLSAI R MEEMGSRTD RL	Secreted
HNRPG_HUMAN	Heterogeneous nuclear ribonucleoprotein G	2	2	42.3	10.06	DMNGKSLDGK AIKVEQATKP	Nucleus
LEG4_HUMAN	Galectin-4	2	2	35.9	9.21	GGRGGSGGTR VGSSGDIALH INPR ITHNPFPGPGQ FFDLSIR	Plasma membrane
LRC59_HUMAN	Leucine-rich repeat-containing protein 59	2	4	34.9	9.61	LQQLPADF	Integral to membrane
LEG3_HUMAN	Galectin-3	2	2	26.2	8.58	LVTLPVSFAQ LK LVTLPVSFAQ LK LVTLPVSFAQ LK QSVFPFESGK PFK IQVLVEPDHF K	Plasma membrane
FAM3C_HUMAN	Protein FAM3C precursor	2	3	24.7	8.52	ICLEDNVLMS GVK	Intracellular region
ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1	2	3	38.8	9.26	LIADLGSTSI TNLGFR LIADLGSTSI TNLGFR LFIGGLSFET TDESLR LFIGGLSFET TDESLR IEVIEIMTDR	Cytoplasm.
HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2	4	4	33.6	4.95	VFIGNLNTLV VK	Ribonucleosomes.
HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0	3	9	38.4	7.61	GFAFVQYVNE R QKVDLSLENL EK MESEGGADDS AEE FGEVVDCTLK FGEVVDCTLK GFGFVLFK GFGFVLFK	Nucleus

						GFGFVLFK		
						GFGFVLFK		
						GFGFVLFK		
						IFVGGLSPDT PEEK		
						IFVGGLSPDT PEEK		
H2A1A_HUMAN	Histone H2A type 1-A	2	3	14.2	10.86	AGLQFPVGR		Nucleus
						AGLQFPVGR		
						LLGGVTIAQG GVLPNIQAV		
						LLGGVTIAQG GVLPNIQAV		
						LLGGVTIAQG GVLPNIQAV		
SOCS7_HUMAN	Suppressor of cytokine signaling 7	2	3	62.9	8.35	DVEAAPEPGP SELLCPR		Plasma membrane
						TKSCNGGSGG GDGTGK		
						TKSCNGGSGG GDGTGK		
ATPK_HUMAN	ATP synthase subunit F	2	2	10.9	9.7	DFSPSGIFGA FQR		Membrane
						GSISGITMVL		
H4_HUMAN	Histone H4	2	2	11.4	11.36	LARRGGVKRI SGL		Nucleus
						TVTAMDVVYA LK		
ILF2_HUMAN	Interleukin enhancer-binding factor 2	2	3	43	5.19	ILPTLEAVAA LGNK		Cytoplasm.
						ILPTLEAVAA LGNK		
						GLFLPGSVGI TDPCEGNFR		
RAB10_HUMAN	Ras-related protein Rab-10	2	6	22.5	8.58	LLIGDSGVG K		plasma membrane
						LLIGDSGVG K		
						AFLTAEEDIL R		
						AFLTAEEDIL R		
						AFLTAEEDIL R		
						AFLTAEEDIL R		
RAB2A_HUMAN	Ras-related protein Rab-2A	3	3	23.5	6.08	YIIIGDTGVG K		Membrane
						TASNVEEAFI NTAK		
						IGPQHAATNA THAGNQGGQQ AGGGCC		
ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A/B	2	3	36.2	8.21	GWTGAAAGAG GATAAP		Nucleus
						GWTGAAAGAG GATAAP		

						FGEVVDCTIK GNRGS GGGGG GGGQSQSW	
ODPAT_HUMAN	Pyruvate dehydrogenase E1 component subunit alpha, testis-specific form	3	7	42.9	8.76	LEEGPPVTTV LTR	Intracellular membrane- bounded organelle
						LEEGPPVTTV LTR LEEGPPVTTV LTR LEEGPPVTTV LTR QGPLGAGIAL ACK GPILMELQTY R GPILMELQTY R YSLEPVAVEL K YSLEPVAVEL K ACANPAAGSV ILLENLR ALESPERPFL AILGGAK ALESPERPFL AILGGAK ALESPERPFL AILGGAK TGQATVASGI PAGW 311mgld	
PGK1_HUMAN	Phosphoglycerate kinase 1	4	7	44.6	8.3		Cytoplasm
ABHD8_HUMAN	Abhydrolase domain- containing protein 8	2	3	47.3	6.54	GSGSGSGSGG R GSGSGSGSGG R SGSGSGSGGR	
CEAM1_HUMAN	Carcinoembryonic antigen- related cell adhesion molecule 1	2	4	57.5	5.65	ELPKPSSSN NSNPVEDK	Integral to plasma membrane
						TLTLLSVTR TLTLLSVTR TLTLLSVTR	
ZN503_HUMAN	Zinc finger protein 503	2	4	62.5	8.94	KEPGGGGGGG GGGGGGGGGV SS KEPGGGGGGG GGGGGGGGGV SS KEPGGGGGGG GGGGGGGGGV SS PGGGGGGGGG GGG	Nucleus
HXD11_HUMAN	Homeobox protein Hox-D11	2	2	35.5	9.43	SPMGAADKGD PR RTGAGGGGGS PCTK	Nucleus

FZD8_HUMAN	Frizzled-8 precursor	2	2	73.3	8.58	AGGAGGAAAG AGAAGAGAGG PGGR	Integral to membrane
						GGAGGAAAGA GAAGAGAGGP GGR	
ZIC2_HUMAN	Zinc finger protein ZIC 2	2	3	55	8.68	SYTHPSSLRK HMK 413vhes GGGSGSGGAG GGSAGGSGSG G GGGSGSGGAG GGSAGGSGSG G	Nucleus
HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L	3	3	60.1	6.65	MAAAGGGGGG GRYYGGGSEG GR TDNAGDQHGG GGGGGGGAGA A HGGGGGGGGG AGAAGGGGGG ENY	Nucleus
FLRT1_HUMAN	Leucine-rich repeat transmembrane protein FLRT1	2	2	71.3	5.95	IPADIPDDAT TLYLQNNQIN NAGIPQDLK LQNLTELSLV RNSLAAPPLN LPSAHLQKLY LQDNAISHIP LQNLTELSLV RNSLAAPPLN LPSAHLQKLY LQDNAISHIP	Integral to membrane
ACTK_HUMAN	Beta-actin-like protein 3	2	4	42	5.91	QAVFPSIVGR PR QAVFPSIVGR PR AVFPSIVGRP R AVFPSIVGRP R	Cytoplasm
DSPP_HUMAN	Dentin sialophosphoprotein precursor	2	2	126.4	3.6	SDSSNSSDSS DSSDSSDSSD SDSSNR NSSDSSDSSD SSDSSDSDSS NR	Extracellular region
CO4A5_HUMAN	Collagen alpha-5(IV) chain	2	2	160.9	7.71	GQAGATGPKG LPGIPGAPGA GLNGMKGDGP LPGVPGFPGM K	Basement membrane
AIM1_HUMAN	Absent in melanoma 1 protein	2	2	188.6	5.61	QPPPASSPTK RK GAPGASDADG LKPR	Unknown
ATP7B_HUMAN	Copper-transporting ATPase 2	2	2	157.2	6.29	MVGTGVAAQN GILIKGGKPL EMAHK LQPWMGSAAM AASSVSVVLS SLQLK	Integral to plasma membrane

PRDM8_HUMAN	PR domain zinc finger protein 8	2	2	71.7	8.21	SGSGSGGGGG HQEAELESPDG IATGGGK	Nucleus
HXB3_HUMAN	Homeobox protein Hox-B3	2	2	44.3	9.27	KLQGAADLNG GCGSLPSGGG GLPK GGSGSGSGGG GGGGGGGDK GGSGSGSGGG GGGGGGGDK	Nucleus
OTUD5_HUMAN	OTU domain-containing protein 5	2	2	60.6	6.1	VGVGGGGTGV GGGDR ASATCSSATA AASS	
CO2A1_HUMAN	Collagen alpha-1(II) chain	3	3	141.7	6.58	TDGPKGASGP AGPPGAQGPP GLQGMPGER GDSGPPGRAG EPGLQGPAGP PG QGDRGEAGAQ GPMGPSGPAG ARGIQGPQ QGDRGEAGAQ GPMGPSGPAG ARGIQGPQ	Basement membrane
CO4A3_HUMAN	Collagen alpha-3(IV) chain	2	2	161.7	9.28	QGAAGLKGSP GSPGNTGL GEPGIPGIGF PGPPGPK	Basement membrane

Supplemental Table 2. Membrane and membrane-associated proteins identified in BxPC-3 cells. Highlighted proteins were only found in BxPC-3 cells.

Accession #	Protein name	Unique peptides	Total peptides	Mr (KDa)	PI	Peptides identified	Subcellular localization
MYOF_HUMAN	Myoferlin	25	43	234.6	5.84	MLRVIVESAS NIPKTK MLRVIVESAS NIPKTK MLRVIVESAS NIPK VIVESASNIP K GPVGTVSEAQ LAR QLSGNNIRPV VK QLSGNNIRPV VK VSMFVLGTGD EPPERR NLVDPFVEVS FAGK NLVDPFVEVS FAGK NLVDPFVEVS FAGK ILVELATFLE K IPANQLAELW LK IPANQLAELW LK SRSLSQIHEA AVR IPAHQVLYST SGENASGK SLLTEADAGH TEFTDEVYQN ESR SLLTEADAGH TEFTDEVYQN ESR VIMELFDNDQ VGKDEFLGR VIMELFDNDQ VGKDEFLGR VIMELFDNDQ VGKDEFLGR TPNFPSSVLF MK TPNFPSSVLF MK VFLPKEELYM PPLVIK	Integral to membrane

						LASTLVHLGE YQAAVDGAR LASTLVHLGE YQAAVDGAR	
PLEC1_HUMAN	Plectin-1	2	4	531.4	5.73	CRPDQLTGLS LLPLSEK	Plasma membrane
						CRPDQLTGLS LLPLSEK APVPASELLA SGVLSR APVPASELLA SGVLSR	
LPPRC_HUMAN	Leucine-rich PPR motif- containing protein	3	3	157.8	5.81	DLPVTEAVFS ALVTGHAR	Membrane
						SYVSEKDVTs AK YAGEPVPFIE PPESFEFYAQ QLRK	
FA62A_HUMAN	Extended synaptotagmin-1	2	3	122.8	5.57	ALTLGALTLP LAR ALTLGALTLP LAR LTPRPTAAEL EEVLQVNSLI QTQK	Membrane
ACTN4_HUMAN	Alpha-actinin-4	23	58	104.8	5.27	KTFTAWCNSH LR	Extracellular region
						FAIQDISVEE TSAKEGLLLW CQR FAIQDISVEE TSAKEGLLLW CQR EGLLLWCQR DGLAFNALIH R DGLAFNALIH R AIMTYVSSFY HAFSGAQKAE TAANR AIMTYVSSFY HAFSGAQKAE TAANR CQLEINFNTL QTK CQLEINFNTL QTK LSNRPAFMPS EGK LSNRPAFMPS EGK VEQIAAIAQE LNELDYYDSH NVNTR VEQIAAIAQE LNELDYYDSH NVNTR	

CQKICDQWDA LGSLTHSR
CQKICDQWDA LGSLTHSR
ICDQWDALGS LTHSR
ICDQWDALGS LTHSR
QLEAIDQLHL EYAKR
QLEAIDQLHL EYAKR
QLEAIDQLHL EYAK
QLEAIDQLHL EYAK
QLEAIDQLHL EYAK
QLEAIDQLHL EYAK
LSGSNPYTTV TPQIINSKWE K
LSGSNPYTTV TPQIINSKWE K
LSGSNPYTTV TPQIINSKWE K
LSGSNPYTTV TPQIINSK
LSGSNPYTTV TPQIINSK
VQQLVPKRDH ALLEEQSK
QFASQANVVG PWIQT
QFASQANVVG PWIQT
QFASQANVVG PWIQT
QFASQANVVG PWIQT
QFASQANVVG PWIQT
QFASQANVVG PWIQT
QFASQANVVG PWIQT
QFASQANVVG PWIQT
QFASQANVVG PWIQT
VGWEQLLTTI AR
VGWEQLLTTI AR
VGWEQLLTTI AR
VGWEQLLTTI AR
VGWEQLLTTI AR

VGWEQLLTTI AR
TINEVENQIL TR
TINEVENQIL TR
GISQEQMQEF R
GISQEQMQEF R
ACLISLGYDV ENDRQGEAEF NR
ACLISLGYDV ENDRQGEAEF NR
ETTDTDADQ VIASF
ETTDTDADQ VIASF
ETTDTDADQ VIASF
ETTDTDADQ VIASF
MAPYQGPDV PGALDYKSFS
TALYGESDL
MAPYQGPDV PGALDYKSFS
TALYGESDL
MAPYQGPDV PGALDYKSFS
TALYGESDL
MAPYQGPDV PGALDYKSFS
TALYGESDL
MAPYQGPDV PGALDYK
MAPYQGPDV PGALDYK

ENPL_HUMAN

Endoplasmin

16

31

92.4

4.76

EGSRTDDEVV QREEEAIQLD GLNASQIR

EGSRTDDEVV QREEEAIQLD GLNASQIR

EGSRTDDEVV QREEEAIQLD GLNASQIR

Endoplasm
reticulum
membrane

EGSRTDDEVV QREEEAIQLD GLNASQIR

EGSRTDDEVV QREEEAIQLD GLNASQIR

EGSRTDDEVV QREEEAIQLD GLNASQIR

TDDEVVQREE EAIQLDGLNA SQIR

TDDEVVQREE EAIQLDGLNA SQIR

ELISNASDAL DKIR

ELISNASDAL DKIR

LISLTDENAL SGNEELTVK

LISLTDENAL SGNEELTVK

SILFVPTSAP R

SILFVPTSAP R

SILFVPTSAP R

GLFDEYGSK

GVVDSDDLPL NVSR

GVVDSDDLPL NVSR

IADDKYNDTF WKEFGTNIK

IADDKYNDTF WKEFGTNIK

FQSSHPTDI TSLDQYVER

FQSSHPTDI TSLDQYVER

KGYEVIYLTE PVDEYCIQAL PEFDGKR

GYEVIYLTEP VDEYCIQALP EFDGKR

GYEVIYLTEP VDEYCIQALP EFDGKR

GYEVIYLTEP VDEYCIQALP EFDGKR

GYEVIYLTEP VDEYCIQALP EFDGKR

EAVEKEFEPL LNWMKDK

ALKDKIEKAV VSQR

						LTESPCALVA SQYGWSGNME R	
						LTESPCALVA SQYGWSGNME R	
						AQAYQTGKDI STNYYSQKK	
						SGYLLPDTK	
ACTN1_HUMAN	Alpha-actinin-1	4	6	103	5.25	KTFTAWCNSH LR	Cytoplasm
						FAIQDISVEE TSAKEGLLLW CQR	
						FAIQDISVEE TSAKEGLLLW CQR	
						EGLLLWCQR	
						LRKDDPLTNL NTAFDVAEK	
						LRKDDPLTNL NTAFDVAEK	
						AIMTYVSSFY HAFSGAQKAE TAANR	
						AIMTYVSSFY HAFSGAQKAE TAANR	
						CQLEINFNTL QTK	
						CQLEINFNTL QTK	
						LAILGIHNEV SK	
						QFGAQANVIG PWIQTk	
						IDQLEGDHQL IQEALIFDNK	
						IDQLEGDHQL IQEALIFDNK	
						VGWEQLLTTI AR	
						VGWEQLLTTI AR	
						VGWEQLLTTI AR	
						VGWEQLLTTI AR	
						VGWEQLLTTI AR	
						VGWEQLLTTI AR	
						TINEVENQIL TR	
						TINEVENQIL TR	
GANAB_HUMAN	Neutral alpha-glucosidase AB	7	10	106.8	5.74	FRIDELEPR	Endoplasmic reticulum
						QYASLTGTQA LPPLFSLGYH QSR	

						QYASLTGTQA LPPLFSLGYH QSR DVHNIYGLYV HMATADGLR HHGPQTLYLP VTLSSIPVFQ R YLPVTLSSIP VFQR VVIIGAGKPA AVVLQTK LSFQHDPETS VLVLRL LSFQHDPETS VLVLRL LSFQHDPETS VLVLRL	
AT1A1_HUMAN	Sodium/potassium-transporting ATPase subunit alpha-1	3	4	112.8	5.13	MSINAEVVV GDLVEVK GVGIISEGNE TVEDIAAR GVGIISEGNE TVEDIAAR LNIPVSQVNP R	Integral to membrane
TERA_HUMAN	Transitional endoplasmic reticulum ATPase	3	6	89.3	5.14	IVSQLLTLMD GLKQR QAAPCVLFFD ELDSIAK QAAPCVLFFD ELDSIAK QAAPCVLFFD ELDSIAK QAAPCVLFFD ELDSIAK LDQLIYIPLP DEK	Endoplasmic reticulum
IMB1_HUMAN	Importin subunit beta-1	3	4	97.1	4.68	MELITILEK MELITILEK LAATNALLNS LEFTK AFGCILEGPE PSQKPLVIQ AMPTLIELMK DPSVVVRDTA AWTVGR	Nucleus envelope
HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2	2	2	85.1	4.85	YGGQPLFSEK FPTLWSGAR YNVLGAETVL NQMR	Nucleus

HXK1_HUMAN	Hexokinase-1	2	3	102.4	6.36	LSDETLIDIM TR LSDETLIDIM TR NHEKNQNVHM ESEVYDTPEN IVHGSGSQLF DHVAECLGDF MEKR NHEKNQNVHM ESEVYDTPEN IVHGSGSQLF DHVAECLGDF MEKR NHEKNQNVHM ESEVYDTPEN IVHGSGSQLF DHVAECLGDF MEKR NHEKNQNVHM ESEVYDTPEN IVHGSGSQLF DHVAECLGDF MEKR	Membrane
LONM_HUMAN	Lon protease homolog	2	2	106.4	6.01	ILEFIAVSQ L R IVSGEAE SVE VTPENLQDFV GKPVFTVER	Mitochondrion
WDR89_HUMAN	WD repeat-containing protein 89	2	2	43.2	5.72	FHPSNPNMVV SGSSDGLVNV FDINIDNEED ALVTTCNSIS SV IHLMNCSMSG LTHVTSLQGG HAATVRSFCW NVQDDSLLTG	
ZN367_HUMAN	Zinc finger protein 367	2	2	38.4	8.07	GRGAPPPAAS ASAAASGGED EE GAPPPAASAS AAASGGE	Nucleus
CALX_HUMAN	Calnexin	6	10	67.5	4.47	APVPTGEVYF ADSFDRG TLS GWILSK APVPTGEVYF ADSFDR APVPTGEVYF ADSFDR GTL SGWILSK GTL SGWILSK LYTLILNPDN SFEILVDQSV VN SGNLL KIPNP DFFED LEPFR KIPNP DFFED LEPFR IPNP DFFEDL EPFR	Integral to membrane

						IPNPdffEDL EPFR	
PDIA4_HUMAN	Protein disulfide-isomerase A4	7	11	72.9	4.96	IANILKDKDP PIPVAK	Endoplasmic reticulum (lumen)
						IDATSASVLA SRFDVSGYPT IK	
						IDATSASVLA SRFDVSGYPT IK	
						FDVSGYPTIK	
						KGQAVDYEGS RTQEEIVAK	
						EVSQPDWTPP PEVTLVLTK	
						EVSQPDWTPP PEVTLVLTK	
						FDVSGYPTLK	
						YGIVDYMIEQ SGPPSKEILT LK	
						YGIVDYMIEQ SGPPSKEILT LK	
						YGIVDYMIEQ SGPPSKEILT LK	
						FAMEPEEFDS DTLREFVTAF K	
NUCL_HUMAN	Nucleolin	5	10	76.6	4.6	QKVEGTEPTT AFNLFVGNLNFN FNK	Cell cortex
						VEGTEPTTAF NLFVGNLNFN K	
						VEGTEPTTAF NLFVGNLNFN K	
						VEGTEPTTAF NLFVGNLNFN K	
						VEGTEPTTAF NLFVGNLNFN K	
						TGISDVFAKN DLAVVDVR	
						TGISDVFAKN DLAVVDVR	
						FGYVDFESAE DLEK	
						NLPYKVTQDE LKEVFEDAAE IR	
						NLPYKVTQDE LKEVFEDAAE IR	
ECHA_HUMAN	Trifunctional enzyme subunit alpha	4	7	82.9	9.16	TVLGTPEVLL GALPGAGGTQ R	Mitochondrial inner membrane.
						TVLGTPEVLL GALPGAGGTQ R	
						MGLVDQLVEP LGPGLKPPEE R	
						MGLVDQLVEP LGPGLKPPEE R	

CEAM6_HUMAN	Carcinoembryonic antigen-related cell adhesion molecule 6	3	5	37.2	5.56	TIEYLEEVAI TFAK TIEYLEEVAI TFAK EVEAVIPDHC IFASNTSALP ISEIAAVSK	Integral to plasma membrane
						VDGNSLIVGY VIGTQQATPG PAYSGR	
						SDPVTNLNVLVY GPDVPTISPS K SDPVTNLNVLVY GPDVPTISPS K PVTNLNVLVYGP DVPTISPSK PVTNLNVLVYGP DVPTISPSK	
4F2_HUMAN	4F2 cell-surface antigen heavy chain	2	4	57.9	5.2	IKVAEDEAEA AAAAK	Integral to membrane
						GQSEDPGSLL SLFR GQSEDPGSLL SLFR GQSEDPGSLL SLFR	
P5CS_HUMAN	Delta-1-pyrroline-5-carboxylate synthetase	2	3	87.2	6.66	SNIPFITVPL SR	Mitochondrial inner membrane.
						GPVGLEGLLT TK GPVGLEGLLT TK	
WDR26_HUMAN	WD repeat-containing protein 26	2	2	72.1	5.74	MQANGAGGGG GGGGGGGGGG GGGGGQGQ MQANGAGGGG GGGGGGGGGG GGGGG	Cytoplasm
GRP78_HUMAN	78 kDa glucose-regulated protein	31	91	72.3	5.07	ITPSYVAFTP EGERLIGDAA K	Integral to endoplasmic reticulum
						ITPSYVAFTP EGERLIGDAA K ITPSYVAFTP EGER ITPSYVAFTP EGER LIGDAAKNQL TSNPENTVFD AKR LIGDAAKNQL TSNPENTVFD AKR	

NQLTSNPENT VFDAK
TWNDPSVQQD IKFLPFK
TWNDPSVQQD IK
KTKPYIQVDI GGGQTK
TKPYIQVDIG GGQTK
TKPYIQVDIG GGQTK
TKPYIQVDIG GGQTK
TFAPEEISAM VLTK
TFAPEEISAM VLTK
TFAPEEISAM VLTK
TFAPEEISAM VLTK
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TFAPEEISAM VLTK
TFAPEEISAM VLTK
TFAPEEISAM VLTK
MKETAEAYLG KK
KVTHAVVTVP AYFNDAQR
VTHAVVTVPA YFNDAQR
VTHAVVTVPA YFNDAQR
QATKDAGTIA GLNVMR
QATKDAGTIA GLNVMR
DAGTIAGLNV MR

IINEPTAAAI AYGLDKR
IINEPTAAAI AYGLDKR
IINEPTAAAI AYGLDK
IINEPTAAAI AYGLDK
IEIESFYEGE DFSETLTR
IEIESFYEGE DFSETLTR
IEIESFYEGE DFSETLTR
IEIESFYEGE DFSETLTR
IEIESFYEGE DFSETLTR
AKFEELNMDL FR
AKFEELNMDL FR
AKFEELNMDL FR
AKFEELNMDL FR
AKFEELNMDL FR
AKFEELNMDL FR
AKFEELNMDL FR
AKFEELNMDL FR
AKFEELNMDL FR
AKFEELNMDL FR
FEELNMDLFR
FEELNMDLFR
FEELNMDLFR
VLEDSDLKKS DIDEIVLVGG STR
VLEDSDLKKS DIDEIVLVGG STR
KSDIDEIVLV GGSTRIPK
IQQLVKEFFN GKEPSR
IQQLVKEFFN GKEPSR
IQQLVKEFFN GKEPSR
IQQLVKEFFN GKEPSR

GRP75_HUMAN	Stress-70 protein	17	55	73.6	5.87	LIPRNTVVPT KKSQIFSTAS DNQPTVTIKV	Cell surface
						YEG 468erpl	
						KSQIFSTASD NQPTVTIK	
						SQIFSTASDN QPTVTIK	
						SQIFSTASDN QPTVTIK	
						SQIFSTASDN QPTVTIK	
						SQIFSTASDN QPTVTIK	
						SQIFSTASDN QPTVTIK	
						DNHLLGTFDL TGIPPAPR	
						DNHLLGTFDL TGIPPAPR	
						DNHLLGTFDL TGIPPAPR	
						DNHLLGTFDL TGIPPAPR	
						DNHLLGTFDL TGIPPAPR	
						DNHLLGTFDL TGIPPAPR	
						DNHLLGTFDL TGIPPAPR	
						DNHLLGTFDL TGIPPAPR	
						DNHLLGTFDL TGIPPAPR	
						DNHLLGTFDL TGIPPAPR	
						ITITNDQNRL TPEEIER	
						IDTRNELESY AYSLK	
						IDTRNELESY AYSLK	
						KKELEEIVQP IISK	
						KKELEEIVQP IISK	
						KKELEEIVQP IISK	
						ELEEIVQPII SK	
						ELEEIVQPII SK	
						LYGSAGPPPT GEEDTAEKDE L	
						LYGSAGPPPT GEEDTAEKDE L	
						TTPSVVAFTA DGERLVGMPA KR	

TTPSVVAFTA DGERLVGMPA KR
TTPSVVAFTA DGERLVGMPA KR
TTPSVVAFTA DGERLVGMPA KR
TTPSVVAFTA DGER
TTPSVVAFTA DGER
QAVTNPNTF YATKR
LYSPSQIGAF VLMK
LYSPSQIGAF VLMK
LYSPSQIGAF VLMK
LYSPSQIGAF VLMK
LYSPSQIGAF VLMK
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LYSPSQIGAF VLMK
LYSPSQIGAF VLMK
LYSPSQIGAF VLMK
MKETAENYLG HTAK
NAVITVPAYF NDSQR
NAVITVPAYF NDSQR
NAVITVPAYF NDSQR
NAVITVPAYF NDSQR
QATKDAGQIS GLNVLR
QATKDAGQIS GLNVLR
DAGQISGLNV LR
DAGQISGLNV LR
GVFEVKSTNG DTFLGGEDFD QALLR
GVFEVKSTNG DTFLGGEDFD QALLR
STNGDTFLGG EDFDQALLR
STNGDTFLGG EDFDQALLR
STNGDTFLGG EDFDQALLR
STNGDTFLGG EDFDQALLR

						STNGDTFLGG EDFDQALLR	
						STNGDTFLGG EDFDQALLR	
						STNGDTFLGG EDFDQALLR	
						AQFEGIVTDL IRR	
						AQFEGIVTDL IRR	
						AQFEGIVTDL IR	
						AQFEGIVTDL IR	
						AQFEGIVTDL IR	
						AQFEGIVTDL IR	
						AQFEGIVTDL IR	
						AMQDAEVSKS DIGEVILVGG MTR	
						AMQDAEVSKS DIGEVILVGG MTR	
						VQQTVQDLFG R	
						VQQTVQDLFG R	
						EMAGDNKLLG QFTLIGIPPA PR	
						EMAGDNKLLG QFTLIGIPPA PR	
						EMAGDNKLLG QFTLIGIPPA PR	
						EMAGDNKLLG QFTLIGIPPA PR	
						EMAGDNKLLG QFTLIGIPPA PR	
						LLGQFTLIGI PPAPR	
						LLGQFTLIGI PPAPR	
						LLGQFTLIGI PPAPR	
						LLGQFTLIGI PPAPR	
						LLGQFTLIGI PPAPR	
						QAASSLQQAS LKLFEMAYKK	
						QAASSLQQAS LKLFEMAYKK	
HSP71_HUMAN	Heat shock 70 kDa protein 1	7	15	70	5.48	TTPSYVAFTD TER	Cytoplasam
						AFYPEEISSM VLTK	
						AFYPEEISSM VLTK	

						MKEIAEAYLG YPVTNAVITV PAYFNDSQR NAVITVPAYF NDSQR NAVITVPAYF NDSQR NAVITVPAYF NDSQR NAVITVPAYF NDSQR QATKDAGVIA GLNVLR QATKDAGVIA GLNVLR QATKDAGVIA GLNVLR QATKDAGVIA GLNVLR DAGVIAGLNV LR IINEPTAAAI AYGLDR IINEPTAAAI AYGLDR IINEPTAAAI AYGLDR IINEPTAAAI AYGLDR ELEQVCNP II SGLYQGAGGP GPGGFQAQGP K ELEQVCNP II SGLYQGAGGP GPGGFQAQGP K	
HSP7C_HUMAN	Heat shock cognate 71 kDa protein	6	11	70.9	5.37	TTPSYVAFTD TER	Cytoplasm
						SFYPEEVSSM VLTK SFYPEEVSSM VLTK SFYPEEVSSM VLTK SFYPEEVSSM VLTK QATKDAGTIA GLNVLR QATKDAGTIA GLNVLR DAGTIAGLNV LR IINEPTAAAI AYGLDK	

						IINEPTAAAI AYGLDK	
						ARFEELNADL FRGTLDPVEK	
						ARFEELNADL FR	
						NTTIPTKQTQ TFTTYSDNQP GVLIQVYEGE	
						R	
						NTTIPTKQTQ TFTTYSDNQP GVLIQVYEGE	
						R	
TRAP1_HUMAN	Heat shock protein 75 kDa	3	8	80.1	8.3	GTITIQDTGI GMTQEELVSN LGTIAR	Mitochondrion
						GTITIQDTGI GMTQEELVSN LGTIAR	
						GTITIQDTGI GMTQEELVSN LGTIAR	
						GTITIQDTGI GMTQEELVSN LGTIAR	
						YESSALPSGQ LTSLSEYASR	
						YESSALPSGQ LTSLSEYASR	
						AQLLQPTLEI NPR	
						AQLLQPTLEI NPR	
RIB1_HUMAN	Dolichyl- diphosphooligosaccharide-- protein glycosyltransferase subunit 1	6	12	68.5	5.96	SSEAPPLINE DVKR	Membrane
						VTAEVVLAHL GGGSTSR	
						VTAEVVLAHL GGGSTSR	
						VTAEVVLAHL GGGSTSR	
						VTAEVVLAHL GGGSTSR	
						ATSFLLALEP ELEAR	
						ATSFLLALEP ELEAR	
						ATSFLLALEP ELEAR	
						ATSFLLALEP ELEAR	
						SEDLLDYGPF R	
						YDYQRQPDSG ISSIR	

						SLETEHKALT SEIALLQSR	
DHSA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit	3	10	72.6	7.06	VSDSISAQYP VVDHEFDAVV VGAGGAGLR	Membrane
						VSDSISAQYP VVDHEFDAVV VGAGGAGLR	
						VSDSISAQYP VVDHEFDAVV VGAGGAGLR	
						VSDSISAQYP VVDHEFDAVV VGAGGAGLR	
						AAFGLSEAGF NTACVTK	
						AAFGLSEAGF NTACVTK	
						LGANSLLDLV VFGR	
						LGANSLLDLV VFGR	
						LGANSLLDLV VFGR	
						LGANSLLDLV VFGR	
ACSL3_HUMAN	Long-chain-fatty-acid--CoA ligase 3	2	3	80.4	8.65	VGAPLVCCEI K	Integral to plasma membrane
						LSPEPWTPET GLVTDAFK	
						LSPEPWTPET GLVTDAFK	
GPDM_HUMAN	Glycerol-3-phosphate dehydrogenase	2	4	80.8	7.23	LVQDYGLESE VAQHLAATYG DK	Mitochondrial inner membrane.
						LVQDYGLESE VAQHLAATYG DK	
						LAFLNVQAAE EALPR	
						LAFLNVQAAE EALPR	
CSMD2_HUMAN	CUB and sushi domain- containing protein 2	2	2	379.8	5.69	PKCEVPCGGN ITSSNGTVYS PGFPSPYSSS QDCVWLITVP IGHGVR	Integral to membrane
						LVINCGDPI PANGLR	

GCN1L_HUMAN	GCN1-like protein 1	2	2	292.6	7.19	ENPGLVEQYL SAILSLEPNQ NYAGMLGLLV QFCTSHKEM LIGNESKGEH VPGF	Cytoplasm
KPYM_HUMAN	Pyruvate kinase isozymes M1/M2	5	7	57.9	7.96	TATESFASDP ILYRPVAVAL DTK TGLIKGSGTA EVELKK GVNLPGAAVD LPAVSEKDIQ DLK LAPITSDPTE ATAVGAVEAS FK LAPITSDPTE ATAVGAVEAS FK LAPITSDPTE ATAVGAVEAS FK GIFPVLCKDP VQEAWAEDVD LR	Cytoplasm
PDIA1_HUMAN	Protein disulfide-isomerase	8	14	57.1	4.76	LAKVDATEES DLAQQYGVR EADDIVNWLK EADDIVNWLK TGPAATTLPD GAAAESLVES SEVAVIGFFK TGPAATTLPD GAAAESLVES SEVAVIGFFK QFLQAAEAID DIPFGITSNS DVFSK QFLQAAEAID DIPFGITSNS DVFSK QFLQAAEAID DIPFGITSNS DVFSK QFLQAAEAID DIPFGITSNS DVFSK HNQLPLVIEF TEQTAPK HNQLPLVIEF TEQTAPK ILEFFGLKKE ECPAVR MDSTANEVEA VKVHSFPTLK FFPASADRTV IDYNGER	Plasma membrane

PDIA3_HUMAN	Protein disulfide-isomerase A3	16	25	56.7	5.98	SDVLELTDDN FESR	Endoplasmic reticulum lumen
						SDVLELTDDN FESR	
						YGVSGYPTLK	
						IFRDGEEAGA YDGPR	
						QAGPASVPLR TEEEFKK	
						FISDKDASIV GFFDDSFSEA HSEFLK	
						FISDKDASIV GFFDDSFSEA HSEFLK	
						FISDKDASIV GFFDDSFSEA HSEFLK	
						VGFFDDSFSE AHSEFLK	
						DLLIAYYDVD YEK	
						DLLIAYYDVD YEK	
						KFLDAGHKLN FAVASR	
						FLDAGHKLN FAVASR	
						KTFSHELSD F GLESTAGEIP VVAIR	
						KTFSHELSD F GLESTAGEIP VVAIR	
						TFSHELSD F GLESTAGEIP VVAIR	
						TFSHELSD F GLESTAGEIP VVAIR	
						FLQDYFDGNL KR	
						LSKDPNIVIA K	
						GFPTIYFSPA NK	
						GFPTIYFSPA NK	
						KYEGGRELS D FISYLQR	
						ELSD F FISYLQ R	
						ELSD F FISYLQ R	
						ELSD F FISYLQ R	
CH60_HUMAN	60 kDa heat shock protein	30	103	61	5.7	ALMLQGV DLL ADAVA VTMGP K	Mitochondrial inner membrane.
						ALMLQGV DLL ADAVA VTMGP K	

ALMLQGVDLL ADAVAVTMGP K
ALMLQGVDLL ADAVAVTMGP K
ALMLQGVDLL ADAVAVTMGP K
ALMLQGVDLL ADAVAVTMGP K
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ALMLQGVDLL ADAVAVTMGP K
ALMLQGVDLL ADAVAVTMGP K
TVIIEQSWGS PK
SIDLKDKYKN IGAK
SIDLKDKYKN IGAK
LVQDVANNTN EEAGDGTTTA TVLAR
LVQDVANNTN EEAGDGTTTA TVLAR

LVQDVANNTN EEAGDGTSTA TVLAR
LVQDVANNTN EEAGDGTSTA TVLAR
LVQDVANNTN EEAGDGTSTA TVLAR
GVMLAVDAVI AELKK
GVMLAVDAVI AELKK
GVMLAVDAVI AELKK
GVMLAVDAVI AELKK
GVMLAVDAVI AELKK
GVMLAVDAVI AELKK
GVMLAVDAVI AELK
QSKPVTTPPE IAQVATISAN GDKEIGNIIS
DAMK
QSKPVTTPPE IAQVATISAN GDKEIGNIIS
DAMK
TLNDELEIIE GMKFDR
TLNDELEIIE GMK
TLNDELEIIE GMK
TLNDELEIIE GMK
TLNDELEIIE GMK
TLNDELEIIE GMK
GQKCEFQDAY VLLSEKK
GQKCEFQDAY VLLSEKK
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KISSIQSIVP ALEIANHR

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ISSIQSIVPA LEIANAHR
KPLVIAEDV DGEALSTLVL NR
KPLVIAEDV DGEALSTLVL NR
KPLVIAEDV DGEALSTLVL NR
KPLVIAEDV DGEALSTLVL NR
KPLVIAEDV DGEALSTLVL NR
VGEVIVTKDD AMLLK
IQEIIEQLDV TTSEYEKEKL NER
IQEIIEQLDV TTSEYEKEKL NER
LSDGVAVLK
VGGTSDVEVN EKKDRVTDAL NATR
VTDALNATR
AAVEEGIVLG GGCALLR
AAVEEGIVLG GGCALLR
AAVEEGIVLG GGCALLR
AAVEEGIVLG GGCALLR
AAVEEGIVLG GGCALLR
AAVEEGIVLG GGCALLR
AAVEEGIVLG GGCALLR
AAVEEGIVLG GGCALLR
CIPALDSLTP ANEDQKIGIE IIKR
CIPALDSLTP ANEDQKIGIE IIKR
CIPALDSLTP ANEDQKIGIE IIKR
CIPALDSLTP ANEDQKIGIE IIKR
CIPALDSLTP ANEDQKIGIE IIKR

CO4A2_HUMAN	Collagen alpha-2(IV) chain precursor	3	3	167.4	8.89	GFPGDAGLPG PPGF GDPGPPGPP GPKGDPGFPG APGTVGA	Basement membrane
EPIPL_HUMAN	Epiplakin	2	2	552.8	5.43	TGSVAGVVLL PEGHK TGCIAGLLLP GSQER	Cytoplasm

NFAC4_HUMAN	Nuclear factor of activated T-cells, cytoplasmic 4	2	2	95.4	5.29	RLGGPGGGAG GAGGGR GAVKAAPGGH P	Nucleus
SFRS1_HUMAN	Splicing factor, arginine/serine-rich 1	3	5	27.7	10.37	GGGGGGGGGA PRG GGGGGGGGGA PR GGGGGGGGAP R GGGGGGGGAP R GGGGGGGGAP R	Nucleus
MDHM_HUMAN	Malate dehydrogenase	3	4	35.5	8.92	LTLYDIAHTP GVAADLSHIE TK TIPLISQCT PK VDFPQDQLTA LTGR VDFPQDQLTA LTGR	Mitochondrion inner membrane
G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase	2	2	36	8.57	LVINGNPITI FQER VPTANVSVD LTGR	Membrane
RAB2A_HUMAN	Ras-related protein Rab-2A	2	3	23.5	6.08	GAAGALLVYD ITR TASNVEEAFI NTAK TASNVEEAFI NTAK	Membrane
CPNS1_HUMAN	Calpain small subunit 1	2	7	28.3	5.05	GGGGGGGGGG GLGGGLGNVL GG GGGGGGGGGG GLGGGLGNVL GG GGGGGGGGGG GLGGGLGNVL GG GGGGGGGGGG GLGG GGGGGGGGGG GLGG GGGGGGGGGG GLGG	Plasma membrane

COGA1_HUMAN	Collagen alpha-1(XVI) chain	2	2	157.7	8.14	GDPGPAGPPG	Extracellular matrix
						GDPGAAGQKG QA	
TRI67_HUMAN	Tripartite motif-containing protein 67	2	2	80.9	6.92	GAGGSAAGGL GGGAGGGGDH ADK	Cytoplasm
						AKHEVKPLGA MWK	
ACTB_HUMAN	Actin, cytoplasmic 1	5	21	41.7	5.29	AVFPSIVGRP R	Cytoplasm
						AVFPSIVGRP R	
						AVFPSIVGRP R	
						AVFPSIVGRP R	
						AVFPSIVGRP R	
						AVFPSIVGR	
						AVFPSIVGR	
						AVFPSIVGR	
						AVFPSIVGR	
						VAPEEHPVLL TEAPLNPK	
						VAPEEHPVLL TEAPLNPK	
						VAPEEHPVLL TEAPLNPK	
						VAPEEHPVLL TEAPLNPK	
						VAPEEHPVLL TEAPLNPK	
						VAPEEHPVLL TEAPLNPK	
						VAPEEHPVLL TEAPLNPK	
						SYELPDGQVI TIGNER	
						SYELPDGQVI TIGNER	
						SYELPDGQVI TIGNER	
						SYELPDGQVI TIGNER	
						QEYDESGPSI VHR	
ADT2_HUMAN	ADP/ATP translocase 2	2	5	32.9	9.76	DFLAGGVAAA ISK	Integral to membrane

						DFLAGGVAAA ISK DFLAGGVAAA ISK YFPTQALNFA FK YFPTQALNFA FK	
PDIA6_HUMAN	Protein disulfide-isomerase A6	2	4	48.1	4.95	LAAVDATVNQ VLASR LAAVDATVNQ VLASR LAAVDATVNQ VLASR GSFSEQGINE FLR	Endoplasmic reticulum lumen
SERPH_HUMAN	Serpin H1	2	4	46.4	8.75	DEEVHAGLGE LLR HLAGLGLTEA IDK HLAGLGLTEA IDK HLAGLGLTEA IDK	Endoplasmic reticulum lumen.
DHX57_HUMAN	Putative ATP-dependent RNA helicase DHX57	2	3	155.5	7.83	GGGGGGGGGG GGNRK GGGGGGGGNR K GGGGGGGGNR K	Endoplasmic reticulum lumen.
IRS2_HUMAN	Insulin receptor substrate 2	2	2	137.2	8.9	AAVPSAGPAG PAPTSAAGR SPKPGAPSGH PVGSLDG	Plasma membrane
ITB4_HUMAN	Integrin beta-4	2	2	202	5.74	LLELQEVDSL LR HRMTTTSAAA YGTHLSPHVP HRVLSTSS	Plasma membrane
PPRC1_HUMAN	Peroxisome proliferator- activated receptor gamma coactivator-related protein 1	5	5	177.4	6.11	SSSSSSSSSS SSSSSSSSSS R SSSSSSSSSS SSSSSSSSSR	Nucleus

						SSSSSSSSSS SSSSSSSR		
						SSSSSSSSSS SSSSR		
						SSSSSSSSSS SSSR		
ATPB_HUMAN	ATP synthase subunit beta	4	13	56.5	5.26	IPVGPETLGR		Mitochondrial inner membrane
						IPVGPETLGR		
						IPVGPETLGR		
						VALTGLTVAE YFR		
						VALTGLTVAE YFR		
						VALTGLTVAE YFR		
						FTQAGSEVSA LLGR		
						FTQAGSEVSA LLGR		
						FTQAGSEVSA LLGR		
						FTQAGSEVSA LLGR		
						FTQAGSEVSA LLGR		
						FTQAGSEVSA LLGR		
						AIAELGIYPA VDPLDSTSR		
CH10_HUMAN	10 kDa heat shock protein	2	9	10.9	8.89	VLQATVVAVG SGSK		Mitochondrion
						VLQATVVAVG SGSK		
						VLQATVVAVG SGSK		
						VLQATVVAVG SGSK		
						VLQATVVAVG SGSK		
						VLQATVVAVG SGSK		
						VLQATVVAVG SGSK		
						VLQATVVAVG SGSK		
						VVLDDKDYFL FR		
ACTK_HUMAN	Beta-actin-like protein 3	3	14	42	5.91	QAVFPSIVGR PR		Cytoplasm
						QAVFPSIVGR PR		
						QAVFPSIVGR PR		

						QAVFPSIVGR PR QAVFPSIVGR PR QAVFPSIVGR PR AVFPSIVGRP R AVFPSIVGRP R AVFPSIVGRP R AVFPSIVGRP R AVFPSIVGRP R AVFPSIVGRP R AVFPSIVGRP R SYELPDGQVI TIGNER	
ATPA_HUMAN	ATP synthase subunit alpha	3	6	59.7	9.16	VLSIGDGIAR	Mitochondrial inner membrane.
						VLSIGDGIAR TGAIVDVPVG EELLGR TGAIVDVPVG EELLGR TGAIVDVPVG EELLGR AVDSLVIPIGR	
CO4A4_HUMAN	Collagen alpha-4(IV) chain precursor	4	4	163.9	8.87	GSRGPPGPPG PQGP GLCACEPGPM GPPGPPGLPG LCACEPGPMG PPGPPGLP GASGLHDVGP PGPV	Basement membrane
ECH1_HUMAN	Delta(3,5)-Delta(2,4)-dienoyl- CoA isomerase	2	6	35.8	8.16	GNQSLVNELA FTAR GNQSLVNELA FTAR GNQSLVNELA FTAR GNQSLVNELA FTAR NQSLVNELAF TAR	Mitochondrion

						NQSLVNELAF TAR	
AATM_HUMAN	Aspartate aminotransferase	2	7	47.4	9.14	EYLPIGGLAE FCK EYLPIGGLAE FCK EYLPIGGLAE FCK EYLPIGGLAE FCK FVTVQTISGT GALR FVTVQTISGT GALR FVTVQTISGT GALR	Plasma membrane
GLYM_HUMAN	Serine hydroxymethyltransferase	2	4	56	8.76	AALEALGSCL NNK AALEALGSCL NNK AALEALGSCL NNK TGLIDYNQLA LTAR	Mitochondrion
HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M	2	2	77.5	8.84	GAPGVPSGNG APGPKGEGER PAQNEK GAPGVPSGNG APGPKGEGER PAQNEK AMQKVMATTG GMGMGPGGPG MITIPPS	Integral to plasma membrane
PO4F2_HUMAN	POU domain, class 4, transcription factor 2	2	2	43.1	9.27	PSSSSNAGGG GGGGGGGGGG GGGR GGGGGGGGGG GGGGGRSSSS SSSGSSGGGG SEAMR	Nucleus
M3K1_HUMAN	Mitogen-activated protein kinase kinase kinase 1	2	2	164.8	8.37	GALKASSAPA AAAGLLR EKMEAEEEEA LAIAM	Membrane fraction
CO4A6_HUMAN	Collagen alpha-6(IV) chain precursor	2	2	163.7	9.31	GDEGIQGLRG PSGVPGLPAL SG GFPGFPGLHG LNGLP	basement membrane

ZO3_HUMAN	Tight junction protein ZO-3	2	2	102.7	6.1	RSPGGGSEAN GLAL SSYDIYRVPS SQSMEDR	Plasma membrane
ANXA2_HUMAN	Annexin A2	2	14	38.6	7.57	STVHEILCK STVHEILCK STVHEILCK STVHEILCK GVDEVTIVNI LTNR GVDEVTIVNI LTNR GVDEVTIVNI LTNR GVDEVTIVNI LTNR GVDEVTIVNI LTNR GVDEVTIVNI LTNR GVDEVTIVNI LTNR GVDEVTIVNI LTNR GVDEVTIVNI LTNR GVDEVTIVNI LTNR	Basement membrane Plasma membrane
M2OM_HUMAN	Mitochondrial 2-oxoglutarate/malate carrier protein	2	2	34	9.92	AVIGMTAGAT GAFVGTPA VIGMTAGATG AFVGTPAEVA L	Integral to plasma membrane
CALR_HUMAN	Calreticulin	9	24	48.1	4.29	EPAVYFKEQF LDGDGWTSR EPAVYFKEQF LDGDGWTSR EPAVYFKEQF LDGDGWTSR EPAVYFKEQF LDGDGWTSR FYGDEEKDKG LQTSQDAR FYALSASFEP FSNK	Cytoplasm

FYALSASFEP FSNK
 LFPNSLDQTD MHGDSEYNIM
 FGPDICGPGT K
 CKDDEFTHLY TLIVRPDNTY EVK
 CKDDEFTHLY TLIVRPDNTY EVK
 CKDDEFTHLY TLIVRPDNTY EVK
 CKDDEFTHLY TLIVRPDNTY EVK
 IDNSQVESGS LEDDWDFLPP KK
 IDNSQVESGS LEDDWDFLPP KK
 IDNSQVESGS LEDDWDFLPP KK
 IDNSQVESGS LEDDWDFLPP KK
 IDNSQVESGS LEDDWDFLPP KK
 IDNSQVESGS LEDDWDFLPP K
 IDNSQVESGS LEDDWDFLPP K
 IKDPDASKPE DWDER

 SGTIFDNFLI TNDEAYAEEF GNETWGVTK

 SGTIFDNFLI TNDEAYAEEF GNETWGVTK

 SGTIFDNFLI TNDEAYAEEF GNETWGVTK

 SGTIFDNFLI TNDEAYAEEF GNETWGVTK

DLDH_HUMAN	Dihydrolipoyl dehydrogenase	5	13	54.1	7.95	ADQPIDADVT VIGSGPGGYV AAIK ADQPIDADVT VIGSGPGGYV AAIK ADQPIDADVT VIGSGPGGYV AAIK ADQPIDADVT VIGSGPGGYV AAIK TVCIEKNETL GGTCLNVGCI PSK TVCIEKNETL GGTCLNVGCI PSK	Mitochondrion
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						NLGLEELGIE LDPR NLGLEELGIE LDPR IPNIYAIGDV VAGPMLAHK IPNIYAIGDV VAGPMLAHK IPNIYAIGDV VAGPMLAHK IPNIYAIGDV VAGPMLAHK VCHAHPTLSE AFR	
ODO2_HUMAN	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	3	6	48.6	9.01	TPAFAESVTE GDVRWEK	Plasma membrane
						TPAFAESVTE GDVRWEK ASAFALQEQP VVNAVIDDTT KEVVYR ASAFALQEQP VVNAVIDDTT KEVVYR ASAFALQEQP VVNAVIDDTT K ASAFALQEQP VVNAVIDDTT K	
HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K	4	8	50.9	5.39	LLIHQSLAGG IIGVK	Nucleus
						LLIHQSLAGG IIGVK IILDLISESP IK IILDLISESP IK GSYGDLGGPI ITTQVTIPK GSYGDLGGPI ITTQVTIPK IITITGTQDQ IQNAQYLLQN SVK IITITGTQDQ IQNAQYLLQN SVK	
QCR1_HUMAN	Cytochrome b-c1 complex subunit 1	3	5	52.6	5.94	DVVFNYLHAT AFQGTPLAQA VEGPSENV DVVFNYLHAT AFQGTPLAQA VEGPSENV	Mitochondrial inner membrane.

						ADLTEYLSTH YKAPR MVLAAAGGVE HQQLDLAQK MVLAAAGGVE HQQLDLAQK	
ENOA_HUMAN	Alpha-enolase	3	5	47.1	7.01	LAMQEFMILP VGAANFR	Plasma membrane
						DATNVGDEGG FAPNILENKE GLELLK DATNVGDEGG FAPNILENKE GLELLK YISPDQLADL YK YISPDQLADL YK	
TBB5_HUMAN	Tubulin beta chain	3	3	49.6	4.78	SGPFGQIFRP DNFVFGQSGA GNNWAK GHYTEGAELV DSVLDVVRK ALTVPELTQQ VFDAK	Microtubule
HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H	2	3	49.2	5.89	STGEAFVQFA SQEIAEK	Nucleus
						STGEAFVQFA SQEIAEK ATENDIYNFF SPLNPVR	
TBA1A_HUMAN	Tubulin alpha-1A chain	2	6	50.1	4.94	AVFVDLEPTV IDEVR AVFVDLEPTV IDEVR AVFVDLEPTV IDEVR AVFVDLEPTV IDEVR IHFPLATYAP VISA EK IHFPLATYAP VISA EK	Microtubule
EFTU_HUMAN	Elongation factor Tu	2	3	49.5	7.26	LLDAVDTYIP VPAR LLDAVDTYIP VPAR DLEKPFLLPV EAVYSVPGR	Mitochondrion
ERO1A_HUMAN	ERO1-like protein alpha precursor	2	3	54.4	5.48	HDDSSDNFCE ADDIQSPEAE YVDLLL NPER HDDSSDNFCE ADDIQSPEAE YVDLLL NPER	Membrane

DHE3_HUMAN	Glutamate dehydrogenase 1	2	2	61.4	7.66	IWNVIYEENC FKPQTIK GASIVEDKLV EDLR	Mitochondrion
OAT_HUMAN	Ornithine aminotransferase	4	6	48.5	6.57	ISGASEKDIV HSGLAYTMER AFYNNVLGEY EEEYITK HQVLFIADDEI QTGLAR WLAVDYENVVR PDIVLLGK WLAVDYENVVR PDIVLLGK VAIAALEVLE EENLAENADK VAIAALEVLE EENLAENADK	Mitochondrion
APMAP_HUMAN	Adipocyte plasma membrane-associated protein	3	5	46.5	5.82	RPLRPQVVTD DDGQAPEAK LFENQLVGPE SIAHIGDVMF TGTADGR LFENQLVGPE SIAHIGDVMF TGTADGR LFENQLVGPE SIAHIGDVMF TGTADGR TRDDEPVCGR PLGIR	Integral to membrane
ACADM_HUMAN	Medium-chain specific acyl-CoA dehydrogenase	2	3	46.6	8.61	AFTGTFIVEAD TPGIQIGRK AFAGDIANQL ATDAVQILGG NGFNTEYPVE K AFAGDIANQL ATDAVQILGG NGFNTEYPVE K	Mitochondrion
TXND4_HUMAN	Thioredoxin domain-containing protein 4 precursor	2	3	46.9	5.09	QQKSDPIQEI RDLAEITTLTD R QQKSDPIQEI RDLAEITTLTD R VANILHDDCA FLSAFGDVSK PER	Endoplasmic reticulum lumen
THIM_HUMAN	3-ketoacyl-CoA thiolase	2	4	41.9	8.32	TPFGAYGGLL KDFTATDLSE FAAK TPFGAYGGLL KDFTATDLSE FAAK VSPETVDSVI MGNVLQSSSD AIYLAR	Mitochondrial inner membrane

TF_HUMAN	Tissue factor	2	3	33	6.64	VSPETVDSVI MGNVLQSSSD AIYLAR TILEWEPKPV NQVYTVQIST K CFYTTDTECD LTDEIVKDVK CFYTTDTECD LTDEIVKDVK	Membrane
PK1L1_HUMAN	Polycystic kidney disease protein 1-like 1	3	3	315.2	6.64	STVVIHHFPS IPSYNVSFIS QTQVGDSQAW HSMTVWYKM STVVIHHFPS IPSYNVSFIS QTQVGDSQAW HSMTVWYKM STVVIHHFPS IPSYNVSFIS QTQVGDSQAW HSMTVWYKM HPCFDSSTAH QLDAAAPTVS FEAQWLSDSY DQFLVMLR EQTVTIKPYS LSSGETYVLQ VSVASKHGLL GKAQLYLTVN PAPR	Integral to membrane
STML2_HUMAN	Stomatin-like protein 2	2	4	38.5	6.87	ILEPGLNILI PVLDR ILEPGLNILI PVLDR ILAAALTQHN GDAAASLTVA EQYVSAFSK ILAAALTQHN GDAAASLTVA EQYVSAFSK	Membrane
L2HDH_HUMAN	L-2-hydroxyglutarate dehydrogenase	2	2	50.3	8.57	AQALDRDGNL VEDFVFDAGV GDIGNR ILHVRNAPSP AATSSIAISG MIADEVQQR ILHVRNAPSP AATSSIAISG MIADEVQQR	Integral to membrane
KCNQ3_HUMAN	Potassium voltage-gated channel subfamily KQT member 3	2	2	96.7	8.98	VGLAPGDVEQ VTLALGAGAD KDGTL	Integral to membrane

						STSEIEDQSM MGKFVKVERQ VQDMGKKLDF LVDMHMQHME R STSEIEDQSM MGKFVKVERQ VQDMGKKLDF LVDMHMQHME R STSEIEDQSM MGKFVKVERQ VQDMGKKLDF LVDMHMQHME R STSEIEDQSM MGKFVKVERQ VQDMGKKLDF LVDMHMQHME R STSEIEDQSM MGKFVKVERQ VQDMGKKLDF LVDMHMQHME R STSEIEDQSM MGKFVKVERQ VQDMGKKLDF LVDMHMQHME R	
TXND5_HUMAN	Thioredoxin domain-containing protein 5 precursor	2	2	47.6	6.63	DLESLREYVE SQLQR GYPTLLLFR	Endoplasmic reticulum lumen
QCR2_HUMAN	Cytochrome b-c1 complex subunit 2	2	2	48.4	8.74	KVKATAAPAG APPQ AVAFQNPQTH VIENLHAAAY R	Mitochondrion inner membrane
HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2	3	9	33.6	4.95	VFIGNLNTLV VK VFIGNLNTLV VK MIAGQVLDIN LAAEPK MIAGQVLDIN LAAEPK MIAGQVLDIN LAAEPK MIAGQVLDIN LAAEPK MIAGQVLDIN LAAEPK MIAGQVLDIN LAAEPK VPPPPPIAR	Ribonucleosomes.

ETFA_HUMAN	Electron transfer flavoprotein subunit alpha	3	7	35.1	8.62	QSTLVIAEHA NDSLAPITLN TITAATR QSTLVIAEHA NDSLAPITLN TITAATR QSTLVIAEHA NDSLAPITLN TITAATR QSTLVIAEHA NDSLAPITLN TITAATR LLYDLADQLH AAVGASR TIVAINKDPE APIFQVADYG IVADLFK TIVAINKDPE APIFQVADYG IVADLFK	Mitochondrion
ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1	3	4	37.4	8.97	LFIGGLSFET TEESLR LFIGGLSFET TEESLR ALSRQEMQEV QSSR GNFGGSRNMG GPYGGGNYGP GGSGGSGGYG GRSRY	Nucleus
ANXA1_HUMAN	Annexin A1	4	5	38.7	6.57	GGPGSAVSPY PTFNPSSDVA ALHK GVDEATIIDI LTKR GVDEATIIDI LTK GLGTDEDTLI EILASR GLGTDEDTLI EILASR	Plasma membrane
ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1	2	3	38.8	9.26	LFIGGLSFET TDESLR LFIGGLSFET TDESLR SSGPYGGGGQ YFAKPR	Cytoplasm
HMOX2_HUMAN	Heme oxygenase 2	2	4	36	5.31	IHYIGQNEPE LLVAHAYTR IHYIGQNEPE LLVAHAYTR ALKLPSTGEG TQFYLFENV D NAQQFK ALKLPSTGEG TQFYLFENV D NAQQFK	Plasma membrane

CDKL2_HUMAN	Cyclin-dependent kinase-like 2	2	2	56	8.45	NPSVAIPPLT HNLSAVAPSI NSGMGTETIP IQGYRVDEK SGMGTTETIPI QGYR	Nucleus
K1542_HUMAN	PHD and RING finger domain- containing protein 1	2	2	178.5	9.15	LPAAVPEPDL EEEPVPDLLG SILSGQSLLM LGSS QTLAPVPAAL TPASEPASQA TAASNSEEK	
GBB2_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	2	4	37.3	5.6	SELEQLRQEA EQLR	Cytoplasm
ECHM_HUMAN	Enoyl-CoA hydratase	3	12	31.4	8.34	SELEQLRQEA EQLR KACGDSTLTQ ITAGLDPVGR KACGDSTLTQ ITAGLDPVGR ALNALCDGLI DELNQALK ALNALCDGLI DELNQALK ALNALCDGLI DELNQALK ALNALCDGLI DELNQALK AQFAQPEILI GTIPGAGGTQ R AQFAQPEILI GTIPGAGGTQ R AQFAQPEILI GTIPGAGGTQ R ICPVETLVEE AIQCAEK ICPVETLVEE AIQCAEK ICPVETLVEE AIQCAEK ICPVETLVEE AIQCAEK ICPVETLVEE AIQCAEK	Mitochondrion
KAD2_HUMAN	Adenylate kinase 2	4	7	26.5	7.67	LVSDVMVVEL IEK LVSDVMVVEL IEK LQAYHTQTTP LIEYYR GIHSAIDASQ TPDVVFASIL AAFSK	Membrane

						GIHSAIDASQ TPDVVFASIL AAFSK GIHSAIDASQ TPDVVFASIL AAFSK QTPDVVFASI LAAFSK	
C1QBP_HUMAN	Complement component 1 Q subcomponent-binding protein	2	3	31.3	4.74	VEEQEPELTS TPNFVVEVIK	Plasma membrane
						ALVLDCHYPE DEVGQEDEAE SDIFSIR ALVLDCHYPE DEVGQEDEAE SDIFSIR	
FAM3C_HUMAN	Protein FAM3C	2	3	24.7	8.52	YFDMWGGDVA PFIEFLKAIQ DGTIVLMGTY DDGATKLNDE ARR LIADLGSTSI TNLGFR LIADLGSTSI TNLGFR	Intracellular region
ALK_HUMAN	ALK tyrosine kinase receptor precursor	2	2	176.3	6.67	MGAIGLLWLL PLLLSTAAVG SGMG TGQRAG SPAAGPPLQP SHGVSVLGIF NLEKDDMLYI LVGQQGEDAC PS	Integral to plasma membrane
PCD16_HUMAN	Protocadherin-16 precursor	2	2	346	4.79	LVLMATDRGS PALVGSATLT VMVIDTNDNR VGAADAGNLS ASVTVSVLVT GEDEYDPVFL APAFHFQVPE GARR	Integral to membrane
PTPRZ_HUMAN	Receptor-type tyrosine-protein phosphatase zeta	2	2	254.4	4.67	VDKISSTMLH LIVSNSASSE NM ATSELSHSAK SDAGLV	Integral to plasma membrane
CO4A5_HUMAN	Collagen alpha-5(IV) chain	3	3	160.9	7.71	GEKGEPGLPG IPGVSGPKGY QGLPGDGPQP GLSGQPGLPG PPGPKGNPG GQKGDGGLPG IPGNPGLPGP KGEPGFHGFPG GVQGPPGPPG SPGPALEGPK GDGGLPGIPG N	Basement membrane

RAB1B_HUMAN	Ras-related protein Rab-1B	3	8	22.2	5.55	VVDNTTAKEF ADSLGIPFLE TSAK VVDNTTAKEF ADSLGIPFLE TSAK VVDNTTAKEF ADSLGIPFLE TSAK EFADSLGIPF LETSAK EFADSLGIPF LETSAK EFADSLGIPF LETSAK EFADSLGIPF LETSAK NATNVEQAFM TMAAEIK	Membrane
ATP5H_HUMAN	ATP synthase subunit d	2	4	18.5	5.21	TIDWVAFAEI IPQNQK TIDWVAFAEI IPQNQK LAALPENPPA IDWAYYK LAALPENPPA IDWAYYK	Mitochondrion inner membrane.
RAB7A_HUMAN	Ras-related protein Rab-7a	2	3	23.5	6.39	DPENFPFVVL GNK EAINVEQAFQ TIAR EAINVEQAFQ TIAR	Intracellular membrane-bound organelle
CDC42_HUMAN	Cell division control protein 42 homolog precursor	2	3	21.3	5.76	TPFLLVGTQI DLRDDPSTIE K TPFLLVGTQI DLRDDPSTIE K TPFLLVGTQI DLR	Plasma membrane
COX2_HUMAN	Cytochrome c oxidase subunit 2	2	4	25.5	4.67	LLDVDNRVVL PIEAPIR LLDVDNRVVL PIEAPIR MMITSQDVLH SWAVPTLGLK MMITSQDVLH SWAVPTLGLK	Membrane
TMEDA_HUMAN	Transmembrane emp24 domain- containing protein 10	2	3	25	6.98	ITDSAGHILY SKEDATK RLEDLSESIV NDFAYMK	Integral to membrane

SSB_HUMAN	Single-stranded DNA-binding protein	2	4	17.2	9.59	RLEDLSESIV NDFAYMK ESETTTSLVL ER	Mitochondrion
TIGD5_HUMAN	Tigger transposable element-derived protein 5	2	2	64.2	6.67	QATTIIADNI IFLSDQTK QATTIIADNI IFLSDQTK QATTIIADNI IFLSDQTK QKRHGISSQR FYGEAGPPAP SPAPGPPVKE EPALPSGAGP LPDR QKRHGISSQR FYGEAGPPAP SPAPGPPVKE EPALPSGAGP LPDR LLPEQAAPPG AGDPGAGGCG RR	Nucleus
F134B_HUMAN	Protein FAM134B	2	2	54.6	4.53	MASPAPPEHA EEGCPAPAAE EQAPPSPPPP QASPAERQQQ EEEAQEAGA	Membrane
SRBP2_HUMAN	Sterol regulatory element-binding protein 2	2	2	123.6	8.72	MASPAPPEHA EEGCPAPAAE EQAPPSPPPP QASPAERQQQ EEEAQ TDGSPVMAAV QNPALTALTT PIQT	Membrane
SSRD_HUMAN	Translocon-associated protein subunit delta precursor	2	3	19	5.76	NPADPIAQVH QA ETVFIVEISL TCKNRVQNMA LYADVGGKQF PVTRGQ NNEDISIIPP LFTVSVDHR NNEDISIIPP LFTVSVDHR	Integral to membrane
S10AB_HUMAN	Protein S100-A11	2	8	11.7	6.56	CIESLIAVFQ K CIESLIAVFQ K CIESLIAVFQ K TEFLSFMNTE LAAFTK TEFLSFMNTE LAAFTK TEFLSFMNTE LAAFTK	Cytoplasm

						TEFLSFMNTE LAAFTK TEFLSFMNTE LAAFTK	
NMES1_HUMAN	Normal mucosa of esophagus-specific gene 1 protein	2	5	9.6	9.45	KKNPEPWETV DPTVPQK	Nucleus
						LITINQQWKP IEELQNVQR LITINQQWKP IEELQNVQR LITINQQWKP IEELQNVQR LITINQQWKP IEELQNVQR LITINQQWKP IEELQNVQR	
CMC2_HUMAN	Calcium-binding mitochondrial carrier protein Aralar2	2	4	74.1	7.14	IAPLEEGTLP FNLAEAQR IAPLEEGTLP FNLAEAQR FGLGSVAGAV GATAVYPIDL VK FGLGSVAGAV GATAVYPIDL VK	Integral to plasam membrane
PPCKM_HUMAN	Phosphoenolpyruvate carboxykinase [GTP]	2	3	70.6	7.56	LGTPVLQALG DGDFVK	Mitochondrion
						LGTPVLQALG DGDFVK GVPLVYEAFN WR	
ACSL4_HUMAN	Long-chain-fatty-acid--CoA ligase 4	2	3	79.1	8.66	KVKALLGGNV RMMLSGGAPL SPQTHRFMNV CF KVKALLGGNV RMMLSGGAPL SPQTHRFMNV CF LSPEPWTPET GLVTDAFK LSPEPWTPET GLVTDAFK	Integral to membrane
TFR1_HUMAN	Transferrin receptor protein 1	2	2	84.8	6.18	SAFSNLFGGE PLSYTR SSGLPNIPVQ TISR	Integral to membrane
HS90A_HUMAN	Heat shock protein HSP 90-alpha	2	2	84.6	4.94	VILHLKEDQT EYLEER	Cytoplasm

						HLEINPDHSI IETLR	
HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U	2	3	90.5	5.76	SSGPTSLFAV TVAPPGAR	Cell surface
						SSGPTSLFAV TVAPPGAR EKPYFPIPEE YTFIQNVPLE DR	
ITAV_HUMAN	Integrin alpha-V	2	2	116	5.45	STGLNAVPSQ ILEGQWAAR	Integral to plasma membrane
						IYIGDDNPLT LIVK	
HYOU1_HUMAN	Hypoxia up-regulated protein 1	5	10	111.3	5.16	LAGLFNEQR	Endoplasmic reticulum
						VEFEELCADL FER VEFEELCADL FER DAVVYPILVE FTR DAVVYPILVE FTR DAVVYPILVE FTR DAVVYPILVE FTR DAVVYPILVE FTR DAVVYPILVE FTR LQDLTLRDLE KQEREK LQDLTLRDLE KQER	
CLCN1_HUMAN	Chloride channel protein	2	2	108.7	5.68	AVIGAAALTG AVSH	Integral to plasma membrane
						ARLAGEGPPG APPG	
CO5A3_HUMAN	Collagen alpha-3(V) chain	2	2	171.9	6.37	DGIPGPLGPL GPPG	Extracellular matrix
						PGADGAQGR	
CODA1_HUMAN	Collagen alpha-1(XIII) chain	2	2	69.9	9.27	HGAKGAPGIA VAGM	Integral to membrane
						GSKGDPGMTG	
ZN503_HUMAN	Zinc finger protein 503	3	3	62.5	8.94	KEPGGGGGGG GGGGGGGGGV SS	Nucleus

						KEPGGGGGGGG GGGGGGGG EPGGGGGGGGG GGGGGGGGV	
EWS_HUMAN	RNA-binding protein EWS	2	2	68.4	9.37	PLRGGPGGPG GPGGPMGR	Plasma membrane
FEZF2_HUMAN	Fez family zinc finger protein 2	2	2	48.8	9.52	GGPGGPGGPG GPM SSLRAGGGGGG GGGGGGGGGG GAPV SLRAGGGGGG GGGGGGGGGG APV	Nucleus
LAMP2_HUMAN	Lysosome-associated membrane glycoprotein 2 precursor	2	3	44.9	5.34	GILTVDELLA IR	Plasma membrane
HXB3_HUMAN	Homeobox protein Hox-B3	3	3	44.3	9.27	GILTVDELLA IR IPLNDLFR EGCGGGGGGGG GGGGSGGSGG GGGGGGGGGDK GGGGGGSGGS GGGGGGGGGG DK GGGSGGSGGG GGGGGGGDK	Nucleus
CO2A1_HUMAN	Collagen alpha-1(II) chain	2	2	141.7	6.58	GPPGPAGAPG PQGFQ	Basement membrane
SODM_HUMAN	Superoxide dismutase [Mn]	2	5	24.7	8.35	PGVMGFPGPK GANGEPGK GDVTAQIALQ PALK AIWNVINWEN VTER AIWNVINWEN VTER AIWNVINWEN VTER AIWNVINWEN VTER	Mitochondrion
CEAM1_HUMAN	Carcinoembryonic antigen-related cell adhesion molecule 1	2	4	57.5	5.65	TLTLLSVTR TLTLLSVTR TLTLLSVTR	Integral to plasma membrane

						NDTGPYECEI QNPVSANRSD PVTNLNVTYGP DTP	
CABL1_HUMAN	CDK5 and ABL1 enzyme substrate 1	2	2	67.6	9.32	GGCIALAAPG TPAAGLAAGS	Cytoplasm
						QSTGAVSLKE IIGLE	
IRX3_HUMAN	Iroquois-class homeodomain protein IRX-3	2	2	52.1	4.88	AAELPIFPQL GAQYELK	Nucleus
						RSPPGAGGSP PGAAVAPS	
CTNA2_HUMAN	Catenin alpha-2	2	2	105.2	5.52	LLEPLVTQVT TLVNTSNK	Plasma membrane
						MAATQIDSLC PQV	
MUC16_HUMAN	Mucin-16	2	2	2351.9		MISAIPTLAV SPTVQGLVTS LVTS	Integral to membrane
						SSVPTTSTGV VSEE	
ATS14_HUMAN	ADAMTS-14 precursor	2	2	133.8	6.81	ASGPNPGPDP GPTSLPPFST PGSPLPGPQD PA	Extracellular matrix
						ASGPNPGPDP GPTSLPP	
BSN_HUMAN	Protein bassoon	2	2	416.2	7.28	KPLGSGPGPG PAPGAKTEPG AR VPSAGADGPL AL	Cellskeleton
COBA1_HUMAN	Collagen alpha-1(XI) chain precursor	2	2	181	5.08	RGPQGPPGPP GDDGMR	Extracellular matrix
						AGPAGSPGED GDKGEIGEPG QK	
PCDAC_HUMAN	Protocadherin alpha-12	2	2	101.6	5.13	IYGELDFEEN NA	Cytoplasm.
						DAGVPPLGSN VTL	
SGOL1_HUMAN	Shugoshin-like 1	2	2	64.1	9.27	SSGMDPNSDD SSR	Nucleus
						SLKDITNVSL YPVVK	
LBXCO_HUMAN	Ladybird homeobox corepressor 1	2	2	99.8	6.11	GSGGQGKGGGA GGGGGGGPGC GAEMAPGPPP HK ASGPAGPGGP GGGAGVR	Nucleus

PAPD5_HUMAN	PAP-associated domain-containing protein 5	2	2	63.2	9.07	AEQRDFLPLE TTNNNNNHHQ PGAWAR	Cytoplasm
						AGSSASSPPS ASSSPHPSAA VPAADPADS	
RSMN_HUMAN	Small nuclear ribonucleoprotein-associated protein N;	2	2	24.6	11.2	AAGRGPVAGV PIPQ	Nucleus
						GTPIGMPPPG MRPP	
COBA2_HUMAN	Collagen alpha-2(XI) chain precursor	2	2	171.7		ERGLPGTAGG PGLK	Extracellular matrix
						GEMGIPGASG PIGP	
ACTG_HUMAN	Actin, cytoplasmic 2	8	23	41.8	5.31	EEEIAALVID NGSGMCK	Cytoplasm
						EEEIAALVID NGSGMCK	
						EEEIAALVID NGSGMCK	
						EEEIAALVID NGSGMCK	
						AVFPSIVGRP R	
						IWHHTFYNEL R	
						VAPEEHPVLL TEAPLNPK	
						VAPEEHPVLL TEAPLNPK	
						VAPEEHPVLL TEAPLNPK	
						LCYVALDFEQ EMATAASSSS LEK	
						LCYVALDFEQ EMATAASSSS LEK	
						LCYVALDFEQ EMATAASSSS LEK	
						LCYVALDFEQ EMATAASSSS LEK	
						LCYVALDFEQ EMATAASSSS LEK	
						LCYVALDFEQ EMATAASSSS LEK	
						LCYVALDFEQ EMATAASSSS LEK	
						LCYVALDFEQ EMATAASSSS LEK	
						FEQEMATAAS SSSLEK	
						SYELPDGQVI TIGNER	

						SYELPDGQVI TIGNER SYELPDGQVI TIGNER SYELPDGQVI TIGNER CDVDIRKDLY ANTVLSGGTT MYPGIADR	
HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F	2	4	45.6	5.38	ITGEAFVQFA SQELAEK ITGEAFVQFA SQELAEK ATENDIYNFF SPLNPVR ATENDIYNFF SPLNPVR	Nucleus
TOM40_HUMAN	Mitochondrial import receptor subunit TOM40 homolog	3	3	37.9	6.79	CKELFPIQME GVK QLSPTEAFPV LVGDMDNSGS LNAQVIHQLG PGLR QLSPTEAFPV LVGDMDNSGS LNAQVIHQLG PGLR SKMAIQTQQS KFVNWQVDGE YR	Integral to membrane
OST48_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	2	2	48.8	5.43	TLVLLDNLNV R	Integral to membrane
ZFHX4_HUMAN	Zinc finger homeobox protein 4	2	2	393.5	5.94	NTLLIAGLQA R PGSATFGMPG MTGMAGSLLE DLK FLFSLTSPSI HFNDKDGHD QSFYITDDPD DNADRSETSS IADPS	Nucleus
SRRM2_HUMAN	Serine/arginine repetitive matrix protein 2	2	2	299.4	12.05	EQNSALPTSS QDEELM	Nucleus
NPM_HUMAN	Nucleophosmin	2	4	32.6	4.64	ASSWGGPHFS PEHK MSVQPTVSLG GFEITPPVVL R	Nucleus

						MSVQPTVSLG GFEITPPVVL R MSVQPTVSLG GFEITPPVVL R SLGGFEITPP VVLR	
GP124_HUMAN	Probable G-protein coupled receptor 124	2	2	141.9	8.75	VPLGGGAPGT R	Integral to membrane
						REGGVPGTRP GSPGQNP	
PHB_HUMAN	Prohibitin	2	4	29.8	5.57	AAELIANSLA TAGDGLIELR AAELIANSLA TAGDGLIELR NITYLPAGQS VLLQLPQ NITYLPAGQS VLLQLPQ	Integral to plasma membrane
PSPC1_HUMAN	Paraspeckle component 1	2	2	58.7	6.26	ATIPGPPMGP GPAMGPEGAA NMGTPMMPDN GAVHNDRFPQ GPPSQMG	Nucleus
						MGSRTGSETP QAPMSGVGPV SGGPGGFGRG SQGGNFEGPN KRR	
CO4A3_HUMAN	Collagen alpha-3(IV) chain	2	2	161.7	9.28	EEDIELDAKG DPGLPGAPGP QGLP	Basement membrane
						PGFFGFPGAM GPRGPKGHMG ERVIGHKGER GVKGLTG	
NELFA_HUMAN	Negative elongation factor A	2	2	59.4	9.06	PTPAAPTSPL TPTTPPAVAP TTQTPPVAMV APQTQAPAQQ QPK ADGQGSTTML VDTVFEMNYA T	Nucleus
CO3A1_HUMAN	Collagen alpha-1(III) chain	2	2	138.5	6.21	GEPGPQGHAG	Extracellular matrix
						GLPGPPGSNG NPGPPGPSGS PGKDGPPGPA GNTGAP	
ODO1_HUMAN	2-oxoglutarate dehydrogenase E1 component	4	4	115.9	6.39	LAVQSLIRAY QIRGHHVAQL DPLGILDADL DSSVPADIIS STDKLGF	Mitochondrial membrane

						SLLRHPEARS SFDEMLPGTH FQRVIPEDGP AAQNPEN LLDTAFDLDV FKNFS LLDTAFDLDV FK	
COX5B_HUMAN	Cytochrome c oxidase subunit 5B	2	2	13.7	9.07	GLDPYNVLAP K	Membrane
						CGAHYKLVLPQ QLAH	
PLEC1_HUMAN	Plectin-1	3	5	531.4	5.73	CRPDQLTGLS LLPLSEK	Plasam membrane
						CRPDQLTGLS LLPLSEK CRPDQLTGLS LLPLSEK APVPASELLA SGVLSR CITDPQTGLC LLPLKEK	
ITA2_HUMAN	Integrin alpha-2 precursor	3	6	129.2	5.16	YNVGLPEAK	Plasam membrane
						IFSGPSSEQF GYAVQQFINP K IFSGPSSEQF GYAVQQFINP K IFSGPSSEQF GYAVQQFINP K FGIAVLGYLN R FGIAVLGYLN R	
ITB1_HUMAN	Integrin beta-1	2	2	88.4	5.3	IGFGSFVEK	Plasma membrane
						NVLSLTNKGE VFNELVGK	
HS90B_HUMAN	Heat shock protein HSP 90-beta	4	6	83.2	4.97	ADLINNLGTI AK	Cytoplasm
						VILHLKEDQT EYLEER SIYYITGESK EQVANSADFVE R SIYYITGESK EQVANSADFVE R HLEINPDHPI VETLR	

EFG1_HUMAN	Elongation factor G 1	3	4	83.4	6.58	HLEINPDHPI VETLR AIYFDGDFGQ IVR AIYFDGDFGQ IVR YGEIPAELR VIGVLEPLDP EDYTKLEFSD ETFGSNIPK	Mitochondrion
BC11B_HUMAN	B-cell lymphoma/leukemia 11B	2	2	95.5	6.1	RGNPMHRLLN PFQSPKSPF LSTPPLPPMP PGGTTPPPQPP AK ENGGGGVPGV PGAGGGGAAKA	Nucleus
GLU2B_HUMAN	Glucosidase 2 subunit beta	2	5	59.4	4.33	SLEDQVEMLR SLEDQVEMLR SLEDQVEMLR SLEDQVEMLR LWEEQLAAAK	Endoplasmic reticulum
CKAP4_HUMAN	Cytoskeleton-associated protein 4	4	5	66	5.63	VQSLQATFGT FESILR VQSLQATFGT FESILR LALQALTEK VQEQVHTLLS QDQAQAAR TAVDSL VAYS VKIETNENNL ESAK TAVDSL VAYS VKIETNENNL ESAK	Integral to membrane
CNDD3_HUMAN	Condensin-2 complex subunit D3	2	2	168.8	7.38	PASQPPPQVR GSVMP SVIR	Nucleus
TBB5_HUMAN	Tubulin beta chain	2	3	49.6	4.78	DLLMEEDDMA LANVVMQEAQ KK ALTVPELTQQ VFDAK ALTVPELTQQ VFDAK YLTVA AVFR	Microtubule

AL7A1_HUMAN	Alpha-aminoadipic semialdehyde dehydrogenase	2	2	55.3	6.44	IQVLGSLVSL EMGK QAVSMFLGAV EEAKK	Mitochondrion
ECHB_HUMAN	Trifunctional enzyme subunit beta, mitochondrial	2	4	51.3	9.45	EVVDYIIFGT VIQEVK EVVDYIIFGT VIQEVK LAAAFVSR LAAAFVSR	Mitochondrion envelope
SCOT_HUMAN	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1	2	5	56.1	7.13	GLTAVSNNAG VDNFGLGLLL R GLTAVSNNAG VDNFGLGLLL R GLTAVSNNAG VDNFGLGLLL R GLTAVSNNAG VDNFGLGLLL R AGGAGVPAFY TPTGYGTLVQ EGGSPIKYNK	Mitochondrion
TBA1B_HUMAN	Tubulin alpha-1B chain	3	7	50.1	4.94	AVFVDLEPTV IDEVR AVFVDLEPTV IDEVR AVFVDLEPTV IDEVR QLFHPEQLIT GKEDAANNYA R QLFHPEQLIT GKEDAANNYA R LISQIVSSIT ASLR LISQIVSSIT ASLR	Microtubule
ITPR1_HUMAN	Inositol 1,4,5-trisphosphate receptor type 1	2	3	313.7	5.71	QDLQQLRSIV EKSELWVYKG QGPDETMDGA SGENEH 1162kkte GAHAVVLELL QIPYEK GAHAVVLELL QIPYEK	Membrane
EAA1_HUMAN	Excitatory amino acid transporter 1	2	2	59.5	8.52	MRMLQMLVLP LISSLVTGM AALDSK TMVIVLTSVG LPTD	Integral to membrane

LG12_HUMAN	Leucine-rich repeat LGI family member 2	2	2	62.3	6.47	GGCGA CTTTDFV VHQ TLPYQSVSVD TFNSK	Extracellular region
BIRC6_HUMAN	Baculoviral IAP repeat-containing protein 6	2	3	527.3	5.66	RLLDYVATVE DEAAAAK RLLDYVATVE DEAAAAK AFHDMGGVQL ICNNMVTSTR AIVNTARSMV	Membrane fraction
RTN4_HUMAN	Reticulon-4	3	3	129.9	4.43	KPAAGLSAAP VPTAPAAGAP LMDFGNDFVP PAPR GPLPAAPPVA PER HQAQIDHYLG LANK	Plasam membrane
ADCL1_HUMAN	Neutral cholesterol ester hydrolase 1	2	4	45.8	6.76	IVQELPQLLD AR SAPLIADQAV LQLLPK SAPLIADQAV LQLLPK SAPLIADQAV LQLLPK	Membrane
CISY_HUMAN	Citrate synthase	3	5	51.7	8.45	ASASSTNLKD ILADLIPKEQ AR ASASSTNLKD ILADLIPKEQ AR ASASSTNLKD ILADLIPK ASASSTNLKD ILADLIPK GLVYETSVLD PDEGIRFR	Mitochondrion
SQRD_HUMAN	Sulfide:quinone oxidoreductase	6	9	49.9	9.18	QLSSSGRPTA SVIPSGVEWI K QLSSSGRPTA SVIPSGVEWI K QLSSSGRPTA SVIPSGVEWI K ALQDFKEGNA IFTFPNTPVK TSPVADAAGW VDVDKETLQH R RYPNVFGIGD CTNLPTSK TAAAVAAQSG ILDR	Membrane

PHB2_HUMAN	Prohibitin-2	4	5	33.3	9.83	EITALAPSTM K EITALAPSTM K IGGVQQDTIL AEGLHFR VLSRPNAQEL PSMYQR QKIVQAEGEA EAAK IYLTADNLVL NLQDESFT IYLTADNLVL NLQDESFT	Membrane
ATPG_HUMAN	ATP synthase subunit gamma	2	3	33	9.23	QAVITKELIE IISGAAALD ELIEIISGAA ALD ELIEIISGAA ALD	Mitochondrial inner membrane.
ANK3_HUMAN	Ankyrin-3	3	3	480.1	6.12	AAPILSKTKN GLSPLHMATQ GDHLNCVQ AAPILSKTKN GLSPLHMATQ GDHLNCVQ ELESNGSGKD NEFGLGLDSP QNEIAQNGNN DQSITECSIA FMLLKKWVTR DGKNATTDAL TSVLTKINR	Membrane
CATD_HUMAN	Cathepsin D	2	3	44.5	6.1	ISVNNVLPVF DNLMQQK ISVNNVLPVF DNLMQQK LVDQNIFSFY LSR	Mitochondrion
ETFB_HUMAN	Electron transfer flavoprotein subunit beta	2	3	27.8	8.25	LGPLQVAR KIEVIKPGDL GVDLTSK KIEVIKPGDL GVDLTSK	Mitochondrion
MTHR_HUMAN	Methylenetetrahydrofolate reductase	2	2	74.5	5.22	VNRQGILTIN SQPNINGKPS SDPIVGWGPS GGYVFQKAYL E	Cytosol

Protein	Function	Length	Number of domains	Weight (kDa)	PI (pI)	Sequence	Location
PGRC1_HUMAN	Membrane-associated progesterone receptor component 1	2	2	21.7	4.56	TIQYIHDNY FLVNLVDNDF PLDNCLWQVV EDTLE GRKFYGPPEGP YGVFAGR	Integral to membrane
RAB14_HUMAN	Ras-related protein Rab-14	2	2	23.9	5.85	FYGPEGPYGV FAGR TGENVEDAFL EAAKK	Plasam membrane
ATPO_HUMAN	ATP synthase subunit O	2	3	23.3	9.97	TGENVEDAFL EAAK LVRPPVQVYG IEGR	Mitochondrion inner membrane
PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase	3	5	27.7	7.68	LVRPPVQVYG IEGR FSPLTTNLIN LLAENGR DYGVLLLEGSG LALR PNGVIKHLVS NDLPVGR HLSVNDLPVG R HLSVNDLPVG R	Mitochondrion