

Table S2. Skeletal muscle proteins separated and purified by 2DGE and identified by tandem mass spectrometry

Mitochondrial fraction of rat quadriceps muscles were prepared by differential centrifugation as described in the Methods. The mitochondrial pellets were used to perform 2DGE for protein purification. The protein serial number sequence is according to Figures 1 and 4. Proteins were identified by tandem mass spectrometry followed by Sequest database search. Proteins are listed with their identification parameters such as accession number, % amino acid (AA) coverage, sequest score and number of specific peptides obtained along with their sub-cellular location and function.

No	Protein name	Accession no	% AA coverage	Sequest Score	Unique Peptides	Subcellular location	Protein function
1	myosin heavy chain, skeletal muscle, adult 1	34870884	13.55	234.32	23	cytoskeleton	muscle contraction
2	myosin, light polypeptide 2	6981238	45.72	90.25	9	cytoskeleton	actin-dependent ATPase activity, calcium ion binding, motor activity
3	tropomodulin 4	34858039	15.94	60.25	6	cytoskeleton	muscle contraction
4	creatine kinase, muscle form	6978661	28.28	138.25	13	cytoplasm	reversibly catalyzes the transfer of phosphate between ATP and various phosphogens
5	Troponin C, skeletal muscle	34860691	30.90	40.26	4	cytoskeleton	regulation of muscle contraction
6	leucine zipper-EF-hand containing transmembrane protein 1	34878524	10.28	70.28	7	mitochondrion, plasma membrane	signal transduction, development
7	3-hydroxyacyl-CoA dehydrogenase type II	7387724	30.33	70.30	6	cytoplasm, mitochondrion, plasma membrane	lipid metabolism
8	coiled-coil-helix-coiled-coil-helixdomaincontaining3	34855114	21.54	80.27	8	mitochondrion	protein binding
9	NAD <sup>+</sup> -isocitrate dehydrogenase, gamma subunit	414185	9.52	48.20	4	mitochondrion	carbohydrate metabolism, tricarboxylic acid cycle
10	pyruvate dehydrogenase (lipoamide) beta	34869518	27.21	90.29	9	mitochondrion,	glucose metabolism, glycolysis, tricarboxylic acid cycle
11	striated muscle alpha tropomyosin	57406	35.26	70.25	7	cytoskeleton	cell motility, regulation of muscle contraction, regulation of heart contraction, fatty acid biosynthesis

12	KCRS_RAT creatine kinase, sarcomeric mitochondrial precursor	125313	11.10	80.22	7	mitochondrion	generation of precursor metabolites and energy, muscle contraction
13	cytochrome c oxidase subunit Vb	16758362	21.86	30.18	3	mitochondrial envelope	electron transport, respiratory gaseous exchange
14	Troponin T, fast skeletal muscle isoforms beta/alpha	136385	9.99	40.25	7	cytoskeleton	regulation of striated muscle contraction
15	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	34875396	9.25	30.26	3	mitochondrion, membrane	electron transport, transcription, regulation of transcription-DNA-dependent, ATP synthesis coupled proton transport, transcription from RNA polymerase II promoter
16	hypothetical protein MGC36907	34868312	4.08	10.22	1		
17	complement component 1 Q subcomponent-binding protein	34870494	5.38	10.24	1	mitochondrial matrix	immune response
18	DNA segment, Chr 10, Johns Hopkins University 81 expressed	27705010	24.22	60.24	6	cell wall, mitochondrion	protein binding
19	prohibitin	34851184	47.23	110.28	11	nucleus, mitochondrial inner membrane,	regulation of progression through cell cycle, DNA replication, signal transduction, histone deacetylation, regulation of apoptosis
20	acyl-Coenzyme A dehydrogenase, very long chain	6978435	6.66	50.28	5	mitochondrion	electron transport, lipid metabolism, fatty acid metabolism, fatty acid beta-oxidation, energy derivation by oxidation of organic compounds
21	malate dehydrogenase 2	13592145	37.39	120.27	11	mitochondrion, mitochondrial matrix	glycolysis, tricarboxylic acid cycle, malate metabolism, tricarboxylic acid cycle intermediate metabolism
22	LRP16 protein	21326475	4.2	10.19	2	mitochondrion	may play a role in cell proliferation
23	pyruvate dehydrogenase (lipoamide) alpha 1	34880551	21.09	80.22	8	extracellular space, mitochondrion	acetyl-CoA metabolism, glycolysis
24	calreticulin	11693172	15.5	60.31	6	endoplasmic reticulum, cytosol, nucleus	regulation of transcription, protein folding, protein export from nucleus, calcium ion homeostasis, regulation of apoptosis
25	NADP+-specific isocitrate dehydrogenase	34857317	39.01	70.26	6	mitochondrion	role in intermediary metabolism and energy production, carbohydrate metabolic process
26	heat shock cognate 71 kDa protein	34876476	9.72	50.24	5	cytoplasm	chaperone, response to unfolded protein, protein binding
27	NAD+-specific isocitrate dehydrogenase b subunit	34858691	19.73	80.23	8	mitochondrion	tricarboxylic acid cycle, isocitrate metabolism

28	ATP synthase subunit d	9506411	29.06	50.24	5	mitochondrion	ion transport, ATP synthesis coupled proton transport
29	peroxiredoxin 5 precursor	16758404	14.35	40.21	4	mitochondrion, peroxisome	inflammatory response, response to oxidative stress
30	hydroxyacyl-Coenzyme A dehydrogenase	18677763	12.50	90.27	9	mitochondrion	lipid metabolism, fatty acid metabolism, fatty acid beta-oxidation
31	mitochondrial aconitase	38541404	22.43	160.27	15	mitochondrion	generation of precursor metabolites and energy, tricarboxylic acid cycle, citrate metabolism
32	unnamed protein product	56691	27.60	70.26	7	mitochondrion	age-dependent response to reactive oxygen species, regulation of transcription from RNA polymerase II promoter, superoxide metabolism, cellular defense response
33	myosin, light polypeptide 3	6981240	38.38	60.26	6	cytoskeleton	muscle contraction
34	Succinyl-Co A ligase beta-chain, mitochondrial	34874487	11.02	40.29	4	mitochondrion	carbohydrate metabolism; tricarboxylic acid cycle
35	prolyl 4-hydroxylase, beta polypeptide	6981324	29.29	160.29	16	extracellular region, endoplasmic reticulum	protein folding, peptidyl-proline hydroxylation to 4-hydroxy-L-proline
36	electron-transfer-flavoprotein, beta polypeptide	27731305	12.58	30.18	3	mitochondrial matrix	electron transport
37	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kD	27667934	34.68	70.20	7	mitochondrial inner membrane	transfer of electrons from NADH to the respiratory chain.
38	Polymerase (RNA) II (DNA directed) polypeptide C	34851240	10.94	30.26	3	nucleus	transcription, transcription from RNA polymerase II promoter
39	Dihydrolipoamide succinyltransferase	266684	3.07	10.24	3	mitochondrion	generation of precursor metabolites and energy, tricarboxylic acid cycle, metabolism
40	alpha 1 actin precursor	4501881	12.9	40.32	4	cytoskeleton	muscle thin filament assembly, skeletal muscle fiber development
41	3-mercaptopyruvate sulfurtransferase	20304123	4.33	10.23	1	mitochondrial matrix	sulfate transport, cyanate catabolism, response to toxin
42	acetyl-Coenzyme A dehydrogenase, long-chain	6978431	14.56	50.31	5	mitochondrion	electron transport, lipid metabolism, fatty acid metabolism
43	ATPase, Ca <sup>++</sup> transporting, cardiac muscle, fast twitch 1	17157987	20.90	90.22	9	smooth endoplasmic reticulum	cation transport, calcium ion transport, regulation of striated muscle contraction, proton transport

44	enoyl Coenzyme A hydratase, short chain 1	17530977	21.97	70.25	7	mitochondrion	generation of precursor metabolites and energy, lipid metabolism, fatty acid metabolism, fatty acid beta-oxidation
45	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, delta subunit	20806153	13.32	20.24	2	mitochondrion, membrane fraction	ion transport, ATP synthesis coupled proton transport, proton transport, ATP biosynthesis
46	fast myosin alkali light chain	13487933	37.56	50.23	7	cytoskeleton	muscle development
47	H(+)-transporting ATP synthase	57029	22.78	78.22	8	mitochondrion, membrane fraction	ion transport, ATP synthesis coupled proton transport, proton transport, ATP biosynthesis
48	dihydrolipoamide dehydrogenase	27717159	11.47	50.33	5	cytoplasm, mitochondrion	electron transport
49	Tu translation elongation factor, mitochondrial	34859187	24.73	80.26	8	mitochondrion, membrane	protein biosynthesis, translational elongation, transport ,
50	NADH dehydrogenase (ubiquinone) Fe-S protein 6	9506913	20.11	30.22	3	mitochondrion	mitochondrial electron transport- NADH to ubiquinone
51	24-kDa subunit of mitochondrial NADH dehydrogenase	34877948	25.29	60.26	6	mitochondrion, membrane fraction	mitochondrial electron transport, NADH to ubiquinone, nervous system development
52	3-hydroxyisobutyrate dehydrogenase	34855881	23.86	100.30	10	mitochondrion	pentose-phosphate shunt, valine metabolism
53	gamma actin-like protein	34856512	14.94	50.25	5	cytoskeleton	structural constituent of cytoskeleton, sarcomere organization
54	Atp5c1 protein	37747914	22.07	88.21	7	membrane fraction, mitochondrion,	generation of precursor metabolites and energy, ion transport, ATP synthesis coupled proton transport, ATP biosynthesis
55	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, beta polypept	34862189	45.73	180.28	18	mitochondrion, integral to membrane,	generation of precursor metabolites and energy, ion transport, ATP synthesis coupled proton transport
56	creatine kinase, sarcomeric mitochondrial precursor	34853112	6.11	30.24	3	mitochondrion inner membrane	Reversibly catalyzes the transfer of phosphate between ATP and various phosphogens (e.g. creatine phosphate).
57	propionyl-Coenzyme A carboxylase, alpha polypeptide	34876107	18.82	90.26	9	mitochondrion; mitochondrial matrix	Carbohydrate metabolism; propanoate metabolism
58	voltage-dependent anion-selective channel protein 1	10720216	22.20	70.25	7	mitochondrial outer membrane	anion transport, apoptotic program, ion transport, apoptosis
59	cytochrome c-1	34866853	12.45	30.23	3	mitochondrion, membrane	electron transport
60	isocitrate dehydrogenase 3 (NAD <sup>+</sup> ) alpha	16758446	24.44	90.22	9	mitochondrion	carbohydrate metabolism, tricarboxylic acid cycle

61	fumarate hydratase 1	8393358	23.69	130.28	12	cytoplasm, mitochondrion	tricarboxylic acid cycle, fumarate metabolism, cell cycle, negative regulation of progression through cell cycle, fumarate metabolism
62	glutamate oxaloacetate transaminase 2	6980972	29.23	170.27	14	mitochondrion	amino acid metabolism, aspartate catabolism
63	NADH dehydrogenase (ubiquinone) flavoprotein 1	34861382	19.82	100.26	10	mitochondrial inner membrane	electron transport, mitochondrial electron transport-NADH to ubiquinone, generation of precursor metabolites and energy
64	lysophospholipase 1	6981362	22.27	40.21	44	membrane fraction	Lipid metabolism, fatty acid metabolism,
65	tropomyosin 4	14134107	4.92	40.25	4	cytoskeleton	cell motility, structural constituent of muscle, calcium dependent regulation of muscle contraction, Binds to actin filaments in muscle and non-muscle cells
66	ubiquinol-cytochrome c reductase binding protein	27677468	41.59	70.20	7	mitochondrial inner membrane	ubiquinol-cytochrome-c reductase activity, electron transport
67	NADH dehydrogenase 1 alpha subcomplex 10-like protein	34877665	14.95	50.25	5	membrane fraction, mitochondrion	generation of precursor metabolites and energy, nucleobase, nucleoside, nucleotide and nucleic acid metabolism
68	methylmalonate semialdehyde dehydrogenase gene	13591997	10.99	60.20	6	mitochondrion	pyrimidine nucleotide metabolism, valine metabolism, thymine metabolism
69	cytochrome c oxidase, subunit Va	24233541	17.93	38.23	4	mitochondrion	electron transport
70	NADH dehydrogenase (ubiquinone) Fe-S protein 2	34880923	12.76	40.24	4	membrane fraction, mitochondrion	electron transport, mitochondrial electron transport-NADH to ubiquinone
71	Mitochondrial H <sup>+</sup> -ATP synthase alpha subunit	38512279	21.99	110.27	11	membrane fraction, mitochondrion	ion transport, ATP synthesis coupled proton transport, proton transport,ATP biosynthesis
72	hydroxyacyl dehydrogenase, subunit B	19424338	13.18	70.20	6	mitochondrial envelope	lipid metabolism, fatty acid metabolism, fatty acid beta-oxidation
73	citrate synthase	18543177	9.28	30.25	3	cytoplasm, mitochondrion	tricarboxylic acid cycle, main pathways of carbohydrate metabolism
74	inner membrane protein	34855983	20.94	128.27	13	mitochondrial inner membrane	critical organizer of the mitochondrial cristae morphology and thus indispensable for normal mitochondrial function
75	ubiquinol-cytochrome c reductase core protein 1	34866355	18.08	80.23	8	mitochondrion, membrane	oxidative phosphorylation, aerobic respiration, electron transport, transport
76	enolase 3, beta; Muscle specific enolase	6978811	8.28	40.23	4	phosphopyruvate	glycolysis

						hydratase complex	
77	electron transfer flavoprotein alpha-subunit	27720225	30.22	80.27	8	mitochondrial matrix	electron transport
78	MD-1 [Rattus norvegicus]	34875250	3.43	10.14	1	plasma membrane	apoptosis, inflammatory response, humoral immune response, signal transduction, cell proliferation, immune response
79	isovaleryl Coenzyme A dehydrogenase	6981112	24.31	110.23	11	mitochondrial matrix	electron transport, metabolism
80	voltage-dependent anion channel 2	13786202	20.26	50.31	5	mitochondrial outer membrane	anion transport, ion transport
81	dihydrolipoamide acetyltransferase	220838	12.72	60.25	6	mitochondrion	acetyl-CoA biosynthesis, glycolysis
82	short chain acyl-coenzyme A dehydrogenase	11968090	16.91	60.24	6	mitochondrion	electron transport, lipid metabolism, fatty acid metabolism, fatty acid beta-oxidation, generation of precursor metabolites and energy
83	dnaK-type molecular chaperone grp75 precursor	2119726	18.86	118.24	12	mitochondrion	Control of cell proliferation and cellular aging. It may also act as a chaperone
84	acetyl-coenzyme A acetyltransferase 1	8392836	21.73	80.29	9	mitochondrion	catalyzes the conversion of 2 acetyl-CoA molecules to acetoacetyl-CoA plus CoA
85	ubiquinol-cytochrome C reductase complex core protein 2	27679580	3.16	10.27	2	mitochondrial inner membrane	electron transport, oxidative phosphorylation, proteolysis, aerobic respiration
86	cytochrome c oxidase, subunit VIa, polypeptide 2	6978691	12.48	10.17	1	mitochondrial envelope	electron transport, generation of precursor metabolites and energy
87	mitochondrial aldehyde dehydrogenase	25990263	29.36	120.28	12	mitochondrion	carbohydrate metabolism, alcohol metabolism, metabolism
88	parvalbumin (calcium binding protein)	11968064	30.41	50.23	5	cytoplasm	calcium-binding protein is involved in muscle relaxation
89	heat shock protein, mitochondrial precursor (Hsp60)	34876438	11.13	128.20	7	mitochondrion matrix	mitochondrial protein import and macromolecular assembly, facilitates correct folding of imported proteins.
90	dihydrolipoamide branched chain transacylase E2	34859889	14.67	60.22	6	mitochondrion matrix	amino acid metabolism
91	hypothetical protein FLJ10759	34860175	21.99	80.29	8	intracellular	transcription regulator activity