Supplemental Table

Table S1. List of protein identification and gene ontological classification by LC-MS/MS

UniProt[a]	UniGene[b]	Protein identified	Gene name	pI[c]	MW (kDa)[d]
Catalytic activity					
F1S6Q7	Ssc:100523423	ATP synthase subunit delta, mitochondrial -like	ATP5D	5.25	17.5
F1RFH9	Ssc.55270	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	ATP2A1	5.29	109.1
F1SLR6	Ssc.5041	Putative ribosomal RNA methyltransferase NOP2	NOP2	9.06	90.2
Q5S1S4	Ssc.10960	Carbonic anhydrase 3	CA3	7.85	29.4
Q9GJT2	Ssc.217	S-formylglutathione hydrolase	ESD	7.02	31.5
F1RFU5	Ssc.3588	Aspartate aminotransferase	GOT2	8.73	24.1
P00355	Ssc.16135	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	8.35	35.8
F1RKI3	Ssc.100518898	histidine triad nucleotide-binding protein 1	HINT1	13.7	6.87
P00339	Ssc.50275	L-lactate dehydrogenase A chain	LDHA	36.6	8.07
Q9TSX9	Ssc.2979	Peroxiredoxin-6	PRDX6	6.01	25
A1X898	Ssc.97027	Procollagen-proline 2-oxoglutarate-4-dioxygenase	P4HA1	6.01	60.9
ATPase activity					
F1S6Q7	Ssc:100523423	ATP synthase subunit delta, mitochondrial -like	ATP5D	5.25	17.5
F1RFH9	Ssc.55270	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	ATP2A1	5.29	109.1
Oxidoreductase activity					
P00355	Ssc.16135	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	8.35	35.8
P00339	Ssc.50275	L-lactate dehydrogenase A chain	LDHA	8.07	36.6

Q9TSX9	Ssc.2979	Peroxiredoxin-6	PRDX6	6.01	25
A1X898	Ssc.97027	Procollagen-proline 2-oxoglutarate-4-dioxygenase	P4HA1	6.01	60.9
Cytoskeletal protein binding					
F1RHL9	Ssc.763	Alpha-actinin-2	ACTN2	5.45	103.7
F1SMN5	Ssc.46794	Filamin-C	FLNC	5.96	290.2
F1RH20	Ssc.83876	Myosin-binding protein C, fast-type	MYBPC2	6.55	127.6
F1RGK5	Ssc.51787	Tropomyosin alpha-3 chain	TPM3	4.75	28.9
Actin binding					
F1RHL9	Ssc.763	Alpha-actinin-2	ACTN2	5.45	103.7
F1SMN5	Ssc.46794	Filamin-C	FLNC	5.96	290.2
F1RH20	Ssc.83876	Myosin-binding protein C, fast-type	MYBPC2	6.55	127.6
F1RGK5	Ssc.51787	Tropomyosin alpha-3 chain	TPM3	4.75	28.9
Calcium ion binding					
F1S6Q7	Ssc:100523423	ATP synthase subunit delta, mitochondrial -like	ATP5D	5.25	17.5
F1RFH9	Ssc.55270	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	ATP2A1	5.29	109.1
F1RHL9	Ssc.763	Alpha-actinin-2	ACTN2	5.45	103.7
F1SKJ8	Ssc.26154	Parvalbumin 1	PVALB1	5.07	12.1
Structural constituent of muscle					
F1RHL9	Ssc.763	Alpha-actinin-2	ACTN2	5.45	103.7
F1RH20	Ssc.83876	Myosin-binding protein C, fast-type	MYBPC2	6.55	127.6

[a]UniProt: Accession number in the UniProt database. [b]UniGene: UniGene number from NCBI (National Center for Biotechnology Information) database. [c]pI: Isoelectric point of the protein. [d]MW (kDa): Molecular weight of the protein.

Table S2. List of protein identification and gene ontological classification by LC-MS/MS

UniProt[a]	UniGene[b]	Protein identified	Gene name	pI[c]	MW (kDa)[d]
Cytoskeletal protein binding					
F1SMN5	Ssc.46794	Filamin-C	FLNC	5.96	290.2
F1RH20	Ssc.83876	Myosin-binding protein C, fast-type	MYBPC2	6.55	127.6
F1RGK5	Ssc.51787	Tropomyosin alpha-3 chain	TPM3	4.75	28.9
Actin binding					
F1SMN5	Ssc.46794	Filamin-C	FLNC	5.96	290.2
F1RH20	Ssc.83876	Myosin-binding protein C, fast-type	MYBPC2	6.55	127.6
F1RGK5	Ssc.51787	Tropomyosin alpha-3 chain	TPM3	4.75	28.9
structural constituent of muscle					
F1RHL9	Ssc.763	Alpha-actinin-2	ACTN2	5.45	103.7
F1RH20	Ssc.83876	Myosin-binding protein C, fast-type	MYBPC2	6.55	`127.6

Table S3. List of protein identification and gene ontological classification by LC-MS/MS

UniProt[a]	UniGene[b]	Protein identified	Gene name	pI[c]	MW (kDa)[d]
Primary metabolic process					
F1S6Q7	Ssc:100523423	ATP synthase subunit delta, mitochondrial -like	ATP5D	5.25	17.5
F1RFH9	Ssc.55270	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	ATP2A1	5.29	109.1
F1SLR6	Ssc.5041	Putative ribosomal RNA methyltransferase NOP2	NOP2	9.06	90.2
F1RFU5	Ssc.3588	Aspartate aminotransferase	GOT2	8.73	24.1
P00355	Ssc.16135	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	8.35	35.8
P00339	Ssc.50275	L-lactate dehydrogenase A chain	LDHA	8.07	36.6
A1X898	Ssc.97027	Procollagen-proline 2-oxoglutarate-4-dioxygenase	P4HA1	6.01	60.9
Cellular metabolic process					
F1S6Q7	Ssc:100523423 Hs.418668	ATP synthase subunit delta, mitochondrial -like	ATP5D	5.25	17.5
F1RFH9	Ssc.55270	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	ATP2A1	5.29	109.1
F1SLR6	Ssc.5041	Putative ribosomal RNA methyltransferase NOP2	NOP2	9.06	90.2
F1RFU5	Ssc.3588	Aspartate aminotransferase	GOT2	8.73	24.1
P00355	Ssc.16135	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	8.35	35.8
P00339	Ssc.50275	L-lactate dehydrogenase A chain	LDHA	8.07	36.6
A1X898	Ssc.97027	Procollagen-proline 2-oxoglutarate-4-dioxygenase	P4HA1	6.01	60.9
Catabolic process					
F1S6Q7	Ssc:100523423 Hs.418668	ATP synthase subunit delta, mitochondrial -like	ATP5D	5.25	17.5
F1RFH9	Ssc.55270	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	ATP2A1	5.29	109.1

F1RFU5	Ssc.3588	Aspartate aminotransferase	GOT2	8.73	24.1
P00355	Ssc.16135	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	8.35	35.8
P00339	Ssc.50275	L-lactate dehydrogenase A chain	LDHA	8.07	36.6
Nitrogen compound metabolic process					
F1S6Q7	Ssc:100523423 Hs.418668	ATP synthase subunit delta, mitochondrial -like	ATP5D	5.25	17.5
F1RFH9	Ssc.55270	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	ATP2A1	5.29	109.1
F1SLR6	Ssc.5041	Putative ribosomal RNA methyltransferase NOP2	NOP2	9.06	90.2
F1RFU5	Ssc.3588	Aspartate aminotransferase	GOT2	8.73	24.1
A1X898	Ssc.97027	Procollagen-proline 2-oxoglutarate-4-dioxygenase	P4HA1	6.01	60.9
Oxidation reduction					
P00355	Ssc.16135	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	8.35	35.8
P00339	Ssc.50275	L-lactate dehydrogenase A chain	LDHA	8.07	36.6
A1X898	Ssc.97027	Procollagen-proline 2-oxoglutarate-4-dioxygenase	P4HA1	6.01	60.9