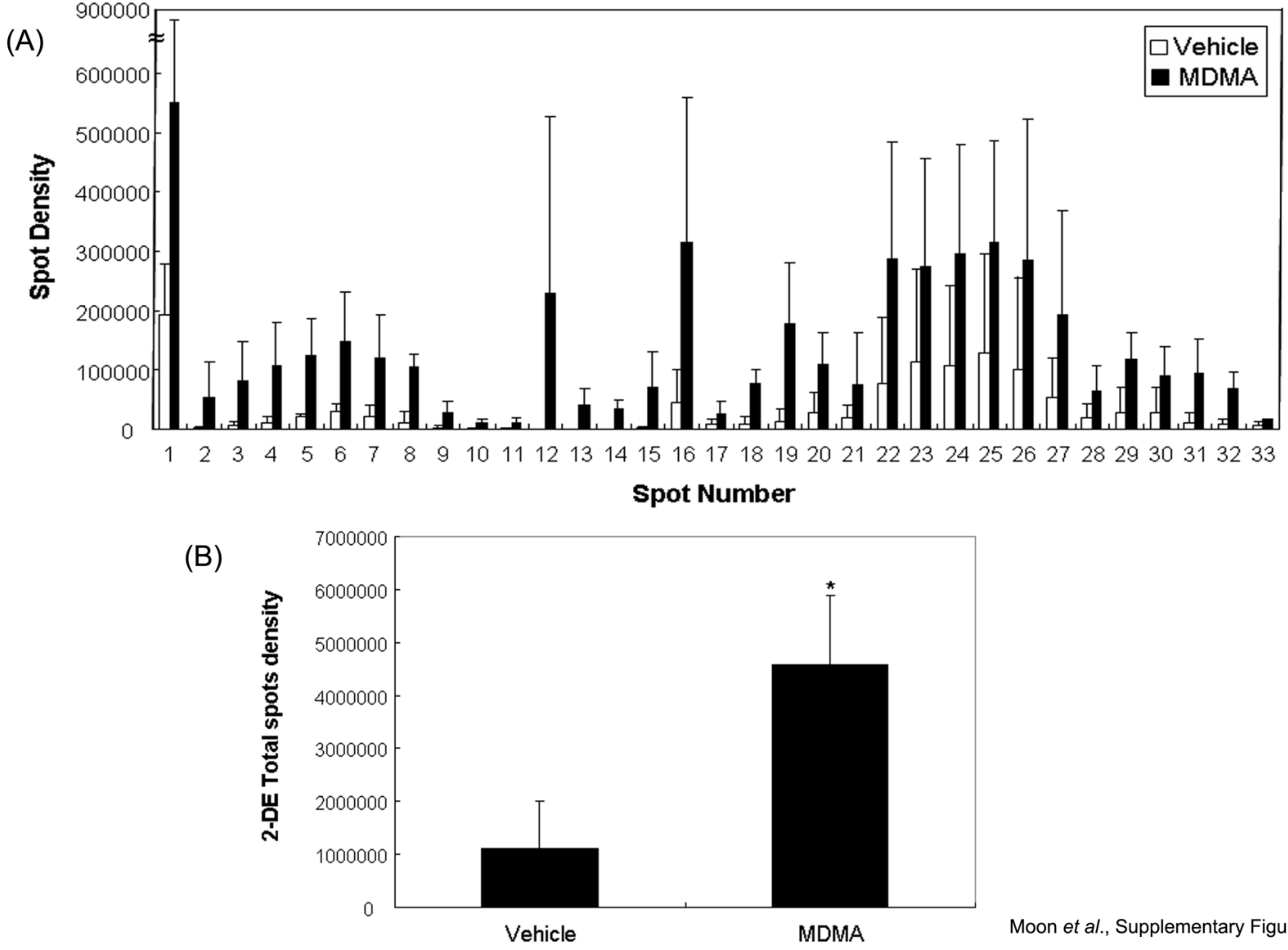

Moon *et al.*, Supplementary Figure 1

Legend for Supplementary Figure 1. Statistical analysis of the densities of individual spots. (A) The densities of individual protein spots from 3 independent 2-D gels as shown in Figure 2C were determined by using a gel digitizing software (UN-SCAN-IT™, Orem, Utah, USA) and compared with statistical analysis. (B) The densities of the entire protein spots in vehicle-treated versus MDMA-exposed samples are calculated and presented as total spot density. *significantly different from the vehicle control ($*p < 0.025$).

Supplementary Table 1. Raw data of LC-MS/MS peptide sequence analyses for oxidized proteins in MDMA treated rat liver mitochondria.

Spot No.	Protein/ Peptide	Detect No. of peptide	Z [a]	X_{corr} [b]	Δ Cn [c]	Swiss-Prot Accession [d]
1						
	60 kDa heat shock protein (Hsp60)					
	R.KPLVIIAEDVDGEALSTLVLNR.L	13	2	7.6207	0.7383	P63039
	K.TLNDELEIIEGMK.F	3	2	4.6498	0.5731	P63039
	K.VGEVIVTK.D	1	2	2.9774	0.3231	P63039
	K.VGGTSDVEVNEKK.D	1	2	2.6078	0.1647	P63039
	K.VTKDGVTVAK.S	3	2	3.453	0.4325	P63039
	R.AAVEEGIVLGGGCALLR.C	1	2	4.9207	0.6328	P63039
	R.CIPALDSLKPANEDQK.I	1	2	3.8211	0.4922	P63039
	R.GVMLAVDAVIAELK.K	2	2	5.0957	0.5004	P63039
	R.GVMLAVDAVIAELKK.Q	1	2	5.3811	0.5273	P63039
	R.GYISPYFINTSK.G	1	2	4.0739	0.5575	P63039
	R.IQEITEQLDITTSEYEKEK.L	1	2	6.0948	0.5976	P63039
	K.VGGTSDVEVNEK.K	4	2	4.0032	0.584	P63039
	R.RGVMLAVDAVIAELK.K	1	2	4.2009	0.4497	P63039
	R.TALLDAAGVASLLTTAEAVVTEIPK.E	4	2	7.3176	0.7573	P63039
	R.TALLDAAGVASLLTTAEAVVTEIPKEEK.D	2	3	5.6631	0.6211	P63039
	R.TVIIEQSWGSPK.V	1	2	3.414	0.4176	P63039
	R.VTDALNATR.A	1	2	3.3133	0.3296	P63039
	K.RIQEITEQLDITTSEYEK.E	1	2	5.7735	0.5697	P63039
	R.IQEITEQLDITTSEYEK.E	6	2	5.6176	0.6097	P63039
	K.IPAMTIAK.N	1	1	2.3153	0.3583	P63039
	K.QSKPVTTPEEIAQVATISANGDK.D	1	2	4.6509	0.5829	P63039
	K.CEFQDAYVLLSEK.K	1	2	3.7654	0.6283	P63039
	K.ILQSSSEVGYDAMLGDFVNMVEK.G	2	2	6.1011	0.6194	P63039
	K.ISSVQSIVPALEIANAHR.K	5	2	4.8671	0.5879	P63039
	K.KISSVQSIVPALEIANAHR.K	2	2	5.484	0.6284	P63039
	K.LNERLAKLSDGVAVLK.V	1	2	3.3701	0.1199	P63039
	K.VGGTSDVEVNEKKDR.V	1	2	3.8491	0.3752	P63039
	K.LSDGVAVLK.V	2	1	3.2674	0.3297	P63039
	K.LVQDVANNTNEEAGDGTTTATVLAR.S	10	2	6.8439	0.7179	P63039
	K.NAGVEGSLIVEK.I	4	1	4.2019	0.512	P63039
	K.DIGNIISDAMK.K	1	2	3.3737	0.422	P63039
	Stress-70 protein (GRP 75)					
	R.EQQIVIQSSGGLSK.D	1	2	3.8664	0.5437	P48721
	K.VQQTVQDLFGR.A	1	2	3.7647	0.4628	P48721
	K.ETAENYLGHTAK.N	1	2	4.2066	0.534	P48721
	K.LKEEISK.M	1	1	2.1789	0.1149	P48721
	K.LLGQFTLIGIPPAPR.G	1	2	3.2741	0.5491	P48721
	K.NAVITVPAYFNDSQR.Q	1	2	3.1442	0.5284	P48721
	K.SDIGEVILVGGMTR.M	1	2	4.7523	0.4914	P48721
	K.DAGQISGLNVLR.V	1	2	3.9935	0.4781	P48721
	R.EGSGSSSTGEQKEDQKEEK.Q	1	2	3.5097	0.5192	P48721
	R.QAASSLQQASLK.L	1	2	3.378	0.5472	P48721
	R.VINEPTAAALAYGLDK.S	1	2	5.6746	0.5878	P48721
	78 kDa glucose-regulated protein (GRP 78)					

K.ELEEIVQPIISK.L	1	2	4.2863	0.3722	P06761
R.IINEPTAAAIAYGLDK.R	1	2	4.1962	0.5961	P06761
K.SQIFSTASDNQPTVTIK.V	1	2	5.0439	0.5914	P06761
K.DNHLLGTFDLTGIPPAPR.G	1	2	4.1005	0.5902	P06761
K.KSDIDEIVLVGGSTR.I	1	2	5.0493	0.5418	P06761

2

Methylmalonate-semialdehyde dehydrogenase (ALDH6)					
K.QGIQFYTQLK.T	1	2	2.6217	0.4372	Q02253
K.ENTLNQLVGAAFGAAGQR.C	1	2	4.7754	0.5517	Q02253
R.AFPAWADTSILSR.Q	1	2	3.9369	0.5361	Q02253
K.EGASILLDGR.K	1	2	2.818	0.4226	Q02253
K.EEIFGPVLVVLETETLDEAIK.I	2	2	5.8385	0.6233	Q02253
R.VNAGDQPGADLGPLITPQAK.E	1	2	6.2929	0.7134	Q02253
K.SDKWIDIHNPATNEVVGR.V	1	3	3.5387	0.3788	Q02253
Aldehyde dehydrogenase 2, mitochondrial (ALDH2)					
R.GYFIQPTVFGDVK.D	1	2	3.8353	0.6029	P11884
K.VAFTGSTEVGHLIQVAAGSSNLK.R	1	2	4.0198	0.4417	P11884
K.VAEQTPLTALYVANLIK.E	1	2	5.3256	0.5512	P11884
Acyl-CoA oxidase 2					
K.VESIIQSDPVFNLK.K	2	2	2.847	0.1619	P97562
Catalase					
R.GPLLVQDVVFTDEMAHFDR.E	1	3	4.1792	0.5142	P04762
R.FNSANEDNVTQVR.T	1	2	2.5848	0.1182	P04762
Glycerol-3-phosphate dehydrogenase					
K.AVKLHNLNAGPSRTVGLFLQGGK.D	2	2	3.8045	0.3153	P35571
cGMP-dependent protein kinase 2					
R.WLNGFNWEGLKAR.S	2	2	3.5242	0.1663	Q64595
Heat shock protein HSP 90-alpha (HSP 86)					
K.VILHLKEDQTEYLEERR.I	2	2	2.6338	0.2387	P82995
Guanine deaminase					
K.RFQSTDVAEEVYTR.V	2	2	2.5856	0.1983	Q9WTT6
Protein S100-A11 (S100 calcium-binding protein A11)					
K.TEFLSFMNTELAAFTK.N	2	2	5.0091	0.5634	Q6B345
Receptor tyrosine kinase					
R.ELQEKYVLEAECAVAGPGANK.E	1	2	2.4108	0.0984	Q9EPA1
R.DSRKIGPAYVSSGGSR.N	1	2	2.7669	0.176	Q9EPA1
Tuberin					
R.MIGQICDVAKTK.K	2	2	3.7459	0.1425	P49816

3

Methylmalonate-semialdehyde dehydrogenase (ALDH6)					
R.VNAGDQPGADLGPLITPQAK.E	3	2	5.7933	0.6404	Q02253
R.LITLEQGK.T	1	2	2.458	0.2473	Q02253
K.TLADAEGDVFR.G	1	2	3.539	0.5064	Q02253
K.AISFVGSNQAGEYIFER.G	2	2	5.5308	0.6281	Q02253
K.EEDATLSSPAVVMPTMGR.-	1	2	4.7709	0.6475	Q02253
K.QGIQFYTQLK.T	1	2	2.5793	0.3445	Q02253
K.IVNDNPYGNGTAIFTTNGAIAR.K	2	3	5.3114	0.5808	Q02253
K.ERVCNLIDSGAK.E	1	2	2.4819	0.1435	Q02253
K.EEIFGPVLVVLETETLDEAIK.I	1	2	6.2128	0.6642	Q02253
K.ENTLNQLVGAAFGAAGQR.C	1	2	5.3873	0.5526	Q02253
K.EGASILLDGR.K	1	2	3.0705	0.4943	Q02253

Glutamate dehydrogenase 1 (GDH)					
K.YNLGLDLR.T	1	2	3.003	0.3352	P10860
K.PISQGGIHGR.I	1	2	3.3418	0.5461	P10860
K.DIVHSGLAYTMER.S	1	2	3.5548	0.5842	P10860
R.DDGSWEVIEGYR.A	1	2	3.3228	0.3989	P10860
R.YSTDVSVDEVK.A	1	2	2.785	0.4962	P10860
K.IIAEGANGPTTPEADK.I	1	2	4.5246	0.6296	P10860
K.HGGTIPVVPTAEFQDR.I	1	2	4.5531	0.5502	P10860
K.GFIGPGIDVPAPDMSTGER.E	1	2	5.0887	0.5675	P10860
K.LQHGSILGFPK.A	1	2	3.0746	0.4256	P10860
Aldehyde dehydrogenase 2, mitochondrial (ALDH2)					
R.TEQGPQVDETQFK.K	1	2	4.1576	0.523	P11884
K.VAEQTPLTALYVANLIK.E	1	2	4.8228	0.5385	P11884

4

Methylmalonate-semialdehyde dehydrogenase (ALDH6)					
K.ERVCNLIDSGAK.E	1	2	3.2637	0.339	Q02253
R.VNAGDQPGADLGPLITPQAK.E	2	2	5.4591	0.6188	Q02253
K.AISFVGSNQAGEYIFER.G	4	2	5.814	0.5721	Q02253
K.EEIFGPVLVVLETETLDEAIK.I	1	2	6.3505	0.6358	Q02253
K.EGASILLDGR.K	1	2	2.8649	0.3499	Q02253
K.GYENGNFVGPTIISNVK.P	1	2	3.4155	0.4081	Q02253
K.IVNDNPYGNGTAIFTTNGAIAR.K	1	2	4.8727	0.3413	Q02253
K.NHGVVMPDANK.E	1	2	2.537	0.4421	Q02253
R.AFPAWADTSILSR.Q	1	2	3.6409	0.5555	Q02253
K.ENTLNQLVGAAFGAAGQR.C	2	2	5.4859	0.5383	Q02253
K.EGASILLDGRK.I	1	2	2.9981	0.2872	Q02253
Glutamate dehydrogenase 1 (GDH)					
R.DSNYHLLMSVQESLER.K	1	2	4.5297	0.556	P10860
K.IIAEGANGPTTPEADKIFLER.N	1	2	5.0072	0.6525	P10860
K.KGFIGPGIDVPAPDMSTGER.E	1	2	4.7312	0.5125	P10860
K.LQHGSILGFPK.A	1	2	3.1139	0.5491	P10860
K.MVEGFFDR.G	1	2	2.9437	0.4398	P10860
K.IIAEGANGPTTPEADK.I	1	2	5.0412	0.5899	P10860
K.PISQGGIHGR.I	1	2	3.2678	0.4616	P10860
K.YNLGLDLR.T	1	2	3.0597	0.3094	P10860
R.GASIVEDKLVEDLK.T	1	2	4.4962	0.3469	P10860
R.YSTDVSVDEVK.A	1	2	3.1399	0.4807	P10860
K.NLNHVSYGR.L	1	2	3.0075	0.3897	P10860
K.VYNEAGVTFT.-	1	2	2.9866	0.4723	P10860
K.GFIGPGIDVPAPDMSTGER.E	1	2	4.1862	0.5906	P10860
K.HGGTIPVVPTAEFQDR.I	1	2	3.9621	0.5865	P10860
UDP-glucose pyrophosphorylase 2					
R.LVEIAQVPK.A	1	2	3.0291	0.457	Q4V8I9
R.IDIPPGAVLENK.I	1	2	2.664	0.4352	Q4V8I9
R.GLPDNISSVLNK.L	1	2	2.9249	0.4374	Q4V8I9
K.TLDGGLNVIQLETAVGAAIK.S	1	2	5.8331	0.6195	Q4V8I9
K.SFENSLGINVPR.S	1	2	3.8766	0.5466	Q4V8I9
Aldehyde dehydrogenase family 7 member A1 (ALDH7)					
R.LFLHESIHDEVVDR.L	1	2	4.4321	0.5237	Q64057
K.QAVSMFVQAVEEAKK.E	1	2	3.1355	0.4121	Q64057
K.QAVSMFVQAVEEAK.K	1	2	2.7107	0.3689	Q64057
Aldehyde dehydrogenase X (ALDH X)					
R.TFVEESIYHEFLER.T	1	2	3.7845	0.4495	Q66HF8
R.EEIFGPVQPLFK.F	1	2	3.8948	0.1438	Q66HF8

K.VAFTGSTEVGHLIQK.A	1	2	4.7423	0.3863	Q66HF8
Voltage-dependent T-type calcium channel subunit alpha-1G (VSCC)					
R.SSPHSPWSAASSWTSR.R	1	2	2.8195	0.0901	O54898
R.LPAPCPGLEPSWAK.D	1	2	2.7095	0.1642	O54898
ATP synthase subunit alpha (α-ATP)					
R.TGAIVDVPVGDELLGR.V	2	2	2.855	0.4351	P15999

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Methylmalonate-semialdehyde dehydrogenase (ALDH6)					
K.EGASILLDGRK.I	1	2	2.7448	0.2658	Q02253
R.AFPAWADTSILSR.Q	1	2	3.6355	0.5766	Q02253
R.VNAGDQPGADLGPLITPQAK.E	3	2	5.0606	0.6325	Q02253
R.CMALSTAVLVGEAK.K	1	2	4.7898	0.4572	Q02253
K.AISFVGSNQAGEYIFER.G	2	2	5.456	0.5528	Q02253
K.DMDLYSYR.L	1	2	3.0057	0.379	Q02253
K.EEIFGPVLVVLETETLDEAIK.I	2	2	6.1454	0.6215	Q02253
K.QGIQFYTQLK.T	1	2	2.508	0.3504	Q02253
K.WIDIHNPATNEVVGR.V	1	2	4.9524	0.5711	Q02253
K.ERVCNLIDSGAK.E	1	2	2.9897	0.3985	Q02253
K.IVNDNPYGNGTAIFTTNGAIAR.K	1	3	4.4385	0.4943	Q02253
K.KWLPELVER.A	1	2	2.4382	0.2147	Q02253
K.NHGVVMPDANK.E	1	2	3.5507	0.5159	Q02253
K.ENTLNQLVGAAFGAAGQR.C	2	2	6.3451	0.5228	Q02253
K.TLADAEGDVFR.G	1	2	3.2427	0.5043	Q02253
K.EEDATLSSPAVVMPTMGR.-	1	2	4.0731	0.651	Q02253
Glutamate dehydrogenase 1 (GDH)					
K.NLNHVSYGR.L	1	2	2.4692	0.4368	P10860
K.YNLGLDLR.T	1	2	2.884	0.357 1	P10860
R.DDGSWEVIEGYR.A	1	2	4.3075	0.5347	P10860
R.DSNYHLLMSVQESLER.K	1	2	5.2476	0.5036	P10860
R.ISATGR.G	1	1	2.1502	0.0949	P10860
K.IIAEGANGPTTPEADKIFLER.N	1	2	4.9451	0.6351	P10860
K.LQHGSILGFPK.A	1	2	2.9395	0.3589	P10860
R.GASIVEDKLVEDLK.T	1	2	4.3938	0.4108	P10860
K.HGGTIPVVPTAEFQDR.I	1	2	4.1241	0.5435	P10860
K.GFIGPGIDVPAPDMSTGER.E	1	2	5.2798	0.6496	P10860
K.IIAEGANGPTTPEADK.I	1	2	5.346	0.5859	P10860
K.PISQGGIHGR.I	1	2	3.1668	0.448	P10860
UDP-glucose pyrophosphorylase 2					
R.IDIPPGAVLENK.I	1	2	3.2596	0.5121	Q4V8I9
R.NENTFLDLTVQQIEHLNK.T	1	2	5.7907	0.3897	Q4V8I9
R.LVEIAQVPK.A	1	2	3.5686	0.4116	Q4V8I9
K.GTVIIIANHGDR.I	1	2	3.4661	0.377	Q4V8I9
R.GLPDNISSVLNK.L	1	2	3.3764	0.4546	Q4V8I9
K.TLDGGLNVIQLETAVGAAIK.S	1	2	5.2171	0.6127	Q4V8I9
K.SFENSLGINVPR.S	1	2	3.8322	0.4939	Q4V8I9
K.IQRPPEDSIQPYEK.I	1	2	4.1281	0.4641	Q4V8I9
ATP synthase subunit alpha (α -ATP)					
R.TGAIVDVPVGDELLGR.V	1	2	4.1188	0.444	P15999
R.ILGADTSVDLEETGR.V	1	2	5.0911	0.6302	P15999
K.AVDSLVPIGR.G	1	2	2.9782	0.4472	P15999
Aldehyde dehydrogenase family 7 member A1 (ALDH 7)					
K.QAVSMFVQAVEEAK.K	1	2	2.9013	0.3912	Q64057
K.QAVSMFVQAVEEAKK.E	1	2	2.9985	0.5163	Q64057
Aldehyde dehydrogenase X (ALDH X)					

K.VAFTGSTEVGHLIQK.A	1	2	4.6674	0.4548	Q66HF8
R.TFVEESIYHEFLER.T	1	2	4.5407	0.4762	Q66HF8
Cytochrome P450 11B1					
K.STTQLMFLPKSLTRWTSTR.V	2	2	3.4692	0.3004	P15393

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Methylmalonate-semialdehyde dehydrogenase (ALDH6)					
K.ENTLNQLVGAAFGAAGQR.C	1	2	5.8084	0.5544	Q02253
R.VNAGDQPGADLGPLITPQAK.E	2	2	5.4206	0.6446	Q02253
R.QQVLLRYQQLIK.E	1	2	3.3912	0.2958	Q02253
R.AKNLRVNAGDQPGADLGPLITPQAK.E	1	3	5.2271	0.4714	Q02253
K.TLADAEGDVFR.G	1	2	2.6734	0.4508	Q02253
K.NLRVNAGDQPGADLGPLITPQAK.E	2	2	5.4553	0.6357	Q02253
K.AISFVGSNQAGEYIFER.G	1	2	5.7451	0.5444	Q02253
K.ERVCNLIDSGAK.E	1	2	3.9622	0.3547	Q02253
K.EGASILLDGRKIK.V	1	2	3.2206	0.3053	Q02253
K.EGASILLDGRK.I	2	2	2.8867	0.3269	Q02253
K.EGASILLDGR.K	1	2	2.661	0.5011	Q02253
R.SSFRGDTNFYGK.Q	1	2	3.6297	0.3385	Q02253
K.LFIDGKFVESK.S	1	2	3.8052	0.465	Q02253
Glutamate dehydrogenase 1 (GDH)					
R.TAAYVNAIEKVFK.V	1	2	4.3373	0.4297	P10860
K.FGKHGGTIPVVPTAEFQDR.I	1	2	4.7397	0.6185	P10860
K.AGVKINPK.N	2	2	2.6889	0.2784	P10860
K.AKIIAEGANGPTTPEADK.I	1	2	6.0673	0.5674	P10860
K.ELEDFKLQHGSILGFPK.A	1	3	3.3256	0.4964	P10860
R.YSTDVSVDEVK.A	1	2	3.3053	0.5119	P10860
R.TAAYVNAIEK.V	1	2	3.4737	0.4997	P10860
R.KFGKHGGTIPVVPTAEFQDR.I	1	2	4.8407	0.6675	P10860
R.GASIVEDKLVEDLK.T	1	2	4.7911	0.4472	P10860
K.HGGTIPVVPTAEFQDR.I	1	2	4.3361	0.5981	P10860
K.NYTDNELEKITR.R	1	2	3.5701	0.4377	P10860
K.INPKNYTDNELEK.I	1	2	3.3767	0.3601	P10860
K.IIAEGANGPTTPEADKIFLER.N	1	2	4.5151	0.6152	P10860
K.VFKVYNEAGVTFT.-	1	2	4.0652	0.6444	P10860
Cytochrome P450 11B1					
K.STTQLMFLPKSLTRWTSTR.V	2	2	3.5586	0.2964	P15393
UDP-glucose pyrophosphorylase 2					
R.INKESLLPIAK.D	1	2	3.4295	0.3682	Q4V8I9
K.SFENSLGINVPR.S	1	2	2.6232	0.2071	Q4V8I9

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Methylmalonate-semialdehyde dehydrogenase (ALDH 6)					
K.EGASILLDGR.K	1	2	2.4317	0.4109	Q02253
K.ERVCNLIDSGAK.E	1	2	3.1361	0.3763	Q02253
K.EGASILLDGRK.I	1	2	2.8884	0.31	Q02253
K.LFIDGKFVESK.S	1	2	3.742	0.4971	Q02253
K.EEIFGPVLVVLETETLDEAIK.I	2	2	6.1282	0.6219	Q02253
K.EEDATLSSPAVVMPTMGR.-	1	2	4.7873	0.6503	Q02253
K.AISFVGSNQAGEYIFER.G	3	2	5.6029	0.6209	Q02253
K.ENTLNQLVGAAFGAAGQR.C	1	2	5.9357	0.5727	Q02253
K.KWLPELVER.A	1	2	2.548	0.2056	Q02253
K.NHGVVMPDANK.E	1	2	3.0354	0.5243	Q02253
K.NHGVVMPDANKENTLNQLVGAAFGAAGQR.C	1	3	3.8942	0.4923	Q02253
K.NLRVNAGDQPGADLGPLITPQAK.E	1	2	4.8182	0.6241	Q02253

K.QGIQFYTQLK.T	1	2	2.609	0.4149	Q02253
K.SDKWIDIHNPATNEVVGR.V	1	2	5.6922	0.4266	Q02253
K.TLADAEGDVFR.G	1	2	2.7528	0.457	Q02253
R.AFPAWADTSILSR.Q	1	2	4.4104	0.5908	Q02253
R.SSFRGDTNFYGK.Q	1	2	3.6436	0.3078	Q02253
R.VNAGDQPGADLGPLITPQAK.E	2	2	5.5936	0.6556	Q02253
R.YQQLIKENLK.E	1	2	3.4173	0.2569	Q02253
K.IVNDNPYGNGTAIFTTNGAIAR.K	1	2	6.1122	0.5022	Q02253
<u>Glutamate dehydrogenase 1 (GDH)</u>					
K.KGFIGPGIDVPAPDMSTGER.E	1	2	5.0357	0.5807	P10860
R.YSTDVSVDEVK.A	1	2	3.0302	0.4353	P10860
R.GASIVEDKLVEDLK.T	1	2	5.2872	0.4192	P10860
K.VFKVYNEAGVTFT.-	1	2	3.8425	0.5116	P10860
K.LQHGSILGFPK.A	1	2	2.7525	0.4542	P10860
K.AGVKINPK.N	1	2	2.8167	0.2034	P10860
K.DIVHSGLAYTMER.S	1	2	3.3943	0.5133	P10860
K.IIAEGANGPTTPEADKIFLER.N	1	2	5.4506	0.6558	P10860
K.IIAEGANGPTTPEADK.I	1	2	5.2667	0.6085	P10860
K.HGGTIPVVPTAEFQDR.I	1	2	4.4727	0.5707	P10860
K.GFIGPGIDVPAPDMSTGER.E	1	2	4.5232	0.5448	P10860
K.ELEDFKLQHGSILGFPK.A	1	2	3.6308	0.5614	P10860
<u>UDP-glucose pyrophosphorylase 2</u>					
K.IQRPPEDSIQPYEK.I	1	2	3.7325	0.435	Q4V8I9
R.LVEIAQVPK.A	1	2	2.9725	0.3593	Q4V8I9
R.INKESLLPIAK.D	1	2	3.424	0.4015	Q4V8I9
K.TLDGGLNVIQLETAVGAAIK.S	1	2	5.9884	0.6492	Q4V8I9
K.SFENSLGINVPR.S	1	2	4.2744	0.52	Q4V8I9
<u>ATP synthase subunit alpha (α -ATP)</u>					
R.ILGADTSVDLEETGR.V	1	2	5.2315	0.6445	P15999
R.VVDALGNAIDGKGPVGSK.I	1	2	4.2976	0.6056	P15999
R.TGAIVDVPVGDELLGR.V	1	2	4.6265	0.4475	P15999
<u>Fumarate hydratase</u>					
R.AAAEVNQEYGLDPK.I	1	2	4.4886	0.4981	P14408
R.IYELAAGGTAVGTGLNTR.I	1	2	5.4665	0.5704	P14408

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<u>Methylmalonate-semialdehyde dehydrogenase (ALDH 6)</u>					
K.LFIDGKFVESK.S	1	2	3.4131	0.3908	Q02253
K.AISFVGSNQAGEYIFER.G	2	2	5.7184	0.5911	Q02253
K.EEIFGPVLVVLETETLDEAIK.I	2	2	6.5744	0.6837	Q02253
K.EGASILLDGR.K	1	2	3.1995	0.5421	Q02253
K.EGASILLDGRK.I	2	2	3.0907	0.2951	Q02253
K.ENTLNQLVGAAFGAAGQR.C	1	2	6.0955	0.5517	Q02253
K.ERVCNLIDSGAK.E	1	2	3.5083	0.3769	Q02253
K.IVNDNPYGNGTAIFTTNGAIAR.K	2	2	6.1896	0.5747	Q02253
R.AFPAWADTSILSR.Q	1	2	4.0197	0.5299	Q02253
R.SSFRGDTNFYGK.Q	1	2	3.4954	0.3515	Q02253
R.VNAGDQPGADLGPLITPQAK.E	2	2	5.4402	0.6252	Q02253
<u>Cytochrome P450 11B1</u>					
K.STTQLMFLPKSLTRWTSTR.V	3	2	3.6317	0.3485	P15393
<u>Fumarate hydratase</u>					
K.VAALTGLPFVTAPNK.F	1	2	2.7815	0.2678	P14408
R.IYELAAGGTAVGTGLNTR.I	1	2	5.4496	0.5782	P14408
R.AAAEVNQEYGLDPK.I	1	2	4.0127	0.5853	P14408
<u>Cytochrome P450 19A1</u>					

K.SSSMVHVMKHSNYISRFGSK.R	2	2	3.0266	0.2423	P22443
9					
Methylmalonate-semialdehyde dehydrogenase (ALDH 6)					
K.ENTLNQLVGAAFGAAGQR.C	1	2	6.124	0.5371	Q02253
K.EGASILLDGRK.I	1	2	2.6735	0.2702	Q02253
K.EGASILLDGR.K	1	2	2.5816	0.4844	Q02253
K.EEIFGPVLVVLETETLDEAIK.I	3	2	6.8553	0.6406	Q02253
K.AISFVGSNQAGEYIFER.G	3	2	5.3742	0.6241	Q02253
K.LFIDGK.F	1	1	2.1902	0.1012	Q02253
K.QGIQFYTQLK.T	1	2	2.6478	0.3513	Q02253
R.VNAGDQPGADLGPLITPQAK.E	1	2	5.4255	0.6336	Q02253
K.TLADAEGDVFR.G	1	2	3.1989	0.5064	Q02253
K.WIDIHNPATNEVVGR.V	1	2	4.3699	0.4962	Q02253
K.ERVCNLIDSGAK.E	1	2	3.5566	0.4576	Q02253
R.AFPAWADTSILSR.Q	1	2	3.4772	0.5163	Q02253
R.SSFRGDTNFYGK.Q	1	2	3.2536	0.2865	Q02253
Cytochrome P450 11B1					
.STTQLMFLPKSLTRWTSTR.V	2	2	3.4541	0.3621	P15393
10					
3-ketoacyl-CoA thiolase					
K.DFTATDLTEFAAR.A	1	2	5.419	0.6942	P13437
K.RTPFGAYGGLLK.D	1	2	2.77	0.1415	P13437
K.SLDLDPSK.T	1	2	2.4202	0.363	P13437
K.TNVSGGAIALGHPLGGSGSR.I	1	2	6.2032	0.5827	P13437
R.ITAHLVHELR.R	1	2	3.6541	0.3645	P13437
R.VGVPTETGALTLNR.L	1	2	3.1396	0.49	P13437
R.GVFIVAAK.R	1	1	2.2057	0.2267	P13437
Methylmalonate-semialdehyde dehydrogenase (ALDH 6)					
K.AISFVGSNQAGEYIFER.G	1	2	5.0246	0.5867	Q02253
R.VNAGDQPGADLGPLITPQAK.E	1	2	4.543	0.596	Q02253
K.ENTLNQLVGAAFGAAGQR.C	2	2	6.2516	0.5482	Q02253
K.EGASILLDGR.K	1	2	2.9068	0.4351	Q02253
K.EEIFGPVLVVLETETLDEAIK.I	1	2	6.6297	0.671	Q02253
Acetyl-CoA dehydrogenase, short chain					
R.LVIAGHLLR.S	1	2	3.1588	0.4164	Q6IMX3
R.ITEIYEGTSEIQR.L	1	2	4.7641	0.5473	Q6IMX3
K.ELVPIAAQLDK.E	1	2	3.2331	0.4552	Q6IMX3
Glutamate dehydrogenase 1 (GDH)					
K.LQHGSILGFPK.A	1	2	2.6833	0.3447	P10860
K.IIAEGANGPTTPEADK.I	1	2	5.2593	0.5752	P10860
Long-chain specific acyl-CoA dehydrogenase					
K.TVAHIQTVQHK.L	1	2	3.3633	0.4431	P15650
R.LPASALLGEENK.G	1	2	4.2927	0.5248	P15650
11					
3-ketoacyl-CoA thiolase					
K.EGTVTAGNASGMSDGAGVVIIASEDAVKK.H	1	3	3.4615	0.4853	P13437
K.DFTATDLTEFAAR.A	1	2	5.3253	0.6616	P13437
K.RTPFGAYGGLLK.D	1	2	3.827	0.3748	P13437
K.AANEAGYFNEEMAPIEVK.T	2	2	4.2768	0.5547	P13437
K.LEDTLWAGLTDQHVK.L	1	2	5.7208	0.5379	P13437
K.LPMGMTAENLAAK.Y	1	2	3.9397	0.4146	P13437

R.TPFGAYGGLLK.D	1	2	3.3644	0.4288	P13437
R.YALQSQQR.W	1	1	2.1982	0.2139	P13437
K.TNVSGGAIALGHPLGGSGSR.I	2	2	6.3526	0.6614	P13437
R.VGVPTETGALTLNR.L	1	2	3.8353	0.4987	P13437
Methylmalonate-semialdehyde dehydrogenase (ALDH 6)					
K.TLADAEGDVFR.G	1	2	3.7866	0.4826	Q02253
K.NHGVVMPDANK.E	1	2	2.9319	0.4123	Q02253
K.IVNDNPYGNGTAIFTTNGAIAR.K	1	2	5.3066	0.4171	Q02253
K.ERVCNLIDSGAK.E	1	2	3.663	0.4259	Q02253
K.ENTLNQLVGAAFGAAGQR.C	1	2	5.6597	0.5631	Q02253
K.EGASILLDGR.K	1	2	2.4038	0.4008	Q02253
K.AISFVGSNQAGEYIFER.G	1	2	5.4729	0.565	Q02253
R.VNAGDQPGADLGPLITPQAK.E	1	2	5.9121	0.6297	Q02253
Glutamate dehydrogenase 1 (GDH)					
K.YNLGLDLR.T	1	2	2.7723	0.42821	P10860
K.LQHGSILGFPK.A	1	2	2.8385	0.3682	P10860
K.IIAEGANGPTTPEADKIFLER.N	1	2	5.1588	0.7178	P10860
K.HGGTIPVVPTAEFQDR.I	1	2	4.4922	0.5341	P10860
Fumarate hydratase					
R.IYELAAGGTAVGTGLNTR.I	1	2	5.7031	0.5611	P14408
R.AAAEVNQEYGLDPK.I	1	2	4.7912	0.4844	P14408
K.AADEVAEGK.L	1	1	2.6719	0.3735	P14408
Acetyl-CoA acetyltransferase					
R.TPIGSFLGSLASQPATK.L	1	2	5.5544	0.6176	P17764
K.FANEITPITISVK.G	1	2	4.0308	0.3902	P17764
Medium-chain specific acyl-CoA dehydrogenase					
K.IYQIYEGTAQIQR.L	1	2	4.8132	0.5532	P08503
R.TRPTVAAGAVGLAQR.A	1	2	4.5159	0.4403	P08503
12					
3-ketoacyl-CoA thiolase					
R.VGVPTETGALTLNR.L	1	2	3.7366	0.4848	P13437
13					
Probable oxidoreductase					
K.INVAVDR.L	1	1	2.2654	0.111	Q68FT3
K.RISQLDTQSPVTK.I	1	2	3.8189	0.4538	Q68FT3
R.ISQLDTQSPVTK.I	1	2	3.9854	0.3707	Q68FT3
R.VQGVVLQGGEEVR.S	1	2	4.4476	0.5192	Q68FT3
3-ketoacyl-CoA thiolase					
R.VGVPTETGALTLNR.L	1	2	3.2398	0.4721	P13437
K.DFTATDLTEFAAR.A	1	2	5.0694	0.6553	P13437
K.TNVSGGAIALGHPLGGSGSR.I	1	2	6.7383	0.6084	P13437
Acetyl-CoA dehydrogenase, short chain					
R.LVIAGHLLR.S	1	2	2.6135	0.3622	Q6IMX3
R.ITEIYEGTSEIQR.L	1	2	4.7519	0.575	Q6IMX3
R.IGIASQALGIAQASLDCAVK.Y	1	2	6.2631	0.6984	Q6IMX3
Protein disulfide-isomerase A6 precursor					
K.LAAVDATVNQVLASR.Y	1	2	5.3954	0.3578	Q63081
K.AASALKDVVK.V	1	2	2.773	0.3279	Q63081
R.TGEAIVDAALSALR.Q	1	2	4.2672	0.4573	Q63081
3-ketoacyl-CoA thiolase A, peroxisomal					
R.IAQFLSGIPETVPLSAVNR.Q	1	2	5.7625	0.6655	P21775
K.AEELGLPILGVLR.S	1	2	4.0844	0.4787	P21775

Peroxisomal delta3, delta2-enoyl-CoA isomerase					
R.QNYVDLVSSLSSSSEASSQGK.G	1	2	5.9388	0.6683	Q5XIC0
K.GILVTSEGGITK.I	1	2	4.3499	0.552	Q5XIC0
14					
Acetyl-CoA dehydrogenase, short chain					
K.ELVPIAAQLDK.E	1	2	2.6214	0.4453	Q6IMX3
R.LVIAGHLLR.S	1	2	3.0022	0.332	Q6IMX3
R.ITEIYEGTSEIQR.L	1	2	4.7853	0.5559	Q6IMX3
R.IGIASQALGIAQASLDCAVK.Y	1	2	5.8309	0.6668	Q6IMX3
3-ketoacyl-CoA thiolase					
K.TNVSGGAIALGHPLGGSGSR.I	1	2	5.6272	0.635	P13437
R.VGVPTETGALTLNR.L	1	2	3.7183	0.4527	P13437
K.DFTATDLTEFAAR.A	1	2	4.6431	0.6813	P13437
Peroxisomal delta3, delta2-enoyl-CoA isomerase					
K.LHAVNEEECTTLR.A	1	2	3.3801	0.3344	Q5XIC0
K.GILVTSEGGITK.I	1	2	4.3336	0.5653	Q5XIC0
R.QNYVDLVSSLSSSSEASSQGK.G	1	2	6.1104	0.6811	Q5XIC0
Glutamate dehydrogenase 1 (GDH)					
K.IIAEGANGPTTPEADK.I	1	2	5.2396	0.5974	P10860
K.NLNHVSYGR.L	1	2	2.9458	0.3735	P10860
Methylmalonate-semialdehyde dehydrogenase (ALDH 6)					
K.AISFVGSNQAGEYIFER.G	1	2	4.5139	0.6086	Q02253
R.VNAGDQPGADLGPLITPQAK.E	1	2	5.4548	0.6104	Q02253
15					
60 kDa heat shock protein (Hsp60)					
K.VGGTSDVEVNEKK.D	1	2	3.7117	0.3804	P63039
R.VTDALNATR.A	1	2	3.3948	0.3582	P63039
K.NAGVEGSLIVEK.I	1	2	4.0535	0.5157	P63039
K.VGGTSDVEVNEK.K	1	2	3.7098	0.5549	P63039
16					
60 kDa heat shock protein (Hsp60)					
K.IGIEIIK.R	1	2	2.8288	0.1015	P63039
R.IQEITEQLDITTSEYEK.E	1	2	5.6175	0.6696	P63039
R.AAVEEGIVLGGGCALLR.C	1	2	4.0266	0.6141	P63039
K.VGGTSDVEVNEKK.D	1	2	3.9021	0.3313	P63039
K.VGGTSDVEVNEK.K	1	2	3.1931	0.4649	P63039
K.VGEVIVTK.D	1	1	2.1555	0.3818	P63039
R.TALLDAAGVASLLTTAEAVVTEIPKEEK.D	1	3	5.3828	0.6509	P63039
R.TALLDAAGVASLLTTAEAVVTEIPK.E	1	2	5.1224	0.6582	P63039
K.IGIEIIKR.A	1	2	3.1164	0.1489	P63039
K.NAGVEGSLIVEK.I	1	2	3.9017	0.4994	P63039
ATP synthase subunit beta (β-ATP)					
R.VALTGLTVAEYFR.D	1	2	4.1921	0.6195	P10719
R.LVLEVAQHLGESTVR.T	1	2	4.5638	0.6099	P10719
17					
Glutamate dehydrogenase 1 (GDH)					
K.AGVKINPK.N	1	2	2.902	0.1954	P10860
R.GASIVEDKLVEDLK.T	1	2	4.7075	0.4873	P10860
R.TAAYVNAIEK.V	1	2	3.1419	0.4924	P10860
R.YSTDVSVDEVK.A	1	2	3.3311	0.4571	P10860

Methylmalonate-semialdehyde dehydrogenase (ALDH 6)					
K.LFIDGKFVESK.S	1	2	3.6418	0.3484	Q02253
K.AISFVGSNQAGEYIFER.G	1	2	5.1768	0.6012	Q02253
18					
Enoyl-CoA hydratase					
K.LFYSTFATDDRR.E	1	2	2.8803	0.2415	P14604
K.NSSVGLIQLNR.P	1	2	3.7529	0.3867	P14604
K.IIVAMAK.E	1	1	2.3402	0.1133	P14604
K.AQFGQPEILLGTIPGAGGTQR.L	1	2	5.339	0.5867	P14604
K.AFAAGADIK.E	1	1	2.7994	0.3958	P14604
K.NSSVGLIQLNRPK.A	1	2	3.8093	0.5287	P14604
19					
Enoyl-CoA hydratase					
K.FLSHWDHITR.I	1	2	3.1879	0.3333	P14604
K.AFAAGADIK.E	1	1	2.9651	0.3874	P14604
K.NSSVGLIQLNRPK.A	2	2	3.7799	0.4564	P14604
K.LFYSTFATDDRR.E	1	2	2.7538	0.2583	P14604
K.KLFYSTFATDDRR.E	1	2	3.211	0.3003	P14604
K.ESVNAAFEMTLTEGNKLEK.K	1	2	2.7675	0.3264	P14604
K.AQFGQPEILLGTIPGAGGTQR.L	1	2	4.8744	0.6113	P14604
K.LFYSTFATDDR.R	1	2	4.3828	0.5384	P14604
Afadin- and alpha-actinin-binding protein (ADIP)					
K.NLLAQESVETQNLK.L	2	2	3.1734	0.1776	Q8CGZ2
Glutamate dehydrogenase 1 (GDH)					
R.YSTDVSVDEVK.A	1	2	3.2148	0.4743	P10860
R.GASIVEDK.L	1	1	2.1628	0.2459	P10860
20					
Electron transfer flavoprotein subunit beta (β-ETF)					
K.EKVDLLFLGK.Q	1	2	2.9981	0.5537	Q68FU3
R.EIDGGLETIR.L	1	2	2.4728	0.3931	Q68FU3
K.VSVISVEEPPQR.L	1	2	3.7147	0.1646	Q68FU3
K.LPAVVTADLR.L	2	2	3.3482	0.5618	Q68FU3
K.SGVVTDGVK.H	1	1	2.2339	0.405	Q68FU3
R.LKLPAVVTADLR.L	1	2	4.0163	0.5582	Q68FU3
R.GIHVEVPGAEAENLGPLQVAR.V	1	2	6.2451	0.6792	Q68FU3
K.VETTEDLVAK.L	1	1	2.2303	0.3292	Q68FU3
3-hydroxyacyl-CoA dehydrogenase 2					
K.GLVAVITGGASGLGLSTAK.R	1	2	5.1952	0.647	O70351
R.VVTIAPGLFATPLLTTLPDK.V	2	2	5.2578	0.6654	O70351
R.VINVNLIGTFNVIR.L	1	2	4.4132	0.5909	O70351
R.NFLASQVPFPSR.L	1	2	3.8556	0.419	O70351
K.NQVHTLEDFQR.V	1	2	3.8086	0.5486	O70351
R.LVGQGATAVLLDVPNSEGETEAK.K	1	2	5.6652	0.5908	O70351
Enoyl-CoA hydratase					
K.ESVNAAFEMTLTEGNKLEK.K	1	2	2.8108	0.2386	P14604
K.LFYSTFATDDR.R	1	2	4.2701	0.6012	P14604
K.LFYSTFATDDRR.E	1	2	2.9527	0.199	P14604
K.NSSVGLIQLNRPK.A	1	2	3.6845	0.524	P14604
K.AFAAGADIK.E	1	1	2.9545	0.394	P14604
Glutamate dehydrogenase 1 (GDH)					
R.GASIVEDK.L	1	1	2.1228	0.3116	P10860

K.IIAEGANGPTTPEADK.I	1	2	5.3819	0.5421	P10860
R.GASIVEDKLVEDLK.T	1	2	4.1037	0.347	P10860
R.YSTDVSVDEVK.A	1	2	2.4318	0.5752	P10860
K.GFIGPGIDVPAPDMSTGER.E	1	2	5.2777	0.621	P10860
21					
<u>Enoyl-CoA hydratase</u>					
K.AFAAGADIK.E	1	1	2.7718	0.27	P14604
K.AQFGQPEILLGTIPGAGGTQR.L	1	2	4.2866	0.5453	P14604
K.NSSVGLIQLNRPK.A	1	2	3.6617	0.4958	P14604
K.LFYSTFATDDRR.E	1	2	2.78	0.2611	P14604
<u>Glutamate dehydrogenase 1 (GDH)</u>					
K.IIAEGANGPTTPEADK.I	1	2	5.2853	0.597	P10860
R.TAAYVNAIEK.V	1	2	3.0451	0.4828	P10860
22					
<u>Enoyl-CoA hydratase</u>					
K.NSSVGLIQLNRPK.A	1	2	2.4712	0.2347	P14604
K.AFAAGADIK.E	2	1	3.073	0.4008	P14604
K.AQFGQPEILLGTIPGAGGTQR.L	2	2	4.5569	0.5716	P14604
<u>Heat shock protein 75 kDa(HSP 75)</u>					
R.VQDVVTK.Y	1	1	2.3869	0.27	Q5XHZ0
K.EELVSNLGTIAR.S	1	2	3.5943	0.558	Q5XHZ0
R.ELISNASDALEK.L	1	2	4.2924	0.4409	Q5XHZ0
K.AFLEALQHQAETSSR.I	1	2	5.115	0.5326	Q5XHZ0
<u>3-hydroxyacyl-CoA dehydrogenase 2</u>					
R.LVGQGATAVLLDVPNSEGETEAK.K	1	2	4.5865	0.5659	O70351
R.VVTIAPGLFATPLLTTLPDK.V	2	2	5.2474	0.6785	O70351
<u>Myosin-Ie</u>					
K.VFIKAPESLFLLEEMR.E	2	2	2.7853	0.1323	Q63356
23					
<u>Enoyl-CoA hydratase</u>					
K.NSSVGLIQLNRPK.A	1	2	3.6478	0.4484	P14604
K.FLSHWDHITR.I	1	2	3.6082	0.4236	P14604
K.AQFGQPEILLGTIPGAGGTQR.L	2	2	4.6237	0.5741	P14604
K.AFAAGADIK.E	1	1	2.6619	0.3284	P14604
24					
<u>Enoyl-CoA hydratase</u>					
K.AQFGQPEILLGTIPGAGGTQR.L	2	2	4.7709	0.6263	P14604
K.NSSVGLIQLNR.P	1	2	3.871	0.4097	P14604
K.AFAAGADIK.E	1	1	3.0459	0.3631	P14604
K.NSSVGLIQLNRPK.A	1	2	2.5897	0.2699	P14604
25					
<u>Enoyl-CoA hydratase</u>					
K.AFAAGADIK.E	1	1	2.8177	0.3417	P14604
K.AQFGQPEILLGTIPGAGGTQR.L	1	2	5.0975	0.6019	P14604
26					
<u>ATP synthase subunit alpha (α -ATP)</u>					
R.EAYPGDVFYLHSR.L	1	2	3.1025	0.4596	P15999
R.VVDALGNAIDGK.G	3	2	4.0277	0.5857	P15999

R.TGAIVDVPVGDELLGR.V	3	2	4.7163	0.4889	P15999
R.FNDGTDEK.K	1	1	2.3105	0.238	P15999
K.TSIAIDTIINQK.R	1	2	3.1848	0.5199	P15999
K.TGTAEMSSILEER.I	1	2	4.0663	0.5226	P15999
K.RFNDGTDEK.K	1	2	3.0653	0.2838	P15999
R.ILGADTSVDLEETGR.V	2	2	5.0254	0.6313	P15999
K.RTGAIVDVPVGDELLGR.V	1	2	4.543	0.4366	P15999
Glutamate dehydrogenase 1 (GDH)					
K.IIAEGANGPTTPEADK.I	1	2	5.0234	0.5591	P10860
K.LQHGSILGFPK.A	1	2	2.8627	0.471	P10860
Phenylalanine-4-hydroxylase					
K.EEVGALAK.V	1	1	2.3603	0.3037	P04176
R.NDIGATVHELSR.D	1	2	3.7814	0.4142	P04176
27					
ATP synthase subunit alpha (α -ATP)					
R.TGAIVDVPVGDELLGR.V	1	2	4.4644	0.4812	P15999
R.ILGADTSVDLEETGR.V	1	2	4.9121	0.6229	P15999
R.EVAAFAQFGSDLDAATQQLLSR.G	1	2	7.226	0.6781	P15999
R.EAYPGDVFYLHSR.L	1	2	3.3349	0.5381	P15999
K.TSIAIDTIINQK.R	1	2	4.3814	0.5085	P15999
K.LELAQYR.E	1	1	2.1069	0.1745	P15999
K.ISEQSDAK.L	1	1	2.3278	0.1796	P15999
K.GIRPAINVGLSVSR.V	1	2	3.8047	0.5525	P15999
Methylmalonate-semialdehyde dehydrogenase (ALDH 6)					
K.ENTLNQLVGAAFGAAGQR.C	1	2	4.8798	0.543	Q02253
K.AISFVGSNQAGEYIFER.G	1	2	5.4146	0.5661	Q02253
28					
ATP synthase subunit alpha (α -ATP)					
K.ISEQSDAK.L	1	1	2.4896	0.0909	P15999
K.TSIAIDTIINQK.R	1	2	4.4971	0.4598	P15999
R.VVDALGNAIDGK.G	1	2	3.3385	0.594	P15999
R.TGAIVDVPVGDELLGR.V	1	2	4.6244	0.5008	P15999
R.EAYPGDVFYLHSR.L	2	2	3.5289	0.5832	P15999
K.EIVTNFLAGFEP.-	1	2	3.7166	0.6176	P15999
R.EVAAFAQFGSDLDAATQQLLSR.G	1	2	2.9732	0.5724	P15999
K.GIRPAINVGLSVSR.V	1	2	4.2434	0.5572	P15999
cAMP-specific 3',5'-cyclic phosphodiesterase 4B (DPDE4)					
R.DSLEETDIDIATEDKSLIDT.-	1	2	2.632	0.1184	P14646
R.DSLEETDIDIATEDK.S	1	2	3.118	0.1348	P14646
29					
ATP synthase subunit alpha (α -ATP)					
K.FESAFLSHVVSQHQSLLGNIR.S	1	2	6.0718	0.6215	P15999
R.VLSIGDGIAR.V	1	2	2.4238	0.2582	P15999
R.VGSAAQTR.A	1	1	2.2165	0.1708	P15999
K.GIRPAINVGLSVSR.V	1	2	3.7678	0.5185	P15999
K.EIVTNFLAGFEP.-	1	2	4.0103	0.5297	P15999
R.EVAAFAQFGSDLDAATQQLLSR.G	1	2	7.3721	0.6619	P15999
Afadin- and alpha-actinin-binding protein (ADIP)					
K.NLLAQESVETQNLK.L	2	2	3.3773	0.1529	Q8CGZ2
ATP synthase D chain					
R.ANVDKPGLVDDFK.N	1	2	4.0452	0.4884	P31399

K.YTALVDAEEKEDVK.N	1	2	4.7678	0.5228	P31399
30					
ATP synthase subunit alpha (α -ATP)					
K.EIVTNFLAGFEP.-	1	2	3.3365	0.5588	P15999
R.EVAAFAQFGSDLDAATQQLLSR.G	1	2	7.2176	0.6516	P15999
R.PAINVGLSVSR.V	1	2	2.8538	0.5013	P15999
R.VGSAAQTR.A	1	1	2.3778	0.2507	P15999
K.ISEQSDAK.L	1	1	2.2456	0.1699	P15999
K.GIRPAINVGLSVSR.V	1	2	4.1348	0.5665	P15999
K.FESAFLSHVVSQHQSLLGNIR.S	1	2	6.7761	0.6161	P15999
31					
Glutamate dehydrogenase 1 (GDH)					
K.IIAEGANGPTTPEADK.I	1	2	5.3963	0.5978	P10860
K.IIAEGANGPTTPEADKIFLER.N	1	2	5.3201	0.638	P10860
K.LQHGSILGFPK.A	1	2	2.94	0.5756	P10860
Methylmalonate-semialdehyde dehydrogenase (ALDH 6)					
K.TLADAEGDVFR.G	1	2	3.7022	0.4517	Q02253
R.LITLEQGK.T	1	1	2.1741	0.2095	Q02253
R.AFPAWADTSILSR.Q	1	2	4.1497	0.5859	Q02253
32					
Methylmalonate-semialdehyde dehydrogenase (ALDH 6)					
K.TLADAEGDVFR.G	1	2	3.415	0.4202	Q02253
R.AFPAWADTSILSR.Q	1	2	3.5938	0.5414	Q02253
33					
60 kDa heat shock protein (Hsp60)					
R.CIPALDSLKPANEDQK.I	1	2	2.7488	0.3279	P63039
K.KISSVQSIVPALEIANAHR.K	1	2	5.4475	0.5664	P63039
K.ISSVQSIVPALEIANAHR.K	2	2	4.6672	0.6229	P63039
K.TLNDELEIIEGMK.F	1	2	4.439	0.5017	P63039
R.VTDALNATR.A	1	2	3.7144	0.4025	P63039
K.VGEVIVTK.D	1	1	2.2298	0.3337	P63039
R.TALLDAAGVASLLTTAEAVVTEIPKEEK.D	2	3	5.4723	0.6527	P63039
R.AAVEEGIVLGGGCALLR.C	1	2	4.3346	0.5455	P63039
R.GVMLAVDAVIAELK.K	1	2	5.1419	0.444	P63039
R.GYISPYFINTSK.G	1	2	3.3973	0.5861	P63039
R.IQEITEQLDITTSEYEK.E	1	2	6.0982	0.6352	P63039
R.KPLVIIAEDVDGEALSTLVLNR.L	3	2	7.5591	0.7389	P63039
R.TALLDAAGVASLLTTAEAVVTEIPK.E	2	2	7.0166	0.7234	P63039
K.LVQDVANNTNEEAGDGTTTATVLAR.S	1	2	6.6826	0.7238	P63039
K.VGLQVVAVK.A	2	1	3.6445	0.306	P63039
Cytochrome b5					
R.EQAGGDATENFEDVGHSTDAR.E	1	2	5.3087	0.6508	P00173
K.FLEEHPGGEEVLR.E	1	2	3.9176	0.44	P00173
K.TYIIGELHPDDR.S	2	2	4.1482	0.5934	P00173
K.YYTLEEIQK.H	1	2	2.9845	0.4535	P00173
Afadin- and alpha-actinin-binding protein (ADIP)					
K.NLLAQESVETQNLK.L	2	1	2.6799	0.1733	Q8CGZ2
cGMP-dependent protein kinase 2					
R.WLNGFNWEGLKAR.S	1	2	3.6077	0.1493	Q64595
K.LITDALNKNQFLK.R	1	2	3.4341	0.2285	Q64595

Glutamate dehydrogenase 1 (GDH)					
K.IIAEGANGPTTPEADK.I	1	2	4.9333	0.592	P10860
K.LQHGSILGFPK.A	1	2	3.3906	0.525	P10860
Thyroid receptor-interacting protein 13					
K.MFQKIQDLIDDK.E	2	2	2.8475	0.1311	Q5XHZ9
10 kDa heat shock protein (Hsp10)					
K.GGEIQPVSVKVGDK.V	2	2	2.507	0.1302	P26772
DNA polymerase subunit gamma 1 (Mitochondrial DNA polymerase catalytic subunit)					
K.MEDGTLQAGPGGAR.G	2	2	2.4528	0.0859	Q9QYV8

a) Charge state of the peptide molecular ion chosen for MS/MS
b) SEQUEST cross correlation score
c) SEQUEST delta correlation score
d) Swiss-Prot protein accession references

In-gel digestion and nanoLC-MS/MS Analysis. The silver-stained 2D gel spots were destained using the destaining solutions from Invitrogen. After destaining, the gel spots were digested with 15 ng/uL of trypsin (Promega, Madison, WI) overnight at 37 °C, and the peptides were extracted by 70% acetonitrile and 0.1% trifluoroacetic acid (TFA) with sonication. The extracted peptides were anlayzed by reversed-phase nanoLC-tandem mass spectrometry (RP nanoLC-MS/MS). RP nanoLC-MS/MS was performed using an Agilent 1100 nanoLC system (Agilent Technologies) coupled online to a linear ion trap mass spectrometer (LTQ, Thermo Electron). Reversed-phase separations of each sample were performed using 75 µm i.d x 360 o.d. x 10 cm long fused silica capillary columns (Polymicro Technologies) that were slurry packed in house with Jupiter 5 µm, 300 Å pore size C18 silica-bonded stationary phase (Phenomenex, Torrance, CA). After injecting 5 µL of sample, the column was washed for 20 min with 98% solvent A (0.1% formic acid in water, v/v) and peptides were eluted at a flow rate of 0.25 µL/min using step linear gradients of 2%-42% solvent B (0.1% formic acid in 100% acetonitrile, v/v) for 40 min and 42%-98% solvent B for 10 min followed by 98% solvent B for 10 min. The mass spectrometer was operated in a data dependent mode in which each full MS scan was followed by 7 MS/MS scans where the 7 most abundant peptide molecular ions were dynamically selected from the prior MS scan for collision-induced dissociation (CID) using a normalized collision energy of 35%. The temperature of the heated capillary and electrospray voltage were 160 °C and 1.5 kV, respectively. The raw MS/MS data were searched using SEQUEST (ThermoFinnigan, San Jose, CA) against a rat protein database from European Bioinformatics Institute (http://www.ebi.ac.uk/proteome/index.html) to identify peptides. False positive rate in peptide identification was evaluated using the method described previously [1], which resulted in a confidence level of more than 95% in positive identifications.

(1) Yu, L.R., Conrads, T.P., Uo, T., Kinoshita, Y., Morrison, R.S., Lucas, D.A., Chan, K.C., Blonder, J., Issaq, H.J., and Veenstra, T.D. (2004) *Mol. Cell. Proteomics*. **3**, 896-907.