

Table S2. Complete list of the myocardial proteins whose levels were not significantly altered after morphine treatment or withdrawal.

# Accession	Protein name	% Cov	Peptides	Fraction
gi 81883737	[Protein ADP-ribosylarginine] hydrolase-like protein 1	26,6	6	CS
gi 61216932	14-3-3 protein epsilon	23,1	2	MT
gi 1051270	14-3-3 zeta isoform	57,1	11	MT
gi 37748456	2,4-dienoyl CoA reductase 1, mitochondrial	60,6	24	MT
gi 67476443	2,4-dienoyl-CoA reductase, mitochondrial	57,9	25	PM
gi 81883712	2-oxoglutarate dehydrogenase E1 component, mitochondrial	40	27	CS
gi 81883712	2-oxoglutarate dehydrogenase E1 component, mitochondrial	61,2	52	PM
gi 81883712	2-oxoglutarate dehydrogenase E1 component, mitochondrial	45,2	35	MT
gi 57333	3-2trans-enoyl-CoA isomerase	53,6	14	CS
gi 57333	3-2trans-enoyl-CoA isomerase	36	9	PM
gi 57333	3-2trans-enoyl-CoA isomerase	26	4	MT
gi 7387724	3-hydroxyacyl-CoA dehydrogenase type-2	82,4	22	CS
gi 7387724	3-hydroxyacyl-CoA dehydrogenase type-2	41,8	5	PM
gi 7387724	3-hydroxyacyl-CoA dehydrogenase type-2	38,7	6	MT
gi 83977457	3-hydroxyisobutyrate dehydrogenase precursor	27,2	6	CS
gi 83977457	3-hydroxyisobutyrate dehydrogenase precursor	17,9	3	PM
gi 149046212	3-hydroxyisobutyryl-Coenzyme A hydrolase	41	10	CS
gi 61556993	3-hydroxyisobutyryl-Coenzyme A hydrolase	13,2	3	PM
gi 38511566	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	38,2	3	CS
gi 54039450	40S ribosomal protein S15a	41,5	2	PM
gi 54039450	40S ribosomal protein S15a	36,2	2	MT
gi 50403620	40S ribosomal protein S18	22,4	2	PM
gi 50403620	40S ribosomal protein S18	34,2	3	MT
gi 50403678	40S ribosomal protein S23	18,9	2	PM
gi 51338623	40S ribosomal protein S28	33,3	2	PM
gi 49065830	40S ribosomal protein S7	22,2	4	PM
gi 49065830	40S ribosomal protein S7	28,4	4	MT
gi 52788199	40S ribosomal protein S9	15	1	PM
gi 52788199	40S ribosomal protein S9	18,6	3	MT
gi 183986025	5'-nucleotidase, cytosolic III	13,8	2	CS
gi 730581	60S acidic ribosomal protein P0	16,4	4	PM
gi 730581	60S acidic ribosomal protein P0	23	5	MT

# Accession	Protein name	% Cov	Peptides	Fraction
gi 50403574	60S ribosomal protein L10	29.4	2	PM
gi 730529	60S ribosomal protein L13	29.4	5	MT
gi 548747	60S ribosomal protein L13a	19.2	2	PM
gi 548747	60S ribosomal protein L13a	13.8	2	MT
gi 2500360	60S ribosomal protein L14	24.8	2	MT
gi 51338615	60S ribosomal protein L23a	12.2	2	PM
gi 51338615	60S ribosomal protein L23a	20.5	3	MT
gi 51704206	60S ribosomal protein L7	20.8	4	PM
gi 51704206	60S ribosomal protein L7	7.3	2	MT
gi 205686171	6-phosphogluconolactonase	39.7	3	CS
gi 91234898	84 kDa heat shock protein	61.9	39	CS
gi 91234898	84 kDa heat shock protein	18.9	6	PM
gi 91234898	84 kDa heat shock protein	26.0	11	MT
gi 33086444	Ab1-021	27.8	19	CS
gi 33086478	Ab1-205	13.4	6	MT
gi 33086478	Ab1-205	13.9	4	PM
gi 33086600	Ab2-371	7.0	4	PM
gi 32264613	Ac1164	23.8	8	PM
gi 32264613	Ac1164	14.7	3	MT
gi 8392836	Acetyl-CoA acetyltransferase 1 precursor	31.4	9	CS
gi 8392836	Acetyl-CoA acetyltransferase 1 precursor	69.8	32	PM
gi 6978429	Acetyl-CoA acyltransferase 1	16.4	2	MT
gi 149027156	Acetyl-CoA acyltransferase 2, isoform CRA_f	82.4	36	CS
gi 149027156	Acetyl-CoA acyltransferase 2, isoform CRA_f	72.5	36	PM
gi 94963134	Acetyl-CoA carboxylase 2	5.8	1	CS
gi 60391194	Aconitate hydratase, mitochondrial	59.9	50	PM
gi 60391194	Aconitate hydratase, mitochondrial	70.8	117	CS
gi 77993370	Actin α , cardiac 1	70.6	27	CS
gi 9506371	Actin, α 1, skeletal muscle	78.5	84	MT
gi 77993368	Acyl-CoA synthetase family member 2 precursor	48.1	27	CS
gi 77993368	Acyl-CoA synthetase family member 2 precursor	28.1	10	PM
gi 77993368	Acyl-CoA synthetase family member 2 precursor	10.2	3	MT
gi 157818027	Acyl-CoA synthetase short-chain family member 1	52.8	29	CS
gi 157818027	Acyl-CoA synthetase short-chain family member 1	6.7	2	MT

# Accession	Protein name	% Cov	Peptides	Fraction
gi 157818027	Acyl-CoA synthetase short-chain family member 1	21.0	6	PM
gi 157817043	Acyl-CoA thioesterase 13	14.3	2	PM
gi 48675862	Acyl-CoA thioesterase 2	63.6	18	CS
gi 62078649	Acyl-CoA thioesterase 9	16.9	4	CS
gi 62078649	Acyl-CoA thioesterase 9	8.4	2	PM
gi 197313734	Acyl-CoA dehydrogenase family, member 9	37.3	10	CS
gi 197313734	Acyl-CoA dehydrogenase family, member 9	26.2	8	MT
gi 149048722	Acyl-CoA dehydrogenase family, member 9, isoform CRA_c	26.5	9	PM
gi 48734846	Acyl-CoA dehydrogenase, C-2 to C-3 short chain	61.8	19	CS
gi 48734846	Acyl-CoA dehydrogenase, C-2 to C-3 short chain	47.6	10	PM
gi 56541110	Acyl-CoA dehydrogenase, very long chain	71.5	54	PM
gi 56541110	Acyl-CoA dehydrogenase, very long chain	59.1	33	MT
gi 6166586	Acyl-CoA thioesterase 2, mitochondrial	24.9	7	PM
gi 6166586	Acyl-CoA thioesterase 2, mitochondrial	22.7	5	MT
gi 188595700	Acylglycerol kinase	8.1	2	PM
gi 157822589	Acylphosphatase 1	39.4	2	CS
gi 281332093	Acylphosphatase 2, muscle type	42.7	4	CS
gi 157823677	Adaptor-related protein complex 2, α 1 subunit	4.7	2	PM
gi 56961624	Adaptor-related protein complex 2, σ 1 subunit	14.1	2	PM
gi 61556832	Adenine phosphoribosyltransferase	60.0	8	CS
gi 52345435	Adenosine kinase	28.0	6	CS
gi 8392878	Adenosylhomocysteinase	8.3	2	CS
gi 77020256	Adenylate kinase 2 isoform b	40.5	8	PM
gi 77020256	Adenylate kinase 2 isoform b	44.0	12	MT
gi 8392885	Adenylate kinase 3-like 1	26.5	5	CS
gi 8918488	Adenylate kinase isozyme 1	28.9	4	PM
gi 8918488	Adenylate kinase isozyme 1	35.6	6	MT
gi 194473622	Adenylosuccinate lyase	20.0	4	CS
gi 54035294	Adh5 protein	18.5	4	CS
gi 5002228	Adipocyte lipid-binding protein	46.7	5	MT
gi 728810	ADP/ATP translocase 2	74.5	68	PM
gi 728810	ADP/ATP translocase 2	79.2	70	MT
gi 149052783	ADP-ribosylation factor 1, isoform CRA_d	21.2	2	MT
gi 57033190	ADP-ribosylation factor 3	37.6	4	CS

# Accession	Protein name	% Cov	Peptides	Fraction
gi 57033190	ADP-ribosylation factor 3	15.5	2	PM
gi 81890516	ADP-ribosylation factor-like protein 8B	23.7	3	PM
gi 58865636	ADP-ribosyltransferase 3	13.9	2	MT
gi 543793	Afamin	16.8	7	CS
gi 198442897	AFG3(ATPase family gene 3)-like 2	25.9	16	PM
gi 198442897	AFG3(ATPase family gene 3)-like 2	32.2	19	MT
gi 39930812	Aflatoxin B1 aldehyde reductase member 2	14.2	3	CS
gi 40352787	Ak3 protein	58.2	7	CS
gi 197927423	Aldehyde dehydrogenase 4A1	33.1	9	CS
gi 75905479	Aldehyde dehydrogenase 9A1	35.6	9	CS
gi 55605	Aldehyde dehydrogenase preprotein	44.9	18	CS
gi 55605	Aldehyde dehydrogenase preprotein	43.7	13	PM
gi 399660	Aldehyde reductase	23.7	4	CS
gi 158138555	Aldo-keto reductase family 1, member C-like 1	36.1	9	CS
gi 55926139	α isoform of regulatory subunit A, protein phosphatase 2	26.7	8	CS
gi 83816939	α -1-inhibitor III precursor	44.8	60	CS
gi 81872093	α -1-macroglobulin	28.9	24	CS
gi 58865362	α -2-antiplasmin precursor	11.6	2	CS
gi 60552688	α -2-HS-glycoprotein	46.6	13	CS
gi 6978477	α -2-HS-glycoprotein precursor	7.7	1	PM
gi 744592	α -B crystallin	53.7	8	PM
gi 744592	α -B crystallin	60.0	9	MT
gi 3462887	α -fodrin	35.1	48	PM
gi 206050	α -propionyl-CoA carboxylase (EC 6.4.1.3)	17.2	9	PM
gi 6094309	α -soluble NSF attachment protein	21.7	4	PM
gi 81884653	Aminoacylase-1A	26.7	5	CS
gi 158749540	Aminopeptidase puromycin sensitive	15.7	7	CS
gi 157819187	Amylo-1,6-glucosidase, 4- α -glucanotransferase	24.9	23	CS
gi 157822539	Ankyrin 1, erythrocytic	8.1	2	PM
gi 6978501	Annexin A1	37.6	6	CS
gi 58865414	Annexin A11	35.4	11	CS
gi 58865414	Annexin A11	14.9	2	PM
gi 9845234	Annexin A2	39.5	8	CS
gi 9845234	Annexin A2	45.7	10	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 9845234	Annexin A2	37.8	7	MT
gi 51980303	Annexin A3	54.9	13	CS
gi 51980303	Annexin A3	18.5	3	PM
gi 51980303	Annexin A3	14.2	2	MT
gi 55742832	Annexin A4	29.8	4	CS
gi 6978505	Annexin A5	41.1	10	PM
gi 6978505	Annexin A5	37.3	8	MT
gi 763181	Annexin VI	19.8	8	MT
gi 6103726	Antioxidant enzyme B166	22.5	2	MT
gi 6103726	Antioxidant enzyme B166	22.5	2	PM
gi 73695330	Ap2b1 protein	9.4	3	PM
gi 73695330	Ap2b1 protein	4.0	1	MT
gi 165971324	Apoa1bp protein	14.9	2	CS
gi 6978515	Apolipoprotein A-I precursor	16.6	2	PM
gi 60552712	Apolipoprotein A-IV	16.9	2	CS
gi 195540026	Apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2	11.6	1	CS
gi 71051103	Apolipoprotein C-I	18.2	1	PM
gi 149041554	Apolipoprotein C-III, isoform CRA_a	46.0	2	PM
gi 295916	Apolipoprotein E	19.9	2	PM
gi 55824759	Apolipoprotein E	18.0	2	MT
gi 57528174	Apolipoprotein H (β -2-glycoprotein I)	23.2	5	PM
gi 62078943	Apolipoprotein O-like	44.1	9	PM
gi 62078943	Apolipoprotein O-like	47.2	8	MT
gi 7619915	Apoptosis-inducing factor	55.7	21	PM
gi 7619915	Apoptosis-inducing factor	52.9	21	MT
gi 6978527	Aquaporin 1	19.3	5	PM
gi 38512104	Arginyl aminopeptidase (aminopeptidase B)	12.3	5	CS
gi 6980972	Aspartate aminotransferase 2	81.6	65	CS
gi 6980972	Aspartate aminotransferase 2	70.5	35	PM
gi 67846036	Aspartyl aminopeptidase	9.5	1	CS
gi 55249793	Asph protein	30.4	6	PM
gi 55249793	Asph protein	23.7	4	MT
gi 54145376	ATP synthase F0 subunit 8	59.7	5	PM
gi 54145376	ATP synthase F0 subunit 8	55.2	5	MT

# Accession	Protein name	% Cov	Peptides	Fraction
gi 157822047	ATP synthase mitochondrial F1 complex assembly factor 2	14.1	2	CS
gi 83300587	ATP synthase subunit α, mitochondrial	79.0	189	MT
gi 461587	ATP synthase subunit e, mitochondrial	84.5	9	PM
gi 461587	ATP synthase subunit e, mitochondrial	84.5	10	MT
gi 543880	ATP synthase subunit O, mitochondrial	74.7	28	PM
gi 39645769	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1	59.8	39	PM
gi 39645769	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1	58.6	38	MT
gi 9506411	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	90.1	52	PM
gi 9506411	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	91.3	44	MT
gi 47058994	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	65.1	9	PM
gi 47058994	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	69.9	17	MT
gi 71681130	ATP synthase, H+ transporting, mitochondrial F1 complex, β polypeptide	79.6	165	PM
gi 149034587	ATP synthase, H+ transporting, mitochondrial F1 complex, δ subunit, isoform CRA_b	74.4	21	PM
gi 149034587	ATP synthase, H+ transporting, mitochondrial F1 complex, δ subunit, isoform CRA_b	59.5	28	MT
gi 34786049	ATP synthase, H+ transporting, mitochondrial F1 complex, ε subunit	82.4	4	PM
gi 34786049	ATP synthase, H+ transporting, mitochondrial F1 complex, ε subunit	92.2	4	MT
gi 39930503	ATP synthase, H+ transporting, mitochondrial F1 complex, γ subunit	59.4	36	MT
gi 149059861	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit, isoform CRA_c	78.1	21	MT
gi 81908923	ATPase family AAA domain-containing protein 1	18.8	3	PM
gi 81908923	ATPase family AAA domain-containing protein 1	20.2	2	MT
gi 77917538	ATPase family, AAA domain containing 3A	28.3	7	PM
gi 77917538	ATPase family, AAA domain containing 3A	26.6	8	MT
gi 77917528	ATPase inhibitory factor 1 precursor	74.8	5	PM
gi 77917528	ATPase inhibitory factor 1 precursor	72.0	6	MT
gi 50927657	ATPase, Na+/K+ transporting, β 1 polypeptide	39.1	13	PM
gi 50927657	ATPase, Na+/K+ transporting, β 1 polypeptide	34.2	9	MT
gi 71152214	ATP-binding cassette sub-family B member 7, mitochondrial	8.1	3	PM
gi 71152214	ATP-binding cassette sub-family B member 7, mitochondrial	7.4	4	MT
gi 81910043	ATP-binding cassette sub-family B member 8, mitochondrial	15.6	4	PM
gi 81910043	ATP-binding cassette sub-family B member 8, mitochondrial	14.9	5	MT
gi 149044979	AU RNA binding protein/enoyl-coenzyme A hydratase (predicted), isoform CRA_a	22.9	3	PM
gi 33086642	Ba2-693	11.2	6	CS
gi 81917434	Basal cell adhesion molecule	7.5	3	PM
gi 7709992	Basigin isoform 2	43.0	11	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 7709992	Basigin isoform 2	28.7	7	MT
gi 38512141	Bcat2 protein	6.2	2	PM
gi 51948420	B-cell receptor-associated protein 31	6.1	1	PM
gi 51948420	B-cell receptor-associated protein 31	12.7	2	MT
gi 9789466	BCL2/adenovirus E1B 19 kDa-interacting protein 3	13.9	2	PM
gi 9789466	BCL2/adenovirus E1B 19 kDa-interacting protein 3	11.8	2	MT
gi 56090628	BCS1-like	8.1	3	PM
gi 56090628	BCS1-like	23.4	5	MT
gi 55575	β-actin	55.7	17	CS
gi 55575	β-actin	62.4	29	PM
gi 56260	β-globin	81.0	58	CS
gi 984679	β-globin	86.4	75	CS
gi 56252	β-globin	84.4	19	PM
gi 984679	β-globin	83.0	22	PM
gi 984679	β-globin	85.7	18	MT
gi 81888008	β-lactamase-like protein 2	25.4	4	CS
gi 50925455	Biliverdin reductase A	20.7	3	CS
gi 81295385	Biphenyl hydrolase-like (serine hydrolase)	22.7	2	CS
gi 81866115	Bone marrow stromal antigen 2	11.6	3	PM
gi 81866115	Bone marrow stromal antigen 2	12.8	2	MT
gi 158187544	Brain glycogen phosphorylase	64.3	47	CS
gi 730248	Brain protein 44	32.3	2	PM
gi 730248	Brain protein 44	40.9	4	MT
gi 66911415	Brain protein 44-like	26.6	3	PM
gi 66911415	Brain protein 44-like	26.6	3	MT
gi 38142418	Brain Y-box binding protein 1	19.6	2	MT
gi 77736548	Branched chain keto acid dehydrogenase E1, α polypeptide	25.1	6	PM
gi 3023378	Branched-chain-amino-acid aminotransferase, mitochondrial	35.1	8	CS
gi 60688421	C9 protein	10.1	1	CS
gi 55249666	Cadherin 13	18.1	6	PM
gi 55249666	Cadherin 13	6.3	1	MT
gi 871525	Calcium binding protein	29.9	5	PM
gi 49522734	Calcium regulated heat stable protein 1	21.1	1	CS
gi 4753894	Calcyclin	25.8	2	CS

# Accession	Protein name	% Cov	Peptides	Fraction
gi 8394168	Calmodulin 2	51.7	2	CS
gi 8394168	Calmodulin 2	72.5	6	PM
gi 8394168	Calmodulin 2	26.9	3	MT
gi 543922	Calnexin	30.0	14	PM
gi 543922	Calnexin	31.0	11	MT
gi 83301638	Calpain small subunit 1	15.9	3	CS
gi 77540019	Calpastatin	12.2	4	CS
gi 988307	Calsequestrin	14.0	3	CS
gi 78099764	Calsequestrin-2	43.1	22	PM
gi 78099764	Calsequestrin-2	34.1	19	MT
gi 158186676	Calumenin isoform a	8.9	3	PM
gi 76559925	Calumenin isoform b	11.1	3	CS
gi 155369271	cAMP-dependent protein kinase catalytic subunit α	19.9	4	CS
gi 83304285	cAMP-dependent protein kinase type II- α regulatory subunit	11.7	2	CS
gi 74355722	Capping protein (actin filament) muscle Z-line, α 2	17.1	3	MT
gi 205687264	Carbonic anhydrase 1	51.0	10	CS
gi 9506445	Carbonic anhydrase II	54.2	8	CS
gi 157818703	Carbonic anhydrase XIV	9.8	2	PM
gi 157818703	Carbonic anhydrase XIV	9.8	2	MT
gi 9506467	Carbonyl reductase 1	49.8	9	CS
gi 205495	Cardiac myosin light chain 2	68.1	8	CS
gi 46577628	Cardiac phospholamban	32.7	2	PM
gi 46577628	Cardiac phospholamban	34.6	2	MT
gi 59797483	Carnitine O-acetyltransferase	8.1	2	CS
gi 59797483	Carnitine O-acetyltransferase	24.1	11	PM
gi 59797483	Carnitine O-acetyltransferase	8.3	4	MT
gi 6978705	Carnitine O-palmitoyltransferase precursor	59.6	27	PM
gi 6978705	Carnitine O-palmitoyltransferase precursor	41.3	19	MT
gi 48735405	Carnitine palmitoyltransferase 1a, liver	11.3	4	PM
gi 48735405	Carnitine palmitoyltransferase 1a, liver	9.8	3	MT
gi 6978607	Catalase	22.0	4	CS
gi 6978607	Catalase	18.8	7	PM
gi 6978607	Catalase	28.5	10	MT
gi 82830420	Cathepsin B preproprotein	9.1	2	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 27465583	Cationic trypsinogen precursor	10.9	2	CS
gi 575380	Caveolin 1	27.4	6	MT
gi 45267819	Caveolin 2	21.0	3	PM
gi 9506465	Caveolin 3	37.1	3	PM
gi 6978635	CD59 molecule, complement regulatory protein precursor	23.0	2	PM
gi 6978639	Cd81 molecule	27.5	3	PM
gi 215275245	CDGSH iron sulfur domain-containing protein 1	44.4	8	PM
gi 215275245	CDGSH iron sulfur domain-containing protein 1	51.9	5	MT
gi 6531681	Cell division cycle 42	20.9	4	CS
gi 6531681	Cell division cycle 42	30.9	4	PM
gi 6531681	Cell division cycle 42	16.8	3	MT
gi 6707016	Cell surface protein CD36	39.2	13	PM
gi 6707016	Cell surface protein CD36	28.8	10	MT
gi 213512607	Citrate lyase β like precursor	26.3	7	CS
gi 56388799	Ckb protein	67.4	42	CS
gi 56388799	Ckb protein	46.6	14	PM
gi 56388799	Ckb protein	35.8	13	MT
gi 9506497	Clathrin, heavy chain (Hc)	10.9	5	CS
gi 9506497	Clathrin, heavy chain (Hc)	13.9	9	PM
gi 38181879	Clu protein	8.9	2	MT
gi 8393101	Cofilin 1	55.4	8	CS
gi 149051244	Cofilin 2, muscle (predicted), isoform CRA_b	56.0	8	CS
gi 62078929	Coiled-coil domain containing 51	26.9	4	PM
gi 62078929	Coiled-coil domain containing 51	20.6	3	MT
gi 157817027	Coiled-coil-helix-coiled-coil-helix domain containing 3	66.1	18	PM
gi 157817027	Coiled-coil-helix-coiled-coil-helix domain containing 3	66.1	18	MT
gi 259016391	Collagen α-1(I) chain	34.3	20	MT
gi 281427229	Collagen, type VI, α 2	10.3	5	MT
gi 48675371	Complement component 1, q subcomponent binding protein precursor	33.3	6	CS
gi 48675371	Complement component 1, q subcomponent binding protein precursor	39.4	7	PM
gi 48675371	Complement component 1, q subcomponent binding protein precursor	17.9	4	MT
gi 158138561	Complement component 3	44.8	53	CS
gi 158138561	Complement component 3	10.6	6	PM
gi 46237589	Complement component 4, gene 1	4.6	2	CS

# Accession	Protein name	% Cov	Peptides	Fraction
gi 56268879	Complement factor B	8.4	4	CS
gi 74353709	Cox15 protein	9.4	2	PM
gi 74353709	Cox15 protein	17.2	3	MT
gi 34849861	Cox6c protein	67.1	15	PM
gi 34849861	Cox6c protein	69.7	9	MT
gi 187469733	Cox7a2l protein	72.6	6	PM
gi 187469733	Cox7a2l protein	61.1	6	MT
gi 847719	CPTI like protein	50.9	30	PM
gi 847719	CPTI like protein	46.2	26	MT
gi 67460125	Cullin-associated NEDD8-dissociated protein 2	8.6	2	CS
gi 737713	Cys-rich protein CRP2	17.3	3	MT
gi 737713	Cys-rich protein CRP2	42.8	6	CS
gi 54036889	Cysteine-rich protein 1	13.0	1	CS
gi 829020	Cytochrome B gene	4.2	3	PM
gi 38303959	Cytochrome b5 reductase 3	38.9	8	PM
gi 38303959	Cytochrome b5 reductase 3	29.2	7	MT
gi 48735409	Cytochrome b5 type B (outer mitochondrial membrane)	65.8	7	PM
gi 149015875	Cytochrome b-5, isoform CRA_e	49.6	5	PM
gi 149015875	Cytochrome b-5, isoform CRA_e	52.5	5	MT
gi 81884378	Cytochrome b-c1 complex subunit 1, mitochondrial	66.9	65	PM
gi 62511137	Cytochrome b-c1 complex subunit 6, mitochondrial	70.8	18	MT
gi 81865392	Cytochrome b-c1 complex subunit 8	54.9	4	PM
gi 81865392	Cytochrome b-c1 complex subunit 8	57.3	6	MT
gi 5851903	Cytochrome C oxidase assembly protein COX17	36.5	2	CS
gi 54145374	Cytochrome c oxidase subunit 1	7.6	3	PM
gi 54145375	Cytochrome c oxidase subunit 2	47.6	10	PM
gi 26983979	Cytochrome c oxidase subunit II	36.6	15	MT
gi 8393180	Cytochrome c oxidase subunit IV isoform 1 precursor	69.2	39	PM
gi 8393180	Cytochrome c oxidase subunit IV isoform 1 precursor	64.5	38	MT
gi 55971	Cytochrome c oxidase subunit Va preprotein	70.6	56	PM
gi 55971	Cytochrome c oxidase subunit Va preprotein	69.2	50	MT
gi 55992	Cytochrome c oxidase subunit VIa (AA 1 - 118)	67.5	32	PM
gi 55992	Cytochrome c oxidase subunit VIa (AA 1 - 118)	61.5	38	MT
gi 56025	Cytochrome c oxidase subunit VIIa	37.4	7	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 56025	Cytochrome c oxidase subunit VIIa	37.4	9	MT
gi 65301490	Cytochrome c oxidase subunit VIIb precursor	16.3	2	PM
gi 65301490	Cytochrome c oxidase subunit VIIb precursor	16.3	1	MT
gi 77736544	Cytochrome c oxidase, subunit VIa, polypeptide 1 precursor	69.4	7	PM
gi 77736544	Cytochrome c oxidase, subunit VIa, polypeptide 1 precursor	44.1	6	MT
gi 223718723	Cytochrome c oxidase, subunit VIb polypeptide 1	81.4	33	PM
gi 197927439	Cytochrome c oxidase, subunit VIIc	36.5	11	PM
gi 197927439	Cytochrome c oxidase, subunit VIIc	39.7	7	MT
gi 6978725	Cytochrome c, somatic	49.5	10	CS
gi 6978725	Cytochrome c, somatic	73.3	22	PM
gi 6978725	Cytochrome c, somatic	72.4	14	MT
gi 149066116	Cytochrome c-1 (predicted), isoform CRA_c	47.6	45	PM
gi 149066116	Cytochrome c-1 (predicted), isoform CRA_c	54.9	45	MT
gi 829025	Cytochrome oxidase III	7.7	3	PM
gi 729378	Cytoplasmic dynein 1 heavy chain 1	5.9	4	PM
gi 157823877	Cytoskeleton-associated protein 4	11.0	2	PM
gi 157823877	Cytoskeleton-associated protein 4	19.0	3	MT
gi 81884348	Cytosol aminopeptidase	22.9	5	CS
gi 537941	Cytosolic NADP-dependent isocitrate dehydrogenase	37.9	11	CS
gi 68837285	D-β-hydroxybutyrate dehydrogenase, mitochondrial	41.1	11	PM
gi 68837285	D-β-hydroxybutyrate dehydrogenase, mitochondrial	41.1	13	MT
gi 56057	Decorin	21.8	5	PM
gi 56057	Decorin	29.7	5	MT
gi 457929	δ subunit of F1F0 ATPase	33.9	2	CS
gi 6015047	δ(3,5)-δ(2,4)-dienoyl-CoA isomerase, mitochondrial	47.4	6	CS
gi 157819621	Deoxyguanosine kinase	20.5	3	CS
gi 38197676	Desmin	8.7	2	CS
gi 149045175	Desmoplakin, isoform CRA_b	13.4	4	MT
gi 56605642	Diablo	14.8	3	MT
gi 54261671	Diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	73.6	5	CS
gi 54261671	Diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	58.6	2	PM
gi 54261671	Diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	51.7	2	MT
gi 183985854	Dihydrolipoamide branched chain transacylase E2	8.5	4	PM
gi 81885266	Dihydrolipoyl dehydrogenase, mitochondrial	44.0	15	CS

# Accession	Protein name	% Cov	Peptides	Fraction
gi 81885266	Dihydrolipoyl dehydrogenase, mitochondrial	48.1	18	PM
gi 81885266	Dihydrolipoyl dehydrogenase, mitochondrial	23.0	7	MT
gi 6012071	Dithiolethione-inducible gene-1	31.9	8	CS
gi 84370227	DnaJ (Hsp40) homolog, subfamily A, member 3 isoform 1	27.9	7	PM
gi 84370227	DnaJ (Hsp40) homolog, subfamily A, member 3 isoform 1	27.5	7	MT
gi 70794764	DnaJ (Hsp40) homolog, subfamily A, member 4	9.9	1	CS
gi 171847074	DnaJ (Hsp40) homolog, subfamily C, member 11	9.7	3	PM
gi 171847074	DnaJ (Hsp40) homolog, subfamily C, member 11	16.6	4	MT
gi 62512124	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	5.7	2	PM
gi 62512124	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	19.5	4	MT
gi 294543	Dynein heavy chain	6.9	3	MT
gi 157823277	Dysferlin	9.6	7	PM
gi 157823277	Dysferlin	5.9	2	MT
gi 149021348	EF hand domain family, member A2	8.0	1	MT
gi 81910618	EH domain-containing protein 1	10.7	3	MT
gi 81908709	EH domain-containing protein 2	22.1	8	PM
gi 81908709	EH domain-containing protein 2	21.4	8	MT
gi 53237076	EH-domain containing 4	8.5	2	PM
gi 53237076	EH-domain containing 4	15.0	3	MT
gi 81884360	Electron transfer flavoprotein subunit β	63.1	26	CS
gi 81884360	Electron transfer flavoprotein subunit β	57.3	14	PM
gi 81884360	Electron transfer flavoprotein subunit β	47.5	9	MT
gi 57527204	Electron-transfer-flavoprotein, α polypeptide precursor	77.8	35	CS
gi 57527204	Electron-transfer-flavoprotein, α polypeptide precursor	70.0	19	PM
gi 57527204	Electron-transfer-flavoprotein, α polypeptide precursor	46.6	12	MT
gi 52138635	Electron-transferring-flavoprotein dehydrogenase precursor	57.8	40	PM
gi 52138635	Electron-transferring-flavoprotein dehydrogenase precursor	58.8	43	MT
gi 50402096	Elongation factor 1-α 2	44.1	14	CS
gi 50402096	Elongation factor 1-α 2	38.4	10	PM
gi 50402096	Elongation factor 1-α 2	24.0	4	MT
gi 190359305	Elongation factor Tu, mitochondrial	62.4	21	PM
gi 190359305	Elongation factor Tu, mitochondrial	44.0	12	MT
gi 77917570	Endonuclease G	23.8	4	MT
gi 38649320	Eno1 protein	24.6	6	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 59808815	Enolase 1, α	26.5	6	MT
gi 54035288	Enolase 3, β , muscle	22.4	6	PM
gi 54035288	Enolase 3, β , muscle	28.3	5	MT
gi 157821153	Enoyl-CoA hydratase domain containing 2	21.6	1	PM
gi 82395853	Epidermal fatty acid binding protein 5	40.6	2	CS
gi 229485399	Erlin-2	13.0	3	PM
gi 197246046	Erythrocyte protein band 4.2	6.1	2	PM
gi 149051496	Erythroid spectrin β	25.0	32	PM
gi 83302472	ES1 protein homolog, mitochondrial	63.2	17	CS
gi 83302472	ES1 protein homolog, mitochondrial	43.2	10	PM
gi 83302472	ES1 protein homolog, mitochondrial	40.2	6	MT
gi 57529187	Esterase 1	22.2	7	CS
gi 81889423	Eukaryotic initiation factor 4A-II	23.6	4	CS
gi 85057089	Eukaryotic translation elongation factor 1 α 1	27.1	9	CS
gi 71051349	Eukaryotic translation elongation factor 1 γ	16.0	4	CS
gi 8393296	Eukaryotic translation elongation factor 2	8.4	2	PM
gi 8393296	Eukaryotic translation elongation factor 2	10.0	2	MT
gi 88909158	Eukaryotic translation initiation factor 3 subunit B	8.3	2	MT
gi 40786436	Eukaryotic translation initiation factor 4A1	28.3	3	CS
gi 91207082	Eukaryotic translation initiation factor 5A-1	55.8	4	CS
gi 91207082	Eukaryotic translation initiation factor 5A-1	20.1	2	PM
gi 81883744	Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	18.4	3	PM
gi 54261546	Fabp4 protein	76.5	23	CS
gi 54261546	Fabp4 protein	37.9	7	PM
gi 81883689	F-actin-capping protein subunit β	15.4	2	MT
gi 72255551	Family with sequence similarity 82, member B	19.4	5	CS
gi 72255551	Family with sequence similarity 82, member B	18.4	4	PM
gi 72255551	Family with sequence similarity 82, member B	23.2	7	MT
gi 204080	Fatty acid binding protein	93.2	56	CS
gi 204080	Fatty acid binding protein	96.2	19	PM
gi 157823017	Ferrochelatase	12.1	2	PM
gi 157823017	Ferrochelatase	13.3	2	MT
gi 6562849	Fetuin-like protein IRL685	23.0	8	CS
gi 4959650	Fibrillin-1	4.4	4	PM

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gi 4959650	Fibrillin-1	4.1	2	MT
gi 790487	Fibrinogen α-E subunit	27.0	12	CS
gi 790487	Fibrinogen α-E subunit	9.7	2	PM
gi 56971493	Fibrinogen β chain	42.2	9	CS
gi 56971493	Fibrinogen β chain	17.5	3	MT
gi 61098186	Fibrinogen γ chain	34.8	9	CS
gi 206725535	FK506 binding protein 3, 25kDa	10.3	1	PM
gi 6978487	Fructose-bisphosphate aldolase A	84.9	52	CS
gi 6978487	Fructose-bisphosphate aldolase A	54.7	18	PM
gi 56541238	Fumarate hydratase 1	44.8	13	PM
gi 73919838	Fumarylacetoacetate hydrolase domain-containing protein 1	27.2	2	CS
gi 229784139	Fumarylacetoacetate hydrolase domain-containing protein 2	15.3	3	CS
gi 51571949	G1 to S phase transition 1	7.4	2	CS
gi 197927125	Galectin-related protein	24.4	2	CS
gi 55741776	γ sarcoglycan	9.6	2	PM
gi 1183937	γ-fibrinogen	9.4	2	PM
gi 6978896	Gap junction protein, α 1	30.9	10	PM
gi 71534276	GDP dissociation inhibitor 1	30.0	4	CS
gi 77799118	GIMAP4	18.0	3	CS
gi 62945328	Glioblastoma amplified sequence	34.2	8	CS
gi 62945328	Glioblastoma amplified sequence	54.8	14	PM
gi 62945328	Glioblastoma amplified sequence	38.4	8	MT
gi 62078447	Globin, α	73.2	10	CS
gi 81892272	Glucose-6-phosphate isomerase	59.7	35	CS
gi 81892272	Glucose-6-phosphate isomerase	14.9	4	PM
gi 81892272	Glucose-6-phosphate isomerase	9.7	2	MT
gi 92090591	Glutamate dehydrogenase 1, mitochondrial	39.3	14	CS
gi 38197390	Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	30.8	8	PM
gi 38197390	Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	34.9	9	MT
gi 66910891	Glutamic-pyruvate transaminase (alanine aminotransferase)	11.1	1	CS
gi 78187979	Glutaredoxin 3	31.5	5	CS
gi 68138297	Glutathione peroxidase	83.6	14	CS
gi 90903249	Glutathione peroxidase 4 isoform A precursor	14.7	2	PM
gi 7188365	Glutathione S-transferase α	16.4	2	CS

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gi 208969735	Glutathione S-transferase α 3	17.1	2	CS
gi 208969713	Glutathione S-transferase α 4	26.1	4	CS
gi 28933457	Glutathione S-transferase μ 2	82.1	18	CS
gi 28933457	Glutathione S-transferase μ 2	20.6	2	PM
gi 28933457	Glutathione S-transferase μ 2	37.2	3	MT
gi 56090550	Glutathione S-transferase ω 1	23.7	3	CS
gi 529588	Glutathione S-transferase Yb3 subunit	67.9	10	CS
gi 9798638	Glyceraldehyde-3-phosphate dehydrogenase	60.7	23	PM
gi 9798638	Glyceraldehyde-3-phosphate dehydrogenase	61.9	17	MT
gi 57527919	Glycerol-3-phosphate dehydrogenase 1 (soluble)	33.5	7	CS
gi 6980978	Glycerol-3-phosphate dehydrogenase 2, mitochondrial precursor	8.4	1	MT
gi 204421	Glycogen phosphorylase	12.5	4	PM
gi 204421	Glycogen phosphorylase	11.9	4	MT
gi 6225463	Glycogenin-1	14.4	3	CS
gi 37589607	Glycoprotein, synaptic 2	9.7	3	PM
gi 37589607	Glycoprotein, synaptic 2	5.8	1	MT
gi 506417	Glycan	19.2	6	PM
gi 506417	Glycan	8.2	3	MT
gi 8928123	GMP reductase 1	25.2	3	CS
gi 253970435	GNAS complex locus XLas	10.1	6	PM
gi 253970435	GNAS complex locus XLas	7.9	4	MT
gi 149038203	Golgi apparatus protein 1	7.5	4	PM
gi 6970046	GPI-anchored ceruloplasmin	17.3	11	CS
gi 8927570	G-protein β -2 subunit	14.7	3	PM
gi 51260133	Group specific component	28.8	5	CS
gi 81883733	Growth hormone-inducible transmembrane protein	11.9	2	MT
gi 67678103	GrpE-like 1, mitochondrial	53.0	6	CS
gi 67678103	GrpE-like 1, mitochondrial	12.9	2	PM
gi 51338593	GTP-binding nuclear protein Ran	35.2	5	CS
gi 9837357	GTP-binding protein RAB11B	31.7	5	CS
gi 9837357	GTP-binding protein RAB11B	33.0	7	PM
gi 9837357	GTP-binding protein RAB11B	28.9	5	MT
gi 9837359	GTP-binding protein RAB7	32.9	4	PM
gi 9837359	GTP-binding protein RAB7	18.4	3	MT

# Accession	Protein name	% Cov	Peptides	Fraction
gi 9910706	Guanine deaminase	30.6	8	CS
gi 71089913	Guanine nucleotide binding protein α inhibiting 2	42.5	11	PM
gi 71089913	guanine nucleotide binding protein α inhibiting 2	19.4	3	MT
gi 54037164	Guanine nucleotide-binding protein subunit β -2-like 1	36.6	4	PM
gi 54037164	Guanine nucleotide-binding protein subunit β -2-like 1	45.7	5	MT
gi 56346	H2B histone	46.4	4	MT
gi 157823683	HD domain containing 2	15.6	1	CS
gi 157819889	HD domain containing 3	24.6	3	CS
gi 6981052	Heat shock 10 kDa protein 1	32.4	2	PM
gi 55977739	Heat shock 70 kDa protein 1A/1B	22.5	9	PM
gi 81886881	Heat shock 70 kDa protein 4	35.6	16	CS
gi 56383	Heat shock protein (hsp60) precursor	49.7	21	PM
gi 56383	Heat shock protein (hsp60) precursor	31.4	12	MT
gi 94400790	Heat shock protein 1	33.2	4	PM
gi 94400790	Heat shock protein 1	35.1	4	MT
gi 81890517	Heat shock protein 105 kDa	14.1	4	CS
gi 38303969	Heat shock protein 5	26.6	13	CS
gi 38303969	Heat shock protein 5	52.8	29	PM
gi 38303969	Heat shock protein 5	46.5	26	MT
gi 71051777	Heat shock protein 8	56.4	41	CS
gi 71051777	Heat shock protein 8	39.5	19	PM
gi 71051777	Heat shock protein 8	43.7	20	MT
gi 54673763	Heat shock protein 90, α (cytosolic), class A member 1	44.5	23	CS
gi 6016269	Heat shock protein β -2	61.0	3	CS
gi 6016271	Heat shock protein β -6	55.6	11	CS
gi 6016271	Heat shock protein β -6	21.0	3	PM
gi 157822045	Hedgehog acyltransferase-like	21.1	10	PM
gi 6981010	Hemoglobin α 1 chain	85.9	78	CS
gi 6981010	Hemoglobin α 1 chain	73.9	30	PM
gi 6981010	Hemoglobin α 1 chain	70.4	23	MT
gi 483109	Hemoglobin α -2 chain - rat (tentative semence)	48.5	14	CS
gi 60688311	Hemopexin	56.1	26	CS
gi 60688311	Hemopexin	19.6	6	PM
gi 60688311	Hemopexin	9.8	1	MT

# Accession	Protein name	% Cov	Peptides	Fraction
gi 52788205	Hepatoma-derived growth factor	18.1	2	CS
gi 149052456	Heterogeneous nuclear ribonucleoprotein H1, isoform CRA_b	9.6	2	CS
gi 48429097	Heterogeneous nuclear ribonucleoprotein K	15.1	1	CS
gi 6981022	Hexokinase 1	36.4	22	PM
gi 6981022	Hexokinase 1	34.9	18	MT
gi 183986567	HIG1 domain family, member 2A	33.0	2	MT
gi 31077132	Histidine rich calcium binding protein	30.2	16	MT
gi 149055944	Histidine rich calcium binding protein, isoform CRA_a	9.6	3	CS
gi 164565401	Histidine triad nucleotide binding protein 2	39.9	3	CS
gi 72679585	Histone cluster 1, H4b	31.1	3	PM
gi 72679585	Histone cluster 1, H4b	45.6	5	MT
gi 281312197	Histone H2A type 2-A	44.6	3	MT
gi 9624483	Hormone-regulated proliferation-associated 20 kDa protein short form	37.4	5	PM
gi 951425	Housekeeping protein	18.9	3	PM
gi 48734844	Hsd17b4 protein	4.9	2	PM
gi 48734844	Hsd17b4 protein	24.8	8	MT
gi 7387725	Hydroxyacyl-CoA dehydrogenase, mitochondrial	34.1	10	PM
gi 7387725	Hydroxyacyl-CoA dehydrogenase, mitochondrial	30.6	6	MT
gi 81907928	Hydroxysteroid dehydrogenase-like protein 2	37.4	11	CS
gi 81907928	Hydroxysteroid dehydrogenase-like protein 2	13.4	4	PM
gi 81907928	Hydroxysteroid dehydrogenase-like protein 2	11.3	4	MT
gi 157787020	Hypothetical protein LOC289278	31.6	3	PM
gi 157787020	Hypothetical protein LOC289278	22.2	2	MT
gi 158262028	Hypothetical protein LOC294231	9.0	1	PM
gi 187282120	Hypothetical protein LOC299909	18.8	2	CS
gi 157819345	Hypothetical protein LOC313776	22.8	7	MT
gi 157822273	Hypothetical protein LOC315463	13.5	2	PM
gi 157822273	Hypothetical protein LOC315463	18.7	2	MT
gi 157817209	Hypothetical protein LOC361606	27.4	2	CS
gi 157817213	Hypothetical protein LOC497874	38.2	2	PM
gi 157817213	Hypothetical protein LOC497874	38.2	4	MT
gi 157817241	Hypothetical protein LOC500694	25.3	2	CS
gi 155369672	Hypothetical protein LOC500874	17.6	4	PM
gi 155369672	Hypothetical protein LOC500874	26.8	3	MT

# Accession	Protein name	% Cov	Peptides	Fraction
gi 169234816	Hypothetical protein LOC681996	12.4	1	CS
gi 68534712	Hypoxanthine phosphoribosyltransferase 1	15.6	2	PM
gi 93279231	Chain A, Acyl-CoA Oxidase Complexed With 3-OH-Dodecanoate	10.9	2	MT
gi 28373861	Chain A, Annexin V K27e Mutant	71.2	18	CS
gi 9257037	Chain A, M-Calpain	18.6	4	CS
gi 93279422	Chain A, Rat Liver F1-Atpase	83.5	189	PM
gi 158428857	Chain A, Rat Phosphatidylethanolamine-Binding Protein	91.6	25	CS
gi 186973052	Chain A, Structure Of Rattus Norvegicus Ntpdase2 In Complex With Calcium And Amppnp	18.2	3	PM
gi 6435548	Chain B, Mammalian 2-Cys Peroxiredoxin, Hbp23	58.3	13	CS
gi 1942646	Chain B, Rat Procathepsin B	29.2	2	CS
gi 3318959	Chain B, Three-Dimensional Structure Of Nadph-Cytochrome P450 Reductase	19.7	7	PM
gi 3318959	Chain B, Three-Dimensional Structure Of Nadph-Cytochrome P450 Reductase	16.4	4	MT
gi 48425083	Chain D, Monoamine Oxidase A	53.9	26	PM
gi 48425083	Chain D, Monoamine Oxidase A	43.5	23	MT
gi 93279424	Chain G, Rat Liver F1-Atpase	56.8	32	PM
gi 81882496	Chaperone activity of bc1 complex-like, mitochondrial	25.0	9	CS
gi 81882496	Chaperone activity of bc1 complex-like, mitochondrial	18.2	6	PM
gi 81882496	Chaperone activity of bc1 complex-like, mitochondrial	11.7	4	MT
gi 149059759	Chaperonin subunit 8 (θ) (predicted), isoform CRA_a	6.9	2	CS
gi 312924	CHIP28k	19.3	1	MT
gi 149024253	Chloride intracellular channel 4, isoform CRA_b	34.0	4	CS
gi 623560	Immunoglobulin γ -2b	15.4	2	CS
gi 501064	Immunophilin FKBP12	40.7	3	CS
gi 149036390	Inner membrane protein, mitochondrial, isoform CRA_a	64.3	51	PM
gi 149036390	Inner membrane protein, mitochondrial, isoform CRA_a	60.1	57	MT
gi 157821079	Inosine triphosphatase	27.8	2	CS
gi 149027464	Insulin-like growth factor 2 receptor, isoform CRA_d	2.8	2	PM
gi 59808174	Inter α -trypsin inhibitor, heavy chain 4	16.9	7	CS
gi 59808174	Inter α -trypsin inhibitor, heavy chain 4	6.1	2	MT
gi 8393899	Inter- α trypsin inhibitor, heavy chain 3 precursor	11.8	7	CS
gi 68051964	Isocitrate dehydrogenase [NAD] subunit β , mitochondrial	24.9	6	PM
gi 68051964	Isocitrate dehydrogenase [NAD] subunit β , mitochondrial	18.7	5	MT
gi 6166247	Isocitrate dehydrogenase [NAD] subunit γ , mitochondrial	11.5	2	MT
gi 62079055	Isocitrate dehydrogenase 2 (NADP+), mitochondrial precursor	69.9	80	CS

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gi 62079055	Isocitrate dehydrogenase 2 (NADP+), mitochondrial precursor	71.2	36	PM
gi 149041699	Isocitrate dehydrogenase 3 (NAD+) α, isoform CRA_a	51.3	17	CS
gi 149041702	Isocitrate dehydrogenase 3 (NAD+) α, isoform CRA_d	35.6	7	PM
gi 149041704	Isocitrate dehydrogenase 3 (NAD+) α, isoform CRA_f	32.4	8	MT
gi 54020666	Isocitrate dehydrogenase 3, γ precursor	44.8	7	CS
gi 54020666	Isocitrate dehydrogenase 3, γ precursor	24.2	4	PM
gi 81863750	Isochorismatase domain-containing protein 1	20.5	1	CS
gi 6981112	Isovaleryl CoA dehydrogenase precursor	52.4	21	CS
gi 6981112	Isovaleryl CoA dehydrogenase precursor	42.0	10	PM
gi 6981112	Isovaleryl CoA dehydrogenase precursor	30.2	6	MT
gi 81885083	Junction plakoglobin	10.3	2	PM
gi 81885083	Junction plakoglobin	15.4	4	MT
gi 83816931	Junctophilin 2	24.1	7	MT
gi 8393610	Karyopherin (importin) β 1	12.9	2	CS
gi 120474989	Keratin 1	30.4	8	MT
gi 73920214	Keratin, type I cytoskeletal 19	18.6	4	MT
gi 81891699	Keratin, type II cytoskeletal 2 epidermal	34.7	7	MT
gi 81891700	Keratin, type II cytoskeletal 73	13.2	4	MT
gi 83776543	Kinesin family member 5B	9.5	2	CS
gi 80861401	Kininogen 1	22.6	7	CS
gi 81861882	Kynurenine--oxoglutarate transaminase 3	10.8	2	CS
gi 157820173	L-2-hydroxyglutarate dehydrogenase	14.3	3	PM
gi 157820173	L-2-hydroxyglutarate dehydrogenase	10.8	2	MT
gi 8393706	Lactate dehydrogenase A	32.2	7	PM
gi 8393706	Lactate dehydrogenase A	23.5	8	MT
gi 81885359	Lactoylglutathione lyase	54.9	4	CS
gi 149048132	Lamin A, isoform CRA_b	11.3	2	MT
gi 8393693	Laminin receptor 1	30.5	4	PM
gi 8393693	Laminin receptor 1	20.0	3	MT
gi 157818227	Laminin, β 1	2.5	2	PM
gi 281371490	Laminin, γ 1	6.5	1	MT
gi 9845261	Lectin, galactoside-binding, soluble, 1	46.7	5	CS
gi 9845261	Lectin, galactoside-binding, soluble, 1	37.0	6	PM
gi 9845261	Lectin, galactoside-binding, soluble, 1	43.0	6	MT

# Accession	Protein name	% Cov	Peptides	Fraction
gi 169234844	Lectin, mannose-binding 2	12.9	1	PM
gi 169234844	Lectin, mannose-binding 2	11.7	2	MT
gi 687712	Lens epithelial protein	23.8	4	CS
gi 62510718	LETM1 and EF-hand domain-containing protein 1, mitochondrial	31.4	10	PM
gi 62510718	LETM1 and EF-hand domain-containing protein 1, mitochondrial	19.4	12	MT
gi 81871846	Leucine-rich PPR motif-containing protein, mitochondrial	22.6	13	CS
gi 149050517	Leucine-rich PPR-motif containing, isoform CRA_b	12.5	4	PM
gi 19424264	Leucyl/cysteinyl aminopeptidase isoform 2	7.9	2	PM
gi 397357	L-iditol 2-dehydrogenase	15.8	3	CS
gi 56676346	LIM and cysteine-rich domains 1	16.4	2	CS
gi 6981168	Lipoprotein lipase precursor	9.7	2	PM
gi 6981168	Lipoprotein lipase precursor	13.3	2	MT
gi 6981146	L-lactate dehydrogenase B	58.4	55	CS
gi 6981146	L-lactate dehydrogenase B	41.0	14	PM
gi 56788960	LOC367586 protein	25.6	6	CS
gi 60688598	LOC367586 protein	16.8	3	PM
gi 68534280	LOC500183 protein	23.5	3	CS
gi 71051822	LOC683313 protein	22.3	5	MT
gi 81916424	Lon protease homolog, mitochondrial	6.5	2	PM
gi 81916424	Lon protease homolog, mitochondrial	5.6	2	MT
gi 6978431	Long-chain acyl-CoA dehydrogenase precursor	63.7	64	CS
gi 6978431	Long-chain acyl-CoA dehydrogenase precursor	56.3	33	PM
gi 5759131	Low molecular weight protein tyrosine phosphatase isoform A	40.5	2	CS
gi 149062241	LRP16 protein	32.8	7	CS
gi 37361818	LRRGT00066	11.0	2	PM
gi 643024	Lumican, secretory interstitial proteoglycan	26.3	4	CS
gi 226694805	LYR motif-containing protein 7	49.0	1	CS
gi 6981362	Lysophospholipase 1	20.0	3	CS
gi 6981144	Lysosomal-associated membrane protein 1 precursor	15.7	2	MT
gi 32129697	MACRO domain-containing protein 1	23.3	2	PM
gi 694108	Macrophage migration inhibitory factor	47.8	4	CS
gi 81884568	Macrophage-capping protein	16.3	3	CS
gi 81861572	Malate dehydrogenase, cytoplasmic	52.1	50	CS
gi 81861572	Malate dehydrogenase, cytoplasmic	43.7	12	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 81861572	Malate dehydrogenase, cytoplasmic	38.6	11	MT
gi 42476181	Malate dehydrogenase, mitochondrial precursor	72.5	47	CS
gi 42476181	Malate dehydrogenase, mitochondrial precursor	71.6	29	PM
gi 42476181	Malate dehydrogenase, mitochondrial precursor	68.3	22	MT
gi 62510703	Mannose-6-phosphate isomerase	9.0	2	CS
gi 8392833	Medium-chain acyl-CoA dehydrogenase precursor	49.6	17	CS
gi 8392833	Medium-chain acyl-CoA dehydrogenase precursor	39.2	15	PM
gi 8392833	Medium-chain acyl-CoA dehydrogenase precursor	18.3	6	MT
gi 62900631	Membrane-associated progesterone receptor component 2	10.6	2	PM
gi 55824737	Mercaptopyruvate sulfurtransferase	42.1	9	CS
gi 56605654	Metaxin 2	36.9	6	PM
gi 56605654	Metaxin 2	28.9	9	MT
gi 81883845	Methylcrotonoyl-CoA carboxylase β chain, mitochondrial	29.3	10	PM
gi 81883845	Methylcrotonoyl-CoA carboxylase β chain, mitochondrial	13.0	2	MT
gi 81882966	Methylcrotonoyl-CoA carboxylase subunit α, mitochondrial	21.7	9	PM
gi 81882966	Methylcrotonoyl-CoA carboxylase subunit α, mitochondrial	13.0	6	MT
gi 400269	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	70.8	50	CS
gi 400269	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	49.2	19	PM
gi 400269	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	29.4	13	MT
gi 157821869	Methylmalonyl CoA epimerase	46.6	4	CS
gi 710563	MHC class I protein	18.9	2	MT
gi 81909845	Microtubule-associated protein 4	8.4	3	CS
gi 2780408	MIPP65	33.2	15	PM
gi 47605758	Mitofusin-1	10.9	4	PM
gi 47605758	Mitofusin-1	8.9	2	MT
gi 166851834	Mitochondria-associated granulocyte macrophage CSF signaling molecule	40.8	3	PM
gi 166851834	Mitochondria-associated granulocyte macrophage CSF signaling molecule	32.0	3	MT
gi 81170680	Mitochondrial antiviral-signaling protein	26.8	3	MT
gi 165971637	Mitochondrial carrier homolog 2	41.3	10	MT
gi 165971637	Mitochondrial carrier homolog 2	28.4	7	PM
gi 94711371	Mitochondrial fission 1 protein	44.1	4	PM
gi 94711371	Mitochondrial fission 1 protein	59.2	6	MT
gi 59800393	Mitochondrial import inner membrane translocase subunit Tim13	41.1	2	CS
gi 59800393	Mitochondrial import inner membrane translocase subunit Tim13	57.9	3	MT

# Accession	Protein name	% Cov	Peptides	Fraction
gi 90110082	Mitochondrial import inner membrane translocase subunit Tim9	47.2	3	PM
gi 90110082	Mitochondrial import inner membrane translocase subunit Tim9	33.7	2	MT
gi 81864913	Mitochondrial import receptor subunit TOM22 homolog	56.3	6	PM
gi 81864912	Mitochondrial import receptor subunit TOM40 homolog	19.4	4	MT
gi 81911805	Mitochondrial import receptor subunit TOM70	21.8	3	PM
gi 81911805	Mitochondrial import receptor subunit TOM70	17.5	4	MT
gi 206597496	Mitochondrial isoleucine tRNA synthetase	17.1	2	CS
gi 206597496	Mitochondrial isoleucine tRNA synthetase	8.9	2	PM
gi 510110	Mitochondrial long-chain 3-ketoacyl-CoA thiolase β subunit	20.4	4	CS
gi 510110	Mitochondrial long-chain 3-ketoacyl-CoA thiolase β subunit	64.2	36	PM
gi 510110	Mitochondrial long-chain 3-ketoacyl-CoA thiolase β subunit	66.3	34	MT
gi 239049264	Mitochondrial malic enzyme 3	27.6	12	CS
gi 239049264	Mitochondrial malic enzyme 3	9.6	3	PM
gi 56553296	Mitochondrial OPA1	67.6	2	MT
gi 599963	Mitochondrial oxidative phosphorylation coupling factor 6	62.0	31	PM
gi 599963	Mitochondrial oxidative phosphorylation coupling factor 6	62.0	32	MT
gi 55741522	Mitochondrial protein 18 kDa	21.1	3	PM
gi 55741522	Mitochondrial protein 18 kDa	19.9	2	MT
gi 71361655	Mitochondrial ribosomal protein L12	12.0	2	PM
gi 157820131	Mitochondrial ribosomal protein S35	10.6	2	PM
gi 149042266	Moesin, isoform CRA_a	35.4	10	PM
gi 32363196	Moesin	10.2	2	MT
gi 81882200	MOSC domain-containing protein 2, mitochondrial	13.3	1	MT
gi 68534595	Mtx1 protein	11.5	3	PM
gi 68534595	Mtx1 protein	8.1	1	MT
gi 81870614	Murinoglobulin-1	42.2	52	CS
gi 81872292	Murinoglobulin-2	7.8	6	PM
gi 6978661	Muscle creatine kinase	84.3	83	CS
gi 6978661	Muscle creatine kinase	70.9	23	PM
gi 6978661	Muscle creatine kinase	57.5	19	MT
gi 158138498	Muscle glycogen phosphorylase	71.1	82	CS
gi 535069	Muscle LIM protein	48.5	5	CS
gi 535069	Muscle LIM protein	19.1	2	PM
gi 81870810	Myeloid-associated differentiation marker	9.4	2	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 197927186	Myofibrillogenesis regulator 1 isoform 3	35.2	3	PM
gi 197927186	Myofibrillogenesis regulator 1 isoform 3	43.0	3	MT
gi 78099013	Myoglobin	94.2	103	CS
gi 78099013	Myoglobin	89.6	24	PM
gi 78099013	Myoglobin	81.8	19	MT
gi 281306803	Myomesin 2	18.4	10	CS
gi 157824043	Myosin binding protein C, cardiac	4.5	2	CS
gi 400429	Myosin I heavy chain	16.6	7	PM
gi 160961485	Myosin light chain kinase 3	30.7	6	CS
gi 149066032	Myosin, heavy polypeptide 9, non-muscle	11.5	2	CS
gi 149066032	Myosin, heavy polypeptide 9, non-muscle	9.1	8	PM
gi 149066032	Myosin, heavy polypeptide 9, non-muscle	12.2	8	MT
gi 266495	Myristoylated alanine-rich C-kinase substrate	25.9	3	MT
gi 6831527	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	22.8	5	CS
gi 6978543	Na+/K+ -ATPase α 1 subunit precursor	49.1	53	PM
gi 6978543	Na+/K+ -ATPase α 1 subunit precursor	28.3	25	MT
gi 6978545	Na+/K+ -ATPase α 2 subunit precursor	28.5	28	PM
gi 6978545	Na+/K+ -ATPase α 2 subunit precursor	18.5	11	MT
gi 81884377	NAD-dependent deacetylase sirtuin-5	22.9	2	CS
gi 6981260	NADH dehydrogenase (ubiquinone) 1 α subcomplex 5	91.4	10	PM
gi 6981260	NADH dehydrogenase (ubiquinone) 1 α subcomplex 5	90.5	8	MT
gi 157818537	NADH dehydrogenase (ubiquinone) 1 α subcomplex, 1	23.3	1	PM
gi 164565371	NADH dehydrogenase (ubiquinone) 1 α subcomplex, 12	82.8	15	PM
gi 164565371	NADH dehydrogenase (ubiquinone) 1 α subcomplex, 12	79.3	12	MT
gi 157817861	NADH dehydrogenase (ubiquinone) 1 α subcomplex, 2	67.0	7	PM
gi 157817861	NADH dehydrogenase (ubiquinone) 1 α subcomplex, 2	76.3	7	MT
gi 189085365	NADH dehydrogenase (ubiquinone) 1 α subcomplex, 4	64.6	31	PM
gi 189085365	NADH dehydrogenase (ubiquinone) 1 α subcomplex, 4	63.4	25	MT
gi 194473636	NADH dehydrogenase (ubiquinone) 1 α subcomplex, 6	73.1	15	PM
gi 194473636	NADH dehydrogenase (ubiquinone) 1 α subcomplex, 6	70.8	15	MT
gi 149038913	NADH dehydrogenase (ubiquinone) 1 α subcomplex, 8	82.0	13	PM
gi 149038913	NADH dehydrogenase (ubiquinone) 1 α subcomplex, 8	82.0	15	MT
gi 157824071	NADH dehydrogenase (ubiquinone) 1 β subcomplex 3	40.4	4	PM
gi 157824071	NADH dehydrogenase (ubiquinone) 1 β subcomplex 3	40.4	3	MT

# Accession	Protein name	% Cov	Peptides	Fraction
gi 82617686	NADH dehydrogenase (ubiquinone) 1 β subcomplex 4	64.3	17	PM
gi 82617686	NADH dehydrogenase (ubiquinone) 1 β subcomplex 4	72.1	15	MT
gi 187469737	NADH dehydrogenase (ubiquinone) 1 β subcomplex 8	57.0	19	PM
gi 187469737	NADH dehydrogenase (ubiquinone) 1 β subcomplex 8	63.4	17	MT
gi 157822175	NADH dehydrogenase (ubiquinone) 1 β subcomplex, 10	80.7	28	PM
gi 157822175	NADH dehydrogenase (ubiquinone) 1 β subcomplex, 10	83.0	29	MT
gi 157822851	NADH dehydrogenase (ubiquinone) 1 β subcomplex, 11	53.6	11	PM
gi 157822851	NADH dehydrogenase (ubiquinone) 1 β subcomplex, 11	71.5	15	MT
gi 219277692	NADH dehydrogenase (ubiquinone) 1 β subcomplex, 2	22.9	2	PM
gi 219277692	NADH dehydrogenase (ubiquinone) 1 β subcomplex, 2	22.9	2	MT
gi 157823387	NADH dehydrogenase (ubiquinone) 1 β subcomplex, 5	33.9	9	PM
gi 157823387	NADH dehydrogenase (ubiquinone) 1 β subcomplex, 5	36.5	8	MT
gi 157820465	NADH dehydrogenase (ubiquinone) 1 β subcomplex, 6	54.7	4	PM
gi 157820465	NADH dehydrogenase (ubiquinone) 1 β subcomplex, 6	59.4	6	MT
gi 157823197	NADH dehydrogenase (ubiquinone) 1 β subcomplex, 7	74.5	17	PM
gi 157823197	NADH dehydrogenase (ubiquinone) 1 β subcomplex, 7	74.5	15	MT
gi 197245756	NADH dehydrogenase (ubiquinone) 1 β subcomplex, 9	73.7	23	PM
gi 197245756	NADH dehydrogenase (ubiquinone) 1 β subcomplex, 9	59.8	23	MT
gi 157820787	NADH dehydrogenase (ubiquinone) 1, α / β subcomplex, 1	36.5	12	PM
gi 57164133	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	50.8	13	PM
gi 57164133	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	55.0	11	MT
gi 157817227	NADH dehydrogenase (ubiquinone) Fe-S protein 3	73.5	24	MT
gi 149022594	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (predicted), isoform CRA_b	65.6	23	PM
gi 72086149	NADH dehydrogenase (ubiquinone) Fe-S protein 5b	73.6	13	PM
gi 72086149	NADH dehydrogenase (ubiquinone) Fe-S protein 5b	72.6	14	MT
gi 56606108	NADH dehydrogenase (ubiquinone) Fe-S protein 7	48.2	17	PM
gi 56606108	NADH dehydrogenase (ubiquinone) Fe-S protein 7	50.0	20	MT
gi 81882328	NADH dehydrogenase [ubiquinone] 1 α subcomplex subunit 10, mitochondrial	84.5	43	PM
gi 52000746	NADH dehydrogenase [ubiquinone] 1 α subcomplex subunit 11	36.2	7	PM
gi 52000746	NADH dehydrogenase [ubiquinone] 1 α subcomplex subunit 11	36.2	8	MT
gi 81882598	NADH dehydrogenase [ubiquinone] 1 α subcomplex subunit 9, mitochondrial	74.9	38	PM
gi 83305118	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	68.6	27	PM
gi 83305118	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	80.7	26	MT
gi 81890431	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	77.8	43	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 81890431	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	73.4	39	MT
gi 81889861	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	65.7	20	PM
gi 81889861	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	44.6	21	MT
gi 228015040	NADH dehydrogenase subunit 4	8.9	4	PM
gi 55741424	NADH dehydrogenase ubiquinone flavoprotein 1 precursor	25.0	4	CS
gi 55741424	NADH dehydrogenase ubiquinone flavoprotein 1 precursor	68.1	46	PM
gi 55741424	NADH dehydrogenase ubiquinone flavoprotein 1 precursor	76.1	42	MT
gi 81882716	NADH-cytochrome b5 reductase 1	24.3	2	PM
gi 81882716	NADH-cytochrome b5 reductase 1	10.8	2	MT
gi 81884209	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	72.6	64	PM
gi 81884209	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	72.4	75	MT
gi 163916626	Ndufa3 protein	49.4	3	PM
gi 163916626	Ndufa3 protein	49.4	2	MT
gi 163915993	Ndufa7 protein	75.0	11	PM
gi 163915993	Ndufa7 protein	75.9	12	MT
gi 165971299	Ndufs8 protein	55.2	14	PM
gi 165971299	Ndufs8 protein	61.8	10	MT
gi 212288176	Neutral cholesterol ester hydrolase 1	10.3	3	PM
gi 212288176	Neutral cholesterol ester hydrolase 1	19.1	4	MT
gi 40538874	Nexilin (F actin binding protein) isoform b	8.9	2	MT
gi 76880449	NFS1 nitrogen fixation 1 homolog	9.8	2	CS
gi 61557127	Nicotinamide nucleotide transhydrogenase	48.4	76	PM
gi 68565643	Nicotinamide phosphoribosyltransferase	23.6	3	CS
gi 77628000	Nitrilase family, member 2	59.1	11	CS
gi 81888874	NLR family member X1	13.3	6	PM
gi 81888874	NLR family member X1	20.5	5	MT
gi 6822247	Nogo-A protein	7.7	5	PM
gi 7839520	NPW16	60.7	6	PM
gi 48734832	NSFL1 (p97) cofactor (p47)	28.1	4	MT
gi 9910324	Nuclear protein E3-3 isoform a	21.1	3	MT
gi 55926145	Nucleoside diphosphate kinase B	88.2	21	CS
gi 55926145	Nucleoside diphosphate kinase B	63.2	8	PM
gi 55926145	Nucleoside diphosphate kinase B	50.0	4	MT
gi 81883766	OCIA domain-containing protein 1	52.2	5	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 81883766	OCIA domain-containing protein 1	50.2	5	MT
gi 83405907	Optic atrophy 1 homolog	30.1	22	PM
gi 83405907	Optic atrophy 1 homolog	34.9	32	MT
gi 38181818	Ornithine aminotransferase	27.8	5	CS
gi 5106930	Outer membrane protein	49.0	6	MT
gi 274318365	Oxidase assembly 1-like	11.6	4	PM
gi 81912692	Paraplegin	11.3	3	PM
gi 81912692	Paraplegin	12.2	3	MT
gi 66911068	Pcbp2 protein	14.9	2	CS
gi 50925459	Pcyt2 protein	17.1	2	CS
gi 60688224	Pdhx protein	24.7	4	CS
gi 8393153	PDZ and LIM domain 1	11.3	2	CS
gi 56268806	Peptidylprolyl isomerase F (cyclophilin F)	56.8	7	CS
gi 56268806	Peptidylprolyl isomerase F (cyclophilin F)	28.2	3	PM
gi 56268806	Peptidylprolyl isomerase F (cyclophilin F)	24.3	2	MT
gi 34849738	Peroxiredoxin 2	62.1	12	CS
gi 149040547	Peroxiredoxin 3	44.8	15	PM
gi 149040547	Peroxiredoxin 3	21.4	5	MT
gi 51261175	Peroxiredoxin 5	62.0	10	CS
gi 5902791	Peroxiredoxin-6	67.4	22	CS
gi 5902791	Peroxiredoxin-6	25.0	4	PM
gi 5902791	Peroxiredoxin-6	22.8	4	MT
gi 6491860	Peroxisomal 2,4-dienoyl CoA reductase	23.1	4	PM
gi 81883743	Peroxisomal 3,2-trans-enoyl-CoA isomerase	17.7	5	CS
gi 81883743	Peroxisomal 3,2-trans-enoyl-CoA isomerase	11.5	4	PM
gi 81883743	Peroxisomal 3,2-trans-enoyl-CoA isomerase	9.7	1	MT
gi 76781470	Peroxisomal short-chain alcohol dehydrogenase	15.1	2	PM
gi 76781470	Peroxisomal short-chain alcohol dehydrogenase	13.3	3	MT
gi 41350889	Pgam1 protein	66.5	22	CS
gi 41350889	Pgam1 protein	18.1	3	PM
gi 118764083	Pgm1 protein	49.9	22	CS
gi 67460102	Phosphatidate cytidylyltransferase 2	10.4	3	PM
gi 67460102	Phosphatidate cytidylyltransferase 2	10.4	3	MT
gi 8393910	Phosphatidylethanolamine binding protein	40.1	4	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 8393910	Phosphatidylethanolamine binding protein	20.9	3	MT
gi 62825891	Phosphofructokinase, muscle	26.2	7	CS
gi 56585024	Phosphoglycerate kinase 1	77.2	42	CS
gi 56585024	Phosphoglycerate kinase 1	30.0	7	PM
gi 56585024	Phosphoglycerate kinase 1	25.7	8	MT
gi 8393948	Phosphoglycerate mutase 2	51.0	29	CS
gi 8393948	Phosphoglycerate mutase 2	35.2	7	PM
gi 164663846	Phosphohistidine phosphatase 1	58.9	6	CS
gi 22654268	Phospholemmann	38.0	3	PM
gi 158341684	Phospholipase A2, activating protein	10.1	2	CS
gi 197246445	Phosphomannomutase 2	26.0	6	CS
gi 171846774	Phosphorylase, glycogen, muscle	13.1	6	PM
gi 157819139	Pitrysin metallopeptidase 1	7.0	2	CS
gi 60688649	Plasminogen	9.0	4	PM
gi 60688649	Plasminogen	10.8	3	MT
gi 51702760	Platelet-activating factor acetylhydrolase IB subunit α	14.4	3	CS
gi 157786694	Polymerase I and transcript release factor	53.3	21	PM
gi 157786694	Polymerase I and transcript release factor	16.6	3	CS
gi 71122474	Ppa1 protein	22.7	3	CS
gi 38541053	Ppib protein	16.7	2	PM
gi 57012987	PRA1 family protein 3	19.7	2	PM
gi 158706096	Pre-B-cell leukemia transcription factor-interacting protein 1	16.5	6	PM
gi 158706096	Pre-B-cell leukemia transcription factor-interacting protein 1	15.1	5	MT
gi 55855	Precursor (AA -17 to 399)	51.2	10	PM
gi 55855	Precursor (AA -17 to 399)	19.7	5	MT
gi 56072	Precursor polypeptide (AA -29 to 261)	48.6	21	CS
gi 56072	Precursor polypeptide (AA -29 to 261)	53.1	12	PM
gi 56164	Precursor polypeptide (AA -32 to 2445)	2.0	1	PM
gi 56164	Precursor polypeptide (AA -32 to 2445)	3.1	3	MT
gi 109511985	PREDICTED: hypothetical protein	29.8	6	PM
gi 109511985	PREDICTED: hypothetical protein	29.5	7	MT
gi 62655115	PREDICTED: similar to 40S ribosomal protein S2	20.3	3	MT
gi 27658914	PREDICTED: similar to 60S ribosomal protein L21	22.6	1	PM
gi 62638415	PREDICTED: similar to 60S ribosomal protein L26 (SIG-20)	22.8	4	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 62638415	PREDICTED: similar to 60S ribosomal protein L26 (SIG-20)	22.8	4	MT
gi 62639430	PREDICTED: similar to 60S ribosomal protein L27a	33.1	2	PM
gi 109490334	PREDICTED: similar to 60S ribosomal protein L3-like	13.0	4	PM
gi 109490334	PREDICTED: similar to 60S ribosomal protein L3-like	24.3	6	MT
gi 62642554	PREDICTED: similar to 60S ribosomal protein L7a	13.9	3	PM
gi 62642554	PREDICTED: similar to 60S ribosomal protein L7a	22.6	4	MT
gi 109463553	PREDICTED: similar to AHNAK nucleoprotein isoform 1 isoform 3	20.7	6	CS
gi 109463555	PREDICTED: similar to AHNAK nucleoprotein isoform 1 isoform 4	20.1	5	PM
gi 62664437	PREDICTED: similar to Aldehyde dehydrogenase family 7, member A1	25.2	6	CS
gi 62648070	PREDICTED: similar to Aldose reductase	11.4	2	PM
gi 109468300	PREDICTED: similar to α-enolase (Enolase 1)	63.4	35	CS
gi 109496584	PREDICTED: similar to ATP synthase F0, H+ transporting, subunit f, isoform 2	29.7	8	PM
gi 109496584	PREDICTED: similar to ATP synthase F0, H+ transporting, subunit f, isoform 2	29.7	9	MT
gi 62646841	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2	43.6	29	PM
gi 62646841	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2	48.2	25	MT
gi 109512256	PREDICTED: similar to Cation-dependent mannose-6-phosphate receptor	17.0	2	PM
gi 109497479	PREDICTED: similar to CG2453-PA	25.1	8	PM
gi 109461675	PREDICTED: similar to Cytochrome c oxidase, subunit VIb polypeptide 1	66.7	32	MT
gi 109511686	PREDICTED: similar to Cytochrome c-type heme lyase	35.8	9	PM
gi 109511686	PREDICTED: similar to Cytochrome c-type heme lyase	36.1	6	MT
gi 109484674	PREDICTED: similar to Dihydrolipoamide S-acetyltransferase	37.1	11	MT
gi 62657092	PREDICTED: similar to Dual specificity protein phosphatase 3 (T-DSP11)	24.0	1	CS
gi 109511865	PREDICTED: similar to Dystrophin, muscular dystrophy	6.3	2	PM
gi 109501906	PREDICTED: similar to F11C1.5a	8.1	5	CS
gi 109501906	PREDICTED: similar to F11C1.5a	6.6	1	PM
gi 62646949	PREDICTED: similar to Filamin-C	10.9	8	CS
gi 62646949	PREDICTED: similar to Filamin-C	5.4	3	MT
gi 62653546	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase	79.6	73	CS
gi 109485458	PREDICTED: similar to Glycerol-3-phosphate dehydrogenase 1-like	32.5	5	CS
gi 109476173	PREDICTED: similar to High mobility group protein 1	31.2	7	CS
gi 109490737	PREDICTED: similar to Histidine triad nucleotide-binding protein 1	55.4	4	CS
gi 27693406	PREDICTED: similar to Histone H2B 291B isoform 2	42.9	5	PM
gi 109501541	PREDICTED: similar to Kinectin 1	7.7	2	MT
gi 109460394	PREDICTED: similar to Laminin α-2 chain precursor	4.9	3	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 62643486	PREDICTED: similar to Large subunit ribosomal protein L36a	17.0	3	PM
gi 62654757	PREDICTED: similar to Methylmalonyl-CoA mutase, mitochondrial precursor	18.9	4	CS
gi 109498993	PREDICTED: similar to Microsomal glutathione S-transferase 3	35.3	6	MT
gi 109466625	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	12.8	1	PM
gi 109477385	PREDICTED: similar to Protein 4.1 (Band 4.1) (P4.1) (4.1R)	8.0	2	PM
gi 62651145	PREDICTED: similar to Protein C14orf159, mitochondrial precursor	15.9	2	CS
gi 109502869	PREDICTED: similar to RAN binding protein 5	9.4	3	CS
gi 27664676	PREDICTED: similar to Ribosomal protein L10	15.4	2	MT
gi 62654783	PREDICTED: similar to Ribosomal protein L10a	18.0	4	PM
gi 62658447	PREDICTED: similar to Ribosomal protein L15	18.6	2	PM
gi 109511626	PREDICTED: similar to Ribosomal protein L21	21.1	2	MT
gi 27680589	PREDICTED: similar to Ribosomal protein L31	31.5	2	MT
gi 62655953	PREDICTED: similar to Ribosomal protein S10	42.4	4	PM
gi 62660444	PREDICTED: similar to Ribosomal protein S23	16.1	2	MT
gi 109482126	PREDICTED: similar to Ribosomal protein S24	20.7	2	PM
gi 109482126	PREDICTED: similar to Ribosomal protein S24	25.2	1	MT
gi 109470913	PREDICTED: similar to Ribosome-binding protein 1	19.3	3	MT
gi 34867677	PREDICTED: similar to Serine protease inhibitor A3M precursor	26.7	9	CS
gi 34854800	PREDICTED: similar to Solute carrier family 25, member 12	33.5	8	PM
gi 109495987	PREDICTED: similar to Tescalcin	34.1	3	CS
gi 109470142	PREDICTED: similar to Titin isoform N2-B	25.4	405	MT
gi 109483017	PREDICTED: similar to Tubulin cofactor a (predicted)	25.7	2	CS
gi 55882	Preprocathepsin D	7.4	2	PM
gi 55882	Preprocathepsin D	11.3	3	MT
gi 77748257	Presenilin associated, rhomboid-like	6.6	1	MT
gi 9653968	Prion protein	16.9	2	PM
gi 5305687	Pro- α -2(I) collagen	23.9	8	MT
gi 73919297	Probable saccharopine dehydrogenase	25.9	3	PM
gi 73919297	Probable saccharopine dehydrogenase	12.4	3	MT
gi 149043683	Procollagen, type VI, α 1 (predicted), isoform CRA_b	14.2	4	PM
gi 149043683	Procollagen, type VI, α 1 (predicted), isoform CRA_b	11.8	5	MT
gi 149037631	Procollagen, type VI, α 3 (predicted), isoform CRA_c	15.0	15	MT
gi 149045856	Procollagen, type XV, isoform CRA_b	5.5	4	PM
gi 149045856	Procollagen, type XV, isoform CRA_b	10.7	3	MT

# Accession	Protein name	% Cov	Peptides	Fraction
gi 51702769	Profilin-1	65.7	6	CS
gi 66911717	Prohibitin	76.5	17	PM
gi 66911717	Prohibitin	76.5	19	MT
gi 76363296	Prohibitin-2	75.9	26	PM
gi 76363296	Prohibitin-2	74.3	23	MT
gi 6981324	Prolyl 4-hydroxylase, β polypeptide	28.4	9	CS
gi 6981324	Prolyl 4-hydroxylase, β polypeptide	17.3	5	PM
gi 6981324	Prolyl 4-hydroxylase, β polypeptide	14.2	3	MT
gi 51260066	Propionyl CoA carboxylase, β polypeptide	44.0	11	CS
gi 51260066	Propionyl CoA carboxylase, β polypeptide	36.8	10	PM
gi 158303308	Propionyl-coenzyme A carboxylase, α polypeptide	28.8	12	CS
gi 157822395	Prostaglandin E synthase 2	48.7	9	PM
gi 157822395	Prostaglandin E synthase 2	39.1	9	MT
gi 38197361	Prostaglandin I2 (prostacyclin) synthase	7.0	2	MT
gi 206558239	Prostaglandin reductase 2	19.9	4	CS
gi 61098214	Protease (prosome, macropain) 28 subunit, α	17.3	4	CS
gi 6981420	Protease, serine, 2 precursor	17.9	20	PM
gi 6981420	Protease, serine, 2 precursor	19.9	18	MT
gi 8394091	Proteasome activator subunit 2	21.0	1	CS
gi 81884895	Protein BAT5	7.9	2	PM
gi 62296810	Protein disulfide-isomerase A6	23.4	6	PM
gi 62296810	Protein disulfide-isomerase A6	21.1	6	MT
gi 56404680	Protein DJ-1	57.7	7	CS
gi 29611707	Protein ERGIC-53	25.7	8	PM
gi 76880465	Protein kinase C and casein kinase substrate in neurons 2	6.4	2	PM
gi 71681475	Protein kinase C and casein kinase substrate in neurons 3	16.8	5	PM
gi 81870080	Protein kinase C δ-binding protein	9.9	2	PM
gi 171846648	Protein kinase C substrate 80K-H	8.2	2	PM
gi 171846648	Protein kinase C substrate 80K-H	8.8	3	MT
gi 6981396	Protein kinase, cAMP dependent regulatory, type I, α	28.1	6	CS
gi 81867103	Protein NDRG2	29.1	5	CS
gi 81867103	Protein NDRG2	49.6	13	PM
gi 81867103	Protein NDRG2	38.5	5	MT
gi 6981388	Protein phosphatase 1, catalytic subunit, β	10.7	3	MT

# Accession	Protein name	% Cov	Peptides	Fraction
gi 8394021	Protein phosphatase 2a, catalytic subunit, β isoform	34.3	3	CS
gi 663080	Protein phosphatase T (PPT)	12.6	1	CS
gi 155369684	Protein tyrosine phosphatase-like, member a	5.2	2	PM
gi 56961640	Protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	40.5	5	CS
gi 73621422	Protein-tyrosine phosphatase mitochondrial 1	16.1	1	PM
gi 4336877	PRx III	23.4	7	PM
gi 205829287	Purine nucleoside phosphorylase	30.1	5	CS
gi 81884356	Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2	8.8	4	PM
gi 81884356	Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2	4.6	2	MT
gi 56268822	Pyridoxine 5'-phosphate oxidase	15.7	2	CS
gi 209529636	Pyrophosphatase (inorganic) 2	39.1	10	CS
gi 209529636	Pyrophosphatase (inorganic) 2	8.5	2	PM
gi 71051030	Pyruvate dehydrogenase (lipoamide) α 1	39.2	10	MT
gi 56090293	Pyruvate dehydrogenase (lipoamide) β precursor	61.0	26	PM
gi 59709473	Pyruvate dehydrogenase kinase 1 precursor	18.2	4	PM
gi 694003	Pyruvate dehydrogenase kinase 2 subunit p45	20.9	2	PM
gi 61889071	RAB10, member RAS oncogene family	15.5	3	PM
gi 61889071	RAB10, member RAS oncogene family	29.0	4	MT
gi 158341664	RAB1B, member RAS oncogene family	68.2	10	PM
gi 158341664	RAB1B, member RAS oncogene family	67.7	8	MT
gi 149061036	RAB2, member RAS oncogene family	23.5	3	MT
gi 149029654	RAB5B, member RAS oncogene family (predicted), isoform CRA_c	16.3	2	PM
gi 149029654	RAB5B, member RAS oncogene family (predicted), isoform CRA_c	11.2	2	MT
gi 165970759	Rab5c protein	19.9	4	MT
gi 54114993	RAP1A, member of RAS oncogene family precursor	54.9	5	PM
gi 54114993	RAP1A, member of RAS oncogene family precursor	49.5	6	MT
gi 157819711	Ras homolog gene family, member T1	7.3	3	MT
gi 206555	Ras protein	45.3	7	PM
gi 56605840	Ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	12.0	2	CS
gi 51338716	Ras-related protein Rab-1A	41.0	6	PM
gi 51338716	Ras-related protein Rab-1A	55.1	6	MT
gi 81884468	Ras-related protein Rab-21	18.4	3	PM
gi 81884468	Ras-related protein Rab-21	20.6	2	MT
gi 54038996	Ras-related protein Ral-A	27.2	2	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 149025373	rCG20813	50.9	4	PM
gi 149025373	rCG20813	63.2	4	MT
gi 149016683	rCG22622	27.3	3	CS
gi 149016272	rCG23940, isoform CRA_g	12.0	2	PM
gi 149016272	rCG23940, isoform CRA_g	26.5	1	MT
gi 149022203	rCG26319	43.7	7	PM
gi 149022203	rCG26319	45.0	9	MT
gi 149044044	rCG27771, isoform CRA_b	59.1	22	CS
gi 149024343	rCG30666, isoform CRA_a	6.5	1	MT
gi 149024657	rCG31394, isoform CRA_b	10.9	2	CS
gi 149052642	rCG33456, isoform CRA_c	67.1	35	CS
gi 149054052	rCG33529, isoform CRA_c	28.5	2	PM
gi 149054052	rCG33529, isoform CRA_c	14.6	1	MT
gi 149053564	rCG35210	28.3	2	CS
gi 149019918	rCG36507, isoform CRA_b	9.8	3	CS
gi 149050264	rCG36968, isoform CRA_c	13.3	3	MT
gi 149035969	rCG38845, isoform CRA_b	59.7	18	PM
gi 149035969	rCG38845, isoform CRA_b	69.4	16	MT
gi 149032791	rCG41951, isoform CRA_a	64.7	18	PM
gi 149032791	rCG41951, isoform CRA_a	69.0	19	MT
gi 149029697	rCG42519, isoform CRA_a	46.1	22	CS
gi 149029697	rCG42519, isoform CRA_a	42.1	22	PM
gi 149059204	rCG44686, isoform CRA_a	56.3	5	PM
gi 149039410	rCG45400	61.4	20	CS
gi 149039134	rCG45607, isoform CRA_a	18.3	16	MT
gi 149058125	rCG46430	42.1	7	PM
gi 149064445	rCG46917, isoform CRA_f	14.4	2	PM
gi 149062343	rCG47621, isoform CRA_a	24.9	3	CS
gi 149061629	rCG47744, isoform CRA_c	31.0	4	PM
gi 149061629	rCG47744, isoform CRA_c	15.5	2	MT
gi 149064836	rCG49984, isoform CRA_a	21.1	2	MT
gi 149056475	rCG54610, isoform CRA_a	30.9	7	PM
gi 149045627	rCG55067	21.2	6	CS
gi 149046922	rCG58516, isoform CRA_a	13.2	3	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 149017560	rCG59263	17.0	2	PM
gi 149048221	rCG62728, isoform CRA_b	44.8	8	PM
gi 149016250	rCG62892	17.0	2	PM
gi 149020707	rCG62940	28.0	4	PM
gi 149068224	rCG63717	30.0	3	PM
gi 149068224	rCG63717	30.0	5	MT
gi 61740635	Related RAS viral (r-ras) oncogene homolog 2	24.0	4	PM
gi 61740635	Related RAS viral (r-ras) oncogene homolog 2	13.2	2	MT
gi 81864134	Reticulon-3	7.9	3	PM
gi 197246916	RGD1306917 protein	22.8	2	PM
gi 197246916	RGD1306917 protein	26.5	2	MT
gi 197246361	RGD1310159 protein	18.5	5	CS
gi 81883710	Rho GDP-dissociation inhibitor 1	54.9	5	CS
gi 736292	Ribophorin I	13.6	5	PM
gi 736292	Ribophorin I	12.9	4	MT
gi 71051098	Ribosomal protein L17	26.6	3	PM
gi 71051098	Ribosomal protein L17	28.3	3	MT
gi 89573867	Ribosomal protein L18	17.0	3	PM
gi 710295	Ribosomal protein L22	29.7	2	MT
gi 56090279	Ribosomal protein L23	11.4	1	MT
gi 560493	Ribosomal protein L24	22.9	3	PM
gi 560493	Ribosomal protein L24	15.3	3	MT
gi 34849736	Ribosomal protein L36	21.0	2	MT
gi 51980641	Ribosomal protein L4	24.5	5	PM
gi 51980641	Ribosomal protein L4	23.0	4	MT
gi 78214309	Ribosomal protein L8	21.0	3	PM
gi 78214309	Ribosomal protein L8	22.6	3	MT
gi 78126139	Ribosomal protein S12	31.1	2	PM
gi 78126139	Ribosomal protein S12	25.0	1	MT
gi 54261703	Ribosomal protein S13	17.2	3	PM
gi 54261703	Ribosomal protein S13	14.6	1	MT
gi 8394215	Ribosomal protein S17	27.4	1	PM
gi 8394215	Ribosomal protein S17	26.7	1	MT
gi 82654220	Ribosomal protein S19	22.1	3	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 82654220	Ribosomal protein S19	31.7	3	MT
gi 78126159	Ribosomal protein S2	13.3	2	PM
gi 56090271	Ribosomal protein S20	16.8	2	PM
gi 56090271	Ribosomal protein S20	26.9	2	MT
gi 483517	Ribosomal protein S21	34.9	2	PM
gi 483517	Ribosomal protein S21	42.2	4	MT
gi 5924385	Ribosomal protein S271	14.3	2	PM
gi 57164151	Ribosomal protein S3	32.5	7	PM
gi 57164151	Ribosomal protein S3	25.9	4	MT
gi 8394221	Ribosomal protein S3a	27.7	7	MT
gi 56090273	Ribosomal protein S4, X-linked	28.1	4	PM
gi 56090273	Ribosomal protein S4, X-linked	17.9	4	MT
gi 8394224	Ribosomal protein S6	12.9	3	PM
gi 8394224	Ribosomal protein S6	37.4	4	MT
gi 71795613	Ribosomal protein, large P2	67.0	5	PM
gi 71795613	Ribosomal protein, large P2	67.0	4	MT
gi 67678203	Rpl6 protein	26.2	6	PM
gi 67678203	Rpl6 protein	28.5	6	MT
gi 54261550	Rps16 protein	25.8	4	PM
gi 54261550	Rps16 protein	10.1	2	MT
gi 165970894	Rps5 protein	13.7	1	MT
gi 189181710	Ryanodine receptor 2, cardiac	17.5	39	PM
gi 189181710	Ryanodine receptor 2, cardiac	18.2	33	MT
gi 206846	S-adenosylmethionine synthetase (EC 2.5.1.6)	12.7	2	CS
gi 149042663	Sarcalumenin (predicted), isoform CRA_a	55.2	38	PM
gi 149042663	Sarcalumenin (predicted), isoform CRA_a	53.1	29	MT
gi 149042664	Sarcalumenin (predicted), isoform CRA_b	15.6	2	CS
gi 157823585	Sarcoglycan, α	7.0	2	PM
gi 189083744	Sarcomeric mitochondrial creatine kinase precursor	71.8	80	PM
gi 189083744	Sarcomeric mitochondrial creatine kinase precursor	74.7	133	MT
gi 57303	Sarcoplasmic reticulum 2+-Ca-ATPase	63.0	105	PM
gi 57303	Sarcoplasmic reticulum 2+-Ca-ATPase	53.8	78	MT
gi 157786908	SCAN domain containing 3	11.1	5	CS
gi 38197654	Scavenger receptor class B, member 2	14.6	2	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 38197654	Scavenger receptor class B, member 2	13.2	1	MT
gi 149022245	Secernin 3, isoform CRA_a	16.0	3	CS
gi 81884646	Secernin-2	15.1	3	CS
gi 274325671	Secretory carrier membrane protein 3	18.3	2	PM
gi 81879451	Selenium-binding protein 1	52.5	20	CS
gi 58865630	Serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1	30.8	7	CS
gi 2507388	Serine protease inhibitor A3N	22.3	4	CS
gi 51036655	Serine protease inhibitor α 1 precursor	54.5	23	CS
gi 51036655	Serine protease inhibitor α 1 precursor	16.3	4	PM
gi 543717	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B α isoform	10.5	4	CS
gi 49065778	Serine/threonine-protein phosphatase PP1-α catalytic subunit	14.9	3	CS
gi 57977275	Serpine1 mRNA binding protein 1	17.6	4	PM
gi 57977275	Serpine1 mRNA binding protein 1	22.2	3	MT
gi 55824765	Serpinh1 protein	9.4	3	PM
gi 81884184	Serum deprivation-response protein	26.1	8	PM
gi 157819445	SET and MYND domain containing 1	17.4	3	CS
gi 193806001	S-formylglutathione hydrolase	39.4	7	CS
gi 78395043	Similar to Basic FGF-repressed Zic-binding protein (mbFZb)	23.1	4	PM
gi 78395043	Similar to Basic FGF-repressed Zic-binding protein (mbFZb)	25.8	5	MT
gi 149038409	Similar to C50H11.1, isoform CRA_a	14.6	2	CS
gi 149053707	Similar to Hypothetical protein MGC18716, isoform CRA_a	14.6	3	CS
gi 149067647	Similar to tripartite motif protein 50 (predicted)	13.4	3	CS
gi 149067647	Similar to tripartite motif protein 50 (predicted)	40.5	11	PM
gi 149067647	Similar to tripartite motif protein 50 (predicted)	21.2	4	MT
gi 417812	Single-stranded DNA-binding protein, mitochondrial	17.2	2	PM
gi 47718004	Slc25a3 protein	54.9	35	PM
gi 47718004	Slc25a3 protein	49.3	34	MT
gi 197246451	Slmap protein	18.8	11	PM
gi 197246451	Slmap protein	18.0	8	MT
gi 5107153	Small zinc finger-like protein	22.7	2	CS
gi 5107153	Small zinc finger-like protein	34.0	2	PM
gi 5107153	Small zinc finger-like protein	76.3	2	MT
gi 5107200	Small zinc finger-like protein	27.0	1	MT
gi 6467898	Small zinc finger-like protein DDP2	28.9	2	MT

# Accession	Protein name	% Cov	Peptides	Fraction
gi 6981542	Solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	15.4	7	PM
gi 6981542	Solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	15.6	5	MT
gi 6980958	Solute carrier family 2 , member 4	10.2	3	PM
gi 6980958	Solute carrier family 2 , member 4	7.9	2	MT
gi 52138624	Solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	46.2	14	PM
gi 52138624	Solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	56.5	14	MT
gi 38014819	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	87.9	118	PM
gi 149053212	Solute carrier family 25 , member 11, isoform CRA_b	62.7	21	PM
gi 149053212	Solute carrier family 25 , member 11, isoform CRA_b	59.9	27	MT
gi 189027101	Solute carrier family 25, member 42	16.7	2	MT
gi 50054324	Solute carrier family 27, member 1	6.3	2	PM
gi 50054324	Solute carrier family 27, member 1	8.8	2	MT
gi 78214331	Solute carrier family 8, member 1 precursor	7.1	2	PM
gi 78214331	Solute carrier family 8, member 1 precursor	4.6	2	MT
gi 158138513	Solute carrier family 9 isoform 3 regulator 2	17.5	3	PM
gi 189491879	Sorcin	10.6	2	CS
gi 81884480	Sorting and assembly machinery component 50 homolog	44.8	13	PM
gi 81884480	Sorting and assembly machinery component 50 homolog	53.9	13	MT
gi 624918	SP120	11.0	2	CS
gi 149044856	Spectrin β 2, isoform CRA_a	26.2	37	PM
gi 158533972	Spectrin α, erythrocytic 1	29.0	39	PM
gi 61557085	Spectrin β, non-erythrocytic 1	8.9	7	MT
gi 157824057	SRA stem-loop-interacting RNA-binding protein	21.6	2	CS
gi 72255527	Stomatin (Epb7.2)-like 2	10.2	2	PM
gi 72255527	Stomatin (Epb7.2)-like 2	14.5	4	MT
gi 116242506	Stress-70 protein, mitochondrial	47.7	26	PM
gi 116242506	Stress-70 protein, mitochondrial	37.0	18	MT
gi 116242506	Stress-70 protein, mitochondrial	48.8	34	CS
gi 54036435	Stress-induced-phosphoprotein 1	19.0	5	CS
gi 52782765	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	75.9	58	PM
gi 52782765	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	13.4	4	CS
gi 209915614	Succinate dehydrogenase complex, subunit B, iron sulfur (Ip) precursor	66.7	20	PM
gi 209915614	Succinate dehydrogenase complex, subunit B, iron sulfur (Ip) precursor	70.2	24	MT
gi 556395	Succinate semialdehyde dehydrogenase	20.5	6	CS

# Accession	Protein name	% Cov	Peptides	Fraction
gi 556395	Succinate semialdehyde dehydrogenase	8.8	2	PM
gi 158749584	Succinate-CoA ligase, ADP-forming, β subunit	38.1	9	MT
gi 223634703	Succinyl-CoA ligase [GDP-forming] subunit α, mitochondrial	22.3	8	PM
gi 223634703	Succinyl-CoA ligase [GDP-forming] subunit α, mitochondrial	28.0	6	MT
gi 187469277	Sucla2 protein	61.9	23	CS
gi 187469277	Sucla2 protein	42.7	14	PM
gi 71681082	Suclg2 protein	30.5	11	CS
gi 71681082	Suclg2 protein	27.3	8	PM
gi 71681082	Suclg2 protein	10.7	3	MT
gi 57241	Sulfated glycoprotein 2	19.0	3	CS
gi 74024923	Sulfite oxidase precursor	13.0	3	CS
gi 8394328	Superoxide dismutase 1, soluble	53.9	14	CS
gi 8394328	Superoxide dismutase 1, soluble	39.0	6	PM
gi 8394331	Superoxide dismutase 2, mitochondrial precursor	41.9	18	CS
gi 8394331	Superoxide dismutase 2, mitochondrial precursor	50.5	12	PM
gi 8394331	Superoxide dismutase 2, mitochondrial precursor	46.4	10	MT
gi 50927605	Suppression of tumorigenicity 13	20.1	3	CS
gi 157823944	Sushi domain containing 2	6.2	1	PM
gi 149067676	Syntaxin 4A (placental), isoform CRA_d	18.5	2	PM
gi 189181726	Talin	8.3	7	CS
gi 189181726	Talin	7.8	1	MT
gi 149032481	Target of myb1 homolog (chicken), isoform CRA_a	19.2	1	CS
gi 209529675	Taxilin β	19.4	4	CS
gi 4325177	Thiopurine S-methyltransferase	16.7	2	CS
gi 34849734	Thioredoxin 1	35.2	4	CS
gi 166796823	Thioredoxin domain containing 17	18.7	2	CS
gi 55250718	Thioredoxin reductase 2	10.1	2	CS
gi 55250718	Thioredoxin reductase 2	6.7	1	PM
gi 81916316	Thioredoxin-like protein 1	16.6	3	CS
gi 83305808	Thiosulfate sulfurtransferase	16.8	2	MT
gi 83305808	Thiosulfate sulfurtransferase	45.1	8	CS
gi 78103212	Thymosin β-4	54.6	4	CS
gi 73918915	TIM21-like protein, mitochondrial	20.0	6	PM
gi 73918915	TIM21-like protein, mitochondrial	25.3	6	MT

# Accession	Protein name	% Cov	Peptides	Fraction
gi 84781723	TNF receptor-associated protein 1 precursor	24.1	8	CS
gi 84781723	TNF receptor-associated protein 1 precursor	10.2	3	PM
gi 84781723	TNF receptor-associated protein 1 precursor	11.3	3	MT
gi 38512111	Tpi1 protein	82.7	41	CS
gi 38512111	Tpi1 protein	43.6	7	PM
gi 38512111	Tpi1 protein	44.4	6	MT
gi 157817646	TraB domain containing	10.6	1	PM
gi 157817646	TraB domain containing	14.1	1	MT
gi 8393848	Trans-2-enoyl-CoA reductase, mitochondrial precursor	10.2	2	CS
gi 92090643	Transaldolase	27.6	3	CS
gi 51317294	Transcription elongation factor B polypeptide 2	36.4	3	CS
gi 9963946	Transcription factor A	11.3	2	PM
gi 61556986	Transferrin precursor	60.0	62	CS
gi 61556986	Transferrin precursor	38.4	16	PM
gi 47605935	Transforming protein RhoA	21.2	4	PM
gi 47605935	Transforming protein RhoA	18.1	5	MT
gi 47605935	Transforming protein RhoA	21.8	2	CS
gi 603877	Transgelin	28.9	3	CS
gi 641973	Transitional endoplasmic reticulum ATPase	57.9	35	PM
gi 641973	Transitional endoplasmic reticulum ATPase	15.1	8	MT
gi 263511729	Translational activator of cytochrome c oxidase 1	20.0	2	CS
gi 60688577	Translocase of inner mitochondrial membrane 10 homolog (yeast)	35.6	2	PM
gi 60688577	Translocase of inner mitochondrial membrane 10 homolog (yeast)	35.6	2	MT
gi 8394449	Translocase of inner mitochondrial membrane 44 homolog precursor	12.6	1	CS
gi 149015617	Translocator of inner mitochondrial membrane 44, isoform CRA_a	26.1	3	MT
gi 149015618	Translocator of inner mitochondrial membrane 44, isoform CRA_b	14.6	3	PM
gi 149030989	Transmembrane 9 superfamily protein member 4, isoform CRA_d	10.6	1	PM
gi 62906896	Transmembrane emp24 domain-containing protein 10	28.3	2	PM
gi 57528337	Transmembrane emp24 protein transport domain containing 9	10.6	2	PM
gi 81884639	Transmembrane protein 109	7.4	1	MT
gi 261244910	Transmembrane protein 11 isoform 2	12.5	1	PM
gi 81882927	Transmembrane protein 126A	18.4	2	PM
gi 81882927	Transmembrane protein 126A	13.3	2	MT
gi 157819597	Transmembrane protein 143	12.5	2	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 157819597	Transmembrane protein 143	14.0	5	MT
gi 6851387	Triadin 1	15.7	3	PM
gi 6851387	Triadin 1	17.8	2	MT
gi 8650526	Tricarboxylate carrier-like protein	13.4	2	MT
gi 60688124	Trifunctional enzyme subunit α, mitochondrial	22.0	8	CS
gi 60688124	Trifunctional enzyme subunit α, mitochondrial	69.7	64	PM
gi 60688124	Trifunctional enzyme subunit α, mitochondrial	67.1	56	MT
gi 52353308	Tropomyosin 3, γ isoform 1	49.0	7	PM
gi 92090646	Tropomyosin α-1 chain	46.8	9	CS
gi 8394469	Troponin 1, type 3	29.9	4	CS
gi 77627992	Troponin C type 1 (slow)	23.0	3	CS
gi 6981666	Troponin T type 2 (cardiac)	21.4	5	PM
gi 55977470	Tubulin α-1A chain	18.9	4	PM
gi 55977470	Tubulin α-1A chain	43.5	11	MT
gi 55976173	Tubulin α-1B chain	59.2	19	CS
gi 81889864	Tubulin α-4A chain	31.5	10	MT
gi 81889864	Tubulin α-4A chain	54.9	19	CS
gi 81892373	Tubulin β-2C chain	21.4	4	PM
gi 81892373	Tubulin β-2C chain	19.8	7	MT
gi 56754676	Tubulin β-5 chain	55.4	17	CS
gi 210032365	Tumor rejection antigen gp96 precursor	12.7	8	PM
gi 210032365	Tumor rejection antigen gp96 precursor	19.2	9	MT
gi 9507243	Tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein, β polypeptide	37.0	8	CS
gi 6981710	Tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein, η polypeptide	56.9	12	CS
gi 9507245	Tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein, γ polypeptide	55.5	12	CS
gi 9507245	Tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein, γ polypeptide	16.6	3	PM
gi 6981712	Tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein, θ polypeptide	39.2	8	CS
gi 84028250	Tyrosine-protein phosphatase non-receptor type 11	11.2	2	CS
gi 187469561	Ube2l3 protein	35.1	3	CS
gi 55741544	Ubiquinol cytochrome c reductase core protein 2 precursor	76.3	64	PM
gi 55741544	Ubiquinol cytochrome c reductase core protein 2 precursor	69.7	59	MT
gi 189011657	Ubiquinol-cytochrome c reductase binding protein	76.6	22	PM
gi 189011657	Ubiquinol-cytochrome c reductase binding protein	85.6	25	MT
gi 281427170	Ubiquinol-cytochrome c reductase complex 7.2kDa protein	57.8	6	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 281427170	Ubiquinol-cytochrome c reductase complex 7.2kDa protein	51.6	3	MT
gi 186910239	Ubiquinol-cytochrome c reductase, 6.4kDa subunit	53.6	1	PM
gi 57114330	Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	74.5	37	PM
gi 57114330	Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	72.6	32	MT
gi 90111989	Ubiquinone biosynthesis methyltransferase COQ5, mitochondrial	19.0	3	MT
gi 90111992	Ubiquinone biosynthesis protein COQ9, mitochondrial	39.1	11	CS
gi 90111992	Ubiquinone biosynthesis protein COQ9, mitochondrial	23.7	3	MT
gi 8394502	Ubiquitin C	84.7	5	PM
gi 8394502	Ubiquitin C	55.1	4	MT
gi 68566104	Ubiquitin carboxyl-terminal hydrolase isozyme L3	43.5	4	CS
gi 157819971	Ubiquitin specific peptidase 5	24.5	6	CS
gi 205829267	Ubiquitin thioesterase OTUB1	23.6	5	CS
gi 77417616	Ubiquitin-conjugating enzyme E2 N	28.3	3	CS
gi 157822205	Ubiquitin-conjugating enzyme E2K	19.5	2	CS
gi 157817518	Ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	25.7	2	CS
gi 51980281	Ubiquitin-like modifier activating enzyme 3	6.5	1	CS
gi 81889667	Ubiquitin-like modifier-activating enzyme 1	25.1	17	CS
gi 67078526	UDP-glucose pyrophosphorylase 2	16.7	6	CS
gi 71043752	UMP-CMP kinase 1	26.9	3	CS
gi 157820137	Unc-45 homolog B	16.9	4	CS
gi 81883788	Uncharacterized protein C18orf19 homolog	27.1	5	PM
gi 81883788	Uncharacterized protein C18orf19 homolog	38.5	5	MT
gi 34784756	Unknown (protein for IMAGE:6890907)	36.8	5	MT
gi 829026	Unknown protein	18.3	1	PM
gi 763179	Unnamed protein product	64.0	12	CS
gi 56929	Unnamed protein product	78.2	51	CS
gi 220659	Unnamed protein product	19.5	6	CS
gi 56336	Unnamed protein product	38.1	9	CS
gi 55985	Unnamed protein product	53.5	11	PM
gi 56929	Unnamed protein product	24.1	8	PM
gi 57139	Unnamed protein product	36.5	5	PM
gi 259435950	Unnamed protein product	59.5	53	PM
gi 57702	Unnamed protein product	13.8	1	PM
gi 57125	Unnamed protein product	23.9	6	PM

# Accession	Protein name	% Cov	Peptides	Fraction
gi 57129	Unnamed protein product	29.1	2	PM
gi 57294	Unnamed protein product	8.4	2	PM
gi 55628	Unnamed protein product	75.0	53	PM
gi 56905	Unnamed protein product	28.2	9	PM
gi 57127	Unnamed protein product	55.2	5	MT
gi 57294	Unnamed protein product	13.2	2	MT
gi 56929	Unnamed protein product	28.4	8	MT
gi 57125	Unnamed protein product	18.2	2	MT
gi 56905	Unnamed protein product	22.8	7	MT
gi 57139	Unnamed protein product	31.7	4	MT
gi 57129	Unnamed protein product	32.5	2	MT
gi 259435950	Unnamed protein product	64.7	56	MT
gi 81884656	UPF0364 protein C6orf211 homolog	16.6	4	CS
gi 81918167	UPF0389 protein FAM162A	51.0	10	PM
gi 81918167	UPF0389 protein FAM162A	54.2	6	MT
gi 81884088	UPF0598 protein C8orf82 homolog	34.9	2	CS
gi 81868653	Up-regulated during skeletal muscle growth protein 5	55.2	4	PM
gi 81868653	Up-regulated during skeletal muscle growth protein 5	55.2	6	MT
gi 73920806	Valyl-tRNA synthetase	6.1	3	CS
gi 4240462	VAMP-associated protein A	27.7	5	PM
gi 4240462	VAMP-associated protein A	14.9	2	MT
gi 4240464	VAMP-associated protein B	14.4	3	PM
gi 71043730	Vanin 1	14.3	6	PM
gi 71043730	Vanin 1	6.4	2	MT
gi 7381163	Vasopressin-activated calcium-mobilizing receptor protein	6.4	1	CS
gi 38051979	Vdac1 protein	94.3	72	PM
gi 76096306	Vesicle amine transport protein 1 homolog (T californica)	17.1	1	PM
gi 57480	Vimentin	21.7	8	MT
gi 205830826	Vinculin	6.5	4	PM
gi 205830826	Vinculin	16.1	7	MT
gi 205830826	Vinculin	36.2	26	CS
gi 76780264	Vitronectin	8.6	2	PM
gi 76780264	Vitronectin	7.1	2	MT
gi 8810245	Voltage-dependent anion channel 1	91.2	69	MT

# Accession	Protein name	% Cov	Peptides	Fraction
gi 8810247	Voltage-dependent anion channel 2	69.2	28	PM
gi 8810249	Voltage-dependent anion channel 3	74.6	27	PM
gi 81910041	WD repeat-containing protein 1	42.1	12	CS

The proteins whose expression levels were not significantly altered after morphine treatment (M) or withdrawal for 3 days (M_w -I) or 6 days (M_w -II) compared to controls were arranged according to their function into several groups. Number of accession (gi numbers from GenBank/EMBL/DDBJ databases) and fraction in which the protein was detected are quoted for each protein (CS, cytosol; PM, plasma membrane-enriched fraction; MT, mitochondria-enriched fraction). %Cov, the percentage of matching amino acids from identified peptides divided by the total number of amino acids in the sequence. Peptides, number of unique peptides per identified protein.