

Supplemental Table.

List of proteins identified with their corresponding peptide sequences, molecular weight (MH+), charge state (z) and Xcorr score (XC). Proteins are listed in an ascending order of their mean FSR values from six rats. The s.no. corresponds to the number in figure 1 and figure 4.

s. no	protein name	FSR \pm SEM	peptide sequence	MH+	z	XC
1	Myosin heavy chain, skeletal muscle, adult 1	0.16 \pm 0.04	K.AITDAAMMAEELKK.E	1553.75550	2	4.17
			K.DIDDLELTLAK.V	1245.65780	2	4.37
			K.IAEKDEEIDQLKR.N	1586.83900	3	5.07
			K.IAEQELLDASER.V	1373.69120	2	4.14
			K.IEDEQALGMQLQK.K	1518.74740	2	5.15
			K.KAITDAAMMAEELKK.E	1681.85040	3	4.29
			K.KMEGDLNEMEIQLNHSNR.M	2189.99190	4	3.45
			K.LAQESTMDVENDKQQLDEK.L	2237.02430	3	3.97
			K.NLTEEMAGLDETIK.L	1650.78960	2	5.39
			R.AEDEEEINAELTAK.K	1561.72330	2	5.05
			R.GKQAFQTQQIEELKR.Q	1675.91310	3	4.99
			R.IEEEEIEAER.A	1488.70700	2	5.01
			R.IQLELNQVK.S	1084.63660	2	3.33
			R.KIAEQELLDASER.V	1501.78620	3	3.80
			R.LDEAEQLALK.G	1129.61050	2	4.08
			R.LDEAEQLALKGGK.K	1371.74840	2	4.47
			R.LEEAGGATSAQIEMNK.K	1664.78010	2	6.37
			R.LINELTAQR.G	1057.60060	2	3.36
			R.LQNEVEDLMIDVER.T	1718.82710	2	5.20
			R.SLSTELFK.I	924.50420	2	2.39
R.TLEDQVSELK.T	1161.60030	2	3.25			
R.VQLLHTQNTSLINTK.K	1709.95500	3	5.33			
R.VVESMQSTLDAEIR.S	1593.77940	2	5.28			
2	myosin, light polypeptide 2	0.20 \pm 0.01	K.EAFTVIDQNR.D	1192.59620	2	4.48
			K.EAFTVIDQNRDGIIDK.E	1833.93470	2	4.68
			K.GADPEDVITGAFK.V	1319.64830	2	4.64
			K.LKGADPEDVITGAFK.V	1560.82730	3	4.65
			K.NICYVITHGDAK.D	1390.70940	2	4.08
			K.NICYVITHGDAKDQE.-	1762.83760	2	5.04
			K.QFLEELLTTQCDR.F	1652.82590	2	4.76
			R.DGIIDKEDLR.D	1173.61150	2	3.09
			R.LNVKNEELDAMMK.E	1566.75070	2	4.53
3	tropomodulin 4	0.27 \pm 0.07	K.ERDDLVPFTGEK.K	1405.69630	2	4.47
			K.ERDDLVPFTGEKK.G	1533.79130	2	4.22
			K.SGDPIANAVADMLR.E	1445.70580	2	5.00
			K.YRDIDEDEILR.T	1436.70210	3	4.61
			R.ENATLTEL.R.V	1046.54820	2	2.87
			R.SFSLVATK.S	852.48310	2	2.57
4	creatine kinase, muscle form	0.30 \pm 0.07	K.DLFDPIIQDR.H	1231.63230	2	2.99
			K.FEEILTR.L	907.48890	2	2.82
			K.GGDDLDPNYVLSSR.V	1507.70290	2	4.96
			K.GQSIDDMIPAQK.-	1318.63130	2	4.21
			K.HKTDLNHENLK.G	1348.69730	3	3.13
			K.IEEIFK.K	778.43510	2	2.21
			K.IEEIFKK.A	906.53000	2	2.89
			K.LMVEMEK.K	911.42180	2	2.39
			K.SQEEYPDLK.H	1195.54830	2	3.62
			K.TDLNHENLK.G	1083.54350	2	3.08
			R.FCVGLQK.I	851.47550	2	2.42
			R.HGGFKPTDK.H	986.50600	2	3.11
			R.RFCVGLQK.I	1007.57660	2	2.64

5	TROPONIN C, SKELETAL MUSCLE	0.32 ± 0.09	K.GKSEEELAEFCR.I	1454.68910	2	4.29
			R.ASGEHVTDEEIESLMK.D	1790.81180	2	5.19
			R.IDFDEFLK.M	1026.51480	2	2.22
			R.SYLSEEMIAEFK.A	1462.67760	2	4.69
6	leucine zipper-EF-hand containing transmembrane protein 1	0.33 ± 0.09	K.ADDKLISEEGVDSLTVK.E	1818.93370	2	5.41
			K.LISEEGVDSLTVK.E	1389.74770	2	4.61
			K.MVDVIPPEILK.D	1356.74480	2	3.02
			K.STLQTLPEIVAK.E	1299.75240	2	3.52
			K.TGDEKYIEESTASKR.L	1713.82950	3	5.66
			R.AMYLPDTLSPADQLK.S	1678.83620	2	4.42
R.FQLTMR.L	811.41360	2	2.01			
7	3-hydroxyacyl-CoA dehydrogenase type II	0.34 ± 0.08	K.EVQAALTLAK.E	1043.61010	2	2.96
			K.GGIVGMTLPIAR.D	1200.67740	2	4.16
			K.LGGNCIFAPANVTSEK.E	1677.85760	2	3.90
			K.NQVHTLEDFQR.V	1386.67660	2	3.83
			R.LVAGVMGQNEPDQGGQR.G	1755.84480	2	6.01
R.NFLASQVPFPSR.L	1362.71700	2	4.23			
8	coiled-coil-helix-coiled-coil-helixdomaincontaining3	0.34 ± 0.06	K.AVANEQLTR.A	1001.53800	2	3.33
			K.ILQCYR.Q	852.47070	2	2.28
			R.KQDAFYK.E	899.46270	2	2.98
			R.LSENVDR.M	945.50050	2	3.19
			R.RVAEELALEQAK.M	1356.74870	2	4.45
			R.VAEELALEQAK.M	1200.64760	2	4.56
			R.YEYHPVCADLQTK.I	1623.77820	3	3.32
			R.YSSVYGASVSDEELK.R	1633.75970	2	5.38
9	NAD⁺-isocitrate dehydrogenase, gamma subunit	0.35 ± 0.06	K.DIDILIVR.E	956.57810	2	2.71
			K.GNIETNHNLPESHK.S	1557.77740	2	4.08
			K.SLPGVVTR.H	828.49430	2	2.13
			R.NAIMAIR.R	804.44020	2	2.47
10	pyruvate dehydrogenase (lipoamide) beta	0.35 ± 0.05	K.DFLIPIGK.A	902.53510	2	2.01
			K.DIIFAIK.K	819.49800	2	2.01
			K.DIIFAIK.T	947.59300	2	2.45
			K.EGIECEVINLR.T	1331.69350	2	3.63
			K.ILEDNSIPQVK.D	1255.68980	2	3.99
			R.EAINQGMDEELERDEK.V	1921.84490	2	4.01
			R.PVGHCLEAAAVLSK.E	1451.79860	3	5.84
			R.TIRPMDIEAIEASVMK.T	1835.92470	3	4.33
R.VTGADVMPYAK.I	1264.62470	2	3.96			
11	striated muscle alpha tropomyosin	0.35 ± 0.10	K.AISEELDHALNDMTSI.-	1774.81690	2	3.53
			K.HIAEDADRKYEEVAR.K	1801.88330	4	2.85
			K.LVIIESDLER.A	1186.66830	2	3.61
			K.MEIQEIQLK.E	1147.60330	2	3.35
			K.SIDDLEDELYAQK.L	1538.72260	2	5.00
			R.AQKDEEKMEIQEIQLK.E	1976.00100	3	4.85
			R.KLVIIESDLER.A	1314.76330	3	4.23
12	KCRS_RAT creatine kinase, sarcomeric mitochondrial precursor	0.36 ± 0.08	K.HPTDL DASK.I	983.47980	2	2.26
			K.ILENLR.L	757.45720	2	2.11
			K.ITHGQFDER.Y	1102.52810	2	2.79
			K.LSEMTEQDQQR.L	1364.61160	2	4.32
			K.VPPPLPQFGR.K	1107.63150	2	2.09
			R.GLSLPPACSR.A	1057.57700	2	2.70
			R.VMKHPTDL DASK.I	1357.67860	2	3.48

13	cytochrome c oxidase subunit Vb	0.37 ± 0.05	K.AASGTKEDPNLVPSVSNK.R	1813.92960	3	3.69
			K.EDPNLVPSVSNK.R	1298.65920	2	2.75
			R.GLDPYNMLPPK.A	1260.62980	2	3.33
14	Troponin T, fast skeletal muscle isoforms beta/alpha	0.37 ± 0.10	K.IPEGEKVDFFDIQK.K	1632.81210	2	5.07
			K.IPEGEKVDFFDIQKK.R	1760.90710	2	4.63
			K.VDFDDIQK.K	979.47360	2	2.56
			R.KKEEEEELIALK.E	1329.76300	2	4.82
15	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	0.38 ± 0.07	K.EIDQEAHAVEVSQLR.D	1586.80260	2	5.25
			K.VPDFSDYR.R	998.45830	2	2.41
			K.VPDFSDYRR.A	1154.55940	2	2.51
16	hypothetical protein MGC36907	0.38 ± 0.05	R.FLEQQNKVLETK.W	1476.80620	2	4.49
17	Complement component 1 Q subcomponent-binding protein	0.38 ± 0.08	K.MSGDWELEVNGTEAK.L	1681.73790	2	4.75
18	DNA segment, Chr 10, Johns Hopkins University 81 expressed	0.38 ± 0.04	K.GVEVTVGHEQEEGGK.W	1554.74000	2	4.63
			K.KPIGLCCIPVLA AK.V	1610.97370	2	4.74
			K.NLSTFAVDGK.D	1051.54240	2	3.38
			K.VLELTGK.-	759.46160	2	2.10
			K.WPYAGTAEAVK.A	1192.60020	2	3.58
			R.NVLAESAR.I	859.46380	2	2.13
19	prohibitin	0.38 ± 0.02	K.DLQNVNITLR.I	1185.65920	2	4.24
			K.EFTEAVEAK.Q	1023.49990	2	2.38
			K.KAAII SAEGDSK.A	1189.64280	2	3.80
			K.VFESIGK.F	779.43030	2	2.42
			R.FDAGELITQR.E	1149.59040	2	4.13
			R.FVVEKAEQQK.K	1205.65300	2	3.17
			R.ILFRPVASQLPR.I	1396.84290	2	3.18
			R.IYTSIGEDYDER.V	1460.65450	2	4.26
			R.KLEAAEDIA YQLSR.S	1606.84410	2	5.67
			R.QVSDDLTER.A	1062.50670	2	2.09
			R.VLPSITTEILK.S	1213.74080	2	2.70
20	acyl-Coenzyme A dehydrogenase, very long chain	0.38 ± 0.07	K.GILLYGTK.A	864.51950	2	2.58
			K.SFAVGMFK.G	902.44460	2	2.51
			K.VEEDTLQGLK.E	1131.58970	2	3.56
			R.FFEEVNDPAK.N	1195.56350	2	4.21
			R.FFEEVNDPAK NDSLEK.V	1881.88700	2	5.57
21	malate dehydrogenase 2	0.39 ± 0.05	K.AGAGSATLSMAYAGAR.F	1454.70620	2	5.30
			K.EGVIECSFVQSK.E	1382.69310	2	3.96
			K.GCDVVVIPAGVPR.K	1338.75090	2	4.60
			K.GYLGPEQLPDCLK.G	1489.76660	2	4.43
			K.HGVYNPNK.I	928.46410	2	3.42
			K.IFGVTTLDIVR.A	1233.72070	2	3.97
			K.IQEAGTEVVK.A	1073.58430	2	3.05
			K.TIIP LISQCTPK.V	1370.80230	2	3.95
			R.ANTFVAELK.G	992.54170	2	3.05
			R.FVFSLV DAMNGK.E	1343.66690	2	3.42
			R.VNVPVIGGHAGK.T	1147.65880	2	3.85
22	LRP16 protein	0.40 ± 0.06	R.AAGSLLTDECR.T	1192.59370	2	3.83
			R.LPHYFPVA.-	943.50	2	2.72

23	Pyruvate dehydrogenase (lipoamide) alpha 1	0.40 ± 0.07	K.LPCIFICENNR.Y	1435.74370	2	4.24
			K.RGDFIPGLR.V	1030.57980	2	3.19
			R.SGKGPILMELQTYR.Y	1608.84190	2	4.32
			R.SKSDPIMLLK.D	1147.63970	2	2.57
			R.SKSDPIMLLKDR.M	1418.76770	2	3.30
			R.TREEIQEVR.S	1159.60710	2	3.44
			R.VDGMDCVLR.E	1193.59640	2	4.01
			R.YHGHSMSDPGVSYR.T	1608.68650	2	3.56
24	calreticulin	0.42 ± 0.09	K.FYGDQEKDKGLQTSQDAR.F	2085.98410	2	6.12
			K.GQTLVVQFTVK.H	1219.70500	2	4.11
			K.IKDPDAAKPEDWDER.A	1784.84550	2	3.98
			K.KVHVIFNYK.G	1147.66280	2	2.90
			K.SDFGKFLSSGK.F	1271.66360	2	4.17
			K.VHVIFNYK.G	1019.56780	2	2.47
			25	NADP+-specific isocitrate dehydrogenase	0.42 ± 0.04	K.LDGNQDLIR.F
K.SSGFVWACK.N	1098.53480	2				4.18
K.TIEAAAHGTVTR.H	1355.69190	2				4.49
K.VCVQTVESGAMTK.D	1425.70230	2				5.17
R.FAQMLEK.V	836.45180	2				2.86
R.GKLDGNQDLIR.F	1228.66500	2				3.97
26	Heat shock cognate 71 kDa protein	0.42 ± 0.04	K.DAGTIAGLNVLRI	1199.67480	2	4.19
			K.MKEIAEAYLGK.T	1268.65600	2	3.82
			K.SFYPEEVSSMVLTK.M	1632.78310	2	4.83
			K.STAGDTHLGGEDFDNR.M	1691.72610	2	4.85
			K.VQVEYKGETK.S	1180.62140	2	3.19
27	NAD+-specific isocitrate dehydrogenase b subunit	0.43 ± 0.13	K.AAAVPVEFK.E	931.52530	2	2.50
			K.EHHLSEVQNMASEEK.L	1783.79210	3	4.51
			K.EHHLSEVQNMASEEK.L	1767.79720	3	3.58
			K.GELASYDMQLR.R	1298.60510	2	3.79
			K.LEQVLSSMK.E	1050.55050	2	3.42
			K.LEQVLSSMKENK.V	1421.73100	2	3.95
			R.EQTEGEYSSLEHESAR.G	1851.79970	2	4.53
			R.HNNLDLVIIR.E	1206.69590	2	4.21
28	ATP synthase subunit d	0.43 ± 0.06	K.NCAQFVTGSQAR.V	1338.65300	2	4.88
			K.SWNETFHTR.L	1177.53900	2	2.85
			K.YNALKIPVPEDK.Y	1386.76330	3	3.70
			R.ANVDKPGLVDDFK.N	1417.73270	2	4.32
			R.ANVDKPGLVDDFKNK.Y	1659.87060	3	4.76
29	peroxiredoxin 5 precursor	0.43 ± 0.09	K.KVNLAELFK.D	1061.63590	2	2.90
			K.VNLAELFK.D	933.54090	2	2.73
			K.VQLLADPTGAFGK.E	1316.72140	2	4.17
			R.FSMVIDK.G	855.42860	2	2.94
30	hydroxyacyl-Coenzyme A dehydrogenase	0.43 ± 0.09	K.DTTASAVAVGLK.Q	1132.62140	2	4.30
			K.GFYIYQSGSK.N	1149.55800	2	3.96
			K.MQLLEIITTDK.T	1320.70850	2	4.10
			K.MQLLEIITTDKTSK.D	1636.88310	2	4.55
			K.VIGMHYFSPVDK.M	1408.69350	2	4.10
			R.C*LAPMMSEVIR.I	1338.65250	2	2.95
			R.FGGGSVELLK.L	1006.55730	2	3.59
			R.FVDLYGAQK.V	1040.54170	2	3.16
			R.LPAKPEVSSDEDIQYR.V	1846.91870	3	5.41

31	Mitochondrial aconitase	0.44 ± 0.05	K.LEAPDADELPR.S	1225.60650	2	4.13
			K.LTGTLSGWTSPPK.D	1247.66360	2	3.58
			K.LTIQGLK.D	772.49330	2	2.17
			K.NTIVTSYNR.N	1067.54850	2	3.25
			K.SQFTITPGSEQIR.A	1463.74940	2	4.17
			K.VAGILTVK.G	800.52460	2	2.57
			R.DGYAQILR.D	935.49510	2	3.13
			R.EHAALPR.H	922.47470	2	2.56
			R.IHETNLK.K	854.47360	2	2.22
			R.LQLLEPFDK.W	1102.61480	2	2.72
			R.NAVTQEFQVPTAR.Y	1601.79240	2	3.27
			R.SDFDPGQDQYQHPPK.D	1731.76140	2	2.45
			R.VDVSPQSQR.L	988.50630	2	2.99
			R.VGLIGSCTNSSYEDMGR.S	1861.83660	2	5.37
			R.WVIGDENYEGSSR.E	1667.76650	2	4.81
32	superoxide dismutase 2, mitochondrial	0.44 ± 0.08	K.GDVTTQVALQPALK.F	1440.80620	3	5.28
			K.GELLEAIK.R	872.50930	2	2.92
			K.GELLEAIKR.D	1028.61040	2	2.97
			K.HHATYVNNLNVTEEK.Y	1768.86180	2	4.52
			K.NVRPDYLK.A	1004.55290	2	2.85
			K.RDFGSFEK.F	985.47430	2	3.09
			K.YHEALAK.G	831.43650	2	2.73
33	myosin, light polypeptide 3	0.45 ± 0.04	K.AAPAPAAAPAAPEPERPK.E	1782.95030	2	5.22
			K.ITYGQCGDVL.R.A	1281.65670	2	3.53
			R.ALGQNPTQAEVLR.V	1396.75480	2	4.55
			R.HVLATLGER.L	995.56380	2	2.96
			R.VFDKEGNGTVMGAELR.H	1738.84340	2	4.97
			R.VLGKPKQEELNSK.M	1469.83280	2	2.62
34	Succinyl-Co A ligase beta-chain, mitochondrial	0.46 ± 0.12	K.INFDSNSAYR.Q	1186.54930	2	3.73
			K.ILACDDLDEAAK.M	1333.66150	2	4.02
			K.YDATMVEINPMVEDADGK.V	2029.87340	2	5.90
			K.LYNLFLK.Y	910.54020	2	2.37
35	prolyl 4-hydroxylase, beta polypeptide	0.46 ± 0.11	K.FFKNGDTASPK.E	1211.60610	2	2.35
			K.FFPASADR.T	910.44230	2	2.26
			K.LGETYKDHENIVIAK.M	1729.91250	3	5.44
			K.MDSTANEVEAVK.V	1309.59460	2	4.17
			K.NFEEVAFDEK.K	1227.55340	2	3.48
			K.NFEEVAFDEKK.N	1355.64830	2	4.09
			K.THILLFLPK.S	1081.67740	2	3.35
			K.VDATEESDLAQQYGVR.G	1780.83530	2	5.74
			K.YKPESDELTAEK.I	1409.68000	3	4.44
			K.YQLDKDGVVLFK.K	1424.77890	2	3.88
			R.ILEFFGLK.K	966.56640	2	2.28
			R.ILEFFGLKK.E	1094.66140	2	2.83
			R.LITLLEEEMTK.Y	1222.62410	2	3.65
			R.NNFEGEITK.E	1051.50600	2	2.73
			R.NNFEGEITKEK.L	1308.64360	2	2.65
R.TVIDYNGER.T	1066.51690	2	2.73			
36	electron-transfer-flavoprotein, beta polypeptide	0.47 ± 0.11	K.AGDLGVDLTSK.V	1075.56350	2	3.58
			K.VETTEDLVAK.L	1104.57880	2	2.93
			K.VSVISVEEPPQR.L	1339.72220	2	3.42
37	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kD	0.47 ± 0.08	K.ELEQFTQVSK.A	1208.61630	2	3.47
			K.VDQEIINIQR.L	1469.79640	2	4.10
			R.EFIEQQHAK.N	1129.56420	2	3.03
			R.EGESALQNCAK.E	1206.57300	2	4.00

			R.RVPDITECK.E	1117.59810	2	2.82
			R.VPDITECK.E	961.49700	2	2.75
			R.YQDLGAYYSAR.K	1306.60680	2	3.97
38	Polymerase (RNA) II (DNA directed) polypeptide C	0.48 ± 0.07	R.LNHVLEEEQK.L	1238.63810	2	2.83
			R.SSEEQRQQPPHSSQQHSETQC	3455.60770	5	2.70
			R.YTDQSGEEEEEDYESEEQIQHR.	2601.05010	3	5.15
39	Dihydrolipoamide succinyltransferase	0.48 ± 0.06	R.NVETMNYADIER.T	1470.65350	2	4.82
			K.VEGGTPLFTRLR.T	1317.75	2	3.03
			K.VEGGTPLFTRLR.K	1189.66	2	3.19
40	alpha 1 actin precursor	0.48 ± 0.08	K.DLYANNVMSGGTTMYPGIADR.	2278.01200	2	5.58
			R.GYSFVTTAER.E	1130.54820	2	3.98
			R.KDLYANNVMSGGTTMYPGIADP	2406.10690	3	6.43
			R.VAPEEHPTLLTEAPLNPK.A	1956.04420	2	4.60
41	3-mercaptopyruvate sulfurtransferase	0.49 ± 0.06	K.THEDILENLDR.R	1425.69740	2	4.51
42	acetyl-Coenzyme A dehydrogenase, long-chain	0.49 ± 0.11	K.CIGAIAMTEPGAGSDLQGVR.T	2018.99450	2	6.25
			K.EQIEQFIPQMTAGK.C	1635.80520	2	5.24
			K.KLTDIGIRR.I	1071.66380	2	2.33
			K.QGLLGINIAEK.H	1155.67370	2	2.30
			R.IFSSEHDIFR.E	1250.61700	2	3.13
43	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	0.49 ± 0.13	K.EVTGSIQLCR.D	1162.61960	2	2.52
			R.DTPPKREEMVLDDSAK.F	1846.88560	2	3.16
			R.EFDDLPLAEQR.E	1332.64360	2	3.56
			R.IGIFSENEEVADR.A	1478.71270	2	4.46
			R.KEVTGSIQLCR.D	1290.71450	2	3.79
			R.RIGIFSENEEVADR.A	1634.81380	2	4.23
			R.VGTTRVPLTGPVK.E	1324.79530	2	4.06
			R.VGTTRVPLTGPVKEK.I	1581.93280	2	3.86
			R.VPLTGPVKEK.I	1067.64650	2	3.12
44	enoyl Coenzyme A hydratase, short chain 1	0.49 ± 0.06	K.AFAAGADIK.E	863.46270	2	2.88
			K.AFAAGADIKEMQNR.T	1537.74330	2	4.89
			K.GKNSSVGLIQLNRPK.A	1610.93420	2	4.97
			K.LFYSTFATDDRR.E	1491.72320	2	2.95
			K.NSSVGLIQLNRPK.A	1425.81780	2	3.68
			K.SLAMEMVLTGDR.I	1354.63460	2	4.35
			R.TFQDCYSGK.F	1105.49300	2	2.98
45	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	0.50 ± 0.09	K.AQSELSGAADEAAR.A	1375.64540	2	4.84
			R.IEANEALVK.A	986.55220	2	3.07
46	fast myosin alkali light chain	0.50 ± 0.10	K.DQGGYEDFVEGLR.V	1484.66580	2	4.41
			K.EAFLLFDR.T	1010.53110	2	2.98
			K.ITLSQVGDVLR.A	1200.69520	2	4.59
			K.VLGNPSNEEMNAK.K	1418.65850	2	3.99
			R.ALGTNPTNAEVK.K	1214.63810	2	3.97
47	H(+)-transporting ATP synthase	0.50 ± 0.07	K.GIRPAINVGLSVSR.V	1438.84940	2	4.25
			K.QVAGTMKLELAQYR.E	1623.85280	2	3.36
			K.QVAGTMKLELAQYR.E	1607.85790	2	2.67
			R.AMKQVAGTMKLELAQYR.E	1970.02030	3	4.35
			R.GVRLTELLK.Q	1028.64680	2	2.26
			R.GYLDKLEPSK.I	1149.61560	2	3.03
			R.GYLDKLEPSKITK.F	1491.84230	2	4.34
			R.LTELLK.Q	716.45580	2	2.31

48	dihydrolipoamide dehydrogenase	0.51 ± 0.07	K.AAQLGFK.T	734.42010	2	2.35
			K.ALTGGIAHLFK.Q	1127.65770	2	3.39
			K.NETLGGTCLNVGCIPSK.A	1819.92930	2	5.45
			K.NQVTATTADGSTQVIGTK.N	1791.90880	2	6.61
			R.GIEIPEVR.L	912.51550	2	2.23
49	Tu translation elongation factor, mitochondrial	0.52 ± 0.10	K.FKKYEEIDNAPEER.A	1767.85530	3	4.16
			K.LLDAVDTYIPVPTR.D	1572.86370	2	3.66
			K.QIGVEHVVVYVVK.A	1483.82730	2	2.87
			R.AEAGDNLGALVR.G	1185.62280	2	4.56
			R.DKPHVNVGTIGHVDHGK.T	1809.93600	4	3.51
			R.GITINAAHVEYSTAAR.H	1673.86110	2	5.27
			R.GLVMVKPGSIQPHQK.V	1634.90520	3	4.28
			R.TVVTGIEMFHK.S	1277.65640	2	3.65
50	NADH dehydrogenase (ubiquinone) Fe-S protein 6	0.52 ± 0.11	K.VYINLDK.E	864.48310	2	2.54
			K.VYINLDKETK.T	1222.66830	2	4.06
			R.IIACDGGGGALGHPK.V	1422.74690	2	4.30
51	24-kDa subunit of mitochondrial NADH dehydrogenase	0.53 ± 0.12	K.VAEVLQVPPMR.V	1254.68800	2	3.44
			R.AAAVLPVLDLAQR.Q	1336.79530	2	4.29
			R.DSDSILETLQR.K	1276.63850	2	4.24
			R.DSDSILETLQRK.L	1404.73340	2	3.72
			R.QNGWLPISAMNK.V	1374.68400	2	4.12
			R.VYEVAIFYTMYNR.K	1672.76810	2	5.25
52	3-hydroxyisobutyrate dehydrogenase	0.53 ± 0.09	K.DLGLAQDSATSTK.T	1306.64900	2	3.22
			K.EAGEQVASSPADVAEK.A	1587.75020	2	4.97
			K.EAGEQVASSPADVAEKADR.I	1929.91540	2	5.13
			K.EFKEAGEQVASSPADVAEK.A	1991.95620	2	5.93
			K.EVEKMGAVFMDAPVSGGVGA ^A	2210.05850	3	4.65
			K.GSLLIDSSTIDPSVSK.E	1618.85400	2	5.58
			K.KGSLLIDSSTIDPSVSK.E	1746.94890	2	4.87
			K.MGAVFMDAPVSGGVGAAR.S	1724.81000	2	5.79
			K.TPILLGSVAHQIYR.M	1567.89600	2	4.51
			K.TPVGFIGLGNMGNPMK.N	1735.85110	2	5.15
53	gamma actin-like protein	0.53 ± 0.13	K.SYELPDGQVITIGNER.F	1790.89250	2	4.93
			R.AVFPSIVGR.P	945.55220	2	2.27
			R.AVFPSIVGRPR.H	1198.70600	2	2.94
			R.DLTDYLMK.I	1014.48180	2	2.41
			R.HQGVMVGMGQKDSYVGDEAQ	2539.16690	4	3.05
54	Atp5c1 protein	0.54 ± 0.08	K.EVMIVGIGEK.I	1090.58180	2	3.02
			K.HLIIGVSSDR.G	1096.61150	2	3.29
			K.NDMAALTAAGK.E	1062.52540	2	3.74
			K.QMKNDMAALTAAGK.E	1465.71430	2	3.66
			R.GLCGAIHSSVAK.Q	1199.65120	2	4.22
			R.THSDQFLVSFK.D	1308.65880	2	4.01
			R.VYGTGSLALYEK.A	1300.67890	2	4.03
55	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, beta polypept	0.54 ± 0.10	K.AHGGYSVFAGVGER.T	1406.68170	2	4.85
			K.IGLFGGAGVGK.T	975.56270	2	3.12
			K.IPVGPETLGR.I	1038.59480	2	2.86
			K.TVLIMELINNVAK.A	1473.83510	2	5.21
			K.VALVYGMNEPPGAR.A	1617.80590	2	4.75
			K.VLDSGAPIKIPVGPETLGR.I	1919.09660	3	4.91
			K.VVDLLAPYAK.G	1088.63560	2	3.61
			R.AIAELGIYPAVDPLDSTSR.I	1988.03400	3	5.34
			R.EGNDLYHEMIESGVINLK.D	2076.99120	2	5.38

			R.FLSQPFQVAEVFTGHMGK.L	2039.00600	2	4.84
			R.FTQAGSEVSALLGR.I	1435.75450	2	5.26
			R.IMDPNIVGSEHYDVAR.G	1831.86490	2	4.83
			R.IMNVIGEPIDER.G	1401.70480	2	4.56
			R.IPSAVGYQPTLATDMGMTQER.	2298.07460	3	5.67
			R.LVLEVAQHLGESTVR.T	1650.91790	2	5.30
			R.TIAMDGTEGLVR.G	1278.63640	2	3.64
			R.TREGNDLYHEMIESGVINLK.D	2334.14000	3	5.45
			R.VALTGLTVAEYFR.D	1439.78980	2	4.81
56	creatine kinase, sarcomeric mitochondrial precursor	0.54 ± 0.10	K.HPTDLTASK.I	983.47980	2	2.22
			R.EVENVAITALEGLK.G	1485.81640	2	4.84
			R.VMKHPTDLTASK.I	1357.67860	2	3.50
57	propionyl-Coenzyme A carboxylase, alpha polypeptide	0.56 ± 0.18	K.AGDTVGEGLLVELE.-	1516.73830	2	4.05
			K.FLSDVYPDGFK.G	1287.62610	2	3.51
			K.LAAELNKFMLEK.V	1422.76660	2	3.86
			K.RMEDALDSYVIR.G	1483.72150	2	2.59
			K.SFGLPSIGR.L	933.51580	2	2.13
			R.DAGGNMSIQFLGTVYK.V	1716.82670	2	5.17
			R.GVTHNIPLLR.E	1119.66380	2	3.19
			R.MEDALDSYVIR.G	1327.62040	2	4.53
			R.VPVIRPDVAK.W	1093.67340	2	3.19
58	Voltage-dependent anion-selective channel protein 1	0.56 ± 0.05	K.LTFDSSFSPNTGK.K	1400.66980	2	4.37
			K.LTFDSSFSPNTGKK.N	1528.76470	2	3.85
			K.LTLSALLDGK.N	1030.61480	2	3.17
			K.SENGLEFTSSGSANTETTK.V	1959.87830	2	5.06
			K.TKSENGLEFTSSGSANTETTK.V	2189.02100	3	4.57
			K.YQVDPDACFSAK.V	1400.64620	2	4.46
			R.VTQSNFAVGYK.T	1213.62170	2	3.92
59	cytochrome c-1	0.57 ± 0.19	R.AANNALPPDLSYIVR.A	1670.88660	2	2.29
			R.GLLSSLDHTSIR.R	1298.70680	2	3.76
			R.HLVGVICYTEEEAK.A	1534.75170	2	4.58
60	isocitrate dehydrogenase 3 (NAD+) alpha	0.57 ± 0.07	K.APIQWEER.N	1028.51650	2	3.04
			K.CSDFTEEICR.R	1316.58620	2	3.91
			K.IEAACFATIK.D	1123.61270	2	3.83
			K.IEAACFATIKDGK.S	1423.75610	2	4.31
			K.TPIAAGHPSMNLRLR.K	1606.87390	2	4.33
			K.TPYTDVNIVTIR.E	1391.75350	2	4.21
			K.WMIPPEAK.E	987.49730	2	2.46
			R.IAEFAFEYAR.N	1216.60020	2	4.24
			R.MSDGLFLQK.C	1054.52430	2	3.44
61	fumarate hydratase 1	0.58 ± 0.06	K.KPVHPNDHVNK.S	1284.68130	2	3.80
			K.LHDALSAK.S	854.47360	2	2.39
			K.NVLHSAR.L	796.44300	2	2.23
			K.RAAAEVNQEYGLDPK.I	1660.82950	3	4.24
			K.SKEFAQVIK.I	1049.59950	3	3.22
			K.VAALTGLPFVTAPNK.F	1498.86330	2	5.03
			K.YYGAQTVR.S	957.47940	2	3.28
			R.AAAEVNQEYGLDPK.I	1504.72840	2	5.04
			R.AIEMLGELGSK.K	1204.62470	2	4.34
			R.IEYDTFGELK.V	1214.59450	2	3.74
			R.IYELAAGGTAVGTGLNTR.I	1763.92920	2	5.57
			R.MPIPVIA.A	813.49080	2	2.19

62	glutamate oxaloacetate transaminase 2	0.58 ± 0.07	K.ASAELALGENSEVLK.S	1530.80150	2	5.14
			K.EFSVYMTK.D	1020.47120	2	2.19
			K.KMNLGVGAYR.D	1124.58860	2	2.82
			K.MNLGVGAYR.D	996.49370	2	3.39
			K.NMGLYGER.V	955.43070	2	3.05
			R.DAGMQLQGYR.Y	1154.52640	2	4.07
			R.DDNGKPYVLPVSR.K	1459.75450	2	2.84
			R.FVTVQTISGTGALR.V	1449.80650	2	5.42
			R.IAATILTSPDLR.K	1270.73710	2	4.24
			R.PLYSNPPLNGAR.I	1298.68570	2	2.57
			R.TQLVSNLK.K	902.53110	2	3.19
			R.TQLVSNLKK.E	1030.62610	2	2.92
			R.VGAFTVVCK.D	980.55440	2	3.54
			R.VGASFLQR.F	877.48960	2	3.31
63	NADH dehydrogenase (ubiquinone) flavoprotein 1	0.58 ± 0.08	K.LVEGCLVGGR.A	1059.59260	2	3.85
			K.YLVVNADEGEPGTCK.D	1651.79430	2	5.30
			K.YLVVNADEGEPGTCKDR.E	1922.92230	2	5.18
			R.AAYIYIR.G	869.48850	2	2.53
			R.EAYEAGLIGK.N	1050.54710	2	2.70
			R.GEFYNEASNLQVAIR.E	1710.84510	2	5.20
			R.GGTWFAGFGR.E	1055.50630	2	2.84
			R.HDPHKLVEGCLVGGR.A	1673.88510	3	4.79
			R.HFRPELEDR.M	1198.59690	3	2.60
			R.LIEFYK.H	812.45580	2	2.27
64	lysophospholipase 1	0.59 ± 0.08	K.ALIDQEVK.N	915.51510	2	2.45
			K.GLVNPANVTFK.V	1159.64750	2	2.91
			K.VYEGMMHSSCQQEMMDVK.Y	2253.88990	3	3.94
			R.ASFSQGPINSANR.D	1348.66090	2	4.29
65	tropomyosin 4	0.60 ± 0.13	K.ATDAEADVASLNR.R	1332.63950	2	4.80
			K.ATDAEADVASLNR.I	1488.74070	2	2.42
			K.KATDAEADVASLNR.R	1460.73450	2	4.91
			K.KATDAEADVASLNR.I	1616.83560	2	2.95
66	ubiquinol-cytochrome c reductase binding protein	0.60 ± 0.07	K.LGLMRDDTMHETEDVK.E	1921.86350	2	3.08
			K.WYYNAAGFNK.L	1233.56930	2	3.52
			R.ALDLSMR.H	805.42420	2	2.20
			R.DDTMHETEDVKEAIR.R	1804.80230	2	4.05
			R.DDTMHETEDVK.E	1319.54250	2	3.03
			R.LPENLYNDR.M	1133.55910	2	3.34
			R.RLPENLYNDR.M	1289.66020	2	3.44
67	NADH dehydrogenase 1 alpha subcomplex 10-like protein	0.60 ± 0.06	K.VVEDIEYLNYNK.G	1498.74290	2	4.95
			K.YAPGYNADVGDK.W	1269.57520	2	2.63
			R.DIAEQLGMK.H	1020.50360	2	3.23
			R.VITVDGNICSGK.N	1262.67200	2	4.00
			R.YGLLASILGDK.T	1149.65190	2	3.86
68	methylmalonate semialdehyde dehydrogenase gene	0.62 ± 0.08	K.DMDLYSYR.L	1078.45150	2	3.25
			K.TLADAEGDVFR.G	1193.58020	2	3.88
			R.VPGATMLLAK.L	1016.58140	2	3.15
			R.VPQSTKAEMEAAVAACK.R	1806.90350	3	2.97
			R.VPQSTKAEMEAAVAACKR.A	1963.00460	3	4.00
R.YQQLIKENLK.E	1276.72650	2	3.43			
69	cytochrome c oxidase, subunit Va	0.64 ± 0.07	K.GMNTLVGYDLVPEPK.I	1648.82560	2	4.56
			R.KGMNTLVGYDLVPEPK.I	1776.92060	3	4.04
			R.LNDFASAVR.I	992.51650	2	3.21
			R.RLNDFASAVR.I	1148.61760	2	3.43

70	NADH dehydrogenase (ubiquinone) Fe-S protein 2	0.66 ± 0.14	K.APGFAHLAGLDK.M	1196.64280	2	4.00
			K.GEFGVYLVSDGSSR.P	1472.70210	2	4.88
			K.TSMESLIHHFK.L	1345.65740	2	3.25
			R.IIEQCLNK.M	1017.57080	2	3.53
71	Mitochondrial H⁺-ATP synthase alpha subunit	0.67 ± 0.11	K.AVDSLVIPIGR.G	1026.59480	2	2.90
			K.LIKEGDIVKR.T	1170.72100	2	3.10
			K.TGTAEMSSILEER.I	1439.66880	2	4.03
			K.TSIAIDTIINQK.R	1316.74260	2	4.32
			R.ILGADTSVDLEETGR.V	1575.78660	2	5.33
			R.ISVREPMQTGIK.A	1374.74150	2	2.96
			R.TGAIVDVPVGDPELLGR.V	1610.87540	2	4.35
			R.VGLKAPGIIPR.I	1120.72060	2	3.33
			R.VLSIGDGIAR.V	1000.57910	2	3.23
			R.VVDALGNAIDGK.G	1171.63230	2	4.45
			R.VVDALGNAIDGKGPVGSK.I	1696.92340	2	5.00
72	hydroxyacyl dehydrogenase, subunit B	0.70 ± 0.12	K.DNGIRPSSLEQMAK.L	1561.76440	3	3.16
			K.DQLLLGPTYATPK.V	1416.77390	2	3.47
			K.VGAPPLEK.F	810.47250	2	2.50
			R.ALAMGYKPK.A	994.53950	2	2.47
			R.DFIYVSQDPK.D	1211.59480	2	3.99
			R.LAAAFVSR.M	905.52090	2	3.75
73	citrate synthase	0.71 ± 0.08	R.FRGYSIPECQK.L	1384.69890	2	4.12
			K.TVVGQITVDMMYGGMR.G	1805.82360	2	5.54
			K.GLVYETSVLDPDEGIR.F	1762.88630	2	4.81
74	inner membrane protein	0.73 ± 0.14	K.AVDEAADALLK.A	1115.59480	2	3.39
			K.FEFEQDLSEK.L	1271.57960	2	3.75
			K.FVNQLKGESR.R	1177.63290	2	2.72
			K.LHSMIVDLDSVVK.K	1471.78300	2	4.71
			K.LHSMIVDLDSVVKK.V	1599.87800	3	4.29
			K.SLEDALNQTATVTR.Q	1518.77640	2	5.08
			K.TSSAEMPTIPLGSAVEAIR.V	1945.99040	2	4.84
			K.VVSQYHELVVQAR.D	1527.82830	2	4.72
			R.EIAGATPYITAAEEK.L	1563.79060	2	3.85
			R.GVYSEETLR.A	1053.52170	2	3.37
			R.KAVDEAADALLK.A	1243.68980	2	4.62
			R.QTITAQNAAVQAVK.A	1442.79670	2	4.70
			R.RKAVDEAADALLK.A	1399.79090	3	4.15
75	ubiquinol-cytochrome c reductase core protein 1	0.76 ± 0.16	K.EVESIGAHLNAYSTR.E	1646.81380	2	4.58
			K.NNGAGYFLEHLAFK.G	1580.78610	2	2.85
			R.IEEVDAQMVR.E	1205.58360	2	3.93
			R.IPLAEWESR.I	1100.57400	2	3.08
			R.NALISHLDGTTVCEDIGR.S	2068.04390	3	3.53
			R.RIPLAEWESR.I	1256.67510	2	3.25
			R.SGMFWLR.F	912.44020	2	2.88
			R.TDLTDYLSR.H	1083.53220	2	3.54
76	enolase 3, beta; Muscle specific enolase	0.77 ± 0.14	K.FMIELDGTENK.S	1312.60950	2	3.66
			K.TLGPALLEK.K	941.56720	2	2.63
			K.TLGPALLEK.L	1069.66210	2	2.51
			K.VVIGMDVAASEFYR.N	1572.77320	2	4.55
77	Electron transfer flavoprotein alpha-subunit	0.79 ± 0.20	K.CDKVVQDLCK.V	1264.66400	2	3.52
			K.LNVAPVSDIIEIK.S	1410.82080	2	4.14
			K.VKVFSVR.G	834.52010	2	2.07
			K.VVPEMTEILKK.K	1302.73430	2	2.06

			R.AAVDAGFVPNDMQVGQTGK.I	1920.91250	2	5.24
			R.GTSFEAAAASGGASSEK.A	1614.72470	2	5.43
			R.LGGEVSCLVAGTK.C	1290.70330	2	5.12
			R.TIYAGNALCTVK.C	1310.70840	2	4.24
78	MD-1 [Rattus norvegicus]	0.79 ± 0.11	R.KLFLDIAFVAK.G	1264.76690	2	2.77
79	isovaleryl Coenzyme A dehydrogenase	0.85 ± 0.17	K.AQEIDQSNDFK.N	1294.59150	2	3.69
			K.FVQENLAPK.A	1045.56820	2	3.50
			K.GVYVLMISGLDLER.L	1467.75170	2	4.36
			K.IGQFQLMQGK.M	1165.60390	2	4.07
			K.LYEIGGGTSEVR.R	1280.64870	2	4.17
			K.LYEIGGGTSEVRR.L	1436.74980	2	2.19
			K.TDLTAVPASR.G	1030.55330	2	3.01
			K.VPAANILSQESK.G	1256.68500	2	4.33
			R.AFNADFR.-	840.40040	2	2.71
			R.GITAFIVEK.D	977.56720	2	3.05
			R.GITAFIVEKDMPGFSTSK.K	1943.97880	2	4.66
80	voltage-dependent anion channel 2	0.86 ± 0.15	K.LTFDITTFSPNTGK.K	1428.70110	2	4.28
			K.LTLSALVDGK.S	1016.59920	2	3.16
			K.SCSGVEFSTSGSSNTDTGK.V	1907.82340	2	6.18
			K.YQLDPTASISAK.V	1293.66910	2	3.92
			R.SNFAVGYR.T	913.45320	2	2.52
81	dihydrolipoamide acetyltransferase	0.87 ± 0.15	K.GFDVASVMSVTLSCDHR.V	1896.88890	2	3.59
			K.GKISVNDFIK.A	1233.72070	2	3.45
			K.GLETIASDVVSLASK.A	1489.81140	2	5.02
			K.ISVNDFIK.A	1048.60430	2	2.37
			K.VPEANSSWMDTVIR.Q	1620.76920	2	4.16
			K.YLEKPVTMLL.-	1222.67570	2	2.80
82	short chain acyl-coenzyme A dehydrogenase	0.88 ± 0.23	K.EHLFPTSQVK.K	1185.62680	2	2.14
			K.ENLLGEPGMGFK.I	1307.63050	2	2.75
			K.LADMALALESAR.L	1276.65710	2	4.80
			R.ASTANLIFEDCR.I	1483.71560	2	4.12
			R.ITEIYEGTSEIQR.L	1538.77020	2	4.82
			R.LVIAGHLLR.S	991.64170	2	3.11
83	dnaK-type molecular chaperone grp75 precursor	0.89 ± 0.16	K.DAGQISGLNVLR.V	1242.68060	2	4.57
			K.LFEMAYK.K	917.44420	2	2.68
			K.LFEMAYKK.M	1045.53920	2	2.08
			K.MKETAENYLGHTAK.N	1608.76920	3	4.76
			K.SDIGEVILVGGMTR.M	1462.75750	2	4.38
			K.VQQTVDLDFGR.A	1290.68060	2	4.24
			R.ASNGDAWVEAHGK.L	1341.61870	2	2.49
			R.ETGVDLTKDNMALQR.V	1706.83830	2	3.56
			R.QAASSLQQASLK.L	1231.66460	2	3.69
			R.QAVTNPNTFYATK.R	1568.77090	2	4.12
			R.QAVTNPNTFYATKR.L	1724.87200	3	2.72
			R.TTPSVVAFTPDGER.L	1476.73340	2	3.99
84	acetyl-coenzyme A acetyltransferase 1	0.90 ± 0.14	K.AGIPKEEVK.E	970.55730	2	2.88
			K.DGLTDVYNK.I	1024.49510	2	3.33
			K.EVYMGNVIQGGEGQAPTR.Q	1921.90780	2	5.38
			K.GKPDVVVK.E	841.51470	2	2.14
			K.IHMGNCAENTAK.K	1361.62470	2	3.50
			K.LEDLIVK.D	829.50350	2	2.53
			K.LGTIAIQGAIEK.A	1213.71560	2	3.93
			K.YAIGSYTR.S	930.46850	2	2.63
			R.SKEAWDAGK.F	991.48490	2	3.25

85	Ubiquinol-cytochrome C reductase complex core protein 2	0.90 ± 0.28	K.AVAQGNLSSADVQAAK.N	1529.79240	2	5.43
			R.GNNTTSLLSQSVAK.G	1419.74	2	4.19
86	cytochrome c oxidase, subunit VIa, polypeptide 2	1.03 ± 0.23	K.GDHGGAGANTWR.L	1198.53540	2	3.40
87	mitochondrial aldehyde dehydrogenase	1.13 ± 0.16	K.EEIFGPVMQILK.F	1419.75570	2	3.57
			K.FKTIEEVVGR.A	1177.65810	2	3.44
			K.LGPALATGNVVVMK.V	1385.78260	2	4.38
			K.TIPIDGDFFSYTR.H	1531.74330	2	2.81
			K.VAEQTPLTALYVANLIK.E	1844.05330	2	5.35
			K.YGLAAAVFTK.D	1040.57810	2	4.02
			R.ELGEYGLQAYTEVK.T	1599.79060	2	4.98
			R.GYFIQPTVFGDVK.D	1470.76330	2	4.09
			R.TEQGPQVDETQFK.K	1506.70760	2	4.72
			R.TEQGPQVDETQFKK.I	1634.80260	2	4.54
			R.TFVQEDVYDEFVER.S	1775.81280	2	5.60
			R.VVGNPFDSR.T	990.50090	2	3.03
			88	Parvalbumin (calcium binding protein)	1.30 ± 0.48	K.AIGAFTAADSFDHK.K
K.AIGAFTAADSFDHKK.F	1578.79160	2				4.69
K.FFQMVGLK.K	985.51810	2				2.61
K.KFFQMVGLK.K	1113.61300	2				2.45
K.VFHILDKDK.S	1114.62610	2				3.11
89	heatshockprotein,mitochondrialprecursor(Hsp60)	1.33 ± 0.37	K.DRVTDALNATR.A	1231.63950	2	3.88
			K.IGIEIIR	785.51370	2	2.68
			K.IGIEIIR.A	941.61480	2	3.13
			K.LSDGVAVLK.V	901.53590	2	3.50
			K.SIDLKDKYK.N	1109.62060	2	2.84
			K.VGLQVVAVK.A	912.58820	2	3.49
			R.GYISPYFINTSK.G	1389.70540	2	4.07
90	dihydrolipoamide branched chain transacylase E2	1.46 ± 0.42	K.AQIMNVSWADHR.V	1530.71230	2	3.90
			K.LREELKPVALAR.G	1394.84840	2	3.48
			K.LSFMPFFLK.A	1145.60690	2	3.09
			K.QTGAILPPSPK.S	1108.63660	2	2.29
			R.ILKEDILNFLEK.Q	1474.85210	2	4.35
			R.SVFEIAMELNR.L	1324.65710	2	3.68
91	hypothetical protein FLJ10759	1.63 ± 0.41	K.GKNSQPLLLVGPDSEQA.-	1752.91320	2	4.26
			K.ILEAHVEAKEPR.A	1391.76470	3	2.80
			K.NSQPLLLVGPDSEQA.-	1567.79680	2	3.24
			K.SVAVLEHQLVEVEETVR.Q	1937.03440	2	5.84
			K.VLEEVADKPQTEFLMK.F	1892.96790	2	5.03
			R.ELSSLNSYLEQLR.Q	1551.80190	2	4.49
			R.MFLAALESSLDR.E	1368.68330	2	4.35
			R.WALGVMAADASR.R	1263.61560	2	4.00