

Appendix C Table 5.2 Peptides identified in oxycysDML experiment.

Acc. No. ^a	Protein Name	Sequence ^b	Light					Heavy					Σ#PSM ^g
			<i>m/z</i>	<i>z</i> ^c	Xcorr ^d	ΔM [ppm] ^e	#PSM ^f	<i>m/z</i>	<i>z</i> ^c	Xcorr ^d	ΔM [ppm] ^e	#PSM ^f	
		AADKDTCFST TEGPNLVTR	680.0060	3	6.01	6.04	284	685.3680	3	3.10	4.66	354	
		TNCDLYEKL GEYGFQNAI LVR	853.7723	3	5.61	4.37	124	859.1350	3	3.24	4.06	99	
		LQTCCDKPL LK	730.4076	2	3.26	4.61	48	742.4744	2	2.59	4.91	120	
		RPCFSALTV DETYVPK	647.0079	3	3.97	5.06	46	652.3710	3	4.14	5.30	85	
		YMCENQATI SSK	752.3436	2	3.08	-1.24	62	760.3883	2	2.72	-0.82	54	
		ENYGELADC CTK	758.3295	2	3.20	4.17	38	766.3748	2	3.20	5.33	76	
		VNKECCHG DLLECADDR AELAK	672.5735	4	3.67	4.99	20	678.6063	4	4.53	4.20	58	
		ECCHGDLLE CADDRAEL AK	773.3463	3	3.20	1.34	23	778.7112	3	3.61	4.00	30	
		NLVKTNCD LYEKLGEYG FQNAILVR	761.1626	4	3.73	5.13	22	767.1951	4	3.72	4.03	30	
		RPCFSALTV DETYVPKEF K	791.0872	3	4.38	4.30	26	799.1318	3	3.37	4.57	20	

P07724	Serum albumin	LVQEVTDFAKTCVADESAANCDK	885.7625	3	4.63	3.25	24	893.8091	3	3.23	5.75	7	1810
		TVMDDFAQFLDTCCK	953.9286	2	4.75	6.06	21	969.9653	2	2.97	0.66	10	
		TCVADESAA NCDK	748.8217	2	2.52	0.35	18	756.8654	2	3.37	-0.62	7	
		ATAEQLKTMDDFAQFLDTCCK	892.7687	3	3.41	7.32	12	906.1417	3	4.41	3.87	9	
		SLHTLFGDKLCAIPNLR	671.0425	3	3.57	-1.46	13	676.4071	3	3.40	1.09	4	
		AETFTFHSDICTLPEKEK	560.0371	4	3.71	4.77	15					0	
		LQTCCDKPL LKK	808.4710	2	3.21	4.51	1	824.5574	2	2.53	1.54	11	
		NLVKTNCDLYEK					0	802.9885	2	2.49	0.77	10	
		SLHTLFGDKLCAIPNLRENYGELADCCTK	870.6884	4	4.60	5.66	5	876.7169	4	3.65	0.17	4	
		YMCENQATISSKLQTCCDKPLLK	967.4855	3	3.26	1.06	7					0	
		KYEATLEKCAEANPPACYGTVLAEFQPLVEEPK					0	1015.0427	4	3.66	-0.81	4	

LPCVEDYLS AILNR	845.9470	2	2.69	1.96	2					0	
TVMDDFAQ FLDTCCKAA DKDTCFSTE GPNLVTR	975.2036	4	3.66	3.14	2					0	
VCLLHEKTP VSEHVTK RHPYFYAPE LLYYAEQY NEILTQCCA EADKESCLT PK	931.8494	5	4.64	5.25	1	0	497.0605	4	3.74	-0.84	2
TCVADESAA NCDKSLHTL FGDKLCAIP NLR					0	871.9659	4	3.73	1.87	1	
VGTKCCTLP EDQRLPCVE DYLSAILNR					0	823.4257	4	4.42	-10.54	1	
YIGGCCGFE PYHIR	586.2701	3	3.90	1.37	270		588.9542	3	3.29	5.73	273
ISGQKVNEA ACDIAR	844.4481	2	2.74	5.51	148		852.4918	2	2.34	4.60	207
GNYVAEKIS GQKVNEAA CDIAR	826.4354	3	5.24	3.93	78		834.4793	3	6.56	3.39	31
QVADEGDA LVAGGVSQ TPSYLSCK	836.7509	3	3.89	3.69	43		842.1092	3	3.72	-1.77	39

O35490	Betaine-- homocysteine S- methyltransfer ase 1	AYLMSQPLA YHTPDCGK	675.3245	3	3.63	-1.40	45	675.3580	3	3.49	1.91	32	1307
		QVADEGDA LVAGGVSQ TPSYLSCKS EVEVK	1069.8820	3	3.40	6.93	24	1077.9246	3	4.07	5.24	21	
		AGASIVGVN CHFDPSVSL QTVK	781.4136	3	3.33	3.75	22	786.7770	3	4.29	4.34	22	
		VNEAACDIA R	573.7821	2	2.77	-0.27	13	577.8044	2	2.40	0.00	4	
		LKAYLMSQP LAYHTPDCG K	759.7313	3	3.31	0.94	13					0	
		QVADEGDA LVAGGVSQ TPSYLSCKS EVEVKK	841.6920	4	3.84	3.16	6	849.7350	4	3.52	1.55	6	
		EAYNLGVR YIGGCCGFE PYHIR	665.5678	4	3.58	-1.92	4	889.7691	3	3.04	-2.29	2	
		AYLMSQPLA YHTPDCGK QGFIDLPEFP FGLEPR					0	967.5027	4	3.63	0.80	3	
		LVKAGASIV GVNCHFDPS VSLQTVK					0	684.4105	4	4.14	-3.38	1	
		VVAVDCGIK NNVIR	806.9676	2	3.69	4.65	101	815.0112	2	3.99	3.63	108	

Q8C196	Carbamoyl-phosphate synthase [ammonia], mitochondrial	SAYALGGLG SGICPNKETL IDLGTK	873.8107	3	5.10	4.31	101	881.8544	3	4.46	3.45	87	1017
		SAYALGGLG SGICPNK	810.9271	2	3.89	3.39	76	818.9715	2	4.36	3.36	49	
		TSACFEPSL DYMVTKIPR	724.3708	3	3.68	4.78	43	729.7348	3	4.48	6.17	54	
		GNPTKVVA VDCGIKNNV IR	713.4120	3	3.75	4.62	40	721.4559	3	5.13	3.90	47	
		GNDVLVIEC NLR	715.3793	2	2.93	3.09	33	719.3987	2	3.12	-0.78	45	
		TSACFEPSL DYMVTK	910.9276	2	2.53	1.79	47	910.9763	2	2.94	3.82	18	
		MCHPSVDGF TPR	716.3312	2	2.50	3.05	4	480.5703	3	3.11	0.76	52	
		QISKCLGLT EAQTR	830.9608	2	2.41	5.55	29	839.0005	2	3.03	-0.03	20	
		CEMASTGE VACFGEGIH TAFLK	1256.0834	2	3.18	9.58	39					0	
		EIGFSDKQIS KCLGLTEAQ TR	822.4437	3	3.55	3.93	8	830.4849	3	3.34	0.07	5	
		SAYALGGLG SGICPNKETL IDLGTKAFA MTNQILVER	999.0425	4	4.50	7.36	5	1005.0776	4	4.96	9.12	5	
		NVMSGK TSA CFEPSLDYM VTKIPR	928.4928	3	3.23	5.99	1					0	

Q91Y97	Fructose-bisphosphate aldolase B	IADQCPSSL AIQENANAL AR	724.0375	3	5.22	2.62	265	726.7185	3	5.37	2.02	313	668
		PSSLAIQENANALAR	870.4686	3	5.26	3.15	45	873.1498	3	6.55	2.93	45	
V9GXA7	Uncharacterized protein	IVSNASCTT NCLAPLAK	938.4921	2	2.48	5.38	322	946.5382	2	4.92	7.21	324	661
		IVSNACCTIS CLAPLAK	973.0009	2	3.14	-0.61	9	947.0322	2	2.87	-0.58	6	
P14152	Malate dehydrogenase, cytoplasmic	VIVVGNPAN TNCLTASK	907.5025	2	4.03	7.50	195	915.5460	2	2.50	6.50	278	587
		SAPSIPKENF SCLTR	881.9648	2	2.56	3.73	13	890.0087	2	2.34	3.15	66	
		SVKVIVVGN PANTNCLTAS K	719.4078	3	3.31	-0.88	8	727.4555	3	3.84	3.67	26	
		KSVKVIVVGN NPANTNCLT ASK	771.4482	3	3.57	-3.08	1					0	
P00329	Alcohol dehydrogenase 1	VIPLFSPQCG ECR	829.9084	2	2.93	3.93	155	833.9312	2	3.03	4.68	203	446
		VCLIGCGFS TGYGSAVK	916.4617	2	3.40	4.37	42	924.5074	2	2.98	5.79	43	
		ICKHPESNFC SR	795.8802	2	2.43	0.94	1	837.9355	2	2.27	-1.63	1	
		IDGASPLDK VCLIGCGFS TGYGSAVK	942.1490	3	3.61	2.24	1					0	
	Succinyl-CoA ligase	LIGPNCFGVI NDCECK	890.9611	2	3.22	3.54	187	899.0083	2	2.93	6.71	210	

Q9WUM1	mgase [ADP/GDP- forming] subunit alpha	IICQGFTGKQ GTFHSQQAL EYGTK	696.6085	4	4.57	-2.28	6	936.5214	3	3.28	-0.78	2	405
P56391	Cytochrome c oxidase subunit 6B1	SLCPVSWVS AWDDR	853.4075	2	3.79	4.36	54	857.4291	2	3.61	3.67	112	404
		GGDVSVCE WYR	678.3094	2	2.91	4.86	52	682.3315	2	2.59	4.78	53	
		NCWQNYLD FHR	527.5773	3	3.75	7.02	25	530.2574	3	3.16	4.33	34	
		VYKSLCPVS WWSAWDDR	708.6946	3	3.44	5.10	28	714.0572	3	3.97	4.64	26	
		SLCPVSWVS AWDDRIAE GTFPGKI	916.4696	3	4.21	2.90	8	921.8358	3	3.29	6.47	11	
		GGDVSVCE WYRR	756.3560	2	2.46	-0.84	1					0	
Q921I1	Serotransferrin	AVSSFFSGS CVPCADPVA FPK	1143.5558	2	3.70	4.74	70	1151.6014	2	5.08	5.83	68	392
		SAGWVIPIG LLFCK	539.6491	3	3.33	5.82	55	817.0101	2	3.84	0.54	66	
		NQQEGVCPE GSIDNSPVK WCALSHLER	792.3846	4	4.08	3.84	28	796.4065	4	3.55	3.40	43	
		KPVDQYED CYLAR	571.6154	3	3.68	0.13	1	576.9811	3	3.36	5.11	16	
		AVLTSQETL FGGSDCTGN FCLFK	1304.6355	2	3.00	8.21	9	875.4469	3	3.75	-1.86	7	
		NQQEGVCPE GSIDNSPVK	1007.4810	2	2.72	0.04	4	1015.5298	2	2.55	4.43	10	

		LYLGHNYV TAIRNQQEG VCPEGSIDN SPVK	854.4359	4	4.17	3.04	3	858.4578	4	3.80	2.78	5	
		NLKQEDFEL LCPDGTR	996.0002	2	2.78	1.44	2	669.6981	3	3.15	0.36	3	
		KPVDQYED CYLARIPSH AVVAR	661.5997	4	3.49	2.11	1					0	
		LLEACTFHK H					0	664.3911	2	2.38	-1.32	1	
P08249	Malate dehydrogenase , mitochondrial	GCDVVVIPA GVPR	683.8837	2	4.13	6.56	51	687.9046	2	3.22	4.61	71	334
		TIPLISQCTP K	713.9241	2	2.51	5.00	40	721.9672	2	3.34	3.09	49	
		GYLGPEQLP DCLK	773.4042	2	2.65	1.93	15	781.4492	2	2.58	2.62	36	
		TIPLISQCTP KVDFPQDQL ATLTGR	990.2137	3	3.70	2.95	27	995.5793	3	5.13	5.70	18	
		ANVKGYL PEQLPDCLK	662.6953	3	3.34	-0.88	11	670.7424	3	3.20	3.24	7	
		ETECTYFST PLLLGKK	986.0276	2	2.64	-1.47	4					0	
		GYLGPEQLP DCLKGCDV VVIPAGVPR	978.5184	3	3.39	4.86	1	961.2063	3	3.87	5.32	2	
		ETECTYFST PLLLGK					0	916.0139	2	2.33	3.91	2	
		FELTCYSLA PQIK	813.4376	2	4.52	4.34	106	821.4811	2	3.79	3.33	131	

		NYDYILSTG CAPPGKNIY YK					0	815.7911	3	3.12	3.93	2	
Q63880-2	Isoform 2 of Carboxylesterase 3A	DASINPPMC LQDVER	894.9202	2	2.47	4.24	77	898.9421	2	2.86	3.92	139	287
		YLQDAGCP VFLYEFQHT	921.1165	3	4.01	0.67	26	926.4869	3	4.95	8.71	43	
		PSSFAK FSAPLPPQP											
		WEGVRDASI NPPMCLQD VER	1112.2220	3	3.73	5.00	1	1114.9037	3	3.22	5.15	1	
P99029-2	Isoform Cytoplasmic+peroxisomal of Peroxi-redoxin-5	GVLEGVVFA ETDCCSV	825.4426	2	2.96	3.58	74	833.4887	2	2.74	5.60	80	272
		ALNVEPDGT GLTCSLAPNI LSQL	804.4255	3	3.39	5.51	63	1210.1624	2	3.90	10.04	55	
Q8VCH0	3-ketoacyl-CoA thiolase B, peroxisomal	QCSSGLQAV ANIAGGIR	577.3077	3	3.52	4.06	78	869.4788	2	3.97	2.61	131	266
		VNPLGGAIA LGHPLGCTG AR	653.6921	3	3.73	1.26	15	656.3752	3	3.33	3.68	31	
		DCLIPMGITS ENVAER	916.9485	2	2.45	0.89	1	920.9740	2	2.79	4.43	9	
		IAQFLSGIPE TVPLSTVNR QCSSGLQAV ANIAGGIR	939.0064	4	3.97	-2.13	1					0	
H3RID2	S-formylglutathi	SVSAFAPICN PVLCSWGK	1025.0210	2	3.29	2.44	101	1033.0725	2	2.57	9.34	139	261

115914	one hydrolase (Fragment)	SVSAFAPICN PVLCSWGK K	735.7255	3	3.20	2.66	13	766.4454	3	3.03	2.73	11	204
Q91X72	Hemopexin	SLPQPQKVN SILGCSQ	906.4937	2	4.29	6.45	81	914.5363	2	2.78	4.39	95	263
		ELGSPPGISL ETIDAAFSCP GSSR	826.0754	3	4.48	3.65	47	828.7552	3	3.84	1.64	33	
		SLGPNTCSS NGSSLYFIH GPNLYCYSS IDKLNAAK	980.7311	4	3.71	0.84	2	986.7569	4	3.72	-6.80	2	
		RLEKELGSP PGISLETIDA AFSCPGSSR	1010.8608	3	4.06	3.69	1	1016.2188	3	3.52	-1.14	2	
P97872	Dimethylaniline monooxygenase [N-oxide- forming] 5	LLLGPCTPV QYR	722.9052	2	3.62	3.39	77	726.9273	2	2.65	3.33	84	249
		IAVIGAGAS GLTCIK	743.9387	2	3.76	2.55	37	751.9845	2	3.25	4.48	49	
		CCLEEGLEP VCFER					0					2	
Q9JKY7	Cytochrome P450 CYP2D22	ALTTPCPYQ LCALPR	894.9657	2	3.21	5.89	111	898.9891	2	2.54	7.25	129	240
		GAQVIENCA VTGIR	758.4049	2	4.96	5.06	70	762.4267	2	4.65	4.52	81	
		RDPLHEELL GQGCVFQER	737.7070	3	3.57	3.95	21	740.3883	3	4.90	3.78	35	
		AAVARGAQ VIENCAVTG IR	662.0327	3	3.54	3.85	7	664.7145	3	3.34	4.48	14	

124270	Catalase	LCENIAGHL KDAQLFIQK					0	552.3386	4	3.66	-2.75	2	
		VANYQRDG PMCMHDNQ GGAPNYYP NSFSAPEQQ R					0	984.6961	4	3.56	4.07	1	
Q8QZR5	Alanine aminotransferase 1	VLCVINPGN PTGQVQTR	941.0060	2	3.63	1.93	75	945.0320	2	2.64	5.90	75	194
		VLTLDTMNP CVR	723.8776	2	2.80	2.38	7	727.9035	2	2.68	7.53	34	
		QVLALCVYP NLLSSPDFPE DAKR	896.8071	3	3.85	-0.01	3					0	
G3UYY2	Selenium- binding protein 2	FLHDPSATQ GFVGCALSS NIQR	811.7409	3	5.58	4.15	77	814.4218	3	6.73	3.47	104	185
		GGSVQVLED QELTCQPEP LVVK	827.7691	3	3.63	0.86	2					0	
		CGPGYPTPL EAMKGPREE IVYLPCIYR	1090.8953	3	3.42	5.19	1					0	
		GGSVQVLED QELTCQPEP LVVKGK	898.8194	3	3.59	1.95	1					0	
		TCLLNETGD EPFQYKN	992.9775	2	3.74	7.89	157	1001.0195	2	5.37	5.39	16	
		TCLLNETGD EPFQYK	935.9493	2	2.77	1.11	5					0	

P15105	Glutamine synthetase	ITGTNAEVM	1366.6731	2	2.70	7.94	2	0	181													
		PAQWEFQIG																				
		PCEGIR																				
		GYFEDRRPS																				
P28474	Alcohol dehydrogenase class-3	ANCDPYAV	1034.5392	2	2.96	6.98	33	1042.5758	25													
		TEAIVR																				
		EFGASECISP																				
		QDFSK																				
G3UYR8	Alpha-aminoadipic semialdehyde dehydrogenase	TGYGAAVN	992.9863	2	3.71	-1.59	18	670.3712	10													
		TAK																				
		AKEFGASEC																				
		ISPQDFSK																				
		LKAGDTVIP	772.0806	3	3.20	3.76	3	0	176													
		LYIPQCGEC																				
		K																				
		GEVITTYCP								966.9842	2	2.56	6.54	30	971.0065	2	2.98	6.67	32			
ANNEPIAR																						
STCTINYSTS																						
LPLAQGIK																						
		STCTINYSTS	1005.5419	2	3.33	9.35	28	1013.5828	2	2.35	5.85	26										
		LPLAQGIKF																				
		Q																				
		GSDCGIVNV																				
		NIPTSGAEIG	1143.1036	2	3.00	6.71	16	1151.1498	2	3.51	8.20	28										
		GAFGGEK																				
		VFANAYLSD											1281.6329	2	2.70	3.13	10	1289.6724	2	3.42	-0.73	5
		LGGCiK																				
			842.4460	2	4.72	4.26	77	567.3302	3	3.43	5.75	49										

P24549	Retinal dehydrogenase 1	YCAGWADK IHGQTIPSDG DIFTYTR	976.8045	3	3.39	0.12	3	982.1733	3	3.21	6.15	29	171
		IGPALSCGN TVVVKPAE QTPLTALHL ASLIK	821.4803	4	4.20	4.15	6	827.5087	4	4.49	-1.88	4	
		LECGGGRW GNKGFFVQP TVFSNVTDE MR	811.9018	4	3.60	5.71	1	815.9191	4	3.88	-0.27	2	
Q61176	Arginase-1	GKFPDVPGF SWVTPCISA K	726.3902	3	4.79	4.40	64	734.4337	3	4.95	3.11	65	170
		TAEVKSTV NTAVALTLA CFGTQR	875.1396	3	4.23	10.79	7	880.4986	3	3.35	6.21	12	
		STVNTAVAL TLACFGTQR					0	973.5307	2	4.07	-0.85	13	
		ELKGKFPDV PGFSWVTPC ISAK	859.1403	3	3.54	2.65	6	869.8669	3	3.94	3.60	3	
		SLVANLAAA NCYKK	803.9557	2	3.07	3.43	53	816.0221	2	2.92	3.20	49	
		SLVANLAAA NCYK	725.8904	2	2.58	0.89	12	733.9362	2	2.90	2.80	26	
		AADAHVDA HYEQNEQP TGCAACIT GGNR	827.1133	4	4.47	-0.62	9	846.1302	4	3.68	-1.48	2	

P55264-2	Isoform Short of Adenosine kinase	SLVANLAAA NCYKKEK	0	642.0874	3	3.32	1.41	4	159				
		KAADAHVD AHYYEQNE QPTGTCAAC ITGGNR	866.1479	4	3.51	2.85	2	870.1672	4	3.84	-0.42	1	
		AATFFGCIGI DKFGEILKR	557.5669	4	3.63	6.68	1					0	
B1B0C7	Basement membrane-specific heparan sulfate proteoglycan core protein	LLQVTFIDS CEVVCB	883.4460	2	3.18	3.31	37	887.4661	2	3.41	0.92	23	158
		LYILQASPA DAGEYVCR	977.4899	2	3.17	-0.70	31	981.5212	2	3.67	8.55	28	
		IASVKPSDA GTYVCQAQ NALGTAQK	888.1334	3	4.17	-0.48	22	896.1841	3	3.94	6.62	17	
E0CXN5	Glycerol-3-phosphate dehydrogenase [NAD(+)]	VCYEGQPV GEFIR	791.3939	2	2.73	4.67	28	795.4154	2	2.38	3.84	60	155
		VCIVGSGNW GSAIAK	787.9243	2	3.33	3.40	38	795.9659	2	2.53	-0.16	29	
P28666	Murinoglobulin-2	LQVTASPQS LCGLR	779.4279	2	2.94	4.26	71	783.4495	2	3.59	3.50	53	155
		ALSCLESSW K	618.8217	2	2.74	5.52	7	626.8657	2	2.63	4.86	24	
O35215	D-dopachrome decarboxylase	LCAATATIL DKPEDR	577.3106	3	3.17	1.09	57	582.6738	3	3.11	1.61	57	143
		STEPCAHLL VSSIGVVGT AEQNR	818.4243	3	3.32	5.22	7	821.1044	3	3.88	3.64	22	
		EIIAVSCGPS QCQETIR	988.4885	2	3.46	6.13	54	1026.5242	2	3.34	6.25	68	

Q9DCW4	Electron transfer flavoprotein subunit beta	KLVKEIIAVS	834.1288	3	3.91	3.64	15	842.1683	3	4.47	-2.19	5	143
		CGPSQCQETIR											
P62889	60S ribosomal protein L30	VCTLAIIDPG	893.4797	2	3.70	5.93	52	897.5005	2	4.50	4.31	35	142
		DSDIIR	691.4059	2	2.85	4.35	23	695.4287	2	2.39	5.25	32	
Q9QXD6	Fructose-1,6-bisphosphatase 1	LLYECNPIAYVMEK	899.9682	2	3.44	9.60	81	908.0118	2	3.65	8.64	31	141
		AQGTGELTQLLNSLCTAIK	1037.5702	2	3.19	5.66	12	1045.6183	2	3.69	9.19	11	
		KAQGTGELTQLLNSLCTAIK	744.0883	3	3.58	1.24	3	752.1343	3	3.60	3.43	3	
Q9DBM2	Peroxisomal bifunctional enzyme	LCNPPVNAISPTVITEVR	1004.5522	2	3.43	3.76	49	1008.5774	2	5.04	6.68	89	138
Q01853	Transitional endoplasmic reticulum ATPase	QAAPCVLFFDELDSIAK	660.6801	3	3.22	5.47	27	998.5630	2	3.02	7.67	29	134
		GVLFGPPGCGK	654.3478	2	2.76	5.11	18	662.3935	2	2.67	6.99	21	
		MTNGFSGADLTEICQR	914.4294	2	2.59	8.21	18	918.4520	2	2.96	8.67	8	
		QAAPCVLFFDELDSIAKAR	736.3918	3	3.58	3.61	5	741.7556	3	3.56	4.66	8	
	Cytochrome b-c1 complex	NALVSHLDGTTPVCEDIGR	694.6828	3	4.06	2.56	44	697.3651	3	3.15	3.69	64	

Q9CZ13	CI complex subunit 1, mitochondrial	VYEEDAVPG	817.4013	2	2.40	3.81	13	821.4206	2	2.36	0.26	5	127					
		LTPCR LCTSATESE VTR	691.3386	2	2.47	5.08	1							0				
H3BLB8	Paraoxonase 1, isoform CRA_c	EVTPVELPN	834.4580	2	2.72	2.99	37	842.5029	2	2.92	3.55	52	126					
		CNLVK LNAFREVTP VELPNCNLV K	1135.1321	2	3.09	8.58	20							762.4508	3	3.20	5.13	17
P38060	Hydroxymethylglutaryl-CoA lyase, mitochondrial	GYVSCALGC	808.8784	2	2.97	2.96	42	850.9371	2	2.51	4.19	58	118					
		PYEGK LLEAGDFIC QALNR	824.4303	2	2.96	0.57	13							828.4507	2	2.44	-1.54	2
		GYVSCALGC PYEGKVSPA K	709.6948	3	3.30	4.01	1							717.7341	3	3.55	-3.10	2
Q07456	Protein AMBP	TIAACNLPIV	849.4476	2	3.90	3.08	34	853.4693	2	3.99	2.53	46	117					
		QGPCR EYCGVPGD GYEELIR	892.9169	2	2.41	5.91	17							896.9324	2	2.71	-1.58	3
		EYCGVPGD GYEELIRS	936.4288	2	2.50	1.24	5							940.4482	2	2.61	-1.79	12
D3YVB6	Ketohexokinase (Fragment)	GGNASNSCT VLSLLGAR	852.9420	2	2.70	3.99	66	856.9626	2	4.26	2.16	45	111					
Q8VBW8	Tetratricopeptide repeat protein 36	QLVLLNPYA	836.9680	2	2.97	4.93	49	840.9899	2	3.28	4.58	50	110					
		ALCNR RQLVLLNPY AALCNR	610.3475	3	3.28	3.48	8							613.0302	3	3.32	5.56	3
		YVDIAIPCN NK	681.8598	2	2.87	2.70	46	689.9057	2	2.52	4.89	28						

P14206	40S ribosomal protein SA	ADHQLTEA SYVNLPTIA LCNTDSPLR	1008.8480	3	3.35	6.52	19	1011.5313	3	3.49	8.37	12	107
		LLVVTDPR DHQPLTEAS YVNLPTIAL CNTDSPLR	980.2636	4	3.79	-2.68	2					0	
Q8VCC2	Liver carboxylesterase 1	AIAQSSVIFN PCLFGR	904.4871	2	4.07	8.04	53					0	104
		HTTSPPLC YQNPEAALR	716.0178	3	3.73	0.04	4	718.6985	3	3.27	-0.98	40	
		FAPPEPAEP WSFVKHTTS YPPLCYQNP EAALR	939.9711	4	4.38	2.83	2	943.9956	4	3.68	5.25	4	
		TTTSAAMV HCLR	459.2336	3	3.23	3.09	1					0	
Q9CPY7-	Isoform 2 of Cytosol aminopeptidase	QVIDCQLAD VNNLGK	871.9617	2	3.07	3.19	28	880.0002	2	2.93	-3.57	16	103
		SAGACTAA AFLR	612.3156	2	2.57	3.08	30	616.3384	2	2.44	4.10	14	
		QVIDCQLAD VNNLGKYR	1031.5419	2	2.88	0.68	1	693.3919	3	3.08	-1.27	8	
		LILADALCY AHTFNP					0	960.0539	2	3.15	-1.52	4	
		ADMGGAAT ICSAIVSAAK	875.4428	2	2.43	-5.22	1	883.4933	2	2.62	1.74	1	

P41317	Mannose-binding protein C	ALCSEFQGS VATPR	775.8869	2	3.72	2.13	49	779.9087	2	2.38	1.61	49	98
F6Y6L6	Cathepsin D (Fragment)	AIGAVPLIQ GEYMIPCEK	1031.0432	2	2.64	1.53	24	1039.0857	2	3.27	-0.30	38	95
		GGCEAIVDT GTSLLVGPV EEVKELQK	938.1756	3	3.44	3.86	16	946.2259	3	3.93	10.09	10	
		AIGAVPLIQ GEYMIPCEK VSSLPTVYL K	1054.2612	3	3.15	9.17	2	1062.3085	3	3.66	11.80	5	
J3QPZ9	Enolase (Fragment)	VNQIGSVTE SLQACK	845.4471	2	2.85	1.74	13	853.4927	2	2.38	3.09	77	93
		SGETEDTFIA DLVVGLCT GQIK					0	809.1068	3	4.41	-2.03	3	
P17742	Peptidyl-prolyl cis-trans isomerase A	IIPGFMCQG GDFTR	813.8950	2	3.70	3.67	23	825.9116	2	2.41	-0.06	29	91
		KITISDCGQL	595.8254	2	2.54	-1.16	2	603.8715	2	2.69	1.69	37	
Q93092	Transaldolase	ALAGCDFLT ISPK	724.8959	2	3.08	1.82	34	732.9410	2	3.42	2.89	57	91
D3Z3P8	Estradiol 17 beta-dehydrogenase 5 (Fragment)	YKPVCNQV ECHPYLNQG K	796.0632	3	3.79	2.79	27	603.3330	4	3.54	3.65	59	86

Q9CRC0	Vitamin K epoxide reductase complex subunit 1	ALCDVGTAI SCSR	719.3481	2	2.44	4.51	40	723.3710	2	2.74	5.37	42	82
Q61838	Alpha-2-macroglobulin	AAPLSLCAL TAVDQSVLL LKPEAK	864.8403	3	3.42	0.71	27	872.8871	3	3.59	3.43	25	80
		FCQEFQHYP AMGGVAPQ ALAVAASGP GSSFR	1089.5300	3	4.88	7.46	11	1092.2073	3	4.14	3.59	9	
		GSGSGCVYL QTSLK					0	764.9327	2	2.52	-2.12	8	
Q8JZR0	Long-chain-fatty-acid-CoA ligase 5	GLAVSDNGP CLGYR	753.8754	2	3.93	4.36	32	757.8976	2	3.32	4.30	33	80
		ADIPVVICDT PQK	756.4091	2	2.72	-1.92	15						
Q8R084	Protein Ugt2b1	ISSEYSDMIE SFCK	876.3997	2	3.05	3.04	29	884.4441	2	3.40	3.08	51	80
O88451	Retinol dehydrogenase 7	VLAACLTEK GAEQLR	857.9771	2	3.40	-3.08	38	866.0271	2	2.71	3.51	40	79
		AIQSLTDTCS DDL SVVTDC MEHALTAC HPR					0	894.6663	4	3.99	3.59	1	
D3YYM6	40S ribosomal protein S5 (Fragment)	VNQAIWLLC TGAR	765.4179	2	2.63	1.81	28	769.4414	2	2.94	3.51	36	78
		TIAECLADE LINA AK	844.4482	2	2.43	-2.59	11	852.4941	2	2.93	-0.85	3	
A2A6F8	60S ribosomal protein L23 (Fragment)	ISLGLPVGA VINCADNTG AK	676.0413	3	3.51	4.52	36	1021.6036	2	4.03	5.33	37	73

Q9D8E6	60S ribosomal protein L4	YAICSALAA SALPALVMS K	997.0544	2	2.79	7.69	23	1005.1016	2	3.21	10.42	42	72
		GPCIYNEDN GIK	831.4285	2	2.75	-4.22	4	839.4789	2	2.98	3.03	2	
		RYAICSALA ASALPALVM SK	1036.5822	2	2.38	-10.55	1					0	
Q9EQ20	methylmalonate- semialdehyde dehydrogenase [acetylating]	VCNLIDSGT KEGASHLD VCNLIDSGT	725.3927	3	3.24	6.85	27	1095.6337	2	2.68	10.35	34	72
		KEGASILLD GRR	777.4232	3	3.39	2.21	4	782.7814	3	3.14	-3.74	7	
D3Z0Y2	Peroxioredoxin- 6	DFTPVCTTE LGR	712.3493	2	2.92	1.88	38	716.3721	2	3.18	2.77	32	71
		DFTPVCTTE LGRAAK					0	869.4940	2	2.39	1.64	1	
D3YWR7	Dihydropteridi ne reductase	GAVHQLCQ SLAGK	712.8905	2	3.03	4.09	36	720.9346	2	2.63	3.62	31	67
O88844	Isocitrate dehydrogenase [NADP] cytoplasmic	EAIICKNIPR	635.3738	2	2.44	4.31	3	643.4175	2	2.48	3.21	49	67
		NILGGTVFR EAIICK	874.0039	2	2.69	3.98	1	882.0421	2	2.86	-3.11	11	
		DLAACIKGL PNVQR	805.9561	2	2.77	0.05	3					0	
P01027	Complement C3	VYSYYNLEE SCTR	856.3884	2	3.18	3.71	17	860.4100	2	2.96	3.02	30	67
		GICVADPYEI R	660.8329	2	2.62	-2.43	4	664.8560	2	2.61	-0.99	7	
		DICEGQVNS LPGSINK	893.9536	2	2.59	-0.35	3	901.9965	2	2.42	-1.97	4	
		DTWVEHWP EAEECQDQK	748.3268	3	3.78	-2.35	2					0	

Q8K3J1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	LCEAICPAQ AITIEAEPR	1035.5306	2	3.11	8.73	41	1039.5499	2	2.85	5.91	26	67	
O35718	Suppressor of cytokine signaling 3	TQSGTKNLR IQCEGGSFSL QSDPR					0	913.4894	3	3.41	2.63	65	65	
Q9DB77	Cytochrome b-c1 complex subunit 2, mitochondrial	NALANPLYC PDYR	797.8909	2	2.65	3.87	28	801.9129	2	3.15	3.66	37	65	
G3UY87	PCTP-like protein (Fragment)	SCVITYLAQ VDPK	775.4202	2	2.41	2.38	40	783.4634	2	2.25	0.87	23	64	
		SCVITYLAQ VDPKGS LPK	1030.5764	2	3.00	-0.27	1					0		
Q8K0E8	Fibrinogen beta chain	TPCTVSCNIP VMSGK	837.9296	2	3.45	-2.05	17	845.9778	2	2.68	2.45	41	63	
		KYCGLPGEY WLGNDKISQ	861.4541	3	3.50	1.59	1	652.3749	4	3.52	0.36	3		
		LTR TPCTVSCNIP												
		VMSGKECEE IIR	868.7678	3	3.24	2.22	1					0		
D3YV43	40S ribosomal protein S3	GLCAIAQAE SLR	658.8557	2	2.74	3.69	27	662.8780	2	2.86	3.90	35	62	
P97742	Carnitine O-palmitoyltransferase 1, liver isoform	LLGSTIPLCS AQWER	879.9664	2	2.47	2.72	30	883.9884	2	2.31	2.47	32	62	

Q8VC81	Group XIIB phospholipase A2-like protein	AACICAE ^{EEE} KEEL	804.3665	2	2.60	-2.23	30	812.4160	2	2.75	4.18	32	62
P05208	Chymotrypsin-like elastase family member 2A	NIQTACLPP AGTILPR	875.4847	2	3.43	-3.36	24	879.5074	2	2.76	-2.82	37	61
P16331	Phenylalanine-4-hydroxylase	ILADSINSEV GILCHALQK	713.0638	3	4.06	3.90	15	718.4281	3	3.56	5.74	26	61
		ILADSINSEV GILCHALQK IKS	624.1108	4	4.40	4.22	2	630.1454	4	4.54	6.19	11	
		AYGAGLLSS FGELQYCLS DKPK	830.0952	3	3.37	-3.31	1	838.1451	3	4.14	3.36	4	
		TACQEYTVT EFQPLYYYVA ESFNDAKEK	1105.8735	3	3.23	8.86	2					0	
Q8BGT5	Alanine aminotransferase 2	VLCIINPGNP TGQVQSR	941.0087	2	3.34	4.79	25	945.0323	2	3.70	6.29	36	61
P97351	40S ribosomal protein S3a	ACQSIYPLH DVFVR	578.3036	3	4.28	7.05	40	580.9846	3	3.22	6.28	20	60
P08228	Superoxide dismutase [Cu-Zn]	AVCVLKGD GPVQGTIHF EQK	756.4161	3	5.08	5.34	27	764.4562	3	5.93	-0.39	30	59
		LACGVIGIA Q					0	519.3148	2	2.37	1.62	2	
Q91WUC	Expressed sequence AU018778	DVRPITEQIA VTAGCK	907.4988	2	2.55	3.46	31	610.6977	3	3.47	3.09	28	59

Q8R0F8	Acylpyruvase FAHD1, mitochondrial	SFTSSCPVSA FVPK	785.4053	2	2.86	3.23	20	793.4503	2	4.30	4.04	38	58
P63038-2	Isoform 2 of 60 kDa heat shock protein, mitochondrial	AAVEEGIVL GGGCALLR	856.9707	2	4.40	-1.37	37	860.9962	2	2.78	2.50	19	56
A2A848	Peroxisomal acyl-coenzyme A oxidase 1 (Fragment)	AFTTWTAN AGIEECR NLCLLYSLY GISQK	877.9139	2	2.68	2.14	30	881.9320	2	3.19	-2.47	11	54
Q5NC80	Nucleoside diphosphate kinase (Fragment)	GDFCIQVGR	540.2698	2	2.83	1.95	31	544.2924	2	2.94	2.66	23	54
P19096	Fatty acid synthase	SLCAFRQAP LLIGSTK ACVDTALEN LSTLK	606.6827	3	3.33	1.64	23	917.5633	2	2.47	-0.06	11	53
F6USD5	Mesencephalic astrocyte- derived neurotrophic factor (Fragment)	LCYYIGATD DAATK	809.3958	2	2.92	0.80	15	817.4441	2	2.67	5.65	37	52
P29788	Vitronectin	SIAQYWLGC PTSEK	848.4249	2	2.82	0.78	28	856.4705	2	3.48	2.21	22	50
Q8R0Y6	Cytosolic 10- formyltetrahyd rofolate dehydrogenase	ECDVLPDDT VSTLYNR TYSTINPTD GSVICQVSL AQVSDVDK AVAAAK	962.9519	2	3.57	0.40	34	966.9796	2	2.55	6.06	5	49
			1131.5896	3	4.02	-2.26	6					0	

	dehydrogenase	TAACLAAG NTVVIKPAQ VTPLTALK	864.8432	3	3.49	-0.30	2	872.8896	3	3.14	2.01	2	
Q8CHT0	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	PCYADKALL ND	713.8811	2	2.53	2.62	10	721.9225	2	2.38	-1.46	13	48
		SAFEYGGQK CSACSR	882.3952	2	2.50	-0.51	10	890.4408	2	2.42	0.87	12	
		LAGECGGK NFHFVHSSA DVDSVVSGLR					0	755.3972	4	3.70	-0.32	3	
Q8CG76	Aflatoxin B1 aldehyde reductase member 2	QVEAELLPCR	678.3743	2	2.52	4.55	19	682.3965	2	2.36	4.48	27	46
Q9WUR2	Isoform 2 of Enoyl-CoA delta isomerase 2, mitochondrial	ATFHTPFSQ LGQSPEACS SYTFPK	915.4412	3	3.63	2.32	16	920.8092	3	3.88	7.88	30	46
Q99LC5	Electron transfer flavoprotein subunit alpha, mitochondrial	TIYAGNALC TVK	683.8754	2	2.63	2.57	28	691.9199	2	2.56	2.72	16	44
P34914-2	Isoform 2 of Bifunctional epoxide hydrolase 2	ACGANLPEN FSISQIFSQA MAAR	837.7461	3	3.60	4.66	12	845.7542	3	3.07	-1.27	26	43
		VTGTQFPEA PLPVPCNPN DVSHGYVT VKPGIR	876.4597	4	4.12	0.43	2	880.4802	4	3.83	-1.41	1	

		GFTTCIVTN NWLDDGDK R					0	728.7169	3	3.51	1.51	2	
Q8VCW8	Acyl-CoA synthetase family member 2, mitochondrial	FLSCYDPINI QFTSGTTGN PK	1208.5980	2	4.84	1.39	20	1216.6525	2	3.28	9.67	23	43
G5E8R3	Pyruvate carboxylase	ADFAQACQ DAGVR	718.8363	2	3.30	4.57	12	722.8585	2	2.67	4.50	30	42
Q8BGD8	Cytochrome c oxidase assembly factor 6 homolog	SSFEASCPQ QWIK	812.3959	2	2.72	0.53	22	820.4418	2	3.12	2.39	20	42
Q8CHR6	Dihydropyrimi dine dehydrogenase [NADP(+)]	GMGLACGQ DPELVR	765.8776	2	2.45	4.86	10	769.9004	2	2.87	5.67	11	41
		IALFGAGPA SISCASFLAR	969.0302	2	2.84	11.15	4	973.0422	2	3.66	0.72	16	
A2AFW6	Mitochondrial carrier homolog 2	LCSGVLGTV VHGK	691.8931	2	2.60	-2.54	7	466.9618	3	3.68	-0.36	33	40
F2Z459	Protein Acat3	VAPEEVSEV IFGHVLTAG CGQNPTR	899.1244	3	3.64	2.84	11	901.8045	3	3.16	1.34	9	39
		AKVAPEEVS EVIFGHVLT AGCGQNPTR	731.3863	4	3.51	3.08	4	980.2090	3	3.39	3.23	15	

P47738	Aldehyde dehydrogenase, mitochondrial	LLCGGGAA ADRGYFIQP TVFGDVK	856.7852	3	3.65	5.01	21	862.1460	3	3.30	2.58	18	39
P68368	Tubulin alpha-4A chain	SIQFVDWCP TGFK	820.9135	2	2.73	3.39	23	828.9570	2	2.47	2.32	16	39
Q8K2B3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit	AAAFGLSEAG	907.4606	2	3.04	-0.77	30	915.5075	2	3.25	1.97	6	39
		FNTACLTKL FPTR	810.0988	3	3.30	5.13	2	815.4612	3	3.15	4.50	1	
D3YUG4	Acyl-protein thioesterase 1 (Fragment)	LAGVTALSC WLPLR	792.9545	2	2.67	5.46	15	796.9720	2	3.99	-0.50	23	38
P05202	Aspartate aminotransferase, mitochondrial	NLDKEYLPI GGLAEFCK	684.3678	3	3.47	0.28	8	692.4147	3	3.72	3.90	26	38
		TCGFDFSGA LEDISK	851.9039	2	2.53	0.66	4					0	
Q64442	Sorbitol dehydrogenase	YCNTWPMA ISMLASK	914.9532	2	2.50	10.77	18	922.9918	2	2.36	4.32	11	38
		VMIKCDPND QNP	743.8591	2	2.48	5.41	3	751.9023	2	2.92	3.74	3	
		VLVCGAGP VGMVTLLV	920.5561	2	2.64	13.55	2					0	
		AK YNLTPTIFFC ATPPDDGNL					0	1288.6207	2	2.27	-0.02	1	
		CR											
D3YZ54	2-hydroxyacyl-CoA lyase 1	NQEAMGAF QEFPQVEAC	1070.4900	2	2.87	6.52	13	1074.5105	2	3.40	4.94	9	37
		R QALQDTSKP CLLNIMIEPQ STR	867.1274	3	3.41	3.63	3	872.4895	3	3.80	2.63	12	37

P21981	Protein-glutamine gamma-glutamyltransferase 2	SEGTYCCGP VSVR	750.3378	2	2.87	4.32	31	788.3666	2	2.28	-4.12	6	37
Q91WGC	Acylcarnitine hydrolase	LSGCEAMDS QALVR	782.8797	2	2.87	3.99	16	786.9011	2	2.67	3.00	20	36
D3Z736	L-lactate dehydrogenase	VIGSGCNLD SAR	638.8224	2	2.56	4.81	9	642.8408	2	2.45	-1.15	25	35
		NRVIGSGCN LDSAR					0	777.9140	2	2.32	0.53	1	
P56593	Cytochrome P450 2A12	MLQGTCGA PIDPTIYLSK	1011.0362	2	2.88	10.11	21	1019.0803	2	2.64	9.79	13	35
		GVEERIQEE AGCLIK					0	902.0184	2	2.29	2.21	1	
Q8K1B3	Gltpd2 protein	LLQLACPGT GEADAR	800.4139	2	2.97	2.87	29	804.4314	2	3.20	-3.02	6	35
B1ASE2	ATP synthase subunit d, mitochondrial (Fragment)	SCAEFVSGS QLR	684.8346	2	2.44	3.09	33	688.8528	2	2.77	-2.65	1	34
O09173	Homogentisate 1,2-dioxygenase	GQNNPQVCP YNLYAEQLS GSAFT CPR	1000.4684	3	3.37	4.35	11	1003.1438	3	3.58	-1.69	14	34
		YISGFGNEC ASEDPR	865.3776	2	2.76	-0.49	8					0	
		MSLQPNEIC VIQR	808.4177	2	2.50	-0.92	1					0	
P11714	Cytochrome P450 2D9	STCNVIASLI FAR	740.4073	2	2.69	5.69	20	744.4303	2	2.54	6.77	14	34

F7C312	Endoplasmic (Fragment)	LTESPCALV ASQYGWSG NMR	1192.5649	2	4.88	9.04	20	803.3904	3	3.71	6.75	13	33
P26443	Glutamate dehydrogenase 1, mitochondrial	VYEGSILEA DCDILIPAAS EK	1175.0968	2	2.69	-1.36	16	1183.1432	2	3.32	0.36	13	33
		IIKPCNHVLS LSFPIR	488.2889	4	3.52	-0.97	3					0	
		IIKPCNHVLS LSFPIRRDDG SWEVIEGYR					0	588.9962	6	3.87	1.39	1	
P40936	Indolethylamine N-methyltransferase	AIQDAGCQV LK	629.8470	2	2.42	3.47	7	637.8919	2	2.49	4.20	26	33
P62983	Ubiquitin-40S ribosomal protein S27a	CCLTYCFNK PEDK	929.9156	2	2.62	3.62	33					0	33
Q91XD4	Formimidoyltransferase-cyclodeaminase	AISQTPGCV LLDVDAGPS TNR	1100.0691	2	2.99	10.64	9	1104.0890	2	2.57	8.53	20	33
		ACALQEGLR	523.2789	2	2.42	4.32	4					0	
P32020	Non-specific lipid-transfer protein	ALEDAQIPY SAVEQACV GYVYGDSTS GQR	1054.8235	3	4.40	-4.00	13	1057.5142	3	5.13	4.73	16	32
		ADCTITMAD SDLLALMTG K					0	1050.0636	2	3.51	9.09	2	

		ADCTITMAD SDLLALMTG KMNPQSAFF QGK					0	1124.2676	3	3.88	10.65	1	
Q60759	Glutaryl-CoA dehydrogenase , mitochondrial	GYGCAGVSS VAYGLLTR	879.9506	2	3.61	5.37	31	883.9695	2	3.44	1.72	1	32
P99028	Cytochrome b- c1 complex subunit 6, mitochondrial	SQTEEDCTE ELFDLHAR	752.3372	3	4.12	2.10	26	755.0212	3	3.37	5.57	5	31
Q9CR00	26S proteasome non-ATPase regulatory subunit 9	GLLGCNIPL QR	691.4054	2	2.51	3.64	3	695.4276	2	2.71	3.66	28	31
Q9Z2V4	Phosphoenolpy ruvate carboxykinase, cytosolic [GTP]	YLAAAFPSA CGK	656.3444	2	2.40	3.67	12	664.3889	2	2.42	3.82	18	30
P39039-2	Isoform 2 of Mannose- binding protein A	SLCTELQGT VAIPR	786.9232	2	2.53	-1.47	8	790.9503	2	2.76	4.68	21	29
Q8VCU1	Carboxylestera se 3B	DASINPPMC LQDVEK	894.9167	2	2.58	-13.71	17	894.9758	2	2.48	-0.10	3	28
		DAGCPVFLY EFQHTPSSF AK	1179.0687	2	2.90	1.28	3	1187.1115	2	2.81	-0.12	5	
Q9CRB3	5- hydroxyisourat e hydrolase	LSRLEAPCQ QWMELR	972.9975	2	2.64	4.82	13	651.6808	3	4.03	2.61	15	28

Q9WTP7	GTP:AMP phosphotransferase AK3, mitochondrial	TLTQCSWLL DGFPR	861.4423	2	3.50	5.43	23	865.4624	2	3.33	2.97	5	28
P00688	Pancreatic alpha-amylase	EVTINADTT CGNDWVCE HR	769.0019	3	4.62	-2.68	13	771.6830	3	3.94	-3.14	13	27
		EFPVPYSA WDFNDKNC NGEIDNYND AYQVR	942.6725	4	3.92	-0.66	1					0	
P27046	Alpha-mannosidase 2	DCLFASQSG SQPR	740.8491	2	3.03	4.05	23	744.8722	2	2.70	5.22	4	27
P85094	isochoismatase domain-containing protein 2A, mitochondrial	ILFESSILFEC DLQEV	981.0370	2	2.67	0.12	10	989.0804	2	2.42	-0.81	15	27
		IIKEPVPDSG LLSLFQGQS PLTSC	881.4795	3	3.66	4.86	2					0	
P68373	Tubulin alpha-1C chain	TIQFVDWCP TGFK	827.9214	2	2.49	3.42	6	835.9669	2	2.97	4.77	20	26
D3Z2P8	Sulfotransferase (Fragment)	IPFLEFSCPG VPPGLETLK	1079.0911	2	2.86	3.86	9	1087.1406	2	3.35	8.60	14	24
		APVYARIPF LEFSCPGVPP GLETLKETP APR	867.2205	4	3.46	-0.13	1					0	
G3X982	Aldehyde oxidase 3	GFGFPQGAF VTETCMSA VAAK	1116.5464	2	3.30	1.17	2	1124.5916	2	2.63	1.87	12	24
		AVQNACQIL MK					0	674.4040	2	2.55	-4.07	6	

		MACEDQFT NLVPQTDSK					0	1028.5187	2	2.62	0.00	4	
P01872	Ig mu chain C region	SILEGSDEYL VCK	784.8983	2	2.48	0.98	2	792.9457	2	2.89	4.82	13	24
		LICEATNFTP KPITVSWLK	768.1006	3	3.94	-0.28	6	776.1466	3	3.08	1.77	3	
P36552	Oxygen- dependent coproporphyrin ogen III	TCALAVVTS VVDRVTV	615.6923	3	3.46	3.65	14	623.7338	3	3.30	-0.90	9	24
		TCAEAVVPS YVPIVK	844.9670	2	2.53	-1.51	1					0	
Q61483	Delta-like protein 1	YQSVYVLSA EKDECVIAT EV	1151.5846	2	2.44	4.14	24					0	24
Q8BWT1	3-ketoacyl- CoA thiolase, mitochondrial	VVG YFVSG CDPTIMGIGP VPAINGALK K	982.2133	3	4.35	7.20	12	990.2577	3	3.24	7.20	4	24
		LCGSGFQSI VSGCQEICS K	1155.0394	2	2.64	4.52	1	1163.0831	2	3.01	3.91	4	
		YAVGSACIG GGQGIALLIQ NTA					0	1085.5901	2	2.85	0.47	2	
		VVG YFVSG CDPTIMGIGP VPAINGALK	1394.7607	2	2.73	13.07	1					0	
Q9DCMC	Persulfide dioxygenase ETHE1, mitochondrial	SLLPGCQSVI SR	672.8699	2	2.43	1.59	24					0	24

P16015	Carbonic anhydrase 3	EAPFTHFDP SCLFPACR	716.6591	3	3.54	-2.43	6	719.3455	3	3.86	4.55	17	23
P50247	Adenosylhomo cysteinase	VAVVAGYG DVGKGCQAQ ALR	974.0340	2	3.36	6.46	8	982.0717	2	2.29	-0.43	7	23
		WSSCNIFST QDHAAAAIA K	1067.5228	2	2.52	-0.14	1	717.3804	3	3.04	-0.32	3	
		SKFDNLYGC R					0	666.3703	2	2.34	-1.35	3	
		GCAQALRGF GAR					0	650.3597	2	2.33	-0.80	1	
D3YTT4	Isobutyryl- CoA dehydrogenase , mitochondrial	AVIFEDCAV PVANR					0	798.9353	2	2.43	2.31	22	22
Q922D8	C-1- tetrahydrofolat e synthase, cytoplasmic	GDLNDCFIP CTPK	830.8904	2	2.62	1.49	7	838.9357	2	2.32	2.57	8	22
		GCLELIKEA GVQIAGR	590.6721	3	3.23	4.13	5	596.0359	3	3.18	5.73	2	
O08573-2	Isoform Short of Galectin-9	FEEGGYVVC NTK	729.8528	2	2.41	3.44	3	737.8970	2	3.41	3.16	18	21
E0CY23	Heat shock 70 kDa protein 4L (Fragment)	GCALQCAIL SPAFK	796.4203	2	2.65	-0.09	11	804.4655	2	2.74	0.90	9	20

Q9CQA3	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	CHTIMNCTQ TCPK	873.8783	2	3.02	3.56	20					0	20
Q9D1Q6	Endoplasmic reticulum resident protein 44	TPADCPVIAI DSFR	795.4037	2	2.70	0.51	6	799.4280	2	2.62	3.22	14	20
Q9ER05	Chymopasin	LQQVVLPLV TVNQCR YTAQVSPVC LASTNEALP SGLTCVTTG WGR ITDAMICAG GSGASSCQG DSGGPLVCQ K	898.0171	2	2.59	0.54	4	902.0370	2	3.56	-2.00	12	20
			1075.5243	3	3.32	-4.11	1	1078.2126	3	3.35	2.30	2	
							0	1400.1877	2	2.44	11.65	1	
E9Q6M6	Mitochondrial glutamate carrier 1	GVNEDTYSG FLDCAR	866.3879	2	3.62	2.39	10	870.4165	2	2.47	9.78	9	19
P14094	Sodium/potassium-transporting ATPase subunit beta-1	YNPNVLPVQ CTGK	773.4065	2	2.49	-2.40	1	781.4561	2	2.50	4.35	18	19
P52760	Ribonuclease UK114	AAGCDFNN VVK NLGEILKAA GCDFNNVV K	625.8123	2	2.51	-1.99	3	633.8600	2	2.42	3.34	14	19
							0	1035.6245	2	2.26	1.60	1	

		QALKNLGEI LKAAGCDF NNVVK				0	849.5377	3	3.13	3.76	1	
Q8QZT1	Acetyl-CoA acetyltransferase, mitochondrial	QATLGAGLP ISTPCTTVN K	993.0414	2	3.09	0.91	2	1001.0840	2	2.76	-0.86	11
		QATLGAGLP ISTPCTTVN KVCASGMK					0	924.1948	3	3.77	2.34	6
A087WP	Mitochondrial amidoxime- reducing component 1	DLLLPIPPA TNPLLQCR	1030.5842	2	2.49	1.86	5	1034.6039	2	2.32	-0.60	7
		DCGEDAAQ WVSSFLK	884.9221	2	2.57	8.94	5	892.9616	2	2.59	3.39	1
A2BIN1	Major urinary protein 8	FAQLCEEHG ILRENIIDLS NANR	685.8494	4	3.73	-2.84	2	687.8629	4	4.38	0.57	11
		FAQLCEEHG ILR	500.9239	3	3.27	-3.81	4					0
		MKMMLLLC LGLTLVCVH AEEASSTGR NFNVEK	1238.9847	3	3.47	1.63	1					0
P17751	Triosephospha te isomerase	IYGGSVTG ATCKELASQ PDVDGFLVG GASLKPEFV DIINAKQ	1145.1200	4	3.77	8.04	8	1153.1672	4	4.33	10.47	3
		IAVAAQNCY K					0	605.3683	2	2.43	4.80	6

		IYGGSVTG ATCK	691.8709	2	2.66	-0.23	1					0	
P54071	Isocitrate dehydrogenase [NADP], mitochondrial	NILGGTVFR EPIICK	887.0048	2	2.58	-3.87	3	895.0556	2	2.73	3.33	13	18
		VCVQTVESG AMTK	733.3749	2	2.43	2.47	1	741.4192	2	2.53	2.28	1	
P58252	Elongation factor 2	RCLYASVLT AQPR					0	785.9510	2	2.49	1.98	15	18
		ETVSEESNV LCLSK	825.9213	2	3.28	5.95	1	833.9598	2	3.33	-1.13	2	
Q8VCF0	Mitochondrial antiviral- signaling protein	ALQICELPG LADQVTR	906.4911	2	2.46	3.54	13	910.5182	2	3.09	8.93	5	18
Q9D8B4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	EKPDDPLNY FIGGCAGGL TLGAR	826.4260	3	3.27	5.68	1	831.7881	3	4.20	4.69	16	17
Q9QZD8	Mitochondrial dicarboxylate carrier	GALVTVGQ LSCYDQAK	883.4583	2	2.63	-3.41	17					0	17
D3YVC1	40S ribosomal protein S2 (Fragment)	GCTATLGNF AK	598.3133	2	2.43	4.42	12	606.3517	2	2.74	-5.41	4	16
D3Z5B9	Protein ERGIC 53 (Fragment)	NNPAIVVIG NNGQINYDH QNDGATQA LASCQR	870.9248	4	3.98	2.86	12	872.9354	4	3.93	2.31	4	16

Q9DCG2	Isoform 2 of CD302 antigen	GDCEISSVE GTLCK		0					785.4149	2	2.50	9.59	16	16
Q9DCJ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	LVNGCALNFR	669.8573	2	2.46	6.39	10		673.8747	2	2.48	-0.76	6	16
E0CX19	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	GCGGVITLNRPK	664.3830	2	2.44	5.41	9		672.4240	2	2.39	0.35	6	15
O08553	Dihydropyrimidinase-related protein 2	SITIANQTNC PLYVTK	940.0032	2	2.69	-0.12	13		948.0449	2	3.74	-2.95	2	15
O70250	Phosphoglycerate mutase 2	DAKIEFDICY TSVLKR	1021.5441	2	2.62	-8.96	15						0	15
P07146	Anionic trypsin-2	VCNYVDWI QNTIADN	926.9358	2	3.87	5.84	6		930.9535	2	2.59	0.99	9	15
P97313	DNA-dependent protein kinase catalytic subunit	CTVLVRIME FTTLLIASP EDCK	920.8260	3	3.10	7.95	15						0	15

Q3UHN9	Isoform 3 of Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1	MPALACLRR LCR	0	782.4400	2	2.26	-6.34	15	15				
Q8VEK0	Cell cycle control protein 50A	EIEIDYTGTE PSSPCNK	998.4702	2	2.59	5.77	9	1006.5069	2	2.71	-1.92	6	15
Q91X79	Chymotrypsin-like elastase family member 1	EGTILANNS PCYITGWGR	1018.9980	2	4.11	1.36	7	1023.0201	2	4.32	1.27	8	15
D3Z2V0	Protein PML (Fragment)	LLPCLHTLC SGCLEAPGL QCPICK	1361.6801	2	2.57	9.91	14					0	14
E9Q1R2	4-hydroxy-2-oxoglutarate aldolase, mitochondrial	LCLTGQWE AAQELQHR	656.6609	3	3.52	-3.85	6	659.3466	3	3.10	2.66	8	14
Q9WVA2	Mitochondrial import inner membrane translocase subunit Tim8 A	AEACFVNCV ER	691.8160	2	2.87	4.05	2	695.8395	2	2.35	5.83	12	14
D21614	Vitamin D-	SCESDAPFP VHPGTPECC TKEGLER	729.8297	4	3.82	0.19	4	733.8517	4	5.01	-0.02	8	13

P21014	binding protein	TSELSVKSC ESDAPFPVH PGTPECCTK EGLER						0	928.9716	4	3.94	0.53	1	13
P52196	Thiosulfate sulfurtransferase	VDSLQPLIA TCR	700.8835	2	2.61	2.15	6						0	13
		KVDLSQPLI ATCR	778.9490	2	2.44	4.96	2	786.9884	2	2.26	-1.37	3		
		AIFQDKKVD LSQPLIATCR	763.0988	3	3.46	-1.16	2					0		
Q99K67	Alpha- aminoadipic semialdehyde synthase, mitochondrial	QLLCDLVGI SR	651.3669	2	2.54	1.42	2	655.3925	2	2.37	6.67	11	13	
D6RHN4	Peroxisomal trans-2-enoyl- CoA reductase	ASLPPSSSAE VSAIQCNI	1008.0129	2	2.88	-2.10	11	1012.0363	2	2.51	-0.91	1	12	
E9Q1S3	Protein transport protein Sec23A	AVLNPLCQV DYR	738.3881	2	2.70	0.95	1	742.4103	2	2.29	0.91	11	12	
G3UX44	Estradiol 17- beta- dehydrogenase 8 (Fragment)	LAAEGAAV AACDLGGA AAQDTR	1122.5503	2	5.13	0.30	6	1126.5743	2	3.70	1.96	6	12	
P20060	Beta- hexosaminidase subunit beta	GIAAQPLYT GYCNYENKI	1066.0287	2	2.70	-1.32	8	1074.0748	2	2.92	0.34	4	12	

P58710	L-gulonolactone oxidase	GDDILLSPCFQR	724.8641	2	2.59	0.40	4	728.8849	2	2.48	-1.40	5	12
		FTRGDDILLSPCFQR					0	930.9948	2	2.41	0.18	2	
		TYGCSPEMY YQPTSVGEV R	1126.5121	2	2.47	7.55	1					0	
		QALAWPDR VALVCTGSE	1044.1970	3	5.06	5.68	1	1046.8717	3	3.87	-0.81	8	
		GSSITNSQLD AR											
		QGFCIPVEP GKPGLLLTK	680.0648	3	3.23	1.32	2	688.1080	3	3.72	-0.38	1	
Q8K480-2	Isoform 2 of Membrane frizzled-related protein	FCQSGGYRD LQWMCDLW K	1183.0464	2	2.43	12.33	12					0	12
Q99KI0	Aconitate hydratase, mitochondrial	VGLIGSCTN SSYEDMGR	937.4279	2	2.70	3.52	11	941.4506	2	2.96	4.06	1	12
Q9D0F9	Phosphoglucosyltransferase-1	TIEEYAICPD LK					0	762.4382	2	2.95	5.91	12	12
D6RHA7	Acetyl-coenzyme A synthetase, cytoplasmic	GATTNICYN VLDR	762.8742	2	3.02	-4.21	7	766.8987	2	2.51	-1.20	4	11
		DIASGLIGPL ILCK	763.4579	2	2.96	4.14	7	771.5024	2	2.79	4.26	3	

G3X9T8	Ceruloplasmin	ADDKVLPG QQYVYVLH ANEPSPGEG DSNCVTR					0	897.7054	4	3.59	-0.38	1	11
Q00519	Xanthine dehydrogenase /oxidase	NKPEPTVEEI ENAFQGNLC R	801.0706	3	3.36	6.40	5	806.4282	3	3.45	-0.15	6	11
Q32P14	Predicted gene, OTTMUSG0000010173	CSECDKCFT QSNLSIHQ R					0	1178.5887	2	2.60	12.07	10	11
		CSECDKCFT KSNLSIHQ R	1178.5884	2	2.50	-3.68	1					0	
Q80Y14	Glutaredoxin-related protein 5, mitochondrial	GTPEQPQCG FSNAVQIL R	1065.0450	2	2.45	0.90	6	1069.0634	2	2.89	-2.73	5	11
Q91X83	S-adenosylmethionine synthase isoform type-1	TACYGHFGR SEFPWEVPK	556.7727	4	3.78	2.02	3	560.7934	4	3.66	-0.67	7	11
		ICDQISDAVL DAHLK					0	590.6714	3	3.21	-2.55	1	
I7HJR3	Beta-2-glycoprotein 1 (Fragment)	VCPFAGILE NGIVR	524.9602	3	3.23	5.92	2	527.6396	3	3.13	1.96	8	10
O09159	Lysosomal alpha-mannosidase	QLAAGWGP CEVLVSNAL AR	1020.5410	2	3.75	2.46	2	1024.5651	2	4.28	4.33	8	10
Q6R653-4	Isoform 4 of UNC5C-like protein	LASHLGLCG MKIRFLSCQ R	1151.5884	2	2.53	-12.48	10					0	10

Q80XN0	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	METYCNSGS TDTSSVINA VTHALTAAT PYTR	1116.5305	3	3.39	7.48	5	1119.2125	3	4.62	7.96	5	10
Q8VCN5	Cystathionine gamma-lyase	LADIGACAQ IVHK					0	489.9704	3	3.27	2.74	10	10
Q9JLJ2	4-trimethylamino butyraldehyde dehydrogenase	EQGATVLCG GEVYVPEDP KLK VIATFACSG EKEVNLAVE NAK					0	799.7949	3	3.49	-0.09	9	10
						0	1179.6873	2	2.52	-1.42	1		
D3Z2B2	Kininogen-1 (Fragment)	ENEFFIVTQT CK	786.4014	2	2.49	11.52	4	794.4359	2	2.28	-1.04	5	9
P28843	Dipeptidyl peptidase 4	YYQLGCWG PGLPLYTLH R	741.3806	3	3.25	2.56	7	744.0620	3	3.15	2.47	2	9
P51881	ADP/ATP translocase 2	EFKGLGDCL VK	450.5903	3	3.22	4.78	9					0	9
P60335	Poly(rC)-binding protein 1	LVVPATQCG SLIGK AITIAGVPQS VTECVK	864.9803	2	2.89	-1.86	2	757.9838	2	2.38	3.48	7	9
A2A817	Protein DJ-1 (Fragment)	VTVAGLAG KDPVQCSR	857.4695	2	2.82	0.06	7	865.5103	2	2.44	-4.10	1	8

A2ATU0	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial	LEELCPFPLD ALQQEMSK	1100.5657	2	2.29	8.28	8				0	8	
D3Z106	Acyl-coenzyme A synthetase ACSM1, mitochondrial (Fragment)	IANVTEQIC GLOOCDIY AIVTTASLV PEVESVASE CPDLKTK AIVTTASLV PEVESVASE CPDLK	874.4695	3	3.12	2.72	2	877.1467	3	3.32	-2.23	2	8
							0	918.2070	3	3.62	1.61	3	
							0	829.7996	3	3.40	0.13	1	
E9Q7D8	Poly(rC)-binding protein 3	LVVPASQCG SLIGK	742.9293	2	2.57	0.44	1	750.9775	2	2.42	5.57	7	8
P35979	60S ribosomal protein L12	EILGTAQSV GCNVDGR	852.4222	2	2.94	-0.58	8					0	8
J8BGA8	isoform 2 of Acyl-coenzyme A synthetase ACSM5, mitochondrial	AANVLEGV GGLQPCDP	842.4276	2	3.15	-0.33	6					0	8
		SIVTSDALAP QVDAISADC PSLQTK	881.7885	3	3.38	-1.47	1	887.1505	3	3.26	-2.49	1	
Q91Z53	Glyoxylate reductase/hydroxypyruvate reductase	NCVILPHIGS ATYK	814.9481	2	2.45	3.63	3	822.9883	2	2.38	-1.45	5	8
	Elongation	WFLTCINQP QFR	819.4142	2	3.05	-2.85	5	823.4404	2	2.47	2.10	2	

Q9D8N0	factor 1-gamma	QAFPNTNR WFLTCINQP QFR					0	858.7838	3	3.37	5.91	1	8
D3Z2D7	Phenazine biosynthesis-like domain-containing protein 1 (Fragment)	GNPAAVCLLER	614.3309	2	2.84	2.53	5	618.3505	2	2.30	-1.68	2	7
D6RFQ4	Protein Rdh16	VLAACLTEK GAEELR					0	866.5150	2	2.96	-1.22	7	7
O35701	Matrilin-3	CALSTHGCE QICVNDR					0					7	7
P51660	Peroxisomal multifunctional enzyme type 2	ICDFSNASKP QTIQUESTGGI VEVLHKVD SEGISPNR	800.2157	5	4.25	3.93	6	1006.0526	4	3.51	5.36	1	7
Q60932-2	Isoform Mt-VDAC1 of Voltage-dependent anion-selective channel protein 1	YQVDPDACF SAK	728.8418	2	2.44	-0.98	5	736.8859	2	2.41	-1.38	2	7
Q6PB66	Leucine-rich PPR motif-containing protein, mitochondrial	VFESTCSSG SPGSNQALL LLR	1126.0695	2	3.69	-3.18	5	1130.0950	2	3.77	-0.23	2	7

Q8BMS1	Trifunctional enzyme subunit alpha, mitochondrial	EVESVTPEH CIFASNTSAL PINQIAAVSK	1056.8810	3	3.97	1.17	3					0	7
		KYESAYGTQ FTPCQLLLD HANNSSK	986.1587	3	3.31	3.55	1	994.1998	3	3.48	0.21	2	
		ALMGLYNG QVLCK					0	769.9567	2	2.32	3.40	1	
Q8K441	ATP-binding cassette sub-family A member 6	SAPLFFLNPT SCFR	842.9312	2	2.97	2.08	2	846.9528	2	2.98	1.39	5	7
Q8R1A8	Ornithine carbamoyltransferase, mitochondrial	VAASDWTF LHCLPR	567.6240	3	3.29	-0.16	5	570.3074	3	3.13	3.16	2	7
Q8R3V2	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	SCENLAPFS TALQLLK	924.5081	2	2.75	8.23	7					0	7
Q9JK53	Prolargin	ECYCPPDFP SALYCDSR	1082.9408	2	2.94	-1.40	4	1086.9644	2	2.91	-0.13	3	7
Q8A087WR	Cathepsin H, isoform CRA_a (Fragment)	MLSLAEQQL VDCAQAFN NHGCK	864.0776	3	3.59	-1.09	1	869.4447	3	3.09	3.69	5	6

A2AAJ9-1	Isoform 2 of Obscurin	FIEDLRQEA TEGATAILR CELSK	903.4571	3	3.59	-13.21	6				0	6		
B7ZMZ7	Dip2c protein	DAGSQQIGF LLGSCGVTV ALTSdachK	912.1273	3	3.31	4.84	6				0	6		
F6Q404	Protein disulfide- isomerase A3 (Fragment)	GIVPLAKVD CTANTNTCN KYGVSgyPT LK VDCTANTN TCNKYGVS GYPTLK	849.7485	3	3.31	3.61	3	0	822.2276	4	3.59	4.58	3	6
Q3UEG6	Alanine-- glyoxylate aminotransfera se 2, mitochondrial	GAYHGCSPY TLGLTNVGI YK GGVCIADeV QTGFGR	743.0452	3	3.40	-0.24	1		748.4128	3	3.23	6.05	4	6
Q62452	UDP- glucuronosyltr ansferase 1-9	GFFELTFSH CR GVFCDYLEE GAQCPSLPS YVPR	476.8966	3	3.33	1.57	3		479.5775	3	3.02	0.41	1	6
Q64374	Regucalcin	IICRWDTVS NQVQR	901.9705	2	3.00	0.38	4		905.9911	2	2.31	-1.34	2	6
Q71RI9-2	Isoform 2 of Kynurenine-- oxoglutarate transaminase 3	LTAIPVSAFC DSK	732.8945	2	2.48	3.44	2		740.9366	2	2.35	0.27	4	6
	Sodium/potassi um- transporting	NIAFFSTNC VEGTAR	857.9087	2	2.72	-6.82	1		861.9357	2	2.68	-1.16	4	

Q8VDN2	transporting ATPase subunit alpha- 1	IISANGCKV DNSSLTGES EPQTR				0	845.7776	3	3.33	-4.44	1	6	
Q9CZN7	Serine hydroxymethyl transferase	AALGALGSC LNNKYSEGY PGKR	621.3234	4	4.01	-1.65					0	6	
		GLELIASENF CSR	762.3771	2	2.43	-3.58	1	766.4018	2	2.44	-0.25		2
Q9JHW2	Omega- amidase NIT2	GCQLLVYPG AFNLTTGPA HWELLQR	957.1742	3	3.74	9.11	3	959.8506	3	3.72	3.80	2	6
		TLSPGDSFST FDTPYCK	989.9624	2	2.87	3.63	1					0	
B1AXW3	Alcohol dehydrogenase [NADP(+)] (Fragment)	HIDCASVYG NETEIGEAL KESVGSGK	945.4722	3	3.39	5.00	4	953.5144	3	4.60	2.72	1	5
B2RS76	Carboxypeptid- ase B1 (Tissue)	EWISPAFCQ WFVR	877.4316	2	2.63	2.29	2	881.4558	2	2.98	4.53	3	5
P10605	Cathepsin B	EQWSNCPTI GQIR					0	812.9162	2	2.31	-2.62	5	5
P52480	Pyruvate kinase PKM	NTGIICTIGP ASR	694.3737	2	2.65	2.80	5					0	5
Q792Z1	MCG140784	VCNYVDWI QNTIAAN	904.9345	2	2.78	-1.06	1	908.9592	2	2.60	1.67	4	5
Q7TPD2-3	Isoform 2 of Protein FAM185A	TCGSSGAQR QGSAPDDSG AGLAR					0	1093.0385	2	2.45	11.51	5	5
Q9D0R2	Threonine-- tRNA ligase, cytoplasmic	TTPYQIACGI SQGLADNTV VAK	788.4124	3	3.22	-2.08	1	1190.1716	2	2.32	8.25	4	5

B1AR28	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial	VASGQALA AFCLTEPSS GSDVASIR	1261.6428	2	2.66	9.00	2	1265.6528	2	2.83	-0.65	2	4
F6Z4J2	Probable phospholipid-transporting ATPase IH (Fragment)	ELFLEICRNC SAVLCCR	1154.0488	2	2.42	6.51	4					0	4
K9J7B2	Protein Ugt1a6b	GFPCSLEHM LGQSPSPVS YVPR	825.0759	3	3.39	5.13	2	827.7582	3	3.18	6.15	2	4
O35308	Monocarboxylate transporter 3	FGCRPVMLA GGLLASAG MILASFASR					0					4	4
P11352	Glutathione peroxidase 1	GLVVLGFPC NQFGHQEN GKNEEILNS LK NALPTPSDD PTALMTDPK YIIWSPVCR	807.1776	4	3.71	4.88	2	1083.9423	3	3.77	2.00	1	4
P31809-3	isoform 3 of Carcinoembryonic antigen-related cell adhesion	EDAGETQCE TENDVCSVD IDPIKREDAG EYQCEISNP VSVR	990.9454	2	2.68	-6.68	2					0	4
P33267	Cytochrome P450 2F2	DFIDCFLTK	607.8098	2	2.47	-0.22	3	615.8564	2	2.31	3.35	1	4
	Electron transfer	ASCDAQTI GICLV					0	728.4115	2	2.51	4.83	2	

Q6PF96	flavoprotein-ubiquinone oxidoreductase	FCPAGVYEF VPLEQGDGFR	0	1112.5541	2	2.48	3.73	2	4				
Q8BH00	Aldehyde dehydrogenase family 8 member A1	ILCGEGVDQ LSLPLR	0	853.4868	2	2.63	-2.16	2	4				
		SSFANQGEI CLCTSR	0	883.4203	2	2.42	-3.21	2					
Q8CIM7	Cytochrome P450 2D26	SLEQWVTEE AGHLCDAFTK	759.7039	3	4.30	5.05	2	765.0663	3	4.19	4.38	2	4
Q91X77-1	Isoform 2 of Cytochrome P450 2C50	DICQSFTNLSK	684.8466	2	2.67	2.29	4					0	4
Q9JHI5	Isovaleryl-CoA dehydrogenase, mitochondrial	ASGAVGLSY GAHSNLCV NQIVR	767.7291	3	3.29	-1.78	1	770.4109	3	3.04	-1.37	3	4
Q9QWK5	Baculoviral IAP repeat-containing protein 1a	CDFLSNCDS LMAVLASCKK	1151.5886	2	2.34	7.57	4					0	4
A087WR	Protein Gm4450	ACQGMSAVI HTAAAIIDPL GAASR	766.0599	3	3.47	5.00	3					0	3
A2A7A8	GDH/6PGL endoplasmic bifunctional protein (Fragment)	LMDKVLESL SCPCK	802.4457	2	2.51	2.64	3					0	3
A8DUK4	Beta-globin	GTFASLSEL HCDKLHVD PENFR					0	661.8492	4	3.81	-0.45	2	3

		GTFASLSEL HCDK				0		512.9476	3	3.34	-1.30	1	
D3YZE7	Erythroid differentiation- related factor 1	SIHQIRPSCA FPVCHDTEE RCR				0		1401.6865	2	2.66	8.66	3	3
D3Z4F9	Protein C-ets-2 (Fragment)	DNLLDSMCP PSATPAALG SELQMLPK	915.1150	3	3.17	-1.76	3					0	3
F6QYF8	Puromycin- sensitive aminopeptidas e (Fragment)	TIQQCCENIL LNAAWLK	1086.0400	2	2.86	-12.00	3					0	3
F8WIE5	E3 ubiquitin- protein ligase HECTD1	LCGKMEPQ DSSLEICVES LSSLLK	1369.7230	2	2.58	-7.76	3					0	3
G3UZ26	Serine hydroxymethyl transferase (Fragment)	LIAGTSCYS R					0	638.8583	2	2.45	-1.37	3	3
G3X9Y6	Aldo-keto reductase family 1, member C19	YKPVCNQV ECHLYLNQR	759.7161	3	3.48	3.10	1	787.7517	3	3.21	-0.48	2	3
O54689	C-C chemokine receptor type 6	GTYAVNFN CGMLLLACI SMDR					0					3	3
P11589	Major urinary protein 2	FAKLCEEHG ILRENIIDLS NANR	685.8536	4	4.11	-10.06	3					0	3

P20918	Plasminogen	NYCRNPDG DVNGPWCY TTNPR QLAAGGVS DCLAK VVGGCVAN PHSWPWQIS LR	673.3612	2	2.67	0.48	1	864.7210	3	3.09	-2.01	1	0	3
P46664	Adenylosuccinate synthetase isozyme 2	VVDLLAQD ADIVCR					0	845.9670	2	2.29	2.39	3		3
Q32Q92-2	Isoform 2 of Acyl-coenzyme A thioesterase 6	SCWDEPLSI AVR	730.8625	2	2.46	-1.69	3					0	3	
Q3UFT3-3	Isoform 2 of GRB2-associated and regulator of MAPK protein	MPCLICMNH RTNESISLPF QCK	1400.1603	2	2.31	-6.03	3					0	3	
Q3UTF4	Protein Zfp114	CEVCGKGFT KLSHLQAHE R	1162.5828	2	2.43	-2.44	3					0	3	
Q63886	UDP-glucuronosyltransferase 1-1	SDFVKDYPR PIMPNMVFI GGINCLQK	781.6642	4	3.72	5.06	1	787.6989	4	3.60	6.71	2	3	
Q64459	Cytochrome P450 3A11	VCKKDVEL NGVYIPK	625.3667	3	3.27	1.87	2	636.0917	3	3.10	0.50	1	3	
Q8QZY2-	Isoform 2 of Glycerate kinase	GPVCLLAGG EPTVQLQGS GK	1012.5475	2	2.60	1.53	2	1020.5890	2	2.56	-1.29	1	3	

Q91X34	Bile acid-CoA:amino acid N-acyltransferase	NWTLLSYPG AGHLIEPPY TPLCQASR	0	993.1910	3	3.69	5.46	3	3				
Q9CZU4	GTPase Era, mitochondrial	MAAPRRYC AGLVR	774.9116	2	2.41	-5.88	3	0	3				
Q9DB29	Isoamyl acetate-hydrolyzing esterase 1 homolog	LNSVVGGEYA NACLQVAR	0	950.5117	2	3.58	1.12	3	3				
Q9DBJ1	Phosphoglycerate mutase 1	YADLTEDQL PSCESLKDTI AR	827.7442	3	3.60	0.08	1	833.1047	3	3.17	-2.77	2	3
Q9QZE5	Coatomer subunit gamma 1	ELAPAVSVL QLFCSSPK	0	959.5724	2	3.25	4.32	3	3				
S4R1W1	Glyceraldehyde-3-phosphate dehydrogenase	IVSNASCTT NCLSPLAK	980.4973	2	2.97	-0.33	3	0	3				
A2ASA8	Inositol 1,4,5-trisphosphate receptor-interacting protein-like 1	CTSSIKAAL CTSSHLDVC KTVQWFR	756.3792	4	3.72	0.06	2	0	2				
Q9ASQ1	Isoform 3 of	FDGPCDPCQ GSMSDLNHI CRVNPTR	0	1028.8116	3	3.37	5.00	1	2				

4275Q1	Agrin	MPPDVCRG MLCGFGAV CEPSVEDPG R	1432.6538	2	2.42	12.05	1				0		
A2CEK9	Major urinary protein 1 (Fragment)	FAQLCEKHG ILRENIIDLS NANR	692.6220	4	3.85	-0.40	1	696.6441	4	4.00	-0.53	1	2
B0R0C0	Nociceptin receptor	KFCCASALH REMQVSDR					0	1152.0836	2	2.45	-3.00	2	2
B1AXJ3	Low-density lipoprotein receptor- related protein 8	SGECVDGG KVCDDQR	812.3495	2	2.57	-11.33	2					0	2
D3YUG9	Quinone oxidoreductase (Fragment)	AGESVLVHG ASGGVGLAT CQIAR	746.7280	3	4.30	1.56	2					0	2
D3YVN5	Signal peptide, CUB and EGF- like domain- containing protein 2	LLMETCAV NNGGCDR	869.3872	2	2.66	-2.67	2					0	2
D3YWM4	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)	MADEAVCV GPAPTSK	794.8898	2	2.46	0.85	1	802.9333	2	2.79	-0.22	1	2
D3Z2J5	Nuclear receptor corepressor 2 (Fragment)	GHVLSYEGG MSVSQCSK	961.4374	2	2.50	-5.58	2					0	2

D3Z3C3	Heparanase	SYWKSQVN HDICRSEPV AAVLR	1369.7189	2	2.36	2.90	2		0	2			
E9Q5F4	Actin, cytoplasmic 1 (Fragment)	LCYVALDFE QEMATAASS SSLEK					0	1311.6665	2	2.60	0.17	2	2
F6VCW7	Nuclear factor of-activated T- cells 5 (Fragment)	SPMLCGQYP VKSEGK	890.9584	2	2.64	6.91	2					0	2
F8VQ40	Laminin subunit alpha- 1	ENAVGPQCS KCQAGTFAL R					0	1151.5929	2	2.39	-4.72	2	2
H3BIX5	Prostaglandin E synthase 2 (Fragment)	IFVEASLNG GCKSQDK	918.9684	2	2.45	-12.52	2					0	2
O35633-2	Isoform 2 of Vesicular inhibitory amino acid transporter	VRDSYVAIA NACCAPR					0	929.9742	2	2.28	-1.74	2	2
P14211	Calreticulin	DMHGDSEY NIMFGPDIC GPGTK	833.0369	3	3.41	5.08	2					0	2
P35700	Peroxiredoxin- 1	SVDEIIRLVQ AFQFTDKHG EVCAPAGWK PGSDTIKPD VNK	754.5729	6	4.01	4.59	2					0	2
P48758	Carbonyl reductase [NADPH] 1	ILLNACCPG WVR	777.9033	2	2.50	4.72	2					0	2

P61922-2	Isoform 2 of 4-aminobutyrate aminotransferase, mitochondrial	GTFCSFDTP DEAIR	822.3744	2	2.82	2.69	2			0	2		
P99024	Tubulin beta-5 chain	MREIVHIQA GQCGNQIGA K					0	728.0782	3	3.08	1.97	2	2
Q08857	Platelet glycoprotein 4	FVLPANAF SPLQNP DNHCFCTEK					0	950.4816	3	3.18	-0.82	2	2
Q3UEJ6	Alpha-1,4 glucan phosphorylase	RWLLLCNPG LADLIAEK	680.0579	3	3.44	3.60	1	685.4243	3	3.21	8.65	1	2
Q3V3R4	Integrin alpha-1	GGFLACGPL YAYR					0	740.8969	2	2.42	4.48	2	2
Q60854	Serpin B6	AFVEVNEEG TEAAAATA GMMTVRCM R					0	1399.1707	2	2.95	6.06	2	2
Q7TR99	Olfactory receptor	NKAISFVGC ATQMWWFG LFVATECFL LAAMAYDR	988.4808	4	3.65	-3.29	1					0	2
Q8BGC4	Zinc-binding alcohol dehydrogenase domain-containing protein 2	DCPVPLPGD GDLLVR					0	829.9530	2	2.30	1.38	2	2

Q8BI84-2	Isoform 2 of Melanoma inhibitory protein 3	ALEDFTGPD CR					0	658.8204	2	2.46	0.21	2	2
Q8BIJ6	Isoleucine--tRNA ligase, mitochondrial	SCQTALAEI LDVLVR	858.4799	2	3.68	9.51	2					0	2
Q8BMS4	Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial	ILDVGC GGG LLTEPLGR					0	882.0007	2	2.75	1.58	2	2
Q8CJ69	BMP-binding endothelial regulator protein	DGEMWSSV NCSICACVK GK	1065.4801	2	2.51	1.95	1					0	2
		NPAEHQGA CCPTCPGCV FEGVQYREG EEFQPEGNK	998.6722	4	3.87	-11.85	1					0	
Q8VCT4	Carboxylesterase 1D	TTTSAVMV HCLR					0	706.3853	2	2.61	3.94	2	2
Q9CPP6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	TTGLVGLAV CDTPHER	585.3029	3	3.24	2.27	2					0	2

Q9D2X5	Isoform 2 of MAU2 chromatid cohesion factor homolog	INPDHSFPVS SHCLRAAAF YVR	0	1262.1459	2	2.33	-10.42	2	2				
Q9DBH5	Vesicular integral-membrane protein VIP36	WSELAGCT ADFR	720.8320	2	2.41	-0.63	1	724.8543	2	2.54	-0.50	1	2
Q9DD20	Methyltransferase-like protein 7B	VTCVDPNPN FEK	738.3653	2	2.55	2.28	1	746.4094	2	2.37	1.85	1	2
Q9Z1T5	Deformed epidermal autoregulatory factor 1 homolog	KEQSCVNCG REAMSECTG CHK	1241.0153	2	2.42	-8.72	2					0	2
S4R2M7	Phosphoglycerate kinase	AAVPSIKFC LDNGAK	837.9626	2	2.63	-4.07	1	850.0325	2	2.32	-0.16	1	2
A087WQ	Influenza virus NS1A-binding protein homolog (Fragment)	WTSCAPLNI RRHQSAVCE LGGYLYIG GAESWNCL NTVER	0	1144.0677	4	3.81	-5.00	1	1				
A087WR	Activating transcription factor 7-interacting protein 1 (Fragment)	ETPCMPNVA VKNKQEDL NSEALSPSIT CDLSSR	940.2158	4	3.48	8.75	1					0	1

A1L317	Keratin, type I cytoskeletal 24	MFCSAQKGS CSSRVSSSG AVGSR	1182.5542	2	2.58	6.64	1		0	1			
A2A592	Protein Gm11939	GYPAPNLKG ISVSTCVEPC ECDPSCC					0	1401.1583	2	2.43	6.97	1	1
A2A6Q5	Cell division cycle protein 27 homolog	NSPEAWCA AGNCFSLQR	969.9458	2	2.57	13.26	1					0	1
A2A7U2	Protein Zmym6	MFMFCSKA CCDEYK	1014.9329	2	2.92	9.29	1					0	1
A2A929	PR domain zinc finger protein 16 (Fragment)	VACSCDDQ NLAMCQINE QIYYK	963.0960	3	3.37	11.37	1					0	1
A2AD25	MCG49690	SYCAEIAHN VSSK	761.3730	2	2.83	1.43	1					0	1
A2AGR4	Oxysterols receptor LXR-alpha	GARYVCHS GGHCPMDT YMRR	1191.5360	2	2.40	7.37	1					0	1
A2AK85	Protein 6330409D20Rik	KPGSQQTPS ALSYLAYCD QPPAYLHIV PSGLQLCSSP GR					0	1096.8374	4	3.88	13.63	1	1
A2ANX6	Very long-chain acyl-CoA synthetase	GEVGLLVC K					0	523.8460	2	2.29	-0.56	1	1
A2AP83	Protein Fnd3c2	VHPLNINNCC EIK					0	790.9211	2	2.70	-9.38	1	1

A2AQT8	Methylmalonic aciduria and homocystinuria type D homolog, mitochondrial (Fragment)	ARLVSYLPG FCSLVK	883.5172	2	2.72	13.45	1	0	1				
A2ARR7	Protein Gm14412	HHDCNQCG KAFARSDDL QK	1185.5984	2	2.39	10.21	1	0	1				
A2ASJ1	Protein Pramef17	RPKSVCFGT YSCYDCDTH CIYGNQTF CECLE	1025.1772	4	3.91	-3.42	1	0	1				
A8Y5J3	Integrator complex subunit 11	AQELCILLET FWERMNLK					0	1183.6647	2	2.47	1.46	1	1
B1AZS9	Peroxiredoxin-4 (Fragment)	SINTEVVAC SVDSQFTHL AWINTPR					0	961.1644	3	3.37	3.19	1	1
B2KF10	BTB/POZ domain-containing protein KCTD20 (Fragment)	CQDLSALLH ELSNDGAHK	1018.4943	2	2.59	-2.59	1	0	1				
B2RR24	Protein Zfp236	EGLSHQCLD CDRAFSSAA VLMHHSK	1399.6753	2	2.51	9.32	1	0	1				

D3YTN9	Exosome complex component RRP45 (Fragment)	CLRNSKCID TESLCVVAG EK	0	1138.6334	2	2.33	-8.07	1	1
D3YTX1	Nephronectin	GQVRCQCPS PGLQLAPDG R	1034.0176	2	2.42	2.68		0	1
D3YXU7	Unconventional myosin-X (Fragment)	CHLGELPPHI FAIANECYR	0					1	1
D3YZY0	Actin, gamma-enteric smooth muscle (Fragment)	LCYVALDFE NEMATAASS SSLEK	1304.6191	2	2.44	5.83		0	1
D3Z0E6	3'(2'),5'-biphosphate nucleotidase 1	ASAYVFASP GCK	657.3322	2	2.56	0.87		0	1
D3Z1M9	Protein BTG3 (Fragment)	ACENSCILY SDLGLPK	0	899.4819	2	2.35	-7.48	1	1
D3Z2G7	Histone deacetylase 11 (Fragment)	GWAINVGPT GTSICCEIFV VRMSLPNIYI FPMTGSSLP PRE	1187.6030	4	3.63	9.89		0	1
D3Z614	Zinc finger protein 30	TPNGEKPYE CGECGK	933.4530	2	2.32	0.22		0	1
D6RCG1	Trifunctional purine biosynthetic protein adenosine-3	QVLVAPGN AGTACAGK	0	793.4771	2	2.34	10.33	1	1

D6RE57	Zinc finger and BTB domain-containing protein 49	IQGLLCDMLVVR	782.4064	2	2.47	-0.03	1	0	1				
E0CY73	Protein 1700112E06Rik	GAFMKVVKPKHHVCCMLPCSHR	908.1270	3	3.13	-3.06	1	0	1				
E0CY90	Proteoglycan 4 (Fragment)	CFESFARGRECDQCK	1214.0095	2	2.26	4.24	1	0	1				
E9PW69	Proteasome subunit alpha type (Fragment)	ATCIGNNSAAVSMLK	832.4299	2	2.52	1.08	1	0	1				
E9PY32	Trypsin	MNLPSCSQVPGLCAPQVGPRLALTSNWARTTPHCVQMLK	769.5556	6	4.16	4.69	1	0	1				
E9PZ00	Prosaposin	GCSFLPDYQK					0	692.3843	2	2.35	4.40	1	1
E9Q1H7	tRNA (guanine-N(7)-methyltransferase non-catalytic subunit WDR4	RTCPEAAGGPMASAGLALCAQTLVVR					0	913.8203	3	3.04	12.00	1	1

E9Q202	Low-density lipoprotein receptor-related protein 1B	SHACEVDA YGMPGGCS HICLLSSSYK TR	1111.1619	3	3.65	-9.68	1	0	1				
E9Q484	5-oxoprolinase (Fragment)	GCTGDLLEI QQPVDLAAL R	1049.0564	2	4.59	2.17	1	0	1				
E9Q4G4	Apolipoprotein B-100 (Fragment)	NLQQCDGF QPISTSVSPL ALIK	1236.6724	2	4.29	8.36	1	0	1				
E9QP09	Cullin-9	CSEEGKVSS EEEKTEHLL MWLSAPEV YANCPMLL R	1046.2615	4	3.80	8.05	1	0	1				
E9QQ26	Ectonucleotide pyrophosphatase/phosphodiesterase family member 1	LSRFVCSCA DDCK					0	816.9079	2	2.41	-1.98	1	1
F2Z494	Myosin-9	VEDMAELT CLNEASVLH NLKER	1312.1527	2	2.34	-10.18	1	0	1				
F6S7U1	RAB6A-GEF complex partner protein 1 (Fragment)	HLLEALWLS CGGAGMK	907.9679	2	2.57	-0.42	1	0	1				

F6XPZ0	Lipoxygenase homology domain- containing protein 1 (Fragment)	KIELGHDGA SPESCWLVE ELCLAVPTQ GTKYTLR	0	963.7697	4	3.73	-12.34	1	1
F6XYI9	TATA-box- binding protein (Fragment)	TTALIFSSGK MVCTGAKS EEQSR	854.1072	3	3.29	12.69	1	0	1
F6Y9P3	Beta- adrenergic receptor kinase 1 (Fragment)	AGCERCSW GLSSILCIRS VMQK	0	1369.7246	2	2.68	8.58	1	1
F6YXH5	Submandibular gland protein C (Fragment)	LMKFKSNDK CCEIGHCEP R	0	793.4059	3	3.05	-2.57	1	1
F7BP94	Protein asunder homolog (Fragment)	XAGVIVKES LTEEDVLNC QK	1185.1259	2	2.49	-7.98	1	0	1
F7CR78	Titin (Fragment)	NESGIERY AFLLVQEPA QIEK	937.8329	3	3.04	2.24	1	0	1
F8VQ15	A disintegrin and metalloprotein ase with thrombospondi n motifs 8	DSDEPICKT KNGSLLWA DGTPCGPGH LCLDGSCVL K	0	1324.6774	3	3.31	10.27	1	1

F8VQE6	Protein Tatdn2	DSSCRSTNS EFATEAEGQ SDAMEEPNK	992.7486	3	3.20	-5.33	1	0	1				
G3UWE8	Hepsin, isoform CRA_c	LLDVISVCD CPR	737.8743	2	2.59	1.31	1	0	1				
G3UXL2	Protein Prps113	VTAVIPCFP YAR	711.3832	2	2.47	-1.28	1	0	1				
G3UYB0	Protein Gm20403	MEDASDSSR GVAPLINNV ALPGSSPSLP VSVTGCKSH PVANK	1097.3384	4	3.54	7.03	1	0	1				
G3UYV1	WD repeat and FYVE domain- containing protein 3 (Fragment)	SQGLSLDAV YHCLNR					0	918.9708	2	2.33	-6.11	1	1
G3UZC7	Protein Gm9268	FSEKNILLG GCNQLINYN CGQK	1361.6819	2	2.49	-4.67	1	0	1				
G5E8G6	Myosin Vb, isoform CRA_c	DEKEYLNN QILCQSK					0	1029.5880	2	2.35	6.98	1	1
G5E8J4	Protein tyrosine phosphatase, non-receptor type 21, isoform CRA_a	SHNPPLLVH CSAGVGRTG VVILSEIMV ACLEHNEVL DIPR					0					1	1

H3BL56	Rho-related GTP-binding protein RhoC	HFCPNVPIL VGNKK	607.3594	3	3.14	1.09	1		0	1			
I7HJS4	Protein Zfp683	SPLLACPEP DLCLCALQK TPLGR	899.1251	3	3.43	-13.91	1		0	1			
J3QNW0	DNA (cytosine-5)-methyltransferase 1	LPQKGDVE MLCGGPPCQ GFSGMNR	924.4327	3	3.40	1.16	1		0	1			
L7N201	Protein Zfp934	CNQCDKAFS QYYSNLQTH R					0	1218.1055	2	2.32	9.48	1	1
M0QW74	MCG9626, isoform CRA_c	ACASDSQSSI SKVSTRNSC R					0	1108.5730	2	2.25	2.44	1	1
O08848	60 kDa SS-A/Ro ribonucleoprotein	QEPLLFALA VCSQCADIN TKQAAFKA VPEVCR	944.4944	4	3.49	-10.56	1					0	1
O89023	Tripeptidyl-peptidase 1	GLTLLFASG DTGAGCWS VSGR					0	1074.5500	2	3.90	-0.38	1	1
P00683	Ribonuclease pancreatic	HIIVACEGNP YVPVHFDAT V					0	1137.5898	2	3.19	-2.00	1	1
P01867-2	Isoform 2 of Ig gamma-2B chain C region	LEPSGPISTI NPCPPCK	961.9877	2	2.78	-1.80	1					0	1

P05622	Platelet-derived growth factor receptor beta	IGSILHIPTAE LSDSGTYTC NVSVSVND HGDEK	1184.5668	3	3.09	-13.94	1		0	1			
P06537-3	Isoform 1-B of Glucocorticoid receptor	LLDSMHDV VENLLSYCF QTFLDK	941.7961	3	3.28	-13.71	1		0	1			
P10649	Glutathione S-transferase Mu 1	MQLIMLCY NPDFEK					0	937.4949	2	3.15	-0.53	1	1
P15409	Rhodopsin	NCMLTTLCC GKNPLGDD DASATASK	909.7437	3	3.21	-10.77	1					0	1
P17427	AP-2 complex subunit alpha-2	ACNQLGQFL QHR					0	503.2733	3	3.16	4.89	1	1
P20852	Cytochrome P450 2A5	IVVLCGQEA VK					0	644.4171	2	2.36	-0.89	1	1
P22315	Ferrochelatase, mitochondrial	AIAFTQYPQ YSCSTTGSS LNAIYR	909.7731	3	3.34	-1.35	1					0	1
P27467	Protein Wnt-3a	SCAEGSAAI CGCSSRLQG SPGEGWK	1249.0630	2	2.90	-3.31	1					0	1
P28798	Granulins	LNTGAWGC CPFAK					0	777.4121	2	2.40	-0.57	1	1
P29699	Alpha-2-HS-glycoprotein	VGQPGAAG PVSPMCPGR	833.4183	2	2.58	5.53	1					0	1

P30115	Glutathione S-transferase A3	FLQPGSQRK PFDDAKCVE SAK	840.7828	3	3.38	2.28	1		0	1			
P33587	Vitamin K-dependent protein C	NVVSENML CAGIIGDTR	938.9610	2	2.41	-5.82	1		0	1			
P35441	Thrombospondin-1	DVDECKEVP DACFNHNG EHRCK					0	1355.6764	2	2.46	11.66	1	1
P35762	CD81 antigen	TFHETLNCC GSNALTTLT TTILR					0					1	1
P40142	Transketolase	TVPFCSTFA AFFTR	840.4185	2	2.57	2.70	1					0	1
P42125	Enoyl-CoA delta isomerase 1, mitochondrial	LYTSNMILV SAINGASPA GGCLLALCC DYRVMADN PK	1001.4979	4	3.43	10.99	1					0	1
P42227-2	Isoform Stat3B of Signal transducer and activator of transcription 3	QQIACIGGPP NICLDR					0	929.9773	2	2.37	-11.99	1	1
P48964	M-phase inducer phosphatase 1	CGLFDSPSP CGSSTRAVL KR	1087.5540	2	2.40	-10.70	1					0	1

P51612	DNA repair protein complementin g XP-C cells homolog	GSQCEPSSFPEASSSSSGCKR	1105.9862	2	2.42	-8.30	1	0	1				
P56677	Suppressor of tumorigenicity 14 protein homolog	CNGKDNCGDGSDEASCD SVNVSCTK	949.0641	3	3.19	13.93	1	0	1				
P58802	TBC1 domain family member 10A	ACQGQYETIEQLRSLSPKIMQEAFVQ EVIELPVTERR	1097.0898	4	3.71	10.51	1	0	1				
P62281	40S ribosomal protein S11	DVQIGDIVTVGECRPLSK	1021.5511	2	2.54	-0.07	1	0	1				
P70351-2	Isoform 2 of Histone-lysine N-methyltransferase EZH1	HPVVSASCSNASASAMAEKKEGDSDR	1392.6399	2	2.29	4.72	1	0	1				
P80313	T-complex protein 1 subunit eta	QLCDNAGFDATNILNKL R	707.0408	3	3.31	5.29	1	0	1				
P80316	T-complex protein 1 subunit epsilon	IAILTCPFEPKPK					0	573.7122	3	3.22	-1.53	1	1

P97789-3	Isoform 3 of 5' 3' exoribonuclease 1	LTAIVKPQPS VSHCSAAPS GHLGGLNHS PQSPFLPTQ VPTK	1075.5786	4	3.76	5.07	1		0	1			
P98064-2	Isoform 2 of Mannan-binding lectin serine protease 1	RSLPTCLPV CGQPSR					0	887.9674	2	2.50	-11.79	1	1
Q07113	Cation-independent mannose-6-phosphate receptor	YYLNVCRPL NPVPGCDR					0					1	1
Q2QI47-2	Isoform 2 of Usherin	FLQSFNGDG CEPCQCNLH GSVNQLCDP LSGQCACK	1027.6792	4	3.80	-6.64	1					0	1
Q3TBA3	Antigen peptide transporter 1	LGSLWAPSG NRDAGDML CR					0	732.6977	3	3.27	3.03	1	1
Q3TTN6	Protein 1700010I14Rik	EELQKICTC NPQQFNR	994.0120	2	2.35	12.51	1					0	1
Q3UHH1	Isoform 5 of Zinc finger SWIM domain-containing protein 8	WCTHVVAL CLFRIHNAS AVCLR	908.1249	3	3.27	-10.63	1					0	1

Q3UHX0	Nucleolar protein 8	SLMENGSKC VNGSSSKLT SCQPAK	903.7863	3	3.25	6.83	1		0	1			
Q3UKZ7	ARL14 effector protein-like	NCLGCFYPC PK					0	812.3931	2	2.43	-9.43	1	1
Q3URI6	Protein Zfp560	ECGKAFTVS SHLSKHVR	971.5259	2	2.42	6.01	1					0	1
Q3UT49	Cytochrome P450 2C29	FIDLLPTSLP HAVTCDIK	699.3902	3	3.31	4.73	1					0	1
Q3V0A6	Uncharacterized protein C2orf78 homolog	AESSIDKDC LSPSQYELPP AGKVK	901.8028	3	3.31	1.02	1					0	1
Q4G0K9	Protein Snhg11	YPELTAWCR GDMR	875.9046	2	2.52	-1.21	1					0	1
Q52KR2	Isoform 2 of Leucine-rich repeats and immunoglobulin-like domains protein 2	LLPAARAGL CPAPCACRL PLLDCSR	908.1312	3	3.28	-12.78	1					0	1
Q571F8	Glutaminase liver isoform, mitochondrial	SNPDLWGVS LCTVDGQR	966.4656	2	3.30	-2.11	1					0	1
Q5DU14	Isoform 3 of Unconventional myosin-XVI	GQAAEERCR LVLQR					0					1	1

Q5DU37	Isoform 2 of Zinc finger FYVE domain-containing protein 26	DPASQPPGV ADAVCGAL QALCCKAEL PESEWRVLC EELLETCR	1196.0812	4	3.52	5.74	1	0	1				
Q5SSE9	ATP-binding cassette sub-family A member 13	FLGGMLAN LSSCVVLDLDR	919.9819	2	2.43	3.30	1	0	1				
Q5SW87	Ras-related protein Rab-1A	LLVGNKCDL TTK	723.4251	2	2.42	2.26	1	0	1				
Q5U465-2	Isoform 2 of Coiled-coil domain-containing protein 125	EQKMGQEE SGFTDVSGL ELAVLGACL CHGPPGGSPC SCAK					0	1047.2793	4	4.18	13.43	1	1
Q5U467	F-box and WD-40 domain protein 12	NVQDRSVIC MVSSMTKL STWDIR	907.8008	3	3.82	-1.30	1	0	1				
Q60662-2	Isoform 2 of A-kinase anchor protein 4	RPEEQCQDN AELDFISGM K	1190.0398	2	2.48	5.49	1	0	1				
Q60841-3	Isoform 3 of Reelin	GAEVSFGCG VLASGKAL VFNK	1063.6012	2	2.61	-14.23	1	0	1				
Q61672	Equilibrative nucleoside transporter 2	WGLFFNPIC CFLLFNVMD WLGR					0	1400.6875	2	2.50	-11.35	1	1

Q69AB2	Thioredoxin domain-containing protein 8	LVVVEFSAK WCGPCK		0	916.0452	2	2.32	-7.93	1	1
Q69ZI1-4	Isoform 4 of E3 ubiquitin-protein ligase SH3RF1	DCLPFAKDD VLTVIRR		0	1029.5902	2	2.42	-12.64	1	1
Q6A065-3	Isoform 3 of Centrosomal protein of 170 kDa	QKSSPVNNH SSPSQTPALC PPETR	1362.1785	2	2.52	-3.79			0	1
Q6NV66	Protein Zfp646	HAGSLMNH QCNPEASRY SCPFCFK		0	1400.1802	2	2.47	11.90	1	1
Q6NZK8	Protein tyrosine phosphatase domain-containing protein 1	HVIPGHMAC SMACGGR		0	868.4127	2	2.48	8.00	1	1
Q6P5H2-3	Isoform 2 of Nestin	TQNHETPGK ENCNSSIEEN SGTVK	1392.6447	2	2.52	2.82			0	1
Q6PDB7	MCG142671, isoform CRA_b	LSGCEAMDS EALVR		0	787.3987	2	2.44	10.13	1	1
Q6XVG2	Cytochrome P450 2C54	DICQSFTNLS R	684.8327	2	2.71	0.33			0	1
Q6ZPS2-3	Isoform 3 of Carnosine synthase 1	CCLGCGLLD GVFNVELK	919.9772	2	2.57	13.95			0	1

Q78JT3	3-hydroxyanthranilate 3,4-dioxygenase	ASFQPPVCNK	602.3164	2	2.76	5.34	1		0	1			
Q7TMY8	Isoform 4 of E3 ubiquitin-protein ligase HUWE1	QQQAATVSMMPVAPHSFLYPPSCTMSSVGVHCPYLVCFCITFAK	973.2700	5	4.05	8.31	1		0	1			
Q80UU9	Membrane-associated progesterone receptor component 2	GLCSGPGAGEESPAATLPR					0	931.9747	2	3.25	-2.00	1	1
Q80ZA4	Isoform 2 of Fibrocystin-L	TKLNCSAMTIQYSVTITSYNC SHNIPMMAVSFGQIITNETK	1145.3145	4	3.44	-8.58	1					0	1
Q8BGA3	Leucine-rich repeat transmembrane neuronal protein 2	SLTTVGLSGLNLWECSPR					0					1	1
Q8BGN9	Uncharacterized protein C1orf115 homolog	AISKGCRYIVIGLQGFAAAYSAPFGVATSVVSFVR	925.5057	4	3.49	-7.11	1					0	1
Q8BGQ7	Alanine--tRNA ligase, cytoplasmic	NVGCLQEALQLATSFAQLR	716.3891	3	3.51	11.60	1					0	1

Q8BIV1	Protein Zfp719	CYPCSDCGK LFLYASDLK	0	1130.0823	2	2.43	-12.99	1	1
Q8BLN6	Protein unc-80 homolog	NFMLESSPA HCSTPGDAG K	1065.4772	2	2.53	-7.55	1	0	1
Q8BLY3	Leucine-rich repeat and fibronectin type-III domain- containing protein 3	CQTQSMPLS VLCPGAGLL FVPPSLDRR	0	762.4159	4	3.52	11.42	1	1
Q8BMF4	Dihydrolipoyll ysine-residue acetyltransfera se component of pyruvate dehydrogenase complex, mitochondrial	YGVRSLCG WSSGSGTVP R	0	981.5060	2	2.28	0.14	1	1
Q8BPN8	Isoform 3 of DmX-like protein 2	CQWLKTGQ FFLSSVTYN LAWDPQDN R	0	798.1561	4	3.64	-11.75	1	1
Q8BPP1	Protein mab-21 like 2	ETDWDEAC LGDRLNGIL LQLISCLQC R	1092.8761	3	3.27	9.95	1	0	1
Q8BSE0	Regulator of microtubule dynamics protein 2	FCNLALLLP VVTK	0	780.5099	2	2.84	-2.71	1	1

Q8BX35	Tumor necrosis factor receptor superfamily member 27	STWGHHRC QTCITCAVIN RVQK	0	1369.7219	2	2.32	-0.34	1	1
Q8CA63	Ephrin type-B receptor 1	CTCKPGYEP ENSVACK	0	981.5067	2	2.40	-3.87	1	1
Q8CCJ9-3	Isoform 3 of PHD finger protein 20-like protein 1	LGPCLPLDL SCGSEVTGS RTPHPHYHG GECPR	866.9006	4	3.73	-9.77		0	1
Q8CGE8	Interferon-activable protein 205-A	QMIEVPNCI TRNANASPK	1078.0458	2	2.43	9.62		0	1
Q8K354	Carbonyl reductase [NADPH] 3	ILLNACCPG WVK	777.9038	2	2.42	-10.83		0	1
Q8K4Z3	NAD(P)H-hydrate epimerase	YQLNLPSYP DTECVYR	0	1027.5088	2	2.62	1.06	1	1
Q8R502	Volume-regulated anion channel subunit LRRC8C	VQFTVDCN VDIQDMTG YK	1093.0358	2	2.36	14.13		0	1
Q8VC12	Urocanate hydratase	AYPIDQYPC R	0	659.8393	2	2.49	5.40	1	1
Q8VCL4	Zfp451 protein	VTFQSEAET CEGKPDWM TSKKR	1370.2296	2	2.49	2.57		0	1

Q8VD73	Potassium voltage-gated channel, shaker-related subfamily, beta member 3	LCGPRPGPG GGNGGPVG GGHGNPPG GGGPSSK	1364.6814	2	2.40	1.45	1	0	1				
Q91W50	Cold shock domain-containing protein E1	EVQDGVEL QAGDEVEFS VILNQRTGK CSACNVWR	988.2275	4	3.85	-7.40	1	0	1				
Q91WE9	Isoform 2 of Protein FAM19A5	EGQLAAGTC EIVTLDR					0	918.9733	2	2.29	-8.72	1	1
Q91WQ3	Tyrosine--tRNA ligase, cytoplasmic	AGCEVTILF ADLHAYLD NMKAPWEL LELRYSYYE NVIK					0	922.8956	5	4.23	-4.23	1	1
Q91X44	Glucokinase regulatory protein	LAAASSVCE VVR	645.3481	2	2.44	0.58	1	0	1				
Q91XE4	N-acyl-aromatic-L-amino acid amidohydrolase (carboxylate-forming)	SCTLTFLGS TATPDDPYE VKR	805.4005	3	3.62	-1.62	1	0	1				

Q921C3	Bromodomain and WD repeat containing protein 1	CATVAANKI KMMCNLK	919.9816	2	2.47	-8.93	1			0	1		
Q921G8	Gamma-tubulin complex component 2	LMSVCVMF TNCMQKFT QSMK	833.3878	3	3.21	-12.84	1			0	1		
Q922B1	O-acetyl-ADP-ribose deacetylase MACROD1	SCYLSSLDL LLEHR					0	581.3174	3	3.24	2.35	1	1
Q99L20	Glutathione S-transferase theta 3	LKLSVQCLL H	422.9281	3	3.21	7.54	1				0	1	
Q99LB2	Dehydrogenase/reductase SDR family member 4	VNCLAPGLI K	570.8436	2	2.43	-0.99	1				0	1	
Q99LC3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	VITVDGNICS GK					0	667.9006	2	2.47	1.17	1	1
Q99MJ6	Na(+)/H(+) exchange regulatory cofactor NHE-RF4	LWQSGDQV TLLVAGLEV EEQCHQLG MPLAAPLAE GWALPAKPR	943.8973	5	3.86	-6.28	1				0	1	

Q99PP6-3	Isoform Gamma of Tripartite motif-containing protein 34A	MASTGLTNI QEKTTCPVC QELLTK	908.1287	3	3.15	-4.00	1		0	1			
Q99PT1	Rho GDP-dissociation inhibitor 1	LTLCVSTAP GPLELDLTG DLESFKK					0	938.2236	3	3.06	6.28	1	1
Q9CPT3	N-acylneuraminat e-9-phosphatase	LSKECFHPY STCITDVRTS HWEEAIQET K	888.6723	4	3.55	-7.35	1					0	1
Q9CPU0	Lactoylglutathi one lyase	GFGHIGIAMP DVYSACK					0	621.6852	3	3.23	0.18	1	1
Q9CR61	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	DSFPNFLAC K					0	635.8581	2	2.31	1.10	1	1
Q9D0C4-3	Isoform 2 of tRNA (guanine(37)-N1)-methyltransferase	EFFTMKCGV YYP	785.3486	2	2.48	-13.90	1					0	1

Q9D0E1-3	Isoform 2 of Heterogeneous nuclear ribonucleoprotein M	GCGVVKFES PEVAER	860.4365	2	2.50	-4.58	1	0	1				
Q9D2L6	Probable G-protein coupled receptor 115	MMAIGFAIG YGCPLVIAVI TVTVTEPGE GYTRK	879.2263	4	3.41	7.75	1	0	1				
Q9D4J3	Discoidin, CUB and LCCL domain-containing protein 1	LQAEELGDG CGHIVTSQD SGTMTSK					0	1355.1763	2	2.35	6.32	1	1
Q9D9N5	Calcium and integrin-binding family member 4	ICRVFSDN VFSFEDVLG MASVFSEQA CPSLK	954.9601	4	3.48	3.03	1	0	1				
Q9DBL1	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ASSTCQLTF ENVKVPETN ILGK	840.7808	3	3.49	-4.04	1	0	1				
Q9DCD2	Pre-mRNA-splicing factor SYF1	VNFKQVDD LASVWCQC GELELR	908.1278	3	3.23	13.23	1	0	1				
Q9EPU0-3	Isoform 2 of Regulator of nonsense transcripts 1	EVTLHKDGP LGETVLECY NCGCR					0	908.1235	3	3.13	-0.45	1	1

Q9EQ06-3	Isoform 2 of Estradiol 17-beta-dehydrogenase 11	TSLCLPNFIN TGFIK				0	922.5077	2	2.75	3.31	1	1
Q9EQ31	Lysophosphatic acid receptor 3	MICCALQDS NTER				0					1	1
Q9ER80	Receptor-transporting protein 4	CQKCFGQF ETPK	864.3983	2	2.45	-3.53					0	1
Q9QXD1	Peroxisomal acyl-coenzyme A oxidase 2	DFSLLPELH ALSTGMKA MSSDFCAQG TEICR				0	889.7023	4	3.50	8.67	1	1
Q9QXX4	Calcium-binding mitochondrial carrier protein Aralar2	AGQTTYNG VTDCFR	809.3711	2	2.84	1.41					0	1
Q9QYES	Protein jagged-2	GRCYDLVN DFYCACDD GWK	1197.0160	2	2.34	2.90					0	1
Q9R229	Bone morphogenetic protein 10	FKYEGMAV SECGCR				0	888.9312	2	2.41	-7.95	1	1
Q9WVF5	Epidermal growth factor receptor	FSNNPILCN MDTIQWR				0	1023.0129	2	2.57	2.97	1	1
Q9WVL6	Exostosin-like 3	CPGCPQALS HDDSHFHER HK	1179.0254	2	2.45	-9.68					0	1

Q9Z117	KRAB-containing zinc finger protein KRAZ1	ECDKSFTEC STLR	902.9276	2	2.29	11.39	1	0	1
S4R1C9	Piezo-type mechanosensitive ion channel component 2 (Fragment)	FGLETCFLM SVNVIGQR	1034.0133	2	2.50	-10.13	1	0	1

^a Accession number provided from the Uniprot mouse database (Jan 7, 2015; 52639 sequences). ^b Peptides are grouped by sequence. ^c Charge. ^d Xcorr is obtained from Proteome Discoverer 1.4. ^e Precursor mass error. ^f Spectra matching number of each peptide group. ^g Total spectra matching number of each protein.