

Analysis Information

Report Type	Protein-Peptide Summary by Spot	Analysis Type	Combined (MS+MS/MS)
Sample Set Name	T056	Database	swissprot
Analysis Name	11-72_MLV_differential spots mouse	Creation Date	12/04/2014 11:38:14
Reported By	12/04/2014 12:38:56 - admin	Last Modified	12/04/2014 12:38:29
MS Acq. : Proc. Methods	(Unspecified) : (Unspecified)		
Interpretation Method	(Unspecified)		

Gel Idx/Pos	129/F4	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9

Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion Score	C. I. %			
1	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform OS=Mus musculus GN=MyI2 PE=1 SV	MLRV_MOUSE	605	18852.4	0	10	100	472	100			
Peptide Information												
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type			
791.3934	791.3932	-0.0002	0	105	111 VFDPEGK				Mascot			
850.4417	850.4464	0.0047	6	51	58 DTFALGR	70	100		Mascot			
850.4417	850.4464	0.0047	6	51	58 DTFALGR				Mascot			
1078.5198	1078.5232	0.0034	3	121	129 EMLTTQAEER				Mascot			
1094.5146	1094.5178	0.0032	3	121	129 EMLTTQAEER	44	99.938	Oxidation (M)[2]	Mascot			
1094.5146	1094.5178	0.0032	3	121	129 EMLTTQAEER				Mascot			
1120.519	1120.5204	0.0014	1	63	71 NEEIDEMIK				Mascot			
1136.514	1136.514	0	0	63	71 NEEIDEMIK				Mascot			
1224.5677	1224.5743	0.0066	5	31	40 EAFITMDQNR	93	100		Mascot			
1224.5677	1224.5743	0.0066	5	31	40 EAFITMDQNR				Mascot			
1240.5627	1240.5669	0.0042	3	31	40 EAFITMDQNR	31	98.99	Oxidation (M)[6]	Mascot			
1240.5627	1240.5669	0.0042	3	31	40 EAFITMDQNR				Mascot			
1389.7485	1389.7448	-0.0037	-3	154	165 NLVHIITGEEK				Mascot			
1404.7006	1404.7015	0.0009	1	92	104 GADPEETILNAFK	83	100		Mascot			
1404.7006	1404.7015	0.0009	1	92	104 GADPEETILNAFK				Mascot			
1998.004	1998.0101	0.0061	3	72	89 EAPGPINFTVLTMFGEK				Mascot			
2013.999	2013.9988	-0.0002	0	72	89 EAPGPINFTVLTMFGEK	76	100	Oxidation (M)[14]	Mascot			
2013.999	2013.9988	-0.0002	0	72	89 EAPGPINFTVLTMFGEK				Mascot			
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	2013.9988								Mascot	1	of	136

	2400.1064	2400.1194	0.013	5	133	153 EEIDQMAFAAPPDVTGNL DYK			Mascot			
	2406.1282	2406.1423	0.0141	6	10	30 IEGGSSNVFSMFQEQIQ EFK			Mascot			
	2416.1013	2416.1104	0.0091	4	133	153 EEIDQMAFAAPPDVTGNL DYK		Oxidation (M)[6]	Mascot			
	2422.123	2422.1292	0.0062	3	10	30 IEGGSSNVFSMFQEQIQ EFK	106	100	Oxidation (M)[11]	Mascot		
	2422.123	2422.1292	0.0062	3	10	30 IEGGSSNVFSMFQEQIQ EFK			Oxidation (M)[11]	Mascot		
2	Myosin regulatory light chain 10 OS=Mus musculus GN=MyI10 PE=2 SV=1	MYL10_MOUSE	273	22668.1	0	4	100	239	100			
Peptide Information												
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type			
850.4417	850.4464	0.0047	6	87	94 DTFALGR	70	100		Mascot			
850.4417	850.4464	0.0047	6	87	94 DTFALGR				Mascot			
1078.5085	1078.5232	0.0147	14	99	107 NEELEAMVK				Mascot			
1224.5677	1224.5743	0.0066	5	67	76 EAFITMDQNR	93	100	Oxidation (M)[7]	Mascot			
1224.5677	1224.5743	0.0066	5	67	76 EAFITMDQNR				Mascot			
1240.5627	1240.5669	0.0042	3	67	76 EAFITMDQNR	31	98.99	Oxidation (M)[6]	Mascot			
1240.5627	1240.5669	0.0042	3	67	76 EAFITMDQNR				Mascot			
1998.004	1998.0101	0.0061	3	108	125 EAPGPINFTVLTMFGEK				Mascot			
2013.999	2013.9988	-0.0002	0	108	125 EAPGPINFTVLTMFGEK	76	100	Oxidation (M)[14]	Mascot			
2013.999	2013.9988	-0.0002	0	108	125 EAPGPINFTVLTMFGEK				Mascot			
ProteomicTO5611-72_MLV_differential spots mouse												
										2	of	136

Gel Idx/Pos	130/F5	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9

Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion Score	C. I. %			
1	Myosin light chain 3 OS=Mus musculus GN=MyI3 PE=1 SV=4	MYL3_MOUSE	677	22521.3	0	12	100	520	100			
Peptide Information												
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type			
896.3995	896.4017	0.0022	2	43	50 EAEDFASK				Mascot			
962.4677	962.4734	0.0057	6	173	180 LTFEDEVK				Mascot			
995.5632	995.5665	0.0033	3	164	172 HVALTGER				Mascot			
1010.5305	1010.5379	0.0074	7	65	72 EAFLLFDR	62	100		Mascot			
1010.5305	1010.5379	0.0074	7	65	72 EAFLLFDR				Mascot			
1233.5892	1233.594	0.0048	4	152	163 EGNQTVMGAELR				Mascot			
1249.5841	1249.5884	0.0043	3	152	163 EGNQTVMGAELR			Oxidation (M)[7]	Mascot			
1281.6256	1281.6316	0.006	5	80	90 IYGGQGDVLR	75	100	Carbamidomethyl (C)[6]	Mascot			
1281.6256	1281.6316	0.006	5	80	90 IYGGQGDVLR				Mascot			
1396.7543	1396.7592	0.0049	4	91	103 ALGONPTQAEVLR	80	100	Carbamidomethyl (C)[6]	Mascot			
1396.7543	1396.7592	0.0049	4	91	103 ALGONPTQAEVLR				Mascot			
1501.6805	1501.6837	0.0032	2	135	147 DTGTYEDFVEGLR	138	100		Mascot			
1501.6805	1501.6837	0.0032	2	135	147 DTGTYEDFVEGLR				Mascot			
1509.7472	1509.744	-0.0032	-2	53	64 IEFTPEQIEEFK	38	99.837		Mascot			
1509.7472	1509.744	-0.0032	-2	53	64 IEFTPEQIEEFK				Mascot			
1983.9377	1983.9365	-0.0012	-1	117	132 MDMFETFLPMLQHSK			Oxidation (M)[11]	Mascot			
1999.9326	1999.9371	0.0045	2	117	132 MDMFETFLPMLQHSK			Oxidation (M)[1,2]	Mascot			
2015.9275	2015.9276	0.0001	0	117	132 MDMFETFLPMLQHSK			Oxidation (M)[1,2,10]	Mascot			
2093.1138	2093.1211	0.0073	3	20	42 AAPAPAAAPAAAPAAPE PERPK	127	100		Mascot			
2093.1138	2093.1211	0.0073	3	20	42 AAPAPAAAPAAAPAAPE PERPK				Mascot			
2145.958	2145.9636	0.0056	3	181	199 LMAQGQEDSNGCINYEAF VK			Carbamidomethyl (C)[11]	Mascot			
2161.9529	2161.9565	0.0036	2	181	199 LMAQGQEDSNGCINYEAF VK			Carbamidomethyl (C)[11], Oxidation (M)[2]	Mascot			
2	Myosin light chain 4 OS=Mus musculus GN=MyI4 PE=2 SV=3	MYL4_MOUSE	81	21259.6	0	1	99.987	75	100			
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Peptide Information												
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type			
1281.6256	1281.6316	0.006	5	69	79 IYGGQGDVLR	75	100	Carbamidomethyl (C)[6]	Mascot			
1281.6256	1281.6316	0.006	5	69	79 IYGGQGDVLR			Carbamidomethyl (C)[6]	Mascot			
3	Myosin light chain 1/3, skeletal muscle isoform OS=Mus musculus GN=MyI1 PE=1 SV=2	MYL1_MOUSE	74	20695.4	0	2	99.931	62	100			
Peptide Information												
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type			
1010.5305	1010.5379	0.0074	7	51	58 EAFLLFDR	62	100		Mascot			
1010.5305	1010.5379	0.0074	7	51	58 EAFLLFDR				Mascot			
1233.5892	1233.594	0.0048	4	136	147 EGNQTVMGAELR				Mascot			
1249.5841	1249.5884	0.0043	3	136	147 EGNQTVMGAELR			Oxidation (M)[7]	Mascot			
ProteomicTO5611-72_MLV_differential spots mouse												
										4	of	136

Gel Idx/Pos	131/F6	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9

Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion Score	C. I. %
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1 Thioredoxin-dependent peroxide reductase, PRDX3_MOUSE 415 28337.5 0 8 100 324 100
mitochondrial OS=Mus musculus GN=Prdx3 PE=1
SV=1

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
715.3297	715.3219	-0.0078	-11	250	254 EYFEK				Mascot
966.4778	966.4796	0.0018	2	85	92 ELSLDDFK				Mascot
1021.5312	1021.5312	0	0	75	84 GTAVNGEFK				Mascot
1206.6599	1206.6626	0.0037	3	198	208 HLSVNDLPVGR	96	100		Mascot
1206.6599	1206.6626	0.0037	3	198	208 HLSVNDLPVGR				Mascot
1271.7358	1271.7339	-0.0019	-1	186	197 GLFIDPVGVK	57	99.998		Mascot
1271.7358	1271.7339	-0.0019	-1	186	197 GLFIDPVGVK				Mascot
1476.8057	1476.8097	0.004	3	172	185 DYGVLLSAGIALR	117	100		Mascot
1476.8057	1476.8097	0.004	3	172	185 DYGVLLSAGIALR				Mascot
1799.932	1799.9253	-0.0057	-3	151	167 NGGLGHMNTLLSDITK	54	99.996	Oxidation (M)[7]	Mascot
1799.932	1799.9253	-0.0057	-3	151	167 NGGLGHMNTLLSDITK			Oxidation (M)[7]	Mascot
3450.6284	3450.6436	0.0152	4	120	149 ANEFHDVNCVAVASVD SHFSLAWINTR			Carbamidomethyl (C)[9]	Mascot

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Gel Idx/Pos 132/F7 Instr./Gel Origin AK139/T056 Process Status Analysis Succeeded
Plate # Name [1] T056P10 Instrument Sample Name Spectra 9

Rank Protein Name Accession No. Protein Score Protein MW Protein PI Pep. Count Protein Total Ion Score C. I. % Total Ion C. I. %

1 Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1 ACTC_MOUSE 264 42334 0 5 100 221 100
Protein Group Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1 ACTA_MOUSE 42380.9 0

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
791.3716	791.3702	-0.0014	-2	287	292 CDIDIR				Mascot
795.4723	795.4716	-0.0007	-1	331	337 IAAPPER	31	99.268	Carbamidomethyl (C)[1]	Mascot
795.4723	795.4716	-0.0007	-1	331	337 IAAPPER				Mascot
1500.7078	1500.7141	0.0063	4	362	374 QEYDEAGPSIVHR	78	100		Mascot
1500.7078	1500.7141	0.0063	4	362	374 QEYDEAGPSIVHR				Mascot
1790.892	1790.8983	0.0063	4	241	256 SYELPDGQVITIGNER	84	100		Mascot
1790.892	1790.8983	0.0063	4	241	256 SYELPDGQVITIGNER				Mascot
2244.0601	2244.0625	0.0024	1	294	314 DLYANNVLSGGTMYPGI ADR	28	98.435	Oxidation (M)[14]	Mascot
2244.0601	2244.0625	0.0024	1	294	314 DLYANNVLSGGTMYPGI ADR			Oxidation (M)[14]	Mascot

2 Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1 ACTS_MOUSE 221 42366 0 4 100 193 100

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
791.3716	791.3702	-0.0014	-2	287	292 CDIDIR				Mascot
795.4723	795.4716	-0.0007	-1	331	337 IAAPPER	31	99.268	Carbamidomethyl (C)[1]	Mascot
795.4723	795.4716	-0.0007	-1	331	337 IAAPPER				Mascot
1500.7078	1500.7141	0.0063	4	362	374 QEYDEAGPSIVHR	78	100		Mascot
1500.7078	1500.7141	0.0063	4	362	374 QEYDEAGPSIVHR				Mascot
1790.892	1790.8983	0.0063	4	241	256 SYELPDGQVITIGNER	84	100		Mascot
1790.892	1790.8983	0.0063	4	241	256 SYELPDGQVITIGNER				Mascot

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3 Myoglobin OS=Mus musculus GN=Mb PE=1 SV=3 MYG_MOUSE 181 17116 0 4 100 132 100

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
748.4352	748.4333	-0.0019	-3	135	140 ALELFR	32	99.425		Mascot
748.4352	748.4333	-0.0019	-3	135	140 ALELFR				Mascot
1494.6278	1494.6293	0.0015	1	120	134 HSGDFGADAQGAMSK			Oxidation (M)[13]	Mascot
1786.9194	1786.9181	-0.0013	-1	81	97 GQHAEEIQPLAQSHTK				Mascot
1896.0225	1896.0195	-0.003	-2	18	35 VEADLAGHGOEVLGLFK	100	100		Mascot
1896.0225	1896.0195	-0.003	-2	18	35 VEADLAGHGOEVLGLFK				Mascot

4 Actin, gamma-enteric smooth muscle OS=Mus musculus GN=Actg2 PE=2 SV=1 ACTH_MOUSE 175 42248.9 0 4 100 143 100

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
791.3716	791.3702	-0.0014	-2	286	291 CDIDIR				Mascot
795.4723	795.4716	-0.0007	-1	330	336 IAAPPER	31	99.268	Carbamidomethyl (C)[1]	Mascot
795.4723	795.4716	-0.0007	-1	330	336 IAAPPER				Mascot
1790.892	1790.8983	0.0063	4	240	255 SYELPDGQVITIGNER	84	100		Mascot
1790.892	1790.8983	0.0063	4	240	255 SYELPDGQVITIGNER				Mascot
2244.0601	2244.0625	0.0024	1	293	313 DLYANNVLSGGTMYPGI ADR	28	98.435	Oxidation (M)[14]	Mascot
2244.0601	2244.0625	0.0024	1	293	313 DLYANNVLSGGTMYPGI ADR			Oxidation (M)[14]	Mascot

5 Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1 ACTG_MOUSE 135 42107.9 0 3 100 115 100

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
795.4723	795.4716	-0.0007	-1	329	335 IAAPPER	31	99.268		Mascot
795.4723	795.4716	-0.0007	-1	329	335 IAAPPER				Mascot
1516.7026	1516.7128	0.0102	7	360	372 QEYDESGPSIVHR				Mascot
1790.892	1790.8983	0.0063	4	239	254 SYELPDGQVITIGNER	84	100		Mascot
1790.892	1790.8983	0.0063	4	239	254 SYELPDGQVITIGNER				Mascot

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6 Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 PE=1 SV=1 ACTBL_MOUSE 127 42319.1 0 2 100 115 100

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
795.4723	795.4716	-0.0007	-1	330	336 IAAPPER	31	99.218		Mascot
795.4723	795.4716	-0.0007	-1	330	336 IAAPPER				Mascot
1790.892	1790.8983	0.0063	4	240	255 SYELPDGQVITIGNER	84	100		Mascot
1790.892	1790.8983	0.0063	4	240	255 SYELPDGQVITIGNER				Mascot

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Gel Idx/Pos 133/F8 Instr./Gel Origin AK139/T056 Process Status Analysis Succeeded
Plate # Name [1] T056P10 Instrument Sample Name Spectra 9

Rank Protein Name Accession No. Protein Score Protein MW Protein PI Pep. Count Protein Total Ion Score C. I. % Total Ion C. I. %

1 Sarcalumenin OS=Mus musculus GN=Srl PE=1 SV=1 SRCA_MOUSE 579 99522.2 0 20 100 378 100

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
761.394	761.3926	-0.0014	-2	830	835 FDLNIR				Mascot
815.4297	815.429	-0.0007	-1	787	792 YLQYIK				Mascot
936.5625	936.5609	-0.0016	-2	779	786 IHALLVDR				Mascot
982.4992	982.5027	0.0035	4	602	609 FGGNFLEK				Mascot
1295.6083	1295.61	0.0017	1	694	704 ADNLATQMLMR			Oxidation (M)[8,10]	Mascot
1349.673	1349.6754	0.0024	2	582	594 TIEGIVMAADSAR	26	97.488	Oxidation (M)[7]	Mascot
1349.673	1349.6754	0.0024	2	582	594 TIEGIVMAADSAR			Oxidation (M)[7]	Mascot

1187,5659	1187,5652	-0.0007	-1	42	52	HQGVMMGMGQK				Oxidation (M)[5]	Mascot
1198,7054	1198,6987	-0.0067	-6	31	41	AVFPSIVGRPR					Mascot
1500,7078	1500,7065	-0.0013	-1	362	374	QEYDEAGPSIVHR	100	100			Mascot
1500,7078	1500,7065	-0.0013	-1	362	374	QEYDEAGPSIVHR					Mascot
1515,7491	1515,7457	-0.0034	-2	87	97	IWHHTFYNELR	66	100			Mascot
1515,7491	1515,7457	-0.0034	-2	87	97	IWHHTFYNELR					Mascot
1790,892	1790,8879	-0.0041	-2	241	256	SYELPDGQVITIGNER	121	100			Mascot
1790,892	1790,8879	-0.0041	-2	241	256	SYELPDGQVITIGNER					Mascot
1956,0437	1956,0325	-0.0112	-6	98	115	VAPEEHPHTLLTEAPLNPK	104	100			Mascot
1956,0437	1956,0325	-0.0112	-6	98	115	VAPEEHPHTLLTEAPLNPK					Mascot
2552,1531	2552,1362	-0.0169	-7	218	240	LCYVALDFENEMATAASS				Carbamidomethyl (C)[2], Oxidation (M)[12]	Mascot
						SSLEK					
3196,6096	3196,5576	-0.052	-16	150	179	TTGIVLDSGDGVTHNVPI					Mascot
						YEGYALPHAIMR					
3212,6045	3212,5852	-0.0193	-6	150	179	TTGIVLDSGDGVTHNVPI				Oxidation (M)[29]	Mascot
						YEGYALPHAIMR					
3220,4636	3220,4685	0.0049	2	259	286	CPETLFPSPFIMGESAGI				Carbamidomethyl (C)[1], Oxidation (M)[13,27]	Mascot
						HETTYNSIMK					

3 Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1 ACTA_MOUSE 667 42380.9 0 13 100 509 100

Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
791,3716	791,3628	-0.0088	-11	292	292	CDIDIR					
795,4723	795,4639	-0.0084	-11	331	337	IAPPER			Carbamidomethyl (C)[1]		Mascot
976,4482	976,4445	-0.0037	-4	21	30	AGFAGDDAPR	57	99,998			Mascot
976,4482	976,4445	-0.0037	-4	21	30	AGFAGDDAPR					Mascot
1130,5476	1130,5458	-0.0018	-2	199	208	GYSFVTTAER	71	100			Mascot

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1130,5476	1130,5458	-0.0018	-2	199	208	GYSFVTTAER					Mascot
1187,5659	1187,5652	-0.0007	-1	42	52	HQGVMMGMGQK			Oxidation (M)[5]		Mascot
1198,7054	1198,6987	-0.0067	-6	31	41	AVFPSIVGRPR					Mascot
1500,7078	1500,7065	-0.0013	-1	362	374	QEYDEAGPSIVHR	100	100			Mascot
1500,7078	1500,7065	-0.0013	-1	362	374	QEYDEAGPSIVHR					Mascot
1790,892	1790,8879	-0.0041	-2	241	256	SYELPDGQVITIGNER	121	100			Mascot
1790,892	1790,8879	-0.0041	-2	241	256	SYELPDGQVITIGNER					Mascot
1956,0437	1956,0325	-0.0112	-6	98	115	VAPEEHPHTLLTEAPLNPK	104	100			Mascot
1956,0437	1956,0325	-0.0112	-6	98	115	VAPEEHPHTLLTEAPLNPK					Mascot
2228,0652	2228,0706	0.0054	2	294	314	DLYANNVLSGGTTMYPGI					Mascot
						ADR					
2244,0601	2244,0474	-0.0127	-6	294	314	DLYANNVLSGGTTMYPGI	55	99,996	Oxidation (M)[14]		Mascot
						ADR					
2244,0601	2244,0474	-0.0127	-6	294	314	DLYANNVLSGGTTMYPGI			Oxidation (M)[14]		Mascot
						ADR					
2552,1531	2552,1362	-0.0169	-7	218	240	LCYVALDFENEMATAASS			Carbamidomethyl (C)[2], Oxidation (M)[12]		Mascot
						SSLEK					
3196,6096	3196,5576	-0.052	-16	150	179	TTGIVLDSGDGVTHNVPI					Mascot
						YEGYALPHAIMR					
3212,6045	3212,5852	-0.0193	-6	150	179	TTGIVLDSGDGVTHNVPI			Oxidation (M)[29]		Mascot
						YEGYALPHAIMR					
3220,4636	3220,4685	0.0049	2	259	286	CPETLFPSPFIMGESAGI			Carbamidomethyl (C)[1], Oxidation (M)[13,27]		Mascot
						HETTYNSIMK					

4 Actin, gamma-enteric smooth muscle OS=Mus musculus GN=Actg2 PE=2 SV=1 ACTH_MOUSE 552 42248.9 0 12 100 409 100

Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
791,3716	791,3628	-0.0088	-11	286	291	CDIDIR					
795,4723	795,4639	-0.0084	-11	330	336	IAPPER			Carbamidomethyl (C)[1]		Mascot
976,4482	976,4445	-0.0037	-4	20	29	AGFAGDDAPR	57	99,998			Mascot
976,4482	976,4445	-0.0037	-4	20	29	AGFAGDDAPR					Mascot
1130,5476	1130,5458	-0.0018	-2	198	207	GYSFVTTAER	71	100			Mascot
1130,5476	1130,5458	-0.0018	-2	198	207	GYSFVTTAER					Mascot
1187,5659	1187,5652	-0.0007	-1	41	51	HQGVMMGMGQK			Oxidation (M)[5]		Mascot
1198,7054	1198,6987	-0.0067	-6	30	40	AVFPSIVGRPR					Mascot
1790,892	1790,8879	-0.0041	-2	240	255	SYELPDGQVITIGNER	121	100			Mascot
1790,892	1790,8879	-0.0041	-2	240	255	SYELPDGQVITIGNER					Mascot
1956,0437	1956,0325	-0.0112	-6	97	114	VAPEEHPHTLLTEAPLNPK	104	100			Mascot
1956,0437	1956,0325	-0.0112	-6	97	114	VAPEEHPHTLLTEAPLNPK					Mascot

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2228,0652	2228,0706	0.0054	2	293	313	DLYANNVLSGGTTMYPGI					Mascot
						ADR					
2244,0601	2244,0474	-0.0127	-6	293	313	DLYANNVLSGGTTMYPGI	55	99,996	Oxidation (M)[14]		Mascot
						ADR					
2244,0601	2244,0474	-0.0127	-6	293	313	DLYANNVLSGGTTMYPGI			Oxidation (M)[14]		Mascot
						ADR					
2552,1531	2552,1362	-0.0169	-7	217	239	LCYVALDFENEMATAASS			Carbamidomethyl (C)[2], Oxidation (M)[12]		Mascot
						SSLEK					
3196,6096	3196,5576	-0.052	-16	149	178	TTGIVLDSGDGVTHNVPI					Mascot
						YEGYALPHAIMR					
3212,6045	3212,5852	-0.0193	-6	149	178	TTGIVLDSGDGVTHNVPI			Oxidation (M)[29]		Mascot
						YEGYALPHAIMR					
3220,4636	3220,4685	0.0049	2	258	285	CPETLFPSPFIMGESAGI			Carbamidomethyl (C)[1], Oxidation (M)[13,27]		Mascot
						HETTYNSIMK					

5 Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1 ACTG_MOUSE 289 42107.9 0 6 100 244 100

Protein Group
Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1 ACTB_MOUSE 42051.9 0

Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
795,4723	795,4639	-0.0084	-11	329	335	IAPPER					Mascot
976,4482	976,4445	-0.0037	-4	19	28	AGFAGDDAPR	57	99,998			Mascot
976,4482	976,4445	-0.0037	-4	19	28	AGFAGDDAPR					Mascot
1187,5659	1187,5652	-0.0007	-1	40	50	HQGVMMGMGQK			Oxidation (M)[5]		Mascot
1198,7054	1198,6987	-0.0067	-6	29	39	AVFPSIVGRPR					Mascot
1515,7491	1515,7457	-0.0034	-2	85	95	IWHHTFYNELR	66	100			Mascot
1515,7491	1515,7457	-0.0034	-2	85	95	IWHHTFYNELR					Mascot
1790,892	1790,8879	-0.0041	-2	239	254	SYELPDGQVITIGNER	121	100			Mascot
1790,892	1790,8879	-0.0041	-2	239	254	SYELPDGQVITIGNER					Mascot

6 Beta-actin-like protein 2 OS=Mus musculus GN=Actb2 PE=1 SV=1 ACTBL_MOUSE 137 42319.1 0 3 100 121 100

Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
795,4723	795,4639	-0.0084	-11	330	336	IAPPER					Mascot
1187,5659	1187,5652	-0.0007	-1	41	51	HQGVMMGMGQK			Oxidation (M)[5]		Mascot
1790,892	1790,8879	-0.0041	-2	240	255	SYELPDGQVITIGNER	121	100			Mascot
1790,892	1790,8879	-0.0041	-2	240	255	SYELPDGQVITIGNER					Mascot

7 Vasculin-like protein 1 OS=Mus musculus GN=Gbbp11 GPBL1_MOUSE 26 52504.4 0 4 0

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Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
1079,4939	1079,522	0.0281	26	439	447	SCSLSSPWR			Carbamidomethyl (C)[2]		Mascot
1531,7289	1531,7374	0.0085	6	61	73	TTGGSWHQRSLFR					Mascot
1561,7142	1561,739	0.0238	15	47	60	HNSSDGDFWLNPLR					Mascot
2307,0862	2307,0979	0.0117	5	1	20	MAQHDVPAWLNFTSQ			Oxidation (M)[1]		Mascot
						SSK					

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Gel Idx/Pos 136/F11 Instr./Gel Origin AK139/T056 Process Status Analysis Succeeded

Plate #	Rank	Protein Name	Instrument Sample Name				Spectra				
[1] T056P10			Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %	9	
1		Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3	ALBU_MOUSE	793	70700.5	0	18	100	596	100	
Peptide Information											
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
		712.3737	712.3704	-0.0033	-5	29	34 SEIAHR				Mascot
		731.441	731.439	-0.002	-3	213	219 ALVSVR				Mascot
		956.5345	956.5366	0.0041	4	98	105 LCAIRNLR			Carbamidomethyl (C)[2]	Mascot
		1017.5363	1017.5423	0.006	6	89	97 SLHTLFGDK				Mascot
		1149.615	1149.6176	0.0026	2	66	75 LVQEVDFAK				Mascot
		1250.5801	1250.5865	0.0064	5	35	44 YNDLGEQHFK				Mascot
		1299.7056	1299.7095	0.0039	3	362	372 HPDYSVSLLLR	92	100		Mascot
		1299.7056	1299.7095	0.0039	3	362	372 HPDYSVSLLLR				Mascot
		1439.7853	1439.7915	0.0062	4	439	452 APQVSTPTLVEAAR	84	100		Mascot
		1479.7954	1479.8076	0.0122	8	422	434 LGEYGFQNALVR	66	100		Mascot
		1479.7954	1479.8076	0.0122	8	422	434 LGEYGFQNALVR			Carbamidomethyl (C)[3]	Mascot
		1596.7323	1596.7406	0.0083	5	589	602 DTCFSTGPNLVTR				Mascot
		1609.7897	1609.7957	0.006	4	348	360 DVFLGFLYEYSR	120	100		Mascot
		1609.7897	1609.7957	0.006	4	348	360 DVFLGFLYEYSR				Mascot
		1662.8519	1662.8571	0.0052	3	470	483 LPCVEDYLSAILNR	120	100	Carbamidomethyl (C)[3]	Mascot
		1662.8519	1662.8571	0.0052	3	470	483 LPCVEDYLSAILNR			Carbamidomethyl (C)[3]	Mascot
		1681.8431	1681.8418	-0.0013	-1	243	257 LSQTFNADFAEITK	40	99.896		Mascot
		1681.8431	1681.8418	-0.0013	-1	243	257 LSQTFNADFAEITK				Mascot
		1866.7708	1866.7728	0.002	1	570	584 TVMDDFAQFLDTCKK			Carbamidomethyl (C)[13,14], Oxidation (M)[3]	Mascot
		1882.9368	1882.9402	0.0034	2	509	524 RPCFSALTYDTEYVPK			Carbamidomethyl (C)[3]	Mascot
		1882.9368	1882.9402	0.0034	2	509	524 RPCFSALTYDTEYVPK			Carbamidomethyl (C)[3]	Mascot
		1895.8844	1895.8838	-0.0006	0	528	543 AETFTFHSIDICTLPEK			Carbamidomethyl (C)[11]	Mascot
		1917.8912	1917.8909	-0.0003	0	153	168 ENPTTFMGHYLHEVAR			Oxidation (M)[7]	Mascot
		2554.1226	2554.1409	0.0183	7	131	152 DDNPSLPPFERPEAEAM CTSFK			Carbamidomethyl (C)[18], Oxidation (M)[17]	Mascot

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Gel Idx/Pos	Rank	Protein Name	Instrument Sample Name				Process Status				
137/F-12			Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %	9	
[1] T056P10			ALBU_MOUSE	566	70700.5	0	12	100	459	100	
Peptide Information											
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
		731.441	731.4224	-0.0186	-25	213	219 ALVSVR				Mascot
		956.5345	956.5401	0.0056	6	98	105 LCAIRNLR			Carbamidomethyl (C)[2]	Mascot
		1149.615	1149.6112	-0.0038	-3	66	75 LVQEVDFAK				Mascot
		1250.5801	1250.5879	0.0078	6	35	44 YNDLGEQHFK				Mascot
		1299.7056	1299.7128	0.0072	6	362	372 HPDYSVSLLLR	86	100		Mascot
		1299.7056	1299.7128	0.0072	6	362	372 HPDYSVSLLLR				Mascot
		1439.7853	1439.7942	0.0089	6	439	452 APQVSTPTLVEAAR	56	99.998		Mascot
		1439.7853	1439.7942	0.0089	6	439	452 APQVSTPTLVEAAR				Mascot
		1479.7954	1479.8101	0.0147	10	422	434 LGEYGFQNALVR	69	100		Mascot
		1479.7954	1479.8101	0.0147	10	422	434 LGEYGFQNALVR				Mascot
		1609.7897	1609.8007	0.011	7	348	360 DVFLGFLYEYSR	124	100		Mascot
		1609.7897	1609.8007	0.011	7	348	360 DVFLGFLYEYSR				Mascot
		1662.8519	1662.8557	0.0038	2	470	483 LPCVEDYLSAILNR	85	100	Carbamidomethyl (C)[3]	Mascot
		1662.8519	1662.8557	0.0038	2	470	483 LPCVEDYLSAILNR			Carbamidomethyl (C)[3]	Mascot
		1681.8431	1681.8461	0.003	2	243	257 LSQTFNADFAEITK	37	99.782		Mascot
		1681.8431	1681.8461	0.003	2	243	257 LSQTFNADFAEITK				Mascot
		1882.9368	1882.934	-0.0028	-1	509	524 RPCFSALTYDTEYVPK			Carbamidomethyl (C)[3]	Mascot
		1917.8912	1917.8903	-0.0009	0	153	168 ENPTTFMGHYLHEVAR			Oxidation (M)[7]	Mascot

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Gel Idx/Pos	Rank	Protein Name	Instrument Sample Name				Process Status				
138/F-13			Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %	9	
[1] T056P10			ALBU_MOUSE	459	70700.5	0	12	100	349	100	
Peptide Information											
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
		956.5345	956.5355	0.001	1	98	105 LCAIRNLR			Carbamidomethyl (C)[2]	Mascot
		1149.615	1149.6056	-0.0094	-8	66	75 LVQEVDFAK				Mascot
		1250.5801	1250.598	0.0179	14	35	44 YNDLGEQHFK				Mascot
		1299.7056	1299.7086	0.003	2	362	372 HPDYSVSLLLR				Mascot
		1439.7853	1439.7883	0.003	2	439	452 APQVSTPTLVEAAR	38	99.825		Mascot
		1439.7853	1439.7883	0.003	2	439	452 APQVSTPTLVEAAR				Mascot
		1479.7954	1479.8064	0.011	7	422	434 LGEYGFQNALVR	68	100		Mascot
		1479.7954	1479.8064	0.011	7	422	434 LGEYGFQNALVR				Mascot
		1609.7897	1609.7986	0.0089	6	348	360 DVFLGFLYEYSR	102	100		Mascot
		1609.7897	1609.7986	0.0089	6	348	360 DVFLGFLYEYSR				Mascot
		1662.8519	1662.8573	0.0054	3	470	483 LPCVEDYLSAILNR	102	100	Carbamidomethyl (C)[3]	Mascot
		1662.8519	1662.8573	0.0054	3	470	483 LPCVEDYLSAILNR			Carbamidomethyl (C)[3]	Mascot
		1681.8431	1681.8405	-0.0026	-2	243	257 LSQTFNADFAEITK	39	99.862		Mascot
		1681.8431	1681.8405	-0.0026	-2	243	257 LSQTFNADFAEITK				Mascot
		1882.9368	1882.938	0.0012	1	509	524 RPCFSALTYDTEYVPK			Carbamidomethyl (C)[3]	Mascot
		1895.8844	1895.9054	0.021	11	528	543 AETFTFHSIDICTLPEK			Carbamidomethyl (C)[11]	Mascot
		1917.8912	1917.8922	0.001	1	153	168 ENPTTFMGHYLHEVAR			Oxidation (M)[7]	Mascot

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Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %			
2	Myosin-6 OS=Mus musculus GN=Myh6 PE=1 SV=2	MYH6_MOUSE	121	224224.8	0	14	100	61	100		
Peptide Information											
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
		931.4843	931.4866	0.0023	2	1692	1699 AVVEQTER				Mascot
		1030.5891	1030.588	-0.0011	-1	1295	1303 EALISQLTR				Mascot
		1060.5171	1060.5215	0.0044	4	1364	1372 ANSEVAQWR				Mascot
		1060.5171	1060.5215	0.0044	4	1366	1374 ANSEVAQWR				Mascot
		1081.5273	1081.5319	0.0046	4	1271	1279 SLNDFTTQR				Mascot

Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %			
3	Myosin-7 OS=Mus musculus GN=Myh7 PE=1 SV=1	MYH7_MOUSE	87	223538.8	0	10	99.997	61	100		
Peptide Information											
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
		931.4843	931.4866	0.0023	2	1690	1697 AVVEQTER				Mascot
		1030.5891	1030.588	-0.0011	-1	1295	1303 EALISQLTR	61	100		Mascot
		1060.5171	1060.5215	0.0044	4	1364	1372 ANSEVAQWR				Mascot
		1090.5891	1090.5865	-0.0026	-2	1561	1569 AGLFENQIK				Mascot
		1417.7169	1417.7261	0.0092	6	1701	1712 LAEQELIETSER				Mascot
		1417.7169	1417.7261	0.0092	6	1701	1712 LAEQELIETSER				Mascot
		1441.7645	1441.7786	0.0141	10	1678	1689 NNLLQAELELR				Mascot
		1581.7426	1581.7568	0.0142	9	1488	1608 MVDSQTSLSDAETR			Oxidation (M)[1]	Mascot
		1608.7838	1608.797	0.0132	8	2	17 ADAEAMAFGAAPFLR			Oxidation (M)[1]	Mascot
		1709.8018	1709.8043	0.0025	1	1486	1499 NAYEESLHLETFK				Mascot
		1718.8265	1718.8296	0.0031	2	1421	1434 LONEIEDLMVDVER			Oxidation (M)[9]	Mascot
		1959.9506	1959.9601	0.0095	5	1506	1523 NLQEEISDLQLGEGGK				Mascot
		2009.8903	2009.8998	0.0095	5	1620	1636 MEGDLNEMEIQLSOANR			Oxidation (M)[1,8]	Mascot

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Gel Idx/Pos	Rank	Protein Name	Instrument Sample Name				Process Status			
139/F-14			Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %	9
[1] T056P10			ALBU_MOUSE	566	70700.5	0	12	100	459	100

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Plate #	Name	[1] T056P10	Instrument Sample Name					Spectra			
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %	9		
1	Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3	ALBU_MOUSE	221	70700.5	0	10	100	135	100		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type	
1250.5801	1250.5901	0.01	8	35	44 YNDLGEQHFK					Mascot	
1299.7056	1299.7056	0.0002	0	362	372 HPDYVSVLLLR					Mascot	
1438.7853	1439.7869	0.0016	1	439	452 APOVSTPTLVEAR					Mascot	
1479.7954	1479.8043	0.0089	6	422	434 LGEYGFQNALVR	58	99.998			Mascot	
1479.7954	1479.8043	0.0089	6	422	434 LGEYGFQNALVR					Mascot	
1609.7897	1609.7942	0.0045	3	348	360 DVFLGFLYEYSR	77	100			Mascot	
1609.7897	1609.7942	0.0045	3	348	360 DVFLGFLYEYSR					Mascot	
1662.8519	1662.8489	-0.003	-2	470	483 LPCVEDYLSAILNR			Carbamidomethyl (C)[3]		Mascot	
1681.8431	1681.8376	-0.0055	-3	243	257 LSQTFMADFAETK			Carbamidomethyl (C)[3]		Mascot	
1882.9368	1882.9343	-0.0025	-1	509	524 RPCFSALTVDVTPPK			Carbamidomethyl (C)[11]		Mascot	
1895.8844	1895.8857	0.0013	1	528	543 AETFTFHSIDCTLPEK			Oxidation (M)[7]		Mascot	
1917.8912	1917.8911	-0.0001	0	153	168 ENPTTFMGHYLHEVAR					Mascot	

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1646.8306	1646.8177	-0.0129	-8	979	993 NLTEEMAGLDEIAK					Mascot
1662.8254	1662.8489	0.0235	14	979	993 NLTEEMAGLDEIAK			Oxidation (M)[9]		Mascot
1709.8018	1709.8026	0.0008	0	1488	1501 NAYEESLEHLETFK					Mascot
1718.8265	1718.8263	-0.0002	0	1423	1436 LONEIEDLMDVDER	36	99.715	Oxidation (M)[9]		Mascot
1718.8265	1718.8263	-0.0002	0	1423	1436 LONEIEDLMDVDER			Oxidation (M)[9]		Mascot
1722.9497	1722.931	-0.0187	-11	1715	1729 VQLLHSQNTSLNOK					Mascot
1959.9506	1959.9485	-0.0021	-1	1506	1523 NLQEEISDLTEQLGEGGK					Mascot
2009.8903	2009.8998	0.0095	5	1620	1636 MEGDLNEMEIQLSOANR			Oxidation (M)[1,8]		Mascot

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928.4305	928.4349	0.0044	5	1338	1344 HDCDLLR			Carbamidomethyl (C)[3]		Mascot
931.4843	931.4861	0.0018	2	1699	1697 AVVEGTER					Mascot
1060.5171	1060.5216	0.0045	4	1364	1372 ANSEVAQWR					Mascot
1090.5891	1090.5868	-0.0023	-2	1561	1569 AGLFNQIK					Mascot
1354.6234	1354.6277	0.0043	3	1901	1911 VQHELDEAER					Mascot
1417.7169	1417.7234	0.0065	5	1703	1714 LAEQELIETSER					Mascot
1441.7645	1441.7743	0.0098	7	1680	1691 NNLLQAELELR	107	100			Mascot
1441.7645	1441.7743	0.0098	7	1680	1691 NNLLQAELELR					Mascot
1581.7426	1581.7675	0.0249	16	1593	1606 MVDLSLQTLSDAETR			Oxidation (M)[1]		Mascot
1709.8018	1709.8026	0.0008	0	1486	1499 NAYEESLEHLETFK					Mascot
1718.8265	1718.8263	-0.0002	0	1421	1434 LONEIEDLMDVDER	36	99.715	Oxidation (M)[9]		Mascot
1718.8265	1718.8263	-0.0002	0	1421	1434 LONEIEDLMDVDER			Oxidation (M)[9]		Mascot
1722.9497	1722.931	-0.0187	-11	1713	1727 VQLLHSQNTSLNOK					Mascot

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809.4515	809.4451	-0.0064	-8	416	422 SLLTYCR					Mascot
912.4396	912.4402	0.0006	1	473	479 SGMFWLR	7	0	Oxidation (M)[3]		Mascot
912.4396	912.4402	0.0006	1	473	479 SGMFWLR			Oxidation (M)[3]		Mascot
1100.5735	1100.5673	-0.0062	-6	424	432 IPLAEWESR					Mascot

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140/F15 Instr./Gel Origin AK139/T056 Process Status Analysis Succeeded

[1] T056P10 Instrument Sample Name Spectra 9

Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %	9	
1	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Mus musculus GN=SdhA PE	DHSA_MOUSE	180	73622.6	0	12	100	72	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
765.3889	765.3835	-0.0054	-7	501	507 FADGSIR					Mascot
1056.5374	1056.5306	-0.0068	-6	616	623 KPFGHEHWR					Mascot
1108.5746	1108.5763	0.0017	2	251	261 NTVIATGGYGR					Mascot
1176.5579	1176.5807	0.0228	19	518	527 SMQNHAAVFR			Oxidation (M)[2]		Mascot
1329.6757	1329.6802	0.0045	3	313	325 GEGGILINSQGER					Mascot
1354.7227	1354.7202	-0.0025	-2	196	207 TGHSLITLVCR					Mascot
1473.8424	1473.8488	0.0064	4	452	465 LGANSLDLVVFGR	72	100			Mascot
1473.8424	1473.8488	0.0064	4	452	465 LGANSLDLVVFGR					Mascot
1539.7948	1539.7915	-0.0033	-2	233	246 GVICLEDGSIHR			Carbamidomethyl (C)[6]		Mascot
1757.8527	1757.875	0.0223	13	76	92 AAFGLSEAGFNACTLTK			Carbamidomethyl (C)[14]		Mascot
1797.8654	1797.8553	-0.0101	-6	601	615 VDEYDYSPKIQGQOK					Mascot
2167.1406	2167.145	0.0044	2	362	379 DHIYVQLHILPFEGLATR					Mascot
2929.469	2929.4612	-0.0078	-3	47	75 VSDAISTQYVVDHEFDAVVGAGGAGLR					Mascot

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Malate dehydrogenase, cytoplasmic OS=Mus musculus MDHC_MOUSE 174 36659.1 0 7 100 113 100

GN=Mdh1 PE=1 SV=3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
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Seq.	Seq.	Score							
795,4471	795,4338	-0.0133	-17	249	255	AIADHIR			
1026,4673	1026,4792	0.0119	12	150	157	ENFSCSLTR			
1178,8165	1178,8212	0.0047	4	221	230	GEFITTVQOR		55	99,997
1178,8165	1178,8212	0.0047	4	221	230	GEFITTVQOR			
1387,725	1387,7285	0.0035	3	80	92	DLDAVVLVGSMPR			
1393,7111	1393,7156	0.0045	3	299	310	FVEGLPINDFSR		59	99,999
1393,7111	1393,7156	0.0045	3	299	310	FVEGLPINDFSR			

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1757,9214	1757,875	-0.0464	-26	126	142	VIVVGNPANTNCLTAK			
2280,1155	2280,1086	-0.0069	-3	180	199	NVIWGNHSSSTQYPDVNHAK			
2280,1155	2280,1086	-0.0069	-3	180	199	NVIWGNHSSSTQYPDVNHAK			

3 Phosphoglucosyltransferase-1 OS=Mus musculus GN=Pgm1 PGM1_MOUSE 68 61664.7 0 6 99,725 29 98,934

Calc. Mass	Obsrv. Mass	Δ da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
878,473	878,4744	0.0014	2	492	499	LIFADGSR				Mascot
1081,5676	1081,562	-0.0056	-5	201	209	NIFDNALK				Mascot
1278,6729	1278,6732	0.0003	0	350	360	IALYETPTGWK				Mascot
1499,7926	1499,799	0.0064	4	65	76	FYMTEAQLIVR		Oxidation (M)[3]		Mascot
1499,7926	1499,799	0.0064	4	65	76	FYMTEAQLIVR		Oxidation (M)[3]		Mascot
1618,8184	1618,8204	0.002	1	9	23	TQAYPDQKPGTSGLR	29	98,934		Mascot
1618,8184	1618,8204	0.002	1	9	23	TQAYPDQKPGTSGLR				Mascot
1652,6571	1652,6759	0.0188	11	278	293	SGEHDGFAAFDGDGR				Mascot

ProteomicTO5611-72_MLV_differential spots mouse 25 of 136

Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %	Process Status	Analysis Succeeded
1	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1	ACTC_MOUSE	642	42334	0	13	100	486	100	9

Calc. Mass	Obsrv. Mass	Δ da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
791,3716	791,3723	0.0007	1	287	292	CDIDIR				Mascot
795,4723	795,4719	-0.0004	-1	331	337	IIAPPER				Mascot
976,4482	976,4516	0.0034	3	21	30	AGFAGDDAPR				Mascot
1130,5476	1130,5537	0.0061	5	199	208	GYSFVTTAER	68	100		Mascot
1130,5476	1130,5537	0.0061	5	199	208	GYSFVTTAER				Mascot
1203,5609	1203,5585	-0.0024	-2	42	52	HQGMVMGMGQK		Oxidation (M)[5,8]		Mascot
1500,7078	1500,7156	0.0078	5	362	374	QEYDEAGPSIVHR	92	100		Mascot
1500,7078	1500,7156	0.0078	5	362	374	QEYDEAGPSIVHR				Mascot
1515,7491	1515,7571	0.008	5	87	97	IWHHTFYNELR	66	100		Mascot
1515,7491	1515,7571	0.008	5	87	97	IWHHTFYNELR				Mascot
1790,892	1790,9004	0.0084	5	241	256	SYELPDGQVITIGNER	121	100		Mascot
1790,892	1790,9004	0.0084	5	241	256	SYELPDGQVITIGNER				Mascot
1956,0437	1956,0455	0.0018	1	98	115	VAPEEHPDLLTEAPLNPK	103	100		Mascot
1956,0437	1956,0455	0.0018	1	98	115	VAPEEHPDLLTEAPLNPK				Mascot
2244,0601	2244,0625	0.0024	1	294	314	DLYANNVLSGGTMYPGIADR	35	99,666		Mascot
2244,0601	2244,0625	0.0024	1	294	314	DLYANNVLSGGTMYPGIADR				Mascot
2552,1531	2552,1523	-0.0008	0	218	240	LCYVALDFENEMATAASSSLEK				Mascot
3212,6045	3212,6033	-0.0012	0	150	179	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR				Mascot
3220,4636	3220,4817	0.0181	6	259	286	CPETLFQPSFGMESAGIHETTYNSIMK				Mascot

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Calc. Mass	Obsrv. Mass	Δ da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
791,3716	791,3723	0.0007	1	287	292	CDIDIR				Mascot
795,4723	795,4719	-0.0004	-1	331	337	IIAPPER				Mascot
976,4482	976,4516	0.0034	3	21	30	AGFAGDDAPR				Mascot
1130,5476	1130,5537	0.0061	5	199	208	GYSFVTTAER	68	100		Mascot
1130,5476	1130,5537	0.0061	5	199	208	GYSFVTTAER				Mascot
1203,5609	1203,5585	-0.0024	-2	42	52	HQGMVMGMGQK		Oxidation (M)[5,8]		Mascot
1500,7078	1500,7156	0.0078	5	362	374	QEYDEAGPSIVHR	92	100		Mascot
1500,7078	1500,7156	0.0078	5	362	374	QEYDEAGPSIVHR				Mascot
1515,7491	1515,7571	0.008	5	87	97	IWHHTFYNELR	66	100		Mascot
1515,7491	1515,7571	0.008	5	87	97	IWHHTFYNELR				Mascot
1790,892	1790,9004	0.0084	5	241	256	SYELPDGQVITIGNER	121	100		Mascot
1790,892	1790,9004	0.0084	5	241	256	SYELPDGQVITIGNER				Mascot
1956,0437	1956,0455	0.0018	1	98	115	VAPEEHPDLLTEAPLNPK	103	100		Mascot
1956,0437	1956,0455	0.0018	1	98	115	VAPEEHPDLLTEAPLNPK				Mascot
2552,1531	2552,1523	-0.0008	0	218	240	LCYVALDFENEMATAASSSLEK				Mascot
3212,6045	3212,6033	-0.0012	0	150	179	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR				Mascot
3220,4636	3220,4817	0.0181	6	259	286	CPETLFQPSFGMESAGIHETTYNSIMK				Mascot

ProteomicTO5611-72_MLV_differential spots mouse 27 of 136

Calc. Mass	Obsrv. Mass	Δ da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
791,3716	791,3723	0.0007	1	287	292	CDIDIR				Mascot
795,4723	795,4719	-0.0004	-1	331	337	IIAPPER				Mascot
976,4482	976,4516	0.0034	3	21	30	AGFAGDDAPR				Mascot
1130,5476	1130,5537	0.0061	5	199	208	GYSFVTTAER	68	100		Mascot
1130,5476	1130,5537	0.0061	5	199	208	GYSFVTTAER				Mascot
1203,5609	1203,5585	-0.0024	-2	42	52	HQGMVMGMGQK		Oxidation (M)[5,8]		Mascot
1500,7078	1500,7156	0.0078	5	362	374	QEYDEAGPSIVHR	92	100		Mascot
1500,7078	1500,7156	0.0078	5	362	374	QEYDEAGPSIVHR				Mascot
1790,892	1790,9004	0.0084	5	241	256	SYELPDGQVITIGNER	121	100		Mascot
1790,892	1790,9004	0.0084	5	241	256	SYELPDGQVITIGNER				Mascot
1956,0437	1956,0455	0.0018	1	98	115	VAPEEHPDLLTEAPLNPK	103	100		Mascot
1956,0437	1956,0455	0.0018	1	98	115	VAPEEHPDLLTEAPLNPK				Mascot
2244,0601	2244,0625	0.0024	1	294	314	DLYANNVLSGGTMYPGIADR	35	99,666		Mascot
2244,0601	2244,0625	0.0024	1	294	314	DLYANNVLSGGTMYPGIADR				Mascot
2552,1531	2552,1523	-0.0008	0	218	240	LCYVALDFENEMATAASSSLEK				Mascot
3212,6045	3212,6033	-0.0012	0	150	179	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR				Mascot
3220,4636	3220,4817	0.0181	6	259	286	CPETLFQPSFGMESAGIHETTYNSIMK				Mascot

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Calc. Mass	Obsrv. Mass	Δ da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
791,3716	791,3723	0.0007	1	286	291	CDIDIR				Mascot

ProteomicTO5611-72_MLV_differential spots mouse 27 of 136

Calc. Mass	Obsrv. Mass	Δ da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
791,3716	791,3723	0.0007	1	286	291	CDIDIR				Mascot

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Plate #	Name	[1] T056P10	Instrument Sample Name					Spectra			9
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pop. Count	Protein Total Ion Score	Total Ion C. I. %			
1	Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3	ALBU_MOUSE	155	70700.5	0	6	100	114	100		
Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence	Ion Score	C. I. %	Modification	Rank Result Type	
	1299,7056	1299,7059	0.0003	0	362	372 HPDYSVSLLLR				Mascot	
	1439,7853	1439,7892	0.0039	3	439	452 APQVSTPTLVEAAR				Mascot	
	1479,7954	1479,8079	0.0125	8	422	434 LGEYGFQNALVR	40	99,881		Mascot	
	1479,7954	1479,8079	0.0125	8	422	434 LGEYGFQNALVR	74	100		Mascot	
	1609,7897	1609,7968	0.0071	4	348	360 DVFLGFLYEYSR				Mascot	
	1609,7897	1609,7968	0.0071	4	348	360 DVFLGFLYEYSR				Mascot	
	1662,8519	1662,8492	-0.0027	-2	470	483 LPCVEDYLSAILNR			Carbamidomethyl (C)[3]	Mascot	
	1917,8912	1917,8998	0.0086	4	153	168 ENPTTFMGHYLHEVAR			Oxidation (M)[7]	Mascot	
2	Myosin-6 OS=Mus musculus GN=Myh6 PE=1 SV=2	MYH6_MOUSE	128	224224.8	0	13	100	65	100		
Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence	Ion Score	C. I. %	Modification	Rank Result Type	
	931,4843	931,4871	0.0028	3	1692	1699 AVVEQTER				Mascot	
	1090,5891	1090,588	-0.0011	-1	1563	1571 AGLFVNOIK				Mascot	
	1130,5801	1130,5564	-0.0237	-21	1282	1291 LOTENGELAR				Mascot	
	1417,7169	1417,7217	0.0048	3	1703	1714 LAEELIETSER				Mascot	
	1441,7645	1441,7722	0.0077	5	1680	1691 NNLLQAELELR	65	100		Mascot	
	1441,7645	1441,7722	0.0077	5	1680	1691 NNLLQAELELR				Mascot	
	1515,7802	1515,75	-0.0302	-20	747	759 LLGSLDIDHMQYK				Mascot	
	1581,7426	1581,7686	0.026	16	1595	1608 MVDLSLQSLDAETR			Oxidation (M)[1]	Mascot	
	1646,8306	1646,8146	-0.016	-10	979	993 NLTEEMAGLDEIAK				Mascot	
	1661,7612	1661,7866	0.0254	15	1883	1897 QAEEAEQANTLNSK				Mascot	
	1662,8254	1662,8492	0.0238	14	979	993 NLTEEMAGLDEIAK			Oxidation (M)[6]	Mascot	
	1709,8018	1709,806	0.0042	2	1488	1501 NAVEEHLLENLFFK				Mascot	
	1722,9497	1722,9473	-0.0024	-1	1715	1728 VQLLHSQNTSLNGK				Mascot	
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	1959,9506	1959,9432	-0.0074	-4	1506	1523 NLQEEISDLTEQLGEGGK				Mascot	
	2009,8903	2009,9022	0.0119	6	1620	1636 MEGDLNEMEIQLSOANR			Oxidation (M)[1,8]	Mascot	
3	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Mus musculus GN=Sucia2 PE=1 SV=2	SUCB1_MOUSE	120	50424.3	0	8	100	58	99,998		
Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence	Ion Score	C. I. %	Modification	Rank Result Type	
	771,4471	771,4449	-0.0022	-3	99	106 AQLVLAGGR				Mascot	
	910,5396	910,528	-0.0116	-13	243	249 LYNFLFK				Mascot	
	1186,5487	1186,5557	0.007	6	275	284 INFDSNSAYR	56	99,997		Mascot	
	1186,5487	1186,5557	0.007	6	275	284 INFDSNSAYR				Mascot	
	1290,6293	1290,6372	0.0079	6	151	160 ICNQLVLCR			Carbamidomethyl (C)[2,8]	Mascot	
	1338,6035	1338,6088	0.0053	4	166	175 EYFAITMER			Oxidation (M)[8]	Mascot	
	1546,8773	1546,8655	-0.0118	-8	370	383 VQAILVNFQGMIR	2	0	Oxidation (M)[13]	Mascot	
	1546,8773	1546,8655	-0.0118	-8	370	383 VQAILVNFQGMIR			Oxidation (M)[13]	Mascot	
	1680,75	1680,7581	0.0081	5	288	300 IFDLGDWQDEDER				Mascot	
	2614,3259	2614,3218	-0.0041	-2	337	362 LHGGTTRAFPLDVGGGAT				Mascot	
						VQVQTEAFK					
4	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1	ACTC_MOUSE	109	42334	0	6	100	57	99,998		
Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence	Ion Score	C. I. %	Modification	Rank Result Type	
	1130,5476	1130,5564	0.0088	8	199	208 GYSFVTTAER				Mascot	
	1500,7078	1500,7161	0.0083	6	362	374 QEYDEAGPSIVHR				Mascot	
	1515,7491	1515,75	0.0009	1	87	97 IWHHTFYNELR				Mascot	
	1790,892	1790,8962	0.0042	2	241	256 SYELPDGQVITIGNER	57	99,998		Mascot	
	1790,892	1790,8962	0.0042	2	241	256 SYELPDGQVITIGNER				Mascot	
	1956,0437	1956,0305	-0.0132	-7	98	115 VAPEEHPHTLLEAPLNPK				Mascot	
	2244,0601	2244,0833	0.0232	10	294	314 DLYANNVLSGGTTMYPGI			Oxidation (M)[14]	Mascot	
						ADR					
5	Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1	ACTA_MOUSE	98	42380.9	0	5	100	57	99,998		
Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence	Ion Score	C. I. %	Modification	Rank Result Type	
	1130,5476	1130,5564	0.0088	8	199	208 GYSFVTTAER				Mascot	
	1500,7078	1500,7161	0.0083	6	362	374 QEYDEAGPSIVHR				Mascot	
	1790,892	1790,8962	0.0042	2	241	256 SYELPDGQVITIGNER	57	99,998		Mascot	
	1790,892	1790,8962	0.0042	2	241	256 SYELPDGQVITIGNER				Mascot	
	1956,0437	1956,0305	-0.0132	-7	98	115 VAPEEHPHTLLEAPLNPK				Mascot	
	2244,0601	2244,0833	0.0232	10	294	314 DLYANNVLSGGTTMYPGI			Oxidation (M)[14]	Mascot	
						ADR					
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	1130,5476	1130,5564	0.0088	8	199	208 GYSFVTTAER				Mascot	
	1500,7078	1500,7161	0.0083	6	362	374 QEYDEAGPSIVHR				Mascot	
	1790,892	1790,8962	0.0042	2	241	256 SYELPDGQVITIGNER	57	99,998		Mascot	
	1790,892	1790,8962	0.0042	2	241	256 SYELPDGQVITIGNER				Mascot	
	1956,0437	1956,0305	-0.0132	-7	98	115 VAPEEHPHTLLEAPLNPK				Mascot	
	2244,0601	2244,0833	0.0232	10	294	314 DLYANNVLSGGTTMYPGI			Oxidation (M)[14]	Mascot	
						ADR					
6	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus musculus GN=Uqcrc1 PE=1 SV=2	QCR1_MOUSE	98	53445.7	0	10	100				
Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence	Ion Score	C. I. %	Modification	Rank Result Type	
	809,4515	809,4438	-0.0077	-10	416	422 SLLTYGR				Mascot	
	912,4396	912,4426	0.003	3	473	479 SGMFWLR			Oxidation (M)[3]	Mascot	
	1110,5426	1110,5447	0.0021	2	214	222 TDLTQYLNLR				Mascot	
	1218,6147	1218,6162	0.0015	1	433	442 IQEVDAGMLR			Oxidation (M)[8]	Mascot	
	1580,7655	1580,7637	-0.0018	-1	86	99 NANGGVYFLHLAFK				Mascot	
	1646,8132	1646,8146	0.0014	1	112	126 EVESGALNAYSTR				Mascot	
	2053,9971	2054,0034	0.0063	3	397	415 NALVSHLDGTFVPCEDIG			Carbamidomethyl (C)[14]	Mascot	
						R					
	2108,1167	2108,1106	-0.0061	-3	229	248 MVLAAAGGVEHQQLDL			Oxidation (M)[1]	Mascot	
						AGK					
	2329,2134	2329,2007	-0.0127	-5	143	163 VVELLADIVONSLSDSQI				Mascot	
						EK					
	2736,2397	2736,239	-0.0007	0	448	470 FYDQCPVAGYGPVIEQL			Carbamidomethyl (C)[6]	Mascot	
						PDYNR					
7	Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1	ACTS_MOUSE	95	42366	0	5	100	57	99,998		
Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence	Ion Score	C. I. %	Modification	Rank Result Type	
	1130,5476	1130,5564	0.0088	8	199	208 GYSFVTTAER				Mascot	
	1500,7078	1500,7161	0.0083	6	362	374 QEYDEAGPSIVHR				Mascot	
	1515,7491	1515,75	0.0009	1	87	97 IWHHTFYNELR				Mascot	
	1790,892	1790,8962	0.0042	2	241	256 SYELPDGQVITIGNER	57	99,998		Mascot	
	1790,892	1790,8962	0.0042	2	241	256 SYELPDGQVITIGNER				Mascot	
	1956,0437	1956,0305	-0.0132	-7	98	115 VAPEEHPHTLLEAPLNPK				Mascot	
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	1130,5476	1130,5564	0.0088	8	199	208 GYSFVTTAER				Mascot	
	1500,7078	1500,7161	0.0083	6	362	374 QEYDEAGPSIVHR				Mascot	
	1790,892	1790,8962	0.0042	2	241	256 SYELPDGQVITIGNER	57	99,998		Mascot	
	1790,892	1790,8962	0.0042	2	241	256 SYELPDGQVITIGNER				Mascot	
	1956,0437	1956,0305	-0.0132	-7	98	115 VAPEEHPHTLLEAPLNPK				Mascot	
8	Myosin-7 OS=Mus musculus GN=Myh7 PE=1 SV=1	MYH7_MOUSE	93	223538.8	0	9	100	65	100		
Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence	Ion Score	C. I. %	Modification	Rank Result Type	
	931,4843	931,4871	0.0028	3	1690	1697 AVVEQTER				Mascot	
	1090,5891	1090,588	-0.0011	-1	1561	1569 AGLFVNOIK				Mascot	
	1417,7169	1417,7217	0.0048	3	1701	1712 LAEELIETSER				Mascot	
	1441,7645	1441,7722	0.0077	5	1678	1689 NNLLQAELELR	65	100		Mascot	
	1441,7645	1441,7722	0.0077	5	1678	1689 NNLLQAELELR				Mascot	
	1515,7802	1515,75	-0.0302	-20	745	757 LLGSLDIDHMQYK				Mascot	
	1581,7426	1581,7686	0.026	16	1593	1606 MVDLSLQSLDAETR			Oxidation (M)[1]	Mascot	
	1661,7612	1661,7866	0.0254	15	1881	1895 QAEEAEQANTLNSK				Mascot	

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1790.892	1790.8934	0.0014	1	240	255 SYELPDGQVITIGNER	43	99.946			Mascot
1790.892	1790.8934	0.0014	1	240	255 SYELPDGQVITIGNER					Mascot
1956.0437	1956.0341	-0.0098	-5	97	114 VAPEEHPTLLTEAPLNPK					Mascot

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Gel Idx/Pos	147/F22	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded
Plate [#] Name	[1] T056P10	Instrument Sample Name		Spectra	9

Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %	
1	Desmin OS=Mus musculus GN=Des PE=1 SV=3	DESM_MOUSE	919	53522.1	0	27	100	574	100

Peptide Information		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
		702.3529	702.351	-0.0019	-3	309	314 NNDALR					Mascot
		751.4097	751.4129	0.0032	4	53	58 VYQVSR					Mascot
		788.4148	788.4162	0.0014	2	369	374 LEEEIR					Mascot
		846.3951	846.399	0.0039	5	429	435 ETSPEQR	44	99.955			Mascot
		846.3951	846.399	0.0039	5	429	435 ETSPEQR					Mascot
		884.4512	884.4559	0.0047	5	118	124 FANYEK					Mascot
		909.4094	909.4156	0.0062	7	339	346 GTNDSLUR			Oxidation (M)[7]		Mascot
		911.4581	911.4663	0.0082	9	241	247 VHEEER					Mascot
		932.4683	932.4755	0.0072	8	407	414 LLEGEESR					Mascot
		1002.5214	1002.5176	-0.0038	-4	212	221 ADVDAATLAR					Mascot
		1018.3968	1018.4017	0.0049	5	318	324 QEMMEYR			Oxidation (M)[3,4]		Mascot
		1028.5735	1028.5806	0.0071	7	193	200 LQEEQLR	66	100			Mascot
		1028.5735	1028.5806	0.0071	7	193	200 LQEEQLR					Mascot
		1032.5432	1032.5499	0.0067	6	59	70 TSGGAGGLGSLR					Mascot
		1086.5902	1086.5972	0.007	6	164	172 QVELTNQR					Mascot
		1101.5535	1101.5609	0.0074	7	180	188 NDLIDLQR					Mascot
		1115.5691	1115.5752	0.0061	5	109	117 VELQELNDR					Mascot
		1263.5964	1263.6046	0.0082	6	201	211 EFAENLAAFR					Mascot
		1268.5828	1268.5848	0.002	2	150	159 VAELYEEMR					Mascot
		1284.5776	1284.582	0.0044	3	150	159 VAELYEEMR			Oxidation (M)[9]		Mascot
		1297.6456	1297.6484	0.0028	2	395	405 MALDVIATYR			Oxidation (M)[1]		Mascot
		1405.7573	1405.7582	0.0009	1	228	239 IESLNEEIAFLK					Mascot
		1555.7135	1555.7207	0.0072	5	355	368 FASEANGYQDNIAR					Mascot
		1633.906	1633.9152	0.0092	6	415	428 INLPIQTFSAINFR	96	100			Mascot
		1633.906	1633.9152	0.0092	6	415	428 INLPIQTFSAINFR					Mascot
		1673.8695	1673.8695	0.009	5	127	141 FLEQQNALAAEVNR	141	100			Mascot

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		1673.8695	1673.8695	0.009	5	127	141 FLEQQNALAAEVNR					Mascot
		1705.8214	1705.8271	0.0057	3	325	338 HQIQSYTCEIDALK			Carbamidomethyl (C)[8]		Mascot
		1768.8348	1768.835	0.0002	0	454	469 DGEVSEATQQQHEVL					Mascot
		2078.0706	2078.0808	0.0102	5	17	37 TFGGAPGFSLGSPLSSP VFR	104	100			Mascot
		2078.0706	2078.0808	0.0102	5	17	37 TFGGAPGFSLGSPLSSP VFR					Mascot
		2755.3574	2755.3633	0.0059	2	79	104 APSYGAGELDFSLADAV NQEFILTR	124	100			Mascot
		2755.3574	2755.3633	0.0059	2	79	104 APSYGAGELDFSLADAV NQEFILTR					Mascot
		3131.5347	3131.5481	0.0134	4	248	274 ELQAQLQEQVQVEMD MSKPDLTAAALR			Oxidation (M)[15,17]		Mascot

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Gel Idx/Pos	148/F23	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded
Plate [#] Name	[1] T056P10	Instrument Sample Name		Spectra	9

Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %	
1	ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2	ATPB_MOUSE	872	56265.5	0	20	100	598	100

Peptide Information		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
		975.5621	975.5546	-0.0075	-8	202	212 IGLFGAGAGVVK					Mascot
		1038.5942	1038.5969	0.0027	3	134	143 IPVGFITLGR					Mascot
		1088.635	1088.6353	0.0003	0	189	198 VDLRLPYAK					Mascot
		1278.6359	1278.6404	0.0045	4	110	121 TIAMDGTGLVLR			Oxidation (M)[4]		Mascot
		1401.7042	1401.7065	0.0023	2	144	155 IMNVIGEPIDR			Oxidation (M)[2]		Mascot
		1406.681	1406.6886	0.0076	5	226	239 AHGYSYVFAVGGER	122	100			Mascot
		1406.681	1406.6886	0.0076	5	226	239 AHGYSYVFAVGGER					Mascot
		1435.7539	1435.761	0.0071	5	311	324 FTDAGSEVSALLGR					Mascot
		1439.7893	1439.7948	0.0055	4	282	294 VALTGLTVAEYR	95	100			Mascot
		1439.7893	1439.7948	0.0055	4	282	294 VALTGLTVAEYR					Mascot
		1473.8345	1473.825	-0.0095	-6	213	225 TVLIMELINNAK			Oxidation (M)[5]		Mascot
		1617.8053	1617.8098	0.0045	3	265	279 VALVYGMNEPPGAR	24	95.654	Oxidation (M)[8]		Mascot
		1617.8053	1617.8098	0.0045	3	265	279 VALVYGMNEPPGAR			Oxidation (M)[8]		Mascot
		1650.9174	1650.9237	0.0063	4	95	109 LVLEVGHILGESTVLR	102	100			Mascot
		1650.9174	1650.9237	0.0063	4	95	109 LVLEVGHILGESTVLR					Mascot
		1858.8752	1858.8757	0.0005	0	407	422 IMDPNVIGNEYDVAR			Oxidation (M)[2]		Mascot
		1921.9655	1921.9722	0.0067	3	295	310 DQEGQDVLFDNIFR	122	100			Mascot
		1921.9655	1921.9722	0.0067	3	295	310 DQEGQDVLFDNIFR					Mascot
		1988.0334	1988.0393	0.0059	3	388	406 AIAELGIYPAVDPLDSTSR	125	100			Mascot
		1988.0334	1988.0393	0.0059	3	388	406 AIAELGIYPAVDPLDSTSR					Mascot
		2039.0055	2039.0058	0.0001	0	463	480 FLSQPFQVAEVFTGHMGK			Oxidation (M)[16]		Mascot
		2076.9907	2076.991	0.0003	0	242	259 EGNLDYHEMIEGVLNPK			Oxidation (M)[9]		Mascot
		2298.074	2298.1169	0.0429	19	325	345 IPSAVGYQPTLATDMGT MQER	8	0	Oxidation (M)[15,18]		Mascot
		2298.074	2298.1169	0.0429	19	325	345 IPSAVGYQPTLATDMGT MQER			Oxidation (M)[15,18]		Mascot
		3042.5491	3042.553	0.0039	1	162	188 FQAPIHAEAFEFIEMSVE			Oxidation (M)[15]		Mascot

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		3366.635	3366.6284	-0.0066	-2	490	519 GFGQLAGEYDHLPEQAF YMVGPTEAAVK			Oxidation (M)[20]		Mascot
		3714.886	3714.8828	-0.0032	-1	352	387 GSITSVQAIYVPADLTD PAPATTFALDATTLSLR					Mascot

2	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1	ACTC_MOUSE	169	42334	0	8	100	97	100
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Peptide Information		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
		795.4723	795.4719	-0.0004	-1	331	337 IAPPER					Mascot
		1130.5476	1130.5516	0.004	4	199	208 GYSFVITAEK					Mascot
		1198.7054	1198.7059	0.0005	0	31	41 AVFVSIVGRPR					Mascot
		1500.7078	1500.7146	0.0068	5	362	374 QEYDEAGPSIVHR					Mascot
		1515.7491	1515.7583	0.0092	9	37	97 IWHFFVNELR					Mascot
		1790.892	1790.8981	0.0061	3	241	256 SYELPDGQVITIGNER	97	100			Mascot
		1790.892	1790.8981	0.0061	3	241	256 SYELPDGQVITIGNER					Mascot
		1956.0437	1956.0409	-0.0028	-1	98	115 VAPEEHPTLLTEAPLNPK					Mascot
		2244.0601	2244.0662	0.0061	3	294	314 DLYANNVLSGGTMYPGIADR			Oxidation (M)[14]		Mascot

3	Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1	ACTA_MOUSE	158	42380.9	0	7	100	97	100
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Peptide Information		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
		795.4723	795.4719	-0.0004	-1	331	337 IAPPER					Mascot
		1130.5476	1130.5516	0.004	4	199	208 GYSFVITAEK					Mascot
		1198.7054	1198.7059	0.0005	0	31	41 AVFVSIVGRPR					Mascot
		1500.7078	1500.7146	0.0068	5	362	374 QEYDEAGPSIVHR					Mascot
		1790.892	1790.8981	0.0061	3	241	256 SYELPDGQVITIGNER	97	100			Mascot
		1790.892	1790.8981	0.0061	3	241	256 SYELPDGQVITIGNER					Mascot

840,4032	840,4194	0,0162	19	407	412 YNQLMR					Oxidation (M)[5]	Mascot
840,4032	840,4194	0,0162	19	407	412 YNQLMR					Oxidation (M)[5]	Mascot
917,4938	917,498	0,0042	5	82	89 LSVVDGDK						Mascot
941,5666	941,5782	0,0116	12	72	80 TLGPALLEK						Mascot
1134,579	1134,5847	0,0057	5	229	239 TAIQAAGYDPK						Mascot
1166,6317	1166,635	0,0033	3	184	193 IGAEVYHHLK						Mascot
1380,7118	1380,6991	-0,0127	-9	16	28 GNPTVEVDLHTAK						Mascot
1519,8301	1519,8248	-0,0053	-3	106	120 FGANAILGVSLAVCK					Carbamidomethyl (C)[14]	Mascot
1556,7777	1556,7796	0,0021	1	240	253 VVIGMDVAASEFYR					Oxidation (M)[10]	Mascot
1557,759	1557,7656	0,0066	4	359	372 LAQSNQGWVMVSHR			6	0	Oxidation (M)[10]	Mascot
1557,759	1557,7656	0,0066	4	359	372 LAQSNQGWVMVSHR					Oxidation (M)[10]	Mascot
1572,7726	1572,7743	0,0017	1	240	253 VVIGMDVAASEFYR			38	99,817	Oxidation (M)[5]	Mascot
1572,7726	1572,7743	0,0017	1	240	253 VVIGMDVAASEFYR					Oxidation (M)[5]	Mascot
1633,8214	1633,8145	-0,0069	-4	344	358 VVIGMDVAASEFYR					Carbamidomethyl (C)[14]	Mascot
1804,944	1804,948	0,004	2	33	50 AAVPSGASTGIYEALER			164	100		Mascot
1804,944	1804,948	0,004	2	33	50 AAVPSGASTGIYEALER						Mascot
1900,9547	1900,949	-0,0057	-3	163	179 LAMQEFMLPGVASSFK			47	99,978	Oxidation (M)[3,7]	Mascot
1900,9547	1900,949	-0,0057	-3	163	179 LAMQEFMLPGVASSFK					Oxidation (M)[3,7]	Mascot
2353,1592	2353,1624	0,0032	1	373	394 SGETEDTFIADLVGLCT					Carbamidomethyl (C)[17]	Mascot
					GQIK						
2743,342	2743,3577	0,0157	6	203	228 DATNVGDEGGFAPNILEN						Mascot
					NEALELLEK						
3007,5747	3007,6113	0,0366	12	133	162 HIADLAGNPDLLVLPVAF						Mascot
					NVINGSGSHAGNK						

2 Gamma-enolase OS=Mus musculus GN=Eno2 PE=1 ENOG_MOUSE 302 47609,1 0 9 100 217 100
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SV=2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
732,3886	732,4073	0,0187	26	10	15 EILDSR					Mascot
800,3824	800,4042	0,0218	27	257	262 YDLDFK					Mascot
840,4032	840,4194	0,0162	19	407	412 YNQLMR			Oxidation (M)[5]		Mascot
840,4032	840,4194	0,0162	19	407	412 YNQLMR			Oxidation (M)[5]		Mascot
1519,8301	1519,8248	-0,0053	-3	106	120 FGANAILGVSLAVCK			53	99,995	Carbamidomethyl (C)[14]
1586,7498	1586,7679	0,0181	11	240	253 VVIGMDVAASEFYR					Mascot
1586,7498	1586,7679	0,0181	11	240	253 VVIGMDVAASEFYR					Mascot
1599,7697	1599,7855	0,0158	10	359	372 LAQSNQGWVMVSHR					Oxidation (M)[10]
1804,944	1804,948	0,004	2	33	50 AAVPSGASTGIYEALER			164	100	Mascot
1804,944	1804,948	0,004	2	33	50 AAVPSGASTGIYEALER					Mascot
1938,9816	1938,9242	-0,0574	-30	163	179 LAMQEFMLPGVASSFR					Mascot
2353,1592	2353,1624	0,0032	1	373	394 SGETEDTFIADLVGLCT					Carbamidomethyl (C)[17]
					GQIK					

3 Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 ENOA_MOUSE 244 47453,3 0 8 100 169 100
 SV=3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
704,4089	704,4275	0,0186	26	127	132 GVPLR					Mascot
800,3824	800,4042	0,0218	27	257	262 YDLDFK					Mascot
1519,8301	1519,8248	-0,0053	-3	106	120 FGANAILGVSLAVCK			6	0	Carbamidomethyl (C)[14]
1557,759	1557,7656	0,0066	4	359	372 LAQSNQGWVMVSHR					Oxidation (M)[10]
1557,759	1557,7656	0,0066	4	359	372 LAQSNQGWVMVSHR					Oxidation (M)[10]
1633,8214	1633,8145	-0,0069	-4	344	358 VVIGMDVAASEFYR					Carbamidomethyl (C)[14]
1804,944	1804,948	0,004	2	33	50 AAVPSGASTGIYEALER			164	100	Mascot
1804,944	1804,948	0,004	2	33	50 AAVPSGASTGIYEALER					Mascot
1928,9608	1928,9626	0,0018	1	163	179 LAMQEFMLPGVASSFR					Oxidation (M)[3,7]
2353,1592	2353,1624	0,0032	1	373	394 SGETEDTFIADLVGLCT					Carbamidomethyl (C)[17]
					GQIK					

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Gel Idx/Pos	157/G8	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded			
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9			
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %
1	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1	ACTC_MOUSE	143	42334	0	7	100	81 100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
795,4723	795,4714	-0,0009	-1	331	337 IAPPER					Mascot
1130,5476	1130,5482	0,0006	1	199	208 GYSFVTTAER					Mascot
1500,7078	1500,7119	0,0041	3	362	374 QEYDEAGSIVHR	58	99,998			Mascot
1500,7078	1500,7119	0,0041	3	362	374 QEYDEAGSIVHR					Mascot
1515,7491	1515,7524	0,0033	2	87	97 IWHHTFYNELR					Mascot
1790,892	1790,8927	0,0007	0	241	256 SYELPDGQVITIGNER	23	92,828			Mascot
1790,892	1790,8927	0,0007	0	241	256 SYELPDGQVITIGNER					Mascot
1956,0437	1956,0289	-0,148	-8	98	115 VAPEEHPTLLTEAPLNPK					Mascot
2244,0601	2244,0784	0,0183	8	294	314 DLVIANVLSGGTMYPGI					Oxidation (M)[14]
					ADR					

2 Serum albumin OS=Mus musculus GN=Ab PE=1 SV=3 ALBU_MOUSE 134 70700,5 0 7 100 80 100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
1439,7853	1439,7775	-0,0078	-5	439	452 APCVSTPTLVEAAR					Mascot
1479,7954	1479,8	0,0046	3	422	434 LGEYGFQNALVR	31	99,061			Mascot
1479,7954	1479,8	0,0046	3	422	434 LGEYGFQNALVR					Mascot
1609,7897	1609,7925	0,0028	2	348	360 DVFLGTFLYEYSR	48	99,98			Mascot
1609,7897	1609,7925	0,0028	2	348	360 DVFLGTFLYEYSR					Mascot
1662,8519	1662,8522	0,0003	0	470	483 LPCVEDVLSALNR					Carbamidomethyl (C)[3]
1681,8431	1681,8179	-0,0252	-15	243	257 LSQTFPNADFAITK					Mascot
1882,9368	1882,9332	-0,0036	-2	509	524 RPCFSALTVDETVPK					Carbamidomethyl (C)[3]
1882,9368	1882,9332	-0,0036	-2	509	524 RPCFSALTVDETVPK					Carbamidomethyl (C)[11]
1895,8844	1895,9244	0,04	21	528	543 AETTFHSDICTLPEK					Mascot

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Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
795,4723	795,4714	-0,0009	-1	331	337 IAPPER					Mascot
1130,5476	1130,5482	0,0006	1	199	208 GYSFVTTAER					Mascot
1500,7078	1500,7119	0,0041	3	362	374 QEYDEAGSIVHR	58	99,998			Mascot
1500,7078	1500,7119	0,0041	3	362	374 QEYDEAGSIVHR					Mascot
1790,892	1790,8927	0,0007	0	241	256 SYELPDGQVITIGNER	23	92,828			Mascot
1790,892	1790,8927	0,0007	0	241	256 SYELPDGQVITIGNER					Mascot
1956,0437	1956,0289	-0,148	-8	98	115 VAPEEHPTLLTEAPLNPK					Mascot
2244,0601	2244,0784	0,0183	8	294	314 DLVIANVLSGGTMYPGI					Oxidation (M)[14]
					ADR					

4 Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1 ACTS_MOUSE 128 42386 0 6 100 81 100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
795,4723	795,4714	-0,0009	-1	331	337 IAPPER					Mascot
1130,5476	1130,5482	0,0006	1	199	208 GYSFVTTAER					Mascot
1500,7078	1500,7119	0,0041	3	362	374 QEYDEAGSIVHR	58	99,998			Mascot
1500,7078	1500,7119	0,0041	3	362	374 QEYDEAGSIVHR					Mascot
1515,7491	1515,7524	0,0033	2	87	97 IWHHTFYNELR					Mascot
1790,892	1790,8927	0,0007	0	241	256 SYELPDGQVITIGNER	23	92,828			Mascot
1790,892	1790,8927	0,0007	0	241	256 SYELPDGQVITIGNER					Mascot
1956,0437	1956,0289	-0,148	-8	98	115 VAPEEHPTLLTEAPLNPK					Mascot

5 Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Mus musculus GN=Suc2g2 PE=2 SUCB2_MOUSE 75 47095,8 0 6 99,943 30 98,698

SV=3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
821.4515	821.4551	0.0036	4	95	102 GVFNGLK				Mascot
1191.6256	1191.6235	-0.0021	-2	192	201 EODIFEGIK				Mascot
1240.5593	1240.5712	0.0119	10	261	270 INFDDNAEFR	30	98.698		Mascot
1340.5593	1240.5712	0.0119	10	261	270 INFDDNAEFR				Mascot
1358.6183	1358.6464	0.0281	21	281	292 SENEPIEAAAR				Mascot

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Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
1556.8279	1556.8077	-0.0202	-13	394	407 LEGTNVQEAQNLK				Mascot
1673.8593	1673.8665	0.0072	4	408	424 SSSLPTSVAVDLEDAAK				Mascot

6 Actin, gamma-enteric smooth muscle OS=Mus musculus GN=Actg2 PE=2 SV=1 ACTH_MOUSE 63 42248.9 0 5 99,171 23 92,828 Mascot

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
795.4723	795.4714	-0.0009	-1	330	336 IAPPER				Mascot
1130.5476	1130.5482	0.0006	1	198	207 GYSFVITTAER				Mascot
1790.8927	1790.8927	0.0007	0	240	255 SYELPDGQVITIGNER	23	92.828		Mascot
1790.8927	1790.8927	0.0007	0	240	255 SYELPDGQVITIGNER				Mascot
1956.0437	1956.0289	-0.0148	-8	97	114 VAPEEHTLLTEAPLNPK				Mascot
2244.0601	2244.0784	0.0183	8	293	313 DLYANNVLSGGTMYPGIADR			Oxidation (M)[14]	Mascot

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Gel Idx/Pos 158/G9 Instr./Gel Origin AK139/T056 Process Status Analysis Succeeded
Plate # Name [1] T056P10 Instrument Sample Name Spectra 9

Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %
1	Troponin T, cardiac muscle OS=Mus musculus GN=Tnn2 PE=1 SV=2	TNNT2_MOUSE	407	35804	0	10	100 304	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
731.3682	731.3765	0.0083	11	281	286 INDNQG				Mascot
732.3635	732.3632	-0.0003	0	204	209 QAQTER				Mascot
779.3934	779.3971	0.0037	5	261	266 FDLQEK	34	99.544		Mascot
906.5043	906.5057	0.0014	2	272	278 YEINLVR				Mascot
906.5043	906.5057	0.0014	2	272	278 YEINLVR				Mascot
1016.4796	1016.4855	0.0059	6	98	105 VDFDIIHR	46	99.965		Mascot
1016.4796	1016.4855	0.0059	6	98	105 VDFDIIHR				Mascot
1171.6544	1171.6478	-0.0066	-6	82	91 LFMPNLVPPK			Oxidation (M)[3]	Mascot
1507.7864	1507.7896	0.0032	2	231	243 ALAIDLHNEQLR	70	100		Mascot
1507.7864	1507.7896	0.0032	2	231	243 ALAIDLHNEQLR				Mascot
1612.761	1612.7889	0.0279	17	190	203 ALSNMMHFGGYIQK			Oxidation (M)[5]	Mascot
1628.756	1628.7664	0.0104	6	190	203 ALSNMMHFGGYIQK	20	88.686	Oxidation (M)[5,6]	Mascot
1628.756	1628.7664	0.0104	6	190	203 ALSNMMHFGGYIQK			Oxidation (M)[5,6]	Mascot
1754.8556	1754.8655	0.0099	6	66	81 DAEEGPEVDTKPKPSR				Mascot
1941.9664	1941.9698	0.0034	2	111	126 DLNELQTLIEAHFENR	133	100		Mascot
1941.9664	1941.9698	0.0034	2	111	126 DLNELQTLIEAHFENR				Mascot

2 Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3 ALBU_MOUSE 197 70700.5 0 8 100 136 100 Mascot

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
1149.615	1149.6084	-0.0066	-6	66	75 LVQEVDFAK				Mascot
1299.7056	1299.703	-0.0026	-2	362	372 HPDYSVSLLLR				Mascot
1439.7853	1439.7859	0.0006	0	439	452 APOVSTPTLVEAAR				Mascot
1479.7954	1479.8052	0.0098	7	422	434 LGEYGFQNALVLR	62	100		Mascot
1479.7954	1479.8052	0.0098	7	422	434 LGEYGFQNALVLR				Mascot

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1609.7897	1609.7959	0.0062	4	348	360 DVFGLFTLYEYSR	74	100		Mascot
1609.7897	1609.7959	0.0062	4	348	360 DVFGLFTLYEYSR				Mascot
1662.8519	1662.8448	-0.0071	-4	470	483 LPCVEDYLSALNLR			Carbamidomethyl (C)[3]	Mascot
1681.8431	1681.8391	-0.004	-2	243	257 LSQTFPNADFAETK				Mascot
1917.8912	1917.9073	0.0161	8	153	168 ENPTTFMGHLYHEVAR			Oxidation (M)[7]	Mascot

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Gel Idx/Pos 159/G10 Instr./Gel Origin AK139/T056 Process Status Analysis Succeeded
Plate # Name [1] T056P10 Instrument Sample Name Spectra 9

Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %
1	Troponin T, cardiac muscle OS=Mus musculus GN=Tnn2 PE=1 SV=2	TNNT2_MOUSE	585	35804	0	12	100 451	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
731.3682	731.3684	0.0002	0	281	286 INDNQG				Mascot
732.3635	732.3669	0.0034	5	204	209 QAQTER				Mascot
779.3934	779.3936	0.0002	0	261	266 FDLQEK				Mascot
805.3322	805.3391	0.0069	9	173	178 EEEENR				Mascot
906.5043	906.5104	0.0061	7	272	278 YEINLVR	34	99.433		Mascot
906.5043	906.5104	0.0061	7	272	278 YEINLVR				Mascot
1016.4796	1016.4879	0.0083	8	98	105 VDFDIIHR	79	100		Mascot
1016.4796	1016.4879	0.0083	8	98	105 VDFDIIHR				Mascot
1155.6594	1155.6593	-0.0001	0	82	91 LFMPNLVPPK			Oxidation (M)[3]	Mascot
1171.6544	1171.6517	-0.0027	-2	82	91 LFMPNLVPPK	23	93.244	Oxidation (M)[3]	Mascot
1171.6544	1171.6517	-0.0027	-2	82	91 LFMPNLVPPK			Oxidation (M)[3]	Mascot
1507.7864	1507.7913	0.0049	3	231	243 ALAIDLHNEQLR	99	100		Mascot
1507.7864	1507.7913	0.0049	3	231	243 ALAIDLHNEQLR				Mascot
1596.8016	1596.7958	-0.0058	-4	248	260 ELWOSIHLEAEK	56	99.997		Mascot
1596.8016	1596.7958	-0.0058	-4	248	260 ELWOSIHLEAEK				Mascot
1612.761	1612.7833	0.0223	14	190	203 ALSNMMHFGGYIQK			Oxidation (M)[5]	Mascot
1628.756	1628.7616	0.0056	3	190	203 ALSNMMHFGGYIQK	25	95.994	Oxidation (M)[5,6]	Mascot
1628.756	1628.7616	0.0056	3	190	203 ALSNMMHFGGYIQK			Oxidation (M)[5,6]	Mascot
1754.8556	1754.8596	0.004	2	66	81 DAEEGPEVDTKPKPSR				Mascot
1941.9664	1941.9722	0.0058	3	111	126 DLNELQTLIEAHFENR	136	100		Mascot
1941.9664	1941.9722	0.0058	3	111	126 DLNELQTLIEAHFENR				Mascot

2 Troponin T, slow skeletal muscle OS=Mus musculus GN=Tnn1 PE=2 SV=3 TNNT1_MOUSE 84 31325.1 0 1 99,993 79 100 Mascot

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
1016.4796	1016.4879	0.0083	8	61	68 VDFDIIHR	79	100		Mascot
1016.4796	1016.4879	0.0083	8	61	68 VDFDIIHR				Mascot

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Gel Idx/Pos 160/G11 Instr./Gel Origin AK139/T056 Process Status Analysis Succeeded
Plate # Name [1] T056P10 Instrument Sample Name Spectra 9

Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %
1	Troponin T, cardiac muscle OS=Mus musculus GN=Tnn2 PE=1 SV=2	TNNT2_MOUSE	524	35804	0	12	100 391	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
731.3682	731.3844	0.0162	22	281	286 INDNQG				Mascot
732.3635	732.3801	0.0166	23	204	209 QAQTER				Mascot
779.3934	779.4079	0.0145	19	261	266 FDLQEK				Mascot

1216.5997	1216.6064	0.0067	6	179	188 IAEFAFEYAR	77	100				Mascot
1216.5997	1216.6064	0.0067	6	179	188 IAEFAFEYAR						Mascot
1316.5247	1316.5297	0.005	4	351	360 CSDFTEICR					Carbamidomethyl (C)[1,9]	Mascot
1391.7529	1391.7567	0.0038	3	135	146 TPYTDVNVITR	93	100				Mascot
1391.7529	1391.7567	0.0038	3	135	146 TPYTDVNVITR						Mascot
1606.8734	1606.8763	0.0029	2	101	115 TPIAAGHPSMNLRL	8	0			Oxidation (M)[10]	Mascot
1606.8734	1606.8763	0.0029	2	101	115 TPIAAGHPSMNLRL					Oxidation (M)[10]	Mascot
1894.9435	1894.9434	-0.0001	0	300	316 DMANPTALLSAVMMLR					Oxidation (M)[2,14,15]	Mascot
1894.9435	1894.9434	-0.0001	0	300	316 DMANPTALLSAVMMLR					Oxidation (M)[2,14,15]	Mascot
2022.0481	2132.0532	0.0051	2	117	134 TFDLVNRPVCSIEGYK					Carbamidomethyl (C)[11]	Mascot
2502.2358	2502.238	0.0022	1	147	169 ENTEGEYSGIEHVVVDGV	73	100				Mascot
					VQSIK						Mascot
2502.2358	2502.238	0.0022	1	147	169 ENTEGEYSGIEHVVVDGV						Mascot
					VQSIK						Mascot

2 Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3 ALBU_MOUSE 90 70700.5 0 6 99,999 50 99,987

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
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1299.7056	1299.7064	0.0008	1	362	372 HPDYSVSLLLR						Mascot
1439.7853	1439.7781	-0.0072	-5	439	452 APOVSTPTLVEAAR						Mascot
1479.7954	1479.8031	0.0077	5	422	434 LGEYGFQNALVR	50	99.988				Mascot
1479.7954	1479.8031	0.0077	5	422	434 LGEYGFQNALVR						Mascot
1609.7897	1609.8182	0.0285	18	348	360 DVFLGFLYEYSR						Mascot
1662.8519	1662.8584	0.0065	4	470	483 LPCVEDLSAILNR					Carbamidomethyl (C)[3]	Mascot
1882.9368	1882.9458	0.009	5	509	524 RPCFSALTYDEVYPK					Carbamidomethyl (C)[3]	Mascot

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165/G16	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded
Plate #1	Instrument Sample Name		Spectra	9

1 Actin, alpha cardiac muscle 1 OS=Mus musculus ACTC_MOUSE 437 42334 0 10 100 329 100

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
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791.3716	791.3797	0.0081	10	287	292 CDIDIR			Carbamidomethyl (C)[1]		Mascot	
795.4723	795.4715	-0.0008	-1	331	337 IAAPPER					Mascot	
1130.5476	1130.5505	0.0029	3	199	208 GYSFVTTAER	54	99.995			Mascot	
1130.5476	1130.5505	0.0029	3	199	208 GYSFVTTAER					Mascot	
1500.7078	1500.7122	0.0044	3	362	374 QEYDEAGPSIVHR	78	100			Mascot	
1500.7078	1500.7122	0.0044	3	362	374 QEYDEAGPSIVHR					Mascot	
1515.7491	1515.7531	0.004	3	87	97 IWHHTFYNELR	52	99.991			Mascot	
1515.7491	1515.7531	0.004	3	87	97 IWHHTFYNELR					Mascot	
1790.892	1790.8965	0.0045	3	241	256 SYELPDGQVITIGNER	83	100			Mascot	
1790.892	1790.8965	0.0045	3	241	256 SYELPDGQVITIGNER					Mascot	
1956.0437	1956.0431	-0.0006	0	98	115 VAPEEHPTLLTEAPLNPK	62	100			Mascot	
1956.0437	1956.0431	-0.0006	0	98	115 VAPEEHPTLLTEAPLNPK					Mascot	
2244.0601	2244.0645	0.0044	2	294	314 DLYANNVLSGGTTMYPGI			Oxidation (M)[14]		Mascot	
					ADR						Mascot
2552.1531	2552.1565	0.0034	1	218	240 LCYVALDFENEMATAASS			Carbamidomethyl (C)[2], Oxidation (M)[12]		Mascot	
					SSLEK						Mascot
3212.6045	3212.6038	-0.0007	0	150	179 TTGIVLDSGDGVTHNVPI			Oxidation (M)[29]		Mascot	
					YEGYALPHAIMR						Mascot

2 Actin, alpha skeletal muscle OS=Mus musculus ACTS_MOUSE 420 42366 0 9 100 329 100

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
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791.3716	791.3797	0.0081	10	287	292 CDIDIR			Carbamidomethyl (C)[1]		Mascot
795.4723	795.4715	-0.0008	-1	331	337 IAAPPER					Mascot
1130.5476	1130.5505	0.0029	3	199	208 GYSFVTTAER	54	99.995			Mascot
1130.5476	1130.5505	0.0029	3	199	208 GYSFVTTAER					Mascot

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1500.7078	1500.7122	0.0044	3	362	374 QEYDEAGPSIVHR	78	100			Mascot	
1500.7078	1500.7122	0.0044	3	362	374 QEYDEAGPSIVHR					Mascot	
1515.7491	1515.7531	0.004	3	87	97 IWHHTFYNELR	52	99.991			Mascot	
1515.7491	1515.7531	0.004	3	87	97 IWHHTFYNELR					Mascot	
1790.892	1790.8965	0.0045	3	241	256 SYELPDGQVITIGNER	83	100			Mascot	
1790.892	1790.8965	0.0045	3	241	256 SYELPDGQVITIGNER					Mascot	
1956.0437	1956.0431	-0.0006	0	98	115 VAPEEHPTLLTEAPLNPK	62	100			Mascot	
1956.0437	1956.0431	-0.0006	0	98	115 VAPEEHPTLLTEAPLNPK					Mascot	
2552.1531	2552.1565	0.0034	1	218	240 LCYVALDFENEMATAASS			Carbamidomethyl (C)[2], Oxidation (M)[12]		Mascot	
					SSLEK						Mascot
3212.6045	3212.6038	-0.0007	0	150	179 TTGIVLDSGDGVTHNVPI			Oxidation (M)[29]		Mascot	
					YEGYALPHAIMR						Mascot

3 Actin, aortic smooth muscle OS=Mus musculus ACTA_MOUSE 372 42380.9 0 9 100 277 100

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
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791.3716	791.3797	0.0081	10	287	292 CDIDIR			Carbamidomethyl (C)[1]		Mascot	
795.4723	795.4715	-0.0008	-1	331	337 IAAPPER					Mascot	
1130.5476	1130.5505	0.0029	3	199	208 GYSFVTTAER	54	99.995			Mascot	
1130.5476	1130.5505	0.0029	3	199	208 GYSFVTTAER					Mascot	
1500.7078	1500.7122	0.0044	3	362	374 QEYDEAGPSIVHR	78	100			Mascot	
1500.7078	1500.7122	0.0044	3	362	374 QEYDEAGPSIVHR					Mascot	
1790.892	1790.8965	0.0045	3	241	256 SYELPDGQVITIGNER	83	100			Mascot	
1790.892	1790.8965	0.0045	3	241	256 SYELPDGQVITIGNER					Mascot	
1956.0437	1956.0431	-0.0006	0	98	115 VAPEEHPTLLTEAPLNPK	62	100			Mascot	
1956.0437	1956.0431	-0.0006	0	98	115 VAPEEHPTLLTEAPLNPK					Mascot	
2244.0601	2244.0645	0.0044	2	294	314 DLYANNVLSGGTTMYPGI			Oxidation (M)[14]		Mascot	
					ADR						Mascot
2552.1531	2552.1565	0.0034	1	218	240 LCYVALDFENEMATAASS			Carbamidomethyl (C)[2], Oxidation (M)[12]		Mascot	
					SSLEK						Mascot
3212.6045	3212.6038	-0.0007	0	150	179 TTGIVLDSGDGVTHNVPI			Oxidation (M)[29]		Mascot	
					YEGYALPHAIMR						Mascot

4 Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3 ALBU_MOUSE 344 70700.5 0 8 100 280 100

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
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1299.7056	1299.7067	0.0011	1	362	372 HPDYSVSLLLR					Mascot
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1439.7853	1439.7866	0.0013	1	439	452 APOVSTPTLVEAAR					Mascot	
1479.7954	1479.802	0.0066	4	422	434 LGEYGFQNALVR	63	100			Mascot	
1479.7954	1479.802	0.0066	4	422	434 LGEYGFQNALVR					Mascot	
1609.7897	1609.7948	0.0051	3	348	360 DVFLGFLYEYSR	117	100			Mascot	
1609.7897	1609.7948	0.0051	3	348	360 DVFLGFLYEYSR					Mascot	
1662.8519	1662.8578	0.0059	4	470	483 LPCVEDLSAILNR	100	100			Carbamidomethyl (C)[3]	Mascot
1662.8519	1662.8578	0.0059	4	470	483 LPCVEDLSAILNR					Carbamidomethyl (C)[3]	Mascot
1866.7708	1866.7714	0.0006	0	570	584 TVMDDFAQLDTCCK			Carbamidomethyl (C)[13,14], Oxidation (M)[3]		Mascot	
1882.9368	1882.9391	0.0023	1	509	524 RPCFSALTYDEVYPK			Carbamidomethyl (C)[3]		Mascot	
1895.8844	1895.8856	0.0012	1	528	543 AETFTFHSIDICTLPEK			Carbamidomethyl (C)[11]		Mascot	

5 Actin, gamma-enteric smooth muscle OS=Mus musculus GN=Actg2 PE=2 SV=1 ACTH_MOUSE 281 42248.9 0 8 100 199 100

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
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791.3716	791.3797	0.0081	10	286	291 CDIDIR			Carbamidomethyl (C)[1]		Mascot
795.4723	795.4715	-0.0008	-1	330	336 IAAPPER					Mascot
1130.5476	1130.5505	0.0029	3	198	207 GYSFVTTAER	54	99.995			Mascot
1130.5476	1130.5505	0.0029	3	198	207 GYSFVTTAER					Mascot
1790.892	1790.8965	0.0045	3	240	255 SYELPDGQVITIGNER	83	100			Mascot
1790.892	1790.8965	0.0045	3	240	255 SYELPDGQVITIGNER					Mascot

1956,0437	1956,0431	-0.0006	0	97	114	VAPEEHPTLLTEAPLNPK	62	100		Mascot
1956,0437	1956,0431	-0.0006	0	97	114	VAPEEHPTLLTEAPLNPK				Mascot
2244,0601	2244,0645	0.0044	2	293	313	DLYANNVLSGGTMYPGI ADR			Oxidation (M)[14]	Mascot
2552,1531	2552,1565	0.0034	1	217	239	LCYVALDFENEMATAASS SSLEK			Carbamidomethyl (C)[2], Oxidation (M)[12]	Mascot
3212,6045	3212,6038	-0.0007	0	149	178	TGIVLSDSGDGVTHNVPI YEGYALPHAIMR			Oxidation (M)[29]	Mascot

6 Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1

ACTG_MOUSE	151	42107.9	0	3	100	134	100
Protein Group							
Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1	ACTB_MOUSE	42051.9	0				

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
795,4723	795,4715	-0.0008	-1	329	335	IAAPPER					Mascot

ProteomicTO5611-72_MLV_d 795,4715 Mascot 86 of 136

1515,7491	1515,7531	0.004	3	85	95	IWHHTFYNELR	52	99,991			Mascot
1515,7491	1515,7531	0.004	3	85	95	IWHHTFYNELR					Mascot
1790,892	1790,8965	0.0045	3	239	254	SYELPDGQVITIGNER	83	100			Mascot
1790,892	1790,8965	0.0045	3	239	254	SYELPDGQVITIGNER					Mascot

7 Beta-actin-like protein 2 OS=Mus musculus GN=Actb2 PE=1 SV=1

ACTB_MOUSE	100	42319.1	0	3	100	83	100
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Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
795,4723	795,4715	-0.0008	-1	330	336	IAAPPER					Mascot
1393,678	1393,7167	0.0387	28	274	285	GIHETTFNSIMK			Oxidation (M)[11]		Mascot
1790,892	1790,8965	0.0045	3	240	255	SYELPDGQVITIGNER	83	100			Mascot
1790,892	1790,8965	0.0045	3	240	255	SYELPDGQVITIGNER					Mascot

8 L-lactate dehydrogenase B chain OS=Mus musculus GN=Ldhb PE=1 SV=2

LDBH_MOUSE	60	36834.1	0	7	98,383		
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Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
742,457	742,4497	-0.0073	-10	108	113	LNLVQR					Mascot
913,5828	913,5828	0	0	92	100	IWVTFQVVR					Mascot
957,6131	957,6087	-0.0044	-5	120	127	FIPQINK					Mascot
1176,5896	1176,5884	-0.0012	-1	320	329	SADTLWDIQK					Mascot
1248,6001	1248,6058	0.0057	5	159	170	VIGSGCNLDSAR					Mascot
1629,8582	1629,8523	-0.0059	-4	44	58	SLADELALVDVLEDK			Carbamidomethyl (C)[6]		Mascot
2312,1414	2312,1531	0.0117	5	280	299	GMYGIENEVFLSLPCLN AR			Carbamidomethyl (C)[15], Oxidation (M)[2]		Mascot

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166IG17	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded
[1] T056P10	Instrument Sample Name		Spectra	9

Rank Protein Name Accession No. Protein Score Protein MW Protein PI Pep. Count Protein Total Ion Score Total Ion C. I. %

1	Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3	ALBU_MOUSE	279	70700.5	0	7	100	227	100
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Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
1299,7056	1299,7095	0.0039	3	362	372	HPDYSVSLLLR					Mascot
1439,7853	1439,7849	-0.0004	0	439	452	APQVSTPTLVEAAR	63	100			Mascot
1439,7853	1439,7849	-0.0004	0	439	452	APQVSTPTLVEAAR					Mascot
1479,7954	1479,8013	0.0059	4	422	434	LGEYGFQNALVR	66	100			Mascot
1479,7954	1479,8013	0.0059	4	422	434	LGEYGFQNALVR					Mascot
1609,7897	1609,7941	0.0044	3	348	360	DVFLGTLVEYSR	99	100			Mascot
1609,7897	1609,7941	0.0044	3	348	360	DVFLGTLVEYSR					Mascot
1662,8519	1662,854	0.0021	1	470	483	LPCEVDLSALNR					Mascot
1882,9368	1882,9359	-0.0009	0	509	524	RPCFSALTVDETVPK			Carbamidomethyl (C)[3]		Mascot
1882,9368	1882,9359	-0.0009	0	509	524	RPCFSALTVDETVPK			Carbamidomethyl (C)[3]		Mascot
1895,8844	1895,8917	0.0073	4	528	543	AETFTFHSIDICTLPEK			Carbamidomethyl (C)[11]		Mascot

2 Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1

ACTC_MOUSE	125	42334	0	6	100	73	100
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Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
1130,5476	1130,5511	0.0035	3	199	208	GYSFVTTAER					Mascot
1500,7078	1500,7123	0.0045	3	362	374	QEYDEAGPSIVHR					Mascot
1515,7491	1515,7488	-0.0003	0	87	97	IWHHTFYNELR					Mascot
1790,892	1790,8975	0.0055	3	241	256	SYELPDGQVITIGNER	73	100			Mascot
1790,892	1790,8975	0.0055	3	241	256	SYELPDGQVITIGNER					Mascot
1956,0437	1956,036	-0.0077	-4	98	115	VAPEEHPTLLTEAPLNPK					Mascot
2244,0601	2244,0706	0.0105	5	294	314	DLYANNVLSGGTMYPGI ADR			Oxidation (M)[14]		Mascot

3 Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1

ACTA_MOUSE	114	42380.9	0	5	100	73	100
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Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
1130,5476	1130,5511	0.0035	3	199	208	GYSFVTTAER					Mascot
1500,7078	1500,7123	0.0045	3	362	374	QEYDEAGPSIVHR					Mascot
1515,7491	1515,7488	-0.0003	0	87	97	IWHHTFYNELR					Mascot
1790,892	1790,8975	0.0055	3	241	256	SYELPDGQVITIGNER	73	100			Mascot
1790,892	1790,8975	0.0055	3	241	256	SYELPDGQVITIGNER					Mascot
1956,0437	1956,036	-0.0077	-4	98	115	VAPEEHPTLLTEAPLNPK					Mascot

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4	Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1	ACTS_MOUSE	111	42366	0	5	100	73	100
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Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
1130,5476	1130,5511	0.0035	3	199	208	GYSFVTTAER					Mascot
1500,7078	1500,7123	0.0045	3	362	374	QEYDEAGPSIVHR					Mascot
1515,7491	1515,7488	-0.0003	0	87	97	IWHHTFYNELR					Mascot
1790,892	1790,8975	0.0055	3	241	256	SYELPDGQVITIGNER	73	100			Mascot
1790,892	1790,8975	0.0055	3	241	256	SYELPDGQVITIGNER					Mascot
1956,0437	1956,036	-0.0077	-4	98	115	VAPEEHPTLLTEAPLNPK					Mascot

5 Actin, gamma-enteric smooth muscle OS=Mus musculus GN=Actg2 PE=2 SV=1

ACTH_MOUSE	105	42248.9	0	4	100	73	100
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Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
1130,5476	1130,5511	0.0035	3	198	207	GYSFVTTAER					Mascot
1790,892	1790,8975	0.0055	3	240	255	SYELPDGQVITIGNER	73	100			Mascot
1790,892	1790,8975	0.0055	3	240	255	SYELPDGQVITIGNER					Mascot
1956,0437	1956,036	-0.0077	-4	97	114	VAPEEHPTLLTEAPLNPK					Mascot
2244,0601	2244,0706	0.0105	5	293	313	DLYANNVLSGGTMYPGI ADR			Oxidation (M)[14]		Mascot

6 Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Mus musculus GN=Pdhb PE=1 SV=1

ODPB_MOUSE	102	39254.1	0	6	100	47	99,983
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Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
1331,6624	1331,6691	0.0067	5	259	269	EGIECEVINLR			Carbamidomethyl (C)[5]		Mascot
1549,6798	1549,7015	0.0217	14	37	49	EAINQGMDEELER			Oxidation (M)[7]		Mascot

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1763.8785	1763.8798	0.0013	1	309	324	IMEGPAFNFLDPAVR	37	99,798	Oxidation (M)[2]	Mascot
1763.8785	1763.8798	0.0013	1	309	324	IMEGPAFNFLDPAVR			Oxidation (M)[2]	Mascot
1801.9006	1801.8887	-0.0119	-7	53	68	VFLGEEVAQYDGYK				Mascot
1835.9242	1835.9111	-0.0131	-7	270	285	TIRPMIDIEAIEASVMK			Oxidation (M)[5,15]	Mascot
1857.9568	1857.9564	-0.0004	0	130	145	TYMSAGLQPVIVFR	11	20,586	Oxidation (M)[4]	Mascot
1857.9568	1857.9564	-0.0004	0	130	145	TYMSAGLQPVIVFR			Oxidation (M)[4]	Mascot
7 Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1										
PE=1 SV=1										
Protein Group										
Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1										
ACTB_MOUSE 42051.9 0										
SV=1										
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
1515.7491	1515.7488	-0.0003	0	85	95	IWHHTFYNELR				Mascot
1790.892	1790.8975	0.0055	3	239	254	SYELPDGQVITIGNER	73	100		Mascot
1790.892	1790.8975	0.0055	3	239	254	SYELPDGQVITIGNER				Mascot
1962.8903	1962.9111	0.0208	11	69	84	YPIEHGIVTWDDMEK			Oxidation (M)[14]	Mascot
8 Beta-actin-like protein 2 OS=Mus musculus GN=Actb2										
PE=1 SV=1										
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
1790.892	1790.8975	0.0055	3	240	255	SYELPDGQVITIGNER	73	100		Mascot
1790.892	1790.8975	0.0055	3	240	255	SYELPDGQVITIGNER				Mascot
1922.8834	1922.9186	0.0352	18	2	19	VDELTAIVDNGSGMK			Carbamidomethyl (C)[17]	Mascot

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Gel Idx/Pos	167/G18	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded					
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9					
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %		
1	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Mus musculus GN=Pdhb PE=1 SV=1	ODPB_MOUSE	353	39254.1	0	10	100	239	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
902.5345	902.5157	-0.0188	-21	220	227	DFLPIGK				Mascot
1231.5953	1231.6117	0.0164	13	174	184	VVSPWNSEDAK				Mascot
1264.6241	1264.6144	-0.0101	-4	325	336	VLEGAIVMIFPAK			Oxidation (M)[8]	Mascot
1331.6624	1331.6665	0.0041	3	259	269	EGIECEVINLR	62	100	Carbamidomethyl (C)[5]	Mascot
1331.6624	1331.6665	0.0041	3	259	269	EGIECEVINLR			Carbamidomethyl (C)[5]	Mascot
1549.6798	1549.6825	0.0027	2	37	49	EAINQGMDEELER	24	95,569	Oxidation (M)[7]	Mascot
1549.6798	1549.6825	0.0027	2	37	49	EAINQGMDEELER			Oxidation (M)[7]	Mascot
1747.8835	1747.8915	0.008	5	309	324	IMEGPAFNFLDPAVR				Mascot
1763.8785	1763.8779	-0.0006	0	309	324	IMEGPAFNFLDPAVR	31	99,081	Oxidation (M)[2]	Mascot
1763.8785	1763.8779	-0.0006	0	309	324	IMEGPAFNFLDPAVR			Oxidation (M)[2]	Mascot
1801.9006	1801.8982	-0.0024	-1	53	68	VFLGEEVAQYDGYK	85	100		Mascot
1801.9006	1801.8982	-0.0024	-1	53	68	VFLGEEVAQYDGYK				Mascot
1835.9242	1835.9199	-0.0043	-2	270	285	TIRPMIDIEAIEASVMK	14	60,867	Oxidation (M)[5,15]	Mascot
1835.9242	1835.9199	-0.0043	-2	270	285	TIRPMIDIEAIEASVMK			Oxidation (M)[5,15]	Mascot
1841.9618	1841.9464	-0.0154	-8	130	145	TYMSAGLQPVIVFR				Mascot
1857.9568	1857.9542	-0.0026	-1	130	145	TYMSAGLQPVIVFR	23	94,697	Oxidation (M)[4]	Mascot
1857.9568	1857.9542	-0.0026	-1	130	145	TYMSAGLQPVIVFR			Oxidation (M)[4]	Mascot
2498.2244	2498.2354	0.011	4	286	308	NHLLVTEGGWPFQVGG AEICAR			Carbamidomethyl (C)[21]	Mascot
2 Adapter molecule crk OS=Mus musculus GN=Crk PE=1										
SV=1										
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
827.4886	827.4872	-0.0014	-2	32	38	HGVFLVR				Mascot
941.4264	941.4295	0.0031	3	11	17	SSWYWR				Mascot

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1023.4741	1023.4817	0.0076	7	131	138	QEEAEYVR				Mascot
1097.564	1097.5681	0.0041	4	284	292	GHPFFTVR				Mascot
1212.6696	1212.6722	0.0026	2	21	31	QEAVALQGR				Mascot
1741.9484	1741.9453	-0.0031	-2	106	120	IHLDTTLLEPVAR				Mascot
1899.8567	1899.8948	0.0381	20	39	56	DSSTSPGDVLSVSENS R				Mascot
3074.6169	3074.623	0.0061	2	57	86	VSHYIINSSGPRPPVPPS PAQFPFGVSPFR				Mascot
3 Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3										
ALBU_MOUSE 76 70700.5 0 4 99,961 53 99,995										
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
1439.7853	1439.7448	-0.0405	-28	439	452	APQVSTPTLVEAAR				Mascot
1479.7954	1479.8004	0.005	3	422	434	LGEYGFQNALVR	53	99,995		Mascot
1479.7954	1479.8004	0.005	3	422	434	LGEYGFQNALVR				Mascot
1609.7897	1609.7944	0.0047	3	348	360	DVFLGTFLEYR				Mascot
1681.8431	1681.847	0.0039	2	243	257	LSQTFPNADFAETK				Mascot

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Gel Idx/Pos	168/G19	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded					
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9					
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %		
1	Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1 PE=1 SV=3	MDHC_MOUSE	282	36659.1	0	8	100	201	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
795.4471	795.4427	-0.0044	-6	249	255	AIADHIR				Mascot
1026.4673	1026.473	0.0057	6	150	157	ENFSCLTR	49	99,987	Carbamidomethyl (C)[5]	Mascot
1026.4673	1026.473	0.0057	6	150	157	ENFSCLTR			Carbamidomethyl (C)[5]	Mascot
1178.6165	1178.6205	0.004	3	221	230	GFETTQQOR	55	99,996		Mascot
1178.6165	1178.6205	0.004	3	221	230	GFETTQQOR				Mascot
1387.725	1387.728	0.003	2	80	92	DLDAVVLVGSMPR			Oxidation (M)[11]	Mascot
1393.7111	1393.7172	0.0061	4	299	310	FVEGLPINDFSR	68	100		Mascot
1393.7111	1393.7172	0.0061	4	299	310	FVEGLPINDFSR				Mascot
1757.9214	1757.9149	-0.0065	-4	126	142	VIVGNPANTNCLTASK			Carbamidomethyl (C)[12]	Mascot
2280.1155	2280.1238	0.0083	4	180	199	NVIWGNHSSTQYPDVNH AK	29	98,45		Mascot
2280.1155	2280.1238	0.0083	4	180	199	NVIWGNHSSTQYPDVNH AK				Mascot
2585.3972	2585.3872	-0.01	-4	7	32	VLVTAAGAQIAYSLYSIG NGSVFGK				Mascot

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Gel Idx/Pos	169/G20	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded					
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9					
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %		
1	Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1 PE=1 SV=3	MDHC_MOUSE	554	36659.1	0	10	100	448	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
795.4471	795.4448	-0.0023	-3	249	255	AIADHIR	29	98,363		Mascot
795.4471	795.4448	-0.0023	-3	249	255	AIADHIR				Mascot

Seq.	Seq.	Score			
720,4039	720,3949	-0.009	-12	36	41 AVIFDR
1149,5898	1149,5986	0.0088	8	134	143 FDAGELITQR
1149,5898	1149,5986	0.0088	8	134	143 FDAGELITQR
1185,6586	1185,6493	-0.0093	-8	84	93 DLQNVNITLR
1396,8423	1396,8312	-0.0111	-8	94	105 ILFRPVASQLPR

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Gel Idx/Pos	173/G24	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9

Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion Score	C. I. %	
1	Prohibitin OS=Mus musculus GN=Pfb PE=1 SV=1	PHB_MOUSE	681	29858.9	0	13	100	508	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
720,4039	720,4	-0.0039	-5	36	41 AVIFDR	33	99,185			Mascot
720,4039	720,4	-0.0039	-5	36	41 AVIFDR					Mascot
1058,5226	1058,5243	0.0017	2	187	195 QVAQOEAEER					Mascot
1062,5062	1062,5133	0.0071	7	149	157 QVSDQLTER					Mascot
1149,5898	1149,5925	0.0027	2	134	143 FDAGELITQR	84	100			Mascot
1149,5898	1149,5925	0.0027	2	134	143 FDAGELITQR					Mascot
1185,6586	1185,6614	0.0028	2	84	93 DLQNVNITLR	56	99,996			Mascot
1185,6586	1185,6614	0.0028	2	84	93 DLQNVNITLR					Mascot
1213,7402	1213,7351	-0.0051	-4	118	128 VLPSITTEIK					Mascot
1396,8423	1396,8423	0	0	94	105 ILFRPVASQLPR	0				Mascot
1460,6539	1460,6566	0.0027	2	106	117 IYTSIGEDYDER					Mascot
1478,7485	1478,7506	0.0021	1	241	253 LEAAEDIAYQLSR					Mascot
1998,0865	1998,0844	-0.0021	-1	220	239 AAELIANSLATAGDGLIELR	146	100			Mascot
1998,0865	1998,0844	-0.0021	-1	220	239 AAELIANSLATAGDGLIELR					Mascot
2119,1433	2119,1365	-0.0068	-3	158	177 AATFGLLDDVSLTHTLFGK					Mascot
2371,2517	2371,2483	-0.0034	-1	12	35 FGLALWAGGVNSALYNVDAGHR	189	100			Mascot
2371,2517	2371,2483	-0.0034	-1	12	35 FGLALWAGGVNSALYNVDAGHR					Mascot
3123,6448	3123,6243	-0.0205	-7	44	70 GVQDIVVGEHTFLIPVWQKPIIFDCR			Carbamidomethyl (C)[26]		Mascot

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Gel Idx/Pos	174/H1	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9

No Confirmed Protein Found

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Gel Idx/Pos	175/H2	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9

Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion Score	C. I. %	
1	Myosin light chain 3 OS=Mus musculus GN=My3 PE=1 SV=4	MYL3_MOUSE	578	22521.3	0	10	100	457	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
896,3995	896,4039	0.0044	5	43	50 EAEFDASK					Mascot
995,5632	995,563	-0.0002	0	164	172 HVLATLGER					Mascot
1010,5305	1010,5357	0.0052	5	65	72 EAFLLFDR	62	100			Mascot
1010,5305	1010,5357	0.0052	5	65	72 EAFLLFDR					Mascot
1249,5841	1249,5973	0.0132	11	152	163 EGNQTVMGAELR			Oxidation (M)[7]		Mascot
1281,6256	1281,63	0.0044	3	80	90 IYTGQGDVLR	67	100	Carbamidomethyl (C)[6]		Mascot
1281,6256	1281,63	0.0044	3	80	90 IYTGQGDVLR			Carbamidomethyl (C)[6]		Mascot
1396,7543	1396,759	0.0047	3	91	103 ALGNQPTQAEVLR	81	100			Mascot
1396,7543	1396,759	0.0047	3	91	103 ALGNQPTQAEVLR					Mascot
1501,8805	1501,8865	0.006	4	135	147 DTGTVEDVPEGLR	109	100			Mascot
1501,8805	1501,8865	0.006	4	135	147 DTGTVEDVPEGLR					Mascot
1509,7472	1509,7452	-0.002	-1	53	64 IEFTPEQIEEFK	43	99,934			Mascot
1509,7472	1509,7452	-0.002	-1	53	64 IEFTPEQIEEFK					Mascot
2015,9275	2015,9241	-0.0034	-2	117	132 MDMFETFLPMLQHSIK			Oxidation (M)[1,2,10]		Mascot
2093,1138	2093,1169	0.0031	1	20	42 AAPAPAAAPAAAPAAPEPERPK	96	100			Mascot
2093,1138	2093,1169	0.0031	1	20	42 AAPAPAAAPAAAPAAPEPERPK					Mascot
2	Apopoprotein A-1 OS=Mus musculus GN=Apoa1 PE=1 SV=1	APOA1_MOUSE	83	30568.7	0	6	99,992	34	99,48	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
1040,5847	1040,5848	0.0001	0	228	236 ARPALDRLR					Mascot
1047,547	1047,5499	0.0029	3	154	172 LSPVAEEFR	34	99,48			Mascot
1047,547	1047,5499	0.0029	3	154	172 LSPVAEEFR					Mascot

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1240,6208	1240,6251	0.0043	3	36	46 DFANVYDVAIK					Mascot
1266,6365	1266,6288	-0.0077	-6	120	129 VQPLYDEFOK					Mascot
1331,6339	1331,6409	0.007	5	206	216 SNPTLNEYHTR					Mascot
1340,7168	1340,7117	-0.0051	-4	142	154 VARFLGAEIQESAR					Mascot

Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion Score	C. I. %	
3	Myosin light chain 1/3, skeletal muscle isoform OS=Mus musculus GN=My11 PE=1 SV=2	MYL1_MOUSE	74	20695.4	0	2	99,936	62	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
1010,5305	1010,5357	0.0052	5	51	58 EAFLLFDR	62	100			Mascot
1010,5305	1010,5357	0.0052	5	51	58 EAFLLFDR					Mascot
1249,5841	1249,5973	0.0132	11	136	147 EGNQTVMGAELR			Oxidation (M)[7]		Mascot
4	Myosin light chain 4 OS=Mus musculus GN=My4 PE=2 SV=3	MYL4_MOUSE	73	21259.6	0	1	99,921	67	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
1281,6256	1281,63	0.0044	3	69	79 IYTGQGDVLR	67	100	Carbamidomethyl (C)[6]		Mascot
1281,6256	1281,63	0.0044	3	69	79 IYTGQGDVLR			Carbamidomethyl (C)[6]		Mascot

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Gel Idx/Pos	176/H3	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9

Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion Score	C. I. %	
1	Transferrin OS=Mus musculus GN=Tr PE=1 SV=1	TTHY_MOUSE	183	15880	0	5	100	117	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
869,4515	869,4535	0.002	2	84	90 FVEGVYR	25	97,138			Mascot
869,4515	869,4535	0.002	2	84	90 FVEGVYR					Mascot
1382,6223	1382,6215	-0.0008	-1	56	68 TSEGSWEPPASGK	10	15,342			Mascot
1382,6223	1382,6215	-0.0008	-1	56	68 TSEGSWEPPASGK					Mascot
1587,7496	1587,75	0.0004	0	69	83 TAESGELHGLTDEK					Mascot
2517,2156	2517,2168	0.0012	0	101	123 TLGSPHFEDADVFTAN	82	100			Mascot

2517.2156	2517.2168	0.0012	0	101	123	DSGHR TLGISPFHEFADVFTAN	Mascot
2597.2883	2597.3054	0.0171	7	124	147	DSGHR HYTIAALLSPYSYSTAVV SNPQN	Mascot

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Gel Idx/Pos	177/H4	Instr./Gel Origin	AK139/T056		Process Status	Analysis Succeeded				
Plate [#] Name	[1] T056P10	Instrument Sample Name			Spectra	9				
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion Score	Total Ion C. I. %	
1	Myosin light chain 3 OS=Mus musculus GN=MyI3 PE=1 SV=4	MYL3_MOUSE	224	22521.3	0	4	100	188	100	
Peptide Information										
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence	Ion Score	C. I. %	Modification	Rank Result Type
	1010.5305	1010.5365	0.006	6	65	72 EAFLLFDR	66	100		Mascot
	1010.5305	1010.5365	0.006	6	65	72 EAFLLFDR				Mascot
	1281.6256	1281.6345	0.0089	7	80	90 IYQGQGVDLR			Carbamidomethyl (C)[6]	Mascot
	1509.7472	1509.7472	0	0	53	64 IEFTPEQIEEFK	40	99.92		Mascot
	1509.7472	1509.7472	0	0	53	64 IEFTPEQIEEFK				Mascot
	2093.1138	2093.1147	0.0009	0	20	42 AAPAPAAAPAAAPAAPE PERPK	82	100		Mascot
	2093.1138	2093.1147	0.0009	0	20	42 AAPAPAAAPAAAPAAPE PERPK				Mascot
2	Fatty acid-binding protein, heart OS=Mus musculus GN=Fabp3 PE=1 SV=5	FABPH_MOUSE	96	14809.7	0	3	100	63	100	
Peptide Information										
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence	Ion Score	C. I. %	Modification	Rank Result Type
	907.4995	907.5024	0.0029	3	23	31 SLGVGFATR				Mascot
	1496.8795	1496.8872	0.0077	5	114	127 LLTLTHGSVSTR				Mascot
	2326.0833	2326.0938	0.0105	5	60	79 NTEINFQLGIEFDEVTTADD R	63	100		Mascot
	2326.0833	2326.0938	0.0105	5	60	79 NTEINFQLGIEFDEVTTADD R				Mascot
3	Myosin light chain 1/3, skeletal muscle isoform OS=Mus musculus GN=MyI1 PE=1 SV=2	MYL1_MOUSE	71	20695.4	0	1	99.872	66	100	
Peptide Information										
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence	Ion Score	C. I. %	Modification	Rank Result Type
	1010.5305	1010.5365	0.006	6	51	58 EAFLLFDR	66	100		Mascot
	1010.5305	1010.5365	0.006	6	51	58 EAFLLFDR				Mascot

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Gel Idx/Pos	178/H5	Instr./Gel Origin	AK139/T056		Process Status	Analysis Succeeded			
Plate [#] Name	[1] T056P10	Instrument Sample Name			Spectra	9			
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion Score	Total Ion C. I. %
No Confirmed Protein Found									

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Gel Idx/Pos	179/H6	Instr./Gel Origin	AK139/T056		Process Status	Analysis Succeeded			
Plate [#] Name	[1] T056P10	Instrument Sample Name			Spectra	9			
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion Score	Total Ion C. I. %
No Confirmed Protein Found									

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Gel Idx/Pos	180/H7	Instr./Gel Origin	AK139/T056		Process Status	Analysis Succeeded				
Plate [#] Name	[1] T056P10	Instrument Sample Name			Spectra	9				
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion Score	Total Ion C. I. %	
1	Apolipoprotein C-III OS=Mus musculus GN=Apoc3 PE=2 SV=2	APOC3_MOUSE	86	10975.5	0	2	99.995	64	100	
Peptide Information										
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence	Ion Score	C. I. %	Modification	Rank Result Type
	1078.4524	1078.4559	0.0035	3	61	68 GWMDNHR			Oxidation (M)[3]	Mascot
	1078.4524	1078.4559	0.0035	3	61	68 GWMDNHR			Oxidation (M)[3]	Mascot
	1988.0294	1988.0402	0.0108	5	42	60 TVQDALSSVQESDIAVA R	64	100		Mascot
	1988.0294	1988.0402	0.0108	5	42	60 TVQDALSSVQESDIAVA R				Mascot

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Gel Idx/Pos	181/H8	Instr./Gel Origin	AK139/T056		Process Status	Analysis Succeeded				
Plate [#] Name	[1] T056P10	Instrument Sample Name			Spectra	9				
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion Score	Total Ion C. I. %	
1	ATP synthase-coupling factor 6, mitochondrial OS=Mus musculus GN=Atp5j PE=1 SV=1	ATP5J_MOUSE	148	12488.6	0	4	100	105	100	
Peptide Information										
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence	Ion Score	C. I. %	Modification	Rank Result Type
	828.4461	828.445	-0.0011	-1	35	41 ELDPVQK				Mascot
	1062.5466	1062.5465	-0.0001	0	100	108 FEVDKPKQS				Mascot
	1188.5242	1188.5295	0.0053	4	85	94 GEMDTFPTFK	29	98.784	Oxidation (M)[3]	Mascot
	1188.5242	1188.5295	0.0053	4	85	94 GEMDTFPTFK			Oxidation (M)[3]	Mascot
	2044.957	2044.9628	0.0058	3	55	73 QASGGPVDIGPEYQQDL DR	76	100		Mascot
	2044.957	2044.9628	0.0058	3	55	73 QASGGPVDIGPEYQQDL DR				Mascot

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Gel Idx/Pos	182/H9	Instr./Gel Origin	AK139/T056		Process Status	Analysis Succeeded				
Plate [#] Name	[1] T056P10	Instrument Sample Name			Spectra	9				
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion Score	Total Ion C. I. %	
1	Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1 PE=1 SV=3	MDHC_MOUSE	179	36859.1	0	6	100	133	100	
Peptide Information										
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence	Ion Score	C. I. %	Modification	Rank Result Type
	795.4471	795.4277	-0.0194	-24	249	255 AIADHIR				Mascot
	1026.4673	1026.4735	0.0062	6	150	157 ENFSCLR			Carbamidomethyl (C)[5]	Mascot
	1178.6165	1178.6191	0.0026	2	221	230 GEFITTVQQR	62	100		Mascot
	1178.6165	1178.6191	0.0026	2	221	230 GEFITTVQQR				Mascot
	1387.725	1387.7247	-0.0003	0	80	92 DLDVAVLGSMPR			Oxidation (M)[11]	Mascot
	1393.7111	1393.7161	0.005	4	299	310 FVEGLPINDFSR	70	100		Mascot
	1393.7111	1393.7161	0.005	4	299	310 FVEGLPINDFSR				Mascot
	2280.1155	2280.1179	0.0024	1	180	199 NVIWMGNHSSTQYPDVNH AK				Mascot
2	Serum albumin OS=Mus musculus GN=Ab PE=1 SV=3	ALBU_MOUSE	90	70700.5	0	7	99.998	42	99.924	

Peptide Information										Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %				
956.5345	956.528	-0.0065	-7	98	105	LCAIPNLR				Carbamidomethyl (C)[2]		Mascot
1149.6115	1149.6062	-0.0088	-8	66	75	LVQEVYDFAK						Mascot
1250.5801	1250.5895	0.0094	8	35	44	YNLDGEGDFK						Mascot
1439.7853	1439.7655	-0.0198	-14	439	452	APQVSTPTLVEAR						Mascot
1479.8569	1479.8304	-0.0265	-18	45	57	GLVLIAFSQYLQK	13	44.035				Mascot
1479.8569	1479.8304	-0.0265	-18	45	57	GLVLIAFSQYLQK						Mascot
1681.8431	1681.8412	-0.0019	-1	243	257	LSQTFPNADFAETK	31	98.931				Mascot
1681.8431	1681.8412	-0.0019	-1	243	257	LSQTFPNADFAETK						Mascot
1917.8912	1917.8931	0.0019	1	153	168	ENPTTFMGHYLHEVAR				Oxidation (M)[7]		Mascot

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Gel Idx/Pos	183/H10	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded				
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9				
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %	Total Ion C. I. %

1	L-lactate dehydrogenase B chain OS=Mus musculus GN=Ldhb PE=1 SV=2	LDHB_MOUSE	413	36834.1	0	16	100	208	100
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Peptide Information										Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %				
720.4039	720.3925	-0.0114	-16	114	119	IVNVFK						Mascot
742.457	742.4539	-0.0031	-4	108	113	LNLVQR	36	99.777				Mascot
742.457	742.4539	-0.0031	-4	108	113	LNLVQR						Mascot
833.3748	833.373	-0.0018	-2	101	107	QQEGESR						Mascot
913.5828	913.5836	0.0008	1	92	100	IVVITAGVR						Mascot
957.6131	957.6152	0.0021	2	120	127	FIFQIVK	30	99.003				Mascot
957.6131	957.6152	0.0021	2	120	127	FIFQIVK						Mascot
1027.5605	1027.5571	-0.0034	-3	271	279	IHPVSTMVK				Oxidation (M)[7]		Mascot
1176.5896	1176.5895	-0.0001	0	320	329	SADTLWDIQK						Mascot
1248.6001	1248.6041	0.004	3	159	170	VIGSGCNLDSAR				Carbamidomethyl (C)[6]		Mascot
1269.6395	1269.6377	-0.0018	-1	234	244	MVVD SAYEVK				Oxidation (M)[1]		Mascot
1626.8334	1626.8412	0.0078	5	8	23	LASVADGEAVPNNK						Mascot
1629.8592	1629.8566	-0.0016	-1	44	58	SLADELALVDVLEDK	50	99.99				Mascot
1629.8592	1629.8566	-0.0016	-1	44	58	SLADELALVDVLEDK						Mascot
1963.9252	1963.9246	-0.0006	0	61	77	GEMMDLQHGSLFLQTPK	31	99.182		Oxidation (M)[3,4]		Mascot
1963.9252	1963.9246	-0.0006	0	61	77	GEMMDLQHGSLFLQTPK				Oxidation (M)[3,4]		Mascot
1989.087	1989.0872	0.0002	0	24	43	ITVVGVGQVGMACASIL				Carbamidomethyl (C)[13], Oxidation (M)[11]		Mascot
2197.1208	2197.1277	0.0069	3	247	266	GVTNWAIGLSVADLIESM				Oxidation (M)[18]		Mascot
2296.1465	2296.1528	0.0063	3	280	299	GMYGIEVEVFLSLPCILN				Carbamidomethyl (C)[15]		Mascot
2312.1414	2312.1445	0.0031	1	280	299	GMYGIEVEVFLSLPCILN	62	100		Carbamidomethyl (C)[15], Oxidation (M)[2]		Mascot
2312.1414	2312.1445	0.0031	1	280	299	GMYGIEVEVFLSLPCILN				Carbamidomethyl (C)[15], Oxidation (M)[2]		Mascot
2683.3687	2683.3682	-0.0005	0	128	150	YSPDCTIIVSNPVDILTY				Carbamidomethyl (C)[5]		Mascot

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Peptide Information										Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %				
742.457	742.4539	-0.0031	-4	107	112	LNLVQR	36	99.809				Mascot
742.457	742.4539	-0.0031	-4	107	112	LNLVQR						Mascot
833.3748	833.373	-0.0018	-2	100	106	QQEGESR						Mascot
913.5829	913.5836	0.0007	1	91	99	LVITAGAR						Mascot
1248.6001	1248.6041	0.004	3	158	169	VIGSGCNLDSAR				Carbamidomethyl (C)[6]		Mascot
1691.8044	1691.8	-0.0044	-3	43	57	DLADELALVDVMEK				Oxidation (M)[12]		Mascot

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Gel Idx/Pos	184/H11	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded				
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9				
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %	Total Ion C. I. %

1	Troponin T, cardiac muscle OS=Mus musculus GN=Tnni2 PE=1 SV=2	TNNT2_MOUSE	158	35804	0	6	100	106	100
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Peptide Information										Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %				
906.5043	906.5074	0.0031	3	272	278	YEINLVR	30	99.23				Mascot
906.5043	906.5074	0.0031	3	272	278	YEINLVR						Mascot
1016.4796	1016.4846	0.005	5	96	105	VDFDIIHR						Mascot
1171.6544	1171.6541	-0.0003	0	82	91	LFMPNLVPPK				Oxidation (M)[3]		Mascot
1507.7864	1507.7855	-0.0009	-1	231	243	ALAIHLNEDQLR	42	99.945				Mascot
1507.7864	1507.7855	-0.0009	-1	231	243	ALAIHLNEDQLR						Mascot
1628.7756	1628.7703	0.0143	9	190	203	ALSNMMHFGGYIQK				Oxidation (M)[5,6]		Mascot
1941.9664	1941.9623	-0.0041	-2	111	126	DLNELQTLIAHFENR	34	99.668				Mascot
1941.9664	1941.9623	-0.0041	-2	111	126	DLNELQTLIAHFENR						Mascot

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Gel Idx/Pos	185/H12	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded				
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9				
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %	Total Ion C. I. %

1	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1	ACTC_MOUSE	382	42334	0	8	100	306	100
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Peptide Information										Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %				
795.4723	795.4704	-0.0019	-2	331	337	IAPPER						Mascot
976.4482	976.4539	0.0057	6	21	30	AGFAGDDAPR						Mascot
1130.5476	1130.5507	0.0031	3	199	208	GYSFVTTAER	50	99.989				Mascot
1130.5476	1130.5507	0.0031	3	199	208	GYSFVTTAER						Mascot
1500.7078	1500.7106	0.0028	2	362	374	QEYDEAGPSIVHR	92	100				Mascot
1500.7078	1500.7106	0.0028	2	362	374	QEYDEAGPSIVHR						Mascot
1515.7491	1515.7515	0.0024	2	87	97	IWHHTFYNELR	56	99.997				Mascot
1515.7491	1515.7515	0.0024	2	87	97	IWHHTFYNELR						Mascot
1790.892	1790.8972	0.0052	3	241	256	SYELPDGQVITIGNER	75	100				Mascot
1790.892	1790.8972	0.0052	3	241	256	SYELPDGQVITIGNER						Mascot
1956.0437	1956.0487	0.005	3	98	115	VAPEEHTLLTEAPLNPK	34	99.516				Mascot
1956.0437	1956.0487	0.005	3	98	115	VAPEEHTLLTEAPLNPK						Mascot
2244.0601	2244.0703	0.0102	5	294	314	DLYANNVLSGGTMYPGI				Oxidation (M)[14]		Mascot
2244.0601	2244.0703	0.0102	5	294	314	DLYANNVLSGGTMYPGI				Oxidation (M)[14]		Mascot

2	Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1	ACTS_MOUSE	365	42366	0	7	100	306	100
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Peptide Information										Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %				
795.4723	795.4704	-0.0019	-2	331	337	IAPPER						Mascot
976.4482	976.4539	0.0057	6	21	30	AGFAGDDAPR						Mascot
1130.5476	1130.5507	0.0031	3	199	208	GYSFVTTAER	50	99.989				Mascot
1130.5476	1130.5507	0.0031	3	199	208	GYSFVTTAER						Mascot
1500.7078	1500.7106	0.0028	2	362	374	QEYDEAGPSIVHR	92	100				Mascot

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852.5665	852.5646	-0.0019	-2	327	334	GLVVPVIR	37	99,858		Mascot
852.5665	852.5646	-0.0019	-2	327	334	GLVVPVIR				Mascot
903.4781	903.479	0.0009	1	347	354	TIMLEGEK				Mascot
1189.6576	1189.6614	0.0038	3	135	145	VEGGTFLFTR	43	99,957		Mascot
1189.6576	1189.6614	0.0038	3	135	145	VEGGTFLFTR				Mascot
1419.7478	1419.7491	0.0013	1	314	326	DYIDISVAVATPR	79	100		Mascot
1419.7478	1419.7491	0.0013	1	314	326	DYIDISVAVATPR				Mascot
1470.653	1470.6584	0.0054	4	335	346	NVETMNVADIER	32	99,522	Oxidation (M)[5]	Mascot
1470.653	1470.6584	0.0054	4	335	346	NVETMNVADIER			Oxidation (M)[5]	Mascot
2011.9728	2011.9675	-0.0053	-3	411	426	VEVRPMYVALTYDHR			Oxidation (M)[6,7]	Mascot
2187.1292	2187.123	-0.0062	-3	288	308	ASAFALQEQPVVNAVDD ATK				Mascot
2248.1091	2248.1128	0.0037	2	69	89	NDVITVOTPAFAESVTEG DVR				Mascot

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Gel Idx/Pos	188/H15	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded					
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9					
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %		

No Confirmed Protein Found

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Gel Idx/Pos	189/H16	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded					
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9					
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %		

1	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=Idh3a PE=1 SV=1	IDH3A_MOUSE	224	40069.2	0	8	100	148	100	
Peptide Information										
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
	1028.516	1028.5197	0.0037	4	59	66 APIQWEER	38	99,829		Mascot
	1028.516	1028.5197	0.0037	4	59	66 APIQWEER				Mascot
	1216.5997	1216.6052	0.0055	5	179	188 IAFAFAFYAR	62	100		Mascot
	1216.5997	1216.6052	0.0055	5	179	188 IAFAFAFYAR				Mascot
	1316.5247	1316.5352	0.0105	8	351	360 CSQFTEEDR			Carbamidomethyl (C)[1,9]	Mascot
	1391.7529	1391.7548	0.0019	1	135	146 TPYTDVNVITIR	39	99,869		Mascot
	1391.7529	1391.7548	0.0019	1	135	146 TPYTDVNVITIR				Mascot
	1606.8734	1606.8732	-0.0002	0	101	115 TPIAAGHPSMNLRL	8	0	Oxidation (M)[10]	Mascot
	1606.8734	1606.8732	-0.0002	0	101	115 TPIAAGHPSMNLRL			Oxidation (M)[10]	Mascot
	1894.9435	1894.9403	-0.0032	-2	300	316 DMANPTALLLSAVMMLR			Oxidation (M)[2,14,15]	Mascot
	1894.9435	1894.9403	-0.0032	-2	300	316 DMANPTALLLSAVMMLR			Oxidation (M)[2,14,15]	Mascot
	2132.0481	2132.0557	0.0076	4	117	134 TFDLVANRVCPSIEGYK			Carbamidomethyl (C)[11]	Mascot
	2502.2358	2502.2422	0.0064	3	147	169 ENTEGEYSIEHVIDGV VQSIK				Mascot

2	Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1 PE=1 SV=3	MDHC_MOUSE	87	36659.1	0	4	99,997	56	99,997	
Peptide Information										
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
	1178.6165	1178.6221	0.0056	5	221	230 GEFITTVQOR	56	99,997		Mascot
	1178.6165	1178.6221	0.0056	5	221	230 GEFITTVQOR				Mascot
	1387.725	1387.7246	-0.0004	0	80	92 DLDAVLVGSMPFR			Oxidation (M)[11]	Mascot
	1393.7111	1393.7351	0.024	17	299	310 FVGLPINDFSR				Mascot
	2280.1155	2280.1345	0.019	8	180	199 NVIIQNGHSSTQYDPVNH AK				Mascot

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Gel Idx/Pos	190/H17	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded					
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9					
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %		

1	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Mus musculus GN=Nduf2 PE=1 SV=2	NDUV2_MOUSE	320	27610	0	10	100	199	100	
Peptide Information										
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
	750.462	750.46	-0.002	-3	212	218 VPKGPPR				Mascot
	902.473	902.4749	0.0019	2	239	248 GPGFGVQAGL				Mascot
	1216.6307	1216.6331	0.0024	2	199	208 DIEIIDLK				Mascot
	1254.6875	1254.692	0.0045	4	100	110 VAELVQVPPMR	17	75,974	Oxidation (M)[10]	Mascot
	1254.6875	1254.692	0.0045	4	100	110 VAELVQVPPMR			Oxidation (M)[10]	Mascot
	1276.6379	1276.6499	0.012	9	143	153 DSQLELEDR				Mascot
	1374.6835	1374.6683	-0.0152	-11	88	99 QNGWLPISAMNK			Oxidation (M)[10]	Mascot
	1656.7727	1656.7993	0.0266	16	111	123 VVEVATFYTMYNR				Mascot
	1672.7676	1672.7736	0.006	4	111	123 VVEVATFYTMYNR	29	98,495	Oxidation (M)[10]	Mascot
	1672.7676	1672.7736	0.006	4	111	123 VVEVATFYTMYNR			Oxidation (M)[10]	Mascot
	1795.8289	1795.8367	0.0078	4	129	142 YHIQVCTTIPCMLR				Mascot
	2162.1353	2162.1428	0.0075	3	68	87 NYPEGHQAALVPLVLDL AQR	122	100	Carbamidomethyl (C)[6,11], Oxidation (M)[12]	Mascot
	2162.1353	2162.1428	0.0075	3	68	87 NYPEGHQAALVPLVLDL AQR				Mascot
	2240.9619	2240.9692	0.0073	3	42	60 DTPENPDTFPDFTPENY K	32	99,334		Mascot
	2240.9619	2240.9692	0.0073	3	42	60 DTPENPDTFPDFTPENY K				Mascot

2	Myosin light chain 3 OS=Mus musculus GN=Myl3 PE=1 SV=4	MYL3_MOUSE	179	22521.3	0	7	100	106	100	
Peptide Information										
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
	995.5632	995.5593	-0.0039	-4	164	172 HVLATLGER				Mascot
	1010.5305	1010.5344	0.0039	4	65	72 EAFLLDR				Mascot
	1281.6256	1281.647	0.0214	17	80	90 ITYGCGDVLRR			Carbamidomethyl (C)[6]	Mascot

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3	Apolipoprotein A-I OS=Mus musculus GN=Apoa1 PE=1 SV=1	APOA1_MOUSE	173	30568.7	0	7	100	112	100	
Peptide Information										
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank Result Type
	1040.5847	1040.5887	0.004	4	228	236 ARPALDLR				Mascot
	1047.547	1047.5508	0.0038	4	164	172 LSPVAEEFR	39	99,849		Mascot
	1047.547	1047.5508	0.0038	4	164	172 LSPVAEEFR				Mascot
	1240.6208	1240.6346	0.0138	11	36	46 DFANVYDVAVK				Mascot
	1266.6365	1266.642	0.0055	4	120	129 VQPYLDEFQK				Mascot
	1313.6267	1313.6494	0.0227	17	184	194 TQLAPHSEQMR			Oxidation (M)[10]	Mascot
	1331.6339	1331.6471	0.0132	10	206	216 SNPTLNEHFSR				Mascot
	1340.7168	1340.7244	0.0076	6	142	154 VAPLGAELQESAR	73	100		Mascot
	1340.7168	1340.7244	0.0076	6	142	154 VAPLGAELQESAR				Mascot

ProteomicTO5611-72_MLV_differential spots mouse 122 of 136

Gel Idx/Pos	191/H18	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded
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Plate #	Name	[1] T056P10	Instrument	Sample Name					Spectra	9
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %		

1	Myosin light chain 3 OS=Mus musculus GN=MyI3 PE=1 SV=4	MYL3_MOUSE	327	22521.3	0	8	100	237	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
995,5632	995,5671	0.0039	4	164	172	HVLATLGER				Mascot
1010,5305	1010,5414	0.0109	11	65	72	EAFLLFDR	59	99,998		Mascot
1261,6256	1261,6335	0.0079	6	80	90	ITYGGQGVLR			Carbamidomethyl (C)[6]	Mascot
1396,7543	1396,7611	0.0068	5	91	103	ALGONPTQAEVLR	57	99,997		Mascot
1396,7543	1396,7611	0.0068	5	91	103	ALGONPTQAEVLR				Mascot
1501,6805	1501,6888	0.0083	6	135	147	DTGTIEDFVEGLR	120	100		Mascot
1501,6805	1501,6888	0.0083	6	135	147	DTGTIEDFVEGLR				Mascot
1509,7472	1509,7551	0.0079	5	53	64	IEFTPEQIEEFK				Mascot
2015,9275	2015,9331	0.0056	3	117	132	MMDFETFLPMLQHSK			Oxidation (M)[1,2,10]	Mascot
2053,1138	2093,1133	-0.0005	0	20	42	AAAPAAPAAPAAAPAE PERPK				Mascot

2	Apolipoprotein A-I OS=Mus musculus GN=Apoa1 PE=1 SV=1	APOA1_MOUSE	320	30568.7	0	11	100	214	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
703,3733	703,38	0.0067	10	195	200	ESLAQR				Mascot
805,3839	805,3915	0.0076	9	101	106	ETDWR				Mascot
843,4683	843,4793	0.011	13	157	163	LOELQGR				Mascot
923,4468	923,4545	0.0077	8	133	139	EDVELYR				Mascot
1040,5947	1040,5939	0.0092	9	228	236	ARPALEDLR				Mascot
1047,547	1047,5579	0.0109	10	164	172	LSPVAEEFR	52	99,99		Mascot
1047,547	1047,5579	0.0109	10	164	172	LSPVAEEFR				Mascot
1240,6208	1240,6287	0.0079	6	36	46	DFANVYDAVK				Mascot
1266,6365	1266,6444	0.0079	6	120	129	VQPYLDFEFOK	45	99,955		Mascot

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1266,6365	1266,6444	0.0079	6	120	129	VQPYLDFEFOK			Oxidation (M)[10]	Mascot		
1313,6267	1313,6323	0.0056	4	184	194	TQLAPHSQEMR				Mascot		
1331,6339	1331,6437	0.0098	7	206	216	SNPTLNEYHTR	41	99,894		Mascot		
1331,6339	1331,6437	0.0098	7	206	216	SNPTLNEYHTR				Mascot		
1340,7168	1340,7251	0.0083	6	142	154	VAPLGAELQESAR	78	100		Mascot		
1340,7168	1340,7251	0.0083	6	142	154	VAPLGAELQESAR				Mascot		

3	Myosin light chain 1/3, skeletal muscle isoform OS=Mus musculus GN=MyI1 PE=1 SV=2	MYL1_MOUSE	72	20695.4	0	2	99,891	59	99,998	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
1010,5305	1010,5414	0.0109	11	51	58	EAFLLFDR	59	99,998		Mascot
1010,5305	1010,5414	0.0109	11	51	58	EAFLLFDR				Mascot
1402,6631	1402,6432	-0.0199	-14	88	100	VLGNPSNEEMNAK				Mascot

Proteomic T05611-72_MLV_differential spots mouse										124	of	136
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Gel Idx/Pos	192/H19	Instrument	Sample Name					Process Status	Analysis Succeeded	
Plate #	Name	[1] T056P10	Instrument	Sample Name					Spectra	9

Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %	
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1	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Mus musculus GN=Sucl2 PE=1 SV=2	SUCB1_MOUSE	543	50424.3	0	16	100	362	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
771,4471	771,4438	-0.0033	-4	99	106	AGVLAGGR				Mascot
810,4355	810,4354	-0.0001	0	109	116	GTFTSGLK				Mascot
887,5196	887,5197	0.0001	0	418	426	ALIADSLK				Mascot
910,5396	910,5394	-0.0002	0	243	249	LYNLFK				Mascot
1019,5407	1019,5432	0.0025	2	121	129	IVFSPEEAK				Mascot
1110,6198	1112,6241	0.0043	4	206	215	EPNDVEGDK				Mascot
1186,5487	1186,558	0.0093	8	275	284	IFDINSAYR	82	100		Mascot
1186,5487	1186,558	0.0093	8	275	284	IFDINSAYR				Mascot
1290,6293	1290,6384	0.0091	7	151	160	ICNQVLCER	63	100	Carbamidomethyl (C)[2,8]	Mascot
1290,6293	1290,6384	0.0091	7	151	160	ICNQVLCER			Carbamidomethyl (C)[2,8]	Mascot
1322,6085	1322,624	0.0155	12	166	175	EYFAITMER				Mascot
1338,6035	1338,6106	0.0071	5	166	175	EYFAITMER	13	53,009	Oxidation (M)[8]	Mascot
1338,6035	1338,6106	0.0071	5	166	175	EYFAITMER			Oxidation (M)[8]	Mascot
1419,7334	1419,7385	0.0051	4	384	396	CDVIAQGVMAVK			Carbamidomethyl (C)[1], Oxidation (M)[10]	Mascot
1530,8824	1530,8866	0.0042	3	370	383	VQAILNIFGGIMR				Mascot
1546,8773	1546,8837	0.0064	4	370	383	VQAILNIFGGIMR	66	100	Oxidation (M)[13]	Mascot
1680,75	1680,7595	0.0095	6	288	300	IFDLGWSGEDER				Mascot
1855,8564	1855,8511	-0.0053	-3	226	242	MGFSPNIVDSAAENMIK				Mascot
2045,8678	2045,8707	0.0029	1	250	267	VDATMVEINFMVSDG K			Oxidation (M)[5,11]	Mascot
2614,3259	2614,3235	-0.0024	-1	337	362	LHGGTPANFLDVGSGAT VQQVTEAFK	138	100		Mascot
2614,3259	2614,3235	-0.0024	-1	337	362	LHGGTPANFLDVGSGAT VQQVTEAFK				Mascot
3009,5527	3009,5398	-0.0129	-4	176	205	SFQGPVLIGSAQGGVNI DVAENPEAIVK				Mascot

Proteomic T05611-72_MLV_differential spots mouse										125	of	136
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GN=Actc1 PE=1 SV=1										
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
795,4723	795,4675	-0.0048	-6	331	337	IIAPPER				Mascot
976,4482	976,4502	0.002	2	21	30	AGFAGDDAPR				Mascot
1130,5476	1130,5538	0.0062	5	199	208	GYSFVITTAER				Mascot
1198,7054	1198,7017	-0.0037	-3	31	41	AVFPSVGRPR				Mascot
1500,7078	1500,7209	0.0131	9	362	374	QEYDEAGPSIVHR				Mascot
1515,7491	1515,7561	0.007	5	87	97	IWHHTFYNELR				Mascot
1790,892	1790,9025	0.0105	6	241	256	SYELPDGQVITIGNER	93	100		Mascot
1790,892	1790,9025	0.0105	6	241	256	SYELPDGQVITIGNER				Mascot
1956,0437	1956,0397	-0.004	-2	98	115	VAPEEHPHTLLEAPLNPK				Mascot
2244,0601	2244,0598	-0.0003	0	294	314	DLYANNVLSGGTTMYPGI ADR			Oxidation (M)[14]	Mascot

3	Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1	ACTA_MOUSE	166	42380.9	0	8	100	93	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
795,4723	795,4675	-0.0048	-6	331	337	IIAPPER				Mascot
976,4482	976,4502	0.002	2	21	30	AGFAGDDAPR				Mascot
1130,5476	1130,5538	0.0062	5	199	208	GYSFVITTAER				Mascot
1198,7054	1198,7017	-0.0037	-3	31	41	AVFPSVGRPR				Mascot
1500,7078	1500,7209	0.0131	9	362	374	QEYDEAGPSIVHR				Mascot
1790,892	1790,9025	0.0105	6	241	256	SYELPDGQVITIGNER	93	100		Mascot
1790,892	1790,9025	0.0105	6	241	256	SYELPDGQVITIGNER				Mascot
1956,0437	1956,0397	-0.004	-2	98	115	VAPEEHPHTLLEAPLNPK				Mascot
2244,0601	2244,0598	-0.0003	0	294	314	DLYANNVLSGGTTMYPGI ADR			Oxidation (M)[14]	Mascot

4	Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1	ACTS_MOUSE	162	42366	0	8	100	93	100
Peptide Information									

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type	
795.4723	795.4675	-0.0048	-6	331	337 IAAPPER					Mascot	
ProteomicTO5611-72_MLV_d											
795.4723	795.4675	-0.0048	-6	330	336 IAAPPER					Mascot	
976.4482	976.4502	0.002	2	21	30 AGFAGDDAPR					Mascot	
1130.5476	1130.5538	0.0062	5	199	208 GYSFVTTAER					Mascot	
1198.7054	1198.7017	-0.0037	-3	31	41 AVFPSVGRPR					Mascot	
1500.7078	1500.7209	0.0131	9	362	374 QEYDEAGPSIVHR					Mascot	
1515.7491	1515.7561	0.007	5	87	97 IWHHTFYNELR					Mascot	
1790.892	1790.9025	0.0105	6	241	256 SYELPDGQVITIGNER	93	100			Mascot	
1790.892	1790.9025	0.0105	6	241	256 SYELPDGQVITIGNER					Mascot	
1956.0437	1956.0397	-0.004	-2	98	115 VAPEEHPDLLTEAPLNPK					Mascot	
5	Actin, gamma-enteric smooth muscle OS=Mus musculus GN=Actg2 PE=2 SV=1			ACTH_MOUSE	154	42248.9	0	7	100	93	100
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type	
795.4723	795.4675	-0.0048	-6	330	336 IAAPPER					Mascot	
976.4482	976.4502	0.002	2	20	29 AGFAGDDAPR					Mascot	
1130.5476	1130.5538	0.0062	5	198	207 GYSFVTTAER					Mascot	
1198.7054	1198.7017	-0.0037	-3	30	40 AVFPSVGRPR					Mascot	
1790.892	1790.9025	0.0105	6	240	255 SYELPDGQVITIGNER	93	100			Mascot	
1790.892	1790.9025	0.0105	6	240	255 SYELPDGQVITIGNER					Mascot	
1956.0437	1956.0397	-0.004	-2	97	114 VAPEEHPDLLTEAPLNPK					Mascot	
2244.0601	2244.0598	-0.0003	0	293	313 DLYANNVLSGGTMYPGIADR			Oxidation (M)[14]		Mascot	
6	Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1			ACTG_MOUSE	138	42107.9	0	6	100	93	100
Protein Group											
Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1											
ACTB_MOUSE 42051.9 0											
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type	
795.4723	795.4675	-0.0048	-6	329	335 IAAPPER					Mascot	
976.4482	976.4502	0.002	2	19	28 AGFAGDDAPR					Mascot	
1198.7054	1198.7017	-0.0037	-3	29	39 AVFPSVGRPR					Mascot	
1515.7491	1515.7561	0.007	5	85	95 IWHHTFYNELR					Mascot	
1516.7026	1516.7474	0.0448	30	360	372 QEYDEAGPSIVHR					Mascot	
1790.892	1790.9025	0.0105	6	239	254 SYELPDGQVITIGNER	93	100			Mascot	
ProteomicTO5611-72_MLV_d											
1790.892	1790.9025	0.0105	6	239	254 SYELPDGQVITIGNER					Mascot	
7	Beta-actin-like protein 2 OS=Mus musculus GN=Actb2 PE=1 SV=1			ACTBL_MOUSE	111	42319.1	0	3	100	93	100
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type	
795.4723	795.4675	-0.0048	-6	330	336 IAAPPER					Mascot	
1510.7285	1510.7064	-0.0221	-15	361	373 QEYDEAGPSIVHR					Mascot	
1790.892	1790.9025	0.0105	6	240	255 SYELPDGQVITIGNER	93	100			Mascot	
1790.892	1790.9025	0.0105	6	240	255 SYELPDGQVITIGNER					Mascot	
ProteomicTO5611-72_MLV_differential spots mouse											
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Col Idx/Pos	193/H20	Instr/Gel Origin	AK139/T056	Process Status	Analysis Succeeded					
Plate [#] Name	[1] T056P10	Instrument Sample Name		Spectra	9					
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %	Total Ion C. I. %	
1	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1	ACTC_MOUSE	528	42334	0	11	100	404	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
795.4723	795.4706	-0.0017	-2	331	337 IAAPPER					Mascot
976.4482	976.4556	0.0074	8	21	30 AGFAGDDAPR					Mascot
1130.5476	1130.5541	0.0065	6	199	208 GYSFVTTAER	63	100			Mascot
1130.5476	1130.5541	0.0065	6	199	208 GYSFVTTAER					Mascot
1198.7054	1198.7111	0.0057	5	31	41 AVFPSVGRPR	40	99.883			Mascot
1198.7054	1198.7111	0.0057	5	31	41 AVFPSVGRPR					Mascot
1500.7078	1500.7164	0.0086	6	362	374 QEYDEAGPSIVHR	93	100			Mascot
1500.7078	1500.7164	0.0086	6	362	374 QEYDEAGPSIVHR					Mascot
1515.7491	1515.7567	0.0076	5	87	97 IWHHTFYNELR					Mascot
1790.892	1790.901	0.009	5	241	256 SYELPDGQVITIGNER	104	100			Mascot
1790.892	1790.901	0.009	5	241	256 SYELPDGQVITIGNER					Mascot
1956.0437	1956.0449	0.0012	1	98	115 VAPEEHPDLLTEAPLNPK	91	100			Mascot
1956.0437	1956.0449	0.0012	1	98	115 VAPEEHPDLLTEAPLNPK					Mascot
2244.0601	2244.0659	0.0058	3	294	314 DLYANNVLSGGTMYPGIADR	13	47.325	Oxidation (M)[14]		Mascot
2244.0601	2244.0659	0.0058	3	294	314 DLYANNVLSGGTMYPGIADR			Oxidation (M)[14]		Mascot
2552.1531	2552.1448	-0.0083	-3	218	240 LCYVALDFENEMATAASSSLEK			Carbamidomethyl (C)[2], Oxidation (M)[12]		Mascot
3212.6045	3212.5989	-0.0056	-2	150	179 TTGIVLDSGDGVTHNVPI YEGYALPHAIMR			Oxidation (M)[29]		Mascot
2	Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1	ACTA_MOUSE	515	42380.9	0	10	100	404	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
795.4723	795.4706	-0.0017	-2	331	337 IAAPPER					Mascot
976.4482	976.4556	0.0074	8	21	30 AGFAGDDAPR					Mascot
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1130.5476	1130.5541	0.0065	6	199	208 GYSFVTTAER	63	100			Mascot
1130.5476	1130.5541	0.0065	6	199	208 GYSFVTTAER					Mascot
1198.7054	1198.7111	0.0057	5	31	41 AVFPSVGRPR	40	99.883			Mascot
1198.7054	1198.7111	0.0057	5	31	41 AVFPSVGRPR					Mascot
1500.7078	1500.7164	0.0086	6	362	374 QEYDEAGPSIVHR	93	100			Mascot
1500.7078	1500.7164	0.0086	6	362	374 QEYDEAGPSIVHR					Mascot
1790.892	1790.901	0.009	5	241	256 SYELPDGQVITIGNER	104	100			Mascot
1790.892	1790.901	0.009	5	241	256 SYELPDGQVITIGNER					Mascot
1956.0437	1956.0449	0.0012	1	98	115 VAPEEHPDLLTEAPLNPK	91	100			Mascot
1956.0437	1956.0449	0.0012	1	98	115 VAPEEHPDLLTEAPLNPK					Mascot
2244.0601	2244.0659	0.0058	3	294	314 DLYANNVLSGGTMYPGIADR	13	47.325	Oxidation (M)[14]		Mascot
2244.0601	2244.0659	0.0058	3	294	314 DLYANNVLSGGTMYPGIADR			Oxidation (M)[14]		Mascot
2552.1531	2552.1448	-0.0083	-3	218	240 LCYVALDFENEMATAASSSLEK			Carbamidomethyl (C)[2], Oxidation (M)[12]		Mascot
3212.6045	3212.5989	-0.0056	-2	150	179 TTGIVLDSGDGVTHNVPI YEGYALPHAIMR			Oxidation (M)[29]		Mascot
3	Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1	ACTS_MOUSE	497	42366	0	10	100	391	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
795.4723	795.4706	-0.0017	-2	331	337 IAAPPER					Mascot
976.4482	976.4556	0.0074	8	21	30 AGFAGDDAPR					Mascot
1130.5476	1130.5541	0.0065	6	199	208 GYSFVTTAER	63	100			Mascot
1130.5476	1130.5541	0.0065	6	199	208 GYSFVTTAER					Mascot
1198.7054	1198.7111	0.0057	5	31	41 AVFPSVGRPR	40	99.883			Mascot
1198.7054	1198.7111	0.0057	5	31	41 AVFPSVGRPR					Mascot
1500.7078	1500.7164	0.0086	6	362	374 QEYDEAGPSIVHR	93	100			Mascot
1500.7078	1500.7164	0.0086	6	362	374 QEYDEAGPSIVHR					Mascot
1515.7491	1515.7567	0.0076	5	87	97 IWHHTFYNELR					Mascot

1790,892	1790,901	0.009	5	241	256 SYELPDGQVITIGNER	104	100	Mascot
1790,892	1790,901	0.009	5	241	256 SYELPDGQVITIGNER	91	100	Mascot
1956,0437	1956,0449	0.0012	1	98	115 VAPEEHPTLLTEARLNPK			Mascot
1956,0437	1956,0449	0.0012	1	98	115 VAPEEHPTLLTEARLNPK			Mascot
2552,1531	2552,1448	-0.0083	-3	218	240 LCYVALDFENEMATAASS SSLEK			Mascot
3212,6045	3212,5989	-0.0056	-2	150	179 TTGIVLDSGDGVTHNVPI			Mascot

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4	Actin, gamma-enteric smooth muscle OS=Mus musculus GN=Actg2 PE=2 SV=1	ACTH_MOUSE	409	42248.9	0	9	100	312	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
795,4723	795,4706	-0.0017	-2	330	336 IAPPER					Mascot
976,4482	976,4556	0.0074	8	20	29 AGFAGDDAPR					Mascot
1130,5476	1130,5541	0.0065	6	198	207 GYSFVTTAER	63	100			Mascot
1130,5476	1130,5541	0.0065	6	198	207 GYSFVTTAER					Mascot
1198,7054	1198,7111	0.0057	5	30	40 AVFSPVGRPR	40	99,883			Mascot
1198,7054	1198,7111	0.0057	5	30	40 AVFSPVGRPR					Mascot
1790,892	1790,901	0.009	5	240	255 SYELPDGQVITIGNER	104	100			Mascot
1790,892	1790,901	0.009	5	240	255 SYELPDGQVITIGNER					Mascot
1956,0437	1956,0449	0.0012	1	97	114 VAPEEHPTLLTEARLNPK	91	100			Mascot
1956,0437	1956,0449	0.0012	1	97	114 VAPEEHPTLLTEARLNPK					Mascot
2244,0601	2244,0659	0.0058	3	293	313 DLYANNVLSGGTMYPGI ADR	13	47,325	Oxidation (M)[14]		Mascot
2244,0601	2244,0659	0.0058	3	293	313 DLYANNVLSGGTMYPGI ADR			Oxidation (M)[14]		Mascot
2552,1531	2552,1448	-0.0083	-3	217	239 LCYVALDFENEMATAASS SSLEK			Carbamidomethyl (C)[2], Oxidation (M)[12]		Mascot
3212,6045	3212,5989	-0.0056	-2	149	178 TTGIVLDSGDGVTHNVPI			Oxidation (M)[29]		Mascot

5	Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1	ACTG_MOUSE	178	42107.9	0	5	100	144	100	
Protein Group										
Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1										
ACTB_MOUSE 42051.9 0										
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
795,4723	795,4706	-0.0017	-2	329	335 IAPPER					Mascot
976,4482	976,4556	0.0074	8	19	28 AGFAGDDAPR					Mascot
1198,7054	1198,7111	0.0057	5	29	39 AVFSPVGRPR	40	99,883			Mascot
1198,7054	1198,7111	0.0057	5	29	39 AVFSPVGRPR					Mascot
1515,7491	1515,7567	0.0076	5	85	95 IWHHTFYNELR					Mascot
1790,892	1790,901	0.009	5	239	254 SYELPDGQVITIGNER	104	100			Mascot
1790,892	1790,901	0.009	5	239	254 SYELPDGQVITIGNER					Mascot

ProteomicT05611-72_MLV_d 1790,901 Mascot 131 of 136

6	Beta-actin-like protein 2 OS=Mus musculus GN=Actb2 PE=1 SV=1	ACTBL_MOUSE	114	42319.1	0	2	100	104	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
795,4723	795,4706	-0.0017	-2	330	336 IAPPER					Mascot
1790,892	1790,901	0.009	5	240	255 SYELPDGQVITIGNER	104	100			Mascot
1790,892	1790,901	0.009	5	240	255 SYELPDGQVITIGNER					Mascot
7	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=Idh3a PE=1 SV=1	IDH3A_MOUSE	112	40069.2	0	7	100	52	99,993	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
1028,516	1028,5231	0.0071	7	59	66 APIQWEER					Mascot
1054,5238	1054,5194	-0.0044	-4	206	214 MSDGLFLQK			Oxidation (M)[1]		Mascot
1216,5997	1216,6082	0.0085	7	179	188 IAFAFAFEYAR	52	99,993			Mascot
1216,5997	1216,6082	0.0085	7	179	188 IAFAFAFEYAR					Mascot
1391,7529	1391,7587	0.0058	4	135	146 TPYTDVNVITR					Mascot
1606,8734	1606,8641	-0.0093	-6	101	115 TRIAAGHPSMNLRLR			Oxidation (M)[10]		Mascot
1894,9435	1894,9399	-0.0036	-2	300	316 DMANPTALLSVMMLR			Oxidation (M)[2,14,15]		Mascot
2502,2358	2502,2312	-0.0046	-2	147	169 ENTEGEYSIEHIVDGV VQSIK					Mascot

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Gel Idx/Pos	194/H21	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded					
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9					
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %		
1	ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2	ATPB_MOUSE	197	56265.5	0	9	100	110	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
1038,5942	1038,5688	-0.0254	-24	134	143 IPVGPETLGR					Mascot
1401,7042	1401,7065	0.0023	2	144	155 IMNVIGEPIDGR			Oxidation (M)[2]		Mascot
1406,681	1406,6866	0.0056	4	226	239 AHGGYSVFAVGGER	59	99,998			Mascot
1435,7539	1435,7719	0.018	13	311	324 FTQAGSEVALLGR					Mascot
1439,7893	1439,7933	0.004	3	282	294 VALTGLTVAEYFR	11	0			Mascot
1439,7893	1439,7933	0.004	3	282	294 VALTGLTVAEYFR					Mascot
1617,8053	1617,8097	0.0044	3	265	279 VALVYGMINEPFGAR	4	0	Oxidation (M)[8]		Mascot
1617,8053	1617,8097	0.0044	3	265	279 VALVYGMINEPFGAR			Oxidation (M)[8]		Mascot
1650,9174	1650,922	0.0046	3	95	109 LVEVAQHLGESTVR					Mascot
1858,8752	1858,8831	0.0079	4	407	422 IMDPNVGNHEDVVAR			Oxidation (M)[2]		Mascot
1988,0334	1988,0347	0.0013	1	388	406 AIAELGIYPAVDPLDSTR	36	99,614			Mascot
1988,0334	1988,0347	0.0013	1	388	406 AIAELGIYPAVDPLDSTR					Mascot

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Gel Idx/Pos	195/H22	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded					
Plate #/Name	[1] T056P10	Instrument Sample Name		Spectra	9					
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %		
1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Mus musculus GN=Ndufs3 PE=1 SV=1	NDUS3_MOUSE	359	30301.6	0	8	100	274	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
881,5428	881,535	-0.0078	-9	43	49 RPTVRR					Mascot
1309,6787	1309,6818	0.0031	2	200	210 DFPLTQVVELR	64	100			Mascot
1309,6787	1309,6818	0.0031	2	200	210 DFPLTQVVELR					Mascot
1357,7322	1357,7283	-0.0039	-3	109	121 SLADLTAVDVPTR					Mascot
1366,7729	1366,7782	0.0053	4	125	135 FEIVYVLLSLR	64	100			Mascot
1366,7729	1366,7782	0.0053	4	125	135 FEIVYVLLSLR					Mascot
1486,79	1486,7955	0.0055	4	218	230 VVAEPVLAQEFR	68	100			Mascot
1486,79	1486,7955	0.0055	4	218	230 VVAEPVLAQEFR					Mascot
1551,759	1551,7668	0.0078	5	186	198 ILTDYGFEGHFFR	77	100			Mascot
1551,759	1551,7668	0.0078	5	186	198 ILTDYGFEGHFFR					Mascot
1664,8894	1664,881	-0.0084	-5	56	70 QLSAFGEYVAELPK					Mascot
1712,8068	1712,8115	0.0047	3	232	245 FDLNVPWEAFPAVR					Mascot
2	ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2	ATPB_MOUSE	161	56265.5	0	7	100	102	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification	Rank	Result Type

Seq.	Seq.	Score	Oxidation (M)[2]	Mascot
1401,7042	1401,714	0,0098	7	144
1406,681	1406,6915	0,0105	7	226
1435,7539	1435,7577	0,0039	3	311
1439,7893	1439,7837	-0,0056	-4	282
1650,9174	1650,915	-0,0024	-1	95
1921,9655	1921,9711	0,0056	3	295
1921,9655	1921,9711	0,0056	3	295
2266,0842	2266,0945	0,0103	5	325

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Gel Idx/Pos	196/H23	Instr./Gel Origin	AK139/T056	Process Status	Analysis Succeeded			
Plate [#] Name	[1] T056P10	Instr./Gel Origin	AK139/T056	Spectra	9			
Rank	Protein Name	Accession No.	Protein Score	Protein MW	Protein PI	Pep. Count	Protein Total Ion Score	Total Ion C. I. %

1 Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 PRDX2_MOUSE 695 21936,1 0 9 100 571 100

SV=3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Ion Score	C. I. %	Modification	Rank	Result Type
789,4101	789,4088	-0,0013	-2	151	157 SVDEALR	39	99,833			Mascot
789,4101	789,4088	-0,0013	-2	151	157 SVDEALR					Mascot
876,5189	876,5177	-0,0012	-1	128	135 GLFIIDAK					Mascot
937,4373	937,4409	0,0036	4	120	127 NDEGIAYR	53	99,994			Mascot
937,4373	937,4409	0,0036	4	120	127 NDEGIAYR					Mascot
1108,5997	1108,6021	0,0024	2	110	119 SLSQNYGVLK	63	100			Mascot
1108,5997	1108,6021	0,0024	2	110	119 SLSQNYGVLK					Mascot
1211,6743	1211,6803	0,006	5	140	150 QITVNDLPVGR	107	100			Mascot
1211,6743	1211,6803	0,006	5	140	150 QITVNDLPVGR					Mascot
1596,7904	1596,7925	0,0021	1	11	26 SAPDFTATAVVDGAFK	89	100			Mascot
1596,7904	1596,7925	0,0021	1	11	26 SAPDFTATAVVDGAFK					Mascot
1706,9688	1706,9688	0	0	93	109 EGGGLGPLNPLADVTK	71	100			Mascot
1706,9688	1706,9688	0	0	93	109 EGGGLGPLNPLADVTK					Mascot
2699,3611	2699,3608	-0,0003	0	68	91 LGCEVLGVSVDQFTHLAWINTPR	150	100	Carbamidomethyl (C)[3]		Mascot
2699,3611	2699,3608	-0,0003	0	68	91 LGCEVLGVSVDQFTHLAWINTPR			Carbamidomethyl (C)[3]		Mascot
3788,7861	3788,782	-0,0041	-1	158	191 LVQAFQYDEHGEVCPAGWKPGSDTIKPNVDDSK			Carbamidomethyl (C)[15]		Mascot

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