Spot	Protein name	Accession number	Total peptides	Sequence coverage	Peptide sequence	Spectrum charge
1	Myosin light polypeptide 3	gi|33563264	11	0.544	EAEFDASK	1, 2
1				0.544	LTEDEVEK	2
1				0.544	HVLATLGER	2
1				0.544	EAFLLFDR	2
1				0.544	NKDTGTYEDFVEGLR	3
1				0.544	EGNGTVMGAELR	2
1				0.544	EGNGTVmGAELR	2
1				0.544	ITYGQcGDVLR	2
1				0.544	AAPAPAAAPAAAPAAAPEPERPK	3
1				0.544	ALGQNPTQAEVLR	2
1				0.544	DTGTYEDFVEGLR	2
1				0.544	VFDKEGNGTVmGAELR	2
1	EF hand domain containing 2	gi|31981086	6	0.317	VFNPYTEFK	2
1				0.317	AAAGELQEDSGLHVLAR	3
1				0.317	DGFIDLmELK	2
1				0.317	LSEIDVSTEGVK	2
1				0.317	SmIQEVDEDFDSK	2
1				0.317	ADLNQGIGEPQSPSR	2
1	Heat shock protein 20-like protein	gi|13507646	5	0.199	RDPFR	2
1				0.199	DSPLSSR	2
1				0.199	FGVPAEGR	2
1				0.199	DGYVEVSGK	2
1				0.199	LSSAWPGTLR	2
1	Tpd52 protein [Mus musculus]	gi|13278549	3	0.189	LGISSLQEFK	2
1				0.189	TSETLSQAGQK	2
1				0.189	ASAAFSSVGSVITK	2
1	Apolipoprotein A-1	gi|74203337	5	0.189	ARPALEDLR	3
1				0.189	LQELQGR	2
1				0.189	DFANVYVDAVK	2
1				0.189	VQPYLDEFQK	2
1				0.189	VAPLGAELQESAR	2
1	Peroxiredoxin-2	gi|56541226	3	0.182	SVDEALR	2
1				0.182	NDEGIAYR	2
1				0.182	SLSQNYGVLK	2
1				0.182	QITVNDLPVGR	2
1	Cytochrome oxidase subunit II	gi|829023	4	0.150	TDAIPGR	2
1				0.150	LLEVDNR	2
1				0.150	LNQATVTSNR	2
1				0.150	VVLPmELPIR	2
1	Lactoylglutathione lyase	gi|21362640	3	0.147	RFEELGVK	2
1				0.147	VLGLTLLQK	2
1				0.147	DFLLQQTmLR	2

1	Phosphatidylethanolamine binding protein	gi|1517864	2	0.112	LYEQLSGK	2
1				0.112	VDYAGVTVDELGK	2
1	Heterochromatin protein 1 beta	gi|48249223	2	0.103	GKVEYLLK	2
1				0.103	NSDEADLVPAK	2
1	Myeloid bactenecin	gi|2071985	2	0.096	YEEIVDR	2
1				0.096	AIEAYNQGR	2
1	Desmin	gi|33563250	3	0.064	ADVDAATLAR	2
1				0.064	QVEVLTNQR	2
1				0.064	EEAENNLAAFR	2
1	Apolipoprotein J	gi|2119394	2	0.054	IDSLLESDR	2
1				0.054	QQSQVLDAmQDSFAR	2, 3
1	PREDICTED: similar to ATP synthase beta chain	gi|73968432	2	0.049	IPVGPETLGR	2
1				0.049	ImDPNIVGNEHYDVAR	3
1	PREDICTED: similar to Actin, cytoplasmic 2 (gam	gi|109489498	2	0.020	LDLAGR	2
1				0.020	DLTDYLmK	2
2	Myosin light chain 2	gi|1709058	11	0.500	DGFIDK	2
2				0.500	VFDPEGK	2
2				0.500	VNVKNEEIDEmIK	2, 3
2				0.500	EMLTTQAER	2
2				0.500	EmLTTQAER	2
2				0.500	NEEIDEMIK	2
2				0.500	NEEIDEmIK	2
2				0.500	DGFIDKNDLR	2
2				0.500	EAFTIMDQNR	2
2				0.500	EAFTImDQNR	2
2				0.500	NLVHIITHGEEK	2
2				0.500	GADPEETILNAFK	2
2				0.500	NLVHIITHGEEKD	2
2				0.500	DTFAALGR	1
2	Myosin light chain,regulatory B-like	gi|71037403	5	0.331	ELLTTmGDR	2
2				0.331	LNGTDPEDVIR	2
2				0.331	EAFNmIDQNR	2
2				0.331	GNFNYIEFTR	2
2				0.331	FTDEEVDELYR	2
2	Cytochrome b5 type B	gi|31542438	2	0.185	QYYIGDVHPSDLKPK	3
2				0.185	VEGSEPSVTYYR	2
2	Myosin light polypeptide 3	gi|33563264	3	0.147	LTEDEVEK	2
2				0.147	HVLATLGER	2
2				0.147	ALGQNPTQAEVLR	2
2	PREDICTED: similar to Actin, cytoplasmic 2 (Gam	gi|109489498	2	0.020	LDLAGR	2
2				0.020	DLTDYLmK	2
3	Malate dehydrogenase 2	gi|31982186	15	0.509	VNVPVIGGHAGK	2, 3
3				0.509	NSPLVSR	2
3				0.509	GcDVVVIPAGVPR	2, 3

3				0.509	TIIPLISQcTPK	2, 3
3				0.509	ANTFVAELK	2
3				0.509	VDFPQDQLATLTGR	2, 3
3				0.509	IQEAGTEVVK	2
3				0.509	MIAEAIPELK	2
3				0.509	mIAEAIPELK	2
3				0.509	ETEcTYFSTPLLLGK	2, 3
3				0.509	IFGVTTLDIVR	2
3				0.509	FVFSLVDAMNGK	2
3				0.509	FVFSLVDAmNGK	2
3				0.509	GcDVVVIPAGVPRKPGMTR	3
3				0.509	EGVVEcSFVQSK	2
3				0.509	AGAGSATLSMAYAGAR	2
3				0.509	AGAGSATLSmAYAGAR	2
3				0.509	GYLGPEQLPDcLK	2
3	ATP synthase alpha subunit precursor	gi|114511	9	0.262	APGIIPR	2
3				0.262	ELIIGDR	2
3				0.262	STVAQLVK	2
3				0.262	VLSIGDGIAR	2
3				0.262	AVDSLVPIGR	2
3				0.262	VVDALGNAIDGK	2
3				0.262	TSIAIDTIINQK	2
3				0.262	TGTAEmSSILEER	2
3				0.262	ILGADTSVDLEETGR	2
3	PREDICTED: similar to glyceraldehyde-3-phospha	gi|109484558	7	0.219	VGVNGFGR	2
3				0.219	ITGmAFR	2
3				0.219	LVNNGKPITIFQER	3
3				0.219	VVDLmAYmASK	2
3				0.219	GAAQNIIPASTGAAK	2
3				0.219	VVDLmAYmASKE	2
3				0.219	IVSNAScTTNcLAPLAK	2
3	Voltage-dependent anion channel 2	gi|6755965	4	0.146	SNFAVGYR	2
3				0.146	LTLSALVDGK	2
3				0.146	YQLDPTASISAK	2
3				0.146	LTFDTTFSPNTGK	2
3	Heterogeneous nuclear ribonucleoprotein A2/B1 is	gi|109134362	4	0.123	LFVGGIK	2
3				0.123	GGNFGFGDSR	2
3				0.123	IDTIEIITDR	2
3				0.123	GGGGNFGPGPGSNFR	2
3	Glyceraldehyde 3-phosphate dehydrogenase	gi|41394411	2	0.121	LTGMAFRVPTPDVSVVDLTcR	3
3				0.121	VPTPDVSVVDLTcR	2
3	PREDICTED: similar to heterogeneous nuclear rib	gi|88953883	2	0.100	EDSQRPGAHLTVK	3
3				0.100	IEVIEImTDR	2
3	Electron transfer flavoprotein subunit alpha	gi|21759113	2	0.093	LGGEVScLVAGTK	2

3				0.093	GTSFEAAATSGGSASSEK	2
3	L-3-hydroxyacyl-coenzyme A dehydrogenase	gi|111038118	3	0.083	AGDEFVEK	2
3				0.083	LKNELFQR	2
3				0.083	TFESLVDFcK	2
3	Lactate dehydrogenase 1, A chain	gi|6754524	2	0.057	LVIITAGAR	2
3				0.057	VTLTPEEEAR	2
3	NONA protein	gi|75022134	2	0.042	GGGGGGGGGGGGGGGGGGGR	3
3				0.042	ESDNERKK	2
3	Hydroxysteroid (17-beta) dehydrogenase 4	gi|31982273	3	0.033	TLGAIVR	2
3				0.033	TALDTFGR	2
3				0.033	AYALAFAER	2
4	Acyl-coenzyme A dehydrogenase, very long chain	gi|23956084	22	0.373	TPIKDAATGAVK	3
4				0.373	IHNFGVIQEK	3
4				0.373	ELVGPVAR	2
4				0.373	GILLYGTK	2
4				0.373	SFAVGmFK	2
4				0.373	SFGGVTHGLPEKK	3
4				0.373	ITAFVVER	2
4				0.373	YYTLNGSK	2
4				0.373	ELTGLGNALK	2
4				0.373	VAVNILNNGR	2
4				0.373	VEDDTLQGLK	2
4				0.373	DFQIEAAISK	2
4				0.373	IFEGANDILR	2
4				0.373	FFEEVNDPAK	2
4				0.373	FGmAATLAGTmK	2
4				0.373	LFVALQGcmDK	2
4				0.373	GIVNEQFLLQR	2
4				0.373	ENmASLQSSPQHQELFR	3
4				0.373	ASNTSEVYFDGVK	2
4				0.373	NPFGNVGLLmGEAGK	2
4				0.373	VPSENVLGEVGDGFK	2
4				0.373	AmVENGGLVTGNPLGI	2
4	Albumin 1	gi|33859506	12	0.209	LATDLTK	2
4				0.209	QTALAELVK	2
4				0.209	KYEATLEK	2
4				0.209	TPVSEHVTK	2
4				0.209	SLHTLFGDK	2
4				0.209	ccSGSLVER	2
4				0.209	LVQEVTDFAK	2
4				0.209	YNDLGEQHFK	2
4				0.209	AADKDTcFSTEGPNLVTR	3
4				0.209	APQVSTPTLVEAAR	2
4				0.209	YmcENQATISSK	2

4				0.209	ENYGELADccTK	2
4	Sdha protein	gi|15030102	12	0.203	AFGGQSLK	2
4				0.203	SmTLEIR	2
4				0.203	ANAGEESVmNLDK	2, 3
4				0.203	ANAGEESVMNLDK	2
4				0.203	GVIALcIEDGSIHR	3
4				0.203	HTLSYVDIK	2
4				0.203	TLNEADcATVPPAIR	2,3
4				0.203	NTVIATGGYGR	2
4				0.203	SmQNHAAVFR	2
4				0.203	VGSVLQEGcEK	2
4				0.203	GEGGILINSQGER	2
4				0.203	VTLEYRPVIDK	2
4				0.203	TGHSLLHTLYGR	2
4	Transferrin	gi|17046471	5	0.067	IPSHAVVAR	3
4				0.067	DSAFGLLR	2
4				0.067	DGGGDVAFVK	2
4				0.067	GYYAVAVVK	2
4				0.067	HTTIFEVLPEK	2
4	Lamin A	gi|1346413	4	0.060	KEGDLLAAQAR	3
4				0.060	LADALQELR	2
4				0.060	SLETENAGLR	2
4				0.060	ITESEEVVSR	2
4	Transketolase	gi|11066098	3	0.047	SGKPAELLK	3
4				0.047	LAVSQVPR	2
4				0.047	IIALDGDTK	2
4	Hypothetical protein	gi|55727397	3	0.042	CLVEILASR	3
4				0.042	ILISLATGNR	2
4				0.042	SELDmLDIR	2
4	Electron transferring flavoprotein, dehydrogenase	gi|21313290	2	0.037	SGSLAAESIFK	2
4				0.037	GAPLNTPVTEDR	2
4	PREDICTED: similar to Actin, cytoplasmic 2 (Gam	gi|109489498	2	0.026	AGFAGDDAPR	2
4				0.026	DLTDYLmK	2
4	Laminin, alpha 2	gi|117647249	2	0.007	LEVHLSSGTR	3
4				0.007	INHADFATVQLR	3
6	Malate dehydrogenase 2	gi|31982186	16	0.530	VNVPVIGGHAGK	2, 3
6				0.530	NSPLVSR	2
6				0.530	ITPFEEK	2
6				0.530	GcDVVVIPAGVPR	2, 3
6				0.530	FVFSLVDAmNGK	2, 3
6				0.530	TIIPLISQcTPK	2, 3
6				0.530	ANTFVAELK	2
6				0.530	VDFPQDQLATLTGR	2, 3
6				0.530	IQEAGTEVVK	2

6				0.530	MIAEAIPELK	2
6				0.530	mIAEAIPELK	2
6				0.530	IFGVTTLDIVR	2
6				0.530	GcDVVVIPAGVPRKPGMTR	3
6				0.530	EGVVEcSFVQSK	2
6				0.530	AGAGSATLSMAYAGAR	2
6				0.530	AGAGSATLSmAYAGAR	2
6				0.530	GYLGPEQLPDcLK	2
6				0.530	ETEcTYFSTPLLLGK	2
6	ATP synthase alpha subunit precursor	gi|114511	7	0.220	STVAQLVK	2
6				0.220	VLSIGDGIAR	2
6				0.220	AVDSLVPIGR	2
6				0.220	VVDALGNAIDGK	2
6				0.220	HALIIYDDLSK	2
6				0.220	TGTAEmSSILEER	2
6				0.220	ILGADTSVDLEETGR	2
6	Heterogeneous nuclear ribonucleoprotein A2/B1 is	gi|109134362	3	0.103	GGNFGFGDSR	2
6				0.103	IDTIEIITDR	2
6				0.103	GGGGNFGPGPGSNFR	2
6	PREDICTED: similar to glyceraldehyde-3-phospha	gi|109484558	4	0.102	ITGmAFR	2
6				0.102	VVDLmAYmASK	2
6				0.102	GAAQNIIPASTGAAK	2
6				0.102	VVDLmAYmASKE	2
6	NADH dehydrogenase (ubiquinone) 1 alpha subco	gi|13384720	4	0.090	GIVNATK	2
6				0.090	YVVNHLGR	2
6				0.090	TFAFTGPNR	2
6				0.090	QPVYVADVSK	2
6	ELAV (embryonic lethal, abnormal vision, Drosoph	gi|31542602	2	0.061	AISTLNGLR	2
6				0.061	VLVDQTTGLSR	2
6	L-3-hydroxyacyl-coenzyme A dehydrogenase	gi|111038118	2	0.054	AGDEFVEK	2
6				0.054	DTPGFIVNR	2
6	Succinate-CoA ligase	gi|9845299	2	0.054	LVGGTTPGK	2
6				0.054	IIcQGFTGK	2
6	Hydroxysteroid (17-beta) dehydrogenase 4	gi|31982273	4	0.048	VVAEIR	2
6				0.048	TALDTFGR	2
6				0.048	AYALAFAER	2
6				0.048	IDVVVNNAGILR	2
6	Elongation factor-1 alpha	gi|85013643	2	0.041	HVDSGK	2
6				0.041	IGGIGTVPVGR	2
7	Acyl-coenzyme A dehydrogenase, medium chain	gi|15488707	11	0.273	KGDEYVINGQK	2, 3
7				0.273	IAmGAFDR	2
7				0.273	GIAFEDVR	2
7				0.273	mWITNGGK	2
7				0.273	TRPTVAAGAVGLAQR	2, 3

7				0.273	AAWEVDSGR	2
7				0.273	NTYYASIAK	2
7				0.273	IYQIYEGTAQIQR	2, 3
7				0.273	SGEYPFPLIK	2
7				0.273	ENVLIGEGAGFK	2
7				0.273	EEIIPVAPEYDK	2
7	Creatine kinase, mitochondrial 2	gi|38259206	10	0.258	GLSLPPAcSR	2
7				0.258	REVENVAITALEGLK	3
7				0.258	ITHGQFDER	2
7				0.258	VPPPLPQFGR	2
7				0.258	GWEFmWNER	2
7				0.258	HNNcmAEcLTPTIYAK	3
7				0.258	LSEMTEQDQQR	2
7				0.258	LFPPSADYPDLR	2
7				0.258	EVENVAITALEGLK	2
7				0.258	LGYILTcPSNLGTGLR	2
7	Phosphoglycerate kinase 1	gi|129903	9	0.249	SLmDEVVK	2
7				0.249	LTLDKLDVK	2
7				0.249	VLPGVDALSNV	2
7				0.249	VADKIQLINNmLDK	3
7				0.249	LGDVYVNDAFGTAHR	3
7				0.249	VSHVSTGGGASLELLEGK	3
7				0.249	IQLINNmLDK	2
7				0.249	YSLEPVAAELK	2
7				0.249	VLNNmEIGTSLYDEEGAK	2
7	Isocitrate dehydrogenase [NADP], mitochondrial p	gi|116242519	10	0.200	FAQTLEK	2
7				0.200	TIEAEAAHGTVTR	3
7				0.200	ATDFVVDR	2
7				0.200	WPLYLSTK	2
7				0.200	LDGNQDLIR	2
7				0.200	YFDLGLPNR	2
7				0.200	cATITPDEAR	2
7				0.200	LIDDmVAQVLK	2
7				0.200	VcVQTVESGAmTK	2
7				0.200	DQTNDQVTIDSALATQK	2
7	Aspartate aminotransferase	gi|6754034	6	0.155	IGADFLGR	2
7				0.155	VGNLTVVGK	2
7				0.155	QVEYLVNEK	2
7				0.155	LVLGDNSPAIR	2
7				0.155	VGGVQSLGGTGALR	2
7				0.155	IVAATLSDPELFK	2
7	Ubiquinol-cytochrome c reductase core protein 2	gi|22267442	5	0.143	YEDSNNLGTSHLLR	3
7				0.143	AVAFQNSQTR	2
7				0.143	ENmAYTVEGIR	2

7				0.143	GNNTTSLLSQSVAK	2
7				0.143	AVAQGNLSSADVQAAK	2
7	Creatine kinase, muscle	gi|6671762	4	0.110	LANLSK	2
7				0.110	DLFDPIIQDR	2
7				0.110	GQSIDDmIPAQK	2
7				0.110	GGDDLDPNYVLSSR	2
7	Pyruvate dehydrogenase E1 alpha 1	gi|6679261	5	0.105	GDFIPGLR	2
7				0.105	AILAELTGR	2
7				0.105	RGDFIPGLR	2
7				0.105	VDGmDILcVR	2
7				0.105	LEEGPPVTTVLTR	2
7	Citrate synthase	gi|13385942	5	0.097	ALGFPLERPK	2, 3
7				0.097	DVLSNLIPK	2
7				0.097	EGSSIGAIDSR	2
7				0.097	NLYREGSSIGAIDSR	3
7				0.097	IVPNILLEQGK	2
7	ATP synthase alpha subunit precursor	gi|114511	3	0.084	STVAQLVK	2
7				0.084	AVDSLVPIGR	2
7				0.084	VVDALGNAIDGK	2
7	47-kDa heat shock protein	gi|303678	2	0.048	AVAISLPK	2
7				0.048	DNQSGSLLFIGR	2
7	Fumarase	gi|227665	2	0.038	FLGSGPR	2
7				0.038	AIEmLGGELGSK	2
11	Aconitase 2	gi|18079339	19	0.262	IHETNLKK	2, 3
11				0.262	qALAHGLK	2
11				0.262	EHAALEPR	2
11				0.262	DGYAQILR	2
11				0.262	DFAPGKPLK	2
11				0.262	EGWPLDIR	2
11				0.262	VDVSPTSQR	2
11				0.262	VAmSHFEPSEYIR	2, 3
11				0.262	NAVTQEFGPVPDTAR	2, 3
11				0.262	DLEDLQILIK	2
11				0.262	LEAPDADELPR	2
11				0.262	LTGSLSGWTSPK	2
11				0.262	VGLIGScTNSSYEDmGR	2, 3
11				0.262	TDIANLAEEFK	2
11				0.262	FNPETDFLTGK	2
11				0.262	SQFTITPGSEQIR	2
11				0.262	FKLEAPDADELPR	2
11				0.262	WVVIGDENYGEGSSR	2
11				0.262	IVYGHLDDPANQEIER	2
16	Transgelin 2	gi|30519911	7	0.357	DGTVLcK	2
16				0.357	GPSYGLSR	2

16				0.357	IQASSmAFK	2
16				0.357	LINSLYPEGQAPVK	2, 3
16				0.357	EDVGQPQPGR	2
16				0.357	TLmNLGGLAVAR	2
16				0.357	NFSDNQLQEGK	2
16	ADP-ribosylation Factor 1	gi|1065361	5	0.278	TTILYK	2
16				0.278	mLAEDELR	2
16				0.278	ILMVGLDAAGK	2
16				0.278	ILmVGLDAAGK	2
16				0.278	DAVLLVFANK	2
16				0.278	QDLPNAmNAAEITDK	2, 3
16	ADP-ribosylation factor 4	gi|6680720	2	0.233	IQEGAAVLQK	2
16				0.233	QDLPNAMAISEMTDK	2
16	Heat shock protein family, member 7 (cardiovascu	gi|31542970	3	0.225	LAADGTVmNTFAHK	2, 3
16				0.225	TLGDAYEFTVDmR	2, 3
16				0.225	ALPAQDPPmEK	2
16	Ferritin light chain 1	gi|120524	4	0.224	LVNLHLR	2
16				0.224	LLEFQNDR	2
16				0.224	TQEAmEAALAmEK	2
16				0.224	QNYSTEVEAAVNR	2
16	Myosin light polypeptide 3	gi|33563264	3	0.216	EAEFDASK	2
16				0.216	AAPAPAAAPAAAPAAAPEPERPK	3
16				0.216	ALGQNPTQAEVLR	2
16	Transgelin	gi|6755714	4	0.179	NGVILSK	2
16				0.179	AAEDYGVIK	2
16				0.179	KYDEELEER	2
16				0.179	VPENPPSmVFK	2
16	Hypothetical protein LOC67939	gi|21312706	3	0.172	QLGVGSGNLR	2
16				0.172	QINLNDLGK	2
16				0.172	FADETAmLEK	2
16	Myosin light chain 2	gi|1709058	3	0.157	VFDPEGK	2
16				0.157	EmLTTQAER	2
16				0.157	EAFTImDQNR	2
16	Peroxiredoxin-3	gi|6680690	3	0.113	ELSLDDFK	2
16				0.113	GTAVVNGEFK	2
16				0.113	HLSVNDLPVGR	2
16	Ubiquinone biosynthesis protein coq7	gi|3806019	2	0.112	TSVGPVIQK	2
16				0.112	IYAGQmAVLGR	2
16	Heat shock protein, alpha-crystallin-related, B6	gi|59958370	2	0.111	LFDQR	2
16				0.111	ASAPLPGFSAPGR	2
16	ATP synthase alpha subunit precursor	gi|114511	3	0.075	APGIIPR	2
16				0.075	VLSIGDGIAR	2
16				0.075	AVDSLVPIGR	2
16	PREDICTED: similar to Actin, cytoplasmic 2 (Gam	gi|109489498	2	0.027	DLTDYLmK	2

16				0.027	EITALAPSTmK	2
17	Ferritin light chain 1	gi|120524	3	0.186	LLEFQNDR	2
17				0.186	TQEAmEAALAmEK	2
17				0.186	QNYSTEVEAAVNR	2
17	Fibronectin 1	gi|46849812	16	0.070	LTAGLTR	2
17				0.070	ITGYIIK	2
17				0.070	LGVRPSQGGEAPR	3
17				0.070	VFAVHQGR	2
17				0.070	APITGYIIR	2
17				0.070	GDSPASSKPVSINYK	3
17				0.070	YEVSVYALK	2
17				0.070	QYNVGPLASK	2
17				0.070	HALQSASAGSGSFTDVR	3
17				0.070	FTNIGPDTmR	2
17				0.070	TVLVTWTPPR	2
17				0.070	TFYScTTEGR	2
17				0.070	VTYSSPEDGIR	2
17				0.070	ATGVFTTLQPLR	2
17				0.070	ESNPLTAQQTTK	2
17				0.070	SYTITGLQPGTDYK	2
17	Actinin alpha 2	gi|21307732	6	0.069	ALDYIASK	2
17				0.069	VIQSYSIR	2
17				0.069	DYESASLTEVR	2
17				0.069	GITQEQmNEFR	2
17				0.069	QSILAIQNEVEK	2
17				0.069	TINEVETQILTR	2
17	PREDICTED: similar to Actin, cytoplasmic 2 (Gam	gi|109489498	5	0.065	LDLAGR	2
17				0.065	AGFAGDDAPR	2
17				0.065	DLTDYLmK	2
17				0.065	GYSFTTTAER	2
17				0.065	DSYVGDEAQSK	2
17	Albumin 1	gi|33859506	4	0.063	ALVSSVR	2
17				0.063	LATDLTK	2
17				0.063	LVQEVTDFAK	2
17				0.063	APQVSTPTLVEAAR	2
17	Tenascin-C	gi|7106435	10	0.042	VPEVTR	2
17				0.042	SIPVSAR	2
17				0.042	SVDLPGLK	2
17				0.042	VSIYGVAR	2
17				0.042	AYAAGFGDR	2
17				0.042	IQALSGSLR	2
17				0.042	FTTDLDSPR	2
17				0.042	APTAQVESFR	2
17				0.042	TPmLSTDVSTAR	2

17				0.042	VSVIAmK	1
17	Procollagen, type VI, alpha 1	gi|6753484	2	0.018	IALVITDGR	2
17				0.018	VPNYQALLR	2
17	PREDICTED: similar to myosin heavy chain 6	gi|109082950	5	0.014	SLSTELFK	2
17				0.014	LQDAEEAVEAVNAK	3
17				0.014	SLNDFTTQR	2
17				0.014	TLEDQANEYR	2
17				0.014	LAEQELIETSER	2
17	Spectrin alpha 2	gi|115496850	2	0.008	GLVSSDELAK	2
17				0.008	SSEEIESAFR	2
18	Triosephosphate isomerase	gi|1864018	7	0.371	TATPQQAQEVHEK	3
18				0.371	RHVFGESDELIGQK	3
18				0.371	IAVAAQNcYK	2
18				0.371	SNVNDGVAQSTR	2
18				0.371	IIYGGSVTGATcK	2
18				0.371	HVFGESDELIGQK	2
18				0.371	VTNGAFTGEISPGmIK	2
18	Growth factor receptor bound protein 2	gi|123228035	6	0.300	DGFIPK	2
18				0.300	FGNDVQHFK	2, 3
18				0.300	QRHDGAFLIR	3
18				0.300	ATADDELSFK	2
18				0.300	ESESAPGDFSLSVK	2
18				0.300	VLNEEcDQNWYK	2
18	Heat shock protein HSP27	gi|424145	6	0.249	AQIGGPEAGK	2
18				0.249	EGVVEITGK	2
18				0.249	DWYPAHSR	2
18				0.249	QLSSGVSEIR	2
18				0.249	LFDQAFGVPR	2
18				0.249	TKEGVVEITGK	2
18				0.249	qLSSGVSEIR	1
18	Peroxiredoxin-6	gi|3219774	6	0.223	VVFIFGPDKK	3
18				0.223	VVFIFGPDK	2
18				0.223	LPFPIIDDK	2
18				0.223	LPFPIIDDKGR	2
18				0.223	DINAYNGETPTEK	2
18				0.223	GESVmVVPTLSEEEAK	2
18	Peroxiredoxin-1	gi|6754976	4	0.221	SVDEIIR	2
18				0.221	DISLSEYK	2
18				0.221	TIAQDYGVLK	2
18				0.221	ATAVmPDGQFK	2
18	GrpE-like 1, mitochondrial	gi|13277394	4	0.171	TLRPALVGVVK	2, 3
18				0.171	AKLEEQLR	2
18				0.171	ALADTENLR	2
18				0.171	LYGIQGFcK	2

18	RNA binding protein gene with multiple splicing isc	gi|33342267	3	0.168	NALNGIR	2
18				0.168	QPVGFVSFDSR	2
18				0.168	ENTPSEANLQEEEVR	2
18	Peroxiredoxin-4	gi|7948999	5	0.168	QGGLGPIR	2
18				0.168	SVDETLR	2
18				0.168	GLFIIDDK	2
18				0.168	IPLLSDLNHQISK	3
18				0.168	LVQAFQYTDK	2
18	Harvey rat sarcoma oncogene, subgroup R	gi|6677819	4	0.165	LVVVGGGGVGK	2
18				0.165	DRDDFPIVLVGNK	2, 3
18				0.165	IcTVDGIPAR	2
18				0.165	VKDRDDFPIVLVGNK	3
18	Ig kappa chain	gi|1083380	3	0.160	TSTSPIVK	2
18				0.160	FSGSGSGTDFTLK	2
18				0.160	QNGVLNSWTDQDSK	2
18	ETHE1 protein	gi|12963539	3	0.146	EAVLIDPVLETAHR	3
18				0.146	SLLPGcQSVISR	2
18				0.146	ScTYTYLLGDR	2
18	Proteasome subunit, beta type 10	gi|13435741	4	0.143	IHFIAPK	2
18				0.143	DGVILGADTR	2
18				0.143	FAPGTTPVLTR	2
18				0.143	ALSTPTEPVQR	2
18	Protein-L-isoaspartate (D-aspartate) O-methyltrans	gi|29436595	5	0.142	KDDPmLLSSGR	3
18				0.142	VIGIDHIK	2
18				0.142	DDPmLLSSGR	2
18				0.142	VFEVmLATDR	2
18				0.142	ELVDDSITNVK	2
18	PDGFA associated protein 1, isoform CRA_a	gi|119597080	2	0.125	VTQLDLDGPK	2
18				0.125	GVEGLIDIENPNR	2
18	Tmed9 protein	gi|48474619	2	0.107	TQLYDK	2
18				0.107	QLVEQVEQIQK	2
18	Dlst protein	gi|23271834	2	0.104	LGFmSAFVK	2
18				0.104	NVETmNYADIER	2
18	Dynactin 6	gi|6756009	2	0.095	GDVTIGPR	2
18				0.095	mGDNNVIESK	2
18	Electron transferring flavoprotein, beta polypeptide	gi|38142460	2	0.082	AGDLGVDLTSK	2
18				0.082	VETTEDLVAK	2
18	Voltage-dependent anion channel 1	gi|10720404	2	0.081	VTQSNFAVGYK	2
18				0.081	LTFDSSFSPNTGK	2
18	PDZ and LIM domain protein 1	gi|78099787	2	0.073	DFEQPLAISR	2
18				0.073	SAmPFTASPAPSTR	2
18	Triosephosphate isomerase	gi|71370922	2	0.067	HVFGESDELIGEK	3
18				0.067	RHVFGESDELIGEK	3
18	Ubiquinol-cytochrome c reductase, Rieske iron-sul	gi|13385168	3	0.062	AEVLDSTK	2

18				0.062	VPDFSDYR	2
18				0.062	RAEVLDSTK	2
18	Albumin 1	gi|33859506	3	0.051	ALVSSVR	2
18				0.051	LVQEVTDFAK	2
18				0.051	APQVSTPTLVEAAR	2
18	Cathepsin D	gi|6753556	2	0.049	QPGIVFVAAK	2
18				0.049	VSSLPTVYLK	2
20	Myosin light chain 2	gi|1709058	7	0.398	VFDPEGK	2
20				0.398	DTFAALGR	2
20				0.398	NLVHIITHGEEKD	3
20				0.398	EmLTTQAER	2
20				0.398	NEEIDEmIK	2
20				0.398	DGFIDKNDLR	2
20				0.398	EAFTImDQNR	2
20	Transgelin 2	gi|30519911	7	0.271	DGTVLcK	2
20				0.271	IQASSmAFK	2
20				0.271	LINSLYPEGQAPVK	2, 3
20				0.271	LINSLYPEGQAPVKK	2, 3
20				0.271	KIQASSmAFK	2
20				0.271	TLmNLGGLAVAR	2
20				0.271	NFSDNQLQEGK	2
20	Heat shock protein, alpha-crystallin-related, B6	gi|59958370	4	0.216	ASAPLPGFSAPGR	2, 3
20				0.216	VVDDHVEVHAR	3
20				0.216	RASAPLPGFSAPGR	3
20				0.216	HFLPEEISVK	2
20	Adp-Ribosylation Factor 1	gi|1065361	3	0.200	ILMVGLDAAGK	2
20				0.200	ILmVGLDAAGK	2
20				0.200	DAVLLVFANK	2
20				0.200	QDLPNAmNAAEITDK	2
20	Hypothetical protein LOC67939	gi|21312706	3	0.172	QLGVGSGNLR	2
20				0.172	QINLNDLGK	2
20				0.172	FADETAmLEK	2
20	Ubiquinone biosynthesis protein coq7	gi|3806019	2	0.112	FNELmIAFR	2
20				0.112	IYAGQmAVLGR	2
20	PREDICTED: similar to Cofilin-1	gi|73946791	2	0.106	AVLFcLSEDKK	3
20				0.106	YALYDATYETK	2
20	Transgelin	gi|6755714	2	0.104	AAEDYGVIK	2
20				0.104	TLmALGSLAVTK	2
20	EF hand domain containing 2	gi|31981086	2	0.088	VQAINVSSR	2
20				0.088	LSEIDVSTEGVK	2
20	Peroxiredoxin-3	gi|6680690	2	0.074	ELSLDDFK	2
20				0.074	HLSVNDLPVGR	2
20	Electron transferring flavoprotein, beta polypeptide	gi|38142460	2	0.067	SGVVTDGVK	2
20				0.067	VDLLFLGK	2

20	PREDICTED: similar to Actin, cytoplasmic 2 (Gam	gi|109489498	2	0.027	DLTDYLmK	2
20				0.027	EITALAPSTmK	2
22	Ubiquinol-cytochrome c reductase, Rieske iron-sul	gi|13385168	5	0.142	VPDFSDYRR	2, 3
22				0.142	LSDIPEGK	2
22				0.142	AEVLDSTK	1, 2
22				0.142	RAEVLDSTK	2
22				0.142	EIDQEAAVEVSQLR	2, 3
22	Ig kappa chain	gi|1083380	2	0.096	TSTSPIVK	2
22				0.096	FSGSGSGTDFTLK	2
22	Es1 protein	gi|20070420	2	0.068	NVLAESAR	2
22				0.068	NLSTFAVDGK	2
23	Hypoxia up-regulated 1	gi|31542333	19	0.186	VLFSR	2
23				0.186	GVGESFK	2
23				0.186	AVLQAAR	2
23				0.186	VITFNR	2
23				0.186	TPVTVTLK	2
23				0.186	LEELTLR	2
23				0.186	KTPVTVTLK	2
23				0.186	EVQYLLNK	2
23				0.186	LcQGLFFR	2
23				0.186	EVEEEPGLR	2
23				0.186	TLGGLEmELR	2
23				0.186	VAIVKPGVPmEIVLNK	3
23				0.186	SRFPEHELIVDPQR	3
23				0.186	FLGDSAAGmAIK	2
23				0.186	EAGmQPQLQIR	2
23				0.186	LPATEKPVLLSK	2
23				0.186	SLAEDFAEQPIK	2
23				0.186	AEPPLNASAGDQEEK	2
23				0.186	LGNTISSLFGGGTSSDAK	2
23	PREDICTED: similar to Actin, cytoplasmic 2 (Gam	gi|109489498	7	0.102	IIAPPERK	2
23				0.102	AGFAGDDAPR	2
23				0.102	QEYDESGPSIVHR	3
23				0.102	DLTDYLmK	2
23				0.102	GYSFTTTAER	2
23				0.102	EITALAPSTmK	2
23				0.102	DSYVGDEAQSK	2
23	PREDICTED: similar to ATP synthase beta chain	gi|73968432	5	0.102	VLDSGAPIK	2
23				0.102	IGLFGGAGVGK	2
23				0.102	IPVGPETLGR	2
23				0.102	TIAmDGTEGLVR	2
23				0.102	ImNVIGEPIDER	2
23	PREDICTED: similar to myosin heavy chain 6	gi|109082950	36	0.094	SLSTELFK	2
23				0.094	SNAAAAALDK	2

23				0.094	KVQHELDEAEER	3
23				0.094	LQDAEEAVEAVNAK	2, 3
23				0.094	YETDAIQR	2
23				0.094	SVNDLTSQR	2
23				0.094	KLAEQELIETSER	2, 3
23				0.094	SNAAAAALDKK	2
23				0.094	ANSEVAQWR	2
23				0.094	ADIAESQVNK	2
23				0.094	SLNDFTTQR	2
23				0.094	IKELTYQTEEDKK	3
23				0.094	AQLEFNQIK	2
23				0.094	QAEEAEEQANTNLSK	2, 3
23				0.094	qAEEAEEQANTNLSK	2
23				0.094	KAITDAAmmAEELKK	3
23				0.094	LDEAEQIALK	2
23				0.094	LQTENGELAR	2
23				0.094	QKYEESQSELESSQK	3
23				0.094	TKYETDAIQR	2
23				0.094	TLEDQANEYR	2
23				0.094	LEQQVDDLEGSLEQEK	3
23				0.094	DIDDLELTLAK	2
23				0.094	DTQIQLDDAVR	2
23				0.094	LQDLVDKLQLK	2
23				0.094	ELENELEAEQK	2
23				0.094	VQHELDEAEER	2
23				0.094	ELTYQTEEDKK	2
23				0.094	LAEQELIETSER	2
23				0.094	IEDEQALGSQLQK	2
23				0.094	ELENELEAEQKR	2
23				0.094	IEELEEELEAER	2
23				0.094	YEESQSELESSQK	2
23				0.094	LEDEEEmNAELTAK	2
23				0.094	NLTEEmAGLDEIIAK	2
23				0.094	LEEAGGATSVQIEmNK	2
23				0.094	qKYEESQSELESSQK	2
23	Desmin	gi|33563250	4	0.083	FANYIEK	2
23				0.083	ADVDAATLAR	2
23				0.083	TSGGAGGLGSLR	2
23				0.083	VSDLTQAANK	2
23	Heat shock protein 1, beta	gi|40556608	5	0.077	YIDQEELNK	2
23				0.077	SIYYITGESK	2
23				0.077	ADLINNLGTIAK	2
23				0.077	EQVANSAFVER	2
23				0.077	GVVDSEDLPLNISR	2

23	Procollagen, type VI, alpha 1	gi|6753484	6	0.064	IALVITDGR	2
23				0.064	GVLYQTVSR	2
23				0.064	VPNYQALLR	2
23				0.064	VAVVQYSGQGQQQPGR	2, 3
23				0.064	GDEGPPGPEGLR	2
23				0.064	TAEYDVAFGER	2
23	Vimentin	gi|2078001	3	0.058	SSVPGVR	2
23				0.058	QVDQLTNDK	2
23				0.058	FADLSEAANR	2
23	NADH dehydrogenase (ubiquinone) Fe-S protein 1	gi|21704020	4	0.052	ILQDIASGR	2
23				0.052	FEAPLFNAR	2
23				0.052	SATYVNTEGR	2
23				0.052	LEEVSPNLVR	2
23	ATP synthase alpha subunit precursor	gi|114511	2	0.047	APGIIPR	2
23				0.047	VLSIGDGIAR	2
23	Valosin containing protein	gi|30023842	3	0.037	GDDLSTAILK	2
23				0.037	mDELQLFR	2
23				0.037	EVDIGIPDATGR	2
23	Albumin 1	gi|33859506	2	0.036	TNcDLYEK	2
23				0.036	APQVSTPTLVEAAR	2
23	Fibronectin 1	gi|46849812	6	0.028	APITGYIIR	2
23				0.028	GDSPASSKPVSINYK	3
23				0.028	STTPDITGYR	2
23				0.028	FTNIGPDTmR	2
23				0.028	ATGVFTTLQPLR	2
23				0.028	ESNPLTAQQTTK	2
23	Spectrin alpha 2	gi|115496850	4	0.019	DLASVQALLR	2
23				0.019	ITALDEFATK	2
23				0.019	TATDEAYKDPSNLQGK	3
23				0.019	VLETAEDIQER	2
23	Hypothetical protein gbs1143	gi|25011194	2	0.017	VAITLK	2
23				0.017	SVEAYNAGVR	2