

A3.4.1. List of proteins identified with 2peptide confidence by gel-free LC-MS/MS analysis in 8 months old whole hearts of ANT overexpressing (ANT-OE) rats

gi Number	Protein Annotation	Mol.Wt (Da)	No. of Peptides	Seq. Coverage (%)
17105350	2,4-dienoyl CoA reductase 1, mitochondrial	36203.8	5	27.2
11693170	2-oxoglutarate carrier	34251.8	4	21.0
13242293	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	34191.8	2	12.9
55742813	3-hydroxybutyrate dehydrogenase (heart, mitochondrial)	38333.0	5	17.4
83977457	3-hydroxyisobutyrate dehydrogenase	35302.7	4	23.3
61556993	3-hydroxyisobutyryl-Coenzyme A hydrolase	34524.9	3	14.5
20304123	3-mercaptopyruvate sulfurtransferase	32940.2	3	20.9
48675845	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	64208.4	3	8.3
8392836	acetyl-coenzyme A acetyltransferase 1	44709.0	6	26.9
18426866	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	41870.9	13	58.9
6978431	acetyl-Coenzyme A dehydrogenase, long-chain	47872.9	11	36.3
8392833	acetyl-coenzyme A dehydrogenase, medium chain	46555.4	6	25.7
40538860	aconitase 2, mitochondrial	85433.4	19	35.5
25742739	acyl-CoA synthetase long-chain family member 1	78178.7	11	24.9
11968090	acyl-coenzyme A dehydrogenase, short chain	44968.0	6	18.8
6978435	acyl-Coenzyme A dehydrogenase, very long chain	70749.3	13	34.4
52345435	adenosine kinase	40132.7	2	11.4
61889092	adenylate kinase 1	21583.8	5	37.6
6978479	adenylate kinase 3	25438.3	2	14.5
8392885	adenylate kinase 3-like 1	25202.9	2	21.5
61556810	ADP-ribosylhydrolase like 1	39877.2	3	11.3
58865636	ADP-ribosyltransferase 3	41712.5	4	27.3
14192933	aldehyde dehydrogenase 2	56488.4	10	25.6
13591997	aldehyde dehydrogenase family 6, subfamily A1	57807.6	11	31.4
75905479	aldehyde dehydrogenase family 9, subfamily A1	54050.1	3	7.4
19705537	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	37597.6	2	7.7
6978487	aldolase A	39351.9	4	25.8
77539778	alpha actinin 4	104915.0	2	8.7
55926139	alpha isoform of regulatory subunit A, protein phosphatase 2	65322.6	3	15.1

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83816939	alpha-1-inhibitor III	163773.3	4	9.3
57527204	alpha-ETF	34951.4	9	45.9
31543764	alpha-spectrin 2	284595.3	24	15.0
6978505	annexin 5	35744.5	6	28.5
58865414	annexin A11	54160.5	3	7.6
9845234	annexin A2	38678.2	3	12.7
13994159	annexin A6	75754.2	12	24.8
6978515	apolipoprotein A-I	30062.1	4	25.5
16758606	Arg/Abl-interacting protein ArgBP2	134053.4	4	6.8
67846036	aspartyl aminopeptidase	52555.2	3	11.6
19705465	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	28868.8	6	28.9
9506411	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	18763.4	4	55.3
17978459	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	8254.6	3	52.1
47058994	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	11460.5	3	41.7
40538742	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1.	59753.6	19	44.8
54792127	ATP synthase, H+ transporting, mitochondrial F1 complex, beta subunit	56353.6	22	63.1
39930503	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma subunit	32996.0	6	24.8
6978543	ATPase, Na+/K+ transporting, alpha 1 polypeptide	113054.3	5	7.3
6978549	ATPase, Na+/K+ transporting, beta 1 polypeptide	35233.6	2	8.2
13929056	basal cell adhesion molecule	67511.7	2	6.1
19705527	basic leucine zipper and W2 domains 2	48049.2	3	14.1
7709992	basigin	29585.5	2	10.3
61556754	B-cell receptor-associated protein 37	33312.4	8	39.1
9845261	beta-galactoside-binding lectin	14856.8	2	17.8
40445397	beta-glo	16037.5	3	35.4
47059181	B-factor, properdin	85120.7	2	4.2
11693174	branched chain aminotransferase 2, mitochondrial	44275.5	6	20.1
29789094	branched chain keto acid dehydrogenase kinase	46390.2	2	8.3

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20302073	cadherin 13	78085.6	2	5.2
13786162	cadherin 2	99811.5	3	6.4
25282419	calnexin	67254.8	3	7.6
11693172	calreticulin	47995.5	3	15.6
76563946	Calsequestrin 2	49402.6	8	30.0
59709467	CAP, adenylate cyclase-associated protein 1	51588.9	2	7.8
57163991	capping protein (actin filament) muscle Z-line, alpha 2	32967.1	5	36.0
9506445	carbonic anhydrase 2	29113.8	4	30.8
9506467	carbonyl reductase	30578.1	3	24.5
31542380	carboxylesterase 3	62147.2	2	7.4
51854229	carnitine acetyltransferase	70800.7	4	11.7
6978703	carnitine palmitoyltransferase 1b	88218.5	5	10.5
6978705	carnitine palmitoyltransferase 2	74110.3	8	21.3
6978607	catalase	59757.2	2	11.6
55742755	catenin (cadherin-associated protein), alpha 1, 102kDa	100236.4	5	12.1
42476045	cathepsin D	44622.6	3	13.0
6978695	ceruloplasmin	120840.7	2	3.4
61557218	chaperone, ABC1 activity of bc1 complex like	72225.6	5	11.6
54400730	chaperonin containing TCP1, subunit 2 (beta)	57458.3	2	7.9
76253725	chaperonin subunit 6a (zeta)	58017.3	2	7.0
18543177	citrate synthase	51866.8	6	18.2
9506497	clathrin, heavy polypeptide (Hc)	191598.7	13	11.3
58865534	coenzyme Q6 homolog	51495.8	3	12.4
48675371	complement component 1, q subcomponent binding protein	30996.9	4	26.5
8393024	complement component 3	186460.4	22	22.3
29789265	complement component 4a	192162.9	2	3.3
16924006	complement component 9	63762.5	3	8.3
8393197	C-reactive protein, petaxin related	25468.0	2	9.6
31542401	creatine kinase, brain	42712.2	10	35.2

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60678254	creatine kinase, mitochondrial 1, ubiquitous	46961.7	3	6.0
6978661	creatine kinase, muscle	43018.9	11	40.4
16905067	crystallin, alpha B	20088.8	4	33.1
16924004	cysteine-rich protein 3	20802.7	2	18.0
13399338	cytochrome b5, outer mitochondrial membrane isoform	16264.9	2	32.2
58615680	cytochrome c oxidase subunit II	25928.3	3	15.9
8393180	cytochrome c oxidase subunit IV isoform 1	19514.6	5	31.4
16758362	cytochrome c oxidase subunit Vb	13914.9	2	14.7
24233541	cytochrome c oxidase, subunit Va	16129.5	3	27.4
25453396	demethyl-Q 7	20140.1	2	11.2
11968118	desmin	53456.7	15	50.3
20302049	diaphorase 1	34174.6	3	15.9
40786469	dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex)	54038.1	6	17.7
78365255	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	80355.3	9	1.8
55742725	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	48925.4	6	20.9
16924002	DJ-1 protein	19974.2	3	32.3
56799412	DnaJ (Hsp40) homolog, subfamily A, member 2	45745.6	2	13.4
84370368	DnaJ (Hsp40) homolog, subfamily A, member 3 isoform 2	35302.7	2	23.3
8393243	dodecenoyl-coenzyme A delta isomerase	32254.4	5	30.1
77917614	dynamamin 1-like	79951.0	4	11.0
31377489	dynein, cytoplasmic, heavy chain 1	532251.7	4	1.6
52630316	dystrophin isoform Dp71ab	40132.7	2	11.4
67846074	EH-domain containing 2	61237.5	6	19.3
21326447	EH-domain containing 4	61467.6	2	6.3
51948412	electron-transfer-flavoprotein, beta polypeptide	27687.4	6	30.2
52138635	electron-transferring-flavoprotein dehydrogenase	68164.1	7	17.2
77917570	endonuclease G	32267.7	2	9.2
16758028	enigma homolog	63201.4	3	6.1
6978809	enolase 1, alpha	74110.3	9	21.3

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6978811	enolase 3, beta	46960.8	3	19.1
12018256	enoyl coenzyme A hydratase 1, peroxisomal	36201.7	6	33.9
17530977	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	31516.4	6	28.6
12621098	epoxide hydrolase 2, cytoplasmic	62340.3	3	9.6
47058982	erythroid spectrin beta	246328.6	5	4.2
51948422	es1 protein	28172.6	2	13.2
15805031	eukaryotic translation elongation factor 1 alpha 2	48574.8	2	2.5
61556967	eukaryotic translation elongation factor 1 delta	72127.6	3	7.5
8393296	eukaryotic translation elongation factor 2	95284.0	5	11.5
16758094	fatty acid binding protein 4	16494.3	3	22.7
56797757	fibrinogen, alpha polypeptide	86656.9	4	9.0
29789106	fibrinogen, beta polypeptide	54303.3	4	14.6
61098186	fibrinogen, gamma polypeptide	49651.7	5	19.0
9506703	fibronectin 1	272511.2	4	2.6
8393358	fumarate hydratase 1	54463.9	10	36.9
40254781	GDP dissociation inhibitor 2	50537.1	5	23.6
51854227	gelsolin	86067.6	4	11.4
46485440	glucose phosphate isomerase	62827.0	9	25.8
8393322	glucose regulated protein, 58 kDa	56589.4	2	4.4
6980956	glutamate dehydrogenase 1	61415.9	8	20.3
6980970	glutamate oxaloacetate transaminase 1	46328.6	8	34.1
6980972	glutamate oxaloacetate transaminase 2	47314.3	10	36.0
30520381	glutathione peroxidase 1	22464.4	4	29.4
31077128	glutathione S-transferase, mitochondrial	25493.0	3	18.6
28933457	glutathione S-transferase, mu 2	25702.6	3	31.7
25453420	glutathione S-transferase, pi	20140.1	2	11.2
13591969	glycogenin 1	37378.1	2	15.0
46485429	glyoxylase 1	20819.6	3	21.2
6978879	group specific component	53544.5	3	12.2

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18543331	guanine nucleotide binding protein, beta polypeptide 2-like 1	35094.8	2	6.6
60097941	haptoglobin	38563.2	4	14.4
13162363	heart fatty acid binding protein	14774.7	3	24.8
18426864	heat shock 27kD protein 2	20346.7	2	18.1
14010865	heat shock 27kDa protein 1	22821.6	2	16.1
25742763	heat shock 70kD protein 5	72347.0	9	22.5
51890229	heat shock 90kDa protein 1, beta	83316.3	2	11.2
11560024	heat shock protein 1 (chaperonin)	60965.5	4	11.7
28467005	heat shock protein 1, alpha	84814.9	2	5.7
24025637	heat shock protein 4	94056.5	4	7.5
20302069	heat shock protein, alpha-crystallin-related, B6	17504.9	5	66.7
6981010	hemoglobin alpha 1 chain	47314.3	4	36.0
17985949	hemoglobin beta chain complex	15979.4	4	27.9
16758014	hemopexin	51290.9	2	5.2
16923998	heterogeneous nuclear ribonucleoprotein K	50976.2	2	9.1
16923996	heterogeneous nuclear ribonucleoprotein U	87748.5	2	5.4
6981022	hexokinase 1	102408.0	6	10.5
13994225	hydroxysteroid (17-beta) dehydrogenase 10	27249.6	5	43.3
62078619	hypothetical protein LOC299354	51698.6	2	5.8
84781656	hypothetical protein LOC304542	35302.7	2	23.3
56912206	hypothetical protein LOC310201	27902.9	2	16.7
53850640	hypothetical protein LOC311430	53804.5	2	8.1
71043858	hypothetical protein LOC313200	58343.9	7	17.6
62078893	hypothetical protein LOC314432	117787.8	4	8.5
62945278	hypothetical protein LOC360975	116295.7	19	34.1
62079055	hypothetical protein LOC361596	50967.3	11	34.5
62945328	hypothetical protein LOC498174	32941.7	4	27.4
78214350	hypothetical protein LOC498909	35145.6	4	24.7

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72255551	hypothetical protein LOC500419	35400.5	5	21.6
77993368	hypothetical protein LOC619561	67886.5	7	22.3
51092266	hypoxanthine guanine phosphoribosyl transferase	24477.2	2	11.0
77917546	inner membrane protein, mitochondrial	67176.8	9	20.9
8393636	integrin beta 1	88494.6	3	6.1
19173772	integrin linked kinase	51373.2	2	4.6
62079215	isochorismatase domain containing 1	32002.5	2	11.4
13928690	isocitrate dehydrogenase 1 (NADP+), soluble	46734.4	5	23.4
16758446	isocitrate dehydrogenase 3 (NAD+) alpha	39613.7	5	21.0
55926203	isocitrate dehydrogenase 3 (NAD+) beta	42353.9	5	19.0
54020666	isocitrate dehydrogenase 3, gamma	42850.5	2	15.8
6981112	isovaleryl Coenzyme A dehydrogenase	46435.5	6	26.2
41529837	junction plakoglobin	81800.8	7	15.6
83816931	junctophilin 2	74258.5	2	3.8
57012436	keratin 10	56505.0	2	5.9
62543563	kynurenine aminotransferase III	51044.1	3	12.6
17105336	L-3-hydroxyacyl-Coenzyme A dehydrogenase	34447.8	7	45.2
6981146	lactate dehydrogenase B	36612.4	9	41.9
57114342	lactate dehydrogenase D	54292.2	2	6.0
50355947	lamin A isoform C2	71899.6	4	10.9
6981142	laminin, beta 2	196473.8	2	2.3
56090371	LEA_4 domain containing protein RGD1359600	31474.4	2	18.3
54400736	leucine zipper-EF-hand containing transmembrane protein 1	83059.8	2	3.7
56605990	leucine-rich protein 157	156652.8	10	10.1
20302022	leukotriene B4 12-hydroxydehydrogenase	35718.4	2	11.2
13591983	lumican	38279.0	2	7.4
15100179	malate dehydrogenase 1, NAD (soluble)	36483.1	8	43.7
42476181	malate dehydrogenase, mitochondrial	35683.6	13	48.8
16758230	malonyl-CoA decarboxylase	54609.9	2	8.1
57528264	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	79329.7	15	34.5

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58865926	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	61517.2	9	23.4
66730360	microtubule-associated protein 4	110300.8	2	3.1
48675862	mitochondrial acyl-CoA thioesterase 1	49629.1	4	35.5
20302061	mitochondrial ATP synthase, O subunit	23397.6	7	48.8
18677763	mitochondrial trifunctional protein, alpha subunit	82512.9	15	38.0
19424338	mitochondrial trifunctional protein, beta subunit	51414.5	11	35.8
12831225	Murinoglobulin 1 homolog	165326.2	2	18.8
11024650	myoglobin	17156.8	5	39.6
8393804	myosin heavy chain, polypeptide 6	223508.4	17	36.5
8393807	myosin heavy chain, polypeptide 7	223083.0	12	10.5
78214305	myosin regulatory light chain 2, ventricular/cardiac muscle isoform	18772.4	2	18.2
6981236	myosin, heavy polypeptide 9	226338.1	4	4.0
6981240	myosin, light polypeptide 3	22156.2	5	46.0
51948400	NAD(P)H dehydrogenase, quinone 2	26275.2	3	18.2
47058992	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11	14854.1	3	35.5
57164133	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	14358.8	2	18.3
53850628	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa	79412.3	18	35.9
58865384	NADH dehydrogenase (ubiquinone) Fe-S protein 2	52561.5	9	30.0
68341995	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	19740.6	4	34.3
55741424	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	50731.0	10	32.5
51092268	NADH dehydrogenase (ubiquinone) flavoprotein 2	27378.3	5	35.5
58615686	NADH dehydrogenase subunit 4	51782.8	3	14.6
58615687	NADH dehydrogenase subunit 5	68618.0	3	8.0
61557127	nicotinamide nucleotide transhydrogenase	113869.4	12	18.3
77628000	nitrilase family, member 2	30701.0	2	11.2
19424278	N-myc downstream regulated gene 2	39270.5	2	21.0
14010837	NSFL1 (p97) cofactor (p47)	40680.0	3	15.9
58865912	nucleosome assembly protein 1-like 4	43916.7	3	11.9
62078483	OCIA domain containing 1	27659.1	2	21.5

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77732522	outer membrane protein	15824.9	2	27.6
16923958	peroxiredoxin 1	22109.4	3	18.6
8394432	peroxiredoxin 2	21783.7	4	23.2
11968132	peroxiredoxin 3	28321.4	4	17.5
16758404	peroxiredoxin 5 precursor	22178.7	3	22.5
16758348	peroxiredoxin 6	24818.6	5	41.1
55741520	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase	43021.4	5	28.6
8393910	phosphatidylethanolamine binding protein	20801.4	5	49.2
13929002	phosphofructokinase, muscle	85559.9	7	13.6
77627971	phosphoglucomutase 1	61390.1	8	22.6
40254752	phosphoglycerate kinase 1	44538.5	2	27.6
16757984	Phosphoglycerate mutase 1	28645.7	4	31.5
8393948	phosphoglycerate mutase 2	28755.0	3	20.2
58865400	pleckstrin homology domain containing, family C (with FERM domain) member 1	77875.5	2	5.0
13540714	plectin 1	533540.0	20	8.8
29293813	pre-B-cell colony enhancing factor 1	55437.9	3	11.4
62650194	PREDICTED: hypothetical protein	51044.1	3	12.6
109511985	PREDICTED: hypothetical protein	298214.2	3	9.3
109504524	PREDICTED: NADH dehydrogenase (ubiquinone) Fe-S protein 6	114585.8	2	2.8
109477971	PREDICTED: ribosomal protein S7	164010.0	3	5.7
109470052	PREDICTED: similar to	143745.1	3	1.5
109481873	PREDICTED: similar to 13kDa differentiation-associated protein	65180.8	3	2.4
109469439	PREDICTED: similar to 14 kDa phosphohistidine phosphatase (Phosphohistidine phosphatase 1)	33056.1	2	8.9
34865350	PREDICTED: similar to 2-oxoisovalerate dehydrogenase beta subunit, mitochondrial precursor	27182.7	2	40.2
109502826	PREDICTED: similar to 60S acidic ribosomal protein P2	37321.3	4	3.8
109471014	PREDICTED: similar to acetyl-CoA synthetase 2-like	168033.8	8	0.7
109489498	PREDICTED: similar to Actin, cytoplasmic 2 (Gamma-actin)	63980.5	2	3.2
109460285	PREDICTED: similar to actin-binding LIM protein 1 isoform a	321328.5	2	23.0

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109506033	PREDICTED: similar to actinin alpha 2	140894.5	19	1.4
109497392	PREDICTED: similar to Actin-related protein 2/3 complex subunit 3	117181.5	2	21.5
109479984	PREDICTED: similar to Adenylosuccinate synthetase isozyme 1 isoform 2	50250.4	2	14.2
109506690	PREDICTED: similar to AFG3-like protein 2 (Paraplegin-like protein)	123188.4	2	1.9
109475727	PREDICTED: similar to aldehyde dehydrogenase 4 family, member A1	164010.0	5	5.7
62664437	PREDICTED: similar to aldehyde dehydrogenase family 7, member A1	109837.9	3	2.1
109506060	PREDICTED: similar to aldo-keto reductase family 1, member C4	140894.5	4	1.4
109487472	PREDICTED: similar to alpha 3 type VI collagen isoform 1 precursor	343536.5	2	15.4
34933197	PREDICTED: similar to Amine oxidase	27182.7	5	40.2
109467489	PREDICTED: similar to amylo-1,6-glucosidase, 4-alpha-glucanotransferase isoform 1	56203.8	6	35.4
109496584	PREDICTED: similar to ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit f, isoform 2	26187.9	3	15.8
34858394	PREDICTED: similar to Bcl-2-like 13 protein (Mil1 protein) (Bcl-rambo)	27182.7	3	40.2
109482276	PREDICTED: similar to C33H5.19	24912.0	2	9.4
109509021	PREDICTED: similar to C50H11.1	93611.4	3	23.2
62646841	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2	51044.1	13	12.6
109491036	PREDICTED: similar to CG7601-PA	58374.9	2	4.0
109473321	PREDICTED: similar to coiled-coil-helix-coiled-coil-helix domain containing 3	542698.9	2	0.5
109509939	PREDICTED: similar to Collagen alpha-1(VI) chain precursor	93611.4	8	23.2
109504497	PREDICTED: similar to Collagen alpha-2(IV) chain precursor	114585.8	2	2.8
109478872	PREDICTED: similar to cytochrome c oxidase subunit VIIa polypeptide 2-like	164010.0	2	5.7
109499760	PREDICTED: similar to cytochrome c oxidase, subunit 7a 3	76688.8	2	2.4
109480910	PREDICTED: similar to cytochrome c-1	157166.1	8	1.0
34856307	PREDICTED: similar to Deoxyguanosine kinase, mitochondrial precursor (dGK)	27182.7	2	40.2
109502634	PREDICTED: similar to Dihydropyrimidinase-related protein 2 (DRP-2)	37321.3	8	3.8
109473741	PREDICTED: similar to Dysferlin (Dystrophy-associated fer-1-like protein)	542698.9	2	0.5
109511865	PREDICTED: similar to dystrophin, muscular dystrophy	298214.2	14	9.3
109463451	PREDICTED: similar to EH-domain-containing protein 1 (mPAST1)	140591.5	5	1.3

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109463542	PREDICTED: similar to Elongation factor 1-gamma (EF-1-gamma)	140591.5	3	1.3
109501906	PREDICTED: similar to F11C1.5a	226223.6	6	5.5
109462323	PREDICTED: similar to Filamin-A (Filamin-1)	321328.5	3	23.0
109473201	PREDICTED: similar to Filamin-C isoform 2	542698.9	2	0.5
34858672	PREDICTED: similar to fumarylacetoacetate hydrolase domain containing 2A	27182.7	2	40.2
109467221	PREDICTED: similar to germinal histone H4 gene	56203.8	3	35.4
109493745	PREDICTED: similar to glucan (1,4-alpha-), branching enzyme 1	19091.6	2	4.8
62665009	PREDICTED: similar to Glutaryl-CoA dehydrogenase, mitochondrial precursor (GCD)	109837.9	3	2.1
34858950	PREDICTED: similar to Glycogen phosphorylase, brain form	27182.7	5	40.2
34861509	PREDICTED: similar to Glycogen phosphorylase, muscle form (Myophosphorylase)	27182.7	11	40.2
109500412	PREDICTED: similar to G-rich sequence factor 1 (GRSF-1)	68552.3	2	22.1
62654513	PREDICTED: similar to Gup1, glycerol uptake/transporter homolog	51044.1	4	12.6
34872418	PREDICTED: similar to heat shock protein family, member 7 (cardiovascular)	27182.7	2	40.2
109459168	PREDICTED: similar to Hemoglobin beta-2 subunit	93168.5	3	3.5
62647260	PREDICTED: similar to Heterogeneous nuclear ribonucleoproteins A2/B1	51044.1	2	12.6
109476409	PREDICTED: similar to Histidine triad nucleotide-binding protein 2	164010.0	2	5.7
109467571	PREDICTED: similar to inorganic pyrophosphatase 2	56203.8	2	35.4
109503793	PREDICTED: similar to Inter-alpha-trypsin inhibitor heavy chain H1 precursor	79854.7	2	20.1
109499222	PREDICTED: similar to isoleucine-tRNA synthetase 2, mitochondrial	112666.3	3	6.3
109460394	PREDICTED: similar to Laminin alpha-2 chain precursor	321328.5	13	23.0
109510183	PREDICTED: similar to Laminin alpha-4 chain precursor	93611.4	2	23.2
109479244	PREDICTED: similar to laminin B1 subunit 1	164010.0	6	5.7
62659497	PREDICTED: similar to Laminin gamma-1 chain precursor (Laminin B2 chain)	109837.9	6	2.1

gi Number	Protein Annotation	Mol.Wt (Da)	No. of Peptides	Seq. Coverage (%)
109503718	PREDICTED: similar to LIM domain binding 3	79854.7	4	20.1
109467479	PREDICTED: similar to Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial precursor	56203.8	4	35.4
109459038	PREDICTED: similar to malic enzyme 3, NADP(+)-dependent, mitochondrial	93168.5	5	3.5
109485854	PREDICTED: similar to Methylmalonyl-CoA mutase, mitochondrial precursor	44784.5	7	3.2
109505530	PREDICTED: similar to Mimecan precursor (Osteoglycin) isoform 3	140894.5	2	1.4
109465995	PREDICTED: similar to mitochondrial ribosomal protein S36	140882.1	2	1.0
109504452	PREDICTED: similar to myomesin 2	114585.8	26	2.8
109495555	PREDICTED: similar to myosin light chain 2, precursor lymphocyte-specific	26187.9	2	15.8
109481431	PREDICTED: similar to myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	157166.1	2	1.0
109487680	PREDICTED: similar to Myosin-11 (Myosin heavy chain, smooth muscle isoform) (SMMHC)	63980.5	4	3.2
109470313	PREDICTED: similar to Myosin-binding protein C, cardiac-type (Cardiac MyBP-C)	168033.8	29	0.7
27695760	PREDICTED: similar to myozenin 2	49670.8	6	6.5
27718097	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	49670.8	4	6.5
27663138	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	49670.8	3	6.5
109469775	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	143745.1	2	1.5
109474252	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	42559.2	10	39.8
62642368	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	51044.1	5	12.6
34856800	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	27182.7	3	40.2
109482288	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	24912.0	2	9.4

gi Number	Protein Annotation	Mol.Wt (Da)	No. of Peptides	Seq. Coverage (%)
27702072	PREDICTED: similar to NADH dehydrogenase (ubiquinone) Fe-S protein 3	49670.8	8	6.5
27661165	PREDICTED: similar to NADH dehydrogenase (ubiquinone) Fe-S protein 8	49670.8	4	6.5
27669100	PREDICTED: similar to NADH-ubiquinone oxidoreductase ESSS subunit, mitochondrial precursor	49670.8	3	6.5
109473144	PREDICTED: similar to NADH-ubiquinone oxidoreductase MLRQ subunit (Complex I-MLRQ)	542698.9	2	0.5
109487851	PREDICTED: similar to NADH-ubiquinone oxidoreductase PDSW subunit (Complex I-PDSW) isoform 1	63980.5	5	3.2
109480121	PREDICTED: similar to Nascent polypeptide-associated complex alpha subunit, muscle-specific form	215361.2	2	3.1
109506129	PREDICTED: similar to Nebulette (Actin-binding Z-disk protein)	140894.5	16	1.4
109505096	PREDICTED: similar to Nidogen-1 precursor (Entactin)	137039.1	2	7.1
109490823	PREDICTED: similar to obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	58374.9	8	4.0
109482588	PREDICTED: similar to parvin, beta	24912.0	2	9.4
27689507	PREDICTED: similar to Polymerase I and transcript release factor	49670.8	4	6.5
27681627	PREDICTED: similar to Probable C->U editing enzyme APOBEC-2	49670.8	4	6.5
109509941	PREDICTED: similar to procollagen, type VI, alpha 2	93611.4	6	23.2
109476383	PREDICTED: similar to procollagen, type XV	164010.0	2	5.7
109502895	PREDICTED: similar to Propionyl-CoA carboxylase alpha chain, mitochondrial precursor	79854.7	10	20.1
27706734	PREDICTED: similar to prostaglandin E synthase 2	49670.8	3	6.5
62665895	PREDICTED: similar to Protein C10orf70	109837.9	2	2.1
62651145	PREDICTED: similar to Protein C14orf159, mitochondrial precursor	51044.1	2	12.6
34869683	PREDICTED: similar to purine-nucleoside phosphorylase	27182.7	3	40.2

gi Number	Protein Annotation	Mol.Wt (Da)	No. of Peptides	Seq. Coverage (%)
109513095	PREDICTED: similar to Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial precursor	298214.2	2	9.3
109510099	PREDICTED: similar to pyrophosphatase	93611.4	2	23.2
109470396	PREDICTED: similar to pyruvate dehydrogenase complex, component X	168033.8	4	0.7
109503594	PREDICTED: similar to Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial precursor isoform 2	79854.7	3	20.1
109510252	PREDICTED: similar to Reticulon-4-interacting protein 1, mitochondrial precursor (NOGO-interacting mitochondrial protein)	93611.4	5	23.2
109489728	PREDICTED: similar to sarcalumenin	83931.4	14	2.0
27714505	PREDICTED: similar to serum deprivation response protein	49670.8	2	6.5
109473648	PREDICTED: similar to SET and MYND domain-containing protein 1 (Zinc-finger protein BOP)	542698.9	4	0.5
34854800	PREDICTED: similar to solute carrier family 25 (mitochondrial carrier, Aralar), member 12	27182.7	4	40.2
109468291	PREDICTED: similar to solute carrier family 25 (mitochondrial carrier, Aralar), member 12	33056.1	2	8.9
109463865	PREDICTED: similar to sorbin and SH3 domain containing 1 isoform 3	43609.3	6	6.9
62664205	PREDICTED: similar to Stress-70 protein, mitochondrial precursor (75 kDa glucose regulated protein) (GRP 75)	109837.9	11	2.1
109477603	PREDICTED: similar to succinate dehydrogenase Ip subunit	164010.0	4	5.7
62661722	PREDICTED: similar to succinate-Coenzyme A ligase, ADP-forming, beta subunit	109837.9	8	2.1
109484980	PREDICTED: similar to talin 2 isoform 2	44784.5	3	3.2
109476401	PREDICTED: similar to Talin-1	164010.0	6	5.7
109472340	PREDICTED: similar to T-complex protein 1 subunit alpha (TCP-1-alpha) (CCT-alpha)	42276.7	2	4.7
109473821	PREDICTED: similar to T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta)	542698.9	2	0.5
27685797	PREDICTED: similar to thioesterase superfamily member 2	49670.8	3	6.5
109470142	PREDICTED: similar to titin isoform N2-B	3703793.8	293	20.9
62641355	PREDICTED: similar to tripartite motif protein 50	51044.1	7	12.6
109462848	PREDICTED: similar to Tu translation elongation factor, mitochondrial	140591.5	4	1.3

gi Number	Protein Annotation	Mol.Wt (Da)	No. of Peptides	Seq. Coverage (%)
109504787	PREDICTED: similar to tubulin, beta 2	114585.8	2	2.8
109458613	PREDICTED: similar to ubiquinol-cytochrome c reductase binding protein	93168.5	2	3.5
109508535	PREDICTED: similar to vacuolar protein sorting 35	93611.4	3	23.2
109464690	PREDICTED: similar to very-long-chain acyl-CoA dehydrogenase VLCAD homolog isoform 1	43609.3	3	6.9
109502103	PREDICTED: similar to Vinculin (Metavinculin)	37321.3	11	3.8
21955142	pregnancy-zone protein	167159.2	13	15.7
42476144	profilin 1	14957.2	3	31.4
25742626	programmed cell death 8	66722.5	10	26.3
6981324	prolyl 4-hydroxylase, beta polypeptide	56864.2	3	7.1
8393913	propionyl Coenzyme A carboxylase, beta polypeptide	58626.2	10	29.4
61098214	protease (prosome, macropain) 28 subunit, alpha	28634.9	2	18.1
19173766	protease, serine, 15	105792.5	9	19.4
72255509	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	100187.6	2	4.5
6981396	protein kinase, cAMP dependent regulatory, type I, alpha	43095.0	3	15.5
29789096	protein kinase, cAMP-dependent, regulatory, type 2, alpha	45540.3	2	9.2
11968062	protein phosphatase 1, catalytic subunit, gamma isoform	44275.5	2	20.1
13929024	protein phosphatase 5, catalytic subunit	56916.7	2	6.4
12018270	pyridoxine 5-phosphate oxidase	30184.4	3	24.1
56090293	pyruvate dehydrogenase (lipoamide) beta	38982.1	9	37.6
16757994	pyruvate kinase, muscle	57817.8	2	37.1
11693160	quinoid dihydropteridine reductase	25552.2	3	23.7
55742827	Rho GDP dissociation inhibitor (GDI) alpha	23407.4	2	15.2
57164151	ribosomal protein S3	26674.3	2	20.2
54633307	RN protein	111248.0	2	3.3
8392878	S-adenosylhomocysteine hydrolase	47538.0	2	7.4

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25742657	sarcosine dehydrogenase	101439.9	2	4.8
18266692	selenium binding protein 2	52532.1	3	12.7
40018548	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6	43018.8	6	31.1
8393057	serine (or cysteine) proteinase inhibitor, clade H, member 1	46517.5	3	13.0
32563565	serine protease inhibitor 2a	68223.4	3	8.8
6981576	serine protease inhibitor 2b	45546.2	3	14.0
13928716	serine protease inhibitor 2c	45554.4	2	16.7
51036655	serine protease inhibitor alpha 1	46121.8	6	22.1
56090257	serum deprivation response protein	46386.4	2	10.1
52138624	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	33070.9	3	14.6
20806141	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	39445.1	5	18.3
32189355	solute carrier family 25, member 4	32989.4	5	19.5
51948454	sorting and assembly machinery component 50 homolog	51960.2	2	10.4
61557085	spectrin beta 2	273586.5	20	13.9
56090475	S-phase kinase-associated protein 1A	18672.0	3	27.0
50054162	statin-like	50454.2	3	14.7
20302113	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	62570.1	2	6.8
18426858	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	71615.2	12	31.1
74024923	sulfite oxidase	60805.8	2	9.0
8394328	superoxide dismutase 1	15911.7	3	24.7
8394331	superoxide dismutase 2	24674.1	2	12.6
13592093	suppression of tumorigenicity 13	41279.5	2	6.0
57528682	thiosulfate sulfurtransferase	33406.7	3	16.5
61556986	transferrin	76395.2	8	15.0

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13928744	transgelin	22602.9	2	16.4
61557028	transgelin 2	22393.4	3	21.6
42476287	transglutaminase 2, C polypeptide	76935.7	9	21.4
21955146	translocase of inner mitochondrial membrane 13 homolog	10457.9	2	25.3
6981684	transthyretin	15747.8	2	25.2
48675841	tropomodulin 1	40454.0	3	22.3
78000203	tropomyosin 1, alpha isoform i	28528.7	3	11.7
8394469	troponin 1, type 3	24159.7	4	20.9
6981666	Troponin T2, cardiac	35730.3	5	20.1
27465535	tubulin, beta 5	49670.8	2	6.5
84781723	tumor necrosis factor type 1 receptor associated protein	80461.2	4	7.5
6981710	tyrosine 3/tryptophan 5 -monooxygenase activation protein, eta polypeptide	28211.7	2	13.4
13928824	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	29121.7	3	23.1
62990183	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	27771.1	3	20.0
51948476	ubiquinol-cytochrome c reductase core protein I	52848.8	10	35.8
55741544	ubiquinol-cytochrome c reductase core protein II	48396.2	11	34.1
57114330	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	29445.7	6	39.1
16758810	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)	57957.1	3	2.1
67078526	UDP-glucose pyrophosphorylase 2	57023.4	2	7.9
17865351	valosin-containing protein	89348.8	8	17.0
14389299	vimentin	53732.7	5	18.5
13786200	voltage-dependent anion channel 1	30755.5	6	55.8
13786202	voltage-dependent anion channel 2	31745.8	6	37.3
13786204	voltage-dependent anion channel 3	30797.8	4	24.0
62543513	zinc binding alcohol dehydrogenase, domain containing 1	29896.9	2	16.7