A3.4.2a. List of proteins identified with 2peptides in mitochondrial fractions of CVB3 infected ANT-OE rats compared to infected WT rats

gi Number	Protein Annotation	No. of Peptides	Mol.Wt (Da)	Seq. Coverage (%)
17105350	2,4-dienoyl CoA reductase 1, mitochondrial	5	36203.8	22.7
11693170	2-oxoglutarate carrier	11	34251.8	39.2
13242293	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	2	34191.8	11.1
55742813	3-hydroxybutyrate dehydrogenase (heart, mitochondrial)	6	38333.0	21.5
83977457	3-hydroxyisobutyrate dehydrogenase	6	35302.7	27.2
61556993	3-hydroxyisobutyryl-Coenzyme A hydrolase	3	34524.9	14.5
20304123	3-mercaptopyruvate sulfurtransferase	2	32940.2	9.8
8392836	acetyl-coenzyme A acetyltransferase 1	11	44709.0	42.2
18426866	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	17	41870.9	54.9
6978431	acetyl-Coenzyme A dehydrogenase, long-chain	12	47872.9	27.2
8392833	acetyl-coenzyme A dehydrogenase, medium chain	9	46555.4	26.8
40538860	aconitase 2, mitochondrial	22	85433.4	38.8
25742739	acyl-CoA synthetase long-chain family member 1	18	78178.7	35.1
11968090	acyl-coenzyme A dehydrogenase, short chain	9	44967.6	32.4
6978435	acyl-Coenzyme A dehydrogenase, very long chain	17	70749.3	37.4
8394149	acyl-Coenzyme A oxidase 1, palmitoyl	4	74678.8	11.6
61889092	adenylate kinase 1	2	21583.8	13.4
13591872	adenylate kinase 2 isoform b	2	46105.7	6.6
6978479	adenylate kinase 3	3	25438.3	17.6
8392885	adenylate kinase 3-like 1	4	25202.9	32.7
13027426	ADP-ribosylation factor-like 6 interacting protein 5	2	21548.6	16.0
19705431	albumin	2	68718.7	3.6
14192933	aldehyde dehydrogenase 2	10	56488.4	25.6

gi Number	Protein Annotation	No. of Peptides	Mol.Wt (Da)	Seq. Coverage (%)
13929028	aldehyde dehydrogenase family 3, subfamily A2	2	54081.6	6.6
13591997	aldehyde dehydrogenase family 6, subfamily A1	12	57807.6	32.7
6978487	aldolase A	3	39351.9	27.7
57527204	alpha-ETF	12	34951.4	53.8
31543764	alpha-spectrin 2	11	284595.3	7.8
9845234	annexin A2	5	38678.2	22.1
13994159	annexin A6	6	75754.2	14.6
6978515	apolipoprotein A-I	2	30062.1	15.1
20301954	apolipoprotein E	3	36037.8	16.1
19705465	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	9	28868.8	41.0
9506411	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	7	18763.4	62.1
17978459	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	4	8254.6	62.0
47058994	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	6	11460.5	60.2
40538742	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1.	24	59753.6	52.8
54792127	ATP synthase, H+ transporting, mitochondrial F1 complex, beta subunit	33	56353.6	77.5
20806153	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit precursor	2	17595.1	13.7
39930503	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma subunit	9	32996.0	29.5
77917538	ATPase family, AAA domain containing 3A	4	66759.0	9.5
6978543	ATPase, Na+/K+ transporting, alpha 1 polypeptide	8	113054.3	19.6
6978549	ATPase, Na+/K+ transporting, beta 1 polypeptide	2	35233.6	8.2
56119152	ATP-binding cassette, sub-family B (MDR/TAP), member 8	3	77770.4	8.7
47058990	ATP-binding cassette, sub-family B, member 7, mitochondrial precursor	5	82557.8	11.3
19705527	basic leucine zipper and W2 domains 2	2	48049.2	7.2
7709992	basigin	3	29585.5	14.3

gi Number	Protein Annotation	No. of Peptides	Mol.Wt (Da)	Seq. Coverage (%)
61556754	B-cell receptor-associated protein 37	10	33312.4	42.5
56090628	BCS1-like	3	47393.2	13.9
40445397	beta-glo	3	16037.5	35.4
19424244	brain protein 44-like	3	12454.6	31.2
11693174	branched chain aminotransferase 2, mitochondrial	6	44275.5	20.1
109461422	branched chain ketoacid dehydrogenase E1, alpha polypeptide	8		
20302073	cadherin 13	3	78085.6	6.9
11693172	calreticulin	3	47995.5	15.6
76563946	calsequestrin 2	10	49402.6	33.3
31542380	carboxylesterase 3	3	62147.2	10.8
51854229	carnitine acetyltransferase	3	70800.7	8.8
6978703	carnitine palmitoyltransferase 1b	10	88218.5	16.1
6978705	carnitine palmitoyltransferase 2	16	74110.3	31.3
6978607	catalase	7	59757.2	17.8
42476045	cathepsin D	4	44622.6	14.0
61557218	chaperone, ABC1 activity of bc1 complex like	6	72225.6	18.6
21489987	chloride ion pump-associated 55 kDa protein	2	56287.6	7.7
18543177	citrate synthase	13	51866.8	38.4
9506497	clathrin, heavy polypeptide (Hc)	3	191598.7	3.4
18158449	coatomer protein complex, subunit beta 1	2	107011.0	3.0
58865534	coenzyme Q6 homolog	3	51495.8	12.4
48675371	complement component 1, q subcomponent binding protein	5	30996.9	37.3
31542401	creatine kinase, brain	2	42712.2	8.4
60678254	creatine kinase, mitochondrial 1, ubiquitous	3	46961.7	7.4

gi Number	Protein Annotation	No. of Peptides	Mol.Wt (Da)	Seq. Coverage (%)
6978661	creatine kinase, muscle	11	43018.9	41.2
16905067	crystallin, alpha B	7	20088.8	55.4
11560046	cytochrome b-5	2	15355.1	24.6
13399338	cytochrome b5, outer mitochondrial membrane isoform	4	16264.9	51.4
58615679	cytochrome c oxidase subunit I	2	56845.0	4.9
58615680	cytochrome c oxidase subunit II	6	25928.3	23.8
8393180	cytochrome c oxidase subunit IV isoform 1	7	19514.6	46.7
16758362	cytochrome c oxidase subunit Vb	4	13914.9	36.4
24233541	cytochrome c oxidase, subunit Va	6	16129.5	52.1
9506509	cytochrome c oxidase, subunit VIc	2	7316.5	35.4
11968118	desmin	8	53456.7	31.3
20302049	diaphorase 1	3	34174.6	16.3
40786469	dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex)	6	54038.1	21.0
109484674	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	10	44784.5	8.3
55742725	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	6	48925.4	17.2
16924002	DJ-1 protein	3	19974.2	32.3
8393243	dodecenoyl-coenzyme A delta isomerase	10	32254.4	45.7
67846074	EH-domain containing 2	9	61237.5	25.6
21326447	EH-domain containing 4	5	61467.6	14.8
51948412	electron-transfer-flavoprotein, beta polypeptide	7	27687.4	42.0
52138635	electron-transferring-flavoprotein dehydrogenase	15	68164.1	29.5
77917570	endonuclease G	3	32267.7	13.6
109468300	enolase 1, alpha	4	33056.1	21.5
12018256	enoyl coenzyme A hydratase 1, peroxisomal	9	36201.7	40.1
17530977	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	8	31516.4	33.8

gi Number	Protein Annotation	No. of Peptides	Mol.Wt (Da)	Seq. Coverage (%)
47058982	erythroid spectrin beta	8	246328.6	6.8
51948422	es1 protein	4	28172.6	24.4
61556967	eukaryotic translation elongation factor 1 delta	2	72127.6	7.4
8393296	eukaryotic translation elongation factor 2	2	95284.0	4.0
16758094	fatty acid binding protein 4	2	16494.3	16.7
56797757	fibrinogen, alpha polypeptide	3	86656.9	4.9
61098186	fibrinogen, gamma polypeptide	2	49651.7	9.8
58865930	fragile X mental retardation gene 1, autosomal homolog	2	63947.4	5.3
8393358	fumarate hydratase 1	11	54463.9	40.6
16758432	G elongation factor	2	83770.1	2.9
6978896	gap junction membrane channel protein alpha 1	3	43031.4	14.4
46485440	glucose phosphate isomerase	2	62827.0	5.4
8393322	glucose regulated protein, 58 kDa	6	56589.4	14.7
6980956	glutamate dehydrogenase 1	13	61415.9	31.9
6980970	glutamate oxaloacetate transaminase 1	4	46328.6	17.4
6980972	glutamate oxaloacetate transaminase 2	12	47314.3	40.7
30520381	glutathione peroxidase 1	3	22464.4	19.9
31077128	glutathione S-transferase, mitochondrial	5	25493.0	40.7
28933457	glutathione S-transferase, mu 2	2	25702.6	19.3
13540622	glypican 1	3	61734.2	10.9
13591955	guanine nucleotide binding protein, alpha inhibiting 2	2	40499.0	12.1
18543331	guanine nucleotide binding protein, beta polypeptide 2-like 1	2	35094.8	7.9
60097941	haptoglobin	2	38563.2	8.4
13162363	heart fatty acid binding protein	5	14774.7	42.1

gi Number	Protein Annotation	No. of Peptides	Mol.Wt (Da)	Seq. Coverage (%)
6981052	heat shock 10 kDa protein 1	4	10875.6	38.2
14010865	heat shock 27kDa protein 1	2	22821.6	14.6
25742763	heat shock 70kD protein 5	10	72347.0	28.1
11560024	heat shock protein 1 (chaperonin)	7	60965.5	13.6
28467005	heat shock protein 1, alpha	2	84814.9	3.8
20302069	heat shock protein, alpha-crystallin-related, B6	3	17504.9	27.2
6981010	hemoglobin alpha 1 chain	6		0.0
17985949	hemoglobin beta chain complex	4	15979.4	27.9
16923998	heterogeneous nuclear ribonucleoprotein K	3	50976.2	10.6
6981022	hexokinase 1	8	102408.0	14.1
31077132	histidine rich calcium binding protein	3	86632.4	8.5
13994225	hydroxysteroid (17-beta) dehydrogenase 10	8	27249.6	55.9
83642822	hypothetical protein LOC288772	4	23249.7	26.1
58585236	hypothetical protein LOC293113	3	21657.3	14.8
62078677	hypothetical protein LOC303606	2	55732.7	8.7
109497479	hypothetical protein LOC304542	3	117181.5	29.5
51948490	hypothetical protein LOC309381	4	62879.1	13.4
53850640	hypothetical protein LOC311430	4	53804.5	13.4
71043858	hypothetical protein LOC313200	5	58343.9	13.0
62078929	hypothetical protein LOC316008	2	42308.1	8.2
62078943	hypothetical protein LOC317191	6	28237.6	33.9
62945278	hypothetical protein LOC360975	18	116295.7	33.2
62079055	hypothetical protein LOC361596	16	50967.3	41.2
56090401	hypothetical protein LOC362946	2	24396.9	13.3
62945328	hypothetical protein LOC498174	5	32941.7	22.4

gi Number	Protein Annotation	No. of Peptides	Mol.Wt (Da)	Seq. Coverage (%)
78214350	hypothetical protein LOC498909	6	35145.6	30.1
72255551	hypothetical protein LOC500419	3	35400.5	19.0
77993368	hypothetical protein LOC619561	5	67886.5	14.3
77404375	hypoxia up-regulated 1	2	23446.2	5.4
77917546	inner membrane protein, mitochondrial	18	67176.8	40.7
16758446	isocitrate dehydrogenase 3 (NAD+) alpha	8	39613.7	31.4
55926203	isocitrate dehydrogenase 3 (NAD+) beta	5	42353.9	20.3
54020666	isocitrate dehydrogenase 3, gamma	4	42850.5	20.6
6981112	isovaleryl Coenzyme A dehydrogenase	8	46435.5	26.4
83816931	junctophilin 2	3	74258.5	9.1
57012436	keratin 10	2	56505.0	9.3
62543563	kynurenine aminotransferase III	2	51044.1	8.8
17105336	L-3-hydroxyacyl-Coenzyme A dehydrogenase	7	34447.8	50.0
6981146	lactate dehydrogenase B	7	36612.4	29.6
8393693	laminin receptor 1	4	32824.1	18.0
54400736	leucine zipper-EF-hand containing transmembrane protein 1	7	83059.8	15.0
56605990	leucine-rich protein 157	6	156652.8	7.2
6981168	lipoprotein lipase	3	53082.4	10.5
68341999	low molecular mass ubiquinone-binding protein	3	9849.4	34.1
21326475	LRP16 protein	2	27078.2	13.6
40254785	lysosomal membrane glycoprotein 2	2	45143.8	4.6
15100179	malate dehydrogenase 1, NAD (soluble)	3	36483.1	13.5
42476181	malate dehydrogenase, mitochondrial	14	35683.6	50.0
16758230	malonyl-CoA decarboxylase	2	54609.9	6.1
56605654	metaxin 2	5	29718.2	30.4

gi Number	Protein Annotation	No. of Peptides	Mol.Wt (Da)	Seq. Coverage (%)
57528264	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	9	79329.7	21.8
58865926	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	8	61517.2	21.3
66730360	microtubule-associated protein 4	4	110300.8	7.8
48675862	mitochondrial acyl-CoA thioesterase 1	4	49629.1	31.8
20302061	mitochondrial ATP synthase, O subunit	9	23397.6	57.3
18677763	mitochondrial trifunctional protein, alpha subunit	20	82512.9	46.0
19424338	mitochondrial trifunctional protein, beta subunit	18	51414.5	47.4
11024650	myoglobin	5	17156.8	41.6
8393804	myosin heavy chain, polypeptide 6	10	223508.4	25.4
8393807	myosin heavy chain, polypeptide 7	8	223083.0	7.4
6981240	myosin, light polypeptide 3	5	22156.2	48.5
40254747	N-acylsphingosine amidohydrolase 1	3	44443.2	11.4
6981260	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 5	5	13411.8	61.2
47058992	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11	4	14854.1	59.6
57164133	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	4	14358.8	32.5
53850628	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa	27	79412.3	47.9
58865384	NADH dehydrogenase (ubiquinone) Fe-S protein 2	17	52561.5	52.9
68341995	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	8	19740.6	52.0
72086149	NADH dehydrogenase (ubiquinone) Fe-S protein 5b	3	12699.8	29.2
56606108	NADH dehydrogenase (ubiquinone) Fe-S protein 7	4	23945.0	30.7
55741424	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	17	50731.0	47.8
51092268	NADH dehydrogenase (ubiquinone) flavoprotein 2	6	27378.3	36.3
58615677	NADH dehydrogenase subunit 1	3	36145.3	11.6
58615678	NADH dehydrogenase subunit 2	2	38652.6	9.5
58615686	NADH dehydrogenase subunit 4	5	51782.8	17.6

gi Number	Protein Annotation	No. of Peptides	Mol.Wt (Da)	Seq. Coverage (%)
58615687	NADH dehydrogenase subunit 5	4	68618.0	9.9
61557127	nicotinamide nucleotide transhydrogenase	29	113869.4	38.6
19424278	N-myc downstream regulated gene 2	3	39270.5	19.0
50582542	nucleolar protein 3	2	24576.7	17.2
62078483	OCIA domain containing 1	3	27659.1	27.5
11968126	peptidylprolyl isomerase B	3	22802.4	16.8
11968132	peroxiredoxin 3	4	28321.4	21.0
16758404	peroxiredoxin 5 precursor	4	22178.7	26.3
55741520	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase	4	43021.4	23.5
13928796	peroxisomal membrane protein 2	2	22577.1	15.5
8393910	phosphatidylethanolamine binding protein	2	20801.4	17.6
8393948	phosphoglycerate mutase 2	4	28755.0	24.9
12083675	phospholamban	2	6094.5	21.2
109477815	PREDICTED: hypothetical protein	6		
109486605	PREDICTED: hypothetical protein	2		
109511985	PREDICTED: hypothetical protein	5		
109460535	PREDICTED: NADH dehydrogenase (ubiquinone) Fe-S protein 6	2		
109490241	PREDICTED: prohibitin	3	29820.1	58.8
59709473	PREDICTED: similar to	6	74207.8	1.6
109480482	PREDICTED: similar to 13kDa differentiation-associated protein	8		
109502826	PREDICTED: similar to 60S acidic ribosomal protein P2	3		
109468951	PREDICTED: similar to acetyl-CoA synthetase 2-like	8		
109489498	PREDICTED: similar to Actin, cytoplasmic 2 (Gamma-actin)	4		
109505063	PREDICTED: similar to actinin alpha 2	6		
109496520	PREDICTED: similar to Acyl carrier protein, mitochondrial precursor (ACP) (NADH-ubiquinone oxidoreductase 9.6 kDa subunit) (CI-SDAP)	2		

gi Number	Protein Annotation	No. of Peptides	Mol.Wt (Da)	Seq. Coverage (%)
109459862	PREDICTED: similar to AHNAK nucleoprotein isoform 1	4		
109475727	PREDICTED: similar to aldehyde dehydrogenase 4 family, member A1	5	164010.0	4.6
109507354	PREDICTED: similar to aldehyde dehydrogenase family 7, member A1	2	92446.5	4.5
109487472	PREDICTED: similar to alpha 3 type VI collagen isoform 1 precursor	2	343536.5	4.2
109511497	PREDICTED: similar to Amine oxidase	11		
109503539	PREDICTED: similar to ankyrin 1, erythroid	4	79854.7	21.7
109487359	PREDICTED: similar to aortic preferentially expressed gene 1	2		
109501003	PREDICTED: similar to ATP binding cassette, sub-family A (ABC1), member 13	2		
109474139	PREDICTED: similar to Bcl-2-like 13 protein (Mil1 protein) (Bcl-rambo)	2		
109498897	PREDICTED: similar to Brain protein 44 (0-44 protein)	2	14257.9	43.3
109482276	PREDICTED: similar to C33H5.19	2	24912.0	9.4
109508252	PREDICTED: similar to C50H11.1	2	92446.5	4.5
109473096	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	14		
109476122	PREDICTED: similar to CG15738-PA	2		
109491914	PREDICTED: similar to CG7319-PC, isoform C	2		
109471895	PREDICTED: similar to coiled-coil-helix-coiled-coil-helix domain containing 3	6	34546.1	3.0
109509326	PREDICTED: similar to Collagen alpha-1(VI) chain precursor	2		
109461624	PREDICTED: similar to Cytochrome c oxidase polypeptide VIIa-heart, mitochondrial precursor isoform 1	2		
109477873	PREDICTED: similar to cytochrome c oxidase subunit VIIa polypeptide 2-like	3		
109499760	PREDICTED: similar to cytochrome c oxidase, subunit 7a 3	2		
109461675	PREDICTED: similar to cytochrome c oxidase, subunit VIb polypeptide 1	2		
109488076	PREDICTED: similar to Cytochrome c, somatic	2		
109482351	PREDICTED: similar to cytochrome c-1	11		
34862422	PREDICTED: similar to cytoskeleton-associated protein 4	2		

gi Number	Protein Annotation	No. of Peptides	Mol.Wt (Da)	Seq. Coverage (%)
109511865	PREDICTED: similar to dystrophin, muscular dystrophy	4	298214.2	2.6
109459775	PREDICTED: similar to EH-domain-containing protein 1 (mPAST1)	8		
109501906	PREDICTED: similar to F11C1.5a	4	226223.6	2.6
109479451	PREDICTED: similar to FK506-binding protein 3 (Peptidyl-prolyl cis-trans isomerase)	2	51144.8	6.6
109508552	PREDICTED: similar to Glutaryl-CoA dehydrogenase, mitochondrial precursor (GCD)	3		
19924091	PREDICTED: similar to glycoprotein, synaptic 2	2	502087.9	0.3
109485542	PREDICTED: similar to Gup1, glycerol uptake/transporter homolog	6		
109459168	PREDICTED: similar to Hemoglobin beta-2 subunit (Hemoglobin beta-2 chain)	2		
109465582	PREDICTED: similar to inorganic pyrophosphatase 2	2		
109461122	PREDICTED: similar to isochorismatase domain containing 2 isoform 1	2		
109499222	PREDICTED: similar to isoleucine-tRNA synthetase 2, mitochondrial	3	112666.3	6.8
109498845	PREDICTED: similar to Laminin gamma-1 chain precursor (Laminin B2 chain)	3		
109465423	PREDICTED: similar to Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex	3		
109479714	PREDICTED: similar to Maleylacetoacetate isomerase (Glutathione S-transferase zeta 1) isoform 4	2		
109462394	PREDICTED: similar to malic enzyme 3, NADP(+)-dependent, mitochondrial	4		
109505493	PREDICTED: similar to Methylglutaconyl-CoA hydratase, mitochondrial precursor	2		
109458869	PREDICTED: similar to Methylmalonyl-CoA epimerase, mitochondrial precursor	3		
109485854	PREDICTED: similar to Methylmalonyl-CoA mutase, mitochondrial precursor (MCM)	3		
109468417	PREDICTED: similar to Mitochondrial carrier homolog 2	6		
109459780	PREDICTED: similar to mitochondrial ribosomal protein L49	2		
109464325	PREDICTED: similar to mitochondrial ribosomal protein S36	3		
109503558	PREDICTED: similar to myomesin 2	4	79854.7	21.7
109468428	PREDICTED: similar to Myosin-binding protein C, cardiac-type (Cardiac MyBP-C)	9		
109481899	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	5		
109507159	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	4		

gi Number	Protein Annotation	No. of Peptides	Mol.Wt (Da)	Seq. Coverage (%)
109482558	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	4	52485.6	2.5
109481717	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	3		
109468091	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	2		
109474252	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	21	42559.2	65.3
109487205	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	2		
109463999	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	6		
109466500	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	3		
109476260	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa isoform 1	2		
109508678	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	4		
109480810	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	3		
109470303	PREDICTED: similar to NADH dehydrogenase (ubiquinone) Fe-S protein 3	7		
109463301	PREDICTED: similar to NADH dehydrogenase (ubiquinone) Fe-S protein 8	8		
109511448	PREDICTED: similar to NADH-ubiquinone oxidoreductase ESSS subunit	5		
109471761	PREDICTED: similar to NADH-ubiquinone oxidoreductase MLRQ subunit (Complex I-MLRQ)	4	34546.1	3.0
109487851	PREDICTED: similar to NADH-ubiquinone oxidoreductase PDSW subunit (Complex I-PDSW) isoform 1	6		
109491901	PREDICTED: similar to Polymerase I and transcript release factor	5		
109465075	PREDICTED: similar to pre-B-cell leukemia transcription factor interacting protein 1	3		
109502895	PREDICTED: similar to Propionyl-CoA carboxylase alpha chain	9	79854.7	21.7
109469545	PREDICTED: similar to prostaglandin E synthase 2	7		
109509802	PREDICTED: similar to Protein C10orf70	3		
109501205	PREDICTED: similar to Protein C14orf166	2		
109486538	PREDICTED: similar to Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial precursor	2		
109468465	PREDICTED: similar to pyruvate dehydrogenase complex, component X	6		

gi Number	Protein Annotation	No. of Peptides	Mol.Wt (Da)	Seq. Coverage (%)
109503594	PREDICTED: similar to Pyruvate dehydrogenase E1 component alpha subunit, somatic form	4		
109511883	PREDICTED: similar to Ras-related protein Rab-1B	3	298214.2	2.6
109509653	PREDICTED: similar to Reticulon-4-interacting protein 1, mitochondrial precursor	3		
109461173	PREDICTED: similar to retinol dehydrogenase 13 (all-trans and 9-cis)	2		
109458180	PREDICTED: similar to ribosomal protein S5	2		
62821815	PREDICTED: similar to ribosomal protein S8	2		
109487785	PREDICTED: similar to sarcalumenin	16		
109502999	PREDICTED: similar to sarcolemma associated protein	3	79854.7	21.7
34854800	PREDICTED: similar to solute carrier family 25 (mitochondrial carrier, Aralar), member 12	6	27182.7	46.5
109468291	PREDICTED: similar to solute carrier family 25 (mitochondrial carrier, Aralar), member 12	4	33056.1	21.5
109507099	PREDICTED: similar to Stress-70 protein, mitochondrial precursor (75 kDa glucose regulated protein)	13		
109475694	PREDICTED: similar to succinate dehydrogenase Ip subunit	9		
109505751	PREDICTED: similar to Succinate semialdehyde dehydrogenase (NAD(+)-dependent succinic semialdehyde dehydrogenase)	4		
109502719	PREDICTED: similar to succinate-Coenzyme A ligase, ADP-forming, beta subunit	12		
109473908	PREDICTED: similar to succinate-Coenzyme A ligase, GDP-forming, beta subunit	7		
109474844	PREDICTED: similar to Talin-1	2	42559.2	65.3
109497169	PREDICTED: similar to tetratricopeptide repeat domain 11	3	49613.7	4.1
109505773	PREDICTED: similar to thioesterase superfamily member 2	3		
109470872	PREDICTED: similar to Thioredoxin domain-containing protein 13 precursor	2		
109461526	PREDICTED: similar to translocase of inner mitochondrial membrane 50 homolog isoform 1	3		
109462948	PREDICTED: similar to tripartite motif protein 50	10		
109459347	PREDICTED: similar to Tu translation elongation factor, mitochondrial	10		
109458613	PREDICTED: similar to ubiquinol-cytochrome c reductase binding protein	4		
109507853	PREDICTED: similar to vacuolar protein sorting 35	2	92446.5	4.5

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109466453	PREDICTED: similar to very-long-chain acyl-CoA dehydrogenase VLCAD homolog isoform 1	6		
109501157	PREDICTED: similar to Vinculin (Metavinculin)	4		
109479478	PREDICTED: similar to Y45G12B.3	3	51144.8	6.6
25742626	programmed cell death 8	12	66722.5	30.7
6981324	prolyl 4-hydroxylase, beta polypeptide	11	56864.2	34.1
8393913	propionyl Coenzyme A carboxylase, beta polypeptide	9	58626.2	24.0
29789096	protein kinase, cAMP-dependent, regulatory, type 2, alpha	2	45540.3	8.2
56090293	pyruvate dehydrogenase (lipoamide) beta	8	38982.1	32.6
61889071	RAB10, member RAS oncogene family	2	22540.9	11.5
13929006	RAB2, member RAS oncogene family	2	23535.5	20.3
12083607	ribosomal protein S14	2	16258.7	15.9
71361655	ribosomal protein, mitochondrial, L12	2	29441.4	9.4
54633307	RN protein	12	111248.0	21.6
62078699	saccharopine dehydrogenase (putative)	5	47088.2	21.4
51036655	serine protease inhibitor alpha 1	2	46121.8	4.9
34328536	single-stranded DNA binding protein 1	2	17454.9	19.9
6981542	solute carrier family 16 (monocarboxylic acid transporters), member 1	2	53238.2	6.5
52138624	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	6	33070.9	19.3
20806141	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	9	39445.1	33.1
32189355	solute carrier family 25, member 4	6	32989.4	22.5
50054324	solute carrier family 27 (fatty acid transporter), member 1	3	71347.1	7.0
76443687	solute carrier family 4, member 1	2	103243.8	10.7
51948454	sorting and assembly machinery component 50 homolog	8	51960.2	25.2
58865394	spectrin alpha 1	3	276621.7	3.0
61557085	spectrin beta 2	4	273586.5	2.7

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50054162	statin-like	5	50454.2	23.1
50356003	sterol carrier protein 2	4	58827.3	8.8
72255527	stomatin (Epb7.2)-like 2	4	38413.9	23.5
18426858	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	25	71615.2	46.6
53850596	succinate dehydrogenase complex, subunit C	4	18202.7	30.8
38454310	succinate dehydrogenase complex, subunit D, integral membrane protein	2	16975.8	10.7
16758586	succinate-CoA ligase, GDP-forming, alpha subunit	4	35031.6	22.2
8394328	superoxide dismutase 1	3	15911.7	24.7
8394331	superoxide dismutase 2	5	24674.1	32.0
57528682	thiosulfate sulfurtransferase	2	33406.7	12.5
47058998	TOM22 protein	2	15490.6	16.2
61556986	transferrin	6	76395.2	12.5
21955146	translocase of inner mitochondrial membrane 13 homolog	3	10457.9	36.8
47058988	translocase of outer mitochondrial membrane 70 homolog A	2	67445.0	4.4
13786206	tripeptidyl peptidase I	3	61332.3	12.8
78000203	tropomyosin 1, alpha isoform i	2	28528.7	11.7
8394469	troponin 1, type 3	4	24159.7	20.9
6981666	troponin T2, cardiac	5	35730.3	24.7
27465535	tubulin, beta 5	2	49670.8	6.1
51948476	ubiquinol-cytochrome c reductase core protein I	16	52848.8	53.3
55741544	ubiquinol-cytochrome c reductase core protein II	17	48396.2	45.1
57164091	ubiquinol-cytochrome c reductase hinge protein	2	10423.6	37.1
57114330	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	5	29445.7	44.5
17865351	valosin-containing protein	18	89348.8	35.1
71043730	vanin 1	2	57013.2	6.4
14389299	vimentin	6	53732.7	21.0
13786200	voltage-dependent anion channel 1	7	30755.5	75.3
13786202	voltage-dependent anion channel 2	7	31745.8	34.9
13786204	voltage-dependent anion channel 3	4	30797.8	29.3